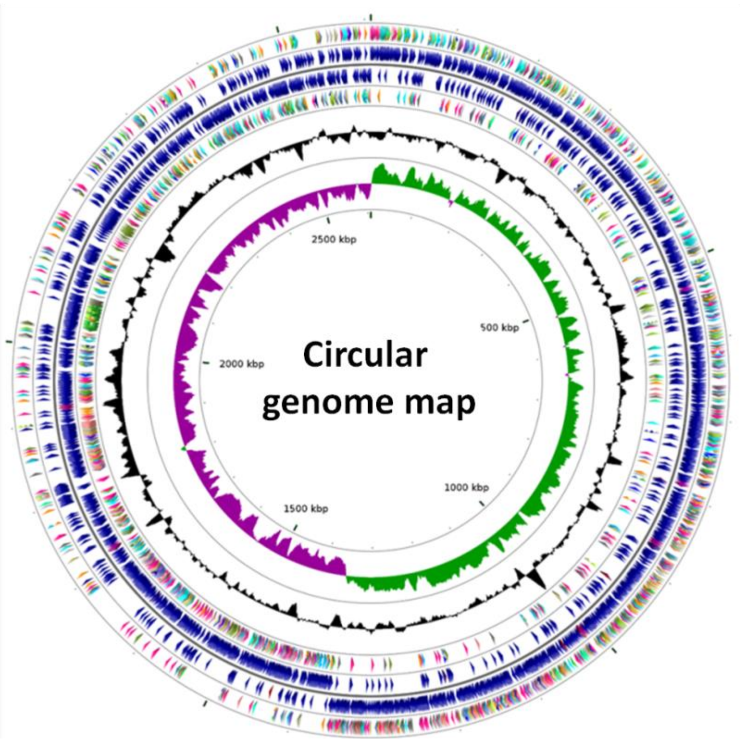
Agricultural University of Athens
Department of Food Science and Human Nutrition
Laboratory of Dairy Research

Whole genome sequencing of the lactic acid bacteria *Lactobacillus zymae, Lactobacillus acidipiscis* and *Lactobacillus rennini*. Physiological, evolutionary and technological implications.



Maria Kazou

PhD Thesis

Thesis supervisor

Prof. Effie Tsakalidou

Athens, 2018

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Περίληψη

Τα οξυγαλακτικά βακτήρια είναι μία από τις πιο σημαντικές ομάδες βακτηρίων για τη βιομηχανία. Τα βακτήρια αυτά χρησιμοποιούνται στην παραγωγή τροφίμων και ζωοτροφών, στη βελτίωση της υγείας του ανθρώπου και των ζώων, στην παραγωγή μακρομορίων, ενζύμων και διαφόρων μεταβολιτών. Τα τελευταία χρόνια, η αλληλούχιση όλο και περισσότερων οξυγαλακτικών βακτηρίων καθώς και η ανάλυσή τους με εργαλεία βιοπληροφορικής μας έχει προσφέρει πρωτοφανείς ευκαιρίες για να ανακαλύψουμε σημαντικά χαρακτηριστικά των βακτηρίων αυτών. Η αλληλούχιση ολόκληρων γονιδιωμάτων μπορούν να παρέχουν σημαντικές πληροφορίες σχετικά με το τεχνολογικό και το προβιοτικό δυναμικό ενός στελέχους. Επιπλέον, η γονιδιωματική ανάλυση ενός στελέχους ή η συγκριτική γονιδιωματική ανάλυση μεταξύ φυλογενετικά κοντινών (ή μη) στελεχών/ειδών μπορεί να προσφέρει σημαντικές γνώσεις, όπως η βακτηριακή ποικιλομορφία και η προσαρμογή σε ποικίλους οικολογικούς θώκους.

Στα πλαίσια της παρούσας διδακτορικής διατριβής, τρία "άγρια" στελέχη οξυγαλακτικών βακτηρίων, ο *Lactobacillus zymae* ACA-DC 3411, ο *Lactobacillus rennini* ACA-DC 565 και ο *Lactobacillus acidipiscis* ACA-DC 1533, τα οποία έχουν απομονωθεί από παραδοσιακά Ελληνικά προϊόντα ζύμωσης και συγκεκριμένα από προζύμι, Μάνα Κοπανιστή και Κοπανιστή, αντιστοίχως, αλληλουχήθηκαν με τεχνικές υψηλής απόδοσης και τα γονιδιώματά τους σχολιάστηκαν χρησιμοποιώντας πληθώρα σύγχρονων εργαλείων βιοπληροφορικής. Αξίζει να σημειωθεί ότι αυτές είναι τα πρώτες ολόκληρες χρωμοσωμικές αλληλουχίες για κάθε ένα από τα αντίστοιχα είδη, καθώς οι υπόλοιπες αλληλουχίες που βρίσκονται στις διάφορες βάσεις δεδομένων είναι μερικώς αλληλουχιμένες.

Η ανάλυση της χρωμοσωμικής αλληλουχίας του στελέχους *L. zymae* ACA-DC 3411 μεγέθους 2,7 Mbp αναγνώρισε ένα σύστημα περιορισμού-τροποποίησης (RM) τύπου I, 19 γονιδιωματικές νήσους που περιείχαν συνολικά 265 γονίδια τα οποία πιθανότατα να προήλθαν από οριζόντια μεταφορά, τέσσερις ημιτελείς και μία υπο αμφισβήτηση αλληλουχίες προφάγων και έξι επιβεβαιωμένα και έξι υπο αμφισβήτηση συστήματα που ονομάζονται συγκεντρωμένες τακτικές παρεμβαλλόμενες σύντομες παλινδρομικές επαναλήψεις (CRISPR). Επιπλέον, η λειτουργική ταξινόμηση των γονιδίων που κωδικοποιούν πρωτεΐνες στις διάφορες ορθόλογες ομάδες γονιδίων (COG) έδειξε ότι 1.930 γονίδια (περίπου 80%) εντοπίστηκαν σε τουλάχιστον μία κατηγορία COG. Η κατηγορία COG με τα περισσότερα γονίδια (14%) σχετίζεται με την αντιγραφή, τον ανασυνδυασμό και την επιδιόρθωση του DNA.

Η ανάλυση της χρωμοσωμικής αλληλουχίας του *L. rennini* ACA-DC 565 μεγέθους 2,4 Mbp αναγνώρισε αρκετές πρωτεΐνες τοξίνης-αντιτοξίνης, ένα σύστημα RM τύπου II και πέντε συστήματα CRISPR με τις σχετικές πρωτεΐνες cas. Επιπλέον, προσδιορίστηκε μια ημιτελής αλληλουχία προφάγου μήκους 17,1 Kbp που περιείχε οκτώ γονίδια φάγων, επτά γονίδια βακτηρίων και δύο γονίδια με υποθετική λειτουργία. Σύμφωνα με τα αποτελέσματα της κατανομής των γονιδίων στις διάφορες λειτουργικές κατηγορίες COG, 1.900 γονίδια (περίπου 87,7%) κατατάχθηκαν κάποια κατηγορία COG, ενώ η κατηγορία COG με τα περισσότερα γονίδια (9,33%) σχετίζεται με τη μεταφορά και το μεταβολισμό των υδατανθράκων.

Ενώ για τα είδη *L. zymae* και *L. rennini*, υπήρχε μόνο ένα γονιδίωμα μερικώς αλληλουχημένο στο Εθνικό Κέντρο Βιοτεχνολογικών Πληροφοριών ο *L. zymae* DSM 19395^T και ο *L. rennini* DSM 20253^T, αντίστοιχα, στην περίπτωση του *L. acidipiscis* υπήρχαν τέσσερα γονιδιώματα μερικώς αλληλουχημένα για τα στελέχη KCTC 13900, DSM 15353, JCM 10692^T και DSM 15836^T. Παρόλαυτά πρέπει να σημειωθεί ότι τα στελέχη KCTC 13900 και DSM 15353 είναι κλώνοι, όπως συμβαίνει και με τα στελέχη στελέχη JCM 10692^T και DSM15836^T το οποίο φάνηκε σε θερμικό χάρτη που υπολογίζει το ποσοστό ομοιότητας μεταξύ 2 αλληλουχιών. Λόγω του ότι η ανάγκη για την εύρεση διαφορών μεταξύ στελεχών γίνεται όλο και πιο απαραίτητη, κάναμε συγκριτική γονιδιωματική ανάλυση μεταξύ των τριών στελεχών του *L. acidipiscis* (ACA-DC 1533, KCTC 13900 και JCM 10692^{T}). Με βάση τα αποτελέσματα της ανάλυσης του παν-γονιδιώματος, του κοινού γονιδιώματος μεταξύ των στελεχών, αλλά και των μοναδικών γονιδίων κάθε στελέχους, τα τρία στελέχη του *L. acidipiscis* παρουσίασαν υψηλό βαθμό συντήρησης σε επίπεδο γονιδιώματος. Επιπλέον, φάνηκε ότι τα στελέχη ACA-DC 1533 και JCM 10692^{T} δεν διαθέτουν συστήματα CRISPR αλλά έχουν δύο παρόμοιες περιοχές προφάγων στα γονιδιώματά τους παρόλο που έχουν απομονωθεί από διαφορετικά οικοσυστήματα, τα οποία είναι η Κοπανιστή και ζυμούμενο ψάρι, αντίστοιχα. Αντίθετα, η ανάλυση των συστημάτων CRISPR του στελέχους KCTC 13900 έδειξε ότι το βακτήριο έχει αποκτήσει ανοσία προφάγους που βρέθηκαν στα άλλα δύο στελέχη του *L. acidipiscis*. Παρόλαυτά, μια αλληλουχία προφάγου που δεν βρέθηκε στα στελέχη ACA-DC 1533 και JCM 10692^{T} βρέθηκε στο στέλεχος KCTC 13900. Τα ευρήματα αυτά υποδηλώνουν την ύπαρξη γενεαλογικού χαρακτήρα εντός του είδους. Από τα παραπάνω μοτίβα παρουσίας/απουσίας γενετικών χαρακτηριστικών στα τρία γονιδιώματα, φαίνεται ότι τα στελέχη ACA-DC 1533 και JCM 10692^{T} είναι περισσότερο κοντά παρόλο που έχουν απομονωθεί από διαφορετικά οικοσυστήματα.

Δεδομένου ότι ο *L. acidipiscis* ανήκει στον κλάδο του *Lactobacillus salivarius*, ο οποίος αποτελείται κυρίως από συμβιωτικά είδη, πραγματοποιήθηκε συγκριτική γονιδιωματική ανάλυση μεταξύ επιλεγμένων στελεχών του κλάδου για να διερευνηθεί το επίπεδο ποικιλομορφίας μεταξύ των γονιδιωμάτων. Η συγκριτική γονιδιωματική ανάλυση μεταξύ των *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 και *Lactobacillus ruminis* ATCC 27782 αποκάλυψε σημαντικές διαφορές στον αριθμό των πρωτεϊνών που σχετίζονται με μεταβολισμό των υδατανθράκων, των πρωτεολυτικών ενζύμων, των μεταφορέων, των αλληλουχιών εισαγωγής και των ρυθμιστικών πρωτεινών. Στη συνέχεια διερευνήθηκε το προβιοτικό δυναμικό του *L. acidipiscis* ACA-DC 1533 σε σύγκριση με τον προβιοτικό *L. salivarius* UCC118, ωστόσο δεν βρέθηκαν προφανή γονιδιωματικά χαρακτηριστικά που να υποστηρίζουν ένα προβιοτικό δυναμικό για το στέλεχος ACA-DC 1533. Επιπλέον, η εύρεση μεταφορέων γλυκίνης- βεταΐνης στο χρωμόσωμα του ACA-DC 1533 θα μπορούσε να εξηγήσει την ικανότητα του στελέχους / είδους να αναπτυχθεί σε ζυμούμενα τρόφιμα με υψηλές συγκεντρώσεις άλατος. Τέλος, εντοπίστηκαν αρκετά γονίδια στο γονιδίωμα του ACA-DC 1533 που κωδικοποιούν ένζυμα κλειδιά τα οποία εμπλέκονται σε μεταβολικά μονοπάτια (κυρίως κατά τον καταβολισμό των αμινοξέων) από τα οποία παράγονται πτητικές ενώσεις, συμβάλλοντας με αυτόν το τρόπο στην ιδιαίτερη πικάντικη γεύση της Κοπανιστής.

Λέξεις κλειδιά: οξυγαλακτικά βακτήρια, Lactobacillus, γονιδιωματική, συγκριτική γονιδιωματική, αλληλούχιση ολόκληρου γονιδιώματος

Abstract

Lactic acid bacteria (LAB) are one of the most industrially important groups of bacteria. They are used in a variety of ways, including food and feed production, health improvement in humans and animals, and production of macromolecules, enzymes and various metabolites. In recent years, the genome sequencing of LAB is booming and the increased amount of published genomics data brings unprecedented opportunity for us to reveal the important traits of LAB. Whole-genome sequences can provide significant information concerning the technological and probiotic potential of a strain. Furthermore, genomic analysis of a strain or comparative genomics among closely related (or not) strains/species could deliver important knowledge, such as bacterial diversity and adaptation to diverse ecological niches.

In the course of the present thesis, three "wild" LAB strains, namely *Lactobacillus zymae* ACA-DC 3411, *Lactobacillus rennini* ACA-DC 565 and *Lactobacillus acidipiscis* ACA-DC 1533, isolated from traditional Greek wheat sourdough, Mana Kopanisti and Kopanisti cheese, respectively, were sequenced by high-throughput sequencing techniques and annotated using a plethora of bioinformatics tools. It is worth noting that these are the first completely sequenced chromosomal assemblies for each of the respective species, since the rest of publicly available genome assemblies are only partially sequenced.

Analysis of the *L. zymae* ACA-DC 3411 chromosomal sequence (2.7 Mbp) identified one type I restriction-modification (RM) system, 19 integrated genomic islands containing a total of 265 genes potentially acquired through horizontal gene transfer, four incomplete and one questionable prophage sequences, as well as six confirmed and six questionable Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) systems. Furthermore, cluster of orthologous groups (COG) functional classification of the *L. zymae* protein-coding genes revealed that 1,930 of them (approximately 80%) were assigned to at least one COG category with the most abundant being related to replication, recombination and repair (14%).

Analysis of the *L. rennini* ACA-DC 565 chromosomal sequence (2.4 Mbp) identified toxin-antitoxin proteins, a type II RM system and five CRISPR systems with their associated cas proteins. Furthermore, an incomplete prophage sequence of 17.1 Kbp length containing eight phage-related, seven bacterial and two hypothetical proteins was also identified. According to the COG results, 1,900 protein-coding genes (approximately 87.7%) were assigned to a putative COG category with the most abundant being related to carbohydrate transport and metabolism (9.33%).

Compared to the species *L. zymae* and *L. rennini*, where only a sole partial genome sequence was available in the beginning of the present thesis (*L. zymae* DSM 19395^T and *L. rennini* DSM 20253^T, respectively) in the National Center for Biotechnology Information database, in the case of *L. acidipiscis* four partially sequenced genome assemblies were reported, namely KCTC 13900, DSM 15353, JCM 10692^T and DSM15836^T. It should be noted though, that *L. acidipiscis* strains KCTC 13900 and DSM 15353 are replicas of the same strain and the same applies for strains JCM 10692^T and DSM15836^T, as confirmed by an average nucleotide identity heat map. Since the need to identify strain-specific differences has become increasingly vital, comparative genomic analysis among three *L. acidipiscis* strains (ACA-DC 1533, KCTC 13900 and JCM 10692^T) was performed. Based on the results of the pan/core-genome and singleton analysis, *L. acidipiscis* strains exhibited a high degree of conservation at the genome level. Furthermore, strains ACA-DC 1533 and JCM 10692^T, which lack CRISPR arrays, carry two similar prophage sequences although they have been isolated from different ecological niches, i.e. Kopanisti cheese and fermented fish, respectively. On the contrary, strain KCTC 13900 seems to have acquired immunity to these prophages based on the sequences of spacers in its CRISPRs. Nevertheless, a prophage sequence that was absent from strains ACA-DC 1533 and JCM 10692^T was identified in strain KCTC 13900. Interestingly, these results suggest a potential existence of lineages within the species. Based on the abovementioned presence/absence patterns of these genomic traits, strains ACA-DC 1533 and JCM 10692^T appeared to be quite related despite the different isolation source.

Since *L. acidipiscis* belongs to the *Lactobacillus salivarius* clade, which is mainly consists of commensal isolates, comparative genomics among representative strains in the clade was performed to investigate the level of their genomic diversity. Thus, comparative genomic analysis among *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *Lactobacillus ruminis* ATCC 27782 revealed significant differences in the number of glycobiome-related proteins, proteolytic enzymes, transporters, insertion sequences and regulatory proteins. Additionally, the probiotic potential of *L. acidipiscis* ACA-DC 1533 was investigated and compared to the extensively studied probiotic *L. salivarius* UCC118 strain; however, no obvious genomic traits supporting a probiotic potential of ACA-DC 1533 strain were found. Furthermore, the detection of glycine-betaine transporters in the ACA-DC 1533 chromosome may explain the ability of the strain/species to grow in fermented foods with high salt concentrations. Finally, *in silico* analysis of the ACA-DC 1533 chromosome identified genes encoding key enzymes involved in metabolic pathways (mainly during the amino acids catabolism) that could underpin the production of major volatile compounds, thus contributing to the distinct piquant flavor of Kopanisti cheese.

Keywords: lactic acid bacteria, *Lactobacillus*, genomics, comparative genomics, whole genome sequencing

Thesis committee

Thesis supervisor
Professor Effie Tsakalidou
Department of Food Science and Human Nutrition
Agricultural University of Athens, Greece

Thesis co-supervisors
Professor Georgios-Ioannis Nychas
Department of Food Science and Human Nutrition
Agricultural University of Athens, Greece

Professor Constantinos E. Vorgias
Department of Biochemistry and Molecular Biology
National and Kapodistrian University of Athens, Greece

Professor Constantinos E. Vorgias was assigned as thesis so-supervisor in the place of Professor Emeritus Stavros-Ioannis Hamodrakas, Department of Cell Biology and Biophysics, National and Kapodistrian University of Athens, who meanwhile retired [decision of the Department of Food Science and Human Nutrition Assembly 537th/05.07.2018, according to Paragraph 3, Article 39, Law No 4485/2017].

Other members
Professor Elias Eliopoulos
Department of Biotechnology
Agricultural University of Athens, Greece

Associate Professor Efstathios Panagou
Department of Food Science and Human Nutrition
Agricultural University of Athens, Greece

Associate Professor Constantinos Ehaliotis
Department of Natural Resources Management & Agricultural Engineering Agricultural
Agricultural University of Athens, Greece

Assistant Professor Konstantinos Papadimitriou
Department of Food Technology
Technological Educational Institute of Peloponnese, Greece

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List of publications

Publications resulting from this thesis

A. Journal papers

1. **Kazou M.**, Alexandraki V., Blom J., Pot B., Tsakalidou E., Papadimitriou K. (2018) Comparative genomics of *Lactobacillus acidipiscis* ACA-DC 1533 isolated from traditional Greek Kopanisti cheese against species within the *Lactobacillus salivarius* clade. *Front Microbiol, 9(1244) doi: 10.3389/fmicb.2018.01244*
2. **Kazou M.**, Alexandraki V., Pot B., Tsakalidou E., Papadimitriou K. (2017) Complete genome sequence of the sourdough isolate *Lactobacillus zymae* ACA-DC 3411. *Genome Announc, 5(30):e00699-17*
3. **Kazou M.,** Alexandraki V., Pot B., Tsakalidou E., Papadimitriou K. (2017) Whole-genome sequence of the cheese isolate *Lactobacillus rennini* ACA-DC 565. *Genome Announc, 5(5):e01579-16*
4. **Kazou M.,** Alexandraki V., Pot B., Tsakalidou E., Papadimitriou K. (2017) Complete genome sequence of the dairy isolate *Lactobacillus acidipiscis* ACA-DC 1533. *Genome Announc, 5(4):e01533-16*

B. International conference papers

1. Papadimitriou K., **Kazou M.,** Alexandraki V., Pot B., Tsakalidou E. "*In silico* analysis of the first complete genome sequence of *Lactobacillus acidipiscis* species". *41st Congress of Federation of European Biochemical Societies (FEBS), 3-8 September 2016, Kusadasi, Turkey (poster)*
2. **Kazou M.,** Alexandraki V., Pot B., Tsakalidou E., Papadimitriou K. "Complete genome sequence of the dairy isolate *Lactobacillus acidipiscis* ACA-DC 1533". *12th International Association for Food Protection (IAFP), 11-13 May 2016, Athens, Greece (poster)*

Other publications during the course of this thesis

A. Journal papers

1. Zoumpopoulou G., Tzouvanou A., Mavrogonatou E., Alexandraki V., Georgalaki M., Anastasiou R., Papadelli M., Manolopoulou E., **Kazou M**., Kletsas D., Papadimitriou K., Tsakalidou E. (2017) Probiotic features of lactic acid bacteria isolated from a diverse pool of traditional Greek dairy products regarding specific strain-host interactions. *Probiotics Antimicrob Proteins, 10(2):313-322 doi: 10.1007/s12602-017-9311-9*
2. Georgalaki M., Zoumpopoulou G., Mavrogonatou E., Driessche G., Alexandraki V., Anastasiou R., Papadelli M., **Kazou M**., Manolopoulou E., Kletsas D., Devreese B., Papadimitriou K., Tsakalidou E. (2017) Evaluation of the antihypertensive angiotensin-converting enzyme inhibitory (ACE-I) activity and other probiotic properties of lactic acid bacteria isolated from traditional Greek dairy products. *Int Dairy J, 75:10-21 doi: 10.1016/j.idairyj.2017.07.003*
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B. Book chapters

1. Papadimitriou K., Zoumpopoulou G., Georgalaki M., Alexandraki V., **Kazou M**., Anastasiou R., Tsakalidou E. (2018) Sourdough bread *In: Innovations in Traditional Foods, C. Galanakis Ed., Woodhead Publishing. In press*
2. Zoumpopoulou G., **Kazou M.,** Alexandraki V., Angelopoulou A., Papadimitriou K., Pot B., Tsakalidou E. (2017) Probiotics and Prebiotics: an Overview on Recent Trends. *In: Probiotics and Prebiotics in Animal Health and Food Safety, p. 1-34, B. Biavati and D. Di Gioia Eds., Springer Publishing*
3. **Kazou M.,** Alexandraki V., Angelopoulou A., Arena M.P., Capozzi V., Russo P., Fiocco D., Spano G., Papadimitriou K., Tsakalidou E. (2016) The Microbiota of non-Cow Milk and Products. In: *Non Cow Milk and Milk Products, p. 117-160, K. Papadimitriou and E. Tsakalidou Eds., Elsevier, San Diego CA US*
4. **Kazou M.** and Papadimitriou K. (2015) Graviera Agrafon. In: *The Oxford Companion to Cheese, pp 327-328, M. Sinsheimer Ed., Oxford University Press USA, NY. (2017 James Beard Award in Reference and Scholarship)*
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6. **Kazou M.** and Papadimitriou K. (2015) San Michali. In: *The Oxford Companion to Cheese, pp 638, M. Sinsheimer Ed., Oxford University Press USA, NY. (2017 James Beard Award in Reference and Scholarship)*

C. International conference papers

1. Papademas P., Mariou M., **Kazou M.,** Alexandraki V., Tsakalidou E. (2018) Reviving a long–forgotten cheese: The case study of Halitzia, a white-brined cheese from Cyprus. *5th International ISEKI_Food Conference, 3-5 July 2018, Stuttgart, Germany (poster)*
2. **Kazou M.,** Alexandraki V., Giolina Chavella G., Marina Koutsoumpou M., Argiro Paximadaki A., Rania Anastasiou R., Marina Georgalaki M., Effie Tsakalidou E., Konstantinos Papadimitriou K. (2017) Culture-dependent *vs* metagenomics approaches to discover the table olives microbial ecosystem. *4th International Conference on Microbial Diversity, 24-26 October 2017, Bari, Italy (poster)*
3. Alexandraki V., **Kazou M.,** Bounenni R., Charmpi C., Georgalaki M., Anastasiou R., Tsakalidou E., Papadimitriou K. (2017) Culture independent omics analysis of Feta cheese microbial ecosystem. *4th International Conference on Microbial Diversity, 24-26 October 2017, Bari, Italy (poster)*
4. **Kazou M.,** Alexandraki V., Giolina Chavella G., Marina Koutsoumpou M., Argiro Paximadaki A., Rania Anastasiou R., Marina Georgalaki M., Effie Tsakalidou E., Konstantinos Papadimitriou K. (2017) Metagenomics analysis of naturally fermented Greek table olives. *12th International Symposium on Lactic Acid Bacteria (LAB12), 27-31 August 2017, Egmond aan Zee, The Netherlands (poster)*
5. Alexandraki V., **Kazou M.,** Bounenni R., Charmpi C., Georgalaki M., Anastasiou R., Tsakalidou E., Papadimitriou K. (2017) Feta cheese microbial ecosystem: a metagenomics approach. *12th International Symposium on Lactic Acid Bacteria (LAB12), 27-31 August 2017, Egmond aan Zee, The Netherlands (poster)*
6. **Kazou M.,** Alexandraki V., Koutsoumpou M., Paximadaki A., Anastasiou R., Georgalaki M., Tsakalidou E., Papadimitriou K. "Exploring the microbial consortia of Greek table olives using culture-dependent and -independent approaches". *12th International Association for Food Protection (IAFP), 11-13 May 2016, Athens, Greece (poster)*
7. Alexandraki V, **Kazou M.,** Pot B., Tsakalidou E., Papadimitriou K. "*In silico* assessment of the technological potential of the dairy *Streptococcus thermophilus* ACA-DC 2 through genome analysis and comparative genomics". *12th International Association for Food Protection (IAFP), 11-13 May 2016, Athens, Greece (poster)*
8. Alexandraki V, **Kazou M.,** Charmpi C., Bounenni RE., Georgalaki M., Anastasiou R., Tsakalidou E., Papadimitriou K. "Metagenomics analysis of the Feta cheese microbial ecosystem". *12th International Association for Food Protection (IAFP), 11-13 May 2016, Athens, Greece (poster)*
9. Georgalaki M., Zoumpopoulou G., Mavrogonatou E., Van Driessche G., Anastasiou R., Alexandraki V., **Kazou M.,** Papadelli M., Manolopoulou E., Papadimitriou K., Kletsas D., Devreese B., Tsakalidou E. "Production of bioactive peptides and probiotic potential of lactic acid bacteria isolated from traditional Greek dairy products". *12th International Association for Food Protection (IAFP), 11-13 May 2016, Athens, Greece (poster)*
10. **Kazou M.,** Alexandraki V., Renault P., Pot B., Tsakalidou E., Papadimitriou K. "Adaptation of *Streptococcus macedonicus* and *Streptococcus thermophilus* in milk. Common strategies, distinct ways". *2nd World Food Day - Mediterranean Food and Nutrition, 16-17 October 2015, Portoroz, Slovenia (poster)*
11. Alexandraki V, **Kazou M.,** Pot B., Tsakalidou E., Papadimitriou K. "Comparative genomic analysis between *Lactobacillus delbreuckii* subsp. *lactis* and *Lactobacillus delbreuckii* subsp. *bulgaricus* of dairy origin". *2nd World Food Day - Mediterranean Food and Nutrition, 16-17 October 2015, Portoroz, Slovenia (poster)*
12. Alexandraki V., **Kazou M**., Renault P, Pot B., Tsakalidou E., Papadimitriou K. "Characterization of the dairy *Streptococcus thermophilus* ACA-DC 29 strain through comparative genomics". *6th Congress of European Microbiologists (FEMS), 7-11 June 2015, Maastricht, Netherlands (poster)*

13. Georgalaki M., **Kazou M**., Alexandraki V., Manolopoulou E., Anastasiou R., Zoumpopoulou G., Papadimitriou K., Papadelli M., Driessche G., Devreese B., Tsakalidou E. "Production of ACE-inhibitory peptides by lactic acid bacteria isolated from traditional Greek dairy products". *6th Congress of European Microbiologists (FEMS), 7-11 June 2015, Maastricht, Netherlands (poster)*
14. Papadimitriou K., **Kazou M**., Alexandraki V., Pot B., Renault P., Tsakalidou E. "Genomics of *Streptococcus macedonicus*: moving from pathogenicity to adaptation to the dairy environment". *6th Congress of European Microbiologists (FEMS), 7-11 June 2015, Maastricht, Netherlands (poster)*
15. Zoumpopoulou G., Alexandraki V., **Kazou M.,** Papadelli M., Tzouvanou A., Manolopoulou E., Anastasiou R., Georgalaki M., Mavrogonatou E., Kletsas D., Papadimitriou K., Tsakalidou E. "Greek traditional dairy and meat products: A biological reservoir for new probiotic strains". *6th Congress of European Microbiologists (FEMS), 7-11 June 2015, Maastricht, Netherlands (poster)*
16. Zoumpopoulou G., Papadelli M., Tzouvanou A., Alexandraki V., **Kazou M.,** Manolopoulou E., Anastasiou R., Georgalaki M., Papadimitriou K., Tsakalidou E. "*In vitro* screening for probiotic potential of lactic acid bacteria isolated from Greek traditional dairy and meat products". *7th IDF International Symposium on Sheep, Goat and other non-Cow Milk, 23-25 March 2015, Limassol, Cyprus (poster)*
17. Georgalaki M., Manolopoulou E., Anastasiou R., Zoumpopoulou G., Alexandraki V., **Kazou M.,** Papadimitriou K., Papadelli M., Driessche G., Devreese B., Tsakalidou E. "Production of ACE-Inhibitory peptides by lactic acid bacteria isolated from Greek traditional yogurt and fermented milk samples". *7th IDF International Symposium on Sheep, Goat and other non-Cow Milk, 23-25 March 2015, Limassol, Cyprus (poster)*
18. Georgalaki M., Manolopoulou E., Anastasiou R., Zoumpopoulou G., Alexandraki V., **Kazou M.,** Tsakalidou E. "Technological and ACE-Inhibitory potential of lactic acid bacteria isolated from Greek traditional yogurt and fermented milk samples". *11th Symposium on Lactic Acid Bacteria - Health, Sustainability, Diversity and Application, 31/8/14 - 4/9/14, Egmond aan Zee, Netherlands (poster)*
19. Zoumpopoulou G., Papadelli M., Tzouvanou A., Alexandraki V., **Kazou M.,** Manolopoulou E., Anastasiou R., Georgalaki M., Papadimitriou K., Tsakalidou E. "Probiotic traits of lactic acid bacteria isolated from Greek traditional dairy and meat products". *International Scientific Conference on Probiotics and Prebiotics, 24-26 June 2014, Budapest, Hungary (poster)*
20. Anastasiou R., **Kazou M.,** Alexandraki V., Tsakalidou E., Papadimitriou K. "Linking stress resistant phenotypes to bacteriocin production under stress conditions: the example of *Streptococcus macedonicus* osmotic stress resistant mutants and macedocin". *4th International Symposium on Antimicrobial Peptides (AMP), 4-6 June 2014, Lorient, France (poster)*
21. Georgalaki M., Zoumpopoulou G., Papadimitriou K., Alexandraki V., **Kazou M.**, Driessche G., Devreese B., Tsakalidou E. "Is the antimicrobial activity exhibited by *Lactobacillus fermentum* ACA-DC 179 attributed to a bacteriocin?" *4th International Symposium on Antimicrobial Peptides (AMP), 4-6 June 2014, Lorient, France (poster)*
22. **Kazou M.**, Zoumpopoulou G., Tarantilis P., Polissiou M., Tsakalidou E., Papadimitriou K. "Assessing global cellular changes in *Lactococcus lactis* during exposure to different stressful conditions with the use of Fourier transform infrared spectroscopy". *5th Congress of European Microbiologists (FEMS), 21-25 July 2013, Leipzig, Germany (poster)*
23. **Kazou M.**, Zoumpopoulou G., Tarantilis P., Polissiou M., Tsakalidou E., Papadimitriou K. "Stress responses of *Lactococcus lactis* subsp. *cremoris* MG1363 and detection of changes in its cellular composition using FT-IR spectroscopy". *XXXII Annual Meeting of the European Culture Collections' Organization (ECCO), 12-14 June 2013, Athens, Greece (poster)*

D. National conference papers

1. Papadimitriou K., Georgalaki M., Zoumpopoulou G., Mavrogonatou E., Van Driessche G., Alexandraki V., Anastasiou R., Papadelli M., **Kazou M.,** Manolopoulou E., Kletsas D., Devreese B., Tsakalidou E. "Evaluation of angiotensin-converting enzyme-inhibitory (ACE-I) activity and other probiotic properties of lactic acid bacteria isolated from traditional Greek dairy products". *67th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 25-27 November 2016, Ioannina, Greece (poster)*
2. Koutsoumpou M., Anastasiou R., Georgalaki M., **Kazou M**., Alexandraki V., Papadimitriou K., Tsakalidou E. "Exploring the microbial ecosystem of naturally fermented Greek table olives". *66th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 10-13 December 2015, Athens, Greece (poster)*
3. Charmpi C., Anastasiou R., Georgalaki M., **Kazou M.**, Alexandraki V., Papadimitriou K., Tsakalidou E. "The microbiota of Greek Feta cheese - Classical and metagenomics approaches". *66th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 10-13 December 2015, Athens, Greece (poster)*
4. Alexandraki V., **Kazou M**., Pot B., Tsakalidou E., Papadimitriou K. "Comparative genomic analysis of *Lactobacillus delbreuckii* subsp. *lactis* and *Lactobacillus delbreuckii* subsp. *bulgaricus* dairy strains". *66th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 10-13 December 2015, Athens, Greece (poster)*
5. Bounenni R.E., Anastasiou R., Georgalaki M., **Kazou M**., Alexandraki V., Papadimitriou K., Tsakalidou E. "Identification of traditional Feta cheese microflora through microbiological and metagenomic analysis". *66th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 10-13 December 2015, Athens, Greece (poster)*
6. **Kazou M.,** Alexandraki V., Sarafianou A., Pot B., Renault P., Tsakalidou E., Papadimitriou K. "Comparative genomic analysis among three dairy *Streptococcus macedonicus* strains". *65th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 28-30 November 2014, Thessaloniki, Greece (poster)*
7. Alexandraki V., **Kazou M.,** Papandreou N.C., Hamodrakas S.J., Pot B. Tsakalidou E., Papadimitriou K. "Comparative genomics among dairy strains of *Streptococcus thermophilus*". *65th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 28-30 November 2014, Thessaloniki, Greece (poster)*
8. Zoumpopoulou G., Alexandraki V., **Kazou M.,** Papadelli M., Tzouvanou A., Manolopoulou E., Anastasiou R., Georgalaki M., Mavrogonatou E., Kletsas D., Papadimitriou K., Tsakalidou E. "*In vitro* evaluation of probiotic attributes of lactic acid bacteria isolated from Greek traditional dairy and meat products". *65th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 28-30 November 2014, Thessaloniki, Greece (poster)*
9. Alexandraki V., Sarafianou A., **Kazou M.,** Anastasiou R., Papandreou N.C., Hamodrakas S.J., Pot B., Renault P., Tsakalidou E., Papadimitriou K. "Comparative genomics among dairy strains of *Streptococcus thermophilus* and *Streptococcus macedonicus*". *9th Conference of the Hellenic Society of Computational Biology and Bionformatics (HSCBB), 10-12 October 2014, Athens, Greece (oral presentation)*
10. **Kazou M.**, Zoumpopoulou G., Tarantilis P., Polissiou M., Tsakalidou E., Papadimitriou K. "Global cellular changes of *Lactococcus lactis* MG1363 during exposure to different stress stimuli assessed by FT-IR spectroscopy". *64th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 6-8 December 2013, Athens, Greece (poster)*
11. **Kazou M.**, Peton V., Jardin J., Gagnaire V., Alexandraki V., Tsakalidou E., Jan G., Papadimitriou K. "Proteome changes of *Lactococcus lactis* MG1363 during exposure to the bacteriocin peptide macedocin produced by *Streptococcus macedonicus* ACA-DC 198". *64th Meeting of the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), 6-8 December 2013, Athens, Greece (poster)*

12. **Kazou M.,** Zoumpopoulou G., Alexandraki V., Tarantilis P.A., Polissiou M., Tsakalidou E., Papadimitriou K. “Global cellular changes of *Lactococcus lactis* subsp. *cremoris* MG1363 during exposure to different stress stimuli assessed by FT-IR spectroscopy”. *8th Meeting of the Hellenic Society for Computational Biology and Bioinformatics (HSCBB), 22-24 November 2013, Lamia, Greece (oral presentation)*
13. **Kazou M**., Zoumpopoulou G., Tarantilis P., Polissiou M., Tsakalidou E., Papadimitriou K. “Stress responses of *Lactococcus lactis* subsp. *cremoris* MG1363 and detection of changes in its cellular composition using FT-IR spectroscopy”. *5th National MikroBiokosmos (MBK) Conference, 13-15 December 2012, Athens, Greece (poster)*

E. Invited lectures

1. **Kazou M.,** Alexandraki V., Papadimitriou K., Tsakalidou E. “Exploring the olive ecosystem. The transition from classical microbiological analysis to metagenomics analysis”. *Workshop on “Bioactive compounds from olive and olive oil” 31 October 2015, Monemvasia, Greece*

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LIST OF ABBREVIATIONS

ABC	ATP-binding cassette
ACA-DC	Agricultural College of Athens-Dairy Culture
AFLP	amplified fragment length polymorphism
ANI	average nucleotide identity
BSH	bile salt hydrolase
CASCADE	CRISPR-associated complex for antiviral defence
CDS	coding sequence
CitP	citrate permease
CL	citrate lyase
COG	cluster of orthologous groups
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
crRNA	CRISPR RNA
crRNA	CRISPR RNA
EMP	Embden-Meyerhof-Parnas
EFSA	European Food Safety Authority
FAO	Food and Agriculture Organization of the United Nations
FDA	Food and Drug Administration
FFA	free fatty acids
GMO	genetically modified organism
GIT	gastrointestinal tract
GRAS	Generally Recognized As Safe
2-HCT	2-hydroxycarboxylate transporter
HGT	horizontal gene transfer
LAB	lactic acid bacteria
LaCOG	*Lactobacillales*-specific COG
LCBs	locally collinear blocks
LPL	lipoprotein lipase
Man-PTS	mannose phosphotransferase system
MGE	mobile genetic element
MTase-REase	methyltransferase-restriction endonuclease
NCBI	National Center for Biotechnology Information
NGS	next-generation sequencing
NSLAB	non-starter lactic acid bacteria
OAD	oxaloacetate decarboxylase
Opp	oligopeptide permease
OxA	oxaloacetate
PacBio	Pacific Biosciences
PAM	protospacer-adjacent motif
PEP/PTS	phosphoenolpyruvate/phosphotransferase

PP	pentose-phosphate
pre-crRNA	precursor-crRNA
PTR	peptide transport
QPS	Qualified Presumption of Safety
RAPD	randomly amplified polymorphic DNA
RCR	rolling-circle replication
RM	restriction modification
SDS-PAGE	sodium dodecyl sulfate-polyacrylamide gel electrophoresis
SMRT	single-molecule real-time
TA	toxin-antitoxin
TGS	third generation sequencers
tracrRNA	trans-activating crRNA
TRD	target recognition domain
WHO	World Health Organisation

CHAPTER 1

General introduction and aim of the thesis

Introduction

1.1.1. Lactic acid bacteria

Lactic acid bacteria (LAB) were first described at the beginning of the 1900s although they first appeared on earth about 3 billion years ago. The first pure culture of *Bacterium lactis* was isolated from milk in 1873 by Lister and it was an earlier synonym of *Lactococcus lactis* (Lister, 1873). More than a century later, we know that LAB constitute a diverse group of microorganisms that are found in a variety of nutrient-rich ecological niches, including food, e.g. dairy products, grain products, meat and fish products, alcoholic drinks, fruits and fruit juices, pickled vegetables, sauerkraut, sourdough, etc., feed, e.g. silage, water, soil, sewage and the oral, respiratory, gastrointestinal and genital tracts of humans and animals (Shalaby, 1996; Carr et al., 2002; Klaenhammer et al., 2002; Leroy and De Vuyst, 2004; Klaenhammer et al., 2005; Pot et al., 2014).

LAB are Gram-positive, non-spore-forming, catalase-negative (although some strains can present a pseudocatalase activity; (Engesser and Hammes, 1994), acid-tolerant, anaerobic or microaerophilic rods and cocci (Orla-Jensen, 1919) and belong to the class III of the phylum *Firmicutes*. LAB are considered as “a rapidly expanding” group of bacteria with currently about 40 genera, among them best known being lactobacilli, lactococci, enterococci, streptococci, leuconostoc and pediococci (Figure 1.1). LAB genera are distributed in six families, namely, *Aerococcaceae* (with 7 genera), *Carnobacteriaceae* (with 16 genera), *Enterococcaceae* (with 7 genera), *Lactobacillaceae* (with 3 genera), *Leuconostoccaceae* (with 4 genera) and *Streptococcaceae* (with 3 genera).

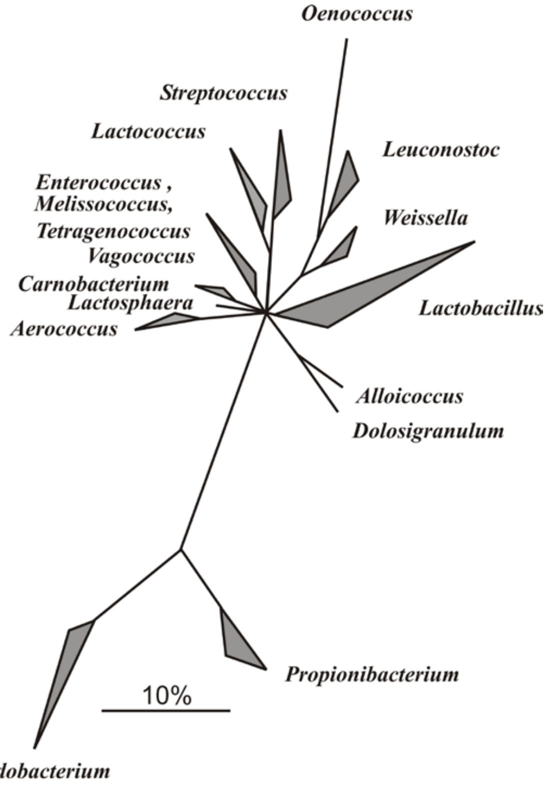

Figure 1.1. Major phylogenetic group of LAB and related Gram-positive bacteria (Stiles and Holzapfel, 1997)

1.1.2. Lactic acid bacteria in food and health applications

Empirical food fermentation by the indigenous microbiota of the raw material (spontaneous fermentation) has been employed for millennia. In particular, spontaneous fermentation of milk allowed the preservation of milk products in a non-perishable and transportable form. The first evidence of dairy fermentation dates back in the 6th millennium BC in Northern Europe with the discovery of potsherds pierced with small holes that have been interpreted as “cheese-strainers” (Salque et al., 2013).

Nowadays, in industrial fermentations, quality, safety and overall acceptability of the final food products have been significantly improved with the use of selected starter cultures, which are mainly LAB species (Holzapfel, 2002). Starters rapidly initiate the acidification of raw material due to the production of lactic acid from lactose and thus ensure the safety and preservation of the final product. A starter culture can be defined as “a microbial preparation of large numbers of cells of at least one microorganism to be added to a raw material to produce a fermented food by accelerating and steering its fermentation process” (Leroy and De Vuyst, 2004). *L. lactis* was the first starter culture used industrially for the production of cheese and sour milk in Germany and Denmark in 1980 (Holzapfel, 1997). Although initially the selection of starters was mainly based on the acidification rate and phage resistance, the increased research in genomics and metabolomics of food microorganisms has led to improved starters' selection based also on their functional properties (Leroy and De Vuyst, 2004; Soro-Yao et al., 2014; Altieri et al., 2017). Safety aspects of starter cultures include specifications such as origin of isolation pathogenic and haemolytic potential, toxin production and side effects in human studies. Moreover, properties like the viability and persistence in the gastrointestinal tract (GIT), survival at different pH values, antibiotic resistance patterns, growth at different NaCl concentration and temperatures are also of importance (Altieri et al., 2017). The LAB species that are mainly used as starter cultures in the production of numerous fermented dairy products (cheese, yoghurt and fermented milks) as well as in other non-dairy fermented foods (fermented sausages, fermented fish, pickles, sourdough and rice wine) are the thermophilic (42 ^{o}C) *Streptococcus thermophilus, Lactobacillus delbrueckii* subsp. bulgaricus and *Lactobacillus helveticus*, as well as the mesophilic (30 ^{o}C) *L. lactis* subsp. *lactis, L. lactis* subsp. *cremoris*, *Leuconostoc mesenteroides* subsp. *cremoris*, *Leuconostoc lactis* (Leroy and De Vuyst, 2004; Bourdichon et al., 2012; Altieri et al., 2017).

Apart from starter cultures, there is a number of LAB species especially in cheese-making that are implicated in the ripening process and referred to as non-starter LAB (NSLAB). NSLAB is a heterogeneous group that mostly includes *Lactobacillus* species, such as *Lactobacillus casei, Lactobacillus paracasei, Lactobacillus plantarum, Lactobacillus pentosus, Lactobacillus curvatus, Lactobacillus rhamnosus, Lactobacillus fermentum, Lactobacillus buchneri, Lactobacillus parabuchneri* and *Lactobacillus brevis*, as well as *Pediococcus acidilactici, Pediococcus pentosaceus, Enterococcus durans, Enterococcus faecalis, Enterococcus faecium* and *Leuconostoc* spp. The addition of NSLAB as adjunct cultures significantly contributes to the organoleptic characteristics of the final product due to the production of a wide range of aromatic compounds or through their proteolytic and peptidolytic activities (Giraffa, 2014). At the beginning of ripening, starter cultures are high in number (about 10^8-10^9 cfu/g) and NSLAB are present at low concentrations, but on completion of the ripening process the initial population of starters gradually decrease (regularly by two or more log cycles) while NSLAB increase (10^7-10^9 cfu/g) (Settanni and Moschetti, 2010; Gobbetti et al., 2015). A combination of starter and non-starter cultures may result in a wide variety of fermented products with a unique sensorial 'identity'. The selection of a suitable combination of starter and adjunct cultures for optimal flavor production can be achieved by the understanding the metabolic processes performed by each strain (Giraffa, 2014). However, it is important to note that random NSLAB population could cause uncontrolled cheese ripening and thus fluctuations in the characteristics of the final product.

Functional starter cultures or NSLAB can contribute to food safety and/or provide organoleptic, technological, nutritional and health advantages to the final product, especially since nowadays consumers prefer healthy food products. The functional properties of LAB include the (i) production of exopolysaccharides, sweeteners and aromatic compounds, (ii) resistance to bacteriophages, freezing and lyophilization, (iii) capacity for adhesion and colonization on the digestive tract mucosa and (iv) production of antimicrobial compounds, such as organic acids (lactic and acetic acids), hydrogen peroxide (H_2O_2), carbon dioxide (CO_2), diacetyl and bacteriocins.

Over a century ago, Elie Metchnikoff suggested that health could be enhanced by modifying the intestinal microbiota with host-friendly bacteria found in yogurt (Metchnikoff, 1910). The term "probiotic" etymologically is derived from the Latin preposition *pro* ("for" or "in support") and the Greek adjective *biotic* from the noun *bios* ("life") meaning "for life" or "in support of life" and was first used by Lilly and Stillwell (Lilly and Stillwell, 1965). According to the most recent definition, probiotics are *"live microorganisms which when administered in adequate amounts confer a health benefit to the host"* (FAO/WHO, 2002). The most commonly used probiotic strains belong to the *Lactobacillus* and *Bifidobacterium* genera, while less often *Enterococcus, Streptococcus, Pediococcus, Leuconostoc, Bacillus, Escherichia* and *Saccharomyces* strains are used (Table 1.1) (Didari et al., 2014; Fijan, 2014; Kim et al., 2016).

Table 1.1. Bacterial species frequently used as probiotics (Leroy et al., 2008)

Lactobacillus **sp.**	***Bifidobacterium*** **sp.**	**Other species**
L. acidophilus	*B. bifidum*	*Enterococcus faecalis*
L. amylovorus	*B. animalis* subsp. *animalis*	*Enterococcus faecium*
L. brevis	*B. animalis* subsp. *lactis*	*Lactococcus lactis*
L. casei	*B. breve*	*Leuconostoc mesenteroides*
L. crispatus	*B. longum*	*Escherichia coli*
L. curvatus	*B. adolescentis*	*Streptococcus thermophilus*
L. delbrueckii subsp. *bulgaricus*		*Bacillus cereus*
L. fermentum		*Bacillus subtilis*
L. salivarius		*Saccharomyces cerevisiae*
L. gasseri		*Saccharomyces boulardii*
L. johnsonii		
L. paracasei		
L. plantarum		
L. reuteri		
L. rhamnosus		

The selection criteria of putative probiotic strains include tolerance to gastrointestinal conditions (gastric acid and bile), ability to adhere to the gastrointestinal mucosa and competitive exclusion of pathogens along with pathogenic potential, toxicity, side effects, antibiotic and phage resistance (Vasiljevic and Shah, 2008; Fontana et al., 2013). Furthermore, a probiotic culture must remain stable during processing and storage conditions and delivered in substantially high concentrations (10^7–10^9 cfu/mL) to confer health benefits to the host (Butel, 2014). Although the mechanisms underlying the beneficial effects of probiotics are still under investigation, they refer to increased adhesion to intestinal mucosa, enhancement of the epithelial barrier, inhibition of pathogen adhesion, competitive exclusion of pathogenic microorganisms, production of antimicrobial substances, and modulation of the immune system (Figure 1.2) (Bermudez-Brito et al., 2012).

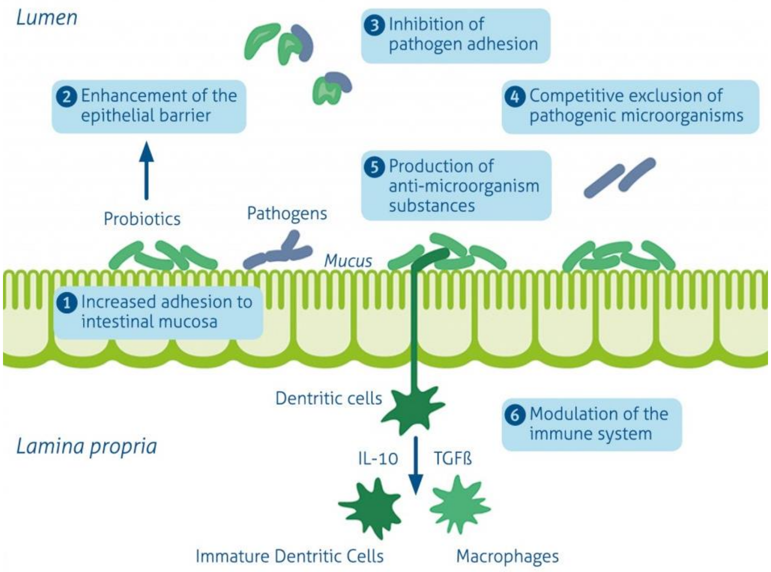

Figure 1.2. Putative modes of action of probiotic strains (Bermudez-Brito et al., 2012)

Based on clinical trials, probiotics have shown to be effective in the prevention or treatment of several health disorders. However, some of their health benefits are better documented than others (Parker et al., 2018). Probiotics are most often used against gastrointestinal disorders, such as diarrhea (acute infectious, antibiotic-associated or *Clostridium difficile*-associated), inflammatory bowel diseases (Crohn's disease, ulcerative colitis and pouchitis), irritable bowel syndrome, constipation and lactose intolerance (Claes et al., 2010; Ringel-Kulka et al., 2011; Kechagia et al., 2013; Cameron et al., 2017). In addition, the use of probiotics in extra-intestinal conditions, such as allergies, infections in upper respiratory tract, atopic diseases (e.g. asthma), obesity, diabetes, cancer, liver disease, urogenital infections and gut-brain axis (e.g. autism), has been also reported (Ljungh and Wadstrom, 2006; Chen et al., 2014; Serban, 2014; Lindsay et al., 2015).

Today, probiotics constitute a multi-billion-dollar global industry. The probiotics market was valued at USD 42.66 billion in 2016 and it is estimated to reach USD 64.02 billion by 2022 (https://www.marketsandmarkets.com). Especially for probiotic *Lactobacillus* strains the global market size is expected to surpass production demand over 8.5 million tonnes by 2024 (https://www.gminsights.com/industry-analysis/probiotics-market). Representative health-enhancing products containing probiotic *Lactobacillus* strains are shown in Table 1.2.

Table 1.2. Representative probiotic *Lactobacillus* strains and health benefits (Saxelin et al., 2005; Siezen and Wilson, 2010)

Strain	**Brand name**	**Claimed effect**
Lactobacillus casei Shirota	Yakult®	Alleviation of acute diarrhoea
Lactobacillus rhamnosus GG	Gefilus®	Immune stimulation, alleviation of atopic eczema, prevention of diarrhoea, aleviation of symptoms associated with irritable bowel syndrome
Lactobacillus acidophilus NCFM	Howaru®	Improvement of intestinal health, alleviation of symptoms associated with irritable bowel syndrome, gastrointestinal ecology
Lactobacillus casei DN114-001	Actimel®	Diarrhoea treatment, gut infections, strengthening of the body's natural defences
Lactobacillus reuteri 55730	Boost®	Alleviation of colic, pathogen inhibition

1.1.3. Metabolism of lactic acid bacteria

1.1.3.1. Carbohydrates metabolism

The primary step in dairy fermentation is the catabolism of carbohydrates by LAB with the main end-product being lactic acid. Lactose fermentation has been extensively studied since it is the major carbohydrate of milk. LAB have developed two different strategies for lactose degradation that depend on the transport system of lactose, either a lactose permease system or a phosphoenolpyruvate/phosphotransferase (PEP/PTS) system (Hickey et al., 1986).

If lactose is transported *via* the PEP/PTS system, enters the cytoplasm as lactose phosphate and cleaved by phospho-β-D-galactosidase (P-β-gal) to generate glucose and galactose-6-phosphate (Figure 1.3). Glucose is further phosphorylated by glucokinase and metabolized either through the Embden-Meyerhof-Parnas (EMP) or pentose-phosphate (PP) pathways according to the type of fermentation per LAB species. In particular, LAB are subdivided into obligate homofermentative (Group A), facultatively heterofermentative (Group B) and obligately heterofermentative species (Group C). Homofermentative LAB are lactococci, enterococci, streptococci, pediococci and some lactobacilli, while obligate heterofermentative LAB are leuconostocs, oenococci, weissellas and group III lactobacilli. Group A species are able to ferment hexoses, such as glucose almost exclusively (>85 %) to lactic acid *via* the EMP pathway. Glycolysis is characterized by the formation of fructose-1,6-diphosphate (FDP) from glucose which is then split by the FDP aldolase into dihydroxyacetone-phosphate and glycerinaldehyde-3-phosphate (Figure 1.3). As a result, 2 moles of lactic acid and a net gain of 2 ATP are generated from 1 mole of glucose. Obligately homofermentative species lack phosphoketolase and therefore, gluconate and pentoses cannot be fermented. In addition, LAB species belonging to Group B are able to ferment hexoses to lactic acid *via* the EMP pathway and are also able to degrade pentoses and often gluconate *via* an inducible phosphoketolase based pathway, since these species possess both the FDP aldolase and the phosphoketolase. Phosphoketolase is an enzyme of the PP pathway resulting in the production of acetic acid or ethanol and CO_2. LAB species belonging to group C lack the glycolytic enzyme FDP aldolase and utilize pentoses and hexoses exclusively *via* the phosphoketolase based pathway (corresponding to the first part of the PP pathway). The key step in heterolactic fermentation is the phosphoketolase split of xylulose-5-phoshate to glycerinaldehyde-3-phosphate (GAP) and acetyl-phosphate. GAP is then converted to lactate whereas acetyl-phosphate to acetate or ethanol (Figure 1.3). Heterolactic fermentation gives in 1 mole each of lactic acid, acetic acid (or ethanol), CO_2 and ATP from 1 mole of glucose (Hammes and Vogel, 1995). On the other hand, galactose-6-phosphate is metabolized through the tagatose-6-phosphate pathway which includes three enzymes, namely galactose-6-phosphate isomerase (LacAB), tagatose-6-phosphate kinase (LacC) and tagatose-1,6-diphosphate aldolase (LacD). In the first step, LacAB converts D-galactose-6-phosphate into D-tagatose-6-phosphate which is then phosphorylated through the ATP-dependent LacC into D-tagatose-1,6-bisphosphate. Finally, LacD cleaves D-tagatose-1,6-bisphosphate to produce glyceraldehyde 3-phosphate and dihydroxyacetone phosphate which enter the glycolytic pathway (Figure 1.3) (Bissett and Anderson, 1974; Hickey et al., 1986).

In the case of uptake *via* a permease, lactose is cleaved by β-galactosidase (β-gal) to generate glucose and β-D-galactose. Glucose is then phosphorylated by glucokinase and metabolized as mentioned above while β-D-galactose is further catabolised *via* the Leloir pathway. Leloir was one of the first central metabolic pathways to be discovered in which β-D-galactose is converted to glucose 1-phosphate by the action of four enzymes (Figure 1.3). In the first step, an aldose 1-epimerase (galactose mutarotase, GalM) epimerizes β-D-galactose to α-D-galactose and subsequently an ATP-dependent galactokinase (GalK) phosphorylates α-D-galactose to galactose 1-phosphate. Furthermore, galactose 1-phosphate-uridyltransferase (GalT) catalyzes the transfer of a UMP group from UDP-glucose to galactose 1-phosphate resulting in glucose 1-phosphate which then enters the glycolytic pathway and UDP-galactose. The resulting UDP-galactose is finally converted to UDP-glucose by UDP-galactose 4-epimerase (GalE) (Bettenbrock and Alpert, 1998; Grossiord et al., 1998; Holden et al., 2003).

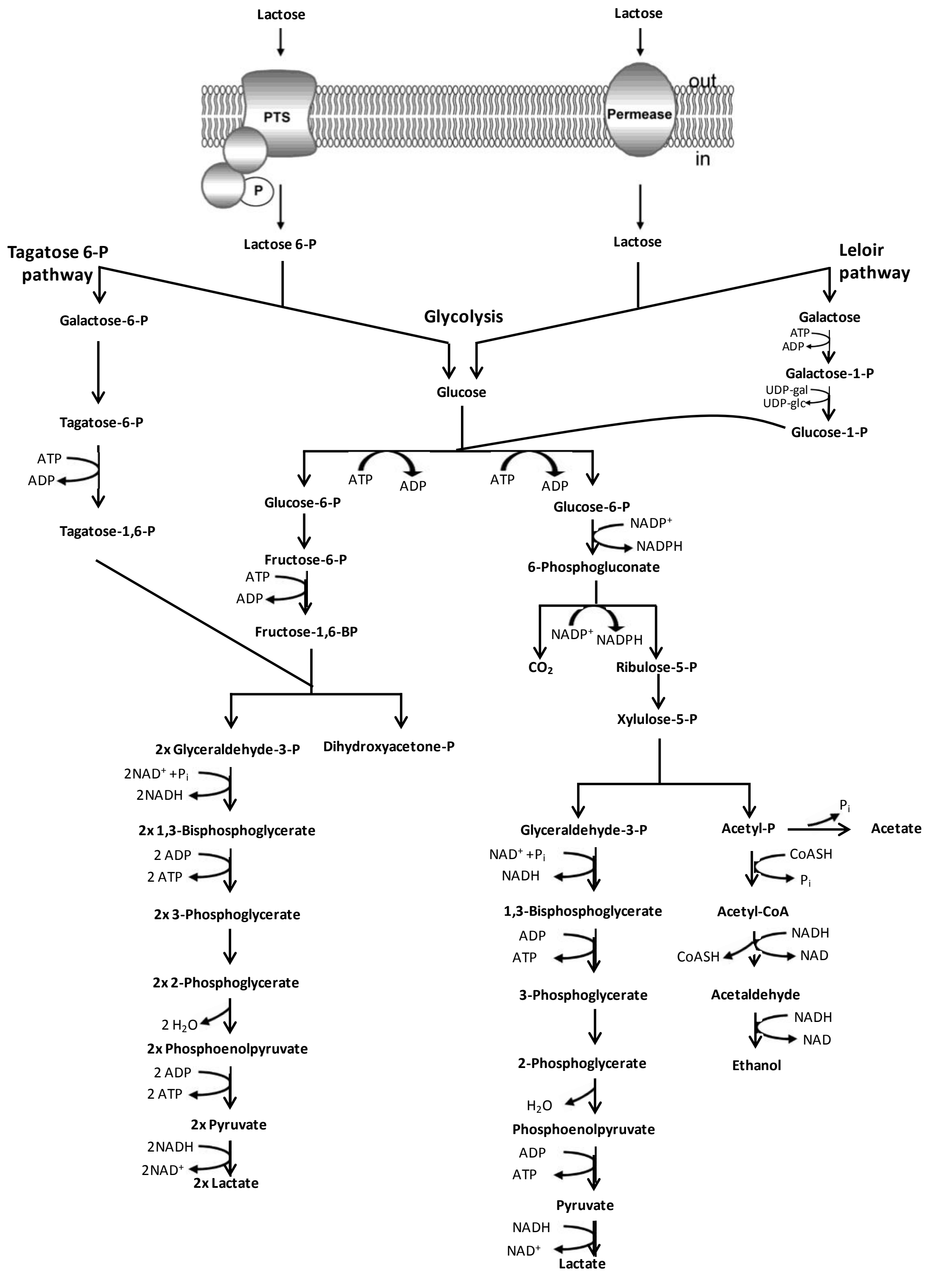

Figure 1.3. Schematic overview of the two alternative pathways for lactose transport and metabolism (Solopova et al., 2012)

1.1.3.2. Citrate fermentation

Citrate is present in several food matrices, such as fruits and vegetables, but also at low concentration in milk (8-9 mM). It can thus serve as energy source for LAB. LAB species that are able to catabolize citrate produce 4-carbon compounds, mainly diacetyl, acetoin and 2,3-butanediol (Figure 1.4), that shape the aroma and taste of the final product. Some of the LAB species that are known as diacetyl/acetoin producers are *L. lactis* subsp. *lactis* biovar. *diacetylactis*, *L. mesenteroides*, *Weissella paramesenteroides*, *E. faecium*, *E. durans*, *L. plantarum* and *Oenococcus oeni* (Bartowsky and Henschke, 2004; de Vos and Hugenholtz, 2004; Hemme and Foucaud-Scheunemann, 2004; Cabral et al., 2007; Minervini et al., 2010; Laëtitia et al., 2014). Among them, *L. mesenteroides, Weissella paramesenteroides* and *L. diacetylactis* are the most frequently used in dairy industry (García-Quintáns et al., 2008). Furthermore, the production of CO_2 during the citrate metabolism contributes to the formation of the characteristic holes of certain cheeses (García-Quintáns et al., 2008).

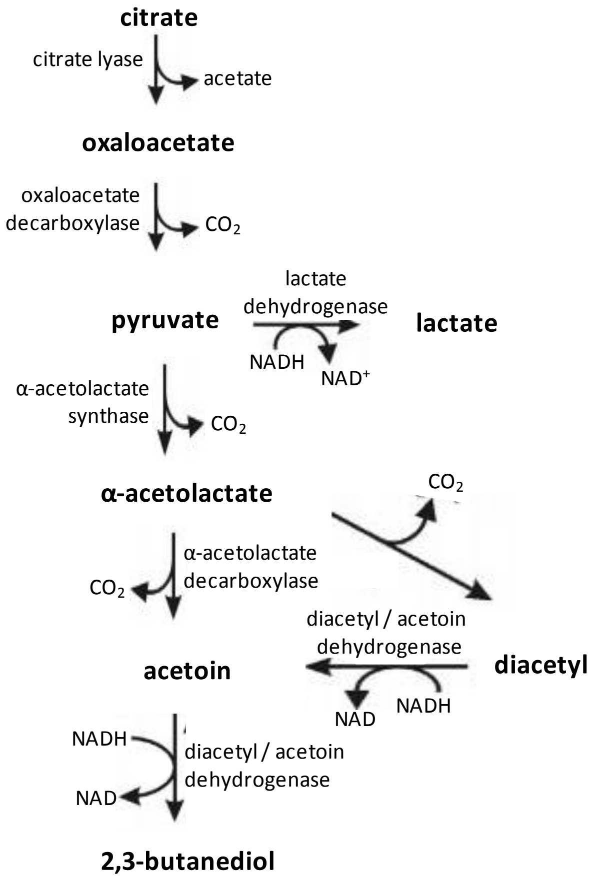

Figure 1.4. Production of 4-carbon aroma compounds during citrate metabolism in LAB (García-Quintáns et al., 2008)

Citrate metabolism takes place in three steps leading to pyruvate formation. First, a citrate permease (CitP) that belongs to the 2-hydroxycarboxylate transporter (2-HCT) family of bacterial citrate transporters is required for the uptake of the extracellular citrate. Then, the internal citrate is cleaved into acetate and oxaloacetate (OxA) by the action of a citrate lyase (CL) and finally OxA is decarboxylated into pyruvate and CO_2 by an oxaloacetate decarboxylase (OAD). Subsequently, pyruvate may be further converted to (i) acetyl CoA through the pyruvate dehydrogenase complex, (ii) formate by the pyruvate formate lyase, (iii) lactate *via* the lactate dehydrogenase and (iv) α-acetolactate by the α-acetolactate synthase, which leads to the 4-carbon compounds acetoin (by α-acetolactate decarboxylate), diacetyl and 2,3-butanediol (by the diacetyl/acetoin reductase).

1.1.3.3. Proteolytic system

LAB require an exogenous source of amino acids since they have limited abilities for amino acid synthesis. Due to the insufficient amounts of free amino acids in most of the raw food materials, LAB have developed an efficient proteolytic system of paramount importance capable of hydrolyzing food proteins, such as caseins, the main milk proteins, to peptides and amino acids that are necessary for their growth. Additionally, the degradation of food proteins also contributes to the organoleptic characteristics of fermented products, i.e. texture, taste and aroma (Pessione et al., 2010). One of the best characterized proteolytic systems is that of *Lactococcus lactis*, which has been a model for all LAB. This system comprises (i) a cell-envelope proteinase (CEP) that initiates the degradation of extracellular casein into oligopeptides, (ii) peptide transporters that take up the degradation products into the cell and (iii) several intracellular peptidases that further degrade peptides into shorter peptides and amino acids (Figure 1.5) (Guédon et al., 2001).

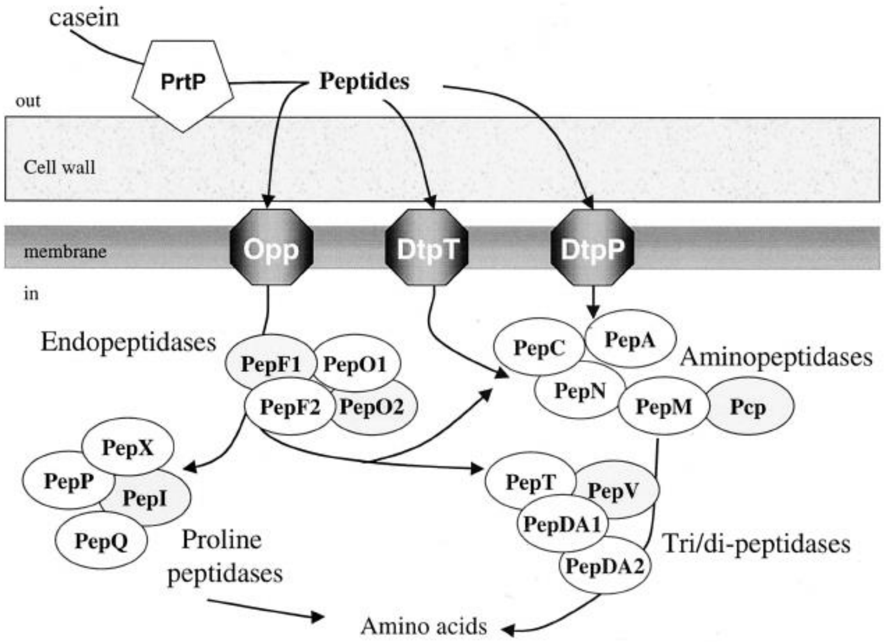

Figure 1.5. Schematic representation of the well-known proteolytic system of *L. lactis* that serves as a model for all LAB (Guédon et al., 2001)

In LAB, five different CEP types have been reported, i.e. PrtP isolated from *L. lactis* and *L. paracasei*, PrtR from *L. rhamnosus*, PrtB from *L. delbrueckii* subsp. *bulgaricus*, PrtH from *L. helveticus* and PrtS from *S. thermophilus* (Savijoki et al., 2006). Among them, PrtP from *L. lactis* subsp. cremoris Wg2 was the first one cloned and characterized (Kok et al., 1988). In lactococci and *L. paracasei*, *prtP* is associated with the upstream-located gene encoding a membrane-bound lipoprotein (PrtM) involved in the maturation of PrtP (Savijoki et al., 2006). Furthermore, although most of LAB possess only one CEP, the presence of two or more genes has been reported for some species, such as *L. helveticus,* in which five *prtH* genes (*prtH1* - *prtH5*) have been identified (Pederson et al., 1999; Smeianov et al., 2007; Sadat-Mekmene et al., 2011; Griffiths and Tellez, 2013; Sun et al., 2015; Guo et al., 2016) . Moreover, lactococcal CEP genes can be either plasmid- or chromosome-encoded, while these from lactobacilli and streptococci have been found only in chromosomes, suggesting higher stability of the trait in these species (Savijoki et al., 2006; Urshev et al., 2014; Tian et al., 2018). According to a comparative genomic analysis among 213 LAB strains with the majority being lactobacilli, an interesting diversity in CEP genes was found (Sun et al., 2015). In total, 60 CEPs were identified in the 213 genomes, ranging from 1,097 to 2,270 amino acids in length. Forty-four of the strains possessed a single CEP, whereas eight encoded two distinct CEPs. In addition, three different anchoring mechanisms were observed for the 60 CEP genes, i.e. (I) a S-layer anchoring (SLAP) domain putatively responsible for non-covalent interactions with the cell wall, (II) a LPXTG motif for covalent linkage to peptidoglycan and (III) a derivative of the LPXTG motif. Finally, 13 out of 60 CEPs had neither a SLAP domain nor a LPXTG-type motif (Sun et al., 2015).

Peptides and amino acids produced by the initial casein degradation are transported into the cell by three types of transporters. Oligopeptide permease (Opp) proteins belong to a superfamily of highly conserved ATP-binding cassette (ABC) transporters. The Opp system typically contains five *opp* genes that are usually organized in a single operon (*oppABCDF*) and is able to transport oligopeptides of 4 to 18 residues. This system consists of an oligopeptide-binding protein (OppA), two integral transmembrane proteins (OppB and OppC) and two nucleotide-binding proteins (OppD and OppF) (Savijoki et al., 2006; Hiron et al., 2007). However, differences among the Opp transport systems of LAB species may occur. According to a comparative genomic analysis by Liu and co-workers, the number of *opp* genes was variable among the proteolytic system of several LAB species/strains (Liu et al., 2010). For example, while most of the examined strains contained a single copy of *oppA*, some strains, such as *S. thermophilus* LMD9, *Lactobacillus acidophilus* NCFM and *Lactobacillus gasseri* ATCC 33323 seemed to contain two, three and four *oppA* copies, respectively (Liu et al., 2010). Other peptide transporters are DtpT belonging to the peptide transport (PTR) family and Dpp (previously referred to as DtpP), an ABC transporter preferring hydrophilic and hydrophobic di-/tripeptides, respectively. Similarly to Opp, the Dpp system consists of five *dpp* genes organized in an operon namely *dppABCDE*. The system contains a peptide-binding protein (DppA), two integral membrane proteins (DppB and DppC) and two nucleotide-binding proteins (DppD and DppF) (Doeven et al., 2005). Oligopeptides are further hydrolyzed into shorter peptides and amino acids by intracellular peptidases classified on the basis of their cleavage specificity. Such peptidases are the general aminopeptidases (PepC and PepN) and the X-prolyl dipeptidyl aminopeptidase (PepX). Although endopeptidases are unable to hydrolyze caseins, they are capable of hydrolyzing internal peptide bonds of casein-derived peptides (Savijoki et al., 2006). Other peptidases are the proline peptidases PepI, PepR, PepL, PepP and PepQ, the dipeptidases PepD and PepV, the tripeptidase PepT, the endopeptidases PepE/PepG, PepO and PepF and the aminopeptidases PepM, PepA and Pcp (Liu et al., 2010).

1.1.3.4. Amino acid catabolism

In addition to proteolysis, bacterial amino acid catabolism results in a number of compounds that contribute to flavor formation during food fermentation. Amino acids can be catabolized in three steps. The first step includes 4 different routes, namely (i) decarboxylation to form amines and CO_2, (ii) transamination for the synthesis of other amino acids, (iii) deamination for the production of α-ketoacids and NH_4 or (iv) hydrolysis of the amino acid side chains. During the second step, the resulting compounds (amines, amino acids and α-ketoacids) are further transformed to aldehydes mainly by deaminases. The final step is the conversion of aldehydes to alcohols (reduction) or acids (oxidation). The catabolism of sulphur-containing amino acids results to the formation of a number of compounds, such as methanethiol and other sulphur derivatives (Figure 1.6) (McSweeney and Sousa, 2000; Liu et al., 2003). Among the compounds produced by amino acid catabolism, these deriving from the branched-chain (isoleucine, leucine and valine), aromatic (tyrosine, phenylalanine and tryptophan) and sulphur-containing (methionine and cysteine) amino acids are of significant interest due to their contribution to the aroma and flavor of fermented dairy products. These metabolic pathways have been extensively studied in *L. lactis* and mesophilic lactobacilli (Helinck et al., 2004).

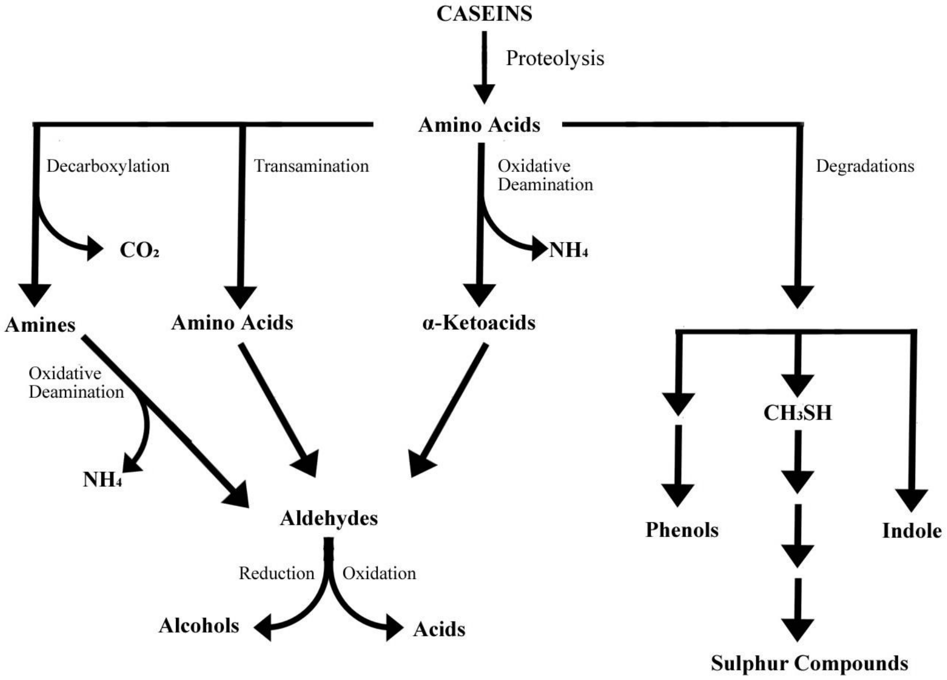

Figure 1.6. General pathways of amino acid catabolism (McSweeney and Sousa, 2000)

1.1.3.5. Lipid metabolism

Lipolysis is performed in two basic steps; first, triglycerides are hydrolyzed in free fatty acids (FFA) and glycerol. Then, FFA are further converted to methyl ketones, lactones, thioesters, keto and hydroxy acids which contribute to the flavor of the final product (Figure 1.7) (Collins et al., 2003). Although lipids may undergo oxidative or hydrolytic degradation, lipid oxidation is rare in cheese (McSweeney and Sousa, 2000).

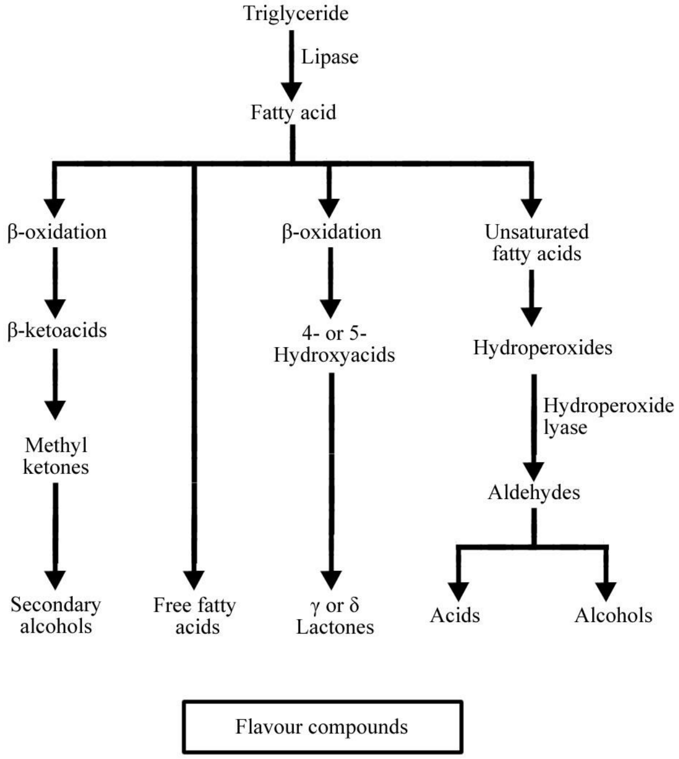

Figure 1.7. General pathways for the catabolism of free fatty acids in cheese (McSweeney and Sousa, 2000)

The main lipolytic agents in cheese originate from the milk and the starter and non-starter bacteria (Collins et al., 2003). Milk contains the lipoprotein lipase (LPL) which involves in the metabolism of plasma triglycerides and its presence in milk results from the leakage of blood through the mammary cell membrane during milking. It should be mentioned that a combination of high-temperature/short-time treatment (72 °C /15 sec) greatly inactivates the enzyme, thus the contribution of LPL is more important in raw milk cheeses (Deeth and Fitz-Gerald, 1983; McSweeney and Sousa, 2000).

On the other hand, LAB possess esterolytic and lipolytic enzymes capable of hydrolysing a range of esters of FFA, tri-, di, and monoacylglyceride substrates. However, despite these enzymes, LAB have generally weak lipolytic activity compared to *Pseudomonas,* *Acinetobacter* and *Flavobacterium* spp. Nevertheless, due to the high numbers of LAB during cheese ripening, they are responsible for the release of considerable amounts of FFA (McSweeney and Sousa, 2000; Collins et al., 2003). To date, several lipases/esterases of LAB have been identified and biochemically characterized mostly from the *Lactococcus, Lactobacillus, Streptococcus, Leuconostoc* and *Enterococcus* genera (Tsakalidou and Kalantzopoulos, 1992; Chich et al., 1997; Fernández et al., 2000; Liu et al., 2001; Katz et al., 2002; Esteban-Torres et al., 2016). Interestingly, it has been shown that the esterolytic activity of thermophilic streptococci is more than double compared to that of lactococcal strains (Crow et al., 1994).

Although many LAB genome sequences are currently available, there is still limited information on the function of genes predicted to encode esterases. Recently, a comparative genomic analysis among 13 *Lactobacillus* species identified several genes encoding lipases all belonging to three families. The most abundant lipase family was PF00561 (family of acid lipases and Pseudomonas-like lipases), followed by PF0785 (family of hormone-sensitive lipases) and PF01734 (family of patatin-like phospholipases). The PF00561 and PF0785 families belong to the alpha/beta hydrolase superfamily, including enzymes with diverse catalytic functions, such as proteases, lipases, peroxidases, esterases and dehalogenases (Drissi et al., 2014).

1.1.4. Defense mechanisms of lactic acid bacteria

1.1.4.1. Bacteriocins

Bacteriocins are small (approximately 30–60 amino acids) ribosomally-synthesized cationic peptides or proteins and usually undergo post-translational modification. Bacteriocins are mostly produced by Gram-positive bacteria and their antimicrobial activity is against related species or even against strains of the same species (Zacharof and Lovitt, 2012; Cotter et al., 2013; Mathur et al., 2017). However, an activity against Gram-negative bacteria such as *Salmonella* has also been reported (Kim et al., 2015; Prudêncio et al., 2015; Mathur et al., 2017; Singh, 2018). It is worth noting that the expression of a specific immunity protein encoded in the bacteriocin operon protects the bacteriocin-producing strain from its own bacteriocin (Mokoena, 2017; Singh, 2018). Bacteriocins are classified based on their primary structures, molecular weights, post-translational modifications and genetic characteristics in three classes.

Class I bacteriocins, called lantibiotics, are characterized by the presence of unusual amino acid residues, such as lanthionine and methyllanthionine resulting from post-translational modifications (Parada et al., 2007). Lantibiotics contain small peptides of 19 to 50 amino acids, their molecular mass is less than 5 kDa and are heat-stable (Yang et al., 2014). Several lantibiotics exhibit strong activity against clinically relevant and food-borne pathogens and some of them have been shown to possess activity against antibiotic-resistant bacteria like vancomycin-resistant enterococci and methicillin-resistant *S. aureus*. Nisin and lactocin are the most known representative lantibiotics (Mathur et al., 2017).

Class II bacteriocins are composed of heat-stable and without post-translational modifications peptides of 20 to 60 amino acids and molecular mass <10 kDa. According to Cotter et al., they are subdivided into five sub-classes (Cotter et al., 2013). Class IIa pediocin-like bacteriocins are *Listeria*-active peptides containing a YGNGV motif (in which N represents any amino acid). Representative class IIa bacteriocins are enterocin NKR-5-3C (Himeno et al., 2012) (Figure 1.10A), pediocin PA-1 (Henderson et al., 1992), enterocin CRL35 (Farias et al., 1996) and carnobacteriocin X (Tulini et al., 2014). Class IIb includes the two-peptide bacteriocins like lactococcin Q (Zendo et al., 2006) (Figure 1.10B), lactacin F (Allison et al., 1994) and ABP-118 (Flynn et al., 2002), while class IIc are the circular ones, such as lactocyclicin Q (Sawa et al., 2009) (Figure 1.10C), carnocyclin A (Gong et al., 2009) and enterocin AS-48 (Martínez-Bueno et al., 1994). In addition, class IId contains the unmodified, linear, non-pediocin-like, single-peptide bacteriocins, such as lacticin Q (Fujita et al., 2007) (Figure 1.10D), epidermicin NI01 (Sandiford and Upton, 2012) and lactococcin A (Holo et al., 1991). Class IIe bacteriocins, formerly known as class IIb microcins, contain a serine-rich carboxy-terminal region with a non-ribosomal siderophore-type modification like microcin E492 (de Lorenzo and Pugsley, 1985). Microcin E492 was isolated from the Gram-negative *Klebsiella pneumonia*, thus class IIe should be categorized to microcins of Gram-negative bacteria (Yang et al., 2014).

Finally, class III bacteriocins are heat-labile proteins with large molecular weight (>30 kDa) which can be further subdivided into two groups. Class IIIa bacteriocins like enterolisin A (Nilsen et al., 2003) inhibit the growth of target strain by lysis of the cell well, while class IIIb bacteriocins are the non-lytic proteins such as helveticin J (Joerger and Klaenhammer, 1986).

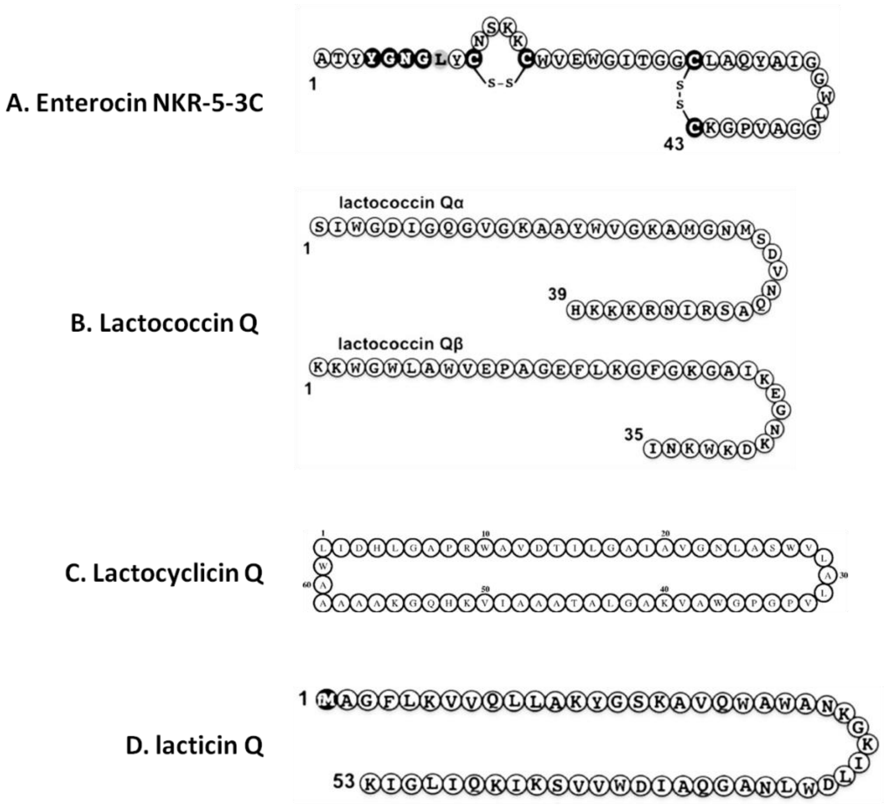

Figure 1.10. Primary structures of representative class II bacteriocins. Enterocin NKR-5-3C is a class IIa (pediocin-like) bacteriocin (A), lactococcin Q a class IIb (two-peptide) bacteriocin which is comprised of the two peptides Qa and Qβ (B), lactocyclicin Q a class IIc (circular) bacteriocin (C), and lacticin Q a class IId bacteriocin with a formylated methionine residue (fM) at the first N-terminal residue (D) (Perez et al., 2014)

The modes of action of bacteriocins can be divided into those that act on the cell envelope and those that affect gene expression (Figure 1.11). Nisin and other lantibiotics target lipid II, which is a key component in the synthesis of the cell wall peptidoglycan and a target for antibacterial compounds such as vancomycin (de Kruijff et al., 2008). These bacteriocins bind lipid II at a different site from the vancomycin-binding site to preserve activity against vancomycin-resistant pathogens and thus inhibit peptidoglycan synthesis. Lipid II can be also used by other lantibiotics for pore formation in the cell membrane and as a consequence the loss of membrane potential. Furthermore, class IIa bacteriocins and several others in class II (e.g. lactococcin A127) bind to the cell envelope-associated mannose phosphotransferase system (Man-PTS) resulting also to pore formation. Other bacteriocins, such as microcin B17, targeting Gram-negative bacteria can kill target cells by interfering with DNA, RNA and protein metabolism (Cotter et al., 2013).

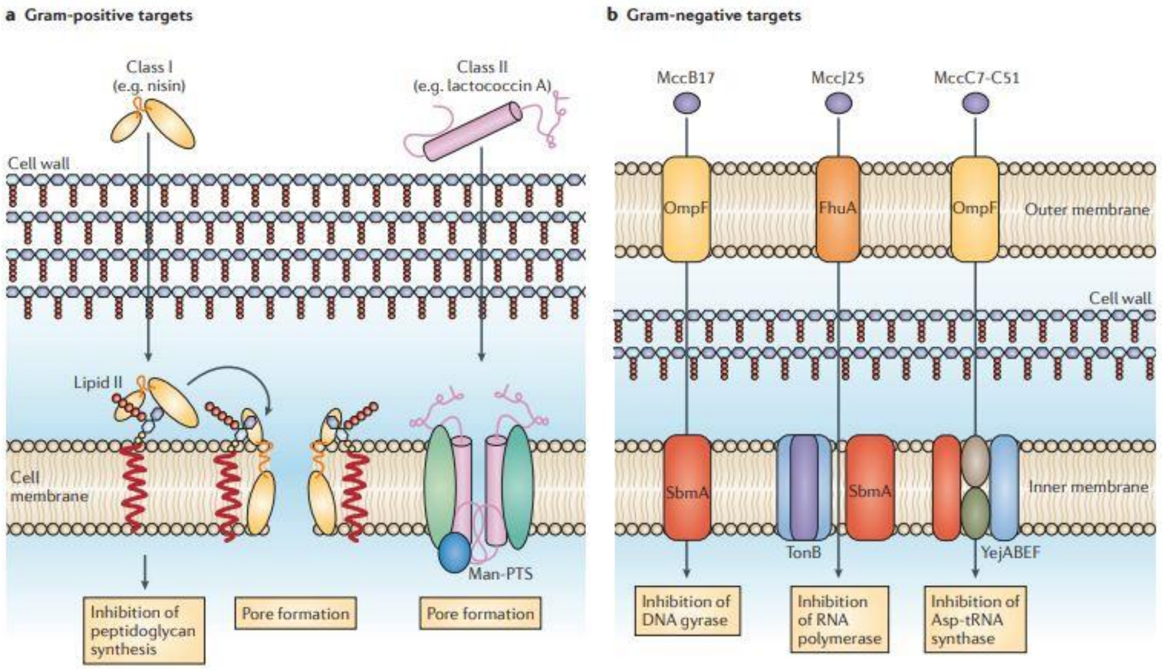

Figure 1.11. Modes of action of represented bacteriocins (Cotter et al., 2013). (a) Some class I bacteriocins target lipid II on the cell membrane and either inhibit peptidoglycan synthesis or form pores. Nisin and some other bacteriocins do both. Class II bacteriocins like lactococcin A bind to the Man-PTS and form pores to inhibit the growth of the target strain. (b) Bacteriocins targeting Gram-negative bacteria like microcin B17 inhibit the growth of target cells by interfering with DNA, RNA and protein metabolism

Although several bacteriocins with potential industrial applications have been isolated and characterized thoroughly, only nisin and pediocin have been approved by the Food and Drug Administration (FDA) and European Food Safety Authority (EFSA) (Müller-Auffermann et al., 2015; Mokoena, 2017). After a long history of safe use, nisin is widely used as a food-preservative (E 234) in over 50 countries and in a broad range of products, including dairy and bakery products, vegetables, meat and fish (Delves-Broughton et al., 1996; Field et al., 2008). Nisin is one of the oldest known antibiotic compounds produced mainly by *L. lactis* subsp. *lactis* (Lubelski et al., 2008). According to several studies, nisin serves as a broad-spectrum bacteriocin against a wide range of mostly Gram-positive bacteria including food spoilage and pathogenic bacteria, such as bacilli, enterococci, staphylococci, streptococci, clostridia, mycobacteria and *Listeria monocytogenes* (McAuliffe et al., 2001; Field et al., 2008; Lubelski et al., 2008). However, recent studies have demonstrated that purified nisin and/or nisin in combination with antibiotics, like polymyxin B, can be effective against also Gram-negative bacteria, such as *Escherichia coli, Salmonella enterica* serovar Typhimurium and *Cronobacter sakazakii (Kuwano et al., 2005; Naghmouchi et al., 2010; Field et al., 2012; Zhou et al., 2016).*

Over the past two decades, the application of nisin has been extended to biomedical applications, including bacterial infections, oral diseases and cancer (Shin et al., 2015). Certain human infectious diseases, such as bacterial skin infections, are prevented and/or treated conventionally with antibiotics. However, the emergence of antibiotic resistance has led to the search for alternative therapies (Zetola et al., 2005). In this perspective, nisin was tested as a potential agent for infectious diseases. Recent studies have reported that nisin can prevent the growth of several antibiotic-resistant bacteria, such as methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant enterococci (Piper et al., 2009; Piper et al., 2011; Balciunas et al., 2013; Shin et al., 2015).

Furthermore, the idea of using nisin to improve oral health was first described by Johnson and co-workers who demonstrated that the number of streptococci was decreased in the dental plaque of monkeys when nisin was added in their food (Johnson et al., 1978). More recently, the results of numerous studies support the antimicrobial properties of nisin against Gram-positive and -negative oral pathogenic bacteria, such as *Streptococcus mutans, Streptococcus sanguinis, Streptococcus sobrinus, Streptococcus gordonii, Porphyromonas gingivalis, Prevotella intermedia, Aggregatibacter actinomycetemcomitans* and *Treponema denticola* (Tong et al., 2010; Tong et al., 2011; Shin et al., 2015).

Finally, the use of nisin has been also extended to control several types of cancer. In particular, many studies have demonstrated the cytotoxic effect of nisin to human breast adenocarcinoma cell line MCF-7, human liver hepatocellular carcinoma cell line HepG2, colon cancer cell lines SW480 and HT29, human T-cell lymphoma Jurkat cells and human adenocarcinoma of colorectum Caco-2 cell line (Maher and McClean, 2006; Begde et al., 2011; Paiva et al., 2012; Ahmadi et al., 2017). Moreover, the cytotoxicity of nisin in head and neck squamous cell carcinoma, as well as the synergistic effect of nisin and doxorubicin against 7,12-dimethylbenz(a)anthracene-induced skin carcinogenesis was also investigated in mice models (Joo et al., 2012; Kamarajan et al., 2015; Preet et al., 2015). Overall, these studies demonstrate the potential of nisin to be used as an anti-cancer agent.

To date, eight natural forms of nisin have been identified, namely nisin A, Z, Q and F produced by *Lactococcus lactis*, U and U2 by *Streptococcus uberis,* H by *Streptococcus hyointestinalis* and P by *Streptococcus gallolyticus* subsp. *pasteurianus* (Figure 1.8) (Shin et al., 2015).

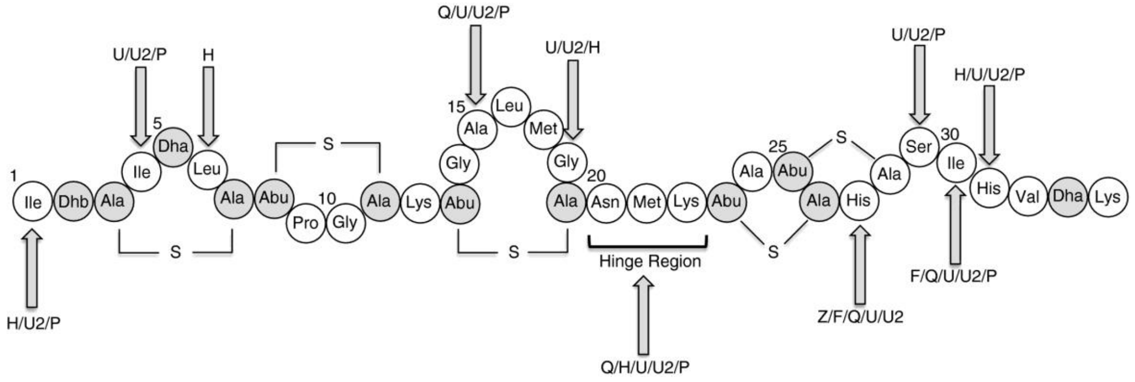

Figure 1.8. Peptide structures of natural variants of nisin. Grey circles indicate post-translational modifications and arrows amino acid differences among the natural variants (Shin et al., 2015)

Nisin regulon contains 11 *nis* genes, *nisABTCIPRKFEG* necessary for nisin production, maturation, immunity and regulation (Figure 1.9). The structural gene, i.e *nisA*, is a lanthionine ring-containing peptide that is ribosomally synthesized as a prepeptide of 57 amino acid residues, containing an N-terminal leader peptide of 23 amino acids. Nisin regulon contains the genes responsible for intracellular post-translational modifications, including dehydration reactions and ring formation (NisBC), transport across the cytoplasmic membrane (NisT) and cleavage of the leader peptide (NisP) before finally becoming biologically active (Kuipers et al., 1993; Lubelski et al., 2008).

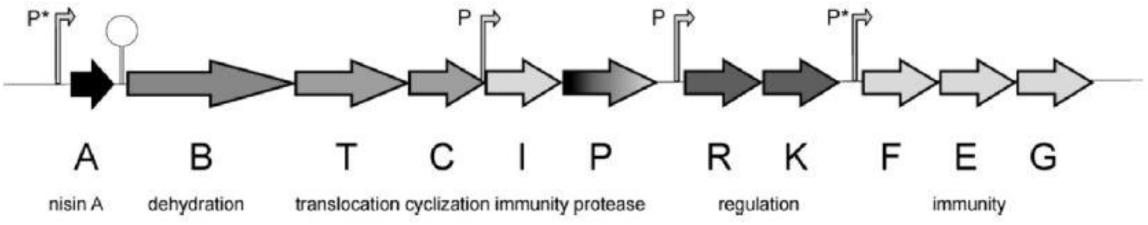

Figure 1.9. Nisin biosynthetic gene cluster *nisABTCIPRKFEG*. Promoters marked with an asterisk (P*) are controlled by the two-component system NisRK (Lubelski et al., 2008)

Nisin biosynthesis is autoregulated by a two-component signal transduction regulatory system, namely NisRK. NisK is a histidine sensor kinase that autophosphorylates a conserved histidine residue in response to the external signal by the fully matured nisin. Afterwards, the phosphoryl group is transferred to a conserved aspartic acid residue of the NisR, which is a transcriptional activator for the induction of the *nisA* and *nisF* promoters of *nisABTCPIRK* and *nisFEG*, respectively. Transcription of these genes is required for nisin biosynthesis and immunity (McAuliffe et al., 2001; Lubelski et al., 2008).

Immunity against the bactericidal activity of nisin is conferred by the lipoprotein NisI and the ABC transporter NisFEG. A knockout approach for each of the two systems revealed that each system alone provided only 5-20% of full immunity demonstrating a strong synergistic action (Siegers and Entian, 1995; Ra et al., 1999). NisFEG proteins form an ABC transporter complex, in which NisF is a cytoplasmic ATP-binding protein and NisE together with NisG are integral membrane proteins (Siegers and Entian, 1995). Interestingly, disruption in *nisI* resulted in a higher level of sensitivity to nisin compared to disruption in *nisFEG* (Siegers and Entian, 1995).

1.1.4.2. Restriction modification systems

Among the bacterial defense mechanisms against foreign DNA, such as that of bacteriophages, restriction modification (RM) systems were discovered first in the early 1950s and studied extensively (Murray, 2000; Rao et al., 2000; Koonin et al., 2017). RM systems contain an endonuclease that recognise specific sequences and catalyse cleavage of double-stranded DNA, and a methyltransferase (mtase) that catalyse the addition of a methyl group to the nucleotide adenine in each strand of the recognition sequence of the bacterial DNA in order to protect self DNA from cleavage (Figure 1.10). The methyl group donor is the *S*-adenosyl-L-methionine (AdoMet) and the potential methylation products are N6-methyladenine, C5-methylcytosine and N4-methylcytosine (Murray, 2000; Dryden et al., 2001). According to the latest classification, RM systems are divided into four types based on the subunit composition, ATP requirement and cleavage mechanism (Koonin et al., 2017).

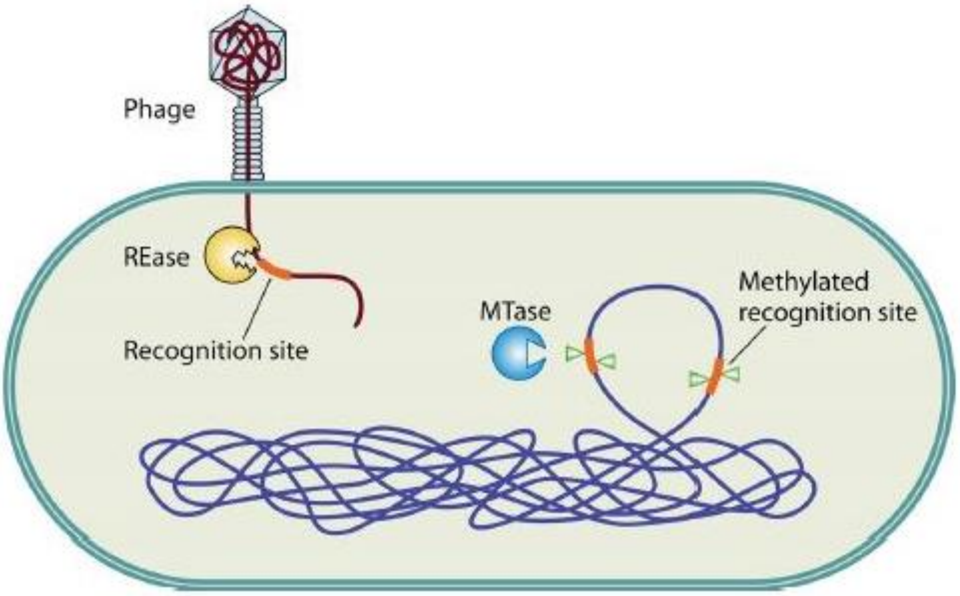

Figure 1.10. Bacterial restriction modification (RM) systems. The methylation status of the recognition sites is maintained by the MTase and sequences lacking methylation are cleaved by the REase (Vasu and Nagaraja, 2013)

The most complex RM system is the ATP-dependent Type I with both restriction and modification functions. These enzymes consist of three subunits, namely HsdS (~50 kDa), HsdM (50-60 kDa) and HsdR (~140 kDa). Usually, Type I enzymes contain one S subunit, two HsdM subunits and two HsdR subunits (Roberts et al., 2003). HsdS contains two target recognition domains (TRDs) of approximately 150 amino acids each to specify the recognition sequences. HsdS also serves as the core subunit to which the other two bind (Fuller-Pace and Murray, 1986). The HsdM subunit includes the binding site for AdoMet and the active site for DNA methylation of the bacterial sequence. Both *hsdM* and *hsdS* are transcribed from the same promoter (Murray, 2000). Finally, HsdR includes the active site for ATP hydrolysis of DNA sequences lacking methylation. DNA cleavage is performed from approximately 100 bp to tens of thousands of bp away from the recognition sequence (Dryden et al., 1997; Dryden et al., 2001). Typical examples of Type I RM systems are *Eco*KI [AAC(N)$_6$GTGC], which is probably the best known (Murray, 2000), *Eco*R124I [GAA(N)$_6$RTCG] and *Eco*AI [GAG(N)$_7$GTCA] (Roberts et al., 2003). Type I RM systems have been found in several LAB species, such as *Lactobacillus salivarius* (Claesson et al., 2006; Raftis et al., 2011), *L. lactis* (Deng et al., 2000; Górecki et al., 2011), *Lactobacillus sakei* (Alpert et al., 2003), *Lactobacillus kefiranofaciens* (Xing et al., 2017), *Lactobacillus reuteri (Ortiz-Velez et al., 2018)*, *L. bulgaricus* (Hao et al., 2011), *S. thermophilus*

(Solow and Somkuti, 2001), *Streptococcus suis* (Willemse and Schultsz, 2016; Xu et al., 2017) and *S. aureus* (Cooper et al., 2017), which are either chromosomal or plasmid encoded.

On the contrary, the simplest, smaller in size and most common RM system is Type II that consists solely of a methyltransferase-restriction endonuclease (MTase-REase) pair that is generally encoded within the same operon. Type II enzymes recognize palindromic DNA sequences of 4-8 bp and cleave DNA within or near these sequences (Pingoud and Jeltsch, 1997; Roberts et al., 2003). Therefore, Type II enzymes are of higly interest for recombinant DNA technology (Roberts et al., 2003). Representative Type II enzyme is *Eco*RI with recognition sequence GAATTC and cleavage site between guanine and adenine (Roberts et al., 2003). Type II RM systems have been found in LAB species, such as *L. lactis* (Davis et al., 1993), *L. bulgaricus* (Hao et al., 2011), *L. kefiranofaciens* (Xing et al., 2017), *S. thermophilus* (Burrus et al., 2001) and *Streptococcus pneumoniae* (Manso et al., 2014).

Additionally, the ATP-dependent Type III RM systems possess both modification and restriction activities. Type III enzymes consist of two different polypeptides, namely Mod (75 kDa) and Res (106 kDa), which recognize specific sequences and cleave DNA approximately 25-27 bp away from the recognition site (Rao et al., 2000). The most well-characterized Type III enzymes are *Eco*P1I and *Eco*P15I from *E. coli* (Roberts et al., 2003). Conserning Gram-positive bacteria, *Lla*FI is the sole one characterized Type III enzyme isolated from *L. lactis* LL42-1 (Su et al., 1999).

Finally, Type IV RM systems are two-subunit complexes contain a GTPase and an endonuclease. The mode of action of Type IV system is completely different from the other three types, since Type IV enzymes cleave non-specifically modified phage DNA containing methylated, hydroxymethylated, or glucosyl-hydroxymethylated bases. These modifications are among the mechanisms employed by phages against conventional REases of Types I, II, and III (Vasu and Nagaraja, 2013). Thus, Type IV RM systems are suitable for such modifications (Roberts et al., 2003; Koonin et al., 2017). The best studied example at both the genetic and biochemical level is *Eco*KMcrBC of *E. coli* K-12 (Raleigh and Wilson, 1986; Stewart et al., 2000).

1.1.4.3. CRISPR-Cas systems

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and their associated *cas* genes provide acquired immunity against foreign genetic elements, such as bacteriophages, viruses and plasmids (Barrangou and Doudna, 2016; Price et al., 2016). CRISPR-Cas systems are found in about 87% of archaeal and 45% of bacterial sequences according to the most recent update of the CRISPR database (http://crispr.i2bc.paris-saclay.fr/) (Grissa et al., 2007a; Grissa et al., 2007b). Although the first CRISPR locus was found in *E. coli* in 1987 (Ishino et al., 1987), the biological function of CRISPRs was clarified many years later when the phage resistance of *S. thermophilus* was studied (Bolotin et al., 2005; Barrangou et al., 2007).

The key role of CRISPR-Cas systems is the protection of host cells against previously encountered bacteriophages, viruses and plasmids (Hidalgo-Cantabrana et al., 2017). CRISPR-Cas systems can be found on both chromosomal and plasmid DNA and contain a leader sequence, usually several hundred nucleotides in length with a high proportion of adenines and thymines, *cas* genes and a CRISPR array (Rath et al., 2015). The CRISPR array is typically formed by a number of short (21 to 50 bp) identical direct repeats separated by spacers (20 to 84 bp) that encode the immunological memory of the CRISPR-Cas system. The sequence and number of direct repeats as well as the leader sequence may vary to an extent among different organisms and/or CRISPR-Cas systems. It is of note that the number of direct repeats per array can range from two to several hundreds, although the majority of loci have around 50 repeats. Similarly, the number of *cas* genes is also depended by the CRISPR-Cas system and usually range from four to 20 different genes (Darmon and Leach, 2014).

CRISPR-Cas systems can be classified as Type I, II and III, with each having several subgroups. These three Types can be distinguished by the presence of unique signature proteins, i.e Cas3, Cas9 and Cas10 for Type I, Type II and Type III, respectively (Makarova et al., 2011). Furthermore, the steps during the CRISPR-Cas immunity process are three: (i) adaptation, (ii) CRISPR RNA (crRNA) expression and (iii) interference (Figure 1.11).

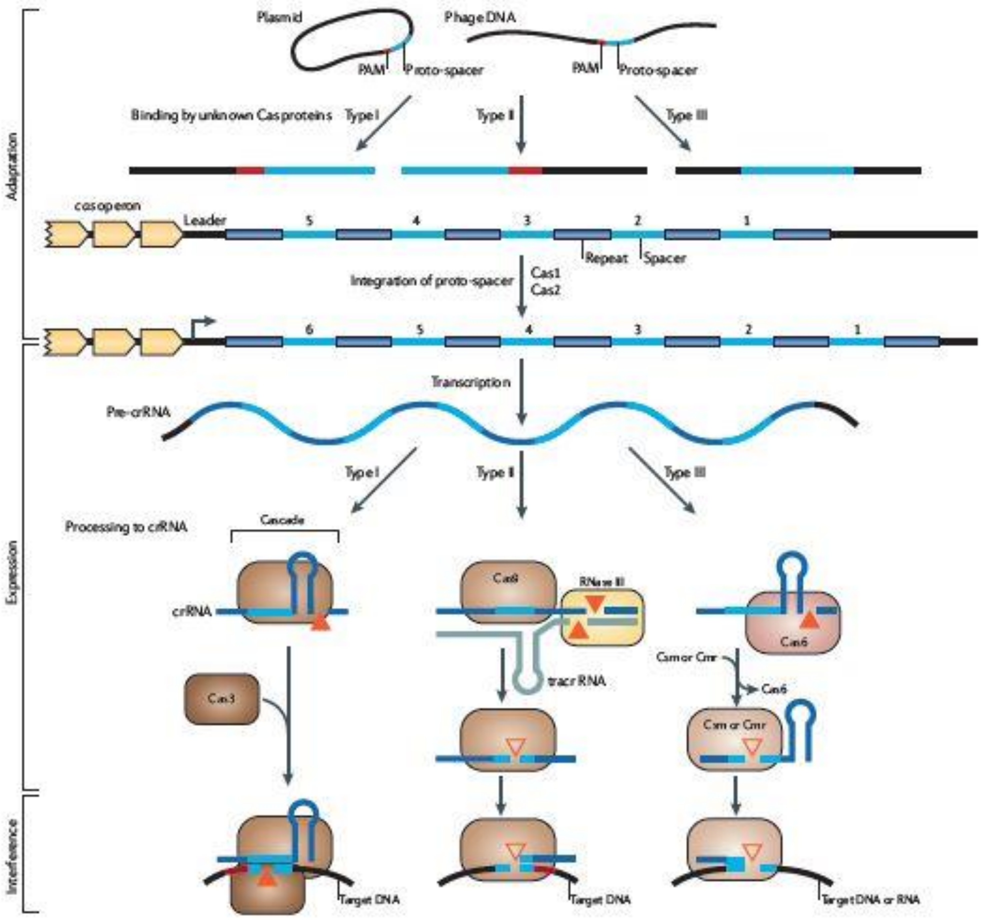

Figure 1.11. The three steps of CRISPR-Cas immunity process, as described for each of the three CRISPR-Cas Types (Makarova et al., 2011)

The first step involves the recognition and assimilation of a foreign DNA sequence by Cas proteins. These proteins are able to identify a specific sequence within the DNA, namely proto-spacer. In Type I and II CRISPR-Cas systems, the selection of proto-spacers depends on a very short sequence (2 to 5 bp) next to the proto-spacer called proto-spacer-adjacent motif (PAM) (Shah et al., 2013). After the initial recognition step, Cas1 and Cas2 proteins incorporate the proto-spacers into the CRISPR array to form a new spacer between the leader sequence and the first repeat of the array after the duplication of a direct repeat.

In a subsequent infection by the same plasmid, bacteriophage or virus, the CRISPR array is transcribed from a promoter in the leader sequence producing a long precursor-crRNA (pre-crRNA) transcript. In Type I, the CRISPR-associated complex for antiviral defence (Cascade) binds the pre-crRNA and Cas6e/Cas6f subunits of subtypes I-E and I-F, respectively, cleave at the junction formed by hairpin loops in the direct repeat. Similar to Type I, Type III also forms hairpin loops in the direct repeats for cleavage. Although Cas6 is responsible for the processing step, crRNA seems to be transferred to a distinct Cas complex namely Csm in subtype III-A and Cmr in subtype III-B, respectively. In subtype III-B systems, the crRNA is further trimmed. In contrast, Type II systems use a trans-activating crRNA (tracrRNA) to form a pair with the repeat fragment of the pre-crRNA and the RNase III cleaves DNA within the repeat sequences in the presence of the Cas9 protein (formerly known as Csn1 or Csx12). In Type II and Type III systems, subsequent maturation might occur by cleavage at a specific distance within the spacers to produce mature crRNAs (Hale et al., 2009; Deltcheva et al., 2011). However, the mechanism of trimming remains unknown (Richter et al., 2013).

In the last step of interference, the invading DNA sequence is cleaved. In Type I systems, the crRNA guides the Cascade complex to foreign DNA that contain the complementary DNA sequence. In this target recognition process, PAM also plays a significant role in Type I systems. Finally, the cleavage of the invading sequence is performed by the Cas3 protein. In Type II systems, crRNA and Cas9 protein form a crRNA-Cas9 complex and directly targets invading DNA for its degradation. Similar to Type I, Type II systems require also the PAM (Haurwitz et al., 2010). On the contrary, Type III systems do not require a PAM for a successful cleavage. The two subtypes of Type III systems, i.e. subtype III-A and subtype III-B, target either DNA or RNA (Marraffini and Sontheimer, 2008; Hale et al., 2009). An updated evolutionary classification of CRISPR-Cas systems identified two putative new Types, namely Type IV and Type V with no subtypes up to date. These new Types are mostly functionally uncharacterized and need further investigation (Makarova et al., 2015).

In order to resist in CRISPR-Cas systems, viruses frequently mutate their genomes by point mutation, deletion or recombination. Bacterial prophages seem to use another strategy, since they have proteins that specifically bind and damage the CRISPR array structure or use anti-CRISPR genes (Bondy-Denomy et al., 2012; Darmon and Leach, 2014).

The high occurrence of CRISPR-Cas systems in LAB genomes reflects their widespread exposure to foreign DNA (Horvath et al., 2009; Chylinski et al., 2013; Hidalgo-Cantabrana et al., 2017). In LAB, eight different CRISPR families have been found. However, these families did not correlate with the phylogeny of LAB species indicating their independent evolution through time. Interestingly, it has been shown that CRISPR systems of distant LAB genera or species are highly similar to *cas* gene content and overall architecture. This could probably be explained by horizontal gene transfer (HGT) events, since they also have different G+C contents compared to the rest of the host genome. Another explanation is the presence of CRISPR loci on plasmids (Horvath et al., 2009). Furthermore, comparative analysis between the CRISPR systems of two closely related species, i.e. *L. helveticus* and *L. casei*, showed that they belong to different families - once again confirming the high level of variability of these systems (Horvath et al., 2009).

Although it has been many years since the discovery of the first CRISPR system (Ishino et al., 1987), our knowledge on CRISPR activity is limited and is mainly based on the model organisms for CRISPRs, which are *Streptococcus pyogenes* and *S. thermophilus* for LAB (Barrangou et al., 2007; Levin et al., 2013; Paez-Espino et al., 2013; Sun et al., 2013; Crawley et al., 2018). The characterized CRISPR loci of *S. thermophilus* are four, namely CRISPR1, CRISPR2, CRISPR3 and CRISPR4, which differ in repeat sequences, *cas* genes and chromosomal location. The four CRISPR systems are included in the three Types proposed by Makarova et al. (Makarova et al., 2011). CRISPR1 and CRISPR3 are attributed to the Csn Type II-A system. Even though the distribution and architecture of *cas* sequences in both CRISPR loci are similar and contain the same number of *cas* genes, the sequence similarities between these genes are low, i.e. 33.6% and 41.3% for *cas1* and *cas2*, respectively (Horvath et al., 2008). Furthermore, CRISPR2 and CRISPR4 belong to the Csm Type III-A and Cse Type I-E systems, respectively (Hao et al., 2018). Comparative genomic analysis of CRISPR systems in streptococci and other bacterial genera and species, showed that CRISPR1 is present in only a few streptococci, CRISPR3 is found in most *Streptococcus* species, CRISPR2 is probably a vestige of a Gram-positive ancestor of *S. thermophilus* and finally CRISPR4 is found only in few *S. thermophilus* strains (Horvath et al., 2008; Hao et al., 2018). In addition, several *S. thermophilus* strains, such as *S. thermophilus* LMD-9, contain more than one CRISPR locus within their genome (Horvath et al., 2008). Moreover, it was recently demonstrated that the *S. thermophilus* CRISPR-Cas9 system (StCas9) can be used for crop improvement and genome editing as a safe alternative to the CRISPR-Cas9 system of *S. pyogenes* (SpCas9) and therefore to be a valuable option for future human gene therapy applications (Ran et al., 2013; Xu et al., 2015; Müller et al., 2016; Arora and Narula, 2017; Jaganathan et al., 2018).

Interestingly, lactobacilli contain CRISPR-Cas systems in their genomes 6-fold (30%) compared to the canonical rate of occurrence for other genera (5%) (Makarova et al., 2015; Sun et al., 2015). The most abundant Type across the genus is Type II and the most dominant subtype is II-A (Sun et al., 2015; Crawley et al., 2018). Genomic analysis among 1,262 *Lactobacillus* strains from 171 different species revealed the presence of CRISPR systems in 59.7% of them (Figure 1.12).

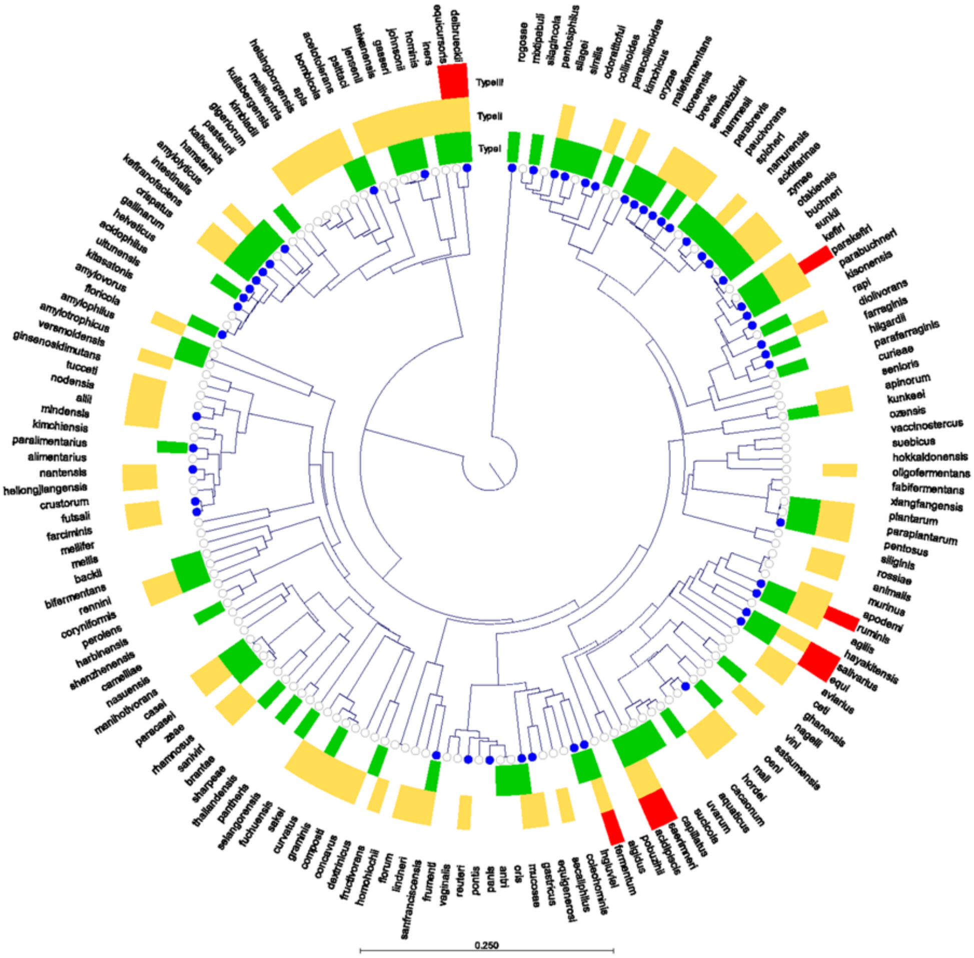

Figure 1.12. Occurrence of CRISPR-Cas systems in lactobacilli. The tree displays the phylogenetic relationship of one representative genome from each of the 171 lactobacilli species used analyzed. Type I systems are in green, Type II in yellow and Type III in red color and the blue nodes are for putative Type V Cas proteins. The species are listed in the outer ring (Crawley et al., 2018)

Notably, *Lactobacillus fermentum* strains NB-22 and MTCC 8711, and *Lactobacillus equicursoris* 66c contained Type I, II and III systems in their genomes, while in other strains/species *cas* genes or CRISPR repeats were missing (Crawley et al., 2018). In addition, comparative genomic analysis among 17 *L. gasseri* strains reveiled that six of them harboured a Type II CRISPR-Cas system. However, these systems were of considerable diversity in array size and spacer content (Sanozky-Dawes et al., 2015; Anderson et al., 2018). Similar analyses have been performed for other *Lactobacillus* species as well, such as *L. buchneri*, *L. paracasei* and *L. rhamnosus* (Douillard et al., 2013; Briner and Barrangou, 2014; Stefanovic and McAuliffe, 2018).

1.1.4.4. Toxin-antitoxin systems

Toxin-antitoxin (TA) systems were originally found in low copy number plasmids (Ogura and Hiraga, 1983). Consequently, they were considered to cause post-segregational killing of host cells ensuring the persistence of a plasmid in a host lineage during replication (Klimina et al., 2013). Normally, TA systems are composed of a gene encoding a small stable toxin protein (<130 amino acids) and its cognate unstable antitoxin, which can be either a protein or an RNA that are co-transcribed and co-translated from a TA operon. Under normal growth conditions, toxin and antitoxin form a stable complex that inhibits toxin activity. On the contrary, under various stress conditions the antitoxin is degraded and the toxin inhibits cell growth by targeting a key molecule in essential cellular processes, such as DNA replication, protein synthesis, cell-wall biosynthesis, mRNA stability and ATP synthesis (Yamaguchi et al., 2011; Darmon and Leach, 2014; Page and Peti, 2016).

The first TA system was found on an *E. coli* plasmid as a control system for cell death. This system provided plasmid maintenance due to the death of cells that did not have the plasmid (Klimina et al., 2017). Similar action of TA systems has been also observed in chromosomal DNA regions that could otherwise be deleted (Christensen-Dalsgaard and Gerdes, 2006). Although these systems are considered to be “selfish” elements promoting their own maintenance at the expense of their host (Van Melderen and Saavedra De Bast, 2009), at the same time they protect their host cell from phages and other mobile elements (Saavedra De Bast et al., 2008).

TA classification is based on the nature of the antitoxin, since the toxin is always a protein, and the mechanisms of its inhibitory action. In type I systems, the antitoxin is a small RNA molecule that regulates toxin expression by inhibiting the toxin expression. Toxin and antitoxin are encoded on opposite DNA strands (Figure 1.13a). In type II systems, which are the most studied, toxin and antitoxin genes (approximately 80-630 bp long) are organized in an operon with a common promoter. The antitoxin is a small unstable protein and the toxin activity is inactivated through a protein complex formation between toxin and antitoxin

(Figure 1.13b). Similarly to type I, the antitoxins of type III are RNAs; however, interaction between toxin and antitoxin occurs through a different mechanism. In type III TA systems, toxin protein is neutralized by direct contact with the antitoxin and the formation of an RNA-protein complex (Figure 1.13c). Type IV systems are similar to type II since toxins and antitoxins are proteins. Unlike the other systems whose toxins and antitoxins interact either as RNAs or proteins, in type IV they do not directly interact (Figure 1.13d). To date, only one TA system belongs to the type V which is the *ghoS/ghoT* system identified in *E. coli*. The antitoxin protein (GhoS) has a sequence specific endoribonuclease activity and cleaves the mRNA of the toxin (GhoT), thus preventing its translation (Figure 1.13e) (Wang et al., 2012; Unterholzner et al., 2013; Klimina et al., 2017).

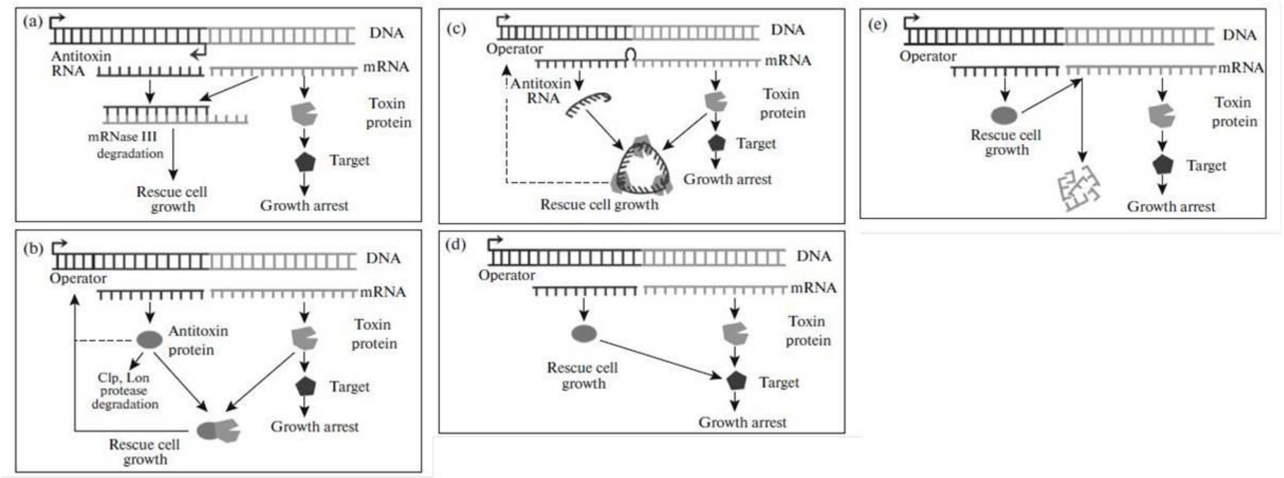

Figure 1.13. Interactions between toxin and antitoxin in types I (a), II (b), III (c), IV (d) and V (e) TA systems (Klimina et al., 2017)

One of the well characterized TA systems is YoeB-YefM, which belongs to the RelBE family of type II systems and has been found in several LAB species, such as *L. rhamnosus*, *E. faecium* and *S. pneumoniae* (Yamaguchi et al., 2011; Chan et al., 2012; Klimina et al., 2013; Krugel et al., 2015). Furthermore, a *relBE* type II TA locus was also identified in plca36 plasmid of *L. casei* Zhang (Zhang et al., 2008). The same TA locus has been also identified in the chromosomes of *Lactobacillus johnsonii* NCC 533 and *L. gasseri* ATCC 33323 (Zhang et al., 2008). It should be mentioned that an orphan *relB* gene has been found in *Lactobacillus brevis* ATCC367 and *L. plantarum* WCFS1 plasmids. However, due to the locasion of the gene in these plasmids, i.e downstream of *repA*, RelB is almost unlikely to be a TA protein (Zhang et al., 2008). In addition, two putative TA systems of the RelBE family have been also reported for the pSF118-44 plasmid of *L. salivarius* UCC118 (Fang et al., 2008). Furthermore, in a second plasmid of strain UCC118, namely pSF118-20, a TA system of the PemIK family was found. Blastp analysis revealed that the TA system of pSF118-20 was identical to that of the p256 plasmid of *L. plantarum* NC7 (Sørvig et al., 2005; Fang et al., 2008). Moreover, comparative genomic analysis among 11 *L. rhamnosus* genomes revealed the presence of six type II TA systems, namely PemK1-A1, PemK2-A2 and PemK3-RelB2, and RelB3-RelE3, YefM-YoeB and RelE1, belonging to the MazE and RelE families, respectively (Klimina et al., 2013). Furthermore, a type I TA system namely Lpt has been identified in *L. casei, L. paracasei* and *L. rhamnosus* plasmids (Folli et al., 2017). Finally, type III TA systems mainly belonging to the ToxIN, CptIN and TenpIN families have been found in the chromosomes and plasmids of several LAB species, such as *L. gasseri, L. helveticus, Lactobacillus jensenii, L. kefiranofaciens and L. lactis* subsp. *lactis* (Blower et al., 2012).

1.1.5. The genus *Lactobacillus*

1.1.5.1. General information

The genus *Lactobacillus* was first proposed in 1901 and over a century later the genus is one of the largest in the order *Lactobacillales* (Beijerinck, 1901). It is also the type genus of the *Lactobacillaceae* family, highly heterogeneous, and currently comprising more than 220 valid species (http://www.bacterio.net/lactobacillus.html) found in an extensive variety of ecological niches (Pot et al., 2014).

Lactobacilli share the common features of LAB, including low G+C content, acid tolerance and conversion of sugars to lactic acid as one of the main end products of metabolism. The majority of lactobacilli are non-motile, facultative anaerobic or microaerophilic microorganisms and usually rod-shaped with the cells often organized in chains. Nevertheless, coccobacilli can also be observed. The optimal growth temperature ranges from 30 to 40 ^{o}C, the pH for growth from 3 to 8 and the DNA G+C content from 32 to 57 mol%. *Lactobacillus* species are present in numerous environments, such as fermented food products (dairy, meat sourdough and wine), plants and both the human and animal GITs. Their ability to ferment raw materials is the basis for their artisanal and industrial usage (Sun et al., 2015). The adaptation of lactobacilli to specific ecological niches as well as their biosynthetic pathways, are reflected by the genome size. Among the *Lactobacillus* species, *Lactobacillus sanfranciscensis* has the smallest genome of 1.23 Mb and *Lactobacillus parakefiri* the largest of 4.91 Mb (Sun et al., 2015). A maximum parsimony reconstruction revealed an extensive loss of ancestral genes during the evolution of *Lactobacillales* (Makarova et al., 2006; Makarova and Koonin, 2007). The results suggest that the common ancestor of *Lactobacillales* had at least ~2,100 to 2,200 genes, lost ~25 to 30% of the genes, i.e. 600 to 1,200 genes and gained <100 genes after the divergence from their *Bacillus* ancestor. Therefore, it was postulated that during the transition in nutritionally rich media, lactobacilli lost a number of genes encoding the biosynthesis of cofactors and conversely, a variety of peptidases were acquired, apparently *via* HGT events (Makarova et al., 2006; Makarova and Koonin, 2007). Examples of lost and gained genes are shown in Table 1.3.

Table 1.3. Examples of lost and gained genes associated with the last common ancestor of *Lactobacillales* (Makarova et al., 2006)

Cluster of orthologous groups (COG)	Enzyme/system name
	Examples of genes/systems gained
Sugar and energy metabolism	Phosphoenolpyruvate carboxylase, ppc Citrate lyase, citCDFE
Amino acid metabolism	Aminopeptidase N, pepN Dipeptidase, pepD Neutral endopeptidase, pepO Pyrrolidone-carboxylate peptidase
Cofactor biosynthesis	Nicotinamide mononucleotide transporter, pnuC Bifunctional Nicotinamide ribose kinase/Nicotinamide mononucleotide adenylyltransferase, nadR
Transporters	K+ transporter, kup
Lipid biosynthesis	3-hydroxy-3-methylglutaryl CoA synthase Hydroxymethylglutaryl-CoA reductase Mevalonate kinase Phosphomevalonate kinase Mevalonate pyrophosphate decarboxylase Isopentenyl diphosphate isomerase
	Examples of genes/systems lost
Sugar and energy metabolism	Heme/copper-type cytochrome/quinol oxidase, CyoABCD Fructose-1,6-bisphosphatase Phosphoglyceromutase
Amino acid metabolism	Glycine cleavage system, gcvTRP Methionine synthase I (cobalamin-dependent), metH Na+/alanine symporter, alsT Na+/proline symporter, putP
Cofactor biosynthesis	Most of heme biosynthesis, hemABCDEFLY Molybdenum cofactor biosynthesis, moaABCDE, mobAB, moeA Panthothenate biosynthesis, panBCD

Plasmids within the *Lactobacillus* genus vary widely in size, gene content and number of different plasmids per strain. Up to date, pLBPp1 plasmid of *L. plantarum* subsp. *plantarum* P-8 is the largest in the genus (51.18 Kbp) (Cui et al., 2015). Although most of the *Lactobacillus* plasmids are cryptic, several others provide host cells with important properties, including antibiotic resistance (Feld et al., 2009), exopolysarccharide biosynthesis (Crowley et al., 2013), bacteriophage resistance (Eguchi et al., 2000), as well as bacteriocin production (Van Reenen et al., 2003) that may sustain its survival in harsh environments (Wegrzyn and Wegrzyn, 2002). Furthermore, several *Lactobacillus* species, such as *L. salivarius, L. acidophilus, Lactobacillus hamster, Lactobacillus intestinalis, Lactobacillus kalixensis, Lactobacillus ingluviei* and *Lactobacillus equi* have been shown to carry megaplasmids ranging from 120–490 Kbp long (Cui et al., 2015). Megaplasmid pMP118 (242 Kbp) of *L. salivarius* UCC118 contain several housekeeping genes or genes encoding important proteins that contribute to the physiology, metabolism, technological and probiotic properties of the strain (Flynn et al., 2002; Claesson et al., 2006; Harris et al., 2017; Lee et al., 2017). Additional genomic analysis of newly sequenced *Lactobacillus* genomes is needed to define the impact of size and gene content variations on the biological and technological properties of the host cells.

1.1.5.2. Lactobacilli in foods

As mentioned above, the significance of fermentation in food production is enormous, as it is among the oldest methods of food preservation worldwide. The rapid growth of lactobacilli and consequently the production of acids and/or antibacterial and antifungal (propionate, phenyl-lactate, hydroxyphenyl-lactate, cyclic dipeptides, phenyllactic acid and 3-hydroxy fatty acids) compounds can inhibit the growth of spoilage and pathogenic microorganisms during food fermentation (Bernardeau et al., 2008; Reis et al., 2012). Due to their history of safe use, the *Lactobacillus* genus includes several Generally Recognized As Safe (GRAS) species according to the FDA (Bourdichon et al., 2012) or species that have been granted the Qualified Presumption of Safety (QPS) status by the EFSA (Hazards, 2017). In order to demonstrate a history of safe use, the microorganism must not infer harm over several generations and in a variety of genetically different human populations. Furthermore, the microorganism must not harbor antimicrobial resistance and in the case of a genetically modified organism (GMO), the differences between the conventional strain and the GMO should be evaluated. The use of lactobacilli in food preservation *via* fermentation alters both the organoleptic characteristics and the nutritional value of the final product (Bernardeau et al., 2006; Fernandez and Zuniga, 2006; Giraffa et al., 2010; Widyastuti and Febrisiantosa, 2014; Afzal et al., 2017). Thus, they are extensively used either artisanally or at industrial scale for the production of fermentated dairy and other food products (Bernardeau et al., 2008; Sun et al., 2015).

Apart from food-related species/strains, the *Lactobacillus* genus also includes commensals and opportunistic pathogens. Commensal lactobacilli, such as *L. rhamnosus*, *L. johnsonii*, *Lactobacillus vaginalis* and *L. acidophilus* can serve as candidate probiotics as well (Walter, 2008; Martín et al., 2013). Furthermore, infections caused by lactobacilli are almost always detected in patients with serious underlying illnesses or the immunocompromised. Lactobacilli have been usually associated with endocarditis and bacteremia, as well as with urinary tract infections and dental caries (Sussman et al., 1986; Husni et al., 1997; Martin et al., 1999; Cannon et al., 2005; Hojo et al., 2007; Nakamoto et al., 2017). *Lactobacillus* endocarditis has been linked to heart diseases and prosthetic valves; however, *Lactobacillus* bacteremia is more frequent compared to *Lactobacillus* endocarditis (Cannon et al., 2005; Salvana and Frank, 2006). The predisposing factors for bacteremia are immunosuppression, prior prolonged hospitalization and prior surgical interventions (Fusco et al., 2018). *Lactobacillus* species that have been associated with such diseases are *L. plantarum*, *L. acidophilus, L. curvatus, L. fermentum, L. jensenii, L. delbrueckii, L. casei, L. rhamnosus* and *L. paracasei (Salvana and Frank, 2006; Encarnacion et al., 2016; Fusco et al., 2018)*. Moreover, other less frequent diseases including meningitis, arteritis, pneumonia, peritonitis, deep abdominal abscesses, pyelonephritis and pancreatitis have been associated with *Lactobacillus* species, mainly *L. rhamnosus* (Fusco et al., 2018).

During the last decades some well-characterized lactobacilli, particularly of human origin, have also served as vaccine carriers (Seegers, 2002; Mohamadzadeh et al., 2009; da Silva et al., 2014) due to their ability to survive transit through the stomach, their immunomodulatory properties and their safe consumption in large amounts or used as probiotics as mentioned above (Sanders, 2008; Goh and Klaenhammer, 2009; Raftis et al., 2011). Health promoting lactobacilli are usually associated with the GIT and the vagina. Examples of these lactobacilli are strains belong to the species *L. rhamnosus, L. casei, L. paracasei, L. salivarius, L. delbrueckii* subsp. *bulgaricus, L. reuteri, L. fermentum, L. johnsonii,* *L. gasseri, L. helveticus, Lactobacillus crispatus, Lactobacillus oeni, L. plantarum* and *Lactobacillus iners* (Pot et al., 2014). Among the aforementioned, *L. rhamnosus* GG (Segers and Lebeer, 2014; Gatej et al., 2018; Uribe et al., 2018) and *L. casei* shirota (Lei et al., 2017; Nagino et al., 2018; Nurul Adilah et al., 2018) are the most comprehensively studied and widely used probiotic strains.

1.1.5.3. Phylogeny and taxonomy

Lactobacilli were initially grouped on the basis of growth temperature and type of hexose fermentation (Orla-Jensen, 1919). Classification and identification of lactobacilli based on their metabolic characteristics is not reliable as they are metabolically very similar to other LAB genera (Hammes and Hertel, 2009).

The first phylogenetic analysis of the genus *Lactobacillus* on the basis of 16S rRNA gene sequencing of 55 species was performed by Collins and co-workers (Figure 1.14A & B) (Collins et al., 1991). The analysis revealed that the majority of the *Lactobacillus* species formed three phylogenetically distinct clusters. The first cluster designated as the *L. delbrueckii* group included the type species of the genus *Lactobacillus* (*L. delbrueckii*) and 11 other obligately homofermentative species. The second cluster designated as *Lactobacillus casei / Pediococcus* group (further divided into four subgroups) (Schleifer and Ludwig, 1995), comprised 32 *Lactobacillus* and five *Pediococcus* species. Although the majority of the species were heterofermentative, a few obligately homofermentative were also included. According to the analysis, this was the largest and phylogenetically most heterogeneous of the three groups. The third cluster designated as the *Leuconostoc paramesenteroides* group included apart from the *L. paramesenteroides*, four *Lactobacillus* species (Collins et al., 1991).

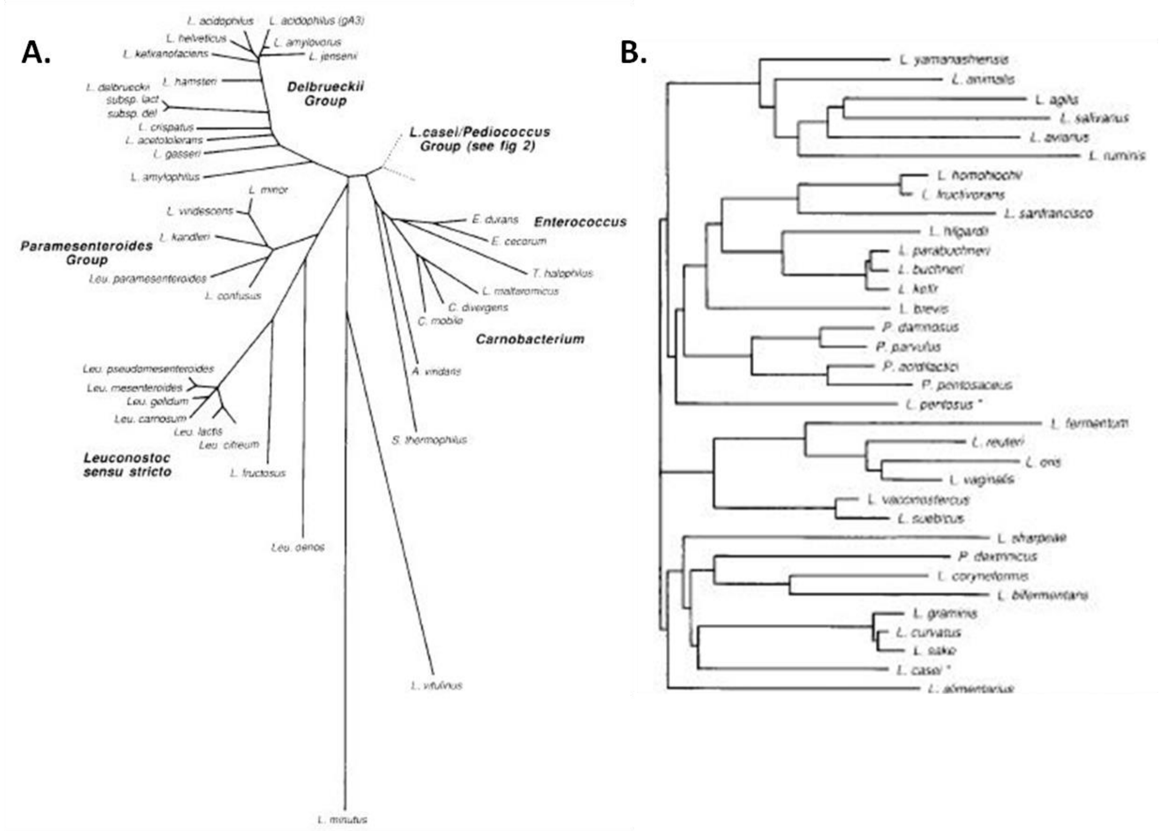

Figure 1.14. Evolutionary distance tree of the *Lactobacillus* genus and other LAB species (A) and the species of the *Lactobacillus casei* / *Pediococcus* group (B) (Collins et al., 1991)

More recently, Salvetti and co-workers have further updated the taxonomy of the *Lactobacillus* genus also on the basis of 16S rRNA gene sequencing (Salvetti et al., 2012). This updated phylogenetic analysis identified 152 validly described *Lactobacillus* species divided into 15 groups of three or more species, four of two species and 10 single lines of descent, as shown in Table 1.4. At the time of writing, the *Lactobacillus* genus comprises 231 species and 29 subspecies including synonyms (http://www.bacterio.net/lactobacillus.html). The 16S rRNA gene sequences and the few genome sequences publicly available revealed that taxonomic and phylogenetic clustering of the *Lactobacillus* genus is not concordant since the genus is unusually diverse and a revised genome-based re-classification is needed (Sun et al., 2015).

Table 1.4. Phylogenetic groups of lactobacilli according to Salvetti et al. (Salvetti et al., 2012)

Groups	**Species**
L. delbrueckii	*L. acetotolerans, L. acidophilus, L. amylolyticus, L. amylophilus, L. amylotrophicus, L. amylovorus, L. crispatus, L. delbrueckii, L. equicursoris, L. fornicalis, L. gallinarum, L. gasseri, L. gigeriorum, L. hamsteri, L. helveticus, L. hominis, L. iners, L. intestinalis, L. jensenii, L. johnsonii, L. kalixensis, L. kefiranofaciens, L. kitasatonis, L. pasteurii, L. psittaci, L. taiwanensis, L. ultunensis*
L. salivarius	*L. acidipiscis, L. agilis, L. animalis, L. apodemi, L. aquaticus, L. aviarius, L. cacaonum, L. capillatus, L. ceti, L. equi, L. ghanensis, L. hayakitensis, L. hordei, L. mali, L. murinus, L. nagelii, L. oeni, L. pobuzihi, L. ruminis, L. saerimneri, L. salivarius, L. sucicola, L. satsumensis, L. uvarum, L. vini*
L. reuteri	*L. alvi, L. antri, L. coleohominis, L. fermentum, L. frumenti, L. equigenerosi, L. gastricus, L. ingluviei, L. mucosae, L. oris, L. panis, L. pontis, L. reuteri, L. secaliphilus, L. vaginalis*
L. buchneri	*L. buchneri, L. dioliovorans, L. farraginis, L. hilgardii, L. kefiri, L. kisonensis, L. otakiensis, L. parabuchneri L. parafarraginis, L. parakefiri, L. rapi, L. sunkii*
L. alimentarius	*L. alimentarius, L. crustorum, L. farciminis, L. futsaii, L. kimchiensis, L. mindensis, L. nantensis, L. nodensis, L. paralimentarius, L. tucceti, L. versmoldensis*
L. brevis	*L. acidifarinae, L. brevis, L. hammesii, L. koreensis, L. namurensis, L. parabrevis, L. paucivorans L. senmaizukei, L. spicheri, L. zymae*
L. collinoides	*L. collinoides, L. kimchicus, L. odoratitofui, L. paracollinoides, L. similis*
L. fructivorans	*L. florum, L. fructivorans, L. homohiochii, L. lindneri, L. sanfranciscensis*
L. plantarum	*L. fabifermentans, L. paraplantarum, L. pentosus, L. plantarum, L. xiangfangensis*
L. sakei	*L. curvatus, L. fuchuensis, L. graminis, L. sakei*
L. casei	*L. casei, L. paracasei, L. rhamnosus*
L. coryniformis	*L. bifermentans, L. coryniformis, L. rennini*
L. manihotivorans	*L. manihotivorans, L. nasuensis, L. porcinae*
L. perolens	*L. harbinensis, L. perolens, L. shenzhenensis*
L. vaccinostercus	*L. oligofermentans, L. suebicus, L. vaccinostercus*
Pediococcus	*P. acidilactici, P. argentinicus, P. cellicola, P. claussenii, P. damnosus, P. ethanolidurans, P. inopinatus, P. lolii, P. parvulus, P. pentosaceus, P. siamensis, P. stilesii*
Couples	*L. kunkeei* and *L. ozensis,* *L. rossiae* and *L. siliginis,* *L. concavus* and *L. dextrinicus,* *L. pantheris* and *L. thailandensis*
Single species	*L. algidus, L. brantae, L. camelliae, L. composti, L. floricola, L. malefermentans, L. saniviri, L. selangorensis, L. senioris, L. sharpeae*

1.1.5.4. *Lactobacillus zymae*

Bread and bakery products are widely consumed worldwide with Greece being among the 50 countries with the largest bread consumption consuming. In 2016, the global production of bread and bakery products was estimated at 130 million tonnes, surpassing USD 200 billion in value (http://bit.ly/2CiwMYd; http://www.bizcommunity.com/Article/1/162/176273.html). The increasing demand of consumers for more natural, tasty and healthy foods has established the use of sourdough in bread production. Sourdough is a mixture of flour (e.g. wheat and rye), water and salt, which is fermented by the naturally occurring microbial ecosystem of LAB and yeasts. The use of sourdough as a natural starter in bread making improves a variety of technological characteristics of the final product, such as shelf-life, nutritional value and organoleptic characteristics through the metabolism of these microorganisms (Arendt et al., 2007). LAB are mainly involved in dough acidification and flavor formation, while yeasts and heterofermentative LAB species participate in the leavening process. The main fermentation end-products contribute to the taste, aroma and volume of sourdough are lactic and acetic acid, ethanol and CO_2 (Corsetti and Settanni, 2007; De Vuyst et al., 2017).

Lactobacilli are among the most significant groups of microorganisms in sourdough fermentation (Gobbetti et al., 2016). Over 90 different *Lactobacillus* species have been found in sourdough, with *Lactobacillus sanfranciscensis*, *L. plantarum*, *L. brevis* and *L. fermentum* being among the most common ones. Apart from lactobacilli, several species belonging to *Weissella, Pediococcus, Leuconostoc, Lactococcus*, *Enterococcus* and *Streptococcus* genera have been also found in sourdough (Gobbetti et al., 2016; De Vuyst et al., 2017). Recently, a number of new *Lactobacillus* species have been isolated from sourdough, such as *Lactobacillus crustorum, Lactobacillus mindensis, Lactobacillus nantensis, Lactobacillus nodensis, Lactobacillus spicheri, Lactobacillus acidifarinae, Lactobacillus siliginis* and *Lactobacillus zymae* (De Vuyst et al., 2002; De Vuyst et al., 2014; Raimondi et al., 2017).

L. zymae is a heterofermentative LAB species also found in a variety of fermented foods, such as Kimchi, a Korean traditional fermented vegetable food (Park et al., 2014), fermented onions (Cheng et al., 2014), fermented cucumbers (Perez-Diaz et al., 2017) and fermented liquid feed (Canibe et al., 2010). The type strain of the species is LMG 22198^T (=CCM 7241^T =CCUG 50163^T =CIP 108703^T =DSM 19395^T =JCM 15957^T; http://www.straininfo.net/strainPassport.action?sort=creationDate&dir=asc&cultureId=388

322) isolated from a Belgian artisanal wheat sourdough (Vancanneyt et al., 2005). *L. zymae* is a Gram-positive, catalase-negative, non spore-forming and non- motile species. Additionally, the optimum growth of the species takes place in MRS medium broth? at 37 °C, although *L. zymae* is also able to grow at 15 °C but not at 45 °C. The rod-shaped cells have a length of 2–20 µm and a width of 1.0 µm.

L. zymae ACA-DC 3411 was isolated from traditional Greek wheat sourdough manufactured without baker's yeast (*Saccharomyces cerevisiae*) (De Vuyst et al., 2002; Vancanneyt et al., 2005). Initially, strain ACA-DC 3411 along with two other isolates were characterized as *L. brevis*-like isolates (De Vuyst et al., 2002), but few years later, Vancanneyt et al. were able to demonstrate that the three *L. brevis*-like isolates represent two novel *Lactobacillus* species namely *L. acidifarinae* (LMG 22200^T) and *L. zymae* (LMG 22198^T and ACA-DC 3411) using SDS-PAGE of whole-cell proteins, 16S rRNA gene sequences, amplified fragment length polymorphism (AFLP) fingerprinting, DNA G+C contents, DNA–DNA hybridizations, growth characteristics and colony morphology, conventional biochemical tests as well as carbohydrate fermentation tests (Vancanneyt et al., 2005). Strain ACA-DC 3411 is deposited in the ACA-DC culture collection of the Agricultural University of Athens, Greece (http://www.aca-dc.gr).

According to a previous phylogenetic analysis of Felis and Dellaglio (Felis and Dellaglio, 2007), *L. zymae* along with other three species (*L. acidifarinae*, *Lactobacillus namurensis* and *L. spicheri*) were grouped into the *L. buchneri* clade. A few years later, an updated phylogenetic analysis performed by Salvetti et al. transferred the four species to the *L. brevis* clade, which currently comprises 10 species (Salvetti et al., 2012). All the species are able to grow between 5 and 10 % of NaCl concentration and the G+C content of the clade ranges between 46 and 55 mol%. At present, only the ACA-DC 3411 genome is completely sequenced and publicly available in the NCBI database while the DSM 19395^T genome is also available but partially sequenced (Table 1.5).

Table 1.5. *Lactobacillus zymae* strains available in the NCBI database

Organism	NCBI Reference Sequence	Isolation source	Sequencing technology	Scaffolds	Reference
L. zymae ACA-DC 3411	NZ_LT854705.1	Wheat sourdough	Illumina HiSeq	1	Kazou et al., 2017c
L. zymae DSM 19395^T	NZ_AZDW00000000.1	Wheat sourdough	Illumina MiSeq/ Illumina HiSeq	59	Sun et al., 2015

1.1.5.5. *Lactobacillus rennini*

Lactobacillus rennini is a salt-tolerant species originally found in spoiled rennet, which when used in cheese production yielded in a final product with several cracks and a phenolic flavor (Chenoll et al., 2006). The type strain of the species is CECT 5922^T (=CIP 109172^T=DSM 20253^T =JCM 14279^T =LMG 23902^T; http://www.straininfo.net/strainPassport.action?sort=creationDate&dir=asc&cultureId=478296) isolated from spoiled rennet (Chenoll et al., 2006). The optimum growth of *L. rennini* takes place in MRS broth at 30 °C under anaerobic conditions and the rod-shaped cells are 1 mm wide by 2-4 mm long. After three days of incubation in MRS agar, colonies are small (up to 1 mm in diameter) and circular (Chenoll et al., 2006). So far, *L. rennini* has been isolated only from spoiled rennet (Chenoll et al., 2006) and Kopanisti cheese (Asteri et al., 2009).

Strain ACA-DC 565 was isolated from a 2-year old traditional Greek Kopanisti cheese (Asteri et al., 2009). This over-mature type of Kopanisti cheese known as Mana Kopanisti is used as inoculum for the back-slopping production of Kopanisti cheese (Donnelly, 2016) and *L. rennini* was the sole microbial species present in Mana Kopanisti. According to Asteri et al. (2009) *L. rennini* produces volatile compounds most probably *via* the secondary catabolism of amino acids (Yvon and Rijnen, 2001) and therefore may contribute to the strong taste of Mana Kopanisti. Strain ACA-DC 565 is deposited in the ACA-DC culture collection of the Agricultural University of Athens, Greece (http://www.aca-dc.gr).

Phylogenetic analysis based on 16S rRNA gene sequencing places *L. rennini* in the *Lactobacillus coryniformis* clade (Pot et al., 2014). The clade consists of four members, namely *L. coryniformis*, *Lactobacillus backii*, *Lactobacillus bifermentans* and *L. rennini*. Previously, *Lactobacillus composti* was also included in the *L. coryniformis* clade but after an updated phylogenetic analysis by Salvetti et al. the species constitutes a single line of descent (Salvetti et al., 2012). According to the NCBI database, only the chromosome of *L. rennini* ACA-DC 565 has has been completely sequenced, while this of strain DSM 20253^T is partially sequenced (Table 1.6).

Table 1.6. *Lactobacillus rennini* strains available in the NCBI database

Organism	Genbank accession	Isolation source	Sequencing technology	Scaffolds	Reference
L. rennini ACA-DC 565	LT634362.1	Kopanisti cheese (Mana Kopanisti)	Illumina HiSeq	1	Kazou et al., 2017b
L. rennini DSM 20253^T	AYYI00000000.1	Rennet	Illumina MiSeq/ Illumina HiSeq	125	Sun et al., 2015

1.1.5.6. *Lactobacillus acidipiscis*

Lactobacillus acidipiscis is a salt-tolerant species (some strains grow at 12% NaCl) originally isolated from fermented fish (Tanasupawat et al., 2000) where the type strain FS60-1^T (=PCU 207^T =NRIC 0300^T =HSCC 1411^T =JCM 10692^T =TISTR 1386^T =DSM 15836^T; http://www.bacterio.net/lactobacillus.html) comes from. The optimum growth takes place in MRS medium at 30 °C within 24 h and the rod-shaped cells have a length of 0,4-0,6 x 1,2-5,0 μm (Tanasupawat et al., 2000). Additionally, although until recently the species was considered as non-motile, Cousin et al. (2015) identified the presence of motility genes in the genome of *L. acidipiscis* KCTC 13900.

Using culture-dependent and -independent approaches, *L. acidipiscis* has been found in several cheeses, e.g. Halloumi (Lawson et al., 2001; Naser et al., 2006; Kim et al., 2011), Cotija (Morales et al., 2011), Minas (Perin et al., 2017) and Chiapas (Morales et al., 2011; Melgar-Lalanne et al., 2013), as well as in fermented fish (An et al., 2010; Tsuda et al., 2012; Thamacharoensuk et al., 2017), fermented meat (Nguyen et al., 2013), sake (Koyanagi et al., 2016), pickles (Arasu et al., 2015), silages (Tohno et al., 2012; Altaher et al., 2015; Khota et al., 2016), Sichuan paocai, a traditional Chinese fermented vegetable (Cao et al., 2017) and table olives (Randazzo et al., 2017). Moreover, *L. acidipiscis* has been found in vinegar and soy sauce, where it is considered to be a spoilage microorganism (Tanasupawat et al., 2002; Cheng et al., 2014b; Li et al., 2014a; Li et al., 2014b).

L. acidipiscis ACA-DC 1533 was isolated from a 3-month-old traditional Greek Kopanisti cheese prepared from raw cow milk, and along with *L. rennini* were the dominant species

(Asteri et al., 2009). Interestingly, both of them exhibited some interesting biochemical properties, especially regarding the production of alcohols and carbonyl compounds that may play a key role to the typical piquant flavor of Kopanisti cheese (Yvon and Rijnen, 2001; Asteri et al., 2009; Donnelly, 2016). Strain ACA-DC 1533 is deposited in the ACA-DC culture collection of the Agricultural University of Athens, Greece (http://www.aca-dc.gr).

Phylogenetic analysis based on 16S rRNA gene sequence places *L. acidipiscis* in the *L. salivarius* clade. *L. salivarius* is the most thoroughly characterized species of this clade and thus gives the name to the clade (Pot et al., 2014). The *L. salivarius* clade contains mainly homofermenters and it is the second largest group with 27 recognized species following this of *L. delbrueckii* group (29 species; Pot et al., 2014). It can be noticed that the *L. salivarius* clade contains the majority of the motile species of the genus, i.e. *L. acidipiscis, Lactobacillus agilis, Lactobacillus aquaticus, Lactobacillus cacaonum, Lactobacillus capillatus, Lactobacillus ghanensis, Lactobacillus hordei, Lactobacillus mali, Lactobacillus nagelii, Lactobacillus oeni, Lactobacillus ruminis, Lactobacillus satsumensis, Lactobacillus sicerae, Lactobacillus sucicola, Lactobacillus uvarum* and *Lactobacillus vini* (Cousin et al., 2015). Furthermore, the *L. salivarius* clade is taxonomically quite heterogeneous and a potential subdivision into different genera could be considered (Pot et al., 2014). This is probably due to the different isolation origin of the strains. The *L. salivarius* clade mainly consists of commensal isolates and in a lesser degree of strains found in naturally fermented foods (Cousin et al., 2015). Several strains belonging to the clade exhibit putative probiotic traits. The most comprehensively studied probiotic *L. salivarius* strain is UCC118 (Harris et al., 2017), which was shown to exhibit (i) prophylactic and therapeutic use against colitis and other inflammatory diseases (Neville and O'Toole, 2010), (ii) strong antimicrobial activity due to the action of its broad-spectrum bacteriocin ABP118, which is located on the pMP118 megaplasmid (Claesson et al., 2006; Flynn et al., 2002), (iii) adhesion capacity to eukaryotic cells by fibronectin-binding and sortase-dependent surface proteins (Collins et al. 2012; van Pijkeren et al., 2006) and (iv) bile-resistant capacity as it harbors two bile salt hydrolase (bsh) genes *bsh-1* and *bsh-2* in pMP118 and chromosome, respectively (Neville and O'Toole, 2010).

Therefore, comparative genomics among members of the *L. salivarius* clade may reveal important aspects, such as niche adaptation, technological potential and probiotic properties (Forde et al., 2011; Raftis et al., 2011; Sun et al., 2015). So far, there is only one *L. acidipiscis* genome with completely sequenced chromosome, i.e. strain ACA-DC 1533 (Kazou et al., 2017a) and four partially sequenced genomes (Kim et al., 2011; Sun et al., 2015) publicly available in the NCBI database. Strain ACA-DC 1533 also contains three plasmids, namely pLAC1, pLAC2 and pLAC3. pLAC1 is fully sequenced and has been previously described by Asteri et al. (2010), while both pLAC2 and pLAC3 are partially sequenced, as shown in Table 1.7.

Table 1.7. *Lactobacillus acidipiscis* strains available in the NCBI database

Organism	NCBI Reference Sequence	Isolation source	Sequencing technology	Scaffolds	Reference
L. acidipiscis ACA-DC 1533 (chromosome)	NZ_LT630287.1	Kopanisti cheese	Illumina HiSeq/ Pacbio RS II	1	Kazou et al., 2017a
L. acidipiscis ACA-DC 1533 (pLAC1 plasmid)	NC_014164.1	Kopanisti cheese	ABI	1	Asteri et al., 2017
L. acidipiscis ACA-DC 1533 (pLAC2 plasmid)	LT996085.1*	Kopanisti cheese	Illumina HiSeq/ Pacbio RS II	-	Kazou et al., 2017
L. acidipiscis ACA-DC 1533 (pLAC3 plasmid)	LT992335.1*	Kopanisti cheese	Illumina HiSeq/ Pacbio RS II	-	Kazou et al., 2017
L. acidipiscis DSM 15836^T	NZ_AZFI00000000.1	Fermented fish	Illumina MiSeq/ Illumina HiSeq	457	Sun et al., 2015
L. acidipiscis JCM 10692^T	NZ_BDQH00000000.1	Fermented fish	Illumina MiSeq	327	-
L. acidipiscis DSM 15353	NZ_JQBK00000000.1	Halloumi cheese	Illumina MiSeq/ Illumina HiSeq	297	Sun et al., 2015
L. acidipiscis KCTC 13900	NZ_BACS00000000.1	Halloumi cheese	Roche 454	487	Kim et al., 2011

*not in RefSeq

1.1.6. Bacterial whole-genome sequencing

In 1976, Fiers et al. established first the complete RNA sequence of bacteriophage MS2 (1976). One year later, Sanger et al. completed the first DNA sequence of bacteriophage phi X174 (1977). In bacteriology, the genomic era began in the mid-1990s, when the first bacterial genome of *Haemophilus influenza* was completed using Sanger sequencing (Fleischmann et al., 1995). Since then, the technical improvements and the sequencing cost decrease have led, as shown in Figure 1.15, to the sequencing of tens of thousands of bacterial genomes providing new insights into microbial diversity (Metzker, 2005; Mardis, 2008; Kant et al., 2011).

For many years, bacterial taxonomic assignment was performed using the 16S rRNA gene sequence. Although this is still used as a reliable taxonomic method, phylogenetic analysis is currently performed at genome scale using reference genomes, sets of conserved proteins or proteomes, since the genetic relationships among bacteria are complex and a single gene comparison is no longer sufficient (Ahrenfeldt et al., 2017; Yokono et al., 2018).

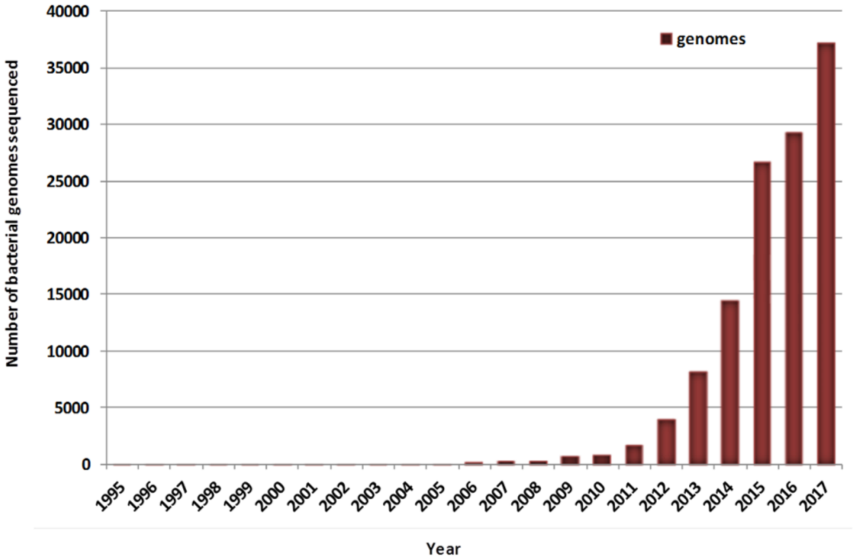

Figure 1.15. Number of bacterial genomes sequenced each year and submitted to the NCBI database (Prokaryotes.txt file downloaded on November 2017)

Furthermore, genome sequencing along with the progress in bioinformatic analysis can deliver important knowledge, such as the evolution, ecology and pathogenesis of bacteria in order to design appropriate therapeutic approaches (Donkor, 2013; Quainoo et al., 2017). In addition, bacterial genomic analysis of a strain or comparative genomic analysis among closely related (or not) strains/species is a powerful tool of a deeper understanding of the mechanisms behind biodiversity and bacterial adaptation to diverse ecological niches (Sun et al., 2015).

In addition, according to a genomic analysis of LAB performed by Schroeter and Klaenhammer, species-to-species variation in the number of pseudogenes (i.e. genes that have lost their protein-coding ability) and in the nutrient uptake and metabolism explains the adaptation of LAB to food matrices and the GIT (Schroeter and Klaenhammer, 2009). Since bacterial diversity continues to expand, comparative genomic analysis of more strains/species is useful to understand the bacterial diversity and plasticity. In 2015, a pan/core-genome analysis of more than 2,000 *E. coli* genomes revealed that the pan-genome (the full set of genes within a group of genomes) of the species was “open”, which means that in every additionally strain that has been sequenced unique gene families are being identified (Land et al., 2015). Even though many of these genomes are draft assemblies and gene calling errors are likely to exist, the number of identified gene families (approximately 90,000) is impressive for a single bacterial species (Figure 1.16).

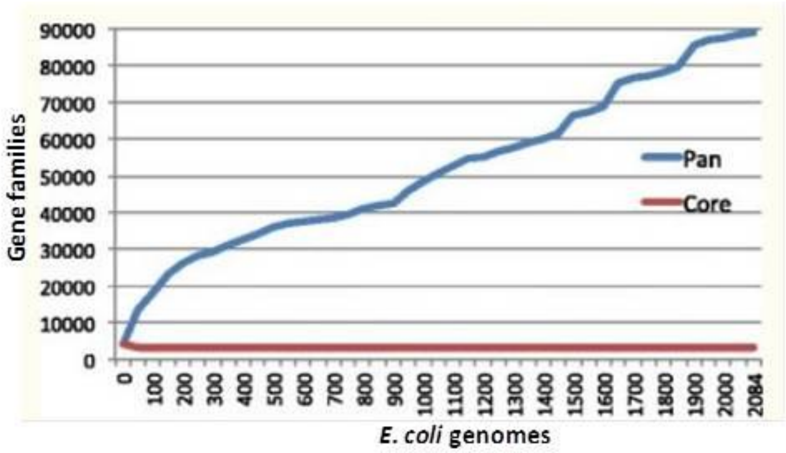

Figure 1.16. Pan/core-genome plots of 2,085 *E. coli* genomes (Land et al., 2015)

However, “closed” pan-genomes have also been reported. According to Tettelin and co-workers, the pan-genome of *Bacillus anthracis* was found to be “closed” since the curve reached a plateau after the addition of only a fourth genome out of the eight analyzed, suggesting that four genome sequences are sufficient to completely characterize the gene content of this species (Tettelin et al., 2005). However, the term “less-open” for similar pan-genomes may be more sufficient due to the presence of mobile genetic elements that can alter the pan-genome of the species at some point (Land et al., 2015). Furthermore, the core-genome (common genes present within a group of genomes) of the 2,085 *E. coli* strains consisted of 3,188 gene families and was quite constant during the addition of each genome (Figure 1.16), since it is related to biological functions that are essential to the basic lifestyle of the species and not to the species diversity (Medini et al., 2005; Land et al., 2015).

1.1.6.1. DNA sequencing technologies

Sequencing technologies can be divided into distinct "generations". Originally, two different DNA sequencing approaches were described, namely (i) the Sanger method that was based on DNA sequencing using chain-terminating inhibitors and (ii) the Maxam-Gilbert method based on base-specific chemical modification and cleavage of the DNA backbone (Maxam and Gilbert, 1977; Sanger et al., 1977; Friedmann, 1979). While the Sanger method is suitable for the sequencing of small genomic regions, both methods are considered as the first-generation sequencing technologies. Despite the wide use of the Sanger method, its low throughput, high cost, time and labour involved for whole genome sequencing projects have limited its use (Metzker, 2010).

To overcome the technological limitations of the Sanger sequencers, second-generation or next-generation sequencing (NGS) technologies were developed based on several innovations, e.g. in the amplification technology and sequencing chemistry, with the first NGS sequencer being available in 2005 (Kchouk et al., 2017). The main NGS platforms currently available are shown in Figure 1.17. Although NGS platforms only generate short sequence reads, they are able to sequence mixtures of DNA molecules in parallel, thus generating millions up to billions of sequence reads in a single run. Thus, NGS technologies are often referred to as "short read" technologies and are distinguished by the third-generation sequencing technologies that provide significantly longer reads. However, these long-read technologies have at present lower throughput and accuracy (Navin et al., 2011; Flaherty et al., 2012; Xu et al., 2012).

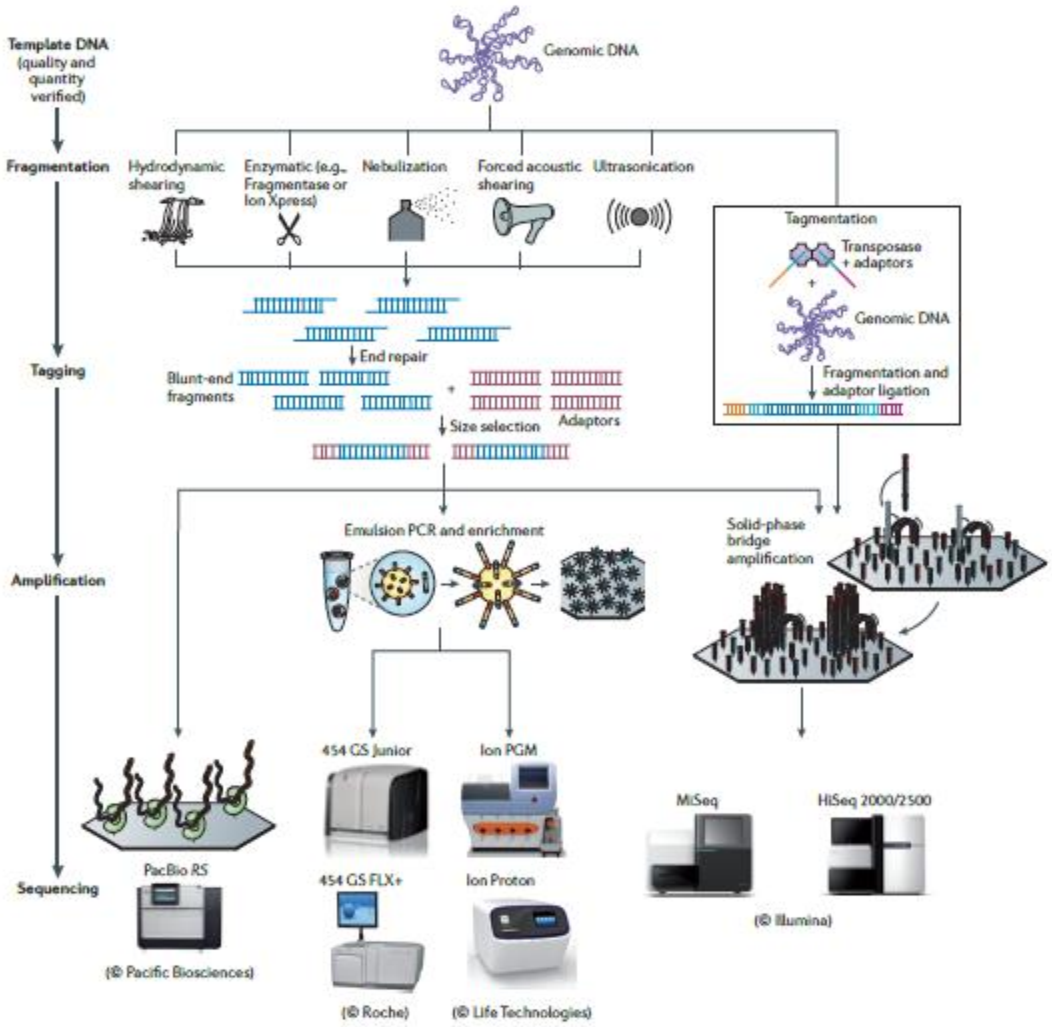

Figure 1.17. The scheme shows the main NGS platforms available and the associated sample preparation and template amplification (Loman et al., 2012)

The 454 FLX pyrosequencing platform (http://www.454.com/) was the first NGS technology developed by 454 Life Sciences (later bought by Roche) and became available in 2005. A few years later, Illumina Genome Analyzer (http://www.illumina.com) and SOLiD™ System (http://www.appliedbiosystems.com) were developed by Solexa GA and Applied Biosystems, respectively (Barzon et al., 2011). Illumina is the most widely used NGS technology, and, although it has higher sequence yield at a relatively low cost per base, it exhibits differences in sequence quality, a higher sequencing error rate and increased single-base errors (Dolan and Denver, 2008; Erlich et al., 2008; Nakamura et al., 2011). Although NGS technologies are improved compared to the Sanger sequencers, they had two main problems: (i) they generally require a PCR amplification step, which is a time-consuming and expensive procedure, and (ii) the genome complexity (e.g. repetitive regions) results in low quality sequences.

To overcome these problems, third generation sequencers (TGS) were developed (Pareek et al., 2011). The TGS (or single-molecule sequencing) eliminate the need of PCR amplification step, providing a lower sequencing cost and shorter execution time, and produce longer reads (several thousand bp) compared to the NGS technologies (a few hundred bp; Kchouk et al., 2017). Pacific Biosciences (PacBio) developed the first genomic sequencer using the Single-Molecule Real-Time (SMRT) approach. Compared to the NGS technology, PacBio has several advantages, such as short time for sample preparation (4 to 6 hours instead of days) and long-read lengths (Kchouk et al., 2017). Unfortunately, PacBio sequencing platforms have a high error rate of about 13%, mostly due to insertions and deletions randomly distributed along the long reads (Koren et al., 2012; Kulski, 2016). Table 1.8 presents a performance comparison of the available sequencing platforms.

Table 1.8. Performance comparison of sequencing platforms (Kchouk et al., 2017)

Platform	Instrument	Reads per run	Average Read length (bp)	Error Type	Error Rate (%)	Data Generated per run (Gb)	Year
First Generation							
ABI Sanger	3730xl	96	400 – 900*	NA	0.3	0.00069 to 0.0021	2002
Second Generation							
454	GS20	200	100	indel	1	0.02	2005
454	GS FLX	400	250	indel	1	0.1	2007
454	GS FLX Titanium	1M	450	indel	1	0.45	2009
454	GS Junior	100	400	indel	1	0.04	2010
454	GS Junior+	100	700	indel	1	0.07	2014
Illumina	MiniSeq	25M (maximum)	150	mismatch	1	7.5 (maximum)	2013
Illumina	MiSeq	25M (maximum)	300	mismatch	0.1	15 (maximum)	2011
Illumina	NextSeq	400M (maximum)	150	mismatch	1	120 (maximum)	2014
Illumina	HiSeq	5B (maximum)	150	mismatch	0.1	1.5Tb (maximum)	2012
Illumina	HiSeq X	6B (maximum)	150	mismatch	0.1	1.8Tb (maximum)	2014
SOLiD	5500 W	3B	75	mismatch	~0.1	160	2011
SOLiD	5500xl W	6B	75	mismatch	~0.1	320	2013
Ion Torrent	PGM 314 chip v2	400.000-550.000	400	indel	1	0.06 to 0.1	2011

Table 1.8. *Continued*

Platform	Instrument	Reads per run	Average Read length (bp)	Error Type	Error Rate (%)	Data Generated per run (Gb)	Year
Ion Torrent	PGM 316 chip v2	2M - 3M	200	indel	1	0.6 to 1	2011
Ion Torrent	PGM 318 chip v2	4M - 5.5M	400	indel	1	1.2 to 2	2013
Ion Torrent	Ion Proton	60M - 80M	200	indel	1	10	2012
Ion Torrent	Ion S5/S5XL 520	3M - 5M	400	indel	1	1.2 to 2	2015
Ion Torrent	Ion S5/S5XL 530	15M-20M	400	indel	1	03 to 05	2015
Ion Torrent	Ion S5/S5XL 540	60M - 80M	400	indel	1	NA	2015
Third Generation							
PacBio	RS C1	432	1300	indel	15	0.54	2011
PacBio	RS C2	432	2500	indel	15	0.5 to 1	2012
PacBio	RS C2 XL	432	4300	indel	15	0.5 to 1	2012
PacBio	RS II C2 XL	564	4600	indel	15	0.5 to 1	2013
PacBio	RS II P5 C3	528	8500	indel	13	0.5 to 1	2014
PacBio	RS II P6 C4	660	13500	indel	12	0.5 to 1	2014
PacBio	Sequel	350	10000	NA	NA	7	2016
Oxford Nanopore	MinION Mk	100	9545	indel/mismatch	12	1.5	2015
Oxford Nanopore	PromethION	NA	9846	NA	NA	2Tb to 4Tb	2016

*depending on run module. NA not available; M: Million; B:Billion; Gb:Gigabytes; Tb: Terabyte

1.1.6.2. Pre-processing of sequencing data

NGS technologies generate large amounts of data that have to be pre-processed in order to convert them to a readable/usable form. This includes the transformation of intensity signals to nucleotides and the assignment of quality scores to each nucleotide base (Sheikh and Erlich, 2012). Quality assessment is an important pre-processing step, which aims at pinpointing poor quality reads. This typically includes the visualization of nucleotide base quality scores, sequence length distributions and nucleotide distributions. Furthermore, a sequence can be improved from data cleaning, such as the trimming of poor quality regions and the adaptor removal (Cox et al., 2010; Haridas et al., 2011).

1.1.6.3. Sequence assembly

de novo assembly is the process of pulling together short reads into longer sequences, namely contigs using computer algorithms (Figure 1.18). For an accurate assembly, it is essential that there is sufficient overlapping between the sequence reads. In order to achieve a sufficient overlapping, high sequencing coverage (read depth) is needed. Generally, sequencing from both ends, namely paired-end sequencing provides further information for the correct assembly. Gaps between contigs or scaffolds (joined contigs) are filled with the character ‘N’ (Flicek and Birney, 2009; Pop, 2009; Miller et al., 2010).

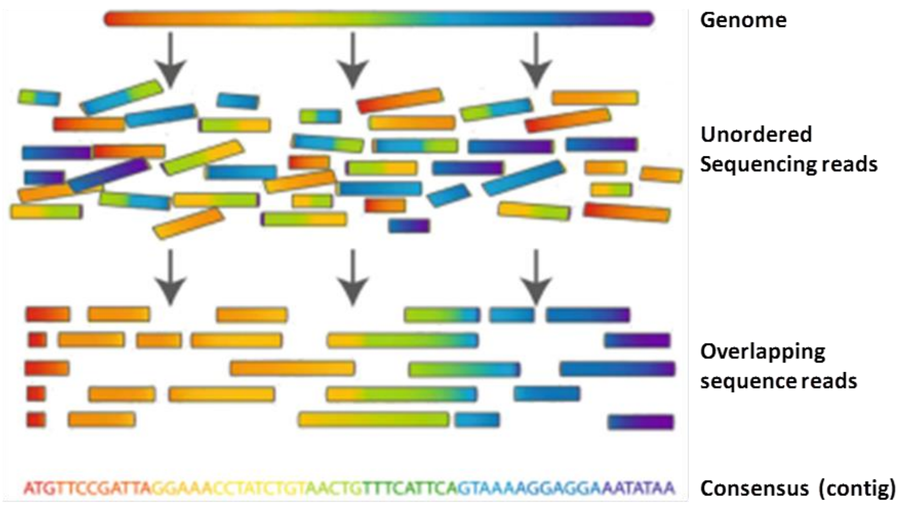

Figure 1.18. Steps of sequence assembly

1.1.6.4. Quality assessment and validation

Once the genome assembly has been completed, assessing its quality remains a challenge since “every draft genome assembly constitutes only a hypothesis of the true underlying genome sequence”. The metrics for testing the assembly can be divided into approaches that require additional information from external data (often not available) and those solely based on information derived from the assembly itself. A standard metric is the N50 length, which is defined as the shortest sequence length at 50% of the set of contigs, kind of similar to the median value. However, the N50 statistics should be used with caution, since they do not contain information on assembly accuracy (Ekblom and Wolf, 2014).

1.1.6.5. Structural genome annotation

Structural annotation consists of the identification of genomic features. Coding sequence (CDS) calling is one of the most important steps of structural annotation since is searching for sufficiently long (≥ 90 bases) DNA sequences between a start and a stop codon, yielding sometimes in incorrect gene predictions (Wang et al., 2004). Bacterial gene finder programs use algorithms with an average accuracy of approximately 90%, and, along with the function assignment given to most of the proteins, it seems that these programs are accurate (Delcher et al., 2007; Hyatt et al., 2010). Prediction of RNA genes is performed using sequence similarity with known RNAs or specific programs, such as the RNAmmer and the tRNAscan-SE (Lagesen et al., 2007; Lowe and Chan, 2016). Apart from the coding regions, a bacterial genome also contains non-coding regions, namely intergenic regions, located between the end of a coding region and the beginning of the following one. Therefore, information about the gene regulation process is present in these regions. Furthermore, intergenic regions are usually annotated for CRISPR arrays (Grissa et al., 2007a; Wang et al., 2016) and contain motifs, which contribute to chromosome replication, DNA segregation, DNA repair and cell division (Touzain et al., 2010). Mobile genetic elements (MGEs) are parts of DNA that encode proteins and facilitate the movement of DNA either within genomes (intracellular mobility) or between bacterial cells (intercellular mobility). These elements significantly affect the transfer, recombination and deletion of host genes. MGEs are present in almost all bacterial genomes (Frost et al., 2005). Examples of MGEs in prokaryotes are shown in Figure 1.19.

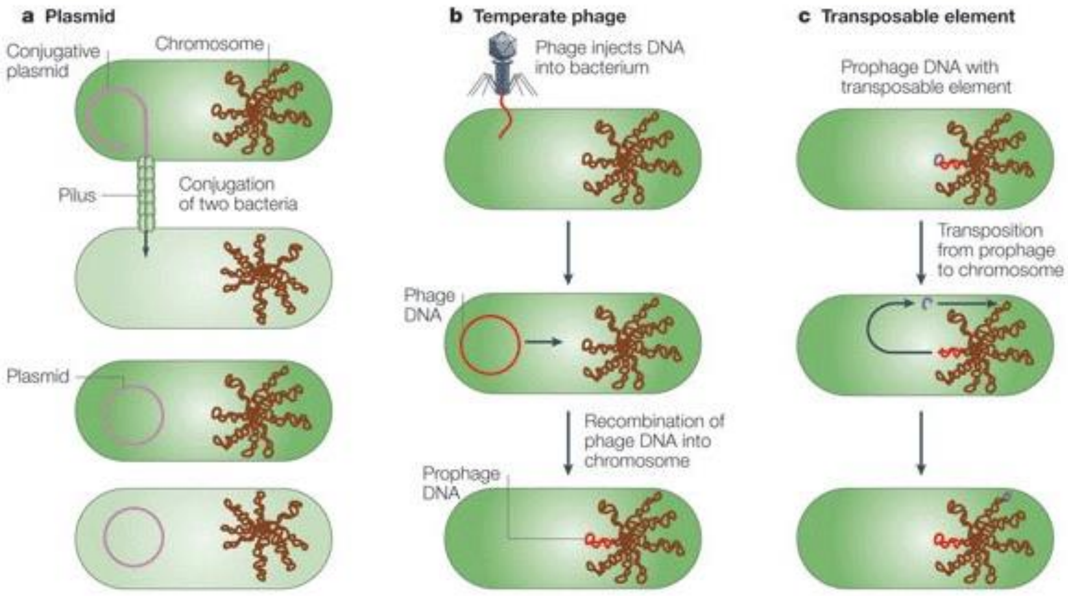

Figure 1.19. The main types of mobile genetic elements in prokaryotes are (a) plasmids that are laterally transferred from a donor bacterial cell to a recipient bacterial cell, (b) temperate phages the DNA of which enters the host cell and integrates into the bacterial genome as a prophage and (c) transposable elements that are embedded within prophage DNA excised and transferred in the bacterial chromosome (Bordenstein and Reznikoff, 2005)

1.1.6.6. Protein function prediction

The analysis of genes and gene products is usually performed in order to discover and/or confirm their function. The functional prediction of the proteins in a genome is quite challenging and the use of automated prediction programs along with manual annotation is preferred. A functional annotation first appeared in databases such as UniProtKB/Swiss-Prot (http://www.uniprot.org/), in which protein entries had an empirically determined role. The conventional approach for protein functional classification is performed by “transferring” the function from sequences with a high degree of similarity (Friedberg, 2006). This type of homology-based functional classification has been shown to be rather accurate and it can assign a function to about 73% of CDSs in a genome (Raes et al., 2007). It should be noted that such an approach is not always correct. Firstly, sequence similarity does not always imply function similarity (Eisen, 1998). Therefore, transferring annotations based on sequence similarity may result in annotation errors (Schnoes et al., 2009). Moreover, “transfering” also fails with the orphan genes, since these are genes without homologues (Tautz and Domazet-Loso, 2011). Thus, the quality of the function prediction depends on the sequence database used, the sequence similarity search method used and the type of function information transferred (Schnoes et al., 2009; Clark and Radivojac, 2011).

1.1.7. Genomics in the genus *Lactobacillus*

The extensive variety as well as the number of applications of LAB has led to the need for correlation between industrially/health-related important features and information obtained from genomic analysis. Thus, comprehensive knowledge concerning the metabolic potential of LAB may improve their use in biotechnological and health-related applications (Stefanovic et al., 2017). The genome sequences of LAB strains are available in online databases, such as the European Nucleotide Archive (ENA) and the NCBI database. Genomic analysis among these species/strains is of significant value for the selection of appropriate cultures for industrial applications (Stefanovic et al., 2017).

The first sequenced *Lactobacillus* genome was that of *L. plantarum* WCFS1 (Kleerebezem et al., 2003) followed by the probiotic *L. johnsonii* NCC 533 (Pridmore et al., 2004) and *L. acidophilus* NCFM (Altermann et al., 2005). Currently (October 2018), there are 1,875 *Lactobacillus* genome assemblies available in the NCBI database.

Genomic analysis is a powerful tool for rapid identification of putative probiotic traits (Chenoll et al., 2006; Federici et al., 2017; Douillard et al., 2018; Jarocki et al., 2018; Petrova et al., 2018). For instance, genomic analysis of the widely used probiotic strain *L. rhamnosus* GG identified among others a pilin-like surface structure that is important for adherence to intestinal mucus and a putative type IIb bacteriocin operon (Kankainen et al., 2009). Another well-known probiotic is *L. salivarius* UCC188 (Neville and O’Toole, 2010). Genomic analysis revealed that the strain encodes fibronectin-binding and sortase-dependent surface proteins that could facilitate bacterial adhesion to eukaryotic cells, as well as bile salt hydrolase (bsh) genes providing strain with a bile-resistant capacity (Neville and O’Toole, 2010). Overall, genomic studies could discover probiotic effector molecules that may be used in novel biotechnological applications.

A recent shifting of bacterial genomics from single-strain genomics to the pan-genomics of a species, or even genus, is of great importance for a better understanding of genomic features, such as bacterial evolution, adaptation and pathogenicity. Comparative genomics among 20 complete *Lactobacillus* genomes representing 14 species revealed that the genome assemblies ranged in size from 1.8 to 3.3 Mbp with a G+C content from 33 to 51% and number of proteins between 1,721 and 3,100. Moreover, the pan-genome consisted of approximately 14,000 protein-coding genes, while the core-genome of 383 genes (Kant et al., 2011). However, in a similar study of Claesson et al. the number of core-genome was lower, i.e. 141 genes, due to the less number of *Lactobacillus* genomes analyzed as well as the use of more strict criteria (Claesson et al., 2008). Interestingly, among the 383 genes of the core-genome, over 100 of them were organized in operon-like clusters that were conserved in the 20 *Lactobacillus* genomes. Therefore, apart from a shared function, these genes had also a conserved organization and control. Taking these into consideration, it is likely that these genes have been derived from a common ancestor since they are also conserved in other Gram-positive bacteria (Kant et al., 2011).

In another study, comparative genomic analysis of 213 *Lactobacillus* with the majority (82%) belonging to the *Lactobacillus* genus revealed that the pan-genome consisted of 44,668 gene families. Although some of the LAB genomes had draft assemblies, their exclusion from the analysis did not alter significantly the pan-genome. However, a negative correlation between the draft genome assemblies and the core-genome was observed. Furthermore, it was interesting the fact that the genomes of the species isolated from animals tended to be smaller compared to species isolated from different ecological niches (Figure 1.20; Sun et al., 2015).

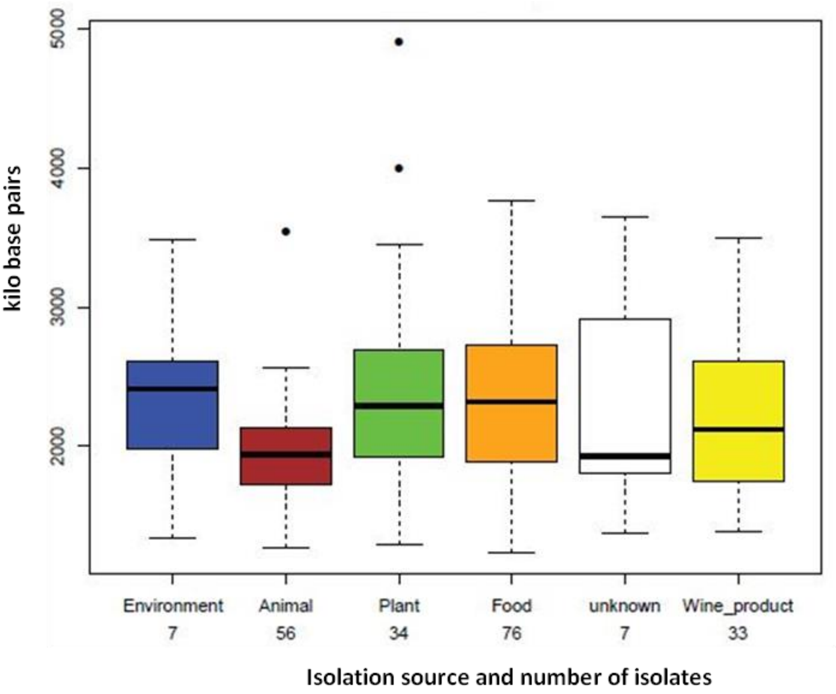

Figure 1.20. Genome assembly size according to the isolation source. Niche categories are shown on the x-axis and the size of the genome assembly on the y-axis. Box-plots represent a five-point summary of the data. From the bottom to the top: the minimum, first quartile, median, third quartile and maximum. Outliers are represented as individual points above or below the box-plot (Sun et al., 2015)

Recently, a comparative genomic analysis among 98 completely sequenced genomes of 32 *Lactobacillus* species was performed (Inglin et al., 2018). The analysis revealed that the pan-genome contains 20,800 genes and can still be considered as "open", since, after the addition of the 98th genome, 50 new genes were added to the pan-genome. In contrast, the core-genome (266 genes) stabilized after the addition of the 70th genome and is therefore considered as "closed" (Inglin et al., 2018). The main resons for the differences observed in the pan-/core-genome analyses among the studies, are likely due to the number of analyzed genomes, the integration of genomes from other genera, the complete or draft nature of genome assemblies and the parameters used.

Furthermore, genome-scale metabolic network reconstruction of lactobacilli identified important aspects, such as their significant degree of auxotrophy for amino acids, and therefore a variety of import functions is needed to include environmental nutrients into their metabolism (Kleerebezem et al., 2010). Niche-specific adaptations are also observed among lactobacilli. The milk-adapted *S. thermophilus, L. bulgaricus* and *L. helveticus* have undergone genome decay to an extent, containing several pseudogenes indicating adaptation to the nutrient-rich milk environment (Makarova et al., 2006; Alexandraki et al., 2017a; Alexandraki et al., 2017b). On the contrary, lactobacilli associated with the intestinal niche encode mucus binding cell-surface proteins and extracellular enzyme complexes probably involved in carbohydrate degradation (Makarova et al., 2006; Kleerebezem et al., 2010). Overall, comparative genomics of lactobacilli confirmed the two general trends observed in other LAB as well, which are the loss of ancestral genes and the reduction of their genome sizes (Makarova et al., 2006).

1.2. Aim of the thesis

The wide variety of lactobacilli in food and health applications, both existing and novel, raises the need to correlate important technological and health-related features with information provided by genome sequencing and annotation. Nowadays, state-of-the-art developments in sequencing technologies and bioinformatic tools provide the means for a more 'knowledge-based' approach for the selection of desirable cultures. Analysis of whole-genome sequences may reveal important information concerning the technological and probiotic potential of a strain, such as the production of antimicrobial peptides and enzymes involved in flavor formation, as well as resistance to foreign DNA. Furthermore, construction of pan-genomes could deliver important knowledge on bacterial evolution, diversity, pathogenicity and adaptability to diverse ecological niches.

For this purpose, the present thesis aimed at investigating the biological, technological and probiotic potential of three LAB strains, namely *L. zymae* ACA-DC 3411, *L. rennini* ACA-DC 565 and *L. acidipiscis* ACA-DC 1533, isolated from traditional Greek wheat sourdough, Mana Kopanisti and Kopanisti cheese, respectively, using high-throughput sequencing techniques and advanced bioinformatics tools.

The strategy employed in order to examine aspects of physiology, metabolism and technological properties for each of the three strains, consisted of the validation of genome assembly, genome annotation, functional annotation of protein-coding genes and comparative genomics among closely related strains and species.

In order to identify clonal relations, shared genomic traits, presence/absence patterns and strain-specific differences, comparative genomic analysis among *L. acidipiscis* ACA-DC 1533 and the publicly available *L. acidipiscis* strains, i.e KCTC 13900, DSM 15353, JCM 10692^T and DSM15836^T was employed. A similar analysis was not feasible for *L. zymae* and *L. rennini* since only a sole partial genome sequence was available in the NCBI database, i.e. *L. zymae* DSM 19395^T and *L. rennini* DSM 20253^T, respectively, in the beginning of the present thesis.

Finally, since *L. acidipiscis* belongs to the *L. salivarius* clade, which is mainly contains commensal isolates, comparative genomics among representative strains, i.e. *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC188 and *L. ruminis* ATCC 27782, was performed to investigate their genomic diversity and to whether *L. acidipiscis* is a commensal that has been transferred to the ecosystem of fermented foods accidentally from the host.

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CHAPTER 2

Materials and Methods

2.1. Bacterial strains and growth conditions

The bacterial strains used in this study were isolated from traditional Greek fermented food products. In particular, *L. zymae* ACA-DC 3411 was isolated from wheat sourdough and grown in MRS medium (Biokar Diagnostics, Beauvais, France) at 37 °C for 48h. *L. rennini* ACA-DC 565 was isolated from a 2-year old Kopanisti cheese known as Mana Kopanisti and grown in GasPak jar with BD GasPak EZ Anaerobe Container System (BD Diagnostic Systems, USA) in MRS at 30 °C at for 48h and *L. acidipiscis* ACA-DC 1533 was isolated from a 3-month-old Kopanisti cheese and grown in MRS at 30 °C at for 48h.

2.2. PCR amplification of 16S rRNA gene

The nearly full-length 16S rRNA gene was amplified for the three strains by using the two specific oligonucleotide primers A_{for}, 5 -GGA GAG TTA GAT CTT GGC TCA G-3 and C_{rev}, 5 -AGA AAG GAG GTG ATC CAG CC-3 for the identification of strains at species level (Ntougias et al., 2006). A reaction mixture (50 ul) containing 1 µl (50 ng/ul) genomic DNA, 25 ul 2xReadyMix (New England, Biolabs, USA), 1 µl of each primer (10 pmol/ul) and 22 ul ddH_2O was prepared per strain. Genomic DNA was amplified using a PTC-200 thermocycler (MJ Research Inc., USA) with a denaturation step of 2 min at 94 °C, followed by 30 cycles of 30 s denaturation at 94 °C, 30 s primer annealing at 56 °C and 1 min DNA chain extension at 72 °C. The PCR was completed by 5 min DNA chain extension at 72 °C. Afterwards, PCR products were purified using NucleoSpin® Gel and PCR Clean-up (Macherey-Nagel, Duren, Germany). Sequencing of purified PCR products was performed in VBC-Biotech Service GmbH (Vienna, Austria).

2.3. Extraction of genomic DNA

Genomic DNA of the three LAB strains, i.e. *L. zymae* ACA-DC 3411, *L. rennini* ACA-DC 565 and *L. acidipiscis* ACA-DC 1533, was extracted according to the protocol of Pitcher et al. (1989). The concentration of the extracted DNA was measured with a UV-Vis spectrophotometer (Q5000, Quawell, San Jose, USA) and its integrity was evaluated electrophoretically in a 0.8% agarose gel.

2.4. Genome sequencing and assembly

Whole-genome sequencing of the three LAB strains was initially performed with the Illumina HiSeq 2000 platform at the Beijing Genomics Institute (BGI Co., Ltd., Hong Kong) using three paired-end libraries with insert sizes of 500 bp, 2,000 bp, and 6,000 bp. To estimate the genome size, k-mer analysis was performed. Afterward, SOAPdenovo v2.04 software was employed to assemble the reads after filtering, placing contigs into super-scaffolds, while SOAPsnp, SOAPindel, and GATK were applied for error correction (Luo et al., 2012; Li et al., 2009). Furthermore, the gapped regions within the super-scaffolds were closed using PCR gap closure and the final step of error correction was performed with the SOAPaligner/soap2 software. The accuracy of the three hybrid assemblies was evaluated through the chromosomal optical maps of the strains, which were generated at Microbion SRL (Verona, Italy) (Latreille et al., 2007). The alignment of each assembly against the respective optical map was created with MapSolver (OpGen Technologies, Inc., Madison, WI). Particularly for *L. acidipiscis* ACA-DC 1533, an additional sequencing platform, i.e. PacBio RS II with one mate pair 5k/6k library was used, due to the high number of repeat sequences in its genome. The Continuous Long Read data collected from the PacBio RS II instrument were processed and filtered using the SMRT Analysis software by read-length, subread-length and read quality.

2.5. Genome annotation

The genome sequences of the three LAB strains were annotated with RAST v2.0 which predicts protein-coding genes, tRNAs and rRNAs (Aziz et al., 2008). Protein-coding genes were also predicted using Prodigal (Hyatt et al., 2010), MetaGeneAnnotator (Noguchi et al., 2008) and FGENESB (Solovyev et al., 2011) for the verification of the obtained coordinates, while putative pseudogenes were identified with GenePRIMP (Pati et al., 2010). All data acquired were combined and subjected to manual curation using Artemis (Carver et al., 2012) and BLAST suite (Altschul et al., 1990).

2.6. Functional anottation

The circular maps of the three LAB genomes were constructed by the DNAPlotter software (Carver et al., 2009). The WebMGA server (Wu et al., 2011) and the EggNog v4.5 (Huerta-Cepas et al., 2016) were used for COG annotation, the Phobius web server for the identification of genes with transmembrane helices and genes with signal peptides (Käll et al., 2007) and the Pfam database for the identification of genes with Pfam domains (Finn et al., 2016). GIs, ISs, putative prophages, CRISPR-Cas, RM, TAs and putative antimicrobial peptides were predicted using the IslandViewer 4 web-based resource (Bertelli et al., 2017), the ISsaga platform (Varani et al., 2011), the PHASTER web server (Arndt et al., 2016), the CRISPRFinder web tool (Grissa et al., 2007), the REBASE database (Roberts et al., 2015), TAfinder (Xie et al., 2018) and BAGEL (van Heel et al., 2013), respectively.

2.7. Phylogenetic analysis

A whole genome phylogenetic tree based on the core genes among representative strains of all species in the *L. salivarius* clade using *L. acidipiscis* ACA-DC 1533 as the reference genome was constructed with the EDGAR software (Blom et al., 2009). It should be noted that whenever available, sequences of type strains were preferred. Core gene sets were aligned using MUSCLE, the individual alignments were concatenated and the resulting genome alignment was used as input for the construction of the phylogenetic tree with the neighbor-joining method as implemented in the PHYLIP package. *Weissella kandleri* DSM 20593^T and *Lactobacillus delbrueckii* subsp. *bulgaricus* ATCC 11842^T were used as outgroups.

2.8. Comparative genomic analysis

To confirm the clonal relation among sequenced strains of *L. acidipiscis* we used an average nucleotide identity (ANI) heat map as calculated with the EDGAR tool. The ANI values were computed as described by Goris et al (2007) and as implemented in the JSpecies package (Richter and Rosselló-Móra, 2009). The resulting phylogenetic distance values were arranged in an ANI matrix, clustered according to their distance patterns and visualized as a colour-coded heatmap, with dark and light orange for high and low similarity regions, respectively. The completeness of partial genome sequences of *L. acidipiscis* strains was assessed using the dataBase of Bacterial Quality scores (dBBQs) (Wanchai et al., 2017). Preliminary evaluation of the presence of plasmids in the partially sequenced *L. acidipiscis* strains was performed with the Related Reference Contig Arrangement (r2cat) tool (Husemann and Stoye, 2010), using as templates the three pLAC plasmid sequences of strain ACA-DC 1533. Comparison of the motility gene clusters among *L. acidipiscis* ACA-DC 1533, KCTC 13900 and *L. curvatus* NRIC 0822 was performed with the Easyfig comparison tool (Sullivan et al., 2011). The GenBank accession numbers for the motility operons of *L. acidipiscis* KCTC 13900 and *L. curvatus* NRIC 0822 are KM886858 and KM886863, respectively (Cousin et al., 2015). Furthermore, full-length chromosome alignments were created by progressiveMAUVE (Darling et al., 2010). Furthermore, pan/core-genome and singleton analysis were conducted with EDGAR. COG frequency heat maps with double hierarchical clustering were generated with the RStudio using the heatmap.2 function included in the Gplots package (http://www.rstudio.org). The glycobiome profile was investigated using the DataBase for automated Carbohydrate-active enzyme Annotation (dbCAN) (Yin et al., 2012) against the Carbohydrate Active EnZymes (CAZy) database (Lombard et al., 2014). Furthermore, transporters were determined using the TransportDB database (Elbourne et al., 2017). Pathways were assigned with the Kyoto Encyclopedia of Genes and Genomes (KEGG) database (Kanehisa et al., 2016). Regulatory proteins including two-component systems, transcription factors and other DNA-binding proteins were detected with the Predicted Prokaryotic Regulatory Proteins (P2RP) web server (Barakat et al., 2013). Finally, the carbohydrate fermentation profile of *L. acidipiscis* ACA-DC 1533 was determined using API 50 CHL stripes (bioMérieux, Marcy-l'Etoile, France).

2.9. References

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CHAPTER 3

Complete genome sequence of the sourdough isolate Lactobacillus zymae ACA-DC 341

PROKARYOTES

Complete Genome Sequence of the Sourdough Isolate *Lactobacillus zymae* ACA-DC 3411

Maria Kazou,[a] Voula Alexandraki,[a] Bruno Pot,[b] Effie Tsakalidou,[a] Konstantinos Papadimitriou[a]

Laboratory of Dairy Research, Department of Food Science and Human Nutrition, Agricultural University of Athens, Athens, Greece[a]; Research Group of Industrial Microbiology and Food Biotechnology (IMDO), Vrije Universiteit Brussel, Brussels, Belgium[b]

ABSTRACT *Lactobacillus zymae* is a Gram-positive lactic acid bacterium belonging to the *Lactobacillus brevis* clade. Here, we report the first complete genome sequence of *L. zymae* ACA-DC 3411, which was isolated from traditional Greek wheat sourdough. Whole-genome analysis may reveal adaptive traits of strain ACA-DC 3411 in the sourdough ecosystem.

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Address correspondence to Konstantinos Papadimitriou, kpapadimitriou@aua.gr.

Lactobacillus zymae is a heterofermentative lactic acid bacterium (LAB) species found in fermented foods (1–4), which was transferred from the *Lactobacillus buchneri* clade to the *Lactobacillus brevis* clade, according to a recent 16S rRNA phylogenetic analysis of lactobacilli (5). *L. zymae* ACA-DC 3411 was isolated from traditional Greek wheat sourdough manufactured without baker's yeast (3, 4). Sourdough has a complex microflora consisting of LAB and yeast species, with lactobacilli being among the most significant group of microorganisms in sourdough fermentation. LAB are mainly involved in dough acidification, whereas yeasts and heterofermentative LAB species participate in the leavening process (6). Analysis of the ACA-DC 3411 genome could prove useful to understand its adaptation in the sourdough environment.

Whole-genome sequencing was performed using the Illumina HiSeq 2000 platform and three paired-end libraries with insert sizes of 500 bp, 2,000 bp, and 6,000 bp at the Beijing Genomics Institute (BGI Co., Ltd., Hong Kong). After filtering, the reads were assembled with the SOAPdenovo version 2.04 software, and the resulting contigs were placed into superscaffolds (7, 8). The assembly was validated using the whole-genome optical map of the strain (9). The map was generated at Microbion SRL (Verona, Italy), and the alignment between the assembly and the optical map was created with the Argus optical mapping system (OpGen Technologies, Inc., Madison, WI). Prediction of protein-coding genes was carried out using Prodigal (10), MetaGeneAnnotator (11) FGENESB (12), and RAST version 2.0, with RAST also being used for the genome annotation and prediction of rRNA and tRNA genes (13). Furthermore, genes were evaluated with the GenePRIMP pipeline for annotation anomalies, including putative pseudogenes (14). Functional annotation of the genome was performed with the WebMGA server (15), the IslandViewer 4 Web-based resource (16), the Phobius Web server (17), and the Pfam database (18) for COG annotation, genomic islands, genes with signal peptides and transmembrane helices, and genes with Pfam domains, respectively.

The genome sequence of ACA-DC 3411 consisted of 2,734,129 bp, with a G+C content of 52.9%. A total of 2,584 genes were identified in the genome, including 2,424 protein-coding genes, 91 potential pseudogenes, 15 rRNA genes, and 54 tRNA genes. According to the COG results, 1,930 protein-coding genes (approximately 80%) were assigned to a putative functional category, with the most abundant being related to replication, recombination, and repair (14%). Moreover, 19 integrated genomic islands were predicted in the ACA-DC 3411 genome, containing a total of 265 genes potentially acquired through horizontal gene transfer. Fifty-six of these genes code for hypothetical proteins, and the rest are of variable function. Additionally, the analysis revealed that the genome contains also 285 protein-coding genes with signal peptides, 545 with transmembrane helices, and 2,012 with Pfam domains. Further analysis of the ACA-DC 3411 genome may reveal the technological potential of the strain for sourdough fermentation.

Accession number(s). The genome sequence of *L. zymae* ACA-DC 3411 is deposited at the European Nucleotide Archive under the accession number LT854705.

ACKNOWLEDGMENTS

We thank Nikos Kyrpides at the Joint Genome Institute (U.S. Department of Energy) for analysis of the ACA-DC 3411 genome with the GenePRIMP server.

The present work was cofinanced by the European Social Fund and the National resources EPEAEK and YPEPTH through the Thales project.

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Supporting information

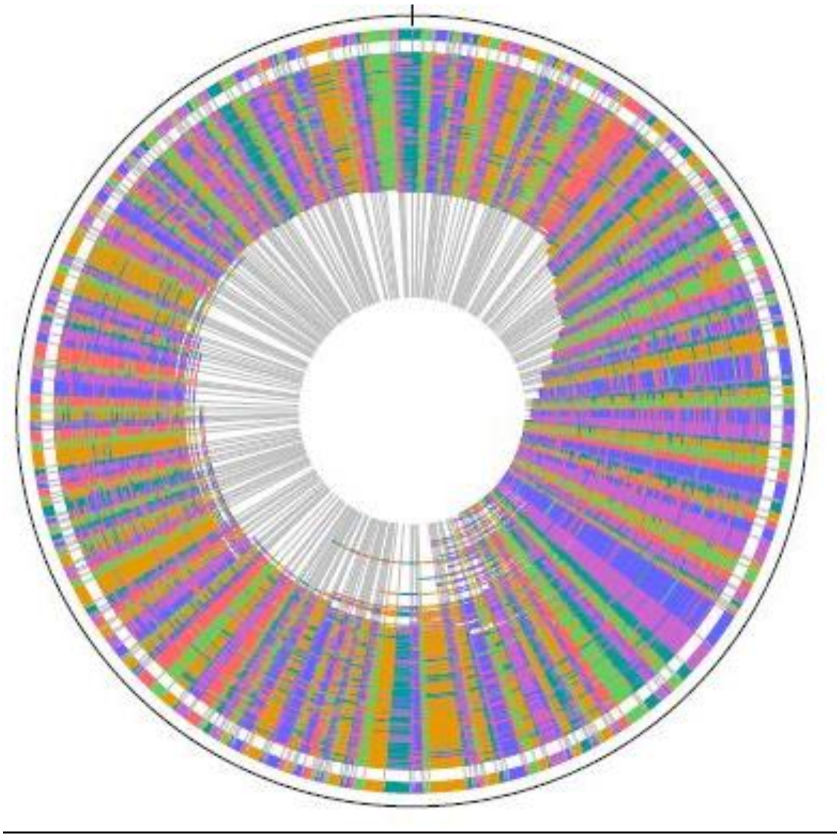

Figure 3.1. Chromosomal DNA of *L. zymae* ACA-DC 3411 was digested by *Afl*II restriction enzyme and the optical map was created with the Argus™ Optical Mapping System (OpGen Technologies, Inc., Madison, WI).

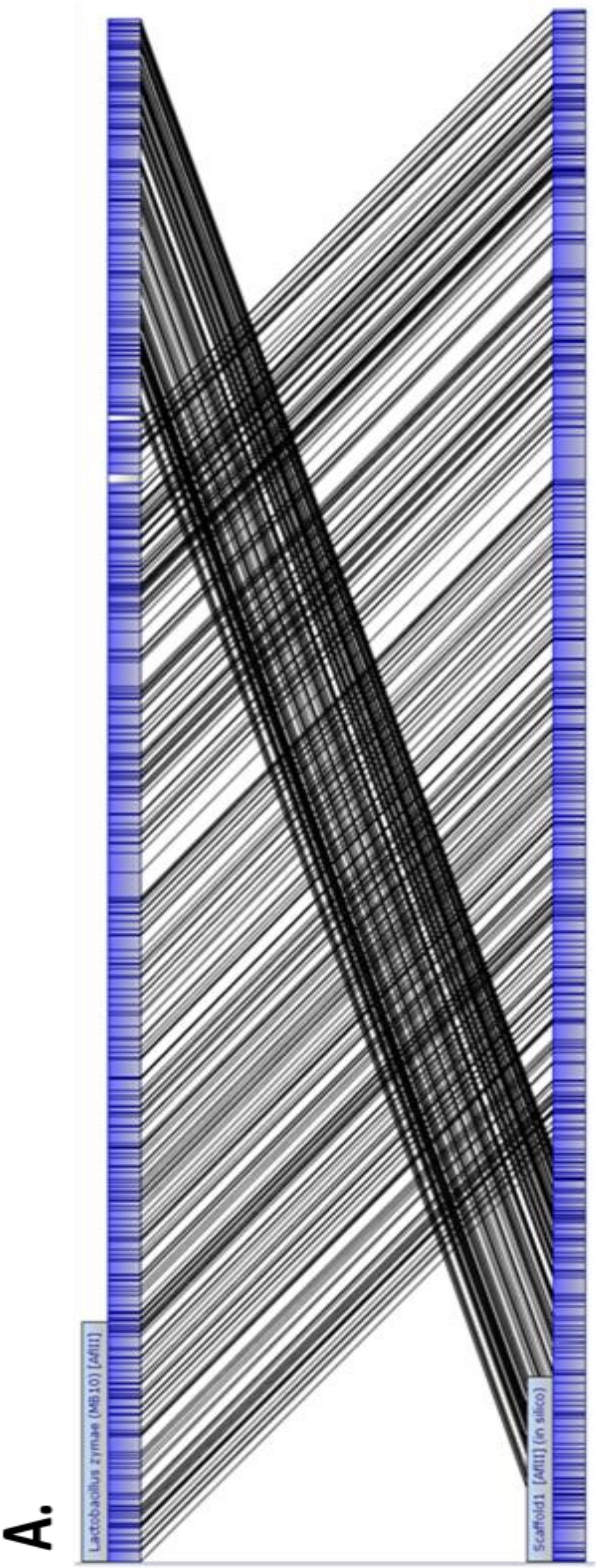

Figure 3.2. (A) Alignment of the optical map to the original contigs.

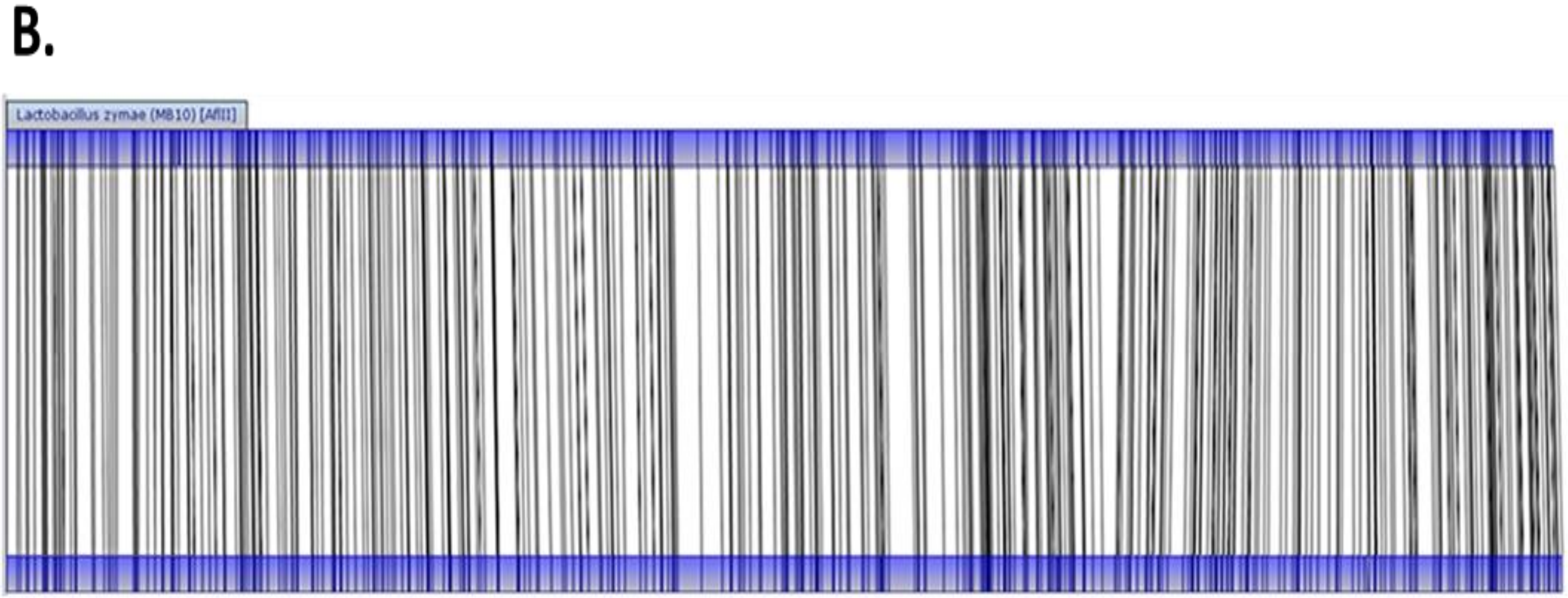

Figure 3.2. (B) Alignment of the optical map to the final assembly for strain ACA-DC 3411.

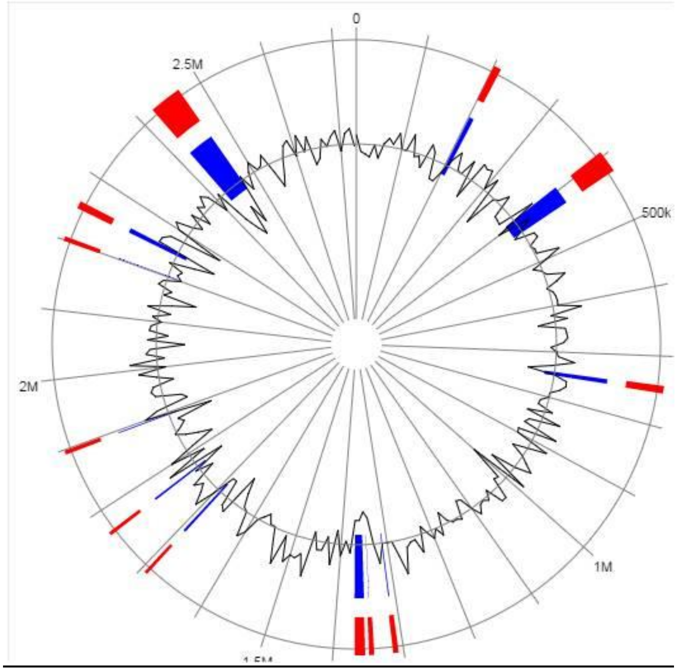

Figure 3.3. Genomic islands (GIs) of *Lactobacillus zymae* ACA-DC 3411 as predicted by the IslandViewer. GIs are colored within the circular map based on the tools used: Orange for SIGI-HMM which predicts GIs based on a hidden Markov model, blue for IslandPath-DIMOB which predicts GIs based on features associated with genomic islands and red for an integration of three methods IslandPath-DIMOB, SIGI-HMM and IslandPick which predicts GIs based on comparative genomics. The black line represents the G+C content (%) of *L. zymae* ACA-DC 3411.

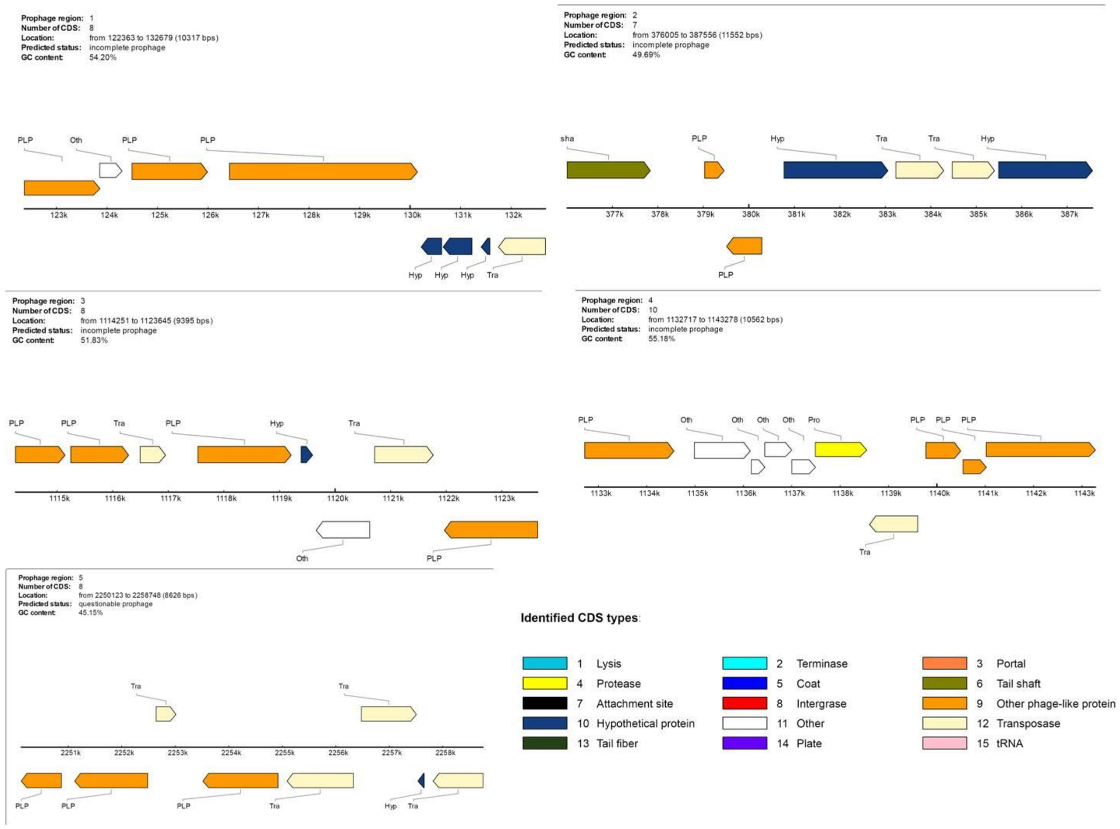

Figure 3.4. Sequence arrangements of predicted prophage regions in *Lactobacillus zymae* ACA-DC 3411 chromosome. Four incomplete and one questionable prophage regions were identified by PHAST.

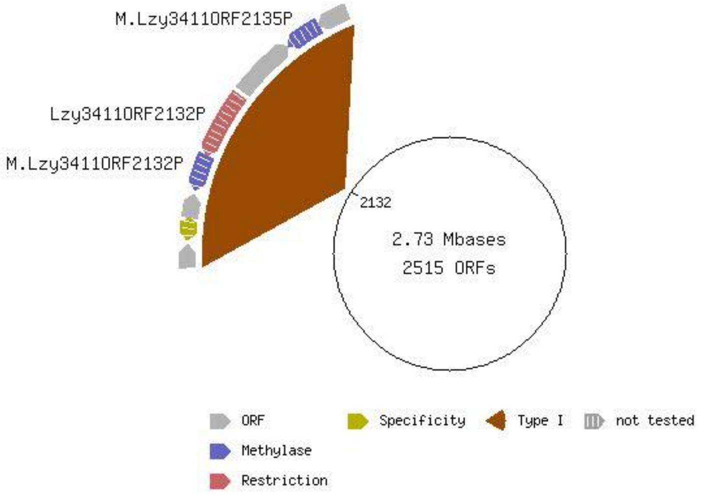

Figure 3.5. A type I restriction-modification system predicted in the *L. zymae* ACA-DC 3411 chromosome by the REBASE database.

Table 3.1. Number of *L. zymae* ACA-DC 3411 proteins associated with general COG functional categories.

COG category	proteins	proteins (%)	Description
C	87	4.13	Energy production and conversion
D	26	1.23	Cell cycle control, cell division, chromosome partitioning
E	162	7.68	Amino acid transport and metabolism
F	94	4.46	Nucleotide transport and metabolism
G	158	7.49	Carbohydrate transport and metabolism
H	66	3.13	Coenzyme transport and metabolism
I	47	2.23	Lipid transport and metabolism
J	142	6.73	Translation, ribosomal structure and biogenesis
K	168	7.97	Transcription
L	296	14.04	Replication, recombination and repair
M	125	5.93	Cell wall/membrane/envelope biogenesis
N	6	0.28	Cell motility
O	51	2.42	Posttranslational modification, protein turnover, chaperones
P	95	4.50	Inorganic ion transport and metabolism
Q	21	1.00	Secondary metabolites biosynthesis, transport and catabolism
R	254	12.04	General function prediction only
S	179	8.49	Function unknown
T	74	3.51	Signal transduction mechanisms
U	22	1.04	Intracellular trafficking, secretion, and vesicular transport
V	36	1.71	Defense mechanisms

CHAPTER 4

Whole-genome sequence of the cheese isolate Lactobacillus rennini ACA-DC 565

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PROKARYOTES

Whole-Genome Sequence of the Cheese Isolate *Lactobacillus rennini* ACA-DC 565

Maria Kazou,[a] Voula Alexandraki,[a] Bruno Pot,[b] Effie Tsakalidou,[a] Konstantinos Papadimitriou[a]

Laboratory of Dairy Research, Department of Food Science and Human Nutrition, Agricultural University of Athens, Athens, Greece[a]; Research Group of Industrial Microbiology and Food Biotechnology (IMDO), Vrije Universiteit Brussel, Brussels, Belgium[b]

ABSTRACT In this study, we present the first complete genome sequence of *Lactobacillus rennini* ACA-DC 565, a strain isolated from a traditional Greek overripened Kopanisti cheese called Mana. Although the species has been associated with cheese spoilage, the strain ACA-DC 565 may contribute to the intense organoleptic characteristics of Mana cheese.

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Address correspondence to Konstantinos Papadimitriou, kpapadimitriou@aua.gr.

Lactobacillus rennini is a Gram-positive homofermentative lactic acid bacterium belonging to the *Lactobacillus coryniformis* clade (1). *L. rennini* was originally found in spoiled rennet that, when used, produced a cheese with defects (2, 3). Strain ACA-DC 565 was isolated from a 2-year-old traditional Greek Kopanisti cheese (4). This overmature type of Kopanisti cheese, referred to as Mana, is used as an inoculum for the back-slopping production of Kopanisti cheese (5). *L. rennini* was the sole isolated microbial species in Mana producing alcohols and carbonyl compounds as major volatile compounds, most probably via the secondary catabolism of amino acids (4, 6). Mana cheese has an intense salty and a distinct piquant flavor (5), and strain ACA-DC 565 may contribute to the strong organoleptic characteristics of this cheese.

The ACA-DC 565 genome was sequenced on the Illumina HiSeq 2000 platform at the Beijing Genomics Institute (BGI Co. Ltd., Hong Kong) using three paired-end libraries with insert sizes of 500 bp, 2,000 bp, and 6,000 bp. Genome size was estimated by k-mer analysis. SOAPdenovo version 2.04 was employed to assemble the reads after filtering, and the resulting contigs were placed into superscaffolds (7, 8). The reads located in gaps were closed using local assembly and PCR gap closure. The final step of error correction was performed with the SOAPaligner/soap2 software. The assembly resulted in one circular chromosome of 2,350,601 bp, with a G+C content of 40.7% and one incomplete plasmid, which is still under sequencing (data not shown). Whole-genome optical mapping of strain ACA-DC 565 was used to validate the hybrid assembly (9). The map was generated at Microbion SRL (Verona, Italy), and the alignment between the assembled genome and an *Afl*II optical map was created with the Argus Optical mapping system (OpGen Technologies, Inc., Madison, WI, USA).

Genome annotation was performed with RAST version 2.0 (10). Genes were predicted combining the results of Prodigal (11), MetaGeneAnnotator (12), and FGENESB (13), while putative pseudogenes were identified with GenePRIMP (14). Finally, the Artemis tool (15) and the BLAST suite (16) were used for the manual curation of the genes. Concerning the functional annotation of the genome, proteins of strain ACA-DC 565 were searched against the Pfam database (17) and the Phobius Web server (18).

The ACA-DC 565 chromosome consists of 2,348 genes, including 2,166 protein-coding genes, 106 potential pseudogenes, 15 rRNAs, and 61 tRNA genes. The existence of potential pseudogenes may suggest genome decay to an extent, which is not unusual for food-related lactic acid bacteria. Furthermore, the chromosome of strain ACA-DC 565 contains 1,875 protein-coding genes with Pfam domains, 180 protein-coding genes with signal peptides, and 495 protein-coding genes with transmembrane helices.

Although *L. rennini* has been associated with cheese spoilage (2, 3), additional analysis of strain ACA-DC 565 may reveal technological properties that render it as a suitable starter or adjunct in Kopanisti cheese production.

Accession number(s). The chromosomal sequence of *L. rennini* ACA-DC 565 is deposited at the European Nucleotide Archive (ENA) under the accession number LT634362.

ACKNOWLEDGMENTS

We thank Dr. Nikos Kyrpides at the Joint Genome Institute (United States Department of Energy) for analysis of the ACA-DC 565 genome with the GenePrimp server.

The present work was cofinanced by the European Social Fund and the National resources EPEAEK and YPEPTH through the Thales project.

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Supporting information

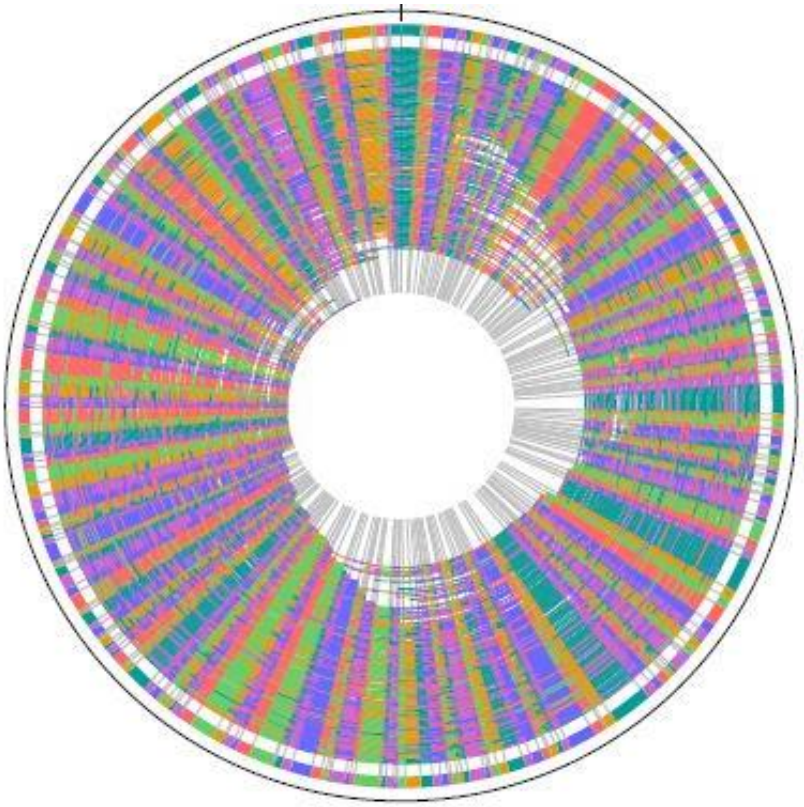

Figure 4.1. Chromosomal DNA of *L. rennini* ACA-DC 1534 was digested by *Afl*II restriction enzyme and the optical map was created with the Argus™ Optical Mapping System (OpGen Technologies, Inc., Madison, WI).

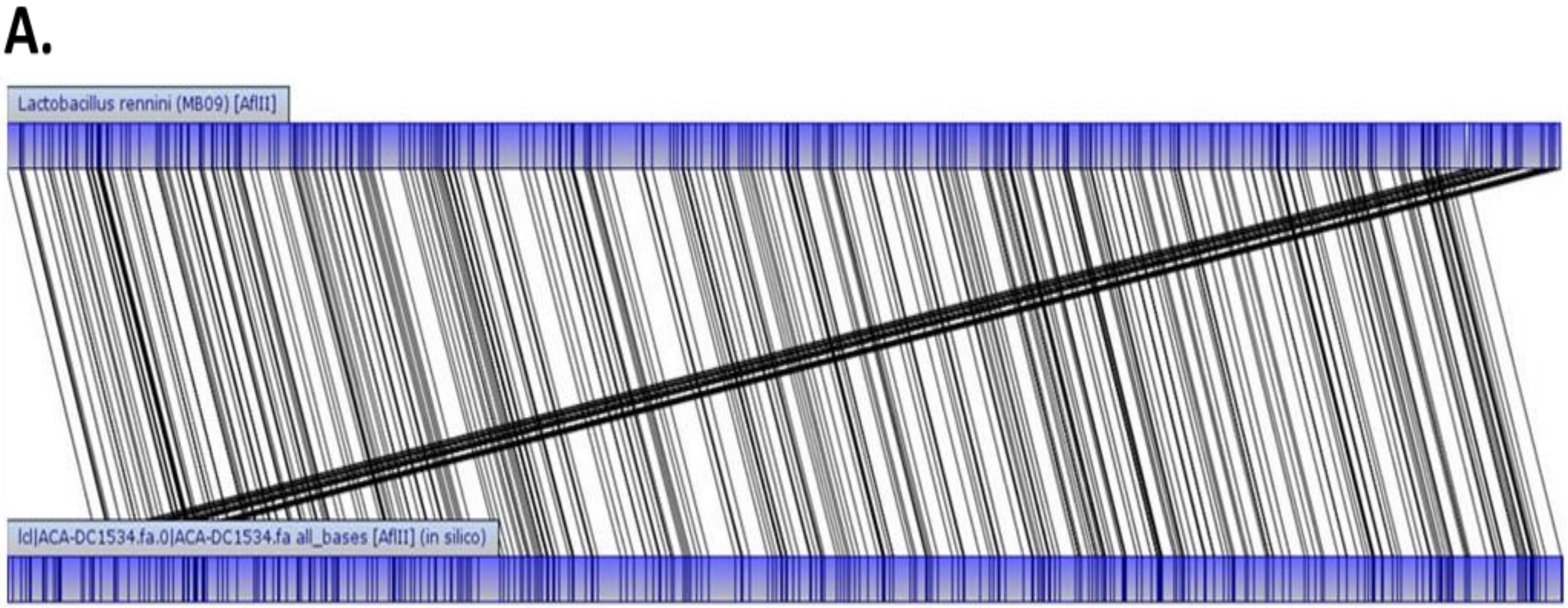

Figure 4.2. (A) Alignment of the optical map to the original contigs.

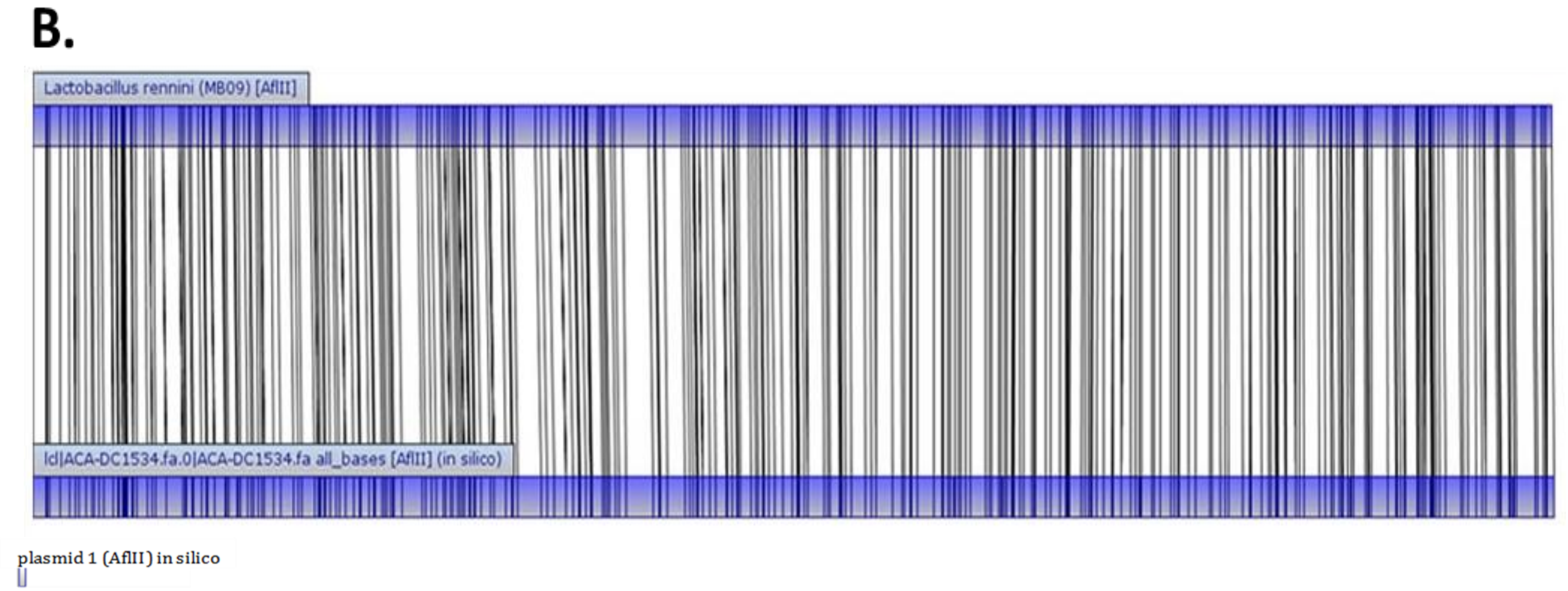

Figure 4.2. (B) Alignment of the optical map to the final assembly for strain ACA-DC 565. The non-aligned contig refers to plasmid sequence.

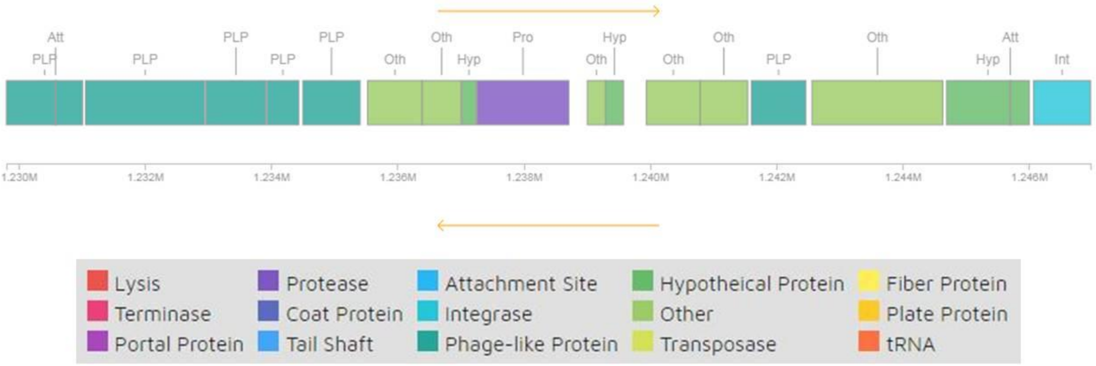

Figure 4.3. Sequence arrangement of predicted incomplete prophage region identified in the *Lactobacillus rennini* ACA-DC 565 chromosome with PHASTER.

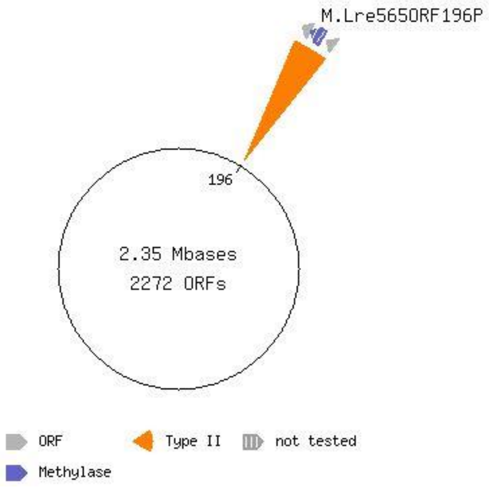

Figure 4.4. A type II restriction-modification system predicted in the *L. rennini* ACA-DC 565 chromosome by the REBASE database.

Table 4.1. Incomplete prophage region identified in the *Lactobacillus rennini* chromosome using PHASTER.

	CDS Position	BLAST Hit	E-Value
1	1229800..1231008	PHAGE_Acidia_virus_NC_029316: poly-A polymerase; LREN565_1191; phage(gi1002166894)	2.10e-23
2	1230571..1230582	attL	0.0
3	1231053..1232939	PHAGE_Plankt_PaV_LD_NC_016564: ABC transporter; LREN565_1192; phage(gi371496158)	4.72e-09
4	1232960..1233907	PHAGE_Staphy_SPbeta_like_NC_029119: thymidylate synthase; LREN565_1193; phage(gi985761245)	5.65e-150
5	1233928..1234428	PHAGE_Staphy_SPbeta_like_NC_029119: dihydrofolate reductase type 1; LREN565_1194; phage(gi985761244)	7.84e-30
6	1234494..1235402	PHAGE_Staphy_SPbeta_like_NC_029119: DegV domain-containing protein; LREN565_1195; phage(gi985761237)	6.62e-30
7	1235519..1236385	FIG006988: Lipase/Acylhydrolase with GDSL-like motif; LREN565_1196	0.0
8	1236382..1236999	YfaA; LREN565_1197	0.0
9	1237011..1237238	FIG00743134: hypothetical protein; LREN565_1198	0.0
10	1237254..1238705	PROPHAGE_Escher_MG1655: carboxy-terminal protease for penicillin-binding protein 3; LREN565_1199; phage(gi16129784)	3.21e-33
11	1238998..1239288	DNA-damage-inducible protein J; LREN565_1200	0.0
12	1239285..1239572	hypothetical protein; LREN565_1201	0.0
13	1239933..1240790	50S ribosomal subunit maturation GTPase RbgA (B. subtilis YlqF); LREN565_1202	0.0
14	1240783..1241538	Ribonuclease HII (EC 3.1.26.4); LREN565_1203	0.0
15	1241596..1242459	PHAGE_Thermu_OH2_NC_021784: SMF family protein; LREN565_1204; phage(gi526118339)	4.47e-27
16	1242556..1244628	DNA topoisomerase I (EC 5.99.1.2); LREN565_1205	0.0
17	1244688..1245998	hypothetical; LREN565_1206	0.0
18	1245690..1245701	attR	0.0
19	1246065..1246967	PHAGE_Thermu_P7426_NC_009804: phage XerD-like integrase; LREN565_1207; phage(gi157265417)	8.80e-24

Table 4.2. Number of *L. rennini* ACA-DC 565 proteins associated with general COG functional categories.

COG functional category	**proteins**	**% proteins**
Energy production and conversion (C)	126	5.82
Cell cycle control, cell division, chromosome partitioning (D)	28	1.29
Amino acid transport and metabolism (E)	133	6.14
Nucleotide transport and metabolism (F)	69	3.19
Carbohydrate transport and metabolism (G)	202	9.33
Coenzyme transport and metabolism (H)	59	2.72
Lipid transport and metabolism (I)	38	1.75
Translation, ribosomal structure and biogenesis (J)	138	6.37
Transcription (K)	153	7.06
Replication, recombination and repair (L)	166	7.66
Cell wall/membrane/envelope biogenesis (M)	126	5.82
Cell motility (N)	3	0.14
Posttranslational modification, protein turnover, chaperones (O)	55	2.54
Inorganic ion transport and metabolism (P)	96	4.43
Secondary metabolites biosynthesis, transport and catabolism (Q)	15	0.69
General function prediction only (R)	0	0.00
Function unknown (S)	392	18.10
Signal transduction mechanisms (T)	54	2.49
Intracellular trafficking, secretion, and vesicular transport (U)	17	0.78
Defense mechanisms (V)	30	1.39

CHAPTER 5

Complete genome sequence of the dairy isolate Lactobacillus acidipiscis ACA-DC 1533

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PROKARYOTES

Complete Genome Sequence of the Dairy Isolate *Lactobacillus acidipiscis* ACA-DC 1533

Maria Kazou,[a] Voula Alexandraki,[a] Bruno Pot,[b] Effie Tsakalidou,[a] Konstantinos Papadimitriou[a]

Laboratory of Dairy Research, Department of Food Science and Human Nutrition, Agricultural University of Athens, Athens, Greece[a]; Research Group of Industrial Microbiology and Food Biotechnology (IMDO), Vrije Universiteit Brussel, Brussels, Belgium[b]

ABSTRACT *Lactobacillus acidipiscis* is a Gram-positive lactic acid bacterium belonging to the *Lactobacillus salivarius* clade. Here, we present the first complete genome sequence of *L. acidipiscis* isolated from traditional Greek Kopanisti cheese. Strain ACA-DC 1533 may play a key role in the strong organoleptic characteristics of Kopanisti cheese.

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Address correspondence to Konstantinos Papadimitriou, kpapadimitriou@aua.gr.

Lactobacillus acidipiscis belongs to the *Lactobacillus salivarius* clade according to the phylogenetic analysis based on the 16S rRNA gene sequence of the *Lactobacillus* genus (1). The clade mainly includes commensals isolated from the intestine/feces of vertebrates and, to a lesser degree, strains isolated from fermented foods (2, 3). *L. acidipiscis* was originally found in fermented fish (4), while strain ACA-DC 1533 was isolated from a 3-month-old traditional Greek Kopanisti cheese prepared from raw cow milk (5). Kopanisti cheese has an intense salty and distinct piquant flavor (6) and strain ACA-DC 1533 may play a key role in the strong organoleptic characteristics of the cheese due to the production of alcohols and carbonyl compounds as major volatile compounds, presumably during secondary amino acid catabolism (5, 7).

Whole-genome sequencing was performed using the Illumina HiSeq 2000 and PacBio RS II platforms at the Beijing Genomics Institute (BGI Co., Ltd., Hong Kong). The libraries used were three Illumina paired-end (500 bp, 2,000 bp, and 6,000 bp inserted size) and one PacBio mate pair 5k/6k. To estimate the genome size, k-mer analysis was performed. Afterward, SOAPdenovo v2.04 software was employed to assemble the reads after filtering, while SOAPsnp, SOAPindel, and GATK were applied for error correction. Furthermore, whole-genome optical mapping generated at Microbion SRL (Verona, Italy) was used to validate the hybrid assembly (8). The alignment of the assembly against the optical map was created with the Argus Optical Mapping System (OpGen Technologies, Inc., Madison, WI). The analysis of the ACA-DC 1533 genome resulted in one circular chromosome of 2,607,423 bp with G+C content of 39.8%. Three plasmid sequences were also detected. Two of them were incomplete and are still under sequencing (data not shown) while the third was plasmid pLAC1 described previously (9).

The chromosomal sequence of ACA-DC 1533 was annotated with RAST v2.0 (10) and prediction of genes was carried out using Prodigal (11), MetaGeneAnnotator (12), and FGENESB (13). GenePRIMP was used for the identification of gene anomalies and putative pseudogenes (14). Manual curation of genes was performed using Artemis (15) and BLAST suite (16). The WebMGA server was used for the identification of genes with Pfam domains (17), whereas signal peptides and transmembrane helices were predicted with the Phobius web server (18). A total of 2,394 genes were annotated in the chromosome of ACA-DC 1533 including 2,262 protein-coding genes, 132 potential pseudogenes, 18 rRNA genes, and 63 tRNA genes. Considering the percentage of potential pseudogenes (approximately 5.5%), it seems that the bacterium has undergone genome decay to an extent, perhaps indicating adaptation to a nutrient-rich environment like that of cheese. The chromosome of ACA-DC 1533 also contains 1,510 protein-coding genes with Pfam domains, 153 with signal peptides, and 427 with transmembrane helices. Further investigation of ACA-DC 1533 may be required to test the applicability of the strain as a starter or adjunct culture according to its technological and probiotic potential.

Accession number(s). The chromosomal sequence of *L. acidipiscis* ACA-DC 1533 was deposited at the European Nucleotide Archive under the accession number LT630287.

ACKNOWLEDGMENTS

We thank Dr. Nikos Kyrpides at the Joint Genome Institute (United States Department of Energy) for the analysis of the ACA-DC 1533 genome with the GenePrimp server. The present work was co-financed by the European Social Fund and the National resources EPEAEK and YPEPTH through the Thales project.

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Supporting information

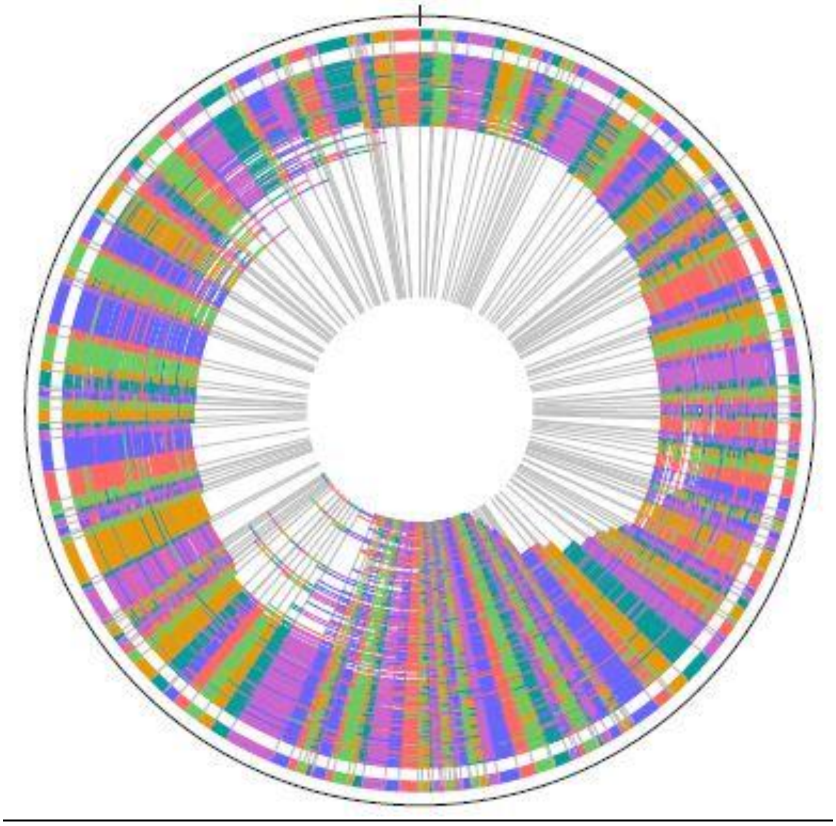

Figure 5.1. Whole-genome *NheI* optical map contigs of the *L. acidipiscis* ACA-DC 1533 genome

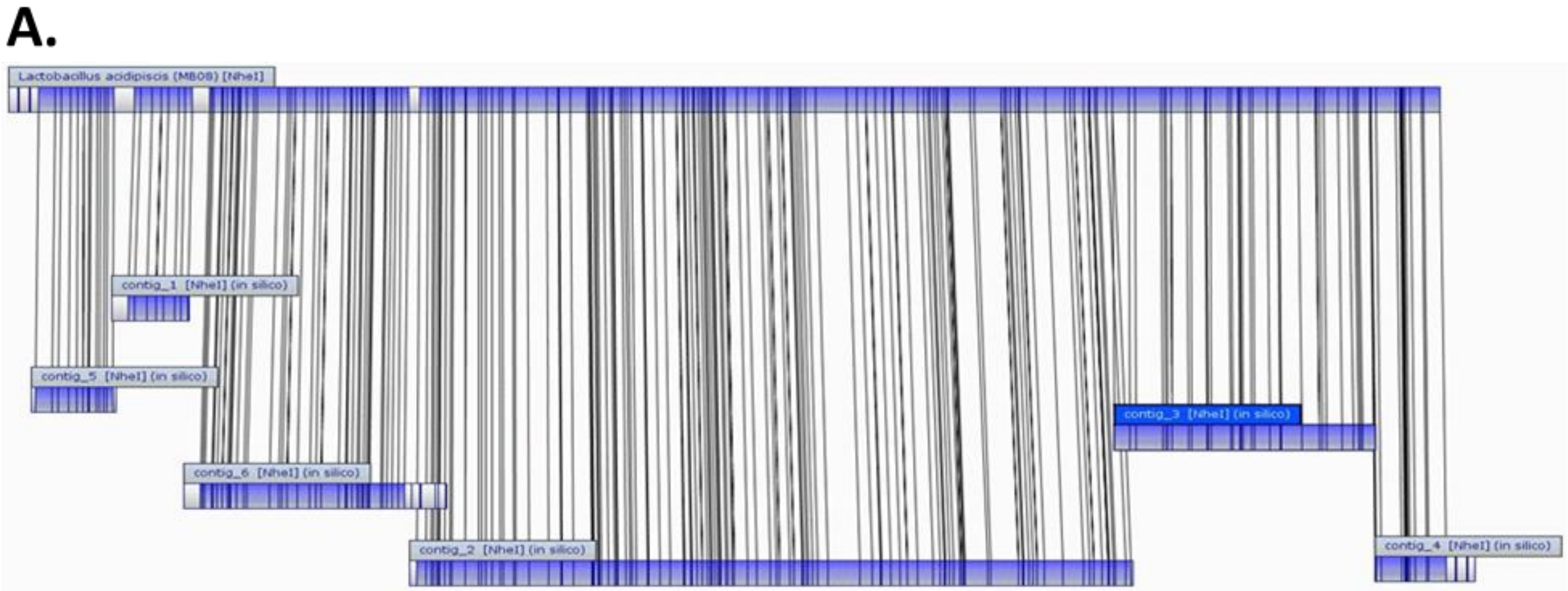

Figure 5.2. (A) Alignment of the optical map to the original contigs.

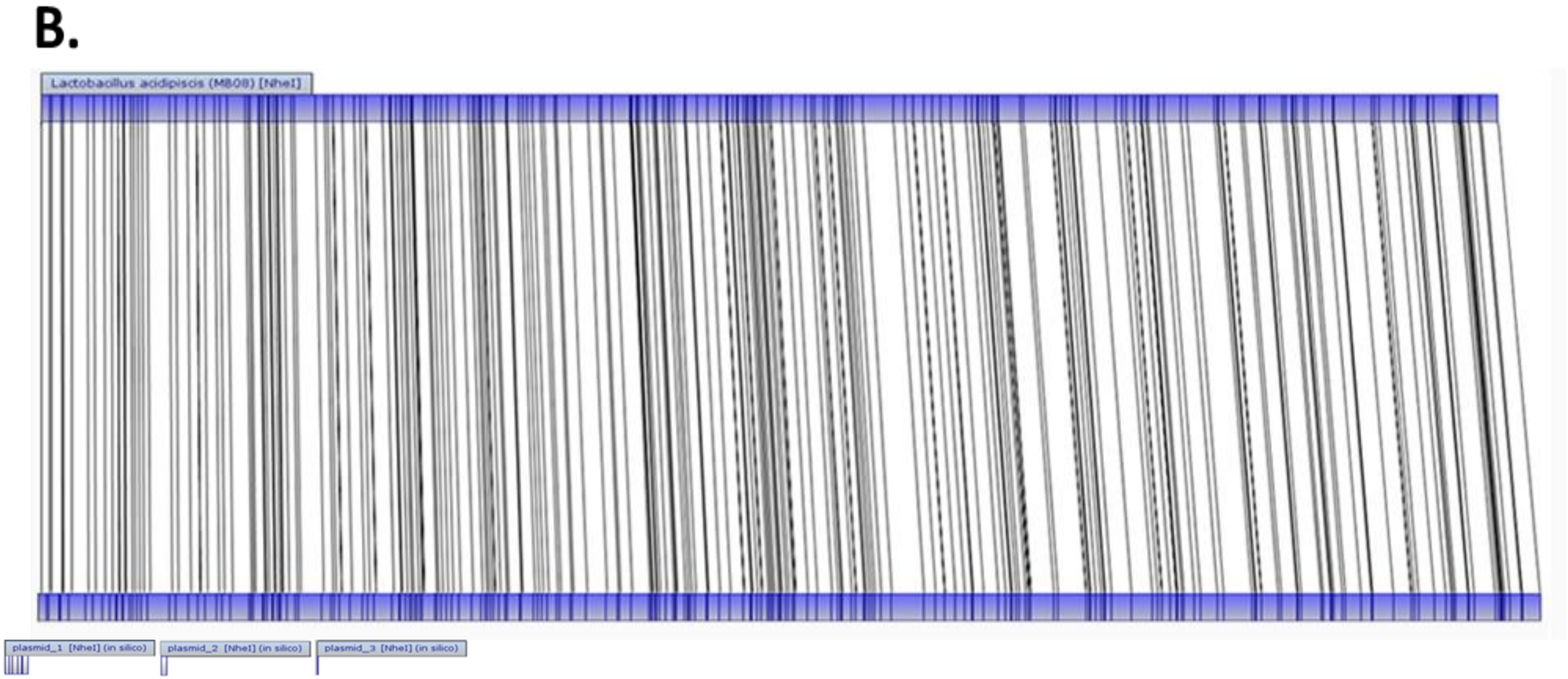

Figure 5.2. (B) Alignment of the optical map to the final assembly for strain ACA-DC 1533. The three non-aligned contigs refer to plasmid sequences.

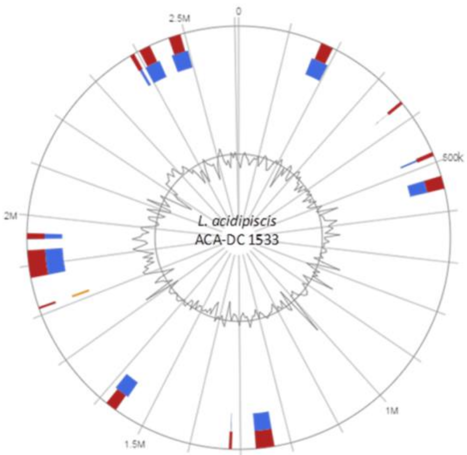

Figure 5.3. Circular map of the *L. acidipiscis* ACA-DC 1533 chromosome as generated by IslandViewer 4. Highlighted regions correspond to GIs. GIs are colored within the circular map according to the prediction method used: GIs in orange were predicted with SIGI-HMM, GIs in blue with IslandPath-DIMOB and the integrated GIs are presented on the periphery in red. The black line plot corresponds to the GC content (%) of the chromosomal sequence.

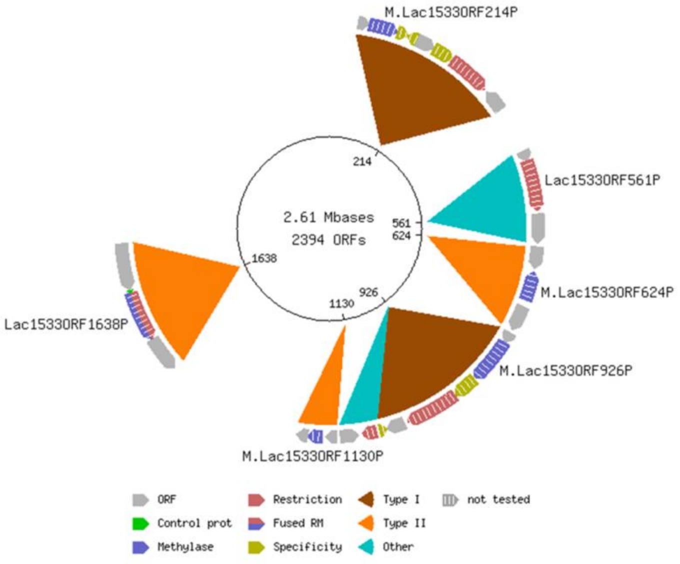

Figure 5.4. Circular map of the *L. acidipiscis* ACA-DC 1533 chromosome highlighting the predicted RM systems by the REBASE database. The symbols are color coded as indicated at the bottom of the figure.

Table 5.1. Number of *L. acidipiscis* ACA-DC 1533 proteins associated with general COG functional categories.

COG functional category	**proteins**	**% proteins**
Energy production and conversion (C)	94	4.11
Cell cycle control, cell division, chromosome partitioning (D)	27	1.18
Amino acid transport and metabolism (E)	124	5.42
Nucleotide transport and metabolism (F)	60	2.62
Carbohydrate transport and metabolism (G)	170	7.43
Coenzyme transport and metabolism (H)	33	1.44
Lipid transport and metabolism (I)	53	2.32
Translation, ribosomal structure and biogenesis (J)	144	6.29
Transcription (K)	140	6.12
Replication, recombination and repair (L)	353	15.43
Cell wall/membrane/envelope biogenesis (M)	107	4.68
Cell motility (N)	34	1.49
Posttranslational modification, protein turnover, chaperones (O)	63	2.75
Inorganic ion transport and metabolism (P)	90	3.93
Secondary metabolites biosynthesis, transport and catabolism (Q)	8	0.35
General function prediction only (R)	0	0.00
Function unknown (S)	416	18.18
Signal transduction mechanisms (T)	51	2.23
Intracellular trafficking, secretion, and vesicular transport (U)	19	0.83
Defense mechanisms (V)	35	1.53

CHAPTER 6

Comparative genomics of Lactobacillus acidipiscis ACA-DC 1533 isolated from traditional Greek Kopanisti cheese against species within the Lactobacillus salivarius clade

frontiers in Microbiology

ORIGINAL RESEARCH
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Comparative Genomics of *Lactobacillus acidipiscis* ACA-DC 1533 Isolated From Traditional Greek Kopanisti Cheese Against Species Within the *Lactobacillus salivarius* Clade

*Maria Kazou[1], Voula Alexandraki[1], Jochen Blom[2], Bruno Pot[3], Effie Tsakalidou[1] and Konstantinos Papadimitriou[1]**

[1] Laboratory of Dairy Research, Department of Food Science and Human Nutrition, Agricultural University of Athens, Athens, Greece, [2] Bioinformatics and Systems Biology, Justus-Liebig-University Giessen, Giessen, Germany, [3] Research Group of Industrial Microbiology and Food Biotechnology (IMDO), Department of Bioengineering Sciences (DBIT), Vrije Universiteit Brussel, Brussels, Belgium

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Fidelity Systems, United States

***Correspondence:**
Konstantinos Papadimitriou
kpapadimitriou@aua.gr

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Lactobacillus acidipiscis belongs to the *Lactobacillus salivarius* clade and it is found in a variety of fermented foods. Strain ACA-DC 1533 was isolated from traditional Greek Kopanisti cheese and among the available *L. acidipiscis* genomes it is the only one with a fully sequenced chromosome. *L. acidipiscis* strains exhibited a high degree of conservation at the genome level. Investigation of the distribution of prophages and Clustered Regularly Interspaced Short Palindromic Repeats (CRISPRs) among the three strains suggests the potential existence of lineages within the species. Based on the presence/absence patterns of these genomic traits, strain ACA-DC 1533 seems to be more related to strain JCM 10692^T than strain KCTC 13900. Interestingly, strains ACA-DC 1533 and JCM 10692^T which lack CRISPRs, carry two similar prophages. In contrast, strain KCTC 13900 seems to have acquired immunity to these prophages according to the sequences of spacers in its CRISPRs. Nonetheless, strain KCTC 13900 has a prophage that is absent from strains ACA-DC 1533 and JCM 10692^T. Furthermore, comparative genomic analysis was performed among *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *Lactobacillus ruminis* ATCC 27782. The chromosomes of the three species lack long-range synteny. Important differences were also determined in the number of glycobiome related proteins, proteolytic enzymes, transporters, insertion sequences and regulatory proteins. Moreover, no obvious genomic traits supporting a probiotic potential of *L. acidipiscis* ACA-DC 1533 were detected when compared to the probiotic *L. salivarius* UCC118. However, the existence of more than one glycine-betaine transporter within the genome of ACA-DC 1533 may explain the ability of *L. acidipiscis* to grow in fermented foods containing high salt concentrations. Finally, *in silico* analysis of the *L. acidipiscis* ACA-DC 1533 genome revealed pathways that could underpin the production of major volatile compounds during the catabolism of amino acids that may contribute to the typical piquant flavors of Kopanisti cheese.

Keywords: *Lactobacillus*, genome, pseudogene, motility, horizontal gene transfer, phage, probiotic, metabolism

INTRODUCTION

The genus *Lactobacillus* constitutes a diverse group of bacteria comprising more than 200 species and subspecies[1] that are ubiquitous and frequently found in a variety of nutrient-rich ecological niches (Pot et al., 2014; Sun Z. et al., 2015). Lactobacilli produce lactic acid as the main end-product of carbohydrate fermentation allowing them to prevail in microbial ecosystems. This attribute along with their safety profile and their ability to shape organoleptic characteristics of the final product are the central reasons for their extensive use in artisanal or industrial food fermentations (Bernardeau et al., 2008; Sun Z. et al., 2015; Reginensi et al., 2016). Apart from food-related lactobacilli, the genus includes many commensals of the human, animal and plant microbiota (Cannon et al., 2005; Duar et al., 2017). The available genomes for *Lactobacillus* species and the close phylogenetic relationship among food- and host-related strains offer a wealth of information that underpin specialized mechanisms of bacterial adaptation to different environments (Sun Z. et al., 2015).

Lactobacillus acidipiscis is a salt-tolerant species originally isolated from fermented fish (Tanasupawat et al., 2000). The species has been also found in a variety of cheeses, i.e., Halloumi (Lawson et al., 2001; Naser et al., 2006; Kim et al., 2011), Cotija (Morales et al., 2011), Minas (Perin et al., 2017), and double cream cheese (Morales et al., 2011; Melgar-Lalanne et al., 2013), as well as in fermented fish (An et al., 2010; Tsuda et al., 2012; Thamacharoensuk et al., 2017), fermented meat (Nguyen et al., 2013), sake (Koyanagi et al., 2016), pickles (Arasu et al., 2015), grasses (Tohno et al., 2012; Khota et al., 2016), mulberry silage (Altaher et al., 2015), sweet paste (Mao et al., 2017), the traditional Chinese fermented vegetable Sichuan paocai, (Cao et al., 2017) and table olives (Randazzo et al., 2017). Moreover, *L. acidipiscis* has also been found in vinegar (Li P. et al., 2014) and soy sauce, where it is considered to be a spoiler (Tanasupawat et al., 2002; Cheng et al., 2014; Li N. et al., 2014). *L. acidipiscis* ACA-DC 1533 was isolated from traditional Greek Kopanisti cheese and along with *Lactobacillus rennini* were the dominant microbiota of this cheese (Asteri et al., 2009). Interestingly, both of them produced alcohols and carbonyl compounds most probably *via* amino acid catabolism that may contribute to the typical piquant flavors of Kopanisti cheese (Yvon and Rijnen, 2001; Asteri et al., 2009; Donnelly, 2016).

Phylogenetic analysis of *L. acidipiscis* places the bacterium in the *Lactobacillus salivarius* clade. The *L. salivarius* clade is the second largest group of lactobacilli with 27 recognized species following that of *Lactobacillus delbrueckii* (29 species; Pot et al., 2014). The *L. salivarius* clade consists mainly of commensal isolates and to a lesser degree of strains found in fermented foods (Cousin et al., 2015). Several strains belonging to the clade exhibit putative probiotic traits (Neville and O'Toole, 2010). Therefore, comparative genomics among members of the *L. salivarius* clade may reveal important aspects, such as niche adaptation, technological potential, and probiotic properties (Forde et al., 2011; Raftis et al., 2011; Sun Z. et al., 2015). So far, there are eight genomes with fully sequenced chromosomes in the *L. salivarius* clade publicly available in the NCBI database, i.e., six from *L. salivarius* (Claesson et al., 2006; Jimenez et al., 2010; Raftis et al., 2014; Chenoll et al., 2016), one from *Lactobacillus ruminis* (Forde et al., 2011) and one from *L. acidipiscis* (Kazou et al., 2017). Furthermore, *L. acidipiscis* JCM 10692^T and DSM 15836^T isolated from fermented fish as well as *L. acidipiscis* DSM 15353 and KCTC 13900 isolated from Halloumi cheese have been partially sequenced (Kim et al., 2011; Sun Z. et al., 2015). In fact, strains JCM 10692^T and DSM 15836^T are replicas of the same strain[2,3] and the same applies for strains DSM 15353 and KCTC 13900[4,5].

The genome sequence of *L. acidipiscis* ACA-DC 1533 has been published (Kazou et al., 2017) and the current study aims to examine aspects of the evolution, physiology, metabolism and technological properties of the species according to the available *L. acidipiscis* genomes. Furthermore, we perform comparative genomics among the species with fully sequenced genomes in the *L. salivarius* clade to shed light to niche adaptation (host or food related, or both). Our analysis reveals technological properties of *L. acidipiscis* ACA-DC 1533 that may support the potential use of the isolate in food fermentations.

MATERIALS AND METHODS

Chromosome-Plasmid Sequences and Annotations

Species/strains employed in phylogenetic analysis and comparative genomics are presented in **Supplementary Table S1**. All annotated sequences derived from RefSeq version 86 with the exception of plasmids pLAC2 and pLAC3 of *L. acidipiscis* ACA-DC 1533 that have not been included in RefSeq yet, so we used their GenBank/ENA versions (Kazou et al., 2017). In the table we present all relevant information to aid the reader assess whether differences or similarities in gene content among strains analyzed may be influenced by differences in sequencing

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[1] http://www.bacterio.net/lactobacillus.html

Abbreviations: ABC, ATP-binding cassette; ANI, average nucleotide identity; CAZy, Carbohydrate Active EnZymes; CBMs, Carbohydrate-Binding Modules; CEs, Carbohydrate Esterases; COG, Clusters of Orthologous Groups; CRISPRs, Clustered Regularly Interspaced Short Palindromic Repeats; dBBQs, dataBase of Bacterial Quality scores; dbCAN, DataBase for automated Carbohydrate-active enzyme Annotation; EPS, Exopolysaccharide; GHs, Glycoside Hydrolases; GIs, Genomic islands; GTs, Glycosyl Transferases; HGT, Horizontal Gene Transfer; HK, Histidine Kinase; ISs, insertion sequences; KEGG, Kyoto Encyclopedia of Genes and Genomes; LCBs, locally collinear blocks; MFS, major facilitator superfamily; OCSs, One-component Systems; ODPs, Other DNA-binding Proteins; PBMCs, peripheral blood mononuclear cells; PEP-PTS, Phosphoenolpyruvate Phosphotransferase System; P2RP, Predicted Prokaryotic Regulatory Proteins; r2cat, Related Reference Contig Arrangement; RM, Restriction-Modification; RPs, Regulatory Proteins; RR, Response Regulator; RSM, reconstituted skim milk; SFs, Sigma Factors; TA, toxin-antitoxin; TCSs, Two-component Systems; TFs, Transcription Factors; TRs, Transcriptional Regulators.

[2] http://www.jcm.riken.jp/cgi-bin/jcm/jcm_number?JCM=10692

[3] https://www.dsmz.de/catalogues/details/culture/DSM-15836.html

[4] https://www.dsmz.de/catalogues/details/culture/DSM-15353.html

[5] http://kctc.kribb.re.kr/En/jsearch/j_sview.aspx?sn=13900

technologies and/or tools used for sequence assembly and annotation.

Phylogenetic Analysis

A whole genome phylogenetic tree based on the core genes among representative strains of all species in the *L. salivarius* clade using *L. acidipiscis* ACA-DC 1533 as the reference genome was constructed with the EDGAR software (Blom et al., 2009). It should be noted that whenever available, sequences of type strains were preferred. Core gene sets were aligned using MUSCLE, the individual alignments were concatenated and the resulting genome alignment was used as input for the construction of the phylogenetic tree with the neighbor-joining method as implemented in the PHYLIP package. *Weissella kandleri* DSM 20593^T and *Lactobacillus delbrueckii* subsp. *bulgaricus* ATCC 11842^T were used as outgroups.

Comparative Genomic Analysis

To confirm the clonal relation among sequenced strains of *L. acidipiscis* as these are deduced from different databases, we used an ANI heat map as calculated with the EDGAR tool. The completeness of partial genome sequences of *L. acidipiscis* strains was assessed using the dBBQs (Wanchai et al., 2017). Preliminary evaluation of the presence of plasmids in the partially sequenced *L. acidipiscis* strains was performed with the r2cat tool (Husemann and Stoye, 2010), using as templates the three pLAC plasmid sequences of strain ACA-DC 1533. The circular map of *L. acidipiscis* ACA-DC 1533 was constructed by the DNAPlotter software (Carver et al., 2009). Pan/core-genome and singleton analysis were conducted with EDGAR. Comparison of the motility gene clusters among *L. acidipiscis* ACA-DC 1533 and KCTC 13900 as well as *Lactobacillus curvatus* NRIC 0822 was performed with the Easyfig comparison tool (Sullivan et al., 2011). The GenBank accession numbers for the motility operons of *L. acidipiscis* KCTC 13900 and *L. curvatus* NRIC 0822 are KM886858 and KM886863, respectively (Cousin et al., 2015). The EggNOG server version 4.5 was used for COG annotation (Huerta-Cepas et al., 2016). COG frequency heat maps with double hierarchical clustering were generated using the RStudio and the package "gplots"[6]. GIs, ISs, putative prophages, CRISPRs, RM systems, TA systems and putative antimicrobial peptides were predicted using the IslandViewer 4 web-based resource (Bertelli et al., 2017), the ISsaga platform (Varani et al., 2011), the PHASTER web server (Arndt et al., 2016), the CRISPRFinder web tool (Grissa et al., 2007), the REBASE database (Roberts et al., 2015), the TAfinder (Xie et al., 2018) and the BAGEL (van Heel et al., 2013), respectively. The glycobiome profile was investigated using the dbCAN (Yin et al., 2012) against the CAZy database (Lombard et al., 2014). Furthermore, transporters were determined using the TransportDB database (Elbourne et al., 2017). Pathways were assigned with the KEGG database (Kanehisa et al., 2016). Regulatory proteins including TCSs, TFs, and ODPs were detected with the P2RP web server (Barakat et al., 2013). Full-length chromosome alignments were created by progressiveMAUVE (Darling et al., 2010). Finally, the carbohydrate fermentation profile of *L. acidipiscis* ACA-DC 1533 was determined using API 50 CHL stripes (bioMérieux, Marcy-l'Etoile, France).

RESULTS AND DISCUSSION

Whole Genome Phylogeny of the *L. salivarius* Clade

The phylogenetic relationship among the species of the *L. salivarius* clade was determined based on whole genome sequences. Analysis with the EDGAR software revealed two major clusters containing 12 and 14 species, respectively (**Figure 1**). *L. acidipiscis* was grouped together with *Lactobacillus pobuzihii* in a cluster, which also included *L. salivarius*. The strains employed in the phylogenetic analysis of the *L. salivarius* clade exhibited a pan genome of 13,470 genes, while the core-genome consisted of 349 genes. Moreover, proteins of the species belonging to the *L. salivarius* clade were distributed into various COG functional categories with a relatively distinct profile for each species. Interestingly, hierarchical clustering of the COG frequency heat map (**Figure 2**) revealed two clusters, which were very similar to the two clusters mentioned above that were obtained in the whole genome phylogenetic tree (**Figure 1**). It should be noted that *L. acidipiscis* ACA-DC 1533 was placed separately from these two clusters most probably due to an increased percentage of genes in the replication, recombination and repair (L) COG category. This difference could arise from a higher number of transposases in the ACA-DC 1533 genome but the number of transposases in the partial genomes employed during this analysis may be severely skewed. Nevertheless, *L. acidipiscis* also exhibited a higher number of transposases when compared to the complete genome sequences of *L. salivarius* and *L. ruminis* (please see below). Both whole genome phylogeny and COG analysis can be influenced by the partial nature of some of the sequences employed as well as differences in pipelines used for genome assembly and annotation. However, the whole genome phylogenetic tree is similar in the overall topology to the 16S rRNA phylogenetic tree of the entire *Lactobacillus* genus published by Pot et al. (2014) which is independent of genome completeness and annotation. The same applies when we compared our whole genome phylogenetic tree to the tree based on the concatenated amino acid sequences of 16 marker genes published by Sun Z. et al. (2015).

General Genomic Features of *L. acidipiscis* Strains

To date, there are five sequenced strains of *L. acidipiscis*, i.e., ACA-DC 1533, KCTC 13900, DSM 15353, JCM 10692^T and DSM 15836^T. As mentioned above, strains KCTC 13900 and DSM 15353 as well as JCM 10692^T and DSM 15836^T are replicas. Since this is not always obvious in the respective literature (Kim et al., 2011; Sun Z. et al., 2015), the relatedness among the two pairs of *L. acidipiscis* strains was also obtained by the ANI performed with

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[6] http://www.rstudio.org

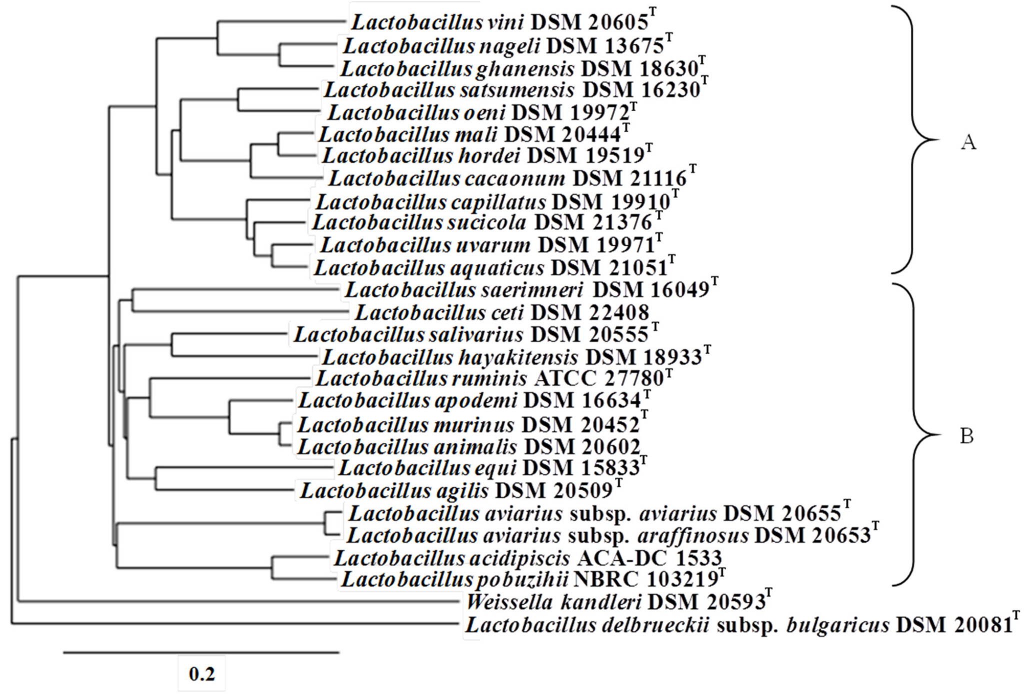

FIGURE 1 | Whole genome phylogenetic tree for representative species of the *L. salivarius* clade. The tree was calculated based on the core-genome and it is presented as a cladogram. Species were separated in two main groups, namely A and B, as depicted in the figure. *Weissella kandleri* DSM 20593^T and *Lactobacillus delbrueckii* subsp. *bulgaricus* ATCC 11842^T were used as outgroups.

EDGAR (**Supplementary Figure S1**). Results obtained confirmed the clonal relationship among the strains. To evaluate the level of completeness between the *L. acidipiscis* genomes in each of the two pairs of replica strains, we used the genome quality scores from the dBBQs based on the sequence completeness, the tRNA and rRNA score, as well as the number of essential genes predicted in the genome sequence (Wanchai et al., 2017). According to these results, strains KCTC 13900 and JCM 10692^T were found to be more complete than strains DSM 15353 and DSM 15836^T, respectively (**Supplementary Table S2**). For this reason, strains KCTC 13900 and JCM 10692^T were employed for further analysis.

The characteristics of the *L. acidipiscis* ACA-DC 1533 genome were described previously (Asteri et al., 2010; Kazou et al., 2017). The complete chromosomal sequence of the strain was recently re-annotated in RefSeq revealing a total of 2,455 genes including 2,199 protein-coding genes and 172 potential pseudogenes mostly due to frame shifting and internal stop codons (**Figure 3**). Among pseudogenes, hypothetical proteins and mobile elements, such as ISs and transposases, were the most common (**Supplementary Table S3**). The genome also includes six rRNA operons distributed throughout the genome and 63 tRNA genes with the majority located around the five rRNA operons (data not shown).

The additional *L. acidipiscis* assemblies of strains JCM 10692^T and KCTC 13900 are fragmented and thus do not allow the determination of their accurate chromosomal size as well as the evaluation of their plasmid content. Nevertheless, in these assemblies we could detect plasmid sequences after analysis with the r2cat tool, using as templates the three pLAC plasmid sequences (data not shown). Strain ACA-DC 1533 exhibits 2,288 protein-coding genes versus 2,126 and 1,969 for the JCM 10692^T and KCTC 13900 strains, respectively. Analysis with EDGAR revealed that the pan-genome consists of 2,722 genes, with 1,569 and 411 genes belonging to the core- and the dispensable genomes, respectively (**Figure 4A** and **Supplementary Tables S4A,B**). Furthermore, the analysis revealed that singletons represented approximately the 18% of the pan-genome. Strain JCM 10692^T carries the highest number of singletons ($n = 197$) followed by strains ACA-DC 1533 ($n = 157$) and KCTC 13900 ($n = 136$) (**Supplementary Table S4C**). However, such differences may not be readily explained given the differences in completeness among these genomes. We would like to mention that the total number of genes for each strain presented in **Figure 4A** is somewhat lower than the total number of genes annotated for the strain. The missing genes are genes that are not part of the 3-genome or 2-genome cores, but also do not appear in the strictly calculated singletons as they have some second-best BLAST hits, or non-reciprocal-BLAST hits or in general show some similarity to other genes in the dataset that rules them out as singletons as calculated by the EDGAR tool. The distribution of proteins into the COG functional categories is shown in a heat map for the three *L. acidipiscis* strains (**Figure 4B**). Despite their differences in completeness, the three genomes present very similar percentages in each of the COG categories. There was only one exception in replication,

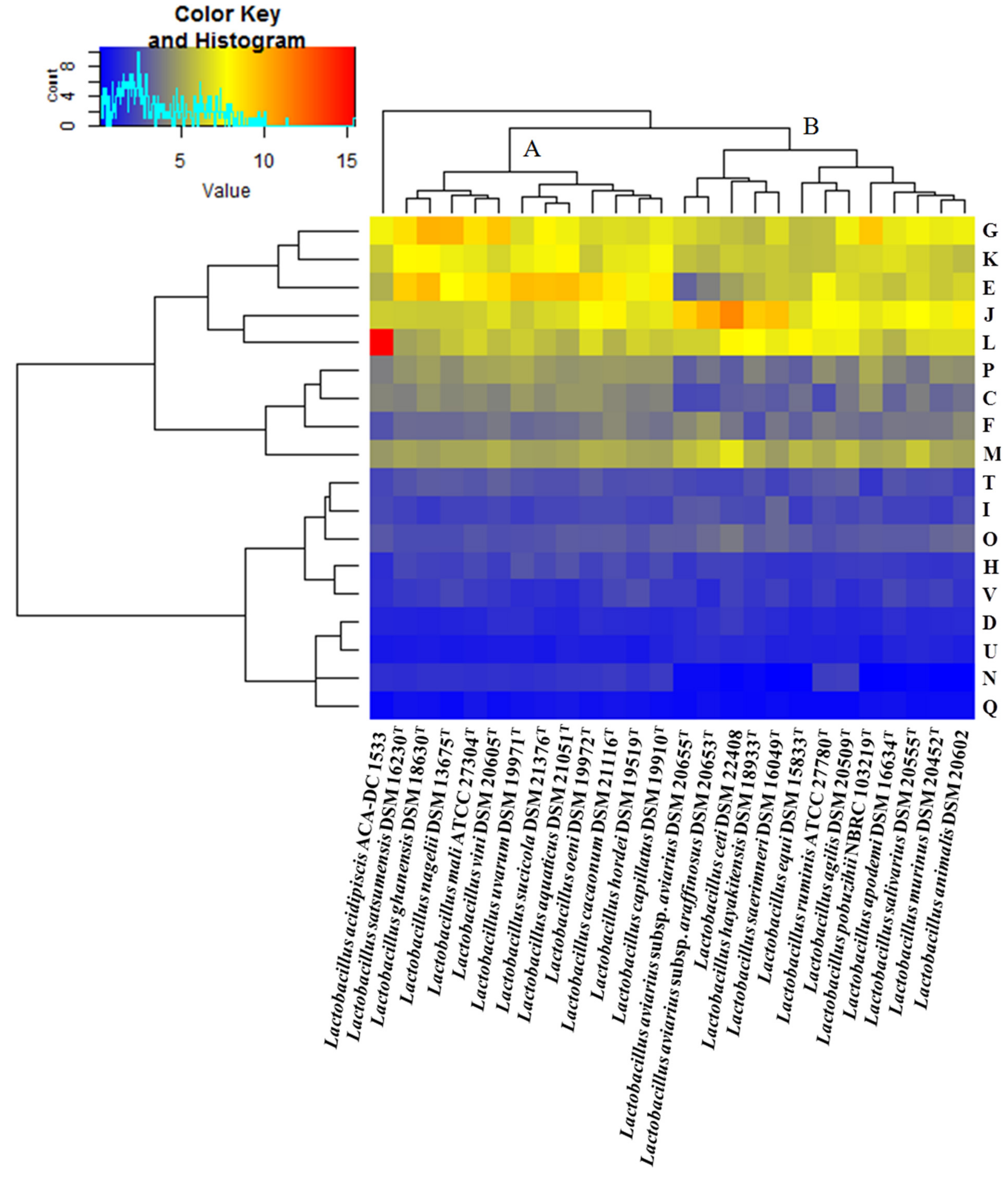

FIGURE 2 | COG frequency heat map based on a two-dimensional hierarchical clustering. The horizontal axis shows the percentage frequency of proteins involved in each functional COG category and the vertical axis the representative strains of the species in the *L. salivarius* clade.

recombination and repair (L) category in which strain ACA-DC 1533 appears to have 15.4% compared to 10.3% and 8.6% for strains JCM 10692^T and KCTC 13900, respectively. As mentioned above, this higher percentage of proteins in the L category for strain ACA-DC 1533 was also evident in the comparison of all species within the *L. salivarius* clade (**Figure 2**). This difference may again reflect the fragmented nature of *L. acidipiscis* JCM 10692^T and KCTC 13900 genome assemblies.

COG functional classification of the singletons is shown in **Figure 5**. We could find singletons of the three strains distributed in all COG categories with the majority associated with replication, recombination and repair (L), cell wall/membrane/envelope biogenesis (M), carbohydrate transport and metabolism (G) and transcription (K). The high prevalence of proteins in the L COG category appears again, this time in all three strains, especially strains ACA-DC 1533 and

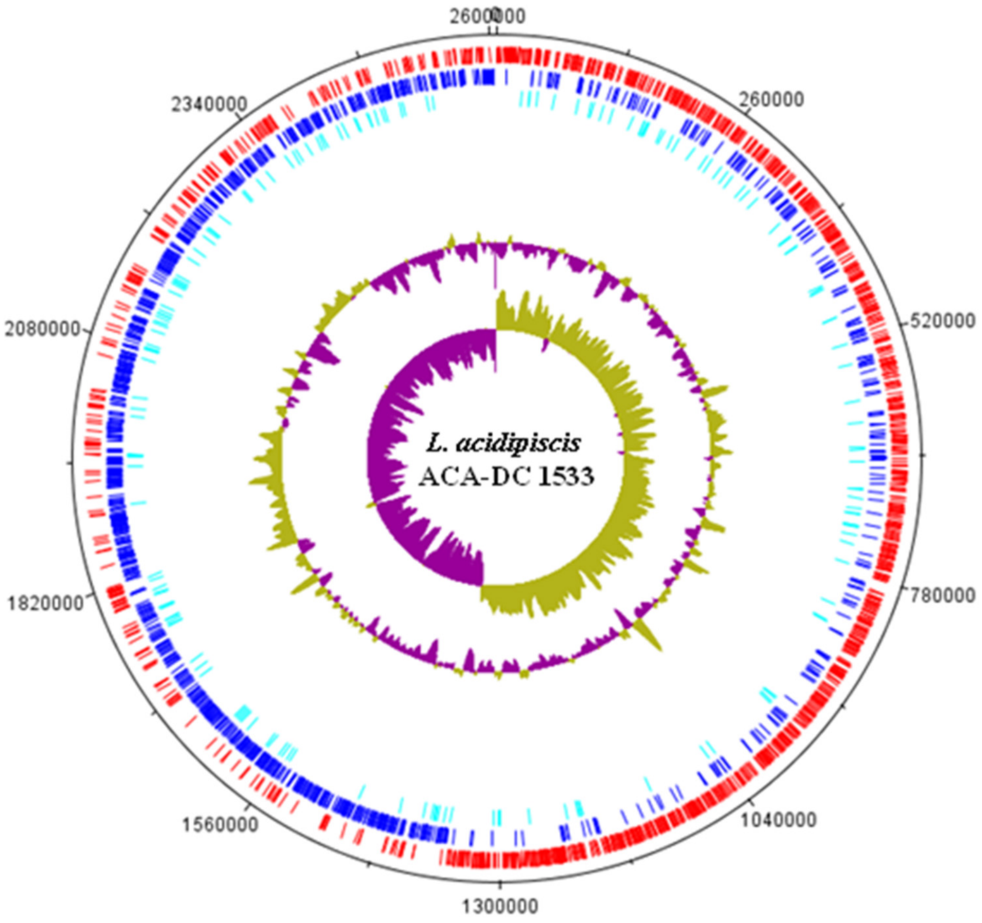

FIGURE 3 | Circular map of the *L. acidipiscis* ACA-DC 1533 chromosome. Labeling from the outside to the inside circle, each ring contains information of the chromosome: CDSs on the forward strand (red); CDSs on the reverse strand (blue); Putative pseudogenes (cyan); tRNA genes (green); rRNA genes (orange); GC content; GC skew.

KCTC 13900. Strain JCM 10692^T appears to have approximately half the singletons in the L COG category, but this may be an artifact deriving from its partial sequence. It is unclear whether genes involved in information storage and processing might have technological implications. It could be suggested though, that the efficiency of central cellular mechanisms like those of the L, M, and K COG categories may provide the strain/species with a competitive advantage in a complex ecosystem. On the contrary, carbohydrate transport and metabolism can have a direct impact on the diversity of ecological niches in which the bacterium can grow.

In Silico Evaluation of Motility of *L. acidipiscis* Strains

From a microbial ecology point of view, motile species may have competitive benefits against non-motile species, regarding e.g., niche colonization and biofilm formation (Neville et al., 2012). Currently, 16 motile *Lactobacillus* species have been recognized in the entire genus, all belonging to the *L. salivarius* clade with the exception of *L. curvatus,* which is a member of the *Lactobacillus sakei* clade (Cousin et al., 2015). Motility of *L. acidipiscis* has been recently described in strain KCTC 13900 revealing that the 54 proteins involved in flagellum regulation, synthesis, export and chemotaxis are organized in a single operon (Cousin et al., 2015). Annotation of ACA-DC 1533 identified 51 motility genes (LAC1533_RS09635-RS09885) producing a functional flagellar apparatus as also observed by *in vivo* experiments (data not shown). Core-genome analysis revealed that the motility operon is also present in strain JCM 10692^T and flanked by the same genes (**Supplementary Table S4B**). As shown in **Figure 6**, alignment of the motility operons of *L. curvatus* NRIC 0822 and *L. acidipiscis* strains KCTC 13900 and ACA-DC 1533 revealed that they are conserved.

GIs Found in *L. acidipiscis* Genomes

HGT is one of the main processes responsible for genome evolution. Genomic fragments acquired by HGT events are characterized as GIs and may have a direct impact on the genome plasticity (Juhas et al., 2009). Here, we focused our analysis in the 13 GIs of the ACA-DC 1533 chromosome identified by

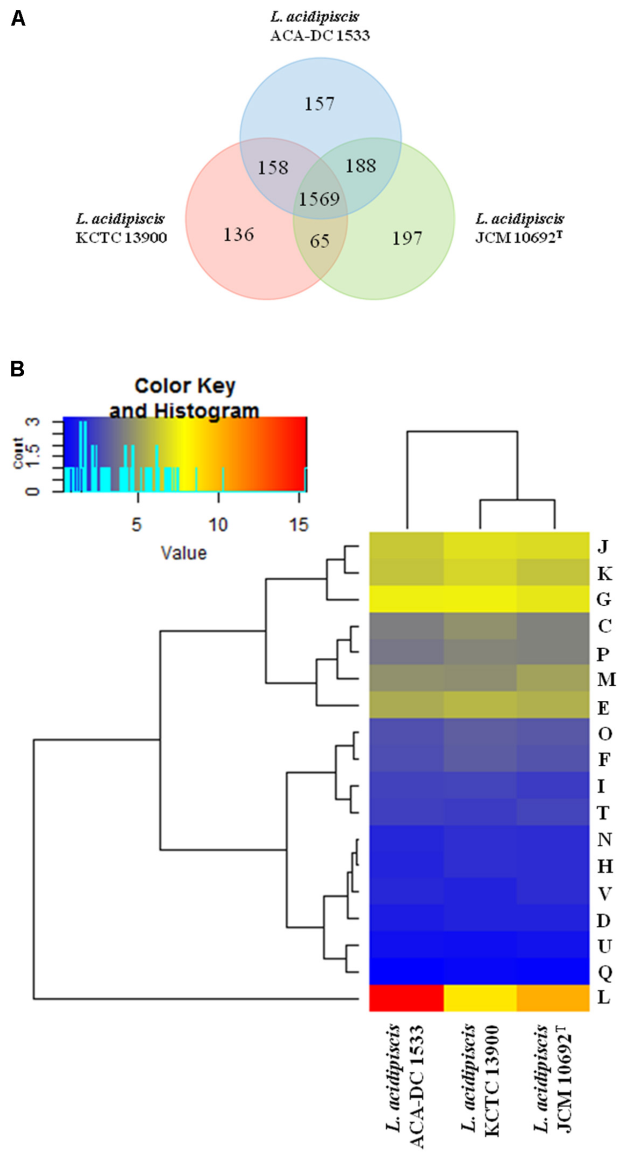

FIGURE 4 | CDS Venn diagram of the three *L. acidipiscis* strains. In the intersection of the three strains we present their total core-genome, in the intersection of each pair of strains we present the corresponding core-genome and finally we present the singleton of each strain all calculated with the EDGAR tool **(A)**. COG frequency heat map based on a two-dimensional hierarchical clustering. The horizontal axis shows the three *L. acidipiscis* strains, namely ACA-DC 1533, KCTC 13900 and JCM 10692^T and the vertical axis the percentage frequency of proteins involved in each functional COG category **(B)**.

the IslandViewer software tool (**Supplementary Figure S2**). Of note, GI 9 contains the genome's array of ribosomal proteins (**Supplementary Table S5**). This is most probably a false positive result, as genes encoding ribosomal proteins have differences in sequence composition compared to regular protein coding genes (Fernández-Gómez et al., 2012) and are thus detected wrongfully by IslandViewer as part of a GI. For this reason, GI 9 was excluded from further analysis. The remaining 12 putative GIs contain a total of 229 genes and the respective lengths ranging from 4,677 to 36,954 bp. Many of these genes are involved in carbohydrate, lipid and amino acid metabolism as well as in membrane transport systems. According to the pan-genome analysis, GIs 3, 7, and 8 are unique for strain ACA-DC 1533 while GIs 1, 4, and 6 are common in all three *L. acidipiscis* strains, indicating acquisition early in the evolution of the species. It is interesting to note that GI 5 is present in strains ACA-DC 1533 and JCM 10692^T but absent in KCTC 13900. Other GIs are shared among the *L. acidipiscis* strains to a variable degree (**Supplementary Table S5**).

Prophage Sequences, CRISPR-Cas Systems, RM Systems and TA Systems of *L. acidipiscis* Strains

PHASTER allowed the identification of one intact (1,228,777-1,272,253 bp, from now on called phage 1) and two incomplete prophage regions (1,575,825-1,586,105 bp and 1,802,666-1,830,756 bp) in the ACA-DC 1533 chromosome. Phage 1 contains 53 CDSs, most of which encode hypothetical proteins (approximately 41.5%). Furthermore, phage tail proteins, capsid proteins and *attL*/*attR* sites flanking the prophage DNA were also identified. Phage 1 is related to several prophages most of which can be found in *Lactobacillus* genomes. Strain JCM 10692^T carries a phage region similar to phage 1 (from now on called phage 2) sharing 30 out of 53 proteins (**Supplementary Table S6A**). Furthermore, strain KCTC 13900 seems to have an intact prophage region (from now on called phage 3) of 40.8 Kbp length related also to *Lactobacillus* phages (**Supplementary Table S6A**).

Three CRISPR sequences (i.e., CRISPR1, 2, and 3) were only identified in strain KCTC 13900 (**Supplementary Table S6B**). BLASTN analysis of all the spacers identified in these three CRISPR-Cas systems showed that several of them, namely spacers 9, 11, 13, 14, 19, 20, and 21 in CRISPR 1 and spacers 5, 14 and 21 in CRISPR 2 had hits in the *Lactobacillus plantarum* virulent phage phiJL-1. Moreover, spacers 22 and 26 in CRISPR 2 had hits in *L. salivarius* plasmids. Since *L. salivarius* strains carrying such plasmids are related to the host environment, this may suggest that *L. acidipiscis* has occupied this niche as well. Most importantly, spacers 1, 3, 5, 6, and 7 in CRISPR 1 and spacer 35 in CRISPR 2 had hits against phage 1 and/or phage 2 genes. Spacers in CRISPRs can reveal aspects of the evolutionary history of their host (Papadimitriou et al., 2014). Thus, it could be hypothesized that strain KCTC 13900 has also been exposed to phage 1 or phage 2 but it was able to acquire immunity through its CRISPR-Cas systems. Our findings may indicate that phages 1 or 2 are abundant in the ecological niches occupied by different *L. acidipiscis* strains or that, despite the different origins of isolation, the three *L. acidipiscis* strains were present in the same ecological niche sometime in the past. Moreover, the presence of phages 1 and 2 in the ACA-DC 1533 and JCM 10692^T genomes, respectively, corroborates with the lack of CRISPR systems in the two strains. However, the presence of prophages in the genomes of *L. acidipiscis* strains may protect them from superinfection by other phages or plasmids (Bondy-Denomy et al., 2016).

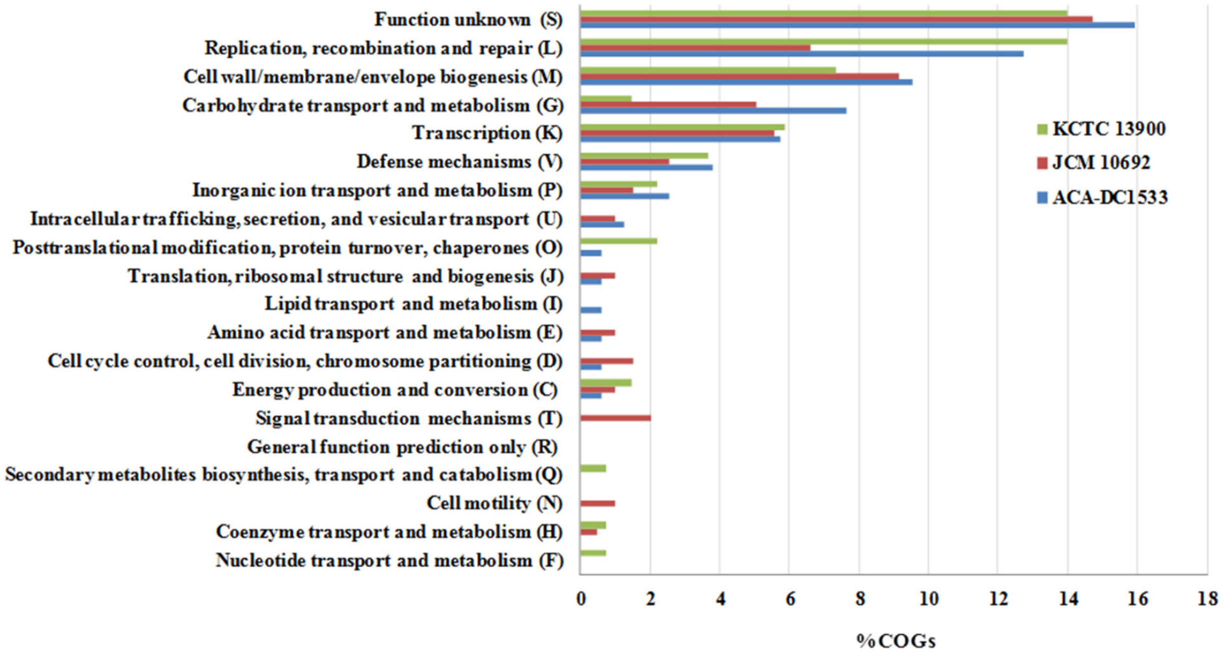

FIGURE 5 | Distribution of singletons in COG functional categories of the three *L. acidipiscis* strains.

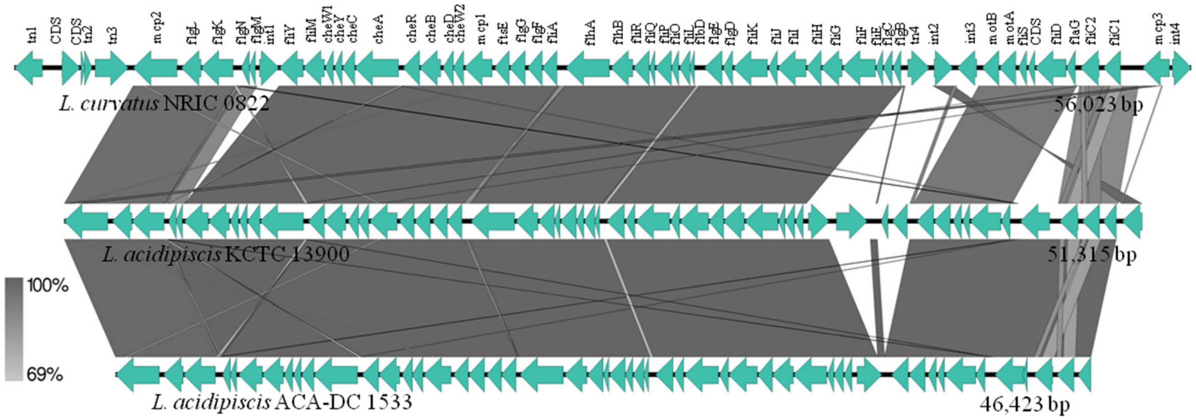

FIGURE 6 | Sequence alignment among the motility gene clusters of *L. curvatus* NRIC 0822, *L. acidipiscis* KCTC 13900 and *L. acidipiscis* ACA-DC 1533. Gray shading corresponds to the % identity of the nucleotide sequences.

Bacterial defense mechanisms against foreign DNA include RM and TA systems (Darmon and Leach, 2014). Strain ACA-DC 1533 has a type I system that seems to be complete, as it contains the DNA-methyltransferase subunit M (LAC1533_RS04765), the specificity subunits S (LAC1533_RS04770) and R (LAC1533_RS04775), as well as a second type I system (LAC1533_RS01110-RS01130) possibly inactivated, since the restriction subunit R is a potential pseudogene (LAC1533_RS01130). According to the REBASE database, the strain also carries three putative type II RM systems (LAC1533_RS03065, LAC1533_RS05790 and LAC1533_RS08450-RS08455) and two type IV RM systems (LAC1533_RS02780 and LAC1533_RS04790) (**Supplementary Figure S3**). Plasmid pLAC3 also carries an *Ava*I RM system. Finally, we looked into TA systems. We concentrated our search on type II TA systems for which TAfinder prediction tool is available. In strain ACA-DC 1533 we found nine TA systems in the chromosome and one in the pLAC2 plasmid (**Supplementary Table S7**).

Comparative Genomics of *L. acidipiscis* Against *L. salivarius* and *L. ruminis*

To further investigate the lifestyle and/or the technological traits of *L. acidipiscis* ACA-DC 1533, we performed comparative genomic analysis against *L. salivarius* UCC118 and *L. ruminis* ATCC 27782. *L. salivarius* UCC118 was chosen as the

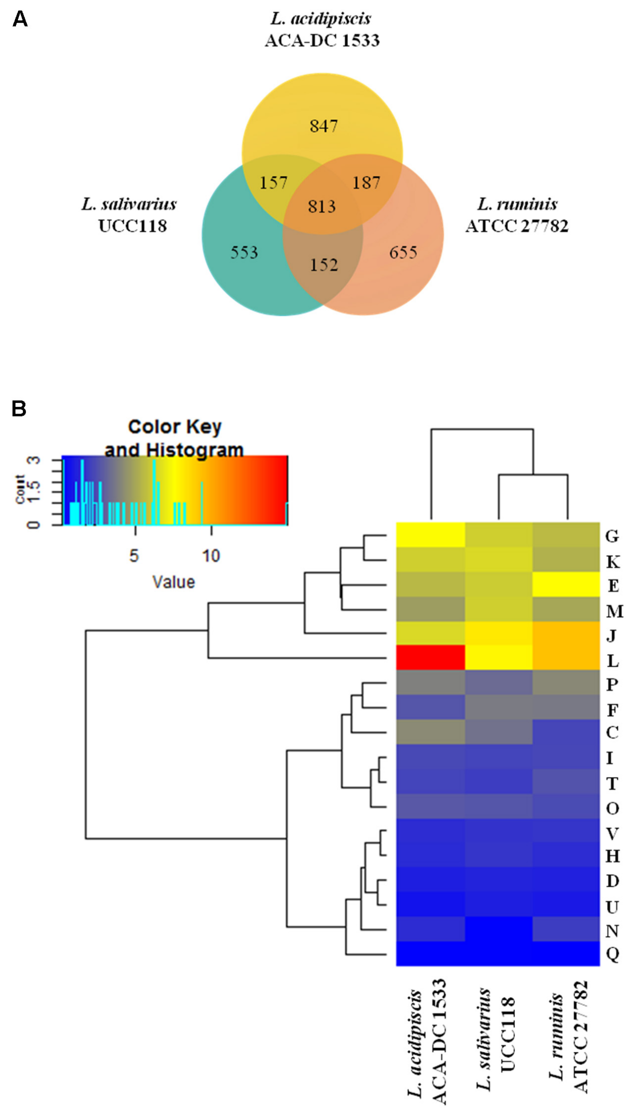

FIGURE 7 | CDS Venn diagram of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 17782. In the intersection of the three strains we present their total core-genome, in the intersection of each pair of strains we present the corresponding core-genome and finally we present the singleton of each strain all calculated with the EDGAR tool **(A)**. COG frequency heat map clustered hierarchically in two dimensions. The vertical axis shows the three genomes. The horizontal axis shows the % frequency of proteins involved in each functional COG category **(B)**.

representative strain of the species since it is the first sequenced and presumably the best characterized strain of the clade (Harris et al., 2017). The comparison was performed initially at the chromosome level since the chromosomes of all three strains are completely sequenced. *L. salivarius* UCC118 was isolated from the human ileal-caecal region and comprises a chromosome of 1.8 Mbp and three plasmids, one of which is a megaplasmid of 242 Kbp (Claesson et al., 2006). *L. ruminis* ATCC 27782 isolated from the bovine rumen has a chromosome size of 2.1 Mbp with no plasmids (Forde et al., 2011). As mention above, *L. acidipiscis* ACA-DC 1533 has a chromosome of 2.6 Mbp, which is the largest among the three species. *L. acidipiscis* ACA-DC 1533 and *L. ruminis* ATCC 27782 exhibited the highest number of potential pseudogenes, i.e., 7.3 and 9.0%, respectively in contrast to the 2.8% of *L. salivarius* UCC188. However, other complete *L. salivarius* chromosomes exhibit a variable percentage of potential pseudogenes, up to 6.6% (**Supplementary Table S8**). Taking this observation into account, it seems that pseudogenes may not be constant among strains of the same species and thus the existence of only one complete chromosomal sequence for *L. acidipiscis* and *L. ruminis* are not enough to comment about their overall genome decay at the species level. Nevertheless, *L. acidipiscis* ACA-DC 1533 and *L. ruminis* ATCC 27782 appear to have undergone genome decay to an extent that is relatively restricted, at least when compared to the genome decay of highly specialized dairy lactobacilli like *L. delbrueckii* subsp. *bulgaricus* (van de Guchte et al., 2006).

Our analysis also revealed that the number of common proteins among the three species is 813, higher than that calculated for the entire *L. salivarius* clade as analyzed above (**Figure 7A** and **Supplementary Table S9A**). *L. acidipiscis* ACA-DC 1533 seems to carry the highest number of unique genes ($n = 847$) mostly encoding hypothetical proteins, transposases, ABC transporters, PEP-PTS and membrane transport proteins (**Supplementary Table S9B**). Similarly to **Figure 4A**, the total number of genes for each strain presented is somewhat lower than the total number of genes annotated for the strain since some genes cannot be assigned neither in the singletons nor in the 3-genome or 2-genome cores for the reason presented above. Furthermore, there is no extensive synteny among the three species as observed during full-length chromosome alignments created by progressiveMAUVE (**Supplementary Figure S4**). The analysis revealed a high number of LCBs with a quite short average length. Several studies based on comparative genomics among *Lactobacillus* species have established the genomic diversity of the *Lactobacillus* genus, which is higher compared to that of a typical bacterial family (Sun Z. et al., 2015; Martino et al., 2016).

The distribution of proteins into the COG functional categories for the three species is shown in **Figure 7B**. As expected, *L. acidipiscis* ACA-DC 1533 chromosome contained more proteins compared to *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 in the L COG category owing to an inflated number of transposases and reverse transcriptases. Inspection of each of the two categories of gene products revealed that they may contain in some instances identical paralogs, but this is not always the case. The biological reason behind this observation is not clear. However, considering that both *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosomes are completely sequenced and that both *L. acidipiscis* ACA-DC 1533 and *L. ruminis* ATCC 27782 are annotated with the same pipeline in RefSeq, the possibility that this difference is some type of artifact is rather unlikely. Another obvious difference was the absence of proteins in the cell motility (N) COG category from the *L. salivarius* UCC118 chromosome. In all other COG categories,

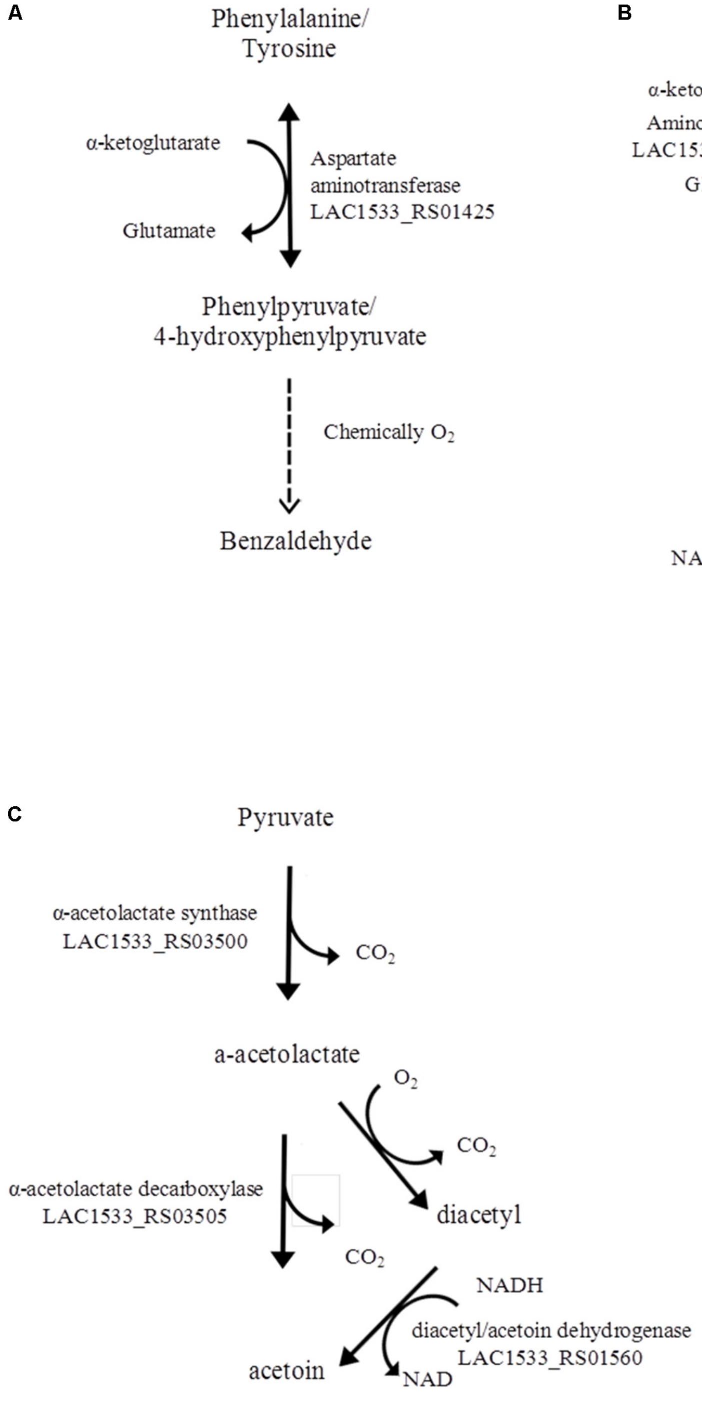

FIGURE 8 | Catabolic pathways of the aromatic amino acids phenylalanine and tyrosine for the production of benzaldehyde **(A)**. Catabolic pathway of the branched chain amino acid leucine for the production of 3-methylbutanol **(B)**. Diacetyl and acetoin synthesis from pyruvate **(C)**.

the distribution of proteins was at a comparable level among the three strains.

We also compared plasmid sequences of *L. acidipiscis* ACA-DC 1533 and *L. salivarius* UCC118. It has been shown for the latter that important housekeeping genes may be carried in its plasmids (Harris et al., 2017). In the case of *L. acidipiscis* plasmids most of the proteins were hypothetical. Nevertheless, we were able to identify some genes encoding proteins that may be important for the physiology, metabolism and/or the technological properties of the strain. For example, we determined the presence of carbohydrate and ion transporters (**Supplementary Table S10**), putative carbohydrate metabolizing enzymes (please see below), and an arsenate reductase. In addition and as mentioned above, plasmids of *L. acidipiscis* ACA-DC 1533 carry an *Ava*I RM system and a type II TA system (**Supplementary Table S7**).

Glycobiome Analysis of *L. acidipiscis*, *L. salivarius*, and *L. ruminis*

The glycobiomes of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 were investigated using dbCAN. According to the analysis, *L. acidipiscis* ACA-DC 1533 had the largest glycobiome with 85 enzymes involved in carbohydrate metabolism, followed by *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 with 78 and 68 enzymes, respectively (**Supplementary Table S11**). Among the 85 enzymes, 37 were identified as GHs, 21 as GTs, 13 as CEs and 14 as CBMs. Compared to the 37 GHs of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 contained 27 and 26 GHs, respectively. Among the GH families identified in the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 genomes, GH 13 was the most pronounced containing mainly enzymes with plant substrate specificity (Crost et al., 2013). Indeed, the carbohydrate fermentation profile of *L. acidipiscis* ACA-DC 1533 using the API 50 CHL stripes (**Supplementary Table S12**) and *L. salivarius* UCC118 (Li et al., 2006) showed that the two strains were able to ferment a number of carbohydrates of plant origin, i.e., L-arabinose, D-ribose, D-cellobiose, D-trehalose, D-glucose, D-fructose, D-mannitol, D-sorbitol, and D-saccharose. Furthermore, several GH families, namely GH 35, GH 38, GH 46, GH 70, and GH 76, were unique for the *L. acidipiscis* ACA-DC 1533 genome indicating that the bacterium presumably requires these enzymes in its ecological niche, which might be different to that of *L. salivarius* UCC118 and *L. ruminis* ATCC 27782. Interestingly, the presence of a beta-galactosidase (GH 35) and two 6-phospho-beta-galactosidase genes (GH 1) in the *L. acidipiscis* ACA-DC 1533 genome could probably be required for growth in milk. *L. acidipiscis* ACA-DC 1533 genome seems to contain also the highest number of CBM modules in family 50 compared to the *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 genomes. CBM 50 modules are commonly found in bacterial lysins having a peptidoglycan binding function and a contribution to cell division (Visweswaran et al., 2013). Similarly to what has been reported previously for *L. salivarius* UCC118 (Harris et al., 2017) and according to our analysis, part of the glycobiome of both *L. salivarius* and *L. acidipiscis* ACA-DC 1533 resides in their plasmids. Specifically for *L. acidipiscis*, we found two GT 4 in plasmid pLAC2. It seems plausible to state that diversity of the plasmid glycobiome in strains of *L. salivarius* is significantly more rich than that of *L. acidipiscis* perhaps due to the presence of the megaplasmid. Moreover, analysis using the TransportDB database identified 47 potential sugar specific PTS transport proteins in the *L. acidipiscis* ACA-DC 1533 genome (3 on pLAC2) and 25 and 16 potential PTS transport proteins for *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 genomes, respectively (**Supplementary Table S10**).

Proteolytic System of *L. acidipiscis*, *L. salivarius*, and *L. ruminis*

The proteolytic system of lactic acid bacteria consists of cell-wall bound proteinases, which initiate the degradation of caseins, peptide and amino acid transport systems and a pool of intracellular peptidases, which further degrade the peptides to shorter peptides and free amino acids (Liu et al., 2010). The proteolytic system of the three *L. acidipiscis* strains, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 was investigated according to the scheme of Liu and co-workers (Liu et al., 2010) (**Supplementary Table S13**). The cell-wall bound proteinase (PrtP), the aminopeptidase A (PepA), the endopeptidases PepE/PepG and the proline peptidase PepL were missing from all strains. It is worth mentioning that PrtP gene is intact in plasmid pR1 of *L. salivarius* strain Ren (Sun E. et al., 2015). The rest of the peptidases were found in up to three copies per genome. Furthermore, *L. acidipiscis* ACA-DC 1533 and *L. ruminis* ATCC 27782 carried one oligopeptide ABC transport system (Opp), which was missing from the *L. salivarius* UCC118 genome. Interestingly, the Opp operon is present in *L. acidipiscis* ACA-DC 1533 and JCM 10692^T but absent in KCTC 13900. On the contrary, a di/tripeptide ABC transport system (Dpp) and a DtpT transporter of di- and tri-peptides were found in the three species (including all three *L. acidipiscis* strains). However, it is worth noting that the DppD protein of *L. acidipiscis* KCTC 13900 is a potential pseudogene inactivating the entire Dpp system which deserves further investigation. Moreover, *L. acidipiscis* ACA-DC 1533 chromosome seems to contain 17 amino acid ABC transport proteins, while *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosomes only 11 and 10, respectively. Even though the five *Lactobacillus* chromosomes and/or genomes carry a number of peptide and amino acid transporters as well as several intracellular peptidases, the absence of PrtP indicates that the strains may not directly hydrolyze large protein molecules, but they may take advantage of peptides and free amino acids already available in their ecological niche.

Miscellaneous Genomic Features Deriving From the Comparison Among *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118, and *L. ruminis* ATCC 27782

We also focused our analysis to IS elements that may contribute in bacterial genome evolution, to transport proteins which allow the transport of the substances in and out of the cell, as well as to RPs that control gene expression.

IS elements of *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 have been previously identified (Claesson et al., 2006) but we have updated the analysis using the latest version of ISsaga and the most recent annotation files for the two strains. In the chromosomes of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782, a total of 53, 10 and 30 IS elements were predicted with ISsaga, respectively (**Supplementary Table S14**). The higher number of IS elements in the chromosome of *L. acidipiscis* ACA-DC 1533 may suggest a higher potential for genome plasticity compared to the *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosome. The majority of IS elements in the *L. acidipiscis* ACA-DC 1533 chromosome belong to the ISL3 and IS982 families which were also previously identified in food related lactobacilli like *Lactobacillus delbrueckii* subsp. *bulgaricus* and *Lactobacillus helveticus*, respectively (Germond et al., 1995; Callanan et al., 2005).

Furthermore, the *L. acidipiscis* ACA-DC 1533 genome contains 287 transport proteins compared to 240 and 238 of *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 genomes, respectively. They mainly belong to the ABC superfamily and to the MFS (**Supplementary Table S10**). Additional analysis of the *L. acidipiscis* ACA-DC 1533 genome revealed 17 potential glycine/betaine transport proteins organized in at least five distinct genomic loci. The glycine/betaine transport system may be necessary to overcome osmotic stress since *L. acidipiscis* is a salt-tolerant species owning strains able to grow in the presence of even 12% NaCl (our unpublished results; Tanasupawat et al., 2000; Romeo et al., 2003; Pot et al., 2014).

RPs include TCSs and TFs. TCSs are the most abundant phosphorylation-dependent signal transduction systems in prokaryotes and typically comprise a membrane-bound HK and a RR (Barakat et al., 2013). On the other hand, TFs contain TRs, OCSs, RRs and SFs. Analysis of *L. acidipiscis* ACA-DC 1533 and *L. salivarius* UCC118 identified six HKs and seven RRs for both strains. Analysis of *L. ruminis* ATCC 27782 chromosome revealed seven HKs and 10 RRs. Furthermore, the *L. acidipiscis* ACA-DC 1533 chromosome contained the highest number of TFs among the three strains analyzed, including 68 TRs, 28 OCSs, five RRs, six SFs and 19 ODPs, most of which were unclassified (**Supplementary Table S15**). The higher number of TFs in the *L. acidipiscis* compared to the other two species may suggest a more intricate regulation of gene expression and perhaps an increased interaction with the environment.

Assessing the Probiotic and Technological Properties of *L. acidipiscis* ACA-DC 1533

Initially, we investigated the probiotic potential of *L. acidipiscis* ACA-DC 1533 based on the available information for *L. salivarius* UCC118 which has been extensively studied as a probiotic strain (Neville and O'Toole, 2010). The *L. salivarius* UCC118 genome contains a bile-salt hydrolase (Claesson et al., 2006) and two EPS clusters associated with the strain's probiotic activity (Harris et al., 2017). These traits were absent from the *L. acidipiscis* ACA-DC 1533 genome. In addition, proteins that may play a role in the interaction of *L. salivarius* UCC118 with the host, may include mucus-, collagen-, salivary agglutinin- and epithelial-binding proteins, as well as enterococcal surface proteins (van Pijkeren et al., 2006; O'Shea et al., 2012). All these proteins are sortase-dependent surface proteins which were either absent from the *L. acidipiscis* ACA-DC 1533 genome or were characterized as potential pseudogenes. The only exception identified was a fibrinogen/fibronectin-binding protein, similar to that of *L. salivarius* UCC118 (Collins et al., 2012) that was also present in the *L. acidipiscis* ACA-DC 1533 genome. Furthermore, analysis of the *L. acidipiscis* ACA-DC 1533 genome with the BAGEL tool did not predict any bacteriocin gene, in contrast to the *L. salivarius* UCC118 genome, which produces the two-component class II bacteriocin Abp118 (Flynn et al., 2002). BAGEL also predicted in *L. acidipiscis* JCM 10692^T three potential structural genes coding for pediocin, sakacin P and carnocin like bacteriocins (the last being a potential pseudogene) and some accessory genes (e.g., immunity, transfer, and maturation) and further experimental testing for their production needs to be performed.

We then investigated aspects of the technological potential of *L. acidipiscis* ACA-DC 1533 taking into account that Asteri and co-workers showed that the major volatile/flavor metabolites produced by this strain when grown in RSM and MRS, were 3-methylbutanal, 3-methylbutanol, benzaldehyde and acetoin (Asteri et al., 2009). The majority of the aforementioned metabolites produced by *L. acidipiscis* ACA-DC 1533 are degradation products of amino acids (**Figure 8**). In particular, benzaldehyde can be formed from two aromatic amino acids, namely phenylalanine and tyrosine, using an enzymatic and a non-enzymatic step (Nierop Groot and de Bont, 1998; Fernandez and Zuniga, 2006). Moreover, 3-methylbutanal and 3-methylbutanol are catabolic products of the branched-chain amino acid leucine (Fernandez and Zuniga, 2006). The α-ketoacid decarboxylase and the alcohol dehydrogenase involved in the leucine catabolism pathway were found to be present in the three *L. acidipiscis* genomes but absent from *L. salivarius* UCC118 and *L. ruminis* ATCC 27782. On the contrary, aspartate aminotransferase, which catalyzes the transamination of phenylalanine and tyrosine, was present in all the *Lactobacillus* genomes analyzed. Many studies have been shown that the amino acid degradation products, especially those deriving from the branched-chain, aromatic and sulfur-containing amino acids, are regarded as significant flavor compounds in several cheese varieties (Ardö, 2006; Liu et al., 2008; Afzal et al., 2017). Furthermore, acetoin, which was produced by *L. acidipiscis* ACA-DC 1533, can be formed from pyruvate using two alternative pathways. Pyruvate, which derives from glycolysis, is converted into a-acetolactate by α-acetolactate synthase (LAC1533_RS03500). α-Acetolactate is then catabolized either to acetoin by α-acetolactate decarboxylase (LAC1533_RS03505) or to diacetyl in the presence of oxygen. Finally, diacetyl/acetoin dehydrogenase (LAC1533_RS01560) catalyzes the conversion of diacetyl to acetoin (Celinska and Grajek, 2009). It should be mentioned that diacetyl was not detected as a volatile metabolite of *L. acidipiscis* ACA-DC 1533 in the work of Asteri et al. (2009). However, the presence of diacetyl/acetoin dehydrogenase in the ACA-DC 1533 genome could probably mean that by the time of sampling diacetyl was fully converted into acetoin. Given that *L. acidipiscis* ACA-DC 1533, along with *L. rennini,* were the only species found in Kopanisti cheese, the production of the above mentioned metabolites by *L. acidipiscis* ACA-DC 1533 *via* amino acid catabolism may contribute to the characteristic piquant flavor of Kopanisti cheese (Yvon and Rijnen, 2001; Asteri et al., 2009; Donnelly, 2016).

CONCLUSION

The *L. salivarius* clade includes mainly commensal species and it has been suggested that several strains may have probiotic properties (Neville and O'Toole, 2010). In this study, we analyzed the available genomes of *L. acidipiscis*, a species within the *L. salivarius* clade that until today has mainly been isolated from fermented foods of dairy or other origin. We wanted to examine whether *L. acidipiscis* is also a commensal that is transferred to the ecosystem of fermented foods accidentally from the host. Furthermore, we wanted to investigate the probiotic and/or the technological potential of the species. We sequenced the genome of strain ACA-DC 1533, originally isolated from Kopanisti, a traditional spread-type cheese that is highly salted and particularly piquant (Kazou et al., 2017). Our investigation suggested that *L. acidipiscis* has a relatively large genome compared to other species of the *L. salivarius* clade (at least those of *L. salivarius* and *L. ruminis*) with a relatively restricted percentage of pseudogenes. These findings along with the observation that *L. acidipiscis* possesses a high number of glycobiome enzymes may indicate an ability to occupy versatile environments and has not been evolved toward a specific ecological niche. Perhaps, adaptation to a nutrient-rich niche would have been more consistent with a smaller genome size, more typically like that of *L. salivarius*. Interestingly, *L. acidipiscis* strains ACA-DC 1533 and JCM 10692^T appear to be more related compared to strain KCTC 13900 based on the presence/absence distribution of a number of genetic traits like prophages and CRISPRs. *L. acidipiscis* ACA-DC 1533 does not seem to present any evident probiotic trait at the genomic level. Besides the absence of several genes that have been related to probiotic properties of *L. salivarius* UCC118 preliminary experiments with strain *L. acidipiscis* ACA-DC 1533 on human PBMCs did not reveal an increased interleucine-10/interleucine-12 ratio, indicative of a potential to stimulate a Treg response (our unpublished results). Some probiotic properties have been suggested for specific *L. acidipiscis* strains like an antiproliferative effect against Caco-2 cells (Thamacharoensuk et al., 2017) or the improvement of feed conversion efficiency in broiler chickens (Altaher et al., 2015). Thus, further *in silico* and/or experimental assessment of the probiotic properties of *L. acidipiscis* may be required. In addition, *L. acidipiscis* is able to grow in the dairy environment since it can ferment lactose, it possesses a complete proteolytic system for the degradation of milk proteins (without carrying a cell-envelope proteinase) and it can produce volatile compounds during the catabolism of amino acids that may contribute to the flavor of the final product. Intriguingly, *L. acidipiscis* is also considered a spoiler in vinegar and soy sauce. For this reason, technological steps to prohibit its growth in certain fermented foods need to be devised. Further research is needed with different species of the *L. salivarius* clade like the newly sequenced *Lactobacillus agilis* to better appreciate the mechanisms underlining the adaptation to the host and/or the food environment. Sequencing of more strains/species would provide invaluable information about the ecology of this important clade within the *Lactobacillus* genus.

AUTHOR CONTRIBUTIONS

MK and VA performed genome analysis and participated in the writing of the manuscript. JB and BP performed genome analysis. ET conceived the project and participated in the writing of the manuscript. KP conceived the project, performed genome analysis, and participated in the writing of the manuscript. All authors read and approved the final manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fmicb.2018.01244/full#supplementary-material

FIGURE S1 | Heat map of ANI values among the five sequenced *L. acidipiscis* strains.

FIGURE S2 | Circular map of the *L. acidipiscis* ACA-DC 1533 chromosome as generated by IslandViewer 4. Highlighted regions correspond to GIs. GIs are colored within the circular map according to the prediction method used: GIs in orange were predicted with SIGI-HMM, GIs in blue with IslandPath-DIMOB and the integrated GIs are presented on the periphery in red. The black line plot corresponds to the GC content (%) of the chromosomal sequence.

FIGURE S3 | Circular map of the *L. acidipiscis* ACA-DC 1533 chromosome highlighting the predicted RM systems by the REBASE database. The symbols are color coded as indicated at the bottom of the figure.

FIGURE S4 | Chromosome alignments among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 strains generated by progressiveMAUVE. Locally collinear blocks (LCBs) of conserved sequences are presented by the same color (white corresponds to the strain-specific regions).

TABLE S1 | General information of the strains analyzed in this study.

TABLE S2 | Level of completeness among the four *L. acidipiscis* strains as calculated by dBBQs.

TABLE S3 | Pseudogenes identified in the *L. acidipiscis* ACA-DC 1533 chromosome.

TABLE S4 | (A) Pan-genome analysis among the three *L. acidipiscis* strains calculated with the EDGAR software. **(B)** Core-genome among the three *L. acidipiscis* strains calculated with the EDGAR software. **(C)** Singletons of the three *L. acidipiscis* strains calculated with the EDGAR software.

TABLE S5 | Genes within genomic islands of *L. acidipiscis* ACA-DC 1533. Common genes within the rest of *L. acidipiscis* strains were predicted from the pan-genome analysis with the EDGAR software.

TABLE S6 | (A) Prophage regions identified in the three *L. acidipiscis* strains using the PHASTER software. **(B)** CRISPR systems identified in the *L. acidipiscis* KCTC 13900 genome using the CRISPRFinder tool.

TABLE S7 | TA systems predicted in the chromosome and pLAC2 plasmid of *L. acidipiscis* ACA-DC 1533 genome.

TABLE S8 | Percentage of potential pseudogenes identified in the chromosomes of the completed sequenced genomes of *L. salivarius* clade.

TABLE S9 | (A) Core-genome among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosomes as calculated with the EDGAR software. **(B)** Singletons among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosomes as calculated with the EDGAR software.

TABLE S10 | Transporters of *L. acidipiscis* ACA-DC 1533 chromosome and pLAC2 plasmid identified by TransportDB.

TABLE S11 | Putative enzymes involved in carbohydrate metabolism of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118, and *L. ruminis* ATCC 27782 chromosomes.

TABLE S12 | Acid production by *L. acidipiscis* ACA-DC 1533 using API 50CHL stripes.

TABLE S13 | The proteolytic system of *L. acidipiscis*, *L. salivarius*, and *L. ruminis* chromosomes and/or genomes.

TABLE S14 | Insertion sequences (ISs) identified among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118, and *L. ruminis* ATCC 27782 chromosomes using the ISsaga platform.

TABLE S15 | Regulatory proteins identified in the chromosomes of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118, and *L. ruminis* ATCC 27782 using P2RP web server.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

CHAPTER 7

Concluding remarks and future perspectives

During the last decades, developments in sequencing technologies and bioinformatics tools have had a profound impact on better understanding microbial ecosystems as well as the functionalities of their members. The genus *Lactobacillus* is the largest and most diverse among LAB genera with significant importance in the food and feed industry as well as in health-related applications. The increasing number of *Lactobacillus* genome sequences available in public databases can provide enormous insights into the biology of this important group of microorganisms.

The present thesis aimed at providing a genetic overview of three “wild” LAB strains, namely *L. zymae* ACA-DC 3411, *L. rennini* ACA-DC 565 and *L. acidipiscis* ACA-DC 1533, isolated from naturally fermented Greek food products. A combination of high-throughput sequencing techniques and whole-genome optical mapping resulted in the first completely sequenced chromosomal assembly for each of the respective species. Additionally, a plethora of bioinformatic tools was used for genome annotation and functional annotation of protein-coding genes.

Analysis of *L. zymae* ACA-DC 3411 and *L. rennini* ACA-DC 565 was limited to their basic genomic features. Nevertheless, important genomic traits and defense mechanisms, were identified in both chromosomal sequences. Future research, which will focus on more extensive analysis of these strains in combination with comparative genomics among closely related species/strains, may reveal technological properties that render them as suitable starter or adjunct cultures in fermented food products.

Analysis of *L. acidipiscis* ACA-DC 1533 revealed that the strain has not been evolved towards a specific ecological niche, although a relatively restricted genome decay was occurred. Furthermore, the existence of one intact prophage sequence in its chromosome indicated the exposure of strain to foreign DNA. Nevertheless, we identified several defence mechanisms although some of them seemed to be inactive due to potential pseudogenes. In addition, strain ACA-DC 1533 does not seem to present any evident probiotic trait. However, since probiotic properties have been suggested for some *L. acidipiscis* strains, further *in silico* and/or *in vitro* and *in vivo* assessment of the probiotic potential of the species may be required. Most importantly, the technological potential of strain ACA-DC 1533 may render it as a promising adjunct culture in the production of dairy products.

In general, whole-genome sequencing of more LAB strains of different species is required so as to perform more extended and reliable genomic analyses, including comparative genomics, which could provide valuable information on the technological and probiotic potential of this important group of microorganisms. Genomics of LAB, can establish the genetic landscape along with genetic criteria for strain selection, improve culture stability by stress preconditioning, provide opportunities for metabolic engineering, elucidate genomic features, such as bacterial evolution, adaptation and pathogenicity, and uncover a mechanistic basis for the beneficial activities of probiotics when delivered in various foods.

In this perspective, optimization of sequencing technologies and development of new bioinformatic tools are expected to contribute as well and facilitate bridging the gap among food, health and medicine fields. However, the major challenge, remains to pursue unlocking the correlation between genotype and phenotype.

APPENDIX

Supplementary Material for the article
Kazou M., Alexandraki V., Blom J., Pot B., Tsakalidou E., Papadimitriou K. (2018) Comparative genomics of *Lactobacillus acidipiscis* ACA-DC 1533 isolated from traditional Greek Kopanisti cheese against species within the *Lactobacillus salivarius* clade. *Front Microbiol, 9(1244) doi: 10.3389/fmicb.2018.01244*
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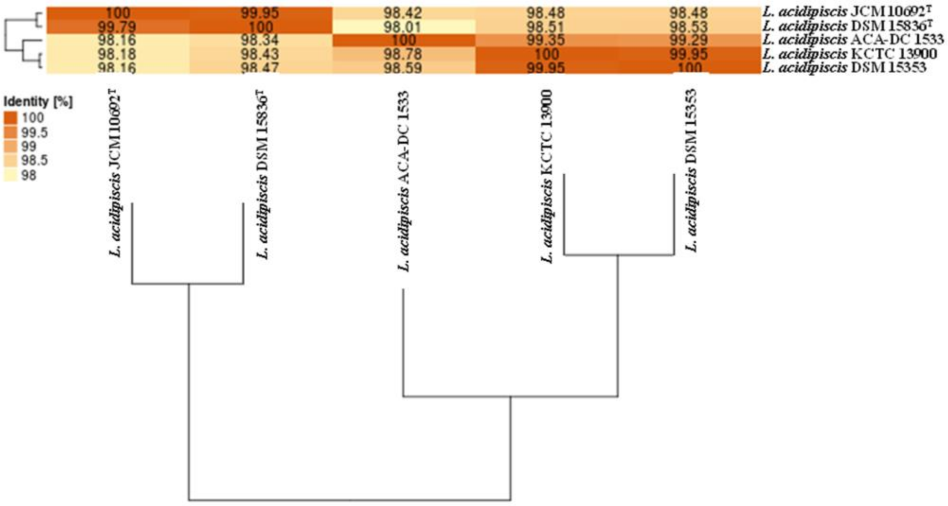
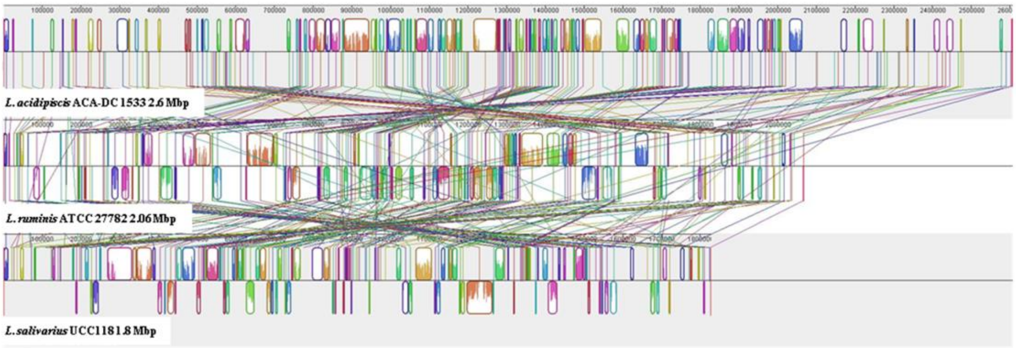


Supplementary figure 1. Heat map of ANI values among the five sequenced *L. acidipiscis* strains.



Supplementary figure 2. Chromosome alignments among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 strains generated by progressiveMAUVE. Locally collinear blocks (LCBs) of conserved sequences are presented by the same color (white corresponds to the strain-specific regions).

Supplementary table S1. General information of the strains analyzed in this study.

Strains	Plasmids	NCBI Reference Sequence	Sequencing technology***	Update Date	Link	Assemby Software****	Annotation Software*****	RefSeq Release
Lactobacillus agilis DSM 20509		NZ_AYYP00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYYP00000000.1?report=girevhist	Canu v. 1/6/2016	NCBI PGAP 4.1	86
Lactobacillus acidipiscis ACA-DC 1533		NZ_LT630287.1	Illumina HiSeq 2000; PacBio RS II	18-MAR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_LT630287.1?report=girevhist	SOAPdenovo v. 2.04	NCBI PGAP 4.1	86
Lactobacillus acidipiscis ACA-DC 1533	pLAC1	NC_014164.1*	ABI	17-DEC-2014	https://www.ncbi.nlm.nih.gov/nuccore/NC_014164.1?report=girevhist	CAP3	GeneMark,FGENESB,MetaGeneAnnotator	86
Lactobacillus acidipiscis ACA-DC 1533	pLAC2	LT996085.1**	Illumina HiSeq 2000; PacBio RS II	13-APR-2018	https://www.ncbi.nlm.nih.gov/nuccore/LT996085.1?report=girevhist	SOAPdenovo v. 2.04	RAST, Prodigal, MetaGeneAnnotator, FGENESB	-
Lactobacillus acidipiscis ACA-DC 1533	pLAC3	LT992335.1**	Illumina HiSeq 2000; PacBio RS II	28-MAR-2018	https://www.ncbi.nlm.nih.gov/nuccore/LT992335.1?report=girevhist	SOAPdenovo v. 2.04	RAST, Prodigal, MetaGeneAnnotator, FGENESB	-
Lactobacillus acidipiscis DSM 15836		NZ_AZFI00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZFI00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus acidipiscis JCM 10692		NZ_BDQH00000000.1	Illumina MiSeq	06-MAY-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_BDQH00000000.1?report=girevhist	Platanus_B v. 1.1.0	NCBI PGAP 4.1	86
Lactobacillus acidipiscis KCTC 13900		NZ_BACS00000000.1	Roche 454	07-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_BACS00000000.1?report=girevhist	Newbler v. 2.3	NCBI PGAP 4.1	86
Lactobacillus acidipiscis DSM 15353		NZ_JQBK00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_JQBK00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus animalis DSM 20602		NZ_AYYW00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYYW00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus apodemi DSM 16634		NZ_AZFT00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZFT00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus aquaticus DSM 21051		NZ_AYZD00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYZD00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus aviarius subsp. *aviarius* DSM 20655		NZ_AYZA00000000.1	Illumina MiSeq; Illumina HiSeq	04-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYZA00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus aviarius subsp. *araffinosus* DSM 20653		NZ_AYYZ00000000.1	Illumina MiSeq; Illumina HiSeq	04-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYYZ00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus cacaonum DSM 21116		NZ_AYZE00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYZE00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus capillatus DSM 19910		NZ_AZEF00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZEF00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus ceti DSM 22408		NZ_AUHP00000000.1	Illumina HiSeq 2000	08-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AUHP00000000.1?report=girevhist	Unknown program v. before 2013-03-07	NCBI PGAP 4.1	86
Lactobacillus equi DSM 15833		NZ_AZFH00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZFH00000000.1?report=girevhist	Newbler v. 2.8	NCBI PGAP 4.1	86
Lactobacillus ghanensis DSM 18630		NZ_AZGB00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZGB00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus hayakitensis DSM 18933		NZ_AZGD00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZGD00000000.1?report=girevhist	Newbler v. 2.8	NCBI PGAP 4.1	86
Lactobacillus hordei DSM 19519		NZ_AZDX00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZDX00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus mali DSM 20444		NZ_AYYH00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYYH00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus murinus DSM 20452		NZ_AYYN00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYYN00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus nagelii DSM 13675		NZ_AZEV00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZEV00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus oeni DSM 19972		NZ_AZEH00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZEH00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus pobuzihii NBRC 103219		NZ_JQCN00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_JQCN00000000.1?report=girevhist	Velvet v. JUN-2012	NCBI PGAP 4.1	86
Lactobacillus ruminis ATCC 27780		NZ_JHAJ00000000.1	Illumina HiSeq	03-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_JHAJ00000000.1?report=girevhist	Velvet v. 1.2.07	NCBI PGAP 4.1	86
Lactobacillus ruminis ATCC 27782		NC_015975.1	454; Illumina	10-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NC_015975.1?report=girevhist	Roche/454 Life Sciences Newbler and Mira	NCBI PGAP 4.1	86
Lactobacillus saerimneri DSM 16049		NZ_AUHQ00000000.1	Illumina HiSeq 2000	08-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AUHQ00000000.1?report=girevhist	Unknown program v. before 2013-04-18	NCBI PGAP 4.1	86
Lactobacillus salivarius DSM 20555		NZ_ACGT00000000.1	454; ABI; Solexa/Illumina	10-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_ACGT00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus salivarius UCC118		NC_007929.1	Sanger	03-AUG-2016	https://www.ncbi.nlm.nih.gov/nuccore/NC_007929.1?report=girevhist	-	NCBI PGAP 3.x	86
Lactobacillus satsumensis DSM 16230		NZ_AZFQ00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZFQ00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus sucicola DSM 21376		NZ_AYZF00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYZF00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus uvarum DSM 19971		NZ_AZEG00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AZEG00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus vini DSM 20605		NZ_AYYX00000000.1	Illumina MiSeq; Illumina HiSeq	11-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_AYYX00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Weissella kandleri DSM 20593		NZ_JQBP00000000.1	Illumina MiSeq; Illumina HiSeq	16-APR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NZ_JQBP00000000.1?report=girevhist	SOAPdenovo v. 2	NCBI PGAP 4.1	86
Lactobacillus delbrueckii subsp. *bulgaricus* DSM 20081		NC_008054.1	Illumina MiSeq; Illumina HiSeq	30-MAR-2017	https://www.ncbi.nlm.nih.gov/nuccore/NC_008054.1?report=girevhist	PHRED/PHRAP/CONSED	NCBI PGAP 4.1	86

*Plasmid pLAC1 also appears with accession number FN667595.1 in GenBank as part of the genome of *Lactobacillus acidipiscis* ACA-DC 1533 (BioProject: PRJEB17511). For the analysis presented in this manuscript the RefSeq annotation was used.

**not in RefSeq

***Not all sequences are accompanied by Sequence Read Archive (SRA) data

****Assembly software as presented in the GenBank assembly record or the relevant paper describing the specified sequence

*****Annotation software as presented in the GenBank file or the relevant paper describing the specified sequence

Supplementary table S2. Level of completeness among the four *L. acidipiscis* strains as calculated by dBBQs.

Strains	**Genome Quality Score**	**Sequence Score**	**rRNA Score**	**tRNA Score**	**Essential Gene Score**
L. acidipiscis KCTC 13900	0.7	0.32	0.6	0.9	1
L. acidipiscis DSM 15353	0.55	0.4	0	0.8	1
L. acidipiscis JCM 10692	0.5	0.41	0.6	1	0
L. acidipiscis DSM 15836	0.38	0.34	0.6	0.6	0

Supplementary table S3. Pseudogenes identified in the *L. acidipiscis* ACA-DC 1533 chromosome.

locus_tag	**start**	**stop**	**annotated function**	**pseudogene type**
LAC1533_RS00135	29053	29259	hypothetical protein	internal stop
LAC1533_RS00175	37845	38265	hypothetical protein	frameshifted
LAC1533_RS00180	<38229	38480	IS200/IS605 family transposase	internal stop and incomplete
LAC1533_RS00235	46786	47757	malate permease	internal stop
LAC1533_RS00320	66569	67879	IS1380 family transposase	internal stop
LAC1533_RS00445	94202	>94414	homoserine dehydrogenase	incomplete
LAC1533_RS00515	109146	>110441	ISL3 family transposase	incomplete
LAC1533_RS00525	111857	112063	hypothetical protein	internal stop
LAC1533_RS00575	123557	123763	hypothetical protein	internal stop
LAC1533_RS00615	135024	136342	Uric acid permease PucJ	frameshifted
LAC1533_RS00745	158652	159895	hypothetical protein	frameshifted
LAC1533_RS00805	172750	>172896	GNAT family N-acetyltransferase	incomplete
LAC1533_RS00810	173009	>173488	transposase	incomplete
LAC1533_RS00820	<175083	175853	transposase	incomplete
LAC1533_RS00830	176631	177008	GNAT family N-acetyltransferase	internal stop
LAC1533_RS00835	177280	177868	site-specific integrase	frameshifted
LAC1533_RS00910	<194544	194810	PTS lactose transporter subunit IIC	frameshifted and incomplete
LAC1533_RS00935	197264	198573	IS1380 family transposase	frameshifted
LAC1533_RS00985	208421	208990	hypothetical protein	internal stop
LAC1533_RS01035	216689	>216870	hypothetical protein	frameshifted and incomplete
LAC1533_RS01130	235903	>238401	DEAD/DEAH box helicase	incomplete
LAC1533_RS01205	253716	255026	IS1380 family transposase	internal stop
LAC1533_RS01225	259583	260893	IS1380 family transposase	internal stop
LAC1533_RS01275	273025	275678	magnesium-transporting ATPase	frameshifted
LAC1533_RS01315	283043	283554	protease	frameshifted
LAC1533_RS01355	289973	290343	hypothetical protein	frameshifted
LAC1533_RS01435	306873	308972	Na+/H+ antiporter	internal stop
LAC1533_RS01460	314071	314277	hypothetical protein	internal stop
LAC1533_RS01525	327491	328677	hypothetical protein	frameshifted
LAC1533_RS01715	365536	>365733	hypothetical protein	incomplete
LAC1533_RS01795	383116	384221	di- and tricarboxylate transporter	frameshifted
LAC1533_RS01805	385119	>386470	hypothetical protein	frameshifted and incomplete
LAC1533_RS01855	396439	397595	MFS transporter	frameshifted
LAC1533_RS01860	397610	398384	IS5/IS1182 family transposase	frameshifted
LAC1533_RS02075	449726	450549	PTS mannose transporter subunit IID	frameshifted
LAC1533_RS02085	452587	452793	hypothetical protein	internal stop
LAC1533_RS02095	454387	>455034	hypothetical protein	incomplete
LAC1533_RS02235	489154	489360	hypothetical protein	internal stop
LAC1533_RS02240	489309	490694	group II intron reverse transcriptase/maturase	internal stop
LAC1533_RS02375	521638	522036	hypothetical protein	internal stop
LAC1533_RS02470	544648	545150	O-acetyl-ADP-ribose deacetylase	frameshifted
LAC1533_RS02650	587406	588783	cell wall anchor protein	frameshifted and internal stop
LAC1533_RS02755	611491	612675	amidohydrolase	internal stop
LAC1533_RS02875	<639655	640458	LytR family transcriptional regulator	internal stop and incomplete
LAC1533_RS02880	640559	>641521	oxidoreductase	incomplete
LAC1533_RS02895	<642684	643698	peptidase M13	frameshifted and incomplete
LAC1533_RS02965	656378	659169	haloacid dehalogenase	frameshifted
LAC1533_RS03090	687171	688136	alcohol dehydrogenase AdhP	frameshifted
LAC1533_RS03095	688636	689813	IS256 family transposase	frameshifted
LAC1533_RS03125	698119	699057	ABC transporter ATP-binding protein	internal stop
LAC1533_RS03185	709747	711093	PTS cellobiose transporter subunit IIC	internal stop
LAC1533_RS03210	715677	716236	ECF transporter S component	frameshifted
LAC1533_RS03215	716243	717966	heme ABC transporter ATP-binding protein	frameshifted and internal stop
LAC1533_RS03270	728814	729020	hypothetical protein	internal stop
LAC1533_RS03280	729554	730329	IS5/IS1182 family transposase	frameshifted
LAC1533_RS03290	731531	732318	hypothetical protein	frameshifted
LAC1533_RS03320	739573	740348	IS5/IS1182 family transposase	frameshifted
LAC1533_RS03370	750678	750884	hypothetical protein	internal stop
LAC1533_RS03480	772276	773582	IS1380 family transposase	frameshifted

LAC1533_RS03695	821398	821604	hypothetical protein	internal stop
LAC1533_RS03775	840948	841154	hypothetical protein	internal stop
LAC1533_RS03790	<842862	844157	ISL3 family transposase	incomplete
LAC1533_RS04275	945708	945914	hypothetical protein	internal stop
LAC1533_RS04285	<947330	948625	ISL3 family transposase	incomplete
LAC1533_RS04305	952393	>953688	ISL3 family transposase	incomplete
LAC1533_RS04315	955104	955310	hypothetical protein	internal stop
LAC1533_RS04800	1038634	1039810	IS256 family transposase	frameshifted
LAC1533_RS04850	1048334	1048540	hypothetical protein	internal stop
LAC1533_RS05185	1122987	1123193	hypothetical protein	internal stop
LAC1533_RS05560	1204915	1205121	hypothetical protein	internal stop
LAC1533_RS05570	<120653	7 1207832	ISL3 family transposase	incomplete
LAC1533_RS05580	1208752	1210051	IS1380 family transposase	frameshifted
LAC1533_RS05585	1210260	1211450	hypothetical protein	internal stop
LAC1533_RS05640	1223035	1223241	hypothetical protein	internal stop
LAC1533_RS05915	1265950	>1266807	hypothetical protein	incomplete
LAC1533_RS06060	1298636	1298842	hypothetical protein	internal stop
LAC1533_RS06065	1298791	1300175	group II intron reverse transcriptase/maturase	frameshifted
LAC1533_RS06070	<130025	7 1301552	ISL3 family transposase	incomplete
LAC1533_RS06085	1306725	1306931	hypothetical protein	internal stop
LAC1533_RS06305	1355289	1356385	NADH-dependent flavin oxidoreductase	frameshifted
LAC1533_RS06345	1362838	1363531	noncanonical pyrimidine nucleotidase, YjjG family	frameshifted and internal stop
LAC1533_RS06380	1369650	1370975	orotidine 5-phosphate decarboxylase	internal stop
LAC1533_RS06390	1371961	1375148	carbamoyl phosphate synthase large subunit	frameshifted
LAC1533_RS06405	1377530	1378479	aspartate carbamoyltransferase	frameshifted
LAC1533_RS06450	1387078	1387284	hypothetical protein	internal stop
LAC1533_RS06575	1414217	1414423	hypothetical protein	internal stop
LAC1533_RS06820	1461785	1464011	polyribonucleotide nucleotidyltransferase	frameshifted
LAC1533_RS07230	1551687	1551893	hypothetical protein	internal stop
LAC1533_RS07250	1556064	1556443	hypothetical protein	frameshifted
LAC1533_RS07285	1562213	1562517	addiction module toxin RelE	frameshifted
LAC1533_RS07315	<156554	9 1565656	hypothetical protein	incomplete
LAC1533_RS07415	1580713	>1581795	IS256 family transposase	incomplete
LAC1533_RS07430	<158394	7 1584045	transposase	incomplete
LAC1533_RS07580	1611204	1611410	hypothetical protein	internal stop
LAC1533_RS07630	1622205	>1623500	ISL3 family transposase	incomplete
LAC1533_RS07640	1624915	1625121	hypothetical protein	internal stop
LAC1533_RS07650	1626806	1627012	hypothetical protein	internal stop
LAC1533_RS07680	1629811	>1631106	ISL3 family transposase	incomplete
LAC1533_RS07690	1632522	1632728	hypothetical protein	internal stop
LAC1533_RS07960	1690320	1690526	hypothetical protein	internal stop
LAC1533_RS08000	1699645	1700312	dithiol-disulfide isomerase	frameshifted
LAC1533_RS08055	1710977	1712107	hypothetical protein	frameshifted and internal stop
LAC1533_RS08305	1758032	1759417	group II intron reverse transcriptase/maturase	internal stop
LAC1533_RS08310	1759366	1759572	hypothetical protein	internal stop
LAC1533_RS08325	1762236	>1763531	ISL3 family transposase	incomplete
LAC1533_RS08335	1764947	1765153	hypothetical protein	internal stop
LAC1533_RS08345	1766838	1767044	hypothetical protein	internal stop
LAC1533_RS08410	<178030	0 1780509	transposase	incomplete
LAC1533_RS08420	1780881	1782266	group II intron reverse transcriptase/maturase	internal stop
LAC1533_RS08425	1782215	1782421	hypothetical protein	internal stop
LAC1533_RS08485	1796209	1797347	nuclease	frameshifted
LAC1533_RS08495	1797956	1799890	hypothetical protein	internal stop
LAC1533_RS08515	1803098	1804440	DEAD/DEAH box helicase	frameshifted and internal stop
LAC1533_RS08570	1813214	1814413	phage portal protein	internal stop
LAC1533_RS08610	1818592	1820250	serine recombinase	internal stop
LAC1533_RS09070	1903055	1903261	hypothetical protein	internal stop
LAC1533_RS09265	1945264	1946913	peptide ABC transporter substrate-binding protein	internal stop
LAC1533_RS09315	1955906	1956112	hypothetical protein	internal stop
LAC1533_RS09325	<1958074	1958388	transposase	incomplete
LAC1533_RS09330	1958378	1958559	hypothetical protein	frameshifted
LAC1533_RS09340	1959171	>1959416	hypothetical protein	incomplete
LAC1533_RS09530	2003013	2003677	methionine ABC transporter permease	frameshifted
LAC1533_RS09570	2011831	2012665	sugar ABC transporter permease	frameshifted
LAC1533_RS09625	2024760	2025120	hypothetical protein	frameshifted and internal stop
LAC1533_RS09870	2069529	2069735	hypothetical protein	internal stop
LAC1533_RS09920	2080304	2084151	alpha-1,2-mannosidase	frameshifted and internal stop
LAC1533_RS09930	2086933	2088027	PTS fructose transporter subunit IIC	internal stop
LAC1533_RS10015	2102849	2103624	tyrosine protein phosphatase	frameshifted

LAC1533_RS10060	2111784	2112693	glycine/betaine ABC transporter	frameshifted
LAC1533_RS10070	2114797	2116755	asparagine synthase (glutamine-hydrolyzing)	internal stop
LAC1533_RS10085	2120129	>2121418	IS1380 family transposase	incomplete
LAC1533_RS10095	2123201	2124169	glycerate dehydrogenase	internal stop
LAC1533_RS10100	2124183	2125079	xylose isomerase	internal stop
LAC1533_RS10125	2127958	2128844	2-hydroxy-3-oxopropionate reductase	frameshifted
LAC1533_RS10155	2133290	2134182	IS982 family transposase	frameshifted
LAC1533_RS10250	2152020	2153326	IS1380 family transposase	frameshifted
LAC1533_RS10280	2160885	>2162180	ISL3 family transposase	incomplete
LAC1533_RS10290	2163596	2163802	hypothetical protein	internal stop
LAC1533_RS10295	2164276	>2165571	ISL3 family transposase	incomplete
LAC1533_RS10305	2166987	2167193	hypothetical protein	internal stop
LAC1533_RS10315	2172272	2173166	IS982 family transposase	frameshifted
LAC1533_RS10410	2194021	2195208	IS256 family transposase	frameshifted
LAC1533_RS10460	2206588	2206846	transcriptional regulator	frameshifted and internal stop
LAC1533_RS10525	2224518	2225458	ferrochelatase	frameshifted
LAC1533_RS10570	2232760	>2234055	ISL3 family transposase	incomplete
LAC1533_RS10580	2235471	2235677	hypothetical protein	internal stop
LAC1533_RS10585	2236181	2237251	hypothetical protein	internal stop
LAC1533_RS10680	2254296	2254502	hypothetical protein	internal stop
LAC1533_RS10850	2291111	2291989	IS982 family transposase	internal stop
LAC1533_RS10860	2293567	2293773	hypothetical protein	internal stop
LAC1533_RS10980	2313121	2314047	alpha/beta hydrolase	internal stop
LAC1533_RS11040	2326607	2327456	short-chain dehydrogenase/reductase	frameshifted
LAC1533_RS11155	2354901	2355585	GTP pyrophosphokinase	frameshifted
LAC1533_RS11205	2363913	2364680	branched-chain amino acid transporter AzlC	internal stop
LAC1533_RS11230	2368066	2370884	ABC transporter permease	frameshifted
LAC1533_RS11275	2381810	2382585	IS5/IS1182 family transposase	frameshifted
LAC1533_RS11340	<239488	7 2395306	transcriptional regulator	incomplete
LAC1533_RS11355	2399119	2400434	IS1380 family transposase	frameshifted
LAC1533_RS11365	<240244	3 2402652	transposase	incomplete
LAC1533_RS11440	2421000	2421206	hypothetical protein	internal stop
LAC1533_RS11485	2428346	2429676	amino acid permease	frameshifted
LAC1533_RS11530	2443155	2443693	LemA family protein	frameshifted
LAC1533_RS11535	2444393	>2445109	glycine/betaine ABC transporter	incomplete
LAC1533_RS11605	2458603	2458975	nucleotide pyrophosphohydrolase	frameshifted
LAC1533_RS11610	2459208	2460394	IS256 family transposase	frameshifted and internal stop
LAC1533_RS11640	2467852	2469351	MFS transporter	internal stop
LAC1533_RS11685	2475505	2476406	hypothetical protein	frameshifted and internal stop
LAC1533_RS11695	2478063	2478269	hypothetical protein	internal stop
LAC1533_RS11785	<249674	5 2497176	helicase	incomplete
LAC1533_RS11815	2500436	2500642	hypothetical protein	internal stop
LAC1533_RS11930	<252761	4 2527853	aspartate - ammonia ligase	incomplete
LAC1533_RS11960	2534558	2535867	IS1380 family transposase	frameshifted

Supplementary table S4A. Pan-genome analysis among the three *L. acidipiscis* strains calculated with the EDGAR software.

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS00005	chromosomal replication initiator protein DnaA	GSS_RS03115	chromosomal replication initiator protein DnaA	Lacidipiscis_RS10985	chromosomal replication initiator protein DnaA
LAC1533_RS00010	DNA polymerase III subunit beta	GSS_RS03110	DNA polymerase III subunit beta	Lacidipiscis_RS10990	DNA polymerase III subunit beta
LAC1533_RS00015	S4 domain-containing protein YaaA	GSS_RS03105	S4 domain-containing protein YaaA	Lacidipiscis_RS10995	S4 domain-containing protein YaaA
LAC1533_RS00020	DNA replication and repair protein RecF	GSS_RS03100	DNA replication and repair protein RecF	Lacidipiscis_RS11000	DNA replication and repair protein RecF
LAC1533_RS00025	DNA topoisomerase (ATP-hydrolyzing) subunit B	GSS_RS03095	DNA topoisomerase (ATP-hydrolyzing) subunit B	Lacidipiscis_RS11005	DNA topoisomerase (ATP-hydrolyzing) subunit B
LAC1533_RS00030	DNA gyrase subunit A	GSS_RS03090	DNA gyrase subunit A	Lacidipiscis_RS11010	DNA gyrase subunit A
LAC1533_RS00035	30S ribosomal protein S6	GSS_RS03085	30S ribosomal protein S6	Lacidipiscis_RS11015	30S ribosomal protein S6
LAC1533_RS00040	single-stranded DNA-binding protein	GSS_RS03080	single-stranded DNA-binding protein	Lacidipiscis_RS11020	single-stranded DNA-binding protein
LAC1533_RS00045	30S ribosomal protein S18	GSS_RS03075	30S ribosomal protein S18	Lacidipiscis_RS11025	30S ribosomal protein S18
LAC1533_RS00050	GntR family transcriptional regulator	GSS_RS03070	GntR family transcriptional regulator	Lacidipiscis_RS11030	GntR family transcriptional regulator
LAC1533_RS00055	beta-galactosidase			Lacidipiscis_RS11045	beta-galactosidase
LAC1533_RS00060	PTS mannose/fructose/sorbose transporter subunit IIB	GSS_RS03060	PTS mannose/fructose/sorbose transporter subunit IIB	Lacidipiscis_RS11050	PTS mannose/fructose/sorbose transporter subunit IIB
LAC1533_RS00065	PTS sugar transporter subunit IIC	GSS_RS03055	PTS sugar transporter subunit IIC		
LAC1533_RS00070	PTS fructose transporter subunit IID	GSS_RS03050	PTS fructose transporter subunit IID		
LAC1533_RS00075	PTS fructose transporter subunit IIA	GSS_RS03045	PTS fructose transporter subunit IIA	Lacidipiscis_RS11055	hypothetical protein
LAC1533_RS00080	SIS domain-containing protein	GSS_RS03040	SIS domain-containing protein	Lacidipiscis_RS11060	SIS domain-containing protein
LAC1533_RS00085	N-acetylglucosamine-6-phosphate deacetylase	GSS_RS03035	N-acetylglucosamine-6-phosphate deacetylase		
LAC1533_RS00090	DeoR/GlpR transcriptional regulator	GSS_RS03030	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS11070	DeoR/GlpR transcriptional regulator
LAC1533_RS00095	ABC transporter ATP-binding protein	GSS_RS03025	ABC transporter ATP-binding protein	Lacidipiscis_RS11075	ABC transporter ATP-binding protein
LAC1533_RS00100	ABC transporter permease			Lacidipiscis_RS11080	ABC transporter permease
LAC1533_RS00105	GntR family transcriptional regulator	GSS_RS03015	GntR family transcriptional regulator	Lacidipiscis_RS11085	GntR family transcriptional regulator
LAC1533_RS00110	ABC transporter ATP-binding protein	GSS_RS03010	ABC transporter ATP-binding protein	Lacidipiscis_RS11090	ABC transporter ATP-binding protein
LAC1533_RS00115	hypothetical protein	GSS_RS03005	hypothetical protein	Lacidipiscis_RS11095	hypothetical protein
LAC1533_RS00120	DHH family phosphoesterase	GSS_RS03000	DHH family phosphoesterase	Lacidipiscis_RS11100	DHH family phosphoesterase
LAC1533_RS00125	50S ribosomal protein L9	GSS_RS02995	50S ribosomal protein L9	Lacidipiscis_RS11105	50S ribosomal protein L9
LAC1533_RS00130	replicative DNA helicase	GSS_RS02990	replicative DNA helicase	Lacidipiscis_RS11110	replicative DNA helicase
LAC1533_RS00140 IDENTICAL PARALOGS LAC1533_RS09865	group II intron reverse transcriptase/maturase				
LAC1533_RS00145	IS1380 family transposase				
LAC1533_RS00150	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein	GSS_RS02985	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein	Lacidipiscis_RS11115	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein
LAC1533_RS00155	phosphonate ABC transporter ATP-binding protein	GSS_RS02980	phosphonate ABC transporter ATP-binding protein	Lacidipiscis_RS11120	phosphonate ABC transporter ATP-binding protein
LAC1533_RS00160	phosphonate ABC transporter, permease protein PhnE	GSS_RS02975	phosphonate ABC transporter, permease protein PhnE	Lacidipiscis_RS11125	phosphonate ABC transporter, permease protein PhnE
LAC1533_RS00165	phosphonate ABC transporter, permease protein PhnE	GSS_RS02970	phosphonate ABC transporter, permease protein PhnE	Lacidipiscis_RS11130	phosphonate ABC transporter, permease protein PhnE
LAC1533_RS00170	bifunctional metallophosphatase/5-nucleotidase	GSS_RS02965	bifunctional metallophosphatase/5-nucleotidase	Lacidipiscis_RS11135	bifunctional metallophosphatase/5-nucleotidase
LAC1533_RS00185	DUF4867 domain-containing protein	GSS_RS02960	DUF4867 domain-containing protein	Lacidipiscis_RS11145	DUF4867 domain-containing protein
LAC1533_RS00190	tagatose-6-phosphate kinase	GSS_RS02955	tagatose-6-phosphate kinase	Lacidipiscis_RS11150	tagatose-6-phosphate kinase
LAC1533_RS00195	PTS sugar transporter subunit IIA	GSS_RS02950	PTS sugar transporter subunit IIA	Lacidipiscis_RS11155	PTS sugar transporter subunit IIA
LAC1533_RS00200	PTS fructose transporter subunit IIB	GSS_RS02945	PTS fructose transporter subunit IIB	Lacidipiscis_RS11160	PTS fructose transporter subunit IIB
LAC1533_RS00205	PTS glucitol transporter subunit IIA	GSS_RS02940	PTS glucitol transporter subunit IIA	Lacidipiscis_RS11165	PTS glucitol transporter subunit IIA
LAC1533_RS00210	hypothetical protein	GSS_RS02935	hypothetical protein	Lacidipiscis_RS11170	hypothetical protein
LAC1533_RS00215	DeoR/GlpR transcriptional regulator	GSS_RS02930	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS11175	DeoR/GlpR transcriptional regulator
LAC1533_RS00220	galactose-6-phosphate isomerase subunit LacA	GSS_RS02925	galactose-6-phosphate isomerase subunit LacA	Lacidipiscis_RS11180	galactose-6-phosphate isomerase subunit LacA
LAC1533_RS00225	galactose-6-phosphate isomerase subunit LacB	GSS_RS02920	galactose-6-phosphate isomerase subunit LacB	Lacidipiscis_RS11185	galactose-6-phosphate isomerase subunit LacB
LAC1533_RS00230	tagatose-bisphosphate aldolase	GSS_RS02915	tagatose-bisphosphate aldolase	Lacidipiscis_RS11190	tagatose-bisphosphate aldolase
LAC1533_RS00240	NAD-dependent malic enzyme			Lacidipiscis_RS11200	NAD-dependent malic enzyme
LAC1533_RS00245	LysR family transcriptional regulator				
LAC1533_RS00250	hypothetical protein			Lacidipiscis_RS11205	LysR family transcriptional regulator
LAC1533_RS00255	PRD domain-containing protein			Lacidipiscis_RS11210	PRD domain-containing protein
LAC1533_RS00260	PTS lactose/cellobiose transporter subunit IIA			Lacidipiscis_RS11215	PTS lactose/cellobiose transporter subunit IIA
LAC1533_RS00265	6-phospho-beta-galactosidase				
LAC1533_RS00270	PTS lactose transporter subunit IIBC	GSS_RS02910	PTS lactose transporter subunit IIBC		
LAC1533_RS00275	LacI family DNA-binding transcriptional regulator	GSS_RS02905	LacI family DNA-binding transcriptional regulator		
LAC1533_RS00280	6-phospho-beta-galactosidase	GSS_RS02900	6-phospho-beta-galactosidase		
LAC1533_RS00285	PTS lactose transporter subunit IIB	GSS_RS02895	PTS lactose transporter subunit IIB		
LAC1533_RS00290	methylglyoxal synthase	GSS_RS02890	methylglyoxal synthase		
LAC1533_RS00295	hypothetical protein				
LAC1533_RS00300 IDENTICAL PARALOGS LAC1533_RS09250	IS30 family transposase	GSS_RS11500	IS30 family transposase	Lacidipiscis_RS04130	IS30 family transposase
LAC1533_RS00305	hypothetical protein	GSS_RS12410	hypothetical protein		
LAC1533_RS00310	hypothetical protein	GSS_RS02875	hypothetical protein		
LAC1533_RS00315	hypothetical protein				

LAC1533_RS00325	hypothetical protein	GSS_RS02870	hypothetical protein		
LAC1533_RS00330	butanediol dehydrogenase	GSS_RS02865	butanediol dehydrogenase	Lacidipiscis_RS02750	butanediol dehydrogenase
LAC1533_RS00335	LysR family transcriptional regulator	GSS_RS02860	LysR family transcriptional regulator	Lacidipiscis_RS02755	LysR family transcriptional regulator
LAC1533_RS00340	class II fumarate hydratase	GSS_RS02855	class II fumarate hydratase	Lacidipiscis_RS02760	class II fumarate hydratase
LAC1533_RS00345	flavocytochrome c	GSS_RS02850	flavocytochrome c	Lacidipiscis_RS02765	flavocytochrome c
LAC1533_RS00350	anion permease	GSS_RS02845	anion permease	Lacidipiscis_RS02770	anion permease
LAC1533_RS00355	LysR family transcriptional regulator	GSS_RS02840	LysR family transcriptional regulator		
LAC1533_RS00360	FAD-binding protein	GSS_RS02835	FAD-binding protein	Lacidipiscis_RS02780	FAD-binding protein
LAC1533_RS00365	SDR family NAD(P)-dependent oxidoreductase	GSS_RS02830	SDR family NAD(P)-dependent oxidoreductase	Lacidipiscis_RS02785	SDR family NAD(P)-dependent oxidoreductase
LAC1533_RS00370	FAD-binding protein	GSS_RS02825	FAD-binding protein	Lacidipiscis_RS02790	FAD-binding protein
LAC1533_RS00375	MFS transporter				
LAC1533_RS00380	MFS transporter				
LAC1533_RS00385	hypothetical protein	GSS_RS02810	hypothetical protein		
LAC1533_RS00390	aldo/keto reductase	GSS_RS02805	aldo/keto reductase	Lacidipiscis_RS02800	aldo/keto reductase
LAC1533_RS00395	NAD(P)-dependent oxidoreductase	GSS_RS02800	NAD(P)-dependent oxidoreductase	Lacidipiscis_RS02805	NAD(P)-dependent oxidoreductase
LAC1533_RS00400	L-lactate oxidase	GSS_RS02795	L-lactate oxidase	Lacidipiscis_RS02810	L-lactate oxidase
LAC1533_RS00405	FAD-binding oxidoreductase	GSS_RS02790	FAD-binding oxidoreductase		
LAC1533_RS00410	LacI family DNA-binding transcriptional regulator	GSS_RS02785	LacI family DNA-binding transcriptional regulator	Lacidipiscis_RS02820	LacI family DNA-binding transcriptional regulator
LAC1533_RS00415	FAD-binding protein	GSS_RS02780	FAD-binding protein	Lacidipiscis_RS02825	FAD-binding protein
LAC1533_RS00420	FAD-binding protein	GSS_RS02775	FAD-binding protein	Lacidipiscis_RS02830	FAD-binding protein
LAC1533_RS00425	hypothetical protein	GSS_RS02770	hypothetical protein	Lacidipiscis_RS02835	hypothetical protein
LAC1533_RS00430	FAD-binding protein	GSS_RS02765	FAD-binding protein	Lacidipiscis_RS02840	FAD-binding protein
LAC1533_RS00435	Cof-type HAD-IIB family hydrolase	GSS_RS02760	Cof-type HAD-IIB family hydrolase		
LAC1533_RS00440	hypothetical protein	GSS_RS13685	hypothetical protein		
LAC1533_RS00450	amino acid ABC transporter permease	GSS_RS02750	amino acid ABC transporter permease		
LAC1533_RS00455	amino acid ABC transporter ATP-binding protein	GSS_RS02745	amino acid ABC transporter ATP-binding protein		
LAC1533_RS00460	amino acid ABC transporter substrate-binding protein	GSS_RS02740	amino acid ABC transporter substrate-binding protein		
LAC1533_RS00465	hypothetical protein	GSS_RS02735	hypothetical protein		
LAC1533_RS00470	cell surface protein	GSS_RS02730	cell surface protein		
LAC1533_RS00475	iron ABC transporter substrate-binding protein	GSS_RS02725	iron ABC transporter substrate-binding protein		
LAC1533_RS00480	iron compound ABC transporter permease	GSS_RS02720	iron compound ABC transporter permease		
LAC1533_RS00485	ABC transporter ATP-binding protein	GSS_RS02715	ABC transporter ATP-binding protein		
LAC1533_RS00490	cytosine deaminase	GSS_RS02710	cytosine deaminase		
LAC1533_RS00495 IDENTICAL PARALOGS LAC1533_RS05535 IDENTICAL PARALOGS LAC1533_RS06750	IS30 family transposase	GSS_RS11395	IS30 family transposase	Lacidipiscis_RS08455	IS30 family transposase
LAC1533_RS00500	MFS transporter				
LAC1533_RS00505	DoxX family membrane protein				
LAC1533_RS00510	glutaryl-CoA dehydrogenase				
LAC1533_RS00520 IDENTICAL PARALOGS LAC1533_RS01465 IDENTICAL PARALOGS LAC1533_RS02090 IDENTICAL PARALOGS LAC1533_RS05565 IDENTICAL PARALOGS LAC1533_RS06445 IDENTICAL PARALOGS LAC1533_RS07575 IDENTICAL PARALOGS LAC1533_RS10300 IDENTICAL PARALOGS LAC1533_RS10575	group II intron reverse transcriptase/maturase				
LAC1533_RS00530	LysR family transcriptional regulator	GSS_RS02705	LysR family transcriptional regulator		
LAC1533_RS00535	acetyl-CoA C-acetyltransferase	GSS_RS02700	acetyl-CoA C-acetyltransferase		
LAC1533_RS00540	acyl-CoA dehydrogenase	GSS_RS02695	acyl-CoA dehydrogenase		
LAC1533_RS00545	3-hydroxybutyryl-CoA dehydrogenase	GSS_RS02690	3-hydroxybutyryl-CoA dehydrogenase		
LAC1533_RS00550	crotonase	GSS_RS02685	crotonase		
LAC1533_RS00555	4-hydroxybutyrate CoA-transferase	GSS_RS12400	4-hydroxybutyrate CoA-transferase		
LAC1533_RS00560	AEC family transporter	GSS_RS02670	AEC family transporter	Lacidipiscis_RS02850	AEC family transporter
LAC1533_RS00565	hypothetical protein	GSS_RS02665	hypothetical protein	Lacidipiscis_RS02855	hypothetical protein
LAC1533_RS00570	adenylosuccinate synthase	GSS_RS02660	adenylosuccinate synthase	Lacidipiscis_RS02860	adenylosuccinate synthase
LAC1533_RS00580	group II intron reverse transcriptase/maturase				
LAC1533_RS00585	ISL3 family transposase	GSS_RS02655	ISL3 family transposase	Lacidipiscis_RS02050	ISL3 family transposase
LAC1533_RS00590	formate C-acetyltransferase	GSS_RS02645	formate C-acetyltransferase	Lacidipiscis_RS02055	formate C-acetyltransferase

LAC1533_RS00595	pyruvate formate lyase-activating protein	GSS_RS02640	pyruvate formate lyase-activating protein	Lacidipiscis_RS02060	pyruvate formate lyase-activating protein
LAC1533_RS00600 IDENTICAL PARALOGS LAC1533_RS06950 IDENTICAL PARALOGS LAC1533_RS07095 IDENTICAL PARALOGS LAC1533_RS12165	transposase				
LAC1533_RS00605 IDENTICAL PARALOGS LAC1533_RS01135 IDENTICAL PARALOGS LAC1533_RS02865 IDENTICAL PARALOGS LAC1533_RS03470 IDENTICAL PARALOGS LAC1533_RS03575 IDENTICAL PARALOGS LAC1533_RS08020	ISL3 family transposase	GSS_RS11420	ISL3 family transposase	Lacidipiscis_RS03185	ISL3 family transposase
LAC1533_RS00610	zinc-binding alcohol dehydrogenase family protein	GSS_RS02630	zinc-binding alcohol dehydrogenase family protein	Lacidipiscis_RS02065	zinc-binding alcohol dehydrogenase family protein
LAC1533_RS00620	sensor protein LytS			Lacidipiscis_RS02075	sensor protein LytS
LAC1533_RS00625	DNA-binding response regulator	GSS_RS02615	DNA-binding response regulator		
LAC1533_RS00630	murein hydrolase regulator LrgA	GSS_RS12390	murein hydrolase regulator LrgA		
LAC1533_RS00635	antiholin	GSS_RS02605	antiholin		
LAC1533_RS00640	2-hydroxyacid dehydrogenase	GSS_RS02600	2-hydroxyacid dehydrogenase	Lacidipiscis_RS07565	hydroxyacid dehydrogenase
LAC1533_RS00645	hypothetical protein	GSS_RS02595	hypothetical protein	Lacidipiscis_RS07570	hypothetical protein
LAC1533_RS00650 IDENTICAL PARALOGS LAC1533_RS09450 IDENTICAL PARALOGS LAC1533_RS12185	IS982 family transposase ISLpl4	GSS_RS11510	IS982 family transposase ISLpl4	Lacidipiscis_RS05750	IS982 family transposase ISLpl4
LAC1533_RS00655	adenine deaminase	GSS_RS12385	adenine deaminase	Lacidipiscis_RS07585	adenine deaminase
LAC1533_RS00660	hypothetical protein	GSS_RS13680	hypothetical protein		
LAC1533_RS00665	metal ABC transporter substrate-binding protein	GSS_RS02585	metal ABC transporter substrate-binding protein	Lacidipiscis_RS07590	metal ABC transporter substrate-binding protein
LAC1533_RS00670	30S ribosomal protein S14	GSS_RS02580	30S ribosomal protein S14	Lacidipiscis_RS07595	30S ribosomal protein S14
LAC1533_RS00675	cysteine synthase family protein	GSS_RS02575	cysteine synthase family protein	Lacidipiscis_RS11450	hypothetical protein
LAC1533_RS00680	PLP-dependent transferase	GSS_RS02570	PLP-dependent transferase	Lacidipiscis_RS11455	PLP-dependent transferase
LAC1533_RS00685	serine acetyltransferase	GSS_RS02565	serine acetyltransferase	Lacidipiscis_RS11460	serine acetyltransferase
LAC1533_RS00690	acyl-CoA thioesterase	GSS_RS02560	acyl-CoA thioesterase	Lacidipiscis_RS11465	acyl-CoA thioesterase
LAC1533_RS00695	threonine/serine exporter	GSS_RS02555	threonine/serine exporter	Lacidipiscis_RS11470	threonine/serine exporter
LAC1533_RS00700	threonine/serine exporter	GSS_RS02550	threonine/serine exporter	Lacidipiscis_RS11475	threonine/serine exporter
LAC1533_RS00705	NupC/NupG family nucleoside CNT transporter	GSS_RS02545	nucleoside transporter	Lacidipiscis_RS11480	nucleoside permease
LAC1533_RS00710	NCS2 family permease	GSS_RS02540	NCS2 family permease	Lacidipiscis_RS11485	NCS2 family permease
LAC1533_RS00715	EAL domain-containing protein	GSS_RS12380	EAL domain-containing protein	Lacidipiscis_RS11490	hypothetical protein
LAC1533_RS00720	hypothetical protein	GSS_RS13995	hypothetical protein		
LAC1533_RS00725	hypothetical protein	GSS_RS02525	hypothetical protein	Lacidipiscis_RS11495	hypothetical protein
LAC1533_RS00730	hypothetical protein				
LAC1533_RS00735	GGDEF domain-containing protein	GSS_RS13675	GGDEF domain-containing protein		
LAC1533_RS00740	IS256 family transposase	GSS_RS11425	IS256 family transposase		
LAC1533_RS00750	peptide ABC transporter substrate-binding protein	GSS_RS02510	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS12325	peptide ABC transporter substrate-binding protein
LAC1533_RS00755	peroxide stress protein YaaA	GSS_RS02505	peroxide stress protein YaaA	Lacidipiscis_RS12320	peroxide stress protein YaaA
LAC1533_RS00760	hypothetical protein	GSS_RS02495	hypothetical protein	Lacidipiscis_RS12315	hypothetical protein
LAC1533_RS00770	NADPH:quinone reductase	GSS_RS02485	NADPH:quinone reductase	Lacidipiscis_RS12305	NADPH:quinone reductase
LAC1533_RS00775	YitT family protein	GSS_RS02480	YitT family protein	Lacidipiscis_RS12300	YitT family protein
LAC1533_RS00780	APC family permease	GSS_RS02475	APC family permease	Lacidipiscis_RS12295	APC family permease
LAC1533_RS00785	ornithine decarboxylase	GSS_RS02470	ornithine decarboxylase	Lacidipiscis_RS12290	ornithine decarboxylase
LAC1533_RS00790	hypothetical protein	GSS_RS13990	hypothetical protein	Lacidipiscis_RS12285	hypothetical protein
LAC1533_RS00795	hypothetical protein	GSS_RS13670	hypothetical protein	Lacidipiscis_RS12280	hypothetical protein
LAC1533_RS00800	DUF2992 domain-containing protein	GSS_RS02455	DUF2992 domain-containing protein	Lacidipiscis_RS12275	DUF2992 domain-containing protein
LAC1533_RS00815 IDENTICAL PARALOGS LAC1533_RS02100 IDENTICAL PARALOGS LAC1533_RS06710 IDENTICAL PARALOGS LAC1533_RS07160 IDENTICAL PARALOGS LAC1533_RS07270 IDENTICAL PARALOGS LAC1533_RS07930 IDENTICAL PARALOGS LAC1533_RS10065 IDENTICAL PARALOGS LAC1533_RS11625 IDENTICAL PARALOGS LAC1533_RS12035	IS1380 family transposase				
LAC1533_RS00825 IDENTICAL PARALOGS LAC1533_RS07320 IDENTICAL PARALOGS LAC1533_RS07425 IDENTICAL PARALOGS LAC1533_RS10245	transposase	GSS_RS11565	ATPase AAA		
LAC1533_RS00840	TetR/AcrR family transcriptional regulator	GSS_RS02430	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS00720	TetR/AcrR family transcriptional regulator
LAC1533_RS00845	ABC transporter permease	GSS_RS02425	ABC transporter permease	Lacidipiscis_RS00725	ABC transporter permease
LAC1533_RS00850	ABC transporter ATP-binding protein	GSS_RS02420	ABC transporter ATP-binding protein	Lacidipiscis_RS07105	ABC transporter ATP-binding protein
LAC1533_RS00855	dihydroxyacetone kinase subunit DhaK	GSS_RS02415	dihydroxyacetone kinase subunit DhaK	Lacidipiscis_RS00735	dihydroxyacetone kinase subunit DhaK

LAC1533_RS00860	dihydroxyacetone kinase subunit L			Lacidipiscis_RS00740	dihydroxyacetone kinase subunit L
LAC1533_RS00865	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM	GSS_RS02405	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM	Lacidipiscis_RS00745	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM
LAC1533_RS00870	glycerol kinase	GSS_RS02400	glycerol kinase	Lacidipiscis_RS00750	glycerol kinase
LAC1533_RS00875	type 1 glycerol-3-phosphate oxidase	GSS_RS02395	type 1 glycerol-3-phosphate oxidase	Lacidipiscis_RS00755	type 1 glycerol-3-phosphate oxidase
LAC1533_RS00880	aquaporin family protein	GSS_RS02390	aquaporin family protein	Lacidipiscis_RS00760	aquaporin family protein
LAC1533_RS00885	GntR family transcriptional regulator	GSS_RS02385	GntR family transcriptional regulator	Lacidipiscis_RS00765	GntR family transcriptional regulator
LAC1533_RS00890	PTS sugar transporter subunit IIC	GSS_RS02380	PTS sugar transporter subunit IIC	Lacidipiscis_RS00770	PTS sugar transporter subunit IIC
LAC1533_RS00895	DUF3284 domain-containing protein	GSS_RS02375	DUF3284 domain-containing protein	Lacidipiscis_RS00775	DUF3284 domain-containing protein
LAC1533_RS00900 IDENTICAL PARALOGS LAC1533_RS01490 IDENTICAL PARALOGS LAC1533_RS03150 IDENTICAL PARALOGS LAC1533_RS04075 IDENTICAL PARALOGS LAC1533_RS04080 IDENTICAL PARALOGS LAC1533_RS04435	hypothetical protein	GSS_RS11350	hypothetical protein		
LAC1533_RS00905	DUF871 domain-containing protein	GSS_RS02370	DUF871 domain-containing protein		
LAC1533_RS00915	hypothetical protein	GSS_RS13980	hypothetical protein	Lacidipiscis_RS00790	PTS sugar transporter subunit IIB
LAC1533_RS00920	GNAT family N-acetyltransferase	GSS_RS13665	GNAT family N-acetyltransferase	Lacidipiscis_RS00795	GNAT family N-acetyltransferase
LAC1533_RS00925	GNAT family N-acetyltransferase	GSS_RS12345	GNAT family N-acetyltransferase		
LAC1533_RS00930	chitosanase				
LAC1533_RS00940	DUF3290 domain-containing protein	GSS_RS02345	DUF3290 domain-containing protein	Lacidipiscis_RS00805	DUF3290 domain-containing protein
LAC1533_RS00945	DUF421 domain-containing protein	GSS_RS02340	DUF421 domain-containing protein	Lacidipiscis_RS00715	DUF421 domain-containing protein
LAC1533_RS00950	hypothetical protein	GSS_RS12335	cytidyltransferase-like domain-containing protein	Lacidipiscis_RS09390	hypothetical protein
LAC1533_RS00955	LysR family transcriptional regulator	GSS_RS13655	LysR family transcriptional regulator	Lacidipiscis_RS09385	LysR family transcriptional regulator
LAC1533_RS00960	glycerol kinase	GSS_RS02320	glycerol kinase	Lacidipiscis_RS09380	glycerol kinase
LAC1533_RS00965	glycerol-3-phosphate dehydrogenase/oxidase	GSS_RS02315	glycerol-3-phosphate dehydrogenase/oxidase	Lacidipiscis_RS09375	glycerol-3-phosphate dehydrogenase/oxidase
LAC1533_RS00970	hypothetical protein	GSS_RS12325	hypothetical protein	Lacidipiscis_RS09370	hypothetical protein
LAC1533_RS00975 IDENTICAL PARALOGS LAC1533_RS01280 IDENTICAL PARALOGS LAC1533_RS01565 IDENTICAL PARALOGS LAC1533_RS01950 IDENTICAL PARALOGS LAC1533_RS02860 IDENTICAL PARALOGS LAC1533_RS05380 IDENTICAL PARALOGS LAC1533_RS07280 IDENTICAL PARALOGS LAC1533_RS08060	transposase				
LAC1533_RS00990	glutamate ABC transporter substrate-binding protein	GSS_RS02290	glutamate ABC transporter substrate-binding protein	Lacidipiscis_RS00875	glutamate ABC transporter substrate-binding protein
LAC1533_RS00995	amino acid ABC transporter permease	GSS_RS02285	amino acid ABC transporter permease	Lacidipiscis_RS00880	amino acid ABC transporter permease
LAC1533_RS01000	aspartate aminotransferase	GSS_RS02280	aspartate aminotransferase	Lacidipiscis_RS00885	aspartate aminotransferase
LAC1533_RS01005	lactate dehydrogenase	GSS_RS02275	lactate dehydrogenase	Lacidipiscis_RS00890	lactate dehydrogenase
LAC1533_RS01010	ZIP family metal transporter	GSS_RS02270	ZIP family metal transporter	Lacidipiscis_RS00895	ZIP family metal transporter
LAC1533_RS01020	histidine phosphatase family protein	GSS_RS02260	histidine phosphatase family protein	Lacidipiscis_RS00905	histidine phosphatase family protein
LAC1533_RS01025	N-acetyltransferase	GSS_RS02255	N-acetyltransferase	Lacidipiscis_RS00910	N-acetyltransferase
LAC1533_RS01030	glycosyltransferase family 8 protein	GSS_RS02250	glycosyltransferase family 8 protein	Lacidipiscis_RS00915	glycosyltransferase family 8 protein
LAC1533_RS01040	hypothetical protein	GSS_RS02240	hypothetical protein	Lacidipiscis_RS00925	hypothetical protein
LAC1533_RS01045	hypothetical protein	GSS_RS02235	membrane protein	Lacidipiscis_RS00930	hypothetical protein
LAC1533_RS01050	pyridoxal kinase	GSS_RS02230	pyridoxal kinase	Lacidipiscis_RS00935	pyridoxal kinase
LAC1533_RS01055	DNA-binding response regulator	GSS_RS02225	DNA-binding response regulator	Lacidipiscis_RS00940	DNA-binding response regulator
LAC1533_RS01060	cell wall metabolism sensor histidine kinase WalK	GSS_RS02220	cell wall metabolism sensor histidine kinase WalK	Lacidipiscis_RS00945	cell wall metabolism sensor histidine kinase WalK
LAC1533_RS01065	hypothetical protein	GSS_RS02215	hypothetical protein	Lacidipiscis_RS00950	hypothetical protein
LAC1533_RS01070	hypothetical protein	GSS_RS02210	hypothetical protein	Lacidipiscis_RS00955	hypothetical protein
LAC1533_RS01075	DUF1634 domain-containing protein	GSS_RS02205	DUF1634 domain-containing protein	Lacidipiscis_RS06485	DUF1634 domain-containing protein
LAC1533_RS01080	sulfite exporter TauE/SafE family protein	GSS_RS02200	sulfite exporter TauE/SafE family protein	Lacidipiscis_RS06490	sulfite exporter TauE/SafE family protein
LAC1533_RS01085	MBL fold metallo-hydrolase	GSS_RS02195	MBL fold metallo-hydrolase	Lacidipiscis_RS06495	MBL fold metallo-hydrolase
LAC1533_RS01090	PDZ domain-containing protein	GSS_RS02190	PDZ domain-containing protein	Lacidipiscis_RS12675	PDZ domain-containing protein

LAC1533_RS01095 IDENTICAL PARALOGS LAC1533_RS01980 IDENTICAL PARALOGS LAC1533_RS08320 IDENTICAL PARALOGS LAC1533_RS10275 IDENTICAL PARALOGS LAC1533_RS11335	IS30 family transposase	GSS_RS11460	IS30 family transposase	Lacidipiscis_RS11325 IDENTICAL PARALOGS Lacidipiscis_RS08300	IS30 family transposase
LAC1533_RS01100	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	GSS_RS02185	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	Lacidipiscis_RS08660	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH
LAC1533_RS01105	SAM-dependent DNA methyltransferase				
LAC1533_RS01110	restriction endonuclease				
LAC1533_RS01115	type I restriction endonuclease	GSS_RS02155	type I restriction modification protein		
LAC1533_RS01120	integrase	GSS_RS02165	integrase		
LAC1533_RS01125	hypothetical protein				
LAC1533_RS01140	DUF3387 domain-containing protein				
LAC1533_RS01145	DUF1516 domain-containing protein	GSS_RS02145	DUF1516 domain-containing protein	Lacidipiscis_RS08665	DUF1516 domain-containing protein
LAC1533_RS01150	hypothetical protein	GSS_RS02140	hypothetical protein		
LAC1533_RS01155	TetR/AcrR family transcriptional regulator	GSS_RS02135	TetR/AcrR family transcriptional regulator		
LAC1533_RS01160	membrane protein	GSS_RS02130	membrane protein	Lacidipiscis_RS00200	hypothetical protein
LAC1533_RS01165	ClC family H(+)/Cl(-) exchange transporter	GSS_RS02125	ClC family H(+)/Cl(-) exchange transporter	Lacidipiscis_RS00205	ClC family H(+)/Cl(-) exchange transporter
LAC1533_RS01170	ATPase	GSS_RS02120	MoxR-like ATPase	Lacidipiscis_RS00210	ATPase
LAC1533_RS01175	hypothetical protein	GSS_RS02115	hypothetical protein	Lacidipiscis_RS00215	hypothetical protein
LAC1533_RS01180	hypothetical protein	GSS_RS02110	hypothetical protein	Lacidipiscis_RS00220	hypothetical protein
LAC1533_RS01185	hypothetical protein	GSS_RS02105	hypothetical protein	Lacidipiscis_RS00225	hypothetical protein
LAC1533_RS01190	NADPH-dependent oxidoreductase	GSS_RS02100	NADPH-dependent oxidoreductase	Lacidipiscis_RS00230	NADPH-dependent oxidoreductase
LAC1533_RS01195	hypothetical protein	GSS_RS02095	hypothetical protein	Lacidipiscis_RS00235	hypothetical protein
LAC1533_RS01200	AraC family transcriptional regulator			Lacidipiscis_RS00240	AraC family transcriptional regulator
LAC1533_RS01210	MFS transporter	GSS_RS02080	MFS transporter	Lacidipiscis_RS00255	MFS transporter
LAC1533_RS01215	50S ribosomal protein L4	GSS_RS13970	50S ribosomal protein L4	Lacidipiscis_RS00250	50S ribosomal protein L4
LAC1533_RS01220	pyruvate oxidase	GSS_RS12305	pyruvate oxidase		
LAC1533_RS01230	amino acid permease	GSS_RS02075	amino acid permease	Lacidipiscis_RS00260	amino acid permease
LAC1533_RS01235	aspartate aminotransferase family protein	GSS_RS02070	aspartate aminotransferase family protein	Lacidipiscis_RS00265	4-aminobutyrate aminotransferase
LAC1533_RS01240	hypothetical protein	GSS_RS02065	hypothetical protein	Lacidipiscis_RS00280	hypothetical protein
LAC1533_RS01245	ABC transporter substrate-binding protein	GSS_RS02060	inosine-uridine nucleoside N-ribohydrolase	Lacidipiscis_RS00285	ABC transporter substrate-binding protein
LAC1533_RS01250	glycine betaine/L-proline ABC transporter ATP-binding protein	GSS_RS02055	glycine betaine/L-proline ABC transporter ATP-binding protein	Lacidipiscis_RS00290	glycine betaine/L-proline ABC transporter ATP-binding protein
LAC1533_RS01255 IDENTICAL PARALOGS LAC1533_RS11550	glycine/betaine ABC transporter	GSS_RS13385	glycine/betaine ABC transporter	Lacidipiscis_RS00295	glycine/betaine ABC transporter
LAC1533_RS01260 IDENTICAL PARALOGS LAC1533_RS11545	glycine/betaine ABC transporter	GSS_RS11315	glycine/betaine ABC transporter	Lacidipiscis_RS00465	glycine/betaine ABC transporter
LAC1533_RS01265	transposase			Lacidipiscis_RS00630	hypothetical protein
LAC1533_RS01270	glycosyltransferase family 1 protein	GSS_RS02050	glycosyltransferase family 1 protein	Lacidipiscis_RS00310	glycosyltransferase family 1 protein
LAC1533_RS01285	IS256 family transposase				
LAC1533_RS01290	magnesium transporter CorA family protein	GSS_RS02040	magnesium transporter CorA family protein	Lacidipiscis_RS00320	magnesium transporter CorA family protein
LAC1533_RS01295	Cof-type HAD-IIB family hydrolase	GSS_RS02035	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS00325	Cof-type HAD-IIB family hydrolase
LAC1533_RS01300	flavoprotein	GSS_RS02030	flavoprotein	Lacidipiscis_RS00330	NADPH-dependent FMN reductase
LAC1533_RS01305	hypothetical protein	GSS_RS13965	hypothetical protein		
LAC1533_RS01310	transcriptional regulator	GSS_RS02020	transcriptional regulator		
LAC1533_RS01320	type 1 glutamine amidotransferase	GSS_RS02010	type 1 glutamine amidotransferase		
LAC1533_RS01325	TetR/AcrR family transcriptional regulator	GSS_RS02005	TetR/AcrR family transcriptional regulator		
LAC1533_RS01330	hypothetical protein	GSS_RS02000	hypothetical protein		
LAC1533_RS01335	ECF transporter S component	GSS_RS01995	ECF transporter S component		
LAC1533_RS01340	hypothetical protein	GSS_RS01985	hypothetical protein		
LAC1533_RS01345	IS30 family transposase				
LAC1533_RS01350	IS256 family transposase				
LAC1533_RS01360	ArsR family transcriptional regulator			Lacidipiscis_RS00345	ArsR family transcriptional regulator
LAC1533_RS01365	IS30 family transposase				
LAC1533_RS01370	DUF1648 domain-containing protein	GSS_RS01970	DUF1648 domain-containing protein	Lacidipiscis_RS00350	DUF1648 domain-containing protein
LAC1533_RS01375	YhgE/Pip domain-containing protein	GSS_RS01965	YhgE/Pip domain-containing protein	Lacidipiscis_RS00355	YhgE/Pip domain-containing protein
LAC1533_RS01380	PAP2 family protein	GSS_RS01955	PAP2 family protein	Lacidipiscis_RS00360	PAP2 family protein
LAC1533_RS01385	patatin family protein	GSS_RS01950	patatin family protein	Lacidipiscis_RS00365	patatin family protein
LAC1533_RS01390	hypothetical protein	GSS_RS01945	hypothetical protein		

LAC1533_RS01395	hypothetical protein	GSS_RS01940	hypothetical protein	Lacidipiscis_RS00375	hypothetical protein
LAC1533_RS01400	LysM domain-containing protein	GSS_RS01930	LysM domain-containing protein	Lacidipiscis_RS00380	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS01405	aspartate kinase	GSS_RS01925	aspartate kinase	Lacidipiscis_RS00385	aspartate kinase
LAC1533_RS01410	phosphatidylglycerophosphatase A	GSS_RS01920	phosphatidylglycerophosphatase A	Lacidipiscis_RS00390	phosphatidylglycerophosphatase A
LAC1533_RS01415	hydrolase	GSS_RS01915	hydrolase	Lacidipiscis_RS00395	hydrolase
LAC1533_RS01420	L-lactate dehydrogenase	GSS_RS01910	L-lactate dehydrogenase	Lacidipiscis_RS00400	L-lactate dehydrogenase
LAC1533_RS01425	branched-chain amino acid aminotransferase	GSS_RS01905	branched-chain amino acid aminotransferase	Lacidipiscis_RS00405	branched-chain amino acid aminotransferase
LAC1533_RS01430	resolvase	GSS_RS12285	resolvase	Lacidipiscis_RS00410	resolvase
LAC1533_RS01440	alpha-glucosidase	GSS_RS01890	alpha-glucosidase	Lacidipiscis_RS00420	alpha-glucosidase
LAC1533_RS01445	PTS sugar transporter subunit IIC	GSS_RS01885	PTS sugar transporter subunit IIC	Lacidipiscis_RS00425	PTS sugar transporter subunit IIC
LAC1533_RS01450	sugar O-acetyltransferase	GSS_RS01880	sugar O-acetyltransferase	Lacidipiscis_RS00430	sugar O-acetyltransferase
LAC1533_RS01455	N-acetyltransferase	GSS_RS01875	N-acetyltransferase	Lacidipiscis_RS00435	N-acetyltransferase
LAC1533_RS01470	hypothetical protein	GSS_RS01870	hypothetical protein	Lacidipiscis_RS07705	hypothetical protein
LAC1533_RS01475	hypothetical protein	GSS_RS01865	hypothetical protein	Lacidipiscis_RS07710	hypothetical protein
LAC1533_RS01480	ATPase	GSS_RS01860	ATPase	Lacidipiscis_RS07715	ATPase
LAC1533_RS01485	DUF3862 domain-containing protein	GSS_RS01855	DUF3862 domain-containing protein	Lacidipiscis_RS07720	DUF3862 domain-containing protein
LAC1533_RS01495	acyl-CoA thioesterase			Lacidipiscis_RS07725	acyl-CoA thioesterase
LAC1533_RS01500	ABC transporter ATP-binding protein			Lacidipiscis_RS07730	ABC transporter ATP-binding protein
LAC1533_RS01505	ABC transporter ATP-binding protein			Lacidipiscis_RS07735	ABC transporter ATP-binding protein
LAC1533_RS01510	ABC transporter permease			Lacidipiscis_RS07740	ABC transporter permease
LAC1533_RS01515	ABC transporter permease			Lacidipiscis_RS07745	ABC transporter permease
LAC1533_RS01520	oligopeptide ABC transporter substrate-binding protein			Lacidipiscis_RS07750	peptide ABC transporter substrate-binding protein
LAC1533_RS01530	multidrug ABC transporter permease/ATP-binding protein			Lacidipiscis_RS07760	multidrug ABC transporter ATP-binding protein
LAC1533_RS01535	ABC transporter ATP-binding protein			Lacidipiscis_RS07765	ABC transporter ATP-binding protein
LAC1533_RS01540	hypothetical protein	GSS_RS01810	hypothetical protein	Lacidipiscis_RS07770	hypothetical protein
LAC1533_RS01545	LysR family transcriptional regulator	GSS_RS12270	LysR family transcriptional regulator		
LAC1533_RS01550	flavocytochrome c	GSS_RS01800	flavocytochrome c	Lacidipiscis_RS07780	flavocytochrome c
LAC1533_RS01555	dipeptide epimerase	GSS_RS01795	dipeptide epimerase	Lacidipiscis_RS07785	dipeptide epimerase
LAC1533_RS01560	3-oxoacyl-ACP reductase			Lacidipiscis_RS07790	3-oxoacyl-ACP reductase
LAC1533_RS01570	oleate hydratase	GSS_RS01785	oleate hydratase	Lacidipiscis_RS07795	oleate hydratase
LAC1533_RS01575	proline iminopeptidase			Lacidipiscis_RS07800	proline iminopeptidase
LAC1533_RS01580	glycine/betaine ABC transporter			Lacidipiscis_RS07805	glycine/betaine ABC transporter
LAC1533_RS01585	hypothetical protein	GSS_RS01770	hypothetical protein	Lacidipiscis_RS07810	hypothetical protein
LAC1533_RS01590	NUDIX domain-containing protein	GSS_RS01765	NUDIX domain-containing protein	Lacidipiscis_RS07815	NUDIX domain-containing protein
LAC1533_RS01595	MFS transporter	GSS_RS01760	MFS transporter	Lacidipiscis_RS07820	MFS transporter
LAC1533_RS01600	phosphoglycolate phosphatase	GSS_RS01755	phosphoglycolate phosphatase	Lacidipiscis_RS07825	HAD family hydrolase
LAC1533_RS01605	NADP-specific glutamate dehydrogenase	GSS_RS01750	NADP-specific glutamate dehydrogenase	Lacidipiscis_RS07830	NADP-specific glutamate dehydrogenase
LAC1533_RS01610	NADP oxidoreductase	GSS_RS12250	NADP oxidoreductase	Lacidipiscis_RS08855	NADP oxidoreductase
LAC1533_RS01615	LLM class flavin-dependent oxidoreductase	GSS_RS01740	LLM class flavin-dependent oxidoreductase	Lacidipiscis_RS08860	LLM class flavin-dependent oxidoreductase
LAC1533_RS01620	IS30 family transposase				
LAC1533_RS01625	LLM class flavin-dependent oxidoreductase				
LAC1533_RS01630	2-hydroxyacid dehydrogenase	GSS_RS01735	2-hydroxyacid dehydrogenase	Lacidipiscis_RS08865	hydroxyacid dehydrogenase
LAC1533_RS01635	Hsp20/alpha crystallin family protein	GSS_RS01730	Hsp20/alpha crystallin family protein	Lacidipiscis_RS08870	Hsp20/alpha crystallin family protein
LAC1533_RS01640	GNAT family N-acetyltransferase	GSS_RS01725	GNAT family N-acetyltransferase	Lacidipiscis_RS08875	GNAT family N-acetyltransferase
LAC1533_RS01645	hypothetical protein	GSS_RS01720	hypothetical protein	Lacidipiscis_RS08880	hypothetical protein
LAC1533_RS01650	hypothetical protein	GSS_RS01715	hypothetical protein	Lacidipiscis_RS08885	hypothetical protein
LAC1533_RS01655	peptide ABC transporter substrate-binding protein	GSS_RS01710	peptide ABC transporter substrate-binding protein		
LAC1533_RS01660	NAD-dependent succinate-semialdehyde dehydrogenase	GSS_RS01705	NAD-dependent succinate-semialdehyde dehydrogenase		
LAC1533_RS01665	hypothetical protein	GSS_RS01700	hypothetical protein	Lacidipiscis_RS04820	hypothetical protein
LAC1533_RS01670	malate permease	GSS_RS01695	malate permease	Lacidipiscis_RS04825	hypothetical protein
LAC1533_RS01675	malate permease	GSS_RS01690	malate permease	Lacidipiscis_RS04830	hypothetical protein
LAC1533_RS01680	hypothetical protein	GSS_RS01685	hypothetical protein	Lacidipiscis_RS04835	hypothetical protein
LAC1533_RS01685	DNA helicase	GSS_RS01680	DNA helicase		
LAC1533_RS01690	hypothetical protein				
LAC1533_RS01695	DNA-binding protein	GSS_RS13455	DNA-binding protein		
LAC1533_RS01700	XRE family transcriptional regulator	GSS_RS11550	XRE family transcriptional regulator		
LAC1533_RS01705	XRE family transcriptional regulator	GSS_RS01675	XRE family transcriptional regulator		
LAC1533_RS01710	ImmA/IrrE family metallo-endopeptidase	GSS_RS01670	ImmA/IrrE family metallo-endopeptidase		
LAC1533_RS01720	DUF5067 domain-containing protein	GSS_RS01655	DUF5067 domain-containing protein		
LAC1533_RS01725	hypothetical protein				

LAC1533_RS01730	IS30 family transposase				
LAC1533_RS01735	SHOCT domain-containing protein	GSS_RS13955	SHOCT domain-containing protein		
LAC1533_RS01740	site-specific integrase	GSS_RS01640	site-specific integrase		
LAC1533_RS01745	aldehyde dehydrogenase	GSS_RS12240	aldehyde dehydrogenase	Lacidipiscis_RS12635	aldehyde dehydrogenase
LAC1533_RS01750	MarR family transcriptional regulator	GSS_RS12235	MarR family transcriptional regulator	Lacidipiscis_RS12640	MarR family transcriptional regulator
LAC1533_RS01755	ABC transporter ATP-binding protein	GSS_RS01625	ABC transporter ATP-binding protein	Lacidipiscis_RS12645	ABC transporter ATP-binding protein
LAC1533_RS01760	ABC transporter ATP-binding protein	GSS_RS01620	ABC transporter ATP-binding protein	Lacidipiscis_RS12650	ABC transporter ATP-binding protein
LAC1533_RS01765	hypothetical protein	GSS_RS01615	hypothetical protein	Lacidipiscis_RS12655	hypothetical protein
LAC1533_RS01770 IDENTICAL PARALOGS LAC1533_RS02220 IDENTICAL PARALOGS LAC1533_RS06075 IDENTICAL PARALOGS LAC1533_RS07310 IDENTICAL PARALOGS LAC1533_RS07955 IDENTICAL PARALOGS LAC1533_RS09890 IDENTICAL PARALOGS LAC1533_RS09960 IDENTICAL PARALOGS LAC1533_RS11060 IDENTICAL PARALOGS LAC1533_RS11955	IS1380 family transposase	GSS_RS11340	IS1380 family transposase		
LAC1533_RS01775	MFS transporter			Lacidipiscis_RS00975	MFS transporter
LAC1533_RS01780	hypothetical protein	GSS_RS01605	MarR family transcriptional regulator	Lacidipiscis_RS00980	MarR family transcriptional regulator
LAC1533_RS01785	IS1380 family transposase				
LAC1533_RS01790	CsbD family protein	GSS_RS01595	CsbD family protein	Lacidipiscis_RS01005	CsbD family protein
LAC1533_RS01800	OsmC family peroxiredoxin			Lacidipiscis_RS01015	OsmC family peroxiredoxin
LAC1533_RS01810 IDENTICAL PARALOGS LAC1533_RS02005 IDENTICAL PARALOGS LAC1533_RS03100 IDENTICAL PARALOGS LAC1533_RS04825 IDENTICAL PARALOGS LAC1533_RS07620 IDENTICAL PARALOGS LAC1533_RS11575	IS1380 family transposase			Lacidipiscis_RS02450	IS1380 family transposase
LAC1533_RS01815	membrane protein	GSS_RS01575	membrane protein	Lacidipiscis_RS01030	membrane protein
LAC1533_RS01820	fructosamine kinase	GSS_RS01565	fructosamine-3-kinase	Lacidipiscis_RS01035	fructosamine kinase
LAC1533_RS01825	AI-2E family transporter	GSS_RS12220	AI-2E family transporter	Lacidipiscis_RS01040	AI-2E family transporter
LAC1533_RS01830	SDR family NAD(P)-dependent oxidoreductase	GSS_RS01555	SDR family NAD(P)-dependent oxidoreductase	Lacidipiscis_RS01045	SDR family NAD(P)-dependent oxidoreductase
LAC1533_RS01835	TrkA family potassium uptake protein	GSS_RS01550	TrkA family potassium uptake protein	Lacidipiscis_RS01050	TrkA family potassium uptake protein
LAC1533_RS01840	Trk family potassium uptake protein	GSS_RS01545	Trk family potassium uptake protein	Lacidipiscis_RS01055	ATP synthase subunit J
LAC1533_RS01845	DeoR/GlpR transcriptional regulator	GSS_RS01540	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS01060	DeoR/GlpR transcriptional regulator
LAC1533_RS01850	DUF159 family protein	GSS_RS01535	DUF159 family protein	Lacidipiscis_RS01065	DUF159 family protein
LAC1533_RS01865	peptide-methionine (R)-S-oxide reductase	GSS_RS01525	peptide-methionine (R)-S-oxide reductase	Lacidipiscis_RS01075	peptide-methionine (R)-S-oxide reductase
LAC1533_RS01870	GntR family transcriptional regulator	GSS_RS01520	GntR family transcriptional regulator	Lacidipiscis_RS01080	GntR family transcriptional regulator
LAC1533_RS01875	ABC transporter ATP-binding protein	GSS_RS01515	ABC transporter ATP-binding protein	Lacidipiscis_RS01085	ABC transporter ATP-binding protein
LAC1533_RS01880	hypothetical protein	GSS_RS01510	hypothetical protein	Lacidipiscis_RS01090	hypothetical protein
LAC1533_RS01885	BMP family ABC transporter substrate-binding protein	GSS_RS01505	BMP family ABC transporter substrate-binding protein	Lacidipiscis_RS01095	BMP family ABC transporter substrate-binding protein
LAC1533_RS01890	ABC transporter ATP-binding protein	GSS_RS12215	ABC transporter ATP-binding protein	Lacidipiscis_RS01100	ABC transporter ATP-binding protein
LAC1533_RS01895	ABC transporter permease	GSS_RS12210	ABC transporter permease	Lacidipiscis_RS01105	ABC transporter permease
LAC1533_RS01900	ABC transporter permease	GSS_RS01490	ABC transporter permease	Lacidipiscis_RS01110	ABC transporter permease
LAC1533_RS01905 IDENTICAL PARALOGS LAC1533_RS03555 IDENTICAL PARALOGS LAC1533_RS03705 IDENTICAL PARALOGS LAC1533_RS04875 IDENTICAL PARALOGS LAC1533_RS05320 IDENTICAL PARALOGS LAC1533_RS10145 IDENTICAL PARALOGS LAC1533_RS12275	hypothetical protein	GSS_RS13400	hypothetical protein		
LAC1533_RS01910	LemA family protein			Lacidipiscis_RS01115	LemA family protein
LAC1533_RS01915	TPM domain-containing protein	GSS_RS01480	TPM domain-containing protein	Lacidipiscis_RS01120	TPM domain-containing protein
LAC1533_RS01920	demethylmenaquinone methyltransferase	GSS_RS01475	demethylmenaquinone methyltransferase	Lacidipiscis_RS01125	demethylmenaquinone methyltransferase
LAC1533_RS01925	antibiotic biosynthesis monooxygenase	GSS_RS01470	antibiotic biosynthesis monooxygenase	Lacidipiscis_RS01130	antibiotic biosynthesis monooxygenase
LAC1533_RS01930	hypothetical protein	GSS_RS01465	hypothetical protein	Lacidipiscis_RS01135	hypothetical protein
LAC1533_RS01935	CPBP family intramembrane metalloprotease	GSS_RS01460	CPBP family intramembrane metalloprotease	Lacidipiscis_RS01140	CPBP family intramembrane metalloprotease
LAC1533_RS01940	MFS transporter	GSS_RS01455	MFS transporter		
LAC1533_RS01945	DUF4811 domain-containing protein	GSS_RS01450	DUF4811 domain-containing protein	Lacidipiscis_RS01150	DUF4811 domain-containing protein
LAC1533_RS01955	DNA polymerase III subunit alpha	GSS_RS08945	DNA polymerase III subunit alpha	Lacidipiscis_RS01155	DNA polymerase III subunit alpha
LAC1533_RS01960	LD-carboxypeptidase	GSS_RS08950	LD-carboxypeptidase	Lacidipiscis_RS01160	LD-carboxypeptidase

LAC1533_RS01965	peptide ABC transporter substrate-binding protein	GSS_RS08955	peptide ABC transporter substrate-binding protein		
LAC1533_RS01970	D-aminopeptidase	GSS_RS08960	D-aminopeptidase	Lacidipiscis_RS06205	aminopeptidase
LAC1533_RS01975	glycerophosphoryl diester phosphodiesterase	GSS_RS08965	glycerophosphoryl diester phosphodiesterase	Lacidipiscis_RS06210	glycerophosphodiester phosphodiesterase
LAC1533_RS01985	sulfate ABC transporter ATP-binding protein			Lacidipiscis_RS03925	sulfate ABC transporter ATP-binding protein
LAC1533_RS01990	APC family permease			Lacidipiscis_RS03930	APC family permease
LAC1533_RS01995 IDENTICAL PARALOGS LAC1533_RS02625 IDENTICAL PARALOGS LAC1533_RS04385 IDENTICAL PARALOGS LAC1533_RS05130 IDENTICAL PARALOGS LAC1533_RS07085 IDENTICAL PARALOGS LAC1533_RS10750 IDENTICAL PARALOGS LAC1533_RS11020	IS1380 family transposase	GSS_RS11335	IS1380 family transposase		
LAC1533_RS02000 IDENTICAL PARALOGS LAC1533_RS08405 IDENTICAL PARALOGS LAC1533_RS11360	hypothetical protein	GSS_RS11495	transposase		
LAC1533_RS02010	IS66 family insertion sequence hypothetical protein	GSS_RS05460	IS66 family insertion sequence hypothetical protein		
LAC1533_RS02015 IDENTICAL PARALOGS LAC1533_RS08415 IDENTICAL PARALOGS LAC1533_RS11370	hypothetical protein	GSS_RS05465	hypothetical protein	Lacidipiscis_RS02640	hypothetical protein
LAC1533_RS02020	L-lactate oxidase	GSS_RS08970	L-lactate oxidase	Lacidipiscis_RS03935	L-lactate oxidase
LAC1533_RS02025	formate-nitrite transporter	GSS_RS08975	formate/nitrite transporter	Lacidipiscis_RS03940	formate/nitrite transporter
LAC1533_RS02030	hypothetical protein	GSS_RS13065	permease domain-containing protein	Lacidipiscis_RS03945	hypothetical protein
LAC1533_RS02035	protein-tyrosine-phosphatase	GSS_RS08990	protein-tyrosine-phosphatase		
LAC1533_RS02040	NAD(P)-dependent alcohol dehydrogenase	GSS_RS08995	NAD(P)-dependent alcohol dehydrogenase	Lacidipiscis_RS05830	NAD(P)-dependent alcohol dehydrogenase
LAC1533_RS02045	hypothetical protein	GSS_RS13800	hypothetical protein		
LAC1533_RS02050	hypothetical protein	GSS_RS13805	hypothetical protein	Lacidipiscis_RS05825	hypothetical protein
LAC1533_RS02055	PRD domain-containing protein	GSS_RS13815	PRD domain-containing protein	Lacidipiscis_RS05820	PRD domain-containing protein
LAC1533_RS02060	PTS fructose IIA component	GSS_RS09005	PTS fructose IIA component	Lacidipiscis_RS04465	PTS fructose IIA subunit
LAC1533_RS02065	PTS mannose/fructose/sorbose transporter subunit IIB	GSS_RS09010	PTS mannose/fructose/sorbose transporter subunit IIB	Lacidipiscis_RS04470	PTS mannose/fructose/sorbose transporter subunit IIB
LAC1533_RS02070	PTS sugar transporter subunit IIC	GSS_RS09015	PTS sugar transporter subunit IIC	Lacidipiscis_RS04475	PTS sugar transporter subunit IIC
LAC1533_RS02080	alpha-glucosidase	GSS_RS09025	alpha-glucosidase	Lacidipiscis_RS04485	alpha-glucosidase
LAC1533_RS02105	hypothetical protein				
LAC1533_RS02110	hypothetical protein	GSS_RS09040	hypothetical protein	Lacidipiscis_RS04500	hypothetical protein
LAC1533_RS02115	hypothetical protein	GSS_RS09045	hypothetical protein	Lacidipiscis_RS04505	hypothetical protein
LAC1533_RS02120	Arc family DNA-binding protein	GSS_RS09050	Arc family DNA-binding protein	Lacidipiscis_RS04510	Arc family DNA-binding protein
LAC1533_RS02125	SPFH domain-containing protein	GSS_RS13085	SPFH domain-containing protein	Lacidipiscis_RS04515	SPFH domain-containing protein
LAC1533_RS02130	hypothetical protein			Lacidipiscis_RS04520	hypothetical protein
LAC1533_RS02135	hypothetical protein	GSS_RS09070	hypothetical protein	Lacidipiscis_RS04525	hypothetical protein
LAC1533_RS02140	cation-translocating P-type ATPase	GSS_RS09075	cation-translocating P-type ATPase	Lacidipiscis_RS04530	cation-translocating P-type ATPase
LAC1533_RS02145	NADH peroxidase	GSS_RS09080	NADH peroxidase	Lacidipiscis_RS04535	NAD(FAD)-dependent dehydrogenase
LAC1533_RS02150	N-acetyltransferase	GSS_RS09085	N-acetyltransferase	Lacidipiscis_RS04540	N-acetyltransferase
LAC1533_RS02155	hypothetical protein	GSS_RS09090	hypothetical protein	Lacidipiscis_RS04545	hypothetical protein
LAC1533_RS02160	Na+/H+ antiporter NhaC	GSS_RS09095	Na+/H+ antiporter NhaC	Lacidipiscis_RS04550	Na+/H+ antiporter NhaC
LAC1533_RS02165	family 65 glycosyl hydrolase			Lacidipiscis_RS04555	maltose phosphorylase
LAC1533_RS02170	beta-phosphoglucomutase	GSS_RS09110	beta-phosphoglucomutase	Lacidipiscis_RS04560	beta-phosphoglucomutase
LAC1533_RS02175	LacI family transcriptional regulator	GSS_RS09115	LacI family transcriptional regulator	Lacidipiscis_RS04565	LacI family transcriptional regulator
LAC1533_RS02180 IDENTICAL PARALOGS LAC1533_RS02620 IDENTICAL PARALOGS LAC1533_RS06625 IDENTICAL PARALOGS LAC1533_RS06775 IDENTICAL PARALOGS LAC1533_RS07495 IDENTICAL PARALOGS LAC1533_RS12225	transposase				
LAC1533_RS02185	alpha-glucosidase	GSS_RS09120	alpha-glucosidase	Lacidipiscis_RS04570	alpha-glucosidase
LAC1533_RS02190	alpha-glycosidase	GSS_RS09125	alpha-glycosidase	Lacidipiscis_RS04575	alpha-glycosidase
LAC1533_RS02195	carbohydrate ABC transporter substrate-binding protein				
LAC1533_RS02200	sugar ABC transporter permease				
LAC1533_RS02205	carbohydrate ABC transporter permease				
LAC1533_RS02210	hypothetical protein				
LAC1533_RS02215	ABC transporter ATP-binding protein	GSS_RS09150	ABC transporter ATP-binding protein	Lacidipiscis_RS04600	ABC transporter ATP-binding protein
LAC1533_RS02225	DJ-1 family protein	GSS_RS09155	DJ-1 family protein	Lacidipiscis_RS04605	DJ-1 family protein
LAC1533_RS02230	hypothetical protein	GSS_RS09160	hypothetical protein	Lacidipiscis_RS04610	hypothetical protein
LAC1533_RS02245	DegV family protein	GSS_RS09165	DegV family protein	Lacidipiscis_RS11685	DegV family protein
LAC1533_RS02250	dipeptidase	GSS_RS09170	dipeptidase	Lacidipiscis_RS11680	dipeptidase
LAC1533_RS02255	NAD(P)H-hydrate epimerase	GSS_RS09175	NAD(P)H-hydrate epimerase	Lacidipiscis_RS04385	NAD(P)H-hydrate epimerase
LAC1533_RS02260	ArsR family transcriptional regulator	GSS_RS09180	ArsR family transcriptional regulator	Lacidipiscis_RS04390	ArsR family transcriptional regulator
LAC1533_RS02265	cation transporter	GSS_RS09185	cation transporter	Lacidipiscis_RS04395	cation transporter
LAC1533_RS02270	hypothetical protein	GSS_RS13820	short-chain dehydrogenase/reductase SDR	Lacidipiscis_RS04400	short-chain dehydrogenase/reductase SDR

LAC1533_RS02275	hypothetical protein	GSS_RS13105	hypothetical protein	Lacidipiscis_RS04180	hypothetical protein
LAC1533_RS02280	alpha/beta hydrolase	GSS_RS09200	alpha/beta hydrolase	Lacidipiscis_RS04185	alpha/beta hydrolase
LAC1533_RS02285	alpha,alpha-phosphotrehalase			Lacidipiscis_RS04190	alpha,alpha-phosphotrehalase
LAC1533_RS02290	trehalose operon repressor			Lacidipiscis_RS04195	trehalose operon repressor
LAC1533_RS02295	hypothetical protein	GSS_RS14175	hypothetical protein	Lacidipiscis_RS04200	hypothetical protein
LAC1533_RS02300	PTS glucose transporter subunit IIBC	GSS_RS13120	PTS glucose transporter subunit IIBC	Lacidipiscis_RS04205	PTS glucose transporter subunit IIBC
LAC1533_RS02305	hypothetical protein	GSS_RS09235	hypothetical protein	Lacidipiscis_RS04210	hypothetical protein
LAC1533_RS02310	NAD(P)-dependent oxidoreductase			Lacidipiscis_RS04215	NAD(P)-dependent oxidoreductase
LAC1533_RS02315	MFS transporter	GSS_RS09245	MFS transporter	Lacidipiscis_RS04220	MFS transporter
LAC1533_RS02320	copper-translocating P-type ATPase	GSS_RS09250	copper-translocating P-type ATPase	Lacidipiscis_RS04225	copper-translocating P-type ATPase
LAC1533_RS02325	glutamate formiminotransferase	GSS_RS09255	glutamate formiminotransferase	Lacidipiscis_RS04230	glutamate formiminotransferase
LAC1533_RS02330	bifunctional 5,10-methylenetetrahydrofolate dehydrogenase/5,10-methenyltetrahydrofolate cyclohydrolase	GSS_RS09260	bifunctional 5,10-methylenetetrahydrofolate dehydrogenase/5,10-methenyltetrahydrofolate cyclohydrolase	Lacidipiscis_RS04235	bifunctional 5,10-methylenetetrahydrofolate dehydrogenase/5,10-methenyltetrahydrofolate cyclohydrolase
LAC1533_RS02335	zinc-binding alcohol dehydrogenase family protein	GSS_RS09265	zinc-binding alcohol dehydrogenase family protein	Lacidipiscis_RS04240	zinc-binding alcohol dehydrogenase family protein
LAC1533_RS02340	o-succinylbenzoate--CoA ligase	GSS_RS09270	o-succinylbenzoate--CoA ligase	Lacidipiscis_RS04245	o-succinylbenzoate--CoA ligase
LAC1533_RS02345	1,4-dihydroxy-2-naphthoyl-CoA synthase	GSS_RS09275	1,4-dihydroxy-2-naphthoyl-CoA synthase	Lacidipiscis_RS04250	1,4-dihydroxy-2-naphthoyl-CoA synthase
LAC1533_RS02350	PaaI family thioesterase	GSS_RS09280	PaaI family thioesterase	Lacidipiscis_RS04255	PaaI family thioesterase
LAC1533_RS02355	replication-associated recombination protein A	GSS_RS09290	replication-associated recombination protein A	Lacidipiscis_RS04260	replication-associated recombination protein A
LAC1533_RS02360	Hsp20/alpha crystallin family protein	GSS_RS09295	Hsp20/alpha crystallin family protein	Lacidipiscis_RS04265	Hsp20/alpha crystallin family protein
LAC1533_RS02365	AarF/ABC1/UbiB kinase family protein	GSS_RS09300	AarF/ABC1/UbiB kinase family protein	Lacidipiscis_RS04270	AarF/ABC1/UbiB kinase family protein
LAC1533_RS02370	peptide ABC transporter substrate-binding protein	GSS_RS09305	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS04275	peptide ABC transporter substrate-binding protein
LAC1533_RS02380	hypothetical protein			Lacidipiscis_RS06190	hypothetical protein
LAC1533_RS02385	carbonic anhydrase	GSS_RS09320	carbonic anhydrase	Lacidipiscis_RS04135	carbonic anhydrase
LAC1533_RS02390	sigma-54-dependent transcriptional regulator	GSS_RS09325	sigma-54-dependent transcriptional regulator	Lacidipiscis_RS04140	sigma-54-dependent transcriptional regulator
LAC1533_RS02395	PTS fructose transporter subunit IIB	GSS_RS09330	PTS fructose transporter subunit IIB	Lacidipiscis_RS04145	PTS fructose transporter subunit IIB
LAC1533_RS02400	PTS mannose transporter subunit IIAB	GSS_RS09335	PTS mannose transporter subunit IIAB	Lacidipiscis_RS04150	PTS mannose transporter subunit IIAB
LAC1533_RS02405	PTS mannose/fructose/sorbose transporter subunit IIC	GSS_RS09340	PTS mannose/fructose/sorbose transporter subunit IIC	Lacidipiscis_RS04155	PTS mannose/fructose/sorbose transporter subunit IIC
LAC1533_RS02410	PTS mannose family transporter subunit IID	GSS_RS09345	PTS mannose transporter subunit IID	Lacidipiscis_RS04160	PTS mannose transporter subunit IID
LAC1533_RS02415	DUF956 domain-containing protein	GSS_RS09350	DUF956 domain-containing protein	Lacidipiscis_RS04165	DUF956 domain-containing protein
LAC1533_RS02435	DUF975 domain-containing protein			Lacidipiscis_RS06995	DUF975 domain-containing protein
LAC1533_RS02440	neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	GSS_RS05675	Neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	Lacidipiscis_RS07000	neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase
LAC1533_RS02445	helix-turn-helix domain-containing protein				
LAC1533_RS02450	hypothetical protein				
LAC1533_RS02455	LysM peptidoglycan-binding domain-containing protein	GSS_RS05680	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS00140	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS02460	LysM peptidoglycan-binding domain-containing protein				
LAC1533_RS02465	uracil-DNA glycosylase	GSS_RS05685	uracil-DNA glycosylase	Lacidipiscis_RS03845	uracil-DNA glycosylase
LAC1533_RS02475	folate family ECF transporter S component	GSS_RS05695	folate family ECF transporter S component	Lacidipiscis_RS03835	folate family ECF transporter S component
LAC1533_RS02480	metal ABC transporter permease	GSS_RS05700	metal ABC transporter permease	Lacidipiscis_RS03830	metal ABC transporter permease
LAC1533_RS02485	ABC transporter ATP-binding protein	GSS_RS05705	ABC transporter ATP-binding protein	Lacidipiscis_RS03825	ABC transporter ATP-binding protein
LAC1533_RS02490	QueT transporter family protein	GSS_RS05710	QueT transporter family protein	Lacidipiscis_RS03820	QueT transporter family protein
LAC1533_RS02495	DUF2829 domain-containing protein	GSS_RS05715	DUF2829 domain-containing protein	Lacidipiscis_RS03815	DUF2829 domain-containing protein
LAC1533_RS02500	3-oxoacyl-ACP reductase	GSS_RS05720	3-oxoacyl-ACP reductase	Lacidipiscis_RS03810	3-oxoacyl-ACP reductase
LAC1533_RS02505	HD domain-containing protein	GSS_RS05725	HD domain-containing protein	Lacidipiscis_RS03805	HD domain-containing protein
LAC1533_RS02510	lipase/esterase	GSS_RS05730	lipase/esterase	Lacidipiscis_RS03800	lipase
LAC1533_RS02515	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	GSS_RS05735	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	Lacidipiscis_RS03795	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG
LAC1533_RS02520	nucleoid occlusion protein	GSS_RS05740	nucleoid occlusion protein	Lacidipiscis_RS03790	nucleoid occlusion protein
LAC1533_RS02525	ParA family protein	GSS_RS05745	ParA family protein	Lacidipiscis_RS03785	ParA family protein
LAC1533_RS02530	chromosome partitioning protein ParB	GSS_RS05750	chromosome partitioning protein ParB	Lacidipiscis_RS03780	chromosome partitioning protein ParB
LAC1533_RS02535	DUF951 domain-containing protein	GSS_RS14060	DUF951 domain-containing protein	Lacidipiscis_RS03775	DUF951 domain-containing protein
LAC1533_RS02540	redox-regulated ATPase YchF	GSS_RS05760	redox-regulated ATPase YchF	Lacidipiscis_RS03770	redox-regulated ATPase YchF
LAC1533_RS02545	DUF1129 domain-containing protein	GSS_RS05765	DUF1129 domain-containing protein	Lacidipiscis_RS03765	DUF1129 domain-containing protein
LAC1533_RS02550	Cof-type HAD-IIB family hydrolase	GSS_RS05770	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS03760	Cof-type HAD-IIB family hydrolase
LAC1533_RS02555	gluconate transporter			Lacidipiscis_RS03755	gluconate transporter
LAC1533_RS02560	excinuclease ABC subunit UvrA	GSS_RS05780	excinuclease ABC subunit UvrA	Lacidipiscis_RS03750	excinuclease ABC subunit UvrA
LAC1533_RS02565	serine hydrolase	GSS_RS05785	serine hydrolase		
LAC1533_RS02570	histidine phosphatase family protein	GSS_RS05795	histidine phosphatase family protein	Lacidipiscis_RS03740	histidine phosphatase family protein
LAC1533_RS02575	histidine phosphatase family protein	GSS_RS05800	histidine phosphatase family protein	Lacidipiscis_RS03735	histidine phosphatase family protein

LAC1533_RS02580	MFS transporter	GSS_RS05805	MFS transporter	Lacidipiscis_RS03730	MFS transporter
LAC1533_RS02585	glutamate 5-kinase	GSS_RS12675	glutamate 5-kinase	Lacidipiscis_RS03725	glutamate 5-kinase
LAC1533_RS02590	glutamate-5-semialdehyde dehydrogenase	GSS_RS05815	glutamate-5-semialdehyde dehydrogenase	Lacidipiscis_RS03720	glutamate-5-semialdehyde dehydrogenase
LAC1533_RS02595	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein			Lacidipiscis_RS03715	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein
LAC1533_RS02600	aldo/keto reductase	GSS_RS05825	aldo/keto reductase	Lacidipiscis_RS01675	aldo/keto reductase
LAC1533_RS02605	endonuclease III	GSS_RS05830	hypothetical protein	Lacidipiscis_RS01670	endonuclease III
LAC1533_RS02610	ribose-phosphate pyrophosphokinase	GSS_RS05835	ribose-phosphate pyrophosphokinase	Lacidipiscis_RS01665	ribose-phosphate pyrophosphokinase
LAC1533_RS02615	aminopeptidase	GSS_RS05840	aminopeptidase	Lacidipiscis_RS01660	aminopeptidase
LAC1533_RS02630	adenosine deaminase	GSS_RS05845	adenosine deaminase	Lacidipiscis_RS01655	adenosine deaminase
LAC1533_RS02635	hypothetical protein	GSS_RS05850	hypothetical protein	Lacidipiscis_RS01650	hypothetical protein
LAC1533_RS02640	cation-translocating P-type ATPase	GSS_RS05855	cation-translocating P-type ATPase	Lacidipiscis_RS01645	cation-translocating P-type ATPase
LAC1533_RS02645	ABC transporter ATP-binding protein	GSS_RS05865	ABC transporter ATP-binding protein	Lacidipiscis_RS01640	ABC transporter ATP-binding protein
LAC1533_RS02655	dipeptidase	GSS_RS05880	dipeptidase		
LAC1533_RS02660	class I SAM-dependent methyltransferase	GSS_RS05885	class I SAM-dependent methyltransferase	Lacidipiscis_RS01625	class I SAM-dependent methyltransferase
LAC1533_RS02665	hypothetical protein	GSS_RS05890	hypothetical protein	Lacidipiscis_RS01620	hypothetical protein
LAC1533_RS02670	MurR/RpiR family transcriptional regulator	GSS_RS05895	MurR/RpiR family transcriptional regulator	Lacidipiscis_RS01615	MurR/RpiR family transcriptional regulator
LAC1533_RS02675	N-acetylmuramic acid 6-phosphate etherase	GSS_RS05900	N-acetylmuramic acid 6-phosphate etherase	Lacidipiscis_RS01610	N-acetylmuramic acid 6-phosphate etherase
LAC1533_RS02680	PTS beta-glucoside transporter subunit EIIBCA	GSS_RS05905	PTS beta-glucoside transporter subunit EIIBCA	Lacidipiscis_RS01605	PTS glucose transporter
LAC1533_RS02685	methionine ABC transporter ATP-binding protein	GSS_RS05910	methionine ABC transporter ATP-binding protein	Lacidipiscis_RS01600	methionine ABC transporter ATP-binding protein
LAC1533_RS02690	ABC transporter permease	GSS_RS05915	ABC transporter permease	Lacidipiscis_RS01595	ABC transporter permease
LAC1533_RS02695	MetQ/NlpA family ABC transporter substrate-binding protein			Lacidipiscis_RS01590	MetQ/NlpA family ABC transporter substrate-binding protein
LAC1533_RS02700	HlyC/CorC family transporter	GSS_RS05930	HlyC/CorC family transporter	Lacidipiscis_RS01585	HlyC/CorC family transporter
LAC1533_RS02705	protein-tyrosine-phosphatase	GSS_RS05935	protein-tyrosine-phosphatase	Lacidipiscis_RS01580	protein-tyrosine-phosphatase
LAC1533_RS02710	methylated-DNA--[protein]-cysteine S-methyltransferase	GSS_RS05940	methylated-DNA--[protein]-cysteine S-methyltransferase	Lacidipiscis_RS01575	methylated-DNA--[protein]-cysteine S-methyltransferase
LAC1533_RS02715	undecaprenyl-diphosphate phosphatase	GSS_RS05945	undecaprenyl-diphosphate phosphatase	Lacidipiscis_RS01570	undecaprenyl-diphosphate phosphatase
LAC1533_RS02720	phosphopyruvate hydratase	GSS_RS05950	phosphopyruvate hydratase	Lacidipiscis_RS01565	phosphopyruvate hydratase
LAC1533_RS02725	hypothetical protein			Lacidipiscis_RS08200	hypothetical protein
LAC1533_RS02730	alpha-galactosidase	GSS_RS05955	alpha-galactosidase	Lacidipiscis_RS10520	alpha-galactosidase
LAC1533_RS02735	hypothetical protein	GSS_RS05960	hypothetical protein	Lacidipiscis_RS10515	hypothetical protein
LAC1533_RS02740	hypothetical protein	GSS_RS05965	hypothetical protein	Lacidipiscis_RS10510	hypothetical protein
LAC1533_RS02745	threonine/serine exporter	GSS_RS05970	threonine/serine exporter	Lacidipiscis_RS10505	threonine/serine exporter
LAC1533_RS02750	threonine/serine exporter	GSS_RS05975	threonine/serine exporter	Lacidipiscis_RS10500	threonine/serine exporter
LAC1533_RS02760	glutamyl-tRNA amidotransferase subunit A	GSS_RS05985	glutamyl-tRNA amidotransferase subunit A	Lacidipiscis_RS10490	glutamyl-tRNA amidotransferase
LAC1533_RS02765	nucleoside-diphosphate kinase	GSS_RS05990	nucleoside-diphosphate kinase	Lacidipiscis_RS10485	nucleoside-diphosphate kinase
LAC1533_RS02770 IDENTICAL PARALOGS LAC1533_RS06930 IDENTICAL PARALOGS LAC1533_RS07625 IDENTICAL PARALOGS LAC1533_RS09480 IDENTICAL PARALOGS LAC1533_RS11780	IS982 family transposase				
LAC1533_RS02775	(deoxy)nucleoside triphosphate pyrophosphohydrolase	GSS_RS05995	(deoxy)nucleoside triphosphate pyrophosphohydrolase	Lacidipiscis_RS10480	(deoxy)nucleoside triphosphate pyrophosphohydrolase
LAC1533_RS02780	DUF3427 domain-containing protein	GSS_RS06000	DUF3427 domain-containing protein	Lacidipiscis_RS10475	DUF3427 domain-containing protein
LAC1533_RS02785	IMP dehydrogenase	GSS_RS06005	IMP dehydrogenase	Lacidipiscis_RS10470	IMP dehydrogenase
LAC1533_RS02790	large-conductance mechanosensitive channel protein MscL	GSS_RS06010	large-conductance mechanosensitive channel protein MscL	Lacidipiscis_RS10465	large-conductance mechanosensitive channel protein MscL
LAC1533_RS02795 IDENTICAL PARALOGS LAC1533_RS03115 IDENTICAL PARALOGS LAC1533_RS04380 IDENTICAL PARALOGS LAC1533_RS07245 IDENTICAL PARALOGS LAC1533_RS10090 IDENTICAL PARALOGS LAC1533_RS10270 IDENTICAL PARALOGS LAC1533_RS10445	IS30 family transposase				
LAC1533_RS02800	nitroreductase	GSS_RS06015	nitroreductase	Lacidipiscis_RS10460	nitroreductase
LAC1533_RS02805	LysM domain-containing protein	GSS_RS06020	LysM domain-containing protein	Lacidipiscis_RS10455	LysM domain-containing protein
LAC1533_RS02810	glyoxalase	GSS_RS06025	glyoxalase	Lacidipiscis_RS10450	glyoxalase
LAC1533_RS02815	hypothetical protein	GSS_RS06030	hypothetical protein	Lacidipiscis_RS10445	hypothetical protein
LAC1533_RS02820	UDP-glucose 4-epimerase GalE	GSS_RS06035	UDP-glucose 4-epimerase GalE	Lacidipiscis_RS10440	UDP-glucose 4-epimerase GalE
LAC1533_RS02825	hypothetical protein	GSS_RS06040	hypothetical protein	Lacidipiscis_RS10435	hypothetical protein
LAC1533_RS02830	hypothetical protein	GSS_RS06045	hypothetical protein	Lacidipiscis_RS10430	hypothetical protein
LAC1533_RS02835	galactose mutarotase	GSS_RS06050	galactose mutarotase	Lacidipiscis_RS10425	galactose mutarotase
LAC1533_RS02840	HAD family hydrolase	GSS_RS06055	HAD family hydrolase	Lacidipiscis_RS03205	HAD family hydrolase
LAC1533_RS02845	AI-2E family transporter	GSS_RS06060	AI-2E family transporter	Lacidipiscis_RS03200	AI-2E family transporter
LAC1533_RS02850	pyridoxal phosphate-dependent aminotransferase	GSS_RS06065	pyridoxal phosphate-dependent aminotransferase	Lacidipiscis_RS03195	pyridoxal phosphate-dependent aminotransferase
LAC1533_RS02855	2,3-diphosphoglycerate-dependent phosphoglycerate mutase	GSS_RS06070	2,3-diphosphoglycerate-dependent phosphoglycerate mutase	Lacidipiscis_RS03190	2,3-diphosphoglycerate-dependent phosphoglycerate mutase
LAC1533_RS02870	hypothetical protein	GSS_RS12705	hypothetical protein	Lacidipiscis_RS05340	hypothetical protein

LAC1533_RS02885	DNA starvation/stationary phase protection protein	GSS_RS06205	DNA starvation/stationary phase protection protein	Lacidipiscis_RS05355	DNA starvation/stationary phase protection protein
LAC1533_RS02890	hypothetical protein			Lacidipiscis_RS05360	hypothetical protein
LAC1533_RS02900	Crp/Fnr family transcriptional regulator	GSS_RS06220	Crp/Fnr family transcriptional regulator	Lacidipiscis_RS05370	Crp/Fnr family transcriptional regulator
LAC1533_RS02905	copper chaperone	GSS_RS06225	copper chaperone	Lacidipiscis_RS05375	copper chaperone
LAC1533_RS02910	DNA starvation/stationary phase protection protein	GSS_RS06230	DNA starvation/stationary phase protection protein	Lacidipiscis_RS05380	DNA starvation/stationary phase protection protein
LAC1533_RS02915	metal-sensitive transcriptional regulator	GSS_RS06240	metal-sensitive transcriptional regulator	Lacidipiscis_RS05385	metal-sensitive transcriptional regulator
LAC1533_RS02920	thioredoxin	GSS_RS06245	thioredoxin	Lacidipiscis_RS05390	thioredoxin
LAC1533_RS02925	aquaporin family protein	GSS_RS06250	aquaporin family protein	Lacidipiscis_RS05395	aquaporin family protein
LAC1533_RS02930	transposase				
LAC1533_RS02935	copper-translocating P-type ATPase			Lacidipiscis_RS05400	copper-translocating P-type ATPase
LAC1533_RS02940	hypothetical protein	GSS_RS14075	hypothetical protein	Lacidipiscis_RS05405	hypothetical protein
LAC1533_RS02945	hypothetical protein	GSS_RS06265	hypothetical protein	Lacidipiscis_RS05410	hypothetical protein
LAC1533_RS02950 IDENTICAL PARALOGS LAC1533_RS04120	IS1380 family transposase				
LAC1533_RS02955	MarR family transcriptional regulator	GSS_RS06280	MarR family transcriptional regulator	Lacidipiscis_RS05415	MarR family transcriptional regulator
LAC1533_RS02960	hypothetical protein				
LAC1533_RS02970	hypothetical protein				
LAC1533_RS02975	IS30 family transposase				
LAC1533_RS02980	bifunctional lysylphosphatidylglycerol flippase/synthetase MprF			Lacidipiscis_RS05430	bifunctional lysylphosphatidylglycerol flippase/synthetase MprF
LAC1533_RS02985	tRNA-dihydrouridine synthase	GSS_RS06305	tRNA-dihydrouridine synthase	Lacidipiscis_RS05435	tRNA-dihydrouridine synthase
LAC1533_RS02990	hypothetical protein	GSS_RS06310	hypothetical protein	Lacidipiscis_RS05440	hypothetical protein
LAC1533_RS02995	succinyl-diaminopimelate desuccinylase	GSS_RS06315	succinyl-diaminopimelate desuccinylase	Lacidipiscis_RS05445	succinyl-diaminopimelate desuccinylase
LAC1533_RS03000	DUF554 domain-containing protein	GSS_RS06320	DUF554 domain-containing protein	Lacidipiscis_RS05450	DUF554 domain-containing protein
LAC1533_RS03005	flavodoxin family protein	GSS_RS06325	flavodoxin family protein	Lacidipiscis_RS05455	flavodoxin family protein
LAC1533_RS03010	DUF4767 domain-containing protein	GSS_RS12740	DUF4767 domain-containing protein	Lacidipiscis_RS05460	DUF4767 domain-containing protein
LAC1533_RS03015	hypothetical protein	GSS_RS06335	hypothetical protein	Lacidipiscis_RS05465	hypothetical protein
LAC1533_RS03020	hypothetical protein	GSS_RS06340	hypothetical protein	Lacidipiscis_RS05470	hypothetical protein
LAC1533_RS03025	RluA family pseudouridine synthase	GSS_RS06350	RluA family pseudouridine synthase	Lacidipiscis_RS05475	RluA family pseudouridine synthase
LAC1533_RS03030	DUF3114 domain-containing protein	GSS_RS12745	DUF3114 domain-containing protein	Lacidipiscis_RS05480	DUF3114 domain-containing protein
LAC1533_RS03035	hypothetical protein	GSS_RS06360	hypothetical protein	Lacidipiscis_RS05485	hypothetical protein
LAC1533_RS03040	OsmC family peroxiredoxin	GSS_RS06365	OsmC family peroxiredoxin	Lacidipiscis_RS05490	OsmC family peroxiredoxin
LAC1533_RS03045	YitT family protein	GSS_RS06370	YitT family protein	Lacidipiscis_RS05495	YitT family protein
LAC1533_RS03050	phosphoketolase family protein	GSS_RS06375	phosphoketolase family protein	Lacidipiscis_RS05500	phosphoketolase family protein
LAC1533_RS03055	hypothetical protein	GSS_RS06380	hypothetical protein	Lacidipiscis_RS05505	hypothetical protein
LAC1533_RS03060	NERD domain-containing protein	GSS_RS06390	NERD domain-containing protein	Lacidipiscis_RS05510	NERD domain-containing protein
LAC1533_RS03065	RNA methylase	GSS_RS06395	RNA methylase	Lacidipiscis_RS05515	RNA methylase
LAC1533_RS03070	YfcC family protein	GSS_RS06400	YfcC family protein	Lacidipiscis_RS05520	YfcC family protein
LAC1533_RS03075	acetylornithine deacetylase	GSS_RS06405	acetylornithine deacetylase	Lacidipiscis_RS05525	acetylornithine deacetylase
LAC1533_RS03080	LemA family protein	GSS_RS06415	LemA family protein	Lacidipiscis_RS05530	LemA family protein
LAC1533_RS03085	heat-shock protein HtpX	GSS_RS06420	heat-shock protein HtpX	Lacidipiscis_RS05535	heat-shock protein HtpX
LAC1533_RS03105	DUF871 domain-containing protein	GSS_RS09780	DUF871 domain-containing protein	Lacidipiscis_RS00850	DUF871 domain-containing protein
LAC1533_RS03110	deoxyribonuclease	GSS_RS09785	deoxyribonuclease	Lacidipiscis_RS00845	deoxyribonuclease
LAC1533_RS03120	TetR/AcrR family transcriptional regulator	GSS_RS13830	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS00840	TetR/AcrR family transcriptional regulator
LAC1533_RS03130	ABC transporter ATP-binding protein	GSS_RS09805	ABC transporter ATP-binding protein	Lacidipiscis_RS00830	ABC transporter ATP-binding protein
LAC1533_RS03135	hypothetical protein	GSS_RS13835	hypothetical protein	Lacidipiscis_RS00825	hypothetical protein
LAC1533_RS03140	glycosyltransferase family 8 protein	GSS_RS09825	glycosyltransferase family 8 protein	Lacidipiscis_RS09505	glycosyltransferase family 8 protein
LAC1533_RS03145	deoxyribose-phosphate aldolase	GSS_RS13210	deoxyribose-phosphate aldolase	Lacidipiscis_RS09500	deoxyribose-phosphate aldolase
LAC1533_RS03155	hypothetical protein				
LAC1533_RS03160	IS982 family transposase	GSS_RS11505	transposase	Lacidipiscis_RS05855	IS982 family transposase
LAC1533_RS03165	IS982 family transposase			Lacidipiscis_RS06900 IDENTICAL PARALOGS Lacidipiscis_RS03210	IS982 family transposase
LAC1533_RS03170	hypothetical protein	GSS_RS13845	hypothetical protein		
LAC1533_RS03175	galactose mutarotase	GSS_RS13850	galactose mutarotase		
LAC1533_RS03180	hypothetical protein	GSS_RS09840	hypothetical protein		
LAC1533_RS03190	PEP phosphonomutase	GSS_RS09850	PEP phosphonomutase		
LAC1533_RS03195	hypothetical protein	GSS_RS09855	hypothetical protein	Lacidipiscis_RS00010	hypothetical protein
LAC1533_RS03200	NADH-dependent alcohol dehydrogenase	GSS_RS09865	NADH-dependent alcohol dehydrogenase	Lacidipiscis_RS00005	NADH-dependent alcohol dehydrogenase
LAC1533_RS03205	HAD family phosphatase	GSS_RS09870	HAD family phosphatase	Lacidipiscis_RS11990	HAD family phosphatase
LAC1533_RS03220	energy-coupling factor transporter transmembrane protein EcfT	GSS_RS09885	energy-coupling factor transporter transmembrane protein EcfT	Lacidipiscis_RS11975	energy-coupling factor transporter transmembrane protein EcfT

LAC1533_RS03225	LysM peptidoglycan-binding domain-containing protein	GSS_RS09890	LysM domain-containing protein	Lacidipiscis_RS11970	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS03230	tRNA epoxyqueuosine(34) reductase QueG	GSS_RS09895	tRNA epoxyqueuosine(34) reductase QueG	Lacidipiscis_RS13315	tRNA epoxyqueuosine(34) reductase QueG
LAC1533_RS03235	DUF4430 domain-containing protein	GSS_RS09900	DUF4430 domain-containing protein	Lacidipiscis_RS13310	DUF4430 domain-containing protein
LAC1533_RS03240	deoxynucleoside kinase	GSS_RS09905	deoxyadenosine kinase	Lacidipiscis_RS13305	deoxyadenosine kinase
LAC1533_RS03245	DUF1440 domain-containing protein	GSS_RS09910	DUF1440 domain-containing protein	Lacidipiscis_RS13300	DUF1440 domain-containing protein
LAC1533_RS03250	MFS transporter	GSS_RS09915	sodium:solute symporter	Lacidipiscis_RS13295	sodium:solute symporter
LAC1533_RS03255	linear amide C-N hydrolase	GSS_RS09920	linear amide C-N hydrolase	Lacidipiscis_RS13290	linear amide C-N hydrolase
LAC1533_RS03260	KR domain-containing protein	GSS_RS09925	KR domain-containing protein		
LAC1533_RS03265	NAD(P)/FAD-dependent oxidoreductase	GSS_RS09930	NAD(P)/FAD-dependent oxidoreductase		
LAC1533_RS03275	maturase				
LAC1533_RS03285	hypothetical protein				
LAC1533_RS03295	cytochrome ubiquinol oxidase subunit I	GSS_RS09935	cytochrome ubiquinol oxidase subunit I	Lacidipiscis_RS04955	cytochrome ubiquinol oxidase subunit I
LAC1533_RS03300	cytochrome d ubiquinol oxidase subunit II	GSS_RS09940	cytochrome d ubiquinol oxidase subunit II	Lacidipiscis_RS04950	cytochrome d ubiquinol oxidase subunit II
LAC1533_RS03305	thiol reductant ABC exporter subunit CydD	GSS_RS09945	thiol reductant ABC exporter subunit CydD	Lacidipiscis_RS04945	thiol reductant ABC exporter subunit CydD
LAC1533_RS03310	thiol reductant ABC exporter subunit CydC	GSS_RS09950	thiol reductant ABC exporter subunit CydC	Lacidipiscis_RS04940	thiol reductant ABC exporter subunit CydC
LAC1533_RS03315	polyprenyl diphosphate synthase			Lacidipiscis_RS04935	polyprenyl diphosphate synthase
LAC1533_RS03325	prenyltransferase	GSS_RS09960	1,4-dihydroxy-2-naphthoate polyprenyltransferase	Lacidipiscis_RS04930	1,4-dihydroxy-2-naphthoate polyprenyltransferase
LAC1533_RS03330	NAD(P)/FAD-dependent oxidoreductase	GSS_RS09965	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS04925	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS03335	D-2-hydroxyacid dehydrogenase	GSS_RS09970	D-2-hydroxyacid dehydrogenase	Lacidipiscis_RS04920	hydroxyacid dehydrogenase
LAC1533_RS03340	metal-dependent hydrolase	GSS_RS09975	metal-dependent hydrolase	Lacidipiscis_RS04915	metal-dependent hydrolase
LAC1533_RS03345	MFS transporter	GSS_RS09980	MFS transporter		
LAC1533_RS03350	hypothetical protein	GSS_RS09985	hypothetical protein	Lacidipiscis_RS04905	hypothetical protein
LAC1533_RS03355	peroxidase	GSS_RS09990	peroxidase	Lacidipiscis_RS04900	peroxidase
LAC1533_RS03360	iron-sulfur cluster biosynthesis family protein	GSS_RS09995	iron-sulfur cluster biosynthesis family protein	Lacidipiscis_RS04895	iron-sulfur cluster biosynthesis family protein
LAC1533_RS03365	PLP-dependent aminotransferase family protein	GSS_RS10000	PLP-dependent aminotransferase family protein	Lacidipiscis_RS04890	PLP-dependent aminotransferase family protein
LAC1533_RS03375 IDENTICAL PARALOGS LAC1533_RS10285	group II intron reverse transcriptase/maturase				
LAC1533_RS03380	CBS domain-containing protein	GSS_RS10005	CBS domain-containing protein	Lacidipiscis_RS04870	CBS domain-containing protein
LAC1533_RS03385	ABC transporter permease	GSS_RS10010	ABC transporter permease	Lacidipiscis_RS04865	ABC transporter permease
LAC1533_RS03390	osmoprotectant ABC transporter substrate-binding protein	GSS_RS10015	osmoprotectant ABC transporter substrate-binding protein	Lacidipiscis_RS04860	osmoprotectant ABC transporter substrate-binding protein
LAC1533_RS03395	ABC transporter permease	GSS_RS10020	ABC transporter permease	Lacidipiscis_RS04855	ABC transporter permease
LAC1533_RS03400	glycosyltransferase family 8 protein	GSS_RS10025	glycosyltransferase family 8 protein	Lacidipiscis_RS04850	glycosyltransferase family 8 protein
LAC1533_RS03405	hypothetical protein	GSS_RS10030	hypothetical protein	Lacidipiscis_RS04845	SAM-dependent methyltransferase
LAC1533_RS03410 IDENTICAL PARALOGS LAC1533_RS04045 IDENTICAL PARALOGS LAC1533_RS04795 IDENTICAL PARALOGS LAC1533_RS06715 IDENTICAL PARALOGS LAC1533_RS07615 IDENTICAL PARALOGS LAC1533_RS11290	IS256 family transposase			Lacidipiscis_RS06475	IS256 family transposase
LAC1533_RS03415	DNA-binding response regulator	GSS_RS10585	DNA-binding response regulator	Lacidipiscis_RS01890	DNA-binding response regulator
LAC1533_RS03420	sensor histidine kinase	GSS_RS10590	sensor histidine kinase	Lacidipiscis_RS01895	sensor histidine kinase
LAC1533_RS03425	D-alanyl-D-alanine carboxypeptidase	GSS_RS10595	D-alanyl-D-alanine carboxypeptidase	Lacidipiscis_RS01900	D-alanyl-D-alanine carboxypeptidase
LAC1533_RS03430	branched-chain amino acid ABC transporter permease	GSS_RS10600	branched-chain amino acid ABC transporter permease	Lacidipiscis_RS01905	branched-chain amino acid ABC transporter permease
LAC1533_RS03435	AzlD domain-containing protein	GSS_RS10605	AzlD domain-containing protein	Lacidipiscis_RS01910	AzlD domain-containing protein
LAC1533_RS03440	alpha/beta hydrolase	GSS_RS10610	alpha/beta hydrolase	Lacidipiscis_RS06445	alpha/beta hydrolase
LAC1533_RS03445	PAP2 family protein	GSS_RS10615	PAP2 family protein		
LAC1533_RS03450	hypothetical protein	GSS_RS10620	hypothetical protein	Lacidipiscis_RS09190	hypothetical protein
LAC1533_RS03455	RluA family pseudouridine synthase	GSS_RS10625	RluA family pseudouridine synthase	Lacidipiscis_RS09195	RluA family pseudouridine synthase
LAC1533_RS03460	metal-dependent transcriptional regulator	GSS_RS10630	metal-dependent transcriptional regulator	Lacidipiscis_RS09200	metal-dependent transcriptional regulator
LAC1533_RS03465	cold-shock protein	GSS_RS10635	cold-shock protein	Lacidipiscis_RS09205	cold-shock protein
LAC1533_RS03475	LytR family transcriptional regulator	GSS_RS10640	LytR family transcriptional regulator	Lacidipiscis_RS09210	LytR family transcriptional regulator
LAC1533_RS03485	DUF805 domain-containing protein	GSS_RS10650	DUF805 domain-containing protein	Lacidipiscis_RS09215	DUF805 domain-containing protein
LAC1533_RS03490	N-acetyltransferase	GSS_RS13320	N-acetyltransferase	Lacidipiscis_RS09220	N-acetyltransferase
LAC1533_RS03495	Rrf2 family transcriptional regulator	GSS_RS10660	Rrf2 family transcriptional regulator	Lacidipiscis_RS09225	Rrf2 family transcriptional regulator
LAC1533_RS03500	acetolactate synthase AlsS	GSS_RS10665	acetolactate synthase AlsS	Lacidipiscis_RS09230	acetolactate synthase AlsS
LAC1533_RS03505	acetolactate decarboxylase	GSS_RS10670	acetolactate decarboxylase	Lacidipiscis_RS09235	acetolactate decarboxylase
LAC1533_RS03510	amino acid permease	GSS_RS10675	amino acid permease	Lacidipiscis_RS09240	amino acid permease
LAC1533_RS03515	serine--tRNA ligase	GSS_RS10680	serine--tRNA ligase	Lacidipiscis_RS09245	serine--tRNA ligase
LAC1533_RS03545	sigma-70 family RNA polymerase sigma factor	GSS_RS04840	sigma-70 family RNA polymerase sigma factor	Lacidipiscis_RS05315	sigma-70 family RNA polymerase sigma factor
LAC1533_RS03560	ATP-dependent DNA helicase	GSS_RS04850	ATP-dependent DNA helicase	Lacidipiscis_RS06410	ATP-dependent DNA helicase
LAC1533_RS03565	tryptophan--tRNA ligase	GSS_RS04855	tryptophan--tRNA ligase	Lacidipiscis_RS06405	tryptophan--tRNA ligase
LAC1533_RS03570	Ppx/GppA family phosphatase	GSS_RS04860	Ppx/GppA family phosphatase	Lacidipiscis_RS06400	exopolyphosphatase
LAC1533_RS03580	hypothetical protein	GSS_RS10285	hypothetical protein	Lacidipiscis_RS06395	hypothetical protein
LAC1533_RS03585	hydroxymethylglutaryl-CoA reductase, degradative	GSS_RS10290	hydroxymethylglutaryl-CoA reductase, degradative	Lacidipiscis_RS06390	hydroxymethylglutaryl-CoA reductase, degradative
LAC1533_RS03590	hypothetical protein	GSS_RS10295	hypothetical protein	Lacidipiscis_RS06385	hypothetical protein
LAC1533_RS03595	NAD-dependent protein deacylase	GSS_RS10300	NAD-dependent protein deacylase	Lacidipiscis_RS06380	NAD-dependent protein deacylase

LAC1533_RS03600	methionine--tRNA ligase	GSS_RS10305	methionine--tRNA ligase	Lacidipiscis_RS06375	methionine--tRNA ligase
LAC1533_RS03605	TatD family deoxyribonuclease	GSS_RS10310	TatD family deoxyribonuclease	Lacidipiscis_RS06370	TatD family deoxyribonuclease
LAC1533_RS03610	ribonuclease M5	GSS_RS10315	ribonuclease M5	Lacidipiscis_RS06365	ribonuclease M5
LAC1533_RS03615	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA			Lacidipiscis_RS06360	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA
LAC1533_RS03620	hypothetical protein	GSS_RS10325	hypothetical protein	Lacidipiscis_RS06355	hypothetical protein
LAC1533_RS03625	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase			Lacidipiscis_RS06350	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase
LAC1533_RS03630	pur operon repressor	GSS_RS10335	pur operon repressor	Lacidipiscis_RS06345	pur operon repressor
LAC1533_RS03635	XRE family transcriptional regulator	GSS_RS10340	XRE family transcriptional regulator	Lacidipiscis_RS06340	XRE family transcriptional regulator
LAC1533_RS03640	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU	GSS_RS10345	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU	Lacidipiscis_RS08340	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU
LAC1533_RS03645	ribose-phosphate pyrophosphokinase	GSS_RS10350	ribose-phosphate pyrophosphokinase	Lacidipiscis_RS08335	ribose-phosphate pyrophosphokinase
LAC1533_RS03650	hypothetical protein	GSS_RS10355	hypothetical protein	Lacidipiscis_RS08330	hypothetical protein
LAC1533_RS03655	biotin--[acetyl-CoA-carboxylase] ligase	GSS_RS10360	biotin--[acetyl-CoA-carboxylase] ligase	Lacidipiscis_RS08325	biotin--[acetyl-CoA-carboxylase] ligase
LAC1533_RS03660	YibE/F family protein			Lacidipiscis_RS09445	YibE/F family protein
LAC1533_RS03665	YibE/F family protein	GSS_RS10370	YibE/F family protein	Lacidipiscis_RS09440	YibE/F family protein
LAC1533_RS03670	hypothetical protein	GSS_RS13295	hypothetical protein	Lacidipiscis_RS09435	hypothetical protein
LAC1533_RS03675	HD domain-containing protein	GSS_RS10385	HD domain-containing protein	Lacidipiscis_RS11385	HD domain-containing protein
LAC1533_RS03680	DUF1934 domain-containing protein	GSS_RS10395	DUF1934 domain-containing protein	Lacidipiscis_RS11380	DUF1934 domain-containing protein
LAC1533_RS03685	DNA-directed RNA polymerase subunit delta	GSS_RS10400	DNA-directed RNA polymerase subunit delta	Lacidipiscis_RS11375	DNA-directed RNA polymerase subunit delta
LAC1533_RS03690	CTP synthase	GSS_RS10405	CTP synthase	Lacidipiscis_RS11370	CTP synthase
LAC1533_RS03700	group II intron reverse transcriptase/maturase				
LAC1533_RS03710	hypothetical protein	GSS_RS10830	hypothetical protein	Lacidipiscis_RS11365	hypothetical protein
LAC1533_RS03715	UDP-N-acetylglucosamine 1-carboxyvinyltransferase			Lacidipiscis_RS11360	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
LAC1533_RS03720	transcription termination factor Rho	GSS_RS10840	transcription termination factor Rho	Lacidipiscis_RS11355	transcription termination factor Rho
LAC1533_RS03725	type B 50S ribosomal protein L31	GSS_RS10845	type B 50S ribosomal protein L31	Lacidipiscis_RS11350	type B 50S ribosomal protein L31
LAC1533_RS03730	hypothetical protein	GSS_RS10850	hypothetical protein	Lacidipiscis_RS13320	hypothetical protein
LAC1533_RS03735	ATP-dependent DNA helicase	GSS_RS10855	ATP-dependent DNA helicase	Lacidipiscis_RS09425	hypothetical protein
LAC1533_RS03740	NCS2 family permease	GSS_RS10860	NCS2 family permease	Lacidipiscis_RS09420	NCS2 family permease
LAC1533_RS03745	dihydrofolate reductase	GSS_RS10865	dihydrofolate reductase	Lacidipiscis_RS09415	dihydrofolate reductase
LAC1533_RS03750	TIGR02452 family protein	GSS_RS10870	TIGR02452 family protein	Lacidipiscis_RS09410	TIGR02452 family protein
LAC1533_RS03755	N-acetyltransferase	GSS_RS10880	N-acetyltransferase	Lacidipiscis_RS09405	N-acetyltransferase
LAC1533_RS03760	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	GSS_RS10885	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	Lacidipiscis_RS09400	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase
LAC1533_RS03765	ATP-dependent helicase	GSS_RS10890	ATP-dependent helicase	Lacidipiscis_RS09395	ATP-dependent helicase
LAC1533_RS03770	transposase				
LAC1533_RS03780	maturase				
LAC1533_RS03785	IS5-like element ISLpl3 family transposase			Lacidipiscis_RS07020	hypothetical protein
LAC1533_RS03795	holo-ACP synthase	GSS_RS10770	holo-ACP synthase	Lacidipiscis_RS03865	holo-ACP synthase
LAC1533_RS03800	alanine racemase	GSS_RS10765	alanine racemase	Lacidipiscis_RS03870	alanine racemase
LAC1533_RS03805	hypothetical protein	GSS_RS10760	hypothetical protein	Lacidipiscis_RS03875	hypothetical protein
LAC1533_RS03810	type II toxin-antitoxin system PemK/MazF family toxin	GSS_RS10755	type II toxin-antitoxin system PemK/MazF family toxin	Lacidipiscis_RS03880	type II toxin-antitoxin system PemK/MazF family toxin
LAC1533_RS03815	hypothetical protein	GSS_RS10750	hypothetical protein	Lacidipiscis_RS03885	hypothetical protein
LAC1533_RS03820	CBS domain-containing protein	GSS_RS10745	CBS domain-containing protein	Lacidipiscis_RS12660	CBS domain-containing protein
LAC1533_RS03825	L-lactate dehydrogenase	GSS_RS10740	L-lactate dehydrogenase	Lacidipiscis_RS04305	L-lactate dehydrogenase
LAC1533_RS03830	aminoacyl-tRNA hydrolase	GSS_RS10735	aminoacyl-tRNA hydrolase	Lacidipiscis_RS04310	aminoacyl-tRNA hydrolase
LAC1533_RS03835	transcription-repair coupling factor	GSS_RS10730	transcription-repair coupling factor	Lacidipiscis_RS04315	transcription-repair coupling factor
LAC1533_RS03840	sugar transporter	GSS_RS10725	PST polysaccharide transporter	Lacidipiscis_RS04320	sugar transporter
LAC1533_RS03845	RNA-binding S4 domain-containing protein	GSS_RS10720	RNA-binding S4 domain-containing protein	Lacidipiscis_RS04325	RNA-binding S4 domain-containing protein
LAC1533_RS03850	septum formation initiator family protein	GSS_RS10715	septum formation initiator family protein	Lacidipiscis_RS05555	septum formation initiator family protein
LAC1533_RS03855	RNA-binding protein S1	GSS_RS10710	S1 RNA-binding domain containing protein	Lacidipiscis_RS05560	RNA-binding protein S1
LAC1533_RS03860	tRNA lysidine(34) synthetase TilS	GSS_RS13870	hypothetical protein	Lacidipiscis_RS05565	tRNA lysidine(34) synthetase TilS
LAC1533_RS03865	hypoxanthine phosphoribosyltransferase	GSS_RS10700	hypoxanthine phosphoribosyltransferase	Lacidipiscis_RS05570	hypoxanthine phosphoribosyltransferase
LAC1533_RS03870	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein	GSS_RS10695	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein	Lacidipiscis_RS05575	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein
LAC1533_RS03875	Hsp33 family molecular chaperone HslO	GSS_RS10690	Hsp33 family molecular chaperone HslO	Lacidipiscis_RS05580	Hsp33 family molecular chaperone HslO
LAC1533_RS03880	lysine--tRNA ligase	GSS_RS10685	lysine--tRNA ligase	Lacidipiscis_RS05585	lysine--tRNA ligase
LAC1533_RS03920	peptide MFS transporter	GSS_RS07250	peptide MFS transporter	Lacidipiscis_RS00675	peptide MFS transporter
LAC1533_RS03935	pyrroline-5-carboxylate reductase	GSS_RS07265	pyrroline-5-carboxylate reductase	Lacidipiscis_RS00690	pyrroline-5-carboxylate reductase
LAC1533_RS03940	N-acetylglucosamine-6-phosphate deacetylase	GSS_RS07270	N-acetylglucosamine-6-phosphate deacetylase	Lacidipiscis_RS00695	N-acetylglucosamine-6-phosphate deacetylase
LAC1533_RS03945	GntR family transcriptional regulator	GSS_RS07275	GntR family transcriptional regulator	Lacidipiscis_RS00700	GntR family transcriptional regulator
LAC1533_RS03950	class 1b ribonucleoside-diphosphate reductase subunit beta	GSS_RS07280	class 1b ribonucleoside-diphosphate reductase subunit beta	Lacidipiscis_RS06780	class 1b ribonucleoside-diphosphate reductase subunit beta
LAC1533_RS03955	class 1b ribonucleoside-diphosphate reductase subunit alpha	GSS_RS12850	class 1b ribonucleoside-diphosphate reductase subunit alpha	Lacidipiscis_RS06775	class 1b ribonucleoside-diphosphate reductase subunit alpha

LAC1533_RS03960	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI	GSS_RS07300	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI	Lacidipiscis_RS06770	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI
LAC1533_RS03965	glutaredoxin-like protein NrdH	GSS_RS07305	glutaredoxin-like protein NrdH	Lacidipiscis_RS06765	glutaredoxin-like protein NrdH
LAC1533_RS03970	class I SAM-dependent methyltransferase	GSS_RS07310	class I SAM-dependent methyltransferase	Lacidipiscis_RS06760	class I SAM-dependent methyltransferase
LAC1533_RS03975	nucleoside deaminase	GSS_RS07315	nucleoside deaminase	Lacidipiscis_RS06755	nucleoside deaminase
LAC1533_RS03985	DNA polymerase III subunit gamma/tau	GSS_RS07320	DNA polymerase III subunit gamma/tau	Lacidipiscis_RS06745	DNA polymerase III subunit gamma/tau
LAC1533_RS03990	YbaB/EbfC family nucleoid-associated protein	GSS_RS07325	nucleoid-associated protein, YbaB/EbfC family	Lacidipiscis_RS06740	nucleoid-associated protein, YbaB/EbfC family
LAC1533_RS03995	recombination protein RecR	GSS_RS07330	recombination protein RecR	Lacidipiscis_RS06735	recombination protein RecR
LAC1533_RS04000	DUF2508 domain-containing protein	GSS_RS07335	DUF2508 domain-containing protein	Lacidipiscis_RS06730	DUF2508 domain-containing protein
LAC1533_RS04005	dTMP kinase			Lacidipiscis_RS06725	dTMP kinase
LAC1533_RS04010	hypothetical protein	GSS_RS07345	hypothetical protein	Lacidipiscis_RS06720	hypothetical protein
LAC1533_RS04015	DNA polymerase III subunit delta	GSS_RS07350	DNA polymerase III subunit delta	Lacidipiscis_RS06715	DNA polymerase III subunit delta
LAC1533_RS04020	DUF972 domain-containing protein	GSS_RS07355	DUF972 domain-containing protein	Lacidipiscis_RS06710	DUF972 domain-containing protein
LAC1533_RS04025	16S rRNA (cytidine(1402)-2-O)-methyltransferase	GSS_RS07360	16S rRNA (cytidine(1402)-2-O)-methyltransferase	Lacidipiscis_RS06705	16S rRNA (cytidine(1402)-2-O)-methyltransferase
LAC1533_RS04030	acyl-ACP thioesterase	GSS_RS07365	acyl-ACP thioesterase	Lacidipiscis_RS06700	acyl-ACP thioesterase
LAC1533_RS04035	IS30 family transposase				
LAC1533_RS04040	asparaginase			Lacidipiscis_RS12555	asparaginase
LAC1533_RS04050	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	GSS_RS07375	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	Lacidipiscis_RS08650	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB
LAC1533_RS04055	N-acetyltransferase	GSS_RS07380	N-acetyltransferase	Lacidipiscis_RS08645	N-acetyltransferase
LAC1533_RS04060	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	GSS_RS07385	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	Lacidipiscis_RS08640	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD
LAC1533_RS04065	multidrug ABC transporter ATP-binding protein			Lacidipiscis_RS08635	multidrug ABC transporter ATP-binding protein
LAC1533_RS04070	redox-sensing transcriptional repressor Rex	GSS_RS07395	redox-sensing transcriptional repressor Rex	Lacidipiscis_RS08630	redox-sensing transcriptional repressor Rex
LAC1533_RS04085	CPBP family intramembrane metalloprotease	GSS_RS07400	CPBP family intramembrane metalloprotease	Lacidipiscis_RS08625	CPBP family intramembrane metalloprotease
LAC1533_RS04090	co-chaperone GroES	GSS_RS07405	co-chaperone GroES	Lacidipiscis_RS08620	co-chaperone GroES
LAC1533_RS04095	chaperonin GroEL	GSS_RS07410	chaperonin GroEL	Lacidipiscis_RS08615	chaperonin GroEL
LAC1533_RS04100	APC family permease	GSS_RS07415	APC family permease	Lacidipiscis_RS06600	APC family permease
LAC1533_RS04105	YigZ family protein	GSS_RS07420	YigZ family protein	Lacidipiscis_RS06605	YigZ family protein
LAC1533_RS04110	DNA/RNA helicase	GSS_RS07425	DNA/RNA helicase	Lacidipiscis_RS06610	DNA/RNA helicase
LAC1533_RS04115	ComF family protein	GSS_RS07430	ComF family protein	Lacidipiscis_RS06615	ComF family protein
LAC1533_RS04125	ribosome-associated translation inhibitor RaiA	GSS_RS07435	ribosome-associated translation inhibitor RaiA	Lacidipiscis_RS06620	ribosome-associated translation inhibitor RaiA
LAC1533_RS04130	preprotein translocase subunit SecA	GSS_RS07440	preprotein translocase subunit SecA	Lacidipiscis_RS06625	preprotein translocase subunit SecA
LAC1533_RS04135	peptide chain release factor 2	GSS_RS07445	peptide chain release factor 2	Lacidipiscis_RS06630	peptide chain release factor 2
LAC1533_RS04140	cell division ATP-binding protein FtsE	GSS_RS07450	cell division ATP-binding protein FtsE	Lacidipiscis_RS06635	cell division ATP-binding protein FtsE
LAC1533_RS04145	ABC transporter permease	GSS_RS07455	ABC transporter permease	Lacidipiscis_RS06640	ABC transporter permease
LAC1533_RS04150	PDZ domain-containing protein	GSS_RS07460	PDZ domain-containing protein	Lacidipiscis_RS07610	PDZ domain-containing protein
LAC1533_RS04155	DNA-binding response regulator	GSS_RS07465	DNA-binding response regulator	Lacidipiscis_RS07615	DNA-binding response regulator
LAC1533_RS04160	two-component sensor histidine kinase	GSS_RS07470	two-component sensor histidine kinase	Lacidipiscis_RS07620	sensor histidine kinase
LAC1533_RS04165	PspC domain-containing protein	GSS_RS07475	PspC domain-containing protein	Lacidipiscis_RS00020	PspC domain-containing protein
LAC1533_RS04170	phage holin family protein	GSS_RS07480	phage holin family protein	Lacidipiscis_RS00025	phage holin family protein
LAC1533_RS04175	HPr kinase/phosphorylase			Lacidipiscis_RS00030	HPr kinase/phosphorylase
LAC1533_RS04180	prolipoprotein diacylglyceryl transferase	GSS_RS07490	prolipoprotein diacylglyceryl transferase	Lacidipiscis_RS00035	prolipoprotein diacylglyceryl transferase
LAC1533_RS04185	thioredoxin-disulfide reductase	GSS_RS07500	thioredoxin-disulfide reductase	Lacidipiscis_RS00040	thioredoxin-disulfide reductase
LAC1533_RS04190 IDENTICAL PARALOGS LAC1533_RS11050	IS256 family transposase			Lacidipiscis_RS00335	IS256 family transposase
LAC1533_RS04195	phospho-sugar mutase	GSS_RS07505	phospho-sugar mutase	Lacidipiscis_RS00045	phospho-sugar mutase
LAC1533_RS04200	excinuclease ABC subunit UvrB	GSS_RS07510	excinuclease ABC subunit UvrB	Lacidipiscis_RS00050	excinuclease ABC subunit UvrB
LAC1533_RS04205	excinuclease ABC subunit UvrA	GSS_RS07515	excinuclease ABC subunit UvrA	Lacidipiscis_RS00055	excinuclease ABC subunit UvrA
LAC1533_RS04210	S-ribosylhomocysteine lyase	GSS_RS07520	S-ribosylhomocysteine lyase	Lacidipiscis_RS00060	S-ribosylhomocysteine lyase
LAC1533_RS04215	serine dehydratase	GSS_RS12875	L-serine ammonia-lyase beta subunit	Lacidipiscis_RS00065	serine dehydratase
LAC1533_RS04220	L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha	GSS_RS07530	L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha	Lacidipiscis_RS00070	L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha
LAC1533_RS04225	RNase adapter RapZ	GSS_RS07535	RNase adapter RapZ	Lacidipiscis_RS00075	RNase adapter RapZ
LAC1533_RS04230	hypothetical protein	GSS_RS07540	hypothetical protein	Lacidipiscis_RS00080	hypothetical protein
LAC1533_RS04235	DNA-binding protein WhiA	GSS_RS07545	DNA-binding protein WhiA	Lacidipiscis_RS00085	DNA-binding protein WhiA
LAC1533_RS04240	ATP-dependent Clp protease proteolytic subunit	GSS_RS07550	ATP-dependent Clp protease proteolytic subunit	Lacidipiscis_RS00090	ATP-dependent Clp protease proteolytic subunit
LAC1533_RS04250	RNA polymerase sigma-54 factor	GSS_RS07560	RNA polymerase sigma-54 factor	Lacidipiscis_RS05880	RNA polymerase sigma-54 factor
LAC1533_RS04255	SorC family transcriptional regulator	GSS_RS07565	SorC family transcriptional regulator	Lacidipiscis_RS05885	SorC family transcriptional regulator
LAC1533_RS04260	type I glyceraldehyde-3-phosphate dehydrogenase	GSS_RS07570	type I glyceraldehyde-3-phosphate dehydrogenase	Lacidipiscis_RS05890	type I glyceraldehyde-3-phosphate dehydrogenase
LAC1533_RS04265	phosphoglycerate kinase			Lacidipiscis_RS05895	phosphoglycerate kinase
LAC1533_RS04270	triose-phosphate isomerase	GSS_RS07580	triose-phosphate isomerase	Lacidipiscis_RS05900	triose-phosphate isomerase
LAC1533_RS04280 IDENTICAL PARALOGS LAC1533_RS07225 IDENTICAL PARALOGS LAC1533_RS10675	group II intron reverse transcriptase/maturase				

LAC1533_RS04290	preprotein translocase subunit SecG	GSS_RS07585	preprotein translocase subunit SecG	Lacidipiscis_RS05905	preprotein translocase subunit SecG
LAC1533_RS04295	ribonuclease R	GSS_RS07595	ribonuclease R	Lacidipiscis_RS05910	ribonuclease R
LAC1533_RS04300	SsrA-binding protein SmpB	GSS_RS07600	SsrA-binding protein SmpB	Lacidipiscis_RS05915	SsrA-binding protein SmpB
LAC1533_RS04310	group II intron reverse transcriptase/maturase			Lacidipiscis_RS03240	group II intron reverse transcriptase/maturase
LAC1533_RS04320	hypothetical protein	GSS_RS07605	hypothetical protein	Lacidipiscis_RS12625	hypothetical protein
LAC1533_RS04325	Cof-type HAD-IIB family hydrolase	GSS_RS07610	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS12620	Cof-type HAD-IIB family hydrolase
LAC1533_RS04330	uracil-DNA glycosylase	GSS_RS07615	uracil-DNA glycosylase	Lacidipiscis_RS12615	uracil-DNA glycosylase
LAC1533_RS04335	phosphate acetyltransferase	GSS_RS07620	phosphate acetyltransferase	Lacidipiscis_RS12610	phosphate acetyltransferase
LAC1533_RS04340	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	GSS_RS07625	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	Lacidipiscis_RS12605	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE
LAC1533_RS04345	exonuclease	GSS_RS07630	exonuclease	Lacidipiscis_RS12600	hypothetical protein
LAC1533_RS04350	UDP-N-acetylmuramate dehydrogenase			Lacidipiscis_RS12595	UDP-N-acetylmuramate dehydrogenase
LAC1533_RS04355	DUF1361 domain-containing protein	GSS_RS07640	DUF1361 domain-containing protein	Lacidipiscis_RS12590	DUF1361 domain-containing protein
LAC1533_RS04360	TIGR00159 family protein	GSS_RS07645	TIGR00159 family protein	Lacidipiscis_RS12585	TIGR00159 family protein
LAC1533_RS04365	hypothetical protein			Lacidipiscis_RS12580	hypothetical protein
LAC1533_RS04370	phosphoglucosamine mutase	GSS_RS07655	phosphoglucosamine mutase	Lacidipiscis_RS12575	phosphoglucosamine mutase
LAC1533_RS04375	hypothetical protein	GSS_RS07660	hypothetical protein	Lacidipiscis_RS12570	hypothetical protein
LAC1533_RS04390	hypothetical protein	GSS_RS07665	hypothetical protein	Lacidipiscis_RS12565	hypothetical protein
LAC1533_RS04395	ABC transporter	GSS_RS07670	ABC transporter	Lacidipiscis_RS09590	ABC transporter
LAC1533_RS04400	phosphate ABC transporter permease subunit PstC	GSS_RS07675	phosphate ABC transporter permease subunit PstC	Lacidipiscis_RS09585	phosphate ABC transporter permease subunit PstC
LAC1533_RS04405	phosphate ABC transporter, permease protein PstA	GSS_RS07680	phosphate ABC transporter, permease protein PstA	Lacidipiscis_RS09580	phosphate ABC transporter, permease protein PstA
LAC1533_RS04410	phosphate ABC transporter ATP-binding protein	GSS_RS07685	phosphate ABC transporter ATP-binding protein	Lacidipiscis_RS09575	phosphate ABC transporter ATP-binding protein
LAC1533_RS04415	phosphate ABC transporter ATP-binding protein	GSS_RS07690	phosphate ABC transporter ATP-binding protein	Lacidipiscis_RS09570	phosphate ABC transporter ATP-binding protein
LAC1533_RS04420	phosphate transport system regulatory protein PhoU	GSS_RS07695	phosphate transport system regulatory protein PhoU	Lacidipiscis_RS09565	phosphate transport system regulatory protein PhoU
LAC1533_RS04425	fructose-1,6-bisphosphate aldolase, class II	GSS_RS07700	fructose-1,6-bisphosphate aldolase, class II	Lacidipiscis_RS09560	fructose-1,6-bisphosphate aldolase, class II
LAC1533_RS04430	IS1182 family transposase	GSS_RS07705	IS1182 family transposase	Lacidipiscis_RS09555	IS5/IS1182 family transposase
LAC1533_RS04440	DUF1836 domain-containing protein	GSS_RS07710	DUF1836 domain-containing protein	Lacidipiscis_RS09545	DUF1836 domain-containing protein
LAC1533_RS04445	hemolysin III	GSS_RS07715	membrane protein	Lacidipiscis_RS09540	hemolysin III
LAC1533_RS04450	ArsR family transcriptional regulator	GSS_RS07720	ArsR family transcriptional regulator	Lacidipiscis_RS09535	ArsR family transcriptional regulator
LAC1533_RS04455	RNase HI	GSS_RS07725	RNase HI	Lacidipiscis_RS09530	RNase HI
LAC1533_RS04460	hypothetical protein	GSS_RS07730	hypothetical protein	Lacidipiscis_RS09525	hypothetical protein
LAC1533_RS04465	hypothetical protein	GSS_RS07735	hypothetical protein	Lacidipiscis_RS09520	hypothetical protein
LAC1533_RS04475	LTA synthase family protein			Lacidipiscis_RS01870	LTA synthase family protein
LAC1533_RS04480	glucose-6-phosphate isomerase	GSS_RS07745	glucose-6-phosphate isomerase	Lacidipiscis_RS09150	glucose-6-phosphate isomerase
LAC1533_RS04485 IDENTICAL PARALOGS LAC1533_RS04735 IDENTICAL PARALOGS LAC1533_RS10420	transposase				
LAC1533_RS04490	CBS domain-containing protein	GSS_RS07750	CBS domain-containing protein	Lacidipiscis_RS11845	CBS domain-containing protein
LAC1533_RS04495	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase			Lacidipiscis_RS11850	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase
LAC1533_RS04500	amidohydrolase	GSS_RS07760	N-acetyldiaminopimelate deacetylase	Lacidipiscis_RS11855	amidohydrolase
LAC1533_RS04505	mechanosensitive ion channel family protein	GSS_RS07765	mechanosensitive ion channel family protein	Lacidipiscis_RS11860	mechanosensitive ion channel family protein
LAC1533_RS04510	DUF948 domain-containing protein	GSS_RS07770	DUF948 domain-containing protein	Lacidipiscis_RS11865	DUF948 domain-containing protein
LAC1533_RS04515	hypothetical protein	GSS_RS07775	hypothetical protein	Lacidipiscis_RS11870	hypothetical protein
LAC1533_RS04520	aminopeptidase P family protein	GSS_RS07780	aminopeptidase P family protein	Lacidipiscis_RS11875	aminopeptidase P family protein
LAC1533_RS04525	catabolite control protein A	GSS_RS07785	catabolite control protein A	Lacidipiscis_RS11880	catabolite control protein A
LAC1533_RS04530	YebC/PmpR family DNA-binding transcriptional regulator	GSS_RS07790	YebC/PmpR family DNA-binding transcriptional regulator	Lacidipiscis_RS11885	YebC/PmpR family DNA-binding transcriptional regulator
LAC1533_RS04535	competence protein ComG	GSS_RS07795	competence protein ComG	Lacidipiscis_RS11890	competence protein ComG
LAC1533_RS04540	competence protein ComG	GSS_RS07800	ComG operon protein 2	Lacidipiscis_RS11895	competence protein ComG
LAC1533_RS04545	prepilin-type N-terminal cleavage/methylation domain-containing protein	GSS_RS07805	prepilin-type N-terminal cleavage/methylation domain-containing protein	Lacidipiscis_RS11900	prepilin-type N-terminal cleavage/methylation domain-containing protein
LAC1533_RS04550	prepilin-type N-terminal cleavage/methylation domain-containing protein	GSS_RS07810	prepilin-type N-terminal cleavage/methylation domain-containing protein	Lacidipiscis_RS11905	prepilin-type N-terminal cleavage/methylation domain-containing protein
LAC1533_RS04555	hypothetical protein	GSS_RS07815	hypothetical protein	Lacidipiscis_RS11910	hypothetical protein
LAC1533_RS04560	type II secretion system protein	GSS_RS07820	type II secretion system protein	Lacidipiscis_RS11915	prepilin-type cleavage/methylation domain-containing protein
LAC1533_RS04565	hypothetical protein	GSS_RS12905	hypothetical protein	Lacidipiscis_RS11920	hypothetical protein
LAC1533_RS04570	class I SAM-dependent methyltransferase	GSS_RS07830	class I SAM-dependent methyltransferase	Lacidipiscis_RS11925	class I SAM-dependent methyltransferase
LAC1533_RS04575	metallophosphatase			Lacidipiscis_RS11930	metallophosphatase
LAC1533_RS04580	multifunctional 2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase	GSS_RS07840	multifunctional 2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase	Lacidipiscis_RS11935	multifunctional 2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase
LAC1533_RS04585	DUF1027 domain-containing protein	GSS_RS07845	DUF1027 domain-containing protein		
LAC1533_RS04590	TIGR01457 family HAD-type hydrolase	GSS_RS07850	TIGR01457 family HAD-type hydrolase	Lacidipiscis_RS13380	TIGR01457 family HAD-type hydrolase
LAC1533_RS04595	TIGR01906 family membrane protein	GSS_RS07855	TIGR01906 family membrane protein	Lacidipiscis_RS13385	TIGR01906 family membrane protein
LAC1533_RS04600	cytochrome o ubiquinol oxidase	GSS_RS07860	membrane protein	Lacidipiscis_RS13390	cytochrome o ubiquinol oxidase
LAC1533_RS04605	NAD(P)/FAD-dependent oxidoreductase	GSS_RS07865	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS13395	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS04610	peptidylprolyl isomerase	GSS_RS07870	peptidyl-prolyl cis-trans isomerase	Lacidipiscis_RS13400	peptidylprolyl isomerase
LAC1533_RS04615	general stress protein	GSS_RS07875	general stress protein	Lacidipiscis_RS13405	general stress protein
LAC1533_RS04740	methionine adenosyltransferase	GSS_RS11040	methionine adenosyltransferase	Lacidipiscis_RS11620	methionine adenosyltransferase

LAC1533_RS04745	LysM peptidoglycan-binding domain-containing protein	GSS_RS13355	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS11630	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS04750	leucine--tRNA ligase	GSS_RS11050	leucine--tRNA ligase	Lacidipiscis_RS11635	leucine--tRNA ligase
LAC1533_RS04755	polysaccharide biosynthesis protein	GSS_RS11055	polysaccharide biosynthesis protein	Lacidipiscis_RS11640	polysaccharide biosynthesis protein
LAC1533_RS04760	hypothetical protein	GSS_RS11060	hypothetical protein	Lacidipiscis_RS11645	hypothetical protein
LAC1533_RS04765	type I restriction-modification system subunit M			Lacidipiscis_RS11650	type I restriction-modification system subunit M
LAC1533_RS04770	restriction endonuclease subunit S			Lacidipiscis_RS11655	restriction endonuclease subunit S
LAC1533_RS04775	type I restriction endonuclease subunit R			Lacidipiscis_RS11660	type I restriction endonuclease subunit R
LAC1533_RS04780	site-specific integrase				
LAC1533_RS04785	type I restriction endonuclease subunit S				
LAC1533_RS04790	restriction endonuclease				
LAC1533_RS04805	IS256 family transposase				
LAC1533_RS04810	NAD(P)H-hydrate dehydratase	GSS_RS04815	NAD(P)H-hydrate dehydratase	Lacidipiscis_RS12805	NAD(P)H-hydrate dehydratase
LAC1533_RS04815	dienelactone hydrolase	GSS_RS04810	dienelactone hydrolase	Lacidipiscis_RS12800	dienelactone hydrolase
LAC1533_RS04830	hypothetical protein	GSS_RS04800	hypothetical protein	Lacidipiscis_RS12790	hypothetical protein
LAC1533_RS04835	universal stress protein	GSS_RS04795	universal stress protein	Lacidipiscis_RS12785	universal stress protein
LAC1533_RS04840	hypothetical protein	GSS_RS04790	hypothetical protein	Lacidipiscis_RS12780	hypothetical protein
LAC1533_RS04845	group II intron reverse transcriptase/maturase				
LAC1533_RS04855	hypothetical protein	GSS_RS04785	hypothetical protein	Lacidipiscis_RS12775	hypothetical protein
LAC1533_RS04860	acetate kinase	GSS_RS04780	acetate kinase	Lacidipiscis_RS12770	acetate kinase
LAC1533_RS04865	hypothetical protein	GSS_RS04775	hypothetical protein	Lacidipiscis_RS12765	hypothetical protein
LAC1533_RS04870	deoxyguanosine kinase	GSS_RS04770	deoxyguanosine kinase	Lacidipiscis_RS12760	deoxyguanosine kinase
LAC1533_RS04880	adenylosuccinate lyase	GSS_RS04765	adenylosuccinate lyase	Lacidipiscis_RS12755	adenylosuccinate lyase
LAC1533_RS04885	LysR family transcriptional regulator	GSS_RS04760	LysR family transcriptional regulator	Lacidipiscis_RS12750	LysR family transcriptional regulator
LAC1533_RS04890	MATE family efflux transporter	GSS_RS04750	MATE family efflux transporter	Lacidipiscis_RS12745	MATE family efflux transporter
LAC1533_RS04895	hypothetical protein	GSS_RS04745	hypothetical protein	Lacidipiscis_RS06335	hypothetical protein
LAC1533_RS04905	arginine--tRNA ligase	GSS_RS04735	arginine--tRNA ligase	Lacidipiscis_RS06325	arginine--tRNA ligase
LAC1533_RS04910	Crp/Fnr family transcriptional regulator	GSS_RS04730	Crp/Fnr family transcriptional regulator	Lacidipiscis_RS08345	Crp/Fnr family transcriptional regulator
LAC1533_RS04915	ArgR family transcriptional regulator	GSS_RS04725	ArgR family transcriptional regulator	Lacidipiscis_RS08350	ArgR family transcriptional regulator
LAC1533_RS04920	carboxypeptidase	GSS_RS04720	carboxypeptidase	Lacidipiscis_RS08355	carboxypeptidase
LAC1533_RS04925	hypothetical protein	GSS_RS04715	hypothetical protein	Lacidipiscis_RS08360	hypothetical protein
LAC1533_RS04930	HD domain-containing protein	GSS_RS04710	HD domain-containing protein	Lacidipiscis_RS08365	HD domain-containing protein
LAC1533_RS04935	peptidylprolyl isomerase	GSS_RS04705	peptidylprolyl isomerase	Lacidipiscis_RS08370	peptidylprolyl isomerase
LAC1533_RS04940	hypothetical protein	GSS_RS04700	hypothetical protein	Lacidipiscis_RS08375	hypothetical protein
LAC1533_RS04945	HIT family protein	GSS_RS04695	HIT family protein	Lacidipiscis_RS08380	HIT family protein
LAC1533_RS04950	ABC transporter ATP-binding protein	GSS_RS12615	ABC transporter ATP-binding protein	Lacidipiscis_RS08385	ABC transporter ATP-binding protein
LAC1533_RS04955	protein ecsB	GSS_RS04685	protein ecsB	Lacidipiscis_RS08390	protein EcsB
LAC1533_RS04960	phosphotransferase	GSS_RS04680	phosphotransferase	Lacidipiscis_RS08395	phosphotransferase
LAC1533_RS04965	tRNA (guanosine(46)-N7)-methyltransferase TrmB	GSS_RS04675	tRNA (guanosine(46)-N7)-methyltransferase TrmB	Lacidipiscis_RS05790	tRNA (guanosine(46)-N7)-methyltransferase TrmB
LAC1533_RS04970	thioredoxin	GSS_RS04670	thioredoxin	Lacidipiscis_RS05785	thioredoxin
LAC1533_RS04975	DUF4479 domain-containing protein	GSS_RS04665	DUF4479 domain-containing protein	Lacidipiscis_RS05780	DUF4479 domain-containing protein
LAC1533_RS04980	DNA translocase FtsK	GSS_RS04660	DNA translocase FtsK	Lacidipiscis_RS05775	DNA translocase FtsK
LAC1533_RS04985	UDP-N-acetylmuramate--L-alanine ligase	GSS_RS04655	UDP-N-acetylmuramate--L-alanine ligase	Lacidipiscis_RS05770	UDP-N-acetylmuramate--L-alanine ligase
LAC1533_RS04990	BAX inhibitor (BI)-1/YccA family protein	GSS_RS04650	BAX inhibitor (BI)-1/YccA family protein	Lacidipiscis_RS05765	BAX inhibitor (BI)-1/YccA family protein

LAC1533_RS04995	DNA polymerase I	GSS_RS04645	DNA polymerase I	Lacidipiscis_RS05760	DNA polymerase I
LAC1533_RS05000	DNA-formamidopyrimidine glycosylase	GSS_RS04635	DNA-formamidopyrimidine glycosylase	Lacidipiscis_RS05755	DNA-formamidopyrimidine glycosylase
LAC1533_RS05005	transcriptional repressor NrdR	GSS_RS04630	transcriptional repressor NrdR	Lacidipiscis_RS05745	transcriptional repressor NrdR
LAC1533_RS05010	chromosome replication initiation / membrane attachment protein	GSS_RS04625	chromosome replication initiation / membrane attachment protein	Lacidipiscis_RS05740	chromosome replication initiation / membrane attachment protein
LAC1533_RS05015	primosomal protein DnaI	GSS_RS04620	primosomal protein DnaI	Lacidipiscis_RS05735	primosomal protein DnaI
LAC1533_RS05020	threonine--tRNA ligase	GSS_RS04615	threonine--tRNA ligase	Lacidipiscis_RS05730	threonine--tRNA ligase
LAC1533_RS05025	translation initiation factor IF-3	GSS_RS04610	translation initiation factor IF-3	Lacidipiscis_RS05725	translation initiation factor IF-3
LAC1533_RS05030	50S ribosomal protein L35	GSS_RS04605	50S ribosomal protein L35	Lacidipiscis_RS05720	50S ribosomal protein L35
LAC1533_RS05035	50S ribosomal protein L20	GSS_RS04600	50S ribosomal protein L20	Lacidipiscis_RS05715	50S ribosomal protein L20
LAC1533_RS05040	YqeG family HAD IIIA-type phosphatase	GSS_RS04595	YqeG family HAD IIIA-type phosphatase	Lacidipiscis_RS05710	YqeG family HAD IIIA-type phosphatase
LAC1533_RS05045	ribosome biogenesis GTPase YqeH	GSS_RS04590	ribosome biogenesis GTPase YqeH	Lacidipiscis_RS05705	ribosome biogenesis GTPase YqeH
LAC1533_RS05050	ribosome assembly RNA-binding protein YhbY	GSS_RS04585	ribosome assembly RNA-binding protein YhbY	Lacidipiscis_RS05700	ribosome assembly RNA-binding protein YhbY
LAC1533_RS05055	nicotinate-nucleotide adenylyltransferase	GSS_RS04580	nicotinate-nucleotide adenylyltransferase	Lacidipiscis_RS05695	nicotinate-nucleotide adenylyltransferase
LAC1533_RS05060	HD domain-containing protein	GSS_RS04570	HD domain-containing protein	Lacidipiscis_RS05690	HD domain-containing protein
LAC1533_RS05065	ribosome silencing factor	GSS_RS04565	ribosome silencing factor	Lacidipiscis_RS05685	ribosome silencing factor
LAC1533_RS05070	class I SAM-dependent methyltransferase	GSS_RS04560	class I SAM-dependent methyltransferase	Lacidipiscis_RS05680	class I SAM-dependent methyltransferase
LAC1533_RS05075	nucleotidyltransferase	GSS_RS04555	nucleotidyltransferase	Lacidipiscis_RS05675	nucleotidyltransferase
LAC1533_RS05080	hypothetical protein	GSS_RS04550	hypothetical protein	Lacidipiscis_RS05670	DNA-binding protein
LAC1533_RS05085	50S ribosomal protein L32	GSS_RS04545	50S ribosomal protein L32	Lacidipiscis_RS05665	50S ribosomal protein L32
LAC1533_RS05090	YihA family ribosome biogenesis GTP-binding protein	GSS_RS04540	YihA family ribosome biogenesis GTP-binding protein	Lacidipiscis_RS05660	YihA family ribosome biogenesis GTP-binding protein
LAC1533_RS05095	nucleotide pyrophosphohydrolase	GSS_RS04535	nucleotide pyrophosphohydrolase	Lacidipiscis_RS05655	nucleotide pyrophosphohydrolase
LAC1533_RS05100	hypothetical protein	GSS_RS12605	hypothetical protein	Lacidipiscis_RS05650	hypothetical protein
LAC1533_RS05105	amino acid ABC transporter ATP-binding protein	GSS_RS04525	amino acid ABC transporter ATP-binding protein	Lacidipiscis_RS05645	amino acid ABC transporter ATP-binding protein
LAC1533_RS05110	excinuclease ABC subunit UvrC			Lacidipiscis_RS05640	excinuclease ABC subunit UvrC
LAC1533_RS05115	GTPase ObgE	GSS_RS04515	GTPase ObgE	Lacidipiscis_RS05635	GTPase ObgE
LAC1533_RS05120	acetyltransferase	GSS_RS04510	acetyltransferase	Lacidipiscis_RS05630	acetyltransferase
LAC1533_RS05125	hypothetical protein	GSS_RS04505	hypothetical protein	Lacidipiscis_RS11440	hypothetical protein
LAC1533_RS05135	ribonuclease Z	GSS_RS04495	ribonuclease Z	Lacidipiscis_RS09595	ribonuclease Z
LAC1533_RS05140	SDR family NAD(P)-dependent oxidoreductase	GSS_RS04490	SDR family NAD(P)-dependent oxidoreductase	Lacidipiscis_RS09600	SDR family NAD(P)-dependent oxidoreductase
LAC1533_RS05145	DUF1049 domain-containing protein	GSS_RS04485	DUF1049 domain-containing protein	Lacidipiscis_RS09605	DUF1049 domain-containing protein
LAC1533_RS05150	single-stranded-DNA-specific exonuclease RecJ	GSS_RS04480	single-stranded-DNA-specific exonuclease RecJ	Lacidipiscis_RS09610	single-stranded-DNA-specific exonuclease RecJ
LAC1533_RS05155	adenine phosphoribosyltransferase	GSS_RS04475	adenine phosphoribosyltransferase	Lacidipiscis_RS09615	adenine phosphoribosyltransferase
LAC1533_RS05160	hypothetical protein	GSS_RS04465	hypothetical protein	Lacidipiscis_RS09160	hypothetical protein
LAC1533_RS05165	helicase-exonuclease AddAB subunit AddA	GSS_RS04460	helicase-exonuclease AddAB subunit AddA	Lacidipiscis_RS09165	helicase-exonuclease AddAB subunit AddA
LAC1533_RS05170	hypothetical protein	GSS_RS04455	hypothetical protein	Lacidipiscis_RS09170	hypothetical protein
LAC1533_RS05175	hypothetical protein	GSS_RS04450	hypothetical protein	Lacidipiscis_RS09175	hypothetical protein
LAC1533_RS05180	50S ribosomal protein L33	GSS_RS04440	50S ribosomal protein L33	Lacidipiscis_RS09640	50S ribosomal protein L33
LAC1533_RS05190	group II intron reverse transcriptase/maturase				
LAC1533_RS05195	5-formyltetrahydrofolate cyclo-ligase	GSS_RS12595	5-formyltetrahydrofolate cyclo-ligase	Lacidipiscis_RS09645	5-formyltetrahydrofolate cyclo-ligase
LAC1533_RS05200	rhomboid family intramembrane serine protease	GSS_RS04425	rhomboid family intramembrane serine protease	Lacidipiscis_RS09650	rhomboid family intramembrane serine protease
LAC1533_RS05205	DUF910 domain-containing protein	GSS_RS04420	DUF910 domain-containing protein	Lacidipiscis_RS09655	DUF910 domain-containing protein
LAC1533_RS05210	glucokinase	GSS_RS04415	glucokinase	Lacidipiscis_RS09660	glucokinase
LAC1533_RS05215	rhodanese-like domain-containing protein	GSS_RS04410	rhodanese-like domain-containing protein	Lacidipiscis_RS09665	rhodanese-like domain-containing protein
LAC1533_RS05220	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	GSS_RS04405	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	Lacidipiscis_RS09670	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA
LAC1533_RS05225	MerR family transcriptional regulator	GSS_RS04400	MerR family transcriptional regulator	Lacidipiscis_RS09675	MerR family transcriptional regulator
LAC1533_RS05230	type I glutamate--ammonia ligase	GSS_RS04395	type I glutamate--ammonia ligase	Lacidipiscis_RS09680	type I glutamate--ammonia ligase
LAC1533_RS05235	hypothetical protein	GSS_RS04390	hypothetical protein		
LAC1533_RS05240	guanylate kinase	GSS_RS04385	guanylate kinase	Lacidipiscis_RS09685	guanylate kinase
LAC1533_RS05245	DNA-directed RNA polymerase subunit omega	GSS_RS04380	DNA-directed RNA polymerase subunit omega	Lacidipiscis_RS09690	DNA-directed RNA polymerase subunit omega
LAC1533_RS05250	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC	GSS_RS12590	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC	Lacidipiscis_RS09695	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC
LAC1533_RS05255	primosomal protein N			Lacidipiscis_RS09700	primosomal protein N
LAC1533_RS05260	methionyl-tRNA formyltransferase	GSS_RS04360	methionyl-tRNA formyltransferase	Lacidipiscis_RS09705	methionyl-tRNA formyltransferase
LAC1533_RS05265	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB	GSS_RS04355	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB	Lacidipiscis_RS09710	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB
LAC1533_RS05270	serine/threonine-protein phosphatase	GSS_RS04350	serine/threonine-protein phosphatase	Lacidipiscis_RS09715	serine/threonine-protein phosphatase
LAC1533_RS05275	serine/threonine protein kinase			Lacidipiscis_RS09720	serine/threonine protein kinase
LAC1533_RS05280	ribosome small subunit-dependent GTPase A	GSS_RS04330	ribosome small subunit-dependent GTPase A	Lacidipiscis_RS09725	ribosome small subunit-dependent GTPase A
LAC1533_RS05285	ribulose-phosphate 3-epimerase	GSS_RS04325	ribulose-phosphate 3-epimerase	Lacidipiscis_RS09730	ribulose-phosphate 3-epimerase
LAC1533_RS05290	thiamine diphosphokinase	GSS_RS04320	thiamine diphosphokinase	Lacidipiscis_RS09735	thiamine diphosphokinase
LAC1533_RS05295	50S ribosomal protein L28	GSS_RS04315	50S ribosomal protein L28	Lacidipiscis_RS09740	50S ribosomal protein L28
LAC1533_RS05300	Asp23/Gls24 family envelope stress response protein	GSS_RS04310	Asp23/Gls24 family envelope stress response protein	Lacidipiscis_RS09745	Asp23/Gls24 family envelope stress response protein
LAC1533_RS05305	DAK2 domain-containing protein	GSS_RS04305	DAK2 domain-containing protein	Lacidipiscis_RS09750	DAK2 domain-containing protein
LAC1533_RS05310	DNA helicase RecG			Lacidipiscis_RS09755	DNA helicase RecG
LAC1533_RS05315	phosphate acyltransferase PlsX	GSS_RS04295	phosphate acyltransferase PlsX	Lacidipiscis_RS09760	phosphate acyltransferase PlsX
LAC1533_RS05325	acyl carrier protein	GSS_RS04290	acyl carrier protein	Lacidipiscis_RS09765	acyl carrier protein
LAC1533_RS05330	ribonuclease III	GSS_RS04275	ribonuclease III	Lacidipiscis_RS09770	ribonuclease III
LAC1533_RS05335	chromosome segregation protein SMC	GSS_RS12570	chromosome segregation protein SMC	Lacidipiscis_RS09775	chromosome segregation protein SMC
LAC1533_RS05340	signal recognition particle-docking protein FtsY	GSS_RS04255	signal recognition particle-docking protein FtsY	Lacidipiscis_RS09780	signal recognition particle-docking protein FtsY
LAC1533_RS05345	putative DNA-binding protein			Lacidipiscis_RS09785	putative DNA-binding protein
LAC1533_RS05350	signal recognition particle protein			Lacidipiscis_RS09790	signal recognition particle protein
LAC1533_RS05355	30S ribosomal protein S16	GSS_RS04240	30S ribosomal protein S16	Lacidipiscis_RS09795	30S ribosomal protein S16
LAC1533_RS05360	KH domain-containing protein	GSS_RS04235	KH domain-containing protein	Lacidipiscis_RS09800	KH domain-containing protein
LAC1533_RS05365	ribosome maturation factor RimM	GSS_RS04230	ribosome maturation factor RimM	Lacidipiscis_RS09805	ribosome maturation factor RimM

LAC1533_RS05370	tRNA (guanosine(37)-N1)-methyltransferase TrmD	GSS_RS04225	tRNA (guanosine(37)-N1)-methyltransferase TrmD	Lacidipiscis_RS09810	tRNA (guanosine(37)-N1)-methyltransferase TrmD
LAC1533_RS05375	50S ribosomal protein L19	GSS_RS04220	50S ribosomal protein L19	Lacidipiscis_RS09815	50S ribosomal protein L19
LAC1533_RS05385	UMP kinase	GSS_RS04215	UMP kinase	Lacidipiscis_RS09820	UMP kinase
LAC1533_RS05390	ribosome recycling factor	GSS_RS04210	ribosome recycling factor	Lacidipiscis_RS09825	ribosome recycling factor
LAC1533_RS05395	isoprenyl transferase	GSS_RS04205	isoprenyl transferase	Lacidipiscis_RS09830	isoprenyl transferase
LAC1533_RS05400	phosphatidate cytidylyltransferase	GSS_RS04200	phosphatidate cytidylyltransferase	Lacidipiscis_RS09835	phosphatidate cytidylyltransferase
LAC1533_RS05405	RIP metalloprotease RseP	GSS_RS04195	RIP metalloprotease RseP	Lacidipiscis_RS09840	RIP metalloprotease RseP
LAC1533_RS05410	proline--tRNA ligase	GSS_RS04190	proline--tRNA ligase	Lacidipiscis_RS09845	proline--tRNA ligase
LAC1533_RS05415	PolC-type DNA polymerase III	GSS_RS04185	PolC-type DNA polymerase III	Lacidipiscis_RS09850	PolC-type DNA polymerase III
LAC1533_RS05420	ribosome maturation factor RimP	GSS_RS04180	ribosome maturation factor RimP	Lacidipiscis_RS09855	ribosome maturation factor RimP
LAC1533_RS05425	transcription termination/antitermination protein NusA	GSS_RS04175	transcription termination/antitermination protein NusA	Lacidipiscis_RS09860	transcription termination/antitermination protein NusA
LAC1533_RS05430	DUF448 domain-containing protein	GSS_RS04170	DUF448 domain-containing protein	Lacidipiscis_RS09865	DUF448 domain-containing protein
LAC1533_RS05435	hypothetical protein	GSS_RS04165	hypothetical protein	Lacidipiscis_RS09870	hypothetical protein
LAC1533_RS05440	translation initiation factor IF-2	GSS_RS04160	translation initiation factor IF-2	Lacidipiscis_RS09875	translation initiation factor IF-2
LAC1533_RS05445	30S ribosome-binding factor RbfA	GSS_RS04155	30S ribosome-binding factor RbfA	Lacidipiscis_RS09880	30S ribosome-binding factor RbfA
LAC1533_RS05450	tRNA pseudouridine(55) synthase TruB	GSS_RS04150	tRNA pseudouridine(55) synthase TruB	Lacidipiscis_RS09885	tRNA pseudouridine(55) synthase TruB
LAC1533_RS05455	riboflavin biosynthesis protein RibF	GSS_RS04145	bifunctional riboflavin kinase/FAD synthetase	Lacidipiscis_RS09890	riboflavin biosynthesis protein RibF
LAC1533_RS05460	heat-inducible transcription repressor HrcA	GSS_RS04140	heat-inducible transcription repressor HrcA	Lacidipiscis_RS09895	heat-inducible transcription repressor HrcA
LAC1533_RS05465	nucleotide exchange factor GrpE	GSS_RS04135	nucleotide exchange factor GrpE	Lacidipiscis_RS09900	nucleotide exchange factor GrpE
LAC1533_RS05470	molecular chaperone DnaK	GSS_RS04130	molecular chaperone DnaK	Lacidipiscis_RS09905	molecular chaperone DnaK
LAC1533_RS05475	molecular chaperone DnaJ	GSS_RS04125	molecular chaperone DnaJ	Lacidipiscis_RS09910	molecular chaperone DnaJ
LAC1533_RS05480	nucleoside deoxyribosyltransferase	GSS_RS04115	nucleoside deoxyribosyltransferase	Lacidipiscis_RS10135	nucleoside 2-deoxyribosyltransferase
LAC1533_RS05485	N-acetyltransferase	GSS_RS04110	N-acetyltransferase	Lacidipiscis_RS00175	N-acetyltransferase
LAC1533_RS05490	alpha/beta hydrolase	GSS_RS04105	alpha/beta hydrolase	Lacidipiscis_RS00170	alpha/beta hydrolase
LAC1533_RS05495	pyruvate oxidase	GSS_RS04100	pyruvate oxidase	Lacidipiscis_RS00160	pyruvate oxidase
LAC1533_RS05500	serine hydroxymethyltransferase	GSS_RS04095	serine hydroxymethyltransferase	Lacidipiscis_RS00155	serine hydroxymethyltransferase
LAC1533_RS05505	N-acetyltransferase	GSS_RS04090	N-acetyltransferase	Lacidipiscis_RS06260	N-acetyltransferase
LAC1533_RS05510	aldo/keto reductase	GSS_RS04085	aldo/keto reductase	Lacidipiscis_RS06265	aldo/keto reductase
LAC1533_RS05515	hypothetical protein	GSS_RS04080	hypothetical protein	Lacidipiscis_RS06270	hypothetical protein
LAC1533_RS05520	TIGR00730 family Rossman fold protein	GSS_RS04075	TIGR00730 family Rossman fold protein	Lacidipiscis_RS06275	TIGR00730 family Rossman fold protein
LAC1533_RS05525	pyruvate oxidase	GSS_RS04070	pyruvate oxidase		
LAC1533_RS05530	elongation factor 4	GSS_RS04060	elongation factor 4	Lacidipiscis_RS06285	elongation factor 4
LAC1533_RS05540	death-on-curing family protein	GSS_RS13715	death-on-curing family protein	Lacidipiscis_RS07940	type II toxin-antitoxin system death-on-curing family toxin
LAC1533_RS05550	IS30 family transposase	GSS_RS04040	IS30 family transposase	Lacidipiscis_RS10055	IS30 family transposase
LAC1533_RS05555	hypothetical protein			Lacidipiscis_RS10050	hypothetical protein
LAC1533_RS05575	hypothetical protein	GSS_RS04025	hypothetical protein	Lacidipiscis_RS10045	hypothetical protein
LAC1533_RS05590	type VI secretion protein ImpB	GSS_RS04010	type VI secretion protein ImpB	Lacidipiscis_RS07640	excinuclease ABC subunit A
LAC1533_RS05595	hypothetical protein	GSS_RS04005	hypothetical protein	Lacidipiscis_RS07645	hypothetical protein
LAC1533_RS05600	RNA methyltransferase	GSS_RS04000	RNA methyltransferase	Lacidipiscis_RS07650	RNA methyltransferase
LAC1533_RS05605	hydrolase	GSS_RS03995	hydrolase	Lacidipiscis_RS07655	hydrolase
LAC1533_RS05610	transcriptional regulator	GSS_RS11445	transcriptional regulator	Lacidipiscis_RS07660	transcriptional regulator
LAC1533_RS05615	phenylalanine--tRNA ligase subunit alpha	GSS_RS03990	phenylalanine--tRNA ligase subunit alpha	Lacidipiscis_RS07665	phenylalanine--tRNA ligase subunit alpha
LAC1533_RS05620	phenylalanine--tRNA ligase subunit beta			Lacidipiscis_RS07670	phenylalanine--tRNA ligase subunit beta
LAC1533_RS05625	endolytic transglycosylase MltG			Lacidipiscis_RS11345	endolytic transglycosylase MltG
LAC1533_RS05630	uridine kinase	GSS_RS03975	uridine kinase	Lacidipiscis_RS11335	uridine kinase
LAC1533_RS05635	transcription elongation factor GreA	GSS_RS03970	transcription elongation factor GreA	Lacidipiscis_RS11330	transcription elongation factor GreA
LAC1533_RS05645	group II intron reverse transcriptase/maturase				
LAC1533_RS05650	NADPH-dependent oxidoreductase	GSS_RS12530	NADPH-dependent oxidoreductase	Lacidipiscis_RS01510	NADPH-dependent oxidoreductase
LAC1533_RS05655	hypothetical protein	GSS_RS03955	hypothetical protein	Lacidipiscis_RS01505	hypothetical protein
LAC1533_RS05660	nucleoside hydrolase	GSS_RS03950	nucleoside hydrolase	Lacidipiscis_RS01500	nucleoside hydrolase
LAC1533_RS05665	50S ribosomal protein L11 methyltransferase			Lacidipiscis_RS01485	50S ribosomal protein L11 methyltransferase
LAC1533_RS05670	16S rRNA (uracil(1498)-N(3))-methyltransferase	GSS_RS03940	16S rRNA (uracil(1498)-N(3))-methyltransferase	Lacidipiscis_RS01480	16S rRNA (uracil(1498)-N(3))-methyltransferase
LAC1533_RS05675	site-specific integrase			Lacidipiscis_RS01475	site-specific integrase
LAC1533_RS05680	hypothetical protein			Lacidipiscis_RS01470	hypothetical protein
LAC1533_RS05685	helix-turn-helix domain-containing protein				
LAC1533_RS05690	XRE family transcriptional regulator				
LAC1533_RS05695	hypothetical protein				
LAC1533_RS05700	DUF2188 domain-containing protein			Lacidipiscis_RS01440	DUF2188 domain-containing protein
LAC1533_RS05705	hypothetical protein			Lacidipiscis_RS01430	hypothetical protein
LAC1533_RS05710	hypothetical protein				
LAC1533_RS05715	hypothetical protein				
LAC1533_RS05720	hypothetical protein			Lacidipiscis_RS01415	hypothetical protein
LAC1533_RS05725	hypothetical protein				
LAC1533_RS05730	hypothetical protein				
LAC1533_RS05735	hypothetical protein				
LAC1533_RS05740	single-stranded DNA-binding protein				
LAC1533_RS05745	hypothetical protein				
LAC1533_RS05750	DNA replication protein				
LAC1533_RS05755	hypothetical protein				
LAC1533_RS05760	hypothetical protein			Lacidipiscis_RS01385	hypothetical protein
LAC1533_RS05765	RusA family crossover junction endodeoxyribonuclease			Lacidipiscis_RS01380	RusA family crossover junction endodeoxyribonuclease
LAC1533_RS05770	hypothetical protein				

LAC1533_RS05775	hypothetical protein			Lacidipiscis_RS01375	hypothetical protein
LAC1533_RS05780	hypothetical protein				
LAC1533_RS05785	hypothetical protein				
LAC1533_RS05790	site-specific DNA-methyltransferase				
LAC1533_RS05795	hypothetical protein				
LAC1533_RS05800	hypothetical protein			Lacidipiscis_RS01365	hypothetical protein
LAC1533_RS05805	terminase small subunit			Lacidipiscis_RS01360	terminase small subunit
LAC1533_RS05810	PBSX family phage terminase large subunit			Lacidipiscis_RS01355	PBSX family phage terminase large subunit
LAC1533_RS05815	phage portal protein			Lacidipiscis_RS01350	phage portal protein
LAC1533_RS05820	minor capsid protein			Lacidipiscis_RS01345	minor capsid protein
LAC1533_RS05825	hypothetical protein			Lacidipiscis_RS01340	hypothetical protein
LAC1533_RS05830	capsid protein			Lacidipiscis_RS01335	hypothetical protein
LAC1533_RS05835	hypothetical protein				
LAC1533_RS05840	hypothetical protein			Lacidipiscis_RS01320	hypothetical protein
LAC1533_RS05845	capsid protein			Lacidipiscis_RS01315	capsid protein
LAC1533_RS05850	capsid protein			Lacidipiscis_RS01310	capsid protein
LAC1533_RS05855	hypothetical protein			Lacidipiscis_RS01305	hypothetical protein
LAC1533_RS05860	capsid protein			Lacidipiscis_RS01300	capsid protein
LAC1533_RS05865	hypothetical protein			Lacidipiscis_RS01295	hypothetical protein
LAC1533_RS05870	hypothetical protein			Lacidipiscis_RS01290	hypothetical protein
LAC1533_RS05875	hypothetical protein			Lacidipiscis_RS01285	hypothetical protein
LAC1533_RS05880	hypothetical protein			Lacidipiscis_RS01280	hypothetical protein
LAC1533_RS05885	hypothetical protein			Lacidipiscis_RS01275	hypothetical protein
LAC1533_RS05890	hypothetical protein			Lacidipiscis_RS01270	hypothetical protein
LAC1533_RS05895	hypothetical protein			Lacidipiscis_RS01265	hypothetical protein
LAC1533_RS05900	collagen-like protein				
LAC1533_RS05905	hypothetical protein				
LAC1533_RS05910	hypothetical protein			Lacidipiscis_RS01260	hypothetical protein
LAC1533_RS05920	hypothetical protein				
LAC1533_RS05925	DUF2335 domain-containing protein				
LAC1533_RS05930	hypothetical protein	GSS_RS03935	hypothetical protein	Lacidipiscis_RS01240	hypothetical protein
LAC1533_RS05935	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	GSS_RS03930	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	Lacidipiscis_RS01235	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase
LAC1533_RS05940	D-tyrosyl-tRNA(Tyr) deacylase	GSS_RS03925	D-tyrosyl-tRNA(Tyr) deacylase	Lacidipiscis_RS01230	D-tyrosyl-tRNA(Tyr) deacylase
LAC1533_RS05945	esterase	GSS_RS03915	alpha/beta hydrolase fold family protein	Lacidipiscis_RS01225	esterase
LAC1533_RS05950	haloacid dehalogenase	GSS_RS03910	haloacid dehalogenase-like hydrolase	Lacidipiscis_RS01220	haloacid dehalogenase
LAC1533_RS05955	N-acetylmuramoyl-L-alanine amidase	GSS_RS03905	N-acetylmuramoyl-L-alanine amidase	Lacidipiscis_RS02320	N-acetylmuramoyl-L-alanine amidase
LAC1533_RS05960	histidine--tRNA ligase	GSS_RS03900	histidine--tRNA ligase	Lacidipiscis_RS02315	histidine--tRNA ligase
LAC1533_RS05965	aspartate--tRNA ligase	GSS_RS03895	aspartate--tRNA ligase	Lacidipiscis_RS02310	aspartate--tRNA ligase
LAC1533_RS05970	YitT family protein	GSS_RS03890	YitT family protein	Lacidipiscis_RS02305	YitT family protein
LAC1533_RS05975	teichoic acid biosynthesis protein	GSS_RS03885	teichoic acid biosynthesis protein	Lacidipiscis_RS02300	teichoic acid biosynthesis protein
LAC1533_RS05980	deoxyribonuclease IV	GSS_RS03880	deoxyribonuclease IV	Lacidipiscis_RS02295	deoxyribonuclease IV
LAC1533_RS05985	kinase/pyrophosphorylase	GSS_RS03875	kinase/pyrophosphorylase	Lacidipiscis_RS02290	kinase/pyrophosphorylase
LAC1533_RS05990	30S ribosomal protein S21	GSS_RS03870	30S ribosomal protein S21	Lacidipiscis_RS02285	30S ribosomal protein S21
LAC1533_RS05995	GatB/YqeY domain-containing protein	GSS_RS03865	GatB/YqeY domain-containing protein	Lacidipiscis_RS02280	GatB/YqeY domain-containing protein
LAC1533_RS06000	PhoH family protein	GSS_RS03860	PhoH family protein	Lacidipiscis_RS04615	PhoH family protein
LAC1533_RS06005	rRNA maturation RNase YbeY	GSS_RS03855	rRNA maturation RNase YbeY	Lacidipiscis_RS04620	rRNA maturation RNase YbeY
LAC1533_RS06010	diacylglycerol kinase	GSS_RS03850	diacylglycerol kinase	Lacidipiscis_RS04625	UDP kinase
LAC1533_RS06015	GTPase Era	GSS_RS03845	GTPase Era	Lacidipiscis_RS04630	GTPase Era
LAC1533_RS06020	DNA repair protein RecO	GSS_RS03840	DNA repair protein RecO	Lacidipiscis_RS04635	DNA repair protein RecO
LAC1533_RS06025	glycine--tRNA ligase subunit alpha	GSS_RS03835	glycine--tRNA ligase subunit alpha	Lacidipiscis_RS07850	glycine--tRNA ligase subunit alpha
LAC1533_RS06030	glycine--tRNA ligase subunit beta	GSS_RS03830	glycine--tRNA ligase subunit beta	Lacidipiscis_RS07845	glycine--tRNA ligase subunit beta
LAC1533_RS06035	DNA primase	GSS_RS03825	DNA primase	Lacidipiscis_RS07840	DNA primase
LAC1533_RS06040	RNA polymerase sigma factor RpoD	GSS_RS03820	RNA polymerase sigma factor RpoD	Lacidipiscis_RS07835	RNA polymerase sigma factor RpoD
LAC1533_RS06045	tRNA (adenine(22)-N(1))-methyltransferase TrmK	GSS_RS03815	tRNA (adenine(22)-N(1))-methyltransferase TrmK	Lacidipiscis_RS11250	SAM-dependent methyltransferase
LAC1533_RS06050	Nif3-like dinuclear metal center hexameric protein	GSS_RS03810	Nif3-like dinuclear metal center hexameric protein	Lacidipiscis_RS11245	Nif3-like dinuclear metal center hexameric protein
LAC1533_RS06055	peptidase T	GSS_RS03805	peptidase T	Lacidipiscis_RS11240	peptidase T

LAC1533_RS06080	ATP-dependent chaperone ClpB	GSS_RS00005	chaperone ClpB	Lacidipiscis_RS11235	ATP-dependent chaperone ClpB
LAC1533_RS06090	group II intron reverse transcriptase/maturase				
LAC1533_RS06095	DUF2929 domain-containing protein			Lacidipiscis_RS10175	DUF2929 domain-containing protein
LAC1533_RS06100	DNA polymerase III subunit alpha	GSS_RS00020	DNA polymerase III subunit alpha	Lacidipiscis_RS10170	DNA polymerase III subunit alpha
LAC1533_RS06105	6-phosphofructokinase	GSS_RS00025	6-phosphofructokinase	Lacidipiscis_RS10165	6-phosphofructokinase
LAC1533_RS06110	pyruvate kinase	GSS_RS00030	pyruvate kinase	Lacidipiscis_RS10160	pyruvate kinase
LAC1533_RS06115	DUF441 domain-containing protein	GSS_RS00035	DUF441 domain-containing protein	Lacidipiscis_RS05240	DUF441 domain-containing protein
LAC1533_RS06120	S1 RNA-binding protein	GSS_RS00040	S1 RNA-binding protein	Lacidipiscis_RS05245	DNA-binding protein
LAC1533_RS06125	transcriptional repressor	GSS_RS00045	transcriptional repressor	Lacidipiscis_RS05250	transcriptional repressor
LAC1533_RS06130	site-specific tyrosine recombinase XerD	GSS_RS11455	site-specific tyrosine recombinase XerD	Lacidipiscis_RS05255	site-specific tyrosine recombinase XerD
LAC1533_RS06135	GNAT family N-acetyltransferase	GSS_RS00050	GNAT family N-acetyltransferase	Lacidipiscis_RS05260	GNAT family N-acetyltransferase
LAC1533_RS06140	rifampin ADP-ribosyl transferase	GSS_RS00055	rifampin ADP-ribosyl transferase	Lacidipiscis_RS05265	rifampin ADP-ribosyl transferase
LAC1533_RS06145	SMC-Scp complex subunit ScpB	GSS_RS00060	SMC-Scp complex subunit ScpB	Lacidipiscis_RS05270	SMC-Scp complex subunit ScpB
LAC1533_RS06150	rRNA pseudouridine synthase	GSS_RS00065	rRNA pseudouridine synthase	Lacidipiscis_RS05275	rRNA pseudouridine synthase
LAC1533_RS06155	hypothetical protein	GSS_RS00070	hypothetical protein	Lacidipiscis_RS05280	hypothetical protein
LAC1533_RS06160	ATP-dependent DNA helicase RecQ	GSS_RS00075	ATP-dependent DNA helicase RecQ	Lacidipiscis_RS05285	ATP-dependent DNA helicase RecQ
LAC1533_RS06165	LysM domain-containing protein	GSS_RS00080	LysM domain-containing protein	Lacidipiscis_RS03645	LysM domain-containing protein
LAC1533_RS06170	(d)CMP kinase			Lacidipiscis_RS03640	(d)CMP kinase
LAC1533_RS06175	30S ribosomal protein S1	GSS_RS00090	30S ribosomal protein S1	Lacidipiscis_RS03635	30S ribosomal protein S1
LAC1533_RS06180	ribosome biogenesis GTPase Der	GSS_RS00095	ribosome biogenesis GTPase Der	Lacidipiscis_RS03630	ribosome biogenesis GTPase Der
LAC1533_RS06185	HU family DNA-binding protein	GSS_RS00100	HU family DNA-binding protein	Lacidipiscis_RS03625	HU family DNA-binding protein
LAC1533_RS06190	tetratricopeptide repeat protein	GSS_RS00105	tetratricopeptide repeat protein	Lacidipiscis_RS03615	tetratricopeptide repeat protein
LAC1533_RS06195 IDENTICAL PARALOGS LAC1533_RS08855	IS30 family transposase			Lacidipiscis_RS00015	IS30 family transposase
LAC1533_RS06200	hypothetical protein	GSS_RS00110	hypothetical protein	Lacidipiscis_RS03610	hypothetical protein
LAC1533_RS06205	4-hydroxy-tetrahydrodipicolinate reductase	GSS_RS00115	4-hydroxy-tetrahydrodipicolinate reductase	Lacidipiscis_RS03595	4-hydroxy-tetrahydrodipicolinate reductase
LAC1533_RS06210	CCA tRNA nucleotidyltransferase	GSS_RS00120	CCA tRNA nucleotidyltransferase	Lacidipiscis_RS03590	CCA tRNA nucleotidyltransferase
LAC1533_RS06215	ABC transporter ATP-binding protein	GSS_RS00125	ABC transporter ATP-binding protein	Lacidipiscis_RS03585	ABC transporter ATP-binding protein
LAC1533_RS06220	thymidylate synthase	GSS_RS00130	thymidylate synthase	Lacidipiscis_RS03580	thymidylate synthase
LAC1533_RS06225	lipase	GSS_RS00135	lipase/acylhydrolase	Lacidipiscis_RS03575	lipase
LAC1533_RS06230	DUF2140 domain-containing protein	GSS_RS00140	DUF2140 domain-containing protein	Lacidipiscis_RS03570	DUF2140 domain-containing protein
LAC1533_RS06235	YozE family protein	GSS_RS13910	hypothetical protein	Lacidipiscis_RS03565	YozE family protein
LAC1533_RS06240	PDZ domain-containing protein	GSS_RS00155	PDZ domain-containing protein	Lacidipiscis_RS03555	PDZ domain-containing protein
LAC1533_RS06245	ribosome biogenesis GTPase YlqF			Lacidipiscis_RS03550	ribosome biogenesis GTPase YlqF
LAC1533_RS06250	ribonuclease HII			Lacidipiscis_RS03545	ribonuclease HII
LAC1533_RS06255	DNA-protecting protein DprA	GSS_RS00170	DNA-protecting protein DprA	Lacidipiscis_RS03540	DNA-protecting protein DprA
LAC1533_RS06260	type I DNA topoisomerase	GSS_RS00180	type I DNA topoisomerase	Lacidipiscis_RS03535	type I DNA topoisomerase
LAC1533_RS06265	tyrosine recombinase XerC	GSS_RS00185	tyrosine recombinase XerC	Lacidipiscis_RS03530	tyrosine recombinase XerC
LAC1533_RS06270	HslU--HslV peptidase proteolytic subunit	GSS_RS00190	HslU--HslV peptidase proteolytic subunit	Lacidipiscis_RS03525	HslU--HslV peptidase proteolytic subunit
LAC1533_RS06275	ATP-dependent protease ATPase subunit HslU	GSS_RS00195	ATP-dependent protease ATPase subunit HslU	Lacidipiscis_RS03520	ATP-dependent protease ATPase subunit HslU
LAC1533_RS06280	aldose 1-epimerase family protein	GSS_RS00200	aldose 1-epimerase family protein	Lacidipiscis_RS03515	aldose 1-epimerase family protein
LAC1533_RS06285	glycerol-3-phosphate acyltransferase	GSS_RS00205	glycerol-3-phosphate acyltransferase	Lacidipiscis_RS03510	glycerol-3-phosphate acyltransferase
LAC1533_RS06290	DNA topoisomerase IV subunit B	GSS_RS11985	DNA topoisomerase IV subunit B	Lacidipiscis_RS03505	DNA topoisomerase IV subunit B
LAC1533_RS06295	DNA topoisomerase IV subunit A	GSS_RS11995	hypothetical protein	Lacidipiscis_RS03500	DNA topoisomerase IV subunit A
LAC1533_RS06300	hypothetical protein	GSS_RS00225	hypothetical protein	Lacidipiscis_RS03495	hypothetical protein
LAC1533_RS06310	signal peptidase I	GSS_RS00235	signal peptidase I	Lacidipiscis_RS01700	signal peptidase I
LAC1533_RS06315	hypothetical protein	GSS_RS00240	hypothetical protein	Lacidipiscis_RS01705	hypothetical protein
LAC1533_RS06320	xylose isomerase	GSS_RS00245	xylose isomerase	Lacidipiscis_RS01710	xylose isomerase
LAC1533_RS06325	DegV family protein	GSS_RS00250	DegV family protein	Lacidipiscis_RS01715	DegV family protein
LAC1533_RS06330	MarR family transcriptional regulator	GSS_RS00255	MarR family transcriptional regulator	Lacidipiscis_RS01720	MarR family transcriptional regulator
LAC1533_RS06335	DUF814 domain-containing protein			Lacidipiscis_RS01725	DUF814 domain-containing protein
LAC1533_RS06340	hypothetical protein	GSS_RS00265	hypothetical protein	Lacidipiscis_RS01730	hypothetical protein
LAC1533_RS06350	GNAT family N-acetyltransferase	GSS_RS00275	GNAT family N-acetyltransferase	Lacidipiscis_RS01740	GNAT family N-acetyltransferase
LAC1533_RS06355	glutamate racemase	GSS_RS00280	glutamate racemase	Lacidipiscis_RS01745	glutamate racemase
LAC1533_RS06360	aminotransferase class V-fold PLP-dependent enzyme	GSS_RS00285	aminotransferase class V-fold PLP-dependent enzyme	Lacidipiscis_RS01750	aminotransferase class V-fold PLP-dependent enzyme
LAC1533_RS06365	DeoR/GlpR transcriptional regulator	GSS_RS00290	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS01755	DeoR/GlpR transcriptional regulator
LAC1533_RS06370	manganese-dependent inorganic pyrophosphatase	GSS_RS00295	manganese-dependent inorganic pyrophosphatase	Lacidipiscis_RS01760	manganese-dependent inorganic pyrophosphatase
LAC1533_RS06375	LysR family transcriptional regulator	GSS_RS00300	LysR family transcriptional regulator	Lacidipiscis_RS01765	LysR family transcriptional regulator
LAC1533_RS06385	dihydroorotate dehydrogenase	GSS_RS00320	dihydroorotate dehydrogenase	Lacidipiscis_RS01775	dihydroorotate dehydrogenase
LAC1533_RS06395	carbamoyl phosphate synthase small subunit	GSS_RS00330	carbamoyl-phosphate synthase small subunit	Lacidipiscis_RS01785	carbamoyl phosphate synthase small subunit

LAC1533_RS06400	dihydroorotase	GSS_RS00335	dihydroorotase	Lacidipiscis_RS01790	dihydroorotase
LAC1533_RS06410	uracil permease			Lacidipiscis_RS01800	uracil permease
LAC1533_RS06415	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR	GSS_RS00350	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR	Lacidipiscis_RS01805	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR
LAC1533_RS06420	RluA family pseudouridine synthase	GSS_RS00355	RluA family pseudouridine synthase	Lacidipiscis_RS01810	RluA family pseudouridine synthase
LAC1533_RS06425	signal peptidase II	GSS_RS00360	signal peptidase II	Lacidipiscis_RS01815	signal peptidase II
LAC1533_RS06430	formate--tetrahydrofolate ligase	GSS_RS00365	formate--tetrahydrofolate ligase	Lacidipiscis_RS01820	formate--tetrahydrofolate ligase
LAC1533_RS06435	hypothetical protein	GSS_RS00370	hypothetical protein	Lacidipiscis_RS01825	hypothetical protein
LAC1533_RS06440	class I SAM-dependent RNA methyltransferase			Lacidipiscis_RS01830	class I SAM-dependent RNA methyltransferase
LAC1533_RS06460	cell division regulator GpsB	GSS_RS00380	cell division regulator GpsB	Lacidipiscis_RS01840	cell division regulator GpsB
LAC1533_RS06465	DUF1273 domain-containing protein	GSS_RS12025	DUF1273 domain-containing protein	Lacidipiscis_RS01845	DUF1273 domain-containing protein
LAC1533_RS06470	Holliday junction resolvase RecU	GSS_RS00390	Holliday junction resolvase RecU	Lacidipiscis_RS01850	Holliday junction resolvase RecU
LAC1533_RS06475	carboxypeptidase			Lacidipiscis_RS01855	carboxypeptidase
LAC1533_RS06480	endonuclease III	GSS_RS00410	endonuclease III	Lacidipiscis_RS10195	endonuclease III
LAC1533_RS06485	DnaD domain protein	GSS_RS00415	DnaD domain protein	Lacidipiscis_RS10200	DnaD domain protein
LAC1533_RS06490	asparagine--tRNA ligase	GSS_RS00420	asparagine--tRNA ligase	Lacidipiscis_RS10205	asparagine--tRNA ligase
LAC1533_RS06495	pyridoxal phosphate-dependent aminotransferase	GSS_RS00425	pyridoxal phosphate-dependent aminotransferase	Lacidipiscis_RS10210	pyridoxal phosphate-dependent aminotransferase
LAC1533_RS06500	hypothetical protein	GSS_RS00430	hypothetical protein	Lacidipiscis_RS10215	hypothetical protein
LAC1533_RS06505	hypothetical protein	GSS_RS13620	hypothetical protein	Lacidipiscis_RS10220	hypothetical protein
LAC1533_RS06510	mevalonate kinase	GSS_RS00440	mevalonate kinase	Lacidipiscis_RS10225	mevalonate kinase
LAC1533_RS06515	diphosphomevalonate decarboxylase			Lacidipiscis_RS10230	diphosphomevalonate decarboxylase
LAC1533_RS06520	phosphomevalonate kinase	GSS_RS00450	phosphomevalonate kinase	Lacidipiscis_RS10235	phosphomevalonate kinase
LAC1533_RS06525	type 2 isopentenyl-diphosphate Delta-isomerase	GSS_RS00455	type 2 isopentenyl-diphosphate Delta-isomerase	Lacidipiscis_RS10240	type 2 isopentenyl-diphosphate Delta-isomerase
LAC1533_RS06530	RNA methyltransferase	GSS_RS00460	23S rRNA methyltransferase	Lacidipiscis_RS10245	RNA methyltransferase
LAC1533_RS06535	hypothetical protein	GSS_RS13625	hypothetical protein	Lacidipiscis_RS10250	hypothetical protein
LAC1533_RS06540	metal-sulfur cluster assembly factor	GSS_RS00470	metal-sulfur cluster assembly factor	Lacidipiscis_RS10255	metal-sulfur cluster assembly factor
LAC1533_RS06545	S9 family serine peptidase	GSS_RS00475	S9 family serine peptidase	Lacidipiscis_RS10260	S9 family serine peptidase
LAC1533_RS06550	Cof-type HAD-IIB family hydrolase	GSS_RS00485	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS10265	Cof-type HAD-IIB family hydrolase
LAC1533_RS06555	diaminopimelate decarboxylase	GSS_RS00490	diaminopimelate decarboxylase	Lacidipiscis_RS10270	diaminopimelate decarboxylase
LAC1533_RS06560	dipeptidase			Lacidipiscis_RS10275	dipeptidase
LAC1533_RS06565	hypothetical protein	GSS_RS13630	hypothetical protein	Lacidipiscis_RS10280	hypothetical protein
LAC1533_RS06570 IDENTICAL PARALOGS LAC1533_RS07645 IDENTICAL PARALOGS LAC1533_RS07685 IDENTICAL PARALOGS LAC1533_RS11435	group II intron reverse transcriptase/maturase				
LAC1533_RS06580	elongation factor Ts	GSS_RS00505	elongation factor Ts	Lacidipiscis_RS10285	elongation factor Ts
LAC1533_RS06585	30S ribosomal protein S2	GSS_RS00510	30S ribosomal protein S2	Lacidipiscis_RS10290	30S ribosomal protein S2
LAC1533_RS06590	lactate dehydrogenase	GSS_RS00515	lactate dehydrogenase	Lacidipiscis_RS10295	lactate dehydrogenase
LAC1533_RS06595	GIY-YIG nuclease family protein	GSS_RS00520	GIY-YIG nuclease family protein	Lacidipiscis_RS10300	GIY-YIG nuclease family protein
LAC1533_RS06600	tRNA1(Val) (adenine(37)-N6)-methyltransferase			Lacidipiscis_RS10305	tRNA1(Val) (adenine(37)-N6)-methyltransferase
LAC1533_RS06605	1-acyl-sn-glycerol-3-phosphate acyltransferase	GSS_RS00530	1-acyl-sn-glycerol-3-phosphate acyltransferase	Lacidipiscis_RS10310	1-acyl-sn-glycerol-3-phosphate acyltransferase
LAC1533_RS06610	hypothetical protein	GSS_RS00535	hypothetical protein	Lacidipiscis_RS10315	hypothetical protein
LAC1533_RS06615	DUF896 family protein	GSS_RS00540	DUF896 family protein	Lacidipiscis_RS10320	DUF896 family protein
LAC1533_RS06620	transcriptional repressor LexA	GSS_RS00545	transcriptional repressor LexA	Lacidipiscis_RS10325	transcriptional repressor LexA
LAC1533_RS06630	DNA repair protein RecN			Lacidipiscis_RS10330	DNA repair protein RecN
LAC1533_RS06635	ArgR family transcriptional regulator	GSS_RS00555	ArgR family transcriptional regulator	Lacidipiscis_RS10335	ArgR family transcriptional regulator
LAC1533_RS06640	TlyA family rRNA (cytidine-2-O)-methyltransferase	GSS_RS00560	TlyA family rRNA (cytidine-2-O)-methyltransferase	Lacidipiscis_RS10340	TlyA family rRNA (cytidine-2-O)-methyltransferase
LAC1533_RS06645	polyprenyl synthetase family protein	GSS_RS00565	polyprenyl synthetase family protein	Lacidipiscis_RS10345	polyprenyl synthetase family protein
LAC1533_RS06650	exodeoxyribonuclease VII small subunit	GSS_RS00570	exodeoxyribonuclease VII small subunit	Lacidipiscis_RS10350	exodeoxyribonuclease VII small subunit
LAC1533_RS06655	exodeoxyribonuclease VII large subunit	GSS_RS00575	exodeoxyribonuclease VII large subunit	Lacidipiscis_RS10355	exodeoxyribonuclease VII large subunit
LAC1533_RS06660	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	GSS_RS00580	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	Lacidipiscis_RS10360	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD
LAC1533_RS06665	transcription antitermination factor NusB	GSS_RS00585	transcription antitermination factor NusB	Lacidipiscis_RS10365	transcription antitermination factor NusB

LAC1533_RS06670	Asp23/Gls24 family envelope stress response protein	GSS_RS00590	Asp23/Gls24 family envelope stress response protein	Lacidipiscis_RS10370	Asp23/Gls24 family envelope stress response protein
LAC1533_RS06675	elongation factor P	GSS_RS00595	elongation factor P	Lacidipiscis_RS10375	elongation factor P
LAC1533_RS06680	aminopeptidase P family protein				
LAC1533_RS06685	50S ribosomal protein L27	GSS_RS00605	50S ribosomal protein L27	Lacidipiscis_RS10385	50S ribosomal protein L27
LAC1533_RS06690	ribosomal-processing cysteine protease Prp	GSS_RS00610	ribosomal-processing cysteine protease Prp	Lacidipiscis_RS10390	ribosomal-processing cysteine protease Prp
LAC1533_RS06695	50S ribosomal protein L21	GSS_RS00615	50S ribosomal protein L21	Lacidipiscis_RS10395	50S ribosomal protein L21
LAC1533_RS06705	1-acyl-sn-glycerol-3-phosphate acyltransferase	GSS_RS12100	1-acyl-sn-glycerol-3-phosphate acyltransferase	Lacidipiscis_RS10405	1-acyl-sn-glycerol-3-phosphate acyltransferase
LAC1533_RS06720	hypothetical protein	GSS_RS00920	hypothetical protein	Lacidipiscis_RS08600	hypothetical protein
LAC1533_RS06725	hypothetical protein	GSS_RS00930	hypothetical protein	Lacidipiscis_RS02095	hypothetical protein
LAC1533_RS06730	hypothetical protein	GSS_RS00935	hypothetical protein	Lacidipiscis_RS02100	hypothetical protein
LAC1533_RS06735	exonuclease SbcC	GSS_RS00940	hypothetical protein	Lacidipiscis_RS02105	hypothetical protein
LAC1533_RS06740	hypothetical protein	GSS_RS00950	hypothetical protein	Lacidipiscis_RS02110	hypothetical protein
LAC1533_RS06745	hydroxymethylglutaryl-CoA synthase			Lacidipiscis_RS02115	hydroxymethylglutaryl-CoA synthase
LAC1533_RS06755	acylphosphatase	GSS_RS00960	acylphosphatase	Lacidipiscis_RS02120	acylphosphatase
LAC1533_RS06760	OxaA precursor			Lacidipiscis_RS02125	OxaA precursor
LAC1533_RS06765	sensor histidine kinase			Lacidipiscis_RS02130	sensor histidine kinase
LAC1533_RS06770	DNA-binding response regulator	GSS_RS00975	DNA-binding response regulator	Lacidipiscis_RS02135	DNA-binding response regulator
LAC1533_RS06780	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	GSS_RS00980	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	Lacidipiscis_RS02140	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)
LAC1533_RS06785	ATP-dependent Clp protease ATP-binding subunit ClpX			Lacidipiscis_RS02145	ATP-dependent Clp protease ATP-binding subunit ClpX
LAC1533_RS06790	trigger factor	GSS_RS12125	trigger factor	Lacidipiscis_RS02150	trigger factor
LAC1533_RS06795	elongation factor Tu	GSS_RS01000	elongation factor Tu	Lacidipiscis_RS02155	elongation factor Tu
LAC1533_RS06800	hypothetical protein	GSS_RS01015	hypothetical protein	Lacidipiscis_RS02160	hypothetical protein
LAC1533_RS06805	ribonuclease J	GSS_RS01020	RNase J family beta-CASP ribonuclease	Lacidipiscis_RS02165	ribonuclease J
LAC1533_RS06810	4-hydroxy-tetrahydrodipicolinate synthase	GSS_RS01025	4-hydroxy-tetrahydrodipicolinate synthase	Lacidipiscis_RS02170	4-hydroxy-tetrahydrodipicolinate synthase
LAC1533_RS06815	aspartate-semialdehyde dehydrogenase	GSS_RS01030	aspartate-semialdehyde dehydrogenase	Lacidipiscis_RS02175	aspartate-semialdehyde dehydrogenase
LAC1533_RS06825	30S ribosomal protein S15	GSS_RS01045	30S ribosomal protein S15	Lacidipiscis_RS02185	30S ribosomal protein S15
LAC1533_RS06830	30S ribosomal protein S20	GSS_RS01050	30S ribosomal protein S20	Lacidipiscis_RS02195	30S ribosomal protein S20
LAC1533_RS06835	DNA polymerase III subunit delta	GSS_RS13470	DNA polymerase III subunit delta	Lacidipiscis_RS02200	DNA polymerase III subunit delta
LAC1533_RS06840	DNA internalization-related competence protein ComEC/Rec2	GSS_RS12145	MBL fold metallo-hydrolase	Lacidipiscis_RS02205	DNA internalization-related competence protein ComEC/Rec2
LAC1533_RS06845	ComE operon protein 2	GSS_RS01070	ComE operon protein 2	Lacidipiscis_RS02210	ComE operon protein 2
LAC1533_RS06850	ComE operon protein 1	GSS_RS01075	ComE operon protein 1	Lacidipiscis_RS02215	ComE operon protein 1
LAC1533_RS06855	PDZ domain-containing protein	GSS_RS01080	PDZ domain-containing protein	Lacidipiscis_RS02220	PDZ domain-containing protein
LAC1533_RS06860	pantetheine-phosphate adenylyltransferase	GSS_RS01090	pantetheine-phosphate adenylyltransferase	Lacidipiscis_RS02225	pantetheine-phosphate adenylyltransferase
LAC1533_RS06865	16S rRNA (guanine(966)-N(2))-methyltransferase RsmD			Lacidipiscis_RS02230	16S rRNA (guanine(966)-N(2))-methyltransferase RsmD
LAC1533_RS06870	DUF2129 domain-containing protein	GSS_RS01100	DUF2129 domain-containing protein	Lacidipiscis_RS02235	DUF2129 domain-containing protein
LAC1533_RS06875	pyruvate carboxylase	GSS_RS12155	pyruvate carboxylase	Lacidipiscis_RS02240	pyruvate carboxylase
LAC1533_RS06880	FtsW/RodA/SpoVE family cell cycle protein	GSS_RS01115	FtsW/RodA/SpoVE family cell cycle protein	Lacidipiscis_RS02245	FtsW/RodA/SpoVE family cell cycle protein
LAC1533_RS06885	DUF1507 domain-containing protein	GSS_RS01120	DUF1507 domain-containing protein	Lacidipiscis_RS02250	DUF1507 domain-containing protein
LAC1533_RS06890	IS982 family transposase				
LAC1533_RS06895	translational GTPase TypA			Lacidipiscis_RS05235	translational GTPase TypA
LAC1533_RS06900	inositol monophosphatase family protein	GSS_RS01130	inositol monophosphatase family protein	Lacidipiscis_RS05230	inositol monophosphatase family protein
LAC1533_RS06905	hypothetical protein	GSS_RS01135	hypothetical protein	Lacidipiscis_RS05225	hypothetical protein
LAC1533_RS06910	lactate dehydrogenase	GSS_RS01140	malate dehydrogenase	Lacidipiscis_RS05220	malate dehydrogenase
LAC1533_RS06915	IS30 family transposase				
LAC1533_RS06920	peptide deformylase	GSS_RS01155	peptide deformylase	Lacidipiscis_RS03290	peptide deformylase
LAC1533_RS06925	hypothetical protein	GSS_RS01160	hypothetical protein	Lacidipiscis_RS03295	hypothetical protein
LAC1533_RS06935	DUF1447 domain-containing protein	GSS_RS01165	DUF1447 domain-containing protein	Lacidipiscis_RS03310	DUF1447 domain-containing protein
LAC1533_RS06940	ribonuclease J	GSS_RS01170	ribonuclease J	Lacidipiscis_RS03315	ribonuclease J
LAC1533_RS06945	transcriptional regulator	GSS_RS01175	transcriptional regulator	Lacidipiscis_RS03320	transcriptional regulator
LAC1533_RS06955	ATP-dependent RecD-like DNA helicase	GSS_RS01180	ATP-dependent RecD-like DNA helicase	Lacidipiscis_RS03325	ATP-dependent RecD-like DNA helicase
LAC1533_RS06960	tetratricopeptide repeat protein	GSS_RS01185	tetratricopeptide repeat protein	Lacidipiscis_RS03330	tetratricopeptide repeat protein
LAC1533_RS06965	histidine phosphatase family protein	GSS_RS01190	histidine phosphatase family protein	Lacidipiscis_RS03335	histidine phosphatase family protein

LAC1533_RS06970	tRNA 2-thiouridine(34) synthase MnmA	GSS_RS01195	tRNA 2-thiouridine(34) synthase MnmA	Lacidipiscis_RS03340	tRNA 2-thiouridine(34) synthase MnmA
LAC1533_RS06975	cysteine desulfurase	GSS_RS01200	cysteine desulfurase	Lacidipiscis_RS03345	cysteine desulfurase
LAC1533_RS06980	cysteine desulfurase			Lacidipiscis_RS03350	cysteine desulfurase
LAC1533_RS06985	5-methylthioadenosine/adenosylhomocysteine nucleosidase	GSS_RS01210	5-methylthioadenosine/adenosylhomocysteine nucleosidase	Lacidipiscis_RS03355	5-methylthioadenosine/adenosylhomocysteine nucleosidase
LAC1533_RS06990	hypothetical protein	GSS_RS01215	hypothetical protein	Lacidipiscis_RS03360	hypothetical protein
LAC1533_RS06995	NUDIX hydrolase	GSS_RS01220	NUDIX hydrolase	Lacidipiscis_RS03365	NUDIX hydrolase
LAC1533_RS07000	diaminopimelate epimerase	GSS_RS12170	diaminopimelate epimerase	Lacidipiscis_RS03370	diaminopimelate epimerase
LAC1533_RS07005	isoleucine--tRNA ligase	GSS_RS01230	isoleucine--tRNA ligase	Lacidipiscis_RS03375	isoleucine--tRNA ligase
LAC1533_RS07010	DivIVA domain-containing protein	GSS_RS01235	DivIVA domain-containing protein	Lacidipiscis_RS03380	DivIVA domain-containing protein
LAC1533_RS07015	RNA-binding protein			Lacidipiscis_RS03385	RNA-binding protein
LAC1533_RS07020	YggT family protein	GSS_RS01245	YggT family protein	Lacidipiscis_RS03390	YggT family protein
LAC1533_RS07025	cell division protein SepF	GSS_RS01250	cell division protein SepF	Lacidipiscis_RS03395	cell division protein SepF
LAC1533_RS07030	cell division protein FtsZ	GSS_RS01255	cell division protein FtsZ	Lacidipiscis_RS03400	cell division protein FtsZ
LAC1533_RS07035	cell division protein FtsA	GSS_RS01260	cell division protein FtsA	Lacidipiscis_RS03405	cell division protein FtsA
LAC1533_RS07040	hypothetical protein	GSS_RS13645	hypothetical protein	Lacidipiscis_RS03410	hypothetical protein
LAC1533_RS07045	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase			Lacidipiscis_RS03415	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
LAC1533_RS07050	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	GSS_RS01270	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	Lacidipiscis_RS03420	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
LAC1533_RS07055	phospho-N-acetylmuramoyl-pentapeptide- transferase	GSS_RS01275	phospho-N-acetylmuramoyl-pentapeptide- transferase	Lacidipiscis_RS03425	phospho-N-acetylmuramoyl-pentapeptide- transferase
LAC1533_RS07060	PASTA domain-containing protein	GSS_RS01280	PASTA domain-containing protein	Lacidipiscis_RS03430	PASTA domain-containing protein
LAC1533_RS07065	cell division protein FtsL	GSS_RS01285	cell division protein FtsL	Lacidipiscis_RS03435	cell division protein FtsL
LAC1533_RS07070	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	GSS_RS01290	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	Lacidipiscis_RS03440	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH
LAC1533_RS07075	transcriptional regulator MraZ	GSS_RS01295	transcriptional regulator MraZ	Lacidipiscis_RS03445	transcriptional regulator MraZ
LAC1533_RS07080	DUF3397 domain-containing protein	GSS_RS01300	DUF3397 domain-containing protein	Lacidipiscis_RS07355	DUF3397 domain-containing protein
LAC1533_RS07090	DUF4044 domain-containing protein	GSS_RS13945	DUF4044 domain-containing protein	Lacidipiscis_RS07360	DUF4044 domain-containing protein
LAC1533_RS07100	alpha/beta hydrolase	GSS_RS01305	alpha/beta hydrolase	Lacidipiscis_RS07365	alpha/beta hydrolase
LAC1533_RS07105	cardiolipin synthase	GSS_RS01310	cardiolipin synthase	Lacidipiscis_RS07370	cardiolipin synthase
LAC1533_RS07110	septum site-determining protein MinD	GSS_RS01320	septum site-determining protein MinD	Lacidipiscis_RS07375	septum site-determining protein MinD
LAC1533_RS07115	cell division inhibitor	GSS_RS01325	cell division inhibitor	Lacidipiscis_RS07380	cell division inhibitor
LAC1533_RS07120	rod shape-determining protein MreD			Lacidipiscis_RS07385	rod shape-determining protein MreD
LAC1533_RS07125	rod shape-determining protein MreC	GSS_RS01335	rod shape-determining protein MreC	Lacidipiscis_RS07390	rod shape-determining protein MreC
LAC1533_RS07130	rod shape-determining protein	GSS_RS01340	rod shape-determining protein	Lacidipiscis_RS07395	rod shape-determining protein
LAC1533_RS07135	cold-shock protein	GSS_RS01345	cold-shock protein	Lacidipiscis_RS07400	cold-shock protein
LAC1533_RS07140	DNA repair protein	GSS_RS01350	DNA repair protein	Lacidipiscis_RS07405	DNA repair protein
LAC1533_RS07145	HAD family phosphatase			Lacidipiscis_RS07410	HAD family phosphatase
LAC1533_RS07150	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	GSS_RS01360	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	Lacidipiscis_RS07415	bifunctional folylpolyglutamate synthase/dihydrofolate synthase
LAC1533_RS07155	valine--tRNA ligase	GSS_RS01365	valine--tRNA ligase	Lacidipiscis_RS07420	valine--tRNA ligase
LAC1533_RS07165	tRNA 4-thiouridine(8) synthase ThiI	GSS_RS01370	tRNA 4-thiouridine(8) synthase ThiI	Lacidipiscis_RS07425	tRNA 4-thiouridine(8) synthase ThiI
LAC1533_RS07170	cysteine desulfurase	GSS_RS01375	cysteine desulfurase	Lacidipiscis_RS07430	cysteine desulfurase
LAC1533_RS07175	septation ring formation regulator EzrA	GSS_RS01380	septation ring formation regulator EzrA	Lacidipiscis_RS07435	septation ring formation regulator EzrA
LAC1533_RS07180	GAF domain-containing protein			Lacidipiscis_RS07440	GAF domain-containing protein
LAC1533_RS07185	30S ribosomal protein S4	GSS_RS01390	30S ribosomal protein S4	Lacidipiscis_RS07445	30S ribosomal protein S4
LAC1533_RS07190	replication-associated recombination protein A	GSS_RS01395	replication-associated recombination protein A	Lacidipiscis_RS07450	replication-associated recombination protein A
LAC1533_RS07195	universal stress protein			Lacidipiscis_RS07455	universal stress protein
LAC1533_RS07200	DNA-3-methyladenine glycosylase I	GSS_RS01405	DNA-3-methyladenine glycosylase I	Lacidipiscis_RS07460	DNA-3-methyladenine glycosylase I
LAC1533_RS07205	aminoglycoside phosphotransferase family protein	GSS_RS01410	aminoglycoside phosphotransferase family protein	Lacidipiscis_RS03460	aminoglycoside phosphotransferase family protein
LAC1533_RS07210	amino acid permease	GSS_RS01415	amino acid permease	Lacidipiscis_RS08405	amino acid permease
LAC1533_RS07215	hypothetical protein				
LAC1533_RS07220	hypothetical protein				
LAC1533_RS07235	GNAT family acetyltransferase	GSS_RS01420	GNAT family acetyltransferase		
LAC1533_RS07240	IS256 family transposase				
LAC1533_RS07255	hypothetical protein				
LAC1533_RS07260	peptide transporter				
LAC1533_RS07265	recombinase family protein				
LAC1533_RS07275	immunity protein	GSS_RS14245	immunity protein		
LAC1533_RS07290	antitoxin RelB	GSS_RS11150	antitoxin RelB	Lacidipiscis_RS12870	RelB
LAC1533_RS07295	site-specific integrase				
LAC1533_RS07300	transcriptional regulator	GSS_RS01425	transcriptional regulator		
LAC1533_RS07305	hypothetical protein				
LAC1533_RS07325 IDENTICAL PARALOGS LAC1533_RS07420 IDENTICAL PARALOGS LAC1533_RS10240	transposase	GSS_RS11365	transposase		

LAC1533_RS07330	hypothetical protein				
LAC1533_RS07335	DUF536 domain-containing protein	GSS_RS11750	DUF536 domain-containing protein		
LAC1533_RS07340	putative holin-like toxin	GSS_RS14255	putative holin-like toxin		
LAC1533_RS07345	LtrC			Lacidipiscis_RS12035	hypothetical protein
LAC1533_RS07350	hypothetical protein			Lacidipiscis_RS12030	hypothetical protein
LAC1533_RS07355	hypothetical protein				
LAC1533_RS07360	type IA DNA topoisomerase			Lacidipiscis_RS12025	type IA DNA topoisomerase
LAC1533_RS07365	hypothetical protein				
LAC1533_RS07370	conjugal transfer protein			Lacidipiscis_RS01950	hypothetical protein
LAC1533_RS07375	hypothetical protein				
LAC1533_RS07380	conjugal transfer protein				
LAC1533_RS07385	conjugal transfer protein				
LAC1533_RS07390	hypothetical protein				
LAC1533_RS07395	IS30 family transposase	GSS_RS11415	IS30 family transposase		
LAC1533_RS07400	hypothetical protein				
LAC1533_RS07405	hypothetical protein				
LAC1533_RS07410	peptidoglycan endopeptidase				
LAC1533_RS07435	Fe-S cluster assembly protein SufB	GSS_RS10410	Fe-S cluster assembly protein SufB	Lacidipiscis_RS03120	Fe-S cluster assembly protein SufB
LAC1533_RS07440	SUF system NifU family Fe-S cluster assembly protein	GSS_RS10415	SUF system NifU family Fe-S cluster assembly protein	Lacidipiscis_RS03125	SUF system NifU family Fe-S cluster assembly protein
LAC1533_RS07445	cysteine desulfurase	GSS_RS10420	cysteine desulfurase	Lacidipiscis_RS03130	cysteine desulfurase
LAC1533_RS07450	Fe-S cluster assembly protein SufD	GSS_RS10425	Fe-S cluster assembly protein SufD	Lacidipiscis_RS03135	Fe-S cluster assembly protein SufD
LAC1533_RS07455	Fe-S cluster assembly ATPase SufC	GSS_RS10430	Fe-S cluster assembly ATPase SufC	Lacidipiscis_RS03140	Fe-S cluster assembly ATPase SufC
LAC1533_RS07460	arsenate reductase family protein	GSS_RS10435	arsenate reductase family protein	Lacidipiscis_RS03145	arsenate reductase family protein
LAC1533_RS07465	rod shape-determining protein RodA	GSS_RS10445	rod shape-determining protein	Lacidipiscis_RS03150	rod shape-determining protein RodA
LAC1533_RS07470	DUF2969 domain-containing protein	GSS_RS10450	DUF2969 domain-containing protein	Lacidipiscis_RS03155	DUF2969 domain-containing protein
LAC1533_RS07475	membrane protein insertion efficiency factor YidD	GSS_RS10455	membrane protein insertion efficiency factor YidD	Lacidipiscis_RS03160	membrane protein insertion efficiency factor YidD
LAC1533_RS07480	rod shape-determining protein	GSS_RS10460	rod shape-determining protein	Lacidipiscis_RS03165	rod shape-determining protein
LAC1533_RS07485	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	GSS_RS10465	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Lacidipiscis_RS03170	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
LAC1533_RS07490	membrane protein	GSS_RS10470	membrane protein	Lacidipiscis_RS03175	membrane protein
LAC1533_RS07500	F0F1 ATP synthase subunit epsilon	GSS_RS10475	F0F1 ATP synthase subunit epsilon	Lacidipiscis_RS06965	F0F1 ATP synthase subunit epsilon
LAC1533_RS07505	F0F1 ATP synthase subunit beta	GSS_RS10480	F0F1 ATP synthase subunit beta	Lacidipiscis_RS06960	F0F1 ATP synthase subunit beta
LAC1533_RS07510	F0F1 ATP synthase subunit gamma	GSS_RS10485	F0F1 ATP synthase subunit gamma	Lacidipiscis_RS06955	F0F1 ATP synthase subunit gamma
LAC1533_RS07515	F0F1 ATP synthase subunit alpha	GSS_RS10490	F0F1 ATP synthase subunit alpha	Lacidipiscis_RS06950	F0F1 ATP synthase subunit alpha
LAC1533_RS07520	F0F1 ATP synthase subunit delta	GSS_RS10500	F0F1 ATP synthase subunit delta	Lacidipiscis_RS06945	F0F1 ATP synthase subunit delta
LAC1533_RS07525	ATP synthase F0 subunit B	GSS_RS10505	ATP synthase F0 subunit B	Lacidipiscis_RS06940	ATP synthase F0 subunit B
LAC1533_RS07530	F0F1 ATP synthase subunit C	GSS_RS10510	F0F1 ATP synthase subunit C	Lacidipiscis_RS06935	F0F1 ATP synthase subunit C
LAC1533_RS07535	F0F1 ATP synthase subunit A	GSS_RS10515	F0F1 ATP synthase subunit A	Lacidipiscis_RS06930	F0F1 ATP synthase subunit A
LAC1533_RS07540	uracil phosphoribosyltransferase	GSS_RS10520	uracil phosphoribosyltransferase	Lacidipiscis_RS06925	uracil phosphoribosyltransferase
LAC1533_RS07545	threonylcarbamoyl-AMP synthase	GSS_RS10525	threonylcarbamoyl-AMP synthase	Lacidipiscis_RS06920	threonylcarbamoyl-AMP synthase
LAC1533_RS07550	peptide chain release factor N(5)-glutamine methyltransferase	GSS_RS10530	peptide chain release factor N(5)-glutamine methyltransferase	Lacidipiscis_RS06915	peptide chain release factor N(5)-glutamine methyltransferase
LAC1533_RS07555	peptide chain release factor 1			Lacidipiscis_RS06910	peptide chain release factor 1
LAC1533_RS07560	thymidine kinase	GSS_RS10540	thymidine kinase	Lacidipiscis_RS06905	thymidine kinase
LAC1533_RS07565	DUF1727 domain-containing protein	GSS_RS10545	DUF1727 domain-containing protein	Lacidipiscis_RS06895	DUF1727 domain-containing protein
LAC1533_RS07570	glutamine amidotransferase	GSS_RS10550	cobyric acid synthase	Lacidipiscis_RS06890	glutamine amidotransferase
LAC1533_RS07585	mannose-6-phosphate isomerase, class I	GSS_RS10555	mannose-6-phosphate isomerase, class I	Lacidipiscis_RS06885	mannose-6-phosphate isomerase, class I
LAC1533_RS07590	transposase				
LAC1533_RS07595	hypothetical protein	GSS_RS10565	hypothetical protein	Lacidipiscis_RS06880	hypothetical protein
LAC1533_RS07600	histidine phosphatase family protein	GSS_RS10570	histidine phosphatase family protein	Lacidipiscis_RS06875	histidine phosphatase family protein
LAC1533_RS07605	hypothetical protein	GSS_RS10575	hypothetical protein	Lacidipiscis_RS06870	hypothetical protein
LAC1533_RS07610	amino acid ABC transporter ATP-binding protein	GSS_RS10580	amino acid ABC transporter ATP-binding protein		
LAC1533_RS07635	group II intron reverse transcriptase/maturase				
LAC1533_RS07660	hypothetical protein	GSS_RS11245	hypothetical protein	Lacidipiscis_RS06685	hypothetical protein
LAC1533_RS07670	XTP/dITP diphosphatase	GSS_RS11255	XTP/dITP diphosphatase	Lacidipiscis_RS06675	XTP/dITP diphosphatase
LAC1533_RS07675	DUF2507 domain-containing protein	GSS_RS11260	DUF2507 domain-containing protein	Lacidipiscis_RS06670	DUF2507 domain-containing protein
LAC1533_RS07695	endonuclease MutS2	GSS_RS09760	endonuclease MutS2	Lacidipiscis_RS06665	endonuclease MutS2
LAC1533_RS07700	CvpA family protein	GSS_RS09755	CvpA family protein	Lacidipiscis_RS06660	CvpA family protein
LAC1533_RS07705	cell division protein ZapA	GSS_RS09750	cell division protein ZapA	Lacidipiscis_RS06655	cell division protein ZapA
LAC1533_RS07710	DUF1292 domain-containing protein	GSS_RS09745	DUF1292 domain-containing protein	Lacidipiscis_RS06225	DUF1292 domain-containing protein
LAC1533_RS07715	Holliday junction resolvase RuvX	GSS_RS09740	Holliday junction resolvase RuvX	Lacidipiscis_RS06230	Holliday junction resolvase RuvX
LAC1533_RS07720	IreB family regulatory phosphoprotein	GSS_RS09735	IreB family regulatory phosphoprotein	Lacidipiscis_RS06235	IreB family regulatory phosphoprotein
LAC1533_RS07725	alanine--tRNA ligase	GSS_RS09725	alanine--tRNA ligase	Lacidipiscis_RS06240	alanine--tRNA ligase
LAC1533_RS07730	ATP-dependent helicase	GSS_RS09720	ATP-dependent helicase	Lacidipiscis_RS06245	ATP-dependent helicase
LAC1533_RS07735	bifunctional oligoribonuclease/PAP phosphatase NrnA	GSS_RS09715	bifunctional oligoribonuclease/PAP phosphatase NrnA	Lacidipiscis_RS06250	bifunctional oligoribonuclease/PAP phosphatase NrnA
LAC1533_RS07740	DNA polymerase IV	GSS_RS09710	DNA polymerase IV	Lacidipiscis_RS13155	DNA polymerase IV
LAC1533_RS07745	glucose-6-phosphate dehydrogenase			Lacidipiscis_RS13150	glucose-6-phosphate dehydrogenase
LAC1533_RS07750	enoyl-[acyl-carrier-protein] reductase FabI	GSS_RS09690	enoyl-[acyl-carrier-protein] reductase FabI	Lacidipiscis_RS13145	enoyl-[acyl-carrier-protein] reductase FabI
LAC1533_RS07755	acetyl-CoA carboxylase carboxyl transferase subunit alpha	GSS_RS09685	acetyl-CoA carboxylase carboxyl transferase subunit alpha	Lacidipiscis_RS13140	acetyl-CoA carboxylase carboxyl transferase subunit alpha
LAC1533_RS07760	acetyl-CoA carboxylase carboxyltransferase subunit beta	GSS_RS09680	acetyl-CoA carboxylase carboxyltransferase subunit beta	Lacidipiscis_RS13135	acetyl-CoA carboxylase carboxyltransferase subunit beta
LAC1533_RS07765	acetyl-CoA carboxylase biotin carboxylase subunit	GSS_RS09675	acetyl-CoA carboxylase biotin carboxylase subunit	Lacidipiscis_RS13130	acetyl-CoA carboxylase biotin carboxylase subunit

LAC1533_RS07770	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	GSS_RS09670	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	Lacidipiscis_RS13125	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
LAC1533_RS07775	acetyl-CoA carboxylase biotin carboxyl carrier protein	GSS_RS09665	acetyl-CoA carboxylase biotin carboxyl carrier protein	Lacidipiscis_RS13120	acetyl-CoA carboxylase biotin carboxyl carrier protein
LAC1533_RS07780	beta-ketoacyl-[acyl-carrier-protein] synthase II	GSS_RS09660	beta-ketoacyl-[acyl-carrier-protein] synthase II	Lacidipiscis_RS13115	beta-ketoacyl-[acyl-carrier-protein] synthase II
LAC1533_RS07785	hypothetical protein			Lacidipiscis_RS13110	hypothetical protein
LAC1533_RS07790	3-oxoacyl-[acyl-carrier-protein] reductase	GSS_RS09655	3-oxoacyl-[acyl-carrier-protein] reductase	Lacidipiscis_RS13105	3-oxoacyl-[acyl-carrier-protein] reductase
LAC1533_RS07795	ACP S-malonyltransferase	GSS_RS09650	ACP S-malonyltransferase	Lacidipiscis_RS13100	ACP S-malonyltransferase
LAC1533_RS07800	acyl carrier protein	GSS_RS09645	acyl carrier protein	Lacidipiscis_RS13095	acyl carrier protein
LAC1533_RS07805	ketoacyl-ACP synthase III	GSS_RS09640	ketoacyl-ACP synthase III	Lacidipiscis_RS13090	ketoacyl-ACP synthase III
LAC1533_RS07810	MarR family transcriptional regulator	GSS_RS09635	MarR family transcriptional regulator	Lacidipiscis_RS13085	MarR family transcriptional regulator
LAC1533_RS07815	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	GSS_RS09630	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	Lacidipiscis_RS13080	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
LAC1533_RS07820	thiol peroxidase	GSS_RS09625	thiol peroxidase	Lacidipiscis_RS13075	thiol peroxidase
LAC1533_RS07825	preprotein translocase subunit YajC	GSS_RS09620	preprotein translocase subunit YajC	Lacidipiscis_RS07910	preprotein translocase subunit YajC
LAC1533_RS07830	tRNA guanosine(34) transglycosylase Tgt	GSS_RS09615	tRNA guanosine(34) transglycosylase Tgt	Lacidipiscis_RS07905	tRNA guanosine(34) transglycosylase Tgt
LAC1533_RS07835	hypothetical protein				
LAC1533_RS07840	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	GSS_RS09605	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	Lacidipiscis_RS07900	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA
LAC1533_RS07845	Holliday junction branch migration DNA helicase RuvB	GSS_RS09600	Holliday junction branch migration DNA helicase RuvB	Lacidipiscis_RS07895	Holliday junction branch migration DNA helicase RuvB
LAC1533_RS07850	Holliday junction branch migration protein RuvA	GSS_RS09595	Holliday junction branch migration protein RuvA	Lacidipiscis_RS07890	Holliday junction branch migration protein RuvA
LAC1533_RS07855	DNA mismatch repair endonuclease MutL	GSS_RS09590	DNA mismatch repair endonuclease MutL	Lacidipiscis_RS07885	DNA mismatch repair endonuclease MutL
LAC1533_RS07860	DNA mismatch repair protein MutS	GSS_RS09585	DNA mismatch repair protein MutS	Lacidipiscis_RS07880	DNA mismatch repair protein MutS
LAC1533_RS07865	TIGR00282 family metallophosphoesterase			Lacidipiscis_RS07875	TIGR00282 family metallophosphoesterase
LAC1533_RS07870	ribonuclease Y	GSS_RS09575	ribonuclease Y	Lacidipiscis_RS07870	ribonuclease Y
LAC1533_RS07875	recombinase RecA	GSS_RS09570	recombinase RecA	Lacidipiscis_RS07865	recombinase RecA
LAC1533_RS07880	competence/damage-inducible protein A	GSS_RS09565	competence/damage-inducible protein A	Lacidipiscis_RS07860	competence/damage-inducible protein A
LAC1533_RS07885	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	GSS_RS09555	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Lacidipiscis_RS01515	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
LAC1533_RS07890	DUF4115 domain-containing protein	GSS_RS13160	DUF4115 domain-containing protein	Lacidipiscis_RS01520	DUF4115 domain-containing protein
LAC1533_RS07895	KR domain-containing protein	GSS_RS09545	KR domain-containing protein	Lacidipiscis_RS01525	KR domain-containing protein
LAC1533_RS07900	insulinase family protein			Lacidipiscis_RS01530	insulinase family protein
LAC1533_RS07905	insulinase family protein	GSS_RS09535	insulinase family protein	Lacidipiscis_RS01535	insulinase family protein
LAC1533_RS07910	DNA translocase FtsK	GSS_RS09530	DNA translocase FtsK	Lacidipiscis_RS01540	DNA translocase FtsK
LAC1533_RS07915	tRNA (cytidine(34)-2-O)-methyltransferase	GSS_RS09525	tRNA (cytidine(34)-2-O)-methyltransferase	Lacidipiscis_RS01545	tRNA (cytidine(34)-2-O)-methyltransferase
LAC1533_RS07920	methyltransferase domain-containing protein	GSS_RS09520	methyltransferase domain-containing protein	Lacidipiscis_RS01550	methyltransferase domain-containing protein
LAC1533_RS07925	aminoacyl-tRNA deacylase	GSS_RS09515	transcriptional regulator	Lacidipiscis_RS01555	aminoacyl-tRNA deacylase
LAC1533_RS07935	GMP reductase	GSS_RS09510	GMP reductase	Lacidipiscis_RS10030	GMP reductase
LAC1533_RS07940	PTS glucose transporter subunit IIA	GSS_RS09505	PTS glucose transporter subunit IIA	Lacidipiscis_RS10025	PTS glucose transporter subunit IIA
LAC1533_RS07945	lactonase family protein	GSS_RS09500	lactonase family protein	Lacidipiscis_RS10020	lactonase family protein
LAC1533_RS07950	copper homeostasis protein CutC	GSS_RS09495	copper homeostasis protein CutC	Lacidipiscis_RS10015	copper homeostasis protein CutC
LAC1533_RS07965	group II intron reverse transcriptase/maturase				
LAC1533_RS07970	UDP-glucose--hexose-1-phosphate uridylyltransferase	GSS_RS09485	galactose-1-phosphate uridylyltransferase	Lacidipiscis_RS10010	UDP-glucose--hexose-1-phosphate uridylyltransferase
LAC1533_RS07975	galactokinase	GSS_RS09480	galactokinase	Lacidipiscis_RS10005	galactokinase
LAC1533_RS07980	LacI family DNA-binding transcriptional regulator	GSS_RS09475	LacI family DNA-binding transcriptional regulator	Lacidipiscis_RS10000	LacI family DNA-binding transcriptional regulator
LAC1533_RS07985	magnesium transporter	GSS_RS09470	magnesium transporter	Lacidipiscis_RS09995	magnesium transporter
LAC1533_RS07990	RluA family pseudouridine synthase	GSS_RS09465	RluA family pseudouridine synthase	Lacidipiscis_RS09990	RluA family pseudouridine synthase
LAC1533_RS07995	NAD kinase	GSS_RS09460	NAD kinase	Lacidipiscis_RS09985	NAD kinase
LAC1533_RS08005	oligoendopeptidase F	GSS_RS09450	oligoendopeptidase F		
LAC1533_RS08010	hypothetical protein	GSS_RS13150	putative competence protein/transcription factor	Lacidipiscis_RS04970	hypothetical protein
LAC1533_RS08015	adapter protein MecA	GSS_RS09440	adapter protein MecA	Lacidipiscis_RS04975	adaptor protein MecA
LAC1533_RS08025	transcriptional regulator Spx	GSS_RS09435	transcriptional regulator Spx	Lacidipiscis_RS04980	transcriptional regulator Spx
LAC1533_RS08030	anaerobic ribonucleoside-triphosphate reductase activating protein	GSS_RS13145	anaerobic ribonucleoside-triphosphate reductase activating protein	Lacidipiscis_RS04985	anaerobic ribonucleoside-triphosphate reductase activating protein
LAC1533_RS08035	anaerobic ribonucleoside-triphosphate reductase	GSS_RS09415	anaerobic ribonucleoside-triphosphate reductase	Lacidipiscis_RS04990	anaerobic ribonucleoside-triphosphate reductase
LAC1533_RS08040	XRE family transcriptional regulator	GSS_RS00890	XRE family transcriptional regulator	Lacidipiscis_RS04995	XRE family transcriptional regulator
LAC1533_RS08045	ImmA/IrrE family metallo-endopeptidase	GSS_RS12095	ImmA/IrrE family metallo-endopeptidase	Lacidipiscis_RS07680	ImmA/IrrE family metallo-endopeptidase
LAC1533_RS08050	hypothetical protein			Lacidipiscis_RS07685	hypothetical protein
LAC1533_RS08140	hypothetical protein	GSS_RS05665	hypothetical protein	Lacidipiscis_RS10925	hypothetical protein
LAC1533_RS08145	LTA synthase family protein	GSS_RS05660	LTA synthase family protein	Lacidipiscis_RS10920	LTA synthase family protein
LAC1533_RS08150	DUF1797 domain-containing protein	GSS_RS05655	DUF1797 domain-containing protein	Lacidipiscis_RS10915	DUF1797 domain-containing protein
LAC1533_RS08155	TIGR00374 family protein	GSS_RS05650	UPF0104 family protein	Lacidipiscis_RS03690	TIGR00374 family protein
LAC1533_RS08160	glycosyl transferase	GSS_RS05645	glycosyl transferase	Lacidipiscis_RS03695	glycosyl transferase
LAC1533_RS08165	glycosyltransferase family 4 protein	GSS_RS05640	glycosyltransferase family 4 protein	Lacidipiscis_RS03700	glycosyltransferase family 4 protein
LAC1533_RS08170	phosphoenolpyruvate--protein phosphotransferase	GSS_RS05635	phosphoenolpyruvate--protein phosphotransferase	Lacidipiscis_RS03705	phosphoenolpyruvate--protein phosphotransferase
LAC1533_RS08175	phosphocarrier protein HPr	GSS_RS05630	phosphocarrier protein HPr	Lacidipiscis_RS03710	phosphocarrier protein HPr
LAC1533_RS08180	hypothetical protein	GSS_RS05625	hypothetical protein	Lacidipiscis_RS03850	hypothetical protein
LAC1533_RS08185	ATP-dependent Clp protease ATP-binding subunit	GSS_RS05620	ATP-dependent Clp protease ATP-binding subunit	Lacidipiscis_RS03855	ATP-dependent Clp protease ATP-binding subunit

LAC1533_RS08190	DUF1827 domain-containing protein	GSS_RS05615	DUF1827 domain-containing protein	Lacidipiscis_RS02505	DUF1827 domain-containing protein
LAC1533_RS08195	hypothetical protein	GSS_RS05610	hypothetical protein	Lacidipiscis_RS02510	hypothetical protein
LAC1533_RS08200	peptide chain release factor 3	GSS_RS05605	peptide chain release factor 3	Lacidipiscis_RS02515	peptide chain release factor 3
LAC1533_RS08205	HlyC/CorC family transporter	GSS_RS05600	HlyC/CorC family transporter	Lacidipiscis_RS02520	HlyC/CorC family transporter
LAC1533_RS08210	LysM peptidoglycan-binding domain-containing protein	GSS_RS05595	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS02525	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS08215	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	GSS_RS05590	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	Lacidipiscis_RS02530	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
LAC1533_RS08220	DUF402 domain-containing protein	GSS_RS05585	DUF402 domain-containing protein	Lacidipiscis_RS02535	DUF402 domain-containing protein
LAC1533_RS08225	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	GSS_RS05580	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	Lacidipiscis_RS02540	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
LAC1533_RS08230	recombination regulator RecX	GSS_RS05575	recombination regulator RecX	Lacidipiscis_RS02545	recombination regulator RecX
LAC1533_RS08235	YihY/virulence factor BrkB family protein	GSS_RS05570	YihY/virulence factor BrkB family protein	Lacidipiscis_RS02550	YihY/virulence factor BrkB family protein
LAC1533_RS08240	LysM peptidoglycan-binding domain-containing protein	GSS_RS05565	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS02555	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS08245	UTP--glucose-1-phosphate uridylyltransferase	GSS_RS05560	UTP--glucose-1-phosphate uridylyltransferase	Lacidipiscis_RS02565	UTP--glucose-1-phosphate uridylyltransferase
LAC1533_RS08250	type I methionyl aminopeptidase	GSS_RS05555	type I methionyl aminopeptidase	Lacidipiscis_RS02570	type I methionyl aminopeptidase
LAC1533_RS08255	flavodoxin	GSS_RS05550	flavodoxin	Lacidipiscis_RS02575	flavodoxin
LAC1533_RS08260	GtrA family protein	GSS_RS05545	GtrA family protein	Lacidipiscis_RS02580	GtrA family protein
LAC1533_RS08265	hypothetical protein	GSS_RS05535	membrane protein	Lacidipiscis_RS02585	hypothetical protein
LAC1533_RS08270	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	GSS_RS05530	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	Lacidipiscis_RS02590	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)
LAC1533_RS08280	DUF3284 domain-containing protein	GSS_RS05515	DUF3284 domain-containing protein	Lacidipiscis_RS02600	DUF3284 domain-containing protein
LAC1533_RS08285	ATP-dependent helicase	GSS_RS05510	ATP-dependent helicase	Lacidipiscis_RS02605	ATP-dependent helicase
LAC1533_RS08290	gfo/Idh/MocA family oxidoreductase	GSS_RS05505	gfo/Idh/MocA family oxidoreductase	Lacidipiscis_RS02610	gfo/Idh/MocA family oxidoreductase
LAC1533_RS08295	Zn-dependent protease	GSS_RS05500	Zn-dependent protease	Lacidipiscis_RS05815	Zn-dependent protease
LAC1533_RS08300	CvpA family protein	GSS_RS05495	CvpA family protein	Lacidipiscis_RS05810	CvpA family protein
LAC1533_RS08315	phosphate ABC transporter substrate-binding protein	GSS_RS05490	phosphate ABC transporter substrate-binding protein	Lacidipiscis_RS05805	phosphate ABC transporter substrate-binding protein
LAC1533_RS08330	group II intron reverse transcriptase/maturase				
LAC1533_RS08340 IDENTICAL PARALOGS LAC1533_RS09310	group II intron reverse transcriptase/maturase				
LAC1533_RS08350	DUF4828 domain-containing protein	GSS_RS05485	DUF4828 domain-containing protein	Lacidipiscis_RS05800	DUF4828 domain-containing protein
LAC1533_RS08355	transposase	GSS_RS11480	ISL3 family transposase		
LAC1533_RS08360	1,3-propanediol dehydrogenase	GSS_RS05480	1,3-propanediol dehydrogenase	Lacidipiscis_RS05850	1,3-propanediol dehydrogenase
LAC1533_RS08365	ECF transporter S component	GSS_RS05475	ECF transporter S component	Lacidipiscis_RS05845	ECF transporter S component
LAC1533_RS08370	hypothetical protein	GSS_RS05470	hypothetical protein		
LAC1533_RS08375	sugar aldolase				
LAC1533_RS08380	hypothetical protein				
LAC1533_RS08385	PTS galactitol transporter subunit IIC				
LAC1533_RS08390	PTS galactitol transporter subunit IIB				
LAC1533_RS08395	PTS galactitol transporter subunit IIA				
LAC1533_RS08400	DeoR/GlpR transcriptional regulator				
LAC1533_RS08430	hypothetical protein				
LAC1533_RS08435	hypothetical protein				
LAC1533_RS08440	hypothetical protein				
LAC1533_RS08445	ATP-dependent helicase				
LAC1533_RS08450	class I SAM-dependent DNA methyltransferase				
LAC1533_RS08455	XRE family transcriptional regulator				
LAC1533_RS08460	helicase				
LAC1533_RS08465	DUF1837 domain-containing protein				
LAC1533_RS08470	sigma-70 family RNA polymerase sigma factor				
LAC1533_RS08475	hypothetical protein				
LAC1533_RS08480	hypothetical protein				
LAC1533_RS08490	DUF2815 domain-containing protein				
LAC1533_RS08500	hypothetical protein				
LAC1533_RS08505	DNA primase				
LAC1533_RS08510	VRR-NUC domain-containing protein				
LAC1533_RS08520	restriction endonuclease				
LAC1533_RS08525	HNH endonuclease				
LAC1533_RS08530	terminase				
LAC1533_RS08535	hypothetical protein				
LAC1533_RS08540 IDENTICAL PARALOGS LAC1533_RS08545	DDE domain-containing protein	GSS_RS11345	DDE domain-containing protein		
LAC1533_RS08550	DUF5049 domain-containing protein				
LAC1533_RS08555	terminase large subunit				
LAC1533_RS08560	hypothetical protein				
LAC1533_RS08565	type II toxin-antitoxin system RelE/ParE family toxin				

LAC1533_RS08575	Clp protease ClpP				
LAC1533_RS08580	phage major capsid protein				
LAC1533_RS08585	phage gp6-like head-tail connector protein				
LAC1533_RS08590	head-tail adaptor protein				
LAC1533_RS08595	DNA primase				
LAC1533_RS08600	1,4-beta-N-acetylmuramidase				
LAC1533_RS08605	hypothetical protein				
LAC1533_RS08615	recombinase family protein				
LAC1533_RS08620	MFS transporter				
LAC1533_RS08625	hypothetical protein				
LAC1533_RS08630	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	GSS_RS05300	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	Lacidipiscis_RS08555	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
LAC1533_RS08635	diacylglycerol kinase	GSS_RS05295	diacylglycerol kinase	Lacidipiscis_RS08560	diacylglycerol kinase
LAC1533_RS08640	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	GSS_RS05290	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	Lacidipiscis_RS08565	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB
LAC1533_RS08645	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA	GSS_RS05285	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA	Lacidipiscis_RS08570	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA
LAC1533_RS08650	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC	GSS_RS05280	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC	Lacidipiscis_RS08575	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC
LAC1533_RS08655	CamS family sex pheromone protein	GSS_RS05275	CamS family sex pheromone protein	Lacidipiscis_RS08580	CamS family sex pheromone protein
LAC1533_RS08660	NAD-dependent DNA ligase LigA	GSS_RS05270	NAD-dependent DNA ligase LigA	Lacidipiscis_RS08585	NAD-dependent DNA ligase LigA
LAC1533_RS08665	DNA helicase PcrA	GSS_RS05265	DNA helicase PcrA	Lacidipiscis_RS08590	DNA helicase PcrA
LAC1533_RS08670	ATP-grasp domain-containing protein	GSS_RS05260	ATP-grasp domain-containing protein	Lacidipiscis_RS05600	ATP-grasp domain-containing protein
LAC1533_RS08675	xanthine phosphoribosyltransferase	GSS_RS05255	xanthine phosphoribosyltransferase	Lacidipiscis_RS05605	xanthine phosphoribosyltransferase
LAC1533_RS08680	lysozyme	GSS_RS05250	lysozyme	Lacidipiscis_RS05610	lysozyme
LAC1533_RS08685	ECF transporter S component	GSS_RS05245	ECF transporter S component	Lacidipiscis_RS05615	ECF transporter S component
LAC1533_RS08690	MarR family transcriptional regulator	GSS_RS05235	MarR family transcriptional regulator	Lacidipiscis_RS08030	MarR family transcriptional regulator
LAC1533_RS08695	DUF454 domain-containing protein	GSS_RS05230	DUF454 domain-containing protein	Lacidipiscis_RS08035	DUF454 domain-containing protein
LAC1533_RS08700	DNA topoisomerase III	GSS_RS05225	DNA topoisomerase III	Lacidipiscis_RS08040	DNA topoisomerase III
LAC1533_RS08705	50S ribosomal protein L7/L12	GSS_RS05220	50S ribosomal protein L7/L12	Lacidipiscis_RS08045	50S ribosomal protein L7/L12
LAC1533_RS08710	50S ribosomal protein L10	GSS_RS05215	50S ribosomal protein L10	Lacidipiscis_RS08050	50S ribosomal protein L10
LAC1533_RS08715	50S ribosomal protein L1	GSS_RS05210	50S ribosomal protein L1	Lacidipiscis_RS08055	50S ribosomal protein L1
LAC1533_RS08720	50S ribosomal protein L11	GSS_RS05205	50S ribosomal protein L11	Lacidipiscis_RS08060	50S ribosomal protein L11
LAC1533_RS08725	transcription termination/antitermination protein NusG	GSS_RS05200	transcription termination/antitermination protein NusG	Lacidipiscis_RS08065	transcription termination/antitermination protein NusG
LAC1533_RS08730	preprotein translocase subunit SecE	GSS_RS05195	preprotein translocase subunit SecE	Lacidipiscis_RS08070	preprotein translocase subunit SecE
LAC1533_RS08735	50S ribosomal protein L33	GSS_RS05190	50S ribosomal protein L33	Lacidipiscis_RS08075	50S ribosomal protein L33
LAC1533_RS08740	NYN domain-containing protein	GSS_RS05185	NYN domain-containing protein	Lacidipiscis_RS08080	NYN domain-containing protein
LAC1533_RS08745	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB	GSS_RS05180	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB	Lacidipiscis_RS08085	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB
LAC1533_RS08750	hypothetical protein	GSS_RS05175	hypothetical protein	Lacidipiscis_RS08090	hypothetical protein
LAC1533_RS08755	cysteine--tRNA ligase	GSS_RS05170	cysteine--tRNA ligase	Lacidipiscis_RS08095	cysteine--tRNA ligase
LAC1533_RS08760	glutamate--tRNA ligase	GSS_RS05165	glutamate--tRNA ligase	Lacidipiscis_RS08100	glutamate--tRNA ligase
LAC1533_RS08765	PIN/TRAM domain-containing protein	GSS_RS05160	PIN/TRAM domain-containing protein	Lacidipiscis_RS08105	PIN/TRAM domain-containing protein
LAC1533_RS08770	DNA repair protein RadA	GSS_RS05155	DNA repair protein RadA	Lacidipiscis_RS08110	DNA repair protein RadA
LAC1533_RS08775	dUTP diphosphatase	GSS_RS05150	dUTP diphosphatase	Lacidipiscis_RS08115	dUTP diphosphatase
LAC1533_RS08780	ribose-5-phosphate isomerase RpiA	GSS_RS05145	ribose-5-phosphate isomerase RpiA	Lacidipiscis_RS08120	ribose-5-phosphate isomerase RpiA
LAC1533_RS08785	aminopeptidase C	GSS_RS05140	aminopeptidase C	Lacidipiscis_RS08125	aminopeptidase
LAC1533_RS08790	phosphoglycerate mutase	GSS_RS05135	phosphoglycerate mutase	Lacidipiscis_RS08130	phosphoglycerate mutase
LAC1533_RS08795	hypothetical protein			Lacidipiscis_RS10130	hypothetical protein
LAC1533_RS08800	hypothetical protein				
LAC1533_RS08805	CHAP domain-containing protein	GSS_RS05120	CHAP domain-containing protein		
LAC1533_RS08810	malate transporter	GSS_RS05115	malate transporter	Lacidipiscis_RS10125	malate transporter
LAC1533_RS08815	LytR family transcriptional regulator	GSS_RS12625	LytR family transcriptional regulator	Lacidipiscis_RS10120	LytR family transcriptional regulator
LAC1533_RS08820	ketoacyl-ACP synthase III	GSS_RS05100	ketoacyl-ACP synthase III	Lacidipiscis_RS10115	ketoacyl-ACP synthase III
LAC1533_RS08830	SprT family protein	GSS_RS05090	SprT family protein	Lacidipiscis_RS10105	SprT family protein
LAC1533_RS08835	DNA helicase RecQ	GSS_RS05085	DNA helicase RecQ	Lacidipiscis_RS10100	DNA helicase RecQ
LAC1533_RS08840	hypothetical protein	GSS_RS05080	hypothetical protein		
LAC1533_RS08845	ammonia-dependent NAD(+) synthetase	GSS_RS05075	ammonia-dependent NAD(+) synthetase	Lacidipiscis_RS10090	ammonia-dependent NAD(+) synthetase
LAC1533_RS08850	glycosyltransferase	GSS_RS05070	glycosyltransferase	Lacidipiscis_RS10085	glycosyltransferase
LAC1533_RS08860	30S ribosomal protein S9	GSS_RS05065	30S ribosomal protein S9	Lacidipiscis_RS05925	30S ribosomal protein S9
LAC1533_RS08865	50S ribosomal protein L13	GSS_RS05060	50S ribosomal protein L13	Lacidipiscis_RS05930	50S ribosomal protein L13
LAC1533_RS08870	tRNA pseudouridine(38-40) synthase TruA	GSS_RS05055	tRNA pseudouridine(38-40) synthase TruA	Lacidipiscis_RS05935	tRNA pseudouridine(38-40) synthase TruA
LAC1533_RS08875	energy-coupling factor transporter transmembrane protein EcfT	GSS_RS05050	energy-coupling factor transporter transmembrane protein EcfT	Lacidipiscis_RS05940	energy-coupling factor transporter transmembrane protein EcfT
LAC1533_RS08880	energy-coupling factor ABC transporter ATP-binding protein	GSS_RS05045	energy-coupling factor transporter ATPase	Lacidipiscis_RS05945	energy-coupling factor ABC transporter ATP-binding protein
LAC1533_RS08885	energy-coupling factor ABC transporter ATP-binding protein	GSS_RS05040	energy-coupling factor ABC transporter ATP-binding protein	Lacidipiscis_RS05950	energy-coupling factor ABC transporter ATP-binding protein

LAC1533_RS08890	50S ribosomal protein L17	GSS_RS05035	50S ribosomal protein L17	Lacidipiscis_RS05955	50S ribosomal protein L17
LAC1533_RS08895	DNA-directed RNA polymerase subunit alpha	GSS_RS05030	DNA-directed RNA polymerase subunit alpha	Lacidipiscis_RS05960	DNA-directed RNA polymerase subunit alpha
LAC1533_RS08900	30S ribosomal protein S11	GSS_RS05025	30S ribosomal protein S11	Lacidipiscis_RS05965	30S ribosomal protein S11
LAC1533_RS08905	30S ribosomal protein S13	GSS_RS05020	30S ribosomal protein S13	Lacidipiscis_RS05970	30S ribosomal protein S13
LAC1533_RS08910	50S ribosomal protein L36	GSS_RS05015	50S ribosomal protein L36	Lacidipiscis_RS05975	50S ribosomal protein L36
LAC1533_RS08915	translation initiation factor IF-1	GSS_RS05010	translation initiation factor IF-1	Lacidipiscis_RS05980	translation initiation factor IF-1
LAC1533_RS08920	adenylate kinase	GSS_RS05005	adenylate kinase	Lacidipiscis_RS05985	adenylate kinase
LAC1533_RS08925	preprotein translocase subunit SecY	GSS_RS05000	preprotein translocase subunit SecY	Lacidipiscis_RS05990	preprotein translocase subunit SecY
LAC1533_RS08930	50S ribosomal protein L15	GSS_RS04995	50S ribosomal protein L15	Lacidipiscis_RS05995	50S ribosomal protein L15
LAC1533_RS08935	50S ribosomal protein L30	GSS_RS04990	50S ribosomal protein L30	Lacidipiscis_RS06000	50S ribosomal protein L30
LAC1533_RS08940	30S ribosomal protein S5	GSS_RS04985	30S ribosomal protein S5	Lacidipiscis_RS06005	30S ribosomal protein S5
LAC1533_RS08945	50S ribosomal protein L18	GSS_RS04980	50S ribosomal protein L18	Lacidipiscis_RS06010	50S ribosomal protein L18
LAC1533_RS08950	50S ribosomal protein L6	GSS_RS04975	50S ribosomal protein L6	Lacidipiscis_RS06015	50S ribosomal protein L6
LAC1533_RS08955	30S ribosomal protein S8	GSS_RS04970	30S ribosomal protein S8	Lacidipiscis_RS06020	30S ribosomal protein S8
LAC1533_RS08960	type Z 30S ribosomal protein S14	GSS_RS04965	type Z 30S ribosomal protein S14	Lacidipiscis_RS06025	type Z 30S ribosomal protein S14
LAC1533_RS08965	50S ribosomal protein L5	GSS_RS04960	50S ribosomal protein L5	Lacidipiscis_RS06030	50S ribosomal protein L5
LAC1533_RS08970	50S ribosomal protein L24	GSS_RS04955	50S ribosomal protein L24	Lacidipiscis_RS06035	50S ribosomal protein L24
LAC1533_RS08975	50S ribosomal protein L14	GSS_RS04950	50S ribosomal protein L14	Lacidipiscis_RS06040	50S ribosomal protein L14
LAC1533_RS08980	30S ribosomal protein S17	GSS_RS04945	30S ribosomal protein S17	Lacidipiscis_RS06045	30S ribosomal protein S17
LAC1533_RS08985	50S ribosomal protein L29	GSS_RS04940	50S ribosomal protein L29	Lacidipiscis_RS06050	50S ribosomal protein L29
LAC1533_RS08990	50S ribosomal protein L16	GSS_RS04935	50S ribosomal protein L16	Lacidipiscis_RS06055	50S ribosomal protein L16
LAC1533_RS08995	30S ribosomal protein S3	GSS_RS04930	30S ribosomal protein S3	Lacidipiscis_RS06060	30S ribosomal protein S3
LAC1533_RS09000	50S ribosomal protein L22	GSS_RS04925	50S ribosomal protein L22	Lacidipiscis_RS06065	50S ribosomal protein L22
LAC1533_RS09005	30S ribosomal protein S19	GSS_RS04920	30S ribosomal protein S19	Lacidipiscis_RS06070	30S ribosomal protein S19
LAC1533_RS09010	50S ribosomal protein L2	GSS_RS04915	50S ribosomal protein L2	Lacidipiscis_RS06075	50S ribosomal protein L2
LAC1533_RS09015	50S ribosomal protein L23	GSS_RS04910	50S ribosomal protein L23	Lacidipiscis_RS06080	50S ribosomal protein L23
LAC1533_RS09020	50S ribosomal protein L4	GSS_RS04905	50S ribosomal protein L4	Lacidipiscis_RS06085	50S ribosomal protein L4
LAC1533_RS09025	50S ribosomal protein L3	GSS_RS04900	50S ribosomal protein L3	Lacidipiscis_RS06090	50S ribosomal protein L3
LAC1533_RS09030	30S ribosomal protein S10	GSS_RS04895	30S ribosomal protein S10	Lacidipiscis_RS06095	30S ribosomal protein S10
LAC1533_RS09035	IS1380 family transposase				
LAC1533_RS09040	cysteine hydrolase	GSS_RS04890	cysteine hydrolase	Lacidipiscis_RS06100	cysteine hydrolase
LAC1533_RS09045	elongation factor G	GSS_RS04885	elongation factor G	Lacidipiscis_RS06105	elongation factor G
LAC1533_RS09050	30S ribosomal protein S7	GSS_RS04880	30S ribosomal protein S7	Lacidipiscis_RS06110	30S ribosomal protein S7
LAC1533_RS09055	30S ribosomal protein S12	GSS_RS04875	30S ribosomal protein S12	Lacidipiscis_RS06115	30S ribosomal protein S12
LAC1533_RS09060	prepilin peptidase	GSS_RS14050	prepilin peptidase	Lacidipiscis_RS06120	prepilin peptidase
LAC1533_RS09065	group II intron reverse transcriptase/maturase				
LAC1533_RS09075	DNA-directed RNA polymerase subunit beta	GSS_RS10275	DNA-directed RNA polymerase subunit beta	Lacidipiscis_RS09300	DNA-directed RNA polymerase subunit beta
LAC1533_RS09080	DNA-directed RNA polymerase subunit beta	GSS_RS10270	DNA-directed RNA polymerase subunit beta	Lacidipiscis_RS09305	DNA-directed RNA polymerase subunit beta
LAC1533_RS09085	ATP-dependent Clp protease ATP-binding subunit	GSS_RS10265	ATP-dependent Clp protease ATP-binding subunit	Lacidipiscis_RS09310	ATP-dependent Clp protease ATP-binding subunit
LAC1533_RS09090	CtsR family transcriptional regulator	GSS_RS10260	CtsR family transcriptional regulator	Lacidipiscis_RS09315	CtsR family transcriptional regulator
LAC1533_RS09095	transposase				
LAC1533_RS09165	tyrosine--tRNA ligase	GSS_RS08515	tyrosine--tRNA ligase	Lacidipiscis_RS07965	tyrosine--tRNA ligase
LAC1533_RS09170	transcriptional repressor	GSS_RS08510	transcriptional repressor	Lacidipiscis_RS07970	transcriptional repressor
LAC1533_RS09175	metal-dependent hydrolase	GSS_RS08505	metal-dependent hydrolase	Lacidipiscis_RS07975	metal-dependent hydrolase
LAC1533_RS09180	SMC family ATPase	GSS_RS08500	SMC family ATPase	Lacidipiscis_RS07980	SMC family ATPase
LAC1533_RS09185	exonuclease SbcCD subunit D	GSS_RS08495	exonuclease SbcCD subunit D	Lacidipiscis_RS07985	exonuclease SbcCD subunit D
LAC1533_RS09190	hypothetical protein	GSS_RS08490	hypothetical protein	Lacidipiscis_RS07990	hypothetical protein
LAC1533_RS09195	hypothetical protein	GSS_RS14125	hypothetical protein	Lacidipiscis_RS04685	hypothetical protein
LAC1533_RS09200	GntR family transcriptional regulator	GSS_RS08485	GntR family transcriptional regulator	Lacidipiscis_RS04690	GntR family transcriptional regulator
LAC1533_RS09205	transposase				
LAC1533_RS09210	class I SAM-dependent methyltransferase	GSS_RS08480	class I SAM-dependent methyltransferase	Lacidipiscis_RS04695	class I SAM-dependent methyltransferase
LAC1533_RS09215	MgtC/SapB family protein	GSS_RS08475	MgtC/SapB family protein	Lacidipiscis_RS04700	MgtC/SapB family protein
LAC1533_RS09220	glycosyltransferase family 4 protein	GSS_RS08470	glycosyltransferase family 4 protein	Lacidipiscis_RS04705	glycosyltransferase family 4 protein
LAC1533_RS09225	protein-tyrosine-phosphatase	GSS_RS08465	protein-tyrosine-phosphatase	Lacidipiscis_RS04710	protein-tyrosine-phosphatase
LAC1533_RS09230	histidine phosphatase family protein	GSS_RS08460	histidine phosphatase family protein	Lacidipiscis_RS04715	histidine phosphatase family protein
LAC1533_RS09235	D-alanine--D-alanine ligase	GSS_RS08455	D-alanine--D-alanine ligase	Lacidipiscis_RS04720	D-alanine--D-alanine ligase
LAC1533_RS09240	hypothetical protein	GSS_RS08450	hypothetical protein	Lacidipiscis_RS04725	hypothetical protein
LAC1533_RS09245	alpha/beta hydrolase	GSS_RS08445	alpha/beta hydrolase	Lacidipiscis_RS04730	alpha/beta hydrolase
LAC1533_RS09255	ASCH domain-containing protein	GSS_RS08440	ASCH domain-containing protein	Lacidipiscis_RS04735	ASCH domain-containing protein
LAC1533_RS09260	peptidase T	GSS_RS08435	peptidase T	Lacidipiscis_RS04740	peptidase T
LAC1533_RS09270	putative N-acetylmannosamine-6-phosphate 2-epimerase	GSS_RS08425	putative N-acetylmannosamine-6-phosphate 2-epimerase	Lacidipiscis_RS04750	putative N-acetylmannosamine-6-phosphate 2-epimerase

LAC1533_RS09275	hypothetical protein	GSS_RS08420	hypothetical protein	Lacidipiscis_RS04755	hypothetical protein
LAC1533_RS09280	hypothetical protein	GSS_RS08415	hypothetical protein	Lacidipiscis_RS04760	hypothetical protein
LAC1533_RS09285	hypothetical protein	GSS_RS08410	hypothetical protein	Lacidipiscis_RS04765	hypothetical protein
LAC1533_RS09290	arginase	GSS_RS08405	arginase	Lacidipiscis_RS04770	arginase
LAC1533_RS09295	OsmC family peroxiredoxin	GSS_RS08400	OsmC family peroxiredoxin	Lacidipiscis_RS04775	OsmC family peroxiredoxin
LAC1533_RS09300	hypothetical protein	GSS_RS08395	hypothetical protein	Lacidipiscis_RS04780	hypothetical protein
LAC1533_RS09305	exodeoxyribonuclease III	GSS_RS08390	exodeoxyribonuclease III	Lacidipiscis_RS04785	exodeoxyribonuclease III
LAC1533_RS09320	IS66 family transposase	GSS_RS08385	IS66 family transposase		
LAC1533_RS09335	sigma-70 family RNA polymerase sigma factor	GSS_RS08370	hypothetical protein		
LAC1533_RS09345	DUF3173 domain-containing protein	GSS_RS08355	DUF3173 domain-containing protein		
LAC1533_RS09350	site-specific integrase	GSS_RS08350	site-specific integrase		
LAC1533_RS09355	glutamine-hydrolyzing GMP synthase	GSS_RS08345	glutamine-hydrolyzing GMP synthase	Lacidipiscis_RS09005	glutamine-hydrolyzing GMP synthase
LAC1533_RS09360	type I pantothenate kinase			Lacidipiscis_RS09010	type I pantothenate kinase
LAC1533_RS09365	lipase	GSS_RS08335	lipase	Lacidipiscis_RS09015	acylhydrolase
LAC1533_RS09370	ATP-dependent DNA helicase	GSS_RS08330	ATP-dependent DNA helicase	Lacidipiscis_RS09020	ATP-dependent DNA helicase
LAC1533_RS09375	potassium transporter	GSS_RS08325	potassium transporter	Lacidipiscis_RS09025	potassium transporter
LAC1533_RS09380	histidine phosphatase family protein	GSS_RS08320	histidine phosphatase family protein	Lacidipiscis_RS09030	histidine phosphatase family protein
LAC1533_RS09385	histidine phosphatase family protein	GSS_RS08315	histidine phosphatase family protein	Lacidipiscis_RS09035	histidine phosphatase family protein
LAC1533_RS09390	hypothetical protein				
LAC1533_RS09395	IS66 family insertion sequence hypothetical protein	GSS_RS11630	IS66 family insertion sequence hypothetical protein		
LAC1533_RS09400	hypothetical protein				
LAC1533_RS09405	NERD domain-containing protein	GSS_RS08300	NERD domain-containing protein	Lacidipiscis_RS09040	NERD domain-containing protein
LAC1533_RS09410	transposase				
LAC1533_RS09415	ABC transporter ATP-binding protein	GSS_RS08295	ABC transporter ATP-binding protein	Lacidipiscis_RS09045	ABC transporter ATP-binding protein
LAC1533_RS09420	ABC transporter ATP-binding protein			Lacidipiscis_RS09050	ABC transporter ATP-binding protein
LAC1533_RS09425	ABC transporter permease	GSS_RS08280	ABC transporter permease	Lacidipiscis_RS09055	ABC transporter permease
LAC1533_RS09430	ABC transporter permease	GSS_RS08275	ABC transporter permease	Lacidipiscis_RS09060	ABC transporter permease
LAC1533_RS09435	peptide ABC transporter substrate-binding protein	GSS_RS08270	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS09065	peptide ABC transporter substrate-binding protein
LAC1533_RS09440	GTPase HflX	GSS_RS08265	GTPase HflX	Lacidipiscis_RS09070	GTPase HflX
LAC1533_RS09445	N-acetyltransferase	GSS_RS08260	N-acetyltransferase	Lacidipiscis_RS09075	N-acetyltransferase
LAC1533_RS09455	amino acid ABC transporter permease	GSS_RS08255	amino acid ABC transporter permease	Lacidipiscis_RS09080	amino acid ABC transporter permease
LAC1533_RS09460	amino acid ABC transporter permease	GSS_RS08250	amino acid ABC transporter permease	Lacidipiscis_RS09085	amino acid ABC transporter permease
LAC1533_RS09465	glutamine ABC transporter substrate-binding protein	GSS_RS08245	glutamine ABC transporter substrate-binding protein	Lacidipiscis_RS09090	glutamine ABC transporter substrate-binding protein
LAC1533_RS09470	amino acid ABC transporter ATP-binding protein	GSS_RS08240	amino acid ABC transporter ATP-binding protein	Lacidipiscis_RS09095	amino acid ABC transporter ATP-binding protein
LAC1533_RS09475	hypothetical protein	GSS_RS08235	hypothetical protein		
LAC1533_RS09485	hypothetical protein	GSS_RS11705	hypothetical protein		
LAC1533_RS09490	transcriptional repressor	GSS_RS08230	transcriptional repressor	Lacidipiscis_RS07285	transcriptional repressor
LAC1533_RS09495	guanylate kinase	GSS_RS12940	guanylate kinase	Lacidipiscis_RS07290	guanylate kinase
LAC1533_RS09500	amino acid permease	GSS_RS08220	amino acid permease	Lacidipiscis_RS07295	amino acid permease
LAC1533_RS09505	hypothetical protein	GSS_RS08215	hypothetical protein	Lacidipiscis_RS07300	hypothetical protein
LAC1533_RS09510 IDENTICAL PARALOGS LAC1533_RS11215	transposase				
LAC1533_RS09515	ECF transporter S component	GSS_RS08210	ECF transporter S component	Lacidipiscis_RS07305	ECF transporter S component
LAC1533_RS09520	Xaa-Pro dipeptidyl-peptidase	GSS_RS08205	Xaa-Pro dipeptidyl-peptidase	Lacidipiscis_RS07310	Xaa-Pro dipeptidyl-peptidase
LAC1533_RS09525	metal ABC transporter substrate-binding protein	GSS_RS08200	metal ABC transporter substrate-binding protein	Lacidipiscis_RS07315	metal ABC transporter substrate-binding protein
LAC1533_RS09535	phosphate ABC transporter ATP-binding protein	GSS_RS08190	methionine ABC transporter ATP-binding protein	Lacidipiscis_RS07325	phosphate ABC transporter ATP-binding protein
LAC1533_RS09540	KR domain-containing protein	GSS_RS08185	KR domain-containing protein	Lacidipiscis_RS07330	KR domain-containing protein
LAC1533_RS09545	prolyl aminopeptidase	GSS_RS08175	prolyl aminopeptidase	Lacidipiscis_RS07335	prolyl aminopeptidase
LAC1533_RS09550	Cof-type HAD-IIB family hydrolase	GSS_RS08170	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS07340	Cof-type HAD-IIB family hydrolase
LAC1533_RS09555	DUF969 domain-containing protein	GSS_RS08165	DUF969 domain-containing protein	Lacidipiscis_RS10825	DUF969 domain-containing protein
LAC1533_RS09560	DUF979 domain-containing protein	GSS_RS08160	DUF979 domain-containing protein	Lacidipiscis_RS10820	DUF979 domain-containing protein
LAC1533_RS09565	pyroglutamyl-peptidase I	GSS_RS08155	pyroglutamyl-peptidase I	Lacidipiscis_RS10815	pyroglutamyl-peptidase I
LAC1533_RS09575	sugar ABC transporter permease	GSS_RS08145	sugar ABC transporter permease	Lacidipiscis_RS10805	sugar ABC transporter permease
LAC1533_RS09580	carbohydrate ABC transporter substrate-binding protein			Lacidipiscis_RS10800	carbohydrate ABC transporter substrate-binding protein
LAC1533_RS09585	ABC transporter ATP-binding protein	GSS_RS08135	ABC transporter ATP-binding protein		
LAC1533_RS09590	putative polysaccharide biosynthesis protein	GSS_RS08130	putative polysaccharide biosynthesis protein	Lacidipiscis_RS10790	putative polysaccharide biosynthesis protein
LAC1533_RS09595	DNA starvation/stationary phase protection protein	GSS_RS08125	DNA starvation/stationary phase protection protein	Lacidipiscis_RS10785	DNA starvation/stationary phase protection protein
LAC1533_RS09600	aldo/keto reductase	GSS_RS08120	aldo/keto reductase	Lacidipiscis_RS10780	aldo/keto reductase
LAC1533_RS09605	glyoxalase	GSS_RS08115	glyoxalase	Lacidipiscis_RS10775	glyoxalase
LAC1533_RS09610	hypothetical protein	GSS_RS08110	hypothetical protein	Lacidipiscis_RS10770	hypothetical protein

LAC1533_RS09615	GTP-binding protein	GSS_RS08100	GTP-binding protein	Lacidipiscis_RS10765	GTP-binding protein
LAC1533_RS09620	LysM domain-containing protein	GSS_RS08095	LysM domain-containing protein	Lacidipiscis_RS10760	LysM domain-containing protein
LAC1533_RS09630	DegV family EDD domain-containing protein	GSS_RS08080	DegV family EDD domain-containing protein	Lacidipiscis_RS10750	DegV family EDD domain-containing protein
LAC1533_RS09635	methyl-accepting chemotaxis protein	GSS_RS08075	methyl-accepting chemotaxis protein	Lacidipiscis_RS10745	methyl-accepting chemotaxis protein
LAC1533_RS09640	flagellin	GSS_RS08070	flagellar hook-associated protein 3	Lacidipiscis_RS10740	flagellar hook-associated protein 3
LAC1533_RS09645	flagellar hook-associated protein FlgK	GSS_RS08065	flagellar hook-associated protein FlgK	Lacidipiscis_RS10735	flagellar hook-associated protein FlgK
LAC1533_RS09650	hypothetical protein	GSS_RS08060	hypothetical protein	Lacidipiscis_RS10730	hypothetical protein
LAC1533_RS09655	flagellar biosynthesis anti-sigma factor FlgM	GSS_RS12920	flagellar biosynthesis anti-sigma factor FlgM	Lacidipiscis_RS10725	flagellar biosynthesis anti-sigma factor FlgM
LAC1533_RS09660	flagellar motor switch phosphatase FliY	GSS_RS08050	flagellar motor switch phosphatase FliY	Lacidipiscis_RS10720	flagellar motor switch phosphatase FliY
LAC1533_RS09665	flagellar motor switch protein FliM	GSS_RS08045	flagellar motor switch protein FliM	Lacidipiscis_RS10715	flagellar motor switch protein FliM
LAC1533_RS09670	hypothetical protein	GSS_RS08040	hypothetical protein	Lacidipiscis_RS10710	hypothetical protein
LAC1533_RS09675	response regulator	GSS_RS08035	response regulator	Lacidipiscis_RS10705	response regulator
LAC1533_RS09680	chemotaxis protein CheC	GSS_RS08030	chemotaxis protein CheC	Lacidipiscis_RS10700	chemotaxis protein CheC
LAC1533_RS09685	chemotaxis protein CheA	GSS_RS08025	chemotaxis protein CheA	Lacidipiscis_RS10695	chemotaxis protein CheA
LAC1533_RS09690	protein-glutamate O-methyltransferase CheR	GSS_RS08020	protein-glutamate O-methyltransferase CheR	Lacidipiscis_RS10690	protein-glutamate O-methyltransferase CheR
LAC1533_RS09695	chemotaxis-specific protein-glutamate methyltransferase CheB	GSS_RS08015	chemotaxis-specific protein-glutamate methyltransferase CheB	Lacidipiscis_RS10685	chemotaxis-specific protein-glutamate methyltransferase CheB
LAC1533_RS09700	chemotaxis protein CheD	GSS_RS08010	chemotaxis protein CheD	Lacidipiscis_RS10680	chemotaxis protein CheD
LAC1533_RS09705	chemotaxis protein CheW	GSS_RS08005	chemotaxis protein CheW	Lacidipiscis_RS10675	chemotaxis protein CheW
LAC1533_RS09710	hypothetical protein	GSS_RS08000	methyl-accepting chemotaxis sensory transducer	Lacidipiscis_RS10670	hypothetical protein
LAC1533_RS09715	cell division protein FtsE	GSS_RS07995	cell division protein FtsE	Lacidipiscis_RS10665	cell division protein FtsE
LAC1533_RS09720	flagellar hook basal-body protein	GSS_RS07990	flagellar hook basal-body protein	Lacidipiscis_RS10660	flagellar hook basal-body protein
LAC1533_RS09725	flagellar hook-basal body protein	GSS_RS07985	flagellar hook-basal body protein	Lacidipiscis_RS10655	flagellar hook-basal body protein
LAC1533_RS09730	FliA/WhiG family RNA polymerase sigma factor	GSS_RS07980	FliA/WhiG family RNA polymerase sigma factor	Lacidipiscis_RS10650	FliA/WhiG family RNA polymerase sigma factor
LAC1533_RS09735	flagellar biosynthesis protein FlhA	GSS_RS07975	flagellar biosynthesis protein FlhA	Lacidipiscis_RS10645	flagellar biosynthesis protein FlhA
LAC1533_RS09740	flagellar type III secretion system protein FlhB	GSS_RS07970	flagellar type III secretion system protein FlhB	Lacidipiscis_RS10640	flagellar type III secretion system protein FlhB
LAC1533_RS09745	type III secretion protein	GSS_RS07965	type III secretion protein	Lacidipiscis_RS10635	flagellar biosynthetic protein FliR
LAC1533_RS09750	flagellar biosynthetic protein FliQ	GSS_RS07960	flagellar biosynthetic protein FliQ	Lacidipiscis_RS10630	flagellar biosynthetic protein FliQ
LAC1533_RS09755	flagellar biosynthetic protein FliP	GSS_RS07955	flagellar biosynthetic protein FliP	Lacidipiscis_RS10625	flagellar biosynthetic protein FliP
LAC1533_RS09760	flagellar biosynthesis protein FliO	GSS_RS12915	flagellar biosynthesis protein FliO	Lacidipiscis_RS10620	hypothetical protein
LAC1533_RS09765	flagellar biosynthesis protein FliL	GSS_RS07945	flagellar biosynthesis protein FliL	Lacidipiscis_RS10615	hypothetical protein
LAC1533_RS09770	flagellar protein FlbD	GSS_RS07940	flagellar protein FlbD	Lacidipiscis_RS10610	endoflagellar protein
LAC1533_RS09775	flagellar hook protein	GSS_RS07935	flagellar hook protein	Lacidipiscis_RS10605	flagellar hook protein
LAC1533_RS09780	flagellar basal body rod modification protein	GSS_RS07930	flagellar basal body rod modification protein	Lacidipiscis_RS10600	hypothetical protein
LAC1533_RS09785	flagellar hook-length control protein FliK	GSS_RS12910	flagellar hook-length control protein FliK	Lacidipiscis_RS10595	flagellar hook-length control protein FliK
LAC1533_RS09790	flagellar export protein FliJ	GSS_RS07915	flagellar export protein FliJ	Lacidipiscis_RS10590	flagellar export protein FliJ
LAC1533_RS09795	flagellar protein export ATPase FliI	GSS_RS07910	flagellar protein export ATPase FliI	Lacidipiscis_RS10585	flagellar protein export ATPase FliI
LAC1533_RS09800	hypothetical protein	GSS_RS07905	flagellar assembly protein FliH	Lacidipiscis_RS10580	hypothetical protein
LAC1533_RS09805	flagellar motor switch protein FliG	GSS_RS07900	flagellar motor switch protein FliG	Lacidipiscis_RS10575	flagellar motor switch protein FliG
LAC1533_RS09810	flagellar M-ring protein FliF	GSS_RS07895	flagellar M-ring protein FliF	Lacidipiscis_RS10570	flagellar M-ring protein FliF
LAC1533_RS09815	flagellar hook-basal body complex protein FliE	GSS_RS07890	flagellar hook-basal body complex protein FliE	Lacidipiscis_RS10565	flagellar hook-basal body complex protein FliE
LAC1533_RS09820	flagellar basal body rod protein FlgC	GSS_RS07885	flagellar basal body rod protein FlgC	Lacidipiscis_RS10560	flagellar basal body rod protein FlgC
LAC1533_RS09825	flagellar basal body rod protein FlgB	GSS_RS07880	flagellar basal body rod protein FlgB	Lacidipiscis_RS10555	flagellar basal body rod protein FlgB
LAC1533_RS09830	IS256 family transposase				
LAC1533_RS09835	hypothetical protein	GSS_RS08520	flagellar motor protein MotB	Lacidipiscis_RS06175	hypothetical protein
LAC1533_RS09840	flagellar motor protein MotA	GSS_RS08525	flagellar motor protein MotA	Lacidipiscis_RS06170	flagellar motor protein MotA
LAC1533_RS09845	flagellar export chaperone FliS	GSS_RS08530	flagellar export chaperone FliS	Lacidipiscis_RS06165	flagellar export chaperone FliS
LAC1533_RS09850	hypothetical protein	GSS_RS08535	hypothetical protein	Lacidipiscis_RS06160	hypothetical protein
LAC1533_RS09855	hypothetical protein	GSS_RS08540	flagellum hook associated protein FliD	Lacidipiscis_RS06155	hypothetical protein
LAC1533_RS09860	flagellar protein FlaG	GSS_RS13755	flagellar protein FlaG	Lacidipiscis_RS06150	hypothetical protein
LAC1533_RS09875	flagellin	GSS_RS08550	flagellin	Lacidipiscis_RS06145	flagellin
LAC1533_RS09880	flagellin	GSS_RS08555	flagellin	Lacidipiscis_RS06140	flagellin
LAC1533_RS09885	LysM domain-containing protein	GSS_RS08560	LysM domain-containing protein	Lacidipiscis_RS06135	LysM domain-containing protein
LAC1533_RS09895	hypothetical protein			Lacidipiscis_RS12250	hypothetical protein
LAC1533_RS09900	hypothetical protein	GSS_RS08575	hypothetical protein	Lacidipiscis_RS12245	hypothetical protein
LAC1533_RS09905	aldo/keto reductase	GSS_RS08580	glyceraldehyde 3-phosphate reductase	Lacidipiscis_RS12240	aldo/keto reductase
LAC1533_RS09910	addiction module antidote protein, HigA family	GSS_RS08585	addiction module antidote protein, HigA family	Lacidipiscis_RS12235	addiction module antidote protein, HigA family
LAC1533_RS09915	plasmid maintenance system killer	GSS_RS08590	plasmid maintenance system killer	Lacidipiscis_RS12230	plasmid maintenance system killer
LAC1533_RS09925	alpha-mannosidase	GSS_RS12990	alpha-mannosidase	Lacidipiscis_RS07550	alpha-mannosidase
LAC1533_RS09935	PTS fructose transporter subunit IIB	GSS_RS08610	PTS fructose transporter subunit IIB	Lacidipiscis_RS07540	PTS fructose transporter subunit IIB
LAC1533_RS09940	hypothetical protein	GSS_RS08615	hypothetical protein	Lacidipiscis_RS07535	hypothetical protein

LAC1533_RS09945	IS30 family transposase				
LAC1533_RS09950	hypothetical protein	GSS_RS13780	hypothetical protein		
LAC1533_RS09955	PRD domain-containing protein	GSS_RS13000	PRD domain-containing protein	Lacidipiscis_RS07530	PRD domain-containing protein
LAC1533_RS09965	glycosyl hydrolase	GSS_RS08625	glycosyl hydrolase	Lacidipiscis_RS07520	hypothetical protein
LAC1533_RS09970	acyltransferase	GSS_RS08630	acyltransferase	Lacidipiscis_RS07515	acyltransferase
LAC1533_RS09975	hypothetical protein	GSS_RS08635	hypothetical protein	Lacidipiscis_RS07510	hypothetical protein
LAC1533_RS09980	PrsW family intramembrane metalloprotease	GSS_RS08640	PrsW family intramembrane metalloprotease	Lacidipiscis_RS07505	PrsW family intramembrane metalloprotease
LAC1533_RS09985	thioredoxin	GSS_RS08645	thioredoxin	Lacidipiscis_RS07500	thioredoxin
LAC1533_RS09990	Cof-type HAD-IIB family hydrolase	GSS_RS08650	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS07495	Cof-type HAD-IIB family hydrolase
LAC1533_RS09995	DUF475 domain-containing protein	GSS_RS08655	DUF475 domain-containing protein	Lacidipiscis_RS07490	DUF475 domain-containing protein
LAC1533_RS10000	hypothetical protein	GSS_RS08660	hypothetical protein	Lacidipiscis_RS07485	hypothetical protein
LAC1533_RS10005	DUF1624 domain-containing protein	GSS_RS14140	DUF1624 domain-containing protein		
LAC1533_RS10010	XRE family transcriptional regulator	GSS_RS08665	XRE family transcriptional regulator	Lacidipiscis_RS06315	XRE family transcriptional regulator
LAC1533_RS10020	hypothetical protein	GSS_RS13790	hypothetical protein	Lacidipiscis_RS04340	LTA synthase family protein
LAC1533_RS10025	L,D-transpeptidase	GSS_RS08690	hypothetical protein	Lacidipiscis_RS04345	L,D-transpeptidase
LAC1533_RS10030	2-dehydropantoate 2-reductase	GSS_RS08700	2-dehydropantoate 2-reductase	Lacidipiscis_RS04350	2-dehydropantoate 2-reductase
LAC1533_RS10035	hypothetical protein	GSS_RS14150	hypothetical protein	Lacidipiscis_RS04355	hypothetical protein
LAC1533_RS10040	MFS transporter	GSS_RS08705	MFS transporter	Lacidipiscis_RS04360	MFS transporter
LAC1533_RS10045	PAS domain S-box protein	GSS_RS08710	PAS domain S-box protein	Lacidipiscis_RS04365	PAS domain S-box protein
LAC1533_RS10050	PAS domain S-box protein			Lacidipiscis_RS03450	PAS domain S-box protein
LAC1533_RS10055	hypothetical protein	GSS_RS08725	hypothetical protein	Lacidipiscis_RS03455	hypothetical protein
LAC1533_RS10075	IS256 family transposase				
LAC1533_RS10080	LysM peptidoglycan-binding domain-containing protein	GSS_RS08745	LysM peptidoglycan-binding domain-containing protein		
LAC1533_RS10105	class II aldolase family protein	GSS_RS08760	class II aldolase family protein		
LAC1533_RS10110	PTS galactitol transporter subunit IIC	GSS_RS08770	PTS Galactitol IIC component		
LAC1533_RS10115	PTS galactitol transporter subunit IIB	GSS_RS08775	PTS galactitol transporter subunit IIB		
LAC1533_RS10120	hypothetical protein	GSS_RS08780	PTS IIA-like nitrogen-regulatory protein PtsN		
LAC1533_RS10130	glycerate kinase	GSS_RS08790	glycerate kinase		
LAC1533_RS10135	hypothetical protein	GSS_RS14230	hypothetical protein		
LAC1533_RS10140	XRE family transcriptional regulator	GSS_RS13410	XRE family transcriptional regulator		
LAC1533_RS10150	hypothetical protein				
LAC1533_RS10160	LytR family transcriptional regulator	GSS_RS08795	LytR family transcriptional regulator	Lacidipiscis_RS10185	transcriptional regulator
LAC1533_RS10165	hypothetical protein				
LAC1533_RS10170	IS1380 family transposase				
LAC1533_RS10175	hypothetical protein	GSS_RS13050	hypothetical protein	Lacidipiscis_RS01255	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS10180	DUF2922 domain-containing protein	GSS_RS08860	DUF2922 domain-containing protein		
LAC1533_RS10185	hypothetical protein	GSS_RS08865	hypothetical protein		
LAC1533_RS10190	peptidase	GSS_RS08870	peptidase		
LAC1533_RS10195	DUF2922 domain-containing protein	GSS_RS08875	DUF2922 domain-containing protein		
LAC1533_RS10200	hypothetical protein	GSS_RS08880	hypothetical protein		
LAC1533_RS10205	sigma-70 family RNA polymerase sigma factor	GSS_RS08885	sigma-70 family RNA polymerase sigma factor		
LAC1533_RS10210	hypothetical protein	GSS_RS08890	hypothetical protein	Lacidipiscis_RS03975	hypothetical protein
LAC1533_RS10215	MurR/RpiR family transcriptional regulator	GSS_RS08895	MurR/RpiR family transcriptional regulator	Lacidipiscis_RS03980	MurR/RpiR family transcriptional regulator
LAC1533_RS10220	PTS sugar transporter subunit IIC	GSS_RS08900	PTS sugar transporter subunit IIC	Lacidipiscis_RS03985	PTS sugar transporter subunit IIC
LAC1533_RS10225	aryl-phospho-beta-D-glucosidase	GSS_RS08905	6-phospho-beta-glucosidase	Lacidipiscis_RS03990	aryl-phospho-beta-D-glucosidase
LAC1533_RS10230	ROK family protein	GSS_RS08910	ROK family protein	Lacidipiscis_RS03995	ROK family protein
LAC1533_RS10235	hypothetical protein				
LAC1533_RS10255	dTDP-glucose 4,6-dehydratase	GSS_RS08915	dTDP-glucose 4,6-dehydratase	Lacidipiscis_RS04005	dTDP-glucose 4,6-dehydratase
LAC1533_RS10260	DegV family protein	GSS_RS08920	DegV family protein	Lacidipiscis_RS04020	DegV family protein
LAC1533_RS10265	cadmium-translocating P-type ATPase	GSS_RS08925	heavy metal translocating P-type ATPase	Lacidipiscis_RS04050	heavy metal translocating P-type ATPase
LAC1533_RS10310	hypothetical protein	GSS_RS13055	hypothetical protein		
LAC1533_RS10320	glycosyltransferase family 2 protein				
LAC1533_RS10325	hypothetical protein				
LAC1533_RS10330	hypothetical protein			Lacidipiscis_RS02465	hypothetical protein
LAC1533_RS10335	hypothetical protein			Lacidipiscis_RS02460	flippase
LAC1533_RS10340	UDP-galactopyranose mutase			Lacidipiscis_RS02455	UDP-galactopyranose mutase
LAC1533_RS10345	hypothetical protein				
LAC1533_RS10350	hypothetical protein				
LAC1533_RS10355	hypothetical protein			Lacidipiscis_RS02480	hypothetical protein
LAC1533_RS10360	hypothetical protein				

LAC1533_RS10365	LicD family protein				
LAC1533_RS10370	DUF4422 domain-containing protein			Lacidipiscis_RS04055	DUF4422 domain-containing protein
LAC1533_RS10375	sugar transferase			Lacidipiscis_RS04060	sugar transferase
LAC1533_RS10380	galactofuranosyltransferase				
LAC1533_RS10385	glycosyltransferase family 2 protein			Lacidipiscis_RS02400	glycosyltransferase family 2 protein
LAC1533_RS10390	hypothetical protein			Lacidipiscis_RS02415	hypothetical protein
LAC1533_RS10395	glycosyltransferase			Lacidipiscis_RS02395	glycosyltransferase
LAC1533_RS10400	hypothetical protein				
LAC1533_RS10405	glycerol-3-phosphate cytidylyltransferase	GSS_RS06455	glycerol-3-phosphate cytidylyltransferase	Lacidipiscis_RS12700	glycerol-3-phosphate cytidylyltransferase
LAC1533_RS10415	GtrA family protein	GSS_RS06505	GtrA family protein	Lacidipiscis_RS12695	GtrA family protein
LAC1533_RS10425	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	GSS_RS06450	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	Lacidipiscis_RS12690	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase
LAC1533_RS10430	IS256 family transposase	GSS_RS11465	IS256 family transposase	Lacidipiscis_RS02665	IS256 family transposase
LAC1533_RS10435	IS30 family transposase				
LAC1533_RS10440	hypothetical protein				
LAC1533_RS10450	hypothetical protein				
LAC1533_RS10455	hypothetical protein				
LAC1533_RS10465	type II toxin-antitoxin system RelE/ParE family toxin	GSS_RS10960	type II toxin-antitoxin system RelE/ParE family toxin	Lacidipiscis_RS12480	type II toxin-antitoxin system RelE/ParE family toxin
LAC1533_RS10470	Cna B-type domain-containing protein				
LAC1533_RS10475	hypothetical protein	GSS_RS06515	hypothetical protein	Lacidipiscis_RS09920	hypothetical protein
LAC1533_RS10480	class A sortase	GSS_RS06520	class A sortase	Lacidipiscis_RS09925	class A sortase
LAC1533_RS10485	TetR/AcrR family transcriptional regulator	GSS_RS06525	TetR/AcrR family transcriptional regulator		
LAC1533_RS10490	sulfite exporter TauE/SafE family protein	GSS_RS06530	sulfite exporter TauE/SafE family protein	Lacidipiscis_RS09935	sulfite exporter TauE/SafE family protein
LAC1533_RS10495	hypothetical protein	GSS_RS06535	hypothetical protein	Lacidipiscis_RS09940	hypothetical protein
LAC1533_RS10500	murein L,D-transpeptidase	GSS_RS06540	murein L,D-transpeptidase	Lacidipiscis_RS09945	murein L,D-transpeptidase
LAC1533_RS10505	hypothetical protein			Lacidipiscis_RS09950	hypothetical protein
LAC1533_RS10510	PTS fructose transporter subunit IIC	GSS_RS06550	PTS fructose transporter subunit IIC	Lacidipiscis_RS09955	PTS fructose transporter subunit IIC
LAC1533_RS10515	1-phosphofructokinase	GSS_RS06555	1-phosphofructokinase	Lacidipiscis_RS09960	1-phosphofructokinase
LAC1533_RS10520	DeoR/GlpR transcriptional regulator	GSS_RS06560	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS09965	DeoR/GlpR transcriptional regulator
LAC1533_RS10530	D-lactate dehydrogenase				
LAC1533_RS10535	CsbD family protein	GSS_RS06575	CsbD family protein	Lacidipiscis_RS02330	CsbD family protein
LAC1533_RS10540	hypothetical protein	GSS_RS13735	hypothetical protein	Lacidipiscis_RS02335	hypothetical protein
LAC1533_RS10545	DUF1694 domain-containing protein	GSS_RS06590	DUF1694 domain-containing protein	Lacidipiscis_RS02340	DUF1694 domain-containing protein
LAC1533_RS10550	hypothetical protein	GSS_RS06595	hypothetical protein	Lacidipiscis_RS02345	hypothetical protein
LAC1533_RS10555	NERD domain-containing protein	GSS_RS14090	NERD domain-containing protein	Lacidipiscis_RS02350	NERD domain-containing protein
LAC1533_RS10560	cation:proton antiporter	GSS_RS06610	cation:proton antiporter	Lacidipiscis_RS02355	cation:proton antiporter
LAC1533_RS10565	metallophosphoesterase	GSS_RS06615	metallophosphoesterase	Lacidipiscis_RS02360	metallophosphoesterase
LAC1533_RS10590	XRE family transcriptional regulator	GSS_RS06625	XRE family transcriptional regulator		
LAC1533_RS10595	hypothetical protein	GSS_RS06630	hypothetical protein	Lacidipiscis_RS05010	hypothetical protein
LAC1533_RS10600	hypothetical protein	GSS_RS06635	hypothetical protein	Lacidipiscis_RS05015	hypothetical protein
LAC1533_RS10605	serine/threonine transporter SstT	GSS_RS06640	serine/threonine transporter SstT	Lacidipiscis_RS05020	serine/threonine transporter SstT
LAC1533_RS10610	organic hydroperoxide resistance protein	GSS_RS06645	organic hydroperoxide resistance protein	Lacidipiscis_RS05025	organic hydroperoxide resistance protein
LAC1533_RS10615	Cof-type HAD-IIB family hydrolase	GSS_RS06655	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS05035	Cof-type HAD-IIB family hydrolase
LAC1533_RS10620	nicotinate phosphoribosyltransferase	GSS_RS06660	nicotinate phosphoribosyltransferase	Lacidipiscis_RS05040	nicotinate phosphoribosyltransferase
LAC1533_RS10625	NUDIX domain-containing protein	GSS_RS06665	NUDIX domain-containing protein	Lacidipiscis_RS05045	NUDIX domain-containing protein
LAC1533_RS10630	NADH-flavin reductase	GSS_RS06675	NADH-flavin reductase	Lacidipiscis_RS05050	NADH-flavin reductase
LAC1533_RS10635	hypothetical protein	GSS_RS06680	hypothetical protein	Lacidipiscis_RS05055	hypothetical protein
LAC1533_RS10640	hypothetical protein	GSS_RS06685	hypothetical protein	Lacidipiscis_RS05060	hypothetical protein
LAC1533_RS10645	peptide-methionine (S)-S-oxide reductase	GSS_RS06690	peptide-methionine (S)-S-oxide reductase	Lacidipiscis_RS05065	peptide-methionine (S)-S-oxide reductase
LAC1533_RS10650	thioredoxin	GSS_RS06695	thioredoxin	Lacidipiscis_RS05070	thioredoxin
LAC1533_RS10655	glutathione peroxidase	GSS_RS06700	glutathione peroxidase	Lacidipiscis_RS05075	glutathione peroxidase
LAC1533_RS10660	DUF488 domain-containing protein	GSS_RS06705	DUF488 domain-containing protein	Lacidipiscis_RS05080	DUF488 domain-containing protein
LAC1533_RS10665	N-acetyltransferase	GSS_RS06710	N-acetyltransferase	Lacidipiscis_RS05085	N-acetyltransferase
LAC1533_RS10670	pyruvate oxidase	GSS_RS06715	pyruvate oxidase	Lacidipiscis_RS05095	pyruvate oxidase
LAC1533_RS10685	glutamine ABC transporter substrate-binding protein				
LAC1533_RS10690	universal stress protein	GSS_RS06730	universal stress protein	Lacidipiscis_RS05105	universal stress protein
LAC1533_RS10695	CPBP family intramembrane metalloprotease	GSS_RS06735	CPBP family intramembrane metalloprotease	Lacidipiscis_RS05110	CPBP family intramembrane metalloprotease
LAC1533_RS10700	deoxyguanosine kinase	GSS_RS06740	deoxyguanosine kinase	Lacidipiscis_RS05115	deoxyguanosine kinase
LAC1533_RS10705	MFS transporter	GSS_RS06745	MFS transporter	Lacidipiscis_RS05120	MFS transporter
LAC1533_RS10710	MarR family transcriptional regulator	GSS_RS06750	MarR family transcriptional regulator	Lacidipiscis_RS05125	MarR family transcriptional regulator
LAC1533_RS10715	aldo/keto reductase	GSS_RS06755	aldo/keto reductase	Lacidipiscis_RS05130	aldo/keto reductase
LAC1533_RS10720	NAD(P)/FAD-dependent oxidoreductase	GSS_RS06760	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS05135	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS10725	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	GSS_RS06765	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	Lacidipiscis_RS05140	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase

LAC1533_RS10730	hypothetical protein	GSS_RS06770	hypothetical protein	Lacidipiscis_RS05145	hypothetical protein
LAC1533_RS10735	aluminum resistance protein	GSS_RS06775	aluminum resistance protein	Lacidipiscis_RS05150	aluminum resistance protein
LAC1533_RS10740	hypothetical protein				
LAC1533_RS10745	hypothetical protein	GSS_RS06785	hypothetical protein	Lacidipiscis_RS05155	hypothetical protein
LAC1533_RS10755	bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase	GSS_RS06790	bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase	Lacidipiscis_RS05160	bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase
LAC1533_RS10760	penicillin-binding protein 2	GSS_RS06795	penicillin-binding protein 2	Lacidipiscis_RS05165	penicillin-binding protein 2
LAC1533_RS10765	aspartate racemase	GSS_RS06800	aspartate racemase	Lacidipiscis_RS05170	aspartate racemase
LAC1533_RS10770	carboxylate--amine ligase	GSS_RS06805	carboxylate--amine ligase	Lacidipiscis_RS05175	carboxylate--amine ligase
LAC1533_RS10775	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase	GSS_RS06810	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase	Lacidipiscis_RS05180	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase
LAC1533_RS10780	hypothetical protein				
LAC1533_RS10785	hypothetical protein	GSS_RS06815	hypothetical protein	Lacidipiscis_RS05185	hypothetical protein
LAC1533_RS10790	universal stress protein	GSS_RS06820	universal stress protein	Lacidipiscis_RS05190	universal stress protein
LAC1533_RS10795	hypothetical protein	GSS_RS06825	hypothetical protein	Lacidipiscis_RS05195	hypothetical protein
LAC1533_RS10800	aldo/keto reductase	GSS_RS06830	aldo/keto reductase	Lacidipiscis_RS05200	aldo/keto reductase
LAC1533_RS10805	peptide ABC transporter substrate-binding protein	GSS_RS06840	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS05205	peptide ABC transporter substrate-binding protein
LAC1533_RS10810	branched-chain amino acid ABC transporter permease	GSS_RS06850	ABC transporter permease	Lacidipiscis_RS05210	branched-chain amino acid ABC transporter permease
LAC1533_RS10815	ABC transporter ATP-binding protein	GSS_RS06855	phosphonate ABC transporter ATP-binding protein	Lacidipiscis_RS05215	ABC transporter ATP-binding protein
LAC1533_RS10820	hypothetical protein	GSS_RS06860	membrane protein	Lacidipiscis_RS08205	hypothetical protein
LAC1533_RS10825	UTP--glucose-1-phosphate uridylyltransferase	GSS_RS06865	UTP--glucose-1-phosphate uridylyltransferase		
LAC1533_RS10830	VanZ family protein	GSS_RS06870	VanZ family protein	Lacidipiscis_RS08215	VanZ family protein
LAC1533_RS10835	4-phosphoerythronate dehydrogenase	GSS_RS06875	4-phosphoerythronate dehydrogenase	Lacidipiscis_RS08220	hydroxyacid dehydrogenase
LAC1533_RS10840	transposase				
LAC1533_RS10845	hypothetical protein	GSS_RS06880	hypothetical protein	Lacidipiscis_RS08225	hypothetical protein
LAC1533_RS10855	group II intron reverse transcriptase/maturase				
LAC1533_RS10865	energy-coupled thiamine transporter ThiT	GSS_RS06885	energy-coupled thiamine transporter ThiT	Lacidipiscis_RS08230	energy-coupled thiamine transporter ThiT
LAC1533_RS10870	energy-coupling factor transporter transmembrane protein EcfT	GSS_RS06890	energy-coupling factor transporter transmembrane protein EcfT	Lacidipiscis_RS08235	energy-coupling factor transporter transmembrane protein EcfT
LAC1533_RS10875	ABC transporter ATP-binding protein	GSS_RS06895	ABC transporter ATP-binding protein	Lacidipiscis_RS08240	ABC transporter ATP-binding protein
LAC1533_RS10880	ABC transporter permease	GSS_RS06900	ABC transporter permease	Lacidipiscis_RS08245	ABC transporter permease
LAC1533_RS10885	PFL family protein	GSS_RS06905	PFL family protein	Lacidipiscis_RS08250	PFL family protein
LAC1533_RS10890	ACT domain-containing protein	GSS_RS06910	ACT domain-containing protein	Lacidipiscis_RS08255	ACT domain-containing protein
LAC1533_RS10895	MFS transporter	GSS_RS06915	MFS transporter	Lacidipiscis_RS08260	MFS transporter
LAC1533_RS10900	N-acetyltransferase	GSS_RS06920	N-acetyltransferase	Lacidipiscis_RS08265	N-acetyltransferase
LAC1533_RS10905	hypothetical protein	GSS_RS13740	hypothetical protein	Lacidipiscis_RS08270	hypothetical protein
LAC1533_RS10910	hypothetical protein	GSS_RS12810	hypothetical protein	Lacidipiscis_RS08275	hypothetical protein
LAC1533_RS10915	hypothetical protein	GSS_RS06930	hypothetical protein	Lacidipiscis_RS08280	hypothetical protein
LAC1533_RS10920	type 1 glutamine amidotransferase	GSS_RS06935	type 1 glutamine amidotransferase	Lacidipiscis_RS08285	type 1 glutamine amidotransferase
LAC1533_RS10925	Rrf2 family transcriptional regulator	GSS_RS06940	Rrf2 family transcriptional regulator	Lacidipiscis_RS08290	Rrf2 family transcriptional regulator
LAC1533_RS10930	hypothetical protein	GSS_RS06945	hypothetical protein	Lacidipiscis_RS08295	NAD(P)-dependent oxidoreductase
LAC1533_RS10935	amino acid ABC transporter permease	GSS_RS06975	amino acid ABC transporter permease	Lacidipiscis_RS08305	amino acid ABC transporter permease
LAC1533_RS10940	amino acid ABC transporter ATP-binding protein	GSS_RS06980	amino acid ABC transporter ATP-binding protein	Lacidipiscis_RS08310	amino acid ABC transporter ATP-binding protein
LAC1533_RS10945	amino acid ABC transporter substrate-binding protein	GSS_RS06985	amino acid ABC transporter substrate-binding protein	Lacidipiscis_RS08315	amino acid ABC transporter substrate-binding protein
LAC1533_RS10950	DUF1541 domain-containing protein	GSS_RS06990	DUF1541 domain-containing protein	Lacidipiscis_RS08915	DUF1541 domain-containing protein
LAC1533_RS10955	PspC domain-containing protein	GSS_RS06995	PspC domain-containing protein	Lacidipiscis_RS08920	PspC domain-containing protein
LAC1533_RS10960	PadR family transcriptional regulator	GSS_RS07000	PadR family transcriptional regulator	Lacidipiscis_RS08925	PadR family transcriptional regulator
LAC1533_RS10965	hypothetical protein	GSS_RS07005	hypothetical protein	Lacidipiscis_RS08930	hypothetical protein
LAC1533_RS10970	DUF1700 domain-containing protein	GSS_RS07010	DUF1700 domain-containing protein	Lacidipiscis_RS08935	DUF1700 domain-containing protein
LAC1533_RS10975	D-alanyl-D-alanine dipeptidase	GSS_RS07020	D-alanyl-D-alanine dipeptidase	Lacidipiscis_RS08940	D-alanyl-D-alanine dipeptidase
LAC1533_RS10985	VOC family protein	GSS_RS07030	VOC family protein	Lacidipiscis_RS08950	VOC family protein
LAC1533_RS10990	MarR family transcriptional regulator	GSS_RS07035	MarR family transcriptional regulator	Lacidipiscis_RS08955	MarR family transcriptional regulator
LAC1533_RS10995	KH domain-containing protein	GSS_RS07040	KH domain-containing protein	Lacidipiscis_RS08960	KH domain-containing protein
LAC1533_RS11000	ribose transporter RbsU	GSS_RS07045	ribose transporter RbsU	Lacidipiscis_RS08965	ribose transporter RbsU
LAC1533_RS11005	D-ribose pyranase	GSS_RS07050	D-ribose pyranase	Lacidipiscis_RS08970	D-ribose pyranase
LAC1533_RS11010	ribokinase	GSS_RS07055	ribokinase	Lacidipiscis_RS08975	ribokinase
LAC1533_RS11015	LacI family transcriptional regulator	GSS_RS12815	hypothetical protein	Lacidipiscis_RS08980	LacI family transcriptional regulator
LAC1533_RS11025	3-oxoacyl-ACP reductase	GSS_RS07070	3-oxoacyl-ACP reductase		
LAC1533_RS11030	phosphoenolpyruvate synthase	GSS_RS07075	phosphoenolpyruvate synthase		
LAC1533_RS11035	N-acetyltransferase	GSS_RS07080	N-acetyltransferase	Lacidipiscis_RS09275	N-acetyltransferase
LAC1533_RS11045	GNAT family N-acetyltransferase	GSS_RS12820	N-acetyltransferase	Lacidipiscis_RS09285	N-acetyltransferase
LAC1533_RS11055	hypothetical protein	GSS_RS07095	hypothetical protein	Lacidipiscis_RS09290	hypothetical protein
LAC1533_RS11065	cadmium-translocating P-type ATPase	GSS_RS07100	copper-translocating P-type ATPase	Lacidipiscis_RS10910	copper-translocating P-type ATPase
LAC1533_RS11070	cupredoxin domain-containing protein	GSS_RS07105	cupredoxin domain-containing protein	Lacidipiscis_RS10905	cupredoxin domain-containing protein
LAC1533_RS11075	copper-binding protein	GSS_RS07110	copper-binding protein	Lacidipiscis_RS10900	copper-binding protein
LAC1533_RS11080	CopY/TcrY family copper transport repressor	GSS_RS07115	CopY/TcrY family copper transport repressor	Lacidipiscis_RS10895	CopY/TcrY family copper transport repressor
LAC1533_RS11085	aldo/keto reductase	GSS_RS07120	aldo/keto reductase	Lacidipiscis_RS10890	aldo/keto reductase

LAC1533_RS11090	M1 family peptidase	GSS_RS07125	M1 family peptidase	Lacidipiscis_RS10885	M1 family peptidase
LAC1533_RS11095	N-acetyltransferase	GSS_RS07130	N-acetyltransferase	Lacidipiscis_RS10880	N-acetyltransferase
LAC1533_RS11100	hypothetical protein				
LAC1533_RS11105	hypothetical protein	GSS_RS14095	hypothetical protein	Lacidipiscis_RS10875	hypothetical protein
LAC1533_RS11110	hypothetical protein	GSS_RS07135	hypothetical protein	Lacidipiscis_RS10870	hypothetical protein
LAC1533_RS11115	KR domain-containing protein	GSS_RS07140	3-oxoacyl-ACP reductase	Lacidipiscis_RS10865	KR domain-containing protein
LAC1533_RS11120	NAD-dependent dehydratase	GSS_RS07145	NAD-dependent dehydratase	Lacidipiscis_RS10860	NAD-dependent dehydratase
LAC1533_RS11125	glycerol dehydrogenase	GSS_RS07150	glycerol dehydrogenase	Lacidipiscis_RS10855	glycerol dehydrogenase
LAC1533_RS11130	glycyl-radical enzyme activating protein	GSS_RS07155	glycyl-radical enzyme activating protein	Lacidipiscis_RS10850	glycyl-radical enzyme activating protein
LAC1533_RS11135	glycyl radical protein	GSS_RS07160	formate C-acetyltransferase/glycerol dehydratase family glycyl radical enzyme	Lacidipiscis_RS10845	formate C-acetyltransferase/glycerol dehydratase family glycyl radical enzyme
LAC1533_RS11140	fructose-bisphosphate aldolase	GSS_RS07165	fructose-bisphosphate aldolase	Lacidipiscis_RS10840	fructose-bisphosphate aldolase
LAC1533_RS11145	peptidase M13	GSS_RS07170	peptidase M13	Lacidipiscis_RS08195	peptidase M13
LAC1533_RS11150	divalent metal cation transporter	GSS_RS07175	divalent metal cation transporter		
LAC1533_RS11160	TetR/AcrR family transcriptional regulator	GSS_RS13745	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS08180	TetR/AcrR family transcriptional regulator
LAC1533_RS11165	1-acyl-sn-glycerol-3-phosphate acyltransferase	GSS_RS12835	1-acyl-sn-glycerol-3-phosphate acyltransferase	Lacidipiscis_RS08175	hypothetical protein
LAC1533_RS11170	glycosyl transferase	GSS_RS07195	glycosyl transferase	Lacidipiscis_RS08170	glycosyltransferase family 8 protein
LAC1533_RS11175	glycosyltransferase family 8 protein	GSS_RS07200	glycosyltransferase family 8 protein	Lacidipiscis_RS08165	glycosyltransferase family 8 protein
LAC1533_RS11180	1-acyl-sn-glycerol-3-phosphate acyltransferase			Lacidipiscis_RS08160	1-acyl-sn-glycerol-3-phosphate acyltransferase
LAC1533_RS11185	universal stress protein	GSS_RS07215	universal stress protein	Lacidipiscis_RS08155	universal stress protein
LAC1533_RS11190	hypothetical protein	GSS_RS07220	hypothetical protein	Lacidipiscis_RS08150	hypothetical protein
LAC1533_RS11195	hypothetical protein	GSS_RS09700	hypothetical protein		
LAC1533_RS11200	hypothetical protein	GSS_RS07225	hypothetical protein	Lacidipiscis_RS08145	hypothetical protein
LAC1533_RS11210	branched-chain amino acid transporter	GSS_RS14100	branched-chain amino acid transporter	Lacidipiscis_RS08135	AzlD domain-containing protein
LAC1533_RS11220	DoxX family membrane protein	GSS_RS07235	DoxX family membrane protein	Lacidipiscis_RS06850	DoxX family membrane protein
LAC1533_RS11225	hypothetical protein	GSS_RS10775	hypothetical protein	Lacidipiscis_RS06840	hypothetical protein
LAC1533_RS11235	ABC transporter ATP-binding protein	GSS_RS10785	ABC transporter ATP-binding protein	Lacidipiscis_RS06830	ABC transporter ATP-binding protein
LAC1533_RS11240	NAD(P)H-dependent oxidoreductase	GSS_RS10790	NAD(P)H-dependent oxidoreductase	Lacidipiscis_RS06825	NAD(P)H-dependent oxidoreductase
LAC1533_RS11245	carbamate kinase	GSS_RS10795	carbamate kinase	Lacidipiscis_RS06820	carbamate kinase
LAC1533_RS11250	amino acid permease	GSS_RS10800	amino acid permease	Lacidipiscis_RS06815	amino acid permease
LAC1533_RS11255	carbamate kinase	GSS_RS10805	carbamate kinase	Lacidipiscis_RS06810	carbamate kinase
LAC1533_RS11260	ornithine carbamoyltransferase	GSS_RS10810	ornithine carbamoyltransferase	Lacidipiscis_RS06805	ornithine carbamoyltransferase
LAC1533_RS11265	arginine deiminase	GSS_RS10815	arginine deiminase	Lacidipiscis_RS06800	arginine deiminase
LAC1533_RS11270	tRNA ligase	GSS_RS10825	tRNA ligase	Lacidipiscis_RS06795	tRNA ligase
LAC1533_RS11280	hypothetical protein	GSS_RS10050	hypothetical protein		
LAC1533_RS11285	GNAT family N-acetyltransferase	GSS_RS13235	GNAT family N-acetyltransferase		
LAC1533_RS11295	amino acid permease	GSS_RS10060	amino acid permease	Lacidipiscis_RS03680	amino acid permease
LAC1533_RS11300	hypothetical protein	GSS_RS13240	ArgR family transcriptional regulator	Lacidipiscis_RS03675	hypothetical protein
LAC1533_RS11305	alpha-glucosidase	GSS_RS10075	alpha-glucosidase	Lacidipiscis_RS03670	alpha-glucosidase
LAC1533_RS11310	fructokinase	GSS_RS10080	fructokinase	Lacidipiscis_RS03665	fructokinase
LAC1533_RS11315	glyoxalase	GSS_RS10085	glyoxalase/bleomycin resistance/dioxygenase family protein	Lacidipiscis_RS03660	glyoxalase/bleomycin resistance/dioxygenase family protein
LAC1533_RS11320	PTS glucose transporter subunit IIABC	GSS_RS10090	PTS glucose transporter subunit IIABC		
LAC1533_RS11325	hypothetical protein	GSS_RS10095	hypothetical protein		
LAC1533_RS11330	SIS domain-containing protein				
LAC1533_RS11345	PTS alpha-glucoside transporter subunit IICB				
LAC1533_RS11350	6-phospho-alpha-glucosidase				
LAC1533_RS11375	mannitol-1-phosphate 5-dehydrogenase			Lacidipiscis_RS07195	mannitol-1-phosphate 5-dehydrogenase
LAC1533_RS11380	PTS mannitol transporter subunit IIA			Lacidipiscis_RS07200	PTS mannitol transporter subunit IIA
LAC1533_RS11385	PTS mannitol transporter subunit IICBA			Lacidipiscis_RS07205	PTS mannitol transporter subunit IICBA
LAC1533_RS11390	esterase family protein			Lacidipiscis_RS07210	esterase family protein
LAC1533_RS11395	PTS fructose transporter subunit IID			Lacidipiscis_RS07215	PTS fructose transporter subunit IID
LAC1533_RS11400	PTS sugar transporter subunit IIC			Lacidipiscis_RS07220	PTS sugar transporter subunit IIC
LAC1533_RS11405	PTS mannose/fructose/sorbose transporter subunit IIB			Lacidipiscis_RS07225	PTS mannose/fructose/sorbose transporter subunit IIB
LAC1533_RS11410	PRD domain-containing protein			Lacidipiscis_RS07230	PRD domain-containing protein
LAC1533_RS11415	hypothetical protein			Lacidipiscis_RS07235	hypothetical protein
LAC1533_RS11420	HTH domain-containing protein			Lacidipiscis_RS09490	HTH domain-containing protein
LAC1533_RS11425	glucosamine-6-phosphate deaminase	GSS_RS10115	glucosamine-6-phosphate deaminase	Lacidipiscis_RS09485	glucosamine-6-phosphate deaminase
LAC1533_RS11430	glutamine--fructose-6-phosphate transaminase (isomerizing)	GSS_RS10120	glutamine--fructose-6-phosphate transaminase (isomerizing)	Lacidipiscis_RS09480	glutamine--fructose-6-phosphate transaminase (isomerizing)
LAC1533_RS11445	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent	GSS_RS10125	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent	Lacidipiscis_RS09475	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent

LAC1533_RS11450	ATP:cob(I)alamin adenosyltransferase	GSS_RS10130	ATP:cob(I)alamin adenosyltransferase	Lacidipiscis_RS09470	ATP:cob(I)alamin adenosyltransferase
LAC1533_RS11455	DUF4430 domain-containing protein	GSS_RS10135	DUF4430 domain-containing protein	Lacidipiscis_RS09465	DUF4430 domain-containing protein
LAC1533_RS11460	aldo/keto reductase	GSS_RS10140	aldo/keto reductase	Lacidipiscis_RS00510	aldo/keto reductase
LAC1533_RS11465	cupin domain-containing protein	GSS_RS10145	cupin domain-containing protein	Lacidipiscis_RS00515	cupin domain-containing protein
LAC1533_RS11470	carboxymuconolactone decarboxylase family protein	GSS_RS10150	carboxymuconolactone decarboxylase family protein	Lacidipiscis_RS00520	carboxymuconolactone decarboxylase family protein
LAC1533_RS11475	DUF2255 domain-containing protein	GSS_RS10155	DUF2255 domain-containing protein	Lacidipiscis_RS00525	DUF2255 domain-containing protein
LAC1533_RS11480	MerR family transcriptional regulator	GSS_RS10160	MerR family transcriptional regulator	Lacidipiscis_RS00530	MerR family transcriptional regulator
LAC1533_RS11490	amino acid ABC transporter ATP-binding protein	GSS_RS10175	amino acid ABC transporter ATP-binding protein		
LAC1533_RS11495	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	GSS_RS10180	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	Lacidipiscis_RS00540	bifunctional acetaldehyde-CoA/alcohol dehydrogenase
LAC1533_RS11500	hypothetical protein				
LAC1533_RS11505	hypothetical protein	GSS_RS13265	carboxylesterase		
LAC1533_RS11510	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	GSS_RS10190	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	Lacidipiscis_RS00500	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG
LAC1533_RS11515	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE	GSS_RS10195	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE	Lacidipiscis_RS00495	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE
LAC1533_RS11520	lipoate--protein ligase	GSS_RS10200	lipoate--protein ligase	Lacidipiscis_RS00490	lipoate--protein ligase
LAC1533_RS11525	MFS transporter	GSS_RS10205	MFS transporter	Lacidipiscis_RS00485	MFS transporter
LAC1533_RS11540	hypothetical protein			Lacidipiscis_RS00470	hypothetical protein
LAC1533_RS11555	glycine betaine/L-proline ABC transporter ATP-binding protein			Lacidipiscis_RS00455	glycine betaine/L-proline ABC transporter ATP-binding protein
LAC1533_RS11560	GlsB/YeaQ/YmgE family stress response membrane protein	GSS_RS10230	GlsB/YeaQ/YmgE family stress response membrane protein	Lacidipiscis_RS00450	GlsB/YeaQ/YmgE family stress response membrane protein
LAC1533_RS11565	PTS cellobiose transporter subunit IIC	GSS_RS10235	PTS cellobiose transporter subunit IIC		
LAC1533_RS11570	hypothetical protein	GSS_RS10240	hypothetical protein	Lacidipiscis_RS03470	hypothetical protein
LAC1533_RS11580	6-phospho-beta-glucosidase	GSS_RS10245	6-phospho-beta-glucosidase	Lacidipiscis_RS03465	aryl-phospho-beta-D-glucosidase
LAC1533_RS11585	MarR family transcriptional regulator	GSS_RS10250	MarR family transcriptional regulator	Lacidipiscis_RS08700	MarR family transcriptional regulator
LAC1533_RS11590	NAD(P)/FAD-dependent oxidoreductase	GSS_RS03800	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS08705	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS11595	DUF3021 domain-containing protein	GSS_RS03795	DUF3021 domain-containing protein	Lacidipiscis_RS08720	DUF3021 domain-containing protein
LAC1533_RS11600	LytTR family transcriptional regulator	GSS_RS03790	LytTR family transcriptional regulator		
LAC1533_RS11615	NCS2 family permease	GSS_RS03780	NCS2 family permease		
LAC1533_RS11620	DegV family protein	GSS_RS03775	DegV family protein	Lacidipiscis_RS07245	DegV family protein
LAC1533_RS11630	glutamate/aspartate:proton symporter GltP	GSS_RS03770	proton glutamate symport protein	Lacidipiscis_RS07250	glutamate:protein symporter
LAC1533_RS11635	DUF4811 domain-containing protein	GSS_RS03765	DUF4811 domain-containing protein		
LAC1533_RS11645	MerR family transcriptional regulator	GSS_RS03755	MerR family transcriptional regulator	Lacidipiscis_RS12730	MerR family transcriptional regulator
LAC1533_RS11650	HAD family hydrolase	GSS_RS11485	HAD family hydrolase	Lacidipiscis_RS12725	HAD family hydrolase
LAC1533_RS11655	CrcB family protein	GSS_RS03750	CrcB family protein	Lacidipiscis_RS00125	CrcB family protein
LAC1533_RS11660	hypothetical protein	GSS_RS03745	camphor resistance protein CrcB	Lacidipiscis_RS04090	hypothetical protein
LAC1533_RS11665	6-phospho-beta-glucosidase	GSS_RS03740	6-phospho-beta-glucosidase	Lacidipiscis_RS04095	6-phospho-beta-glucosidase
LAC1533_RS11670	PTS lactose/cellobiose transporter subunit IIA	GSS_RS03735	PTS lactose/cellobiose transporter subunit IIA	Lacidipiscis_RS04100	PTS lactose/cellobiose transporter subunit IIA
LAC1533_RS11675	PTS sugar transporter subunit IIB	GSS_RS03730	PTS sugar transporter subunit IIB	Lacidipiscis_RS04105	PTS sugar transporter subunit IIB
LAC1533_RS11680	GntR family transcriptional regulator			Lacidipiscis_RS04110	GntR family transcriptional regulator
LAC1533_RS11690	group II intron reverse transcriptase/maturase				
LAC1533_RS11700	hypothetical protein				
LAC1533_RS11705	nucleotide sugar dehydrogenase			Lacidipiscis_RS02425	nucleotide sugar dehydrogenase
LAC1533_RS11710	hypothetical protein				
LAC1533_RS11715	hypothetical protein				
LAC1533_RS11720	hypothetical protein				
LAC1533_RS11725	hypothetical protein				
LAC1533_RS11730	hypothetical protein				
LAC1533_RS11735	glycosyltransferase family 2 protein				
LAC1533_RS11740	UDP-phosphate N-acetylgalactosaminyl-1-phosphate transferase	GSS_RS03700	sugar transferase	Lacidipiscis_RS00600	UDP-phosphate N-acetylgalactosaminyl-1-phosphate transferase
LAC1533_RS11745	epimerase	GSS_RS03695	epimerase	Lacidipiscis_RS00605	epimerase
LAC1533_RS11750	tyrosine protein phosphatase	GSS_RS03685	tyrosine protein phosphatase	Lacidipiscis_RS00610	hypothetical protein
LAC1533_RS11755	exopolysaccharide biosynthesis protein	GSS_RS03680	exopolysaccharide biosynthesis protein	Lacidipiscis_RS00615	exopolysaccharide biosynthesis protein
LAC1533_RS11760	chain-length determining protein	GSS_RS03675	polysaccharide biosynthesis protein	Lacidipiscis_RS00620	chain-length determining protein
LAC1533_RS11765	serine hydrolase	GSS_RS03670	serine hydrolase	Lacidipiscis_RS00625	serine hydrolase
LAC1533_RS11770	aryl-sulfate sulfotransferase	GSS_RS03665	aryl-sulfate sulfotransferase	Lacidipiscis_RS00635	aryl-sulfate sulfotransferase
LAC1533_RS11775	glucosamine-6-phosphate deaminase	GSS_RS03660	glucosamine-6-phosphate deaminase	Lacidipiscis_RS00640	glucosamine-6-phosphate deaminase
LAC1533_RS11790	type II toxin-antitoxin system PemK/MazF family toxin			Lacidipiscis_RS03220	type II toxin-antitoxin system PemK/MazF family toxin
LAC1533_RS11795	PbsX family transcriptional regulator			Lacidipiscis_RS03225	PbsX family transcriptional regulator
LAC1533_RS11800	site-specific integrase			Lacidipiscis_RS03230	site-specific integrase
LAC1533_RS11805	hypothetical protein			Lacidipiscis_RS03235	hypothetical protein

LAC1533_RS11810	group II intron reverse transcriptase/maturase				
LAC1533_RS11820	NAD(P)-dependent alcohol dehydrogenase			Lacidipiscis_RS03250	NAD(P)-dependent alcohol dehydrogenase
LAC1533_RS11825	ABC-F type ribosomal protection protein			Lacidipiscis_RS03255	ABC-F type ribosomal protection protein
LAC1533_RS11830	hypothetical protein	GSS_RS03655	hypothetical protein	Lacidipiscis_RS03260	hypothetical protein
LAC1533_RS11835	hypothetical protein	GSS_RS03650	hypothetical protein	Lacidipiscis_RS03265	hypothetical protein
LAC1533_RS11840	hypothetical protein	GSS_RS03645	hypothetical protein	Lacidipiscis_RS03270	hypothetical protein
LAC1533_RS11845	NAD(P)/FAD-dependent oxidoreductase	GSS_RS03640	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS03275	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS11850	ABC transporter ATP-binding protein	GSS_RS03635	ABC transporter ATP-binding protein	Lacidipiscis_RS03280	ABC transporter ATP-binding protein
LAC1533_RS11855	glycine/betaine ABC transporter permease	GSS_RS03630	glycine/betaine ABC transporter permease	Lacidipiscis_RS03285	glycine/betaine ABC transporter permease
LAC1533_RS11860	DUF975 domain-containing protein	GSS_RS03625	DUF975 domain-containing protein	Lacidipiscis_RS11770	DUF975 domain-containing protein
LAC1533_RS11865	metal-dependent transcriptional regulator	GSS_RS03620	metal-dependent transcriptional regulator	Lacidipiscis_RS11765	metal-dependent transcriptional regulator
LAC1533_RS11870	divalent metal cation transporter	GSS_RS03615	divalent metal cation transporter	Lacidipiscis_RS11760	divalent metal cation transporter
LAC1533_RS11875	universal stress protein	GSS_RS03610	universal stress protein	Lacidipiscis_RS11755	universal stress protein
LAC1533_RS11880	MurR/RpiR family transcriptional regulator	GSS_RS03605	MurR/RpiR family transcriptional regulator	Lacidipiscis_RS11750	MurR/RpiR family transcriptional regulator
LAC1533_RS11885	gluconate permease	GSS_RS03595	gluconate permease	Lacidipiscis_RS11745	gluconate permease
LAC1533_RS11890	gluconokinase	GSS_RS03590	gluconokinase	Lacidipiscis_RS11740	gluconokinase
LAC1533_RS11895	6-phosphogluconate dehydrogenase (decarboxylating)	GSS_RS03585	6-phosphogluconate dehydrogenase (decarboxylating)	Lacidipiscis_RS11735	6-phosphogluconate dehydrogenase (decarboxylating)
LAC1533_RS11900	pyridine nucleotide-disulfide oxidoreductase	GSS_RS03580	pyridine nucleotide-disulfide oxidoreductase	Lacidipiscis_RS11730	pyridine nucleotide-disulfide oxidoreductase
LAC1533_RS11905	3-hydroxyacyl-CoA dehydrogenase family protein	GSS_RS12510	hypothetical protein		
LAC1533_RS11910	IS256 family transposase				
LAC1533_RS11915	hypothetical protein	GSS_RS14035	hypothetical protein	Lacidipiscis_RS06470	hypothetical protein
LAC1533_RS11920	MFS transporter	GSS_RS03555	MFS transporter	Lacidipiscis_RS06465	MFS transporter
LAC1533_RS11925	copper oxidase	GSS_RS03550	multicopper oxidase	Lacidipiscis_RS06460	copper oxidase
LAC1533_RS11935	hypothetical protein	GSS_RS03445	hypothetical protein	Lacidipiscis_RS01975	hypothetical protein
LAC1533_RS11940	succinate-semialdehyde dehydrogenase	GSS_RS03440	succinate-semialdehyde dehydrogenase	Lacidipiscis_RS01980	succinate-semialdehyde dehydrogenase
LAC1533_RS11945	HIT family protein	GSS_RS12465	HIT family protein	Lacidipiscis_RS01985	HIT family protein
LAC1533_RS11950	glutamate/gamma-aminobutyrate family transporter YjeM	GSS_RS12460	glutamate/gamma-aminobutyrate family transporter YjeM	Lacidipiscis_RS01990	glutamate/gamma-aminobutyrate family transporter YjeM
LAC1533_RS11965	DedA family protein	GSS_RS03415	DedA family protein	Lacidipiscis_RS02260	DedA family protein
LAC1533_RS11970	hypothetical protein	GSS_RS03410	hypothetical protein		
LAC1533_RS11975	hypothetical protein	GSS_RS13690	hypothetical protein		
LAC1533_RS11980	ribonucleoside hydrolase RihC	GSS_RS03400	ribonucleoside hydrolase RihC	Lacidipiscis_RS12365	ribonucleoside hydrolase RihC
LAC1533_RS11985	aldo/keto reductase	GSS_RS03395	aldo/keto reductase	Lacidipiscis_RS12360	aldo/keto reductase
LAC1533_RS11990	magnesium transporter CorA family protein				
LAC1533_RS11995	N-acetyltransferase	GSS_RS12440	N-acetyltransferase	Lacidipiscis_RS12350	N-acetyltransferase
LAC1533_RS12000	type I methionyl aminopeptidase	GSS_RS03380	type I methionyl aminopeptidase	Lacidipiscis_RS12345	type I methionyl aminopeptidase
LAC1533_RS12005	GntR family transcriptional regulator	GSS_RS03375	GntR family transcriptional regulator	Lacidipiscis_RS12340	GntR family transcriptional regulator
LAC1533_RS12010	amino acid permease	GSS_RS03370	amino acid permease	Lacidipiscis_RS12335	amino acid permease
LAC1533_RS12015	ABC transporter ATP-binding protein			Lacidipiscis_RS08435	ABC transporter ATP-binding protein
LAC1533_RS12020	iron ABC transporter permease	GSS_RS03355	iron ABC transporter permease	Lacidipiscis_RS08440	iron ABC transporter permease
LAC1533_RS12025	iron ABC transporter permease	GSS_RS03350	iron ABC transporter permease	Lacidipiscis_RS08445	iron ABC transporter permease
LAC1533_RS12030	iron-siderophore ABC transporter substrate-binding protein	GSS_RS03345	iron-siderophore ABC transporter substrate-binding protein		
LAC1533_RS12040	catalase	GSS_RS03335	catalase		
LAC1533_RS12045	biotin transporter BioY	GSS_RS03330	biotin transporter BioY	Lacidipiscis_RS08465	biotin transporter BioY
LAC1533_RS12050	dephospho-CoA kinase	GSS_RS03325	dephospho-CoA kinase	Lacidipiscis_RS08470	dephospho-CoA kinase
LAC1533_RS12055	Cof-type HAD-IIB family hydrolase	GSS_RS03320	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS08475	Cof-type HAD-IIB family hydrolase
LAC1533_RS12060	MFS transporter	GSS_RS03315	MFS transporter		
LAC1533_RS12065	hypothetical protein	GSS_RS03310	hypothetical protein	Lacidipiscis_RS08485	hypothetical protein
LAC1533_RS12070	hypothetical protein	GSS_RS03305	pyridoxine 5-phosphate oxidase V	Lacidipiscis_RS08785	hypothetical protein
LAC1533_RS12075	argininosuccinate lyase	GSS_RS03300	argininosuccinate lyase	Lacidipiscis_RS08790	argininosuccinate lyase
LAC1533_RS12080	argininosuccinate synthase	GSS_RS03295	argininosuccinate synthase	Lacidipiscis_RS08795	argininosuccinate synthase
LAC1533_RS12085	peptide-methionine (S)-S-oxide reductase	GSS_RS03290	peptide-methionine (S)-S-oxide reductase	Lacidipiscis_RS08800	peptide-methionine (S)-S-oxide reductase
LAC1533_RS12090	N-acetyltransferase	GSS_RS03285	N-acetyltransferase	Lacidipiscis_RS08805	N-acetyltransferase
LAC1533_RS12095	polysaccharide biosynthesis protein	GSS_RS03280	polysaccharide biosynthesis protein	Lacidipiscis_RS08810	polysaccharide biosynthesis protein
LAC1533_RS12100	hypothetical protein	GSS_RS03275	hypothetical protein	Lacidipiscis_RS08815	hypothetical protein
LAC1533_RS12105	hypothetical protein	GSS_RS03270	hypothetical protein	Lacidipiscis_RS08820	hypothetical protein
LAC1533_RS12110	hypothetical protein	GSS_RS03260	hypothetical protein	Lacidipiscis_RS08825	hypothetical protein
LAC1533_RS12115	dihydrofolate reductase	GSS_RS03255	dihydrofolate reductase	Lacidipiscis_RS08830	dihydrofolate reductase
LAC1533_RS12120	iron export ABC transporter permease subunit FetB	GSS_RS03250	iron export ABC transporter permease subunit FetB	Lacidipiscis_RS08835	iron export ABC transporter permease subunit FetB
LAC1533_RS12125	putrescine/spermidine ABC transporter ATP-binding protein	GSS_RS03245	putrescine/spermidine ABC transporter ATP-binding protein	Lacidipiscis_RS08840	spermidine/putrescine ABC transporter ATP-binding protein
LAC1533_RS12130	glutathione peroxidase	GSS_RS03240	glutathione peroxidase	Lacidipiscis_RS04460	glutathione peroxidase
LAC1533_RS12135	IS30 family transposase				
LAC1533_RS12140	hypothetical protein			Lacidipiscis_RS04455	hypothetical protein
LAC1533_RS12145	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha	GSS_RS03230	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha	Lacidipiscis_RS04450	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha
LAC1533_RS12150	alpha-ketoacid dehydrogenase subunit beta	GSS_RS03225	alpha-ketoacid dehydrogenase subunit beta	Lacidipiscis_RS04445	alpha-ketoacid dehydrogenase subunit beta

LAC1533_RS12155	dihydrolipoamide acetyltransferase	GSS_RS03220	dihydrolipoamide acetyltransferase	Lacidipiscis_RS04440	dienelactone hydrolase
LAC1533_RS12160	dihydrolipoyl dehydrogenase	GSS_RS03215	dihydrolipoyl dehydrogenase	Lacidipiscis_RS04435	dihydrolipoyl dehydrogenase
LAC1533_RS12170	lipoate--protein ligase A	GSS_RS03210	lipoate--protein ligase A	Lacidipiscis_RS04430	lipoate--protein ligase
LAC1533_RS12175	FAD:protein FMN transferase	GSS_RS03205	FAD:protein FMN transferase	Lacidipiscis_RS04425	FAD:protein FMN transferase
LAC1533_RS12180	fructose-bisphosphatase class III	GSS_RS03200	fructose-bisphosphatase class III	Lacidipiscis_RS04420	fructose-bisphosphatase class III
LAC1533_RS12190	hypothetical protein	GSS_RS03195	hypothetical protein	Lacidipiscis_RS04415	hypothetical protein
LAC1533_RS12195	hypothetical protein	GSS_RS03190	hypothetical protein	Lacidipiscis_RS04410	hypothetical protein
LAC1533_RS12200	metal-dependent transcriptional regulator	GSS_RS03185	metal-dependent transcriptional regulator	Lacidipiscis_RS11780	metal-dependent transcriptional regulator
LAC1533_RS12205	divalent metal cation transporter	GSS_RS03180	divalent metal cation transporter	Lacidipiscis_RS11785	divalent metal cation transporter
LAC1533_RS12210	universal stress protein	GSS_RS03175	universal stress protein	Lacidipiscis_RS11790	universal stress protein
LAC1533_RS12215	hypothetical protein	GSS_RS03170	hypothetical protein	Lacidipiscis_RS02630	hypothetical protein
LAC1533_RS12220	hypothetical protein	GSS_RS03165	hypothetical protein		
LAC1533_RS12230	L-arabinose isomerase			Lacidipiscis_RS11285	L-arabinose isomerase
LAC1533_RS12235	L-ribulose-5-phosphate 4-epimerase AraD	GSS_RS03155	L-ribulose-5-phosphate 4-epimerase AraD	Lacidipiscis_RS11290	L-ribulose-5-phosphate 4-epimerase AraD
LAC1533_RS12240	ATPase	GSS_RS03150	ATPase	Lacidipiscis_RS11295	ATPase
LAC1533_RS12245	sugar porter family MFS transporter	GSS_RS03145	sugar porter family MFS transporter		
LAC1533_RS12250	GntR family transcriptional regulator	GSS_RS03140	GntR family transcriptional regulator	Lacidipiscis_RS11305	GntR family transcriptional regulator
LAC1533_RS12255	acetate kinase	GSS_RS03135	acetate kinase	Lacidipiscis_RS10965	acetate kinase
LAC1533_RS12260	membrane protein	GSS_RS03130	membrane protein	Lacidipiscis_RS10970	hypothetical protein
LAC1533_RS12265	ribonuclease P protein component	GSS_RS03125	ribonuclease P protein component	Lacidipiscis_RS10975	ribonuclease P protein component
LAC1533_RS12270	50S ribosomal protein L34	GSS_RS03120	50S ribosomal protein L34	Lacidipiscis_RS10980	50S ribosomal protein L34
pLAC1_p1	replication protein			Lacidipiscis_RS10145	replication protein
pLAC1_p2	hypothetical protein				
pLAC1_p3	hypothetical protein				
pLAC1_p4	mobilization protein				
PLAC3_P01	hypothetical protein				
PLAC3_P02	hypothetical protein				
PLAC3_P03	hypothetical protein				
PLAC3_P04	hypothetical protein				
PLAC3_P05	hypothetical protein				
PLAC3_P06	RLX protein				
PLAC3_P07	hypothetical protein				
PLAC3_P08	hypothetical protein				
PLAC3_P09	hypothetical protein			Lacidipiscis_RS13190	replication initiation protein
PLAC3_P10	hypothetical protein	GSS_RS11225	hypothetical protein	Lacidipiscis_RS13185	hypothetical protein
PLAC3_P11	nisin resistance protein (putative)				
PLAC3_P12	Type II restriction enzyme AvaI				
PLAC3_P13	Modification methylase AvaI				
PLAC3_P14	hypothetical protein				
PLAC3_P15	integrase/recombinase plasmid associated, putative				
PLAC3_P16	Retron-type RNA-directed DNA polymerase				
PLAC3_P17	hypothetical protein				
PLAC2_P01	Plasmid replication initiation protein	GSS_RS11190	replication initiation protein	Lacidipiscis_RS12825	replication initiation protein
PLAC2_P02	hypothetical protein	GSS_RS11185	hypothetical protein	Lacidipiscis_RS12820	hypothetical protein
PLAC2_P03	hypothetical protein	GSS_RS11180	hypothetical protein	Lacidipiscis_RS10955	hypothetical protein
PLAC2_P04	Mobile element protein				
PLAC2_P05	FIG00742586: hypothetical protein	GSS_RS11300	hypothetical protein	Lacidipiscis_RS12835	hypothetical protein
PLAC2_P06	replication protein			Lacidipiscis_RS02690	plasmid replication initiation protein
PLAC2_P07	hypothetical protein	GSS_RS11265	hypothetical protein		
PLAC2_P08	hypothetical protein	GSS_RS11270	hypothetical protein	Lacidipiscis_RS12090	hypothetical protein
PLAC2_P09	putative plasmid partition protein	GSS_RS11275	ParA family protein	Lacidipiscis_RS12095	ParA family protein
PLAC2_P10	Site-specific recombinase, DNA invertase Pin related protein	GSS_RS11280	recombinase family protein	Lacidipiscis_RS07005	recombinase family protein
PLAC2_P11	Mobile element protein				
PLAC2_P12	hypothetical protein				
PLAC2_P13	UPF0236 protein TTE2489				
PLAC2_P14	holin				
PLAC2_P15	Arsenate reductase			Lacidipiscis_RS09140	arsenate reductase (thioredoxin)
PLAC2_P16	transposase				
PLAC2_P17	Alpha-1,4-N-acetylgalactosamine transferase PglH				

PLAC2_P18	Alpha-1,4-N-acetylgalactosamine transferase PglH				
PLAC2_P19	transposase				
PLAC2_P20	Mobile element protein				
PLAC2_P21	hypothetical protein				
PLAC2_P22	hypothetical protein				
PLAC2_P23	Mobile element protein				
PLAC2_P24	hypothetical protein				
PLAC2_P25	Mobile element protein				
PLAC2_P26	Mobile element protein				
PLAC2_P27	Transcriptional regulator of D-allose utilization, LacI family				
PLAC2_P28	Transaldolase				
PLAC2_P29	PTS system, sorbose-specific IID component				
PLAC2_P30	PTS system, mannose-specific IIA component				
PLAC2_P31	PTS system, mannose-specific IIB component				
PLAC2_P32	Mobile element protein				
PLAC2_P33	Mobile element protein				
PLAC2_P34	putative resolvase	GSS_RS11015	recombinase family protein	Lacidipiscis_RS12395	recombinase family protein
PLAC2_P35	hypothetical protein				
PLAC2_P36	hypothetical protein				
PLAC2_P37	hypothetical protein	GSS_RS11000	hypothetical protein	Lacidipiscis_RS12140	hypothetical protein
PLAC2_P38	hypothetical protein				
PLAC2_P39	Predicted pyrophosphatase	GSS_RS10995	hypothetical protein	Lacidipiscis_RS12145	hypothetical protein
PLAC2_P40	hypothetical protein				
PLAC2_P41	hypothetical protein	GSS_RS10985	hypothetical protein	Lacidipiscis_RS12155	hypothetical protein
PLAC2_P42	Retron-type RNA-directed DNA polymerase	GSS_RS11125	RNA-directed DNA polymerase	Lacidipiscis_RS12165	maturase
PLAC2_P43	membrane protein, MmpL family	GSS_RS11135	MMPL family transporter	Lacidipiscis_RS12170	MMPL family transporter
PLAC2_P44	predicted transcriptional regulator	GSS_RS11140	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS12175	TetR/AcrR family transcriptional regulator
PLAC2_P45	hypothetical protein			Lacidipiscis_RS12875	type II toxin-antitoxin system mRNA interferase toxin, RelE/StbE family
PLAC2_P46	hypothetical protein				
PLAC2_P47	integrase/recombinase plasmid associated, putative			Lacidipiscis_RS12865	site-specific integrase
PLAC2_P48	Glyoxalase	GSS_RS11165	VOC family protein	Lacidipiscis_RS12860	VOC family protein
PLAC2_P49	Na(+)/H(+) antiporter	GSS_RS11170	cation:proton antiporter	Lacidipiscis_RS12855	cation:proton antiporter
PLAC2_P50	cation-transporting ATPase, E1-E2 family	GSS_RS11175	magnesium-transporting ATPase	Lacidipiscis_RS12850	magnesium-transporting ATPase
PLAC2_P51	hypothetical protein				
PLAC2_P52	hypothetical protein				
PLAC2_P53	hypothetical protein			Lacidipiscis_RS11435	hypothetical protein
PLAC2_P54	hypothetical protein	GSS_RS13550	plasmid mobilization relaxosome protein MobC	Lacidipiscis_RS11430	hypothetical protein
PLAC2_P55	MobA	GSS_RS13895	putative plasmid mobilization protein	Lacidipiscis_RS11425	hypothetical protein
PLAC2_P56	hypothetical protein			Lacidipiscis_RS11420	hypothetical protein
PLAC2_P57	hypothetical protein			Lacidipiscis_RS11415	hypothetical protein
PLAC2_P58	hypothetical protein	GSS_RS11115	RepB family plasmid replication initiator protein	Lacidipiscis_RS11410	replication initiation protein
PLAC2_P59	Transcriptional regulator OrfX	GSS_RS11110	hypothetical protein	Lacidipiscis_RS11400	hypothetical protein
PLAC2_P60	hypothetical protein	GSS_RS11105	hypothetical protein	Lacidipiscis_RS12815	hypothetical protein
PLAC2_P61	FIG00742765: hypothetical protein	GSS_RS11100	site-specific integrase		
PLAC2_P62	hypothetical protein	GSS_RS11095	hypothetical protein		
PLAC2_P63	hypothetical protein	GSS_RS11090	hypothetical protein		
PLAC2_P64	hypothetical protein	GSS_RS11085	hypothetical protein		
PLAC2_P65	hypothetical protein	GSS_RS11200	bacteriocin immunity protein		
PLAC2_P66	hypothetical protein				
PLAC2_P67	hypothetical protein				
PLAC2_P68	hypothetical protein				
		GSS_RS13595	reverse transcriptase	Lacidipiscis_RS02045	reverse transcriptase
		GSS_RS14265	IS256 family transposase		
		GSS_RS11720	hypothetical protein		
		GSS_RS11575	CRISPR system precrRNA processing endoribonuclease RAMP protein Cas6	Lacidipiscis_RS06570	CRISPR system precrRNA processing endoribonuclease RAMP protein Cas6
		GSS_RS13900	hypothetical protein	Lacidipiscis_RS13215	hypothetical protein
		GSS_RS11435	XRE family transcriptional regulator	Lacidipiscis_RS10140	XRE family transcriptional regulator
		GSS_RS11410	ISL3 family transposase		
		GSS_RS11385	hypothetical protein	Lacidipiscis_RS13220	hypothetical protein
		GSS_RS11355	prenyltransferase		
		GSS_RS14220	hypothetical protein		
		GSS_RS11285	hypothetical protein	Lacidipiscis_RS10950	hypothetical protein
		GSS_RS11290	replication initiation protein	Lacidipiscis_RS10945	replication initiation protein

		GSS_RS11215	site-specific DNA-methyltransferase		
		GSS_RS13375	hypothetical protein		
		GSS_RS11230	RepB family plasmid replication initiator protein		
		GSS_RS11160	hypothetical protein		
		GSS_RS13890	plasmid mobilization relaxosome protein MobC		
		GSS_RS11075	type II toxin-antitoxin system Phd/YefM family antitoxin	Lacidipiscis_RS12840	type II toxin-antitoxin system Phd/YefM family antitoxin
		GSS_RS11080	Txe/YoeB family addiction module toxin	Lacidipiscis_RS12845	Txe/YoeB family addiction module toxin
		GSS_RS13885	LysM peptidoglycan-binding domain-containing protein		
		GSS_RS11020	PRD domain-containing protein		
		GSS_RS11025	PTS beta-glucoside transporter subunit EIIBCA		
		GSS_RS11030	glycoside hydrolase family 1 protein		
		GSS_RS11035	ISL3 family transposase		
		GSS_RS10900	plasmid mobilization relaxosome protein MobC		
		GSS_RS10910	hypothetical protein		
		GSS_RS10915	NADH oxidase		
		GSS_RS10920	hypothetical protein		
		GSS_RS10930	XRE family transcriptional regulator		
		GSS_RS10935	HTH domain-containing protein	Lacidipiscis_RS12505	HTH domain-containing protein
		GSS_RS10940	type II toxin-antitoxin system PemK/MazF family toxin	Lacidipiscis_RS12500	type II toxin-antitoxin system PemK/MazF family toxin
		GSS_RS10945	hypothetical protein	Lacidipiscis_RS12495	hypothetical protein
		GSS_RS10950	hypothetical protein	Lacidipiscis_RS12490	hypothetical protein
		GSS_RS10955	XRE family transcriptional regulator	Lacidipiscis_RS12485	XRE family transcriptional regulator
		GSS_RS10965	hypothetical protein	Lacidipiscis_RS12475	hypothetical protein
		GSS_RS10970	hypothetical protein		
		GSS_RS10975	hypothetical protein		
		GSS_RS13875	tRNA lysidine(34) synthetase TilS		
		GSS_RS10280	amino acid ABC transporter substrate-binding protein		
		GSS_RS10220	glycine/betaine ABC transporter substrate-binding protein		
		GSS_RS13245	MurR/RpiR family transcriptional regulator		
		GSS_RS13855	hypothetical protein		
		GSS_RS14195	hypothetical protein		
		GSS_RS10040	hypothetical protein		
		GSS_RS09875	DUF3816 family protein	Lacidipiscis_RS11985	DUF3816 family protein
		GSS_RS13840	hypothetical protein		
		GSS_RS14180	DUF3427 domain-containing protein		
		GSS_RS14185	DUF3427 domain-containing protein		
		GSS_RS13185	NgoFVII family restriction endonuclease		
		GSS_RS09610	hypothetical protein		
		GSS_RS09490	hypothetical protein		
		GSS_RS09455	hypothetical protein	Lacidipiscis_RS09980	dithiol-disulfide isomerase
		GSS_RS09410	ammonium transporter		
		GSS_RS13825	hypothetical protein		
		GSS_RS09130	sugar ABC transporter substrate-binding protein	Lacidipiscis_RS04580	sugar ABC transporter substrate-binding protein
		GSS_RS09135	sugar ABC transporter permease	Lacidipiscis_RS04585	sugar ABC transporter permease
		GSS_RS09140	sugar ABC transporter permease	Lacidipiscis_RS04590	sugar ABC transporter permease
		GSS_RS09145	maltodextrose utilization protein MalA	Lacidipiscis_RS04595	hypothetical protein
		GSS_RS09035	hypothetical protein	Lacidipiscis_RS04490	hypothetical protein
		GSS_RS13810	hypothetical protein		
		GSS_RS13795	hypothetical protein		
		GSS_RS14170	hypothetical protein		
		GSS_RS08800	hypothetical protein		
		GSS_RS08805	hypothetical protein		
		GSS_RS08815	minor teichoic acid biosynthesis protein		
		GSS_RS08820	teichoic acid biosynthesis protein B		
		GSS_RS08825	CDP-glycerol glycerophosphotransferase family protein	Lacidipiscis_RS04645	CDP-glycerol glycerophosphotransferase family protein
		GSS_RS08830	CDP-glycerol glycerophosphotransferase	Lacidipiscis_RS04650	CDP-glycerol glycerophosphotransferase

		GSS_RS08835	ABC transporter permease	Lacidipiscis_RS04665	ABC transporter permease
		GSS_RS08755	endonuclease		
		GSS_RS08740	asparagine synthase (glutamine-hydrolyzing)	Lacidipiscis_RS04370	asparagine synthase (glutamine-hydrolyzing)
		GSS_RS14160	glycine/betaine/carnitine ABC transporter, substrate-binding lipoprotein precursor(ProX)		
		GSS_RS14165	glycine/betaine/carnitine ABC transporter, substrate-binding lipoprotein precursor(ProX)		
		GSS_RS08195	ABC transporter permease	Lacidipiscis_RS07320	ABC transporter permease
		GSS_RS13750	hypothetical protein		
		GSS_RS07085	KR domain-containing protein	Lacidipiscis_RS09280	KR domain-containing protein
		GSS_RS07025	alpha/beta hydrolase	Lacidipiscis_RS08945	alpha/beta hydrolase
		GSS_RS06965	DUF536 domain-containing protein		
		GSS_RS06970	hypothetical protein		
		GSS_RS06950	hypothetical protein		
		GSS_RS06955	hypothetical protein	Lacidipiscis_RS12405	hypothetical protein
		GSS_RS06835	hypothetical protein		
		GSS_RS12795	hypothetical protein	Lacidipiscis_RS05090	hypothetical protein
		GSS_RS06565	ferrochelatase	Lacidipiscis_RS09970	ferrochelatase
		GSS_RS06510	hypothetical protein		
		GSS_RS06465	hypothetical protein		
		GSS_RS12760	hypothetical protein		
		GSS_RS06475	ABC transporter permease		
		GSS_RS12765	LysM peptidoglycan-binding domain-containing protein		
		GSS_RS06485	hypothetical protein		
		GSS_RS14085	hypothetical protein		
		GSS_RS06495	glycerol-3-phosphate cytidylyltransferase		
		GSS_RS12770	hypothetical protein		
		GSS_RS06445	glycosyltransferase		
		GSS_RS06435	hypothetical protein		
		GSS_RS06385	hypothetical protein		
		GSS_RS06345	hypothetical protein		
		GSS_RS06160	DUF4365 domain-containing protein		
		GSS_RS06165	hypothetical protein		
		GSS_RS14065	phosphoglyceromutase		
		GSS_RS14070	teichoic acid D-Ala incorporation-associated protein DltX	Lacidipiscis_RS05325	teichoic acid D-Ala incorporation-associated protein DltX
		GSS_RS06180	hypothetical protein	Lacidipiscis_RS05330	hypothetical protein
		GSS_RS06185	hypothetical protein	Lacidipiscis_RS05335	hypothetical protein
		GSS_RS06200	gfo/Idh/MocA family oxidoreductase		
		GSS_RS06085	hypothetical protein		
		GSS_RS06090	hypothetical protein		
		GSS_RS06095	hypothetical protein		
		GSS_RS06100	primase		
		GSS_RS06105	DNA-binding protein		
		GSS_RS06110	site-specific integrase		
		GSS_RS06115	hypothetical protein		
		GSS_RS06120	DNA repair protein RadC		
		GSS_RS06125	hypothetical protein		
		GSS_RS12700	DUF1643 domain-containing protein		
		GSS_RS06140	site-specific integrase		
		GSS_RS06145	helicase		
		GSS_RS06150	hypothetical protein		
		GSS_RS05690	O-acetyl-ADP-ribose deacetylase	Lacidipiscis_RS03840	O-acetyl-ADP-ribose deacetylase
		GSS_RS05435	hypothetical protein	Lacidipiscis_RS06540	hypothetical protein
		GSS_RS05440	hypothetical protein	Lacidipiscis_RS06535	hypothetical protein
		GSS_RS05445	hypothetical protein		
		GSS_RS05400	type III-A CRISPR-associated protein Cas10/Csm1	Lacidipiscis_RS06565	type III-A CRISPR-associated protein Cas10/Csm1
		GSS_RS05405	type III-A CRISPR-associated protein Csm2	Lacidipiscis_RS06560	type III-A CRISPR-associated protein Csm2
		GSS_RS05410	type III-A CRISPR-associated RAMP protein Csm3	Lacidipiscis_RS06555	type III-A CRISPR-associated RAMP protein Csm3
		GSS_RS05415	type III-A CRISPR-associated RAMP protein Csm4	Lacidipiscis_RS06550	type III-A CRISPR-associated RAMP protein Csm4
		GSS_RS05420	type III-A CRISPR-associated RAMP protein Csm5	Lacidipiscis_RS06545	type III-A CRISPR-associated RAMP protein Csm5
		GSS_RS05385	type II CRISPR-associated endonuclease Cas1	Lacidipiscis_RS06580	type II CRISPR-associated endonuclease Cas1

		GSS_RS05390	CRISPR-associated endonuclease Cas2	Lacidipiscis_RS06575	CRISPR-associated endonuclease Cas2
		GSS_RS05375	IS30 family transposase	Lacidipiscis_RS04130	IS30 family transposase
		GSS_RS05380	IS30 family transposase		
		GSS_RS05350	cytosine permease		
		GSS_RS05355	DUF4162 domain-containing protein		
		GSS_RS05360	ABC transporter permease		
		GSS_RS05305	hypothetical protein		
		GSS_RS05310	hypothetical protein		
		GSS_RS12640	TetR/AcrR family transcriptional regulator		
		GSS_RS05320	hypothetical protein		
		GSS_RS05330	TetR/AcrR family transcriptional regulator		
		GSS_RS05335	hypothetical protein		
		GSS_RS04870	hypothetical protein		
		GSS_RS04820	2-dehydropantoate 2-reductase		
		GSS_RS04825	PTS sugar transporter subunit IIC		
		GSS_RS12580	PASTA domain-containing protein		
		GSS_RS03965	IS4 family transposase	Lacidipiscis_RS11505	IS4 family transposase
		GSS_RS03785	nucleotide pyrophosphohydrolase	Lacidipiscis_RS08730	nucleotide pyrophosphohydrolase
		GSS_RS03760	MFS transporter		
		GSS_RS03710	O-antigen ligase domain-containing protein		
		GSS_RS03715	toxin		
		GSS_RS03720	capsule biosynthesis protein CapK		
		GSS_RS12520	polysaccharide biosynthesis protein		
		GSS_RS03705	glycosyl transferase family 2		
		GSS_RS03480	type I-E CRISPR-associated protein Cse1/CasA		
		GSS_RS03485	CRISPR-associated protein Cse2		
		GSS_RS03490	type I-E CRISPR-associated protein Cas7/Cse4/CasC		
		GSS_RS03500	type I-E CRISPR-associated protein Cas6/Cse3/CasE		
		GSS_RS03505	type I-E CRISPR-associated endonuclease Cas1		
		GSS_RS03510	type I-E CRISPR-associated endoribonuclease Cas2		
		GSS_RS12490	hypothetical protein		
		GSS_RS13710	hypothetical protein		
		GSS_RS03530	transposase	Lacidipiscis_RS00560	transposase
		GSS_RS03535	IS3 family transposase	Lacidipiscis_RS00555	IS3 family transposase
		GSS_RS12470	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS01960	TetR/AcrR family transcriptional regulator
		GSS_RS13705	hypothetical protein		
		GSS_RS03450	aspartate--ammonia ligase	Lacidipiscis_RS01970	aspartate--ammonia ligase
		GSS_RS13695	hypothetical protein		
		GSS_RS14020	hypothetical protein		
		GSS_RS02625	purine permease	Lacidipiscis_RS02070	purine permease
		GSS_RS02530	NAD(P)/FAD-dependent oxidoreductase		
		GSS_RS02325	hypothetical protein		
		GSS_RS13660	hypothetical protein		
		GSS_RS02180	hypothetical protein		
		GSS_RS02150	type I restriction endonuclease subunit R		
		GSS_RS02160	type I restriction endonuclease subunit S		
		GSS_RS02170	restriction endonuclease subunit S		
		GSS_RS02045	magnesium-transporting ATPase	Lacidipiscis_RS00315	magnesium-transporting ATPase
		GSS_RS01825	OsmC family peroxiredoxin		
		GSS_RS01830	OsmC family peroxiredoxin		
		GSS_RS01835	MarR family transcriptional regulator		
		GSS_RS01840	hypothetical protein		
		GSS_RS01815	hypothetical protein		
		GSS_RS01660	hypothetical protein		
		GSS_RS01665	hypothetical protein		
		GSS_RS01530	MFS transporter	Lacidipiscis_RS01070	MFS transporter
		GSS_RS13950	permease		
		GSS_RS01580	hypothetical protein	Lacidipiscis_RS01025	hypothetical protein
		GSS_RS01590	di- and tricarboxylate transporter	Lacidipiscis_RS01010	di- and tricarboxylate transporter
		GSS_RS01430	hypothetical protein		
		GSS_RS01435	cytochrome P450		
		GSS_RS01440	transposase		
		GSS_RS01445	IS3 family transposase		
		GSS_RS12160	hypothetical protein		
		GSS_RS12140	polyribonucleotide nucleotidyltransferase	Lacidipiscis_RS02180	polyribonucleotide nucleotidyltransferase
		GSS_RS00900	hypothetical protein		
		GSS_RS00905	TM2 domain-containing protein		

		GSS_RS00910	site-specific integrase	Lacidipiscis_RS07690	site-specific integrase
		GSS_RS00625	LysM peptidoglycan-binding domain-containing protein		
		GSS_RS00630	hypothetical protein		
		GSS_RS00635	hypothetical protein		
		GSS_RS00640	hypothetical protein		
		GSS_RS00645	hypothetical protein		
		GSS_RS00655	hypothetical protein		
		GSS_RS00660	phage protein		
		GSS_RS00665	phage protein		
		GSS_RS13640	phage tail tape measure protein		
		GSS_RS00685	phage-related major tail protein		
		GSS_RS00690	hypothetical protein		
		GSS_RS00695	hypothetical protein		
		GSS_RS00700	phage head-tail joining protein		
		GSS_RS00705	DNA-packaging protein		
		GSS_RS00710	hypothetical protein		
		GSS_RS00720	HK97 family phage prohead protease		
		GSS_RS00725	phage portal protein		
		GSS_RS00730	hypothetical protein		
		GSS_RS00735	terminase large subunit		
		GSS_RS00740	terminase		
		GSS_RS00745	HNH endonuclease		
		GSS_RS00750	hypothetical protein		
		GSS_RS00755	hypothetical protein		
		GSS_RS00770	hypothetical protein		
		GSS_RS00775	hypothetical protein		
		GSS_RS00780	hypothetical protein		
		GSS_RS00785	hypothetical protein		
		GSS_RS00790	hypothetical protein		
		GSS_RS00800	RusA family crossover junction endodeoxyribonuclease		
		GSS_RS00805	hypothetical protein		
		GSS_RS00810	hypothetical protein		
		GSS_RS00815	hypothetical protein		
		GSS_RS00820	hypothetical protein		
		GSS_RS00830	ATP-dependent helicase		
		GSS_RS00835	DUF4145 domain-containing protein		
		GSS_RS00840	hypothetical protein		
		GSS_RS00845	hypothetical protein		
		GSS_RS00850	hypothetical protein		
		GSS_RS00855	hypothetical protein		
		GSS_RS00860	chromosome segregation protein SMC		
		GSS_RS00875	DUF771 domain-containing protein		
		GSS_RS00880	hypothetical protein		
		GSS_RS00885	hypothetical protein		
		GSS_RS13615	hypothetical protein		
		GSS_RS00325	carbamoyl-phosphate synthase large subunit	Lacidipiscis_RS01780	carbamoyl-phosphate synthase large subunit
		GSS_RS00340	aspartate carbamoyltransferase catalytic subunit	Lacidipiscis_RS01795	aspartate carbamoyltransferase catalytic subunit
		GSS_RS00270	noncanonical pyrimidine nucleotidase, YjjG family		
				Lacidipiscis_RS13350	hypothetical protein
				Lacidipiscis_RS13330	IS30 family transposase
				Lacidipiscis_RS13270	site-specific integrase
				Lacidipiscis_RS13175	hypothetical protein
				Lacidipiscis_RS13180	bacteriocin immunity protein
				Lacidipiscis_RS13195	hypothetical protein
				Lacidipiscis_RS13200	hypothetical protein
				Lacidipiscis_RS13205	hypothetical protein
				Lacidipiscis_RS13210	hypothetical protein
				Lacidipiscis_RS13225	site-specific integrase
				Lacidipiscis_RS13230	CPBP family intramembrane metalloprotease
				Lacidipiscis_RS13235	hypothetical protein
				Lacidipiscis_RS13240	bacteriocin immunity protein
				Lacidipiscis_RS13250	CPBP family intramembrane metalloprotease
				Lacidipiscis_RS13255	peptide cleavage/export ABC transporter
				Lacidipiscis_RS13260	bacteriocin secretion accessory protein
				Lacidipiscis_RS13070	IS1380 family transposase
				Lacidipiscis_RS13020	hypothetical protein
				Lacidipiscis_RS13025	hypothetical protein
				Lacidipiscis_RS13030	hypothetical protein
				Lacidipiscis_RS12965	XRE family transcriptional regulator
				Lacidipiscis_RS12975	LacI family transcriptional regulator

				Lacidipiscis_RS12980	MFS transporter
				Lacidipiscis_RS12985	alpha-glucosidase
				Lacidipiscis_RS12990	alpha-glucosidase
				Lacidipiscis_RS12995	sugar O-acetyltransferase
				Lacidipiscis_RS12830	hypothetical protein
				Lacidipiscis_RS12705	hypothetical protein
				Lacidipiscis_RS12710	hypothetical protein
				Lacidipiscis_RS12510	hypothetical protein
				Lacidipiscis_RS12515	helix-turn-helix domain-containing protein
				Lacidipiscis_RS12390	IS30 family transposase
				Lacidipiscis_RS12410	copper-translocating P-type ATPase
				Lacidipiscis_RS12415	copper chaperone
				Lacidipiscis_RS12420	DNA-binding protein
				Lacidipiscis_RS12430	hypothetical protein
				Lacidipiscis_RS12435	nickase
				Lacidipiscis_RS12440	hypothetical protein
				Lacidipiscis_RS12445	hypothetical protein
				Lacidipiscis_RS12450	hypothetical protein
				Lacidipiscis_RS12455	type II toxin-antitoxin system antitoxin, RelB/DinJ family
				Lacidipiscis_RS12465	hypothetical protein
				Lacidipiscis_RS12470	hypothetical protein
				Lacidipiscis_RS12330	helix-turn-helix domain-containing protein
				Lacidipiscis_RS12225	transposase
				Lacidipiscis_RS12085	transposase
				Lacidipiscis_RS12105	ABC transporter ATP-binding protein
				Lacidipiscis_RS12110	ABC transporter permease
				Lacidipiscis_RS12115	TetR/AcrR family transcriptional regulator
				Lacidipiscis_RS12120	hypothetical protein
				Lacidipiscis_RS12130	recombinase family protein
				Lacidipiscis_RS12060	APC family permease
				Lacidipiscis_RS12065	hypothetical protein
				Lacidipiscis_RS12010	hypothetical protein
				Lacidipiscis_RS12015	hypothetical protein
				Lacidipiscis_RS12020	nickase
				Lacidipiscis_RS11960	IS30 family transposase
				Lacidipiscis_RS11720	hypothetical protein
				Lacidipiscis_RS11625	hypothetical protein
				Lacidipiscis_RS11405	hypothetical protein
				Lacidipiscis_RS11320	hypothetical protein
				Lacidipiscis_RS11340	IS982-like element ISLpl4 family transposase
				Lacidipiscis_RS11260	hypothetical protein
				Lacidipiscis_RS11265	ParA family protein
				Lacidipiscis_RS11270	hypothetical protein
				Lacidipiscis_RS11275	hypothetical protein
				Lacidipiscis_RS11140	RNA 2-phosphotransferase
				Lacidipiscis_RS10935	glycine/betaine ABC transporter
				Lacidipiscis_RS10940	hypothetical protein
				Lacidipiscis_RS10190	hypothetical protein
				Lacidipiscis_RS10150	XRE family transcriptional regulator
				Lacidipiscis_RS10075	transporter
				Lacidipiscis_RS10035	reverse transcriptase
				Lacidipiscis_RS09635	hypothetical protein
				Lacidipiscis_RS09260	hypothetical protein
				Lacidipiscis_RS09115	recombinase family protein
				Lacidipiscis_RS09120	ArsR family transcriptional regulator
				Lacidipiscis_RS09125	arsenical pump-driving ATPase
				Lacidipiscis_RS09130	arsenical efflux pump membrane protein ArsB
				Lacidipiscis_RS09135	arsenical resistance operon transcriptional repressor ArsD
				Lacidipiscis_RS09145	IS256 family transposase
				Lacidipiscis_RS08905	GlsB/YeaQ/YmgE family stress response membrane protein
				Lacidipiscis_RS08845	hypothetical protein
				Lacidipiscis_RS08745	hypothetical protein
				Lacidipiscis_RS08750	ISL3 family transposase
				Lacidipiscis_RS08755	hypothetical protein
				Lacidipiscis_RS08765	hypothetical protein
				Lacidipiscis_RS08770	NADPH-dependent oxidoreductase
				Lacidipiscis_RS08780	IS6-like element IS1216 family transposase
				Lacidipiscis_RS08710	hypothetical protein
				Lacidipiscis_RS08715	ABC transporter ATP-binding protein
				Lacidipiscis_RS08675	hypothetical protein
				Lacidipiscis_RS08680	hypothetical protein

				Lacidipiscis_RS08685	hypothetical protein
				Lacidipiscis_RS08500	glycosyltransferase
				Lacidipiscis_RS08505	glycosyltransferase family 39 protein
				Lacidipiscis_RS08510	GtrA family protein
				Lacidipiscis_RS08515	DNA-binding response regulator
				Lacidipiscis_RS08535	hypothetical protein
				Lacidipiscis_RS08540	hypothetical protein
				Lacidipiscis_RS08545	hypothetical protein
				Lacidipiscis_RS08550	hypothetical protein
				Lacidipiscis_RS08495	hypothetical protein
				Lacidipiscis_RS08410	IS1380 family transposase
				Lacidipiscis_RS08420	hypothetical protein
				Lacidipiscis_RS08425	hypothetical protein
				Lacidipiscis_RS08185	GTP pyrophosphokinase
				Lacidipiscis_RS08015	transposase
				Lacidipiscis_RS08020	transposase
				Lacidipiscis_RS07945	IS30 family transposase
				Lacidipiscis_RS07920	type II CRISPR RNA-guided endonuclease Cas9
				Lacidipiscis_RS07930	CRISPR-associated endonuclease Cas2
				Lacidipiscis_RS07935	type II-A CRISPR-associated protein Csn2
				Lacidipiscis_RS07635	hypothetical protein
				Lacidipiscis_RS07575	LysM peptidoglycan-binding domain-containing protein
				Lacidipiscis_RS07580	NCS2 family permease
				Lacidipiscis_RS07525	hypothetical protein
		GSS_RS05465	hypothetical protein	Lacidipiscis_RS07190	hypothetical protein
				Lacidipiscis_RS07125	fructokinase
				Lacidipiscis_RS07130	ketose-bisphosphate aldolase
				Lacidipiscis_RS07135	fructose-bisphosphate aldolase
				Lacidipiscis_RS07140	PTS fructose transporter subunit IIC
				Lacidipiscis_RS07145	PTS fructose transporter subunit IIB
				Lacidipiscis_RS07150	PTS mannose transporter subunit IIAB
				Lacidipiscis_RS07155	transcription antiterminator
				Lacidipiscis_RS07160	oleate hydratase
				Lacidipiscis_RS07165	hypothetical protein
				Lacidipiscis_RS07170	TetR/AcrR family transcriptional regulator
				Lacidipiscis_RS07175	recombinase family protein
				Lacidipiscis_RS07025	Crp/Fnr family transcriptional regulator
				Lacidipiscis_RS07030	copper resistance protein CopZ
				Lacidipiscis_RS07035	DNA starvation/stationary phase protection protein
				Lacidipiscis_RS07040	hypothetical protein
				Lacidipiscis_RS07045	metal-sensitive transcriptional regulator
				Lacidipiscis_RS07050	thioredoxin
				Lacidipiscis_RS07055	PbsX family transcriptional regulator
				Lacidipiscis_RS07065	copper-translocating P-type ATPase
				Lacidipiscis_RS07070	IS3 family transposase
				Lacidipiscis_RS07075	transposase
				Lacidipiscis_RS07080	IS3 family transposase
				Lacidipiscis_RS07085	IS6 family transposase
				Lacidipiscis_RS07095	TetR/AcrR family transcriptional regulator
				Lacidipiscis_RS07100	ABC transporter permease
				Lacidipiscis_RS06515	PTS N-acetylglucosamine transporter subunit IIBC
				Lacidipiscis_RS06585	IS256 family transposase
				Lacidipiscis_RS06420	hypothetical protein
				Lacidipiscis_RS06425	zinc ribbon domain-containing protein
				Lacidipiscis_RS06430	zinc ribbon domain-containing protein
				Lacidipiscis_RS06435	zinc ribbon domain-containing protein
				Lacidipiscis_RS06305	hypothetical protein
				Lacidipiscis_RS06310	hypothetical protein
				Lacidipiscis_RS06185	hypothetical protein
				Lacidipiscis_RS05860	hypothetical protein
				Lacidipiscis_RS05870	hypothetical protein
				Lacidipiscis_RS05030	hypothetical protein
				Lacidipiscis_RS04875	hypothetical protein
				Lacidipiscis_RS04880	group II intron reverse transcriptase/maturase
				Lacidipiscis_RS04805	IS982 family transposase
				Lacidipiscis_RS04745	peptide ABC transporter substrate-binding protein
				Lacidipiscis_RS04675	transposase
				Lacidipiscis_RS04495	6-phospho-beta-glucosidase
				Lacidipiscis_RS04125	hypothetical protein

				Lacidipiscis_RS04070	hypothetical protein
				Lacidipiscis_RS04075	IS3 family transposase
				Lacidipiscis_RS03955	hypothetical protein
				Lacidipiscis_RS04000	dTDP-4-dehydrorhamnose reductase
				Lacidipiscis_RS04010	dTDP-4-dehydrorhamnose 3,5-epimerase
				Lacidipiscis_RS04015	glucose-1-phosphate thymidylyltransferase
				Lacidipiscis_RS04025	phosphatase PAP2 family protein
				Lacidipiscis_RS04030	6-phospho-beta-glucosidase
				Lacidipiscis_RS04035	hypothetical protein
				Lacidipiscis_RS04040	hypothetical protein
				Lacidipiscis_RS04045	PRD domain-containing protein
				Lacidipiscis_RS03560	IS982 family transposase
				Lacidipiscis_RS03305	transposase
				Lacidipiscis_RS02880	LysM peptidoglycan-binding domain-containing protein
				Lacidipiscis_RS02885	hypothetical protein
				Lacidipiscis_RS02890	hypothetical protein
				Lacidipiscis_RS02895	hypothetical protein
				Lacidipiscis_RS02900	SGNH/GDSL hydrolase family protein
				Lacidipiscis_RS02905	hypothetical protein
				Lacidipiscis_RS02910	hypothetical protein
				Lacidipiscis_RS02915	hypothetical protein
				Lacidipiscis_RS02920	hypothetical protein
				Lacidipiscis_RS02925	hypothetical protein
				Lacidipiscis_RS02930	hypothetical protein
				Lacidipiscis_RS02935	phage major tail protein, TP901-1 family
				Lacidipiscis_RS02940	hypothetical protein
				Lacidipiscis_RS02945	hypothetical protein
				Lacidipiscis_RS02950	hypothetical protein
				Lacidipiscis_RS02955	hypothetical protein
				Lacidipiscis_RS02960	phage capsid protein
				Lacidipiscis_RS02965	DNA methyltransferase
				Lacidipiscis_RS02970	hypothetical protein
				Lacidipiscis_RS02975	hypothetical protein
				Lacidipiscis_RS02980	phage portal protein
				Lacidipiscis_RS02985	terminase
				Lacidipiscis_RS02990	terminase
				Lacidipiscis_RS02995	hypothetical protein
				Lacidipiscis_RS03000	hypothetical protein
				Lacidipiscis_RS03005	hypothetical protein
				Lacidipiscis_RS03010	hypothetical protein
				Lacidipiscis_RS03015	hypothetical protein
				Lacidipiscis_RS03020	hypothetical protein
				Lacidipiscis_RS03025	DnaD domain protein
				Lacidipiscis_RS03030	hypothetical protein
				Lacidipiscis_RS03035	hypothetical protein
				Lacidipiscis_RS03040	hypothetical protein
				Lacidipiscis_RS03045	hypothetical protein
				Lacidipiscis_RS03050	hypothetical protein
				Lacidipiscis_RS03055	DNA-binding protein
				Lacidipiscis_RS03060	hypothetical protein
				Lacidipiscis_RS03065	oxidoreductase
				Lacidipiscis_RS03070	hypothetical protein
		GSS_RS00890	XRE family transcriptional regulator	Lacidipiscis_RS03075	XRE family transcriptional regulator
				Lacidipiscis_RS03080	ImmA/IrrE family metallo-endopeptidase
				Lacidipiscis_RS03085	SHOCT domain-containing protein
				Lacidipiscis_RS03090	hypothetical protein
				Lacidipiscis_RS03095	hypothetical protein
				Lacidipiscis_RS03100	hypothetical protein
				Lacidipiscis_RS03105	hypothetical protein
				Lacidipiscis_RS03110	hypothetical protein
				Lacidipiscis_RS03115	site-specific integrase
				Lacidipiscis_RS02715	gfo/Idh/MocA family oxidoreductase
				Lacidipiscis_RS02720	glucose transporter GlcU
				Lacidipiscis_RS02725	FeoB-associated Cys-rich membrane protein
				Lacidipiscis_RS02735	iron transporter FeoA
				Lacidipiscis_RS02740	thioredoxin-disulfide reductase
				Lacidipiscis_RS02745	glutathione peroxidase
				Lacidipiscis_RS02660	hypothetical protein
				Lacidipiscis_RS02670	hypothetical protein
				Lacidipiscis_RS02675	recombinase family protein

				Lacidipiscis_RS02680	hypothetical protein
				Lacidipiscis_RS02685	ParA family protein
				Lacidipiscis_RS02695	hypothetical protein
				Lacidipiscis_RS02700	toxin zeta
				Lacidipiscis_RS02560	hypothetical protein
				Lacidipiscis_RS02405	hypothetical protein
				Lacidipiscis_RS02420	IS256 family transposase
				Lacidipiscis_RS02430	glycosyltransferase family 2 protein
				Lacidipiscis_RS02435	hypothetical protein
				Lacidipiscis_RS02440	hypothetical protein
				Lacidipiscis_RS02445	LicD family protein
				Lacidipiscis_RS02470	glycosyl transferase family 2
				Lacidipiscis_RS02475	glycosyl transferase family 2
				Lacidipiscis_RS02485	L-Rha 1,3-L-rhamnosyltransferase
				Lacidipiscis_RS02490	hypothetical protein
				Lacidipiscis_RS02495	hypothetical protein
				Lacidipiscis_RS02380	hypothetical protein
				Lacidipiscis_RS02265	group II intron reverse transcriptase/maturase
				Lacidipiscis_RS02255	IS982 family transposase
				Lacidipiscis_RS02190	hypothetical protein
				Lacidipiscis_RS02025	hypothetical protein
				Lacidipiscis_RS02030	hypothetical protein
				Lacidipiscis_RS02035	hypothetical protein
				Lacidipiscis_RS02000	group II intron reverse transcriptase/maturase
				Lacidipiscis_RS01935	hypothetical protein
				Lacidipiscis_RS01940	type IA DNA topoisomerase
				Lacidipiscis_RS01945	hypothetical protein
				Lacidipiscis_RS01955	hypothetical protein
				Lacidipiscis_RS01965	hypothetical protein
				Lacidipiscis_RS01865	transposase
				Lacidipiscis_RS01875	hypothetical protein
				Lacidipiscis_RS01245	DUF3037 domain-containing protein
				Lacidipiscis_RS01250	hypothetical protein
				Lacidipiscis_RS01325	hypothetical protein
				Lacidipiscis_RS01370	hypothetical protein
				Lacidipiscis_RS01390	ATP-binding protein
				Lacidipiscis_RS01395	hypothetical protein
				Lacidipiscis_RS01400	hypothetical protein
				Lacidipiscis_RS01405	hypothetical protein
				Lacidipiscis_RS01410	phage recombination protein Bet
				Lacidipiscis_RS01420	hypothetical protein
				Lacidipiscis_RS01425	hypothetical protein
				Lacidipiscis_RS01435	hypothetical protein
				Lacidipiscis_RS01445	hypothetical protein
				Lacidipiscis_RS01450	hypothetical protein
				Lacidipiscis_RS01455	DUF3102 domain-containing protein
				Lacidipiscis_RS01460	XRE family transcriptional regulator
				Lacidipiscis_RS01465	XRE family transcriptional regulator
				Lacidipiscis_RS01205	hypothetical protein
				Lacidipiscis_RS01190	IS30 family transposase
				Lacidipiscis_RS00970	IS30 family transposase
				Lacidipiscis_RS01000	group II intron reverse transcriptase/maturase
				Lacidipiscis_RS01020	hypothetical protein
				Lacidipiscis_RS00960	reverse transcriptase
				Lacidipiscis_RS00860	reverse transcriptase
				Lacidipiscis_RS00870	N-acetyltransferase
				Lacidipiscis_RS00800	hypothetical protein
				Lacidipiscis_RS00835	ABC transporter ATP-binding protein
				Lacidipiscis_RS00550	hypothetical protein
				Lacidipiscis_RS00565	hypothetical protein
				Lacidipiscis_RS00570	hypothetical protein
				Lacidipiscis_RS00575	hypothetical protein
				Lacidipiscis_RS00580	hypothetical protein
				Lacidipiscis_RS00595	hypothetical protein
		GSS_RS13385	glycine/betaine ABC transporter	Lacidipiscis_RS00460	glycine/betaine ABC transporter
				Lacidipiscis_RS00185	type II-A CRISPR-associated protein Csn2
				Lacidipiscis_RS00190	hypothetical protein
				Lacidipiscis_RS00195	hypothetical protein
				Lacidipiscis_RS00275	hypothetical protein
				Lacidipiscis_RS00300	glycine/betaine ABC transporter
				Lacidipiscis_RS00305	hypothetical protein
				Lacidipiscis_RS00145	peptidoglycan endopeptidase
				Lacidipiscis_RS00095	hypothetical protein
				Lacidipiscis_RS00100	class I SAM-dependent DNA methyltransferase
				Lacidipiscis_RS00115	MATE family efflux transporter

Supplementary table S4B. Core-genome among the three *L. acidipiscis* strains calculated with the EDGAR software.

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^{T}**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS00005	chromosomal replication initiator protein DnaA	GSS_RS03115	chromosomal replication initiator protein DnaA	Lacidipiscis_RS10985	chromosomal replication initiator protein DnaA
LAC1533_RS00010	DNA polymerase III subunit beta	GSS_RS03110	DNA polymerase III subunit beta	Lacidipiscis_RS10990	DNA polymerase III subunit beta
LAC1533_RS00015	S4 domain-containing protein YaaA	GSS_RS03105	S4 domain-containing protein YaaA	Lacidipiscis_RS10995	S4 domain-containing protein YaaA
LAC1533_RS00020	DNA replication and repair protein RecF	GSS_RS03100	DNA replication and repair protein RecF	Lacidipiscis_RS11000	DNA replication and repair protein RecF
LAC1533_RS00025	DNA topoisomerase (ATP-hydrolyzing) subunit B	GSS_RS03095	DNA topoisomerase (ATP-hydrolyzing) subunit B	Lacidipiscis_RS11005	DNA topoisomerase (ATP-hydrolyzing) subunit B
LAC1533_RS00030	DNA gyrase subunit A	GSS_RS03090	DNA gyrase subunit A	Lacidipiscis_RS11010	DNA gyrase subunit A
LAC1533_RS00035	30S ribosomal protein S6	GSS_RS03085	30S ribosomal protein S6	Lacidipiscis_RS11015	30S ribosomal protein S6
LAC1533_RS00040	single-stranded DNA-binding protein	GSS_RS03080	single-stranded DNA-binding protein	Lacidipiscis_RS11020	single-stranded DNA-binding protein
LAC1533_RS00045	30S ribosomal protein S18	GSS_RS03075	30S ribosomal protein S18	Lacidipiscis_RS11025	30S ribosomal protein S18
LAC1533_RS00050	GntR family transcriptional regulator	GSS_RS03070	GntR family transcriptional regulator	Lacidipiscis_RS11030	GntR family transcriptional regulator
LAC1533_RS00060	PTS mannose/fructose/sorbose transporter subunit IIB	GSS_RS03060	PTS mannose/fructose/sorbose transporter subunit IIB	Lacidipiscis_RS11050	PTS mannose/fructose/sorbose transporter subunit IIB
LAC1533_RS00075	PTS fructose transporter subunit IIA	GSS_RS03045	PTS fructose transporter subunit IIA	Lacidipiscis_RS11055	hypothetical protein
LAC1533_RS00080	SIS domain-containing protein	GSS_RS03040	SIS domain-containing protein	Lacidipiscis_RS11060	SIS domain-containing protein
LAC1533_RS00090	DeoR/GlpR transcriptional regulator	GSS_RS03030	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS11070	DeoR/GlpR transcriptional regulator
LAC1533_RS00095	ABC transporter ATP-binding protein	GSS_RS03025	ABC transporter ATP-binding protein	Lacidipiscis_RS11075	ABC transporter ATP-binding protein
LAC1533_RS00105	GntR family transcriptional regulator	GSS_RS03015	GntR family transcriptional regulator	Lacidipiscis_RS11085	GntR family transcriptional regulator
LAC1533_RS00110	ABC transporter ATP-binding protein	GSS_RS03010	ABC transporter ATP-binding protein	Lacidipiscis_RS11090	ABC transporter ATP-binding protein
LAC1533_RS00115	hypothetical protein	GSS_RS03005	hypothetical protein	Lacidipiscis_RS11095	hypothetical protein
LAC1533_RS00120	DHH family phosphoesterase	GSS_RS03000	DHH family phosphoesterase	Lacidipiscis_RS11100	DHH family phosphoesterase
LAC1533_RS00125	50S ribosomal protein L9	GSS_RS02995	50S ribosomal protein L9	Lacidipiscis_RS11105	50S ribosomal protein L9
LAC1533_RS00130	replicative DNA helicase	GSS_RS02990	replicative DNA helicase	Lacidipiscis_RS11110	replicative DNA helicase
LAC1533_RS00150	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein	GSS_RS02985	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein	Lacidipiscis_RS11115	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein
LAC1533_RS00155	phosphonate ABC transporter ATP-binding protein	GSS_RS02980	phosphonate ABC transporter ATP-binding protein	Lacidipiscis_RS11120	phosphonate ABC transporter ATP-binding protein
LAC1533_RS00160	phosphonate ABC transporter, permease protein PhnE	GSS_RS02975	phosphonate ABC transporter, permease protein PhnE	Lacidipiscis_RS11125	phosphonate ABC transporter, permease protein PhnE
LAC1533_RS00165	phosphonate ABC transporter, permease protein PhnE	GSS_RS02970	phosphonate ABC transporter, permease protein PhnE	Lacidipiscis_RS11130	phosphonate ABC transporter, permease protein PhnE
LAC1533_RS00170	bifunctional metallophosphatase/5-nucleotidase	GSS_RS02965	bifunctional metallophosphatase/5-nucleotidase	Lacidipiscis_RS11135	bifunctional metallophosphatase/5-nucleotidase
LAC1533_RS00185	DUF4867 domain-containing protein	GSS_RS02960	DUF4867 domain-containing protein	Lacidipiscis_RS11145	DUF4867 domain-containing protein
LAC1533_RS00190	tagatose-6-phosphate kinase	GSS_RS02955	tagatose-6-phosphate kinase	Lacidipiscis_RS11150	tagatose-6-phosphate kinase
LAC1533_RS00195	PTS sugar transporter subunit IIA	GSS_RS02950	PTS sugar transporter subunit IIA	Lacidipiscis_RS11155	PTS sugar transporter subunit IIA
LAC1533_RS00200	PTS fructose transporter subunit IIB	GSS_RS02945	PTS fructose transporter subunit IIB	Lacidipiscis_RS11160	PTS fructose transporter subunit IIB
LAC1533_RS00205	PTS glucitol transporter subunit IIA	GSS_RS02940	PTS glucitol transporter subunit IIA	Lacidipiscis_RS11165	PTS glucitol transporter subunit IIA
LAC1533_RS00210	hypothetical protein	GSS_RS02935	hypothetical protein	Lacidipiscis_RS11170	hypothetical protein
LAC1533_RS00215	DeoR/GlpR transcriptional regulator	GSS_RS02930	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS11175	DeoR/GlpR transcriptional regulator
LAC1533_RS00220	galactose-6-phosphate isomerase subunit LacA	GSS_RS02925	galactose-6-phosphate isomerase subunit LacA	Lacidipiscis_RS11180	galactose-6-phosphate isomerase subunit LacA
LAC1533_RS00225	galactose-6-phosphate isomerase subunit LacB	GSS_RS02920	galactose-6-phosphate isomerase subunit LacB	Lacidipiscis_RS11185	galactose-6-phosphate isomerase subunit LacB
LAC1533_RS00230	tagatose-bisphosphate aldolase	GSS_RS02915	tagatose-bisphosphate aldolase	Lacidipiscis_RS11190	tagatose-bisphosphate aldolase
LAC1533_RS00300 IDENTICAL PARALOGS LAC1533_RS09250	IS30 family transposase	GSS_RS11500	IS30 family transposase	Lacidipiscis_RS04130	IS30 family transposase
LAC1533_RS00330	butanediol dehydrogenase	GSS_RS02865	butanediol dehydrogenase	Lacidipiscis_RS02750	butanediol dehydrogenase
LAC1533_RS00335	LysR family transcriptional regulator	GSS_RS02860	LysR family transcriptional regulator	Lacidipiscis_RS02755	LysR family transcriptional regulator
LAC1533_RS00340	class II fumarate hydratase	GSS_RS02855	class II fumarate hydratase	Lacidipiscis_RS02760	class II fumarate hydratase
LAC1533_RS00345	flavocytochrome c	GSS_RS02850	flavocytochrome c	Lacidipiscis_RS02765	flavocytochrome c
LAC1533_RS00350	anion permease	GSS_RS02845	anion permease	Lacidipiscis_RS02770	anion permease
LAC1533_RS00360	FAD-binding protein	GSS_RS02835	FAD-binding protein	Lacidipiscis_RS02780	FAD-binding protein
LAC1533_RS00365	SDR family NAD(P)-dependent oxidoreductase	GSS_RS02830	SDR family NAD(P)-dependent oxidoreductase	Lacidipiscis_RS02785	SDR family NAD(P)-dependent oxidoreductase
LAC1533_RS00370	FAD-binding protein	GSS_RS02825	FAD-binding protein	Lacidipiscis_RS02790	FAD-binding protein
LAC1533_RS00390	aldo/keto reductase	GSS_RS02805	aldo/keto reductase	Lacidipiscis_RS02800	aldo/keto reductase
LAC1533_RS00395	NAD(P)-dependent oxidoreductase	GSS_RS02800	NAD(P)-dependent oxidoreductase	Lacidipiscis_RS02805	NAD(P)-dependent oxidoreductase
LAC1533_RS00400	L-lactate oxidase	GSS_RS02795	L-lactate oxidase	Lacidipiscis_RS02810	L-lactate oxidase
LAC1533_RS00410	LacI family DNA-binding transcriptional regulator	GSS_RS02785	LacI family DNA-binding transcriptional regulator	Lacidipiscis_RS02820	LacI family DNA-binding transcriptional regulator
LAC1533_RS00415	FAD-binding protein	GSS_RS02780	FAD-binding protein	Lacidipiscis_RS02825	FAD-binding protein
LAC1533_RS00420	FAD-binding protein	GSS_RS02775	FAD-binding protein	Lacidipiscis_RS02830	FAD-binding protein
LAC1533_RS00425	hypothetical protein	GSS_RS02770	hypothetical protein	Lacidipiscis_RS02835	hypothetical protein
LAC1533_RS00430	FAD-binding protein	GSS_RS02765	FAD-binding protein	Lacidipiscis_RS02840	FAD-binding protein
LAC1533_RS00495 IDENTICAL PARALOGS LAC1533_RS05535 IDENTICAL PARALOGS LAC1533_RS06750	IS30 family transposase	GSS_RS11395	IS30 family transposase	Lacidipiscis_RS08455	IS30 family transposase
LAC1533_RS00560	AEC family transporter	GSS_RS02670	AEC family transporter	Lacidipiscis_RS02850	AEC family transporter
LAC1533_RS00565	hypothetical protein	GSS_RS02665	hypothetical protein	Lacidipiscis_RS02855	hypothetical protein
LAC1533_RS00570	adenylosuccinate synthase	GSS_RS02660	adenylosuccinate synthase	Lacidipiscis_RS02860	adenylosuccinate synthase
LAC1533_RS00585	ISL3 family transposase	GSS_RS02655	ISL3 family transposase	Lacidipiscis_RS02050	ISL3 family transposase
LAC1533_RS00590	formate C-acetyltransferase	GSS_RS02645	formate C-acetyltransferase	Lacidipiscis_RS02055	formate C-acetyltransferase

LAC1533_RS00595	pyruvate formate lyase-activating protein	GSS_RS02640	pyruvate formate lyase-activating protein	Lacidipiscis_RS02060	pyruvate formate lyase-activating protein
LAC1533_RS00605 IDENTICAL PARALOGS LAC1533_RS01135 IDENTICAL PARALOGS LAC1533_RS02865 IDENTICAL PARALOGS LAC1533_RS03470 IDENTICAL PARALOGS LAC1533_RS03575 IDENTICAL PARALOGS LAC1533_RS08020	ISL3 family transposase	GSS_RS11420	ISL3 family transposase	Lacidipiscis_RS03185	ISL3 family transposase
LAC1533_RS00610	zinc-binding alcohol dehydrogenase family protein	GSS_RS02630	zinc-binding alcohol dehydrogenase family protein	Lacidipiscis_RS02065	zinc-binding alcohol dehydrogenase family protein
LAC1533_RS00640	2-hydroxyacid dehydrogenase	GSS_RS02600	2-hydroxyacid dehydrogenase	Lacidipiscis_RS07565	hydroxyacid dehydrogenase
LAC1533_RS00645	hypothetical protein	GSS_RS02595	hypothetical protein	Lacidipiscis_RS07570	hypothetical protein
LAC1533_RS00650 IDENTICAL PARALOGS LAC1533_RS09450 IDENTICAL PARALOGS LAC1533_RS12185	IS982 family transposase ISLpl4	GSS_RS11510	IS982 family transposase ISLpl4	Lacidipiscis_RS05750	IS982 family transposase ISLpl4
LAC1533_RS00655	adenine deaminase	GSS_RS12385	adenine deaminase	Lacidipiscis_RS07585	adenine deaminase
LAC1533_RS00665	metal ABC transporter substrate-binding protein	GSS_RS02585	metal ABC transporter substrate-binding protein	Lacidipiscis_RS07590	metal ABC transporter substrate-binding protein
LAC1533_RS00670	30S ribosomal protein S14	GSS_RS02580	30S ribosomal protein S14	Lacidipiscis_RS07595	30S ribosomal protein S14
LAC1533_RS00675	cysteine synthase family protein	GSS_RS02575	cysteine synthase family protein	Lacidipiscis_RS11450	hypothetical protein
LAC1533_RS00680	PLP-dependent transferase	GSS_RS02570	PLP-dependent transferase	Lacidipiscis_RS11455	PLP-dependent transferase
LAC1533_RS00685	serine acetyltransferase	GSS_RS02565	serine acetyltransferase	Lacidipiscis_RS11460	serine acetyltransferase
LAC1533_RS00690	acyl-CoA thioesterase	GSS_RS02560	acyl-CoA thioesterase	Lacidipiscis_RS11465	acyl-CoA thioesterase
LAC1533_RS00695	threonine/serine exporter	GSS_RS02555	threonine/serine exporter	Lacidipiscis_RS11470	threonine/serine exporter
LAC1533_RS00700	threonine/serine exporter	GSS_RS02550	threonine/serine exporter	Lacidipiscis_RS11475	threonine/serine exporter
LAC1533_RS00705	NupC/NupG family nucleoside CNT transporter	GSS_RS02545	nucleoside transporter	Lacidipiscis_RS11480	nucleoside permease
LAC1533_RS00710	NCS2 family permease	GSS_RS02540	NCS2 family permease	Lacidipiscis_RS11485	NCS2 family permease
LAC1533_RS00715	EAL domain-containing protein	GSS_RS12380	EAL domain-containing protein	Lacidipiscis_RS11490	hypothetical protein
LAC1533_RS00725	hypothetical protein	GSS_RS02525	hypothetical protein	Lacidipiscis_RS11495	hypothetical protein
LAC1533_RS00750	peptide ABC transporter substrate-binding protein	GSS_RS02510	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS12325	peptide ABC transporter substrate-binding protein
LAC1533_RS00755	peroxide stress protein YaaA	GSS_RS02505	peroxide stress protein YaaA	Lacidipiscis_RS12320	peroxide stress protein YaaA
LAC1533_RS00760	hypothetical protein	GSS_RS02495	hypothetical protein	Lacidipiscis_RS12315	hypothetical protein
LAC1533_RS00770	NADPH:quinone reductase	GSS_RS02485	NADPH:quinone reductase	Lacidipiscis_RS12305	NADPH:quinone reductase
LAC1533_RS00775	YitT family protein	GSS_RS02480	YitT family protein	Lacidipiscis_RS12300	YitT family protein
LAC1533_RS00780	APC family permease	GSS_RS02475	APC family permease	Lacidipiscis_RS12295	APC family permease
LAC1533_RS00785	ornithine decarboxylase	GSS_RS02470	ornithine decarboxylase	Lacidipiscis_RS12290	ornithine decarboxylase
LAC1533_RS00790	hypothetical protein	GSS_RS13990	hypothetical protein	Lacidipiscis_RS12285	hypothetical protein
LAC1533_RS00795	hypothetical protein	GSS_RS13670	hypothetical protein	Lacidipiscis_RS12280	hypothetical protein
LAC1533_RS00800	DUF2992 domain-containing protein	GSS_RS02455	DUF2992 domain-containing protein	Lacidipiscis_RS12275	DUF2992 domain-containing protein
LAC1533_RS00840	TetR/AcrR family transcriptional regulator	GSS_RS02430	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS00720	TetR/AcrR family transcriptional regulator
LAC1533_RS00845	ABC transporter permease	GSS_RS02425	ABC transporter permease	Lacidipiscis_RS00725	ABC transporter permease
LAC1533_RS00850	ABC transporter ATP-binding protein	GSS_RS02420	ABC transporter ATP-binding protein	Lacidipiscis_RS07105	ABC transporter ATP-binding protein
LAC1533_RS00855	dihydroxyacetone kinase subunit DhaK	GSS_RS02415	dihydroxyacetone kinase subunit DhaK	Lacidipiscis_RS00735	dihydroxyacetone kinase subunit DhaK
LAC1533_RS00865	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM	GSS_RS02405	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM	Lacidipiscis_RS00745	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM
LAC1533_RS00870	glycerol kinase	GSS_RS02400	glycerol kinase	Lacidipiscis_RS00750	glycerol kinase
LAC1533_RS00875	type 1 glycerol-3-phosphate oxidase	GSS_RS02395	type 1 glycerol-3-phosphate oxidase	Lacidipiscis_RS00755	type 1 glycerol-3-phosphate oxidase
LAC1533_RS00880	aquaporin family protein	GSS_RS02390	aquaporin family protein	Lacidipiscis_RS00760	aquaporin family protein
LAC1533_RS00885	GntR family transcriptional regulator	GSS_RS02385	GntR family transcriptional regulator	Lacidipiscis_RS00765	GntR family transcriptional regulator
LAC1533_RS00890	PTS sugar transporter subunit IIC	GSS_RS02380	PTS sugar transporter subunit IIC	Lacidipiscis_RS00770	PTS sugar transporter subunit IIC
LAC1533_RS00895	DUF3284 domain-containing protein	GSS_RS02375	DUF3284 domain-containing protein	Lacidipiscis_RS00775	DUF3284 domain-containing protein
LAC1533_RS00915	hypothetical protein	GSS_RS13980	hypothetical protein	Lacidipiscis_RS00790	PTS sugar transporter subunit IIB
LAC1533_RS00920	GNAT family N-acetyltransferase	GSS_RS13665	GNAT family N-acetyltransferase	Lacidipiscis_RS00795	GNAT family N-acetyltransferase
LAC1533_RS00940	DUF3290 domain-containing protein	GSS_RS02345	DUF3290 domain-containing protein	Lacidipiscis_RS00805	DUF3290 domain-containing protein
LAC1533_RS00945	DUF421 domain-containing protein	GSS_RS02340	DUF421 domain-containing protein	Lacidipiscis_RS00715	DUF421 domain-containing protein
LAC1533_RS00950	hypothetical protein	GSS_RS12335	cytidyltransferase-like domain-containing protein	Lacidipiscis_RS09390	hypothetical protein
LAC1533_RS00955	LysR family transcriptional regulator	GSS_RS13655	LysR family transcriptional regulator	Lacidipiscis_RS09385	LysR family transcriptional regulator
LAC1533_RS00960	glycerol kinase	GSS_RS02320	glycerol kinase	Lacidipiscis_RS09380	glycerol kinase
LAC1533_RS00965	glycerol-3-phosphate dehydrogenase/oxidase	GSS_RS02315	glycerol-3-phosphate dehydrogenase/oxidase	Lacidipiscis_RS09375	glycerol-3-phosphate dehydrogenase/oxidase
LAC1533_RS00970	hypothetical protein	GSS_RS12325	hypothetical protein	Lacidipiscis_RS09370	hypothetical protein
LAC1533_RS00990	glutamate ABC transporter substrate-binding protein	GSS_RS02290	glutamate ABC transporter substrate-binding protein	Lacidipiscis_RS00875	glutamate ABC transporter substrate-binding protein
LAC1533_RS00995	amino acid ABC transporter permease	GSS_RS02285	amino acid ABC transporter permease	Lacidipiscis_RS00880	amino acid ABC transporter permease
LAC1533_RS01000	aspartate aminotransferase	GSS_RS02280	aspartate aminotransferase	Lacidipiscis_RS00885	aspartate aminotransferase
LAC1533_RS01005	lactate dehydrogenase	GSS_RS02275	lactate dehydrogenase	Lacidipiscis_RS00890	lactate dehydrogenase
LAC1533_RS01010	ZIP family metal transporter	GSS_RS02270	ZIP family metal transporter	Lacidipiscis_RS00895	ZIP family metal transporter
LAC1533_RS01020	histidine phosphatase family protein	GSS_RS02260	histidine phosphatase family protein	Lacidipiscis_RS00905	histidine phosphatase family protein
LAC1533_RS01025	N-acetyltransferase	GSS_RS02255	N-acetyltransferase	Lacidipiscis_RS00910	N-acetyltransferase

LAC1533_RS01030	glycosyltransferase family 8 protein	GSS_RS02250	glycosyltransferase family 8 protein	Lacidipiscis_RS00915	glycosyltransferase family 8 protein
LAC1533_RS01040	hypothetical protein	GSS_RS02240	hypothetical protein	Lacidipiscis_RS00925	hypothetical protein
LAC1533_RS01045	hypothetical protein	GSS_RS02235	membrane protein	Lacidipiscis_RS00930	hypothetical protein
LAC1533_RS01050	pyridoxal kinase	GSS_RS02230	pyridoxal kinase	Lacidipiscis_RS00935	pyridoxal kinase
LAC1533_RS01055	DNA-binding response regulator	GSS_RS02225	DNA-binding response regulator	Lacidipiscis_RS00940	DNA-binding response regulator
LAC1533_RS01060	cell wall metabolism sensor histidine kinase WalK	GSS_RS02220	cell wall metabolism sensor histidine kinase WalK	Lacidipiscis_RS00945	cell wall metabolism sensor histidine kinase WalK
LAC1533_RS01065	hypothetical protein	GSS_RS02215	hypothetical protein	Lacidipiscis_RS00950	hypothetical protein
LAC1533_RS01070	hypothetical protein	GSS_RS02210	hypothetical protein	Lacidipiscis_RS00955	hypothetical protein
LAC1533_RS01075	DUF1634 domain-containing protein	GSS_RS02205	DUF1634 domain-containing protein	Lacidipiscis_RS06485	DUF1634 domain-containing protein
LAC1533_RS01080	sulfite exporter TauE/SafE family protein	GSS_RS02200	sulfite exporter TauE/SafE family protein	Lacidipiscis_RS06490	sulfite exporter TauE/SafE family protein
LAC1533_RS01085	MBL fold metallo-hydrolase	GSS_RS02195	MBL fold metallo-hydrolase	Lacidipiscis_RS06495	MBL fold metallo-hydrolase
LAC1533_RS01090	PDZ domain-containing protein	GSS_RS02190	PDZ domain-containing protein	Lacidipiscis_RS12675	PDZ domain-containing protein
LAC1533_RS01095 IDENTICAL PARALOGS LAC1533_RS01980 IDENTICAL PARALOGS LAC1533_RS08320 IDENTICAL PARALOGS LAC1533_RS10275 IDENTICAL PARALOGS LAC1533_RS11335	IS30 family transposase	GSS_RS11460	IS30 family transposase	Lacidipiscis_RS11325 IDENTICAL PARALOGS Lacidipiscis_RS08300	IS30 family transposase
LAC1533_RS01100	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	GSS_RS02185	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	Lacidipiscis_RS08660	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH
LAC1533_RS01145	DUF1516 domain-containing protein	GSS_RS02145	DUF1516 domain-containing protein	Lacidipiscis_RS08665	DUF1516 domain-containing protein
LAC1533_RS01160	membrane protein	GSS_RS02130	membrane protein	Lacidipiscis_RS00200	hypothetical protein
LAC1533_RS01165	ClC family H(+)/Cl(-) exchange transporter	GSS_RS02125	ClC family H(+)/Cl(-) exchange transporter	Lacidipiscis_RS00205	ClC family H(+)/Cl(-) exchange transporter
LAC1533_RS01170	ATPase	GSS_RS02120	MoxR-like ATPase	Lacidipiscis_RS00210	ATPase
LAC1533_RS01175	hypothetical protein	GSS_RS02115	hypothetical protein	Lacidipiscis_RS00215	hypothetical protein
LAC1533_RS01180	hypothetical protein	GSS_RS02110	hypothetical protein	Lacidipiscis_RS00220	hypothetical protein
LAC1533_RS01185	hypothetical protein	GSS_RS02105	hypothetical protein	Lacidipiscis_RS00225	hypothetical protein
LAC1533_RS01190	NADPH-dependent oxidoreductase	GSS_RS02100	NADPH-dependent oxidoreductase	Lacidipiscis_RS00230	NADPH-dependent oxidoreductase
LAC1533_RS01195	hypothetical protein	GSS_RS02095	hypothetical protein	Lacidipiscis_RS00235	hypothetical protein
LAC1533_RS01210	MFS transporter	GSS_RS02080	MFS transporter	Lacidipiscis_RS00255	MFS transporter
LAC1533_RS01215	50S ribosomal protein L4	GSS_RS13970	50S ribosomal protein L4	Lacidipiscis_RS00250	50S ribosomal protein L4
LAC1533_RS01230	amino acid permease	GSS_RS02075	amino acid permease	Lacidipiscis_RS00260	amino acid permease
LAC1533_RS01235	aspartate aminotransferase family protein	GSS_RS02070	aspartate aminotransferase family protein	Lacidipiscis_RS00265	4-aminobutyrate aminotransferase
LAC1533_RS01240	hypothetical protein	GSS_RS02065	hypothetical protein	Lacidipiscis_RS00280	hypothetical protein
LAC1533_RS01245	ABC transporter substrate-binding protein	GSS_RS02060	inosine-uridine nucleoside N-ribohydrolase	Lacidipiscis_RS00285	ABC transporter substrate-binding protein
LAC1533_RS01250	glycine betaine/L-proline ABC transporter ATP-binding protein	GSS_RS02055	glycine betaine/L-proline ABC transporter ATP-binding protein	Lacidipiscis_RS00290	glycine betaine/L-proline ABC transporter ATP-binding protein
LAC1533_RS01255 IDENTICAL PARALOGS LAC1533_RS11550	glycine/betaine ABC transporter	GSS_RS13385	glycine/betaine ABC transporter	Lacidipiscis_RS00295	glycine/betaine ABC transporter
LAC1533_RS01260 IDENTICAL PARALOGS LAC1533_RS11545	glycine/betaine ABC transporter	GSS_RS11315	glycine/betaine ABC transporter	Lacidipiscis_RS00465	glycine/betaine ABC transporter
LAC1533_RS01270	glycosyltransferase family 1 protein	GSS_RS02050	glycosyltransferase family 1 protein	Lacidipiscis_RS00310	glycosyltransferase family 1 protein
LAC1533_RS01290	magnesium transporter CorA family protein	GSS_RS02040	magnesium transporter CorA family protein	Lacidipiscis_RS00320	magnesium transporter CorA family protein
LAC1533_RS01295	Cof-type HAD-IIB family hydrolase	GSS_RS02035	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS00325	Cof-type HAD-IIB family hydrolase
LAC1533_RS01300	flavoprotein	GSS_RS02030	flavoprotein	Lacidipiscis_RS00330	NADPH-dependent FMN reductase
LAC1533_RS01370	DUF1648 domain-containing protein	GSS_RS01970	DUF1648 domain-containing protein	Lacidipiscis_RS00350	DUF1648 domain-containing protein
LAC1533_RS01375	YhgE/Pip domain-containing protein	GSS_RS01965	YhgE/Pip domain-containing protein	Lacidipiscis_RS00355	YhgE/Pip domain-containing protein
LAC1533_RS01380	PAP2 family protein	GSS_RS01955	PAP2 family protein	Lacidipiscis_RS00360	PAP2 family protein
LAC1533_RS01385	patatin family protein	GSS_RS01950	patatin family protein	Lacidipiscis_RS00365	patatin family protein
LAC1533_RS01395	hypothetical protein	GSS_RS01940	hypothetical protein	Lacidipiscis_RS00375	hypothetical protein
LAC1533_RS01400	LysM domain-containing protein	GSS_RS01930	LysM domain-containing protein	Lacidipiscis_RS00380	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS01405	aspartate kinase	GSS_RS01925	aspartate kinase	Lacidipiscis_RS00385	aspartate kinase
LAC1533_RS01410	phosphatidylglycerophosphatase A	GSS_RS01920	phosphatidylglycerophosphatase A	Lacidipiscis_RS00390	phosphatidylglycerophosphatase A
LAC1533_RS01415	hydrolase	GSS_RS01915	hydrolase	Lacidipiscis_RS00395	hydrolase
LAC1533_RS01420	L-lactate dehydrogenase	GSS_RS01910	L-lactate dehydrogenase	Lacidipiscis_RS00400	L-lactate dehydrogenase
LAC1533_RS01425	branched-chain amino acid aminotransferase	GSS_RS01905	branched-chain amino acid aminotransferase	Lacidipiscis_RS00405	branched-chain amino acid aminotransferase
LAC1533_RS01430	resolvase	GSS_RS12285	resolvase	Lacidipiscis_RS00410	resolvase
LAC1533_RS01440	alpha-glucosidase	GSS_RS01890	alpha-glucosidase	Lacidipiscis_RS00420	alpha-glucosidase
LAC1533_RS01445	PTS sugar transporter subunit IIC	GSS_RS01885	PTS sugar transporter subunit IIC	Lacidipiscis_RS00425	PTS sugar transporter subunit IIC
LAC1533_RS01450	sugar O-acetyltransferase	GSS_RS01880	sugar O-acetyltransferase	Lacidipiscis_RS00430	sugar O-acetyltransferase
LAC1533_RS01455	N-acetyltransferase	GSS_RS01875	N-acetyltransferase	Lacidipiscis_RS00435	N-acetyltransferase
LAC1533_RS01470	hypothetical protein	GSS_RS01870	hypothetical protein	Lacidipiscis_RS07705	hypothetical protein
LAC1533_RS01475	hypothetical protein	GSS_RS01865	hypothetical protein	Lacidipiscis_RS07710	hypothetical protein
LAC1533_RS01480	ATPase	GSS_RS01860	ATPase	Lacidipiscis_RS07715	ATPase
LAC1533_RS01485	DUF3862 domain-containing protein	GSS_RS01855	DUF3862 domain-containing protein	Lacidipiscis_RS07720	DUF3862 domain-containing protein
LAC1533_RS01540	hypothetical protein	GSS_RS01810	hypothetical protein	Lacidipiscis_RS07770	hypothetical protein

LAC1533_RS01550	flavocytochrome c	GSS_RS01800	flavocytochrome c	Lacidipiscis_RS07780	flavocytochrome c
LAC1533_RS01555	dipeptide epimerase	GSS_RS01795	dipeptide epimerase	Lacidipiscis_RS07785	dipeptide epimerase
LAC1533_RS01570	oleate hydratase	GSS_RS01785	oleate hydratase	Lacidipiscis_RS07795	oleate hydratase
LAC1533_RS01585	hypothetical protein	GSS_RS01770	hypothetical protein	Lacidipiscis_RS07810	hypothetical protein
LAC1533_RS01590	NUDIX domain-containing protein	GSS_RS01765	NUDIX domain-containing protein	Lacidipiscis_RS07815	NUDIX domain-containing protein
LAC1533_RS01595	MFS transporter	GSS_RS01760	MFS transporter	Lacidipiscis_RS07820	MFS transporter
LAC1533_RS01600	phosphoglycolate phosphatase	GSS_RS01755	phosphoglycolate phosphatase	Lacidipiscis_RS07825	HAD family hydrolase
LAC1533_RS01605	NADP-specific glutamate dehydrogenase	GSS_RS01750	NADP-specific glutamate dehydrogenase	Lacidipiscis_RS07830	NADP-specific glutamate dehydrogenase
LAC1533_RS01610	NADP oxidoreductase	GSS_RS12250	NADP oxidoreductase	Lacidipiscis_RS08855	NADP oxidoreductase
LAC1533_RS01615	LLM class flavin-dependent oxidoreductase	GSS_RS01740	LLM class flavin-dependent oxidoreductase	Lacidipiscis_RS08860	LLM class flavin-dependent oxidoreductase
LAC1533_RS01630	2-hydroxyacid dehydrogenase	GSS_RS01735	2-hydroxyacid dehydrogenase	Lacidipiscis_RS08865	hydroxyacid dehydrogenase
LAC1533_RS01635	Hsp20/alpha crystallin family protein	GSS_RS01730	Hsp20/alpha crystallin family protein	Lacidipiscis_RS08870	Hsp20/alpha crystallin family protein
LAC1533_RS01640	GNAT family N-acetyltransferase	GSS_RS01725	GNAT family N-acetyltransferase	Lacidipiscis_RS08875	GNAT family N-acetyltransferase
LAC1533_RS01645	hypothetical protein	GSS_RS01720	hypothetical protein	Lacidipiscis_RS08880	hypothetical protein
LAC1533_RS01650	hypothetical protein	GSS_RS01715	hypothetical protein	Lacidipiscis_RS08885	hypothetical protein
LAC1533_RS01665	hypothetical protein	GSS_RS01700	hypothetical protein	Lacidipiscis_RS04820	hypothetical protein
LAC1533_RS01670	malate permease	GSS_RS01695	malate permease	Lacidipiscis_RS04825	hypothetical protein
LAC1533_RS01675	malate permease	GSS_RS01690	malate permease	Lacidipiscis_RS04830	hypothetical protein
LAC1533_RS01680	hypothetical protein	GSS_RS01685	hypothetical protein	Lacidipiscis_RS04835	hypothetical protein
LAC1533_RS01745	aldehyde dehydrogenase	GSS_RS12240	aldehyde dehydrogenase	Lacidipiscis_RS12635	aldehyde dehydrogenase
LAC1533_RS01750	MarR family transcriptional regulator	GSS_RS12235	MarR family transcriptional regulator	Lacidipiscis_RS12640	MarR family transcriptional regulator
LAC1533_RS01755	ABC transporter ATP-binding protein	GSS_RS01625	ABC transporter ATP-binding protein	Lacidipiscis_RS12645	ABC transporter ATP-binding protein
LAC1533_RS01760	ABC transporter ATP-binding protein	GSS_RS01620	ABC transporter ATP-binding protein	Lacidipiscis_RS12650	ABC transporter ATP-binding protein
LAC1533_RS01765	hypothetical protein	GSS_RS01615	hypothetical protein	Lacidipiscis_RS12655	hypothetical protein
LAC1533_RS01780	hypothetical protein	GSS_RS01605	MarR family transcriptional regulator	Lacidipiscis_RS00980	MarR family transcriptional regulator
LAC1533_RS01790	CsbD family protein	GSS_RS01595	CsbD family protein	Lacidipiscis_RS01005	CsbD family protein
LAC1533_RS01815	membrane protein	GSS_RS01575	membrane protein	Lacidipiscis_RS01030	membrane protein
LAC1533_RS01820	fructosamine kinase	GSS_RS01565	fructosamine-3-kinase	Lacidipiscis_RS01035	fructosamine kinase
LAC1533_RS01825	AI-2E family transporter	GSS_RS12220	AI-2E family transporter	Lacidipiscis_RS01040	AI-2E family transporter
LAC1533_RS01830	SDR family NAD(P)-dependent oxidoreductase	GSS_RS01555	SDR family NAD(P)-dependent oxidoreductase	Lacidipiscis_RS01045	SDR family NAD(P)-dependent oxidoreductase
LAC1533_RS01835	TrkA family potassium uptake protein	GSS_RS01550	TrkA family potassium uptake protein	Lacidipiscis_RS01050	TrkA family potassium uptake protein
LAC1533_RS01840	Trk family potassium uptake protein	GSS_RS01545	Trk family potassium uptake protein	Lacidipiscis_RS01055	ATP synthase subunit J
LAC1533_RS01845	DeoR/GlpR transcriptional regulator	GSS_RS01540	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS01060	DeoR/GlpR transcriptional regulator
LAC1533_RS01850	DUF159 family protein	GSS_RS01535	DUF159 family protein	Lacidipiscis_RS01065	DUF159 family protein
LAC1533_RS01865	peptide-methionine (R)-S-oxide reductase	GSS_RS01525	peptide-methionine (R)-S-oxide reductase	Lacidipiscis_RS01075	peptide-methionine (R)-S-oxide reductase
LAC1533_RS01870	GntR family transcriptional regulator	GSS_RS01520	GntR family transcriptional regulator	Lacidipiscis_RS01080	GntR family transcriptional regulator
LAC1533_RS01875	ABC transporter ATP-binding protein	GSS_RS01515	ABC transporter ATP-binding protein	Lacidipiscis_RS01085	ABC transporter ATP-binding protein
LAC1533_RS01880	hypothetical protein	GSS_RS01510	hypothetical protein	Lacidipiscis_RS01090	hypothetical protein
LAC1533_RS01885	BMP family ABC transporter substrate-binding protein	GSS_RS01505	BMP family ABC transporter substrate-binding protein	Lacidipiscis_RS01095	BMP family ABC transporter substrate-binding protein
LAC1533_RS01890	ABC transporter ATP-binding protein	GSS_RS12215	ABC transporter ATP-binding protein	Lacidipiscis_RS01100	ABC transporter ATP-binding protein
LAC1533_RS01895	ABC transporter permease	GSS_RS12210	ABC transporter permease	Lacidipiscis_RS01105	ABC transporter permease
LAC1533_RS01900	ABC transporter permease	GSS_RS01490	ABC transporter permease	Lacidipiscis_RS01110	ABC transporter permease
LAC1533_RS01915	TPM domain-containing protein	GSS_RS01480	TPM domain-containing protein	Lacidipiscis_RS01120	TPM domain-containing protein
LAC1533_RS01920	demethylmenaquinone methyltransferase	GSS_RS01475	demethylmenaquinone methyltransferase	Lacidipiscis_RS01125	demethylmenaquinone methyltransferase
LAC1533_RS01925	antibiotic biosynthesis monooxygenase	GSS_RS01470	antibiotic biosynthesis monooxygenase	Lacidipiscis_RS01130	antibiotic biosynthesis monooxygenase
LAC1533_RS01930	hypothetical protein	GSS_RS01465	hypothetical protein	Lacidipiscis_RS01135	hypothetical protein
LAC1533_RS01935	CPBP family intramembrane metalloprotease	GSS_RS01460	CPBP family intramembrane metalloprotease	Lacidipiscis_RS01140	CPBP family intramembrane metalloprotease
LAC1533_RS01945	DUF4811 domain-containing protein	GSS_RS01450	DUF4811 domain-containing protein	Lacidipiscis_RS01150	DUF4811 domain-containing protein
LAC1533_RS01955	DNA polymerase III subunit alpha	GSS_RS08945	DNA polymerase III subunit alpha	Lacidipiscis_RS01155	DNA polymerase III subunit alpha
LAC1533_RS01960	LD-carboxypeptidase	GSS_RS08950	LD-carboxypeptidase	Lacidipiscis_RS01160	LD-carboxypeptidase
LAC1533_RS01970	D-aminopeptidase	GSS_RS08960	D-aminopeptidase	Lacidipiscis_RS06205	aminopeptidase
LAC1533_RS01975	glycerophosphoryl diester phosphodiesterase	GSS_RS08965	glycerophosphoryl diester phosphodiesterase	Lacidipiscis_RS06210	glycerophosphodiester phosphodiesterase
LAC1533_RS02015 IDENTICAL PARALOGS LAC1533_RS08415 IDENTICAL PARALOGS LAC1533_RS11370	hypothetical protein	GSS_RS05465	hypothetical protein	Lacidipiscis_RS02640	hypothetical protein
LAC1533_RS02020	L-lactate oxidase	GSS_RS08970	L-lactate oxidase	Lacidipiscis_RS03935	L-lactate oxidase

LAC1533_RS02025	formate-nitrite transporter	GSS_RS08975	formate/nitrite transporter	Lacidipiscis_RS03940	formate/nitrite transporter
LAC1533_RS02030	hypothetical protein	GSS_RS13065	permease domain-containing protein	Lacidipiscis_RS03945	hypothetical protein
LAC1533_RS02040	NAD(P)-dependent alcohol dehydrogenase	GSS_RS08995	NAD(P)-dependent alcohol dehydrogenase	Lacidipiscis_RS05830	NAD(P)-dependent alcohol dehydrogenase
LAC1533_RS02050	hypothetical protein	GSS_RS13805	hypothetical protein	Lacidipiscis_RS05825	hypothetical protein
LAC1533_RS02055	PRD domain-containing protein	GSS_RS13815	PRD domain-containing protein	Lacidipiscis_RS05820	PRD domain-containing protein
LAC1533_RS02060	PTS fructose IIA component	GSS_RS09005	PTS fructose IIA component	Lacidipiscis_RS04465	PTS fructose IIA subunit
LAC1533_RS02065	PTS mannose/fructose/sorbose transporter subunit IIB	GSS_RS09010	PTS mannose/fructose/sorbose transporter subunit IIB	Lacidipiscis_RS04470	PTS mannose/fructose/sorbose transporter subunit IIB
LAC1533_RS02070	PTS sugar transporter subunit IIC	GSS_RS09015	PTS sugar transporter subunit IIC	Lacidipiscis_RS04475	PTS sugar transporter subunit IIC
LAC1533_RS02080	alpha-glucosidase	GSS_RS09025	alpha-glucosidase	Lacidipiscis_RS04485	alpha-glucosidase
LAC1533_RS02110	hypothetical protein	GSS_RS09040	hypothetical protein	Lacidipiscis_RS04500	hypothetical protein
LAC1533_RS02115	hypothetical protein	GSS_RS09045	hypothetical protein	Lacidipiscis_RS04505	hypothetical protein
LAC1533_RS02120	Arc family DNA-binding protein	GSS_RS09050	Arc family DNA-binding protein	Lacidipiscis_RS04510	Arc family DNA-binding protein
LAC1533_RS02125	SPFH domain-containing protein	GSS_RS13085	SPFH domain-containing protein	Lacidipiscis_RS04515	SPFH domain-containing protein
LAC1533_RS02135	hypothetical protein	GSS_RS09070	hypothetical protein	Lacidipiscis_RS04525	hypothetical protein
LAC1533_RS02140	cation-translocating P-type ATPase	GSS_RS09075	cation-translocating P-type ATPase	Lacidipiscis_RS04530	cation-translocating P-type ATPase
LAC1533_RS02145	NADH peroxidase	GSS_RS09080	NADH peroxidase	Lacidipiscis_RS04535	NAD(FAD)-dependent dehydrogenase
LAC1533_RS02150	N-acetyltransferase	GSS_RS09085	N-acetyltransferase	Lacidipiscis_RS04540	N-acetyltransferase
LAC1533_RS02155	hypothetical protein	GSS_RS09090	hypothetical protein	Lacidipiscis_RS04545	hypothetical protein
LAC1533_RS02160	Na+/H+ antiporter NhaC	GSS_RS09095	Na+/H+ antiporter NhaC	Lacidipiscis_RS04550	Na+/H+ antiporter NhaC
LAC1533_RS02170	beta-phosphoglucomutase	GSS_RS09110	beta-phosphoglucomutase	Lacidipiscis_RS04560	beta-phosphoglucomutase
LAC1533_RS02175	LacI family transcriptional regulator	GSS_RS09115	LacI family transcriptional regulator	Lacidipiscis_RS04565	LacI family transcriptional regulator
LAC1533_RS02185	alpha-glucosidase	GSS_RS09120	alpha-glucosidase	Lacidipiscis_RS04570	alpha-glucosidase
LAC1533_RS02190	alpha-glycosidase	GSS_RS09125	alpha-glycosidase	Lacidipiscis_RS04575	alpha-glycosidase
LAC1533_RS02215	ABC transporter ATP-binding protein	GSS_RS09150	ABC transporter ATP-binding protein	Lacidipiscis_RS04600	ABC transporter ATP-binding protein
LAC1533_RS02225	DJ-1 family protein	GSS_RS09155	DJ-1 family protein	Lacidipiscis_RS04605	DJ-1 family protein
LAC1533_RS02230	hypothetical protein	GSS_RS09160	hypothetical protein	Lacidipiscis_RS04610	hypothetical protein
LAC1533_RS02245	DegV family protein	GSS_RS09165	DegV family protein	Lacidipiscis_RS11685	DegV family protein
LAC1533_RS02250	dipeptidase	GSS_RS09170	dipeptidase	Lacidipiscis_RS11680	dipeptidase
LAC1533_RS02255	NAD(P)H-hydrate epimerase	GSS_RS09175	NAD(P)H-hydrate epimerase	Lacidipiscis_RS04385	NAD(P)H-hydrate epimerase
LAC1533_RS02260	ArsR family transcriptional regulator	GSS_RS09180	ArsR family transcriptional regulator	Lacidipiscis_RS04390	ArsR family transcriptional regulator
LAC1533_RS02265	cation transporter	GSS_RS09185	cation transporter	Lacidipiscis_RS04395	cation transporter
LAC1533_RS02270	hypothetical protein	GSS_RS13820	short-chain dehydrogenase/reductase SDR	Lacidipiscis_RS04400	short-chain dehydrogenase/reductase SDR
LAC1533_RS02275	hypothetical protein	GSS_RS13105	hypothetical protein	Lacidipiscis_RS04180	hypothetical protein
LAC1533_RS02280	alpha/beta hydrolase	GSS_RS09200	alpha/beta hydrolase	Lacidipiscis_RS04185	alpha/beta hydrolase
LAC1533_RS02295	hypothetical protein	GSS_RS14175	hypothetical protein	Lacidipiscis_RS04200	hypothetical protein
LAC1533_RS02300	PTS glucose transporter subunit IIBC	GSS_RS13120	PTS glucose transporter subunit IIBC	Lacidipiscis_RS04205	PTS glucose transporter subunit IIBC
LAC1533_RS02305	hypothetical protein	GSS_RS09235	hypothetical protein	Lacidipiscis_RS04210	hypothetical protein
LAC1533_RS02315	MFS transporter	GSS_RS09245	MFS transporter	Lacidipiscis_RS04220	MFS transporter
LAC1533_RS02320	copper-translocating P-type ATPase	GSS_RS09250	copper-translocating P-type ATPase	Lacidipiscis_RS04225	copper-translocating P-type ATPase
LAC1533_RS02325	glutamate formiminotransferase	GSS_RS09255	glutamate formiminotransferase	Lacidipiscis_RS04230	glutamate formiminotransferase
LAC1533_RS02330	bifunctional 5,10-methylenetetrahydrofolate dehydrogenase/5,10-methenyltetrahydrofolate cyclohydrolase	GSS_RS09260	bifunctional 5,10-methylenetetrahydrofolate dehydrogenase/5,10-methenyltetrahydrofolate cyclohydrolase	Lacidipiscis_RS04235	bifunctional 5,10-methylenetetrahydrofolate dehydrogenase/5,10-methenyltetrahydrofolate cyclohydrolase
LAC1533_RS02335	zinc-binding alcohol dehydrogenase family protein	GSS_RS09265	zinc-binding alcohol dehydrogenase family protein	Lacidipiscis_RS04240	zinc-binding alcohol dehydrogenase family protein
LAC1533_RS02340	o-succinylbenzoate--CoA ligase	GSS_RS09270	o-succinylbenzoate--CoA ligase	Lacidipiscis_RS04245	o-succinylbenzoate--CoA ligase
LAC1533_RS02345	1,4-dihydroxy-2-naphthoyl-CoA synthase	GSS_RS09275	1,4-dihydroxy-2-naphthoyl-CoA synthase	Lacidipiscis_RS04250	1,4-dihydroxy-2-naphthoyl-CoA synthase
LAC1533_RS02350	PaaI family thioesterase	GSS_RS09280	PaaI family thioesterase	Lacidipiscis_RS04255	PaaI family thioesterase
LAC1533_RS02355	replication-associated recombination protein A	GSS_RS09290	replication-associated recombination protein A	Lacidipiscis_RS04260	replication-associated recombination protein A
LAC1533_RS02360	Hsp20/alpha crystallin family protein	GSS_RS09295	Hsp20/alpha crystallin family protein	Lacidipiscis_RS04265	Hsp20/alpha crystallin family protein
LAC1533_RS02365	AarF/ABC1/UbiB kinase family protein	GSS_RS09300	AarF/ABC1/UbiB kinase family protein	Lacidipiscis_RS04270	AarF/ABC1/UbiB kinase family protein
LAC1533_RS02370	peptide ABC transporter substrate-binding protein	GSS_RS09305	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS04275	peptide ABC transporter substrate-binding protein
LAC1533_RS02385	carbonic anhydrase	GSS_RS09320	carbonic anhydrase	Lacidipiscis_RS04135	carbonic anhydrase
LAC1533_RS02390	sigma-54-dependent transcriptional regulator	GSS_RS09325	sigma-54-dependent transcriptional regulator	Lacidipiscis_RS04140	sigma-54-dependent transcriptional regulator
LAC1533_RS02395	PTS fructose transporter subunit IIB	GSS_RS09330	PTS fructose transporter subunit IIB	Lacidipiscis_RS04145	PTS fructose transporter subunit IIB
LAC1533_RS02400	PTS mannose transporter subunit IIAB	GSS_RS09335	PTS mannose transporter subunit IIAB	Lacidipiscis_RS04150	PTS mannose transporter subunit IIAB
LAC1533_RS02405	PTS mannose/fructose/sorbose transporter subunit IIC	GSS_RS09340	PTS mannose/fructose/sorbose transporter subunit IIC	Lacidipiscis_RS04155	PTS mannose/fructose/sorbose transporter subunit IIC
LAC1533_RS02410	PTS mannose family transporter subunit IID	GSS_RS09345	PTS mannose transporter subunit IID	Lacidipiscis_RS04160	PTS mannose transporter subunit IID
LAC1533_RS02415	DUF956 domain-containing protein	GSS_RS09350	DUF956 domain-containing protein	Lacidipiscis_RS04165	DUF956 domain-containing protein
LAC1533_RS02440	neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	GSS_RS05675	Neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	Lacidipiscis_RS07000	neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase
LAC1533_RS02455	LysM peptidoglycan-binding domain-containing protein	GSS_RS05680	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS00140	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS02465	uracil-DNA glycosylase	GSS_RS05685	uracil-DNA glycosylase	Lacidipiscis_RS03845	uracil-DNA glycosylase
LAC1533_RS02475	folate family ECF transporter S component	GSS_RS05695	folate family ECF transporter S component	Lacidipiscis_RS03835	folate family ECF transporter S component
LAC1533_RS02480	metal ABC transporter permease	GSS_RS05700	metal ABC transporter permease	Lacidipiscis_RS03830	metal ABC transporter permease
LAC1533_RS02485	ABC transporter ATP-binding protein	GSS_RS05705	ABC transporter ATP-binding protein	Lacidipiscis_RS03825	ABC transporter ATP-binding protein
LAC1533_RS02490	QueT transporter family protein	GSS_RS05710	QueT transporter family protein	Lacidipiscis_RS03820	QueT transporter family protein

LAC1533_RS02495	DUF2829 domain-containing protein	GSS_RS05715	DUF2829 domain-containing protein	Lacidipiscis_RS03815	DUF2829 domain-containing protein
LAC1533_RS02500	3-oxoacyl-ACP reductase	GSS_RS05720	3-oxoacyl-ACP reductase	Lacidipiscis_RS03810	3-oxoacyl-ACP reductase
LAC1533_RS02505	HD domain-containing protein	GSS_RS05725	HD domain-containing protein	Lacidipiscis_RS03805	HD domain-containing protein
LAC1533_RS02510	lipase/esterase	GSS_RS05730	lipase/esterase	Lacidipiscis_RS03800	lipase
LAC1533_RS02515	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	GSS_RS05735	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	Lacidipiscis_RS03795	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG
LAC1533_RS02520	nucleoid occlusion protein	GSS_RS05740	nucleoid occlusion protein	Lacidipiscis_RS03790	nucleoid occlusion protein
LAC1533_RS02525	ParA family protein	GSS_RS05745	ParA family protein	Lacidipiscis_RS03785	ParA family protein
LAC1533_RS02530	chromosome partitioning protein ParB	GSS_RS05750	chromosome partitioning protein ParB	Lacidipiscis_RS03780	chromosome partitioning protein ParB
LAC1533_RS02535	DUF951 domain-containing protein	GSS_RS14060	DUF951 domain-containing protein	Lacidipiscis_RS03775	DUF951 domain-containing protein
LAC1533_RS02540	redox-regulated ATPase YchF	GSS_RS05760	redox-regulated ATPase YchF	Lacidipiscis_RS03770	redox-regulated ATPase YchF
LAC1533_RS02545	DUF1129 domain-containing protein	GSS_RS05765	DUF1129 domain-containing protein	Lacidipiscis_RS03765	DUF1129 domain-containing protein
LAC1533_RS02550	Cof-type HAD-IIB family hydrolase	GSS_RS05770	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS03760	Cof-type HAD-IIB family hydrolase
LAC1533_RS02560	excinuclease ABC subunit UvrA	GSS_RS05780	excinuclease ABC subunit UvrA	Lacidipiscis_RS03750	excinuclease ABC subunit UvrA
LAC1533_RS02570	histidine phosphatase family protein	GSS_RS05795	histidine phosphatase family protein	Lacidipiscis_RS03740	histidine phosphatase family protein
LAC1533_RS02575	histidine phosphatase family protein	GSS_RS05800	histidine phosphatase family protein	Lacidipiscis_RS03735	histidine phosphatase family protein
LAC1533_RS02580	MFS transporter	GSS_RS05805	MFS transporter	Lacidipiscis_RS03730	MFS transporter
LAC1533_RS02585	glutamate 5-kinase	GSS_RS12675	glutamate 5-kinase	Lacidipiscis_RS03725	glutamate 5-kinase
LAC1533_RS02590	glutamate-5-semialdehyde dehydrogenase	GSS_RS05815	glutamate-5-semialdehyde dehydrogenase	Lacidipiscis_RS03720	glutamate-5-semialdehyde dehydrogenase
LAC1533_RS02600	aldo/keto reductase	GSS_RS05825	aldo/keto reductase	Lacidipiscis_RS01675	aldo/keto reductase
LAC1533_RS02605	endonuclease III	GSS_RS05830	hypothetical protein	Lacidipiscis_RS01670	endonuclease III
LAC1533_RS02610	ribose-phosphate pyrophosphokinase	GSS_RS05835	ribose-phosphate pyrophosphokinase	Lacidipiscis_RS01665	ribose-phosphate pyrophosphokinase
LAC1533_RS02615	aminopeptidase	GSS_RS05840	aminopeptidase	Lacidipiscis_RS01660	aminopeptidase
LAC1533_RS02630	adenosine deaminase	GSS_RS05845	adenosine deaminase	Lacidipiscis_RS01655	adenosine deaminase
LAC1533_RS02635	hypothetical protein	GSS_RS05850	hypothetical protein	Lacidipiscis_RS01650	hypothetical protein
LAC1533_RS02640	cation-translocating P-type ATPase	GSS_RS05855	cation-translocating P-type ATPase	Lacidipiscis_RS01645	cation-translocating P-type ATPase
LAC1533_RS02645	ABC transporter ATP-binding protein	GSS_RS05865	ABC transporter ATP-binding protein	Lacidipiscis_RS01640	ABC transporter ATP-binding protein
LAC1533_RS02660	class I SAM-dependent methyltransferase	GSS_RS05885	class I SAM-dependent methyltransferase	Lacidipiscis_RS01625	class I SAM-dependent methyltransferase
LAC1533_RS02665	hypothetical protein	GSS_RS05890	hypothetical protein	Lacidipiscis_RS01620	hypothetical protein
LAC1533_RS02670	MurR/RpiR family transcriptional regulator	GSS_RS05895	MurR/RpiR family transcriptional regulator	Lacidipiscis_RS01615	MurR/RpiR family transcriptional regulator
LAC1533_RS02675	N-acetylmuramic acid 6-phosphate etherase	GSS_RS05900	N-acetylmuramic acid 6-phosphate etherase	Lacidipiscis_RS01610	N-acetylmuramic acid 6-phosphate etherase
LAC1533_RS02680	PTS beta-glucoside transporter subunit EIIBCA	GSS_RS05905	PTS beta-glucoside transporter subunit EIIBCA	Lacidipiscis_RS01605	PTS glucose transporter
LAC1533_RS02685	methionine ABC transporter ATP-binding protein	GSS_RS05910	methionine ABC transporter ATP-binding protein	Lacidipiscis_RS01600	methionine ABC transporter ATP-binding protein
LAC1533_RS02690	ABC transporter permease	GSS_RS05915	ABC transporter permease	Lacidipiscis_RS01595	ABC transporter permease
LAC1533_RS02700	HlyC/CorC family transporter	GSS_RS05930	HlyC/CorC family transporter	Lacidipiscis_RS01585	HlyC/CorC family transporter
LAC1533_RS02705	protein-tyrosine-phosphatase	GSS_RS05935	protein-tyrosine-phosphatase	Lacidipiscis_RS01580	protein-tyrosine-phosphatase
LAC1533_RS02710	methylated-DNA--[protein]-cysteine S-methyltransferase	GSS_RS05940	methylated-DNA--[protein]-cysteine S-methyltransferase	Lacidipiscis_RS01575	methylated-DNA--[protein]-cysteine S-methyltransferase
LAC1533_RS02715	undecaprenyl-diphosphate phosphatase	GSS_RS05945	undecaprenyl-diphosphate phosphatase	Lacidipiscis_RS01570	undecaprenyl-diphosphate phosphatase
LAC1533_RS02720	phosphopyruvate hydratase	GSS_RS05950	phosphopyruvate hydratase	Lacidipiscis_RS01565	phosphopyruvate hydratase
LAC1533_RS02730	alpha-galactosidase	GSS_RS05955	alpha-galactosidase	Lacidipiscis_RS10520	alpha-galactosidase
LAC1533_RS02735	hypothetical protein	GSS_RS05960	hypothetical protein	Lacidipiscis_RS10515	hypothetical protein
LAC1533_RS02740	hypothetical protein	GSS_RS05965	hypothetical protein	Lacidipiscis_RS10510	hypothetical protein
LAC1533_RS02745	threonine/serine exporter	GSS_RS05970	threonine/serine exporter	Lacidipiscis_RS10505	threonine/serine exporter
LAC1533_RS02750	threonine/serine exporter	GSS_RS05975	threonine/serine exporter	Lacidipiscis_RS10500	threonine/serine exporter
LAC1533_RS02760	glutamyl-tRNA amidotransferase subunit A	GSS_RS05985	glutamyl-tRNA amidotransferase subunit A	Lacidipiscis_RS10490	glutamyl-tRNA amidotransferase
LAC1533_RS02765	nucleoside-diphosphate kinase	GSS_RS05990	nucleoside-diphosphate kinase	Lacidipiscis_RS10485	nucleoside-diphosphate kinase
LAC1533_RS02775	(deoxy)nucleoside triphosphate pyrophosphohydrolase	GSS_RS05995	(deoxy)nucleoside triphosphate pyrophosphohydrolase	Lacidipiscis_RS10480	(deoxy)nucleoside triphosphate pyrophosphohydrolase
LAC1533_RS02780	DUF3427 domain-containing protein	GSS_RS06000	DUF3427 domain-containing protein	Lacidipiscis_RS10475	DUF3427 domain-containing protein
LAC1533_RS02785	IMP dehydrogenase	GSS_RS06005	IMP dehydrogenase	Lacidipiscis_RS10470	IMP dehydrogenase
LAC1533_RS02790	large-conductance mechanosensitive channel protein MscL	GSS_RS06010	large-conductance mechanosensitive channel protein MscL	Lacidipiscis_RS10465	large-conductance mechanosensitive channel protein MscL
LAC1533_RS02800	nitroreductase	GSS_RS06015	nitroreductase	Lacidipiscis_RS10460	nitroreductase
LAC1533_RS02805	LysM domain-containing protein	GSS_RS06020	LysM domain-containing protein	Lacidipiscis_RS10455	LysM domain-containing protein
LAC1533_RS02810	glyoxalase	GSS_RS06025	glyoxalase	Lacidipiscis_RS10450	glyoxalase
LAC1533_RS02815	hypothetical protein	GSS_RS06030	hypothetical protein	Lacidipiscis_RS10445	hypothetical protein
LAC1533_RS02820	UDP-glucose 4-epimerase GalE	GSS_RS06035	UDP-glucose 4-epimerase GalE	Lacidipiscis_RS10440	UDP-glucose 4-epimerase GalE
LAC1533_RS02825	hypothetical protein	GSS_RS06040	hypothetical protein	Lacidipiscis_RS10435	hypothetical protein
LAC1533_RS02830	hypothetical protein	GSS_RS06045	hypothetical protein	Lacidipiscis_RS10430	hypothetical protein
LAC1533_RS02835	galactose mutarotase	GSS_RS06050	galactose mutarotase	Lacidipiscis_RS10425	galactose mutarotase
LAC1533_RS02840	HAD family hydrolase	GSS_RS06055	HAD family hydrolase	Lacidipiscis_RS03205	HAD family hydrolase
LAC1533_RS02845	AI-2E family transporter	GSS_RS06060	AI-2E family transporter	Lacidipiscis_RS03200	AI-2E family transporter
LAC1533_RS02850	pyridoxal phosphate-dependent aminotransferase	GSS_RS06065	pyridoxal phosphate-dependent aminotransferase	Lacidipiscis_RS03195	pyridoxal phosphate-dependent aminotransferase
LAC1533_RS02855	2,3-diphosphoglycerate-dependent phosphoglycerate mutase	GSS_RS06070	2,3-diphosphoglycerate-dependent phosphoglycerate mutase	Lacidipiscis_RS03190	2,3-diphosphoglycerate-dependent phosphoglycerate mutase
LAC1533_RS02870	hypothetical protein	GSS_RS12705	hypothetical protein	Lacidipiscis_RS05340	hypothetical protein
LAC1533_RS02885	DNA starvation/stationary phase protection protein	GSS_RS06205	DNA starvation/stationary phase protection protein	Lacidipiscis_RS05355	DNA starvation/stationary phase protection protein
LAC1533_RS02900	Crp/Fnr family transcriptional regulator	GSS_RS06220	Crp/Fnr family transcriptional regulator	Lacidipiscis_RS05370	Crp/Fnr family transcriptional regulator
LAC1533_RS02905	copper chaperone	GSS_RS06225	copper chaperone	Lacidipiscis_RS05375	copper chaperone
LAC1533_RS02910	DNA starvation/stationary phase protection protein	GSS_RS06230	DNA starvation/stationary phase protection protein	Lacidipiscis_RS05380	DNA starvation/stationary phase protection protein
LAC1533_RS02915	metal-sensitive transcriptional regulator	GSS_RS06240	metal-sensitive transcriptional regulator	Lacidipiscis_RS05385	metal-sensitive transcriptional regulator

LAC1533_RS02920	thioredoxin	GSS_RS06245	thioredoxin	Lacidipiscis_RS05390	thioredoxin
LAC1533_RS02925	aquaporin family protein	GSS_RS06250	aquaporin family protein	Lacidipiscis_RS05395	aquaporin family protein
LAC1533_RS02940	hypothetical protein	GSS_RS14075	hypothetical protein	Lacidipiscis_RS05405	hypothetical protein
LAC1533_RS02945	hypothetical protein	GSS_RS06265	hypothetical protein	Lacidipiscis_RS05410	hypothetical protein
LAC1533_RS02955	MarR family transcriptional regulator	GSS_RS06280	MarR family transcriptional regulator	Lacidipiscis_RS05415	MarR family transcriptional regulator
LAC1533_RS02985	tRNA-dihydrouridine synthase	GSS_RS06305	tRNA-dihydrouridine synthase	Lacidipiscis_RS05435	tRNA-dihydrouridine synthase
LAC1533_RS02990	hypothetical protein	GSS_RS06310	hypothetical protein	Lacidipiscis_RS05440	hypothetical protein
LAC1533_RS02995	succinyl-diaminopimelate desuccinylase	GSS_RS06315	succinyl-diaminopimelate desuccinylase	Lacidipiscis_RS05445	succinyl-diaminopimelate desuccinylase
LAC1533_RS03000	DUF554 domain-containing protein	GSS_RS06320	DUF554 domain-containing protein	Lacidipiscis_RS05450	DUF554 domain-containing protein
LAC1533_RS03005	flavodoxin family protein	GSS_RS06325	flavodoxin family protein	Lacidipiscis_RS05455	flavodoxin family protein
LAC1533_RS03010	DUF4767 domain-containing protein	GSS_RS12740	DUF4767 domain-containing protein	Lacidipiscis_RS05460	DUF4767 domain-containing protein
LAC1533_RS03015	hypothetical protein	GSS_RS06335	hypothetical protein	Lacidipiscis_RS05465	hypothetical protein
LAC1533_RS03020	hypothetical protein	GSS_RS06340	hypothetical protein	Lacidipiscis_RS05470	hypothetical protein
LAC1533_RS03025	RluA family pseudouridine synthase	GSS_RS06350	RluA family pseudouridine synthase	Lacidipiscis_RS05475	RluA family pseudouridine synthase
LAC1533_RS03030	DUF3114 domain-containing protein	GSS_RS12745	DUF3114 domain-containing protein	Lacidipiscis_RS05480	DUF3114 domain-containing protein
LAC1533_RS03035	hypothetical protein	GSS_RS06360	hypothetical protein	Lacidipiscis_RS05485	hypothetical protein
LAC1533_RS03040	OsmC family peroxiredoxin	GSS_RS06365	OsmC family peroxiredoxin	Lacidipiscis_RS05490	OsmC family peroxiredoxin
LAC1533_RS03045	YitT family protein	GSS_RS06370	YitT family protein	Lacidipiscis_RS05495	YitT family protein
LAC1533_RS03050	phosphoketolase family protein	GSS_RS06375	phosphoketolase family protein	Lacidipiscis_RS05500	phosphoketolase family protein
LAC1533_RS03055	hypothetical protein	GSS_RS06380	hypothetical protein	Lacidipiscis_RS05505	hypothetical protein
LAC1533_RS03060	NERD domain-containing protein	GSS_RS06390	NERD domain-containing protein	Lacidipiscis_RS05510	NERD domain-containing protein
LAC1533_RS03065	RNA methylase	GSS_RS06395	RNA methylase	Lacidipiscis_RS05515	RNA methylase
LAC1533_RS03070	YfcC family protein	GSS_RS06400	YfcC family protein	Lacidipiscis_RS05520	YfcC family protein
LAC1533_RS03075	acetylornithine deacetylase	GSS_RS06405	acetylornithine deacetylase	Lacidipiscis_RS05525	acetylornithine deacetylase
LAC1533_RS03080	LemA family protein	GSS_RS06415	LemA family protein	Lacidipiscis_RS05530	LemA family protein
LAC1533_RS03085	heat-shock protein HtpX	GSS_RS06420	heat-shock protein HtpX	Lacidipiscis_RS05535	heat-shock protein HtpX
LAC1533_RS03105	DUF871 domain-containing protein	GSS_RS09780	DUF871 domain-containing protein	Lacidipiscis_RS00850	DUF871 domain-containing protein
LAC1533_RS03110	deoxyribonuclease	GSS_RS09785	deoxyribonuclease	Lacidipiscis_RS00845	deoxyribonuclease
LAC1533_RS03120	TetR/AcrR family transcriptional regulator	GSS_RS13830	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS00840	TetR/AcrR family transcriptional regulator
LAC1533_RS03130	ABC transporter ATP-binding protein	GSS_RS09805	ABC transporter ATP-binding protein	Lacidipiscis_RS00830	ABC transporter ATP-binding protein
LAC1533_RS03135	hypothetical protein	GSS_RS13835	hypothetical protein	Lacidipiscis_RS00825	hypothetical protein
LAC1533_RS03140	glycosyltransferase family 8 protein	GSS_RS09825	glycosyltransferase family 8 protein	Lacidipiscis_RS09505	glycosyltransferase family 8 protein
LAC1533_RS03145	deoxyribose-phosphate aldolase	GSS_RS13210	deoxyribose-phosphate aldolase	Lacidipiscis_RS09500	deoxyribose-phosphate aldolase
LAC1533_RS03160	IS982 family transposase	GSS_RS11505	transposase	Lacidipiscis_RS05855	IS982 family transposase
LAC1533_RS03195	hypothetical protein	GSS_RS09855	hypothetical protein	Lacidipiscis_RS00010	hypothetical protein
LAC1533_RS03200	NADH-dependent alcohol dehydrogenase	GSS_RS09865	NADH-dependent alcohol dehydrogenase	Lacidipiscis_RS00005	NADH-dependent alcohol dehydrogenase
LAC1533_RS03205	HAD family phosphatase	GSS_RS09870	HAD family phosphatase	Lacidipiscis_RS11990	HAD family phosphatase
LAC1533_RS03220	energy-coupling factor transporter transmembrane protein EcfT	GSS_RS09885	energy-coupling factor transporter transmembrane protein EcfT	Lacidipiscis_RS11975	energy-coupling factor transporter transmembrane protein EcfT
LAC1533_RS03225	LysM peptidoglycan-binding domain-containing protein	GSS_RS09890	LysM domain-containing protein	Lacidipiscis_RS11970	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS03230	tRNA epoxyqueuosine(34) reductase QueG	GSS_RS09895	tRNA epoxyqueuosine(34) reductase QueG	Lacidipiscis_RS13315	tRNA epoxyqueuosine(34) reductase QueG
LAC1533_RS03235	DUF4430 domain-containing protein	GSS_RS09900	DUF4430 domain-containing protein	Lacidipiscis_RS13310	DUF4430 domain-containing protein
LAC1533_RS03240	deoxynucleoside kinase	GSS_RS09905	deoxyadenosine kinase	Lacidipiscis_RS13305	deoxyadenosine kinase
LAC1533_RS03245	DUF1440 domain-containing protein	GSS_RS09910	DUF1440 domain-containing protein	Lacidipiscis_RS13300	DUF1440 domain-containing protein
LAC1533_RS03250	MFS transporter	GSS_RS09915	sodium:solute symporter	Lacidipiscis_RS13295	sodium:solute symporter
LAC1533_RS03255	linear amide C-N hydrolase	GSS_RS09920	linear amide C-N hydrolase	Lacidipiscis_RS13290	linear amide C-N hydrolase
LAC1533_RS03295	cytochrome ubiquinol oxidase subunit I	GSS_RS09935	cytochrome ubiquinol oxidase subunit I	Lacidipiscis_RS04955	cytochrome ubiquinol oxidase subunit I
LAC1533_RS03300	cytochrome d ubiquinol oxidase subunit II	GSS_RS09940	cytochrome d ubiquinol oxidase subunit II	Lacidipiscis_RS04950	cytochrome d ubiquinol oxidase subunit II
LAC1533_RS03305	thiol reductant ABC exporter subunit CydD	GSS_RS09945	thiol reductant ABC exporter subunit CydD	Lacidipiscis_RS04945	thiol reductant ABC exporter subunit CydD
LAC1533_RS03310	thiol reductant ABC exporter subunit CydC	GSS_RS09950	thiol reductant ABC exporter subunit CydC	Lacidipiscis_RS04940	thiol reductant ABC exporter subunit CydC
LAC1533_RS03325	prenyltransferase	GSS_RS09960	1,4-dihydroxy-2-naphthoate polyprenyltransferase	Lacidipiscis_RS04930	1,4-dihydroxy-2-naphthoate polyprenyltransferase
LAC1533_RS03330	NAD(P)/FAD-dependent oxidoreductase	GSS_RS09965	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS04925	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS03335	D-2-hydroxyacid dehydrogenase	GSS_RS09970	D-2-hydroxyacid dehydrogenase	Lacidipiscis_RS04920	hydroxyacid dehydrogenase
LAC1533_RS03340	metal-dependent hydrolase	GSS_RS09975	metal-dependent hydrolase	Lacidipiscis_RS04915	metal-dependent hydrolase
LAC1533_RS03350	hypothetical protein	GSS_RS09985	hypothetical protein	Lacidipiscis_RS04905	hypothetical protein
LAC1533_RS03355	peroxidase	GSS_RS09990	peroxidase	Lacidipiscis_RS04900	peroxidase
LAC1533_RS03360	iron-sulfur cluster biosynthesis family protein	GSS_RS09995	iron-sulfur cluster biosynthesis family protein	Lacidipiscis_RS04895	iron-sulfur cluster biosynthesis family protein
LAC1533_RS03365	PLP-dependent aminotransferase family protein	GSS_RS10000	PLP-dependent aminotransferase family protein	Lacidipiscis_RS04890	PLP-dependent aminotransferase family protein
LAC1533_RS03380	CBS domain-containing protein	GSS_RS10005	CBS domain-containing protein	Lacidipiscis_RS04870	CBS domain-containing protein
LAC1533_RS03385	ABC transporter permease	GSS_RS10010	ABC transporter permease	Lacidipiscis_RS04865	ABC transporter permease
LAC1533_RS03390	osmoprotectant ABC transporter substrate-binding protein	GSS_RS10015	osmoprotectant ABC transporter substrate-binding protein	Lacidipiscis_RS04860	osmoprotectant ABC transporter substrate-binding protein
LAC1533_RS03395	ABC transporter permease	GSS_RS10020	ABC transporter permease	Lacidipiscis_RS04855	ABC transporter permease

LAC1533_RS03400	glycosyltransferase family 8 protein	GSS_RS10025	glycosyltransferase family 8 protein	Lacidipiscis_RS04850	glycosyltransferase family 8 protein
LAC1533_RS03405	hypothetical protein	GSS_RS10030	hypothetical protein	Lacidipiscis_RS04845	SAM-dependent methyltransferase
LAC1533_RS03415	DNA-binding response regulator	GSS_RS10585	DNA-binding response regulator	Lacidipiscis_RS01890	DNA-binding response regulator
LAC1533_RS03420	sensor histidine kinase	GSS_RS10590	sensor histidine kinase	Lacidipiscis_RS01895	sensor histidine kinase
LAC1533_RS03425	D-alanyl-D-alanine carboxypeptidase	GSS_RS10595	D-alanyl-D-alanine carboxypeptidase	Lacidipiscis_RS01900	D-alanyl-D-alanine carboxypeptidase
LAC1533_RS03430	branched-chain amino acid ABC transporter permease	GSS_RS10600	branched-chain amino acid ABC transporter permease	Lacidipiscis_RS01905	branched-chain amino acid ABC transporter permease
LAC1533_RS03435	AzlD domain-containing protein	GSS_RS10605	AzlD domain-containing protein	Lacidipiscis_RS01910	AzlD domain-containing protein
LAC1533_RS03440	alpha/beta hydrolase	GSS_RS10610	alpha/beta hydrolase	Lacidipiscis_RS06445	alpha/beta hydrolase
LAC1533_RS03450	hypothetical protein	GSS_RS10620	hypothetical protein	Lacidipiscis_RS09190	hypothetical protein
LAC1533_RS03455	RluA family pseudouridine synthase	GSS_RS10625	RluA family pseudouridine synthase	Lacidipiscis_RS09195	RluA family pseudouridine synthase
LAC1533_RS03460	metal-dependent transcriptional regulator	GSS_RS10630	metal-dependent transcriptional regulator	Lacidipiscis_RS09200	metal-dependent transcriptional regulator
LAC1533_RS03465	cold-shock protein	GSS_RS10635	cold-shock protein	Lacidipiscis_RS09205	cold-shock protein
LAC1533_RS03475	LytR family transcriptional regulator	GSS_RS10640	LytR family transcriptional regulator	Lacidipiscis_RS09210	LytR family transcriptional regulator
LAC1533_RS03485	DUF805 domain-containing protein	GSS_RS10650	DUF805 domain-containing protein	Lacidipiscis_RS09215	DUF805 domain-containing protein
LAC1533_RS03490	N-acetyltransferase	GSS_RS13320	N-acetyltransferase	Lacidipiscis_RS09220	N-acetyltransferase
LAC1533_RS03495	Rrf2 family transcriptional regulator	GSS_RS10660	Rrf2 family transcriptional regulator	Lacidipiscis_RS09225	Rrf2 family transcriptional regulator
LAC1533_RS03500	acetolactate synthase AlsS	GSS_RS10665	acetolactate synthase AlsS	Lacidipiscis_RS09230	acetolactate synthase AlsS
LAC1533_RS03505	acetolactate decarboxylase	GSS_RS10670	acetolactate decarboxylase	Lacidipiscis_RS09235	acetolactate decarboxylase
LAC1533_RS03510	amino acid permease	GSS_RS10675	amino acid permease	Lacidipiscis_RS09240	amino acid permease
LAC1533_RS03515	serine--tRNA ligase	GSS_RS10680	serine--tRNA ligase	Lacidipiscis_RS09245	serine--tRNA ligase
LAC1533_RS03545	sigma-70 family RNA polymerase sigma factor	GSS_RS04840	sigma-70 family RNA polymerase sigma factor	Lacidipiscis_RS05315	sigma-70 family RNA polymerase sigma factor
LAC1533_RS03560	ATP-dependent DNA helicase	GSS_RS04850	ATP-dependent DNA helicase	Lacidipiscis_RS06410	ATP-dependent DNA helicase
LAC1533_RS03565	tryptophan--tRNA ligase	GSS_RS04855	tryptophan--tRNA ligase	Lacidipiscis_RS06405	tryptophan--tRNA ligase
LAC1533_RS03570	Ppx/GppA family phosphatase	GSS_RS04860	Ppx/GppA family phosphatase	Lacidipiscis_RS06400	exopolyphosphatase
LAC1533_RS03580	hypothetical protein	GSS_RS10285	hypothetical protein	Lacidipiscis_RS06395	hypothetical protein
LAC1533_RS03585	hydroxymethylglutaryl-CoA reductase, degradative	GSS_RS10290	hydroxymethylglutaryl-CoA reductase, degradative	Lacidipiscis_RS06390	hydroxymethylglutaryl-CoA reductase, degradative
LAC1533_RS03590	hypothetical protein	GSS_RS10295	hypothetical protein	Lacidipiscis_RS06385	hypothetical protein
LAC1533_RS03595	NAD-dependent protein deacylase	GSS_RS10300	NAD-dependent protein deacylase	Lacidipiscis_RS06380	NAD-dependent protein deacylase
LAC1533_RS03600	methionine--tRNA ligase	GSS_RS10305	methionine--tRNA ligase	Lacidipiscis_RS06375	methionine--tRNA ligase
LAC1533_RS03605	TatD family deoxyribonuclease	GSS_RS10310	TatD family deoxyribonuclease	Lacidipiscis_RS06370	TatD family deoxyribonuclease
LAC1533_RS03610	ribonuclease M5	GSS_RS10315	ribonuclease M5	Lacidipiscis_RS06365	ribonuclease M5
LAC1533_RS03620	hypothetical protein	GSS_RS10325	hypothetical protein	Lacidipiscis_RS06355	hypothetical protein
LAC1533_RS03630	pur operon repressor	GSS_RS10335	pur operon repressor	Lacidipiscis_RS06345	pur operon repressor
LAC1533_RS03635	XRE family transcriptional regulator	GSS_RS10340	XRE family transcriptional regulator	Lacidipiscis_RS06340	XRE family transcriptional regulator
LAC1533_RS03640	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU	GSS_RS10345	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU	Lacidipiscis_RS08340	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU
LAC1533_RS03645	ribose-phosphate pyrophosphokinase	GSS_RS10350	ribose-phosphate pyrophosphokinase	Lacidipiscis_RS08335	ribose-phosphate pyrophosphokinase
LAC1533_RS03650	hypothetical protein	GSS_RS10355	hypothetical protein	Lacidipiscis_RS08330	hypothetical protein
LAC1533_RS03655	biotin--[acetyl-CoA-carboxylase] ligase	GSS_RS10360	biotin--[acetyl-CoA-carboxylase] ligase	Lacidipiscis_RS08325	biotin--[acetyl-CoA-carboxylase] ligase
LAC1533_RS03665	YibE/F family protein	GSS_RS10370	YibE/F family protein	Lacidipiscis_RS09440	YibE/F family protein
LAC1533_RS03670	hypothetical protein	GSS_RS13295	hypothetical protein	Lacidipiscis_RS09435	hypothetical protein
LAC1533_RS03675	HD domain-containing protein	GSS_RS10385	HD domain-containing protein	Lacidipiscis_RS11385	HD domain-containing protein
LAC1533_RS03680	DUF1934 domain-containing protein	GSS_RS10395	DUF1934 domain-containing protein	Lacidipiscis_RS11380	DUF1934 domain-containing protein
LAC1533_RS03685	DNA-directed RNA polymerase subunit delta	GSS_RS10400	DNA-directed RNA polymerase subunit delta	Lacidipiscis_RS11375	DNA-directed RNA polymerase subunit delta
LAC1533_RS03690	CTP synthase	GSS_RS10405	CTP synthase	Lacidipiscis_RS11370	CTP synthase
LAC1533_RS03710	hypothetical protein	GSS_RS10830	hypothetical protein	Lacidipiscis_RS11365	hypothetical protein
LAC1533_RS03720	transcription termination factor Rho	GSS_RS10840	transcription termination factor Rho	Lacidipiscis_RS11355	transcription termination factor Rho
LAC1533_RS03725	type B 50S ribosomal protein L31	GSS_RS10845	type B 50S ribosomal protein L31	Lacidipiscis_RS11350	type B 50S ribosomal protein L31
LAC1533_RS03730	hypothetical protein	GSS_RS10850	hypothetical protein	Lacidipiscis_RS13320	hypothetical protein
LAC1533_RS03735	ATP-dependent DNA helicase	GSS_RS10855	ATP-dependent DNA helicase	Lacidipiscis_RS09425	hypothetical protein
LAC1533_RS03740	NCS2 family permease	GSS_RS10860	NCS2 family permease	Lacidipiscis_RS09420	NCS2 family permease
LAC1533_RS03745	dihydrofolate reductase	GSS_RS10865	dihydrofolate reductase	Lacidipiscis_RS09415	dihydrofolate reductase
LAC1533_RS03750	TIGR02452 family protein	GSS_RS10870	TIGR02452 family protein	Lacidipiscis_RS09410	TIGR02452 family protein
LAC1533_RS03755	N-acetyltransferase	GSS_RS10880	N-acetyltransferase	Lacidipiscis_RS09405	N-acetyltransferase
LAC1533_RS03760	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	GSS_RS10885	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	Lacidipiscis_RS09400	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase
LAC1533_RS03765	ATP-dependent helicase	GSS_RS10890	ATP-dependent helicase	Lacidipiscis_RS09395	ATP-dependent helicase
LAC1533_RS03795	holo-ACP synthase	GSS_RS10770	holo-ACP synthase	Lacidipiscis_RS03865	holo-ACP synthase
LAC1533_RS03800	alanine racemase	GSS_RS10765	alanine racemase	Lacidipiscis_RS03870	alanine racemase
LAC1533_RS03805	hypothetical protein	GSS_RS10760	hypothetical protein	Lacidipiscis_RS03875	hypothetical protein
LAC1533_RS03810	type II toxin-antitoxin system PemK/MazF family toxin	GSS_RS10755	type II toxin-antitoxin system PemK/MazF family toxin	Lacidipiscis_RS03880	type II toxin-antitoxin system PemK/MazF family toxin

LAC1533_RS03815	hypothetical protein	GSS_RS10750	hypothetical protein	Lacidipiscis_RS03885	hypothetical protein
LAC1533_RS03820	CBS domain-containing protein	GSS_RS10745	CBS domain-containing protein	Lacidipiscis_RS12660	CBS domain-containing protein
LAC1533_RS03825	L-lactate dehydrogenase	GSS_RS10740	L-lactate dehydrogenase	Lacidipiscis_RS04305	L-lactate dehydrogenase
LAC1533_RS03830	aminoacyl-tRNA hydrolase	GSS_RS10735	aminoacyl-tRNA hydrolase	Lacidipiscis_RS04310	aminoacyl-tRNA hydrolase
LAC1533_RS03835	transcription-repair coupling factor	GSS_RS10730	transcription-repair coupling factor	Lacidipiscis_RS04315	transcription-repair coupling factor
LAC1533_RS03840	sugar transporter	GSS_RS10725	PST polysaccharide transporter	Lacidipiscis_RS04320	sugar transporter
LAC1533_RS03845	RNA-binding S4 domain-containing protein	GSS_RS10720	RNA-binding S4 domain-containing protein	Lacidipiscis_RS04325	RNA-binding S4 domain-containing protein
LAC1533_RS03850	septum formation initiator family protein	GSS_RS10715	septum formation initiator family protein	Lacidipiscis_RS05555	septum formation initiator family protein
LAC1533_RS03855	RNA-binding protein S1	GSS_RS10710	S1 RNA-binding domain containing protein	Lacidipiscis_RS05560	RNA-binding protein S1
LAC1533_RS03860	tRNA lysidine(34) synthetase TilS	GSS_RS13870	hypothetical protein	Lacidipiscis_RS05565	tRNA lysidine(34) synthetase TilS
LAC1533_RS03865	hypoxanthine phosphoribosyltransferase	GSS_RS10700	hypoxanthine phosphoribosyltransferase	Lacidipiscis_RS05570	hypoxanthine phosphoribosyltransferase
LAC1533_RS03870	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein	GSS_RS10695	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein	Lacidipiscis_RS05575	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein
LAC1533_RS03875	Hsp33 family molecular chaperone HslO	GSS_RS10690	Hsp33 family molecular chaperone HslO	Lacidipiscis_RS05580	Hsp33 family molecular chaperone HslO
LAC1533_RS03880	lysine--tRNA ligase	GSS_RS10685	lysine--tRNA ligase	Lacidipiscis_RS05585	lysine--tRNA ligase
LAC1533_RS03920	peptide MFS transporter	GSS_RS07250	peptide MFS transporter	Lacidipiscis_RS00675	peptide MFS transporter
LAC1533_RS03935	pyrroline-5-carboxylate reductase	GSS_RS07265	pyrroline-5-carboxylate reductase	Lacidipiscis_RS00690	pyrroline-5-carboxylate reductase
LAC1533_RS03940	N-acetylglucosamine-6-phosphate deacetylase	GSS_RS07270	N-acetylglucosamine-6-phosphate deacetylase	Lacidipiscis_RS00695	N-acetylglucosamine-6-phosphate deacetylase
LAC1533_RS03945	GntR family transcriptional regulator	GSS_RS07275	GntR family transcriptional regulator	Lacidipiscis_RS00700	GntR family transcriptional regulator
LAC1533_RS03950	class 1b ribonucleoside-diphosphate reductase subunit beta	GSS_RS07280	class 1b ribonucleoside-diphosphate reductase subunit beta	Lacidipiscis_RS06780	class 1b ribonucleoside-diphosphate reductase subunit beta
LAC1533_RS03955	class 1b ribonucleoside-diphosphate reductase subunit alpha	GSS_RS12850	class 1b ribonucleoside-diphosphate reductase subunit alpha	Lacidipiscis_RS06775	class 1b ribonucleoside-diphosphate reductase subunit alpha
LAC1533_RS03960	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI	GSS_RS07300	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI	Lacidipiscis_RS06770	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI
LAC1533_RS03965	glutaredoxin-like protein NrdH	GSS_RS07305	glutaredoxin-like protein NrdH	Lacidipiscis_RS06765	glutaredoxin-like protein NrdH
LAC1533_RS03970	class I SAM-dependent methyltransferase	GSS_RS07310	class I SAM-dependent methyltransferase	Lacidipiscis_RS06760	class I SAM-dependent methyltransferase
LAC1533_RS03975	nucleoside deaminase	GSS_RS07315	nucleoside deaminase	Lacidipiscis_RS06755	nucleoside deaminase
LAC1533_RS03985	DNA polymerase III subunit gamma/tau	GSS_RS07320	DNA polymerase III subunit gamma/tau	Lacidipiscis_RS06745	DNA polymerase III subunit gamma/tau
LAC1533_RS03990	YbaB/EbfC family nucleoid-associated protein	GSS_RS07325	nucleoid-associated protein, YbaB/EbfC family	Lacidipiscis_RS06740	nucleoid-associated protein, YbaB/EbfC family
LAC1533_RS03995	recombination protein RecR	GSS_RS07330	recombination protein RecR	Lacidipiscis_RS06735	recombination protein RecR
LAC1533_RS04000	DUF2508 domain-containing protein	GSS_RS07335	DUF2508 domain-containing protein	Lacidipiscis_RS06730	DUF2508 domain-containing protein
LAC1533_RS04010	hypothetical protein	GSS_RS07345	hypothetical protein	Lacidipiscis_RS06720	hypothetical protein
LAC1533_RS04015	DNA polymerase III subunit delta	GSS_RS07350	DNA polymerase III subunit delta	Lacidipiscis_RS06715	DNA polymerase III subunit delta
LAC1533_RS04020	DUF972 domain-containing protein	GSS_RS07355	DUF972 domain-containing protein	Lacidipiscis_RS06710	DUF972 domain-containing protein
LAC1533_RS04025	16S rRNA (cytidine(1402)-2-O)-methyltransferase	GSS_RS07360	16S rRNA (cytidine(1402)-2-O)-methyltransferase	Lacidipiscis_RS06705	16S rRNA (cytidine(1402)-2-O)-methyltransferase
LAC1533_RS04030	acyl-ACP thioesterase	GSS_RS07365	acyl-ACP thioesterase	Lacidipiscis_RS06700	acyl-ACP thioesterase
LAC1533_RS04050	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	GSS_RS07375	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	Lacidipiscis_RS08650	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB
LAC1533_RS04055	N-acetyltransferase	GSS_RS07380	N-acetyltransferase	Lacidipiscis_RS08645	N-acetyltransferase
LAC1533_RS04060	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	GSS_RS07385	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	Lacidipiscis_RS08640	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD
LAC1533_RS04070	redox-sensing transcriptional repressor Rex	GSS_RS07395	redox-sensing transcriptional repressor Rex	Lacidipiscis_RS08630	redox-sensing transcriptional repressor Rex
LAC1533_RS04085	CPBP family intramembrane metalloprotease	GSS_RS07400	CPBP family intramembrane metalloprotease	Lacidipiscis_RS08625	CPBP family intramembrane metalloprotease
LAC1533_RS04090	co-chaperone GroES	GSS_RS07405	co-chaperone GroES	Lacidipiscis_RS08620	co-chaperone GroES
LAC1533_RS04095	chaperonin GroEL	GSS_RS07410	chaperonin GroEL	Lacidipiscis_RS08615	chaperonin GroEL
LAC1533_RS04100	APC family permease	GSS_RS07415	APC family permease	Lacidipiscis_RS06600	APC family permease
LAC1533_RS04105	YigZ family protein	GSS_RS07420	YigZ family protein	Lacidipiscis_RS06605	YigZ family protein
LAC1533_RS04110	DNA/RNA helicase	GSS_RS07425	DNA/RNA helicase	Lacidipiscis_RS06610	DNA/RNA helicase
LAC1533_RS04115	ComF family protein	GSS_RS07430	ComF family protein	Lacidipiscis_RS06615	ComF family protein
LAC1533_RS04125	ribosome-associated translation inhibitor RaiA	GSS_RS07435	ribosome-associated translation inhibitor RaiA	Lacidipiscis_RS06620	ribosome-associated translation inhibitor RaiA
LAC1533_RS04130	preprotein translocase subunit SecA	GSS_RS07440	preprotein translocase subunit SecA	Lacidipiscis_RS06625	preprotein translocase subunit SecA
LAC1533_RS04135	peptide chain release factor 2	GSS_RS07445	peptide chain release factor 2	Lacidipiscis_RS06630	peptide chain release factor 2
LAC1533_RS04140	cell division ATP-binding protein FtsE	GSS_RS07450	cell division ATP-binding protein FtsE	Lacidipiscis_RS06635	cell division ATP-binding protein FtsE
LAC1533_RS04145	ABC transporter permease	GSS_RS07455	ABC transporter permease	Lacidipiscis_RS06640	ABC transporter permease
LAC1533_RS04150	PDZ domain-containing protein	GSS_RS07460	PDZ domain-containing protein	Lacidipiscis_RS07610	PDZ domain-containing protein
LAC1533_RS04155	DNA-binding response regulator	GSS_RS07465	DNA-binding response regulator	Lacidipiscis_RS07615	DNA-binding response regulator
LAC1533_RS04160	two-component sensor histidine kinase	GSS_RS07470	two-component sensor histidine kinase	Lacidipiscis_RS07620	sensor histidine kinase
LAC1533_RS04165	PspC domain-containing protein	GSS_RS07475	PspC domain-containing protein	Lacidipiscis_RS00020	PspC domain-containing protein
LAC1533_RS04170	phage holin family protein	GSS_RS07480	phage holin family protein	Lacidipiscis_RS00025	phage holin family protein
LAC1533_RS04180	prolipoprotein diacylglyceryl transferase	GSS_RS07490	prolipoprotein diacylglyceryl transferase	Lacidipiscis_RS00035	prolipoprotein diacylglyceryl transferase
LAC1533_RS04185	thioredoxin-disulfide reductase	GSS_RS07500	thioredoxin-disulfide reductase	Lacidipiscis_RS00040	thioredoxin-disulfide reductase
LAC1533_RS04195	phospho-sugar mutase	GSS_RS07505	phospho-sugar mutase	Lacidipiscis_RS00045	phospho-sugar mutase
LAC1533_RS04200	excinuclease ABC subunit UvrB	GSS_RS07510	excinuclease ABC subunit UvrB	Lacidipiscis_RS00050	excinuclease ABC subunit UvrB
LAC1533_RS04205	excinuclease ABC subunit UvrA	GSS_RS07515	excinuclease ABC subunit UvrA	Lacidipiscis_RS00055	excinuclease ABC subunit UvrA
LAC1533_RS04210	S-ribosylhomocysteine lyase	GSS_RS07520	S-ribosylhomocysteine lyase	Lacidipiscis_RS00060	S-ribosylhomocysteine lyase
LAC1533_RS04215	serine dehydratase	GSS_RS12875	L-serine ammonia-lyase beta subunit	Lacidipiscis_RS00065	serine dehydratase
LAC1533_RS04220	L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha	GSS_RS07530	L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha	Lacidipiscis_RS00070	L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha
LAC1533_RS04225	RNase adapter RapZ	GSS_RS07535	RNase adapter RapZ	Lacidipiscis_RS00075	RNase adapter RapZ
LAC1533_RS04230	hypothetical protein	GSS_RS07540	hypothetical protein	Lacidipiscis_RS00080	hypothetical protein

LAC1533_RS04235	DNA-binding protein WhiA	GSS_RS07545	DNA-binding protein WhiA	Lacidipiscis_RS00085	DNA-binding protein WhiA
LAC1533_RS04240	ATP-dependent Clp protease proteolytic subunit	GSS_RS07550	ATP-dependent Clp protease proteolytic subunit	Lacidipiscis_RS00090	ATP-dependent Clp protease proteolytic subunit
LAC1533_RS04250	RNA polymerase sigma-54 factor	GSS_RS07560	RNA polymerase sigma-54 factor	Lacidipiscis_RS05880	RNA polymerase sigma-54 factor
LAC1533_RS04255	SorC family transcriptional regulator	GSS_RS07565	SorC family transcriptional regulator	Lacidipiscis_RS05885	SorC family transcriptional regulator
LAC1533_RS04260	type I glyceraldehyde-3-phosphate dehydrogenase	GSS_RS07570	type I glyceraldehyde-3-phosphate dehydrogenase	Lacidipiscis_RS05890	type I glyceraldehyde-3-phosphate dehydrogenase
LAC1533_RS04270	triose-phosphate isomerase	GSS_RS07580	triose-phosphate isomerase	Lacidipiscis_RS05900	triose-phosphate isomerase
LAC1533_RS04290	preprotein translocase subunit SecG	GSS_RS07585	preprotein translocase subunit SecG	Lacidipiscis_RS05905	preprotein translocase subunit SecG
LAC1533_RS04295	ribonuclease R	GSS_RS07595	ribonuclease R	Lacidipiscis_RS05910	ribonuclease R
LAC1533_RS04300	SsrA-binding protein SmpB	GSS_RS07600	SsrA-binding protein SmpB	Lacidipiscis_RS05915	SsrA-binding protein SmpB
LAC1533_RS04320	hypothetical protein	GSS_RS07605	hypothetical protein	Lacidipiscis_RS12625	hypothetical protein
LAC1533_RS04325	Cof-type HAD-IIB family hydrolase	GSS_RS07610	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS12620	Cof-type HAD-IIB family hydrolase
LAC1533_RS04330	uracil-DNA glycosylase	GSS_RS07615	uracil-DNA glycosylase	Lacidipiscis_RS12615	uracil-DNA glycosylase
LAC1533_RS04335	phosphate acetyltransferase	GSS_RS07620	phosphate acetyltransferase	Lacidipiscis_RS12610	phosphate acetyltransferase
LAC1533_RS04340	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	GSS_RS07625	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	Lacidipiscis_RS12605	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE
LAC1533_RS04345	exonuclease	GSS_RS07630	exonuclease	Lacidipiscis_RS12600	hypothetical protein
LAC1533_RS04355	DUF1361 domain-containing protein	GSS_RS07640	DUF1361 domain-containing protein	Lacidipiscis_RS12590	DUF1361 domain-containing protein
LAC1533_RS04360	TIGR00159 family protein	GSS_RS07645	TIGR00159 family protein	Lacidipiscis_RS12585	TIGR00159 family protein
LAC1533_RS04370	phosphoglucosamine mutase	GSS_RS07655	phosphoglucosamine mutase	Lacidipiscis_RS12575	phosphoglucosamine mutase
LAC1533_RS04375	hypothetical protein	GSS_RS07660	hypothetical protein	Lacidipiscis_RS12570	hypothetical protein
LAC1533_RS04390	hypothetical protein	GSS_RS07665	hypothetical protein	Lacidipiscis_RS12565	hypothetical protein
LAC1533_RS04395	ABC transporter	GSS_RS07670	ABC transporter	Lacidipiscis_RS09590	ABC transporter
LAC1533_RS04400	phosphate ABC transporter permease subunit PstC	GSS_RS07675	phosphate ABC transporter permease subunit PstC	Lacidipiscis_RS09585	phosphate ABC transporter permease subunit PstC
LAC1533_RS04405	phosphate ABC transporter, permease protein PstA	GSS_RS07680	phosphate ABC transporter, permease protein PstA	Lacidipiscis_RS09580	phosphate ABC transporter, permease protein PstA
LAC1533_RS04410	phosphate ABC transporter ATP-binding protein	GSS_RS07685	phosphate ABC transporter ATP-binding protein	Lacidipiscis_RS09575	phosphate ABC transporter ATP-binding protein
LAC1533_RS04415	phosphate ABC transporter ATP-binding protein	GSS_RS07690	phosphate ABC transporter ATP-binding protein	Lacidipiscis_RS09570	phosphate ABC transporter ATP-binding protein
LAC1533_RS04420	phosphate transport system regulatory protein PhoU	GSS_RS07695	phosphate transport system regulatory protein PhoU	Lacidipiscis_RS09565	phosphate transport system regulatory protein PhoU
LAC1533_RS04425	fructose-1,6-bisphosphate aldolase, class II	GSS_RS07700	fructose-1,6-bisphosphate aldolase, class II	Lacidipiscis_RS09560	fructose-1,6-bisphosphate aldolase, class II
LAC1533_RS04430	IS1182 family transposase	GSS_RS07705	IS1182 family transposase	Lacidipiscis_RS09555	IS5/IS1182 family transposase
LAC1533_RS04440	DUF1836 domain-containing protein	GSS_RS07710	DUF1836 domain-containing protein	Lacidipiscis_RS09545	DUF1836 domain-containing protein
LAC1533_RS04445	hemolysin III	GSS_RS07715	membrane protein	Lacidipiscis_RS09540	hemolysin III
LAC1533_RS04450	ArsR family transcriptional regulator	GSS_RS07720	ArsR family transcriptional regulator	Lacidipiscis_RS09535	ArsR family transcriptional regulator
LAC1533_RS04455	RNase HI	GSS_RS07725	RNase HI	Lacidipiscis_RS09530	RNase HI
LAC1533_RS04460	hypothetical protein	GSS_RS07730	hypothetical protein	Lacidipiscis_RS09525	hypothetical protein
LAC1533_RS04465	hypothetical protein	GSS_RS07735	hypothetical protein	Lacidipiscis_RS09520	hypothetical protein
LAC1533_RS04480	glucose-6-phosphate isomerase	GSS_RS07745	glucose-6-phosphate isomerase	Lacidipiscis_RS09150	glucose-6-phosphate isomerase
LAC1533_RS04490	CBS domain-containing protein	GSS_RS07750	CBS domain-containing protein	Lacidipiscis_RS11845	CBS domain-containing protein
LAC1533_RS04500	amidohydrolase	GSS_RS07760	N-acetyldiaminopimelate deacetylase	Lacidipiscis_RS11855	amidohydrolase
LAC1533_RS04505	mechanosensitive ion channel family protein	GSS_RS07765	mechanosensitive ion channel family protein	Lacidipiscis_RS11860	mechanosensitive ion channel family protein
LAC1533_RS04510	DUF948 domain-containing protein	GSS_RS07770	DUF948 domain-containing protein	Lacidipiscis_RS11865	DUF948 domain-containing protein
LAC1533_RS04515	hypothetical protein	GSS_RS07775	hypothetical protein	Lacidipiscis_RS11870	hypothetical protein
LAC1533_RS04520	aminopeptidase P family protein	GSS_RS07780	aminopeptidase P family protein	Lacidipiscis_RS11875	aminopeptidase P family protein
LAC1533_RS04525	catabolite control protein A	GSS_RS07785	catabolite control protein A	Lacidipiscis_RS11880	catabolite control protein A
LAC1533_RS04530	YebC/PmpR family DNA-binding transcriptional regulator	GSS_RS07790	YebC/PmpR family DNA-binding transcriptional regulator	Lacidipiscis_RS11885	YebC/PmpR family DNA-binding transcriptional regulator
LAC1533_RS04535	competence protein ComG	GSS_RS07795	competence protein ComG	Lacidipiscis_RS11890	competence protein ComG

LAC1533_RS04540	competence protein ComG	GSS_RS07800	ComG operon protein 2	Lacidipiscis_RS11895	competence protein ComG
LAC1533_RS04545	prepilin-type N-terminal cleavage/methylation domain-containing protein	GSS_RS07805	prepilin-type N-terminal cleavage/methylation domain-containing protein	Lacidipiscis_RS11900	prepilin-type N-terminal cleavage/methylation domain-containing protein
LAC1533_RS04550	prepilin-type N-terminal cleavage/methylation domain-containing protein	GSS_RS07810	prepilin-type N-terminal cleavage/methylation domain-containing protein	Lacidipiscis_RS11905	prepilin-type N-terminal cleavage/methylation domain-containing protein
LAC1533_RS04555	hypothetical protein	GSS_RS07815	hypothetical protein	Lacidipiscis_RS11910	hypothetical protein
LAC1533_RS04560	type II secretion system protein	GSS_RS07820	type II secretion system protein	Lacidipiscis_RS11915	prepilin-type cleavage/methylation domain-containing protein
LAC1533_RS04565	hypothetical protein	GSS_RS12905	hypothetical protein	Lacidipiscis_RS11920	hypothetical protein
LAC1533_RS04570	class I SAM-dependent methyltransferase	GSS_RS07830	class I SAM-dependent methyltransferase	Lacidipiscis_RS11925	class I SAM-dependent methyltransferase
LAC1533_RS04580	multifunctional 2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase	GSS_RS07840	multifunctional 2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase	Lacidipiscis_RS11935	multifunctional 2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase
LAC1533_RS04590	TIGR01457 family HAD-type hydrolase	GSS_RS07850	TIGR01457 family HAD-type hydrolase	Lacidipiscis_RS13380	TIGR01457 family HAD-type hydrolase
LAC1533_RS04595	TIGR01906 family membrane protein	GSS_RS07855	TIGR01906 family membrane protein	Lacidipiscis_RS13385	TIGR01906 family membrane protein
LAC1533_RS04600	cytochrome o ubiquinol oxidase	GSS_RS07860	membrane protein	Lacidipiscis_RS13390	cytochrome o ubiquinol oxidase
LAC1533_RS04605	NAD(P)/FAD-dependent oxidoreductase	GSS_RS07865	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS13395	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS04610	peptidylprolyl isomerase	GSS_RS07870	peptidyl-prolyl cis-trans isomerase	Lacidipiscis_RS13400	peptidylprolyl isomerase
LAC1533_RS04615	general stress protein	GSS_RS07875	general stress protein	Lacidipiscis_RS13405	general stress protein
LAC1533_RS04740	methionine adenosyltransferase	GSS_RS11040	methionine adenosyltransferase	Lacidipiscis_RS11620	methionine adenosyltransferase
LAC1533_RS04745	LysM peptidoglycan-binding domain-containing protein	GSS_RS13355	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS11630	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS04750	leucine--tRNA ligase	GSS_RS11050	leucine--tRNA ligase	Lacidipiscis_RS11635	leucine--tRNA ligase
LAC1533_RS04755	polysaccharide biosynthesis protein	GSS_RS11055	polysaccharide biosynthesis protein	Lacidipiscis_RS11640	polysaccharide biosynthesis protein
LAC1533_RS04760	hypothetical protein	GSS_RS11060	hypothetical protein	Lacidipiscis_RS11645	hypothetical protein
LAC1533_RS04810	NAD(P)H-hydrate dehydratase	GSS_RS04815	NAD(P)H-hydrate dehydratase	Lacidipiscis_RS12805	NAD(P)H-hydrate dehydratase
LAC1533_RS04815	dienelactone hydrolase	GSS_RS04810	dienelactone hydrolase	Lacidipiscis_RS12800	dienelactone hydrolase
LAC1533_RS04830	hypothetical protein	GSS_RS04800	hypothetical protein	Lacidipiscis_RS12790	hypothetical protein
LAC1533_RS04835	universal stress protein	GSS_RS04795	universal stress protein	Lacidipiscis_RS12785	universal stress protein
LAC1533_RS04840	hypothetical protein	GSS_RS04790	hypothetical protein	Lacidipiscis_RS12780	hypothetical protein
LAC1533_RS04855	hypothetical protein	GSS_RS04785	hypothetical protein	Lacidipiscis_RS12775	hypothetical protein
LAC1533_RS04860	acetate kinase	GSS_RS04780	acetate kinase	Lacidipiscis_RS12770	acetate kinase
LAC1533_RS04865	hypothetical protein	GSS_RS04775	hypothetical protein	Lacidipiscis_RS12765	hypothetical protein
LAC1533_RS04870	deoxyguanosine kinase	GSS_RS04770	deoxyguanosine kinase	Lacidipiscis_RS12760	deoxyguanosine kinase
LAC1533_RS04880	adenylosuccinate lyase	GSS_RS04765	adenylosuccinate lyase	Lacidipiscis_RS12755	adenylosuccinate lyase
LAC1533_RS04885	LysR family transcriptional regulator	GSS_RS04760	LysR family transcriptional regulator	Lacidipiscis_RS12750	LysR family transcriptional regulator
LAC1533_RS04890	MATE family efflux transporter	GSS_RS04750	MATE family efflux transporter	Lacidipiscis_RS12745	MATE family efflux transporter
LAC1533_RS04895	hypothetical protein	GSS_RS04745	hypothetical protein	Lacidipiscis_RS06335	hypothetical protein
LAC1533_RS04905	arginine--tRNA ligase	GSS_RS04735	arginine--tRNA ligase	Lacidipiscis_RS06325	arginine--tRNA ligase
LAC1533_RS04910	Crp/Fnr family transcriptional regulator	GSS_RS04730	Crp/Fnr family transcriptional regulator	Lacidipiscis_RS08345	Crp/Fnr family transcriptional regulator
LAC1533_RS04915	ArgR family transcriptional regulator	GSS_RS04725	ArgR family transcriptional regulator	Lacidipiscis_RS08350	ArgR family transcriptional regulator
LAC1533_RS04920	carboxypeptidase	GSS_RS04720	carboxypeptidase	Lacidipiscis_RS08355	carboxypeptidase
LAC1533_RS04925	hypothetical protein	GSS_RS04715	hypothetical protein	Lacidipiscis_RS08360	hypothetical protein
LAC1533_RS04930	HD domain-containing protein	GSS_RS04710	HD domain-containing protein	Lacidipiscis_RS08365	HD domain-containing protein
LAC1533_RS04935	peptidylprolyl isomerase	GSS_RS04705	peptidylprolyl isomerase	Lacidipiscis_RS08370	peptidylprolyl isomerase
LAC1533_RS04940	hypothetical protein	GSS_RS04700	hypothetical protein	Lacidipiscis_RS08375	hypothetical protein
LAC1533_RS04945	HIT family protein	GSS_RS04695	HIT family protein	Lacidipiscis_RS08380	HIT family protein
LAC1533_RS04950	ABC transporter ATP-binding protein	GSS_RS12615	ABC transporter ATP-binding protein	Lacidipiscis_RS08385	ABC transporter ATP-binding protein
LAC1533_RS04955	protein ecsB	GSS_RS04685	protein ecsB	Lacidipiscis_RS08390	protein EcsB
LAC1533_RS04960	phosphotransferase	GSS_RS04680	phosphotransferase	Lacidipiscis_RS08395	phosphotransferase
LAC1533_RS04965	tRNA (guanosine(46)-N7)-methyltransferase TrmB	GSS_RS04675	tRNA (guanosine(46)-N7)-methyltransferase TrmB	Lacidipiscis_RS05790	tRNA (guanosine(46)-N7)-methyltransferase TrmB
LAC1533_RS04970	thioredoxin	GSS_RS04670	thioredoxin	Lacidipiscis_RS05785	thioredoxin
LAC1533_RS04975	DUF4479 domain-containing protein	GSS_RS04665	DUF4479 domain-containing protein	Lacidipiscis_RS05780	DUF4479 domain-containing protein
LAC1533_RS04980	DNA translocase FtsK	GSS_RS04660	DNA translocase FtsK	Lacidipiscis_RS05775	DNA translocase FtsK
LAC1533_RS04985	UDP-N-acetylmuramate--L-alanine ligase	GSS_RS04655	UDP-N-acetylmuramate--L-alanine ligase	Lacidipiscis_RS05770	UDP-N-acetylmuramate--L-alanine ligase
LAC1533_RS04990	BAX inhibitor (BI)-1/YccA family protein	GSS_RS04650	BAX inhibitor (BI)-1/YccA family protein	Lacidipiscis_RS05765	BAX inhibitor (BI)-1/YccA family protein
LAC1533_RS04995	DNA polymerase I	GSS_RS04645	DNA polymerase I	Lacidipiscis_RS05760	DNA polymerase I
LAC1533_RS05000	DNA-formamidopyrimidine glycosylase	GSS_RS04635	DNA-formamidopyrimidine glycosylase	Lacidipiscis_RS05755	DNA-formamidopyrimidine glycosylase
LAC1533_RS05005	transcriptional repressor NrdR	GSS_RS04630	transcriptional repressor NrdR	Lacidipiscis_RS05745	transcriptional repressor NrdR
LAC1533_RS05010	chromosome replication initiation / membrane attachment protein	GSS_RS04625	chromosome replication initiation / membrane attachment protein	Lacidipiscis_RS05740	chromosome replication initiation / membrane attachment protein
LAC1533_RS05015	primosomal protein DnaI	GSS_RS04620	primosomal protein DnaI	Lacidipiscis_RS05735	primosomal protein DnaI
LAC1533_RS05020	threonine--tRNA ligase	GSS_RS04615	threonine--tRNA ligase	Lacidipiscis_RS05730	threonine--tRNA ligase
LAC1533_RS05025	translation initiation factor IF-3	GSS_RS04610	translation initiation factor IF-3	Lacidipiscis_RS05725	translation initiation factor IF-3
LAC1533_RS05030	50S ribosomal protein L35	GSS_RS04605	50S ribosomal protein L35	Lacidipiscis_RS05720	50S ribosomal protein L35
LAC1533_RS05035	50S ribosomal protein L20	GSS_RS04600	50S ribosomal protein L20	Lacidipiscis_RS05715	50S ribosomal protein L20
LAC1533_RS05040	YqeG family HAD IIIA-type phosphatase	GSS_RS04595	YqeG family HAD IIIA-type phosphatase	Lacidipiscis_RS05710	YqeG family HAD IIIA-type phosphatase
LAC1533_RS05045	ribosome biogenesis GTPase YqeH	GSS_RS04590	ribosome biogenesis GTPase YqeH	Lacidipiscis_RS05705	ribosome biogenesis GTPase YqeH
LAC1533_RS05050	ribosome assembly RNA-binding protein YhbY	GSS_RS04585	ribosome assembly RNA-binding protein YhbY	Lacidipiscis_RS05700	ribosome assembly RNA-binding protein YhbY
LAC1533_RS05055	nicotinate-nucleotide adenylyltransferase	GSS_RS04580	nicotinate-nucleotide adenylyltransferase	Lacidipiscis_RS05695	nicotinate-nucleotide adenylyltransferase
LAC1533_RS05060	HD domain-containing protein	GSS_RS04570	HD domain-containing protein	Lacidipiscis_RS05690	HD domain-containing protein
LAC1533_RS05065	ribosome silencing factor	GSS_RS04565	ribosome silencing factor	Lacidipiscis_RS05685	ribosome silencing factor
LAC1533_RS05070	class I SAM-dependent methyltransferase	GSS_RS04560	class I SAM-dependent methyltransferase	Lacidipiscis_RS05680	class I SAM-dependent methyltransferase
LAC1533_RS05075	nucleotidyltransferase	GSS_RS04555	nucleotidyltransferase	Lacidipiscis_RS05675	nucleotidyltransferase

LAC1533_RS05080	hypothetical protein	GSS_RS04550	hypothetical protein	Lacidipiscis_RS05670	DNA-binding protein
LAC1533_RS05085	50S ribosomal protein L32	GSS_RS04545	50S ribosomal protein L32	Lacidipiscis_RS05665	50S ribosomal protein L32
LAC1533_RS05090	YihA family ribosome biogenesis GTP-binding protein	GSS_RS04540	YihA family ribosome biogenesis GTP-binding protein	Lacidipiscis_RS05660	YihA family ribosome biogenesis GTP-binding protein
LAC1533_RS05095	nucleotide pyrophosphohydrolase	GSS_RS04535	nucleotide pyrophosphohydrolase	Lacidipiscis_RS05655	nucleotide pyrophosphohydrolase
LAC1533_RS05100	hypothetical protein	GSS_RS12605	hypothetical protein	Lacidipiscis_RS05650	hypothetical protein
LAC1533_RS05105	amino acid ABC transporter ATP-binding protein	GSS_RS04525	amino acid ABC transporter ATP-binding protein	Lacidipiscis_RS05645	amino acid ABC transporter ATP-binding protein
LAC1533_RS05115	GTPase ObgE	GSS_RS04515	GTPase ObgE	Lacidipiscis_RS05635	GTPase ObgE
LAC1533_RS05120	acetyltransferase	GSS_RS04510	acetyltransferase	Lacidipiscis_RS05630	acetyltransferase
LAC1533_RS05125	hypothetical protein	GSS_RS04505	hypothetical protein	Lacidipiscis_RS11440	hypothetical protein
LAC1533_RS05135	ribonuclease Z	GSS_RS04495	ribonuclease Z	Lacidipiscis_RS09595	ribonuclease Z
LAC1533_RS05140	SDR family NAD(P)-dependent oxidoreductase	GSS_RS04490	SDR family NAD(P)-dependent oxidoreductase	Lacidipiscis_RS09600	SDR family NAD(P)-dependent oxidoreductase
LAC1533_RS05145	DUF1049 domain-containing protein	GSS_RS04485	DUF1049 domain-containing protein	Lacidipiscis_RS09605	DUF1049 domain-containing protein
LAC1533_RS05150	single-stranded-DNA-specific exonuclease RecJ	GSS_RS04480	single-stranded-DNA-specific exonuclease RecJ	Lacidipiscis_RS09610	single-stranded-DNA-specific exonuclease RecJ
LAC1533_RS05155	adenine phosphoribosyltransferase	GSS_RS04475	adenine phosphoribosyltransferase	Lacidipiscis_RS09615	adenine phosphoribosyltransferase
LAC1533_RS05160	hypothetical protein	GSS_RS04465	hypothetical protein	Lacidipiscis_RS09160	hypothetical protein
LAC1533_RS05165	helicase-exonuclease AddAB subunit AddA	GSS_RS04460	helicase-exonuclease AddAB subunit AddA	Lacidipiscis_RS09165	helicase-exonuclease AddAB subunit AddA
LAC1533_RS05170	hypothetical protein	GSS_RS04455	hypothetical protein	Lacidipiscis_RS09170	hypothetical protein
LAC1533_RS05175	hypothetical protein	GSS_RS04450	hypothetical protein	Lacidipiscis_RS09175	hypothetical protein
LAC1533_RS05180	50S ribosomal protein L33	GSS_RS04440	50S ribosomal protein L33	Lacidipiscis_RS09640	50S ribosomal protein L33
LAC1533_RS05195	5-formyltetrahydrofolate cyclo-ligase	GSS_RS12595	5-formyltetrahydrofolate cyclo-ligase	Lacidipiscis_RS09645	5-formyltetrahydrofolate cyclo-ligase
LAC1533_RS05200	rhomboid family intramembrane serine protease	GSS_RS04425	rhomboid family intramembrane serine protease	Lacidipiscis_RS09650	rhomboid family intramembrane serine protease
LAC1533_RS05205	DUF910 domain-containing protein	GSS_RS04420	DUF910 domain-containing protein	Lacidipiscis_RS09655	DUF910 domain-containing protein
LAC1533_RS05210	glucokinase	GSS_RS04415	glucokinase	Lacidipiscis_RS09660	glucokinase
LAC1533_RS05215	rhodanese-like domain-containing protein	GSS_RS04410	rhodanese-like domain-containing protein	Lacidipiscis_RS09665	rhodanese-like domain-containing protein
LAC1533_RS05220	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	GSS_RS04405	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	Lacidipiscis_RS09670	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA
LAC1533_RS05225	MerR family transcriptional regulator	GSS_RS04400	MerR family transcriptional regulator	Lacidipiscis_RS09675	MerR family transcriptional regulator
LAC1533_RS05230	type I glutamate--ammonia ligase	GSS_RS04395	type I glutamate--ammonia ligase	Lacidipiscis_RS09680	type I glutamate--ammonia ligase
LAC1533_RS05240	guanylate kinase	GSS_RS04385	guanylate kinase	Lacidipiscis_RS09685	guanylate kinase
LAC1533_RS05245	DNA-directed RNA polymerase subunit omega	GSS_RS04380	DNA-directed RNA polymerase subunit omega	Lacidipiscis_RS09690	DNA-directed RNA polymerase subunit omega
LAC1533_RS05250	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC	GSS_RS12590	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC	Lacidipiscis_RS09695	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC
LAC1533_RS05260	methionyl-tRNA formyltransferase	GSS_RS04360	methionyl-tRNA formyltransferase	Lacidipiscis_RS09705	methionyl-tRNA formyltransferase
LAC1533_RS05265	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB	GSS_RS04355	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB	Lacidipiscis_RS09710	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB
LAC1533_RS05270	serine/threonine-protein phosphatase	GSS_RS04350	serine/threonine-protein phosphatase	Lacidipiscis_RS09715	serine/threonine-protein phosphatase
LAC1533_RS05280	ribosome small subunit-dependent GTPase A	GSS_RS04330	ribosome small subunit-dependent GTPase A	Lacidipiscis_RS09725	ribosome small subunit-dependent GTPase A
LAC1533_RS05285	ribulose-phosphate 3-epimerase	GSS_RS04325	ribulose-phosphate 3-epimerase	Lacidipiscis_RS09730	ribulose-phosphate 3-epimerase
LAC1533_RS05290	thiamine diphosphokinase	GSS_RS04320	thiamine diphosphokinase	Lacidipiscis_RS09735	thiamine diphosphokinase
LAC1533_RS05295	50S ribosomal protein L28	GSS_RS04315	50S ribosomal protein L28	Lacidipiscis_RS09740	50S ribosomal protein L28
LAC1533_RS05300	Asp23/Gls24 family envelope stress response protein	GSS_RS04310	Asp23/Gls24 family envelope stress response protein	Lacidipiscis_RS09745	Asp23/Gls24 family envelope stress response protein
LAC1533_RS05305	DAK2 domain-containing protein	GSS_RS04305	DAK2 domain-containing protein	Lacidipiscis_RS09750	DAK2 domain-containing protein
LAC1533_RS05315	phosphate acyltransferase PlsX	GSS_RS04295	phosphate acyltransferase PlsX	Lacidipiscis_RS09760	phosphate acyltransferase PlsX
LAC1533_RS05325	acyl carrier protein	GSS_RS04290	acyl carrier protein	Lacidipiscis_RS09765	acyl carrier protein
LAC1533_RS05330	ribonuclease III	GSS_RS04275	ribonuclease III	Lacidipiscis_RS09770	ribonuclease III
LAC1533_RS05335	chromosome segregation protein SMC	GSS_RS12570	chromosome segregation protein SMC	Lacidipiscis_RS09775	chromosome segregation protein SMC
LAC1533_RS05340	signal recognition particle-docking protein FtsY	GSS_RS04255	signal recognition particle-docking protein FtsY	Lacidipiscis_RS09780	signal recognition particle-docking protein FtsY
LAC1533_RS05355	30S ribosomal protein S16	GSS_RS04240	30S ribosomal protein S16	Lacidipiscis_RS09795	30S ribosomal protein S16
LAC1533_RS05360	KH domain-containing protein	GSS_RS04235	KH domain-containing protein	Lacidipiscis_RS09800	KH domain-containing protein
LAC1533_RS05365	ribosome maturation factor RimM	GSS_RS04230	ribosome maturation factor RimM	Lacidipiscis_RS09805	ribosome maturation factor RimM
LAC1533_RS05370	tRNA (guanosine(37)-N1)-methyltransferase TrmD	GSS_RS04225	tRNA (guanosine(37)-N1)-methyltransferase TrmD	Lacidipiscis_RS09810	tRNA (guanosine(37)-N1)-methyltransferase TrmD
LAC1533_RS05375	50S ribosomal protein L19	GSS_RS04220	50S ribosomal protein L19	Lacidipiscis_RS09815	50S ribosomal protein L19
LAC1533_RS05385	UMP kinase	GSS_RS04215	UMP kinase	Lacidipiscis_RS09820	UMP kinase
LAC1533_RS05390	ribosome recycling factor	GSS_RS04210	ribosome recycling factor	Lacidipiscis_RS09825	ribosome recycling factor
LAC1533_RS05395	isoprenyl transferase	GSS_RS04205	isoprenyl transferase	Lacidipiscis_RS09830	isoprenyl transferase
LAC1533_RS05400	phosphatidate cytidylyltransferase	GSS_RS04200	phosphatidate cytidylyltransferase	Lacidipiscis_RS09835	phosphatidate cytidylyltransferase
LAC1533_RS05405	RIP metalloprotease RseP	GSS_RS04195	RIP metalloprotease RseP	Lacidipiscis_RS09840	RIP metalloprotease RseP
LAC1533_RS05410	proline--tRNA ligase	GSS_RS04190	proline--tRNA ligase	Lacidipiscis_RS09845	proline--tRNA ligase
LAC1533_RS05415	PolC-type DNA polymerase III	GSS_RS04185	PolC-type DNA polymerase III	Lacidipiscis_RS09850	PolC-type DNA polymerase III
LAC1533_RS05420	ribosome maturation factor RimP	GSS_RS04180	ribosome maturation factor RimP	Lacidipiscis_RS09855	ribosome maturation factor RimP
LAC1533_RS05425	transcription termination/antitermination protein NusA	GSS_RS04175	transcription termination/antitermination protein NusA	Lacidipiscis_RS09860	transcription termination/antitermination protein NusA
LAC1533_RS05430	DUF448 domain-containing protein	GSS_RS04170	DUF448 domain-containing protein	Lacidipiscis_RS09865	DUF448 domain-containing protein
LAC1533_RS05435	hypothetical protein	GSS_RS04165	hypothetical protein	Lacidipiscis_RS09870	hypothetical protein
LAC1533_RS05440	translation initiation factor IF-2	GSS_RS04160	translation initiation factor IF-2	Lacidipiscis_RS09875	translation initiation factor IF-2
LAC1533_RS05445	30S ribosome-binding factor RbfA	GSS_RS04155	30S ribosome-binding factor RbfA	Lacidipiscis_RS09880	30S ribosome-binding factor RbfA
LAC1533_RS05450	tRNA pseudouridine(55) synthase TruB	GSS_RS04150	tRNA pseudouridine(55) synthase TruB	Lacidipiscis_RS09885	tRNA pseudouridine(55) synthase TruB
LAC1533_RS05455	riboflavin biosynthesis protein RibF	GSS_RS04145	bifunctional riboflavin kinase/FAD synthetase	Lacidipiscis_RS09890	riboflavin biosynthesis protein RibF
LAC1533_RS05460	heat-inducible transcription repressor HrcA	GSS_RS04140	heat-inducible transcription repressor HrcA	Lacidipiscis_RS09895	heat-inducible transcription repressor HrcA
LAC1533_RS05465	nucleotide exchange factor GrpE	GSS_RS04135	nucleotide exchange factor GrpE	Lacidipiscis_RS09900	nucleotide exchange factor GrpE
LAC1533_RS05470	molecular chaperone DnaK	GSS_RS04130	molecular chaperone DnaK	Lacidipiscis_RS09905	molecular chaperone DnaK

LAC1533_RS05475	molecular chaperone DnaJ	GSS_RS04125	molecular chaperone DnaJ	Lacidipiscis_RS09910	molecular chaperone DnaJ
LAC1533_RS05480	nucleoside deoxyribosyltransferase	GSS_RS04115	nucleoside deoxyribosyltransferase	Lacidipiscis_RS10135	nucleoside 2-deoxyribosyltransferase
LAC1533_RS05485	N-acetyltransferase	GSS_RS04110	N-acetyltransferase	Lacidipiscis_RS00175	N-acetyltransferase
LAC1533_RS05490	alpha/beta hydrolase	GSS_RS04105	alpha/beta hydrolase	Lacidipiscis_RS00170	alpha/beta hydrolase
LAC1533_RS05495	pyruvate oxidase	GSS_RS04100	pyruvate oxidase	Lacidipiscis_RS00160	pyruvate oxidase
LAC1533_RS05500	serine hydroxymethyltransferase	GSS_RS04095	serine hydroxymethyltransferase	Lacidipiscis_RS00155	serine hydroxymethyltransferase
LAC1533_RS05505	N-acetyltransferase	GSS_RS04090	N-acetyltransferase	Lacidipiscis_RS06260	N-acetyltransferase
LAC1533_RS05510	aldo/keto reductase	GSS_RS04085	aldo/keto reductase	Lacidipiscis_RS06265	aldo/keto reductase
LAC1533_RS05515	hypothetical protein	GSS_RS04080	hypothetical protein	Lacidipiscis_RS06270	hypothetical protein
LAC1533_RS05520	TIGR00730 family Rossman fold protein	GSS_RS04075	TIGR00730 family Rossman fold protein	Lacidipiscis_RS06275	TIGR00730 family Rossman fold protein
LAC1533_RS05530	elongation factor 4	GSS_RS04060	elongation factor 4	Lacidipiscis_RS06285	elongation factor 4
LAC1533_RS05540	death-on-curing family protein	GSS_RS13715	death-on-curing family protein	Lacidipiscis_RS07940	type II toxin-antitoxin system death-on-curing family toxin
LAC1533_RS05550	IS30 family transposase	GSS_RS04040	IS30 family transposase	Lacidipiscis_RS10055	IS30 family transposase
LAC1533_RS05575	hypothetical protein	GSS_RS04025	hypothetical protein	Lacidipiscis_RS10045	hypothetical protein
LAC1533_RS05590	type VI secretion protein ImpB	GSS_RS04010	type VI secretion protein ImpB	Lacidipiscis_RS07640	excinuclease ABC subunit A
LAC1533_RS05595	hypothetical protein	GSS_RS04005	hypothetical protein	Lacidipiscis_RS07645	hypothetical protein
LAC1533_RS05600	RNA methyltransferase	GSS_RS04000	RNA methyltransferase	Lacidipiscis_RS07650	RNA methyltransferase
LAC1533_RS05605	hydrolase	GSS_RS03995	hydrolase	Lacidipiscis_RS07655	hydrolase
LAC1533_RS05610	transcriptional regulator	GSS_RS11445	transcriptional regulator	Lacidipiscis_RS07660	transcriptional regulator
LAC1533_RS05615	phenylalanine--tRNA ligase subunit alpha	GSS_RS03990	phenylalanine--tRNA ligase subunit alpha	Lacidipiscis_RS07665	phenylalanine--tRNA ligase subunit alpha
LAC1533_RS05630	uridine kinase	GSS_RS03975	uridine kinase	Lacidipiscis_RS11335	uridine kinase
LAC1533_RS05635	transcription elongation factor GreA	GSS_RS03970	transcription elongation factor GreA	Lacidipiscis_RS11330	transcription elongation factor GreA
LAC1533_RS05650	NADPH-dependent oxidoreductase	GSS_RS12530	NADPH-dependent oxidoreductase	Lacidipiscis_RS01510	NADPH-dependent oxidoreductase
LAC1533_RS05655	hypothetical protein	GSS_RS03955	hypothetical protein	Lacidipiscis_RS01505	hypothetical protein
LAC1533_RS05660	nucleoside hydrolase	GSS_RS03950	nucleoside hydrolase	Lacidipiscis_RS01500	nucleoside hydrolase
LAC1533_RS05670	16S rRNA (uracil(1498)-N(3))-methyltransferase	GSS_RS03940	16S rRNA (uracil(1498)-N(3))-methyltransferase	Lacidipiscis_RS01480	16S rRNA (uracil(1498)-N(3))-methyltransferase
LAC1533_RS05930	hypothetical protein	GSS_RS03935	hypothetical protein	Lacidipiscis_RS01240	hypothetical protein
LAC1533_RS05935	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	GSS_RS03930	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	Lacidipiscis_RS01235	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase
LAC1533_RS05940	D-tyrosyl-tRNA(Tyr) deacylase	GSS_RS03925	D-tyrosyl-tRNA(Tyr) deacylase	Lacidipiscis_RS01230	D-tyrosyl-tRNA(Tyr) deacylase
LAC1533_RS05945	esterase	GSS_RS03915	alpha/beta hydrolase fold family protein	Lacidipiscis_RS01225	esterase
LAC1533_RS05950	haloacid dehalogenase	GSS_RS03910	haloacid dehalogenase-like hydrolase	Lacidipiscis_RS01220	haloacid dehalogenase
LAC1533_RS05955	N-acetylmuramoyl-L-alanine amidase	GSS_RS03905	N-acetylmuramoyl-L-alanine amidase	Lacidipiscis_RS02320	N-acetylmuramoyl-L-alanine amidase
LAC1533_RS05960	histidine--tRNA ligase	GSS_RS03900	histidine--tRNA ligase	Lacidipiscis_RS02315	histidine--tRNA ligase
LAC1533_RS05965	aspartate--tRNA ligase	GSS_RS03895	aspartate--tRNA ligase	Lacidipiscis_RS02310	aspartate--tRNA ligase
LAC1533_RS05970	YitT family protein	GSS_RS03890	YitT family protein	Lacidipiscis_RS02305	YitT family protein
LAC1533_RS05975	teichoic acid biosynthesis protein	GSS_RS03885	teichoic acid biosynthesis protein	Lacidipiscis_RS02300	teichoic acid biosynthesis protein
LAC1533_RS05980	deoxyribonuclease IV	GSS_RS03880	deoxyribonuclease IV	Lacidipiscis_RS02295	deoxyribonuclease IV
LAC1533_RS05985	kinase/pyrophosphorylase	GSS_RS03875	kinase/pyrophosphorylase	Lacidipiscis_RS02290	kinase/pyrophosphorylase
LAC1533_RS05990	30S ribosomal protein S21	GSS_RS03870	30S ribosomal protein S21	Lacidipiscis_RS02285	30S ribosomal protein S21
LAC1533_RS05995	GatB/YqeY domain-containing protein	GSS_RS03865	GatB/YqeY domain-containing protein	Lacidipiscis_RS02280	GatB/YqeY domain-containing protein
LAC1533_RS06000	PhoH family protein	GSS_RS03860	PhoH family protein	Lacidipiscis_RS04615	PhoH family protein
LAC1533_RS06005	rRNA maturation RNase YbeY	GSS_RS03855	rRNA maturation RNase YbeY	Lacidipiscis_RS04620	rRNA maturation RNase YbeY
LAC1533_RS06010	diacylglycerol kinase	GSS_RS03850	diacylglycerol kinase	Lacidipiscis_RS04625	UDP kinase
LAC1533_RS06015	GTPase Era	GSS_RS03845	GTPase Era	Lacidipiscis_RS04630	GTPase Era
LAC1533_RS06020	DNA repair protein RecO	GSS_RS03840	DNA repair protein RecO	Lacidipiscis_RS04635	DNA repair protein RecO
LAC1533_RS06025	glycine--tRNA ligase subunit alpha	GSS_RS03835	glycine--tRNA ligase subunit alpha	Lacidipiscis_RS07850	glycine--tRNA ligase subunit alpha
LAC1533_RS06030	glycine--tRNA ligase subunit beta	GSS_RS03830	glycine--tRNA ligase subunit beta	Lacidipiscis_RS07845	glycine--tRNA ligase subunit beta
LAC1533_RS06035	DNA primase	GSS_RS03825	DNA primase	Lacidipiscis_RS07840	DNA primase
LAC1533_RS06040	RNA polymerase sigma factor RpoD	GSS_RS03820	RNA polymerase sigma factor RpoD	Lacidipiscis_RS07835	RNA polymerase sigma factor RpoD
LAC1533_RS06045	tRNA (adenine(22)-N(1))-methyltransferase TrmK	GSS_RS03815	tRNA (adenine(22)-N(1))-methyltransferase TrmK	Lacidipiscis_RS11250	SAM-dependent methyltransferase
LAC1533_RS06050	Nif3-like dinuclear metal center hexameric protein	GSS_RS03810	Nif3-like dinuclear metal center hexameric protein	Lacidipiscis_RS11245	Nif3-like dinuclear metal center hexameric protein
LAC1533_RS06055	peptidase T	GSS_RS03805	peptidase T	Lacidipiscis_RS11240	peptidase T
LAC1533_RS06080	ATP-dependent chaperone ClpB	GSS_RS00005	chaperone ClpB	Lacidipiscis_RS11235	ATP-dependent chaperone ClpB
LAC1533_RS06100	DNA polymerase III subunit alpha	GSS_RS00020	DNA polymerase III subunit alpha	Lacidipiscis_RS10170	DNA polymerase III subunit alpha
LAC1533_RS06105	6-phosphofructokinase	GSS_RS00025	6-phosphofructokinase	Lacidipiscis_RS10165	6-phosphofructokinase
LAC1533_RS06110	pyruvate kinase	GSS_RS00030	pyruvate kinase	Lacidipiscis_RS10160	pyruvate kinase
LAC1533_RS06115	DUF441 domain-containing protein	GSS_RS00035	DUF441 domain-containing protein	Lacidipiscis_RS05240	DUF441 domain-containing protein
LAC1533_RS06120	S1 RNA-binding protein	GSS_RS00040	S1 RNA-binding protein	Lacidipiscis_RS05245	DNA-binding protein
LAC1533_RS06125	transcriptional repressor	GSS_RS00045	transcriptional repressor	Lacidipiscis_RS05250	transcriptional repressor
LAC1533_RS06130	site-specific tyrosine recombinase XerD	GSS_RS11455	site-specific tyrosine recombinase XerD	Lacidipiscis_RS05255	site-specific tyrosine recombinase XerD
LAC1533_RS06135	GNAT family N-acetyltransferase	GSS_RS00050	GNAT family N-acetyltransferase	Lacidipiscis_RS05260	GNAT family N-acetyltransferase
LAC1533_RS06140	rifampin ADP-ribosyl transferase	GSS_RS00055	rifampin ADP-ribosyl transferase	Lacidipiscis_RS05265	rifampin ADP-ribosyl transferase
LAC1533_RS06145	SMC-Scp complex subunit ScpB	GSS_RS00060	SMC-Scp complex subunit ScpB	Lacidipiscis_RS05270	SMC-Scp complex subunit ScpB
LAC1533_RS06150	rRNA pseudouridine synthase	GSS_RS00065	rRNA pseudouridine synthase	Lacidipiscis_RS05275	rRNA pseudouridine synthase
LAC1533_RS06155	hypothetical protein	GSS_RS00070	hypothetical protein	Lacidipiscis_RS05280	hypothetical protein
LAC1533_RS06160	ATP-dependent DNA helicase RecQ	GSS_RS00075	ATP-dependent DNA helicase RecQ	Lacidipiscis_RS05285	ATP-dependent DNA helicase RecQ
LAC1533_RS06165	LysM domain-containing protein	GSS_RS00080	LysM domain-containing protein	Lacidipiscis_RS03645	LysM domain-containing protein
LAC1533_RS06175	30S ribosomal protein S1	GSS_RS00090	30S ribosomal protein S1	Lacidipiscis_RS03635	30S ribosomal protein S1
LAC1533_RS06180	ribosome biogenesis GTPase Der	GSS_RS00095	ribosome biogenesis GTPase Der	Lacidipiscis_RS03630	ribosome biogenesis GTPase Der
LAC1533_RS06185	HU family DNA-binding protein	GSS_RS00100	HU family DNA-binding protein	Lacidipiscis_RS03625	HU family DNA-binding protein
LAC1533_RS06190	tetratricopeptide repeat protein	GSS_RS00105	tetratricopeptide repeat protein	Lacidipiscis_RS03615	tetratricopeptide repeat protein
LAC1533_RS06200	hypothetical protein	GSS_RS00110	hypothetical protein	Lacidipiscis_RS03610	hypothetical protein
LAC1533_RS06205	4-hydroxy-tetrahydrodipicolinate reductase	GSS_RS00115	4-hydroxy-tetrahydrodipicolinate reductase	Lacidipiscis_RS03595	4-hydroxy-tetrahydrodipicolinate reductase

LAC1533_RS06210	CCA tRNA nucleotidyltransferase	GSS_RS00120	CCA tRNA nucleotidyltransferase	Lacidipiscis_RS03590	CCA tRNA nucleotidyltransferase
LAC1533_RS06215	ABC transporter ATP-binding protein	GSS_RS00125	ABC transporter ATP-binding protein	Lacidipiscis_RS03585	ABC transporter ATP-binding protein
LAC1533_RS06220	thymidylate synthase	GSS_RS00130	thymidylate synthase	Lacidipiscis_RS03580	thymidylate synthase
LAC1533_RS06225	lipase	GSS_RS00135	lipase/acylhydrolase	Lacidipiscis_RS03575	lipase
LAC1533_RS06230	DUF2140 domain-containing protein	GSS_RS00140	DUF2140 domain-containing protein	Lacidipiscis_RS03570	DUF2140 domain-containing protein
LAC1533_RS06235	YozE family protein	GSS_RS13910	hypothetical protein	Lacidipiscis_RS03565	YozE family protein
LAC1533_RS06240	PDZ domain-containing protein	GSS_RS00155	PDZ domain-containing protein	Lacidipiscis_RS03555	PDZ domain-containing protein
LAC1533_RS06255	DNA-protecting protein DprA	GSS_RS00170	DNA-protecting protein DprA	Lacidipiscis_RS03540	DNA-protecting protein DprA
LAC1533_RS06260	type I DNA topoisomerase	GSS_RS00180	type I DNA topoisomerase	Lacidipiscis_RS03535	type I DNA topoisomerase
LAC1533_RS06265	tyrosine recombinase XerC	GSS_RS00185	tyrosine recombinase XerC	Lacidipiscis_RS03530	tyrosine recombinase XerC
LAC1533_RS06270	HslU--HslV peptidase proteolytic subunit	GSS_RS00190	HslU--HslV peptidase proteolytic subunit	Lacidipiscis_RS03525	HslU--HslV peptidase proteolytic subunit
LAC1533_RS06275	ATP-dependent protease ATPase subunit HslU	GSS_RS00195	ATP-dependent protease ATPase subunit HslU	Lacidipiscis_RS03520	ATP-dependent protease ATPase subunit HslU
LAC1533_RS06280	aldose 1-epimerase family protein	GSS_RS00200	aldose 1-epimerase family protein	Lacidipiscis_RS03515	aldose 1-epimerase family protein
LAC1533_RS06285	glycerol-3-phosphate acyltransferase	GSS_RS00205	glycerol-3-phosphate acyltransferase	Lacidipiscis_RS03510	glycerol-3-phosphate acyltransferase
LAC1533_RS06290	DNA topoisomerase IV subunit B	GSS_RS11985	DNA topoisomerase IV subunit B	Lacidipiscis_RS03505	DNA topoisomerase IV subunit B
LAC1533_RS06295	DNA topoisomerase IV subunit A	GSS_RS11995	hypothetical protein	Lacidipiscis_RS03500	DNA topoisomerase IV subunit A
LAC1533_RS06300	hypothetical protein	GSS_RS00225	hypothetical protein	Lacidipiscis_RS03495	hypothetical protein
LAC1533_RS06310	signal peptidase I	GSS_RS00235	signal peptidase I	Lacidipiscis_RS01700	signal peptidase I
LAC1533_RS06315	hypothetical protein	GSS_RS00240	hypothetical protein	Lacidipiscis_RS01705	hypothetical protein
LAC1533_RS06320	xylose isomerase	GSS_RS00245	xylose isomerase	Lacidipiscis_RS01710	xylose isomerase
LAC1533_RS06325	DegV family protein	GSS_RS00250	DegV family protein	Lacidipiscis_RS01715	DegV family protein
LAC1533_RS06330	MarR family transcriptional regulator	GSS_RS00255	MarR family transcriptional regulator	Lacidipiscis_RS01720	MarR family transcriptional regulator
LAC1533_RS06340	hypothetical protein	GSS_RS00265	hypothetical protein	Lacidipiscis_RS01730	hypothetical protein
LAC1533_RS06350	GNAT family N-acetyltransferase	GSS_RS00275	GNAT family N-acetyltransferase	Lacidipiscis_RS01740	GNAT family N-acetyltransferase
LAC1533_RS06355	glutamate racemase	GSS_RS00280	glutamate racemase	Lacidipiscis_RS01745	glutamate racemase
LAC1533_RS06360	aminotransferase class V-fold PLP-dependent enzyme	GSS_RS00285	aminotransferase class V-fold PLP-dependent enzyme	Lacidipiscis_RS01750	aminotransferase class V-fold PLP-dependent enzyme
LAC1533_RS06365	DeoR/GlpR transcriptional regulator	GSS_RS00290	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS01755	DeoR/GlpR transcriptional regulator
LAC1533_RS06370	manganese-dependent inorganic pyrophosphatase	GSS_RS00295	manganese-dependent inorganic pyrophosphatase	Lacidipiscis_RS01760	manganese-dependent inorganic pyrophosphatase
LAC1533_RS06375	LysR family transcriptional regulator	GSS_RS00300	LysR family transcriptional regulator	Lacidipiscis_RS01765	LysR family transcriptional regulator
LAC1533_RS06385	dihydroorotate dehydrogenase	GSS_RS00320	dihydroorotate dehydrogenase	Lacidipiscis_RS01775	dihydroorotate dehydrogenase
LAC1533_RS06395	carbamoyl phosphate synthase small subunit	GSS_RS00330	carbamoyl-phosphate synthase small subunit	Lacidipiscis_RS01785	carbamoyl phosphate synthase small subunit
LAC1533_RS06400	dihydroorotase	GSS_RS00335	dihydroorotase	Lacidipiscis_RS01790	dihydroorotase
LAC1533_RS06415	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR	GSS_RS00350	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR	Lacidipiscis_RS01805	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR
LAC1533_RS06420	RluA family pseudouridine synthase	GSS_RS00355	RluA family pseudouridine synthase	Lacidipiscis_RS01810	RluA family pseudouridine synthase
LAC1533_RS06425	signal peptidase II	GSS_RS00360	signal peptidase II	Lacidipiscis_RS01815	signal peptidase II
LAC1533_RS06430	formate--tetrahydrofolate ligase	GSS_RS00365	formate--tetrahydrofolate ligase	Lacidipiscis_RS01820	formate--tetrahydrofolate ligase
LAC1533_RS06435	hypothetical protein	GSS_RS00370	hypothetical protein	Lacidipiscis_RS01825	hypothetical protein
LAC1533_RS06460	cell division regulator GpsB	GSS_RS00380	cell division regulator GpsB	Lacidipiscis_RS01840	cell division regulator GpsB
LAC1533_RS06465	DUF1273 domain-containing protein	GSS_RS12025	DUF1273 domain-containing protein	Lacidipiscis_RS01845	DUF1273 domain-containing protein
LAC1533_RS06470	Holliday junction resolvase RecU	GSS_RS00390	Holliday junction resolvase RecU	Lacidipiscis_RS01850	Holliday junction resolvase RecU
LAC1533_RS06480	endonuclease III	GSS_RS00410	endonuclease III	Lacidipiscis_RS10195	endonuclease III
LAC1533_RS06485	DnaD domain protein	GSS_RS00415	DnaD domain protein	Lacidipiscis_RS10200	DnaD domain protein
LAC1533_RS06490	asparagine--tRNA ligase	GSS_RS00420	asparagine--tRNA ligase	Lacidipiscis_RS10205	asparagine--tRNA ligase
LAC1533_RS06495	pyridoxal phosphate-dependent aminotransferase	GSS_RS00425	pyridoxal phosphate-dependent aminotransferase	Lacidipiscis_RS10210	pyridoxal phosphate-dependent aminotransferase
LAC1533_RS06500	hypothetical protein	GSS_RS00430	hypothetical protein	Lacidipiscis_RS10215	hypothetical protein
LAC1533_RS06505	hypothetical protein	GSS_RS13620	hypothetical protein	Lacidipiscis_RS10220	hypothetical protein
LAC1533_RS06510	mevalonate kinase	GSS_RS00440	mevalonate kinase	Lacidipiscis_RS10225	mevalonate kinase
LAC1533_RS06520	phosphomevalonate kinase	GSS_RS00450	phosphomevalonate kinase	Lacidipiscis_RS10235	phosphomevalonate kinase
LAC1533_RS06525	type 2 isopentenyl-diphosphate Delta-isomerase	GSS_RS00455	type 2 isopentenyl-diphosphate Delta-isomerase	Lacidipiscis_RS10240	type 2 isopentenyl-diphosphate Delta-isomerase
LAC1533_RS06530	RNA methyltransferase	GSS_RS00460	23S rRNA methyltransferase	Lacidipiscis_RS10245	RNA methyltransferase
LAC1533_RS06535	hypothetical protein	GSS_RS13625	hypothetical protein	Lacidipiscis_RS10250	hypothetical protein
LAC1533_RS06540	metal-sulfur cluster assembly factor	GSS_RS00470	metal-sulfur cluster assembly factor	Lacidipiscis_RS10255	metal-sulfur cluster assembly factor
LAC1533_RS06545	S9 family serine peptidase	GSS_RS00475	S9 family serine peptidase	Lacidipiscis_RS10260	S9 family serine peptidase
LAC1533_RS06550	Cof-type HAD-IIB family hydrolase	GSS_RS00485	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS10265	Cof-type HAD-IIB family hydrolase
LAC1533_RS06555	diaminopimelate decarboxylase	GSS_RS00490	diaminopimelate decarboxylase	Lacidipiscis_RS10270	diaminopimelate decarboxylase
LAC1533_RS06565	hypothetical protein	GSS_RS13630	hypothetical protein	Lacidipiscis_RS10280	hypothetical protein
LAC1533_RS06580	elongation factor Ts	GSS_RS00505	elongation factor Ts	Lacidipiscis_RS10285	elongation factor Ts
LAC1533_RS06585	30S ribosomal protein S2	GSS_RS00510	30S ribosomal protein S2	Lacidipiscis_RS10290	30S ribosomal protein S2
LAC1533_RS06590	lactate dehydrogenase	GSS_RS00515	lactate dehydrogenase	Lacidipiscis_RS10295	lactate dehydrogenase
LAC1533_RS06595	GIY-YIG nuclease family protein	GSS_RS00520	GIY-YIG nuclease family protein	Lacidipiscis_RS10300	GIY-YIG nuclease family protein
LAC1533_RS06605	1-acyl-sn-glycerol-3-phosphate acyltransferase	GSS_RS00530	1-acyl-sn-glycerol-3-phosphate acyltransferase	Lacidipiscis_RS10310	1-acyl-sn-glycerol-3-phosphate acyltransferase
LAC1533_RS06610	hypothetical protein	GSS_RS00535	hypothetical protein	Lacidipiscis_RS10315	hypothetical protein
LAC1533_RS06615	DUF896 family protein	GSS_RS00540	DUF896 family protein	Lacidipiscis_RS10320	DUF896 family protein
LAC1533_RS06620	transcriptional repressor LexA	GSS_RS00545	transcriptional repressor LexA	Lacidipiscis_RS10325	transcriptional repressor LexA
LAC1533_RS06635	ArgR family transcriptional regulator	GSS_RS00555	ArgR family transcriptional regulator	Lacidipiscis_RS10335	ArgR family transcriptional regulator
LAC1533_RS06640	TlyA family rRNA (cytidine-2-O)-methyltransferase	GSS_RS00560	TlyA family rRNA (cytidine-2-O)-methyltransferase	Lacidipiscis_RS10340	TlyA family rRNA (cytidine-2-O)-methyltransferase
LAC1533_RS06645	polyprenyl synthetase family protein	GSS_RS00565	polyprenyl synthetase family protein	Lacidipiscis_RS10345	polyprenyl synthetase family protein
LAC1533_RS06650	exodeoxyribonuclease VII small subunit	GSS_RS00570	exodeoxyribonuclease VII small subunit	Lacidipiscis_RS10350	exodeoxyribonuclease VII small subunit

LAC1533_RS06655	exodeoxyribonuclease VII large subunit	GSS_RS00575	exodeoxyribonuclease VII large subunit	Lacidipiscis_RS10355	exodeoxyribonuclease VII large subunit
LAC1533_RS06660	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	GSS_RS00580	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	Lacidipiscis_RS10360	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD
LAC1533_RS06665	transcription antitermination factor NusB	GSS_RS00585	transcription antitermination factor NusB	Lacidipiscis_RS10365	transcription antitermination factor NusB
LAC1533_RS06670	Asp23/Gls24 family envelope stress response protein	GSS_RS00590	Asp23/Gls24 family envelope stress response protein	Lacidipiscis_RS10370	Asp23/Gls24 family envelope stress response protein
LAC1533_RS06675	elongation factor P	GSS_RS00595	elongation factor P	Lacidipiscis_RS10375	elongation factor P
LAC1533_RS06685	50S ribosomal protein L27	GSS_RS00605	50S ribosomal protein L27	Lacidipiscis_RS10385	50S ribosomal protein L27
LAC1533_RS06690	ribosomal-processing cysteine protease Prp	GSS_RS00610	ribosomal-processing cysteine protease Prp	Lacidipiscis_RS10390	ribosomal-processing cysteine protease Prp
LAC1533_RS06695	50S ribosomal protein L21	GSS_RS00615	50S ribosomal protein L21	Lacidipiscis_RS10395	50S ribosomal protein L21
LAC1533_RS06705	1-acyl-sn-glycerol-3-phosphate acyltransferase	GSS_RS12100	1-acyl-sn-glycerol-3-phosphate acyltransferase	Lacidipiscis_RS10405	1-acyl-sn-glycerol-3-phosphate acyltransferase
LAC1533_RS06720	hypothetical protein	GSS_RS00920	hypothetical protein	Lacidipiscis_RS08600	hypothetical protein
LAC1533_RS06725	hypothetical protein	GSS_RS00930	hypothetical protein	Lacidipiscis_RS02095	hypothetical protein
LAC1533_RS06730	hypothetical protein	GSS_RS00935	hypothetical protein	Lacidipiscis_RS02100	hypothetical protein
LAC1533_RS06735	exonuclease SbcC	GSS_RS00940	hypothetical protein	Lacidipiscis_RS02105	hypothetical protein
LAC1533_RS06740	hypothetical protein	GSS_RS00950	hypothetical protein	Lacidipiscis_RS02110	hypothetical protein
LAC1533_RS06755	acylphosphatase	GSS_RS00960	acylphosphatase	Lacidipiscis_RS02120	acylphosphatase
LAC1533_RS06770	DNA-binding response regulator	GSS_RS00975	DNA-binding response regulator	Lacidipiscis_RS02135	DNA-binding response regulator
LAC1533_RS06780	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	GSS_RS00980	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	Lacidipiscis_RS02140	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)
LAC1533_RS06790	trigger factor	GSS_RS12125	trigger factor	Lacidipiscis_RS02150	trigger factor
LAC1533_RS06795	elongation factor Tu	GSS_RS01000	elongation factor Tu	Lacidipiscis_RS02155	elongation factor Tu
LAC1533_RS06800	hypothetical protein	GSS_RS01015	hypothetical protein	Lacidipiscis_RS02160	hypothetical protein
LAC1533_RS06805	ribonuclease J	GSS_RS01020	RNase J family beta-CASP ribonuclease	Lacidipiscis_RS02165	ribonuclease J
LAC1533_RS06810	4-hydroxy-tetrahydrodipicolinate synthase	GSS_RS01025	4-hydroxy-tetrahydrodipicolinate synthase	Lacidipiscis_RS02170	4-hydroxy-tetrahydrodipicolinate synthase
LAC1533_RS06815	aspartate-semialdehyde dehydrogenase	GSS_RS01030	aspartate-semialdehyde dehydrogenase	Lacidipiscis_RS02175	aspartate-semialdehyde dehydrogenase
LAC1533_RS06825	30S ribosomal protein S15	GSS_RS01045	30S ribosomal protein S15	Lacidipiscis_RS02185	30S ribosomal protein S15
LAC1533_RS06830	30S ribosomal protein S20	GSS_RS01050	30S ribosomal protein S20	Lacidipiscis_RS02195	30S ribosomal protein S20
LAC1533_RS06835	DNA polymerase III subunit delta	GSS_RS13470	DNA polymerase III subunit delta	Lacidipiscis_RS02200	DNA polymerase III subunit delta
LAC1533_RS06840	DNA internalization-related competence protein ComEC/Rec2	GSS_RS12145	MBL fold metallo-hydrolase	Lacidipiscis_RS02205	DNA internalization-related competence protein ComEC/Rec2
LAC1533_RS06845	ComE operon protein 2	GSS_RS01070	ComE operon protein 2	Lacidipiscis_RS02210	ComE operon protein 2
LAC1533_RS06850	ComE operon protein 1	GSS_RS01075	ComE operon protein 1	Lacidipiscis_RS02215	ComE operon protein 1
LAC1533_RS06855	PDZ domain-containing protein	GSS_RS01080	PDZ domain-containing protein	Lacidipiscis_RS02220	PDZ domain-containing protein
LAC1533_RS06860	pantetheine-phosphate adenylyltransferase	GSS_RS01090	pantetheine-phosphate adenylyltransferase	Lacidipiscis_RS02225	pantetheine-phosphate adenylyltransferase
LAC1533_RS06870	DUF2129 domain-containing protein	GSS_RS01100	DUF2129 domain-containing protein	Lacidipiscis_RS02235	DUF2129 domain-containing protein
LAC1533_RS06875	pyruvate carboxylase	GSS_RS12155	pyruvate carboxylase	Lacidipiscis_RS02240	pyruvate carboxylase
LAC1533_RS06880	FtsW/RodA/SpoVE family cell cycle protein	GSS_RS01115	FtsW/RodA/SpoVE family cell cycle protein	Lacidipiscis_RS02245	FtsW/RodA/SpoVE family cell cycle protein
LAC1533_RS06885	DUF1507 domain-containing protein	GSS_RS01120	DUF1507 domain-containing protein	Lacidipiscis_RS02250	DUF1507 domain-containing protein
LAC1533_RS06900	inositol monophosphatase family protein	GSS_RS01130	inositol monophosphatase family protein	Lacidipiscis_RS05230	inositol monophosphatase family protein
LAC1533_RS06905	hypothetical protein	GSS_RS01135	hypothetical protein	Lacidipiscis_RS05225	hypothetical protein
LAC1533_RS06910	lactate dehydrogenase	GSS_RS01140	malate dehydrogenase	Lacidipiscis_RS05220	malate dehydrogenase
LAC1533_RS06920	peptide deformylase	GSS_RS01155	peptide deformylase	Lacidipiscis_RS03290	peptide deformylase
LAC1533_RS06925	hypothetical protein	GSS_RS01160	hypothetical protein	Lacidipiscis_RS03295	hypothetical protein
LAC1533_RS06935	DUF1447 domain-containing protein	GSS_RS01165	DUF1447 domain-containing protein	Lacidipiscis_RS03310	DUF1447 domain-containing protein
LAC1533_RS06940	ribonuclease J	GSS_RS01170	ribonuclease J	Lacidipiscis_RS03315	ribonuclease J
LAC1533_RS06945	transcriptional regulator	GSS_RS01175	transcriptional regulator	Lacidipiscis_RS03320	transcriptional regulator
LAC1533_RS06955	ATP-dependent RecD-like DNA helicase	GSS_RS01180	ATP-dependent RecD-like DNA helicase	Lacidipiscis_RS03325	ATP-dependent RecD-like DNA helicase
LAC1533_RS06960	tetratricopeptide repeat protein	GSS_RS01185	tetratricopeptide repeat protein	Lacidipiscis_RS03330	tetratricopeptide repeat protein
LAC1533_RS06965	histidine phosphatase family protein	GSS_RS01190	histidine phosphatase family protein	Lacidipiscis_RS03335	histidine phosphatase family protein
LAC1533_RS06970	tRNA 2-thiouridine(34) synthase MnmA	GSS_RS01195	tRNA 2-thiouridine(34) synthase MnmA	Lacidipiscis_RS03340	tRNA 2-thiouridine(34) synthase MnmA
LAC1533_RS06975	cysteine desulfurase	GSS_RS01200	cysteine desulfurase	Lacidipiscis_RS03345	cysteine desulfurase
LAC1533_RS06985	5-methylthioadenosine/adenosylhomocysteine nucleosidase	GSS_RS01210	5-methylthioadenosine/adenosylhomocysteine nucleosidase	Lacidipiscis_RS03355	5-methylthioadenosine/adenosylhomocysteine nucleosidase
LAC1533_RS06990	hypothetical protein	GSS_RS01215	hypothetical protein	Lacidipiscis_RS03360	hypothetical protein
LAC1533_RS06995	NUDIX hydrolase	GSS_RS01220	NUDIX hydrolase	Lacidipiscis_RS03365	NUDIX hydrolase
LAC1533_RS07000	diaminopimelate epimerase	GSS_RS12170	diaminopimelate epimerase	Lacidipiscis_RS03370	diaminopimelate epimerase
LAC1533_RS07005	isoleucine--tRNA ligase	GSS_RS01230	isoleucine--tRNA ligase	Lacidipiscis_RS03375	isoleucine--tRNA ligase
LAC1533_RS07010	DivIVA domain-containing protein	GSS_RS01235	DivIVA domain-containing protein	Lacidipiscis_RS03380	DivIVA domain-containing protein
LAC1533_RS07020	YggT family protein	GSS_RS01245	YggT family protein	Lacidipiscis_RS03390	YggT family protein
LAC1533_RS07025	cell division protein SepF	GSS_RS01250	cell division protein SepF	Lacidipiscis_RS03395	cell division protein SepF
LAC1533_RS07030	cell division protein FtsZ	GSS_RS01255	cell division protein FtsZ	Lacidipiscis_RS03400	cell division protein FtsZ
LAC1533_RS07035	cell division protein FtsA	GSS_RS01260	cell division protein FtsA	Lacidipiscis_RS03405	cell division protein FtsA
LAC1533_RS07040	hypothetical protein	GSS_RS13645	hypothetical protein	Lacidipiscis_RS03410	hypothetical protein
LAC1533_RS07050	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	GSS_RS01270	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	Lacidipiscis_RS03420	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
LAC1533_RS07055	phospho-N-acetylmuramoyl-pentapeptide- transferase	GSS_RS01275	phospho-N-acetylmuramoyl-pentapeptide- transferase	Lacidipiscis_RS03425	phospho-N-acetylmuramoyl-pentapeptide- transferase
LAC1533_RS07060	PASTA domain-containing protein	GSS_RS01280	PASTA domain-containing protein	Lacidipiscis_RS03430	PASTA domain-containing protein
LAC1533_RS07065	cell division protein FtsL	GSS_RS01285	cell division protein FtsL	Lacidipiscis_RS03435	cell division protein FtsL
LAC1533_RS07070	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	GSS_RS01290	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	Lacidipiscis_RS03440	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH
LAC1533_RS07075	transcriptional regulator MraZ	GSS_RS01295	transcriptional regulator MraZ	Lacidipiscis_RS03445	transcriptional regulator MraZ

LAC1533_RS07080	DUF3397 domain-containing protein	GSS_RS01300	DUF3397 domain-containing protein	Lacidipiscis_RS07355	DUF3397 domain-containing protein
LAC1533_RS07090	DUF4044 domain-containing protein	GSS_RS13945	DUF4044 domain-containing protein	Lacidipiscis_RS07360	DUF4044 domain-containing protein
LAC1533_RS07100	alpha/beta hydrolase	GSS_RS01305	alpha/beta hydrolase	Lacidipiscis_RS07365	alpha/beta hydrolase
LAC1533_RS07105	cardiolipin synthase	GSS_RS01310	cardiolipin synthase	Lacidipiscis_RS07370	cardiolipin synthase
LAC1533_RS07110	septum site-determining protein MinD	GSS_RS01320	septum site-determining protein MinD	Lacidipiscis_RS07375	septum site-determining protein MinD
LAC1533_RS07115	cell division inhibitor	GSS_RS01325	cell division inhibitor	Lacidipiscis_RS07380	cell division inhibitor
LAC1533_RS07125	rod shape-determining protein MreC	GSS_RS01335	rod shape-determining protein MreC	Lacidipiscis_RS07390	rod shape-determining protein MreC
LAC1533_RS07130	rod shape-determining protein	GSS_RS01340	rod shape-determining protein	Lacidipiscis_RS07395	rod shape-determining protein
LAC1533_RS07135	cold-shock protein	GSS_RS01345	cold-shock protein	Lacidipiscis_RS07400	cold-shock protein
LAC1533_RS07140	DNA repair protein	GSS_RS01350	DNA repair protein	Lacidipiscis_RS07405	DNA repair protein
LAC1533_RS07150	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	GSS_RS01360	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	Lacidipiscis_RS07415	bifunctional folylpolyglutamate synthase/dihydrofolate synthase
LAC1533_RS07155	valine--tRNA ligase	GSS_RS01365	valine--tRNA ligase	Lacidipiscis_RS07420	valine--tRNA ligase
LAC1533_RS07165	tRNA 4-thiouridine(8) synthase ThiI	GSS_RS01370	tRNA 4-thiouridine(8) synthase ThiI	Lacidipiscis_RS07425	tRNA 4-thiouridine(8) synthase ThiI
LAC1533_RS07170	cysteine desulfurase	GSS_RS01375	cysteine desulfurase	Lacidipiscis_RS07430	cysteine desulfurase
LAC1533_RS07175	septation ring formation regulator EzrA	GSS_RS01380	septation ring formation regulator EzrA	Lacidipiscis_RS07435	septation ring formation regulator EzrA
LAC1533_RS07185	30S ribosomal protein S4	GSS_RS01390	30S ribosomal protein S4	Lacidipiscis_RS07445	30S ribosomal protein S4
LAC1533_RS07190	replication-associated recombination protein A	GSS_RS01395	replication-associated recombination protein A	Lacidipiscis_RS07450	replication-associated recombination protein A
LAC1533_RS07200	DNA-3-methyladenine glycosylase I	GSS_RS01405	DNA-3-methyladenine glycosylase I	Lacidipiscis_RS07460	DNA-3-methyladenine glycosylase I
LAC1533_RS07205	aminoglycoside phosphotransferase family protein	GSS_RS01410	aminoglycoside phosphotransferase family protein	Lacidipiscis_RS03460	aminoglycoside phosphotransferase family protein
LAC1533_RS07210	amino acid permease	GSS_RS01415	amino acid permease	Lacidipiscis_RS08405	amino acid permease
LAC1533_RS07290	antitoxin RelB	GSS_RS11150	antitoxin RelB	Lacidipiscis_RS12870	RelB
LAC1533_RS07435	Fe-S cluster assembly protein SufB	GSS_RS10410	Fe-S cluster assembly protein SufB	Lacidipiscis_RS03120	Fe-S cluster assembly protein SufB
LAC1533_RS07440	SUF system NifU family Fe-S cluster assembly protein	GSS_RS10415	SUF system NifU family Fe-S cluster assembly protein	Lacidipiscis_RS03125	SUF system NifU family Fe-S cluster assembly protein
LAC1533_RS07445	cysteine desulfurase	GSS_RS10420	cysteine desulfurase	Lacidipiscis_RS03130	cysteine desulfurase
LAC1533_RS07450	Fe-S cluster assembly protein SufD	GSS_RS10425	Fe-S cluster assembly protein SufD	Lacidipiscis_RS03135	Fe-S cluster assembly protein SufD
LAC1533_RS07455	Fe-S cluster assembly ATPase SufC	GSS_RS10430	Fe-S cluster assembly ATPase SufC	Lacidipiscis_RS03140	Fe-S cluster assembly ATPase SufC
LAC1533_RS07460	arsenate reductase family protein	GSS_RS10435	arsenate reductase family protein	Lacidipiscis_RS03145	arsenate reductase family protein
LAC1533_RS07465	rod shape-determining protein RodA	GSS_RS10445	rod shape-determining protein	Lacidipiscis_RS03150	rod shape-determining protein RodA
LAC1533_RS07470	DUF2969 domain-containing protein	GSS_RS10450	DUF2969 domain-containing protein	Lacidipiscis_RS03155	DUF2969 domain-containing protein
LAC1533_RS07475	membrane protein insertion efficiency factor YidD	GSS_RS10455	membrane protein insertion efficiency factor YidD	Lacidipiscis_RS03160	membrane protein insertion efficiency factor YidD
LAC1533_RS07480	rod shape-determining protein	GSS_RS10460	rod shape-determining protein	Lacidipiscis_RS03165	rod shape-determining protein
LAC1533_RS07485	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	GSS_RS10465	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Lacidipiscis_RS03170	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
LAC1533_RS07490	membrane protein	GSS_RS10470	membrane protein	Lacidipiscis_RS03175	membrane protein
LAC1533_RS07500	F0F1 ATP synthase subunit epsilon	GSS_RS10475	F0F1 ATP synthase subunit epsilon	Lacidipiscis_RS06965	F0F1 ATP synthase subunit epsilon
LAC1533_RS07505	F0F1 ATP synthase subunit beta	GSS_RS10480	F0F1 ATP synthase subunit beta	Lacidipiscis_RS06960	F0F1 ATP synthase subunit beta
LAC1533_RS07510	F0F1 ATP synthase subunit gamma	GSS_RS10485	F0F1 ATP synthase subunit gamma	Lacidipiscis_RS06955	F0F1 ATP synthase subunit gamma
LAC1533_RS07515	F0F1 ATP synthase subunit alpha	GSS_RS10490	F0F1 ATP synthase subunit alpha	Lacidipiscis_RS06950	F0F1 ATP synthase subunit alpha
LAC1533_RS07520	F0F1 ATP synthase subunit delta	GSS_RS10500	F0F1 ATP synthase subunit delta	Lacidipiscis_RS06945	F0F1 ATP synthase subunit delta
LAC1533_RS07525	ATP synthase F0 subunit B	GSS_RS10505	ATP synthase F0 subunit B	Lacidipiscis_RS06940	ATP synthase F0 subunit B
LAC1533_RS07530	F0F1 ATP synthase subunit C	GSS_RS10510	F0F1 ATP synthase subunit C	Lacidipiscis_RS06935	F0F1 ATP synthase subunit C
LAC1533_RS07535	F0F1 ATP synthase subunit A	GSS_RS10515	F0F1 ATP synthase subunit A	Lacidipiscis_RS06930	F0F1 ATP synthase subunit A
LAC1533_RS07540	uracil phosphoribosyltransferase	GSS_RS10520	uracil phosphoribosyltransferase	Lacidipiscis_RS06925	uracil phosphoribosyltransferase
LAC1533_RS07545	threonylcarbamoyl-AMP synthase	GSS_RS10525	threonylcarbamoyl-AMP synthase	Lacidipiscis_RS06920	threonylcarbamoyl-AMP synthase
LAC1533_RS07550	peptide chain release factor N(5)-glutamine methyltransferase	GSS_RS10530	peptide chain release factor N(5)-glutamine methyltransferase	Lacidipiscis_RS06915	peptide chain release factor N(5)-glutamine methyltransferase
LAC1533_RS07560	thymidine kinase	GSS_RS10540	thymidine kinase	Lacidipiscis_RS06905	thymidine kinase
LAC1533_RS07565	DUF1727 domain-containing protein	GSS_RS10545	DUF1727 domain-containing protein	Lacidipiscis_RS06895	DUF1727 domain-containing protein
LAC1533_RS07570	glutamine amidotransferase	GSS_RS10550	cobyric acid synthase	Lacidipiscis_RS06890	glutamine amidotransferase
LAC1533_RS07585	mannose-6-phosphate isomerase, class I	GSS_RS10555	mannose-6-phosphate isomerase, class I	Lacidipiscis_RS06885	mannose-6-phosphate isomerase, class I
LAC1533_RS07595	hypothetical protein	GSS_RS10565	hypothetical protein	Lacidipiscis_RS06880	hypothetical protein
LAC1533_RS07600	histidine phosphatase family protein	GSS_RS10570	histidine phosphatase family protein	Lacidipiscis_RS06875	histidine phosphatase family protein
LAC1533_RS07605	hypothetical protein	GSS_RS10575	hypothetical protein	Lacidipiscis_RS06870	hypothetical protein
LAC1533_RS07660	hypothetical protein	GSS_RS11245	hypothetical protein	Lacidipiscis_RS06685	hypothetical protein
LAC1533_RS07670	XTP/dITP diphosphatase	GSS_RS11255	XTP/dITP diphosphatase	Lacidipiscis_RS06675	XTP/dITP diphosphatase
LAC1533_RS07675	DUF2507 domain-containing protein	GSS_RS11260	DUF2507 domain-containing protein	Lacidipiscis_RS06670	DUF2507 domain-containing protein
LAC1533_RS07695	endonuclease MutS2	GSS_RS09760	endonuclease MutS2	Lacidipiscis_RS06665	endonuclease MutS2
LAC1533_RS07700	CvpA family protein	GSS_RS09755	CvpA family protein	Lacidipiscis_RS06660	CvpA family protein
LAC1533_RS07705	cell division protein ZapA	GSS_RS09750	cell division protein ZapA	Lacidipiscis_RS06655	cell division protein ZapA
LAC1533_RS07710	DUF1292 domain-containing protein	GSS_RS09745	DUF1292 domain-containing protein	Lacidipiscis_RS06225	DUF1292 domain-containing protein
LAC1533_RS07715	Holliday junction resolvase RuvX	GSS_RS09740	Holliday junction resolvase RuvX	Lacidipiscis_RS06230	Holliday junction resolvase RuvX
LAC1533_RS07720	IreB family regulatory phosphoprotein	GSS_RS09735	IreB family regulatory phosphoprotein	Lacidipiscis_RS06235	IreB family regulatory phosphoprotein
LAC1533_RS07725	alanine--tRNA ligase	GSS_RS09725	alanine--tRNA ligase	Lacidipiscis_RS06240	alanine--tRNA ligase
LAC1533_RS07730	ATP-dependent helicase	GSS_RS09720	ATP-dependent helicase	Lacidipiscis_RS06245	ATP-dependent helicase
LAC1533_RS07735	bifunctional oligoribonuclease/PAP phosphatase NrnA	GSS_RS09715	bifunctional oligoribonuclease/PAP phosphatase NrnA	Lacidipiscis_RS06250	bifunctional oligoribonuclease/PAP phosphatase NrnA
LAC1533_RS07740	DNA polymerase IV	GSS_RS09710	DNA polymerase IV	Lacidipiscis_RS13155	DNA polymerase IV
LAC1533_RS07750	enoyl-[acyl-carrier-protein] reductase FabI	GSS_RS09690	enoyl-[acyl-carrier-protein] reductase FabI	Lacidipiscis_RS13145	enoyl-[acyl-carrier-protein] reductase FabI
LAC1533_RS07755	acetyl-CoA carboxylase carboxyl transferase subunit alpha	GSS_RS09685	acetyl-CoA carboxylase carboxyl transferase subunit alpha	Lacidipiscis_RS13140	acetyl-CoA carboxylase carboxyl transferase subunit alpha

LAC1533_RS07760	acetyl-CoA carboxylase carboxyltransferase subunit beta	GSS_RS09680	acetyl-CoA carboxylase carboxyltransferase subunit beta	Lacidipiscis_RS13135	acetyl-CoA carboxylase carboxyltransferase subunit beta
LAC1533_RS07765	acetyl-CoA carboxylase biotin carboxylase subunit	GSS_RS09675	acetyl-CoA carboxylase biotin carboxylase subunit	Lacidipiscis_RS13130	acetyl-CoA carboxylase biotin carboxylase subunit
LAC1533_RS07770	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	GSS_RS09670	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	Lacidipiscis_RS13125	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
LAC1533_RS07775	acetyl-CoA carboxylase biotin carboxyl carrier protein	GSS_RS09665	acetyl-CoA carboxylase biotin carboxyl carrier protein	Lacidipiscis_RS13120	acetyl-CoA carboxylase biotin carboxyl carrier protein
LAC1533_RS07780	beta-ketoacyl-[acyl-carrier-protein] synthase II	GSS_RS09660	beta-ketoacyl-[acyl-carrier-protein] synthase II	Lacidipiscis_RS13115	beta-ketoacyl-[acyl-carrier-protein] synthase II
LAC1533_RS07790	3-oxoacyl-[acyl-carrier-protein] reductase	GSS_RS09655	3-oxoacyl-[acyl-carrier-protein] reductase	Lacidipiscis_RS13105	3-oxoacyl-[acyl-carrier-protein] reductase
LAC1533_RS07795	ACP S-malonyltransferase	GSS_RS09650	ACP S-malonyltransferase	Lacidipiscis_RS13100	ACP S-malonyltransferase
LAC1533_RS07800	acyl carrier protein	GSS_RS09645	acyl carrier protein	Lacidipiscis_RS13095	acyl carrier protein
LAC1533_RS07805	ketoacyl-ACP synthase III	GSS_RS09640	ketoacyl-ACP synthase III	Lacidipiscis_RS13090	ketoacyl-ACP synthase III
LAC1533_RS07810	MarR family transcriptional regulator	GSS_RS09635	MarR family transcriptional regulator	Lacidipiscis_RS13085	MarR family transcriptional regulator
LAC1533_RS07815	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	GSS_RS09630	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	Lacidipiscis_RS13080	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
LAC1533_RS07820	thiol peroxidase	GSS_RS09625	thiol peroxidase	Lacidipiscis_RS13075	thiol peroxidase
LAC1533_RS07825	preprotein translocase subunit YajC	GSS_RS09620	preprotein translocase subunit YajC	Lacidipiscis_RS07910	preprotein translocase subunit YajC
LAC1533_RS07830	tRNA guanosine(34) transglycosylase Tgt	GSS_RS09615	tRNA guanosine(34) transglycosylase Tgt	Lacidipiscis_RS07905	tRNA guanosine(34) transglycosylase Tgt
LAC1533_RS07840	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	GSS_RS09605	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	Lacidipiscis_RS07900	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA
LAC1533_RS07845	Holliday junction branch migration DNA helicase RuvB	GSS_RS09600	Holliday junction branch migration DNA helicase RuvB	Lacidipiscis_RS07895	Holliday junction branch migration DNA helicase RuvB
LAC1533_RS07850	Holliday junction branch migration protein RuvA	GSS_RS09595	Holliday junction branch migration protein RuvA	Lacidipiscis_RS07890	Holliday junction branch migration protein RuvA
LAC1533_RS07855	DNA mismatch repair endonuclease MutL	GSS_RS09590	DNA mismatch repair endonuclease MutL	Lacidipiscis_RS07885	DNA mismatch repair endonuclease MutL
LAC1533_RS07860	DNA mismatch repair protein MutS	GSS_RS09585	DNA mismatch repair protein MutS	Lacidipiscis_RS07880	DNA mismatch repair protein MutS
LAC1533_RS07870	ribonuclease Y	GSS_RS09575	ribonuclease Y	Lacidipiscis_RS07870	ribonuclease Y
LAC1533_RS07875	recombinase RecA	GSS_RS09570	recombinase RecA	Lacidipiscis_RS07865	recombinase RecA
LAC1533_RS07880	competence/damage-inducible protein A	GSS_RS09565	competence/damage-inducible protein A	Lacidipiscis_RS07860	competence/damage-inducible protein A
LAC1533_RS07885	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	GSS_RS09555	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Lacidipiscis_RS01515	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
LAC1533_RS07890	DUF4115 domain-containing protein	GSS_RS13160	DUF4115 domain-containing protein	Lacidipiscis_RS01520	DUF4115 domain-containing protein
LAC1533_RS07895	KR domain-containing protein	GSS_RS09545	KR domain-containing protein	Lacidipiscis_RS01525	KR domain-containing protein
LAC1533_RS07905	insulinase family protein	GSS_RS09535	insulinase family protein	Lacidipiscis_RS01535	insulinase family protein
LAC1533_RS07910	DNA translocase FtsK	GSS_RS09530	DNA translocase FtsK	Lacidipiscis_RS01540	DNA translocase FtsK
LAC1533_RS07915	tRNA (cytidine(34)-2-O)-methyltransferase	GSS_RS09525	tRNA (cytidine(34)-2-O)-methyltransferase	Lacidipiscis_RS01545	tRNA (cytidine(34)-2-O)-methyltransferase
LAC1533_RS07920	methyltransferase domain-containing protein	GSS_RS09520	methyltransferase domain-containing protein	Lacidipiscis_RS01550	methyltransferase domain-containing protein
LAC1533_RS07925	aminoacyl-tRNA deacylase	GSS_RS09515	transcriptional regulator	Lacidipiscis_RS01555	aminoacyl-tRNA deacylase
LAC1533_RS07935	GMP reductase	GSS_RS09510	GMP reductase	Lacidipiscis_RS10030	GMP reductase
LAC1533_RS07940	PTS glucose transporter subunit IIA	GSS_RS09505	PTS glucose transporter subunit IIA	Lacidipiscis_RS10025	PTS glucose transporter subunit IIA
LAC1533_RS07945	lactonase family protein	GSS_RS09500	lactonase family protein	Lacidipiscis_RS10020	lactonase family protein
LAC1533_RS07950	copper homeostasis protein CutC	GSS_RS09495	copper homeostasis protein CutC	Lacidipiscis_RS10015	copper homeostasis protein CutC
LAC1533_RS07970	UDP-glucose--hexose-1-phosphate uridylyltransferase	GSS_RS09485	galactose-1-phosphate uridylyltransferase	Lacidipiscis_RS10010	UDP-glucose--hexose-1-phosphate uridylyltransferase
LAC1533_RS07975	galactokinase	GSS_RS09480	galactokinase	Lacidipiscis_RS10005	galactokinase
LAC1533_RS07980	LacI family DNA-binding transcriptional regulator	GSS_RS09475	LacI family DNA-binding transcriptional regulator	Lacidipiscis_RS10000	LacI family DNA-binding transcriptional regulator
LAC1533_RS07985	magnesium transporter	GSS_RS09470	magnesium transporter	Lacidipiscis_RS09995	magnesium transporter
LAC1533_RS07990	RluA family pseudouridine synthase	GSS_RS09465	RluA family pseudouridine synthase	Lacidipiscis_RS09990	RluA family pseudouridine synthase
LAC1533_RS07995	NAD kinase	GSS_RS09460	NAD kinase	Lacidipiscis_RS09985	NAD kinase
LAC1533_RS08010	hypothetical protein	GSS_RS13150	putative competence protein/transcription factor	Lacidipiscis_RS04970	hypothetical protein
LAC1533_RS08015	adapter protein MecA	GSS_RS09440	adapter protein MecA	Lacidipiscis_RS04975	adaptor protein MecA
LAC1533_RS08025	transcriptional regulator Spx	GSS_RS09435	transcriptional regulator Spx	Lacidipiscis_RS04980	transcriptional regulator Spx
LAC1533_RS08030	anaerobic ribonucleoside-triphosphate reductase activating protein	GSS_RS13145	anaerobic ribonucleoside-triphosphate reductase activating protein	Lacidipiscis_RS04985	anaerobic ribonucleoside-triphosphate reductase activating protein
LAC1533_RS08035	anaerobic ribonucleoside-triphosphate reductase	GSS_RS09415	anaerobic ribonucleoside-triphosphate reductase	Lacidipiscis_RS04990	anaerobic ribonucleoside-triphosphate reductase
LAC1533_RS08040	XRE family transcriptional regulator	GSS_RS00890	XRE family transcriptional regulator	Lacidipiscis_RS04995	XRE family transcriptional regulator
LAC1533_RS08045	ImmA/IrrE family metallo-endopeptidase	GSS_RS12095	ImmA/IrrE family metallo-endopeptidase	Lacidipiscis_RS07680	ImmA/IrrE family metallo-endopeptidase
LAC1533_RS08140	hypothetical protein	GSS_RS05665	hypothetical protein	Lacidipiscis_RS10925	hypothetical protein
LAC1533_RS08145	LTA synthase family protein	GSS_RS05660	LTA synthase family protein	Lacidipiscis_RS10920	LTA synthase family protein
LAC1533_RS08150	DUF1797 domain-containing protein	GSS_RS05655	DUF1797 domain-containing protein	Lacidipiscis_RS10915	DUF1797 domain-containing protein
LAC1533_RS08155	TIGR00374 family protein	GSS_RS05650	UPF0104 family protein	Lacidipiscis_RS03690	TIGR00374 family protein
LAC1533_RS08160	glycosyl transferase	GSS_RS05645	glycosyl transferase	Lacidipiscis_RS03695	glycosyl transferase
LAC1533_RS08165	glycosyltransferase family 4 protein	GSS_RS05640	glycosyltransferase family 4 protein	Lacidipiscis_RS03700	glycosyltransferase family 4 protein
LAC1533_RS08170	phosphoenolpyruvate--protein phosphotransferase	GSS_RS05635	phosphoenolpyruvate--protein phosphotransferase	Lacidipiscis_RS03705	phosphoenolpyruvate--protein phosphotransferase
LAC1533_RS08175	phosphocarrier protein HPr	GSS_RS05630	phosphocarrier protein HPr	Lacidipiscis_RS03710	phosphocarrier protein HPr
LAC1533_RS08180	hypothetical protein	GSS_RS05625	hypothetical protein	Lacidipiscis_RS03850	hypothetical protein
LAC1533_RS08185	ATP-dependent Clp protease ATP-binding subunit	GSS_RS05620	ATP-dependent Clp protease ATP-binding subunit	Lacidipiscis_RS03855	ATP-dependent Clp protease ATP-binding subunit
LAC1533_RS08190	DUF1827 domain-containing protein	GSS_RS05615	DUF1827 domain-containing protein	Lacidipiscis_RS02505	DUF1827 domain-containing protein
LAC1533_RS08195	hypothetical protein	GSS_RS05610	hypothetical protein	Lacidipiscis_RS02510	hypothetical protein
LAC1533_RS08200	peptide chain release factor 3	GSS_RS05605	peptide chain release factor 3	Lacidipiscis_RS02515	peptide chain release factor 3
LAC1533_RS08205	HlyC/CorC family transporter	GSS_RS05600	HlyC/CorC family transporter	Lacidipiscis_RS02520	HlyC/CorC family transporter

LAC1533_RS08210	LysM peptidoglycan-binding domain-containing protein	GSS_RS05595	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS02525	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS08215	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	GSS_RS05590	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	Lacidipiscis_RS02530	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
LAC1533_RS08220	DUF402 domain-containing protein	GSS_RS05585	DUF402 domain-containing protein	Lacidipiscis_RS02535	DUF402 domain-containing protein
LAC1533_RS08225	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	GSS_RS05580	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	Lacidipiscis_RS02540	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
LAC1533_RS08230	recombination regulator RecX	GSS_RS05575	recombination regulator RecX	Lacidipiscis_RS02545	recombination regulator RecX
LAC1533_RS08235	YihY/virulence factor BrkB family protein	GSS_RS05570	YihY/virulence factor BrkB family protein	Lacidipiscis_RS02550	YihY/virulence factor BrkB family protein
LAC1533_RS08240	LysM peptidoglycan-binding domain-containing protein	GSS_RS05565	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS02555	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS08245	UTP--glucose-1-phosphate uridylyltransferase	GSS_RS05560	UTP--glucose-1-phosphate uridylyltransferase	Lacidipiscis_RS02565	UTP--glucose-1-phosphate uridylyltransferase
LAC1533_RS08250	type I methionyl aminopeptidase	GSS_RS05555	type I methionyl aminopeptidase	Lacidipiscis_RS02570	type I methionyl aminopeptidase
LAC1533_RS08255	flavodoxin	GSS_RS05550	flavodoxin	Lacidipiscis_RS02575	flavodoxin
LAC1533_RS08260	GtrA family protein	GSS_RS05545	GtrA family protein	Lacidipiscis_RS02580	GtrA family protein
LAC1533_RS08265	hypothetical protein	GSS_RS05535	membrane protein	Lacidipiscis_RS02585	hypothetical protein
LAC1533_RS08270	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	GSS_RS05530	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	Lacidipiscis_RS02590	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)
LAC1533_RS08280	DUF3284 domain-containing protein	GSS_RS05515	DUF3284 domain-containing protein	Lacidipiscis_RS02600	DUF3284 domain-containing protein
LAC1533_RS08285	ATP-dependent helicase	GSS_RS05510	ATP-dependent helicase	Lacidipiscis_RS02605	ATP-dependent helicase
LAC1533_RS08290	gfo/Idh/MocA family oxidoreductase	GSS_RS05505	gfo/Idh/MocA family oxidoreductase	Lacidipiscis_RS02610	gfo/Idh/MocA family oxidoreductase
LAC1533_RS08295	Zn-dependent protease	GSS_RS05500	Zn-dependent protease	Lacidipiscis_RS05815	Zn-dependent protease
LAC1533_RS08300	CvpA family protein	GSS_RS05495	CvpA family protein	Lacidipiscis_RS05810	CvpA family protein
LAC1533_RS08315	phosphate ABC transporter substrate-binding protein	GSS_RS05490	phosphate ABC transporter substrate-binding protein	Lacidipiscis_RS05805	phosphate ABC transporter substrate-binding protein
LAC1533_RS08350	DUF4828 domain-containing protein	GSS_RS05485	DUF4828 domain-containing protein	Lacidipiscis_RS05800	DUF4828 domain-containing protein
LAC1533_RS08360	1,3-propanediol dehydrogenase	GSS_RS05480	1,3-propanediol dehydrogenase	Lacidipiscis_RS05850	1,3-propanediol dehydrogenase
LAC1533_RS08365	ECF transporter S component	GSS_RS05475	ECF transporter S component	Lacidipiscis_RS05845	ECF transporter S component
LAC1533_RS08630	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	GSS_RS05300	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	Lacidipiscis_RS08555	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
LAC1533_RS08635	diacylglycerol kinase	GSS_RS05295	diacylglycerol kinase	Lacidipiscis_RS08560	diacylglycerol kinase
LAC1533_RS08640	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	GSS_RS05290	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	Lacidipiscis_RS08565	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB
LAC1533_RS08645	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA	GSS_RS05285	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA	Lacidipiscis_RS08570	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA
LAC1533_RS08650	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC	GSS_RS05280	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC	Lacidipiscis_RS08575	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC
LAC1533_RS08655	CamS family sex pheromone protein	GSS_RS05275	CamS family sex pheromone protein	Lacidipiscis_RS08580	CamS family sex pheromone protein
LAC1533_RS08660	NAD-dependent DNA ligase LigA	GSS_RS05270	NAD-dependent DNA ligase LigA	Lacidipiscis_RS08585	NAD-dependent DNA ligase LigA
LAC1533_RS08665	DNA helicase PcrA	GSS_RS05265	DNA helicase PcrA	Lacidipiscis_RS08590	DNA helicase PcrA
LAC1533_RS08670	ATP-grasp domain-containing protein	GSS_RS05260	ATP-grasp domain-containing protein	Lacidipiscis_RS05600	ATP-grasp domain-containing protein
LAC1533_RS08675	xanthine phosphoribosyltransferase	GSS_RS05255	xanthine phosphoribosyltransferase	Lacidipiscis_RS05605	xanthine phosphoribosyltransferase
LAC1533_RS08680	lysozyme	GSS_RS05250	lysozyme	Lacidipiscis_RS05610	lysozyme
LAC1533_RS08685	ECF transporter S component	GSS_RS05245	ECF transporter S component	Lacidipiscis_RS05615	ECF transporter S component
LAC1533_RS08690	MarR family transcriptional regulator	GSS_RS05235	MarR family transcriptional regulator	Lacidipiscis_RS08030	MarR family transcriptional regulator
LAC1533_RS08695	DUF454 domain-containing protein	GSS_RS05230	DUF454 domain-containing protein	Lacidipiscis_RS08035	DUF454 domain-containing protein
LAC1533_RS08700	DNA topoisomerase III	GSS_RS05225	DNA topoisomerase III	Lacidipiscis_RS08040	DNA topoisomerase III
LAC1533_RS08705	50S ribosomal protein L7/L12	GSS_RS05220	50S ribosomal protein L7/L12	Lacidipiscis_RS08045	50S ribosomal protein L7/L12
LAC1533_RS08710	50S ribosomal protein L10	GSS_RS05215	50S ribosomal protein L10	Lacidipiscis_RS08050	50S ribosomal protein L10
LAC1533_RS08715	50S ribosomal protein L1	GSS_RS05210	50S ribosomal protein L1	Lacidipiscis_RS08055	50S ribosomal protein L1
LAC1533_RS08720	50S ribosomal protein L11	GSS_RS05205	50S ribosomal protein L11	Lacidipiscis_RS08060	50S ribosomal protein L11
LAC1533_RS08725	transcription termination/antitermination protein NusG	GSS_RS05200	transcription termination/antitermination protein NusG	Lacidipiscis_RS08065	transcription termination/antitermination protein NusG
LAC1533_RS08730	preprotein translocase subunit SecE	GSS_RS05195	preprotein translocase subunit SecE	Lacidipiscis_RS08070	preprotein translocase subunit SecE
LAC1533_RS08735	50S ribosomal protein L33	GSS_RS05190	50S ribosomal protein L33	Lacidipiscis_RS08075	50S ribosomal protein L33
LAC1533_RS08740	NYN domain-containing protein	GSS_RS05185	NYN domain-containing protein	Lacidipiscis_RS08080	NYN domain-containing protein
LAC1533_RS08745	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB	GSS_RS05180	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB	Lacidipiscis_RS08085	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB
LAC1533_RS08750	hypothetical protein	GSS_RS05175	hypothetical protein	Lacidipiscis_RS08090	hypothetical protein
LAC1533_RS08755	cysteine--tRNA ligase	GSS_RS05170	cysteine--tRNA ligase	Lacidipiscis_RS08095	cysteine--tRNA ligase
LAC1533_RS08760	glutamate--tRNA ligase	GSS_RS05165	glutamate--tRNA ligase	Lacidipiscis_RS08100	glutamate--tRNA ligase
LAC1533_RS08765	PIN/TRAM domain-containing protein	GSS_RS05160	PIN/TRAM domain-containing protein	Lacidipiscis_RS08105	PIN/TRAM domain-containing protein
LAC1533_RS08770	DNA repair protein RadA	GSS_RS05155	DNA repair protein RadA	Lacidipiscis_RS08110	DNA repair protein RadA
LAC1533_RS08775	dUTP diphosphatase	GSS_RS05150	dUTP diphosphatase	Lacidipiscis_RS08115	dUTP diphosphatase
LAC1533_RS08780	ribose-5-phosphate isomerase RpiA	GSS_RS05145	ribose-5-phosphate isomerase RpiA	Lacidipiscis_RS08120	ribose-5-phosphate isomerase RpiA
LAC1533_RS08785	aminopeptidase C	GSS_RS05140	aminopeptidase C	Lacidipiscis_RS08125	aminopeptidase
LAC1533_RS08790	phosphoglycerate mutase	GSS_RS05135	phosphoglycerate mutase	Lacidipiscis_RS08130	phosphoglycerate mutase
LAC1533_RS08810	malate transporter	GSS_RS05115	malate transporter	Lacidipiscis_RS10125	malate transporter
LAC1533_RS08815	LytR family transcriptional regulator	GSS_RS12625	LytR family transcriptional regulator	Lacidipiscis_RS10120	LytR family transcriptional regulator
LAC1533_RS08820	ketoacyl-ACP synthase III	GSS_RS05100	ketoacyl-ACP synthase III	Lacidipiscis_RS10115	ketoacyl-ACP synthase III
LAC1533_RS08830	SprT family protein	GSS_RS05090	SprT family protein	Lacidipiscis_RS10105	SprT family protein
LAC1533_RS08835	DNA helicase RecQ	GSS_RS05085	DNA helicase RecQ	Lacidipiscis_RS10100	DNA helicase RecQ
LAC1533_RS08845	ammonia-dependent NAD(+) synthetase	GSS_RS05075	ammonia-dependent NAD(+) synthetase	Lacidipiscis_RS10090	ammonia-dependent NAD(+) synthetase
LAC1533_RS08850	glycosyltransferase	GSS_RS05070	glycosyltransferase	Lacidipiscis_RS10085	glycosyltransferase
LAC1533_RS08860	30S ribosomal protein S9	GSS_RS05065	30S ribosomal protein S9	Lacidipiscis_RS05925	30S ribosomal protein S9
LAC1533_RS08865	50S ribosomal protein L13	GSS_RS05060	50S ribosomal protein L13	Lacidipiscis_RS05930	50S ribosomal protein L13
LAC1533_RS08870	tRNA pseudouridine(38-40) synthase TruA	GSS_RS05055	tRNA pseudouridine(38-40) synthase TruA	Lacidipiscis_RS05935	tRNA pseudouridine(38-40) synthase TruA
LAC1533_RS08875	energy-coupling factor transporter transmembrane protein EcfT	GSS_RS05050	energy-coupling factor transporter transmembrane protein EcfT	Lacidipiscis_RS05940	energy-coupling factor transporter transmembrane protein EcfT

LAC1533_RS08880	energy-coupling factor ABC transporter ATP-binding protein	GSS_RS05045	energy-coupling factor transporter ATPase	Lacidipiscis_RS05945	energy-coupling factor ABC transporter ATP-binding protein
LAC1533_RS08885	energy-coupling factor ABC transporter ATP-binding protein	GSS_RS05040	energy-coupling factor ABC transporter ATP-binding protein	Lacidipiscis_RS05950	energy-coupling factor ABC transporter ATP-binding protein
LAC1533_RS08890	50S ribosomal protein L17	GSS_RS05035	50S ribosomal protein L17	Lacidipiscis_RS05955	50S ribosomal protein L17
LAC1533_RS08895	DNA-directed RNA polymerase subunit alpha	GSS_RS05030	DNA-directed RNA polymerase subunit alpha	Lacidipiscis_RS05960	DNA-directed RNA polymerase subunit alpha
LAC1533_RS08900	30S ribosomal protein S11	GSS_RS05025	30S ribosomal protein S11	Lacidipiscis_RS05965	30S ribosomal protein S11
LAC1533_RS08905	30S ribosomal protein S13	GSS_RS05020	30S ribosomal protein S13	Lacidipiscis_RS05970	30S ribosomal protein S13
LAC1533_RS08910	50S ribosomal protein L36	GSS_RS05015	50S ribosomal protein L36	Lacidipiscis_RS05975	50S ribosomal protein L36
LAC1533_RS08915	translation initiation factor IF-1	GSS_RS05010	translation initiation factor IF-1	Lacidipiscis_RS05980	translation initiation factor IF-1
LAC1533_RS08920	adenylate kinase	GSS_RS05005	adenylate kinase	Lacidipiscis_RS05985	adenylate kinase
LAC1533_RS08925	preprotein translocase subunit SecY	GSS_RS05000	preprotein translocase subunit SecY	Lacidipiscis_RS05990	preprotein translocase subunit SecY
LAC1533_RS08930	50S ribosomal protein L15	GSS_RS04995	50S ribosomal protein L15	Lacidipiscis_RS05995	50S ribosomal protein L15
LAC1533_RS08935	50S ribosomal protein L30	GSS_RS04990	50S ribosomal protein L30	Lacidipiscis_RS06000	50S ribosomal protein L30
LAC1533_RS08940	30S ribosomal protein S5	GSS_RS04985	30S ribosomal protein S5	Lacidipiscis_RS06005	30S ribosomal protein S5
LAC1533_RS08945	50S ribosomal protein L18	GSS_RS04980	50S ribosomal protein L18	Lacidipiscis_RS06010	50S ribosomal protein L18
LAC1533_RS08950	50S ribosomal protein L6	GSS_RS04975	50S ribosomal protein L6	Lacidipiscis_RS06015	50S ribosomal protein L6
LAC1533_RS08955	30S ribosomal protein S8	GSS_RS04970	30S ribosomal protein S8	Lacidipiscis_RS06020	30S ribosomal protein S8
LAC1533_RS08960	type Z 30S ribosomal protein S14	GSS_RS04965	type Z 30S ribosomal protein S14	Lacidipiscis_RS06025	type Z 30S ribosomal protein S14
LAC1533_RS08965	50S ribosomal protein L5	GSS_RS04960	50S ribosomal protein L5	Lacidipiscis_RS06030	50S ribosomal protein L5
LAC1533_RS08970	50S ribosomal protein L24	GSS_RS04955	50S ribosomal protein L24	Lacidipiscis_RS06035	50S ribosomal protein L24
LAC1533_RS08975	50S ribosomal protein L14	GSS_RS04950	50S ribosomal protein L14	Lacidipiscis_RS06040	50S ribosomal protein L14
LAC1533_RS08980	30S ribosomal protein S17	GSS_RS04945	30S ribosomal protein S17	Lacidipiscis_RS06045	30S ribosomal protein S17
LAC1533_RS08985	50S ribosomal protein L29	GSS_RS04940	50S ribosomal protein L29	Lacidipiscis_RS06050	50S ribosomal protein L29
LAC1533_RS08990	50S ribosomal protein L16	GSS_RS04935	50S ribosomal protein L16	Lacidipiscis_RS06055	50S ribosomal protein L16
LAC1533_RS08995	30S ribosomal protein S3	GSS_RS04930	30S ribosomal protein S3	Lacidipiscis_RS06060	30S ribosomal protein S3
LAC1533_RS09000	50S ribosomal protein L22	GSS_RS04925	50S ribosomal protein L22	Lacidipiscis_RS06065	50S ribosomal protein L22
LAC1533_RS09005	30S ribosomal protein S19	GSS_RS04920	30S ribosomal protein S19	Lacidipiscis_RS06070	30S ribosomal protein S19
LAC1533_RS09010	50S ribosomal protein L2	GSS_RS04915	50S ribosomal protein L2	Lacidipiscis_RS06075	50S ribosomal protein L2
LAC1533_RS09015	50S ribosomal protein L23	GSS_RS04910	50S ribosomal protein L23	Lacidipiscis_RS06080	50S ribosomal protein L23
LAC1533_RS09020	50S ribosomal protein L4	GSS_RS04905	50S ribosomal protein L4	Lacidipiscis_RS06085	50S ribosomal protein L4
LAC1533_RS09025	50S ribosomal protein L3	GSS_RS04900	50S ribosomal protein L3	Lacidipiscis_RS06090	50S ribosomal protein L3
LAC1533_RS09030	30S ribosomal protein S10	GSS_RS04895	30S ribosomal protein S10	Lacidipiscis_RS06095	30S ribosomal protein S10
LAC1533_RS09040	cysteine hydrolase	GSS_RS04890	cysteine hydrolase	Lacidipiscis_RS06100	cysteine hydrolase
LAC1533_RS09045	elongation factor G	GSS_RS04885	elongation factor G	Lacidipiscis_RS06105	elongation factor G
LAC1533_RS09050	30S ribosomal protein S7	GSS_RS04880	30S ribosomal protein S7	Lacidipiscis_RS06110	30S ribosomal protein S7
LAC1533_RS09055	30S ribosomal protein S12	GSS_RS04875	30S ribosomal protein S12	Lacidipiscis_RS06115	30S ribosomal protein S12
LAC1533_RS09060	prepilin peptidase	GSS_RS14050	prepilin peptidase	Lacidipiscis_RS06120	prepilin peptidase
LAC1533_RS09075	DNA-directed RNA polymerase subunit beta	GSS_RS10275	DNA-directed RNA polymerase subunit beta	Lacidipiscis_RS09300	DNA-directed RNA polymerase subunit beta
LAC1533_RS09080	DNA-directed RNA polymerase subunit beta	GSS_RS10270	DNA-directed RNA polymerase subunit beta	Lacidipiscis_RS09305	DNA-directed RNA polymerase subunit beta
LAC1533_RS09085	ATP-dependent Clp protease ATP-binding subunit	GSS_RS10265	ATP-dependent Clp protease ATP-binding subunit	Lacidipiscis_RS09310	ATP-dependent Clp protease ATP-binding subunit
LAC1533_RS09090	CtsR family transcriptional regulator	GSS_RS10260	CtsR family transcriptional regulator	Lacidipiscis_RS09315	CtsR family transcriptional regulator
LAC1533_RS09165	tyrosine--tRNA ligase	GSS_RS08515	tyrosine--tRNA ligase	Lacidipiscis_RS07965	tyrosine--tRNA ligase
LAC1533_RS09170	transcriptional repressor	GSS_RS08510	transcriptional repressor	Lacidipiscis_RS07970	transcriptional repressor
LAC1533_RS09175	metal-dependent hydrolase	GSS_RS08505	metal-dependent hydrolase	Lacidipiscis_RS07975	metal-dependent hydrolase
LAC1533_RS09180	SMC family ATPase	GSS_RS08500	SMC family ATPase	Lacidipiscis_RS07980	SMC family ATPase
LAC1533_RS09185	exonuclease SbcCD subunit D	GSS_RS08495	exonuclease SbcCD subunit D	Lacidipiscis_RS07985	exonuclease SbcCD subunit D
LAC1533_RS09190	hypothetical protein	GSS_RS08490	hypothetical protein	Lacidipiscis_RS07990	hypothetical protein
LAC1533_RS09195	hypothetical protein	GSS_RS14125	hypothetical protein	Lacidipiscis_RS04685	hypothetical protein
LAC1533_RS09200	GntR family transcriptional regulator	GSS_RS08485	GntR family transcriptional regulator	Lacidipiscis_RS04690	GntR family transcriptional regulator
LAC1533_RS09210	class I SAM-dependent methyltransferase	GSS_RS08480	class I SAM-dependent methyltransferase	Lacidipiscis_RS04695	class I SAM-dependent methyltransferase
LAC1533_RS09215	MgtC/SapB family protein	GSS_RS08475	MgtC/SapB family protein	Lacidipiscis_RS04700	MgtC/SapB family protein
LAC1533_RS09220	glycosyltransferase family 4 protein	GSS_RS08470	glycosyltransferase family 4 protein	Lacidipiscis_RS04705	glycosyltransferase family 4 protein
LAC1533_RS09225	protein-tyrosine-phosphatase	GSS_RS08465	protein-tyrosine-phosphatase	Lacidipiscis_RS04710	protein-tyrosine-phosphatase
LAC1533_RS09230	histidine phosphatase family protein	GSS_RS08460	histidine phosphatase family protein	Lacidipiscis_RS04715	histidine phosphatase family protein
LAC1533_RS09235	D-alanine--D-alanine ligase	GSS_RS08455	D-alanine--D-alanine ligase	Lacidipiscis_RS04720	D-alanine--D-alanine ligase
LAC1533_RS09240	hypothetical protein	GSS_RS08450	hypothetical protein	Lacidipiscis_RS04725	hypothetical protein
LAC1533_RS09245	alpha/beta hydrolase	GSS_RS08445	alpha/beta hydrolase	Lacidipiscis_RS04730	alpha/beta hydrolase
LAC1533_RS09255	ASCH domain-containing protein	GSS_RS08440	ASCH domain-containing protein	Lacidipiscis_RS04735	ASCH domain-containing protein
LAC1533_RS09260	peptidase T	GSS_RS08435	peptidase T	Lacidipiscis_RS04740	peptidase T
LAC1533_RS09270	putative N-acetylmannosamine-6-phosphate 2-epimerase	GSS_RS08425	putative N-acetylmannosamine-6-phosphate 2-epimerase	Lacidipiscis_RS04750	putative N-acetylmannosamine-6-phosphate 2-epimerase
LAC1533_RS09275	hypothetical protein	GSS_RS08420	hypothetical protein	Lacidipiscis_RS04755	hypothetical protein
LAC1533_RS09280	hypothetical protein	GSS_RS08415	hypothetical protein	Lacidipiscis_RS04760	hypothetical protein
LAC1533_RS09285	hypothetical protein	GSS_RS08410	hypothetical protein	Lacidipiscis_RS04765	hypothetical protein
LAC1533_RS09290	arginase	GSS_RS08405	arginase	Lacidipiscis_RS04770	arginase
LAC1533_RS09295	OsmC family peroxiredoxin	GSS_RS08400	OsmC family peroxiredoxin	Lacidipiscis_RS04775	OsmC family peroxiredoxin

LAC1533_RS09300	hypothetical protein	GSS_RS08395	hypothetical protein	Lacidipiscis_RS04780	hypothetical protein
LAC1533_RS09305	exodeoxyribonuclease III	GSS_RS08390	exodeoxyribonuclease III	Lacidipiscis_RS04785	exodeoxyribonuclease III
LAC1533_RS09355	glutamine-hydrolyzing GMP synthase	GSS_RS08345	glutamine-hydrolyzing GMP synthase	Lacidipiscis_RS09005	glutamine-hydrolyzing GMP synthase
LAC1533_RS09365	lipase	GSS_RS08335	lipase	Lacidipiscis_RS09015	acylhydrolase
LAC1533_RS09370	ATP-dependent DNA helicase	GSS_RS08330	ATP-dependent DNA helicase	Lacidipiscis_RS09020	ATP-dependent DNA helicase
LAC1533_RS09375	potassium transporter	GSS_RS08325	potassium transporter	Lacidipiscis_RS09025	potassium transporter
LAC1533_RS09380	histidine phosphatase family protein	GSS_RS08320	histidine phosphatase family protein	Lacidipiscis_RS09030	histidine phosphatase family protein
LAC1533_RS09385	histidine phosphatase family protein	GSS_RS08315	histidine phosphatase family protein	Lacidipiscis_RS09035	histidine phosphatase family protein
LAC1533_RS09405	NERD domain-containing protein	GSS_RS08300	NERD domain-containing protein	Lacidipiscis_RS09040	NERD domain-containing protein
LAC1533_RS09415	ABC transporter ATP-binding protein	GSS_RS08295	ABC transporter ATP-binding protein	Lacidipiscis_RS09045	ABC transporter ATP-binding protein
LAC1533_RS09425	ABC transporter permease	GSS_RS08280	ABC transporter permease	Lacidipiscis_RS09055	ABC transporter permease
LAC1533_RS09430	ABC transporter permease	GSS_RS08275	ABC transporter permease	Lacidipiscis_RS09060	ABC transporter permease
LAC1533_RS09435	peptide ABC transporter substrate-binding protein	GSS_RS08270	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS09065	peptide ABC transporter substrate-binding protein
LAC1533_RS09440	GTPase HflX	GSS_RS08265	GTPase HflX	Lacidipiscis_RS09070	GTPase HflX
LAC1533_RS09445	N-acetyltransferase	GSS_RS08260	N-acetyltransferase	Lacidipiscis_RS09075	N-acetyltransferase
LAC1533_RS09455	amino acid ABC transporter permease	GSS_RS08255	amino acid ABC transporter permease	Lacidipiscis_RS09080	amino acid ABC transporter permease
LAC1533_RS09460	amino acid ABC transporter permease	GSS_RS08250	amino acid ABC transporter permease	Lacidipiscis_RS09085	amino acid ABC transporter permease
LAC1533_RS09465	glutamine ABC transporter substrate-binding protein	GSS_RS08245	glutamine ABC transporter substrate-binding protein	Lacidipiscis_RS09090	glutamine ABC transporter substrate-binding protein
LAC1533_RS09470	amino acid ABC transporter ATP-binding protein	GSS_RS08240	amino acid ABC transporter ATP-binding protein	Lacidipiscis_RS09095	amino acid ABC transporter ATP-binding protein
LAC1533_RS09490	transcriptional repressor	GSS_RS08230	transcriptional repressor	Lacidipiscis_RS07285	transcriptional repressor
LAC1533_RS09495	guanylate kinase	GSS_RS12940	guanylate kinase	Lacidipiscis_RS07290	guanylate kinase
LAC1533_RS09500	amino acid permease	GSS_RS08220	amino acid permease	Lacidipiscis_RS07295	amino acid permease
LAC1533_RS09505	hypothetical protein	GSS_RS08215	hypothetical protein	Lacidipiscis_RS07300	hypothetical protein
LAC1533_RS09515	ECF transporter S component	GSS_RS08210	ECF transporter S component	Lacidipiscis_RS07305	ECF transporter S component
LAC1533_RS09520	Xaa-Pro dipeptidyl-peptidase	GSS_RS08205	Xaa-Pro dipeptidyl-peptidase	Lacidipiscis_RS07310	Xaa-Pro dipeptidyl-peptidase
LAC1533_RS09525	metal ABC transporter substrate-binding protein	GSS_RS08200	metal ABC transporter substrate-binding protein	Lacidipiscis_RS07315	metal ABC transporter substrate-binding protein
LAC1533_RS09535	phosphate ABC transporter ATP-binding protein	GSS_RS08190	methionine ABC transporter ATP-binding protein	Lacidipiscis_RS07325	phosphate ABC transporter ATP-binding protein
LAC1533_RS09540	KR domain-containing protein	GSS_RS08185	KR domain-containing protein	Lacidipiscis_RS07330	KR domain-containing protein
LAC1533_RS09545	prolyl aminopeptidase	GSS_RS08175	prolyl aminopeptidase	Lacidipiscis_RS07335	prolyl aminopeptidase
LAC1533_RS09550	Cof-type HAD-IIB family hydrolase	GSS_RS08170	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS07340	Cof-type HAD-IIB family hydrolase
LAC1533_RS09555	DUF969 domain-containing protein	GSS_RS08165	DUF969 domain-containing protein	Lacidipiscis_RS10825	DUF969 domain-containing protein
LAC1533_RS09560	DUF979 domain-containing protein	GSS_RS08160	DUF979 domain-containing protein	Lacidipiscis_RS10820	DUF979 domain-containing protein
LAC1533_RS09565	pyroglutamyl-peptidase I	GSS_RS08155	pyroglutamyl-peptidase I	Lacidipiscis_RS10815	pyroglutamyl-peptidase I
LAC1533_RS09575	sugar ABC transporter permease	GSS_RS08145	sugar ABC transporter permease	Lacidipiscis_RS10805	sugar ABC transporter permease
LAC1533_RS09590	putative polysaccharide biosynthesis protein	GSS_RS08130	putative polysaccharide biosynthesis protein	Lacidipiscis_RS10790	putative polysaccharide biosynthesis protein
LAC1533_RS09595	DNA starvation/stationary phase protection protein	GSS_RS08125	DNA starvation/stationary phase protection protein	Lacidipiscis_RS10785	DNA starvation/stationary phase protection protein
LAC1533_RS09600	aldo/keto reductase	GSS_RS08120	aldo/keto reductase	Lacidipiscis_RS10780	aldo/keto reductase
LAC1533_RS09605	glyoxalase	GSS_RS08115	glyoxalase	Lacidipiscis_RS10775	glyoxalase
LAC1533_RS09610	hypothetical protein	GSS_RS08110	hypothetical protein	Lacidipiscis_RS10770	hypothetical protein
LAC1533_RS09615	GTP-binding protein	GSS_RS08100	GTP-binding protein	Lacidipiscis_RS10765	GTP-binding protein
LAC1533_RS09620	LysM domain-containing protein	GSS_RS08095	LysM domain-containing protein	Lacidipiscis_RS10760	LysM domain-containing protein
LAC1533_RS09630	DegV family EDD domain-containing protein	GSS_RS08080	DegV family EDD domain-containing protein	Lacidipiscis_RS10750	DegV family EDD domain-containing protein
LAC1533_RS09635	methyl-accepting chemotaxis protein	GSS_RS08075	methyl-accepting chemotaxis protein	Lacidipiscis_RS10745	methyl-accepting chemotaxis protein
LAC1533_RS09640	flagellin	GSS_RS08070	flagellar hook-associated protein 3	Lacidipiscis_RS10740	flagellar hook-associated protein 3
LAC1533_RS09645	flagellar hook-associated protein FlgK	GSS_RS08065	flagellar hook-associated protein FlgK	Lacidipiscis_RS10735	flagellar hook-associated protein FlgK
LAC1533_RS09650	hypothetical protein	GSS_RS08060	hypothetical protein	Lacidipiscis_RS10730	hypothetical protein
LAC1533_RS09655	flagellar biosynthesis anti-sigma factor FlgM	GSS_RS12920	flagellar biosynthesis anti-sigma factor FlgM	Lacidipiscis_RS10725	flagellar biosynthesis anti-sigma factor FlgM
LAC1533_RS09660	flagellar motor switch phosphatase FliY	GSS_RS08050	flagellar motor switch phosphatase FliY	Lacidipiscis_RS10720	flagellar motor switch phosphatase FliY
LAC1533_RS09665	flagellar motor switch protein FliM	GSS_RS08045	flagellar motor switch protein FliM	Lacidipiscis_RS10715	flagellar motor switch protein FliM
LAC1533_RS09670	hypothetical protein	GSS_RS08040	hypothetical protein	Lacidipiscis_RS10710	hypothetical protein
LAC1533_RS09675	response regulator	GSS_RS08035	response regulator	Lacidipiscis_RS10705	response regulator
LAC1533_RS09680	chemotaxis protein CheC	GSS_RS08030	chemotaxis protein CheC	Lacidipiscis_RS10700	chemotaxis protein CheC
LAC1533_RS09685	chemotaxis protein CheA	GSS_RS08025	chemotaxis protein CheA	Lacidipiscis_RS10695	chemotaxis protein CheA
LAC1533_RS09690	protein-glutamate O-methyltransferase CheR	GSS_RS08020	protein-glutamate O-methyltransferase CheR	Lacidipiscis_RS10690	protein-glutamate O-methyltransferase CheR
LAC1533_RS09695	chemotaxis-specific protein-glutamate methyltransferase CheB	GSS_RS08015	chemotaxis-specific protein-glutamate methyltransferase CheB	Lacidipiscis_RS10685	chemotaxis-specific protein-glutamate methyltransferase CheB
LAC1533_RS09700	chemotaxis protein CheD	GSS_RS08010	chemotaxis protein CheD	Lacidipiscis_RS10680	chemotaxis protein CheD
LAC1533_RS09705	chemotaxis protein CheW	GSS_RS08005	chemotaxis protein CheW	Lacidipiscis_RS10675	chemotaxis protein CheW
LAC1533_RS09710	hypothetical protein	GSS_RS08000	methyl-accepting chemotaxis sensory transducer	Lacidipiscis_RS10670	hypothetical protein
LAC1533_RS09715	cell division protein FtsE	GSS_RS07995	cell division protein FtsE	Lacidipiscis_RS10665	cell division protein FtsE
LAC1533_RS09720	flagellar hook basal-body protein	GSS_RS07990	flagellar hook basal-body protein	Lacidipiscis_RS10660	flagellar hook basal-body protein
LAC1533_RS09725	flagellar hook-basal body protein	GSS_RS07985	flagellar hook-basal body protein	Lacidipiscis_RS10655	flagellar hook-basal body protein
LAC1533_RS09730	FliA/WhiG family RNA polymerase sigma factor	GSS_RS07980	FliA/WhiG family RNA polymerase sigma factor	Lacidipiscis_RS10650	FliA/WhiG family RNA polymerase sigma factor
LAC1533_RS09735	flagellar biosynthesis protein FlhA	GSS_RS07975	flagellar biosynthesis protein FlhA	Lacidipiscis_RS10645	flagellar biosynthesis protein FlhA
LAC1533_RS09740	flagellar type III secretion system protein FlhB	GSS_RS07970	flagellar type III secretion system protein FlhB	Lacidipiscis_RS10640	flagellar type III secretion system protein FlhB
LAC1533_RS09745	type III secretion protein	GSS_RS07965	type III secretion protein	Lacidipiscis_RS10635	flagellar biosynthetic protein FliR
LAC1533_RS09750	flagellar biosynthetic protein FliQ	GSS_RS07960	flagellar biosynthetic protein FliQ	Lacidipiscis_RS10630	flagellar biosynthetic protein FliQ
LAC1533_RS09755	flagellar biosynthetic protein FliP	GSS_RS07955	flagellar biosynthetic protein FliP	Lacidipiscis_RS10625	flagellar biosynthetic protein FliP
LAC1533_RS09760	flagellar biosynthesis protein FliO	GSS_RS12915	flagellar biosynthesis protein FliO	Lacidipiscis_RS10620	hypothetical protein
LAC1533_RS09765	flagellar biosynthesis protein FliL	GSS_RS07945	flagellar biosynthesis protein FliL	Lacidipiscis_RS10615	hypothetical protein
LAC1533_RS09770	flagellar protein FlbD	GSS_RS07940	flagellar protein FlbD	Lacidipiscis_RS10610	endoflagellar protein
LAC1533_RS09775	flagellar hook protein	GSS_RS07935	flagellar hook protein	Lacidipiscis_RS10605	flagellar hook protein

LAC1533_RS09780	flagellar basal body rod modification protein	GSS_RS07930	flagellar basal body rod modification protein	Lacidipiscis_RS10600	hypothetical protein
LAC1533_RS09785	flagellar hook-length control protein FliK	GSS_RS12910	flagellar hook-length control protein FliK	Lacidipiscis_RS10595	flagellar hook-length control protein FliK
LAC1533_RS09790	flagellar export protein FliJ	GSS_RS07915	flagellar export protein FliJ	Lacidipiscis_RS10590	flagellar export protein FliJ
LAC1533_RS09795	flagellar protein export ATPase FliI	GSS_RS07910	flagellar protein export ATPase FliI	Lacidipiscis_RS10585	flagellar protein export ATPase FliI
LAC1533_RS09800	hypothetical protein	GSS_RS07905	flagellar assembly protein FliH	Lacidipiscis_RS10580	hypothetical protein
LAC1533_RS09805	flagellar motor switch protein FliG	GSS_RS07900	flagellar motor switch protein FliG	Lacidipiscis_RS10575	flagellar motor switch protein FliG
LAC1533_RS09810	flagellar M-ring protein FliF	GSS_RS07895	flagellar M-ring protein FliF	Lacidipiscis_RS10570	flagellar M-ring protein FliF
LAC1533_RS09815	flagellar hook-basal body complex protein FliE	GSS_RS07890	flagellar hook-basal body complex protein FliE	Lacidipiscis_RS10565	flagellar hook-basal body complex protein FliE
LAC1533_RS09820	flagellar basal body rod protein FlgC	GSS_RS07885	flagellar basal body rod protein FlgC	Lacidipiscis_RS10560	flagellar basal body rod protein FlgC
LAC1533_RS09825	flagellar basal body rod protein FlgB	GSS_RS07880	flagellar basal body rod protein FlgB	Lacidipiscis_RS10555	flagellar basal body rod protein FlgB
LAC1533_RS09835	hypothetical protein	GSS_RS08520	flagellar motor protein MotB	Lacidipiscis_RS06175	hypothetical protein
LAC1533_RS09840	flagellar motor protein MotA	GSS_RS08525	flagellar motor protein MotA	Lacidipiscis_RS06170	flagellar motor protein MotA
LAC1533_RS09845	flagellar export chaperone FliS	GSS_RS08530	flagellar export chaperone FliS	Lacidipiscis_RS06165	flagellar export chaperone FliS
LAC1533_RS09850	hypothetical protein	GSS_RS08535	hypothetical protein	Lacidipiscis_RS06160	hypothetical protein
LAC1533_RS09855	hypothetical protein	GSS_RS08540	flagellum hook associated protein FliD	Lacidipiscis_RS06155	hypothetical protein
LAC1533_RS09860	flagellar protein FlaG	GSS_RS13755	flagellar protein FlaG	Lacidipiscis_RS06150	hypothetical protein
LAC1533_RS09875	flagellin	GSS_RS08550	flagellin	Lacidipiscis_RS06145	flagellin
LAC1533_RS09880	flagellin	GSS_RS08555	flagellin	Lacidipiscis_RS06140	flagellin
LAC1533_RS09885	LysM domain-containing protein	GSS_RS08560	LysM domain-containing protein	Lacidipiscis_RS06135	LysM domain-containing protein
LAC1533_RS09900	hypothetical protein	GSS_RS08575	hypothetical protein	Lacidipiscis_RS12245	hypothetical protein
LAC1533_RS09905	aldo/keto reductase	GSS_RS08580	glyceraldehyde 3-phosphate reductase	Lacidipiscis_RS12240	aldo/keto reductase
LAC1533_RS09910	addiction module antidote protein, HigA family	GSS_RS08585	addiction module antidote protein, HigA family	Lacidipiscis_RS12235	addiction module antidote protein, HigA family
LAC1533_RS09915	plasmid maintenance system killer	GSS_RS08590	plasmid maintenance system killer	Lacidipiscis_RS12230	plasmid maintenance system killer
LAC1533_RS09925	alpha-mannosidase	GSS_RS12990	alpha-mannosidase	Lacidipiscis_RS07550	alpha-mannosidase
LAC1533_RS09935	PTS fructose transporter subunit IIB	GSS_RS08610	PTS fructose transporter subunit IIB	Lacidipiscis_RS07540	PTS fructose transporter subunit IIB
LAC1533_RS09940	hypothetical protein	GSS_RS08615	hypothetical protein	Lacidipiscis_RS07535	hypothetical protein
LAC1533_RS09955	PRD domain-containing protein	GSS_RS13000	PRD domain-containing protein	Lacidipiscis_RS07530	PRD domain-containing protein
LAC1533_RS09965	glycosyl hydrolase	GSS_RS08625	glycosyl hydrolase	Lacidipiscis_RS07520	hypothetical protein
LAC1533_RS09970	acyltransferase	GSS_RS08630	acyltransferase	Lacidipiscis_RS07515	acyltransferase
LAC1533_RS09975	hypothetical protein	GSS_RS08635	hypothetical protein	Lacidipiscis_RS07510	hypothetical protein
LAC1533_RS09980	PrsW family intramembrane metalloprotease	GSS_RS08640	PrsW family intramembrane metalloprotease	Lacidipiscis_RS07505	PrsW family intramembrane metalloprotease
LAC1533_RS09985	thioredoxin	GSS_RS08645	thioredoxin	Lacidipiscis_RS07500	thioredoxin
LAC1533_RS09990	Cof-type HAD-IIB family hydrolase	GSS_RS08650	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS07495	Cof-type HAD-IIB family hydrolase
LAC1533_RS09995	DUF475 domain-containing protein	GSS_RS08655	DUF475 domain-containing protein	Lacidipiscis_RS07490	DUF475 domain-containing protein
LAC1533_RS10000	hypothetical protein	GSS_RS08660	hypothetical protein	Lacidipiscis_RS07485	hypothetical protein
LAC1533_RS10010	XRE family transcriptional regulator	GSS_RS08665	XRE family transcriptional regulator	Lacidipiscis_RS06315	XRE family transcriptional regulator
LAC1533_RS10020	hypothetical protein	GSS_RS13790	hypothetical protein	Lacidipiscis_RS04340	LTA synthase family protein
LAC1533_RS10025	L,D-transpeptidase	GSS_RS08690	hypothetical protein	Lacidipiscis_RS04345	L,D-transpeptidase
LAC1533_RS10030	2-dehydropantoate 2-reductase	GSS_RS08700	2-dehydropantoate 2-reductase	Lacidipiscis_RS04350	2-dehydropantoate 2-reductase
LAC1533_RS10035	hypothetical protein	GSS_RS14150	hypothetical protein	Lacidipiscis_RS04355	hypothetical protein
LAC1533_RS10040	MFS transporter	GSS_RS08705	MFS transporter	Lacidipiscis_RS04360	MFS transporter
LAC1533_RS10045	PAS domain S-box protein	GSS_RS08710	PAS domain S-box protein	Lacidipiscis_RS04365	PAS domain S-box protein
LAC1533_RS10055	hypothetical protein	GSS_RS08725	hypothetical protein	Lacidipiscis_RS03455	hypothetical protein
LAC1533_RS10160	LytR family transcriptional regulator	GSS_RS08795	LytR family transcriptional regulator	Lacidipiscis_RS10185	transcriptional regulator
LAC1533_RS10175	hypothetical protein	GSS_RS13050	hypothetical protein	Lacidipiscis_RS01255	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS10210	hypothetical protein	GSS_RS08890	hypothetical protein	Lacidipiscis_RS03975	hypothetical protein
LAC1533_RS10215	MurR/RpiR family transcriptional regulator	GSS_RS08895	MurR/RpiR family transcriptional regulator	Lacidipiscis_RS03980	MurR/RpiR family transcriptional regulator
LAC1533_RS10220	PTS sugar transporter subunit IIC	GSS_RS08900	PTS sugar transporter subunit IIC	Lacidipiscis_RS03985	PTS sugar transporter subunit IIC
LAC1533_RS10225	aryl-phospho-beta-D-glucosidase	GSS_RS08905	6-phospho-beta-glucosidase	Lacidipiscis_RS03990	aryl-phospho-beta-D-glucosidase
LAC1533_RS10230	ROK family protein	GSS_RS08910	ROK family protein	Lacidipiscis_RS03995	ROK family protein
LAC1533_RS10255	dTDP-glucose 4,6-dehydratase	GSS_RS08915	dTDP-glucose 4,6-dehydratase	Lacidipiscis_RS04005	dTDP-glucose 4,6-dehydratase
LAC1533_RS10260	DegV family protein	GSS_RS08920	DegV family protein	Lacidipiscis_RS04020	DegV family protein
LAC1533_RS10265	cadmium-translocating P-type ATPase	GSS_RS08925	heavy metal translocating P-type ATPase	Lacidipiscis_RS04050	heavy metal translocating P-type ATPase
LAC1533_RS10405	glycerol-3-phosphate cytidylyltransferase	GSS_RS06455	glycerol-3-phosphate cytidylyltransferase	Lacidipiscis_RS12700	glycerol-3-phosphate cytidylyltransferase
LAC1533_RS10415	GtrA family protein	GSS_RS06505	GtrA family protein	Lacidipiscis_RS12695	GtrA family protein
LAC1533_RS10425	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	GSS_RS06450	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	Lacidipiscis_RS12690	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase
LAC1533_RS10430	IS256 family transposase	GSS_RS11465	IS256 family transposase	Lacidipiscis_RS02665	IS256 family transposase
LAC1533_RS10465	type II toxin-antitoxin system RelE/ParE family toxin	GSS_RS10960	type II toxin-antitoxin system RelE/ParE family toxin	Lacidipiscis_RS12480	type II toxin-antitoxin system RelE/ParE family toxin
LAC1533_RS10475	hypothetical protein	GSS_RS06515	hypothetical protein	Lacidipiscis_RS09920	hypothetical protein
LAC1533_RS10480	class A sortase	GSS_RS06520	class A sortase	Lacidipiscis_RS09925	class A sortase
LAC1533_RS10490	sulfite exporter TauE/SafE family protein	GSS_RS06530	sulfite exporter TauE/SafE family protein	Lacidipiscis_RS09935	sulfite exporter TauE/SafE family protein
LAC1533_RS10495	hypothetical protein	GSS_RS06535	hypothetical protein	Lacidipiscis_RS09940	hypothetical protein
LAC1533_RS10500	murein L,D-transpeptidase	GSS_RS06540	murein L,D-transpeptidase	Lacidipiscis_RS09945	murein L,D-transpeptidase
LAC1533_RS10510	PTS fructose transporter subunit IIC	GSS_RS06550	PTS fructose transporter subunit IIC	Lacidipiscis_RS09955	PTS fructose transporter subunit IIC

LAC1533_RS10515	1-phosphofructokinase	GSS_RS06555	1-phosphofructokinase	Lacidipiscis_RS09960	1-phosphofructokinase
LAC1533_RS10520	DeoR/GlpR transcriptional regulator	GSS_RS06560	DeoR/GlpR transcriptional regulator	Lacidipiscis_RS09965	DeoR/GlpR transcriptional regulator
LAC1533_RS10535	CsbD family protein	GSS_RS06575	CsbD family protein	Lacidipiscis_RS02330	CsbD family protein
LAC1533_RS10540	hypothetical protein	GSS_RS13735	hypothetical protein	Lacidipiscis_RS02335	hypothetical protein
LAC1533_RS10545	DUF1694 domain-containing protein	GSS_RS06590	DUF1694 domain-containing protein	Lacidipiscis_RS02340	DUF1694 domain-containing protein
LAC1533_RS10550	hypothetical protein	GSS_RS06595	hypothetical protein	Lacidipiscis_RS02345	hypothetical protein
LAC1533_RS10555	NERD domain-containing protein	GSS_RS14090	NERD domain-containing protein	Lacidipiscis_RS02350	NERD domain-containing protein
LAC1533_RS10560	cation:proton antiporter	GSS_RS06610	cation:proton antiporter	Lacidipiscis_RS02355	cation:proton antiporter
LAC1533_RS10565	metallophosphoesterase	GSS_RS06615	metallophosphoesterase	Lacidipiscis_RS02360	metallophosphoesterase
LAC1533_RS10595	hypothetical protein	GSS_RS06630	hypothetical protein	Lacidipiscis_RS05010	hypothetical protein
LAC1533_RS10600	hypothetical protein	GSS_RS06635	hypothetical protein	Lacidipiscis_RS05015	hypothetical protein
LAC1533_RS10605	serine/threonine transporter SstT	GSS_RS06640	serine/threonine transporter SstT	Lacidipiscis_RS05020	serine/threonine transporter SstT
LAC1533_RS10610	organic hydroperoxide resistance protein	GSS_RS06645	organic hydroperoxide resistance protein	Lacidipiscis_RS05025	organic hydroperoxide resistance protein
LAC1533_RS10615	Cof-type HAD-IIB family hydrolase	GSS_RS06655	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS05035	Cof-type HAD-IIB family hydrolase
LAC1533_RS10620	nicotinate phosphoribosyltransferase	GSS_RS06660	nicotinate phosphoribosyltransferase	Lacidipiscis_RS05040	nicotinate phosphoribosyltransferase
LAC1533_RS10625	NUDIX domain-containing protein	GSS_RS06665	NUDIX domain-containing protein	Lacidipiscis_RS05045	NUDIX domain-containing protein
LAC1533_RS10630	NADH-flavin reductase	GSS_RS06675	NADH-flavin reductase	Lacidipiscis_RS05050	NADH-flavin reductase
LAC1533_RS10635	hypothetical protein	GSS_RS06680	hypothetical protein	Lacidipiscis_RS05055	hypothetical protein
LAC1533_RS10640	hypothetical protein	GSS_RS06685	hypothetical protein	Lacidipiscis_RS05060	hypothetical protein
LAC1533_RS10645	peptide-methionine (S)-S-oxide reductase	GSS_RS06690	peptide-methionine (S)-S-oxide reductase	Lacidipiscis_RS05065	peptide-methionine (S)-S-oxide reductase
LAC1533_RS10650	thioredoxin	GSS_RS06695	thioredoxin	Lacidipiscis_RS05070	thioredoxin
LAC1533_RS10655	glutathione peroxidase	GSS_RS06700	glutathione peroxidase	Lacidipiscis_RS05075	glutathione peroxidase
LAC1533_RS10660	DUF488 domain-containing protein	GSS_RS06705	DUF488 domain-containing protein	Lacidipiscis_RS05080	DUF488 domain-containing protein
LAC1533_RS10665	N-acetyltransferase	GSS_RS06710	N-acetyltransferase	Lacidipiscis_RS05085	N-acetyltransferase
LAC1533_RS10670	pyruvate oxidase	GSS_RS06715	pyruvate oxidase	Lacidipiscis_RS05095	pyruvate oxidase
LAC1533_RS10690	universal stress protein	GSS_RS06730	universal stress protein	Lacidipiscis_RS05105	universal stress protein
LAC1533_RS10695	CPBP family intramembrane metalloprotease	GSS_RS06735	CPBP family intramembrane metalloprotease	Lacidipiscis_RS05110	CPBP family intramembrane metalloprotease
LAC1533_RS10700	deoxyguanosine kinase	GSS_RS06740	deoxyguanosine kinase	Lacidipiscis_RS05115	deoxyguanosine kinase
LAC1533_RS10705	MFS transporter	GSS_RS06745	MFS transporter	Lacidipiscis_RS05120	MFS transporter
LAC1533_RS10710	MarR family transcriptional regulator	GSS_RS06750	MarR family transcriptional regulator	Lacidipiscis_RS05125	MarR family transcriptional regulator
LAC1533_RS10715	aldo/keto reductase	GSS_RS06755	aldo/keto reductase	Lacidipiscis_RS05130	aldo/keto reductase
LAC1533_RS10720	NAD(P)/FAD-dependent oxidoreductase	GSS_RS06760	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS05135	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS10725	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase	GSS_RS06765	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase	Lacidipiscis_RS05140	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase
LAC1533_RS10730	hypothetical protein	GSS_RS06770	hypothetical protein	Lacidipiscis_RS05145	hypothetical protein
LAC1533_RS10735	aluminum resistance protein	GSS_RS06775	aluminum resistance protein	Lacidipiscis_RS05150	aluminum resistance protein
LAC1533_RS10745	hypothetical protein	GSS_RS06785	hypothetical protein	Lacidipiscis_RS05155	hypothetical protein
LAC1533_RS10755	bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase	GSS_RS06790	bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase	Lacidipiscis_RS05160	bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase
LAC1533_RS10760	penicillin-binding protein 2	GSS_RS06795	penicillin-binding protein 2	Lacidipiscis_RS05165	penicillin-binding protein 2
LAC1533_RS10765	aspartate racemase	GSS_RS06800	aspartate racemase	Lacidipiscis_RS05170	aspartate racemase
LAC1533_RS10770	carboxylate--amine ligase	GSS_RS06805	carboxylate--amine ligase	Lacidipiscis_RS05175	carboxylate--amine ligase
LAC1533_RS10775	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase	GSS_RS06810	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase	Lacidipiscis_RS05180	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase
LAC1533_RS10785	hypothetical protein	GSS_RS06815	hypothetical protein	Lacidipiscis_RS05185	hypothetical protein
LAC1533_RS10790	universal stress protein	GSS_RS06820	universal stress protein	Lacidipiscis_RS05190	universal stress protein
LAC1533_RS10795	hypothetical protein	GSS_RS06825	hypothetical protein	Lacidipiscis_RS05195	hypothetical protein
LAC1533_RS10800	aldo/keto reductase	GSS_RS06830	aldo/keto reductase	Lacidipiscis_RS05200	aldo/keto reductase
LAC1533_RS10805	peptide ABC transporter substrate-binding protein	GSS_RS06840	peptide ABC transporter substrate-binding protein	Lacidipiscis_RS05205	peptide ABC transporter substrate-binding protein
LAC1533_RS10810	branched-chain amino acid ABC transporter permease	GSS_RS06850	ABC transporter permease	Lacidipiscis_RS05210	branched-chain amino acid ABC transporter permease
LAC1533_RS10815	ABC transporter ATP-binding protein	GSS_RS06855	phosphonate ABC transporter ATP-binding protein	Lacidipiscis_RS05215	ABC transporter ATP-binding protein
LAC1533_RS10820	hypothetical protein	GSS_RS06860	membrane protein	Lacidipiscis_RS08205	hypothetical protein
LAC1533_RS10830	VanZ family protein	GSS_RS06870	VanZ family protein	Lacidipiscis_RS08215	VanZ family protein
LAC1533_RS10835	4-phosphoerythronate dehydrogenase	GSS_RS06875	4-phosphoerythronate dehydrogenase	Lacidipiscis_RS08220	hydroxyacid dehydrogenase
LAC1533_RS10845	hypothetical protein	GSS_RS06880	hypothetical protein	Lacidipiscis_RS08225	hypothetical protein
LAC1533_RS10865	energy-coupled thiamine transporter ThiT	GSS_RS06885	energy-coupled thiamine transporter ThiT	Lacidipiscis_RS08230	energy-coupled thiamine transporter ThiT
LAC1533_RS10870	energy-coupling factor transporter transmembrane protein EcfT	GSS_RS06890	energy-coupling factor transporter transmembrane protein EcfT	Lacidipiscis_RS08235	energy-coupling factor transporter transmembrane protein EcfT
LAC1533_RS10875	ABC transporter ATP-binding protein	GSS_RS06895	ABC transporter ATP-binding protein	Lacidipiscis_RS08240	ABC transporter ATP-binding protein
LAC1533_RS10880	ABC transporter permease	GSS_RS06900	ABC transporter permease	Lacidipiscis_RS08245	ABC transporter permease
LAC1533_RS10885	PFL family protein	GSS_RS06905	PFL family protein	Lacidipiscis_RS08250	PFL family protein
LAC1533_RS10890	ACT domain-containing protein	GSS_RS06910	ACT domain-containing protein	Lacidipiscis_RS08255	ACT domain-containing protein
LAC1533_RS10895	MFS transporter	GSS_RS06915	MFS transporter	Lacidipiscis_RS08260	MFS transporter
LAC1533_RS10900	N-acetyltransferase	GSS_RS06920	N-acetyltransferase	Lacidipiscis_RS08265	N-acetyltransferase
LAC1533_RS10905	hypothetical protein	GSS_RS13740	hypothetical protein	Lacidipiscis_RS08270	hypothetical protein
LAC1533_RS10910	hypothetical protein	GSS_RS12810	hypothetical protein	Lacidipiscis_RS08275	hypothetical protein
LAC1533_RS10915	hypothetical protein	GSS_RS06930	hypothetical protein	Lacidipiscis_RS08280	hypothetical protein
LAC1533_RS10920	type 1 glutamine amidotransferase	GSS_RS06935	type 1 glutamine amidotransferase	Lacidipiscis_RS08285	type 1 glutamine amidotransferase
LAC1533_RS10925	Rrf2 family transcriptional regulator	GSS_RS06940	Rrf2 family transcriptional regulator	Lacidipiscis_RS08290	Rrf2 family transcriptional regulator
LAC1533_RS10930	hypothetical protein	GSS_RS06945	hypothetical protein	Lacidipiscis_RS08295	NAD(P)-dependent oxidoreductase
LAC1533_RS10935	amino acid ABC transporter permease	GSS_RS06975	amino acid ABC transporter permease	Lacidipiscis_RS08305	amino acid ABC transporter permease
LAC1533_RS10940	amino acid ABC transporter ATP-binding protein	GSS_RS06980	amino acid ABC transporter ATP-binding protein	Lacidipiscis_RS08310	amino acid ABC transporter ATP-binding protein

LAC1533_RS10945	amino acid ABC transporter substrate-binding protein	GSS_RS06985	amino acid ABC transporter substrate-binding protein	Lacidipiscis_RS08315	amino acid ABC transporter substrate-binding protein
LAC1533_RS10950	DUF1541 domain-containing protein	GSS_RS06990	DUF1541 domain-containing protein	Lacidipiscis_RS08915	DUF1541 domain-containing protein
LAC1533_RS10955	PspC domain-containing protein	GSS_RS06995	PspC domain-containing protein	Lacidipiscis_RS08920	PspC domain-containing protein
LAC1533_RS10960	PadR family transcriptional regulator	GSS_RS07000	PadR family transcriptional regulator	Lacidipiscis_RS08925	PadR family transcriptional regulator
LAC1533_RS10965	hypothetical protein	GSS_RS07005	hypothetical protein	Lacidipiscis_RS08930	hypothetical protein
LAC1533_RS10970	DUF1700 domain-containing protein	GSS_RS07010	DUF1700 domain-containing protein	Lacidipiscis_RS08935	DUF1700 domain-containing protein
LAC1533_RS10975	D-alanyl-D-alanine dipeptidase	GSS_RS07020	D-alanyl-D-alanine dipeptidase	Lacidipiscis_RS08940	D-alanyl-D-alanine dipeptidase
LAC1533_RS10985	VOC family protein	GSS_RS07030	VOC family protein	Lacidipiscis_RS08950	VOC family protein
LAC1533_RS10990	MarR family transcriptional regulator	GSS_RS07035	MarR family transcriptional regulator	Lacidipiscis_RS08955	MarR family transcriptional regulator
LAC1533_RS10995	KH domain-containing protein	GSS_RS07040	KH domain-containing protein	Lacidipiscis_RS08960	KH domain-containing protein
LAC1533_RS11000	ribose transporter RbsU	GSS_RS07045	ribose transporter RbsU	Lacidipiscis_RS08965	ribose transporter RbsU
LAC1533_RS11005	D-ribose pyranase	GSS_RS07050	D-ribose pyranase	Lacidipiscis_RS08970	D-ribose pyranase
LAC1533_RS11010	ribokinase	GSS_RS07055	ribokinase	Lacidipiscis_RS08975	ribokinase
LAC1533_RS11015	LacI family transcriptional regulator	GSS_RS12815	hypothetical protein	Lacidipiscis_RS08980	LacI family transcriptional regulator
LAC1533_RS11035	N-acetyltransferase	GSS_RS07080	N-acetyltransferase	Lacidipiscis_RS09275	N-acetyltransferase
LAC1533_RS11045	GNAT family N-acetyltransferase	GSS_RS12820	N-acetyltransferase	Lacidipiscis_RS09285	N-acetyltransferase
LAC1533_RS11055	hypothetical protein	GSS_RS07095	hypothetical protein	Lacidipiscis_RS09290	hypothetical protein
LAC1533_RS11065	cadmium-translocating P-type ATPase	GSS_RS07100	copper-translocating P-type ATPase	Lacidipiscis_RS10910	copper-translocating P-type ATPase
LAC1533_RS11070	cupredoxin domain-containing protein	GSS_RS07105	cupredoxin domain-containing protein	Lacidipiscis_RS10905	cupredoxin domain-containing protein
LAC1533_RS11075	copper-binding protein	GSS_RS07110	copper-binding protein	Lacidipiscis_RS10900	copper-binding protein
LAC1533_RS11080	CopY/TcrY family copper transport repressor	GSS_RS07115	CopY/TcrY family copper transport repressor	Lacidipiscis_RS10895	CopY/TcrY family copper transport repressor
LAC1533_RS11085	aldo/keto reductase	GSS_RS07120	aldo/keto reductase	Lacidipiscis_RS10890	aldo/keto reductase
LAC1533_RS11090	M1 family peptidase	GSS_RS07125	M1 family peptidase	Lacidipiscis_RS10885	M1 family peptidase
LAC1533_RS11095	N-acetyltransferase	GSS_RS07130	N-acetyltransferase	Lacidipiscis_RS10880	N-acetyltransferase
LAC1533_RS11105	hypothetical protein	GSS_RS14095	hypothetical protein	Lacidipiscis_RS10875	hypothetical protein
LAC1533_RS11110	hypothetical protein	GSS_RS07135	hypothetical protein	Lacidipiscis_RS10870	hypothetical protein
LAC1533_RS11115	KR domain-containing protein	GSS_RS07140	3-oxoacyl-ACP reductase	Lacidipiscis_RS10865	KR domain-containing protein
LAC1533_RS11120	NAD-dependent dehydratase	GSS_RS07145	NAD-dependent dehydratase	Lacidipiscis_RS10860	NAD-dependent dehydratase
LAC1533_RS11125	glycerol dehydrogenase	GSS_RS07150	glycerol dehydrogenase	Lacidipiscis_RS10855	glycerol dehydrogenase
LAC1533_RS11130	glycyl-radical enzyme activating protein	GSS_RS07155	glycyl-radical enzyme activating protein	Lacidipiscis_RS10850	glycyl-radical enzyme activating protein
LAC1533_RS11135	glycyl radical protein	GSS_RS07160	formate C-acetyltransferase/glycerol dehydratase family glycyl radical enzyme	Lacidipiscis_RS10845	formate C-acetyltransferase/glycerol dehydratase family glycyl radical enzyme
LAC1533_RS11140	fructose-bisphosphate aldolase	GSS_RS07165	fructose-bisphosphate aldolase	Lacidipiscis_RS10840	fructose-bisphosphate aldolase
LAC1533_RS11145	peptidase M13	GSS_RS07170	peptidase M13	Lacidipiscis_RS08195	peptidase M13
LAC1533_RS11160	TetR/AcrR family transcriptional regulator	GSS_RS13745	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS08180	TetR/AcrR family transcriptional regulator
LAC1533_RS11165	1-acyl-sn-glycerol-3-phosphate acyltransferase	GSS_RS12835	1-acyl-sn-glycerol-3-phosphate acyltransferase	Lacidipiscis_RS08175	hypothetical protein
LAC1533_RS11170	glycosyl transferase	GSS_RS07195	glycosyl transferase	Lacidipiscis_RS08170	glycosyltransferase family 8 protein
LAC1533_RS11175	glycosyltransferase family 8 protein	GSS_RS07200	glycosyltransferase family 8 protein	Lacidipiscis_RS08165	glycosyltransferase family 8 protein
LAC1533_RS11185	universal stress protein	GSS_RS07215	universal stress protein	Lacidipiscis_RS08155	universal stress protein
LAC1533_RS11190	hypothetical protein	GSS_RS07220	hypothetical protein	Lacidipiscis_RS08150	hypothetical protein
LAC1533_RS11200	hypothetical protein	GSS_RS07225	hypothetical protein	Lacidipiscis_RS08145	hypothetical protein
LAC1533_RS11210	branched-chain amino acid transporter	GSS_RS14100	branched-chain amino acid transporter	Lacidipiscis_RS08135	AzlD domain-containing protein
LAC1533_RS11220	DoxX family membrane protein	GSS_RS07235	DoxX family membrane protein	Lacidipiscis_RS06850	DoxX family membrane protein
LAC1533_RS11225	hypothetical protein	GSS_RS10775	hypothetical protein	Lacidipiscis_RS06840	hypothetical protein
LAC1533_RS11235	ABC transporter ATP-binding protein	GSS_RS10785	ABC transporter ATP-binding protein	Lacidipiscis_RS06830	ABC transporter ATP-binding protein
LAC1533_RS11240	NAD(P)H-dependent oxidoreductase	GSS_RS10790	NAD(P)H-dependent oxidoreductase	Lacidipiscis_RS06825	NAD(P)H-dependent oxidoreductase
LAC1533_RS11245	carbamate kinase	GSS_RS10795	carbamate kinase	Lacidipiscis_RS06820	carbamate kinase
LAC1533_RS11250	amino acid permease	GSS_RS10800	amino acid permease	Lacidipiscis_RS06815	amino acid permease
LAC1533_RS11255	carbamate kinase	GSS_RS10805	carbamate kinase	Lacidipiscis_RS06810	carbamate kinase
LAC1533_RS11260	ornithine carbamoyltransferase	GSS_RS10810	ornithine carbamoyltransferase	Lacidipiscis_RS06805	ornithine carbamoyltransferase
LAC1533_RS11265	arginine deiminase	GSS_RS10815	arginine deiminase	Lacidipiscis_RS06800	arginine deiminase
LAC1533_RS11270	tRNA ligase	GSS_RS10825	tRNA ligase	Lacidipiscis_RS06795	tRNA ligase
LAC1533_RS11295	amino acid permease	GSS_RS10060	amino acid permease	Lacidipiscis_RS03680	amino acid permease
LAC1533_RS11300	hypothetical protein	GSS_RS13240	ArgR family transcriptional regulator	Lacidipiscis_RS03675	hypothetical protein
LAC1533_RS11305	alpha-glucosidase	GSS_RS10075	alpha-glucosidase	Lacidipiscis_RS03670	alpha-glucosidase
LAC1533_RS11310	fructokinase	GSS_RS10080	fructokinase	Lacidipiscis_RS03665	fructokinase
LAC1533_RS11315	glyoxalase	GSS_RS10085	glyoxalase/bleomycin resistance/dioxygenase family protein	Lacidipiscis_RS03660	glyoxalase/bleomycin resistance/dioxygenase family protein
LAC1533_RS11425	glucosamine-6-phosphate deaminase	GSS_RS10115	glucosamine-6-phosphate deaminase	Lacidipiscis_RS09485	glucosamine-6-phosphate deaminase
LAC1533_RS11430	glutamine--fructose-6-phosphate transaminase (isomerizing)	GSS_RS10120	glutamine--fructose-6-phosphate transaminase (isomerizing)	Lacidipiscis_RS09480	glutamine--fructose-6-phosphate transaminase (isomerizing)
LAC1533_RS11445	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent	GSS_RS10125	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent	Lacidipiscis_RS09475	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent
LAC1533_RS11450	ATP:cob(I)alamin adenosyltransferase	GSS_RS10130	ATP:cob(I)alamin adenosyltransferase	Lacidipiscis_RS09470	ATP:cob(I)alamin adenosyltransferase
LAC1533_RS11455	DUF4430 domain-containing protein	GSS_RS10135	DUF4430 domain-containing protein	Lacidipiscis_RS09465	DUF4430 domain-containing protein
LAC1533_RS11460	aldo/keto reductase	GSS_RS10140	aldo/keto reductase	Lacidipiscis_RS00510	aldo/keto reductase
LAC1533_RS11465	cupin domain-containing protein	GSS_RS10145	cupin domain-containing protein	Lacidipiscis_RS00515	cupin domain-containing protein
LAC1533_RS11470	carboxymuconolactone decarboxylase family protein	GSS_RS10150	carboxymuconolactone decarboxylase family protein	Lacidipiscis_RS00520	carboxymuconolactone decarboxylase family protein
LAC1533_RS11475	DUF2255 domain-containing protein	GSS_RS10155	DUF2255 domain-containing protein	Lacidipiscis_RS00525	DUF2255 domain-containing protein

LAC1533_RS11480	MerR family transcriptional regulator	GSS_RS10160	MerR family transcriptional regulator	Lacidipiscis_RS00530	MerR family transcriptional regulator
LAC1533_RS11495	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	GSS_RS10180	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	Lacidipiscis_RS00540	bifunctional acetaldehyde-CoA/alcohol dehydrogenase
LAC1533_RS11510	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	GSS_RS10190	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	Lacidipiscis_RS00500	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG
LAC1533_RS11515	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE	GSS_RS10195	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE	Lacidipiscis_RS00495	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE
LAC1533_RS11520	lipoate--protein ligase	GSS_RS10200	lipoate--protein ligase	Lacidipiscis_RS00490	lipoate--protein ligase
LAC1533_RS11525	MFS transporter	GSS_RS10205	MFS transporter	Lacidipiscis_RS00485	MFS transporter
LAC1533_RS11560	GlsB/YeaQ/YmgE family stress response membrane protein	GSS_RS10230	GlsB/YeaQ/YmgE family stress response membrane protein	Lacidipiscis_RS00450	GlsB/YeaQ/YmgE family stress response membrane protein
LAC1533_RS11570	hypothetical protein	GSS_RS10240	hypothetical protein	Lacidipiscis_RS03470	hypothetical protein
LAC1533_RS11580	6-phospho-beta-glucosidase	GSS_RS10245	6-phospho-beta-glucosidase	Lacidipiscis_RS03465	aryl-phospho-beta-D-glucosidase
LAC1533_RS11585	MarR family transcriptional regulator	GSS_RS10250	MarR family transcriptional regulator	Lacidipiscis_RS08700	MarR family transcriptional regulator
LAC1533_RS11590	NAD(P)/FAD-dependent oxidoreductase	GSS_RS03800	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS08705	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS11595	DUF3021 domain-containing protein	GSS_RS03795	DUF3021 domain-containing protein	Lacidipiscis_RS08720	DUF3021 domain-containing protein
LAC1533_RS11620	DegV family protein	GSS_RS03775	DegV family protein	Lacidipiscis_RS07245	DegV family protein
LAC1533_RS11630	glutamate/aspartate:proton symporter GltP	GSS_RS03770	proton glutamate symport protein	Lacidipiscis_RS07250	glutamate:protein symporter
LAC1533_RS11645	MerR family transcriptional regulator	GSS_RS03755	MerR family transcriptional regulator	Lacidipiscis_RS12730	MerR family transcriptional regulator
LAC1533_RS11650	HAD family hydrolase	GSS_RS11485	HAD family hydrolase	Lacidipiscis_RS12725	HAD family hydrolase
LAC1533_RS11655	CrcB family protein	GSS_RS03750	CrcB family protein	Lacidipiscis_RS00125	CrcB family protein
LAC1533_RS11660	hypothetical protein	GSS_RS03745	camphor resistance protein CrcB	Lacidipiscis_RS04090	hypothetical protein
LAC1533_RS11665	6-phospho-beta-glucosidase	GSS_RS03740	6-phospho-beta-glucosidase	Lacidipiscis_RS04095	6-phospho-beta-glucosidase
LAC1533_RS11670	PTS lactose/cellobiose transporter subunit IIA	GSS_RS03735	PTS lactose/cellobiose transporter subunit IIA	Lacidipiscis_RS04100	PTS lactose/cellobiose transporter subunit IIA
LAC1533_RS11675	PTS sugar transporter subunit IIB	GSS_RS03730	PTS sugar transporter subunit IIB	Lacidipiscis_RS04105	PTS sugar transporter subunit IIB
LAC1533_RS11740	UDP-phosphate N-acetylgalactosaminyl-1-phosphate transferase	GSS_RS03700	sugar transferase	Lacidipiscis_RS00600	UDP-phosphate N-acetylgalactosaminyl-1-phosphate transferase
LAC1533_RS11745	epimerase	GSS_RS03695	epimerase	Lacidipiscis_RS00605	epimerase
LAC1533_RS11750	tyrosine protein phosphatase	GSS_RS03685	tyrosine protein phosphatase	Lacidipiscis_RS00610	hypothetical protein
LAC1533_RS11755	exopolysaccharide biosynthesis protein	GSS_RS03680	exopolysaccharide biosynthesis protein	Lacidipiscis_RS00615	exopolysaccharide biosynthesis protein
LAC1533_RS11760	chain-length determining protein	GSS_RS03675	polysaccharide biosynthesis protein	Lacidipiscis_RS00620	chain-length determining protein
LAC1533_RS11765	serine hydrolase	GSS_RS03670	serine hydrolase	Lacidipiscis_RS00625	serine hydrolase
LAC1533_RS11770	aryl-sulfate sulfotransferase	GSS_RS03665	aryl-sulfate sulfotransferase	Lacidipiscis_RS00635	aryl-sulfate sulfotransferase
LAC1533_RS11775	glucosamine-6-phosphate deaminase	GSS_RS03660	glucosamine-6-phosphate deaminase	Lacidipiscis_RS00640	glucosamine-6-phosphate deaminase
LAC1533_RS11830	hypothetical protein	GSS_RS03655	hypothetical protein	Lacidipiscis_RS03260	hypothetical protein
LAC1533_RS11835	hypothetical protein	GSS_RS03650	hypothetical protein	Lacidipiscis_RS03265	hypothetical protein
LAC1533_RS11840	hypothetical protein	GSS_RS03645	hypothetical protein	Lacidipiscis_RS03270	hypothetical protein
LAC1533_RS11845	NAD(P)/FAD-dependent oxidoreductase	GSS_RS03640	NAD(P)/FAD-dependent oxidoreductase	Lacidipiscis_RS03275	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS11850	ABC transporter ATP-binding protein	GSS_RS03635	ABC transporter ATP-binding protein	Lacidipiscis_RS03280	ABC transporter ATP-binding protein
LAC1533_RS11855	glycine/betaine ABC transporter permease	GSS_RS03630	glycine/betaine ABC transporter permease	Lacidipiscis_RS03285	glycine/betaine ABC transporter permease
LAC1533_RS11860	DUF975 domain-containing protein	GSS_RS03625	DUF975 domain-containing protein	Lacidipiscis_RS11770	DUF975 domain-containing protein
LAC1533_RS11865	metal-dependent transcriptional regulator	GSS_RS03620	metal-dependent transcriptional regulator	Lacidipiscis_RS11765	metal-dependent transcriptional regulator
LAC1533_RS11870	divalent metal cation transporter	GSS_RS03615	divalent metal cation transporter	Lacidipiscis_RS11760	divalent metal cation transporter
LAC1533_RS11875	universal stress protein	GSS_RS03610	universal stress protein	Lacidipiscis_RS11755	universal stress protein
LAC1533_RS11880	MurR/RpiR family transcriptional regulator	GSS_RS03605	MurR/RpiR family transcriptional regulator	Lacidipiscis_RS11750	MurR/RpiR family transcriptional regulator
LAC1533_RS11885	gluconate permease	GSS_RS03595	gluconate permease	Lacidipiscis_RS11745	gluconate permease
LAC1533_RS11890	gluconokinase	GSS_RS03590	gluconokinase	Lacidipiscis_RS11740	gluconokinase
LAC1533_RS11895	6-phosphogluconate dehydrogenase (decarboxylating)	GSS_RS03585	6-phosphogluconate dehydrogenase (decarboxylating)	Lacidipiscis_RS11735	6-phosphogluconate dehydrogenase (decarboxylating)
LAC1533_RS11900	pyridine nucleotide-disulfide oxidoreductase	GSS_RS03580	pyridine nucleotide-disulfide oxidoreductase	Lacidipiscis_RS11730	pyridine nucleotide-disulfide oxidoreductase
LAC1533_RS11915	hypothetical protein	GSS_RS14035	hypothetical protein	Lacidipiscis_RS06470	hypothetical protein
LAC1533_RS11920	MFS transporter	GSS_RS03555	MFS transporter	Lacidipiscis_RS06465	MFS transporter
LAC1533_RS11925	copper oxidase	GSS_RS03550	multicopper oxidase	Lacidipiscis_RS06460	copper oxidase
LAC1533_RS11935	hypothetical protein	GSS_RS03445	hypothetical protein	Lacidipiscis_RS01975	hypothetical protein
LAC1533_RS11940	succinate-semialdehyde dehydrogenase	GSS_RS03440	succinate-semialdehyde dehydrogenase	Lacidipiscis_RS01980	succinate-semialdehyde dehydrogenase
LAC1533_RS11945	HIT family protein	GSS_RS12465	HIT family protein	Lacidipiscis_RS01985	HIT family protein
LAC1533_RS11950	glutamate/gamma-aminobutyrate family transporter YjeM	GSS_RS12460	glutamate/gamma-aminobutyrate family transporter YjeM	Lacidipiscis_RS01990	glutamate/gamma-aminobutyrate family transporter YjeM
LAC1533_RS11965	DedA family protein	GSS_RS03415	DedA family protein	Lacidipiscis_RS02260	DedA family protein
LAC1533_RS11980	ribonucleoside hydrolase RihC	GSS_RS03400	ribonucleoside hydrolase RihC	Lacidipiscis_RS12365	ribonucleoside hydrolase RihC
LAC1533_RS11985	aldo/keto reductase	GSS_RS03395	aldo/keto reductase	Lacidipiscis_RS12360	aldo/keto reductase
LAC1533_RS11995	N-acetyltransferase	GSS_RS12440	N-acetyltransferase	Lacidipiscis_RS12350	N-acetyltransferase
LAC1533_RS12000	type I methionyl aminopeptidase	GSS_RS03380	type I methionyl aminopeptidase	Lacidipiscis_RS12345	type I methionyl aminopeptidase
LAC1533_RS12005	GntR family transcriptional regulator	GSS_RS03375	GntR family transcriptional regulator	Lacidipiscis_RS12340	GntR family transcriptional regulator
LAC1533_RS12010	amino acid permease	GSS_RS03370	amino acid permease	Lacidipiscis_RS12335	amino acid permease
LAC1533_RS12020	iron ABC transporter permease	GSS_RS03355	iron ABC transporter permease	Lacidipiscis_RS08440	iron ABC transporter permease
LAC1533_RS12025	iron ABC transporter permease	GSS_RS03350	iron ABC transporter permease	Lacidipiscis_RS08445	iron ABC transporter permease
LAC1533_RS12045	biotin transporter BioY	GSS_RS03330	biotin transporter BioY	Lacidipiscis_RS08465	biotin transporter BioY
LAC1533_RS12050	dephospho-CoA kinase	GSS_RS03325	dephospho-CoA kinase	Lacidipiscis_RS08470	dephospho-CoA kinase
LAC1533_RS12055	Cof-type HAD-IIB family hydrolase	GSS_RS03320	Cof-type HAD-IIB family hydrolase	Lacidipiscis_RS08475	Cof-type HAD-IIB family hydrolase
LAC1533_RS12065	hypothetical protein	GSS_RS03310	hypothetical protein	Lacidipiscis_RS08485	hypothetical protein
LAC1533_RS12070	hypothetical protein	GSS_RS03305	pyridoxine 5-phosphate oxidase V	Lacidipiscis_RS08785	hypothetical protein

LAC1533_RS12075	argininosuccinate lyase	GSS_RS03300	argininosuccinate lyase	Lacidipiscis_RS08790	argininosuccinate lyase
LAC1533_RS12080	argininosuccinate synthase	GSS_RS03295	argininosuccinate synthase	Lacidipiscis_RS08795	argininosuccinate synthase
LAC1533_RS12085	peptide-methionine (S)-S-oxide reductase	GSS_RS03290	peptide-methionine (S)-S-oxide reductase	Lacidipiscis_RS08800	peptide-methionine (S)-S-oxide reductase
LAC1533_RS12090	N-acetyltransferase	GSS_RS03285	N-acetyltransferase	Lacidipiscis_RS08805	N-acetyltransferase
LAC1533_RS12095	polysaccharide biosynthesis protein	GSS_RS03280	polysaccharide biosynthesis protein	Lacidipiscis_RS08810	polysaccharide biosynthesis protein
LAC1533_RS12100	hypothetical protein	GSS_RS03275	hypothetical protein	Lacidipiscis_RS08815	hypothetical protein
LAC1533_RS12105	hypothetical protein	GSS_RS03270	hypothetical protein	Lacidipiscis_RS08820	hypothetical protein
LAC1533_RS12110	hypothetical protein	GSS_RS03260	hypothetical protein	Lacidipiscis_RS08825	hypothetical protein
LAC1533_RS12115	dihydrofolate reductase	GSS_RS03255	dihydrofolate reductase	Lacidipiscis_RS08830	dihydrofolate reductase
LAC1533_RS12120	iron export ABC transporter permease subunit FetB	GSS_RS03250	iron export ABC transporter permease subunit FetB	Lacidipiscis_RS08835	iron export ABC transporter permease subunit FetB
LAC1533_RS12125	putrescine/spermidine ABC transporter ATP-binding protein	GSS_RS03245	putrescine/spermidine ABC transporter ATP-binding protein	Lacidipiscis_RS08840	spermidine/putrescine ABC transporter ATP-binding protein
LAC1533_RS12130	glutathione peroxidase	GSS_RS03240	glutathione peroxidase	Lacidipiscis_RS04460	glutathione peroxidase
LAC1533_RS12145	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha	GSS_RS03230	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha	Lacidipiscis_RS04450	pyruvate dehydrogenase (acetyl-transferring) E1 component subunit alpha
LAC1533_RS12150	alpha-ketoacid dehydrogenase subunit beta	GSS_RS03225	alpha-ketoacid dehydrogenase subunit beta	Lacidipiscis_RS04445	alpha-ketoacid dehydrogenase subunit beta
LAC1533_RS12155	dihydrolipoamide acetyltransferase	GSS_RS03220	dihydrolipoamide acetyltransferase	Lacidipiscis_RS04440	dienelactone hydrolase
LAC1533_RS12160	dihydrolipoyl dehydrogenase	GSS_RS03215	dihydrolipoyl dehydrogenase	Lacidipiscis_RS04435	dihydrolipoyl dehydrogenase
LAC1533_RS12170	lipoate--protein ligase A	GSS_RS03210	lipoate--protein ligase A	Lacidipiscis_RS04430	lipoate--protein ligase
LAC1533_RS12175	FAD:protein FMN transferase	GSS_RS03205	FAD:protein FMN transferase	Lacidipiscis_RS04425	FAD:protein FMN transferase
LAC1533_RS12180	fructose-bisphosphatase class III	GSS_RS03200	fructose-bisphosphatase class III	Lacidipiscis_RS04420	fructose-bisphosphatase class III
LAC1533_RS12190	hypothetical protein	GSS_RS03195	hypothetical protein	Lacidipiscis_RS04415	hypothetical protein
LAC1533_RS12195	hypothetical protein	GSS_RS03190	hypothetical protein	Lacidipiscis_RS04410	hypothetical protein
LAC1533_RS12200	metal-dependent transcriptional regulator	GSS_RS03185	metal-dependent transcriptional regulator	Lacidipiscis_RS11780	metal-dependent transcriptional regulator
LAC1533_RS12205	divalent metal cation transporter	GSS_RS03180	divalent metal cation transporter	Lacidipiscis_RS11785	divalent metal cation transporter
LAC1533_RS12210	universal stress protein	GSS_RS03175	universal stress protein	Lacidipiscis_RS11790	universal stress protein
LAC1533_RS12215	hypothetical protein	GSS_RS03170	hypothetical protein	Lacidipiscis_RS02630	hypothetical protein
LAC1533_RS12235	L-ribulose-5-phosphate 4-epimerase AraD	GSS_RS03155	L-ribulose-5-phosphate 4-epimerase AraD	Lacidipiscis_RS11290	L-ribulose-5-phosphate 4-epimerase AraD
LAC1533_RS12240	ATPase	GSS_RS03150	ATPase	Lacidipiscis_RS11295	ATPase
LAC1533_RS12250	GntR family transcriptional regulator	GSS_RS03140	GntR family transcriptional regulator	Lacidipiscis_RS11305	GntR family transcriptional regulator
LAC1533_RS12255	acetate kinase	GSS_RS03135	acetate kinase	Lacidipiscis_RS10965	acetate kinase
LAC1533_RS12260	membrane protein	GSS_RS03130	membrane protein	Lacidipiscis_RS10970	hypothetical protein
LAC1533_RS12265	ribonuclease P protein component	GSS_RS03125	ribonuclease P protein component	Lacidipiscis_RS10975	ribonuclease P protein component
LAC1533_RS12270	50S ribosomal protein L34	GSS_RS03120	50S ribosomal protein L34	Lacidipiscis_RS10980	50S ribosomal protein L34
PLAC3_P10	hypothetical protein	GSS_RS11225	hypothetical protein	Lacidipiscis_RS13185	hypothetical protein
PLAC2_P01	Plasmid replication initiation protein	GSS_RS11190	replication initiation protein	Lacidipiscis_RS12825	replication initiation protein
PLAC2_P02	hypothetical protein	GSS_RS11185	hypothetical protein	Lacidipiscis_RS12820	hypothetical protein
PLAC2_P03	hypothetical protein	GSS_RS11180	hypothetical protein	Lacidipiscis_RS10955	hypothetical protein
PLAC2_P05	FIG00742586: hypothetical protein	GSS_RS11300	hypothetical protein	Lacidipiscis_RS12835	hypothetical protein
PLAC2_P08	hypothetical protein	GSS_RS11270	hypothetical protein	Lacidipiscis_RS12090	hypothetical protein
PLAC2_P09	putative plasmid partition protein	GSS_RS11275	ParA family protein	Lacidipiscis_RS12095	ParA family protein
PLAC2_P10	Site-specific recombinase, DNA invertase Pin related protein	GSS_RS11280	recombinase family protein	Lacidipiscis_RS07005	recombinase family protein
PLAC2_P34	putative resolvase	GSS_RS11015	recombinase family protein	Lacidipiscis_RS12395	recombinase family protein
PLAC2_P37	hypothetical protein	GSS_RS11000	hypothetical protein	Lacidipiscis_RS12140	hypothetical protein
PLAC2_P39	Predicted pyrophosphatase	GSS_RS10995	hypothetical protein	Lacidipiscis_RS12145	hypothetical protein
PLAC2_P41	hypothetical protein	GSS_RS10985	hypothetical protein	Lacidipiscis_RS12155	hypothetical protein
PLAC2_P42	Retron-type RNA-directed DNA polymerase	GSS_RS11125	RNA-directed DNA polymerase	Lacidipiscis_RS12165	maturase
PLAC2_P43	membrane protein, MmpL family	GSS_RS11135	MMPL family transporter	Lacidipiscis_RS12170	MMPL family transporter
PLAC2_P44	predicted transcriptional regulator	GSS_RS11140	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS12175	TetR/AcrR family transcriptional regulator
PLAC2_P48	Glyoxalase	GSS_RS11165	VOC family protein	Lacidipiscis_RS12860	VOC family protein
PLAC2_P49	Na(+)/H(+) antiporter	GSS_RS11170	cation:proton antiporter	Lacidipiscis_RS12855	cation:proton antiporter
PLAC2_P50	cation-transporting ATPase, E1-E2 family	GSS_RS11175	magnesium-transporting ATPase	Lacidipiscis_RS12850	magnesium-transporting ATPase
PLAC2_P54	hypothetical protein	GSS_RS13550	plasmid mobilization relaxosome protein MobC	Lacidipiscis_RS11430	hypothetical protein
PLAC2_P55	MobA	GSS_RS13895	putative plasmid mobilization protein	Lacidipiscis_RS11425	hypothetical protein
PLAC2_P58	hypothetical protein	GSS_RS11115	RepB family plasmid replication initiator protein	Lacidipiscis_RS11410	replication initiation protein
PLAC2_P59	Transcriptional regulator OrfX	GSS_RS11110	hypothetical protein	Lacidipiscis_RS11400	hypothetical protein
PLAC2_P60	hypothetical protein	GSS_RS11105	hypothetical protein	Lacidipiscis_RS12815	hypothetical protein

Supplementary table S4C. Singletons of the three *L. acidipiscis* strains calculated with the EDGAR software.

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS00295	hypothetical protein	GSS_RS00270	noncanonical pyrimidine nucleotidase, YjjG family	Lacidipiscis_RS00095	hypothetical protein
LAC1533_RS00375	MFS transporter	GSS_RS00625	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS00100	class I SAM-dependent DNA methyltransferase
LAC1533_RS00380	MFS transporter	GSS_RS00630	hypothetical protein	Lacidipiscis_RS00185	type II-A CRISPR-associated protein Csn2
LAC1533_RS00500	MFS transporter	GSS_RS00635	hypothetical protein	Lacidipiscis_RS00305	hypothetical protein
LAC1533_RS00510	glutaryl-CoA dehydrogenase	GSS_RS00640	hypothetical protein	Lacidipiscis_RS00550	hypothetical protein
LAC1533_RS00730	hypothetical protein	GSS_RS00645	hypothetical protein	Lacidipiscis_RS00565	hypothetical protein
LAC1533_RS00930	chitosanase	GSS_RS00655	hypothetical protein	Lacidipiscis_RS00570	hypothetical protein
LAC1533_RS01105	SAM-dependent DNA methyltransferase	GSS_RS00660	phage protein	Lacidipiscis_RS00575	hypothetical protein
LAC1533_RS01110	restriction endonuclease	GSS_RS00665	phage protein	Lacidipiscis_RS00580	hypothetical protein
LAC1533_RS01125	hypothetical protein	GSS_RS00685	phage-related major tail protein	Lacidipiscis_RS00800	hypothetical protein
LAC1533_RS01690	hypothetical protein	GSS_RS00690	hypothetical protein	Lacidipiscis_RS00870	N-acetyltransferase
LAC1533_RS01725	hypothetical protein	GSS_RS00695	hypothetical protein	Lacidipiscis_RS01245	DUF3037 domain-containing protein
LAC1533_RS02195	carbohydrate ABC transporter substrate-binding protein	GSS_RS00700	phage head-tail joining protein	Lacidipiscis_RS01250	hypothetical protein
LAC1533_RS02205	carbohydrate ABC transporter permease	GSS_RS00705	DNA-packaging protein	Lacidipiscis_RS01325	hypothetical protein
LAC1533_RS02210	hypothetical protein	GSS_RS00710	hypothetical protein	Lacidipiscis_RS01370	hypothetical protein
LAC1533_RS02445	helix-turn-helix domain-containing protein	GSS_RS00720	HK97 family phage prohead protease	Lacidipiscis_RS01390	ATP-binding protein
LAC1533_RS02450	hypothetical protein	GSS_RS00725	phage portal protein	Lacidipiscis_RS01395	hypothetical protein
LAC1533_RS04780	site-specific integrase	GSS_RS00730	hypothetical protein	Lacidipiscis_RS01400	hypothetical protein
LAC1533_RS04785	type I restriction endonuclease subunit S	GSS_RS00735	terminase large subunit	Lacidipiscis_RS01405	hypothetical protein
LAC1533_RS04790	restriction endonuclease	GSS_RS00740	terminase	Lacidipiscis_RS01410	phage recombination protein Bet
LAC1533_RS05685	helix-turn-helix domain-containing protein	GSS_RS00745	HNH endonuclease	Lacidipiscis_RS01420	hypothetical protein
LAC1533_RS05690	XRE family transcriptional regulator	GSS_RS00750	hypothetical protein	Lacidipiscis_RS01425	hypothetical protein
LAC1533_RS05695	hypothetical protein	GSS_RS00755	hypothetical protein	Lacidipiscis_RS01435	hypothetical protein
LAC1533_RS05715	hypothetical protein	GSS_RS00770	hypothetical protein	Lacidipiscis_RS01445	hypothetical protein
LAC1533_RS05725	hypothetical protein	GSS_RS00775	hypothetical protein	Lacidipiscis_RS01450	hypothetical protein
LAC1533_RS05730	hypothetical protein	GSS_RS00780	hypothetical protein	Lacidipiscis_RS01455	DUF3102 domain-containing protein
LAC1533_RS05735	hypothetical protein	GSS_RS00785	hypothetical protein	Lacidipiscis_RS01460	XRE family transcriptional regulator
LAC1533_RS05745	hypothetical protein	GSS_RS00790	hypothetical protein	Lacidipiscis_RS01465	XRE family transcriptional regulator
LAC1533_RS05750	DNA replication protein	GSS_RS00800	RusA family crossover junction endodeoxyribonuclease	Lacidipiscis_RS01875	hypothetical protein
LAC1533_RS05755	hypothetical protein	GSS_RS00805	hypothetical protein	Lacidipiscis_RS01945	hypothetical protein
LAC1533_RS05770	hypothetical protein	GSS_RS00810	hypothetical protein	Lacidipiscis_RS01955	hypothetical protein
LAC1533_RS05780	hypothetical protein	GSS_RS00815	hypothetical protein	Lacidipiscis_RS01965	hypothetical protein
LAC1533_RS05785	hypothetical protein	GSS_RS00820	hypothetical protein	Lacidipiscis_RS02380	hypothetical protein
LAC1533_RS05790	site-specific DNA-methyltransferase	GSS_RS00830	ATP-dependent helicase	Lacidipiscis_RS02405	hypothetical protein
LAC1533_RS05795	hypothetical protein	GSS_RS00835	DUF4145 domain-containing protein	Lacidipiscis_RS02430	glycosyltransferase family 2 protein
LAC1533_RS05835	hypothetical protein	GSS_RS00840	hypothetical protein	Lacidipiscis_RS02435	hypothetical protein
LAC1533_RS05900	collagen-like protein	GSS_RS00845	hypothetical protein	Lacidipiscis_RS02440	hypothetical protein
LAC1533_RS05905	hypothetical protein	GSS_RS00850	hypothetical protein	Lacidipiscis_RS02445	LicD family protein
LAC1533_RS05920	hypothetical protein	GSS_RS00855	hypothetical protein	Lacidipiscis_RS02470	glycosyl transferase family 2
LAC1533_RS05925	DUF2335 domain-containing protein	GSS_RS00860	chromosome segregation protein SMC	Lacidipiscis_RS02475	glycosyl transferase family 2
LAC1533_RS06680	aminopeptidase P family protein	GSS_RS00875	DUF771 domain-containing protein	Lacidipiscis_RS02485	L-Rha 1,3-L-rhamnosyltransferase
LAC1533_RS07255	hypothetical protein	GSS_RS00880	hypothetical protein	Lacidipiscis_RS02660	hypothetical protein
LAC1533_RS07330	hypothetical protein	GSS_RS00885	hypothetical protein	Lacidipiscis_RS02670	hypothetical protein
LAC1533_RS07355	hypothetical protein	GSS_RS00900	hypothetical protein	Lacidipiscis_RS02680	hypothetical protein
LAC1533_RS07365	hypothetical protein	GSS_RS00905	TM2 domain-containing protein	Lacidipiscis_RS02685	ParA family protein
LAC1533_RS07375	hypothetical protein	GSS_RS01430	hypothetical protein	Lacidipiscis_RS02695	hypothetical protein
LAC1533_RS07380	conjugal transfer protein	GSS_RS01435	cytochrome P450	Lacidipiscis_RS02700	toxin zeta
LAC1533_RS07385	conjugal transfer protein	GSS_RS01660	hypothetical protein	Lacidipiscis_RS02715	gfo/Idh/MocA family oxidoreductase
LAC1533_RS07390	hypothetical protein	GSS_RS01665	hypothetical protein	Lacidipiscis_RS02720	glucose transporter GlcU
LAC1533_RS07400	hypothetical protein	GSS_RS01815	hypothetical protein	Lacidipiscis_RS02725	FeoB-associated Cys-rich membrane protein
LAC1533_RS07405	hypothetical protein	GSS_RS01825	OsmC family peroxiredoxin	Lacidipiscis_RS02735	iron transporter FeoA
LAC1533_RS07410	peptidoglycan endopeptidase	GSS_RS01830	OsmC family peroxiredoxin	Lacidipiscis_RS02880	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS07835	hypothetical protein	GSS_RS01835	MarR family transcriptional regulator	Lacidipiscis_RS02885	hypothetical protein
LAC1533_RS08375	sugar aldolase	GSS_RS01840	hypothetical protein	Lacidipiscis_RS02890	hypothetical protein
LAC1533_RS08380	hypothetical protein	GSS_RS02150	type I restriction endonuclease subunit R	Lacidipiscis_RS02895	hypothetical protein
LAC1533_RS08390	PTS galactitol transporter subunit IIB	GSS_RS02160	type I restriction endonuclease subunit S	Lacidipiscis_RS02900	SGNH/GDSL hydrolase family protein
LAC1533_RS08395	PTS galactitol transporter subunit IIA	GSS_RS02170	restriction endonuclease subunit S	Lacidipiscis_RS02905	hypothetical protein
LAC1533_RS08400	DeoR/GlpR transcriptional regulator	GSS_RS02180	hypothetical protein	Lacidipiscis_RS02910	hypothetical protein
LAC1533_RS08430	hypothetical protein	GSS_RS03480	type I-E CRISPR-associated protein Cse1/CasA	Lacidipiscis_RS02915	hypothetical protein
LAC1533_RS08435	hypothetical protein	GSS_RS03485	CRISPR-associated protein Cse2	Lacidipiscis_RS02920	hypothetical protein
LAC1533_RS08440	hypothetical protein	GSS_RS03490	type I-E CRISPR-associated protein Cas7/Cse4/CasC	Lacidipiscis_RS02925	hypothetical protein
LAC1533_RS08445	ATP-dependent helicase	GSS_RS03500	type I-E CRISPR-associated protein Cas6/Cse3/CasE	Lacidipiscis_RS02930	hypothetical protein

LAC1533_RS08450	class I SAM-dependent DNA methyltransferase	GSS_RS03505	type I-E CRISPR-associated endonuclease Cas1	Lacidipiscis_RS02935	phage major tail protein, TP901-1 family
LAC1533_RS08455	XRE family transcriptional regulator	GSS_RS03510	type I-E CRISPR-associated endoribonuclease Cas2	Lacidipiscis_RS02940	hypothetical protein
LAC1533_RS08460	helicase	GSS_RS03705	glycosyl transferase family 2	Lacidipiscis_RS02945	hypothetical protein
LAC1533_RS08465	DUF1837 domain-containing protein	GSS_RS03710	O-antigen ligase domain-containing protein	Lacidipiscis_RS02950	hypothetical protein
LAC1533_RS08470	sigma-70 family RNA polymerase sigma factor	GSS_RS03715	toxin	Lacidipiscis_RS02955	hypothetical protein
LAC1533_RS08475	hypothetical protein	GSS_RS03720	capsule biosynthesis protein CapK	Lacidipiscis_RS02960	phage capsid protein
LAC1533_RS08480	hypothetical protein	GSS_RS04825	PTS sugar transporter subunit IIC	Lacidipiscis_RS02965	DNA methyltransferase
LAC1533_RS08490	DUF2815 domain-containing protein	GSS_RS04870	hypothetical protein	Lacidipiscis_RS02970	hypothetical protein
LAC1533_RS08500	hypothetical protein	GSS_RS05305	hypothetical protein	Lacidipiscis_RS02975	hypothetical protein
LAC1533_RS08505	DNA primase	GSS_RS05310	hypothetical protein	Lacidipiscis_RS02980	phage portal protein
LAC1533_RS08510	VRR-NUC domain-containing protein	GSS_RS05320	hypothetical protein	Lacidipiscis_RS02985	terminase
LAC1533_RS08520	restriction endonuclease	GSS_RS05330	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS02990	terminase
LAC1533_RS08525	HNH endonuclease	GSS_RS05335	hypothetical protein	Lacidipiscis_RS02995	hypothetical protein
LAC1533_RS08530	terminase	GSS_RS05350	cytosine permease	Lacidipiscis_RS03005	hypothetical protein
LAC1533_RS08535	hypothetical protein	GSS_RS05355	DUF4162 domain-containing protein	Lacidipiscis_RS03010	hypothetical protein
LAC1533_RS08550	DUF5049 domain-containing protein	GSS_RS05360	ABC transporter permease	Lacidipiscis_RS03015	hypothetical protein
LAC1533_RS08555	terminase large subunit	GSS_RS05380	IS30 family transposase	Lacidipiscis_RS03020	hypothetical protein
LAC1533_RS08560	hypothetical protein	GSS_RS06085	hypothetical protein	Lacidipiscis_RS03025	DnaD domain protein
LAC1533_RS08565	type II toxin-antitoxin system RelE/ParE family toxin	GSS_RS06090	hypothetical protein	Lacidipiscis_RS03030	hypothetical protein
LAC1533_RS08575	Clp protease ClpP	GSS_RS06095	hypothetical protein	Lacidipiscis_RS03035	hypothetical protein
LAC1533_RS08580	phage major capsid protein	GSS_RS06100	primase	Lacidipiscis_RS03040	hypothetical protein
LAC1533_RS08585	phage gp6-like head-tail connector protein	GSS_RS06105	DNA-binding protein	Lacidipiscis_RS03045	hypothetical protein
LAC1533_RS08590	head-tail adaptor protein	GSS_RS06110	site-specific integrase	Lacidipiscis_RS03050	hypothetical protein
LAC1533_RS08595	DNA primase	GSS_RS06115	hypothetical protein	Lacidipiscis_RS03055	DNA-binding protein
LAC1533_RS08600	1,4-beta-N-acetylmuramidase	GSS_RS06120	DNA repair protein RadC	Lacidipiscis_RS03060	hypothetical protein
LAC1533_RS08605	hypothetical protein	GSS_RS06125	hypothetical protein	Lacidipiscis_RS03065	oxidoreductase
LAC1533_RS08615	recombinase family protein	GSS_RS06140	site-specific integrase	Lacidipiscis_RS03070	hypothetical protein
LAC1533_RS08620	MFS transporter	GSS_RS06145	helicase	Lacidipiscis_RS03080	ImmA/IrrE family metallo-endopeptidase
LAC1533_RS08625	hypothetical protein	GSS_RS06150	hypothetical protein	Lacidipiscis_RS03085	SHOCT domain-containing protein
LAC1533_RS10150	hypothetical protein	GSS_RS06160	DUF4365 domain-containing protein	Lacidipiscis_RS03090	hypothetical protein
LAC1533_RS10235	hypothetical protein	GSS_RS06165	hypothetical protein	Lacidipiscis_RS03095	hypothetical protein
LAC1533_RS10320	glycosyltransferase family 2 protein	GSS_RS06200	gfo/Idh/MocA family oxidoreductase	Lacidipiscis_RS03100	hypothetical protein
LAC1533_RS10325	hypothetical protein	GSS_RS06385	hypothetical protein	Lacidipiscis_RS03105	hypothetical protein
LAC1533_RS10345	hypothetical protein	GSS_RS06435	hypothetical protein	Lacidipiscis_RS03110	hypothetical protein
LAC1533_RS10350	hypothetical protein	GSS_RS06445	glycosyltransferase	Lacidipiscis_RS04000	dTDP-4-dehydrorhamnose reductase
LAC1533_RS10360	hypothetical protein	GSS_RS06465	hypothetical protein	Lacidipiscis_RS04010	dTDP-4-dehydrorhamnose 3,5-epimerase
LAC1533_RS10365	LicD family protein	GSS_RS06475	ABC transporter permease	Lacidipiscis_RS04015	glucose-1-phosphate thymidylyltransferase
LAC1533_RS10400	hypothetical protein	GSS_RS06485	hypothetical protein	Lacidipiscis_RS04025	phosphatase PAP2 family protein
LAC1533_RS10440	hypothetical protein	GSS_RS06835	hypothetical protein	Lacidipiscis_RS04040	hypothetical protein
LAC1533_RS10450	hypothetical protein	GSS_RS06965	DUF536 domain-containing protein	Lacidipiscis_RS04045	PRD domain-containing protein
LAC1533_RS10455	hypothetical protein	GSS_RS06970	hypothetical protein	Lacidipiscis_RS04070	hypothetical protein
LAC1533_RS10470	Cna B-type domain-containing protein	GSS_RS08755	endonuclease	Lacidipiscis_RS04125	hypothetical protein
LAC1533_RS10530	D-lactate dehydrogenase	GSS_RS08800	hypothetical protein	Lacidipiscis_RS04495	6-phospho-beta-glucosidase
LAC1533_RS10685	glutamine ABC transporter substrate-binding protein	GSS_RS08805	hypothetical protein	Lacidipiscis_RS05030	hypothetical protein
LAC1533_RS10740	hypothetical protein	GSS_RS08815	minor teichoic acid biosynthesis protein	Lacidipiscis_RS05860	hypothetical protein
LAC1533_RS11330	SIS domain-containing protein	GSS_RS08820	teichoic acid biosynthesis protein B	Lacidipiscis_RS05870	hypothetical protein
LAC1533_RS11345	PTS alpha-glucoside transporter subunit IICB	GSS_RS09410	ammonium transporter	Lacidipiscis_RS06185	hypothetical protein
LAC1533_RS11350	6-phospho-alpha-glucosidase	GSS_RS09610	hypothetical protein	Lacidipiscis_RS06420	hypothetical protein
LAC1533_RS11700	hypothetical protein	GSS_RS10910	hypothetical protein	Lacidipiscis_RS06425	zinc ribbon domain-containing protein
LAC1533_RS11710	hypothetical protein	GSS_RS10915	NADH oxidase	Lacidipiscis_RS06430	zinc ribbon domain-containing protein
LAC1533_RS11715	hypothetical protein	GSS_RS10920	hypothetical protein	Lacidipiscis_RS06435	zinc ribbon domain-containing protein
LAC1533_RS11720	hypothetical protein	GSS_RS10930	XRE family transcriptional regulator	Lacidipiscis_RS06515	PTS N-acetylglucosamine transporter subunit IIBC
LAC1533_RS11725	hypothetical protein	GSS_RS10970	hypothetical protein	Lacidipiscis_RS07040	hypothetical protein
LAC1533_RS11730	hypothetical protein	GSS_RS10975	hypothetical protein	Lacidipiscis_RS07055	PbsX family transcriptional regulator
LAC1533_RS11735	glycosyltransferase family 2 protein	GSS_RS11020	PRD domain-containing protein	Lacidipiscis_RS07085	IS6 family transposase
LAC1533_RS11990	magnesium transporter CorA family protein	GSS_RS11025	PTS beta-glucoside transporter subunit EIIBCA	Lacidipiscis_RS07095	TetR/AcrR family transcriptional regulator
pLAC1_p2	hypothetical protein	GSS_RS11035	ISL3 family transposase	Lacidipiscis_RS07130	ketose-bisphosphate aldolase
pLAC1_p3	hypothetical protein	GSS_RS11215	site-specific DNA-methyltransferase	Lacidipiscis_RS07135	fructose-bisphosphate aldolase
pLAC1_p4	mobilization protein	GSS_RS11230	RepB family plasmid replication initiator protein	Lacidipiscis_RS07140	PTS fructose transporter subunit IIC
PLAC2_P12	hypothetical protein	GSS_RS11355	prenyltransferase	Lacidipiscis_RS07150	PTS mannose transporter subunit IIAB
PLAC2_P17	Alpha-1,4-N-acetylgalactosamine transferase PglH	GSS_RS12490	hypothetical protein	Lacidipiscis_RS07155	transcription antiterminator
PLAC2_P18	Alpha-1,4-N-acetylgalactosamine transferase PglH	GSS_RS12520	polysaccharide biosynthesis protein	Lacidipiscis_RS07165	hypothetical protein

PLAC2_P21	hypothetical protein	GSS_RS12640	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS07170	TetR/AcrR family transcriptional regulator
PLAC2_P22	hypothetical protein	GSS_RS12700	DUF1643 domain-containing protein	Lacidipiscis_RS07575	LysM peptidoglycan-binding domain-containing protein
PLAC2_P25	Mobile element protein	GSS_RS12760	hypothetical protein	Lacidipiscis_RS07580	NCS2 family permease
PLAC2_P26	Mobile element protein	GSS_RS12765	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS07635	hypothetical protein
PLAC2_P27	Transcriptional regulator of D-allose utilization, LacI family	GSS_RS12770	hypothetical protein	Lacidipiscis_RS07920	type II CRISPR RNA-guided endonuclease Cas9
PLAC2_P28	Transaldolase	GSS_RS13245	MurR/RpiR family transcriptional regulator	Lacidipiscis_RS07930	CRISPR-associated endonuclease Cas2
PLAC2_P29	PTS system, sorbose-specific IID component	GSS_RS13375	hypothetical protein	Lacidipiscis_RS07935	type II-A CRISPR-associated protein Csn2
PLAC2_P30	PTS system, mannose-specific IIA component	GSS_RS13640	phage tail tape measure protein	Lacidipiscis_RS08185	GTP pyrophosphokinase
PLAC2_P31	PTS system, mannose-specific IIB component	GSS_RS13710	hypothetical protein	Lacidipiscis_RS08420	hypothetical protein
PLAC2_P32	Mobile element protein	GSS_RS14085	hypothetical protein	Lacidipiscis_RS08425	hypothetical protein
PLAC2_P33	Mobile element protein	GSS_RS14180	DUF3427 domain-containing protein	Lacidipiscis_RS08500	glycosyltransferase
PLAC2_P35	hypothetical protein	GSS_RS14185	DUF3427 domain-containing protein	Lacidipiscis_RS08505	glycosyltransferase family 39 protein
PLAC2_P36	hypothetical protein			Lacidipiscis_RS08510	GtrA family protein
PLAC2_P38	hypothetical protein			Lacidipiscis_RS08515	DNA-binding response regulator
PLAC2_P51	hypothetical protein			Lacidipiscis_RS08535	hypothetical protein
PLAC2_P52	hypothetical protein			Lacidipiscis_RS08540	hypothetical protein
PLAC2_P66	hypothetical protein			Lacidipiscis_RS08545	hypothetical protein
PLAC2_P67	hypothetical protein			Lacidipiscis_RS08550	hypothetical protein
PLAC2_P68	hypothetical protein			Lacidipiscis_RS08675	hypothetical protein
PLAC3_P01	hypothetical protein			Lacidipiscis_RS08685	hypothetical protein
PLAC3_P02	hypothetical protein			Lacidipiscis_RS08710	hypothetical protein
PLAC3_P03	hypothetical protein			Lacidipiscis_RS08715	ABC transporter ATP-binding protein
PLAC3_P04	hypothetical protein			Lacidipiscis_RS08745	hypothetical protein
PLAC3_P05	hypothetical protein			Lacidipiscis_RS08755	hypothetical protein
PLAC3_P06	RLX protein			Lacidipiscis_RS08765	hypothetical protein
PLAC3_P07	hypothetical protein			Lacidipiscis_RS08780	IS6-like element IS1216 family transposase
PLAC3_P08	hypothetical protein			Lacidipiscis_RS09115	recombinase family protein
PLAC3_P11	nisin resistance protein (putative)			Lacidipiscis_RS09120	ArsR family transcriptional regulator
PLAC3_P12	Type II restriction enzyme AvaI			Lacidipiscis_RS09125	arsenical pump-driving ATPase
PLAC3_P13	Modification methylase AvaI			Lacidipiscis_RS09130	arsenical efflux pump membrane protein ArsB
PLAC3_P14	hypothetical protein			Lacidipiscis_RS09135	arsenical resistance operon transcriptional repressor ArsD
PLAC3_P16	Retron-type RNA-directed DNA polymerase			Lacidipiscis_RS09260	hypothetical protein
PLAC3_P17	hypothetical protein			Lacidipiscis_RS10075	transporter
				Lacidipiscis_RS11140	RNA 2-phosphotransferase
				Lacidipiscis_RS11260	hypothetical protein
				Lacidipiscis_RS11265	ParA family protein
				Lacidipiscis_RS11270	hypothetical protein
				Lacidipiscis_RS11275	hypothetical protein
				Lacidipiscis_RS11625	hypothetical protein
				Lacidipiscis_RS11720	hypothetical protein
				Lacidipiscis_RS12010	hypothetical protein
				Lacidipiscis_RS12015	hypothetical protein
				Lacidipiscis_RS12020	nickase
				Lacidipiscis_RS12060	APC family permease
				Lacidipiscis_RS12065	hypothetical protein
				Lacidipiscis_RS12110	ABC transporter permease
				Lacidipiscis_RS12115	TetR/AcrR family transcriptional regulator
				Lacidipiscis_RS12120	hypothetical protein
				Lacidipiscis_RS12430	hypothetical protein
				Lacidipiscis_RS12435	nickase
				Lacidipiscis_RS12440	hypothetical protein
				Lacidipiscis_RS12445	hypothetical protein
				Lacidipiscis_RS12450	hypothetical protein
				Lacidipiscis_RS12455	type II toxin-antitoxin system antitoxin, RelB/DinJ family
				Lacidipiscis_RS12465	hypothetical protein
				Lacidipiscis_RS12510	hypothetical protein
				Lacidipiscis_RS12515	helix-turn-helix domain-containing protein
				Lacidipiscis_RS12710	hypothetical protein
				Lacidipiscis_RS12965	XRE family transcriptional regulator

				Lacidipiscis_RS12975	LacI family transcriptional regulator
				Lacidipiscis_RS12980	MFS transporter
				Lacidipiscis_RS12995	sugar O-acetyltransferase
				Lacidipiscis_RS13020	hypothetical protein
				Lacidipiscis_RS13025	hypothetical protein
				Lacidipiscis_RS13030	hypothetical protein
				Lacidipiscis_RS13175	hypothetical protein
				Lacidipiscis_RS13180	bacteriocin immunity protein
				Lacidipiscis_RS13230	CPBP family intramembrane metalloprotease
				Lacidipiscis_RS13240	bacteriocin immunity protein
				Lacidipiscis_RS13250	CPBP family intramembrane metalloprotease
				Lacidipiscis_RS13255	peptide cleavage/export ABC transporter
				Lacidipiscis_RS13260	bacteriocin secretion accessory protein
				Lacidipiscis_RS13350	hypothetical protein

Supplementary table S5. Genes within genomic islands of *L. acidipiscis* ACA-DC 1533. Common genes within the rest of *L. acidipiscis* strains were predicted from the pan-genome analysis with the EDGAR software.

Genomic island 1 (genomic coordinates: 166,530-191,640; size: 25,110 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag*	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS00780	APC family permease	GSS_RS02475	APC family permease	Lacidipiscis_RS12295	APC family permease
LAC1533_RS00785	ornithine decarboxylase	GSS_RS02470	ornithine decarboxylase	Lacidipiscis_RS12290	ornithine decarboxylase
LAC1533_RS00790	hypothetical protein	GSS_RS13990	hypothetical protein	Lacidipiscis_RS12285	hypothetical protein
LAC1533_RS00795	hypothetical protein	GSS_RS13670	hypothetical protein	Lacidipiscis_RS12280	hypothetical protein
LAC1533_RS00800	DUF2992 domain-containing protein	GSS_RS02455	DUF2992 domain-containing protein	Lacidipiscis_RS12275	DUF2992 domain-containing protein
LAC1533_RS00805	GNAT family N-acetyltransferase	-	-	-	-
LAC1533_RS00810	transposase	-	-	-	-
LAC1533_RS00815	IS1380 family transposase	-	-	-	-
LAC1533_RS00820	transposase	-	-	-	-
LAC1533_RS00825	transposase	GSS_RS11565	ATPase AAA	-	-
LAC1533_RS00830	GNAT family N-acetyltransferase	-	-	-	-
LAC1533_RS00835	site-specific integrase	-	-	-	-
LAC1533_RS00840	TetR/AcrR family transcriptional regulator	GSS_RS02430	TetR/AcrR family transcriptional regulator	Lacidipiscis_RS00720	TetR/AcrR family transcriptional regulator
LAC1533_RS00845	ABC transporter permease	GSS_RS02425	ABC transporter permease	Lacidipiscis_RS00725	ABC transporter permease
LAC1533_RS00850	ABC transporter ATP-binding protein	GSS_RS02420	ABC transporter ATP-binding protein	Lacidipiscis_RS07105	ABC transporter ATP-binding protein
LAC1533_RS00855	dihydroxyacetone kinase subunit DhaK	GSS_RS02415	dihydroxyacetone kinase subunit DhaK	Lacidipiscis_RS00735	dihydroxyacetone kinase subunit DhaK
LAC1533_RS00860	dihydroxyacetone kinase subunit L	-	-	Lacidipiscis_RS00740	dihydroxyacetone kinase subunit L
LAC1533_RS00865	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM	GSS_RS02405	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM	Lacidipiscis_RS00745	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM
LAC1533_RS00870	glycerol kinase	GSS_RS02400	glycerol kinase	Lacidipiscis_RS00750	glycerol kinase
LAC1533_RS00875	type 1 glycerol-3-phosphate oxidase	GSS_RS02395	type 1 glycerol-3-phosphate oxidase	Lacidipiscis_RS00755	type 1 glycerol-3-phosphate oxidase
LAC1533_RS00880	aquaporin family protein	GSS_RS02390	aquaporin family protein	Lacidipiscis_RS00760	aquaporin family protein
LAC1533_RS00885	GntR family transcriptional regulator	GSS_RS02385	GntR family transcriptional regulator	Lacidipiscis_RS00765	GntR family transcriptional regulator
LAC1533_RS00890	PTS sugar transporter subunit IIC	GSS_RS02380	PTS sugar transporter subunit IIC	Lacidipiscis_RS00770	PTS sugar transporter subunit IIC
LAC1533_RS00895	DUF3284 domain-containing protein	GSS_RS02375	DUF3284 domain-containing protein	Lacidipiscis_RS00775	DUF3284 domain-containing protein

Genomic island 2 (genomic coordinates: 361,412-368,010; size: 6,598 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS01675	malate permease	GSS_RS01690	malate permease	Lacidipiscis_RS04830	hypothetical protein
LAC1533_RS01680	hypothetical protein	GSS_RS01685	hypothetical protein	Lacidipiscis_RS04835	hypothetical protein
LAC1533_RS01685	DNA helicase	GSS_RS01680	DNA helicase	-	-
LAC1533_RS01690	hypothetical protein		-	-	-
LAC1533_RS01695	DNA-binding protein	GSS_RS13455	DNA-binding protein	-	-
LAC1533_RS01700	XRE family transcriptional regulator	GSS_RS11550	XRE family transcriptional regulator	-	-
LAC1533_RS01705	XRE family transcriptional regulator	GSS_RS01675	XRE family transcriptional regulator	-	-
LAC1533_RS01710	ImmA/IrrE family metallo-endopeptidase	GSS_RS01670	ImmA/IrrE family metallo-endopeptidase	-	-
LAC1533_RS01715	hypothetical protein	-	-	-	-
LAC1533_RS01720	DUF5067 domain-containing protein	GSS_RS01655	DUF5067 domain-containing protein	-	-
LAC1533_RS01725	hypothetical protein	-	-	-	-
LAC1533_RS01730	IS30 family transposase	-	-	-	-

Genomic island 3 (genomic coordinates: 478,668-487,028; size: 8,360 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS02190	alpha-glycosidase	GSS_RS09125	alpha-glycosidase	Lacidipiscis_RS04575	alpha-glycosidase
LAC1533_RS02195	sugar ABC transporter substrate-binding protein	-	-	-	-
LAC1533_RS02200	ABC transporter permease	-	-	-	-
LAC1533_RS02205	sugar ABC transporter permease	-	-	-	-
LAC1533_RS02210	hypothetical protein	-	-	-	-
LAC1533_RS02215	sugar ABC transporter ATP-binding protein	GSS_RS09150	ABC transporter ATP-binding protein	Lacidipiscis_RS04600	ABC transporter ATP-binding protein
LAC1533_RS02220	IS1380 family transposase	-	-	-	-

Genomic island 4 (genomic coordinates: 528,365-554,586; size: 26,221 bp)

Lactobacillus acidipiscis ACA-DC 1533		*Lactobacillus acidipiscis* KCTC 13900		*Lactobacillus acidipiscis* JCM 10692^{T}	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS02405	PTS mannose/fructose/sorbose transporter subunit IIC	GSS_RS09340	PTS mannose/fructose/sorbose transporter subunit IIC	Lacidipiscis_RS04155	PTS mannose/fructose/sorbose transporter subunit IIC
LAC1533_RS02410	PTS mannose family transporter subunit IID	GSS_RS09345	PTS mannose transporter subunit IID	Lacidipiscis_RS04160	PTS mannose transporter subunit IID
LAC1533_RS02415	DUF956 domain-containing protein	GSS_RS09350	DUF956 domain-containing protein	Lacidipiscis_RS04165	DUF956 domain-containing protein
LAC1533_RS02435	DUF975 domain-containing protein	-	-	Lacidipiscis_RS06995	DUF975 domain-containing protein
LAC1533_RS02440	neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	GSS_RS05675	Neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	Lacidipiscis_RS07000	neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase
LAC1533_RS02445	helix-turn-helix domain-containing protein	-	-	-	-
LAC1533_RS02450	hypothetical protein	-	-	-	-
LAC1533_RS02455	LysM peptidoglycan-binding domain-containing protein	GSS_RS05680	LysM peptidoglycan-binding domain-containing protein	Lacidipiscis_RS00140	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS02460	LysM peptidoglycan-binding domain-containing protein	-	-	-	-
LAC1533_RS02465	uracil-DNA glycosylase	GSS_RS05685	uracil-DNA glycosylase	Lacidipiscis_RS03845	uracil-DNA glycosylase
LAC1533_RS02475	folate family ECF transporter S component	GSS_RS05695	folate family ECF transporter S component	Lacidipiscis_RS03835	folate family ECF transporter S component
LAC1533_RS02480	metal ABC transporter permease	GSS_RS05700	metal ABC transporter permease	Lacidipiscis_RS03830	metal ABC transporter permease
LAC1533_RS02485	ABC transporter ATP-binding protein	GSS_RS05705	ABC transporter ATP-binding protein	Lacidipiscis_RS03825	ABC transporter ATP-binding protein
LAC1533_RS02490	QueT transporter family protein	GSS_RS05710	QueT transporter family protein	Lacidipiscis_RS03820	QueT transporter family protein
LAC1533_RS02495	DUF2829 domain-containing protein	GSS_RS05715	DUF2829 domain-containing protein	Lacidipiscis_RS03815	DUF2829 domain-containing protein
LAC1533_RS02500	3-oxoacyl-ACP reductase	GSS_RS05720	3-oxoacyl-ACP reductase	Lacidipiscis_RS03810	3-oxoacyl-ACP reductase
LAC1533_RS02505	HD domain-containing protein	GSS_RS05725	HD domain-containing protein	Lacidipiscis_RS03805	HD domain-containing protein
LAC1533_RS02510	lipase/esterase	GSS_RS05730	lipase/esterase	Lacidipiscis_RS03800	lipase
LAC1533_RS02515	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	GSS_RS05735	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	Lacidipiscis_RS03795	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG
LAC1533_RS02520	nucleoid occlusion protein	GSS_RS05740	nucleoid occlusion protein	Lacidipiscis_RS03790	nucleoid occlusion protein
LAC1533_RS02525	ParA family protein	GSS_RS05745	ParA family protein	Lacidipiscis_RS03785	ParA family protein
LAC1533_RS02530	chromosome partitioning protein ParB	GSS_RS05750	chromosome partitioning protein ParB	Lacidipiscis_RS03780	chromosome partitioning protein ParB

Genomic island 5 (genomic coordinates: 1,232,888-1,269,842; size: 36,954 bp)

Lactobacillus acidipiscis ACA-DC 1533		*Lactobacillus acidipiscis* KCTC 13900		*Lactobacillus acidipiscis* JCM 10692^{T}	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS05700	DUF2188 domain-containing protein	-	-	Lacidipiscis_RS01440	DUF2188 domain-containing protein
LAC1533_RS05705	hypothetical protein	-	-	Lacidipiscis_RS01430	hypothetical protein
LAC1533_RS05710	hypothetical protein	-	-	-	-
LAC1533_RS05715	hypothetical protein	-	-	-	-
LAC1533_RS05720	hypothetical protein	-	-	Lacidipiscis_RS01415	hypothetical protein
LAC1533_RS05725	hypothetical protein	-	-	-	-
LAC1533_RS05730	hypothetical protein	-	-	-	-
LAC1533_RS05735	hypothetical protein	-	-	-	-
LAC1533_RS05740	single-stranded DNA-binding protein	-	-	-	-
LAC1533_RS05745	hypothetical protein	-	-	-	-
LAC1533_RS05750	DNA replication protein	-	-	-	-
LAC1533_RS05755	hypothetical protein	-	-	-	-
LAC1533_RS05760	hypothetical protein	-	-	Lacidipiscis_RS01385	hypothetical protein
LAC1533_RS05765	RusA family crossover junction endodeoxyribonuclease	-	-	Lacidipiscis_RS01380	RusA family crossover junction endodeoxyribonuclease
LAC1533_RS05770	hypothetical protein	-	-	-	-
LAC1533_RS05775	hypothetical protein	-	-	Lacidipiscis_RS01375	hypothetical protein
LAC1533_RS05780	hypothetical protein	-	-	-	-
LAC1533_RS05785	hypothetical protein	-	-	-	-
LAC1533_RS05790	site-specific DNA-methyltransferase	-	-	-	-
LAC1533_RS05795	hypothetical protein	-	-	-	-
LAC1533_RS05800	hypothetical protein	-	-	Lacidipiscis_RS01365	hypothetical protein
LAC1533_RS05805	terminase small subunit	-	-	Lacidipiscis_RS01360	terminase small subunit
LAC1533_RS05810	PBSX family phage terminase large subunit	-	-	Lacidipiscis_RS01355	PBSX family phage terminase large subunit
LAC1533_RS05815	phage portal protein	-	-	Lacidipiscis_RS01350	phage portal protein
LAC1533_RS05820	minor capsid protein	-	-	Lacidipiscis_RS01345	minor capsid protein
LAC1533_RS05825	hypothetical protein	-	-	Lacidipiscis_RS01340	hypothetical protein
LAC1533_RS05830	capsid protein	-	-	Lacidipiscis_RS01335	hypothetical protein
LAC1533_RS05835	hypothetical protein	-	-	-	-
LAC1533_RS05840	hypothetical protein	-	-	Lacidipiscis_RS01320	hypothetical protein
LAC1533_RS05845	capsid protein	-	-	Lacidipiscis_RS01315	capsid protein
LAC1533_RS05850	capsid protein	-	-	Lacidipiscis_RS01310	capsid protein
LAC1533_RS05855	hypothetical protein	-	-	Lacidipiscis_RS01305	hypothetical protein
LAC1533_RS05860	capsid protein	-	-	Lacidipiscis_RS01300	capsid protein
LAC1533_RS05865	hypothetical protein	-	-	Lacidipiscis_RS01295	hypothetical protein
LAC1533_RS05870	hypothetical protein	-	-	Lacidipiscis_RS01290	hypothetical protein
LAC1533_RS05875	hypothetical protein	-	-	Lacidipiscis_RS01285	hypothetical protein
LAC1533_RS05880	hypothetical protein	-	-	Lacidipiscis_RS01280	hypothetical protein
LAC1533_RS05885	hypothetical protein	-	-	Lacidipiscis_RS01275	hypothetical protein
LAC1533_RS05890	hypothetical protein	-	-	Lacidipiscis_RS01270	hypothetical protein
LAC1533_RS05895	hypothetical protein	-	-	Lacidipiscis_RS01265	hypothetical protein
LAC1533_RS05900	collagen-like protein	-	-	-	-
LAC1533_RS05905	hypothetical protein	-	-	-	-
LAC1533_RS05910	hypothetical protein	-	-	Lacidipiscis_RS01260	hypothetical protein
LAC1533_RS05915	hypothetical protein	-	-	-	-
LAC1533_RS05920	hypothetical protein	-	-	-	-
LAC1533_RS05925	DUF2335 domain-containing protein	-	-	-	-
LAC1533_RS05930	hypothetical protein	GSS_RS03935	hypothetical protein	Lacidipiscis_RS01240	hypothetical protein

Genomic island 6 (genomic coordinates: 1,317,124-1,323,132; size: 6,008 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^{T}**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS06125	transcriptional repressor	GSS_RS00045	transcriptional repressor	Lacidipiscis_RS05250	transcriptional repressor
LAC1533_RS06130	site-specific tyrosine recombinase XerD	GSS_RS11455	site-specific tyrosine recombinase XerD	Lacidipiscis_RS05255	site-specific tyrosine recombinase XerD
LAC1533_RS06135	GNAT family N-acetyltransferase	GSS_RS00050	GNAT family N-acetyltransferase	Lacidipiscis_RS05260	GNAT family N-acetyltransferase
LAC1533_RS06140	rifampin ADP-ribosyl transferase	GSS_RS00055	rifampin ADP-ribosyl transferase	Lacidipiscis_RS05265	rifampin ADP-ribosyl transferase
LAC1533_RS06145	SMC-Scp complex subunit ScpB	GSS_RS00060	SMC-Scp complex subunit ScpB	Lacidipiscis_RS05270	SMC-Scp complex subunit ScpB
LAC1533_RS06150	rRNA pseudouridine synthase	GSS_RS00065	rRNA pseudouridine synthase	Lacidipiscis_RS05275	rRNA pseudouridine synthase
LAC1533_RS06155	hypothetical protein	GSS_RS00070	hypothetical protein	Lacidipiscis_RS05280	hypothetical protein
LAC1533_RS06160	ATP-dependent DNA helicase RecQ	GSS_RS00075	ATP-dependent DNA helicase RecQ	Lacidipiscis_RS05285	ATP-dependent DNA helicase RecQ

Genomic island 7 (genomic coordinates: 1,560,818-1,583,886; size: 23,068 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^{T}**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS07280	hypothetical protein	-	-	-	-
LAC1533_RS07285	addiction module toxin RelE	-	-	-	-
LAC1533_RS07290	antitoxin RelB	GSS_RS11150	antitoxin RelB	Lacidipiscis_RS12870	RelB
LAC1533_RS07295	site-specific integrase	-	-	-	-
LAC1533_RS07300	transcriptional regulator	GSS_RS01425	transcriptional regulator	-	-
LAC1533_RS07305	hypothetical protein	-	-	-	-
LAC1533_RS07310	IS1380 family transposase	-	-	-	-
LAC1533_RS07315	hypothetical protein	-	-	-	-
LAC1533_RS07320	transposase	-	-	-	-
LAC1533_RS07325	transposase	GSS_RS11365	transposase	-	-
LAC1533_RS07330	hypothetical protein	-	-	-	-
LAC1533_RS07335	DUF536 domain-containing protein	GSS_RS11750	DUF536 domain-containing protein	-	-
LAC1533_RS07340	putative holin-like toxin	GSS_RS14255	putative holin-like toxin	-	-
LAC1533_RS07345	LtrC	-	-	Lacidipiscis_RS12035	hypothetical protein
LAC1533_RS07350	hypothetical protein	-	-	Lacidipiscis_RS12030	hypothetical protein
LAC1533_RS07355	hypothetical protein	-	-	-	-
LAC1533_RS07360	type IA DNA topoisomerase	-	-	Lacidipiscis_RS12025	type IA DNA topoisomerase
LAC1533_RS07365	hypothetical protein	-	-	-	-
LAC1533_RS07370	conjugal transfer protein	-	-	Lacidipiscis_RS01950	hypothetical protein
LAC1533_RS07375	hypothetical protein	-	-	-	-
LAC1533_RS07380	conjugal transfer protein	-	-	-	-
LAC1533_RS07385	conjugal transfer protein	-	-	-	-
LAC1533_RS07390	hypothetical protein	-	-	-	-
LAC1533_RS07395	IS30 family transposase	GSS_RS11415	IS30 family transposase	-	-
LAC1533_RS07400	hypothetical protein	-	-	-	-
LAC1533_RS07405	hypothetical protein	-	-	-	-
LAC1533_RS07410	peptidoglycan endopeptidase	-	-	-	-
LAC1533_RS07415	IS256 family transposase	-	-	-	-
LAC1533_RS07420	transposase	-	-	-	-
LAC1533_RS07425	transposase	-	-	-	-

Genomic island 8 (genomic coordinates: 1,812,682-1,817,359; size: 4,677 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* DSM 15836^{T}**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS08565	addiction module toxin RelE	-	-	-	-
LAC1533_RS08570	phage portal protein	-	-	-	-
LAC1533_RS08575	peptidase	-	-	-	-
LAC1533_RS08580	phage major capsid protein	-	-	-	-
LAC1533_RS08585	hypothetical protein	-	-	-	-
LAC1533_RS08590	head-tail adaptor	-	-	-	-
LAC1533_RS08595	DNA primase	-	-	-	-
LAC1533_RS08600	1,4-beta-N-acetylmuramidase	-	-	-	-

Genomic island 9 (genomic coordinates: 1,876,064-1,930,970; size: 54,906 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS08865	50S ribosomal protein L13	GSS_RS05060	50S ribosomal protein L13	Lacidipiscis_RS05930	50S ribosomal protein L13
LAC1533_RS08870	tRNA pseudouridine(38-40) synthase TruA	GSS_RS05055	tRNA pseudouridine(38-40) synthase TruA	Lacidipiscis_RS05935	tRNA pseudouridine(38-40) synthase TruA
LAC1533_RS08875	energy-coupling factor transporter transmembrane protein EcfT	GSS_RS05050	energy-coupling factor transporter transmembrane protein EcfT	Lacidipiscis_RS05940	energy-coupling factor transporter transmembrane protein EcfT
LAC1533_RS08880	energy-coupling factor ABC transporter ATP-binding protein	GSS_RS05045	energy-coupling factor transporter ATPase	Lacidipiscis_RS05945	energy-coupling factor ABC transporter ATP-binding protein
LAC1533_RS08885	energy-coupling factor ABC transporter ATP-binding protein	GSS_RS05040	energy-coupling factor ABC transporter ATP-binding protein	Lacidipiscis_RS05950	energy-coupling factor ABC transporter ATP-binding protein
LAC1533_RS08890	50S ribosomal protein L17	GSS_RS05035	50S ribosomal protein L17	Lacidipiscis_RS05955	50S ribosomal protein L17
LAC1533_RS08895	DNA-directed RNA polymerase subunit alpha	GSS_RS05030	DNA-directed RNA polymerase subunit alpha	Lacidipiscis_RS05960	DNA-directed RNA polymerase subunit alpha
LAC1533_RS08900	30S ribosomal protein S11	GSS_RS05025	30S ribosomal protein S11	Lacidipiscis_RS05965	30S ribosomal protein S11
LAC1533_RS08905	30S ribosomal protein S13	GSS_RS05020	30S ribosomal protein S13	Lacidipiscis_RS05970	30S ribosomal protein S13
LAC1533_RS08910	50S ribosomal protein L36	GSS_RS05015	50S ribosomal protein L36	Lacidipiscis_RS05975	50S ribosomal protein L36
LAC1533_RS08915	translation initiation factor IF-1	GSS_RS05010	translation initiation factor IF-1	Lacidipiscis_RS05980	translation initiation factor IF-1
LAC1533_RS08920	adenylate kinase	GSS_RS05005	adenylate kinase	Lacidipiscis_RS05985	adenylate kinase
LAC1533_RS08925	preprotein translocase subunit SecY	GSS_RS05000	preprotein translocase subunit SecY	Lacidipiscis_RS05990	preprotein translocase subunit SecY
LAC1533_RS08930	50S ribosomal protein L15	GSS_RS04995	50S ribosomal protein L15	Lacidipiscis_RS05995	50S ribosomal protein L15
LAC1533_RS08935	50S ribosomal protein L30	GSS_RS04990	50S ribosomal protein L30	Lacidipiscis_RS06000	50S ribosomal protein L30
LAC1533_RS08940	30S ribosomal protein S5	GSS_RS04985	30S ribosomal protein S5	Lacidipiscis_RS06005	30S ribosomal protein S5
LAC1533_RS08945	50S ribosomal protein L18	GSS_RS04980	50S ribosomal protein L18	Lacidipiscis_RS06010	50S ribosomal protein L18
LAC1533_RS08950	50S ribosomal protein L6	GSS_RS04975	50S ribosomal protein L6	Lacidipiscis_RS06015	50S ribosomal protein L6
LAC1533_RS08955	30S ribosomal protein S8	GSS_RS04970	30S ribosomal protein S8	Lacidipiscis_RS06020	30S ribosomal protein S8
LAC1533_RS08960	type Z 30S ribosomal protein S14	GSS_RS04965	type Z 30S ribosomal protein S14	Lacidipiscis_RS06025	type Z 30S ribosomal protein S14
LAC1533_RS08965	50S ribosomal protein L5	GSS_RS04960	50S ribosomal protein L5	Lacidipiscis_RS06030	50S ribosomal protein L5
LAC1533_RS08970	50S ribosomal protein L24	GSS_RS04955	50S ribosomal protein L24	Lacidipiscis_RS06035	50S ribosomal protein L24
LAC1533_RS08975	50S ribosomal protein L14	GSS_RS04950	50S ribosomal protein L14	Lacidipiscis_RS06040	50S ribosomal protein L14
LAC1533_RS08980	30S ribosomal protein S17	GSS_RS04945	30S ribosomal protein S17	Lacidipiscis_RS06045	30S ribosomal protein S17
LAC1533_RS08985	50S ribosomal protein L29	GSS_RS04940	50S ribosomal protein L29	Lacidipiscis_RS06050	50S ribosomal protein L29
LAC1533_RS08990	50S ribosomal protein L16	GSS_RS04935	50S ribosomal protein L16	Lacidipiscis_RS06055	50S ribosomal protein L16
LAC1533_RS08995	30S ribosomal protein S3	GSS_RS04930	30S ribosomal protein S3	Lacidipiscis_RS06060	30S ribosomal protein S3
LAC1533_RS09000	50S ribosomal protein L22	GSS_RS04925	50S ribosomal protein L22	Lacidipiscis_RS06065	50S ribosomal protein L22
LAC1533_RS09005	30S ribosomal protein S19	GSS_RS04920	30S ribosomal protein S19	Lacidipiscis_RS06070	30S ribosomal protein S19
LAC1533_RS09010	50S ribosomal protein L2	GSS_RS04915	50S ribosomal protein L2	Lacidipiscis_RS06075	50S ribosomal protein L2
LAC1533_RS09015	50S ribosomal protein L23	GSS_RS04910	50S ribosomal protein L23	Lacidipiscis_RS06080	50S ribosomal protein L23
LAC1533_RS09020	50S ribosomal protein L4	GSS_RS04905	50S ribosomal protein L4	Lacidipiscis_RS06085	50S ribosomal protein L4
LAC1533_RS09025	50S ribosomal protein L3	GSS_RS04900	50S ribosomal protein L3	Lacidipiscis_RS06090	50S ribosomal protein L3
LAC1533_RS09030	30S ribosomal protein S10	GSS_RS04895	30S ribosomal protein S10	Lacidipiscis_RS06095	30S ribosomal protein S10

Genomic island 10 (genomic coordinates: 1,952,756-1,964,615; size: 11,859 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS09300	hypothetical protein	GSS_RS08395	hypothetical protein	Lacidipiscis_RS04780	hypothetical protein
LAC1533_RS09305	exodeoxyribonuclease III	GSS_RS08390	exodeoxyribonuclease III	Lacidipiscis_RS04785	exodeoxyribonuclease III
LAC1533_RS09310	group II intron reverse transcriptase/maturase	-	-	-	-
LAC1533_RS09315	hypothetical protein	-	-	-	-
LAC1533_RS09320	IS66 family transposase	GSS_RS08385	IS66 family transposase		
LAC1533_RS09325	transposase	-	-	-	-
LAC1533_RS09330	hypothetical protein	-	-	-	-
LAC1533_RS09335	sigma-70 family RNA polymerase sigma factor	GSS_RS08370	hypothetical protein	-	-
LAC1533_RS09340	hypothetical protein	-	-	-	-
LAC1533_RS09345	DUF3173 domain-containing protein	GSS_RS08355	DUF3173 domain-containing protein	-	-
LAC1533_RS09350	site-specific integrase	GSS_RS08350	site-specific integrase	-	-
LAC1533_RS09355	glutamine-hydrolyzing GMP synthase	GSS_RS08345	glutamine-hydrolyzing GMP synthase	Lacidipiscis_RS09005	glutamine-hydrolyzing GMP synthase
LAC1533_RS09360	type I pantothenate kinase	-	-	Lacidipiscis_RS09010	type I pantothenate kinase
LAC1533_RS09365	lipase	GSS_RS08335	lipase	Lacidipiscis_RS09015	acylhydrolase

Genomic island 11 (genomic coordinates: 2,383,526-2,392,933; size: 9,407 bp)

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^T**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS11280	hypothetical protein	GSS_RS10050	hypothetical protein	-	-
LAC1533_RS11285	GNAT family N-acetyltransferase	GSS_RS13235	GNAT family N-acetyltransferase	-	-
LAC1533_RS11290	IS256 family transposase	-	-	-	-
LAC1533_RS11295	amino acid permease	GSS_RS10060	amino acid permease	Lacidipiscis_RS03680	amino acid permease
LAC1533_RS11300	hypothetical protein	GSS_RS13240	ArgR family transcriptional regulator	Lacidipiscis_RS03675	hypothetical protein
LAC1533_RS11305	alpha-glucosidase	GSS_RS10075	alpha-glucosidase	Lacidipiscis_RS03670	alpha-glucosidase
LAC1533_RS11310	fructokinase	GSS_RS10080	fructokinase	Lacidipiscis_RS03665	fructokinase
LAC1533_RS11315	glyoxalase	GSS_RS10085	glyoxalase/bleomycin resistance/dioxygenase family protein	Lacidipiscis_RS03660	glyoxalase/bleomycin resistance/dioxygenase family protein
LAC1533_RS11320	PTS glucose transporter subunit IIABC	GSS_RS10090	PTS glucose transporter subunit IIABC	-	-

Genomic island 12 (genomic coordinates: 2,404,281-2,427,642; size: 23,361 bp)					
***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^{T}**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS11380	PTS mannitol transporter subunit IIA	-	-	Lacidipiscis_RS07200	PTS mannitol transporter subunit IIA
LAC1533_RS11385	PTS mannitol transporter subunit IICBA	-	-	Lacidipiscis_RS07205	PTS mannitol transporter subunit IICBA
LAC1533_RS11390	esterase family protein	-	-	Lacidipiscis_RS07210	esterase family protein
LAC1533_RS11395	PTS fructose transporter subunit IID	-	-	Lacidipiscis_RS07215	PTS fructose transporter subunit IID
LAC1533_RS11400	PTS sugar transporter subunit IIC	-	-	Lacidipiscis_RS07220	PTS sugar transporter subunit IIC
LAC1533_RS11405	PTS mannose/fructose/sorbose transporter subunit IIB	-	-	Lacidipiscis_RS07225	PTS mannose/fructose/sorbose transporter subunit IIB
LAC1533_RS11410	PRD domain-containing protein	-	-	Lacidipiscis_RS07230	PRD domain-containing protein
LAC1533_RS11415	hypothetical protein	-	-	Lacidipiscis_RS07235	hypothetical protein
LAC1533_RS11420	HTH domain-containing protein	-	-	Lacidipiscis_RS09490	HTH domain-containing protein
LAC1533_RS11425	glucosamine-6-phosphate deaminase	GSS_RS10115	glucosamine-6-phosphate deaminase	Lacidipiscis_RS09485	glucosamine-6-phosphate deaminase
LAC1533_RS11430	glutamine--fructose-6-phosphate transaminase (isomerizing)	GSS_RS10120	glutamine--fructose-6-phosphate transaminase (isomerizing)	Lacidipiscis_RS09480	glutamine--fructose-6-phosphate transaminase (isomerizing)
LAC1533_RS11435	group II intron reverse transcriptase/maturase	-	-	-	-
LAC1533_RS11440	hypothetical protein	-	-	-	-
LAC1533_RS11445	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent	GSS_RS10125	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent	Lacidipiscis_RS09475	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent
LAC1533_RS11450	ATP:cob(I)alamin adenosyltransferase	GSS_RS10130	ATP:cob(I)alamin adenosyltransferase	Lacidipiscis_RS09470	ATP:cob(I)alamin adenosyltransferase
LAC1533_RS11455	DUF4430 domain-containing protein	GSS_RS10135	DUF4430 domain-containing protein	Lacidipiscis_RS09465	DUF4430 domain-containing protein
LAC1533_RS11460	aldo/keto reductase	GSS_RS10140	aldo/keto reductase	Lacidipiscis_RS00510	aldo/keto reductase
LAC1533_RS11465	cupin domain-containing protein	GSS_RS10145	cupin domain-containing protein	Lacidipiscis_RS00515	cupin domain-containing protein
LAC1533_RS11470	carboxymuconolactone decarboxylase family protein	GSS_RS10150	carboxymuconolactone decarboxylase family protein	Lacidipiscis_RS00520	carboxymuconolactone decarboxylase family protein
LAC1533_RS11475	DUF2255 domain-containing protein	GSS_RS10155	DUF2255 domain-containing protein	Lacidipiscis_RS00525	DUF2255 domain-containing protein
LAC1533_RS11480	MerR family transcriptional regulator	GSS_RS10160	MerR family transcriptional regulator	Lacidipiscis_RS00530	MerR family transcriptional regulator
Genomic island 13 (genomic coordinates: 2,467,112-2,491,877; size: 24,765 bp)					
***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus acidipiscis* KCTC 13900**		***Lactobacillus acidipiscis* JCM 10692^{T}**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS11635	DUF4811 domain-containing protein	GSS_RS03765	DUF4811 domain-containing protein	-	-
LAC1533_RS11640	MFS transporter	-	-	-	-
LAC1533_RS11645	MerR family transcriptional regulator	GSS_RS03755	MerR family transcriptional regulator	Lacidipiscis_RS12730	MerR family transcriptional regulator
LAC1533_RS11650	HAD family hydrolase	GSS_RS11485	HAD family hydrolase	Lacidipiscis_RS12725	HAD family hydrolase
LAC1533_RS11655	CrcB family protein	GSS_RS03750	CrcB family protein	Lacidipiscis_RS00125	CrcB family protein
LAC1533_RS11660	hypothetical protein	GSS_RS03745	camphor resistance protein CrcB	Lacidipiscis_RS04090	hypothetical protein
LAC1533_RS11665	6-phospho-beta-glucosidase	GSS_RS03740	6-phospho-beta-glucosidase	Lacidipiscis_RS04095	6-phospho-beta-glucosidase
LAC1533_RS11670	PTS lactose/cellobiose transporter subunit IIA	GSS_RS03735	PTS lactose/cellobiose transporter subunit IIA	Lacidipiscis_RS04100	PTS lactose/cellobiose transporter subunit IIA
LAC1533_RS11675	PTS sugar transporter subunit IIB	GSS_RS03730	PTS sugar transporter subunit IIB	Lacidipiscis_RS04105	PTS sugar transporter subunit IIB
LAC1533_RS11680	GntR family transcriptional regulator	-	-	Lacidipiscis_RS04110	GntR family transcriptional regulator
LAC1533_RS11685	hypothetical protein	-	-	-	-
LAC1533_RS11690	group II intron reverse transcriptase/maturase	-	-	-	-
LAC1533_RS11695	hypothetical protein	-	-	-	-
LAC1533_RS11700	hypothetical protein	-	-		
LAC1533_RS11705	nucleotide sugar dehydrogenase	-	-	Lacidipiscis_RS02425	nucleotide sugar dehydrogenase
LAC1533_RS11710	hypothetical protein	-	-	-	-
LAC1533_RS11715	hypothetical protein	-	-	-	-
LAC1533_RS11720	hypothetical protein	-	-	-	-
LAC1533_RS11725	hypothetical protein	-	-	-	-
LAC1533_RS11730	hypothetical protein	-	-	-	-
LAC1533_RS11735	glycosyltransferase family 2 protein	-	-	-	-
LAC1533_RS11740	UDP-phosphate N-acetylgalactosaminyl-1-phosphate transferase	GSS_RS03700	sugar transferase	Lacidipiscis_RS00600	UDP-phosphate N-acetylgalactosaminyl-1-phosphate transferase
LAC1533_RS11745	epimerase	GSS_RS03695	epimerase	Lacidipiscis_RS00605	epimerase
LAC1533_RS11750	tyrosine protein phosphatase	GSS_RS03685	tyrosine protein phosphatase	Lacidipiscis_RS00610	hypothetical protein
LAC1533_RS11755	exopolysaccharide biosynthesis protein	GSS_RS03680	exopolysaccharide biosynthesis protein	Lacidipiscis_RS00615	exopolysaccharide biosynthesis protein
LAC1533_RS11760	chain-length determining protein	GSS_RS03675	polysaccharide biosynthesis protein	Lacidipiscis_RS00620	chain-length determining protein
LAC1533_RS11765	serine hydrolase	GSS_RS03670	serine hydrolase	Lacidipiscis_RS00625	serine hydrolase
* Blue colour genes represent pseudogenes within strain ACA-DC 1533					

Supplementary table S6A. Prophage regions identified in the three *L. acidipiscis* strains using the PHASTER software.

				***Lactobacillus acidipiscis* ACA-DC 1533**			***Lactobacillus acidipiscis* JCM 10692^T**	***Lactobacillus acidipiscis* KCTC 13900**
Region Length	**Completeness**	**Region Position**	**Most common phages (hit genes count)**	**BLAST Hit**	**E-Value**	**locus_tag**	**locus_tag**	**locus_tag**
43.4 Kbp	intact	1,228,777-1,272,253	*Lactobacillus* phage phig1e (9)	attL	0	-	-	-
			Aggregatibacter phage S1249 (9)	PROPHAGE_Oceano_HTE831: integrase;phage(gi23097608)	4.04E-82	LAC1533_RS05675	Lacidipiscis_RS01475	-
			Lactobacillus phage phiJB (9)	PHAGE_Propio_PFR1_NC_031076: hypothetical protein; phage(gi100027)	2.88E-32	LAC1533_RS05680	Lacidipiscis_RS01470	-
			Lactobacillus phage LL-H (6)	PHAGE_Lactob_Sha1_NC_019489: bifunctional S24 family peptidase/transcriptional regulator; phage(gi418489831)	8.16E-64	LAC1533_RS05685	-	-
			Streptococcus phage 5093 (6)	PHAGE_Lactoc_98201_NC_031064: putative Cro/Cl-type repressor; phage(gi100005)	2.28E-29	LAC1533_RS05690	-	-
			Lactobacillus phage PLE2 (5)	PHAGE_Lactob_Sha1_NC_019489: phage-related antirepressor; phage(gi418489833)	3.39E-70	LAC1533_RS05695	-	-
			Lactobacillus phage Sha1 (5)	PHAGE_Gordon_Schwabeltier_NC_031255: putative head morphogenesis protein; phage(gi100034)	3.89E-08	LAC1533_RS05700	Lacidipiscis_RS01440	-
			Bacillus phage BCJA1c (5)	hypothetical protein	0	LAC1533_RS05705	Lacidipiscis_RS01430	-
			Lactobacillus phage iLp1308 (4)	hypothetical protein	0	LAC1533_RS05710	-	-
			Lactobacillus phage CL1 (4)	hypothetical protein	0	LAC1533_RS05715	-	-
				hypothetical protein	0	LAC1533_RS05720	Lacidipiscis_RS01415	-
				PHAGE_Lactob_Sha1_NC_019489: phage protein; phage(gi418489843)	2.40E-28	LAC1533_RS05725	-	-
				PHAGE_Strept_SMP_NC_008721: hypothetical protein; phage(gi119953766)	6.41E-48	LAC1533_RS05730	-	-
				PHAGE_Lactob_PL_1_NC_022757: hypothetical protein; phage(gi557308025)	2.44E-73	LAC1533_RS05735	-	-
				PHAGE_Lactob_Lv_1_NC_011801: single stranded DNA binding protein; phage(gi219563233)	1.68E-33	LAC1533_RS05740	-	-
				hypothetical protein	0	LAC1533_RS05745	-	-
				PHAGE_Strept_APCM01_NC_029030: replisome organizer; phage(gi971767293)	4.60E-84	LAC1533_RS05750	-	-
				PHAGE_Lactob_phiAQ113_NC_019782: DNA replication protein; phage(gi446730275)	6.15E-17	LAC1533_RS05755	-	-
				hypothetical protein	0	LAC1533_RS05760	Lacidipiscis_RS01385	-
				PHAGE_Lactob_Lc_Nu_NC_007501: putative Holliday junction resolvase; phage(gi78000012)	1.83E-36	LAC1533_RS05765	Lacidipiscis_RS01380	-
				PHAGE_Geobac_E3_NC_029073: hypothetical protein; phage(gi985758435)	1.03E-24	LAC1533_RS05770	-	-
				hypothetical protein	0	LAC1533_RS05775	Lacidipiscis_RS01375	-
				PHAGE_Lactob_Lrm1_NC_011104: hypothetical protein; phage(gi195661244)	4.48E-05	LAC1533_RS05780	-	-
				PHAGE_Strept_phiARI0468_4_NC_031915: general stress protein; phage(gi100019)	1.46E-30	LAC1533_RS05785	-	-
				PHAGE_Lactob_Lrm1_NC_011104: DNA methylase; phage(gi195661243)	2.55E-149	LAC1533_RS05790	-	-
				hypothetical protein	0	LAC1533_RS05795	-	-
				PHAGE_Lactob_Sha1_NC_019489: phage transcriptional activator RinA; phage(gi418489798)	5.82E-06	LAC1533_RS05800	Lacidipiscis_RS01365	-
				PHAGE_Lactob_PLE3_NC_031125: serine recombinase; phage(gi100001)	1.95E-41	LAC1533_RS05805	Lacidipiscis_RS01360	-
				PHAGE_Lister_A500_NC_009810: TerL; phage(gi157324962)	2.74E-151	LAC1533_RS05810	Lacidipiscis_RS01355	-
				PHAGE_Lactob_phig1e_NC_004305: minor capsid protein; phage(gi23455800)	1.26E-161	LAC1533_RS05815	Lacidipiscis_RS01350	-
				PHAGE_Lactob_phig1e_NC_004305: minor capsid protein; phage(gi23455801)	3.28E-97	LAC1533_RS05820	Lacidipiscis_RS01345	-
				PHAGE_Lister_vB_LmoS_293_NC_028929: capsid scaffolding protein; phage(gi971756881)	3.55E-26	LAC1533_RS05825	Lacidipiscis_RS01340	-
				PHAGE_Lactob_phiJB_NC_022775: major capsid protein; phage(gi571797882)	3.60E-124	LAC1533_RS05830	Lacidipiscis_RS01335	-
				hypothetical protein	0	LAC1533_RS05835	-	-
				PHAGE_Strept_phiARI0468_4_NC_031915: hypothetical protein; phage(gi100013)	5.89E-08	LAC1533_RS05840	Lacidipiscis_RS01320	-
				PHAGE_Lactob_phig1e_NC_004305: minor capsid protein; phage(gi23455805)	1.22E-39	LAC1533_RS05845	Lacidipiscis_RS01315	-
				PHAGE_Lactob_phig1e_NC_004305: minor capsid protein; phage(gi23455806)	2.36E-26	LAC1533_RS05850	Lacidipiscis_RS01310	-
				PHAGE_Lactob_phig1e_NC_004305: minor capsid protein; phage(gi23455807)	3.44E-06	LAC1533_RS05855	Lacidipiscis_RS01305	-
				PHAGE_Lactoc_98201_NC_031064: hypothetical protein; phage(gi100041)	1.08E-14	LAC1533_RS05860	Lacidipiscis_RS01300	-
				PHAGE_Lactob_phig1e_NC_004305: minor capsid protein; phage(gi23455809)	1.43E-05	LAC1533_RS05865	Lacidipiscis_RS01295	-
				PHAGE_Lactob_phig1e_NC_004305: hypothetical protein; phage(gi23455810)	5.33E-34	LAC1533_RS05870	Lacidipiscis_RS01290	-
				PHAGE_Oenoco_phiS13_NC_023560: Phage tail length tape-measure protein; phage(gi589286259)	3.06E-98	LAC1533_RS05875	Lacidipiscis_RS01285	-
				PHAGE_Clostr_phiCD146_NC_028958: Tail component protein; phage(gi971820172)	4.86E-06	LAC1533_RS05880	Lacidipiscis_RS01280	-
				PHAGE_Clostr_phi8074_B1_NC_019924: putative phage tail protein; phage(gi431810378)	9.47E-26	LAC1533_RS05885	Lacidipiscis_RS01275	-
				PHAGE_Entero_vB_IME197_NC_028671: glycerophosphoryl diester phosphodiesterase; phage(gi966199029)	1.79E-63	LAC1533_RS05890	Lacidipiscis_RS01270	-
				hypothetical protein	0	LAC1533_RS05895	Lacidipiscis_RS01265	-
				PHAGE_Lactob_iLp1308_NC_028911: hypothetical protein; phage(gi971754938)	0	LAC1533_RS05900	-	-
				PHAGE_Lactob_CL2_NC_028835: tail fiber protein; phage(gi971748035)	4.66E-12	LAC1533_RS05905	-	-
				PHAGE_Entero_EFC_1_NC_025453: holin; phage(gi725950567)	5.76E-27	LAC1533_RS05910	Lacidipiscis_RS01260	-
				PHAGE_Lactob_Ld3_NC_025421: putative endolysin; phage(gi712912341)	2.69E-77	LAC1533_RS05915	-	-
				hypothetical protein	0	LAC1533_RS05920	-	-
				PHAGE_Pseudo_MD8_NC_031091: hypothetical protein; phage(gi100029)	7.80E-11	LAC1533_RS05925	-	-
				attR	0	-	-	-
				hypothetical protein	0	LAC1533_RS05930	Lacidipiscis_RS01240	GSS_RS03935
				PHAGE_Aggreg_S1249_NC_013597: XRE family transcriptional regulator; phage(gi100024)	8.74E-09	LAC1533_RS05935	Lacidipiscis_RS01235	GSS_RS03930

				***Lactobacillus acidipiscis* KCTC 13900**			***Lactobacillus acidipiscis* ACA-DC 1533**	***Lactobacillus acidipiscis* JCM 10692^{T}**
Region Length	**Completeness**	**Region Position**	**Most common phages (hit genes count)**	**BLAST Hit**	**E-Value**	**locus_tag**	**locus_tag**	**locus_tag**
40.8Kb	intact	-	*Lactobacillus* phage PL-1 (15)	attL	0	-	-	-
			Lactobacillus phage J-1 (14)	PHAGE_Strept_315.4_NC_004587: hypothetical protein; phage(gi28876329)	7.15E-77	GSS_RS00660	-	-
			Lactobacillus phage Lrm1 (11)	PHAGE_Clostr_phiCT19406C_NC_029006: tail protein; phage(gi971821558)	3.00E-14	GSS_RS00665	-	-
			Lactobacillus phage LF1 (10)	PHAGE_Lactob_PL_1_NC_022757: tape measure; phage(gi557308006)	0	GSS_RS13640	-	-
			Lactobacillus phage A2 (9)	PHAGE_Lactob_PL_1_NC_022757: major tail protein; phage(gi557308004)	4.85E-86	GSS_RS00685	-	-
			Enterococcus phage EFC-1 (7)	PHAGE_Lactob_PL_1_NC_022757: hypothetical protein; phage(gi557308003)	6.51E-27	GSS_RS00690	-	-
			Bacillus phage BCJA1c (6)	PHAGE_Lactob_PL_1_NC_022757: hypothetical protein; phage(gi557308002)	5.90E-30	GSS_RS00695	-	-
			Lactobacillus phage phiPYB5 (6)	PHAGE_Lactob_PL_1_NC_022757: head tail joining protein; phage(gi557308001)	1.47E-31	GSS_RS00700	-	-
				PHAGE_Lactob_PL_1_NC_022757: head tail joining protein; phage(gi557308000)	8.32E-23	GSS_RS00705	-	-
				PHAGE_Lactob_PL_1_NC_022757: major capsid L; phage(gi557308050)	1.31E-12	GSS_RS00710	-	-
				PHAGE_Lactob_PL_1_NC_022757: capsid maturation protease; phage(gi557307998)	8.37E-79	GSS_RS00720	-	-
				PHAGE_Lactob_PL_1_NC_022757: portal protein; phage(gi557307997)	1.05E-145	GSS_RS00725	-	-
				hypothetical protein	0	GSS_RS00730	-	-
				PHAGE_Lactob_PL_1_NC_022757: terminase large subunit; phage(gi557307995)	0	GSS_RS00735	-	-
				PHAGE_Lactob_PL_1_NC_022757: terminase small subunit; phage(gi557307994)	1.41E-50	GSS_RS00740	-	-
				PHAGE_Lactob_PL_1_NC_022757: hypothetical protein; phage(gi557308049)	2.28E-106	GSS_RS00745	-	-
				hypothetical protein	0.00E+00	GSS_RS00750	-	-
				hypothetical protein	0	GSS_RS00755	-	-
				PHAGE_Entero_phiFL1A_NC_013646: hypothetical protein; phage(gi281416358)	7.15E-47	GSS_RS00770	-	-
				PHAGE_Thermu_OH2_NC_021784: phage transcriptional regulator, ArpU; phage(gi526118340)	1.05E-14	GSS_RS00775	-	-
				hypothetical protein	0.00E+00	GSS_RS00780	-	-
				hypothetical protein	0	GSS_RS00785	-	-
				hypothetical protein	0	GSS_RS00790	-	-
				PHAGE_Entero_EFC_1_NC_025453: endodeoxyribonuclease RusA; phage(gi725950541)	1.74E-61	GSS_RS00800	-	-
				hypothetical protein	0	GSS_RS00805	-	-
				PHAGE_Entero_EFC_1_NC_025453: primase2; phage(gi725950538)	0	GSS_RS00810	-	-
				hypothetical protein	0.00E+00	GSS_RS00815	-	-
				hypothetical protein	0.00E+00	GSS_RS00820	-	-
				PHAGE_Entero_EFC_1_NC_025453: DEAD/DEAH box helicase; Type; phage III restriction enzme; -(gi725950530)	0.00E+00	GSS_RS00830	-	-
				PHAGE_Strept_SM1_NC_004996: gp14; phage(gi32469445)	5.22E-27	GSS_RS00835	-	-
				hypothetical protein	0.00E+00	GSS_RS00840	-	-
				PHAGE_Entero_EFC_1_NC_025453: replication terminator protein; phage(gi725950528)	2.21E-34	GSS_RS00845	-	-
				PHAGE_Paenib_Vegas_NC_028767: hypothetical protein; phage(gi971741647)	3.34E-20	GSS_RS00850	-	-
				PHAGE_Bacill_BCJA1c_NC_006557: hypothetical protein; phage(gi56694882)	3.02E-112	GSS_RS00855	-	-
				PHAGE_Paenib_Vegas_NC_028767: chromosome segregation protein SMC; phage(gi971741645)	0.00E+00	GSS_RS00860	-	-
				PHAGE_Lactob_Lv_1_NC_011801: hypothetical protein; phage(gi219563228)	1.41E-15	GSS_RS00875	-	-
				hypothetical protein	0.00E+00	GSS_RS00880	-	-
				PHAGE_Lactob_phiadh_NC_000896: hypothetical protein; phage(gi9633012)	1.01E-16	GSS_RS00885	-	-
				PHAGE_Lactoc_PLgT_1_NC_031016: N-acetylmuramoyl-L-alanine amidase; phage(gi100063)	9.04E-23	GSS_RS00890	-	Lacidipiscis_RS03075
				hypothetical protein	0	GSS_RS00900	-	-
				PHAGE_Bacill_SP_15_NC_031245: hypothetical protein; phage(gi100313)	3.91E-15	GSS_RS00905	-	-
				PHAGE_Lactob_Sha1_NC_019489: phage integrase; phage(gi418489824)	1.79E-125	GSS_RS00910	-	Lacidipiscis_RS07690
				attR	0	-	-	-

Supplementary table S6B. CRISPR systems identified in the *L. acidipiscis* KCTC 13900 genome using the CRISPRFinder tool.

CRISPR1 (contig 102)	
Direct Repeat	**Spacers***
GTATTCCCCACGCATGTGGGGGTGATCC	>spacer1
	TCTGATAGTTGTAGCCACCTTCTTTTGCAGGTA
	>spacer2
	TGAATAATGGATATTAACACAACGAGACTAGCT
	>spacer3
	CATTTGGGGACAAAAACTACGGTGGATCAAATT
	>spacer4
	CAACGCAATTCGAGATGGTTACGTTAAACTGCA
	>spacer5
	CAAAATGGACGGCTTAATGCAGCCTAAAGAATA
	>spacer6
	TATAAATCGCTCATGCCTAAGGTGTCAGCAATC
	>spacer7
	TATAAATCGCTCATGCCTAAGGTGTCAGCAATC
	>spacer8
	CGTGAGTCAGAAGTTGGAACCAAACAAACGACC
	>spacer9
	CTTGTTCAATCTTAGATCCTACGTTTGGCTGCA
	>spacer10
	CAATCATTGATGGTACACTCAGATCCCTTAAAG
	>spacer11
	TTTGGTGATAACGCACGGCCATGATCGGTTGTG
	>spacer12
	TTATGGAAAAGGCATCCGGACATTGACAGCATT
	>spacer13
	TTACCGTGTGTACGATGTGGCCGACGTAAAATA
	>spacer14
	TCACAAAGCATTCGGATTGCCAATTACAGCCGA
	>spacer15
	TATGTTGACGCAATGGGTGCTGTCAAGGCTGGG
	>spacer16
	CGACAGTACAAGGTAGCGATGGATAACCAATAT
	>spacer17
	TAAATATCGTAAGGTTAAGGAAAAAGGCAAAAA
	>spacer18
	CTTTGACATCTGGATAAGCAGTTGATATTTTGA
	>spacer19
	CTGTCGCACCGTCAAGGATAGCCTTTGCCTCCCA
	>spacer20
	TAGTGATAAGGAAAAGAATGAAAATCAATTATC
	>spacer21
	TTCAATCCATGGCGATTGGACGTTTGATCCGCA
	>spacer22
	TAATGAAATCCAATCCGGTTGGCAAAGTCGATT
	>spacer23
	CAATATTGGCACGTGTGTATATCAGGCGCGTCA
	>spacer24
	TATCATCGCGCTGTTTTTTTGCTTTAGTAGTTG
	>spacer25
	TTACCGGAACTGATGATCGTATCACCCAGTTCG

CRISPR2 (contig 158 & 370)	
Direct Repeat	**Spacers**
GTTCTCGTCCCCTATTACCGGGGATCATCTAATACC	>spacer1
	AATACCTTAACCAACACAATGCAGGTAAATTTCG
	>spacer2
	ATACGACTAAAGATGATGATGAAAATGTGCCATTCT
	>spacer3
	AGGGGGCTTCTAAGAGCAAACAGCAAAAGACCAATA
	>spacer4
	TAAATTACCTGATTTTACATTTGATGAGCTTAACG
	>spacer5
	TGAACATGCTTGTTAAACCGTTGAAGAAAGAAAA
	>spacer6
	GTGAATCGCTTTGAATAAGTAAAGGAGAAATAACA
	>spacer7
	ATAAATTGATGGGAATCCGTAAAGAGCATCAAG
	>spacer8
	TGACCGCGTCAATGAACAAATCGCTTAGATGGTCAA
	>spacer9
	CCGAAGTTAATTTGATCTTTTCTCCTATGCCCAGCGC
	>spacer10
	TAAAATATTCAATATAGCAGTAAAAAAAGCCAAC
	>spacer11
	ACAAGATACAAATATTCATGTGGCGTCAACTCACG
	>spacer12
	ACCAAAAAGGAGATTTTATTATGTATACAATATACG
	>spacer13
	TGATAGCAGAGTAAAACACATTGATAACCGGCCAATG
	>spacer14
	AATGCTAGGATTCGCACCATCGACAGGTAAAACAAT
	>spacer15
	TGAGAAAATTGAGGTAACTGATGATAGACGCGGTTAA
	>spacer16
	AGATTTTATCATGTATACAATTTATGAATATCAGC
	>spacer17
	TGAAAGACTATCAGGCATATATTGAAGAAACAGATA
	>spacer18
	GCAAAAAATTGTAGATATGGCAATGGAAAACGA
	>spacer19
	AAAGAGTTGGCAAGGCAAAACGATTTGGAGTACAC
	>spacer20
	TAAAAGCACAGGAAAACGGTTGGAACGAGTGGCATA
	>spacer21
	AAAAATGGGACTGTTAGATAAGATTAAGGAAAACG
	>spacer22
	ACAAAAACCAGTGGCATTGTTAGAGAATCTTATTT
	>spacer23
	CGTAAATCAGCACGGTAATCATATCCACAAGATCCAGG
	>spacer24
	TGATTCAGCAGATAGTAGTAAGCATTATGGCGGTAGTCG
	>spacer25
	GATGATTACATGACTATAAGAGATGATTTTTTACA
	>spacer26
	TAAAGGAGATTTTATCATGGATAAAAAAGCTTTAATT
	>spacer27
	TTTAGTGATCGTCCGTGGATGATCCTTGTCGCC
	>spacer28
	CCAATATTTCTTTTAAAAGATCTTCGTCAGCGTTTGA
	>spacer29
	ATGGAGGACGAGAAAATGGAAAATAAAAATATA
	>spacer30
	ATAAAGAACGCGGACTATTAGGATTTACAGGGGAA
	>spacer31
	TAACTGACTACATGGTTAGTGTAGAGTATGATAGCG

	>spacer32
	AAAATTCAAATGCGATGAACTATCAGACAAGCAAATCG
	>spacer33
	TCATGCTAGCGACGACAGTTTCAAGAGGGCAATTA
	>spacer34
	TGGGACTTAGCAGCAAACGGAGATAATGCAAAGTGC
	>spacer35
	AATTTTGCAAAACAAACTATGACTCAAGATAATTTCA
	>spacer36
	CTGCTGAAGCGTTGGGTATTAAGGTTGACGATATTT
CRISPR3 (contig 155)	
Direct Repeat	**Spacers**
GTTCTCGTCCCCTATTACTGGGGATACTCTATTAC	>spacer1
	CCCTTAATAGCGATCAAACCTATAACAAATTTAT
	>spacer2
	CAAAAAGTTAAACAAAAAGGAGTAACGAAAATGAAA
	>spacer3
	CATGGATATCGGAGAATGGTTGGATTTGTTGGCAGC
	>spacer4
	CATGAAAATCAGAAAAGAAATTTTTGCCTTAACAGT
	>spacer5
	CGTGAAGGAGATTTTAACAATGAAAATGTGGACACC
	>spacer6
	AAAGGGGAAATAACAATGAAAATATGGACGCCCGAA
	>spacer7
	TGATAGTATTAAAGAGTAGTAAAAAACAAACAAGT

* Grey colour spacers had hits against phage 1 and/or phage 2 proteins.

Supplementary table S7. TA systems predicted in the chromosome and pLAC2 plasmid of *L. acidipiscis* ACA-DC 1533 genome.

Chromosome

TA_no.	**ID**	**T/A**	**Locus_tag**	**Location**	**Len(a.a.)**	**Strand**	**Family**	**Domain**
TA_1	6339955564	T	LAC1533_RS01710	365105..365533	142	+	COG2856like_domain	NULL
	6339955563	AT	LAC1533_RS01705	364755..365105	116	+	Xrelike_domain	NULL
TA_2	6339955577	T	LAC1533_RS01775	378757..380181	474	-	NULL	pfam12568
	6339955578	AT	LAC1533_RS01780	380171..380617	148	-	NULL	COG1733
TA_3	6339955917	T	LAC1533_RS03490	774869..775402	177	+	NULL	PRK10809
	6339955918	AT	LAC1533_RS03495	775407..775901	164	+	NULL	pfam02082
TA_4	6339955975	T	LAC1533_RS03810	846278..846655	125	+	MazFlike_domain	NULL
	6339955974	AT	LAC1533_RS03805	845997..846239	80	+	RHHlike_domain	NULL
TA_5	6339956314	T	LAC1533_RS05695	1231999..1232736	245	+	Brolike_domain	NULL
	6339956313	AT	LAC1533_RS05690	1231754..1231984	76	+	Xrelike_domain	NULL
TA_6	6339956780	T	LAC1533_RS08045	1709932..1710339	135	+	COG2856like_domain	COG2856
	6339956779	AT	LAC1533_RS08040	1709617..1709931	104	+	Xrelike_domain	TIGR02684
TA_7	6339956868	T	LAC1533_RS08565	1812682..1812960	92	+	relElike_domain	COG2026
	6339956867	AT	LAC1533_RS08560	1812452..1812679	75	+	RHHlike_domain	COG4453
TA_8	6339957124	T	LAC1533_RS09915	2079481..2079768	95	-	relElike_domain	COG3549
	6339957123	AT	LAC1533_RS09910	2079173..2079466	97	-	higA	COG5499
TA_9	6339957499	T	LAC1533_RS11790	2497320..2497664	114	-	MazFlike_domain	PRK09812
	6339957500	AT	LAC1533_RS11795	2497658..2497921	87	-	AbrBlike_domain	smart00966

pLAC2 plasmid

TA_no.	**ID**	**T/A**	**Locus_tag**	**Location**	**Len(a.a.)**	**Strand**	**Family**	**Domain**
TA_1	7573185672	T	PLAC2_P45	35522..35752	76	-	NULL	COG3041
	7573185673	AT	PLAC2_P46	35757..36020	87	-	NULL	COG5304

Supplementary Table S8. Percentage of potential pseudogenes identified in the chromosomes of the completed sequenced genomes of *L. salivarius* clade.

Strain	**CDSs**	**pseudogenes**	**%**
L. salivarius str. Ren	1661	39	2.35
L. salivarius UCC118	1717	49	2.85
L. salivarius LPM01	1677	59	3.52
L. salivarius CICC 23174	1627	73	4.49
L. salivarius JCM104	1703	113	6.64
L. acidipiscis ACA-DC 1533	2371	172	7.25
L. ruminis ATCC 27782	2047	185	9.04

Supplementary table S9A. Core-genome among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosomes as calculated with the EDGAR software.

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus salivarius* UCC118**		***Lactobacillus ruminis* ATCC 27782**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS00005	chromosomal replication initiator protein DnaA	LSL_0001	chromosomal replication initiation protein	LRC_RS00010	chromosomal replication initiator protein DnaA
LAC1533_RS00010	DNA polymerase III subunit beta	LSL_0002	DNA polymerase III subunit beta	LRC_RS00015	DNA polymerase III subunit beta
LAC1533_RS00015	S4 domain-containing protein YaaA	LSL_0003	hypothetical protein	LRC_RS00020	S4 domain-containing protein YaaA
LAC1533_RS00020	DNA replication and repair protein RecF	LSL_0004	recombination protein F	LRC_RS00025	DNA replication and repair protein RecF
LAC1533_RS00025	DNA topoisomerase (ATP-hydrolyzing) subunit B	LSL_0005	DNA gyrase subunit B	LRC_RS00030	DNA topoisomerase (ATP-hydrolyzing) subunit B
LAC1533_RS00030	DNA gyrase subunit A	LSL_0006	DNA gyrase subunit A	LRC_RS00035	DNA gyrase subunit A
LAC1533_RS00035	30S ribosomal protein S6	LSL_0007	30S ribosomal protein S6	LRC_RS00040	30S ribosomal protein S6
LAC1533_RS00040	single-stranded DNA-binding protein	LSL_0008	single-strand DNA binding protein	LRC_RS00045	single-stranded DNA-binding protein
LAC1533_RS00045	30S ribosomal protein S18	LSL_0009	30S ribosomal protein S18	LRC_RS00050	30S ribosomal protein S18
LAC1533_RS00120	DHH family phosphoesterase	LSL_1728	phosphoesterase, DHH family protein	LRC_RS00065	DHH family phosphoesterase
LAC1533_RS00125	50S ribosomal protein L9	LSL_1727	50S ribosomal protein L9	LRC_RS00070	50S ribosomal protein L9
LAC1533_RS00130	replicative DNA helicase	LSL_1726	replicative DNA helicase	LRC_RS00075	replicative DNA helicase
LAC1533_RS00345	flavocytochrome c	LSL_1326	fumarate reductase flavoprotein subunit	LRC_RS01705	flavocytochrome c
LAC1533_RS00570	adenylosuccinate synthase	LSL_1724	adenylosuccinate synthetase	LRC_RS00165	adenylosuccinate synthase
LAC1533_RS00665	metal ABC transporter substrate-binding protein	LSL_1587	ABC transporter substrate-binding protein	LRC_RS09535	metal ABC transporter substrate-binding protein
LAC1533_RS00675	cysteine synthase family protein	LSL_0026	cysteine synthase	LRC_RS00140	cysteine synthase A
LAC1533_RS00690	acyl-CoA thioesterase	LSL_1721	acyl-CoA thioesterase	LRC_RS00180	acyl-CoA thioesterase
LAC1533_RS00700	threonine/serine exporter	LSL_1479	hypothetical protein	LRC_RS01235	threonine/serine exporter
LAC1533_RS00705	NupC/NupG family nucleoside CNT transporter	LSL_1735	nucleoside transport protein	LRC_RS00185	nucleoside transporter
LAC1533_RS00775	YitT family protein	LSL_0704	hypothetical protein	LRC_RS05220	YitT family protein
LAC1533_RS00780	APC family permease	LSL_0168	amino acid permease	LRC_RS06060	amino acid permease
LAC1533_RS00855	dihydroxyacetone kinase subunit DhaK	LSL_1633	dihydroxyacetone kinase subunit DhaK	LRC_RS09165	dihydroxyacetone kinase subunit DhaK
LAC1533_RS00860	dihydroxyacetone kinase subunit L	LSL_1632	dihydroxyacetone kinase	LRC_RS09170	dihydroxyacetone kinase subunit L
LAC1533_RS00865	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM	LSL_1631	hypothetical protein	LRC_RS09175	PTS-dependent dihydroxyacetone kinase phosphotransferase subunit DhaM
LAC1533_RS00880	aquaporin family protein	LSL_0112	glycerol uptake facilitator protein	LRC_RS09180	aquaporin family protein
LAC1533_RS01055	DNA-binding response regulator	LSL_0035	two-component response regulator	LRC_RS00210	DNA-binding response regulator
LAC1533_RS01060	cell wall metabolism sensor histidine kinase WalK	LSL_0036	two-component sensor kinase yycG	LRC_RS00215	cell wall metabolism sensor histidine kinase WalK
LAC1533_RS01070	hypothetical protein	LSL_0038	hypothetical protein	LRC_RS00225	hypothetical protein
LAC1533_RS01075	DUF1634 domain-containing protein	LSL_0181	hypothetical protein	LRC_RS01275	DUF1634 domain-containing protein
LAC1533_RS01080	sulfite exporter TauE/SafE family protein	LSL_0182	hypothetical protein	LRC_RS01280	sulfite exporter TauE/SafE family protein
LAC1533_RS01085	MBL fold metallo-hydrolase	LSL_0041	zinc-dependent hydrolase	LRC_RS00230	MBL fold metallo-hydrolase
LAC1533_RS01090	PDZ domain-containing protein	LSL_0042	endopeptidase	LRC_RS00235	PDZ domain-containing protein
LAC1533_RS01100	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	LSL_0043	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	LRC_RS00240	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH
LAC1533_RS01160	membrane protein	LSL_0022	hypothetical protein	LRC_RS01685	membrane protein
LAC1533_RS01165	ClC family H(+)/Cl(-) exchange transporter	LSL_1158	chloride channel protein	LRC_RS03450	ClC family H(+)/Cl(-) exchange transporter
LAC1533_RS01400	LysM domain-containing protein	LSL_1036	peptidoglycan binding protein	LRC_RS08470	LysM domain-containing protein
LAC1533_RS01420	L-lactate dehydrogenase	LSL_1600	L-2-hydroxyisocaproate dehydrogenase	LRC_RS01695	L-lactate dehydrogenase
LAC1533_RS01425	branched-chain amino acid aminotransferase	LSL_0063	branched-chain amino acid aminotransferase	LRC_RS00305	branched-chain amino acid aminotransferase
LAC1533_RS01595	MFS transporter	LSL_1515	multidrug resistance efflux pump	LRC_RS07150	MFS transporter
LAC1533_RS01755	ABC transporter ATP-binding protein	LSL_0212	multidrug ABC transporter permease/ATP-binding protein	LRC_RS01730	ABC transporter ATP-binding protein
LAC1533_RS01815	membrane protein	LSL_0167	hypothetical protein	LRC_RS02515	membrane protein
LAC1533_RS02165	family 65 glycosyl hydrolase	LSL_1280	maltose phosphorylase	LRC_RS09835	maltose phosphorylase
LAC1533_RS02170	beta-phosphoglucomutase	LSL_1279	beta-phosphoglucomutase / glucose-1-phosphate phosphodismutase	LRC_RS09830	beta-phosphoglucomutase
LAC1533_RS02190	alpha-glycosidase	LSL_1295	neopullulanase / cyclomaltodextrinase / maltogenic alpha-amylase	LRC_RS09625	alpha-glycosidase
LAC1533_RS02225	DJ-1 family protein	LSL_1604	4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis protein	LRC_RS09820	DJ-1 family protein
LAC1533_RS02230	hypothetical protein	LSL_1588	hypothetical protein	LRC_RS00450	hypothetical protein
LAC1533_RS02400	PTS mannose transporter subunit IIAB	LSL_0654	PTS system mannose-specific transporter subunit IIAB	LRC_RS09700	PTS mannose transporter subunit IIAB
LAC1533_RS02405	PTS mannose/fructose/sorbose transporter subunit IIC	LSL_0655	PTS system mannose-specific transporter subunit IIC	LRC_RS09695	PTS mannose/fructose/sorbose transporter subunit IIC
LAC1533_RS02410	PTS mannose family transporter subunit IID	LSL_0656	PTS system mannose-specific transporter subunit IID	LRC_RS09690	PTS mannose transporter subunit IID
LAC1533_RS02415	DUF956 domain-containing protein	LSL_0560	hypothetical protein	LRC_RS09685	DUF956 domain-containing protein
LAC1533_RS02435	DUF975 domain-containing protein	LSL_0158	integral membrane protein	LRC_RS05985	DUF975 domain-containing protein
LAC1533_RS02465	uracil-DNA glycosylase	LSL_0093	Uracil DNA glycosylase superfamily protein	LRC_RS04690	uracil-DNA glycosylase
LAC1533_RS02475	folate family ECF transporter S component	LSL_1584	hypothetical protein	LRC_RS09555	folate family ECF transporter S component
LAC1533_RS02480	metal ABC transporter permease	LSL_1585	ABC transporter permease	LRC_RS09545	metal ABC transporter permease
LAC1533_RS02485	ABC transporter ATP-binding protein	LSL_1586	ABC transporter ATP-binding protein	LRC_RS09540	ABC transporter ATP-binding protein
LAC1533_RS02490	QueT transporter family protein	LSL_1470	hypothetical protein	LRC_RS00860	QueT transporter family protein
LAC1533_RS02495	DUF2829 domain-containing protein	LSL_1469	hypothetical protein	LRC_RS00855	DUF2829 domain-containing protein
LAC1533_RS02500	3-oxoacyl-ACP reductase	LSL_1468	3-ketoacyl-ACP reductase	LRC_RS00850	3-oxoacyl-ACP reductase
LAC1533_RS02515	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	LSL_1599	16S rRNA methyltransferase GidB	LRC_RS09490	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG

LAC1533_RS02520	nucleoid occlusion protein	LSL_1598	chromosome partitioning protein	LRC_RS09485	nucleoid occlusion protein
LAC1533_RS02525	ParA family protein	LSL_1597	chromosome partitioning protein parA	LRC_RS09480	ParA family protein
LAC1533_RS02530	chromosome partitioning protein ParB	LSL_1596	chromosome partitioning protein, DNA-binding protein	LRC_RS09475	chromosome partitioning protein ParB
LAC1533_RS02535	DUF951 domain-containing protein	LSL_1595	hypothetical protein	LRC_RS09470	DUF951 domain-containing protein
LAC1533_RS02540	redox-regulated ATPase YchF	LSL_1594	GTP-dependent nucleic acid-binding protein EngD	LRC_RS09465	redox-regulated ATPase YchF
LAC1533_RS02545	DUF1129 domain-containing protein	LSL_1593	hypothetical protein	LRC_RS09460	DUF1129 domain-containing protein
LAC1533_RS02585	glutamate 5-kinase	LSL_1612	glutamate 5-kinase	LRC_RS01040	glutamate 5-kinase
LAC1533_RS02590	glutamate-5-semialdehyde dehydrogenase	LSL_1611	gamma-glutamyl phosphate reductase	LRC_RS01045	glutamate-5-semialdehyde dehydrogenase
LAC1533_RS02610	ribose-phosphate pyrophosphokinase	LSL_1610	ribose-phosphate pyrophosphokinase	LRC_RS08630	ribose-phosphate pyrophosphokinase
LAC1533_RS02655	dipeptidase	LSL_0179	dipeptidase A	LRC_RS08555	dipeptidase
LAC1533_RS02690	ABC transporter permease	LSL_0140	ABC transporter permease	LRC_RS08530	ABC transporter permease
LAC1533_RS02695	MetQ/NlpA family ABC transporter substrate-binding protein	LSL_0141	ABC transporter substrate-binding protein	LRC_RS08525	methionine ABC transporter substrate-binding protein
LAC1533_RS02700	HlyC/CorC family transporter	LSL_1455	magnesium and cobalt efflux protein corC	LRC_RS08520	HlyC/CorC family transporter
LAC1533_RS02705	protein-tyrosine-phosphatase	LSL_1454	protein tyrosine phosphatase	LRC_RS08515	protein-tyrosine-phosphatase
LAC1533_RS02720	phosphopyruvate hydratase	LSL_1163	phosphopyruvate hydratase	LRC_RS03445	phosphopyruvate hydratase
LAC1533_RS02775	(deoxy)nucleoside triphosphate pyrophosphohydrolase	LSL_1014	7,8-dihydro-8-oxoguanine-triphosphatase	LRC_RS03045	(deoxy)nucleoside triphosphate pyrophosphohydrolase
LAC1533_RS02780	DUF3427 domain-containing protein	LSL_1453	DNA/RNA helicase	LRC_RS03050	DUF3427 domain-containing protein
LAC1533_RS02785	IMP dehydrogenase	LSL_1452	inosine 5-monophosphate dehydrogenase	LRC_RS08510	IMP dehydrogenase
LAC1533_RS02820	UDP-glucose 4-epimerase GalE	LSL_1507	UDP-glucose 4-epimerase	LRC_RS09035	UDP-glucose 4-epimerase GalE
LAC1533_RS02835	galactose mutarotase	LSL_1503	aldose 1-epimerase	LRC_RS09025	galactose mutarotase
LAC1533_RS02845	AI-2E family transporter	LSL_1500	hypothetical protein	LRC_RS09015	AI-2E family transporter
LAC1533_RS02850	pyridoxal phosphate-dependent aminotransferase	LSL_1499	aminotransferase	LRC_RS09010	putative C-S lyase
LAC1533_RS02855	2,3-diphosphoglycerate-dependent phosphoglycerate mutase	LSL_1498	phosphoglyceromutase	LRC_RS09005	2,3-diphosphoglycerate-dependent phosphoglycerate mutase
LAC1533_RS02925	aquaporin family protein	LSL_0466	glycerol uptake facilitator protein	LRC_RS07785	aquaporin family protein
LAC1533_RS02980	bifunctional lysylphosphatidylglycerol flippase/synthetase MprF	LSL_1234	hypothetical protein	LRC_RS02205	bifunctional lysylphosphatidylglycerol flippase/synthetase MprF
LAC1533_RS03000	DUF554 domain-containing protein	LSL_0081	hypothetical protein	LRC_RS10040	DUF554 domain-containing protein
LAC1533_RS03050	phosphoketolase family protein	LSL_1509	phosphoketolase	LRC_RS09050	phosphoketolase family protein
LAC1533_RS03080	LemA family protein	LSL_0214	LemA protein	LRC_RS01765	LemA family protein
LAC1533_RS03405	hypothetical protein	LSL_0364	hypothetical protein	LRC_RS01070	hypothetical protein
LAC1533_RS03415	DNA-binding response regulator	LSL_0205	two-component response regulator	LRC_RS01075	DNA-binding response regulator
LAC1533_RS03420	sensor histidine kinase	LSL_0206	two component system histidine kinase	LRC_RS01080	GHKL domain-containing protein
LAC1533_RS03425	D-alanyl-D-alanine carboxypeptidase	LSL_0075	D-alanyl-D-alanine serine-type carboxypeptidase	LRC_RS01085	D-alanyl-D-alanine carboxypeptidase
LAC1533_RS03430	branched-chain amino acid ABC transporter permease	LSL_1488	branched chain amino acid ABC transporter	LRC_RS01115	branched-chain amino acid ABC transporter permease
LAC1533_RS03435	AzlD domain-containing protein	LSL_1487	hypothetical protein	LRC_RS01120	AzlD domain-containing protein
LAC1533_RS03440	alpha/beta hydrolase	LSL_1486	endo-1,4-beta-xylanase	LRC_RS01125	alpha/beta hydrolase
LAC1533_RS03455	RluA family pseudouridine synthase	LSL_1482	ribosomal large subunit pseudouridine synthase D	LRC_RS01215	RluA family pseudouridine synthase
LAC1533_RS03460	metal-dependent transcriptional regulator	LSL_1481	Iron-dependent repressor	LRC_RS01220	metal-dependent transcriptional regulator
LAC1533_RS03465	cold-shock protein	LSL_1480	cold shock protein	LRC_RS01225	cold-shock protein
LAC1533_RS03475	LytR family transcriptional regulator	LSL_0180	LytR family transcriptional regulator	LRC_RS01270	LytR family transcriptional regulator
LAC1533_RS03510	amino acid permease	LSL_0188	lysine-specific permease	LRC_RS01295	amino acid permease
LAC1533_RS03515	serine--tRNA ligase	LSL_0189	seryl-tRNA synthetase	LRC_RS01300	serine--tRNA ligase
LAC1533_RS03560	ATP-dependent DNA helicase	LSL_0216	ATP-dependent DNA helicase	LRC_RS02295	ATP-dependent DNA helicase
LAC1533_RS03565	tryptophan--tRNA ligase	LSL_0218	tryptophanyl-tRNA synthetase II	LRC_RS02310	tryptophan--tRNA ligase
LAC1533_RS03570	Ppx/GppA family phosphatase	LSL_0219	exopolyphosphatase	LRC_RS02315	exopolyphosphatase
LAC1533_RS03585	hydroxymethylglutaryl-CoA reductase, degradative	LSL_0224	3-hydroxy-3-methylglutaryl-coenzyme A reductase / 3-hydroxy-3-methylglutaryl-coenzyme Auctase	LRC_RS02380	hydroxymethylglutaryl-CoA reductase, degradative
LAC1533_RS03600	methionine--tRNA ligase	LSL_0226	methionyl-tRNA synthetase / protein secretion chaperonin CsaA	LRC_RS02395	methionine--tRNA ligase
LAC1533_RS03605	TatD family deoxyribonuclease	LSL_0227	TatD family deoxyribonuclease	LRC_RS02400	TatD family deoxyribonuclease
LAC1533_RS03610	ribonuclease M5	LSL_0228	ribonuclease M5	LRC_RS02405	ribonuclease M5
LAC1533_RS03615	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA	LSL_0229	dimethyladenosine transferase	LRC_RS02410	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA
LAC1533_RS03620	hypothetical protein	LSL_0230	VEG protein	LRC_RS02415	hypothetical protein
LAC1533_RS03625	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase	LSL_0234	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	LRC_RS02440	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase
LAC1533_RS03630	pur operon repressor	LSL_0315	pur operon repressor	LRC_RS02465	pur operon repressor
LAC1533_RS03640	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU	LSL_0317	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	LRC_RS02470	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU
LAC1533_RS03645	ribose-phosphate pyrophosphokinase	LSL_0318	ribose-phosphate pyrophosphokinase	LRC_RS02475	ribose-phosphate pyrophosphokinase

LAC1533_RS03650	hypothetical protein	LSL_0321	hypothetical protein	LRC_RS02510	hypothetical protein
LAC1533_RS03655	biotin--[acetyl-CoA-carboxylase] ligase	LSL_0325	biotin operon repressor / biotin--[acetyl-CoA-carboxylase] synthetase	LRC_RS02550	biotin--[acetyl-CoA-carboxylase] ligase
LAC1533_RS03660	YibE/F family protein	LSL_0326	hypothetical protein	LRC_RS02555	YibE/F family protein
LAC1533_RS03665	YibE/F family protein	LSL_0327	hypothetical protein	LRC_RS02560	YibE/F family protein
LAC1533_RS03675	HD domain-containing protein	LSL_0338	hydrolase	LRC_RS02575	HD domain-containing protein
LAC1533_RS03685	DNA-directed RNA polymerase subunit delta	LSL_0341	DNA-directed RNA polymerase subunit delta	LRC_RS02585	DNA-directed RNA polymerase subunit delta
LAC1533_RS03715	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	LSL_0345	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	LRC_RS02605	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
LAC1533_RS03720	transcription termination factor Rho	LSL_0346	transcription termination factor Rho	LRC_RS02610	transcription termination factor Rho
LAC1533_RS03725	type B 50S ribosomal protein L31	LSL_0347	50S ribosomal protein L31 type B	LRC_RS02615	type B 50S ribosomal protein L31
LAC1533_RS03730	hypothetical protein	LSL_0348	hypothetical protein	LRC_RS02645	hypothetical protein
LAC1533_RS03735	ATP-dependent DNA helicase	LSL_0349	superfamily II DNA/RNA helicase	LRC_RS01720	ATP-dependent DNA helicase
LAC1533_RS03740	NCS2 family permease	LSL_0353	guanine-hypoxanthine permease	LRC_RS00155	NCS2 family permease
LAC1533_RS03750	TIGR02452 family protein	LSL_0354	hypothetical protein	LRC_RS01725	TIGR02452 family protein
LAC1533_RS03760	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	LSL_0355	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	LRC_RS01775	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase
LAC1533_RS03765	ATP-dependent helicase	LSL_0356	ATP-dependent RNA helicase	LRC_RS01780	ATP-dependent helicase
LAC1533_RS03795	holo-ACP synthase	LSL_0357	Holo-[acyl-carrier protein] synthase	LRC_RS01785	holo-ACP synthase
LAC1533_RS03800	alanine racemase	LSL_0358	alanine racemase	LRC_RS01790	alanine racemase
LAC1533_RS03810	type II toxin-antitoxin system PemK/MazF family toxin	LSL_0360	PemK family transcriptional regulator	LRC_RS01800	type II toxin-antitoxin system PemK/MazF family toxin
LAC1533_RS03820	CBS domain-containing protein	LSL_1364	hypothetical protein	LRC_RS01815	CBS domain-containing protein
LAC1533_RS03825	L-lactate dehydrogenase	LSL_1362	L-lactate dehydrogenase	LRC_RS01830	L-lactate dehydrogenase
LAC1533_RS03830	aminoacyl-tRNA hydrolase	LSL_1361	peptidyl-tRNA hydrolase	LRC_RS01835	aminoacyl-tRNA hydrolase
LAC1533_RS03835	transcription-repair coupling factor	LSL_1360	transcription-repair coupling factor	LRC_RS01840	transcription-repair coupling factor
LAC1533_RS03840	sugar transporter	LSL_1359	polysaccharides export protein	LRC_RS01845	polysaccharide biosynthesis protein
LAC1533_RS03845	RNA-binding S4 domain-containing protein	LSL_1358	heat shock protein 15	LRC_RS01850	RNA-binding S4 domain-containing protein
LAC1533_RS03855	RNA-binding protein S1	LSL_1356	hypothetical protein	LRC_RS01860	RNA-binding protein
LAC1533_RS03860	tRNA lysidine(34) synthetase TilS	LSL_1355	tRNA(Ile)-lysidine synthase TilS	LRC_RS01870	tRNA lysidine(34) synthetase TilS
LAC1533_RS03865	hypoxanthine phosphoribosyltransferase	LSL_1354	hypoxanthine-guanine phosphoribosyltransferase	LRC_RS01875	hypoxanthine phosphoribosyltransferase
LAC1533_RS03870	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein	LSL_1353	cell division protein	LRC_RS01880	ATP-dependent metallopeptidase FtsH/Yme1/Tma family protein
LAC1533_RS03880	lysine--tRNA ligase	LSL_1351	lysyl-tRNA synthetase	LRC_RS01900	lysine--tRNA ligase
LAC1533_RS03920	peptide MFS transporter	LSL_1265	di-/tripeptide transporter	LRC_RS01990	peptide MFS transporter
LAC1533_RS03935	pyrroline-5-carboxylate reductase	LSL_1264	pyrroline-5-carboxylate reductase	LRC_RS02005	pyrroline-5-carboxylate reductase
LAC1533_RS03940	N-acetylglucosamine-6-phosphate deacetylase	LSL_1466	N-acetylglucosamine-6-phosphate deacetylase	LRC_RS02010	N-acetylglucosamine-6-phosphate deacetylase
LAC1533_RS03945	GntR family transcriptional regulator	LSL_1263	GntR family transcriptional regulator	LRC_RS02015	GntR family transcriptional regulator
LAC1533_RS03950	class 1b ribonucleoside-diphosphate reductase subunit beta	LSL_1233	ribonucleotide-diphosphate reductase subunit beta	LRC_RS08060	class 1b ribonucleoside-diphosphate reductase subunit beta
LAC1533_RS03955	class 1b ribonucleoside-diphosphate reductase subunit alpha	LSL_1232	ribonucleotide-diphosphate reductase subunit alpha	LRC_RS08065	class 1b ribonucleoside-diphosphate reductase subunit alpha
LAC1533_RS03960	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI	LSL_1231	ribonucleotide reductase stimulatory protein	LRC_RS08070	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI
LAC1533_RS03965	glutaredoxin-like protein NrdH	LSL_1230	glutaredoxin	LRC_RS08075	glutaredoxin family protein
LAC1533_RS03975	nucleoside deaminase	LSL_1229	cytosine/adenosine deaminase	LRC_RS03135	nucleoside deaminase
LAC1533_RS03985	DNA polymerase III subunit gamma/tau	LSL_1228	DNA polymerase III subunit gamma/tau	LRC_RS03140	DNA polymerase III subunit gamma/tau
LAC1533_RS03990	YbaB/EbfC family nucleoid-associated protein	LSL_1227	hypothetical protein	LRC_RS03145	nucleoid-associated protein, YbaB/EbfC family
LAC1533_RS03995	recombination protein RecR	LSL_1226	recombination protein RecR	LRC_RS03150	recombination protein RecR
LAC1533_RS04000	DUF2508 domain-containing protein	LSL_1225	hypothetical protein	LRC_RS03155	DUF2508 domain-containing protein
LAC1533_RS04005	dTMP kinase	LSL_1224	thymidylate kinase	LRC_RS03160	dTMP kinase
LAC1533_RS04015	DNA polymerase III subunit delta	LSL_1223	DNA polymerase III subunit delta	LRC_RS03170	DNA polymerase III subunit delta
LAC1533_RS04020	DUF972 domain-containing protein	LSL_1222	initiation-control protein	LRC_RS03175	DUF972 domain-containing protein
LAC1533_RS04025	16S rRNA (cytidine(1402)-2-O)-methyltransferase	LSL_1221	tetrapyrrole (Corrin/Porphyrin) methylase family protein	LRC_RS03180	16S rRNA (cytidine(1402)-2-O)-methyltransferase
LAC1533_RS04030	acyl-ACP thioesterase	LSL_1220	acyl-acyl carrier protein thioesterase	LRC_RS03185	acyl-ACP thioesterase
LAC1533_RS04050	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	LSL_1218	glycoprotein endopeptidase	LRC_RS03205	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB
LAC1533_RS04060	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	LSL_1216	O-sialoglycoprotein endopeptidase	LRC_RS03215	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD
LAC1533_RS04065	multidrug ABC transporter ATP-binding protein	LSL_1215	ABC transporter ATP-binding protein	LRC_RS03220	ABC transporter ATP-binding protein
LAC1533_RS04070	redox-sensing transcriptional repressor Rex	LSL_1214	redox-sensing transcriptional repressor Rex	LRC_RS03225	redox-sensing transcriptional repressor Rex
LAC1533_RS04085	CPBP family intramembrane metalloprotease	LSL_1213	CAAX family protease	LRC_RS03230	CPBP family intramembrane metalloprotease
LAC1533_RS04090	co-chaperone GroES	LSL_1212	molecular chaperone GroES	LRC_RS03235	co-chaperone GroES
LAC1533_RS04095	chaperonin GroEL	LSL_1211	molecular chaperone GroEL	LRC_RS03240	chaperonin GroEL
LAC1533_RS04100	APC family permease	LSL_1209	amino acid permease	LRC_RS03245	APC family permease
LAC1533_RS04105	YigZ family protein	LSL_1576	hypothetical protein	LRC_RS03270	YigZ family protein
LAC1533_RS04110	DNA/RNA helicase	LSL_1207	ComF operon protein 1	LRC_RS03275	DNA/RNA helicase
LAC1533_RS04115	ComF family protein	LSL_1206	ComF operon protein 3	LRC_RS03280	amidophosphoribosyltransferase
LAC1533_RS04125	ribosome-associated translation inhibitor RaiA	LSL_1188	ribosome-associated factor Y	LRC_RS03285	ribosome-associated translation inhibitor RaiA
LAC1533_RS04130	preprotein translocase subunit SecA	LSL_1186	preprotein translocase subunit SecA	LRC_RS03290	preprotein translocase subunit SecA
LAC1533_RS04135	peptide chain release factor 2	LSL_1185	peptide chain release factor 2	LRC_RS03295	peptide chain release factor 2

LAC1533_RS04150	PDZ domain-containing protein	LSL_1183	hypothetical protein	LRC_RS03315	PDZ domain-containing protein
LAC1533_RS04155	DNA-binding response regulator	LSL_1182	alkaline phosphatase synthesis transcriptional regulatory protein PhoP	LRC_RS03320	DNA-binding response regulator
LAC1533_RS04160	two-component sensor histidine kinase	LSL_1181	two component system histidine kinase	LRC_RS03325	two-component sensor histidine kinase
LAC1533_RS04170	phage holin family protein	LSL_1179	hypothetical protein	LRC_RS03335	phage holin family protein
LAC1533_RS04175	HPr kinase/phosphorylase	LSL_1178	HPr kinase/phosphorylase	LRC_RS03340	HPr kinase/phosphorylase
LAC1533_RS04180	prolipoprotein diacylglyceryl transferase	LSL_1177	prolipoprotein diacylglyceryl transferase	LRC_RS03345	prolipoprotein diacylglyceryl transferase
LAC1533_RS04185	thioredoxin-disulfide reductase	LSL_1722	thioredoxin reductase	LRC_RS10105	thioredoxin-disulfide reductase
LAC1533_RS04195	phospho-sugar mutase	LSL_1176	phosphoglucomutase	LRC_RS03350	phospho-sugar mutase
LAC1533_RS04200	excinuclease ABC subunit UvrB	LSL_1175	excinuclease ABC subunit B	LRC_RS03355	excinuclease ABC subunit UvrB
LAC1533_RS04205	excinuclease ABC subunit UvrA	LSL_1174	excinuclease ABC subunit A	LRC_RS03360	excinuclease ABC subunit UvrA
LAC1533_RS04210	S-ribosylhomocysteine lyase	LSL_1173	S-ribosylhomocysteinase	LRC_RS03365	S-ribosylhomocysteine lyase
LAC1533_RS04225	RNase adapter RapZ	LSL_1171	hypothetical protein	LRC_RS03380	RNase adapter RapZ
LAC1533_RS04230	hypothetical protein	LSL_1170	hypothetical protein	LRC_RS03385	YvcK family protein
LAC1533_RS04240	ATP-dependent Clp protease proteolytic subunit	LSL_1168	ATP-dependent Clp protease proteolytic subunit	LRC_RS03410	ATP-dependent Clp endopeptidase, proteolytic subunit ClpP
LAC1533_RS04255	SorC family transcriptional regulator	LSL_1167	central glycolytic genes regulator	LRC_RS03425	SorC family transcriptional regulator
LAC1533_RS04260	type I glyceraldehyde-3-phosphate dehydrogenase	LSL_1166	glyceraldehyde 3-phosphate dehydrogenase	LRC_RS03430	type I glyceraldehyde-3-phosphate dehydrogenase
LAC1533_RS04265	phosphoglycerate kinase	LSL_1165	phosphoglycerate kinase	LRC_RS03435	phosphoglycerate kinase
LAC1533_RS04270	triose-phosphate isomerase	LSL_1164	triosephosphate isomerase	LRC_RS03440	triose-phosphate isomerase
LAC1533_RS04290	preprotein translocase subunit SecG	LSL_1157	preprotein translocase subunit SecG	LRC_RS03455	preprotein translocase subunit SecG
LAC1533_RS04295	ribonuclease R	LSL_1156	ribonuclease R 1	LRC_RS03460	ribonuclease R
LAC1533_RS04300	SsrA-binding protein SmpB	LSL_1155	SsrA-binding protein	LRC_RS03465	SsrA-binding protein SmpB
LAC1533_RS04320	hypothetical protein	LSL_1154	hypothetical protein	LRC_RS03485	hypothetical protein
LAC1533_RS04325	Cof-type HAD-IIB family hydrolase	LSL_1153	HAD superfamily hydrolase	LRC_RS03490	Cof-type HAD-IIB family hydrolase
LAC1533_RS04330	uracil-DNA glycosylase	LSL_1152	uracil-DNA glycosylase	LRC_RS03495	uracil-DNA glycosylase
LAC1533_RS04335	phosphate acetyltransferase	LSL_1151	phosphate acetyltransferase	LRC_RS03500	phosphate acetyltransferase
LAC1533_RS04340	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	LSL_1150	ATP/GTP hydrolase	LRC_RS03505	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE
LAC1533_RS04345	exonuclease	LSL_1149	DNA-directed DNA polymerase III subunit epsilon	LRC_RS03510	exonuclease
LAC1533_RS04350	UDP-N-acetylmuramate dehydrogenase	LSL_1148	UDP-N-acetylenolpyruvoylglucosamine reductase	LRC_RS03585	UDP-N-acetylmuramate dehydrogenase
LAC1533_RS04355	DUF1361 domain-containing protein	LSL_1147	hypothetical protein	LRC_RS08050	DUF1361 domain-containing protein
LAC1533_RS04360	TIGR00159 family protein	LSL_1146	hypothetical protein	LRC_RS08045	TIGR00159 family protein
LAC1533_RS04365	hypothetical protein	LSL_1145	hypothetical protein	LRC_RS08040	hypothetical protein
LAC1533_RS04370	phosphoglucosamine mutase	LSL_1144	phosphoglucosamine mutase	LRC_RS08035	phosphoglucosamine mutase
LAC1533_RS04390	hypothetical protein	LSL_1300	hypothetical protein	LRC_RS07995	hypothetical protein
LAC1533_RS04400	phosphate ABC transporter permease subunit PstC	LSL_0401	phosphate ABC transporter permease	LRC_RS07955	phosphate ABC transporter permease subunit PstC
LAC1533_RS04405	phosphate ABC transporter, permease protein PstA	LSL_0402	phosphate ABC transporter permease	LRC_RS07950	phosphate ABC transporter, permease protein PstA
LAC1533_RS04410	phosphate ABC transporter ATP-binding protein	LSL_0403	phosphate ABC transporter ATP-binding protein	LRC_RS07945	phosphate ABC transporter ATP-binding protein
LAC1533_RS04415	phosphate ABC transporter ATP-binding protein	LSL_0404	phosphate ABC transporter ATP-binding protein	LRC_RS07940	phosphate ABC transporter ATP-binding protein
LAC1533_RS04420	phosphate transport system regulatory protein PhoU	LSL_0405	phosphate transporter PhoU	LRC_RS07935	phosphate transport system regulatory protein PhoU
LAC1533_RS04425	fructose-1,6-bisphosphate aldolase, class II	LSL_0406	fructose-bisphosphate aldolase	LRC_RS07930	fructose-1,6-bisphosphate aldolase, class II
LAC1533_RS04445	hemolysin III	LSL_0412	hypothetical protein	LRC_RS07875	hemolysin III
LAC1533_RS04450	ArsR family transcriptional regulator	LSL_0413	ArsR family transcriptional regulator	LRC_RS07870	ArsR family transcriptional regulator
LAC1533_RS04455	RNase HI	LSL_0415	ribonuclease HI	LRC_RS07865	RNase HI
LAC1533_RS04475	LTA synthase family protein	LSL_0465	sulfatase family protein	LRC_RS07810	LTA synthase family protein
LAC1533_RS04480	glucose-6-phosphate isomerase	LSL_0464	glucose-6-phosphate isomerase	LRC_RS07800	glucose-6-phosphate isomerase
LAC1533_RS04490	CBS domain-containing protein	LSL_0467	hypothetical protein	LRC_RS07780	CBS domain-containing protein
LAC1533_RS04495	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	LSL_0468	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	LRC_RS07775	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase
LAC1533_RS04500	amidohydrolase	LSL_0469	N-acetyldiaminopimelate deacetylase	LRC_RS07770	N-acetyldiaminopimelate deacetylase
LAC1533_RS04505	mechanosensitive ion channel family protein	LSL_0470	mechanosensitive ion channel	LRC_RS07760	mechanosensitive ion channel family protein
LAC1533_RS04510	DUF948 domain-containing protein	LSL_0417	hypothetical protein	LRC_RS07755	DUF948 domain-containing protein
LAC1533_RS04520	aminopeptidase P family protein	LSL_0419	Xaa-Pro aminopeptidase	LRC_RS07740	aminopeptidase P family protein
LAC1533_RS04525	catabolite control protein A	LSL_0420	catabolite control protein A	LRC_RS07735	catabolite control protein A
LAC1533_RS04530	YebC/PmpR family DNA-binding transcriptional regulator	LSL_0422	hypothetical protein	LRC_RS07725	YebC/PmpR family DNA-binding transcriptional regulator
LAC1533_RS04535	competence protein ComG	LSL_0424	ComG operon protein 1	LRC_RS07715	competence protein ComG
LAC1533_RS04540	competence protein ComG	LSL_0425	ComG operon protein 2	LRC_RS07710	competence protein ComG
LAC1533_RS04545	prepilin-type N-terminal cleavage/methylation domain-containing protein	LSL_0426	ComG operon protein 3	LRC_RS07705	prepilin-type N-terminal cleavage/methylation domain-containing protein
LAC1533_RS04585	DUF1027 domain-containing protein	LSL_0435	hypothetical protein	LRC_RS07650	DUF1027 domain-containing protein
LAC1533_RS04590	TIGR01457 family HAD-type hydrolase	LSL_0436	N-acetylglucosamine catabolic protein	LRC_RS07645	TIGR01457 family HAD-type hydrolase
LAC1533_RS04600	cytochrome o ubiquinol oxidase	LSL_0438	DedA family protein	LRC_RS07630	membrane protein
LAC1533_RS04605	NAD(P)/FAD-dependent oxidoreductase	LSL_0439	thioredoxin reductase	LRC_RS07625	NAD(P)/FAD-dependent oxidoreductase
LAC1533_RS04610	peptidylprolyl isomerase	LSL_0055	peptidyl-prolyl cis-trans isomerase	LRC_RS07620	peptidyl-prolyl cis-trans isomerase
LAC1533_RS04615	general stress protein	LSL_0440	polyribonucleotide nucleotidyltransferase	LRC_RS07615	general stress protein
LAC1533_RS04740	methionine adenosyltransferase	LSL_0441	S-adenosylmethionine synthetase	LRC_RS07490	methionine adenosyltransferase
LAC1533_RS04750	leucine--tRNA ligase	LSL_0442	leucyl-tRNA synthetase	LRC_RS07480	leucine--tRNA ligase

LAC1533_RS04810	NAD(P)H-hydrate dehydratase	LSL_0446	sugar kinase	LRC_RS07465	NAD(P)H-hydrate dehydratase
LAC1533_RS04835	universal stress protein	LSL_1120	universal stress protein	LRC_RS07450	universal stress protein
LAC1533_RS04880	adenylosuccinate lyase	LSL_0517	adenylosuccinate lyase	LRC_RS05965	adenylosuccinate lyase
LAC1533_RS04885	LysR family transcriptional regulator	LSL_0674	LysR family transcriptional regulator	LRC_RS05900	LysR family transcriptional regulator
LAC1533_RS04895	hypothetical protein	LSL_0675	hypothetical protein	LRC_RS05890	hypothetical protein
LAC1533_RS04905	arginine--tRNA ligase	LSL_0677	arginyl-tRNA synthetase	LRC_RS05880	arginine--tRNA ligase
LAC1533_RS04925	hypothetical protein	LSL_0473	hypothetical protein	LRC_RS05855	YlbF family regulator
LAC1533_RS04930	HD domain-containing protein	LSL_0474	CMP-binding factor	LRC_RS05850	3-5 exoribonuclease YhaM
LAC1533_RS04935	peptidylprolyl isomerase	LSL_0475	peptidyl-prolyl isomerase	LRC_RS05800	peptidylprolyl isomerase
LAC1533_RS04945	HIT family protein	LSL_0477	bis(5-nucleosyl)-tetraphosphatase	LRC_RS05790	HIT family protein
LAC1533_RS04950	ABC transporter ATP-binding protein	LSL_0478	ABC transporter ATP-binding protein	LRC_RS05785	ABC transporter ATP-binding protein
LAC1533_RS04960	phosphotransferase	LSL_0480	phosphotransferase family protein	LRC_RS05775	phosphotransferase
LAC1533_RS04965	tRNA (guanosine(46)-N7)-methyltransferase TrmB	LSL_0481	tRNA (m(7)G46) methyltransferase	LRC_RS05770	tRNA (guanosine(46)-N7)-methyltransferase TrmB
LAC1533_RS04970	thioredoxin	LSL_0483	thioredoxin	LRC_RS05760	thioredoxin
LAC1533_RS04975	DUF4479 domain-containing protein	LSL_0484	tRNA-binding domain-containing protein	LRC_RS05755	DUF4479 domain-containing protein
LAC1533_RS04985	UDP-N-acetylmuramate--L-alanine ligase	LSL_0485	UDP-N-acetylmuramate--L-alanine ligase	LRC_RS05745	UDP-N-acetylmuramate--L-alanine ligase
LAC1533_RS04990	BAX inhibitor (BI)-1/YccA family protein	LSL_0487	integral membrane protein	LRC_RS05730	BAX inhibitor (BI)-1/YccA family protein
LAC1533_RS04995	DNA polymerase I	LSL_0488	DNA polymerase I	LRC_RS05720	DNA polymerase I
LAC1533_RS05000	DNA-formamidopyrimidine glycosylase	LSL_0489	formamidopyrimidine-DNA glycosylase	LRC_RS05715	DNA-formamidopyrimidine glycosylase
LAC1533_RS05005	transcriptional repressor NrdR	LSL_0491	NrdR family transcriptional regulator	LRC_RS05705	transcriptional repressor NrdR
LAC1533_RS05015	primosomal protein DnaI	LSL_0493	primosomal protein DnaI	LRC_RS05695	primosomal protein DnaI
LAC1533_RS05020	threonine--tRNA ligase	LSL_0494	threonyl-tRNA synthetase	LRC_RS05690	threonine--tRNA ligase
LAC1533_RS05025	translation initiation factor IF-3	LSL_0495	translation initiation factor IF-3	LRC_RS05685	translation initiation factor IF-3
LAC1533_RS05030	50S ribosomal protein L35	LSL_0496	50S ribosomal protein L35	LRC_RS05680	50S ribosomal protein L35
LAC1533_RS05035	50S ribosomal protein L20	LSL_0497	50S ribosomal protein L20	LRC_RS05675	50S ribosomal protein L20
LAC1533_RS05040	YqeG family HAD IIIA-type phosphatase	LSL_0499	HAD superfamily hydrolase	LRC_RS05670	YqeG family HAD IIIA-type phosphatase
LAC1533_RS05045	ribosome biogenesis GTPase YqeH	LSL_0500	GTP-binding protein YqeH	LRC_RS05665	ribosome biogenesis GTPase YqeH
LAC1533_RS05050	ribosome assembly RNA-binding protein YhbY	LSL_0501	hypothetical protein	LRC_RS05660	ribosome assembly RNA-binding protein YhbY
LAC1533_RS05055	nicotinate-nucleotide adenylyltransferase	LSL_0502	nicotinate-nucleotide adenylyltransferase	LRC_RS05655	nicotinate-nucleotide adenylyltransferase
LAC1533_RS05060	HD domain-containing protein	LSL_0503	hypothetical protein	LRC_RS05650	HD domain-containing protein
LAC1533_RS05065	ribosome silencing factor	LSL_0504	Iojap-related protein	LRC_RS05645	ribosome silencing factor
LAC1533_RS05075	nucleotidyltransferase	LSL_0505	hypothetical protein	LRC_RS05635	nucleotidyltransferase
LAC1533_RS05080	hypothetical protein	LSL_0506	hypothetical protein	LRC_RS05630	DNA-binding protein
LAC1533_RS05085	50S ribosomal protein L32	LSL_0507	50S ribosomal protein L32	LRC_RS10595	50S ribosomal protein L32
LAC1533_RS05090	YihA family ribosome biogenesis GTP-binding protein	LSL_0543	GTP-binding protein	LRC_RS05625	YihA family ribosome biogenesis GTP-binding protein
LAC1533_RS05095	nucleotide pyrophosphohydrolase	LSL_0544	hypothetical protein	LRC_RS05620	nucleotide pyrophosphohydrolase
LAC1533_RS05105	amino acid ABC transporter ATP-binding protein	LSL_1540	ABC transporter ATP-binding protein	LRC_RS05615	amino acid ABC transporter ATP-binding protein
LAC1533_RS05110	excinuclease ABC subunit UvrC	LSL_1098	excinuclease ABC subunit C	LRC_RS05610	excinuclease ABC subunit UvrC
LAC1533_RS05115	GTPase ObgE	LSL_1097	GTPase ObgE	LRC_RS05600	GTPase ObgE
LAC1533_RS05120	acetyltransferase	LSL_1096	acyltransferase	LRC_RS05595	acetyltransferase
LAC1533_RS05135	ribonuclease Z	LSL_1093	ribonuclease Z	LRC_RS05585	ribonuclease Z
LAC1533_RS05140	SDR family NAD(P)-dependent oxidoreductase	LSL_1092	short-chain dehydrogenase	LRC_RS05580	SDR family NAD(P)-dependent oxidoreductase
LAC1533_RS05155	adenine phosphoribosyltransferase	LSL_1090	adenine phosphoribosyltransferase	LRC_RS05565	adenine phosphoribosyltransferase
LAC1533_RS05170	hypothetical protein	LSL_1089	hypothetical protein	LRC_RS06475	membrane protein
LAC1533_RS05180	50S ribosomal protein L33	LSL_0548	50S ribosomal protein L33	LRC_RS06465	50S ribosomal protein L33
LAC1533_RS05195	5-formyltetrahydrofolate cyclo-ligase	LSL_0549	5-formyltetrahydrofolate cyclo-ligase	LRC_RS06460	5-formyltetrahydrofolate cyclo-ligase
LAC1533_RS05200	rhomboid family intramembrane serine protease	LSL_0550	rhomboid family integral membrane protein	LRC_RS06455	rhomboid family intramembrane serine protease
LAC1533_RS05205	DUF910 domain-containing protein	LSL_0551	hypothetical protein	LRC_RS06450	DUF910 domain-containing protein
LAC1533_RS05210	glucokinase	LSL_0552	glucokinase	LRC_RS06445	glucokinase
LAC1533_RS05215	rhodanese-like domain-containing protein	LSL_0553	hypothetical protein	LRC_RS06440	rhodanese-like domain-containing protein
LAC1533_RS05220	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	LSL_0555	tRNA delta(2)-isopentenylpyrophosphate transferase	LRC_RS06435	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA
LAC1533_RS05225	MerR family transcriptional regulator	LSL_0557	glutamine synthetase	LRC_RS06425	MerR family transcriptional regulator
LAC1533_RS05230	type I glutamate--ammonia ligase	LSL_0558	glutamine synthetase	LRC_RS06420	type I glutamate--ammonia ligase
LAC1533_RS05240	guanylate kinase	LSL_0611	guanylate kinase	LRC_RS06400	guanylate kinase
LAC1533_RS05245	DNA-directed RNA polymerase subunit omega	LSL_0612	DNA-directed RNA polymerase subunit omega	LRC_RS06395	DNA-directed RNA polymerase subunit omega
LAC1533_RS05250	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC	LSL_0613	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase	LRC_RS06390	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC
LAC1533_RS05255	primosomal protein N	LSL_0613b	primosomal protein n-prim	LRC_RS06385	primosomal protein N
LAC1533_RS05260	methionyl-tRNA formyltransferase	LSL_0614	methionyl-tRNA formyltransferase	LRC_RS06380	methionyl-tRNA formyltransferase

LAC1533_RS05265	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB	LSL_0615	16S rRNA (cytosine(967)-C(5))-methyltransferase	LRC_RS06375	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB
LAC1533_RS05270	serine/threonine-protein phosphatase	LSL_0616	protein phosphatase 2C	LRC_RS06370	serine/threonine-protein phosphatase
LAC1533_RS05280	ribosome small subunit-dependent GTPase A	LSL_0617	GTPase	LRC_RS06360	ribosome small subunit-dependent GTPase A
LAC1533_RS05290	thiamine diphosphokinase	LSL_0618	thiamin pyrophosphokinase	LRC_RS06350	thiamine diphosphokinase
LAC1533_RS05295	50S ribosomal protein L28	LSL_0619	50S ribosomal protein L28	LRC_RS06345	50S ribosomal protein L28
LAC1533_RS05300	Asp23/Gls24 family envelope stress response protein	LSL_0620	hypothetical protein	LRC_RS06340	Asp23/Gls24 family envelope stress response protein
LAC1533_RS05305	DAK2 domain-containing protein	LSL_0621	hypothetical protein	LRC_RS06335	DAK2 domain-containing protein
LAC1533_RS05310	DNA helicase RecG	LSL_0622	ATP-dependent DNA helicase	LRC_RS06330	DNA helicase RecG
LAC1533_RS05315	phosphate acyltransferase PlsX	LSL_0623	Fatty acid/phospholipid synthesis protein	LRC_RS06325	phosphate acyltransferase PlsX
LAC1533_RS05325	acyl carrier protein	LSL_0624	acyl carrier protein	LRC_RS06320	acyl carrier protein
LAC1533_RS05330	ribonuclease III	LSL_0625	ribonuclease III	LRC_RS06315	ribonuclease III
LAC1533_RS05335	chromosome segregation protein SMC	LSL_0626	chromosome partition protein	LRC_RS06310	chromosome segregation protein SMC
LAC1533_RS05340	signal recognition particle-docking protein FtsY	LSL_0627	cell division protein	LRC_RS06305	signal recognition particle-docking protein FtsY
LAC1533_RS05345	putative DNA-binding protein	LSL_0628	signal recognition particle associated protein	LRC_RS06300	putative DNA-binding protein
LAC1533_RS05350	signal recognition particle protein	LSL_0629	signal recognition particle protein	LRC_RS06295	signal recognition particle protein
LAC1533_RS05355	30S ribosomal protein S16	LSL_0630	30S ribosomal protein S16	LRC_RS06290	30S ribosomal protein S16
LAC1533_RS05360	KH domain-containing protein	LSL_0631	RNA binding protein	LRC_RS06285	KH domain-containing protein
LAC1533_RS05365	ribosome maturation factor RimM	LSL_0632	16S rRNA processing protein	LRC_RS06280	ribosome maturation factor RimM
LAC1533_RS05370	tRNA (guanosine(37)-N1)-methyltransferase TrmD	LSL_0633	tRNA (guanine-N(1)-)-methyltransferase	LRC_RS06275	tRNA (guanosine(37)-N1)-methyltransferase TrmD
LAC1533_RS05375	50S ribosomal protein L19	LSL_0636	50S ribosomal protein L19	LRC_RS04425	50S ribosomal protein L19
LAC1533_RS05385	UMP kinase	LSL_0561	uridylate kinase	LRC_RS04610	UMP kinase
LAC1533_RS05390	ribosome recycling factor	LSL_0562	ribosome recycling factor	LRC_RS04615	ribosome recycling factor
LAC1533_RS05395	isoprenyl transferase	LSL_0563	undecaprenyl pyrophosphate synthetase	LRC_RS04620	isoprenyl transferase
LAC1533_RS05400	phosphatidate cytidylyltransferase	LSL_0564	phosphatidate cytidylyltransferase	LRC_RS04625	CDP-archaeol synthase
LAC1533_RS05405	RIP metalloprotease RseP	LSL_0565	M50 family membrane endopeptidase	LRC_RS04630	RIP metalloprotease RseP
LAC1533_RS05410	proline--tRNA ligase	LSL_0566	prolyl-tRNA synthetase	LRC_RS04635	proline--tRNA ligase
LAC1533_RS05415	PolC-type DNA polymerase III	LSL_0567	DNA polymerase III PolC	LRC_RS05350	PolC-type DNA polymerase III
LAC1533_RS05420	ribosome maturation factor RimP	LSL_0568	hypothetical protein	LRC_RS05345	ribosome maturation factor RimP
LAC1533_RS05425	transcription termination/antitermination protein NusA	LSL_0569	transcription elongation factor NusA	LRC_RS05340	transcription termination/antitermination protein NusA
LAC1533_RS05430	DUF448 domain-containing protein	LSL_0570	hypothetical protein	LRC_RS05335	DUF448 domain-containing protein
LAC1533_RS05435	hypothetical protein	LSL_0571	50S ribosomal protein L7AE	LRC_RS05330	hypothetical protein
LAC1533_RS05440	translation initiation factor IF-2	LSL_0572	translation initiation factor IF-2	LRC_RS05325	translation initiation factor IF-2
LAC1533_RS05445	30S ribosome-binding factor RbfA	LSL_0573	ribosome-binding factor A	LRC_RS05320	30S ribosome-binding factor RbfA
LAC1533_RS05450	tRNA pseudouridine(55) synthase TruB	LSL_0574	tRNA pseudouridine synthase B	LRC_RS05315	tRNA pseudouridine(55) synthase TruB
LAC1533_RS05455	riboflavin biosynthesis protein RibF	LSL_0575	riboflavin kinase/FMN adenylyltransferase	LRC_RS05310	riboflavin biosynthesis protein RibF
LAC1533_RS05460	heat-inducible transcription repressor HrcA	LSL_0576	heat-inducible transcription repressor	LRC_RS04660	heat-inducible transcriptional repressor HrcA
LAC1533_RS05465	nucleotide exchange factor GrpE	LSL_0577	GrpE protein HSP-70 cofactor	LRC_RS04665	nucleotide exchange factor GrpE
LAC1533_RS05470	molecular chaperone DnaK	LSL_0578	molecular chaperone DnaK	LRC_RS04670	molecular chaperone DnaK
LAC1533_RS05475	molecular chaperone DnaJ	LSL_0579	chaperone protein	LRC_RS04675	molecular chaperone DnaJ
LAC1533_RS05530	elongation factor 4	LSL_0580	GTP-binding protein LepA	LRC_RS05520	elongation factor 4
LAC1533_RS05600	RNA methyltransferase	LSL_0810	23S rRNA methyltransferase	LRC_RS05305	RNA methyltransferase
LAC1533_RS05605	hydrolase	LSL_0811	HD superfamily hydrolase	LRC_RS06185	hydrolase
LAC1533_RS05610	transcriptional regulator	LSL_0812	MarR family transcriptional regulator	LRC_RS06180	transcriptional regulator
LAC1533_RS05615	phenylalanine--tRNA ligase subunit alpha	LSL_0813	phenylalanyl-tRNA synthetase subunit alpha	LRC_RS06175	phenylalanine--tRNA ligase subunit alpha
LAC1533_RS05625	endolytic transglycosylase MltG	LSL_0815	hypothetical protein	LRC_RS06165	endolytic transglycosylase MltG
LAC1533_RS05630	uridine kinase	LSL_0816	uridine kinase	LRC_RS06160	uridine kinase
LAC1533_RS05635	transcription elongation factor GreA	LSL_0817	transcription elongation factor	LRC_RS06155	transcription elongation factor GreA
LAC1533_RS05650	NADPH-dependent oxidoreductase	LSL_1376	nitro/flavin reductase	LRC_RS01050	NADPH-dependent oxidoreductase
LAC1533_RS05655	hypothetical protein	LSL_0818	hypothetical protein	LRC_RS06145	hypothetical protein
LAC1533_RS05660	nucleoside hydrolase	LSL_0819	inosine-uridine preferring nucleoside hydrolase	LRC_RS06140	nucleoside hydrolase
LAC1533_RS05935	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	LSL_0822	GTP pyrophosphokinase	LRC_RS06115	bifunctional (p)ppGpp synthetase/guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase
LAC1533_RS05940	D-tyrosyl-tRNA(Tyr) deacylase	LSL_0823	D-tyrosyl-tRNA(Tyr) deacylase	LRC_RS06110	D-tyrosyl-tRNA(Tyr) deacylase
LAC1533_RS05950	haloacid dehalogenase	LSL_0824	phosphoglycolate phosphatase	LRC_RS06100	phosphoglycolate phosphatase
LAC1533_RS05955	N-acetylmuramoyl-L-alanine amidase	LSL_0899	N-acetylmuramoyl-L-alanine amidase	LRC_RS04595	N-acetylmuramoyl-L-alanine amidase
LAC1533_RS05960	histidine--tRNA ligase	LSL_0852	histidyl-tRNA synthetase	LRC_RS04580	histidine--tRNA ligase
LAC1533_RS05965	aspartate--tRNA ligase	LSL_0853	aspartyl-tRNA synthetase	LRC_RS04585	aspartate--tRNA ligase
LAC1533_RS05970	YitT family protein	LSL_0693	hypothetical protein	LRC_RS06090	YitT family protein
LAC1533_RS05985	kinase/pyrophosphorylase	LSL_0699	hypothetical protein	LRC_RS06055	kinase/pyrophosphorylase
LAC1533_RS05990	30S ribosomal protein S21	LSL_0700	30S ribosomal protein S21	LRC_RS06050	30S ribosomal protein S21
LAC1533_RS05995	GatB/YqeY domain-containing protein	LSL_0701	GatB/Yqey domain-containing protein	LRC_RS06045	GatB/YqeY domain-containing protein
LAC1533_RS06000	PhoH family protein	LSL_0898	PhoH protein	LRC_RS06040	phosphate starvation-inducible protein PhoH
LAC1533_RS06005	rRNA maturation RNase YbeY	LSL_0897	hypothetical protein	LRC_RS06035	rRNA maturation RNase YbeY
LAC1533_RS06010	diacylglycerol kinase	LSL_0896	diacylglycerol kinase	LRC_RS06030	UDP kinase
LAC1533_RS06015	GTPase Era	LSL_0895	GTP-binding protein Era	LRC_RS06025	GTPase Era
LAC1533_RS06020	DNA repair protein RecO	LSL_0894	DNA repair protein	LRC_RS06020	DNA repair protein RecO
LAC1533_RS06025	glycine--tRNA ligase subunit alpha	LSL_0912	glycyl-tRNA synthetase subunit alpha	LRC_RS06015	glycine--tRNA ligase subunit alpha
LAC1533_RS06030	glycine--tRNA ligase subunit beta	LSL_0911	glycyl-tRNA synthetase subunit beta	LRC_RS06010	glycine--tRNA ligase subunit beta

LAC1533_RS06035	DNA primase	LSL_0910	DNA primase	LRC_RS04380	DNA primase
LAC1533_RS06040	RNA polymerase sigma factor RpoD	LSL_0909	RNA polymerase sigma factor RpoD	LRC_RS04385	RNA polymerase sigma factor RpoD
LAC1533_RS06045	tRNA (adenine(22)-N(1))-methyltransferase TrmK	LSL_0846	hypothetical protein	LRC_RS05515	tRNA (adenine(22)-N(1))-methyltransferase TrmK
LAC1533_RS06055	peptidase T	LSL_0848	peptidase T	LRC_RS05505	peptidase T
LAC1533_RS06080	ATP-dependent chaperone ClpB	LSL_0863	chaperone	LRC_RS05490	ATP-dependent chaperone ClpB
LAC1533_RS06095	DUF2929 domain-containing protein	LSL_0864	hypothetical protein	LRC_RS05475	DUF2929 domain-containing protein
LAC1533_RS06100	DNA polymerase III subunit alpha	LSL_0865	DNA polymerase III subunit alpha	LRC_RS05470	DNA polymerase III subunit alpha
LAC1533_RS06105	6-phosphofructokinase	LSL_0866	6-phosphofructokinase	LRC_RS04410	6-phosphofructokinase
LAC1533_RS06110	pyruvate kinase	LSL_0867	pyruvate kinase	LRC_RS04415	pyruvate kinase
LAC1533_RS06115	DUF441 domain-containing protein	LSL_0936	hypothetical protein	LRC_RS09240	DUF441 domain-containing protein
LAC1533_RS06120	S1 RNA-binding protein	LSL_0935	hypothetical protein	LRC_RS06270	S1 RNA-binding protein
LAC1533_RS06130	site-specific tyrosine recombinase XerD	LSL_0934	integrase/recombinase XerD/RipX family	LRC_RS06260	site-specific tyrosine recombinase XerD
LAC1533_RS06135	GNAT family N-acetyltransferase	LSL_0941	RibT protein	LRC_RS06255	hypothetical protein
LAC1533_RS06140	rifampin ADP-ribosyl transferase	LSL_0940	segregation and condensation protein ScpA	LRC_RS06250	rifampin ADP-ribosyl transferase
LAC1533_RS06145	SMC-Scp complex subunit ScpB	LSL_0939	segregation and condensation protein ScpB	LRC_RS06245	SMC-Scp complex subunit ScpB
LAC1533_RS06150	rRNA pseudouridine synthase	LSL_0938	ribosomal large subunit pseudouridine synthase B	LRC_RS06240	rRNA pseudouridine synthase
LAC1533_RS06160	ATP-dependent DNA helicase RecQ	LSL_0902	ATP-dependent DNA helicase	LRC_RS06220	ATP-dependent DNA helicase RecQ
LAC1533_RS06165	LysM domain-containing protein	LSL_0901	hypothetical protein	LRC_RS06215	LysM domain-containing protein
LAC1533_RS06170	(d)CMP kinase	LSL_0900	cytidylate kinase	LRC_RS06210	(d)CMP kinase
LAC1533_RS06180	ribosome biogenesis GTPase Der	LSL_0886	GTP-binding protein EngA	LRC_RS06200	ribosome biogenesis GTPase Der
LAC1533_RS06185	HU family DNA-binding protein	LSL_0885	DNA-binding protein HU	LRC_RS06195	HU family DNA-binding protein
LAC1533_RS06190	tetratricopeptide repeat protein	LSL_0851	hypothetical protein	LRC_RS04680	tetratricopeptide repeat protein
LAC1533_RS06200	hypothetical protein	LSL_0703	integrase/recombinase xerD	LRC_RS04685	integrase
LAC1533_RS06205	4-hydroxy-tetrahydrodipicolinate reductase	LSL_0705	4-hydroxy-tetrahydrodipicolinate reductase	LRC_RS05205	4-hydroxy-tetrahydrodipicolinate reductase
LAC1533_RS06210	CCA tRNA nucleotidyltransferase	LSL_0706	tRNA CCA-pyrophosphorylase	LRC_RS05200	CCA tRNA nucleotidyltransferase
LAC1533_RS06215	ABC transporter ATP-binding protein	LSL_0707	ABC transporter ATP-binding protein	LRC_RS05195	ABC transporter ATP-binding protein
LAC1533_RS06220	thymidylate synthase	LSL_0708	thymidylate synthase	LRC_RS05190	thymidylate synthase
LAC1533_RS06225	lipase	LSL_0714	lipase/acylhydrolase	LRC_RS05175	lipase/acylhydrolase
LAC1533_RS06230	DUF2140 domain-containing protein	LSL_0715	hypothetical protein	LRC_RS05170	DUF2140 domain-containing protein
LAC1533_RS06235	YozE family protein	LSL_0716	hypothetical protein	LRC_RS05165	YozE family protein
LAC1533_RS06245	ribosome biogenesis GTPase YlqF	LSL_0717	GTP-binding protein	LRC_RS05150	ribosome biogenesis GTPase YlqF
LAC1533_RS06250	ribonuclease HII	LSL_0718	ribonuclease HII	LRC_RS05145	ribonuclease HII
LAC1533_RS06255	DNA-protecting protein DprA	LSL_0719	DNA processing protein	LRC_RS05140	DNA-protecting protein DprA
LAC1533_RS06260	type I DNA topoisomerase	LSL_0720	DNA topoisomerase I	LRC_RS05135	type I DNA topoisomerase
LAC1533_RS06265	tyrosine recombinase XerC	LSL_0948	XerC/CodV family integrase/recombinase	LRC_RS05115	tyrosine recombinase XerC
LAC1533_RS06270	HslU--HslV peptidase proteolytic subunit	LSL_0947	ATP-dependent protease peptidase subunit	LRC_RS05110	ATP-dependent protease subunit HslV
LAC1533_RS06275	ATP-dependent protease ATPase subunit HslU	LSL_0946	ATP-dependent protease ATP-binding subunit HslU	LRC_RS05105	ATP-dependent protease ATPase subunit HslU
LAC1533_RS06280	aldose 1-epimerase family protein	LSL_0207	galactose mutarotase	LRC_RS05100	aldose 1-epimerase family protein
LAC1533_RS06285	glycerol-3-phosphate acyltransferase	LSL_0870	hypothetical protein	LRC_RS05090	glycerol-3-phosphate 1-O-acyltransferase PlsY
LAC1533_RS06290	DNA topoisomerase IV subunit B	LSL_0871	DNA topoisomerase IV subunit B	LRC_RS05085	DNA topoisomerase IV subunit B
LAC1533_RS06295	DNA topoisomerase IV subunit A	LSL_0872	DNA topoisomerase IV subunit A	LRC_RS05080	DNA topoisomerase IV subunit A
LAC1533_RS06310	signal peptidase I	LSL_0876	signal peptidase I	LRC_RS05055	signal peptidase I
LAC1533_RS06325	DegV family protein	LSL_0875	DegV family protein	LRC_RS05070	DegV family protein
LAC1533_RS06335	DUF814 domain-containing protein	LSL_0873	fibronectin-binding protein / fibrinogen-binding protein	LRC_RS05075	DUF814 domain-containing protein
LAC1533_RS06350	GNAT family N-acetyltransferase	LSL_1673	acetyltransferase	LRC_RS05010	N-acetyltransferase
LAC1533_RS06355	glutamate racemase	LSL_0836	glutamate racemase	LRC_RS05005	glutamate racemase
LAC1533_RS06360	aminotransferase class V-fold PLP-dependent enzyme	LSL_0835	aromatic amino acid aminotransferase	LRC_RS04990	aminotransferase A
LAC1533_RS06365	DeoR/GlpR transcriptional regulator	LSL_0834	DeoR family transcriptional regulator	LRC_RS04985	DeoR/GlpR transcriptional regulator
LAC1533_RS06370	manganese-dependent inorganic pyrophosphatase	LSL_0833	manganese-dependent inorganic pyrophosphatase	LRC_RS04980	manganese-dependent inorganic pyrophosphatase
LAC1533_RS06375	LysR family transcriptional regulator	LSL_0832	LysR family transcriptional regulator	LRC_RS04975	LysR family transcriptional regulator
LAC1533_RS06385	dihydroorotate dehydrogenase	LSL_0194	dihydroorotate dehydrogenase 1B	LRC_RS04955	dihydroorotate dehydrogenase
LAC1533_RS06395	carbamoyl phosphate synthase small subunit	LSL_0192	carbamoyl phosphate synthase small subunit	LRC_RS04945	carbamoyl-phosphate synthase small subunit
LAC1533_RS06400	dihydroorotase	LSL_0191	dihydroorotase	LRC_RS04940	dihydroorotase
LAC1533_RS06415	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR	LSL_0827	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase	LRC_RS04930	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR
LAC1533_RS06420	RluA family pseudouridine synthase	LSL_0826	ribosomal large subunit pseudouridine synthase D	LRC_RS04925	RluA family pseudouridine synthase
LAC1533_RS06425	signal peptidase II	LSL_0825	lipoprotein signal peptidase	LRC_RS04920	signal peptidase II
LAC1533_RS06430	formate--tetrahydrofolate ligase	LSL_0842	formate--tetrahydrofolate ligase	LRC_RS04910	formate--tetrahydrofolate ligase
LAC1533_RS06435	hypothetical protein	LSL_0841	hypothetical protein	LRC_RS04905	hypothetical protein
LAC1533_RS06440	class I SAM-dependent RNA methyltransferase	LSL_0839	hypothetical protein	LRC_RS04895	class I SAM-dependent RNA methyltransferase
LAC1533_RS06460	cell division regulator GpsB	LSL_0838	cell division protein GpsB	LRC_RS04890	cell division regulator GpsB
LAC1533_RS06465	DUF1273 domain-containing protein	LSL_0930	hypothetical protein	LRC_RS04885	DUF1273 domain-containing protein

LAC1533_RS06470	Holliday junction resolvase RecU	LSL_0932	Holliday junction-specific endonuclease	LRC_RS04880	Holliday junction resolvase RecU
LAC1533_RS06475	carboxypeptidase	LSL_0933	multimodular transpeptidase-transglycosylase PBP 1A	LRC_RS04875	penicillin-binding protein
LAC1533_RS06480	endonuclease III	LSL_0691	endonuclease III	LRC_RS04870	endonuclease III
LAC1533_RS06485	DnaD domain protein	LSL_0690	DNA replication protein dnaD	LRC_RS04865	DnaD domain protein
LAC1533_RS06490	asparagine--tRNA ligase	LSL_0689	asparaginyl-tRNA synthetase	LRC_RS04860	asparagine--tRNA ligase
LAC1533_RS06495	pyridoxal phosphate-dependent aminotransferase	LSL_0688	aspartate aminotransferase	LRC_RS04855	pyridoxal phosphate-dependent aminotransferase
LAC1533_RS06500	hypothetical protein	LSL_0687	hypothetical protein	LRC_RS04850	hypothetical protein
LAC1533_RS06505	hypothetical protein	LSL_0686	ATP-dependent helicase DinG	LRC_RS04845	ATP-dependent helicase
LAC1533_RS06510	mevalonate kinase	LSL_0685	mevalonate kinase	LRC_RS04840	mevalonate kinase
LAC1533_RS06515	diphosphomevalonate decarboxylase	LSL_0684	diphosphomevalonate decarboxylase	LRC_RS04835	diphosphomevalonate decarboxylase
LAC1533_RS06520	phosphomevalonate kinase	LSL_0683	phosphomevalonate kinase	LRC_RS04830	phosphomevalonate kinase
LAC1533_RS06525	type 2 isopentenyl-diphosphate Delta-isomerase	LSL_0682	isopentenyl pyrophosphate isomerase	LRC_RS04825	type 2 isopentenyl-diphosphate Delta-isomerase
LAC1533_RS06530	RNA methyltransferase	LSL_0999	23S rRNA m(5)C methyltransferase	LRC_RS04815	23S rRNA methyltransferase
LAC1533_RS06535	hypothetical protein	LSL_1000	hypothetical protein	LRC_RS04810	hypothetical protein
LAC1533_RS06545	S9 family serine peptidase	LSL_1001	hypothetical protein	LRC_RS04800	S9 family serine peptidase
LAC1533_RS06550	Cof-type HAD-IIB family hydrolase	LSL_1002	HAD superfamily hydrolase	LRC_RS04720	Cof-type HAD-IIB family hydrolase
LAC1533_RS06555	diaminopimelate decarboxylase	LSL_1004	diaminopimelate decarboxylase	LRC_RS04710	diaminopimelate decarboxylase
LAC1533_RS06560	dipeptidase	LSL_1006	dipeptidase A	LRC_RS04700	dipeptidase
LAC1533_RS06580	elongation factor Ts	LSL_0512	elongation factor Ts	LRC_RS04405	elongation factor Ts
LAC1533_RS06585	30S ribosomal protein S2	LSL_0511	30S ribosomal protein S2	LRC_RS04400	30S ribosomal protein S2
LAC1533_RS06595	GIY-YIG nuclease family protein	LSL_0510	hypothetical protein	LRC_RS04560	GIY-YIG nuclease family protein
LAC1533_RS06600	tRNA1(Val) (adenine(37)-N6)-methyltransferase	LSL_0509	methyltransferase	LRC_RS04555	tRNA1(Val) (adenine(37)-N6)-methyltransferase
LAC1533_RS06605	1-acyl-sn-glycerol-3-phosphate acyltransferase	LSL_0508	1-acyl-sn-glycerol-3-phosphate acyltransferase	LRC_RS04550	1-acyl-sn-glycerol-3-phosphate acyltransferase
LAC1533_RS06610	hypothetical protein	LSL_0542	hypothetical protein	LRC_RS04525	hypothetical protein
LAC1533_RS06615	DUF896 family protein	LSL_0541	hypothetical protein	LRC_RS04520	DUF896 family protein
LAC1533_RS06620	transcriptional repressor LexA	LSL_0540	LexA repressor	LRC_RS04515	transcriptional repressor LexA
LAC1533_RS06630	DNA repair protein RecN	LSL_0539	DNA repair protein	LRC_RS04510	DNA repair protein RecN
LAC1533_RS06635	ArgR family transcriptional regulator	LSL_0538	arginine repressor	LRC_RS04505	ArgR family transcriptional regulator
LAC1533_RS06640	TlyA family rRNA (cytidine-2-O)-methyltransferase	LSL_0537	hemolysin	LRC_RS04500	TlyA family rRNA (cytidine-2-O)-methyltransferase
LAC1533_RS06645	polyprenyl synthetase family protein	LSL_0536	geranyltranstransferase	LRC_RS04495	polyprenyl synthetase family protein
LAC1533_RS06650	exodeoxyribonuclease VII small subunit	LSL_0535	exodeoxyribonuclease VII small subunit	LRC_RS04490	exodeoxyribonuclease VII small subunit
LAC1533_RS06655	exodeoxyribonuclease VII large subunit	LSL_0534	exodeoxyribonuclease VII large subunit	LRC_RS04485	exodeoxyribonuclease VII large subunit
LAC1533_RS06660	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	LSL_0533	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	LRC_RS04480	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD
LAC1533_RS06665	transcription antitermination factor NusB	LSL_0532	transcription antitermination protein NusB	LRC_RS04475	transcription antitermination factor NusB
LAC1533_RS06670	Asp23/Gls24 family envelope stress response protein	LSL_0531	alkaline shock protein	LRC_RS04470	Asp23/Gls24 family envelope stress response protein
LAC1533_RS06675	elongation factor P	LSL_0530	protein translation elongation factor P	LRC_RS04465	elongation factor P
LAC1533_RS06680	aminopeptidase P family protein	LSL_1084	Xaa-Pro dipeptidase	LRC_RS04460	aminopeptidase P family protein
LAC1533_RS06685	50S ribosomal protein L27	LSL_0954	50S ribosomal protein L27	LRC_RS04440	50S ribosomal protein L27
LAC1533_RS06690	ribosomal-processing cysteine protease Prp	LSL_0955	ribosomal protein	LRC_RS04435	ribosomal-processing cysteine protease Prp
LAC1533_RS06695	50S ribosomal protein L21	LSL_0956	50S ribosomal protein L21	LRC_RS04430	50S ribosomal protein L21
LAC1533_RS06730	hypothetical protein	LSL_0528	hypothetical protein	LRC_RS05530	hypothetical protein
LAC1533_RS06735	exonuclease SbcC	LSL_0527	hypothetical protein	LRC_RS05535	hypothetical protein
LAC1533_RS06745	hydroxymethylglutaryl-CoA synthase	LSL_0526	hydroxymethylglutaryl-CoA synthase	LRC_RS05545	hydroxymethylglutaryl-CoA synthase
LAC1533_RS06755	acylphosphatase	LSL_0525	acylphosphatase	LRC_RS05550	acylphosphatase
LAC1533_RS06760	OxaA precursor	LSL_0524	60 kDa inner membrane protein	LRC_RS05555	membrane protein
LAC1533_RS06770	DNA-binding response regulator	LSL_0522	two-component response regulator	LRC_RS06485	DNA-binding response regulator
LAC1533_RS06780	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	LSL_0645	6-phosphogluconate dehydrogenase	LRC_RS06490	phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)
LAC1533_RS06785	ATP-dependent Clp protease ATP-binding subunit ClpX	LSL_0644	ATP-dependent protease ATP-binding subunit ClpX	LRC_RS06495	ATP-dependent Clp protease ATP-binding subunit ClpX
LAC1533_RS06790	trigger factor	LSL_0643	trigger factor, PPIase	LRC_RS06500	trigger factor
LAC1533_RS06795	elongation factor Tu	LSL_0642	elongation factor Tu	LRC_RS06505	elongation factor Tu
LAC1533_RS06805	ribonuclease J	LSL_0640	metallo-beta-lactamase superfamily protein	LRC_RS06515	RNase J family beta-CASP ribonuclease
LAC1533_RS06810	4-hydroxy-tetrahydrodipicolinate synthase	LSL_0639	4-hydroxy-tetrahydrodipicolinate synthase	LRC_RS06520	4-hydroxy-tetrahydrodipicolinate synthase
LAC1533_RS06825	30S ribosomal protein S15	LSL_0638	30S ribosomal protein S15	LRC_RS06525	30S ribosomal protein S15
LAC1533_RS06830	30S ribosomal protein S20	LSL_0637	30S ribosomal protein S20	LRC_RS06530	30S ribosomal protein S20
LAC1533_RS06835	DNA polymerase III subunit delta	LSL_0681	DNA polymerase III subunit delta	LRC_RS06540	DNA polymerase III subunit delta
LAC1533_RS06840	DNA internalization-related competence protein ComEC/Rec2	LSL_0680	ComE operon protein 3	LRC_RS06545	DNA internalization-related competence protein ComEC/Rec2
LAC1533_RS06845	ComE operon protein 2	LSL_0679	ComE operon protein 2	LRC_RS06550	ComE operon protein 2
LAC1533_RS06850	ComE operon protein 1	LSL_0678	ComE operon protein 1	LRC_RS06555	competence protein ComEA
LAC1533_RS06855	PDZ domain-containing protein	LSL_0662	ATP-dependent protease La	LRC_RS06560	PDZ domain-containing protein
LAC1533_RS06860	pantetheine-phosphate adenylyltransferase	LSL_0661	phosphopantetheine adenylyltransferase	LRC_RS06565	pantetheine-phosphate adenylyltransferase
LAC1533_RS06865	16S rRNA (guanine(966)-N(2))-methyltransferase RsmD	LSL_0660	methyltransferase	LRC_RS06570	16S rRNA (guanine(966)-N(2))-methyltransferase RsmD
LAC1533_RS06870	DUF2129 domain-containing protein	LSL_0659	hypothetical protein	LRC_RS06575	DUF2129 domain-containing protein
LAC1533_RS06875	pyruvate carboxylase	LSL_0658	pyruvate carboxylase	LRC_RS06585	pyruvate carboxylase
LAC1533_RS06880	FtsW/RodA/SpoVE family cell cycle protein	LSL_0657	cell division protein	LRC_RS06590	cell division protein FtsW
LAC1533_RS06895	translational GTPase TypA	LSL_0653	GTP-binding protein	LRC_RS06600	translational GTPase TypA

LAC1533_RS06900	inositol monophosphatase family protein	LSL_0652	myo-inositol-1(or 4)-monophosphatase	LRC_RS06605	inositol monophosphatase family protein
LAC1533_RS06905	hypothetical protein	LSL_0651	hypothetical protein	LRC_RS06610	hypothetical protein
LAC1533_RS06920	peptide deformylase	LSL_0649	peptide deformylase	LRC_RS06615	peptide deformylase
LAC1533_RS06935	DUF1447 domain-containing protein	LSL_0647	hypothetical protein	LRC_RS06625	DUF1447 domain-containing protein
LAC1533_RS06940	ribonuclease J	LSL_0646	metallo-beta-lactamase superfamily protein	LRC_RS06630	ribonuclease J
LAC1533_RS06945	transcriptional regulator	LSL_0950	transcriptional regulator	LRC_RS06635	transcriptional regulator
LAC1533_RS06955	ATP-dependent RecD-like DNA helicase	LSL_0728	exodeoxyribonuclease V subunit alpha	LRC_RS06640	ATP-dependent RecD-like DNA helicase
LAC1533_RS06960	tetratricopeptide repeat protein	LSL_0727	hypothetical protein	LRC_RS06645	tetratricopeptide repeat protein
LAC1533_RS06965	histidine phosphatase family protein	LSL_0726	phosphoglycerate mutase	LRC_RS06650	histidine phosphatase family protein
LAC1533_RS06970	tRNA 2-thiouridine(34) synthase MnmA	LSL_0862	tRNA (5-methyl aminomethyl-2-thiouridylate)-methyltransferase	LRC_RS06655	tRNA 2-thiouridine(34) synthase MnmA
LAC1533_RS06975	cysteine desulfurase	LSL_0861	hypothetical protein	LRC_RS06660	cysteine desulfurase
LAC1533_RS06980	cysteine desulfurase	LSL_0860	cysteine desulfurase / selenocysteine lyase	LRC_RS06665	cysteine desulfurase
LAC1533_RS06985	5-methylthioadenosine/adenosylhomocysteine nucleosidase	LSL_0859	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase	LRC_RS06670	5-methylthioadenosine/adenosylhomocysteine nucleosidase
LAC1533_RS06995	NUDIX hydrolase	LSL_0857	ADP-ribose pyrophosphatase	LRC_RS06680	NUDIX hydrolase
LAC1533_RS07000	diaminopimelate epimerase	LSL_0856	diaminopimelate epimerase	LRC_RS06685	diaminopimelate epimerase
LAC1533_RS07010	DivIVA domain-containing protein	LSL_1043	cell division initiation protein	LRC_RS06695	DivIVA domain-containing protein
LAC1533_RS07015	RNA-binding protein	LSL_1044	RNA binding protein	LRC_RS06700	RNA-binding protein
LAC1533_RS07020	YggT family protein	LSL_1045	integral membrane protein	LRC_RS06705	YggT family protein
LAC1533_RS07025	cell division protein SepF	LSL_1046	hypothetical protein	LRC_RS06710	DUF552 domain-containing protein
LAC1533_RS07035	cell division protein FtsA	LSL_1048	cell division protein	LRC_RS06720	cell division protein FtsA
LAC1533_RS07045	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	LSL_1050	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	LRC_RS06730	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
LAC1533_RS07050	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	LSL_1051	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	LRC_RS06735	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
LAC1533_RS07055	phospho-N-acetylmuramoyl-pentapeptide- transferase	LSL_1052	phospho-N-acetylmuramoyl-pentapeptide- transferase	LRC_RS06740	phospho-N-acetylmuramoyl-pentapeptide- transferase
LAC1533_RS07060	PASTA domain-containing protein	LSL_1053	penicillin binding protein 2B	LRC_RS06750	PASTA domain-containing protein
LAC1533_RS07070	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	LSL_1055	S-adenosyl-methyltransferase MraW	LRC_RS06760	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH
LAC1533_RS07075	transcriptional regulator MraZ	LSL_1056	cell division protein MraZ	LRC_RS06765	transcriptional regulator MraZ
LAC1533_RS07090	DUF4044 domain-containing protein	LSL_1059	hypothetical protein	LRC_RS10650	DUF4044 domain-containing protein
LAC1533_RS07100	alpha/beta hydrolase	LSL_1060	cell surface hydrolase, membrane-bound	LRC_RS06790	alpha/beta hydrolase
LAC1533_RS07105	cardiolipin synthase	LSL_0673	cardiolipin synthetase	LRC_RS06795	cardiolipin synthase
LAC1533_RS07110	septum site-determining protein MinD	LSL_1064	cell division inhibitor	LRC_RS06815	septum site-determining protein MinD
LAC1533_RS07115	cell division inhibitor	LSL_1065	cell division inhibitor	LRC_RS06820	cell division inhibitor
LAC1533_RS07120	rod shape-determining protein MreD	LSL_1066	rod shape-determining protein	LRC_RS06825	rod shape-determining protein MreD
LAC1533_RS07125	rod shape-determining protein MreC	LSL_1067	rod shape-determining protein MreC	LRC_RS06830	rod shape-determining protein MreC
LAC1533_RS07130	rod shape-determining protein	LSL_1068	rod shape-determining protein MreB	LRC_RS06835	rod shape-determining protein
LAC1533_RS07135	cold-shock protein	LSL_1069	cold shock protein	LRC_RS06840	cold-shock protein
LAC1533_RS07140	DNA repair protein	LSL_1070	DNA repair protein	LRC_RS06845	DNA repair protein RadC
LAC1533_RS07145	HAD family phosphatase	LSL_1577	HAD superfamily hydrolase	LRC_RS06850	HAD family phosphatase
LAC1533_RS07150	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	LSL_1071	folylpolyglutamate synthase / dihydrofolate synthase	LRC_RS06855	bifunctional folylpolyglutamate synthase/dihydrofolate synthase
LAC1533_RS07155	valine--tRNA ligase	LSL_1072	valyl-tRNA synthetase	LRC_RS06865	valine--tRNA ligase
LAC1533_RS07165	tRNA 4-thiouridine(8) synthase ThiI	LSL_1073	thiamine biosynthesis protein	LRC_RS06870	tRNA 4-thiouridine(8) synthase ThiI
LAC1533_RS07170	cysteine desulfurase	LSL_1074	cysteine desulfurase / selenocysteine lyase	LRC_RS06875	cysteine desulfurase
LAC1533_RS07175	septation ring formation regulator EzrA	LSL_1075	septation ring formation regulator EzrA	LRC_RS06880	selenide, water dikinase
LAC1533_RS07180	GAF domain-containing protein	LSL_1076	GAF domain-containing protein	LRC_RS06885	GAF domain-containing protein
LAC1533_RS07185	30S ribosomal protein S4	LSL_1077	30S ribosomal protein S4	LRC_RS06890	30S ribosomal protein S4
LAC1533_RS07190	replication-associated recombination protein A	LSL_1079	recombination factor protein RarA	LRC_RS06905	replication-associated recombination protein A
LAC1533_RS07195	universal stress protein	LSL_1081	universal stress protein	LRC_RS06915	universal stress protein
LAC1533_RS07200	DNA-3-methyladenine glycosylase I	LSL_1082	DNA-3-methyladenine glycosylase	LRC_RS06920	DNA-3-methyladenine glycosylase I
LAC1533_RS07205	aminoglycoside phosphotransferase family protein	LSL_0610	hypothetical protein	LRC_RS06950	hypothetical protein
LAC1533_RS07210	amino acid permease	LSL_1278	amino acid permease	LRC_RS08930	amino acid permease
LAC1533_RS07465	rod shape-determining protein RodA	LSL_0607	rod shape determining protein	LRC_RS07025	rod shape-determining protein RodA
LAC1533_RS07470	DUF2969 domain-containing protein	LSL_0606	hypothetical protein	LRC_RS07030	DUF2969 domain-containing protein
LAC1533_RS07475	membrane protein insertion efficiency factor YidD	LSL_0605	hypothetical protein	LRC_RS10665	membrane protein insertion efficiency factor YidD
LAC1533_RS07480	rod shape-determining protein	LSL_0604	rod shape-determining protein MreB	LRC_RS07040	rod shape-determining protein
LAC1533_RS07485	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	LSL_0603	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	LRC_RS07045	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
LAC1533_RS07490	membrane protein	LSL_0602	hypothetical protein	LRC_RS07050	DUF1146 domain-containing protein
LAC1533_RS07500	F0F1 ATP synthase subunit epsilon	LSL_0601	ATP synthase subunit epsilon	LRC_RS07055	F0F1 ATP synthase subunit epsilon
LAC1533_RS07505	F0F1 ATP synthase subunit beta	LSL_0600	F0F1 ATP synthase subunit beta	LRC_RS07060	F0F1 ATP synthase subunit beta
LAC1533_RS07510	F0F1 ATP synthase subunit gamma	LSL_0599	F0F1 ATP synthase subunit gamma	LRC_RS07065	F0F1 ATP synthase subunit gamma
LAC1533_RS07515	F0F1 ATP synthase subunit alpha	LSL_0598	F0F1 ATP synthase subunit alpha	LRC_RS07070	F0F1 ATP synthase subunit alpha
LAC1533_RS07520	F0F1 ATP synthase subunit delta	LSL_0597	ATP synthase subunit delta	LRC_RS07075	F0F1 ATP synthase subunit delta
LAC1533_RS07525	ATP synthase F0 subunit B	LSL_0596	ATP synthase subunit B	LRC_RS07080	ATP synthase F0 subunit B
LAC1533_RS07530	F0F1 ATP synthase subunit C	LSL_0595	ATP synthase subunit C	LRC_RS07085	F0F1 ATP synthase subunit C
LAC1533_RS07535	F0F1 ATP synthase subunit A	LSL_0594	F0F1 ATP synthase subunit A	LRC_RS07090	F0F1 ATP synthase subunit A

LAC1533_RS07535	F0F1 ATP synthase subunit A	LSL_0594	F0F1 ATP synthase subunit A	LRC_RS07090	F0F1 ATP synthase subunit A
LAC1533_RS07540	uracil phosphoribosyltransferase	LSL_0593	uracil phosphoribosyltransferase	LRC_RS07095	uracil phosphoribosyltransferase
LAC1533_RS07545	threonylcarbamoyl-AMP synthase	LSL_0592	Sua5/YciO/YrdC/YwlC family protein	LRC_RS07100	threonylcarbamoyl-AMP synthase
LAC1533_RS07550	peptide chain release factor N(5)-glutamine methyltransferase	LSL_0591	peptide chain release factor-glutamine N5-methyltransferase	LRC_RS07105	peptide chain release factor N(5)-glutamine methyltransferase
LAC1533_RS07555	peptide chain release factor 1	LSL_0590	peptide chain release factor 1	LRC_RS07110	peptide chain release factor 1
LAC1533_RS07560	thymidine kinase	LSL_0589	thymidine kinase	LRC_RS07115	thymidine kinase
LAC1533_RS07565	DUF1727 domain-containing protein	LSL_0588	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	LRC_RS07120	DUF1727 domain-containing protein
LAC1533_RS07570	glutamine amidotransferase	LSL_0587	cobyric acid synthase	LRC_RS07125	glutamine amidotransferase
LAC1533_RS07585	mannose-6-phosphate isomerase, class I	LSL_1613	mannose-6-phosphate isomerase	LRC_RS07130	mannose-6-phosphate isomerase, class I
LAC1533_RS07595	hypothetical protein	LSL_0584	beta-lactamase family protein	LRC_RS07135	hypothetical protein
LAC1533_RS07610	amino acid ABC transporter ATP-binding protein	LSL_0582	glutamine transport ATP-binding protein	LRC_RS07160	amino acid ABC transporter ATP-binding protein
LAC1533_RS07660	hypothetical protein	LSL_0513	hypothetical protein	LRC_RS07205	hypothetical protein
LAC1533_RS07670	XTP/dITP diphosphatase	LSL_1102	HAM1 protein	LRC_RS07220	XTP/dITP diphosphatase
LAC1533_RS07675	DUF2507 domain-containing protein	LSL_1103	hypothetical protein	LRC_RS07225	DUF2507 domain-containing protein
LAC1533_RS07695	endonuclease MutS2	LSL_1105	DNA mismatch repair protein	LRC_RS07235	endonuclease MutS2
LAC1533_RS07700	CvpA family protein	LSL_1106	hypothetical protein	LRC_RS07240	CvpA family protein
LAC1533_RS07705	cell division protein ZapA	LSL_1107	hypothetical protein	LRC_RS07245	cell division protein ZapA
LAC1533_RS07710	DUF1292 domain-containing protein	LSL_1108	hypothetical protein	LRC_RS07250	DUF1292 domain-containing protein
LAC1533_RS07715	Holliday junction resolvase RuvX	LSL_1109	Holliday junction resolvase-like protein	LRC_RS07255	Holliday junction resolvase RuvX
LAC1533_RS07720	IreB family regulatory phosphoprotein	LSL_1110	hypothetical protein	LRC_RS07260	IreB family regulatory phosphoprotein
LAC1533_RS07725	alanine--tRNA ligase	LSL_1111	alanyl-tRNA synthetase	LRC_RS07265	alanine--tRNA ligase
LAC1533_RS07730	ATP-dependent helicase	LSL_1112	ATP-dependent RNA helicase	LRC_RS07270	ATP-dependent helicase
LAC1533_RS07735	bifunctional oligoribonuclease/PAP phosphatase NrnA	LSL_1113	phosphoesterase, DHH family protein	LRC_RS07275	bifunctional oligoribonuclease/PAP phosphatase NrnA
LAC1533_RS07740	DNA polymerase IV	LSL_1162	DNA polymerase IV	LRC_RS07280	DNA polymerase IV
LAC1533_RS07745	glucose-6-phosphate dehydrogenase	LSL_0462	glucose-6-phosphate 1-dehydrogenase	LRC_RS07285	glucose-6-phosphate dehydrogenase
LAC1533_RS07750	enoyl-[acyl-carrier-protein] reductase FabI	LSL_0461	enoyl-ACP reductase	LRC_RS07290	enoyl-[acyl-carrier-protein] reductase FabI
LAC1533_RS07755	acetyl-CoA carboxylase carboxyl transferase subunit alpha	LSL_0460	acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	LRC_RS07295	acetyl-CoA carboxylase carboxyl transferase subunit alpha
LAC1533_RS07760	acetyl-CoA carboxylase carboxyltransferase subunit beta	LSL_0459	acetyl-CoA carboxylase carboxyltransferase subunit beta	LRC_RS07300	acetyl-CoA carboxylase carboxyltransferase subunit beta
LAC1533_RS07765	acetyl-CoA carboxylase biotin carboxylase subunit	LSL_0458	acetyl-CoA carboxylase biotin carboxylase subunit	LRC_RS07305	acetyl-CoA carboxylase biotin carboxylase subunit
LAC1533_RS07770	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	LSL_0457	(3R)-hydroxymyristoyl-ACP dehydratase	LRC_RS07310	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
LAC1533_RS07775	acetyl-CoA carboxylase biotin carboxyl carrier protein	LSL_0456	acetyl-CoA carboxylase, biotin carboxyl carrier protein	LRC_RS07315	acetyl-CoA carboxylase biotin carboxyl carrier protein
LAC1533_RS07780	beta-ketoacyl-[acyl-carrier-protein] synthase II	LSL_0455	3-oxoacyl-ACP synthase	LRC_RS07320	beta-ketoacyl-[acyl-carrier-protein] synthase II
LAC1533_RS07790	3-oxoacyl-[acyl-carrier-protein] reductase	LSL_0454	3-oxoacyl-ACP reductase	LRC_RS07325	3-oxoacyl-[acyl-carrier-protein] reductase
LAC1533_RS07795	ACP S-malonyltransferase	LSL_0453	malonyl-CoA-[acyl-carrier-protein] transacylase	LRC_RS07330	ACP S-malonyltransferase
LAC1533_RS07800	acyl carrier protein	LSL_0452	acyl carrier protein	LRC_RS07335	acyl carrier protein
LAC1533_RS07805	ketoacyl-ACP synthase III	LSL_0451	3-oxoacyl-ACP synthase	LRC_RS07340	ketoacyl-ACP synthase III
LAC1533_RS07810	MarR family transcriptional regulator	LSL_0450	MarR family transcriptional regulator	LRC_RS07345	MarR family transcriptional regulator
LAC1533_RS07815	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	LSL_0449	(3R)-hydroxyacyl-ACP dehydratase	LRC_RS07350	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ
LAC1533_RS07825	preprotein translocase subunit YajC	LSL_1122	protein translocase subunit	LRC_RS07355	preprotein translocase subunit YajC
LAC1533_RS07830	tRNA guanosine(34) transglycosylase Tgt	LSL_1123	queuine tRNA-ribosyltransferase	LRC_RS07360	tRNA guanosine(34) transglycosylase Tgt
LAC1533_RS07840	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	LSL_1124	S-adenosylmethionine--tRNA ribosyltransferase-isomerase	LRC_RS07365	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
LAC1533_RS07845	Holliday junction branch migration DNA helicase RuvB	LSL_1125	Holliday junction DNA helicase RuvB	LRC_RS07370	Holliday junction branch migration DNA helicase RuvB
LAC1533_RS07850	Holliday junction branch migration protein RuvA	LSL_1126	Holliday junction DNA helicase RuvA	LRC_RS07375	Holliday junction branch migration protein RuvA
LAC1533_RS07855	DNA mismatch repair endonuclease MutL	LSL_1127	DNA mismatch repair protein	LRC_RS07380	DNA mismatch repair endonuclease MutL
LAC1533_RS07860	DNA mismatch repair protein MutS	LSL_1128	DNA mismatch repair protein MutS	LRC_RS07385	DNA mismatch repair protein MutS
LAC1533_RS07875	recombinase RecA	LSL_1130	recombinase A	LRC_RS04290	recombinase RecA
LAC1533_RS07885	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	LSL_1131	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	LRC_RS04280	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
LAC1533_RS07890	DUF4115 domain-containing protein	LSL_1132	transcriptional regulator	LRC_RS04275	DUF4115 domain-containing protein
LAC1533_RS07895	KR domain-containing protein	LSL_1133	3-oxoacyl-ACP reductase	LRC_RS04270	KR domain-containing protein
LAC1533_RS07900	insulinase family protein	LSL_1134	M16 family peptidase	LRC_RS04265	insulinase family protein
LAC1533_RS07910	DNA translocase FtsK	LSL_1135	cell division protein	LRC_RS04255	DNA translocase FtsK
LAC1533_RS07915	tRNA (cytidine(34)-2-O)-methyltransferase	LSL_1136	23S rRNA methyltransferase	LRC_RS04250	tRNA (uridine(34)/cytosine(34)/5-carboxymethylaminomethyluridine(34)-2-O)- methyltransferase TrmL
LAC1533_RS07925	aminoacyl-tRNA deacylase	LSL_1138	transcriptional regulator	LRC_RS04240	aminoacyl-tRNA deacylase
LAC1533_RS07935	GMP reductase	LSL_1139	guanosine 5-monophosphate oxidoreductase	LRC_RS04235	GMP reductase
LAC1533_RS07945	lactonase family protein	LSL_1142	6-phosphogluconolactonase	LRC_RS04225	lactonase family protein
LAC1533_RS07970	UDP-glucose--hexose-1-phosphate uridylyltransferase	LSL_0383	galactose-1-phosphate uridylyltransferase	LRC_RS04125	UDP-glucose--hexose-1-phosphate uridylyltransferase
LAC1533_RS07975	galactokinase	LSL_0381	galactokinase	LRC_RS04120	galactokinase
LAC1533_RS07980	LacI family DNA-binding transcriptional regulator	LSL_0380	galactose operon repressor	LRC_RS05825	LacI family DNA-binding transcriptional regulator

LAC1533_RS07985	magnesium transporter	LSL_1302	Mg2+ transporter	LRC_RS04210	magnesium transporter
LAC1533_RS07990	RluA family pseudouridine synthase	LSL_1303	ribosomal large subunit pseudouridine synthase D	LRC_RS04205	RluA family pseudouridine synthase
LAC1533_RS07995	NAD kinase	LSL_1304	inorganic polyphosphate/ATP-NAD kinase	LRC_RS04200	NAD kinase
LAC1533_RS08005	oligoendopeptidase F	LSL_0398	oligoendopeptidase F	LRC_RS04185	oligoendopeptidase F
LAC1533_RS08015	adapter protein MecA	LSL_0396	adaptor protein MecA	LRC_RS04175	adaptor protein MecA
LAC1533_RS08025	transcriptional regulator Spx	LSL_1330	arsenate reductase	LRC_RS04170	transcriptional regulator Spx
LAC1533_RS08030	anaerobic ribonucleoside-triphosphate reductase activating protein	LSL_1331	anaerobic ribonucleoside-triphosphate reductase activating protein	LRC_RS04160	anaerobic ribonucleoside-triphosphate reductase activating protein
LAC1533_RS08035	anaerobic ribonucleoside-triphosphate reductase	LSL_1332	anaerobic ribonucleoside triphosphate reductase	LRC_RS04155	anaerobic ribonucleoside-triphosphate reductase
LAC1533_RS08145	LTA synthase family protein	LSL_0394	sulfatase family protein	LRC_RS03745	LTA synthase family protein
LAC1533_RS08150	DUF1797 domain-containing protein	LSL_0393	hypothetical protein	LRC_RS03740	DUF1797 domain-containing protein
LAC1533_RS08155	TIGR00374 family protein	LSL_0392	hypothetical protein	LRC_RS03735	UPF0104 family protein
LAC1533_RS08160	glycosyl transferase	LSL_0391	glycosyltransferase	LRC_RS03730	glycosyl transferase
LAC1533_RS08165	glycosyltransferase family 4 protein	LSL_0390	glycosyltransferase	LRC_RS03725	glycosyltransferase family 4 protein
LAC1533_RS08170	phosphoenolpyruvate--protein phosphotransferase	LSL_0389	phosphoenolpyruvate-protein phosphotransferase	LRC_RS03720	phosphoenolpyruvate--protein phosphotransferase
LAC1533_RS08175	phosphocarrier protein HPr	LSL_0388	phosphocarrier protein HPr	LRC_RS03715	phosphocarrier protein HPr
LAC1533_RS08180	hypothetical protein	LSL_0387	hypothetical protein	LRC_RS03710	hypothetical protein
LAC1533_RS08185	ATP-dependent Clp protease ATP-binding subunit	LSL_0386	ATP-dependent Clp protease ATP-binding subunit	LRC_RS03705	ATP-dependent Clp protease ATP-binding subunit
LAC1533_RS08190	DUF1827 domain-containing protein	LSL_0385	hypothetical protein	LRC_RS03700	DUF1827 domain-containing protein
LAC1533_RS08200	peptide chain release factor 3	LSL_0374	peptide chain release factor 3	LRC_RS03685	peptide chain release factor 3
LAC1533_RS08210	LysM peptidoglycan-binding domain-containing protein	LSL_0373	teichoic acid translocation ATP-binding protein	LRC_RS03675	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS08215	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	LSL_0372	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	LRC_RS03660	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
LAC1533_RS08220	DUF402 domain-containing protein	LSL_0370	hypothetical protein	LRC_RS03650	DUF402 domain-containing protein
LAC1533_RS08225	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	LSL_0369	23S rRNA (uracil-5-)-methyltransferase RumA	LRC_RS03645	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
LAC1533_RS08230	recombination regulator RecX	LSL_0368	recombination regulator RecX	LRC_RS03635	recombination regulator RecX
LAC1533_RS08235	YihY/virulence factor BrkB family protein	LSL_1266	ribonuclease BN	LRC_RS03630	YihY/virulence factor BrkB family protein
LAC1533_RS08245	UTP--glucose-1-phosphate uridylyltransferase	LSL_1268	UTP--glucose-1-phosphate uridylyltransferase	LRC_RS03620	UTP--glucose-1-phosphate uridylyltransferase
LAC1533_RS08250	type I methionyl aminopeptidase	LSL_1269	methionine aminopeptidase	LRC_RS03615	type I methionyl aminopeptidase
LAC1533_RS08255	flavodoxin	LSL_1270	flavodoxin	LRC_RS03610	flavodoxin
LAC1533_RS08265	hypothetical protein	LSL_1272	hypothetical protein	LRC_RS03605	membrane protein
LAC1533_RS08270	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	LSL_1276	UDP-N-acetylglucosamine 2-epimerase	LRC_RS03600	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)
LAC1533_RS08280	DUF3284 domain-containing protein	LSL_1285	hypothetical protein	LRC_RS03120	DUF3284 domain-containing protein
LAC1533_RS08285	ATP-dependent helicase	LSL_1286	ATP-dependent RNA helicase	LRC_RS03115	ATP-dependent helicase
LAC1533_RS08290	gfo/Idh/MocA family oxidoreductase	LSL_1287	oxidoreductase	LRC_RS03110	gfo/Idh/MocA family oxidoreductase
LAC1533_RS08315	phosphate ABC transporter substrate-binding protein	LSL_0400	phosphate-binding protein	LRC_RS07960	phosphate ABC transporter substrate-binding protein
LAC1533_RS08350	DUF4828 domain-containing protein	LSL_1288	hypothetical protein	LRC_RS03105	DUF4828 domain-containing protein
LAC1533_RS08630	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	LSL_1341	23S rRNA (uracil-5-)-methyltransferase RumA	LRC_RS02760	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
LAC1533_RS08635	diacylglycerol kinase	LSL_1343	lipid kinase	LRC_RS02735	diacylglycerol kinase
LAC1533_RS08640	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	LSL_1344	aspartyl/glutamyl-tRNA amidotransferase subunit B	LRC_RS02730	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB
LAC1533_RS08645	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA	LSL_1345	aspartyl/glutamyl-tRNA amidotransferase subunit A	LRC_RS02725	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA
LAC1533_RS08650	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC	LSL_1346	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	LRC_RS02720	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC
LAC1533_RS08655	CamS family sex pheromone protein	LSL_1347	lipoprotein, pheromone precursor	LRC_RS02715	CamS family sex pheromone protein
LAC1533_RS08660	NAD-dependent DNA ligase LigA	LSL_1348	NAD-dependent DNA ligase	LRC_RS02710	NAD-dependent DNA ligase LigA
LAC1533_RS08665	DNA helicase PcrA	LSL_1349	ATP-dependent DNA helicase	LRC_RS02705	DNA helicase PcrA
LAC1533_RS08670	ATP-grasp domain-containing protein	LSL_1350	phosphoribosylaminoimidazole carboxylase NCAIR mutase subunit	LRC_RS02695	ATP-grasp domain-containing protein
LAC1533_RS08675	xanthine phosphoribosyltransferase	LSL_1309	xanthine phosphoribosyltransferase	LRC_RS02685	xanthine phosphoribosyltransferase
LAC1533_RS08680	lysozyme	LSL_1310	muramidase	LRC_RS02680	lysozyme
LAC1533_RS08685	ECF transporter S component	LSL_1311	hypothetical protein	LRC_RS02675	ECF transporter S component
LAC1533_RS08695	DUF454 domain-containing protein	LSL_1328	hypothetical protein	LRC_RS01670	DUF454 domain-containing protein
LAC1533_RS08700	DNA topoisomerase III	LSL_1306	DNA topoisomerase III	LRC_RS01660	DNA topoisomerase 3
LAC1533_RS08705	50S ribosomal protein L7/L12	LSL_1237	50S ribosomal protein L7/L12	LRC_RS02195	50S ribosomal protein L7/L12
LAC1533_RS08710	50S ribosomal protein L10	LSL_1238	50S ribosomal protein L10	LRC_RS02190	50S ribosomal protein L10
LAC1533_RS08715	50S ribosomal protein L1	LSL_1239	50S ribosomal protein L1	LRC_RS02185	50S ribosomal protein L1
LAC1533_RS08720	50S ribosomal protein L11	LSL_1240	50S ribosomal protein L11	LRC_RS02180	50S ribosomal protein L11
LAC1533_RS08725	transcription termination/antitermination protein NusG	LSL_1241	transcription antitermination protein	LRC_RS02165	transcription termination/antitermination protein NusG
LAC1533_RS08730	preprotein translocase subunit SecE	LSL_1242	protein translocase subunit secE	LRC_RS02160	preprotein translocase subunit SecE
LAC1533_RS08735	50S ribosomal protein L33	LSL_1243	50S ribosomal protein L33	LRC_RS02155	50S ribosomal protein L33
LAC1533_RS08740	NYN domain-containing protein	LSL_1244	hypothetical protein	LRC_RS02150	NYN domain-containing protein
LAC1533_RS08745	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB	LSL_1245	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB	LRC_RS02145	23S rRNA (guanosine(2251)-2-O)-methyltransferase RlmB
LAC1533_RS08750	hypothetical protein	LSL_1246	hypothetical protein	LRC_RS02140	ribonuclease III
LAC1533_RS08755	cysteine--tRNA ligase	LSL_1247	cysteinyl-tRNA synthetase	LRC_RS02135	cysteine--tRNA ligase
LAC1533_RS08760	glutamate--tRNA ligase	LSL_1248	glutamyl-tRNA synthetase	LRC_RS02130	glutamate--tRNA ligase
LAC1533_RS08765	PIN/TRAM domain-containing protein	LSL_1249	PilT family ATPase	LRC_RS02125	PIN/TRAM domain-containing protein
LAC1533_RS08770	DNA repair protein RadA	LSL_1250	DNA repair protein RadA	LRC_RS02120	DNA repair protein RadA

LAC1533_RS08775	dUTP diphosphatase	LSL_1251	deoxyuridine 5-triphosphate nucleotidohydrolase	LRC_RS02115	dUTP diphosphatase
LAC1533_RS08785	aminopeptidase C	LSL_1253	aminopeptidase C	LRC_RS02100	aminopeptidase C
LAC1533_RS08790	phosphoglycerate mutase	LSL_1255	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	LRC_RS02095	phosphoglycerate mutase
LAC1533_RS08810	malate transporter	LSL_1256	malate permease	LRC_RS02075	malate transporter
LAC1533_RS08820	ketoacyl-ACP synthase III	LSL_1257	3-oxoacyl-ACP synthase	LRC_RS02060	ketoacyl-ACP synthase III
LAC1533_RS08830	SprT family protein	LSL_1258	hypothetical protein	LRC_RS02045	SprT family protein
LAC1533_RS08845	ammonia-dependent NAD(+) synthetase	LSL_1260	NAD synthetase	LRC_RS02030	ammonia-dependent NAD(+) synthetase
LAC1533_RS08850	glycosyltransferase	LSL_1262	N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase	LRC_RS02025	glycosyltransferase
LAC1533_RS08860	30S ribosomal protein S9	LSL_1402	30S ribosomal protein S9	LRC_RS01640	30S ribosomal protein S9
LAC1533_RS08865	50S ribosomal protein L13	LSL_1403	50S ribosomal protein L13	LRC_RS01635	50S ribosomal protein L13
LAC1533_RS08870	tRNA pseudouridine(38-40) synthase TruA	LSL_1404	tRNA pseudouridine synthase A	LRC_RS01630	tRNA pseudouridine(38-40) synthase TruA
LAC1533_RS08875	energy-coupling factor transporter transmembrane protein EcfT	LSL_1405	cobalt transport permease	LRC_RS01625	energy-coupling factor transporter transmembrane protein EcfT
LAC1533_RS08880	energy-coupling factor ABC transporter ATP-binding protein	LSL_1406	cobalt transport ATP-binding protein	LRC_RS01620	energy-coupling factor transporter ATPase
LAC1533_RS08885	energy-coupling factor ABC transporter ATP-binding protein	LSL_1407	cobalt transport ATP-binding protein	LRC_RS01615	energy-coupling factor ABC transporter ATP-binding protein
LAC1533_RS08890	50S ribosomal protein L17	LSL_1408	50S ribosomal protein L17	LRC_RS01605	50S ribosomal protein L17
LAC1533_RS08895	DNA-directed RNA polymerase subunit alpha	LSL_1409	DNA-directed RNA polymerase subunit alpha	LRC_RS01600	DNA-directed RNA polymerase subunit alpha
LAC1533_RS08900	30S ribosomal protein S11	LSL_1410	30S ribosomal protein S11	LRC_RS01595	30S ribosomal protein S11
LAC1533_RS08905	30S ribosomal protein S13	LSL_1411	30S ribosomal protein S13	LRC_RS01590	30S ribosomal protein S13
LAC1533_RS08910	50S ribosomal protein L36	LSL_1412	50S ribosomal protein L36	LRC_RS01585	50S ribosomal protein L36
LAC1533_RS08915	translation initiation factor IF-1	LSL_1413	translation initiation factor IF-1	LRC_RS01580	translation initiation factor IF-1
LAC1533_RS08920	adenylate kinase	LSL_1414	adenylate kinase	LRC_RS01575	adenylate kinase
LAC1533_RS08925	preprotein translocase subunit SecY	LSL_1415	preprotein translocase subunit SecY	LRC_RS01570	preprotein translocase subunit SecY
LAC1533_RS08930	50S ribosomal protein L15	LSL_1416	50S ribosomal protein L15	LRC_RS01565	50S ribosomal protein L15
LAC1533_RS08935	50S ribosomal protein L30	LSL_1417	50S ribosomal protein L30	LRC_RS01560	50S ribosomal protein L30
LAC1533_RS08940	30S ribosomal protein S5	LSL_1418	30S ribosomal protein S5	LRC_RS01555	30S ribosomal protein S5
LAC1533_RS08945	50S ribosomal protein L18	LSL_1419	50S ribosomal protein L18	LRC_RS01550	50S ribosomal protein L18
LAC1533_RS08950	50S ribosomal protein L6	LSL_1420	50S ribosomal protein L6	LRC_RS01545	50S ribosomal protein L6
LAC1533_RS08955	30S ribosomal protein S8	LSL_1421	30S ribosomal protein S8	LRC_RS01540	30S ribosomal protein S8
LAC1533_RS08960	type Z 30S ribosomal protein S14	LSL_1422	30S ribosomal protein S14	LRC_RS10380	type Z 30S ribosomal protein S14
LAC1533_RS08965	50S ribosomal protein L5	LSL_1423	50S ribosomal protein L5	LRC_RS01535	50S ribosomal protein L5
LAC1533_RS08970	50S ribosomal protein L24	LSL_1424	50S ribosomal protein L24	LRC_RS01530	50S ribosomal protein L24
LAC1533_RS08975	50S ribosomal protein L14	LSL_1425	50S ribosomal protein L14	LRC_RS01525	50S ribosomal protein L14
LAC1533_RS08980	30S ribosomal protein S17	LSL_1426	30S ribosomal protein S17	LRC_RS01520	30S ribosomal protein S17
LAC1533_RS08985	50S ribosomal protein L29	LSL_1427	50S ribosomal protein L29	LRC_RS01515	50S ribosomal protein L29
LAC1533_RS08990	50S ribosomal protein L16	LSL_1428	50S ribosomal protein L16	LRC_RS01510	50S ribosomal protein L16
LAC1533_RS08995	30S ribosomal protein S3	LSL_1429	30S ribosomal protein S3	LRC_RS01505	30S ribosomal protein S3
LAC1533_RS09005	30S ribosomal protein S19	LSL_1431	30S ribosomal protein S19	LRC_RS01495	30S ribosomal protein S19
LAC1533_RS09010	50S ribosomal protein L2	LSL_1432	50S ribosomal protein L2	LRC_RS01490	50S ribosomal protein L2
LAC1533_RS09015	50S ribosomal protein L23	LSL_1433	50S ribosomal protein L23	LRC_RS01485	50S ribosomal protein L23
LAC1533_RS09020	50S ribosomal protein L4	LSL_1434	50S ribosomal protein L4	LRC_RS01480	50S ribosomal protein L4
LAC1533_RS09025	50S ribosomal protein L3	LSL_1435	50S ribosomal protein L3	LRC_RS01475	50S ribosomal protein L3
LAC1533_RS09030	30S ribosomal protein S10	LSL_1436	30S ribosomal protein S10	LRC_RS01470	30S ribosomal protein S10
LAC1533_RS09040	cysteine hydrolase	LSL_1510	pyrazinamidase / nicotinamidase	LRC_RS01465	cysteine hydrolase
LAC1533_RS09045	elongation factor G	LSL_0202	elongation factor G	LRC_RS01420	elongation factor G
LAC1533_RS09050	30S ribosomal protein S7	LSL_0201	30S ribosomal protein S7	LRC_RS01415	30S ribosomal protein S7
LAC1533_RS09055	30S ribosomal protein S12	LSL_0200	30S ribosomal protein S12	LRC_RS01410	30S ribosomal protein S12
LAC1533_RS09075	DNA-directed RNA polymerase subunit beta	LSL_0198	DNA-directed RNA polymerase subunit beta	LRC_RS01395	DNA-directed RNA polymerase subunit beta
LAC1533_RS09080	DNA-directed RNA polymerase subunit beta	LSL_0197	DNA-directed RNA polymerase subunit beta	LRC_RS01390	DNA-directed RNA polymerase subunit beta
LAC1533_RS09085	ATP-dependent Clp protease ATP-binding subunit	LSL_0196	negative regulator of genetic competence	LRC_RS01385	ATP-dependent Clp protease ATP-binding subunit
LAC1533_RS09090	CtsR family transcriptional regulator	LSL_0195	transcriptional regulator ctsR	LRC_RS01380	CtsR family transcriptional regulator
LAC1533_RS09165	tyrosine--tRNA ligase	LSL_1366	tyrosyl-tRNA synthetase	LRC_RS02235	tyrosine--tRNA ligase
LAC1533_RS09170	transcriptional repressor	LSL_1367	ferric uptake regulation protein	LRC_RS02230	transcriptional repressor
LAC1533_RS09175	metal-dependent hydrolase	LSL_1368	hypothetical protein	LRC_RS02225	metal-dependent hydrolase
LAC1533_RS09185	exonuclease SbcCD subunit D	LSL_1370	exonuclease	LRC_RS02215	exonuclease SbcCD subunit D
LAC1533_RS09200	GntR family transcriptional regulator	LSL_1508	GntR family transcriptional regulator	LRC_RS09040	GntR family transcriptional regulator
LAC1533_RS09210	class I SAM-dependent methyltransferase	LSL_0949	cyclopropane-fatty-acyl-phospholipid synthase	LRC_RS01680	class I SAM-dependent methyltransferase
LAC1533_RS09230	histidine phosphatase family protein	LSL_1511	phosphoglycerate mutase	LRC_RS09055	histidine phosphatase family protein
LAC1533_RS09255	ASCH domain-containing protein	LSL_0877	hypothetical protein	LRC_RS08935	ASCH domain-containing protein
LAC1533_RS09305	exodeoxyribonuclease III	LSL_1490	exodeoxyribonuclease III	LRC_RS03515	exodeoxyribonuclease III
LAC1533_RS09355	glutamine-hydrolyzing GMP synthase	LSL_1537	GMP synthase	LRC_RS09350	glutamine-hydrolyzing GMP synthase
LAC1533_RS09360	type I pantothenate kinase	LSL_1538	pantothenate kinase	LRC_RS09355	type I pantothenate kinase
LAC1533_RS09370	ATP-dependent DNA helicase	LSL_1377	ATP-dependent DNA helicase	LRC_RS09380	ATP-dependent DNA helicase
LAC1533_RS09375	potassium transporter	LSL_1378	Na+/H+ antiporter	LRC_RS09385	potassium transporter
LAC1533_RS09385	histidine phosphatase family protein	LSL_0125	phosphoglycerate mutase	LRC_RS09390	histidine phosphatase family protein
LAC1533_RS09415	ABC transporter ATP-binding protein	LSL_1695	oligopeptide transport ATP-binding protein oppF	LRC_RS01005	ABC transporter ATP-binding protein
LAC1533_RS09420	ABC transporter ATP-binding protein	LSL_1696	oligopeptide transport ATP-binding protein	LRC_RS01000	ABC transporter ATP-binding protein
LAC1533_RS09425	ABC transporter permease	LSL_1697	oligopeptide transport system permease	LRC_RS00995	ABC transporter permease
LAC1533_RS09430	ABC transporter permease	LSL_1698	oligopeptide transport system permease	LRC_RS00990	ABC transporter permease

LAC1533_RS09435	peptide ABC transporter substrate-binding protein	LSL_1699	oligopeptide-binding protein oppA	LRC_RS00985	peptide ABC transporter substrate-binding protein
LAC1533_RS09440	GTPase HflX	LSL_1437	GTP-binding protein	LRC_RS00980	GTPase HflX
LAC1533_RS09445	N-acetyltransferase	LSL_1441	hypothetical protein	LRC_RS00975	N-acetyltransferase
LAC1533_RS09475	hypothetical protein	LSL_1448	hypothetical protein	LRC_RS00970	hypothetical protein
LAC1533_RS09485	hypothetical protein	LSL_1449	hypothetical protein	LRC_RS00965	hypothetical protein
LAC1533_RS09490	transcriptional repressor	LSL_1450	ferric uptake regulation protein	LRC_RS00960	transcriptional repressor
LAC1533_RS09500	amino acid permease	LSL_1451	amino acid permease	LRC_RS00930	amino acid permease
LAC1533_RS09515	ECF transporter S component	LSL_0937	hypothetical protein	LRC_RS06235	ECF transporter S component
LAC1533_RS09520	Xaa-Pro dipeptidyl-peptidase	LSL_1534	x-prolyl-dipeptidyl aminopeptidase	LRC_RS00920	Xaa-Pro dipeptidyl-peptidase
LAC1533_RS09605	glyoxalase	LSL_1463	lactoylglutathione lyase family protein	LRC_RS00890	glyoxalase
LAC1533_RS09990	Cof-type HAD-IIB family hydrolase	LSL_1476	HAD superfamily hydrolase	LRC_RS00805	Cof-type HAD-IIB family hydrolase
LAC1533_RS09995	DUF475 domain-containing protein	LSL_1621	tellurium resistance protein	LRC_RS00790	DUF475 domain-containing protein
LAC1533_RS10025	L,D-transpeptidase	LSL_0176	ErfK family protein	LRC_RS08570	L,D-transpeptidase
LAC1533_RS10130	glycerate kinase	LSL_1707	glycerate kinase	LRC_RS02445	glycerate kinase
LAC1533_RS10160	LytR family transcriptional regulator	LSL_1551	LytR family transcriptional regulator	LRC_RS04970	LytR family transcriptional regulator
LAC1533_RS10195	DUF2922 domain-containing protein	LSL_0960	hypothetical protein	LRC_RS00885	DUF2922 domain-containing protein
LAC1533_RS10255	dTDP-glucose 4,6-dehydratase	LSL_1570	dTDP-glucose 4,6-dehydratase	LRC_RS00585	dTDP-glucose 4,6-dehydratase
LAC1533_RS10265	cadmium-translocating P-type ATPase	LSL_0169	lead, cadmium, zinc and mercury transporting ATPase	LRC_RS00765	heavy metal translocating P-type ATPase
LAC1533_RS10335	hypothetical protein	LSL_1547	oligosaccharide translocase	LRC_RS00730	hypothetical protein
LAC1533_RS10340	UDP-galactopyranose mutase	LSL_1548	UDP-galactopyranose mutase	LRC_RS00735	UDP-galactopyranose mutase
LAC1533_RS10355	hypothetical protein	LSL_0694	hypothetical protein	LRC_RS00610	beta-1,6-galactofuranosyltransferase
LAC1533_RS10370	DUF4422 domain-containing protein	LSL_1574	glycosyltransferase	LRC_RS00740	DUF4422 domain-containing protein
LAC1533_RS10395	glycosyltransferase	LSL_0171	glycosyltransferase	LRC_RS00630	glycosyltransferase
LAC1533_RS10425	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase	LSL_1208	undecaprenyl-phosphate alpha-N-acetylglucosaminephosphotransferase	LRC_RS03255	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase
LAC1533_RS10510	PTS fructose transporter subunit IIC	LSL_0165	PTS system fructose-specific transporter subunit IIABC	LRC_RS00420	PTS fructose transporter subunit IIC
LAC1533_RS10515	1-phosphofructokinase	LSL_0164	1-phosphofructokinase	LRC_RS00415	1-phosphofructokinase
LAC1533_RS10520	DeoR/GlpR transcriptional regulator	LSL_0163	transcription regulator of fructose operon	LRC_RS00410	DeoR/GlpR transcriptional regulator
LAC1533_RS10560	cation:proton antiporter	LSL_1533	Na+/H+ antiporter	LRC_RS00935	cation:proton antiporter
LAC1533_RS10620	nicotinate phosphoribosyltransferase	LSL_1261	nicotinate phosphoribosyltransferase	LRC_RS00365	nicotinate phosphoribosyltransferase
LAC1533_RS10635	hypothetical protein	LSL_0160	hypothetical protein	LRC_RS00355	hypothetical protein
LAC1533_RS10645	peptide-methionine (S)-S-oxide reductase	LSL_0692	peptide methionine sulfoxide reductase	LRC_RS06095	peptide-methionine (S)-S-oxide reductase
LAC1533_RS10650	thioredoxin	LSL_1104	thioredoxin	LRC_RS07230	thioredoxin
LAC1533_RS10685	glutamine ABC transporter substrate-binding protein	LSL_0062	glutamine-binding protein / glutamine transport system permease	LRC_RS07165	glutamine ABC transporter substrate-binding protein
LAC1533_RS10690	universal stress protein	LSL_0060	universal stress protein	LRC_RS00295	universal stress protein
LAC1533_RS10700	deoxyguanosine kinase	LSL_1642	deoxyguanosine kinase	LRC_RS00290	deoxyguanosine kinase
LAC1533_RS10725	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	LSL_0129	5-methyltetrahydropteroyltriglutamate/homocysteine S-methyltransferase	LRC_RS08940	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
LAC1533_RS10735	aluminum resistance protein	LSL_0556	aluminum resistance protein	LRC_RS06430	aluminum resistance protein
LAC1533_RS10760	penicillin-binding protein 2	LSL_1088	penicillin-binding protein	LRC_RS06470	penicillin-binding protein 2
LAC1533_RS10805	peptide ABC transporter substrate-binding protein	LSL_0117	ABC transporter substrate-binding protein	LRC_RS07835	ABC transporter substrate-binding protein
LAC1533_RS10810	branched-chain amino acid ABC transporter permease	LSL_0118	ABC transporter permease	LRC_RS07840	branched-chain amino acid ABC transporter permease
LAC1533_RS10885	PFL family protein	LSL_0162	hypothetical protein	LRC_RS00390	PFL family protein
LAC1533_RS10890	ACT domain-containing protein	LSL_0161	hypothetical protein	LRC_RS00385	ACT domain-containing protein
LAC1533_RS10920	type 1 glutamine amidotransferase	LSL_0339	GMP synthase	LRC_RS10115	type 1 glutamine amidotransferase
LAC1533_RS10935	amino acid ABC transporter permease	LSL_1063	polar amino acid ABC transporter permease	LRC_RS06810	amino acid ABC transporter permease
LAC1533_RS10940	amino acid ABC transporter ATP-binding protein	LSL_1062	polar amino acid ABC transporter ATP-binding protein	LRC_RS06805	amino acid ABC transporter ATP-binding protein
LAC1533_RS10945	amino acid ABC transporter substrate-binding protein	LSL_1061	polar amino acid ABC transporter substrate-binding protein	LRC_RS06800	amino acid ABC transporter substrate-binding protein
LAC1533_RS10955	PspC domain-containing protein	LSL_0108	stress-responsive transcriptional regulator PspC	LRC_RS09905	PspC domain-containing protein
LAC1533_RS10960	PadR family transcriptional regulator	LSL_0105	PadR family transcriptional regulator	LRC_RS09920	PadR family transcriptional regulator
LAC1533_RS10970	DUF1700 domain-containing protein	LSL_0106	hypothetical protein	LRC_RS09915	DUF1700 domain-containing protein
LAC1533_RS10975	D-alanyl-D-alanine dipeptidase	LSL_1373	D-alanyl-D-alanine dipeptidase	LRC_RS04165	D-alanyl-D-alanine dipeptidase
LAC1533_RS10990	MarR family transcriptional regulator	LSL_1646	MarR family transcriptional regulator	LRC_RS09940	MarR family transcriptional regulator
LAC1533_RS10995	KH domain-containing protein	LSL_1647	hypothetical protein	LRC_RS09945	protein jag
LAC1533_RS11010	ribokinase	LSL_0423	ribokinase	LRC_RS07720	ribokinase
LAC1533_RS11035	N-acetyltransferase	LSL_0998	acetyltransferase	LRC_RS03010	N-acetyltransferase
LAC1533_RS11065	cadmium-translocating P-type ATPase	LSL_1704	cation transport ATPases	LRC_RS02625	cadmium-translocating P-type ATPase
LAC1533_RS11145	peptidase M13	LSL_1669	oligoendopeptidase O	LRC_RS09950	peptidase M13
LAC1533_RS11310	fructokinase	LSL_1461	fructokinase	LRC_RS00895	fructokinase
LAC1533_RS11430	glutamine--fructose-6-phosphate transaminase (isomerizing)	LSL_1627	glucosamine--fructose-6-phosphate aminotransferase	LRC_RS09125	glutamine--fructose-6-phosphate transaminase (isomerizing)
LAC1533_RS11510	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	LSL_0124	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	LRC_RS10050	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG
LAC1533_RS11515	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE	LSL_0123	tRNA modification GTPase TrmE	LRC_RS10055	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE
LAC1533_RS11660	hypothetical protein	LSL_1473	CrcB family protein	LRC_RS00820	fluoride efflux transporter CrcB
LAC1533_RS11705	nucleotide sugar dehydrogenase	LSL_0979	UDP-glucose 6-dehydrogenase	LRC_RS00570	nucleotide sugar dehydrogenase

LAC1533_RS11750	tyrosine protein phosphatase	LSL_1552	phosphotyrosine-protein phosphatase	LRC_RS00465	tyrosine protein phosphatase
LAC1533_RS11755	exopolysaccharide biosynthesis protein	LSL_1553	tyrosine-protein kinase	LRC_RS00460	exopolysaccharide biosynthesis protein
LAC1533_RS12010	amino acid permease	LSL_0443	amino acid permease	LRC_RS07475	amino acid permease
LAC1533_RS12045	biotin transporter BioY	LSL_0074	BioY protein	LRC_RS03090	biotin transporter BioY
LAC1533_RS12050	dephospho-CoA kinase	LSL_0490	dephospho-CoA kinase	LRC_RS05710	dephospho-CoA kinase
LAC1533_RS12075	argininosuccinate lyase	LSL_0305	argininosuccinate lyase	LRC_RS02450	argininosuccinate lyase
LAC1533_RS12080	argininosuccinate synthase	LSL_0306	argininosuccinate synthase	LRC_RS02455	argininosuccinate synthase
LAC1533_RS12120	iron export ABC transporter permease subunit FetB	LSL_1683	hypothetical protein	LRC_RS01010	iron export ABC transporter permease subunit FetB
LAC1533_RS12175	FAD:protein FMN transferase	LSL_1520	Iron-sulfur cluster assembly/repair protein	LRC_RS10140	FAD:protein FMN transferase
LAC1533_RS12260	membrane protein	LSL_1736	60 kDa inner membrane protein	LRC_RS10190	membrane protein
LAC1533_RS12265	ribonuclease P protein component	LSL_1737	ribonuclease P	LRC_RS10195	ribonuclease P protein component
LAC1533_RS12270	50S ribosomal protein L34	LSL_1738	50S ribosomal protein L34	LRC_RS11060	50S ribosomal protein L34

Supplementary table S9B. Singletons among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosomes as calculated with the EDGAR software.

***Lactobacillus acidipiscis* ACA-DC 1533**		***Lactobacillus salivarius* UCC118**		***Lactobacillus ruminis* ATCC 27782**	
locus_tag	**annotated function**	**locus_tag**	**annotated function**	**locus_tag**	**annotated function**
LAC1533_RS00050	GntR family transcriptional regulator	LSL_0015	hypothetical protein	LRC_RS00005	hypothetical protein
LAC1533_RS00055	beta-galactosidase	LSL_0020	TetR family transcriptional regulator	LRC_RS00060	nicotinamide mononucleotide transporter
LAC1533_RS00065	PTS sugar transporter subunit IIC	LSL_0021	glucose uptake protein	LRC_RS00080	hypothetical protein
LAC1533_RS00070	PTS fructose transporter subunit IID	LSL_0024	drug/metabolite exporter family protein	LRC_RS00090	hypothetical protein
LAC1533_RS00075	PTS fructose transporter subunit IIA	LSL_0030	DNA-damage-inducible protein J	LRC_RS00095	MFS transporter
LAC1533_RS00080	SIS domain-containing protein	LSL_0031	MarR family transcriptional regulator	LRC_RS00110	amidase
LAC1533_RS00085	N-acetylglucosamine-6-phosphate deacetylase	LSL_0037	hypothetical protein	LRC_RS00120	hypothetical protein
LAC1533_RS00090	DeoR/GlpR transcriptional regulator	LSL_0044	oxidoreductase	LRC_RS00125	cytosine permease
LAC1533_RS00100	ABC transporter permease	LSL_0045	hypothetical protein	LRC_RS00145	hypothetical protein
LAC1533_RS00115	hypothetical protein	LSL_0046	short-chain dehydrogenase	LRC_RS00150	hypothetical protein
LAC1533_RS00140	group II intron reverse transcriptase/maturase	LSL_0047	hypothetical protein	LRC_RS00220	hypothetical protein
LAC1533_RS00145	IS1380 family transposase	LSL_0048	glycerol-3-phosphate transporter	LRC_RS00250	YitT family protein
LAC1533_RS00150	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein	LSL_0049	IS1223 family transposase	LRC_RS00255	lactoylglutathione lyase
LAC1533_RS00155	phosphonate ABC transporter ATP-binding protein	LSL_0050	IS200 family transposase	LRC_RS00260	IS200/IS605 family transposase
LAC1533_RS00160	phosphonate ABC transporter, permease protein PhnE	LSL_0051	hypothetical protein	LRC_RS00270	cytidine deaminase
LAC1533_RS00165	phosphonate ABC transporter, permease protein PhnE	LSL_0052	Na+ driven multidrug efflux pump	LRC_RS00300	PTS sugar transporter subunit IIC
LAC1533_RS00170	bifunctional metallophosphatase/5-nucleotidase	LSL_0054	hypothetical protein	LRC_RS00310	hypothetical protein
LAC1533_RS00185	DUF4867 domain-containing protein	LSL_0056	glutamine amidotransferase	LRC_RS00320	isopeptide-forming domain-containing fimbrial protein
LAC1533_RS00190	tagatose-6-phosphate kinase	LSL_0057	glutamate--cysteine ligase	LRC_RS00325	class C sortase
LAC1533_RS00195	PTS sugar transporter subunit IIA	LSL_0061	hypothetical protein	LRC_RS00335	hypothetical protein
LAC1533_RS00200	PTS fructose transporter subunit IIB	LSL_0067	neopullulanase / cyclomaltodextrinase / maltogenic alpha-amylase	LRC_RS00340	hypothetical protein
LAC1533_RS00205	PTS glucitol transporter subunit IIA	LSL_0068	potassium uptake protein ktrB	LRC_RS00345	ATPase
LAC1533_RS00210	hypothetical protein	LSL_0070	Zn-dependent protease	LRC_RS00350	hypothetical protein
LAC1533_RS00215	DeoR/GlpR transcriptional regulator	LSL_0071	N-acetylglucosaminyltransferase	LRC_RS00370	hypothetical protein
LAC1533_RS00220	galactose-6-phosphate isomerase subunit LacA	LSL_0072	hypothetical protein	LRC_RS00395	aspartate ammonia-lyase
LAC1533_RS00225	galactose-6-phosphate isomerase subunit LacB	LSL_0073	hypothetical protein	LRC_RS00400	Lrp/AsnC family transcriptional regulator
LAC1533_RS00230	tagatose-bisphosphate aldolase	LSL_0077	hypothetical protein	LRC_RS00405	hypothetical protein
LAC1533_RS00255	PRD domain-containing protein	LSL_0082	sugar-binding protein	LRC_RS00425	type II toxin-antitoxin system RelB/DinJ family antitoxin
LAC1533_RS00265	6-phospho-beta-galactosidase	LSL_0083	two-component response regulator	LRC_RS00430	type II toxin-antitoxin system YafQ family toxin
LAC1533_RS00270	PTS lactose transporter subunit IIBC	LSL_0084	two component system histidine kinase	LRC_RS00435	hypothetical protein
LAC1533_RS00280	6-phospho-beta-galactosidase	LSL_0085	D-ribose-binding protein	LRC_RS00440	RloB domain-containing protein
LAC1533_RS00285	PTS lactose transporter subunit IIB	LSL_0090	hypothetical protein	LRC_RS00445	ATP-binding protein
LAC1533_RS00290	methylglyoxal synthase	LSL_0095	hypothetical protein	LRC_RS00475	aldolase
LAC1533_RS00295	hypothetical protein	LSL_0096	hypothetical protein	LRC_RS00480	pyridoxal-dependent decarboxylase
LAC1533_RS00300	IS30 family transposase	LSL_0097	hypothetical protein	LRC_RS00485	sugar transferase

LAC1533_RS00305	hypothetical protein	LSL_0098	CRISPR-associated protein	LRC_RS00490	branched-chain amino acid transaminase
LAC1533_RS00310	hypothetical protein	LSL_0099	CRISPR-associated protein	LRC_RS00495	glycosyltransferase family 2 protein
LAC1533_RS00315	hypothetical protein	LSL_0100	CRISPR-associated Csn2 family protein	LRC_RS00500	hypothetical protein
LAC1533_RS00325	hypothetical protein	LSL_0107	hypothetical protein	LRC_RS00505	NAD(P)-dependent oxidoreductase
LAC1533_RS00330	butanediol dehydrogenase	LSL_0109	hypothetical protein	LRC_RS00510	acyltransferase
LAC1533_RS00355	LysR family transcriptional regulator	LSL_0114	spermidine/putrescine ABC transporter permease	LRC_RS00515	glycosyl transferase
LAC1533_RS00360	FAD-binding protein	LSL_0122	hypothetical protein	LRC_RS00520	glycosyl transferase
LAC1533_RS00365	SDR family NAD(P)-dependent oxidoreductase	LSL_0126	CAAX amino protease	LRC_RS00525	oligosaccharide repeat unit polymerase
LAC1533_RS00370	FAD-binding protein	LSL_0127	flavodoxin	LRC_RS00530	hypothetical protein
LAC1533_RS00375	MFS transporter	LSL_0130	ABC transporter substrate-binding protein	LRC_RS00535	flippase
LAC1533_RS00380	MFS transporter	LSL_0133	succinyl-diaminopimelate desuccinylase	LRC_RS00540	acetyltransferase
LAC1533_RS00385	hypothetical protein	LSL_0134	NAD(P)H-dependent quinone reductase	LRC_RS00555	ATP-binding protein
LAC1533_RS00390	aldo/keto reductase	LSL_0135	acetoacetate decarboxylase	LRC_RS00560	transposase
LAC1533_RS00395	NAD(P)-dependent oxidoreductase	LSL_0136	3-hydroxybutyryl-CoA dehydrogenase	LRC_RS00565	hypothetical protein
LAC1533_RS00400	L-lactate oxidase	LSL_0139	hypothetical protein	LRC_RS00600	hypothetical protein
LAC1533_RS00405	FAD-binding oxidoreductase	LSL_0142	hypothetical protein	LRC_RS00625	GtrA family protein
LAC1533_RS00410	LacI family DNA-binding transcriptional regulator	LSL_0143	hypothetical protein	LRC_RS00635	hypothetical protein
LAC1533_RS00415	FAD-binding protein	LSL_0144	glucose-1-dehydrogenase	LRC_RS00640	IS256 family transposase
LAC1533_RS00420	FAD-binding protein	LSL_0146	LysR family transcriptional regulator	LRC_RS00645	hypothetical protein
LAC1533_RS00425	hypothetical protein	LSL_0148	short-chain dehydrogenase	LRC_RS00655	hypothetical protein
LAC1533_RS00435	Cof-type HAD-IIB family hydrolase	LSL_0149	hypothetical protein	LRC_RS00660	hypothetical protein
LAC1533_RS00440	hypothetical protein	LSL_0150	hypothetical protein	LRC_RS00665	hypothetical protein
LAC1533_RS00465	hypothetical protein	LSL_0159	hypothetical protein	LRC_RS00670	hypothetical protein
LAC1533_RS00470	cell surface protein	LSL_0166	hypothetical protein	LRC_RS00675	acyltransferase
LAC1533_RS00475	iron ABC transporter substrate-binding protein	LSL_0183	LysR family transcriptional regulator	LRC_RS00680	hypothetical protein
LAC1533_RS00480	iron compound ABC transporter permease	LSL_0184	phosphatase	LRC_RS00700	hypothetical protein
LAC1533_RS00485	ABC transporter ATP-binding protein	LSL_0185	acetyltransferase	LRC_RS00710	glycosyltransferase
LAC1533_RS00495	IS30 family transposase	LSL_0204	class I and II aminotransferase	LRC_RS00715	glycosyl transferase family 2
LAC1533_RS00500	MFS transporter	LSL_0208	hypothetical protein	LRC_RS00720	LicD family protein
LAC1533_RS00505	DoxX family membrane protein	LSL_0209	1-deoxy-D-xylulose-5-phosphate synthase	LRC_RS00745	sugar transferase
LAC1533_RS00510	glutaryl-CoA dehydrogenase	LSL_0211	TetR family transcriptional regulator	LRC_RS00750	glycosyltransferase family 2 protein
LAC1533_RS00520	group II intron reverse transcriptase/maturase	LSL_0213	ATPase associated with chromosome architecture/replication	LRC_RS00755	hypothetical protein
LAC1533_RS00530	LysR family transcriptional regulator	LSL_0222	TetR family transcriptional regulator	LRC_RS00760	ATP-binding protein
LAC1533_RS00535	acetyl-CoA C-acetyltransferase	LSL_0223	amino acid ABC transporter substrate-binding protein	LRC_RS00770	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
LAC1533_RS00540	acyl-CoA dehydrogenase	LSL_0231	hypothetical protein	LRC_RS00775	nucleotide sugar dehydratase
LAC1533_RS00545	3-hydroxybutyryl-CoA dehydrogenase	LSL_0232	transaminase	LRC_RS00795	hypothetical protein
LAC1533_RS00550	crotonase	LSL_0236	phage integrase	LRC_RS00800	N-acetyltransferase
LAC1533_RS00555	4-hydroxybutyrate CoA-transferase	LSL_0237	hypothetical protein	LRC_RS00825	DegV family EDD domain-containing protein
LAC1533_RS00580	group II intron reverse transcriptase/maturase	LSL_0238	hypothetical protein	LRC_RS00830	DNA-binding response regulator
LAC1533_RS00600	transposase	LSL_0239	hypothetical protein	LRC_RS00835	sensor histidine kinase
LAC1533_RS00605	ISL3 family transposase	LSL_0240	cII-like protein, phage associated	LRC_RS00845	ABC transporter permease
LAC1533_RS00610	zinc-binding alcohol dehydrogenase family protein	LSL_0241	hypothetical protein	LRC_RS00865	hypothetical protein
LAC1533_RS00620	sensor protein LytS	LSL_0242	cI-like repressor, phage associated	LRC_RS00900	GntR family transcriptional regulator
LAC1533_RS00625	DNA-binding response regulator	LSL_0243	hypothetical protein	LRC_RS00910	linear amide C-N hydrolase
LAC1533_RS00630	murein hydrolase regulator LrgA	LSL_0244	hypothetical protein	LRC_RS00925	peptide ABC transporter substrate-binding protein
LAC1533_RS00635	antiholin	LSL_0245	hypothetical protein	LRC_RS00940	hypothetical protein
LAC1533_RS00640	2-hydroxyacid dehydrogenase	LSL_0246	hypothetical protein	LRC_RS00950	hypothetical protein
LAC1533_RS00645	hypothetical protein	LSL_0248	hypothetical protein	LRC_RS01020	transposase
LAC1533_RS00650	IS982 family transposase ISLpl4	LSL_0249	hypothetical protein	LRC_RS01030	PTS sugar transporter subunit IIC
LAC1533_RS00655	adenine deaminase	LSL_0250	Cro-like protein, phage associated	LRC_RS01055	transposase
LAC1533_RS00660	hypothetical protein	LSL_0251	phage antirepressor protein	LRC_RS01060	transposase
LAC1533_RS00670	30S ribosomal protein S14	LSL_0252	hypothetical protein	LRC_RS01095	DegV family protein
LAC1533_RS00685	serine acetyltransferase	LSL_0253	hypothetical protein	LRC_RS01100	DUF1836 domain-containing protein

LAC1533_RS00715	EAL domain-containing protein	LSL_0254	hypothetical protein	LRC_RS01110	Ktr system potassium uptake protein D
LAC1533_RS00720	hypothetical protein	LSL_0255	hypothetical protein	LRC_RS01130	hypothetical protein
LAC1533_RS00725	hypothetical protein	LSL_0256	hypothetical protein	LRC_RS01140	GntR family transcriptional regulator
LAC1533_RS00730	hypothetical protein	LSL_0257	replisome organizer, phage associated	LRC_RS01150	glycoside hydrolase family 1 protein
LAC1533_RS00735	GGDEF domain-containing protein	LSL_0258	hypothetical protein	LRC_RS01155	PTS sugar transporter subunit IIC
LAC1533_RS00740	IS256 family transposase	LSL_0259	hypothetical protein	LRC_RS01170	transposase
LAC1533_RS00760	hypothetical protein	LSL_0260	replication terminator protein, phage associated	LRC_RS01175	ROK family protein
LAC1533_RS00770	NADPH:quinone reductase	LSL_0261	hypothetical protein	LRC_RS01180	glycoside hydrolase family 1 protein
LAC1533_RS00790	hypothetical protein	LSL_0262	hypothetical protein	LRC_RS01210	hypothetical protein
LAC1533_RS00795	hypothetical protein	LSL_0263	hypothetical protein	LRC_RS01265	hypothetical protein
LAC1533_RS00800	DUF2992 domain-containing protein	LSL_0264	hypothetical protein	LRC_RS01285	DUF805 domain-containing protein
LAC1533_RS00815	IS1380 family transposase	LSL_0265	hypothetical protein	LRC_RS01305	histidine phosphatase family protein
LAC1533_RS00840	TetR/AcrR family transcriptional regulator	LSL_0266	hypothetical protein	LRC_RS01425	hypothetical protein
LAC1533_RS00890	PTS sugar transporter subunit IIC	LSL_0267	hypothetical protein	LRC_RS01445	MFS transporter
LAC1533_RS00895	DUF3284 domain-containing protein	LSL_0268	hypothetical protein	LRC_RS01450	carboxylate--amine ligase
LAC1533_RS00900	hypothetical protein	LSL_0270	hypothetical protein	LRC_RS01455	ATP-grasp domain-containing protein
LAC1533_RS00905	DUF871 domain-containing protein	LSL_0271	hypothetical protein	LRC_RS01460	hypothetical protein
LAC1533_RS00915	hypothetical protein	LSL_0272	hypothetical protein	LRC_RS01610	hypothetical protein
LAC1533_RS00920	GNAT family N-acetyltransferase	LSL_0273	hypothetical protein	LRC_RS01645	alpha/beta hydrolase
LAC1533_RS00925	GNAT family N-acetyltransferase	LSL_0274	hypothetical protein	LRC_RS01665	hypothetical protein
LAC1533_RS00930	chitosanase	LSL_0275	hypothetical protein	LRC_RS01710	ABC transporter ATP-binding protein
LAC1533_RS00940	DUF3290 domain-containing protein	LSL_0277	DNA packaging, phage associated	LRC_RS01715	ABC transporter ATP-binding protein
LAC1533_RS00950	hypothetical protein	LSL_0278	hypothetical protein	LRC_RS01745	hypothetical protein
LAC1533_RS00955	LysR family transcriptional regulator	LSL_0279	phage endonuclease	LRC_RS01755	alpha/beta hydrolase
LAC1533_RS00970	hypothetical protein	LSL_0280	phage terminase small subunit	LRC_RS01795	hypothetical protein
LAC1533_RS00975	transposase	LSL_0281	terminase large subunit	LRC_RS01905	hypothetical protein
LAC1533_RS01000	aspartate aminotransferase	LSL_0282	phage head-tail joining protein	LRC_RS01910	hypothetical protein
LAC1533_RS01010	ZIP family metal transporter	LSL_0283	portal protein	LRC_RS01915	TnpV protein
LAC1533_RS01020	histidine phosphatase family protein	LSL_0284	ATP-dependent Clp protease proteolytic subunit	LRC_RS01920	hypothetical protein
LAC1533_RS01025	N-acetyltransferase	LSL_0285	major head protein	LRC_RS01925	hypothetical protein
LAC1533_RS01030	glycosyltransferase family 8 protein	LSL_0286	DNA packaging, phage associated	LRC_RS01930	hypothetical protein
LAC1533_RS01040	hypothetical protein	LSL_0287	phage head-tail joining protein	LRC_RS01940	TIR domain-containing protein
LAC1533_RS01065	hypothetical protein	LSL_0288	phage head-tail joining protein	LRC_RS01945	hypothetical protein
LAC1533_RS01095	IS30 family transposase	LSL_0289	phage tail protein	LRC_RS01985	asparaginase
LAC1533_RS01105	SAM-dependent DNA methyltransferase	LSL_0290	phage major tail protein	LRC_RS02080	hypothetical protein
LAC1533_RS01110	restriction endonuclease	LSL_0291	hypothetical protein	LRC_RS02085	FIST domain containing protein
LAC1533_RS01115	type I restriction endonuclease	LSL_0292	hypothetical protein	LRC_RS02090	methyl-accepting chemotaxis protein
LAC1533_RS01120	integrase	LSL_0293	hypothetical protein	LRC_RS02200	hypothetical protein
LAC1533_RS01125	hypothetical protein	LSL_0294	phage tail tape mesure	LRC_RS02220	SMC family ATPase
LAC1533_RS01140	DUF3387 domain-containing protein	LSL_0295	hypothetical protein	LRC_RS02270	glutamate synthase large subunit
LAC1533_RS01145	DUF1516 domain-containing protein	LSL_0296	phage lysin	LRC_RS02275	glutamate synthase subunit beta
LAC1533_RS01150	hypothetical protein	LSL_0297	hypothetical protein	LRC_RS02280	sigma-70 family RNA polymerase sigma factor
LAC1533_RS01155	TetR/AcrR family transcriptional regulator	LSL_0298	hypothetical protein	LRC_RS02285	XRE family transcriptional regulator
LAC1533_RS01170	ATPase	LSL_0299	hypothetical protein	LRC_RS02305	hypothetical protein
LAC1533_RS01175	hypothetical protein	LSL_0300	hypothetical protein	LRC_RS02320	transposase
LAC1533_RS01180	hypothetical protein	LSL_0301	hypothetical protein	LRC_RS02325	transposase
LAC1533_RS01185	hypothetical protein	LSL_0302	hypothetical protein	LRC_RS02330	hypothetical protein
LAC1533_RS01190	NADPH-dependent oxidoreductase	LSL_0303	hypothetical protein	LRC_RS02340	hypothetical protein
LAC1533_RS01195	hypothetical protein	LSL_0304	phage lysin	LRC_RS02350	hypothetical protein
LAC1533_RS01200	AraC family transcriptional regulator	LSL_0311	mucus binding protein	LRC_RS02355	transposase
LAC1533_RS01215	50S ribosomal protein L4	LSL_0314	MerR family transcriptional regulator	LRC_RS02360	hypothetical protein
LAC1533_RS01235	aspartate aminotransferase family protein	LSL_0316	macrolide-efflux protein	LRC_RS02370	transposase
LAC1533_RS01240	hypothetical protein	LSL_0319	ribosomal-protein-serine acetyltransferase	LRC_RS02375	amino acid ABC transporter substrate-binding protein
LAC1533_RS01250	glycine betaine/L-proline ABC transporter ATP-binding protein	LSL_0322	phosphorylase Pnp/Udp family protein	LRC_RS02420	TetR/AcrR family transcriptional regulator
LAC1533_RS01255	glycine/betaine ABC transporter	LSL_0328	hypothetical protein	LRC_RS02425	shikimate dehydrogenase

LAC1533_RS01260	glycine/betaine ABC transporter	LSL_0329	ATPase	LRC_RS02430	type I 3-dehydroquinate dehydratase
LAC1533_RS01265	transposase	LSL_0330	hypothetical protein	LRC_RS02435	hypothetical protein
LAC1533_RS01270	glycosyltransferase family 1 protein	LSL_0331	hypothetical protein	LRC_RS02525	hypothetical protein
LAC1533_RS01285	IS256 family transposase	LSL_0332	hypothetical protein	LRC_RS02535	hypothetical protein
LAC1533_RS01290	magnesium transporter CorA family protein	LSL_0333	hypothetical protein	LRC_RS02565	hypothetical protein
LAC1533_RS01295	Cof-type HAD-IIB family hydrolase	LSL_0334	hypothetical protein	LRC_RS02620	mercury(II) reductase
LAC1533_RS01310	transcriptional regulator	LSL_0335	hypothetical protein	LRC_RS02640	AraC family transcriptional regulator
LAC1533_RS01320	type 1 glutamine amidotransferase	LSL_0336	hypothetical protein	LRC_RS02650	transketolase
LAC1533_RS01325	TetR/AcrR family transcriptional regulator	LSL_0344	hypothetical protein	LRC_RS02655	3-deoxy-7-phosphoheptulonate synthase
LAC1533_RS01330	hypothetical protein	LSL_0350	hypothetical protein	LRC_RS02660	3-dehydroquinate synthase
LAC1533_RS01335	ECF transporter S component	LSL_0351	hypothetical protein	LRC_RS02670	YbaK/EbsC family protein
LAC1533_RS01345	IS30 family transposase	LSL_0352	hypothetical protein	LRC_RS02700	IS256 family transposase
LAC1533_RS01350	IS256 family transposase	LSL_0359	hypothetical protein	LRC_RS02745	hypothetical protein
LAC1533_RS01360	ArsR family transcriptional regulator	LSL_0361	hypothetical protein	LRC_RS02750	Crp/Fnr family transcriptional regulator
LAC1533_RS01365	IS30 family transposase	LSL_0365	hypothetical protein	LRC_RS02755	ClbS/DfsB family four-helix bundle protein
LAC1533_RS01370	DUF1648 domain-containing protein	LSL_0367	sigma-70 factor family protein	LRC_RS02770	integrase
LAC1533_RS01380	PAP2 family protein	LSL_0375	hypothetical protein	LRC_RS02775	integrase
LAC1533_RS01390	hypothetical protein	LSL_0376	beta-galactosidase	LRC_RS02780	hypothetical protein
LAC1533_RS01395	hypothetical protein	LSL_0408	hypothetical protein	LRC_RS02785	PcfB family protein
LAC1533_RS01410	phosphatidylglycerophosphatase A	LSL_0409	hypothetical protein	LRC_RS02790	hypothetical protein
LAC1533_RS01415	hydrolase	LSL_0410	hypothetical protein	LRC_RS02805	hypothetical protein
LAC1533_RS01430	resolvase	LSL_0416	hypothetical protein	LRC_RS02810	hypothetical protein
LAC1533_RS01450	sugar O-acetyltransferase	LSL_0418	hypothetical protein	LRC_RS02825	hypothetical protein
LAC1533_RS01470	hypothetical protein	LSL_0427	hypothetical protein	LRC_RS02830	hypothetical protein
LAC1533_RS01475	hypothetical protein	LSL_0428	hypothetical protein	LRC_RS02835	hypothetical protein
LAC1533_RS01480	ATPase	LSL_0429	hypothetical protein	LRC_RS02855	DUF3791 domain-containing protein
LAC1533_RS01485	DUF3862 domain-containing protein	LSL_0430	hypothetical protein	LRC_RS02860	DUF3990 domain-containing protein
LAC1533_RS01495	acyl-CoA thioesterase	LSL_0431	hypothetical protein	LRC_RS02865	hypothetical protein
LAC1533_RS01540	hypothetical protein	LSL_0437	hypothetical protein	LRC_RS02870	RNA helicase
LAC1533_RS01545	LysR family transcriptional regulator	LSL_0471	Crp family transcriptional regulator	LRC_RS02875	quinolinate synthase NadA
LAC1533_RS01550	flavocytochrome c	LSL_0476	hypothetical protein	LRC_RS02880	L-aspartate oxidase
LAC1533_RS01555	dipeptide epimerase	LSL_0482	hypothetical protein	LRC_RS02885	nicotinate-nucleotide diphosphorylase (carboxylating)
LAC1533_RS01560	3-oxoacyl-ACP reductase	LSL_0492	chromosome replication initiation / membrane attachment protein	LRC_RS02890	transcription repressor NadR
LAC1533_RS01580	glycine/betaine ABC transporter	LSL_0519	hypothetical protein	LRC_RS02900	hypothetical protein
LAC1533_RS01585	hypothetical protein	LSL_0520	hypothetical protein	LRC_RS02905	hypothetical protein
LAC1533_RS01590	NUDIX domain-containing protein	LSL_0521	hypothetical protein	LRC_RS02910	hypothetical protein
LAC1533_RS01600	phosphoglycolate phosphatase	LSL_0545	hypothetical protein	LRC_RS02915	toxin/antitoxin system Toxin component
LAC1533_RS01610	NADP oxidoreductase	LSL_0546	IS3 family transposase	LRC_RS02920	addiction module antidote protein, HigA family
LAC1533_RS01615	LLM class flavin-dependent oxidoreductase	LSL_0547	hypothetical protein	LRC_RS02925	hypothetical protein
LAC1533_RS01620	IS30 family transposase	LSL_0559	O6-methylguanine-DNA methyltransferase	LRC_RS02930	phosphatase PAP2 family protein
LAC1533_RS01640	GNAT family N-acetyltransferase	LSL_0585	IS3 family transposase	LRC_RS02940	XRE family transcriptional regulator
LAC1533_RS01645	hypothetical protein	LSL_0586	IS3 family transposase	LRC_RS02945	hypothetical protein
LAC1533_RS01650	hypothetical protein	LSL_0641	hypothetical protein	LRC_RS02950	YkgJ family cysteine cluster protein
LAC1533_RS01665	hypothetical protein	LSL_0648	hypothetical protein	LRC_RS02955	cardiolipin synthetase
LAC1533_RS01680	hypothetical protein	LSL_0650	lactate/malate dehydrogenase	LRC_RS02965	hypothetical protein
LAC1533_RS01685	DNA helicase	LSL_0672	hypothetical protein	LRC_RS02970	MFS transporter
LAC1533_RS01690	hypothetical protein	LSL_0695	glycosyltransferase	LRC_RS02980	N-acetyltransferase
LAC1533_RS01695	DNA-binding protein	LSL_0697	hypothetical protein	LRC_RS02990	hypothetical protein
LAC1533_RS01700	XRE family transcriptional regulator	LSL_0698	hypothetical protein	LRC_RS02995	homoserine O-succinyltransferase
LAC1533_RS01705	XRE family transcriptional regulator	LSL_0702	hypothetical protein	LRC_RS03000	hypothetical protein
LAC1533_RS01710	ImmA/IrrE family metallo-endopeptidase	LSL_0711	MerR family transcriptional regulator	LRC_RS03015	hypothetical protein
LAC1533_RS01720	DUF5067 domain-containing protein	LSL_0713	hypothetical protein	LRC_RS03025	Zn-dependent alcohol dehydrogenase
LAC1533_RS01725	hypothetical protein	LSL_0722	PTS system galactitol-specific transporter subunit IIC	LRC_RS03030	lipase
LAC1533_RS01730	IS30 family transposase	LSL_0723	TetR family transcriptional regulator	LRC_RS03040	HNH endonuclease

LAC1533_RS01735	SHOCT domain-containing protein	LSL_0724	ABC transporter ATP-binding protein	LRC_RS03055	YccF domain-containing protein
LAC1533_RS01740	site-specific integrase	LSL_0725	ABC transporter permease	LRC_RS03060	MFS transporter
LAC1533_RS01745	aldehyde dehydrogenase	LSL_0730	hypothetical protein	LRC_RS03065	ABC transporter ATP-binding protein
LAC1533_RS01750	MarR family transcriptional regulator	LSL_0731	hypothetical protein	LRC_RS03190	aconitate hydratase AcnA
LAC1533_RS01765	hypothetical protein	LSL_0732	IS200/IS605 family transposase	LRC_RS03195	methylcitrate synthase
LAC1533_RS01770	IS1380 family transposase	LSL_0733	IS200/IS605 family transposase	LRC_RS03200	NADP-dependent isocitrate dehydrogenase
LAC1533_RS01780	hypothetical protein	LSL_0734	hypothetical protein	LRC_RS03250	hypothetical protein
LAC1533_RS01785	IS1380 family transposase	LSL_0735	hypothetical protein	LRC_RS03260	hypothetical protein
LAC1533_RS01790	CsbD family protein	LSL_0736	hypothetical protein	LRC_RS03330	PspC domain-containing protein
LAC1533_RS01800	OsmC family peroxiredoxin	LSL_0737	hypothetical protein	LRC_RS03395	hypothetical protein
LAC1533_RS01810	IS1380 family transposase	LSL_0738	hypothetical protein	LRC_RS03405	ABC transporter ATP-binding protein
LAC1533_RS01820	fructosamine kinase	LSL_0739	hypothetical protein	LRC_RS03470	cell surface protein
LAC1533_RS01825	AI-2E family transporter	LSL_0741	phage cI like repressor	LRC_RS03480	N-acetyltransferase
LAC1533_RS01830	SDR family NAD(P)-dependent oxidoreductase	LSL_0742	Cro/CI family phage transcriptional regulator	LRC_RS03520	PHP domain-containing protein
LAC1533_RS01840	Trk family potassium uptake protein	LSL_0743	hypothetical protein	LRC_RS03525	hypothetical protein
LAC1533_RS01845	DeoR/GlpR transcriptional regulator	LSL_0745	phage antirepressor	LRC_RS03530	ATP phosphoribosyltransferase regulatory subunit
LAC1533_RS01850	DUF159 family protein	LSL_0746	phage antirepressor	LRC_RS03535	ATP phosphoribosyltransferase
LAC1533_RS01870	GntR family transcriptional regulator	LSL_0747	hypothetical protein	LRC_RS03540	histidinol dehydrogenase
LAC1533_RS01875	ABC transporter ATP-binding protein	LSL_0749	hypothetical protein	LRC_RS03545	imidazoleglycerol-phosphate dehydratase HisB
LAC1533_RS01880	hypothetical protein	LSL_0750	hypothetical protein	LRC_RS03550	imidazole glycerol phosphate synthase subunit HisH
LAC1533_RS01905	hypothetical protein	LSL_0751	hypothetical protein	LRC_RS03555	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4- carboxamide isomerase
LAC1533_RS01910	LemA family protein	LSL_0752	phage helicase	LRC_RS03560	imidazole glycerol phosphate synthase subunit HisF
LAC1533_RS01915	TPM domain-containing protein	LSL_0753	hypothetical protein	LRC_RS03565	phosphoribosyl-AMP cyclohydrolase
LAC1533_RS01920	demethylmenaquinone methyltransferase	LSL_0754	hypothetical protein	LRC_RS03570	phosphoribosyl-ATP diphosphatase
LAC1533_RS01925	antibiotic biosynthesis monooxygenase	LSL_0755	hypothetical protein	LRC_RS03575	histidinol-phosphate transaminase
LAC1533_RS01930	hypothetical protein	LSL_0756	phage NTP-binding protein	LRC_RS03580	N-acetyltransferase
LAC1533_RS01935	CPBP family intramembrane metalloprotease	LSL_0757	hypothetical protein	LRC_RS03625	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS01945	DUF4811 domain-containing protein	LSL_0758	phage DNA polymerase	LRC_RS03690	hypothetical protein
LAC1533_RS01955	DNA polymerase III subunit alpha	LSL_0759	phage primase	LRC_RS03860	DUF1828 domain-containing protein
LAC1533_RS01960	LD-carboxypeptidase	LSL_0760	phage DNA primase	LRC_RS03865	hypothetical protein
LAC1533_RS01970	D-aminopeptidase	LSL_0761	hypothetical protein	LRC_RS03870	ImmA/IrrE family metallo-endopeptidase
LAC1533_RS01985	sulfate ABC transporter ATP-binding protein	LSL_0762	hypothetical protein	LRC_RS03875	XRE family transcriptional regulator
LAC1533_RS01990	APC family permease	LSL_0763	hypothetical protein	LRC_RS03885	antirepressor
LAC1533_RS01995	IS1380 family transposase	LSL_0764	hypothetical protein	LRC_RS03890	hypothetical protein
LAC1533_RS02000	hypothetical protein	LSL_0765	phage integrase	LRC_RS03910	hypothetical protein
LAC1533_RS02015	hypothetical protein	LSL_0766	hypothetical protein	LRC_RS03915	hypothetical protein
LAC1533_RS02020	L-lactate oxidase	LSL_0767	hypothetical protein	LRC_RS03920	hypothetical protein
LAC1533_RS02025	formate-nitrite transporter	LSL_0768	hypothetical protein	LRC_RS03930	helix-turn-helix domain-containing protein
LAC1533_RS02030	hypothetical protein	LSL_0769	hypothetical protein	LRC_RS03940	DUF1064 domain-containing protein
LAC1533_RS02035	protein-tyrosine-phosphatase	LSL_0770	hypothetical protein	LRC_RS03950	hypothetical protein
LAC1533_RS02040	NAD(P)-dependent alcohol dehydrogenase	LSL_0771	hypothetical protein	LRC_RS03955	transposase
LAC1533_RS02045	hypothetical protein	LSL_0772	hypothetical protein	LRC_RS03965	HNH endonuclease
LAC1533_RS02050	hypothetical protein	LSL_0773	hypothetical protein	LRC_RS03970	hypothetical protein
LAC1533_RS02055	PRD domain-containing protein	LSL_0774	hypothetical protein	LRC_RS03980	hypothetical protein
LAC1533_RS02060	PTS fructose IIA component	LSL_0775	hypothetical protein	LRC_RS03985	terminase
LAC1533_RS02065	PTS mannose/fructose/sorbose transporter subunit IIB	LSL_0776	hypothetical protein	LRC_RS03990	DUF4355 domain-containing protein
LAC1533_RS02070	PTS sugar transporter subunit IIC	LSL_0777	hypothetical protein	LRC_RS03995	phage major capsid protein
LAC1533_RS02105	hypothetical protein	LSL_0778	hypothetical protein	LRC_RS04000	hypothetical protein
LAC1533_RS02110	hypothetical protein	LSL_0780	hypothetical protein	LRC_RS04005	hypothetical protein
LAC1533_RS02115	hypothetical protein	LSL_0781	phage endonuclease	LRC_RS04010	hypothetical protein
LAC1533_RS02120	Arc family DNA-binding protein	LSL_0782	phage terminase small subunit	LRC_RS04015	hypothetical protein
LAC1533_RS02125	SPFH domain-containing protein	LSL_0783	terminase large subunit	LRC_RS04020	hypothetical protein
LAC1533_RS02130	hypothetical protein	LSL_0784	portal protein	LRC_RS04025	hypothetical protein
LAC1533_RS02135	hypothetical protein	LSL_0785	ATP-dependent Clp protease proteolytic subunit	LRC_RS04030	hypothetical protein

LAC1533_RS02140	cation-translocating P-type ATPase	LSL_0786	phage prohead protease	LRC_RS04035	hypothetical protein
LAC1533_RS02150	N-acetyltransferase	LSL_0787	phage DNA packaging	LRC_RS04040	phage tail protein
LAC1533_RS02155	hypothetical protein	LSL_0788	phage head-tail joining protein	LRC_RS04045	hypothetical protein
LAC1533_RS02180	transposase	LSL_0789	phage head-tail joining protein	LRC_RS04050	hypothetical protein
LAC1533_RS02195	carbohydrate ABC transporter substrate-binding protein	LSL_0790	phage head-tail joining protein	LRC_RS04055	hypothetical protein
LAC1533_RS02200	sugar ABC transporter permease	LSL_0791	phage major tail protein	LRC_RS04065	LysM peptidoglycan-binding domain-containing protein
LAC1533_RS02205	carbohydrate ABC transporter permease	LSL_0792	hypothetical protein	LRC_RS04075	hypothetical protein
LAC1533_RS02210	hypothetical protein	LSL_0793	hypothetical protein	LRC_RS04090	hypothetical protein
LAC1533_RS02255	NAD(P)H-hydrate epimerase	LSL_0794	phage tail tape mesure protein	LRC_RS04095	hypothetical protein
LAC1533_RS02265	cation transporter	LSL_0795	hypothetical protein	LRC_RS04100	hypothetical protein
LAC1533_RS02270	hypothetical protein	LSL_0796	hypothetical protein	LRC_RS04105	hypothetical protein
LAC1533_RS02275	hypothetical protein	LSL_0797	phage lysin	LRC_RS04115	hypothetical protein
LAC1533_RS02280	alpha/beta hydrolase	LSL_0798	hypothetical protein	LRC_RS04130	iron transporter FeoA
LAC1533_RS02305	hypothetical protein	LSL_0799	phage minor head protein	LRC_RS04135	ferrous iron transport protein B
LAC1533_RS02315	MFS transporter	LSL_0800	hypothetical protein	LRC_RS04245	hypothetical protein
LAC1533_RS02320	copper-translocating P-type ATPase	LSL_0801	hypothetical protein	LRC_RS04300	hypothetical protein
LAC1533_RS02325	glutamate formiminotransferase	LSL_0803	hypothetical protein	LRC_RS04305	anthranilate synthase component I family protein
LAC1533_RS02330	bifunctional 5,10-methylenetetrahydrofolate dehydrogenase/5,10-methenyltetrahydrofolate cyclohydrolase	LSL_0804	hypothetical protein	LRC_RS04310	type 1 glutamine amidotransferase
LAC1533_RS02335	zinc-binding alcohol dehydrogenase family protein	LSL_0805	phage lysin	LRC_RS04315	anthranilate phosphoribosyltransferase
LAC1533_RS02355	replication-associated recombination protein A	LSL_0806	hypothetical protein	LRC_RS04320	indole-3-glycerol phosphate synthase TrpC
LAC1533_RS02380	hypothetical protein	LSL_0807	hypothetical protein	LRC_RS04325	phosphoribosylanthranilate isomerase
LAC1533_RS02385	carbonic anhydrase	LSL_0808	hypothetical protein	LRC_RS04330	tryptophan synthase subunit beta
LAC1533_RS02445	helix-turn-helix domain-containing protein	LSL_0809	hypothetical protein	LRC_RS04335	tryptophan synthase subunit alpha
LAC1533_RS02455	LysM peptidoglycan-binding domain-containing protein	LSL_0837	hypothetical protein	LRC_RS04340	PAP2 superfamily protein
LAC1533_RS02460	LysM peptidoglycan-binding domain-containing protein	LSL_0843	hypothetical protein	LRC_RS04350	CDP-diacylglycerol--serine O-phosphatidyltransferase
LAC1533_RS02510	lipase/esterase	LSL_0844	hypothetical protein	LRC_RS04365	hypothetical protein
LAC1533_RS02550	Cof-type HAD-IIB family hydrolase	LSL_0845	hypothetical protein	LRC_RS04370	transposase
LAC1533_RS02555	gluconate transporter	LSL_0849	hypothetical protein	LRC_RS04375	transposase
LAC1533_RS02560	excinuclease ABC subunit UvrA	LSL_0850	drug/metabolite exporter family protein	LRC_RS04390	GntR family transcriptional regulator
LAC1533_RS02565	serine hydrolase	LSL_0854	magnesium/cobalt transporter CorA	LRC_RS04420	hypothetical protein
LAC1533_RS02580	MFS transporter	LSL_0868	hypothetical protein	LRC_RS04445	branched-chain amino acid ABC transporter substrate-binding protein
LAC1533_RS02595	phosphate/phosphite/phosphonate ABC transporter substrate-binding protein	LSL_0869	hypothetical protein	LRC_RS04455	transposase
LAC1533_RS02600	aldo/keto reductase	LSL_0879	phosphoesterase	LRC_RS04540	helix-turn-helix domain-containing protein
LAC1533_RS02605	endonuclease III	LSL_0880	drug/metabolite exporter family protein	LRC_RS04545	transposase
LAC1533_RS02630	adenosine deaminase	LSL_0883	hypothetical protein	LRC_RS04570	hypothetical protein
LAC1533_RS02635	hypothetical protein	LSL_0884	hypothetical protein	LRC_RS04575	hypothetical protein
LAC1533_RS02660	class I SAM-dependent methyltransferase	LSL_0888	arsenate reductase	LRC_RS04590	hypothetical protein
LAC1533_RS02670	MurR/RpiR family transcriptional regulator	LSL_0903	hypothetical protein	LRC_RS04645	pyridoxal 5-phosphate synthase glutaminase subunit PdxT
LAC1533_RS02675	N-acetylmuramic acid 6-phosphate etherase	LSL_0905	6-pyruvoyl-tetrahydropterin synthase	LRC_RS04650	pyridoxal 5-phosphate synthase lyase subunit PdxS
LAC1533_RS02680	PTS beta-glucoside transporter subunit EIIBCA	LSL_0906	hypothetical protein	LRC_RS04655	PLP-dependent aminotransferase family protein
LAC1533_RS02710	methylated-DNA--[protein]-cysteine S-methyltransferase	LSL_0907	hypothetical protein	LRC_RS04695	hypothetical protein
LAC1533_RS02725	hypothetical protein	LSL_0908	hypothetical protein	LRC_RS04715	hypothetical protein
LAC1533_RS02735	hypothetical protein	LSL_0914	PTS system cellobiose transporter subunit IIC	LRC_RS04725	site-specific DNA-methyltransferase
LAC1533_RS02740	hypothetical protein	LSL_0915	type I restriction-modification system specificity subunit	LRC_RS04730	type III restriction-modification system endonuclease
LAC1533_RS02745	threonine/serine exporter	LSL_0916	type I restriction-modification system specificity subunit	LRC_RS04735	hypothetical protein
LAC1533_RS02750	threonine/serine exporter	LSL_0918	type I restriction-modification system specificity subunit	LRC_RS04740	helicase
LAC1533_RS02760	glutamyl-tRNA amidotransferase subunit A	LSL_0920	type I restriction-modification system restriction subunit	LRC_RS04745	hypothetical protein
LAC1533_RS02765	nucleoside-diphosphate kinase	LSL_0921	hypothetical protein	LRC_RS04755	transposase

LAC1533_RS02770	IS982 family transposase	LSL_0922	phosphohydrolase, MutT/nudix family protein	LRC_RS04765	hypothetical protein
LAC1533_RS02795	IS30 family transposase	LSL_0923	phosphatidylglycerophosphatase B	LRC_RS04775	hypothetical protein
LAC1533_RS02800	nitroreductase	LSL_0925	hypothetical protein	LRC_RS04780	hypothetical protein
LAC1533_RS02810	glyoxalase	LSL_0926	zwittermicin A resistance protein zmaR	LRC_RS04785	DUF4065 domain-containing protein
LAC1533_RS02815	hypothetical protein	LSL_0927	hypothetical protein	LRC_RS04790	hypothetical protein
LAC1533_RS02825	hypothetical protein	LSL_0929	adenine deaminase	LRC_RS04795	hypothetical protein
LAC1533_RS02870	hypothetical protein	LSL_0942	hypothetical protein	LRC_RS04820	hypothetical protein
LAC1533_RS02890	hypothetical protein	LSL_0943	hypothetical protein	LRC_RS04915	hypothetical protein
LAC1533_RS02900	Crp/Fnr family transcriptional regulator	LSL_0944	hypothetical protein	LRC_RS04995	hypothetical protein
LAC1533_RS02905	copper chaperone	LSL_0945	hypothetical protein	LRC_RS05000	DUF5052 domain-containing protein
LAC1533_RS02910	DNA starvation/stationary phase protection protein	LSL_0951	hypothetical protein	LRC_RS05045	8-oxo-dGTP diphosphatase
LAC1533_RS02915	metal-sensitive transcriptional regulator	LSL_0952	hypothetical protein	LRC_RS05050	hypothetical protein
LAC1533_RS02930	transposase	LSL_0953	hypothetical protein	LRC_RS05060	hypothetical protein
LAC1533_RS02940	hypothetical protein	LSL_0957	hypothetical protein	LRC_RS05095	hypothetical protein
LAC1533_RS02945	hypothetical protein	LSL_0958	hypothetical protein	LRC_RS05120	MFS transporter
LAC1533_RS02950	IS1380 family transposase	LSL_0959	hypothetical protein	LRC_RS05155	signal peptidase I
LAC1533_RS02960	hypothetical protein	LSL_0962	hypothetical protein	LRC_RS05180	hypothetical protein
LAC1533_RS02975	IS30 family transposase	LSL_0963	hypothetical protein	LRC_RS05210	MarR family transcriptional regulator
LAC1533_RS02985	tRNA-dihydrouridine synthase	LSL_0966	acetyltransferase	LRC_RS05215	multidrug transporter MatE
LAC1533_RS02995	succinyl-diaminopimelate desuccinylase	LSL_0967	hypothetical protein	LRC_RS05235	XRE family transcriptional regulator
LAC1533_RS03010	DUF4767 domain-containing protein	LSL_0968	hypothetical protein	LRC_RS05240	Crp/Fnr family transcriptional regulator
LAC1533_RS03015	hypothetical protein	LSL_0969	hypothetical protein	LRC_RS05255	hypothetical protein
LAC1533_RS03020	hypothetical protein	LSL_0970	quinone oxidoreductase	LRC_RS05260	hypothetical protein
LAC1533_RS03030	DUF3114 domain-containing protein	LSL_0975	hypothetical protein	LRC_RS05265	CRISPR-associated endonuclease Cas2
LAC1533_RS03035	hypothetical protein	LSL_0977	glycosyltransferase	LRC_RS05270	type II CRISPR-associated endonuclease Cas1
LAC1533_RS03040	OsmC family peroxiredoxin	LSL_0978	glycosyltransferase	LRC_RS05275	type III-A CRISPR-associated RAMP protein Csm5
LAC1533_RS03055	hypothetical protein	LSL_0980	UDP-glucuronate 4-epimerase	LRC_RS05280	type III-A CRISPR-associated RAMP protein Csm4
LAC1533_RS03060	NERD domain-containing protein	LSL_0981	oligosaccharide translocase	LRC_RS05285	type III-A CRISPR-associated RAMP protein Csm3
LAC1533_RS03065	RNA methylase	LSL_0982	glycosyltransferase	LRC_RS05290	type III-A CRISPR-associated protein Csm2
LAC1533_RS03070	YfcC family protein	LSL_0983	glycosyltransferase	LRC_RS05295	type III-A CRISPR-associated protein Cas10/Csm1
LAC1533_RS03075	acetylornithine deacetylase	LSL_0984	glycosyltransferase	LRC_RS05300	CRISPR system precrRNA processing endoribonuclease RAMP protein Cas6
LAC1533_RS03085	heat-shock protein HtpX	LSL_0985	hypothetical protein	LRC_RS05360	serine/threonine protein kinase
LAC1533_RS03105	DUF871 domain-containing protein	LSL_0986	glycosyltransferase	LRC_RS05380	hypothetical protein
LAC1533_RS03120	TetR/AcrR family transcriptional regulator	LSL_0987	glycosyltransferase	LRC_RS05390	CRISPR-associated endonuclease Cas2
LAC1533_RS03130	ABC transporter ATP-binding protein	LSL_0988	glycosyltransferase	LRC_RS05395	type I-B CRISPR-associated endonuclease Cas1
LAC1533_RS03135	hypothetical protein	LSL_0989	glycosyltransferase	LRC_RS05400	CRISPR-associated protein Cas4
LAC1533_RS03140	glycosyltransferase family 8 protein	LSL_0990	glycosyltransferase	LRC_RS05405	CRISPR-associated helicase/endonuclease Cas3
LAC1533_RS03145	deoxyribose-phosphate aldolase	LSL_0991	glycosyltransferase	LRC_RS05410	CRISPR-associated protein Cas5
LAC1533_RS03155	hypothetical protein	LSL_0992	acetyltransferase	LRC_RS05415	type I-B CRISPR-associated protein Cas7/Cst2/DevR
LAC1533_RS03160	IS982 family transposase	LSL_0994	aminotransferase	LRC_RS05420	type I-B CRISPR-associated protein Cas8b1/Cst1
LAC1533_RS03165	IS982 family transposase	LSL_0997	chain length regulator	LRC_RS05425	CRISPR-associated endoribonuclease Cas6
LAC1533_RS03170	hypothetical protein	LSL_1003	acetyltransferase	LRC_RS05430	DUF3862 domain-containing protein
LAC1533_RS03175	galactose mutarotase	LSL_1007	hypothetical protein	LRC_RS05435	HNH endonuclease
LAC1533_RS03180	hypothetical protein	LSL_1008	AraC family transcriptional regulator	LRC_RS05445	transposase
LAC1533_RS03190	PEP phosphonomutase	LSL_1009	hypothetical protein	LRC_RS05450	hypothetical protein
LAC1533_RS03195	hypothetical protein	LSL_1011	hypothetical protein	LRC_RS05485	transposase
LAC1533_RS03200	NADH-dependent alcohol dehydrogenase	LSL_1012	acetyltransferase	LRC_RS05500	ATP-dependent helicase
LAC1533_RS03205	HAD family phosphatase	LSL_1016	hypothetical protein	LRC_RS05525	hypothetical protein
LAC1533_RS03220	energy-coupling factor transporter transmembrane protein EcfT	LSL_1017	hypothetical protein	LRC_RS05540	hypothetical protein
LAC1533_RS03230	tRNA epoxyqueuosine(34) reductase QueG	LSL_1018	cellulose synthase catalytic subunit	LRC_RS05590	hypothetical protein
LAC1533_RS03235	DUF4430 domain-containing protein	LSL_1019	N-acetylglucosaminyltransferase	LRC_RS05700	chromosome replication initiation / membrane attachment protein

LAC1533_RS03245	DUF1440 domain-containing protein	LSL_1020	hypothetical protein	LRC_RS05725	polysaccharide deacetylase
LAC1533_RS03250	MFS transporter	LSL_1021	hypothetical protein	LRC_RS05740	cupin
LAC1533_RS03260	KR domain-containing protein	LSL_1022	hypothetical protein	LRC_RS05765	hypothetical protein
LAC1533_RS03265	NAD(P)/FAD-dependent oxidoreductase	LSL_1023	hypothetical protein	LRC_RS05780	ABC transporter permease
LAC1533_RS03275	maturase	LSL_1024	response regulator	LRC_RS05795	hypothetical protein
LAC1533_RS03285	hypothetical protein	LSL_1033	asparagine synthetase AsnA	LRC_RS05805	hypothetical protein
LAC1533_RS03335	D-2-hydroxyacid dehydrogenase	LSL_1034	peptidoglycan binding protein	LRC_RS05810	hypothetical protein
LAC1533_RS03350	hypothetical protein	LSL_1035	rhodanese-related sulfurtransferases	LRC_RS05845	methyl-accepting chemotaxis protein
LAC1533_RS03375	group II intron reverse transcriptase/maturase	LSL_1038	hypothetical protein	LRC_RS05960	ROK family protein
LAC1533_RS03380	CBS domain-containing protein	LSL_1039	hypothetical protein	LRC_RS05990	TrkA family potassium uptake protein
LAC1533_RS03385	ABC transporter permease	LSL_1040	ADP-ribosylglycohydrolase	LRC_RS05995	potassium transporter TrkH
LAC1533_RS03390	osmoprotectant ABC transporter substrate-binding protein	LSL_1054	cell division protein ftsL	LRC_RS06000	transposase
LAC1533_RS03395	ABC transporter permease	LSL_1057	hypothetical protein	LRC_RS06005	transposase
LAC1533_RS03410	IS256 family transposase	LSL_1085	surface protein	LRC_RS06070	hypothetical protein
LAC1533_RS03445	PAP2 family protein	LSL_1087	hypothetical protein	LRC_RS06085	glycosyl transferase
LAC1533_RS03450	hypothetical protein	LSL_1094	hypothetical protein	LRC_RS06150	ion transporter
LAC1533_RS03490	N-acetyltransferase	LSL_1095	hypothetical protein	LRC_RS06190	hypothetical protein
LAC1533_RS03545	sigma-70 family RNA polymerase sigma factor	LSL_1100	hypothetical protein	LRC_RS06225	hypothetical protein
LAC1533_RS03580	hypothetical protein	LSL_1115	hypothetical protein	LRC_RS06510	hypothetical protein
LAC1533_RS03635	XRE family transcriptional regulator	LSL_1116	iron-sulfur cluster-binding protein	LRC_RS06580	hypothetical protein
LAC1533_RS03700	group II intron reverse transcriptase/maturase	LSL_1117	hypothetical protein	LRC_RS06620	hypothetical protein
LAC1533_RS03745	dihydrofolate reductase	LSL_1119	hypothetical protein	LRC_RS06675	hypothetical protein
LAC1533_RS03770	transposase	LSL_1121	hypothetical protein	LRC_RS06745	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase
LAC1533_RS03780	maturase	LSL_1141	copper homeostasis protein cutC	LRC_RS06755	cell division protein FtsL
LAC1533_RS03785	IS5-like element ISLpl3 family transposase	LSL_1159	multidrug resistance protein	LRC_RS06770	DUF3397 domain-containing protein
LAC1533_RS03805	hypothetical protein	LSL_1172	oxidoreductase	LRC_RS06900	hypothetical protein
LAC1533_RS04035	IS30 family transposase	LSL_1180	stress-responsive transcriptional regulator PspC	LRC_RS06925	glycerophosphodiester phosphodiesterase
LAC1533_RS04055	N-acetyltransferase	LSL_1187	major facilitator superfamily transporter	LRC_RS06935	hypothetical protein
LAC1533_RS04165	PspC domain-containing protein	LSL_1189	phage integrase	LRC_RS06940	RNA degradosome polyphosphate kinase
LAC1533_RS04190	IS256 family transposase	LSL_1190	hypothetical protein	LRC_RS07170	acylphosphatase
LAC1533_RS04280	group II intron reverse transcriptase/maturase	LSL_1191	Cro/CI family phage transcriptional regulator	LRC_RS07175	hypothetical protein
LAC1533_RS04310	group II intron reverse transcriptase/maturase	LSL_1192	phage repressor proteins	LRC_RS07415	hypothetical protein
LAC1533_RS04375	hypothetical protein	LSL_1193	phage immunity repressor	LRC_RS07420	TIGR00730 family Rossman fold protein
LAC1533_RS04430	IS1182 family transposase	LSL_1194	hypothetical protein	LRC_RS07425	hypothetical protein
LAC1533_RS04460	hypothetical protein	LSL_1195	hypothetical protein	LRC_RS07440	hypothetical protein
LAC1533_RS04465	hypothetical protein	LSL_1196	hypothetical protein	LRC_RS07445	hypothetical protein
LAC1533_RS04485	transposase	LSL_1197	hypothetical protein	LRC_RS07635	MFS transporter
LAC1533_RS04515	hypothetical protein	LSL_1198	hypothetical protein	LRC_RS07660	asparagine synthase B
LAC1533_RS04550	prepilin-type N-terminal cleavage/methylation domain-containing protein	LSL_1199	hypothetical protein	LRC_RS07675	hypothetical protein
LAC1533_RS04555	hypothetical protein	LSL_1200	hypothetical protein	LRC_RS07680	hypothetical protein
LAC1533_RS04560	type II secretion system protein	LSL_1201	hypothetical protein	LRC_RS07685	hypothetical protein
LAC1533_RS04565	hypothetical protein	LSL_1202	DNA primase	LRC_RS07690	transposase
LAC1533_RS04580	multifunctional 2,3-cyclic-nucleotide 2-phosphodiesterase/5-nucleotidase/3-nucleotidase	LSL_1203	hypothetical protein	LRC_RS07695	IS200/IS605 family transposase
LAC1533_RS04760	hypothetical protein	LSL_1204	hypothetical protein	LRC_RS07700	type II secretion system protein
LAC1533_RS04765	type I restriction-modification system subunit M	LSL_1205	hypothetical protein	LRC_RS07750	hypothetical protein
LAC1533_RS04770	restriction endonuclease subunit S	LSL_1217	ribosomal-protein-S18-alanine acetyltransferase	LRC_RS07790	gfo/Idh/MocA family oxidoreductase
LAC1533_RS04775	type I restriction endonuclease subunit R	LSL_1254	bacteriocin immunity protein	LRC_RS07795	CPBP family intramembrane metalloprotease
LAC1533_RS04790	restriction endonuclease	LSL_1267	hypothetical protein	LRC_RS07805	glucose transporter GlcU

LAC1533_RS04805	IS256 family transposase	LSL_1273	ornithine cyclodeaminase	LRC_RS07825	hypothetical protein
LAC1533_RS04815	dienelactone hydrolase	LSL_1274	hypothetical protein	LRC_RS07830	hypothetical protein
LAC1533_RS04830	hypothetical protein	LSL_1275	transcriptional regulator	LRC_RS07850	transposase
LAC1533_RS04845	group II intron reverse transcriptase/maturase	LSL_1281	aldose 1-epimerase	LRC_RS07855	transposase
LAC1533_RS04910	Crp/Fnr family transcriptional regulator	LSL_1282	sugar transporter	LRC_RS07860	universal stress protein
LAC1533_RS04940	hypothetical protein	LSL_1284	Kup system potassium uptake protein	LRC_RS07895	hypothetical protein
LAC1533_RS05010	chromosome replication initiation / membrane attachment protein	LSL_1290	glycogen phosphorylase	LRC_RS07900	multidrug ABC transporter ATP-binding protein
LAC1533_RS05100	hypothetical protein	LSL_1293	glucose-1-phosphate adenylyltransferase	LRC_RS07905	hypothetical protein
LAC1533_RS05125	hypothetical protein	LSL_1296	hypothetical protein	LRC_RS07910	hypothetical protein
LAC1533_RS05160	hypothetical protein	LSL_1299	acetyltransferase	LRC_RS07915	hypothetical protein
LAC1533_RS05175	hypothetical protein	LSL_1329	pyridine nucleotide-disulfide oxidoreductase family protein	LRC_RS07920	hypothetical protein
LAC1533_RS05190	group II intron reverse transcriptase/maturase	LSL_1334	acetyltransferase	LRC_RS07925	hypothetical protein
LAC1533_RS05235	hypothetical protein	LSL_1335	mucus binding protein	LRC_RS08000	hypothetical protein
LAC1533_RS05480	nucleoside deoxyribosyltransferase	LSL_1336	acetyltransferase	LRC_RS08055	nitroreductase
LAC1533_RS05485	N-acetyltransferase	LSL_1337	hypothetical protein	LRC_RS08085	hypothetical protein
LAC1533_RS05490	alpha/beta hydrolase	LSL_1338	DNA-binding protein	LRC_RS08090	hypothetical protein
LAC1533_RS05505	N-acetyltransferase	LSL_1340	hypothetical protein	LRC_RS08105	MFS transporter
LAC1533_RS05515	hypothetical protein	LSL_1363	hypothetical protein	LRC_RS08110	IS30 family transposase
LAC1533_RS05540	death-on-curing family protein	LSL_1365	2-dehydropantoate 2-reductase	LRC_RS08120	hypothetical protein
LAC1533_RS05550	IS30 family transposase	LSL_1369	exonuclease	LRC_RS08125	glycerol-3-phosphate cytidiltransferase
LAC1533_RS05555	hypothetical protein	LSL_1379	hypothetical protein	LRC_RS08130	hypothetical protein
LAC1533_RS05575	hypothetical protein	LSL_1382	hypothetical protein	LRC_RS08135	alanine--glyoxylate aminotransferase family protein
LAC1533_RS05590	type VI secretion protein ImpB	LSL_1383	ABC transporter	LRC_RS08145	LicD family protein
LAC1533_RS05595	hypothetical protein	LSL_1384	ABC transporter ATP-binding protein	LRC_RS08150	NAD/NADP octopine/nopaline dehydrogenase
LAC1533_RS05645	group II intron reverse transcriptase/maturase	LSL_1385	response regulator receiver	LRC_RS08160	glycosyltransferase family 2 protein
LAC1533_RS05675	site-specific integrase	LSL_1387	hypothetical protein	LRC_RS08170	hypothetical protein
LAC1533_RS05690	XRE family transcriptional regulator	LSL_1388	death on curing protein	LRC_RS08180	flagellar protein FlaG
LAC1533_RS05695	hypothetical protein	LSL_1389	hypothetical protein	LRC_RS08185	family 2 glycosyl transferase
LAC1533_RS05705	hypothetical protein	LSL_1390	hypothetical protein	LRC_RS08195	hypothetical protein
LAC1533_RS05710	hypothetical protein	LSL_1391	hypothetical protein	LRC_RS08200	hypothetical protein
LAC1533_RS05715	hypothetical protein	LSL_1392	hypothetical protein	LRC_RS08205	tetratricopeptide repeat protein
LAC1533_RS05720	hypothetical protein	LSL_1393	hypothetical protein	LRC_RS08215	hypothetical protein
LAC1533_RS05725	hypothetical protein	LSL_1394	hypothetical protein	LRC_RS08220	sigma-70 family RNA polymerase sigma factor
LAC1533_RS05730	hypothetical protein	LSL_1395	hypothetical protein	LRC_RS08225	hypothetical protein
LAC1533_RS05735	hypothetical protein	LSL_1396	hypothetical protein	LRC_RS08245	flagellar biosynthesis anti-sigma factor FlgM
LAC1533_RS05745	hypothetical protein	LSL_1397	dehydrogenase	LRC_RS08370	flagellar protein
LAC1533_RS05750	DNA replication protein	LSL_1399	hypothetical protein	LRC_RS08380	flagellar hook-length control protein FliK
LAC1533_RS05755	hypothetical protein	LSL_1400	hypothetical protein	LRC_RS08395	flagellar biosynthesis protein
LAC1533_RS05760	hypothetical protein	LSL_1401	hypothetical protein	LRC_RS08435	chemotaxis protein
LAC1533_RS05765	RusA family crossover junction endodeoxyribonuclease	LSL_1439	ribose 5-phosphate isomerase	LRC_RS08450	hypothetical protein
LAC1533_RS05770	hypothetical protein	LSL_1442	amino acid permease	LRC_RS08455	membrane protein
LAC1533_RS05775	hypothetical protein	LSL_1447	hypothetical protein	LRC_RS08460	hypothetical protein
LAC1533_RS05780	hypothetical protein	LSL_1460	hypothetical protein	LRC_RS08475	TVP38/TMEM64 family protein
LAC1533_RS05785	hypothetical protein	LSL_1462	Na+ driven multidrug efflux pump	LRC_RS08480	hypothetical protein
LAC1533_RS05790	site-specific DNA-methyltransferase	LSL_1467	succinyl-diaminopimelate desuccinylase	LRC_RS08490	MFS transporter
LAC1533_RS05795	hypothetical protein	LSL_1472	DegV family protein	LRC_RS08500	cupin domain-containing protein
LAC1533_RS05800	hypothetical protein	LSL_1483	hypothetical protein	LRC_RS08540	hypothetical protein
LAC1533_RS05805	terminase small subunit	LSL_1485	hypothetical protein	LRC_RS08545	membrane protein
LAC1533_RS05810	PBSX family phage terminase large subunit	LSL_1492	hypothetical protein	LRC_RS08550	hypothetical protein
LAC1533_RS05815	phage portal protein	LSL_1493	hypothetical protein	LRC_RS08560	L,D-transpeptidase
LAC1533_RS05820	minor capsid protein	LSL_1494	hypothetical protein	LRC_RS08565	hypothetical protein
LAC1533_RS05825	hypothetical protein	LSL_1495	hypothetical protein	LRC_RS08600	ribose-5-phosphate isomerase
LAC1533_RS05830	capsid protein	LSL_1496	hypothetical protein	LRC_RS08665	peptidase
LAC1533_RS05835	hypothetical protein	LSL_1497	hypothetical protein	LRC_RS08670	O-acetylhomoserine aminocarboxypropyltransferase/cysteine synthase
LAC1533_RS05840	hypothetical protein	LSL_1501	drug/metabolite exporter family protein	LRC_RS08680	alpha/beta hydrolase
LAC1533_RS05845	capsid protein	LSL_1504	FMN reductase	LRC_RS08685	hypothetical protein
LAC1533_RS05850	capsid protein	LSL_1505	luciferase-like monooxygenase	LRC_RS08695	hypothetical protein
LAC1533_RS05855	hypothetical protein	LSL_1506	MarR family transcriptional regulator	LRC_RS08700	sensor histidine kinase

LAC1533_RS05860	capsid protein	LSL_1516	N-acetylmuramoyl-L-alanine amidase	LRC_RS08710	hypothetical protein
LAC1533_RS05865	hypothetical protein	LSL_1517	glucosyltransferase-S	LRC_RS08720	ABC transporter ATP-binding protein
LAC1533_RS05870	hypothetical protein	LSL_1522	hypothetical protein	LRC_RS08725	ABC transporter ATP-binding protein
LAC1533_RS05875	hypothetical protein	LSL_1523	hypothetical protein	LRC_RS08730	branched-chain amino acid ABC transporter permease
LAC1533_RS05880	hypothetical protein	LSL_1526	polysachharide biosynthesis protein	LRC_RS08735	branched-chain amino acid ABC transporter permease
LAC1533_RS05885	hypothetical protein	LSL_1527	O-acetyl transferase	LRC_RS08740	branched-chain amino acid ABC transporter substrate-binding protein
LAC1533_RS05890	hypothetical protein	LSL_1528	inosine-uridine preferring nucleoside hydrolase	LRC_RS08745	carbon-nitrogen family hydrolase
LAC1533_RS05895	hypothetical protein	LSL_1529	hypothetical protein	LRC_RS08750	hypothetical protein
LAC1533_RS05900	collagen-like protein	LSL_1530	oxidoreductase	LRC_RS08755	hypothetical protein
LAC1533_RS05905	hypothetical protein	LSL_1532	D-alanyl-D-alanine serine-type carboxypeptidase	LRC_RS08765	hypothetical protein
LAC1533_RS05920	hypothetical protein	LSL_1535	hypothetical protein	LRC_RS08775	ABC transporter substrate-binding protein
LAC1533_RS05975	teichoic acid biosynthesis protein	LSL_1536	hypothetical protein	LRC_RS08780	carbohydrate ABC transporter permease
LAC1533_RS06090	group II intron reverse transcriptase/maturase	LSL_1541	amino acid ABC transporter	LRC_RS08785	sugar ABC transporter permease
LAC1533_RS06155	hypothetical protein	LSL_1543	hypothetical protein	LRC_RS08795	IS256 family transposase
LAC1533_RS06195	IS30 family transposase	LSL_1544	multidrug resistance efflux pump	LRC_RS08800	pyridoxal phosphate-dependent aminotransferase
LAC1533_RS06300	hypothetical protein	LSL_1545	hypothetical protein	LRC_RS08820	hypothetical protein
LAC1533_RS06315	hypothetical protein	LSL_1546	hypothetical protein	LRC_RS08825	thiol reductase thioredoxin
LAC1533_RS06565	hypothetical protein	LSL_1555	polysacharide biosyntheis protein	LRC_RS08830	bacteriocin
LAC1533_RS06570	group II intron reverse transcriptase/maturase	LSL_1556	glycosyltransferase	LRC_RS08835	hypothetical protein
LAC1533_RS06705	1-acyl-sn-glycerol-3-phosphate acyltransferase	LSL_1557	hypothetical protein	LRC_RS08840	GHKL domain-containing protein
LAC1533_RS06720	hypothetical protein	LSL_1558	capsular polysaccharide synthesis protein	LRC_RS08845	DNA-binding response regulator
LAC1533_RS06740	hypothetical protein	LSL_1559	glycosyltransferase	LRC_RS08850	peptide cleavage/export ABC transporter
LAC1533_RS06800	hypothetical protein	LSL_1560	glycosyltransferase	LRC_RS08855	hypothetical protein
LAC1533_RS06815	aspartate-semialdehyde dehydrogenase	LSL_1561	glycosyltransferase	LRC_RS08890	aspartate aminotransferase family protein
LAC1533_RS06890	IS982 family transposase	LSL_1562	hypothetical protein	LRC_RS08915	nitrate reductase
LAC1533_RS06910	lactate dehydrogenase	LSL_1564	DNA helicase	LRC_RS08920	peptidase M20
LAC1533_RS06915	IS30 family transposase	LSL_1565	hypothetical protein	LRC_RS08925	dehydrogenase
LAC1533_RS06925	hypothetical protein	LSL_1566	hypothetical protein	LRC_RS08945	cobalt ABC transporter permease
LAC1533_RS06990	hypothetical protein	LSL_1567	hypothetical protein	LRC_RS08960	ABC transporter permease
LAC1533_RS07065	cell division protein FtsL	LSL_1573	glycosyltransferase	LRC_RS08965	ABC transporter ATP-binding protein
LAC1533_RS07080	DUF3397 domain-containing protein	LSL_1575	hypothetical protein	LRC_RS08970	hypothetical protein
LAC1533_RS07215	hypothetical protein	LSL_1579	hypothetical protein	LRC_RS08975	TetR/AcrR family transcriptional regulator
LAC1533_RS07220	hypothetical protein	LSL_1581	MerR family transcriptional regulator	LRC_RS08980	amino acid ABC transporter substrate-binding protein
LAC1533_RS07235	GNAT family acetyltransferase	LSL_1601	glycerophosphodiester phosphodiesterase	LRC_RS08990	amino acid ABC transporter permease
LAC1533_RS07240	IS256 family transposase	LSL_1602	calcium-transporting ATPase	LRC_RS09000	MFS transporter
LAC1533_RS07255	hypothetical protein	LSL_1605	hypothetical protein	LRC_RS09065	hypothetical protein
LAC1533_RS07260	peptide transporter	LSL_1609	hypothetical protein	LRC_RS09095	TetR/AcrR family transcriptional regulator
LAC1533_RS07265	recombinase family protein	LSL_1614	hypothetical protein	LRC_RS09100	2-hydroxyglutaryl-CoA dehydratase
LAC1533_RS07275	immunity protein	LSL_1615	hypothetical protein	LRC_RS09105	hypothetical protein
LAC1533_RS07290	antitoxin RelB	LSL_1629	Na+/H+ antiporter	LRC_RS09110	hypothetical protein
LAC1533_RS07295	site-specific integrase	LSL_1637	hypothetical protein	LRC_RS09120	hypothetical protein
LAC1533_RS07300	transcriptional regulator	LSL_1641	myosin-cross-reactive antigen	LRC_RS09135	hypothetical protein
LAC1533_RS07305	hypothetical protein	LSL_1644	branched chain amino acid ABC transporter	LRC_RS09195	flavodoxin
LAC1533_RS07330	hypothetical protein	LSL_1648	phage integrase	LRC_RS09205	amino acid transporter
LAC1533_RS07335	DUF536 domain-containing protein	LSL_1649	Cro/CI family transcriptional regulator	LRC_RS09210	4a-hydroxytetrahydrobiopterin dehydratase
LAC1533_RS07340	putative holin-like toxin	LSL_1650	antirepressor	LRC_RS09220	acetylornithine transaminase
LAC1533_RS07345	LtrC	LSL_1651	hypothetical protein	LRC_RS09225	acetylglutamate kinase
LAC1533_RS07350	hypothetical protein	LSL_1652	hypothetical protein	LRC_RS09230	bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ
LAC1533_RS07355	hypothetical protein	LSL_1653	hypothetical protein	LRC_RS09235	N-acetyl-gamma-glutamyl-phosphate reductase
LAC1533_RS07360	type IA DNA topoisomerase	LSL_1654	hypothetical protein	LRC_RS09245	MATE family efflux transporter
LAC1533_RS07365	hypothetical protein	LSL_1655	hypothetical protein	LRC_RS09250	phosphoglycolate phosphatase
LAC1533_RS07370	conjugal transfer protein	LSL_1656	hypothetical protein	LRC_RS09255	hypothetical protein
LAC1533_RS07375	hypothetical protein	LSL_1657	hypothetical protein	LRC_RS09260	DUF368 domain-containing protein

LAC1533_RS07380	conjugal transfer protein	LSL_1658	DNA primase	LRC_RS09265	thioredoxin-dependent thiol peroxidase
LAC1533_RS07385	conjugal transfer protein	LSL_1659	hypothetical protein	LRC_RS09270	N-acetyltransferase
LAC1533_RS07390	hypothetical protein	LSL_1660	hypothetical protein	LRC_RS09275	WYL domain-containing protein
LAC1533_RS07395	IS30 family transposase	LSL_1661	hypothetical protein	LRC_RS09280	hypothetical protein
LAC1533_RS07400	hypothetical protein	LSL_1662	hypothetical protein	LRC_RS09290	GNAT family N-acetyltransferase
LAC1533_RS07405	hypothetical protein	LSL_1663	hypothetical protein	LRC_RS09295	PadR family transcriptional regulator
LAC1533_RS07410	peptidoglycan endopeptidase	LSL_1664	hypothetical protein	LRC_RS09300	hypothetical protein
LAC1533_RS07590	transposase	LSL_1665	hypothetical protein	LRC_RS09315	IS200/IS605 family transposase
LAC1533_RS07635	group II intron reverse transcriptase/maturase	LSL_1666	hypothetical protein	LRC_RS09320	cysteine hydrolase
LAC1533_RS07785	hypothetical protein	LSL_1667	TetR family transcriptional regulator	LRC_RS09325	putative heavy metal-binding protein
LAC1533_RS07835	hypothetical protein	LSL_1668	hypothetical protein	LRC_RS09340	abortive phage infection protein
LAC1533_RS07965	group II intron reverse transcriptase/maturase	LSL_1670	D-alanine aminotransferase	LRC_RS09345	hypothetical protein
LAC1533_RS08010	hypothetical protein	LSL_1671	hypothetical protein	LRC_RS09365	MFS transporter
LAC1533_RS08040	XRE family transcriptional regulator	LSL_1672	hypothetical protein	LRC_RS09370	AraC family transcriptional regulator
LAC1533_RS08045	ImmA/IrrE family metallo-endopeptidase	LSL_1674	agmatine deiminase	LRC_RS09395	nucleoside deoxyribosyltransferase
LAC1533_RS08050	hypothetical protein	LSL_1675	ABC transporter permease	LRC_RS09400	DUF3021 domain-containing protein
LAC1533_RS08140	hypothetical protein	LSL_1677	TetR family transcriptional regulator	LRC_RS09405	LytTR family transcriptional regulator
LAC1533_RS08195	hypothetical protein	LSL_1678	hypothetical protein	LRC_RS09410	ABC transporter
LAC1533_RS08295	Zn-dependent protease	LSL_1679	PPE repeat-containing protein	LRC_RS09415	ABC transporter ATP-binding protein
LAC1533_RS08300	CvpA family protein	LSL_1680	glyoxalase	LRC_RS09425	hypothetical protein
LAC1533_RS08330	group II intron reverse transcriptase/maturase	LSL_1682	MarR family transcriptional regulator	LRC_RS09430	LytTR family transcriptional regulator
LAC1533_RS08340	group II intron reverse transcriptase/maturase	LSL_1685	major facilitator superfamily permease	LRC_RS09440	Fis family transcriptional regulator
LAC1533_RS08355	transposase	LSL_1687	hypothetical protein	LRC_RS09445	hypothetical protein
LAC1533_RS08360	1,3-propanediol dehydrogenase	LSL_1688	TetR family transcriptional regulator	LRC_RS09495	alpha/beta hydrolase
LAC1533_RS08365	ECF transporter S component	LSL_1690	hypothetical protein	LRC_RS09500	hypothetical protein
LAC1533_RS08370	hypothetical protein	LSL_1691	hypothetical protein	LRC_RS09505	ABC transporter ATP-binding protein
LAC1533_RS08375	sugar aldolase	LSL_1692	homocysteine methyltransferase	LRC_RS09510	hypothetical protein
LAC1533_RS08380	hypothetical protein	LSL_1694	phosphate-starvation-inducible protein PsiE	LRC_RS09515	hypothetical protein
LAC1533_RS08385	PTS galactitol transporter subunit IIC	LSL_1700	amino acid permease	LRC_RS09520	hypothetical protein
LAC1533_RS08390	PTS galactitol transporter subunit IIB	LSL_1708	ArsR family transcriptional regulator	LRC_RS09525	hypothetical protein
LAC1533_RS08395	PTS galactitol transporter subunit IIA	LSL_1709	ThiJ/PfpI family protein	LRC_RS09530	XRE family transcriptional regulator
LAC1533_RS08400	DeoR/GlpR transcriptional regulator	LSL_1710	glycerophosphodiester phosphodiesterase	LRC_RS09550	membrane protein
LAC1533_RS08430	hypothetical protein	LSL_1711	LacI family transcriptional regulator	LRC_RS09600	neopullulanase
LAC1533_RS08435	hypothetical protein	LSL_1713	PTS system N-acetylgalactosamine-specific transporter subunit IIA	LRC_RS09605	maltodextrose utilization protein MalA
LAC1533_RS08440	hypothetical protein	LSL_1714	PTS system mannose-specific transporter subunit IID	LRC_RS09610	sugar ABC transporter permease
LAC1533_RS08445	ATP-dependent helicase	LSL_1715	PTS system mannose-specific transporter subunit IIC	LRC_RS09615	sugar ABC transporter permease
LAC1533_RS08450	class I SAM-dependent DNA methyltransferase	LSL_1720	hypothetical protein	LRC_RS09620	sugar ABC transporter substrate-binding protein
LAC1533_RS08455	XRE family transcriptional regulator	LSL_1723	hypothetical protein	LRC_RS09655	endonuclease/exonuclease/phosphatase
LAC1533_RS08460	helicase	LSL_1725	hypothetical protein	LRC_RS09660	PTS glucose transporter subunit IIABC
LAC1533_RS08465	DUF1837 domain-containing protein	LSL_1729	hypothetical protein	LRC_RS09710	PTS beta-glucoside transporter subunit IIC
LAC1533_RS08470	sigma-70 family RNA polymerase sigma factor	LSL_1731	polysaccharide deacetylase	LRC_RS09735	shikimate kinase
LAC1533_RS08475	hypothetical protein	LSL_1732	hypothetical protein	LRC_RS09740	prephenate dehydrogenase
LAC1533_RS08480	hypothetical protein	LSL_1733	LysR family transcriptional regulator	LRC_RS09745	3-phosphoshikimate 1-carboxyvinyltransferase
LAC1533_RS08490	DUF2815 domain-containing protein	LSL_1734	hypothetical protein	LRC_RS09750	hypothetical protein
LAC1533_RS08500	hypothetical protein			LRC_RS09755	chorismate synthase
LAC1533_RS08505	DNA primase			LRC_RS09760	maltose acetyltransferase
LAC1533_RS08510	VRR-NUC domain-containing protein			LRC_RS09765	ABC transporter ATP-binding protein
LAC1533_RS08520	restriction endonuclease			LRC_RS09800	methyl-accepting chemotaxis protein
LAC1533_RS08525	HNH endonuclease			LRC_RS09805	ABC transporter substrate-binding protein
LAC1533_RS08530	terminase			LRC_RS09815	DUF3955 domain-containing protein
LAC1533_RS08535	hypothetical protein			LRC_RS09825	endonuclease

LAC1533_RS08540	DDE domain-containing protein			LRC_RS09890	hypothetical protein
LAC1533_RS08550	DUF5049 domain-containing protein			LRC_RS09900	hypothetical protein
LAC1533_RS08555	terminase large subunit			LRC_RS09910	hypothetical protein
LAC1533_RS08560	hypothetical protein			LRC_RS09930	Cof-type HAD-IIB family hydrolase
LAC1533_RS08565	type II toxin-antitoxin system RelE/ParE family toxin			LRC_RS09955	hypothetical protein
LAC1533_RS08575	Clp protease ClpP			LRC_RS09975	MFS transporter
LAC1533_RS08580	phage major capsid protein			LRC_RS09980	MFS transporter
LAC1533_RS08585	phage gp6-like head-tail connector protein			LRC_RS09990	hypothetical protein
LAC1533_RS08590	head-tail adaptor protein			LRC_RS09995	hypothetical protein
LAC1533_RS08595	DNA primase			LRC_RS10000	DUF2207 domain-containing protein
LAC1533_RS08600	1,4-beta-N-acetylmuramidase			LRC_RS10010	XRE family transcriptional regulator
LAC1533_RS08605	hypothetical protein			LRC_RS10015	hypothetical protein
LAC1533_RS08625	hypothetical protein			LRC_RS10020	hypothetical protein
LAC1533_RS08800	hypothetical protein			LRC_RS10030	transposase
LAC1533_RS08805	CHAP domain-containing protein			LRC_RS10035	IS200/IS605 family transposase
LAC1533_RS08835	DNA helicase RecQ			LRC_RS10060	XRE family transcriptional regulator
LAC1533_RS08840	hypothetical protein			LRC_RS10095	DUF2207 domain-containing protein
LAC1533_RS09035	IS1380 family transposase			LRC_RS10120	ArsR family transcriptional regulator
LAC1533_RS09060	prepilin peptidase			LRC_RS10135	NAD(P)H-dependent oxidoreductase
LAC1533_RS09065	group II intron reverse transcriptase/maturase			LRC_RS10145	ABC transporter ATP-binding protein
LAC1533_RS09095	transposase			LRC_RS10150	ABC transporter ATP-binding protein
LAC1533_RS09180	SMC family ATPase			LRC_RS10155	ABC transporter permease
LAC1533_RS09190	hypothetical protein			LRC_RS10160	hypothetical protein
LAC1533_RS09205	transposase			LRC_RS10170	N-acetylmuramoyl-L-alanine amidase
LAC1533_RS09215	MgtC/SapB family protein			LRC_RS10180	transposase
LAC1533_RS09220	glycosyltransferase family 4 protein			LRC_RS10205	hypothetical protein
LAC1533_RS09235	D-alanine--D-alanine ligase			LRC_RS10210	hypothetical protein
LAC1533_RS09240	hypothetical protein			LRC_RS10235	DnaD domain protein
LAC1533_RS09245	alpha/beta hydrolase			LRC_RS10240	DUF4065 domain-containing protein
LAC1533_RS09270	putative N-acetylmannosamine-6-phosphate 2-epimerase			LRC_RS10245	XRE family transcriptional regulator
LAC1533_RS09275	hypothetical protein			LRC_RS10275	hypothetical protein
LAC1533_RS09280	hypothetical protein			LRC_RS10290	GNAT family acetyltransferase
LAC1533_RS09285	hypothetical protein			LRC_RS10295	vitamin B12-binding protein
LAC1533_RS09290	arginase			LRC_RS10300	hypothetical protein
LAC1533_RS09295	OsmC family peroxiredoxin			LRC_RS10305	hypothetical protein
LAC1533_RS09300	hypothetical protein			LRC_RS10310	hypothetical protein
LAC1533_RS09320	IS66 family transposase			LRC_RS10320	vitamin B12-binding protein
LAC1533_RS09335	sigma-70 family RNA polymerase sigma factor			LRC_RS10325	hypothetical protein
LAC1533_RS09345	DUF3173 domain-containing protein			LRC_RS10335	vitamin B12-binding protein
LAC1533_RS09350	site-specific integrase			LRC_RS10345	YhgE/Pip domain-containing protein
LAC1533_RS09390	hypothetical protein			LRC_RS10355	hypothetical protein
LAC1533_RS09400	hypothetical protein			LRC_RS10375	transposase
LAC1533_RS09405	NERD domain-containing protein			LRC_RS10395	vitamin B12-binding protein
LAC1533_RS09410	transposase			LRC_RS10400	vitamin B12-binding protein
LAC1533_RS09505	hypothetical protein			LRC_RS10405	tRNA-binding protein
LAC1533_RS09510	transposase			LRC_RS10420	hypothetical protein
LAC1533_RS09525	metal ABC transporter substrate-binding protein			LRC_RS10430	hypothetical protein
LAC1533_RS09540	KR domain-containing protein			LRC_RS10460	vitamin B12-binding protein
LAC1533_RS09550	Cof-type HAD-IIB family hydrolase			LRC_RS10485	hypothetical protein
LAC1533_RS09555	DUF969 domain-containing protein			LRC_RS10520	transposase
LAC1533_RS09560	DUF979 domain-containing protein			LRC_RS10530	FeoB-associated Cys-rich membrane protein
LAC1533_RS09575	sugar ABC transporter permease			LRC_RS10535	hypothetical protein
LAC1533_RS09580	carbohydrate ABC transporter substrate-binding protein			LRC_RS10540	hypothetical protein
LAC1533_RS09590	putative polysaccharide biosynthesis protein			LRC_RS10575	amino acid-binding protein
LAC1533_RS09610	hypothetical protein			LRC_RS10580	IS66 family transposase
LAC1533_RS09620	LysM domain-containing protein			LRC_RS10600	HTH domain-containing protein

LAC1533_RS09630	DegV family EDD domain-containing protein			LRC_RS10605	hypothetical protein
LAC1533_RS09655	flagellar biosynthesis anti-sigma factor FlgM			LRC_RS10625	hypothetical protein
LAC1533_RS09785	flagellar hook-length control protein FliK			LRC_RS10670	hypothetical protein
LAC1533_RS09830	IS256 family transposase			LRC_RS10675	hypothetical protein
LAC1533_RS09850	hypothetical protein			LRC_RS10680	hypothetical protein
LAC1533_RS09895	hypothetical protein			LRC_RS10695	hypothetical protein
LAC1533_RS09900	hypothetical protein			LRC_RS10710	hypothetical protein
LAC1533_RS09905	aldo/keto reductase			LRC_RS10715	hypothetical protein
LAC1533_RS09910	addiction module antidote protein, HigA family			LRC_RS10720	hypothetical protein
LAC1533_RS09915	plasmid maintenance system killer			LRC_RS10725	hypothetical protein
LAC1533_RS09925	alpha-mannosidase			LRC_RS10730	hypothetical protein
LAC1533_RS09940	hypothetical protein			LRC_RS10740	hypothetical protein
LAC1533_RS09945	IS30 family transposase			LRC_RS10745	hypothetical protein
LAC1533_RS09950	hypothetical protein			LRC_RS10760	hypothetical protein
LAC1533_RS09955	PRD domain-containing protein			LRC_RS10780	hypothetical protein
LAC1533_RS09965	glycosyl hydrolase			LRC_RS10795	vitamin B12-binding protein
LAC1533_RS09970	acyltransferase			LRC_RS10800	vitamin B12-binding protein
LAC1533_RS09975	hypothetical protein			LRC_RS10810	vitamin B12-binding protein
LAC1533_RS09980	PrsW family intramembrane metalloprotease			LRC_RS10815	vitamin B12-binding protein
LAC1533_RS10000	hypothetical protein			LRC_RS10830	IS66 family transposase
LAC1533_RS10020	hypothetical protein			LRC_RS10835	vitamin B12-binding protein
LAC1533_RS10030	2-dehydropantoate 2-reductase			LRC_RS10840	vitamin B12-binding protein
LAC1533_RS10035	hypothetical protein			LRC_RS10850	hypothetical protein
LAC1533_RS10040	MFS transporter			LRC_RS10865	vitamin B12-binding protein
LAC1533_RS10045	PAS domain S-box protein			LRC_RS10890	hypothetical protein
LAC1533_RS10050	PAS domain S-box protein			LRC_RS10895	flotillin family protein
LAC1533_RS10055	hypothetical protein			LRC_RS10900	hypothetical protein
LAC1533_RS10075	IS256 family transposase			LRC_RS10935	hypothetical protein
LAC1533_RS10080	LysM peptidoglycan-binding domain-containing protein			LRC_RS10940	hypothetical protein
LAC1533_RS10105	class II aldolase family protein			LRC_RS10950	vitamin B12-binding protein
LAC1533_RS10110	PTS galactitol transporter subunit IIC			LRC_RS10955	vitamin B12-binding protein
LAC1533_RS10115	PTS galactitol transporter subunit IIB			LRC_RS10960	vitamin B12-binding protein
LAC1533_RS10120	hypothetical protein			LRC_RS10970	vitamin B12-binding protein
LAC1533_RS10135	hypothetical protein			LRC_RS10995	hypothetical protein
LAC1533_RS10150	hypothetical protein			LRC_RS11000	vitamin B12-binding protein
LAC1533_RS10165	hypothetical protein			LRC_RS11005	vitamin B12-binding protein
LAC1533_RS10170	IS1380 family transposase			LRC_RS11015	hypothetical protein
LAC1533_RS10175	hypothetical protein			LRC_RS11040	hypothetical protein
LAC1533_RS10180	DUF2922 domain-containing protein			LRC_RS11050	hypothetical protein
LAC1533_RS10190	peptidase				
LAC1533_RS10205	sigma-70 family RNA polymerase sigma factor				
LAC1533_RS10210	hypothetical protein				
LAC1533_RS10215	MurR/RpiR family transcriptional regulator				
LAC1533_RS10220	PTS sugar transporter subunit IIC				
LAC1533_RS10230	ROK family protein				
LAC1533_RS10235	hypothetical protein				
LAC1533_RS10310	hypothetical protein				
LAC1533_RS10320	glycosyltransferase family 2 protein				
LAC1533_RS10325	hypothetical protein				
LAC1533_RS10350	hypothetical protein				
LAC1533_RS10360	hypothetical protein				
LAC1533_RS10365	LicD family protein				
LAC1533_RS10385	glycosyltransferase family 2 protein				
LAC1533_RS10390	hypothetical protein				
LAC1533_RS10430	IS256 family transposase				
LAC1533_RS10435	IS30 family transposase				
LAC1533_RS10440	hypothetical protein				

LAC1533_RS10450	hypothetical protein				
LAC1533_RS10455	hypothetical protein				
LAC1533_RS10465	type II toxin-antitoxin system RelE/ParE family toxin				
LAC1533_RS10470	Cna B-type domain-containing protein				
LAC1533_RS10475	hypothetical protein				
LAC1533_RS10480	class A sortase				
LAC1533_RS10485	TetR/AcrR family transcriptional regulator				
LAC1533_RS10490	sulfite exporter TauE/SafE family protein				
LAC1533_RS10505	hypothetical protein				
LAC1533_RS10530	D-lactate dehydrogenase				
LAC1533_RS10535	CsbD family protein				
LAC1533_RS10540	hypothetical protein				
LAC1533_RS10550	hypothetical protein				
LAC1533_RS10555	NERD domain-containing protein				
LAC1533_RS10590	XRE family transcriptional regulator				
LAC1533_RS10595	hypothetical protein				
LAC1533_RS10600	hypothetical protein				
LAC1533_RS10605	serine/threonine transporter SstT				
LAC1533_RS10610	organic hydroperoxide resistance protein				
LAC1533_RS10630	NADH-flavin reductase				
LAC1533_RS10640	hypothetical protein				
LAC1533_RS10655	glutathione peroxidase				
LAC1533_RS10660	DUF488 domain-containing protein				
LAC1533_RS10665	N-acetyltransferase				
LAC1533_RS10695	CPBP family intramembrane metalloprotease				
LAC1533_RS10705	MFS transporter				
LAC1533_RS10710	MarR family transcriptional regulator				
LAC1533_RS10720	NAD(P)/FAD-dependent oxidoreductase				
LAC1533_RS10730	hypothetical protein				
LAC1533_RS10740	hypothetical protein				
LAC1533_RS10745	hypothetical protein				
LAC1533_RS10780	hypothetical protein				
LAC1533_RS10785	hypothetical protein				
LAC1533_RS10790	universal stress protein				
LAC1533_RS10795	hypothetical protein				
LAC1533_RS10820	hypothetical protein				
LAC1533_RS10830	VanZ family protein				
LAC1533_RS10835	4-phosphoerythronate dehydrogenase				
LAC1533_RS10840	transposase				
LAC1533_RS10855	group II intron reverse transcriptase/maturase				
LAC1533_RS10865	energy-coupled thiamine transporter ThiT				
LAC1533_RS10870	energy-coupling factor transporter transmembrane protein EcfT				
LAC1533_RS10895	MFS transporter				
LAC1533_RS10900	N-acetyltransferase				
LAC1533_RS10905	hypothetical protein				
LAC1533_RS10910	hypothetical protein				
LAC1533_RS10915	hypothetical protein				
LAC1533_RS10950	DUF1541 domain-containing protein				
LAC1533_RS10965	hypothetical protein				
LAC1533_RS11000	ribose transporter RbsU				
LAC1533_RS11005	D-ribose pyranase				
LAC1533_RS11025	3-oxoacyl-ACP reductase				
LAC1533_RS11030	phosphoenolpyruvate synthase				
LAC1533_RS11045	GNAT family N-acetyltransferase				
LAC1533_RS11055	hypothetical protein				
LAC1533_RS11100	hypothetical protein				
LAC1533_RS11105	hypothetical protein				
LAC1533_RS11110	hypothetical protein				
LAC1533_RS11115	KR domain-containing protein				
LAC1533_RS11120	NAD-dependent dehydratase				
LAC1533_RS11125	glycerol dehydrogenase				
LAC1533_RS11130	glycyl-radical enzyme activating protein				

LAC1533_RS11135	glycyl radical protein				
LAC1533_RS11140	fructose-bisphosphate aldolase				
LAC1533_RS11160	TetR/AcrR family transcriptional regulator				
LAC1533_RS11165	1-acyl-sn-glycerol-3-phosphate acyltransferase				
LAC1533_RS11170	glycosyl transferase				
LAC1533_RS11175	glycosyltransferase family 8 protein				
LAC1533_RS11180	1-acyl-sn-glycerol-3-phosphate acyltransferase				
LAC1533_RS11190	hypothetical protein				
LAC1533_RS11195	hypothetical protein				
LAC1533_RS11200	hypothetical protein				
LAC1533_RS11220	DoxX family membrane protein				
LAC1533_RS11225	hypothetical protein				
LAC1533_RS11245	carbamate kinase				
LAC1533_RS11250	amino acid permease				
LAC1533_RS11255	carbamate kinase				
LAC1533_RS11265	arginine deiminase				
LAC1533_RS11270	tRNA ligase				
LAC1533_RS11280	hypothetical protein				
LAC1533_RS11285	GNAT family N-acetyltransferase				
LAC1533_RS11315	glyoxalase				
LAC1533_RS11325	hypothetical protein				
LAC1533_RS11330	SIS domain-containing protein				
LAC1533_RS11345	PTS alpha-glucoside transporter subunit IICB				
LAC1533_RS11350	6-phospho-alpha-glucosidase				
LAC1533_RS11390	esterase family protein				
LAC1533_RS11395	PTS fructose transporter subunit IID				
LAC1533_RS11400	PTS sugar transporter subunit IIC				
LAC1533_RS11405	PTS mannose/fructose/sorbose transporter subunit IIB				
LAC1533_RS11410	PRD domain-containing protein				
LAC1533_RS11415	hypothetical protein				
LAC1533_RS11445	ribonucleoside-triphosphate reductase, adenosylcobalamin-dependent				
LAC1533_RS11450	ATP:cob(I)alamin adenosyltransferase				
LAC1533_RS11455	DUF4430 domain-containing protein				
LAC1533_RS11475	DUF2255 domain-containing protein				
LAC1533_RS11480	MerR family transcriptional regulator				
LAC1533_RS11500	hypothetical protein				
LAC1533_RS11505	hypothetical protein				
LAC1533_RS11520	lipoate--protein ligase				
LAC1533_RS11525	MFS transporter				
LAC1533_RS11555	glycine betaine/L-proline ABC transporter ATP-binding protein				
LAC1533_RS11590	NAD(P)/FAD-dependent oxidoreductase				
LAC1533_RS11595	DUF3021 domain-containing protein				
LAC1533_RS11615	NCS2 family permease				
LAC1533_RS11635	DUF4811 domain-containing protein				
LAC1533_RS11645	MerR family transcriptional regulator				
LAC1533_RS11650	HAD family hydrolase				
LAC1533_RS11690	group II intron reverse transcriptase/maturase				
LAC1533_RS11700	hypothetical protein				
LAC1533_RS11710	hypothetical protein				
LAC1533_RS11715	hypothetical protein				
LAC1533_RS11720	hypothetical protein				
LAC1533_RS11725	hypothetical protein				
LAC1533_RS11730	hypothetical protein				
LAC1533_RS11735	glycosyltransferase family 2 protein				
LAC1533_RS11740	UDP-phosphate N-acetylgalactosaminyl-1-phosphate transferase				
LAC1533_RS11760	chain-length determining protein				
LAC1533_RS11765	serine hydrolase				
LAC1533_RS11770	aryl-sulfate sulfotransferase				

LAC1533_RS11790	type II toxin-antitoxin system PemK/MazF family toxin				
LAC1533_RS11795	PbsX family transcriptional regulator				
LAC1533_RS11800	site-specific integrase				
LAC1533_RS11805	hypothetical protein				
LAC1533_RS11810	group II intron reverse transcriptase/maturase				
LAC1533_RS11820	NAD(P)-dependent alcohol dehydrogenase				
LAC1533_RS11835	hypothetical protein				
LAC1533_RS11840	hypothetical protein				
LAC1533_RS11845	NAD(P)/FAD-dependent oxidoreductase				
LAC1533_RS11850	ABC transporter ATP-binding protein				
LAC1533_RS11855	glycine/betaine ABC transporter permease				
LAC1533_RS11860	DUF975 domain-containing protein				
LAC1533_RS11865	metal-dependent transcriptional regulator				
LAC1533_RS11880	MurR/RpiR family transcriptional regulator				
LAC1533_RS11885	gluconate permease				
LAC1533_RS11890	gluconokinase				
LAC1533_RS11895	6-phosphogluconate dehydrogenase (decarboxylating)				
LAC1533_RS11900	pyridine nucleotide-disulfide oxidoreductase				
LAC1533_RS11905	3-hydroxyacyl-CoA dehydrogenase family protein				
LAC1533_RS11910	IS256 family transposase				
LAC1533_RS11915	hypothetical protein				
LAC1533_RS11925	copper oxidase				
LAC1533_RS11935	hypothetical protein				
LAC1533_RS11970	hypothetical protein				
LAC1533_RS11975	hypothetical protein				
LAC1533_RS11990	magnesium transporter CorA family protein				
LAC1533_RS11995	N-acetyltransferase				
LAC1533_RS12015	ABC transporter ATP-binding protein				
LAC1533_RS12020	iron ABC transporter permease				
LAC1533_RS12025	iron ABC transporter permease				
LAC1533_RS12030	iron-siderophore ABC transporter substrate-binding protein				
LAC1533_RS12040	catalase				
LAC1533_RS12055	Cof-type HAD-IIB family hydrolase				
LAC1533_RS12065	hypothetical protein				
LAC1533_RS12070	hypothetical protein				
LAC1533_RS12085	peptide-methionine (S)-S-oxide reductase				
LAC1533_RS12090	N-acetyltransferase				
LAC1533_RS12100	hypothetical protein				
LAC1533_RS12105	hypothetical protein				
LAC1533_RS12110	hypothetical protein				
LAC1533_RS12130	glutathione peroxidase				
LAC1533_RS12135	IS30 family transposase				
LAC1533_RS12140	hypothetical protein				
LAC1533_RS12180	fructose-bisphosphatase class III				
LAC1533_RS12190	hypothetical protein				
LAC1533_RS12195	hypothetical protein				
LAC1533_RS12200	metal-dependent transcriptional regulator				
LAC1533_RS12215	hypothetical protein				
LAC1533_RS12220	hypothetical protein				
LAC1533_RS12230	L-arabinose isomerase				
LAC1533_RS12235	L-ribulose-5-phosphate 4-epimerase AraD				
LAC1533_RS12240	ATPase				
LAC1533_RS12245	sugar porter family MFS transporter				
LAC1533_RS12250	GntR family transcriptional regulator				

Supplementary table S10. Transporters of *L. acidipiscis* ACA-DC 1533 chromosome and pLAC2 plasmid identified by TransportDB.

Chromosome

locus_tag	Transporter Family	Subfamily	Substrate/Function
LAC1533_RS00060	Sugar Specific PTS	EnzymeIIB	mannose/fructose
LAC1533_RS00065	Sugar Specific PTS	EnzymeIIC	mannose/fructose
LAC1533_RS00070	Sugar Specific PTS	EnzymeIID	mannose/fructose
LAC1533_RS00075	Sugar Specific PTS	EnzymeIIA	mannose/fructose
LAC1533_RS00095	The ATP-binding Cassette (ABC) Superfamily	binding	lipoprotein
LAC1533_RS00100	The ATP-binding Cassette (ABC) Superfamily	membrane	
LAC1533_RS00110	The ATP-binding Cassette (ABC) Superfamily	binding	daunorubicin
LAC1533_RS00150	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonates
LAC1533_RS00155	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonate
LAC1533_RS00160	The ATP-binding Cassette (ABC) Superfamily	membrane	phosphonate
LAC1533_RS00165	The ATP-binding Cassette (ABC) Superfamily	membrane	phosphonate
LAC1533_RS00195	Sugar Specific PTS	EnzymeIIA	fructose
LAC1533_RS00200	Sugar Specific PTS	EnzymeIIB	galactitol
LAC1533_RS00205	Sugar Specific PTS	EnzymeIIC	galactitol
LAC1533_RS00260	Sugar Specific PTS	EnzymeIIA	cellobiose
LAC1533_RS00270	Sugar Specific PTS	EnzymeIIABC	cellobiose
LAC1533_RS00285	Sugar Specific PTS	EnzymeIIBC	cellobiose
LAC1533_RS00350	The Divalent Anion:Na+ Symporter (DASS) Family		sodium ion:dicarboxylate/sulfate
LAC1533_RS00375	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS00380	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS00450	The ATP-binding Cassette (ABC) Superfamily	membrane	amino aicd (glutamine/glutamate/aspartate?)
LAC1533_RS00455	The ATP-binding Cassette (ABC) Superfamily	binding	phosphate
LAC1533_RS00460	The ATP-binding Cassette (ABC) Superfamily	binding protein	amino acid (glutamine/glutamate/aspartate?)
LAC1533_RS00475	The ATP-binding Cassette (ABC) Superfamily	binding	heme
LAC1533_RS00480	The ATP-binding Cassette (ABC) Superfamily	membrane	cobalamin/Fe3+-siderophores
LAC1533_RS00485	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonate
LAC1533_RS00500	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS00560	The Auxin Efflux Carrier (AEC) Family		
LAC1533_RS00665	The ATP-binding Cassette (ABC) Superfamily	binding	zinc
LAC1533_RS00700	The Threonine/Serine Exporter (ThrE) Family		
LAC1533_RS00705	The Concentrative Nucleoside Transporter (CNT) Family		sodium ion:nucleoside symporter
LAC1533_RS00710	The Nucleobase:Cation Symporter-2 (NCS2) Family		xanthine/uracil
LAC1533_RS00750	The ATP-binding Cassette (ABC) Superfamily	binding protein	oligopeptide
LAC1533_RS00780	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS00845	The ATP-binding Cassette (ABC) Superfamily	membrane	multidrug
LAC1533_RS00850	The ATP-binding Cassette (ABC) Superfamily	ABC	multidrug
LAC1533_RS00880	The Major Intrinsic Protein (MIP) Family		glycerol uptake
LAC1533_RS00890	Sugar Specific PTS	EnzymeIIC	cellobiose
LAC1533_RS00915	Sugar Specific PTS	EnzymeIIC	cellobiose
LAC1533_RS00990	The ATP-binding Cassette (ABC) Superfamily	binding protein	amino acid (glutamine/glutamate/aspartate?)
LAC1533_RS00995	The ATP-binding Cassette (ABC) Superfamily	membrane	amino aicd (glutamine/glutamate/aspartate?)
LAC1533_RS01010	The Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP) Family		zinc ion
LAC1533_RS01060	The Solute:Sodium Symporter (SSS) Family		sodium ion:proline symporter
LAC1533_RS01160	The Threonine/Serine Exporter (ThrE) Family		
LAC1533_RS01210	The Major Facilitator Superfamily (MFS)		multidrug efflux (EmrB/QacA subfamily)
LAC1533_RS01230	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS01250	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS01255	The ATP-binding Cassette (ABC) Superfamily	membrane	glycine betaine/L-proline
LAC1533_RS01260	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS01290	The CorA Metal Ion Transporter (MIT) Family		magnesium/cobalt ion
LAC1533_RS01335	The Riboflavin Transporter (RFT) Family		riboflavin uptake
LAC1533_RS01370	The SdpC (Peptide-Antibiotic Killer Factor) Immunity Protein, SdpI (SdpI) Family		protein export
LAC1533_RS01500	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS01505	The ATP-binding Cassette (ABC) Superfamily	binding	D-methionine
LAC1533_RS01510	The ATP-binding Cassette (ABC) Superfamily	membrane	dipeptide/oligopeptide
LAC1533_RS01515	The ATP-binding Cassette (ABC) Superfamily	membrane	dipeptide/oligopeptide
LAC1533_RS01520	The ATP-binding Cassette (ABC) Superfamily	binding protein	dipeptide/oligopeptide
LAC1533_RS01530	The ATP-binding Cassette (ABC) Superfamily	ABC+ membrane	multidrug
LAC1533_RS01535	The ATP-binding Cassette (ABC) Superfamily	binding	lipid A
LAC1533_RS01580	The Betaine/Carnitine/Choline Transporter (BCCT) Family		glycine betaine/carnitine/choline
LAC1533_RS01595	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS01655	The ATP-binding Cassette (ABC) Superfamily	binding protein	oligopeptide

LAC1533_RS01670	The Auxin Efflux Carrier (AEC) Family		
LAC1533_RS01675	The Auxin Efflux Carrier (AEC) Family		
LAC1533_RS01755	The ATP-binding Cassette (ABC) Superfamily	binding	lipid A
LAC1533_RS01760	The ATP-binding Cassette (ABC) Superfamily	binding	lipid A
LAC1533_RS01775	The Major Facilitator Superfamily (MFS)		multidrug efflux (EmrB/QacA subfamily)
LAC1533_RS01825	The Autoinducer-2 Exporter (AI-2E) Family (Formerly the PerM Family, TC #9.B.22)		Autoinducer-2 export
LAC1533_RS01840	The K+ Transporter (Trk) Family		potassium ion uptake
LAC1533_RS01875	The ATP-binding Cassette (ABC) Superfamily	binding	daunorubicin
LAC1533_RS01890	The ATP-binding Cassette (ABC) Superfamily	ABC	sugar
LAC1533_RS01895	The ATP-binding Cassette (ABC) Superfamily	membrane	sugar
LAC1533_RS01900	The ATP-binding Cassette (ABC) Superfamily	membrane	sugar
LAC1533_RS01940	The Major Facilitator Superfamily (MFS)		multidrug efflux (EmrB/QacA subfamily)
LAC1533_RS01965	The ATP-binding Cassette (ABC) Superfamily	binding protein	oligopeptide
LAC1533_RS01985	The ATP-binding Cassette (ABC) Superfamily	binding	lipoprotein
LAC1533_RS01990	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS02025	The Formate-Nitrite Transporter (FNT) Family		formate/nitrite
LAC1533_RS02030	The ATP-binding Cassette (ABC) Superfamily	membrane	efflux (antimicrobial peptide?)
LAC1533_RS02060	Sugar Specific PTS	EnzymeIIA	mannose/fructose
LAC1533_RS02065	Sugar Specific PTS	EnzymeIIB	mannose/fructose
LAC1533_RS02070	Sugar Specific PTS	EnzymeIIC	mannose/fructose
LAC1533_RS02140	The P-type ATPase (P-ATPase) Superfamily		calcium ion/manganese ion
LAC1533_RS02160	The NhaC Na+:H+ Antiporter (NhaC) Family		sodium ion:proton antiporter
LAC1533_RS02195	The ATP-binding Cassette (ABC) Superfamily	binding protein	sugar
LAC1533_RS02200	The ATP-binding Cassette (ABC) Superfamily	membrane	sugar
LAC1533_RS02205	The ATP-binding Cassette (ABC) Superfamily	membrane	sugar
LAC1533_RS02215	The ATP-binding Cassette (ABC) Superfamily	binding	polyamine
LAC1533_RS02265	The Cation Diffusion Facilitator (CDF) Family		cation efflux
LAC1533_RS02295	Sugar Specific PTS	EnzymeIIABC	glucose
LAC1533_RS02300	Sugar Specific PTS	EnzymeIIABC	glucose/maltose/N-acetylglucosamine
LAC1533_RS02315	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS02320	The P-type ATPase (P-ATPase) Superfamily		copper ion
LAC1533_RS02370	The ATP-binding Cassette (ABC) Superfamily	binding protein	oligopeptide
LAC1533_RS02395	Sugar Specific PTS	EnzymeIIB	mannose/fructose
LAC1533_RS02400	Sugar Specific PTS	EnzymeIIAB	mannose/fructose
LAC1533_RS02405	Sugar Specific PTS	EnzymeIIC	mannose/fructose
LAC1533_RS02410	Sugar Specific PTS	EnzymeIID	mannose/fructose
LAC1533_RS02480	The ATP-binding Cassette (ABC) Superfamily	membrane	manganese/zinc ion
LAC1533_RS02485	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonate
LAC1533_RS02555	The Gluconate:H+ Symporter (GntP) Family		gluconate
LAC1533_RS02580	The Major Facilitator Superfamily (MFS)		metabolite
LAC1533_RS02595	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonates
LAC1533_RS02640	The P-type ATPase (P-ATPase) Superfamily		calcium ion/manganese ion
LAC1533_RS02645	The ATP-binding Cassette (ABC) Superfamily	binding	heme
LAC1533_RS02680	Sugar Specific PTS	EnzymeIIABC	glucose/maltose/N-acetylglucosamine
LAC1533_RS02685	The ATP-binding Cassette (ABC) Superfamily	binding	D-methionine
LAC1533_RS02690	The ATP-binding Cassette (ABC) Superfamily	membrane	D-methionine
LAC1533_RS02695	The ATP-binding Cassette (ABC) Superfamily	binding	methionine
LAC1533_RS02700	The HlyC/CorC (HCC) Family		hemolysin C (HlyC) homolog
LAC1533_RS02745	The Threonine/Serine Exporter (ThrE) Family		
LAC1533_RS02785	The Mg2+ Transporter-E (MgtE) Family		magnesium ion
LAC1533_RS02790	The Large Conductance Mechanosensitive Ion Channel (MscL) Family		large-conductance mechanosensitive ion chan
LAC1533_RS02845	The Autoinducer-2 Exporter (AI-2E) Family (Formerly the PerM Family, TC #9.B.22)		Autoinducer-2 export
LAC1533_RS02925	The Major Intrinsic Protein (MIP) Family		glycerol uptake
LAC1533_RS02935	The P-type ATPase (P-ATPase) Superfamily		zinc/cadmium/cobalt ion
LAC1533_RS02980	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS03070	The C4-dicarboxylate Uptake C (DcuC) Family		C4-dicarboxylate
LAC1533_RS03130	The ATP-binding Cassette (ABC) Superfamily	binding	daunorubicin
LAC1533_RS03135	The ATP-binding Cassette (ABC) Superfamily	membrane	multidrug
LAC1533_RS03220	The ATP-binding Cassette (ABC) Superfamily	membrane	cobalt ion
LAC1533_RS03250	The Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter Family		multidrug efflux
LAC1533_RS03305	The ATP-binding Cassette (ABC) Superfamily	ABC+ membrane	CydC/CydD homolog
LAC1533_RS03310	The ATP-binding Cassette (ABC) Superfamily	binding	lipid A

LAC1533_RS03345	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS03380	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS03385	The ATP-binding Cassette (ABC) Superfamily	membrane	glycine betaine/L-proline/carnitine/choline
LAC1533_RS03390	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS03395	The ATP-binding Cassette (ABC) Superfamily	membrane	glycine betaine/L-proline/carnitine/choline
LAC1533_RS03420	The Solute:Sodium Symporter (SSS) Family		sodium ion:proline symporter
LAC1533_RS03430	The Branched Chain Amino Acid Exporter (LIV-E) Family	AzlC	branched-chain amino acid efflux (AzlC)
LAC1533_RS03450	The P-type ATPase (P-ATPase) Superfamily		
LAC1533_RS03510	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS03580	The ATP-binding Cassette (ABC) Superfamily	binding protein	amino acid (glutamine/glutamate/aspartate)
LAC1533_RS03740	The Nucleobase:Cation Symporter-2 (NCS2) Family		xanthine/uracil
LAC1533_RS03840	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	PST	polysaccharide export
LAC1533_RS03920	The Proton-dependent Oligopeptide Transporter (POT) Family		proton:dipeptide/tripeptide symporter
LAC1533_RS04065	The ATP-binding Cassette (ABC) Superfamily	binding	heme
LAC1533_RS04100	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS04140	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonate
LAC1533_RS04145	The ATP-binding Cassette (ABC) Superfamily	membrane	cell division
LAC1533_RS04160	The Solute:Sodium Symporter (SSS) Family		sodium ion:proline symporter
LAC1533_RS04400	The ATP-binding Cassette (ABC) Superfamily	membrane	phosphate
LAC1533_RS04405	The ATP-binding Cassette (ABC) Superfamily	membrane	phosphate
LAC1533_RS04410	The ATP-binding Cassette (ABC) Superfamily	binding	phosphate
LAC1533_RS04415	The ATP-binding Cassette (ABC) Superfamily	binding	phosphate
LAC1533_RS04505	The Small Conductance Mechanosensitive Ion Channel (MscS) Family		small-conductance mechanosensitive ion channel
LAC1533_RS04755	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	PST	polysaccharide export
LAC1533_RS04890	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	MATE	multidrug efflux
LAC1533_RS04950	The ATP-binding Cassette (ABC) Superfamily	binding	daunorubicin
LAC1533_RS04955	The ATP-binding Cassette (ABC) Superfamily	membrane	multidrug/exoprotein (EcsBA homolog)
LAC1533_RS05105	The ATP-binding Cassette (ABC) Superfamily	binding	phosphate
LAC1533_RS06215	The ATP-binding Cassette (ABC) Superfamily	binding	heme
LAC1533_RS06310	The Type IV (Conjugal DNA-Protein Transfer or VirB) Secretory Pathway (IVSP) Family		
LAC1533_RS06410	The Nucleobase:Cation Symporter-2 (NCS2) Family		xanthine/uracil
LAC1533_RS06760	The Cytochrome Oxidase Biogenesis (Oxa1) Family		60 KD inner membrane protein OxaA homolog
LAC1533_RS06840	The Bacterial Competence-related DNA Transformation Transporter (DNA-T) Family		
LAC1533_RS06850	The Bacterial Competence-related DNA Transformation Transporter (DNA-T) Family		
LAC1533_RS07020	The YggT or Fanciful K+ Uptake-B (FkuB; YggT) Family		potassium ion uptake
LAC1533_RS07210	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS07370	The Type IV (Conjugal DNA-Protein Transfer or VirB) Secretory Pathway (IVSP) Family		
LAC1533_RS07435	The ATP-binding Cassette (ABC) Superfamily	membrane	(Fe-S assembly/SufBCD system)
LAC1533_RS07450	The ATP-binding Cassette (ABC) Superfamily	membrane	(Fe-S assembly/SufBCD system)
LAC1533_RS07455	The ATP-binding Cassette (ABC) Superfamily	ABC	(Fe-S assembly/SufBCD system)
LAC1533_RS07500	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07505	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07510	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07515	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07520	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07525	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07530	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07535	The H+- or Na+-translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily		protons
LAC1533_RS07610	The ATP-binding Cassette (ABC) Superfamily	binding	phosphate
LAC1533_RS07940	Sugar Specific PTS	EnzymeIIA	glucitol/sorbitol
LAC1533_RS07985	The Mg2+ Transporter-E (MgtE) Family		magnesium ion
LAC1533_RS08170	General PTS	EnzymeI	
LAC1533_RS08175	General PTS	HPr	
LAC1533_RS08205	The HlyC/CorC (HCC) Family		hemolysin C (HlyC) homolog
LAC1533_RS08210	The ATP-binding Cassette (ABC) Superfamily	binding	daunorubicin
LAC1533_RS08385	Sugar Specific PTS	EnzymeIIC	galactitol
LAC1533_RS08395	Sugar Specific PTS	EnzymeIIA	fructose
LAC1533_RS08620	The Major Facilitator Superfamily (MFS)		multidrug efflux (EmrB/QacA subfamily)
LAC1533_RS08685	The Sulfate Permease (SulP) Family		sulfate
LAC1533_RS08810	The Auxin Efflux Carrier (AEC) Family		
LAC1533_RS08875	The ATP-binding Cassette (ABC) Superfamily	membrane	cobalt ion
LAC1533_RS08880	The ATP-binding Cassette (ABC) Superfamily	binding	cobalt

LAC1533_RS08885	The ATP-binding Cassette (ABC) Superfamily	binding	cobalt
LAC1533_RS09375	The Monovalent Cation:Proton Antiporter-2 (CPA2) Family		potassium/sodium ion:proton antiporter
LAC1533_RS09415	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS09420	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS09425	The ATP-binding Cassette (ABC) Superfamily	membrane	dipeptide/oligopeptide
LAC1533_RS09430	The ATP-binding Cassette (ABC) Superfamily	membrane	dipeptide/oligopeptide
LAC1533_RS09435	The ATP-binding Cassette (ABC) Superfamily	binding protein	oligopeptide
LAC1533_RS09455	The ATP-binding Cassette (ABC) Superfamily	membrane	amino aicd (glutamine/glutamate/aspartate)
LAC1533_RS09460	The ATP-binding Cassette (ABC) Superfamily	membrane	amino aicd (glutamine/glutamate/aspartate)
LAC1533_RS09465	The ATP-binding Cassette (ABC) Superfamily	binding protein	amino aicd (glutamine/glutamate/aspartate)
LAC1533_RS09470	The ATP-binding Cassette (ABC) Superfamily	binding	phosphate
LAC1533_RS09500	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS09515	The Riboflavin Transporter (RFT) Family		riboflavin uptake
LAC1533_RS09525	The ATP-binding Cassette (ABC) Superfamily	binding	methionine
LAC1533_RS09535	The ATP-binding Cassette (ABC) Superfamily	binding	D-methionine
LAC1533_RS09575	The ATP-binding Cassette (ABC) Superfamily	membrane	sugar
LAC1533_RS09580	The ATP-binding Cassette (ABC) Superfamily	binding protein	sugar
LAC1533_RS09585	The ATP-binding Cassette (ABC) Superfamily	binding	polyamine
LAC1533_RS09715	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonate
LAC1533_RS09735	The Type III (Virulence-related) Secretory Pathway (IIISP) Family		
LAC1533_RS09740	The Type III (Virulence-related) Secretory Pathway (IIISP) Family		
LAC1533_RS09745	The Type III (Virulence-related) Secretory Pathway (IIISP) Family		
LAC1533_RS09750	The Type III (Virulence-related) Secretory Pathway (IIISP) Family		
LAC1533_RS09755	The Type III (Virulence-related) Secretory Pathway (IIISP) Family		
LAC1533_RS09810	The Type III (Virulence-related) Secretory Pathway (IIISP) Family		
LAC1533_RS09835	The OmpA-OmpF Porin (OOP) Family		
LAC1533_RS09840	The H+- or Na+-translocating Bacterial Flagellar Motor 1ExbBD Outer Membrane Transport Energizer (Mo		
LAC1533_RS09935	Sugar Specific PTS	EnzymeIIB	fructose
LAC1533_RS09940	Sugar Specific PTS	EnzymeIIA	fructose
LAC1533_RS09950	Sugar Specific PTS	EnzymeIIA	fructose
LAC1533_RS09995	The Resistance to Homoserine/Threonine (RhtB) Family		tellurium ion efflux
LAC1533_RS10035	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS10040	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS10110	Sugar Specific PTS	EnzymeIIC	galactitol
LAC1533_RS10115	Sugar Specific PTS	EnzymeIIB	galactitol
LAC1533_RS10120	Sugar Specific PTS	EnzymeIIA	fructose
LAC1533_RS10220	Sugar Specific PTS	EnzymeIIABC	cellobiose
LAC1533_RS10265	The P-type ATPase (P-ATPase) Superfamily		zinc/cadmium/cobalt ion
LAC1533_RS10335	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	PST	polysaccharide export
LAC1533_RS10510	Sugar Specific PTS	EnzymeIIABC	fructose
LAC1533_RS10560	The Monovalent Cation:Proton Antiporter-2 (CPA2) Family		potassium/sodium ion:proton antiporter
LAC1533_RS10605	The Dicarboxylate/Amino Acid:Cation (Na+ or H+) Symporter (DAACS) Family		sodium ion:serine/threonine symporter
LAC1533_RS10685	The ATP-binding Cassette (ABC) Superfamily	membrane	amino aicd (glutamine/glutamate/aspartate)
LAC1533_RS10705	The Major Facilitator Superfamily (MFS)		multidrug efflux (EmrB/QacA subfamily)
LAC1533_RS10805	The ATP-binding Cassette (ABC) Superfamily	binding protein	
LAC1533_RS10810	The ATP-binding Cassette (ABC) Superfamily	membrane	
LAC1533_RS10815	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonate
LAC1533_RS10865	The Biotin Uptake Transporter (BUT) Family		
LAC1533_RS10870	The ATP-binding Cassette (ABC) Superfamily	membrane	cobalt ion
LAC1533_RS10875	The ATP-binding Cassette (ABC) Superfamily	binding	cobalt
LAC1533_RS10880	The ATP-binding Cassette (ABC) Superfamily	membrane	
LAC1533_RS10895	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS10935	The ATP-binding Cassette (ABC) Superfamily	membrane	amino aicd (glutamine/glutamate/aspartate)
LAC1533_RS10940	The ATP-binding Cassette (ABC) Superfamily	binding	sulfate
LAC1533_RS10945	The ATP-binding Cassette (ABC) Superfamily	binding protein	amino acid (glutamine/glutamate/aspartate)
LAC1533_RS11000	The Drug/Metabolite Transporter (DMT) Superfamily	GRP	glucose uptake (GRP subfamily)
LAC1533_RS11065	The P-type ATPase (P-ATPase) Superfamily		copper ion
LAC1533_RS11150	The Metal Ion (Mn2+-iron) Transporter (Nramp) Family		manganese/iron ion
LAC1533_RS11235	The ATP-binding Cassette (ABC) Superfamily	binding	lipoprotein
LAC1533_RS11250	The Amino Acid-Polyamine-Organocation (APC) Family		arginine:ornithine antiporter
LAC1533_RS11295	The Amino Acid-Polyamine-Organocation (APC) Family		amino acid
LAC1533_RS11320	Sugar Specific PTS	EnzymeIIABC	glucose
LAC1533_RS11345	Sugar Specific PTS	EnzymeIIABC	glucose/maltose/N-acetylglucosamine
LAC1533_RS11380	Sugar Specific PTS	EnzymeIIA	mannitol/fructose
LAC1533_RS11385	Sugar Specific PTS	EnzymeIIABC	mannitol
LAC1533_RS11395	Sugar Specific PTS	EnzymeIID	mannose/fructose

LAC1533_RS11400	Sugar Specific PTS	EnzymeIIC	mannose/fructose
LAC1533_RS11405	Sugar Specific PTS	EnzymeIIB	mannose/fructose
LAC1533_RS11415	Sugar Specific PTS	EnzymeIIA	mannose/fructose
LAC1533_RS11490	The ATP-binding Cassette (ABC) Superfamily	binding	phosphate
LAC1533_RS11525	The Major Facilitator Superfamily (MFS)		multidrug efflux (EmrB/QacA subfamily)
LAC1533_RS11545	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS11550	The ATP-binding Cassette (ABC) Superfamily	membrane	glycine betaine/L-proline
LAC1533_RS11555	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS11565	Sugar Specific PTS	EnzymeIIC	cellobiose
LAC1533_RS11615	The Nucleobase:Cation Symporter-2 (NCS2) Family		xanthine/uracil
LAC1533_RS11630	The Dicarboxylate/Amino Acid:Cation (Na+ or H+) Symporter (DAACS) Family		proton/sodium ion:glutamate/aspartate symporter
LAC1533_RS11670	Sugar Specific PTS	EnzymeIIA	cellobiose
LAC1533_RS11675	Sugar Specific PTS	EnzymeIIB	cellobiose
LAC1533_RS11710	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	PST	polysaccharide export
LAC1533_RS11825	The ATP-binding Cassette (ABC) Superfamily	binding	heme
LAC1533_RS11850	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS11855	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS11870	The Metal Ion (Mn2+-iron) Transporter (Nramp) Family		manganese/iron ion
LAC1533_RS11885	The Gluconate:H+ Symporter (GntP) Family		gluconate
LAC1533_RS11920	The Major Facilitator Superfamily (MFS)		multidrug efflux (EmrB/QacA subfamily)
LAC1533_RS11950	The Amino Acid-Polyamine-Organocation (APC) Family		glutamate:GABA antiporter
LAC1533_RS11990	The CorA Metal Ion Transporter (MIT) Family		magnesium/cobalt ion
LAC1533_RS12010	The Amino Acid-Polyamine-Organocation (APC) Family		GABA
LAC1533_RS12015	The ATP-binding Cassette (ABC) Superfamily	binding	phosphonate
LAC1533_RS12020	The ATP-binding Cassette (ABC) Superfamily	membrane	cobalamin/Fe3+-siderophores
LAC1533_RS12025	The ATP-binding Cassette (ABC) Superfamily	membrane	cobalamin/Fe3+-siderophores
LAC1533_RS12030	The ATP-binding Cassette (ABC) Superfamily	binding	iron-hydroxamate
LAC1533_RS12045	The Biotin Uptake Transporter (BUT) Family		biotin uptake
LAC1533_RS12060	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS12095	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	PST	polysaccharide export
LAC1533_RS12120	The ATP-binding Cassette (ABC) Superfamily	membrane	
LAC1533_RS12125	The ATP-binding Cassette (ABC) Superfamily	binding	glycine betaine
LAC1533_RS12205	The Metal Ion (Mn2+-iron) Transporter (Nramp) Family		manganese/iron ion
LAC1533_RS12245	The Major Facilitator Superfamily (MFS)		multidrug efflux
LAC1533_RS12260	The Cytochrome Oxidase Biogenesis (Oxa1) Family		60 KD inner membrane protein OxaA homolog
pLAC2			
locus_tag	**Transporter Family**	**Subfamily**	**Substrate/Function**
PLAC2_P29	Sugar Specific PTS	EnzymeIICD	mannose/fructose
PLAC2_P30	Sugar Specific PTS	EnzymeIIA	mannose/fructose
PLAC2_P31	Sugar Specific PTS	EnzymeIIB	mannose/fructose
PLAC2_P43	The Resistance-Nodulation-Cell Division (RND) Superfamily	HAE2	multidrug/solvent efflux (MmpL homolog/HAE2 subfamily)
PLAC2_P49	The Monovalent Cation:Proton Antiporter-2 (CPA2) Family		potassium/sodium ion:proton antiporter
PLAC2_P50	The P-type ATPase (P-ATPase) Superfamily		calcium ion

Supplementary table S11. Putative enzymes involved in carbohydrate metabolism of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 genomes.

Glycoside Hydrolases	***Lactobacillus acidipiscis*** **ACA-DC 1533**	***Lactobacillus salivarius*** **UCC118**	***Lactobacillus ruminis*** **ATCC27782**
Enzyme family	**No. of enzymes***		
GH1	5	0	4
GH2	0	1	0
GH3	0	1	1
GH4	2	1	0
GH9	0	1	1
GH13	7	6	6
GH20	2	3	3
GH23	1	0	0
GH25	4	4	2
GH29	1	1	0
GH31	4	1	2
GH32	0	1	1
GH35	1	0	0
GH36	1	1	0
GH38	1	0	0
GH46	1	0	0
GH65	1	1	1
GH70	1	0	0
GH73	2	2	2
GH76	1	0	0
GH109	2	2	3
GH126	0	1	0
Total	**37**	**27**	**26**
Glycosyl Transferases	***Lactobacillus acidipiscis ACA-DC 1533***	***Lactobacillus salivarius*** **UCC118**	***Lactobacillus ruminis*** **ATCC27782**
Enzyme family	**No. of enzymes**		
GT2	5	9	11
GT4	6	13	2
GT5	0	1	1
GT8	5	0	1
GT14	0	1	2
GT26	1	1	1
GT28	1	1	1
GT32	1	2	0
GT35	0	1	0
GT51	2	2	1
Total	**21**	**31**	**20**

Carbohydrate Esterases	***Lactobacillus acidipiscis*** **ACA-DC 1533**	***Lactobacillus salivarius*** **UCC118**	***Lactobacillus ruminis*** **ATCC27782**
Enzyme family	**No. of enzymes**		
CE1	6	2	4
CE3	1	0	1
CE4	0	1	1
CE9	2	1	1
CE10	3	1	4
CE12	1	2	0
Total	**13**	**7**	**11**
Carbohydrate-Binding Modules	***Lactobacillus acidipiscis*** **ACA-DC 1533**	***Lactobacillus salivarius*** **UCC118**	***Lactobacillus ruminis*** **ATCC27782**
Enzyme family	**No. of enzymes**		
CBM34	2	3	3
CBM48	0	1	1
CBM50	12	9	7
Total	**14**	**13**	**11**

*To identify enzymes involved in carbohydrate metabolism we used E-value < 1e − 3 as the cutoff for alignments shorter than 80 amino acids and E-value < 1e − 5 for alignments longer than 80 amino acids according to the instructions in the dbCAN cite.

Supplemetnaty table S12. Acid production by *L. acidi*

Substrate	**Abbrev.**	**Values**
Negative control		-
Glycerol	GLY	-
Erythritol	ERY	-
D-Arabinose	DARA	-
L-Arabinose	LARA	+
D-Ribose	RIB	+
D-Xylose	DXYL	-
L-Xylose	LXYL	-
D-adonitol	ADO	-
Methyl-βD-Xylopyranoside	MDX	-
D-Galactose	GAL	+
D-Glucose	GLU	+
D-Fructose	FRU	+
D-Mannose	MNE	+
L-Sorbose	SBE	-
L-Rhamnose	RHA	-
Dulcitol	DUL	-
Inositol	INO	-
D-Mannitol	MAN	+
D-Sorbitol	SOR	-
Methyl-αD-mannopyranoside	MDM	-
Methyl-αD-glucopyranoside	MDG	-
N-acetyl-glucosamine	NAG	+

Amygdalin	AMY	+
Arbutin	ARB	-
Esculin	ESC	+
Salicin	SAL	-
D-Cellobiose	CEL	+
D-Maltose	MAL	+
D-Lactose	LAC	+
D-Melibiose	MEL	-
D-Saccharose	SAC	-
D-Trehalose	TRE	+
Inulin	INU	-
D-Melezitose	MLZ	-
D-Raffinose	RAF	-
Amidon (starch)	AMD	-
Glycogen	GLYG	-
Xylitol	XLT	-
β-gentiobiose	GEN	+
D-Tyranose	TUR	-
D-Lyxose	LYX	-
D-Tagatose	TAG	-
D-Fucose	DFUC	-
L-Fucose	LFUC	-
D-Arabitol	DARL	-
L-Arabitol	LARL	-
Gluconate	GNT	-
2-ketogluconate	2KG	-
5-ketogluconate	5KG	-

Supplementary table S13. The proteolytic system of *L. acidipiscis*, *L. salivarius* and *L. ruminis* chromosomes and/or genomes.

Description	**Gene**	***Lactobacillus acidipiscis* ACA-DC 1533**	***Lactobacillus acidipiscis* KCTC 13900**	***Lactobacillus acidipiscis* JCM 10692^T**	***Lactobacillus salivarius* UCC118**	***Lactobacillus ruminis* ATCC 27782**
Cell-wall bound proteinase	*prtP*	-	-	-	-	-
Oligopeptide ABC transporter, substrate-binding protein	*oppA*	LAC1533_RS01520	-	Lacidipiscis_RS07750	-	LRC_RS09070
Oligopeptide ABC transporter, permease protein	*oppB*	LAC1533_RS01515	-	Lacidipiscis_RS07745	-	LRC_RS09075
Oligopeptide ABC transporter, permease protein	*oppC*	LAC1533_RS01510	-	Lacidipiscis_RS07740	-	LRC_RS09080
Oligopeptide ABC transporter, ATP-binding protein	*oppD*	LAC1533_RS01505	-	Lacidipiscis_RS07735	-	LRC_RS09085
Oligopeptide ABC transporter, ATP-binding protein	*oppF*	LAC1533_RS01500	-	Lacidipiscis_RS07730	-	LRC_RS09090
Di/tripeptide ABC transporter, substrate-binding protein	*dppA/P*	LAC1533_RS09435	GSS_RS08270	Lacidipiscis_RS09065	LSL_1699	LRC_RS00985
Di/tripeptide ABC transporter, permease protein	*dppB*	LAC1533_RS09430	GSS_RS08275	Lacidipiscis_RS09060	LSL_1698	LRC_RS00990
Di/tripeptide ABC transporter, permease protein	*dppC*	LAC1533_RS09425	GSS_RS08280	Lacidipiscis_RS09055	LSL_1697	LRC_RS00995
Di/tripeptide ABC transporter, ATP-binding protein	*dppD*	LAC1533_RS09420	-	Lacidipiscis_RS09050	LSL_1696	LRC_RS01000
Di/tripeptide ABC transporter, ATP-binding protein	*dppF*	LAC1533_RS09415	GSS_RS08295	Lacidipiscis_RS09045	LSL_1695	LRC_RS01005
Di-/tripeptide transporter	*dtpT*	LAC1533_RS03920	GSS_RS07250	Lacidipiscis_RS00675	LSL_1265	LRC_RS01990
Cysteine aminopeptidase C	*pepC*	LAC1533_RS08785	GSS_RS05140	Lacidipiscis_RS08125	LSL_1253	LRC_RS02100
Aminopeptidase N	*pepN*	LAC1533_RS11090	GSS_RS07125	Lacidipiscis_RS10885	LSL_1745	LRC_RS05905
Methionine aminopeptidase	*pepM*	LAC1533_RS08250	GSS_RS05555	Lacidipiscis_RS02570	LSL_1269	LRC_RS03615
		LAC1533_RS12000	GSS_RS03380	Lacidipiscis_RS12345	-	-
Aminopeptidase A	*pepA*	-	-	-	-	-
Pyroglutamyl aminopeptidase	*pcp*	LAC1533_RS09565	GSS_RS08155	Lacidipiscis_RS10815	-	LRC_RS00085
Endopeptidase	*pepE/pepG*	-	-	-	-	-
Endopeptidase	*pepO*	LAC1533_RS11145	GSS_RS07170	Lacidipiscis_RS08195	LSL_1669	LRC_RS09950
Oligoendopeptidase	*pepF*	LAC1533_RS08005	GSS_RS09450	-	LSL_0398	LRC_RS04185
		-	-	-	LSL_0025	LRC_RS00115
Dipeptidase	*pepD*	LAC1533_RS02250	GSS_RS09170	Lacidipiscis_RS11680	-	-
		LAC1533_RS02655	GSS_RS05880	-	LSL_0179	LRC_RS08555
		LAC1533_RS06560	-	Lacidipiscis_RS10275	LSL_1006	LRC_RS04700
Xaa-His dipeptidase	*pepV*	-	-	-	LSL_0447	LRC_RS07460
Peptidase T	*pepT*	LAC1533_RS06055	GSS_RS03805	Lacidipiscis_RS11240	LSL_0848	LRC_RS05505
		LAC1533_RS09260	GSS_RS08435	Lacidipiscis_RS04740	-	-
X-prolyl-dipeptidyl aminopeptidase	*pepX*	LAC1533_RS09520	GSS_RS08205	Lacidipiscis_RS07310	LSL_1534	LRC_RS00920
Proline peptidase	*pepI*	LAC1533_RS01575	-	Lacidipiscis_RS07800	-	LRC_RS00245
Proline peptidase	*pepR*	LAC1533_RS09545	GSS_RS08175	Lacidipiscis_RS07335	-	LRC_RS00905
Proline peptidase	*pepL*	-	-	-	-	-
Aminopeptidase P	*pepP*	LAC1533_RS06680	-	-	LSL_1084	LRC_RS04460
Xaa-proline dipeptidase	*pepQ*	LAC1533_RS04520	GSS_RS07780	Lacidipiscis_RS11875	LSL_0419	LRC_RS07740

Supplementary table S14. Insertion sequences (ISs) identified among the *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 chromosomes using the ISsaga platform.

***Lactobacillus acidipiscis* ACA-DC 1533**				***Lactobacillus salivarius* UCC118**				***Lactobacillus ruminis* ATCC 27782**			
IS Family	**Subgroup**	**ORFs Distribution***	**Different IS(s)**	**IS Family**	**Subgroup**	**ORFs Distribution***	**Different IS(s)**	**IS Family**	**Subgroup**	**ORFs Distribution***	**Different IS(s)**
ISL3		[37 / 1 / 13 / 7]	10	ISL3		[0 / 2 / 6 / 17]	2	IS200_IS605	ssgr_IS1341	[6 / 4 / 0 / 4]	7
IS5	ssgr_IS427	[1 / 0 / 4 / 0]	1	IS200_IS605	ssgr_IS200	[1 / 0 / 1 / 0]	1	ISL3		[0 / 2 / 0 / 3]	4
IS3	Issgr_IS3	[0 / 1 / 0 / 0]	1	IS256		[0 / 0 / 1 / 0]	1	IS607		[0 / 1 / 0 / 0]	1
IS6		[0 / 0 / 0 / 2]	1	IS30		[0 / 0 / 1 / 0]	1	IS256		[8 / 5 / 0 / 0]	1
ISLre2		[0 / 0 / 0 / 8]	2	IS3	ssgr_IS150	[2 / 1 / 1 / 1]	2	IS4	ssgr_ISPepr1	[0 / 3 / 0 / 1]	3
IS200_IS605	ssgr_IS200	[0 / 0 / 1 / 0]	1	IS200_IS605		[2 / 0 / 0 / 0]	2	IS66		[4 / 3 / 0 / 10]	1
IS256		[17 / 0 / 5 / 0]	4	IS110		[0 / 0 / 1 / 0]	1	IS30		[0 / 0 / 0 / 1]	1
IS4	ssgr_ISPepr1	[7 / 0 / 1 / 0]	1	**Total**			**10**	IS3	ssgr_IS150	[7 / 3 / 0 / 15]	2
IS66		[1 / 0 / 3 / 5]	3					IS200_IS605		[2 / 7 / 0 / 7]	9
IS30		[29 / 0 / 0 / 2]	6					IS21		[5 / 2 / 0 / 0]	1
IS3	ssgr_IS150	[0 / 3 / 0 / 2]	3					**Total**			**30**
IS1182		[1 / 1 / 0 / 1]	3								
IS982		[11 / 2 / 4 / 3]	9								
IS21		[7 / 0 / 2 / 0]	1								
IS1380		[37 / 1 / 11 / 1]	5								
ISNCY**		[1 / 0 / 0 / 1]	2								
Total			**53**								

*[Complete / Partial / Pseudogene / unknown]

**group of unclassified elements

Supplementary table S15. Regulatory proteins identified in the chromosomes of *L. acidipiscis* ACA-DC 1533, *L. salivarius* UCC118 and *L. ruminis* ATCC 27782 using P2RP web server.

	Two-Component Systems		**Transcription Factors**				
Strains	**Histidine Kinases**	**Response Regulators**	**Transcriptional Regulators**	**One-Component Systems**	**Response Regulators**	**Sigma Factors**	**Other DNA-binding Proteins**
***L. acidipiscis* ACA-DC 1533**	6	7	68	28	5	6	19
***L. salivarius* UCC118**	6	7	58	19	6	2	6
***L. ruminis* ATCC 27782**	7	10	50	22	8	3	6