

## GeDiPNet Cluster 341 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax\_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build\_cluster\_go\_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 14:59:52

| GO Term                                                    | GO ID      | Overlap Genes | Overlap Gene Names  | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|------------------------------------------------------------|------------|---------------|---------------------|-----------------|--------------------|-----------------|-----------|-------------|
| 'de novo' UMP biosynthetic process                         | GO:0044205 | 3             | CAD, DHODH, UMPS    | 3               | 15                 | 1245.80         | 4.184e-10 | 1.043e-7    |
| UDP biosynthetic process                                   | GO:0006225 | 3             | CAD, DHODH, UMPS    | 5               | 15                 | 747.48          | 4.180e-9  | 7.865e-7    |
| 'de novo' pyrimidine nucleobase biosynthetic process       | GO:0006207 | 3             | CAD, DHODH, UMPS    | 6               | 15                 | 622.90          | 8.356e-9  | 1.446e-6    |
| pyrimidine nucleotide biosynthetic process                 | GO:0006221 | 3             | CAD, DHODH, UMPS    | 9               | 15                 | 415.27          | 3.505e-8  | 4.925e-6    |
| positive regulation of protein localization to cell cortex | GO:1904778 | 2             | GPSM2, EPB41        | 5               | 15                 | 498.32          | 6.006e-6  | 3.503e-4    |
| actin filament capping                                     | GO:0051693 | 2             | SPTB, SPTA1         | 19              | 15                 | 131.14          | 1.020e-4  | 3.073e-3    |
| protein localization to plasma membrane                    | GO:0072659 | 3             | MYO5A, SLC4A1, ANK1 | 152             | 15                 | 24.59           | 2.234e-4  | 5.448e-3    |
| actin cytoskeleton organization                            | GO:0030036 | 3             | SPTB, EPB41, SPTA1  | 234             | 15                 | 15.97           | 7.891e-4  | 1.311e-2    |
| pH elevation                                               | GO:0045852 | 1             | SLC4A1              | 1               | 15                 | 1245.80         | 8.027e-4  | 1.318e-2    |
| regulation of intestinal absorption                        | GO:1904478 | 1             | EPB41               | 2               | 15                 | 622.90          | 1.605e-3  | 2.014e-2    |
| pyrimidine-containing compound biosynthetic process        | GO:0072528 | 1             | CAD                 | 2               | 15                 | 622.90          | 1.605e-3  | 2.014e-2    |
| chloride transport                                         | GO:0006821 | 2             | CLCC1, SLC4A1       | 81              | 15                 | 30.76           | 1.878e-3  | 2.225e-2    |
| pyrimidine ribonucleotide biosynthetic process             | GO:0009220 | 1             | DHODH               | 3               | 15                 | 415.27          | 2.406e-3  | 2.543e-2    |
| UMP biosynthetic process                                   | GO:0006222 | 1             | UMPS                | 3               | 15                 | 415.27          | 2.406e-3  | 2.543e-2    |
| pyrimidine nucleobase biosynthetic process                 | GO:0019856 | 1             | UMPS                | 3               | 15                 | 415.27          | 2.406e-3  | 2.543e-2    |