

ociations (−log(qval)*sign(coeff))

amino_acid_biosynthesis_l_methionine_biosynthesis_via_de_novo_pathway_l_cystathionine_from_o_succinyl_l_homoserine_step_1_1
organic_acid_metabolism_propanoate_degradation
nitrogen_metabolism_nitric_oxide_reduction
polyol_metabolism_1_2_propanediol_degradation
amino_acid_degradation_l_threonine_degradation_via_oxido_reductase_pathway_glycine_from_l_threonine_step_1_2
amino_acid_biosynthesis_l_methionine_biosynthesis_via_de_novo_pathway_o_succinyl_l_homoserine_from_l_homoserine_step_1_1
carbohydrate_acid_metabolism_galactarate_degradation_d_glycerate_from_galactarate_step_1_3
purine_metabolism_imp_biosynthesis_via_de_novo_pathway_n_1_5_phospho_d_ribosyl_glycinamide_from_5_phospho_alpha_d_ribose_1_diphosphate_step_1_2
carbohydrate_acid_metabolism_galactarate_degradation_d_glycerate_from_galactarate_step_3_3
carbohydrate_metabolism_d_sorbitol_degradation_d_fructose_6_phosphate_from_d_sorbitol_6_phosphate_step_1_1
capsule_biogenesis_capsule_polysaccharide_biosynthesis
carbohydrate_degradation_2_deoxy_d_ribose_1_phosphate_degradation_d_glyceraldehyde_3_phosphate_and_acetaldehyde_from_2_deoxy_alpha_d_ribose_1_phosphate_step_2_2
carbohydrate_metabolism_entner_doudoroff_pathway
amino_acid_biosynthesis_l_arginine_biosynthesis_n_2_acetyl_l_ornithine_from_l_glutamate_step_1_4
amino_acid_biosynthesis_l_serine_biosynthesis_l_serine_from_3_phospho_d_glycerate_step_1_3
metabolic_intermediate_biosynthesis_chorismate_biosynthesis_chorismate_from_d_erythrose_4_phosphate_and_phosphoenolpyruvate_step_1_7
amine_and_polyamine_metabolism_carnitine_metabolism
aromatic_compound_metabolism_4_hydroxyphenylacetate_degradation_pyruvate_and_succinate_semialdehyde_from_4_hydroxyphenylacetate_step_6_7
purine_metabolism_pp_gpp_biosynthesis_pp_gpp_from_gdp_step_1_1
cofactor_biosynthesis_pyridoxine_5_phosphate_biosynthesis_pyridoxine_5_phosphate_from_d_erythrose_4_phosphate_step_2_5
porphyrin_containing_compound_metabolism_heme_o_biosynthesis_heme_o_from_protoheme_step_1_1
aromatic_compound_metabolism_phenylacetate_degradation
carbohydrate_metabolism_d_ribose_degradation_d_ribose_5_phosphate_from_beta_d_ribofuranose_step_1_2
carbohydrate_degradation_pentose_phosphate_pathway_d_ribulose_5_phosphate_from_d_glucose_6_phosphate_oxidative_stage_step_2_3
amine_and_polyamine_biosynthesis_betaine_biosynthesis_via_choline_pathway_betaine_from_betaine_aldehyde_step_1_1
purine_metabolism_imp_biosynthesis_via_de_novo_pathway_5_amino_1_5_phospho_d_ribosyl_imidazole_from_n_2_formyl_n_1_5_phospho_d_ribosyl_glycinamide_step_1_2
porphyrin_containing_compound_metabolism_protoheme_biosynthesis
amino_acid_biosynthesis_l_isoleucine_biosynthesis_2_oxobutanoate_from_l_threonine_step_1_1
glycan_metabolism_osmoregulated_periplasmic_glycan_opg_biosynthesis
sulfur_metabolism_hydrogen_sulfide_biosynthesis_sulfite_from_sulfate_step_3_3
porphyrin_containing_compound_metabolism_protoporphyrin_ix_biosynthesis_protoporphyrinogen_ix_from_coproporphyrinogen_iii_o2_route_step_1_1
carbohydrate_degradation_pentose_phosphate_pathway_d_ribulose_5_phosphate_from_d_glucose_6_phosphate_oxidative_stage_step_1_3
amine_and_polyamine_degradation_ethanolamine_degradation
purine_metabolism_imp_biosynthesis_via_salvage_pathway_imp_from_inosine_step_1_1
glycan_biosynthesis_sucrose_metabolism
phospholipid_metabolism_phosphatidylglycerol_biosynthesis_phosphatidylglycerol_from_cdp_diacylglycerol_step_1_2
cofactor_biosynthesis_nad_biosynthesis_nad_from_nicotinamide_d_ribonucleotide_step_1_1
cofactor_biosynthesis_nad_biosynthesis_regulation
cell_wall_biogenesis_peptidoglycan_recycling
carbohydrate_degradation_glycolysis_pyruvate_from_d_glyceraldehyde_3_phosphate_step_5_5
energy_metabolism_oxidative_phosphorylation
amino_acid_biosynthesis_l_lysine_biosynthesis_via_dap_pathway_s_tetrahydronicotinate_from_l_aspartate_step_1_4
carbohydrate_metabolism_tricarboxylic_acid_cycle_oxaloacetate_from_s_malate_quinone_route_step_1_1
carbohydrate_metabolism_tricarboxylic_acid_cycle_isocitrate_from_oxaloacetate_step_1_2
amino_acid_biosynthesis_d_alanine_biosynthesis_d_alanine_from_l_alanine_step_1_1
amino_acid_biosynthesis_l_lysine_biosynthesis_via_dap_pathway_s_tetrahydronicotinate_from_l_aspartate_step_2_4
cofactor_biosynthesis_molybdopterin_biosynthesis
carbohydrate_acid_metabolism_d_gluconate_degradation_regulation
amino_acid_biosynthesis_l_asparagine_biosynthesis_l_asparagine_from_l_aspartate_l_gln_route_step_1_1
genetic_information_processing_dna_replication