sly00020: Citrate cycle (TCA cycle)
sly00040: Pentose and glucuronate interconversions
sly00051: Fructose and mannose metabolism

Frequency

P-score

0.0 0.2 0.4 0.6 0.8 1.0
sly00053: Ascorbate and aldarate metabolism

Frequency

$P$-score
sly00061: Fatty acid biosynthesis
sly00062: Fatty acid elongation
sly00071: Fatty acid degradation
sly00073: Cutin, suberine and wax biosynthesis
sly00100: Steroid biosynthesis

Frequency

P-score
sly00130: Ubiquinone and other terpenoid-quinone biosynthesis
sly00190: Oxidative phosphorylation
sly00195: Photosynthesis

![Histogram of P-scores](image-url)
P-score

sly00220: Arginine biosynthesis
sly00230: Purine metabolism
sly00250: Alanine, aspartate and glutamate metabolism
sly00260: Glycine, serine and threonine metabolism

Frequency

P-score

0.0 0.2 0.4 0.6 0.8 1.0
sly00270: Cysteine and methionine metabolism
sly00280: Valine, leucine and isoleucine degradation

![Bar chart showing frequency distribution of P-scores for valine, leucine, and isoleucine degradation process. The x-axis represents P-scores ranging from 0.0 to 1.0, and the y-axis represents frequency.]
sly00330: Arginine and proline metabolism
sly00350: Tyrosine metabolism
sly00380: Tryptophan metabolism

![Histogram showing frequency distribution of P-scores for Tryptophan metabolism.](image)
sly00400: Phenylalanine, tyrosine and tryptophan biosynthesis
sly00410: beta-Alanine metabolism

Frequency

$P$-score

0.0 0.2 0.4 0.6 0.8 1.0
sly00480: Glutathione metabolism

P-score

Frequency
sly00510: N-Glycan biosynthesis

Frequency

P-score

0.0 0.2 0.4 0.6 0.8 1.0
sly00520: Amino sugar and nucleotide sugar metabolism
sly00562: Inositol phosphate metabolism
sly00565: Ether lipid metabolism
sly00592: alpha-Linolenic acid metabolism
sly00630: Glyoxylate and dicarboxylate metabolism
sly00670: One carbon pool by folate

Frequency

$P$-score

0.0 0.2 0.4 0.6 0.8 1.0
sly00770: Pantothenate and CoA biosynthesis
sly00900: Terpenoid backbone biosynthesis

Frequency

P-score

0.0 0.2 0.4 0.6 0.8 1.0
sly00906: Carotenoid biosynthesis

![Bar chart showing frequency distribution of P-scores for Carotenoid biosynthesis related to sly00906. The x-axis represents P-scores ranging from 0.0 to 1.0, and the y-axis represents frequency ranging from 0 to 600.]
sly00910: Nitrogen metabolism

Frequency

P-score
sly00920: Sulfur metabolism

Frequency vs $P$-score bar chart.
sly00940: Phenylpropanoid biosynthesis
sly00941: Flavonoid biosynthesis
sly00945: Stilbenoid, diarylheptanoid and gingerol biosynthesis
sly00960: Tropane, piperidine and pyridine alkaloid biosynthesis

![Bar chart showing frequency distribution of P-scores for sly00960 involving tropane, piperidine, and pyridine alkaloid biosynthesis.]
sly00970: Aminoacyl-tRNA biosynthesis
sly01040: Biosynthesis of unsaturated fatty acids
sly01200: Carbon metabolism
sly01210: 2-Oxocarboxylic acid metabolism
sly01212: Fatty acid metabolism
sly01230: Biosynthesis of amino acids

Frequency

P-score

0.0 0.2 0.4 0.6 0.8 1.0
sly03008: Ribosome biogenesis in eukaryotes
sly03015: mRNA surveillance pathway

Frequency

$P$-score
sly03020: RNA polymerase
sly03022: Basal transcription factors
sly03050: Proteasome

Frequency vs. P-score graph.
sly03410: Base excision repair

![Bar graph showing frequency distribution for P-score values ranging from 0.0 to 1.0. The y-axis represents frequency, and the x-axis represents P-score values. The graph illustrates the distribution of base excision repair events across different P-score values.](image-url)
sly03420: Nucleotide excision repair

Frequency

P-score

0.0 0.2 0.4 0.6 0.8 1.0
sly03430: Mismatch repair
sly03440: Homologous recombination

Frequency vs. P-score graph.
sly04070: Phosphatidylinositol signaling system
sly04075: Plant hormone signal transduction
sly04120: Ubiquitin mediated proteolysis
sly04140: Regulation of autophagy
sly04141: Protein processing in endoplasmic reticulum
sly04145: Phagosome
sly04146: Peroxisome
sly04626: Plant-pathogen interaction