



- PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)|g_Herbaspirillum.s_Herbaspirillum_seropedicae
PWY-7221: guanosine ribonucleotides de novo biosynthesis|g_Lactobacillus.s_Lactobacillus_delbrueckii
PWY-1042: glycolysis IV|g_Lactobacillus.s_Lactobacillus_delbrueckii
ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)|g_Lactobacillus.s_Lactobacillus_delbrueckii
PWY-5384: sucrose degradation IV (sucrose phosphorylase)|g_Lactobacillus.s_Lactobacillus_delbrueckii
PWY-621: sucrose degradation III (sucrose invertase)|g_Lactobacillus.s_Lactobacillus_delbrueckii
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)|g_Lactobacillus.s_Lactobacillus_delbrueckii
PWY-5686: UMP biosynthesis II|g_Lactobacillus.s_Lactobacillus_delbrueckii
PWY-7663: gondoate biosynthesis (anaerobic)|g_Lactobacillus.s_Lactobacillus_delbrueckii
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)|g_Lactobacillus.s_Lactobacillus_delbrueckii
PWY-7791: UMP biosynthesis III|g_Lactobacillus.s_Lactobacillus_avarius
PWY-5686: UMP biosynthesis II|g_Lactobacillus.s_Lactobacillus_avarius
PWY-7790: UMP biosynthesis II|g_Lactobacillus.s_Lactobacillus_avarius
PWY-3841: folate transformations II (plants)|g_Lactobacillus.s_Lactobacillus_fermentum
COA-PWY-1: superpathway of coenzyme A biosynthesis III (mammals)|g_Lactobacillus.s_Lactobacillus_fermentum
COA-PWY: coenzyme A biosynthesis I (prokaryotic)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-7851: coenzyme A biosynthesis II (eukaryotic)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-5973: cis-vaccenate biosynthesis|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-7663: gondoate biosynthesis (anaerobic)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis|g_Lactobacillus.s_Lactobacillus_fermentum
SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
GLUTORN-PWY: L-ornithine biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-7953: UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)|g_Lactobacillus.s_Lactobacillus_fermentum
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-5154: L-arginine biosynthesis III (via N-acetyl-L-citrulline)|g_Lactobacillus.s_Lactobacillus_fermentum
ARGSYNSUB-PWY: L-arginine biosynthesis II (acetyl cycle)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6897: thiamine diphosphate salvage II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-724: superpathway of L-lysine, L-threonine and L-methionine biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-2942: L-lysine biosynthesis III|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-7357: thiamine phosphate formation from pyrimidine and oxythiamine (yeast)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-5097: L-lysine biosynthesis VI|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-2941: L-lysine biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-5384: sucrose degradation IV (sucrose phosphorylase)|g_Lactobacillus.s_Lactobacillus_avarius
PWY-6527: stachyose degradation|g_Lactobacillus.s_Lactobacillus_avarius
PWY-8187: L-arginine degradation XIII (reductive Stickland reaction)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-7356: thiamine diphosphate salvage IV (yeast)|g_Lactobacillus.s_Lactobacillus_fermentum
ARGSYN-PWY: L-arginine biosynthesis I (via L-ornithine)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6385: peptidoglycan biosynthesis III (mycobacteria)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY66-429: fatty acid biosynthesis initiation (mitochondria)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-7400: L-arginine biosynthesis IV (archaeobacteria)|g_Lactobacillus.s_Lactobacillus_fermentum
HISTSYN-PWY: L-histidine biosynthesis|g_Lactobacillus.s_Lactobacillus_fermentum
P124-PWY: Bifidobacterium shunt|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6797: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (Methanocaldococcus)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6151: S-adenosyl-L-methionine salvage II|g_Lactobacillus.s_Lactobacillus_fermentum
UDPNACETYLGALSIN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
TRNA-CHARGING-PWY: tRNA charging|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6470: peptidoglycan biosynthesis V (β-lactam resistance)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6471: peptidoglycan biosynthesis IV (Enterococcus faecium)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6124: inosine-5'-phosphate biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6123: inosine-5'-phosphate biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-7234: inosine-5'-phosphate biosynthesis III|g_Lactobacillus.s_Lactobacillus_fermentum
UDPNAGSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis II|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6936: seleno-amino acid biosynthesis (plants)|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6527: stachyose degradation|g_Lactobacillus.s_Lactobacillus_fermentum
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II|g_Lactobacillus.s_Lactobacillus_avarius
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PWY-7234: inosine-5'-phosphate biosynthesis III|g_Lactobacillus.s_Lactobacillus_avarius

Taxon