| Function | FDR | Genes in network | Genes in genome |
|---|---|---|---|
| pyruvate metabolic process | 5.0477256900470695e-17 | 13 | 120 |
| glucose catabolic process to pyruvate | 5.041941332576316e-11 | 7 | 27 |
| glycolytic process through fructose-6-phosphate | 5.041941332576316e-11 | 7 | 27 |
| glycolytic process through glucose-6-phosphate | 5.041941332576316e-11 | 7 | 27 |
| NADH regeneration | 5.041941332576316e-11 | 7 | 27 |
| glucose catabolic process | 5.595931688546885e-11 | 7 | 28 |
| NADH metabolic process | 8.475967750771954e-11 | 7 | 31 |
| ADP metabolic process | 8.475967750771954e-11 | 9 | 102 |
| ATP generation from ADP | 8.475967750771954e-11 | 9 | 100 |
| nucleoside diphosphate phosphorylation | 8.475967750771954e-11 | 9 | 101 |
| NAD metabolic process | 8.475967750771954e-11 | 7 | 31 |
| purine ribonucleoside diphosphate metabolic process | 9.500928283081697e-11 | 9 | 105 |
| carbohydrate catabolic process | 9.500928283081697e-11 | 10 | 163 |
| purine nucleoside diphosphate metabolic process | 9.50806703677266e-11 | 9 | 106 |
| nucleotide phosphorylation | 1.0767084448518332e-10 | 9 | 109 |
| ribonucleoside diphosphate metabolic process | 1.0767084448518332e-10 | 9 | 109 |
| nucleoside diphosphate metabolic process | 2.859500112182678e-10 | 9 | 122 |
| glucose metabolic process | 3.3749469782171394e-10 | 9 | 125 |
| hexose catabolic process | 1.2524384215830424e-9 | 7 | 49 |
| monosaccharide catabolic process | 4.123166888851958e-9 | 7 | 58 |
| hexose metabolic process | 4.270882754614213e-9 | 9 | 168 |
| monosaccharide metabolic process | 2.7872626709518085e-8 | 9 | 208 |
| glycolytic process | 1.1726144505704904e-7 | 7 | 94 |
| ATP metabolic process | 1.2271846911307626e-7 | 9 | 248 |
| regulation of purine nucleotide biosynthetic process | 7.129260992185925e-7 | 5 | 29 |
| neutral amino acid transmembrane transporter activity | 7.129260992185925e-7 | 5 | 29 |
| hexose biosynthetic process | 7.585082866671209e-7 | 6 | 67 |
| regulation of nucleotide biosynthetic process | 7.934957289228299e-7 | 5 | 30 |
| regulation of sulfur metabolic process | 8.117507698921346e-7 | 4 | 10 |
| monosaccharide biosynthetic process | 0.000001062719807807525 | 6 | 72 |
| acetyl-CoA biosynthetic process from pyruvate | 0.000001191954151667838 | 4 | 11 |
| acetyl-CoA biosynthetic process | 0.000034906724321122 34 | 4 | 14 |
| regulation of purine nucleotide metabolic process | 0.000006319813923384256 | 6 | 98 |
| thioester biosynthetic process | 0.00000726457575838 2187 | 5 | 48 |
| acyl-CoA biosynthetic process | 0.00000726457575838 2187 | 5 | 48 |
| regulation of nucleotide metabolic process | 0.000007264575758382187 | 6 | 101 |
| hydro-lyase activity | 0.000007862449255990296 | 5 | 49 |
| L-amino acid transmembrane transporter activity | 0.000008496437880662527 | 5 | 50 |
| organic acid transmembrane transport | 0.000013670815338884064 | 6 | 115 |
| carboxylic acid transmembrane transport | 0.000013670815338884064 | 6 | 115 |
| purine nucleoside bisphosphate biosynthetic process | 0.000022619466279085233 | 5 | 62 |
| nucleoside bisphosphate biosynthetic process | 0.000022619466279085233 | 5 | 62 |
| ribonucleoside bisphosphate biosynthetic process | 0.000022619466279085233 | 5 | 62 |
| acetyl-CoA metabolic process | 0.000031683118505805166 | 4 | 25 |
| carbon-oxygen lyase activity | 0.000032074124899833164 | 5 | 67 |
| amino acid transmembrane transporter activity | 0.000036429534008423635 | 5 | 69 |
| purine ribonucleotide biosynthetic process | 0.000039339388040932845 | 6 | 141 |
| acyl-CoA metabolic process | 0.00004644662514625086 | 5 | 73 |
| purine nucleotide biosynthetic process | 0.000048350612493134956 | 6 | 148 |
| ribonucleotide biosynthetic process | 0.000048350612493134956 | 6 | 148 |
| lyase activity | 0.000048350612493134956 | 6 | 148 |
| ribose phosphate biosynthetic process | 0.00005775055031303625 | 6 | 153 |
| carboxylic acid transmembrane transporter activity | 0.00006119300567027089 | 6 | 155 |
| organic acid transmembrane transporter activity | 0.00006239130855766887 | 6 | 156 |
| carbohydrate biosynthetic process | 0.00006605490304159608 | 6 | 158 |
| purine-containing compound biosynthetic process | 0.00009323342563131641 | 6 | 168 |
| neutral amino acid transport | 0.00011246898674767384 | 4 | 36 |
| thioester metabolic process | 0.00013713779967614606 | 5 | 94 |

| | | | | | |
|---|---|---|---|---|---|
| alanine transport | 0.0001547410866956381 | 3 | 10 | | |
| anion transmembrane transport | 0.0001967386915477776 | 6 | 193 | | |
| amino acid transport | 0.00023745243836534126 | 5 | 106 | | |
| nucleotide biosynthetic process | 0.00024149184345745295 | 6 | 201 | | |
| regulation of vacuole organization | 0.00025476536721776217 | 4 | 45 | | |
| nucleoside phosphate biosynthetic process | 0.00031064203775212177 | 6 | 211 | | |
| organic anion transmembrane transporter activity | 0.00033210400404607186 | 6 | 214 | | |
| ribonucleoside bisphosphate metabolic process | 0.000521683913052866 | 5 | 127 | | |
| nucleoside bisphosphate metabolic process | 0.000521683913052866 | 5 | 127 | | |
| purine nucleoside bisphosphate metabolic process | 0.000521683913052866 | 5 | 127 | | |
| carboxylic acid transport | 0.0011268892431192097 | 6 | 267 | | |
| organic acid transport | 0.0012099535034297082 | 6 | 271 | | |
| regulation of fatty acid metabolic process | 0.0014312342412799248 | 4 | 71 | | |
| sulfur compound biosynthetic process | 0.002116699543293243 | 5 | 171 | | |
| amino acid import across plasma membrane | 0.00299176657162186 | 3 | 27 | | |
| secondary active transmembrane transporter activity | 0.003346560509465978 | 5 | 189 | | |
| L-alpha-amino acid transmembrane transport | 0.007650529764730285 | 3 | 37 | | |
| basolateral plasma membrane | 0.008187956525796512 | 3 | 38 | | |
| amino acid import | 0.00944409634704563 | 3 | 40 | | |
| basal part of cell | 0.010808941860991609 | 3 | 42 | | |
| organelle fusion | 0.011692993473643776 | 4 | 124 | | |
| L-amino acid transport | 0.015773101481639837 | 3 | 48 | | |
| amino acid transmembrane transport | 0.021922767855097655 | 3 | 54 | | |
| vacuole organization | 0.021922767855097655 | 4 | 147 | | |
| active transmembrane transporter activity | 0.022292678100388135 | 5 | 288 | | |
| regulation of cellular ketone metabolic process | 0.026174859305093827 | 4 | 155 | | |
| microvillus | 0.03228319798646687 | 2 | 11 | | |
| CD4-positive, alpha-beta T cell activation | 0.04672863011334898 | 3 | 71 | | |
| cartilage development | 0.04672863011334898 | 3 | 71 | | |
| regulation of alpha-beta T cell activation | 0.0587365110591952 | 3 | 77 | | |
| regulation of CD8-positive, alpha-beta T cell activation | 0.0814957145177767 | 2 | 18 | | |
| cellular ketone metabolic process | 0.0814957145177767 | 4 | 212 | | |
| vascular transport | 0.0814957145177767 | 3 | 87 | | |
| negative regulation of alpha-beta T cell differentiation | 0.0814957145177767 | 2 | 18 | | |
| regulation of oxidoreductase activity | 0.0814957145177767 | 3 | 88 | | |
| cytosol | 0.0814957145177767 | 4 | 214 | | |
| apical part of cell | 0.08978362592515551 | 4 | 221 | | |