**Full list of enriched KEGG pathways in each level FDR < 0.05**

| L1 | L2 | L3 | L4 | L5 | L6 | L7 | L8 | L9 | KEGG | Pathway name |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa00970 | Aminoacyl-tRNA biosynthesis |
| 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa03410 | Base excision repair |
| 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa03030 | DNA replication |
| 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa03460 | Fanconi anemia pathway |
| 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa03440 | Homologous recombination |
| 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa04114 | Oocyte meiosis |
| 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa00230 | Purine metabolism |
| 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa04110 | Cell cycle |
| 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa03430 | Mismatch repair |
| 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa03420 | Nucleotide excision repair |
| 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa00240 | Pyrimidine metabolism |
| 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa03008 | Ribosome biogenesis in eukaryotes |
| 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa03050 | Proteasome |
| 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa03013 | RNA transport |
| 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa03040 | Spliceosome |
| 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | hsa04914 | Progesterone-mediated oocyte maturation |
| 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa04210 | Apoptosis |
| 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa03022 | Basal transcription factors |
| 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa03015 | mRNA surveillance pathway |
| 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa03018 | RNA degradation |
| 0 | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | hsa01100 | Metabolic pathways |
| 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa00510 | N-Glycan biosynthesis |
| 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa01130 | Biosynthesis of antibiotics |
| 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa00310 | Lysine degradation |
| 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | hsa04141 | Protein processing in endoplasmic reticulum |
| 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | hsa03020 | RNA polymerase |
| 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | hsa04120 | Ubiquitin mediated proteolysis |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa05231 | Choline metabolism in cancer |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa00020 | Citrate cycle (TCA cycle) |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa00563 | Glycosylphosphatidylinositol(GPI)-anchor biosynthesis |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa04146 | Peroxisome |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa04070 | Phosphatidylinositol signaling system |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa03060 | Protein export |
| 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa05211 | Renal cell carcinoma |
| 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | hsa05100 | Bacterial invasion of epithelial cells |
| 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | hsa05120 | Epithelial cell signaling in Helicobacter pylori infection |
| 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | hsa05131 | Shigellosis |
| 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | hsa04722 | Neurotrophin signaling pathway |
| 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | 0 | hsa05016 | Huntington's disease |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | hsa05010 | Alzheimer's disease |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | hsa05012 | Parkinson's disease |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | hsa04932 | Non-alcoholic fatty liver disease (NAFLD) |
| 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | hsa00190 | Oxidative phosphorylation |
| 0 | 0 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | hsa04142 | Lysosome |
| 0 | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | hsa03010 | Ribosome |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | hsa04520 | Adherens junction |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | hsa04360 | Axon guidance |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | hsa00531 | Glycosaminoglycan degradation |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04270 | Vascular smooth muscle contraction |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04512 | ECM-receptor interaction |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04510 | Focal adhesion |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04066 | HIF-1 signaling pathway |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04910 | Insulin signaling pathway |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa00511 | Other glycan degradation |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04921 | Oxytocin signaling pathway |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04145 | Phagosome |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04611 | Platelet activation |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04015 | Rap1 signaling pathway |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | hsa04810 | Regulation of actin cytoskeleton |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | hsa04514 | Cell adhesion molecules (CAMs) |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | hsa05414 | Dilated cardiomyopathy |
| 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | 1 | hsa05410 | Hypertrophic cardiomyopathy (HCM) |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | hsa04152 | AMPK signaling pathway |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | hsa01040 | Biosynthesis of unsaturated fatty acids |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | hsa04068 | FoxO signaling pathway |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | hsa04670 | Leukocyte transendothelial migration |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | hsa04010 | MAPK signaling pathway |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | hsa04530 | Tight junction |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 | hsa05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) |

| Term | Pathway name | P Value | FDR (Benjamini-Hochberg method) | Level |
|---|---|---|---|---|
| hsa00970 | Aminoacyl-tRNA biosynthesis | 5.69E-04 | 0.01152069 | L1 |
| hsa03410 | Base excision repair | 1.68E-04 | 0.003990091 | L1 |
| hsa04110 | Cell cycle | 6.88E-15 | 1.96E-12 | L1 |
| hsa03030 | DNA replication | 2.70E-14 | 3.86E-12 | L1 |
| hsa03460 | Fanconi anemia pathway | 1.93E-07 | 9.16E-06 | L1 |
| hsa03440 | Homologous recombination | 1.46E-04 | 0.003787921 | L1 |
| hsa03430 | Mismatch repair | 4.11E-05 | 0.001301931 | L1 |
| hsa03420 | Nucleotide excision repair | 1.02E-04 | 0.002907191 | L1 |
| hsa04114 | Oocyte meiosis | 3.14E-05 | 0.001116311 | L1 |
| hsa03050 | Proteasome | 4.90E-04 | 0.01068541 | L1 |
| hsa00230 | Purine metabolism | 9.29E-04 | 0.017510916 | L1 |
| hsa00240 | Pyrimidine metabolism | 1.02E-07 | 5.81E-06 | L1 |
| hsa03008 | Ribosome biogenesis in eukaryotes | 5.35E-08 | 3.81E-06 | L1 |
| hsa03013 | RNA transport | 2.55E-06 | 1.04E-04 | L1 |
| hsa03040 | Spliceosome | 6.83E-10 | 6.49E-08 | L1 |
| hsa04110 | Cell cycle | 4.97E-15 | 1.44E-12 | L2 |
| hsa03030 | DNA replication | 1.73E-14 | 1.67E-12 | L2 |
| hsa03460 | Fanconi anemia pathway | 6.57E-10 | 3.80E-08 | L2 |
| hsa03440 | Homologous recombination | 3.14E-05 | 6.48E-04 | L2 |
| hsa03430 | Mismatch repair | 2.53E-07 | 7.32E-06 | L2 |
| hsa03420 | Nucleotide excision repair | 2.60E-07 | 6.84E-06 | L2 |
| hsa04114 | Oocyte meiosis | 1.27E-07 | 4.60E-06 | L2 |
| hsa04914 | Progesterone-mediated oocyte maturation | 0.001946419 | 0.026456265 | L2 |
| hsa03050 | Proteasome | 2.00E-07 | 6.42E-06 | L2 |
| hsa00230 | Purine metabolism | 8.73E-05 | 0.001681189 | L2 |
| hsa00240 | Pyrimidine metabolism | 8.74E-09 | 3.61E-07 | L2 |
| hsa03008 | Ribosome biogenesis in eukaryotes | 7.06E-10 | 3.40E-08 | L2 |
| hsa03018 | RNA degradation | 7.63E-06 | 1.70E-04 | L2 |
| hsa03013 | RNA transport | 2.70E-12 | 1.95E-10 | L2 |
| hsa03040 | Spliceosome | 7.95E-15 | 1.16E-12 | L2 |
| hsa00970 | Aminoacyl-tRNA biosynthesis | 0.00163523 | 0.02337098 | L2 |
| hsa04210 | Apoptosis | 5.39E-04 | 0.008612076 | L2 |
| hsa03022 | Basal transcription factors | 3.22E-04 | 0.005459108 | L2 |
| hsa03410 | Base excision repair | 2.75E-04 | 0.004950544 | L2 |
| hsa01100 | Metabolic pathways | 8.73E-04 | 0.01319934 | L2 |
| hsa03015 | mRNA surveillance pathway | 4.87E-06 | 1.17E-04 | L2 |
| hsa04210 | Apoptosis | 2.30E-04 | 0.006659435 | L3 |
| hsa03022 | Basal transcription factors | 4.37E-07 | 4.22E-05 | L3 |
| hsa01130 | Biosynthesis of antibiotics | 3.85E-04 | 0.010096169 | L3 |
| hsa00310 | Lysine degradation | 0.001366431 | 0.030042252 | L3 |
| hsa00510 | N-Glycan biosynthesis | 0.001432656 | 0.029261075 | L3 |
| hsa04110 | Cell cycle | 0.003164692 | 0.049785528 | L3 |
| hsa01100 | Metabolic pathways | 2.52E-05 | 0.001042067 | L3 |
| hsa03430 | Mismatch repair | 0.002053433 | 0.038961223 | L3 |
| hsa03015 | mRNA surveillance pathway | 2.11E-06 | 1.22E-04 | L3 |
| hsa03420 | Nucleotide excision repair | 7.66E-05 | 0.00246381 | L3 |
| hsa03050 | Proteasome | 1.97E-05 | 9.52E-04 | L3 |
| hsa04141 | Protein processing in endoplasmic reticulum | 3.98E-04 | 0.009576996 | L3 |
| hsa00240 | Pyrimidine metabolism | 0.002297159 | 0.040827068 | L3 |
| hsa03008 | Ribosome biogenesis in eukaryotes | 1.48E-06 | 1.08E-04 | L3 |
| hsa03020 | RNA polymerase | 0.002339763 | 0.03917248 | L3 |
| hsa03013 | RNA transport | 2.26E-09 | 3.28E-07 | L3 |
| hsa03040 | Spliceosome | 4.82E-14 | 1.40E-11 | L3 |
| hsa04120 | Ubiquitin mediated proteolysis | 4.27E-05 | 0.001545895 | L3 |
| hsa05100 | Bacterial invasion of epithelial cells | 1.69E-06 | 7.06E-05 | L4 |
| hsa05231 | Choline metabolism in cancer | 0.001288296 | 0.019683387 | L4 |
| hsa00020 | Citrate cycle (TCA cycle) | 0.003642659 | 0.040290759 | L4 |
| hsa04144 | Endocytosis | 4.77E-09 | 1.40E-06 | L4 |
| hsa05120 | Epithelial cell signaling in Helicobacter pylori infection | 4.56E-04 | 0.007395635 | L4 |
| hsa00563 | Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | 0.00526481 | 0.048668216 | L4 |
| hsa03015 | mRNA surveillance pathway | 8.83E-08 | 6.47E-06 | L4 |
| hsa04146 | Peroxisome | 0.004477181 | 0.045870329 | L4 |
| hsa04070 | Phosphatidylinositol signaling system | 0.002826704 | 0.035418297 | L4 |
| hsa03060 | Protein export | 0.002176061 | 0.028595923 | L4 |
| hsa04141 | Protein processing in endoplasmic reticulum | 5.33E-08 | 5.21E-06 | L4 |
| hsa05211 | Renal cell carcinoma | 0.004527505 | 0.044812171 | L4 |
| hsa03020 | RNA polymerase | 4.83E-05 | 0.001087215 | L4 |
| hsa05131 | Shigellosis | 2.15E-05 | 5.25E-04 | L4 |
| hsa04071 | Sphingolipid signaling pathway | 0.001780124 | 0.024552655 | L4 |
| hsa05010 | Alzheimer's disease | 6.25E-06 | 1.66E-04 | L4 |
| hsa03022 | Basal transcription factors | 0.003160244 | 0.037905316 | L4 |

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|---|---|---|---|---|
| hsa01130 | Biosynthesis of antibiotics | 0.00134308 | 0.019496785 | L4 |
| hsa05016 | Huntington's disease | 1.05E-08 | 1.54E-06 | L4 |
| hsa00310 | Lysine degradation | 0.003737926 | 0.039824708 | L4 |
| hsa01100 | Metabolic pathways | 1.75E-06 | 6.40E-05 | L4 |
| hsa04722 | Neurotrophin signaling pathway | 0.00332709 | 0.038305555 | L4 |
| hsa04932 | Non-alcoholic fatty liver disease (NAFLD) | 2.30E-04 | 0.003959359 | L4 |
| hsa00190 | Oxidative phosphorylation | 3.70E-06 | 1.08E-04 | L4 |
| hsa05012 | Parkinson's disease | 3.06E-06 | 9.97E-05 | L4 |
| hsa03050 | Proteasome | 8.02E-05 | 0.001564515 | L4 |
| hsa05205 | Proteoglycans in cancer | 0.005150172 | 0.049179507 | L4 |
| hsa03018 | RNA degradation | 8.11E-05 | 0.00148374 | L4 |
| hsa03013 | RNA transport | 1.52E-06 | 7.44E-05 | L4 |
| hsa03040 | Spliceosome | 8.89E-08 | 5.21E-06 | L4 |
| hsa04120 | Ubiquitin mediated proteolysis | 5.11E-05 | 0.001069003 | L4 |
| hsa04120 | Ubiquitin mediated proteolysis | 9.10E-09 | 6.57E-07 | L5 |
| hsa05010 | Alzheimer's disease | 1.72E-06 | 4.96E-05 | L5 |
| hsa05100 | Bacterial invasion of epithelial cells | 0.00257882 | 0.045569164 | L5 |
| hsa04144 | Endocytosis | 2.58E-08 | 1.49E-06 | L5 |
| hsa05120 | Epithelial cell signaling in Helicobacter pylori infection | 0.002105935 | 0.049504073 | L5 |
| hsa05016 | Huntington's disease | 7.54E-08 | 3.63E-06 | L5 |
| hsa04142 | Lysosome | 1.97E-04 | 0.005164404 | L5 |
| hsa01100 | Metabolic pathways | 5.31E-07 | 1.92E-05 | L5 |
| hsa04722 | Neurotrophin signaling pathway | 0.002537554 | 0.047773485 | L5 |
| hsa04932 | Non-alcoholic fatty liver disease (NAFLD) | 1.54E-06 | 4.94E-05 | L5 |
| hsa00190 | Oxidative phosphorylation | 7.95E-15 | 2.31E-12 | L5 |
| hsa05012 | Parkinson's disease | 2.14E-09 | 2.07E-07 | L5 |
| hsa04141 | Protein processing in endoplasmic reticulum | 4.19E-07 | 1.73E-05 | L5 |
| hsa03010 | Ribosome | 7.29E-11 | 1.05E-08 | L5 |
| hsa03020 | RNA polymerase | 0.002157884 | 0.046888369 | L5 |
| hsa05131 | Shigellosis | 0.002288203 | 0.046188462 | L5 |
| hsa05010 | Alzheimer's disease | 3.92E-11 | 3.81E-09 | L6 |
| hsa05016 | Huntington's disease | 4.33E-10 | 2.53E-08 | L6 |
| hsa01100 | Metabolic pathways | 3.61E-09 | 1.76E-07 | L6 |
| hsa04722 | Neurotrophin signaling pathway | 8.73E-05 | 0.002546359 | L6 |
| hsa04932 | Non-alcoholic fatty liver disease (NAFLD) | 3.04E-07 | 1.27E-05 | L6 |
| hsa00190 | Oxidative phosphorylation | 4.06E-16 | 6.48E-14 | L6 |
| hsa05012 | Parkinson's disease | 2.45E-10 | 1.79E-08 | L6 |
| hsa03010 | Ribosome | 3.61E-33 | 1.05E-30 | L6 |
| hsa04144 | Endocytosis | 7.17E-07 | 2.62E-05 | L6 |
| hsa04142 | Lysosome | 5.14E-05 | 0.00166602 | L6 |
| hsa04071 | Sphingolipid signaling pathway | 0.001478141 | 0.038505988 | L6 |
| hsa04520 | Adherens junction | 0.00369944 | 0.042507928 | L7 |
| hsa04360 | Axon guidance | 0.003091287 | 0.038673623 | L7 |
| hsa04512 | ECM-receptor interaction | 3.25E-05 | 0.001191119 | L7 |
| hsa00531 | Glycosaminoglycan degradation | 0.002910087 | 0.038069976 | L7 |
| hsa04066 | HIF-1 signaling pathway | 2.02E-04 | 0.004909463 | L7 |
| hsa04142 | Lysosome | 4.39E-06 | 3.22E-04 | L7 |
| hsa00511 | Other glycan degradation | 0.001593658 | 0.024295485 | L7 |
| hsa04145 | Phagosome | 3.00E-04 | 0.006263096 | L7 |
| hsa05205 | Proteoglycans in cancer | 0.003260011 | 0.039080186 | L7 |
| hsa04810 | Regulation of actin cytoskeleton | 2.29E-05 | 9.60E-04 | L7 |
| hsa05010 | Alzheimer's disease | 6.75E-05 | 0.002194021 | L7 |
| hsa04514 | Cell adhesion molecules (CAMs) | 2.09E-04 | 0.004697069 | L7 |
| hsa05414 | Dilated cardiomyopathy | 4.46E-04 | 0.008133322 | L7 |
| hsa04144 | Endocytosis | 1.51E-06 | 2.21E-04 | L7 |
| hsa04510 | Focal adhesion | 1.93E-05 | 9.43E-04 | L7 |
| hsa05410 | Hypertrophic cardiomyopathy (HCM) | 9.97E-04 | 0.017049157 | L7 |
| hsa04910 | Insulin signaling pathway | 0.001208265 | 0.019487375 | L7 |
| hsa01100 | Metabolic pathways | 1.51E-04 | 0.004026929 | L7 |
| hsa04932 | Non-alcoholic fatty liver disease (NAFLD) | 1.10E-05 | 6.45E-04 | L7 |
| hsa00190 | Oxidative phosphorylation | 2.03E-06 | 1.98E-04 | L7 |
| hsa04921 | Oxytocin signaling pathway | 0.001840064 | 0.025369573 | L7 |
| hsa05012 | Parkinson's disease | 2.09E-04 | 0.004697069 | L7 |
| hsa04611 | Platelet activation | 0.001638173 | 0.02373276 | L7 |
| hsa04015 | Rap1 signaling pathway | 1.43E-04 | 0.004169934 | L7 |
| hsa03010 | Ribosome | 8.38E-23 | 2.46E-20 | L7 |
| hsa04270 | Vascular smooth muscle contraction | 4.03E-04 | 0.007845315 | L7 |
| hsa04152 | AMPK signaling pathway | 0.002764207 | 0.037123199 | L8 |
| hsa01040 | Biosynthesis of unsaturated fatty acids | 0.001392946 | 0.026317766 | L8 |
| hsa04514 | Cell adhesion molecules (CAMs) | 4.76E-06 | 3.41E-04 | L8 |
| hsa05414 | Dilated cardiomyopathy | 7.91E-06 | 4.54E-04 | L8 |
| hsa04510 | Focal adhesion | 1.05E-06 | 3.02E-04 | L8 |

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|---|---|---|---|---|
| hsa04068 | FoxO signaling pathway | 0.003916002 | 0.047781571 | L8 |
| hsa05410 | Hypertrophic cardiomyopathy (HCM) | 1.13E-06 | 1.61E-04 | L8 |
| hsa04910 | Insulin signaling pathway | 2.63E-04 | 0.00628188 | L8 |
| hsa04670 | Leukocyte transendothelial migration | 0.002985044 | 0.038248806 | L8 |
| hsa04010 | MAPK signaling pathway | 7.33E-04 | 0.014926529 | L8 |
| hsa04921 | Oxytocin signaling pathway | 1.15E-05 | 5.51E-04 | L8 |
| hsa04611 | Platelet activation | 1.27E-04 | 0.004052049 | L8 |
| hsa04015 | Rap1 signaling pathway | 2.26E-06 | 2.17E-04 | L8 |
| hsa04530 | Tight junction | 0.001735084 | 0.028892142 | L8 |
| hsa04270 | Vascular smooth muscle contraction | 2.33E-04 | 0.00605894 | L8 |
| hsa05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 9.12E-05 | 0.003267151 | L8 |
| hsa04512 | ECM-receptor interaction | 1.33E-04 | 0.003807655 | L8 |
| hsa04144 | Endocytosis | 5.05E-04 | 0.011090252 | L8 |
| hsa04066 | HIF-1 signaling pathway | 0.002032358 | 0.030263152 | L8 |
| hsa00511 | Other glycan degradation | 0.002604038 | 0.036725324 | L8 |
| hsa04145 | Phagosome | 0.00177796 | 0.027975061 | L8 |
| hsa04810 | Regulation of actin cytoskeleton | 3.98E-05 | 0.001630149 | L8 |
| hsa03010 | Ribosome | 0.001498573 | 0.026542218 | L8 |
| hsa05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 1.53E-05 | 0.002036824 | L9 |
| hsa04514 | Cell adhesion molecules (CAMs) | 2.84E-06 | 7.58E-04 | L9 |
| hsa05414 | Dilated cardiomyopathy | 2.39E-04 | 0.015839575 | L9 |
| hsa05410 | Hypertrophic cardiomyopathy (HCM) | 1.01E-04 | 0.008910191 | L9 |