	Random-Forest Score (error rate = 100%)
Xylene_degradationPATH.ko00622. Vitamin_B6_metabolismPATH.ko00750. Valineleucine_and_isoleucine_degradationPATH.ko00280.	•
Valineleucine_and_isoleucine_biosynthesisPATH.ko00290. Unclassified_viral_proteins Ubiquitin_systemBR.ko04121. Ubiquinone_and_other_terpenoid.quinone_biosynthesisPATH.ko00130.	
Tyrosine_metabolismPATH.ko00350. Type_I_diabetes_mellitusPATH.ko04940. Two.component_systemPATH.ko02020.	
Two.component_systemBR.ko02022. • TuberculosisPATH.ko05152. • Tryptophan_metabolismPATH.ko00380. • Tropanepiperidine_and_pyridine_alkaloid_biosynthesisPATH.ko00960. •	
TransportersBR.ko02000. · Transport · Translation_factorsBR.ko03012. ·	
Translation • Transfer_RNA_biogenesisBR.ko03016.• Transcription_machineryBR.ko03021.• Transcription_factorsBR.ko03000.•	•
Transcription - Toluene_degradationPATH.ko00623. Thyroid_hormone_synthesisPATH.ko04918.	•
Thiamine_metabolismPATH.ko00730. Terpenoid_backbone_biosynthesisPATH.ko00900. Taurine_and_hypotaurine_metabolismPATH.ko00430. Synthesis_and_degradation_of_ketone_bodiesPATH.ko00072.	
Sulfur_relay_systemPATH.ko00920. Sulfur_metabolismPATH.ko00920. Styrene_degradationPATH.ko00643.	
Structural_proteins - Streptomycin_biosynthesisPATH.ko00521 Steroid_hormone_biosynthesisPATH.ko00140 Steroid_degradationPATH.ko00984	
Staurosporine_biosynthesisPATH.ko00404 Starch_and_sucrose_metabolismPATH.ko00500 Staphylococcus_aureus_infectionPATH.ko05150	
Sphingolipid_signaling_pathwayPATH.ko04071. Sphingolipid_metabolismPATH.ko00600. Signaling_proteins Sesquiterpenoid_and_triterpenoid_biosynthesisPATH.ko00909.	
Selenocompound_metabolismPATH.ko00450. Secretion_systemBR.ko02044. Secondary_metabolism	
Secondary_bile_acid_biosynthesisPATH.ko00121. Salmonella_infectionPATH.ko05132. RIG.I.like_receptor_signaling_pathwayPATH.ko04622. Ribosome_biogenesisBR.ko03009.	
RibosomeBR.ko03011. Riboflavin_metabolismPATH.ko00740. Replication_and_repair	
Quorum_sensingPATH.ko02024. • Pyruvate_metabolismPATH.ko00620. • Pyrimidine_metabolismPATH.ko00240. • Purine_metabolismPATH.ko00230. •	•
Protein_processing · Protein_phosphatases_and_associated_proteinsBR.ko01009. · Protein_kinasesBR.ko01001. ·	
ProteasomeBR.ko03051 Propanoate_metabolismPATH.ko00640 Prolactin_signaling_pathwayPATH.ko04917 Prokaryotic_defense_systemBR.ko02048	•
Prion_diseasesPATH.ko05020. Primary_immunodeficiencyPATH.ko05340. PrenyltransferasesBR.ko01006.	
PPAR_signaling_pathwayPATH.ko03320. • Porphyrin_and_chlorophyll_metabolismPATH.ko00860. • Polyketide_sugar_unit_biosynthesisPATH.ko00523. • Polyketide_biosynthesis_proteinsBR.ko01008. •	
Polycyclic_aromatic_hydrocarbon_degradationPATH.ko00624. Platinum_drug_resistancePATH.ko01524. Plant.pathogen_interactionPATH.ko04626.	
Photosynthesis_proteinsBR.ko00194. Phosphonate_and_phosphinate_metabolismPATH.ko00440. Phosphatidylinositol_signaling_systemPATH.ko04070. Phenylpropanoid_biosynthesisPATH.ko00940.	
Phenylalaninetyrosine_and_tryptophan_biosynthesisPATH.ko00400. Phenylalanine_metabolismPATH.ko00360. PertussisPATH.ko05133.	
PeroxisomePATH.ko04146 Peptidoglycan_biosynthesis_and_degradation_proteinsBR.ko01011 Peptidoglycan_biosynthesisPATH.ko00550 PeptidasesBR.ko01002	•
Pentose_phosphate_pathwayPATH.ko00030. Pentose_and_glucuronate_interconversionsPATH.ko00040. Penicillin_and_cephalosporin_biosynthesisPATH.ko00311.	
Pantothenate_and_CoA_biosynthesisPATH.ko00770. · Oxidative_phosphorylationPATH.ko00190. · Others · Other_glycan_degradationPATH.ko00511. ·	
One_carbon_pool_by_folatePATH.ko00670. Nucleotide_metabolism · Novobiocin_biosynthesisPATH.ko00401.	
Nonribosomal_peptide_structuresPATH.ko01054. Non.alcoholic_fatty_liver_diseaseNAFLDPATH.ko04932. Nitrotoluene_degradationPATH.ko00633. Nitrogen_metabolismPATH.ko00910.	
Nicotinate_and_nicotinamide_metabolismPATH.ko00760. Neomycinkanamycin_and_gentamicin_biosynthesisPATH.ko00524. Naphthalene_degradationPATH.ko00626.	
Monobactam_biosynthesisPATH.ko00261. Mitochondrial_biogenesisBR.ko03029. Mineral_absorptionPATH.ko04978. Methane_metabolismPATH.ko00680.	
Messenger_RNA_biogenesisBR.ko03019. Membrane_traffickingBR.ko04131. MelanogenesisPATH.ko04916. LysosomePATH.ko04142.	
Lysine_degradationPATH.ko00310. Lysine_biosynthesisPATH.ko00300. Longevity_regulating_pathwaymultiple_speciesPATH.ko04213.	
Lipopolysaccharide_biosynthesis_proteinsBR.ko01005. Lipopolysaccharide_biosynthesisPATH.ko00540. Lipoic_acid_metabolismPATH.ko00785. Lipid_metabolism	
Lipid_biosynthesis_proteinsBR.ko01004. · Limonene_and_pinene_degradationPATH.ko00903. · LegionellosisPATH.ko05134. ·	
Isoquinoline_alkaloid_biosynthesisPATH.ko00950. Insulin_resistancePATH.ko04931. Inositol_phosphate_metabolismPATH.ko00562. Huntington_diseasePATH.ko05016.	
Histidine_metabolismPATH.ko00340. GTP.binding_proteinsBR.ko04031. Glyoxylate_and_dicarboxylate_metabolismPATH.ko00630. GlycosyltransferasesBR.ko01003.	
GlycosylphosphatidylinositolGPIanchored_proteinsBR.ko00537. Glycosphingolipid_biosynthesisglobo_and_isoglobo_seriesPATH.ko00603. Glycosaminoglycan_binding_proteinsBR.ko00536.	
GlycolysisGluconeogenesisPATH.ko00010 Glycineserine_and_threonine_metabolismPATH.ko00260 Glycerophospholipid_metabolismPATH.ko00564 Glycerolipid_metabolismPATH.ko00561	
Glycan_metabolism - Glutathione_metabolismPATH.ko00480 Glucosinolate_biosynthesisPATH.ko00966 Global_maps_only -	
Geraniol_degradationPATH.ko00281. General_function_prediction_only Galactose_metabolismPATH.ko00052.	
Furfural_degradationPATH.ko00365. Function_unknown Fructose_and_mannose_metabolismPATH.ko00051. Folate_biosynthesisPATH.ko00790.	
Fluid_shear_stress_and_atherosclerosisPATH.ko05418. Flavonoid_biosynthesisPATH.ko00941. FerroptosisPATH.ko04216.	
Fatty_acid_degradationPATH.ko00071. Fatty_acid_biosynthesisPATH.ko00061. ExosomeBR.ko04147. Ethylbenzene_degradationPATH.ko00642.	•
Epithelial_cell_signaling_in_Helicobacter_pylori_infectionPATH.ko05120. Enzymes_with_EC_numbers · Energy_metabolism ·	•
Drug_metabolismother_enzymesPATH.ko00983. Drug_metabolismcytochrome_P450PATH.ko00982. DNA_replication_proteinsBR.ko03032. DNA_repair_and_recombination_proteinsBR.ko03400.	
Dioxin_degradationPATH.ko00621. D.Arginine_and_D.ornithine_metabolismPATH.ko00472. Cytoskeleton_proteinsBR.ko04812.	
Cytochrome_P450BR.ko00199. Cysteine_and_methionine_metabolismPATH.ko00270. Cyanoamino_acid_metabolismPATH.ko00460. Cushing_syndromePATH.ko04934.	
Cofactor_metabolism · Citrate_cycleTCA_cyclePATH.ko00020. · Chromosome_and_associated_proteinsBR.ko03036. · Choline_metabolism_in_cancerPATH.ko05231. ·	
Chlorocyclohexane_and_chlorobenzene_degradationPATH.ko00361. Chloroalkane_and_chloroalkene_degradationPATH.ko00625. Chemical_carcinogenesisPATH.ko05204.	
Chaperones_and_folding_catalystsBR.ko03110. • Central_carbon_metabolism_in_cancerPATH.ko05230. • Cell_motility • Cell_growth •	
Cell_cycleCaulobacterPATH.ko04112. Cell_adhesion_moleculesBR.ko04515. CD_moleculesBR.ko04090.	
Cationic_antimicrobial_peptideCAMPresistancePATH.ko01503. · Carotenoid_biosynthesisPATH.ko00906. · Carbon_fixation_pathways_in_prokaryotesPATH.ko00720. · Carbon_fixation_in_photosynthetic_organismsPATH.ko00710. ·	
Carbohydrate_metabolism · Carbohydrate_metabolism · Carbohydrate_digestion_and_absorptionPATH.ko04973. · Carbapenem_biosynthesisPATH.ko00332. · Caprolactam_degradationPATH.ko00930. ·	
C5.Branched_dibasic_acid_metabolismPATH.ko00660. Butanoate_metabolismPATH.ko00650. Bladder_cancerPATH.ko05219.	•
Bisphenol_degradationPATH.ko00363. Biotin_metabolismPATH.ko00780. Biosynthesis_of_type_II_polyketide_productsPATH.ko01057. Biosynthesis_of_siderophore_group_nonribosomal_peptidesPATH.ko01053.	
Biosynthesis_of_secondary_metabolitesunclassifiedPATH.ko00999. Biosynthesis_of_ansamycinsPATH.ko01051. Biofilm_formationVibrio_choleraePATH.ko05111.	
Biofilm_formationPseudomonas_aeruginosaPATH.ko02025. · Biofilm_formationEscherichia_coliPATH.ko02026. · Betalain_biosynthesisPATH.ko00965. · beta.Lactam_resistancePATH.ko01501. ·	
beta.Alanine_metabolismPATH.ko00410. Benzoate_degradationPATH.ko00362. Bacterial_toxinsBR.ko02042.	•
Bacterial_motility_proteinsBR.ko02035. Bacterial_invasion_of_epithelial_cellsPATH.ko05100. Atrazine_degradationPATH.ko00791. Ascorbate_and_aldarate_metabolismPATH.ko00053.	
Arginine_biosynthesisPATH.ko00220. Arginine_and_proline_metabolismPATH.ko00330. Arachidonic_acid_metabolismPATH.ko00590.	
Arabinogalactan_biosynthesisMycobacteriumPATH.ko00572. Antimicrobial_resistance_genesBR.ko01504. Antifolate_resistancePATH.ko01523. Amyotrophic_lateral_sclerosisALSPATH.ko05014.	
AmoebiasisPATH.ko05146 Aminobenzoate_degradationPATH.ko00627 Aminoacyl.tRNA_biosynthesisPATH.ko00970 Amino_sugar_and_nucleotide_sugar_metabolismPATH.ko00520	
Amino_acid_related_enzymesBR.ko01007. Amino_acid_metabolism - Amino_acid_related_enzymesBR.ko01007.	
AlcoholismPATH.ko05034. Alanineaspartate_and_glutamate_metabolismPATH.ko00250. African_trypanosomiasisPATH.ko05143. Acarbose_and_validamycin_biosynthesisPATH.ko00525.	
ABC_transportersPATH.ko02010.	050 -0.025 0.000 0.025 0.050
	Importance (mean decrease in accuracy)