

| | Enriched gained GO terms | P-value | Enriched lost GO terms | P-value |
|---|--|--------------------|---|-------------------|
| all eukaryotes except Metamonada | <ul style="list-style-type: none"> oxidation reduction folic acid and derivative biosynthetic process | 2.0E-6 3.4E-4 | | |
| all eukaryotes except Metamonada, Naegleria | <ul style="list-style-type: none"> sulfate assimilation GPI anchor biosynthetic process | 1.6E-4 2.9E-4 | | |
| all eukaryotes except Metamonada, Naegleria, Entamoeba | <ul style="list-style-type: none"> ATP synthesis coupled electron transport Mo-molybdopterin cofactor biosynthetic process | 1.3E-5 9.5E-5 | <ul style="list-style-type: none"> polysaccharide biosynthetic process | 8.0E-3 |
| all eukaryotes except Metamonada, Naegleria, Entamoeba, Dictyostelium | <ul style="list-style-type: none"> photosynthesis histidine biosynthetic process | 3.9E-20 2.8E-8 | | |
| Opisthokonta & Viridplantae & Oomyces | <ul style="list-style-type: none"> lipopolysaccharide biosynthetic process carbohydrate metabolic process | 9.3E-4 2.9E-3 | <ul style="list-style-type: none"> asparagine biosynthetic process pathogenesis | 2.5E-3 2.4E-2 |
| Opisthokonta & Viridplantae | <ul style="list-style-type: none"> protein secretion ciliary or flagellar motility | 2.7E-6 3.5E-3 | | |
| Opisthokonta | <ul style="list-style-type: none"> regulation of primary metabolic process | 3.1E-2 | <ul style="list-style-type: none"> photosynthesis glycolipid biosynthetic process | 2.0E-28 8.0E-3 |
| Metazoa & Choanoflagellata | <ul style="list-style-type: none"> signal transduction cell-cell signaling | 2.9E-4 2.9E-3 | <ul style="list-style-type: none"> protein-chromophore linkage glucan biosynthetic process | 5.4E-4 5.2E-3 |
| Metazoa | <ul style="list-style-type: none"> regulation of transcription, DNA-dependent cell-matrix adhesion | 2.3E-7 4.6E-4 | <ul style="list-style-type: none"> histidine biosynthetic process tyrosine biosynthetic process | 1.8E-3 9.5E-3 |
| Bilaterian & Cnidaria | <ul style="list-style-type: none"> apoptosis peptide cross-linking | 3.1E-4 4.7E-4 | <ul style="list-style-type: none"> protein folding transcription initiation | 1.8E-3 3.8E-3 |
| Bilateria | <ul style="list-style-type: none"> mitochondrial electron transport, NADH to ubiquinone Wnt receptor signaling pathway | 8.3E-6 2.8E-4 | <ul style="list-style-type: none"> branched chain family amino acid biosynthetic process histidine biosynthetic process | 3.36E-4 2.3E-3 |
| Deuterostomia | | | <ul style="list-style-type: none"> cellular amino acid biosynthetic process phosphoenolpyruvate-dependent sugar phosphotransferase system | 6.7E-4 3.1E-3 |
| Chordata | <ul style="list-style-type: none"> lipid catabolic process activation of MAPKK activity | 3.3E-3 6.8E-3 | <ul style="list-style-type: none"> proteolysis | 1.6E-2 |
| Urochordata & Vertebrata | <ul style="list-style-type: none"> antigen processing and presentation response to stimulus | 5.5E-3 8.6E-3 | <ul style="list-style-type: none"> folic acid and derivative metabolic process cellular amide metabolic process | 2.2E-3 6.57E-3 |
| Vertebrata | <ul style="list-style-type: none"> immune response G-protein coupled receptor protein signaling pathway | 5.14E-11 1.8E-5 | <ul style="list-style-type: none"> DNA topological change carbohydrate metabolic process | 2.0E-3 3.0E-3 |
| Tetrapoda | <ul style="list-style-type: none"> regulation of growth synaptic transmission | 1.4E-2 2.0E-2 | <ul style="list-style-type: none"> valyl-tRNA aminoacylation response to water | 4.3E-3 8.6E-3 |
| Amniota | <ul style="list-style-type: none"> defense response immune response | 1.7E-3 1.8E-3 | <ul style="list-style-type: none"> regulation of transcription, DNA-dependent riboflavin biosynthetic process | 8.6E-8 1.0E-3 |
| Mammalia | <ul style="list-style-type: none"> hemopoiesis reciprocal meiotic recombination | 2.8E-3 8.3E-3 | <ul style="list-style-type: none"> aromatic amino acid family biosynthetic process | 1.1E-2 |