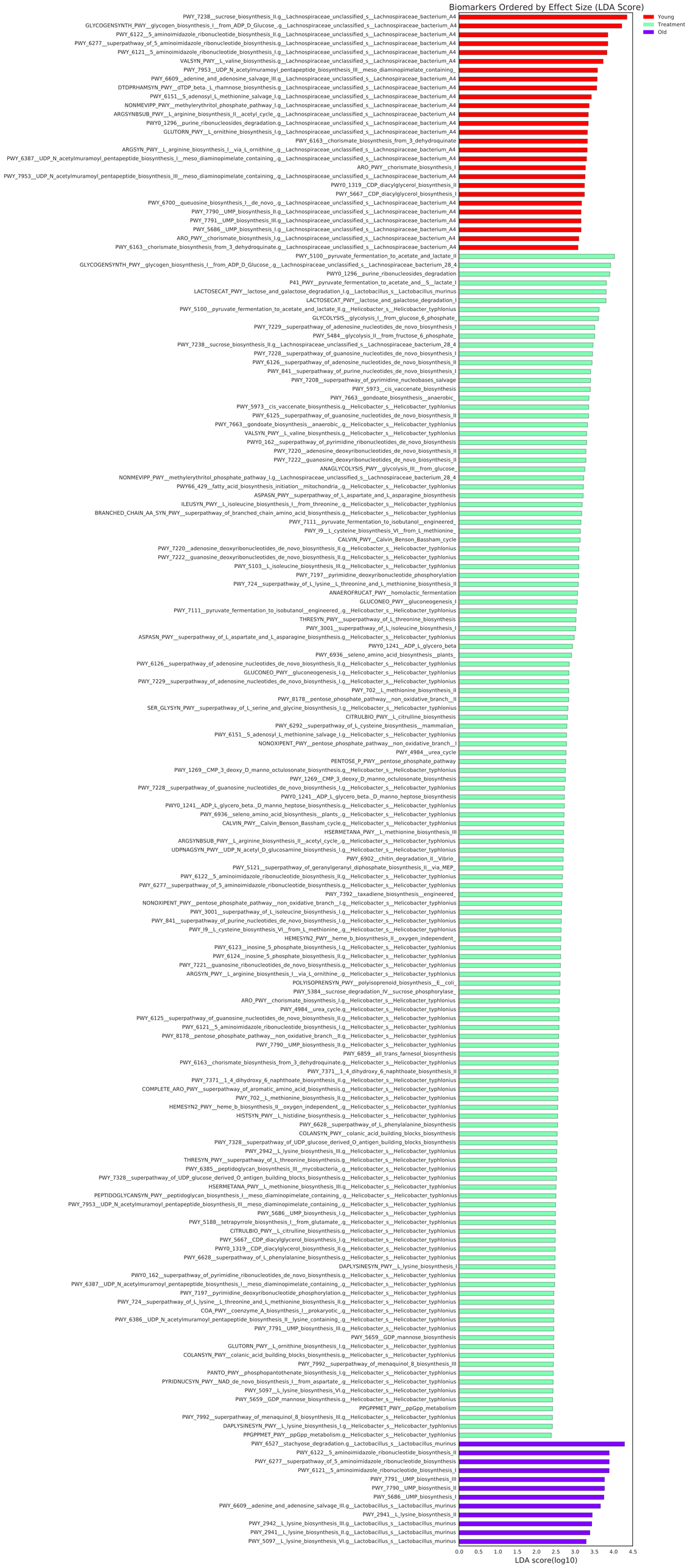
Biomarkers Ordered by Effect Size (LDA Score)
Young
Treatment
Old
PWY_7238__sucrose_biosynthesis_II.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
VALSYN_PWY__L_valine_biosynthesis.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_7953__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_III__meso_diaminopimelate_containing_
PWY_6609__adenine_and_adenosine_salvage_III.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
DTDPRHAMSYN_PWY__dTDP_beta._L_rhamnose_biosynthesis.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_6151__S_adenosyl_L_methionine_salvage_I.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
ARGSYNBSUB_PWY__L_arginine_biosynthesis_II__acetyl_cycle_.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY0_1296__purine_ribonucleosides_degradation.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
GLUTORN_PWY__L_ornithine_biosynthesis_I.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_6163__chorismate_biosynthesis_from_3_dehydroquinate
ARGSYN_PWY__L_arginine_biosynthesis_I__via_L_ornithine_.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
ARO_PWY__chorismate_biosynthesis_I
PWY_7953__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_III__meso_diaminopimelate_containing_.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY0_1319__CDP_diacylglycerol_biosynthesis_II
PWY_5667__CDP_diacylglycerol_biosynthesis_I
PWY_6700__queuosine_biosynthesis_I__de_novo_.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_7790__UMP_biosynthesis_II.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_7791__UMP_biosynthesis_III.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_5686__UMP_biosynthesis_I.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
ARO_PWY__chorismate_biosynthesis_I.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_6163__chorismate_biosynthesis_from_3_dehydroquinate.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_A4
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II
GLYCOGENSYNTH_PWY__glycogen_biosynthesis_I__from_ADP_D_Glucose_.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_28_4
PWY0_1296__purine_ribonucleosides_degradation
P41_PWY__pyruvate_fermentation_to_acetate_and__S__lactate_I
LACTOSECAT_PWY__lactose_and_galactose_degradation_I.g__Lactobacillus_s__Lactobacillus_murinus
LACTOSECAT_PWY__lactose_and_galactose_degradation_I
PWY_5100__pyruvate_fermentation_to_acetate_and_lactate_II.g__Helicobacter_s__Helicobacter_typhlonius
GLYCOLYSIS__glycolysis_I__from_glucose_6_phosphate_
PWY_7229__superpathway_of_adenosine_nucleotides_de_novo_biosynthesis_I
PWY_5484__glycolysis_II__from_fructose_6_phosphate_
PWY_7238__sucrose_biosynthesis_II.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_28_4
PWY_7228__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_I
PWY_6126__superpathway_of_adenosine_nucleotides_de_novo_biosynthesis_II
PWY_841__superpathway_of_purine_nucleotides_de_novo_biosynthesis_I
PWY_7208__superpathway_of_pyrimidine_nucleobases_salvage
PWY_5973__cis_vaccenate_biosynthesis
PWY_7663__gondoate_biosynthesis__anaerobic_
PWY_5973__cis_vaccenate_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6125__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_II
PWY_7663__gondoate_biosynthesis__anaerobic_.g__Helicobacter_s__Helicobacter_typhlonius
VALSYN_PWY__L_valine_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY0_162__superpathway_of_pyrimidine_ribonucleotides_de_novo_biosynthesis
PWY_7220__adenosine_deoxyribonucleotides_de_novo_biosynthesis_II
PWY_7222__guanosine_deoxyribonucleotides_de_novo_biosynthesis_II
ANAGLYCOLYSIS_PWY__glycolysis_III__from_glucose_
NONMEVIPP_PWY__methylerythritol_phosphate_pathway_I.g__Lachnospiraceae_unclassified_s__Lachnospiraceae_bacterium_28_4
PWY66_429__fatty_acid_biosynthesis_initiation__mitochondria_.g__Helicobacter_s__Helicobacter_typhlonius
ASPASN_PWY__superpathway_of_L_aspartate_and_L_asparagine_biosynthesis
ILEUSYN_PWY__L_isoleucine_biosynthesis_I__from_threonine_.g__Helicobacter_s__Helicobacter_typhlonius
BRANCHED_CHAIN_AA_SYN_PWY__superpathway_of_branched_chain_amino_acid_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_
PWY_I9__L_cysteine_biosynthesis_VI__from_L_methionine_
CALVIN_PWY__Calvin_Benson_Bassham_cycle
PWY_7220__adenosine_deoxyribonucleotides_de_novo_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7222__guanosine_deoxyribonucleotides_de_novo_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_5103__L_isoleucine_biosynthesis_III.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7197__pyrimidine_deoxyribonucleotide_phosphorylation
PWY_724__superpathway_of_L_lysine__L_threonine_and_L_methionine_biosynthesis_II
ANAEROFRUCAT_PWY__homolactic_fermentation
GLUCONEO_PWY__gluconeogenesis_I
PWY_7111__pyruvate_fermentation_to_isobutanol__engineered_.g__Helicobacter_s__Helicobacter_typhlonius
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis
PWY_3001__superpathway_of_L_isoleucine_biosynthesis_I
ASPASN_PWY__superpathway_of_L_aspartate_and_L_asparagine_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY0_1241__ADP_L_glycero_beta
PWY_6936__seleno_amino_acid_biosynthesis__plants_
PWY_6126__superpathway_of_adenosine_nucleotides_de_novo_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
GLUCONEO_PWY__gluconeogenesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7229__superpathway_of_adenosine_nucleotides_de_novo_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_702__L_methionine_biosynthesis_II
PWY_8178__pentose_phosphate_pathway__non_oxidative_branch__II
SER_GLYSYN_PWY__superpathway_of_L_serine_and_glycine_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
CITRULBIO_PWY__L_citrulline_biosynthesis
PWY_6292__superpathway_of_L_cysteine_biosynthesis__mammalian_
PWY_6151__S_adenosyl_L_methionine_salvage_I.g__Helicobacter_s__Helicobacter_typhlonius
NONOXIPENT_PWY__pentose_phosphate_pathway__non_oxidative_branch__I
PWY_4984__urea_cycle
PENTOSE_P_PWY__pentose_phosphate_pathway
PWY_1269__CMP_3_deoxy_D_manno_octulosonate_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_1269__CMP_3_deoxy_D_manno_octulosonate_biosynthesis
PWY_7228__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY0_1241__ADP_L_glycero_beta._D_manno_heptose_biosynthesis
PWY0_1241__ADP_L_glycero_beta._D_manno_heptose_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6936__seleno_amino_acid_biosynthesis__plants_.g__Helicobacter_s__Helicobacter_typhlonius
CALVIN_PWY__Calvin_Benson_Bassham_cycle.g__Helicobacter_s__Helicobacter_typhlonius
HSERMETANA_PWY__L_methionine_biosynthesis_III
ARGSYNBSUB_PWY__L_arginine_biosynthesis_II__acetyl_cycle_.g__Helicobacter_s__Helicobacter_typhlonius
UDPNAGSYN_PWY__UDP_N_acetyl_D_glucosamine_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6902__chitin_degradation_II__Vibrio_
PWY_5121__superpathway_of_geranylgeranyl_diphosphate_biosynthesis_II__via_MEP_
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7392__taxadiene_biosynthesis__engineered_
NONOXIPENT_PWY__pentose_phosphate_pathway__non_oxidative_branch__I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_3001__superpathway_of_L_isoleucine_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_841__superpathway_of_purine_nucleotides_de_novo_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_I9__L_cysteine_biosynthesis_VI__from_L_methionine_.g__Helicobacter_s__Helicobacter_typhlonius
HEMESYN2_PWY__heme_b_biosynthesis_II__oxygen_independent_
PWY_6123__inosine_5_phosphate_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6124__inosine_5_phosphate_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7221__guanosine_ribonucleotides_de_novo_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
ARGSYN_PWY__L_arginine_biosynthesis_I__via_L_ornithine_.g__Helicobacter_s__Helicobacter_typhlonius
POLYISOPRENSYN_PWY__polyisoprenoid_biosynthesis__E__coli_
PWY_5384__sucrose_degradation_IV__sucrose_phosphorylase_
ARO_PWY__chorismate_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_4984__urea_cycle.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6125__superpathway_of_guanosine_nucleotides_de_novo_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_8178__pentose_phosphate_pathway__non_oxidative_branch__II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7790__UMP_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6859__all_trans_farnesol_biosynthesis
PWY_6163__chorismate_biosynthesis_from_3_dehydroquinate.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7371__1_4_dihydroxy_6_naphthoate_biosynthesis_II
PWY_7371__1_4_dihydroxy_6_naphthoate_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
COMPLETE_ARO_PWY__superpathway_of_aromatic_amino_acid_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_702__L_methionine_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
HEMESYN2_PWY__heme_b_biosynthesis_II__oxygen_independent_.g__Helicobacter_s__Helicobacter_typhlonius
HISTSYN_PWY__L_histidine_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6628__superpathway_of_L_phenylalanine_biosynthesis
COLANSYN_PWY__colanic_acid_building_blocks_biosynthesis
PWY_7328__superpathway_of_UDP_glucose_derived_O_antigen_building_blocks_biosynthesis
PWY_2942__L_lysine_biosynthesis_III.g__Helicobacter_s__Helicobacter_typhlonius
THRESYN_PWY__superpathway_of_L_threonine_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6385__peptidoglycan_biosynthesis_III__mycobacteria_.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7328__superpathway_of_UDP_glucose_derived_O_antigen_building_blocks_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
HSERMETANA_PWY__L_methionine_biosynthesis_III.g__Helicobacter_s__Helicobacter_typhlonius
PEPTIDOGLYCANSYN_PWY__peptidoglycan_biosynthesis_I__meso_diaminopimelate_containing_.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7953__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_III__meso_diaminopimelate_containing_.g__Helicobacter_s__Helicobacter_typhlonius
PWY_5686__UMP_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY_5188__tetrapyrrole_biosynthesis_I__from_glutamate_.g__Helicobacter_s__Helicobacter_typhlonius
CITRULBIO_PWY__L_citrulline_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_5667__CDP_diacylglycerol_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PWY0_1319__CDP_diacylglycerol_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6628__superpathway_of_L_phenylalanine_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I
PWY0_162__superpathway_of_pyrimidine_ribonucleotides_de_novo_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6387__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_I__meso_diaminopimelate_containing_.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7197__pyrimidine_deoxyribonucleotide_phosphorylation.g__Helicobacter_s__Helicobacter_typhlonius
PWY_724__superpathway_of_L_lysine__L_threonine_and_L_methionine_biosynthesis_II.g__Helicobacter_s__Helicobacter_typhlonius
COA_PWY__coenzyme_A_biosynthesis_I__prokaryotic_.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6386__UDP_N_acetylmuramoyl_pentapeptide_biosynthesis_II__lysine_containing_.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7791__UMP_biosynthesis_III.g__Helicobacter_s__Helicobacter_typhlonius
PWY_5659__GDP_mannose_biosynthesis
GLUTORN_PWY__L_ornithine_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
COLANSYN_PWY__colanic_acid_building_blocks_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PWY_7992__superpathway_of_menaquinol_8_biosynthesis_III
PANTO_PWY__phosphopantothenate_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PYRIDNUCSYN_PWY__NAD_de_novo_biosynthesis_I__from_aspartate_.g__Helicobacter_s__Helicobacter_typhlonius
PWY_5097__L_lysine_biosynthesis_VI.g__Helicobacter_s__Helicobacter_typhlonius
PWY_5659__GDP_mannose_biosynthesis.g__Helicobacter_s__Helicobacter_typhlonius
PPGPPMET_PWY__ppGpp_metabolism
PWY_7992__superpathway_of_menaquinol_8_biosynthesis_III.g__Helicobacter_s__Helicobacter_typhlonius
DAPLYSINESYN_PWY__L_lysine_biosynthesis_I.g__Helicobacter_s__Helicobacter_typhlonius
PPGPPMET_PWY__ppGpp_metabolism.g__Helicobacter_s__Helicobacter_typhlonius
PWY_6527__stachyose_degradation.g__Lactobacillus_s__Lactobacillus_murinus
PWY_6122__5_aminoimidazole_ribonucleotide_biosynthesis_II
PWY_6277__superpathway_of_5_aminoimidazole_ribonucleotide_biosynthesis
PWY_6121__5_aminoimidazole_ribonucleotide_biosynthesis_I
PWY_7791__UMP_biosynthesis_III
PWY_7790__UMP_biosynthesis_II
PWY_5686__UMP_biosynthesis_I
PWY_6609__adenine_and_adenosine_salvage_III.g__Lactobacillus_s__Lactobacillus_murinus
PWY_2941__L_lysine_biosynthesis_II
PWY_2942__L_lysine_biosynthesis_III.g__Lactobacillus_s__Lactobacillus_murinus
PWY_2941__L_lysine_biosynthesis_II.g__Lactobacillus_s__Lactobacillus_murinus
PWY_5097__L_lysine_biosynthesis_VI.g__Lactobacillus_s__Lactobacillus_murinus
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
LDA score(log10)