

## GeDiPNet Cluster 365 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 13:28:06

| GO Term                                                 | GO ID      | Overlap Genes | Overlap Gene Names | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|---------------------------------------------------------|------------|---------------|--------------------|-----------------|--------------------|-----------------|----------|-------------|
| uracil catabolic process                                | GO:0006212 | 2             | DPYD, DPYS         | 2               | 7                  | 2669.57         | 1.203e-7 | 1.406e-5    |
| thymine catabolic process                               | GO:0006210 | 2             | DPYD, DPYS         | 3               | 7                  | 1779.71         | 3.608e-7 | 3.548e-5    |
| CMP catabolic process                                   | GO:0006248 | 2             | DPYD, DPYS         | 5               | 7                  | 1067.83         | 1.202e-6 | 9.607e-5    |
| dCMP catabolic process                                  | GO:0006249 | 2             | DPYD, DPYS         | 6               | 7                  | 889.86          | 1.803e-6 | 1.327e-4    |
| UMP catabolic process                                   | GO:0046050 | 2             | DPYD, DPYS         | 6               | 7                  | 889.86          | 1.803e-6 | 1.327e-4    |
| dUMP catabolic process                                  | GO:0046079 | 2             | DPYD, DPYS         | 6               | 7                  | 889.86          | 1.803e-6 | 1.327e-4    |
| pyrimidine nucleobase catabolic process                 | GO:0006208 | 2             | DPYD, DPYS         | 7               | 7                  | 762.73          | 2.524e-6 | 1.734e-4    |
| purine nucleobase catabolic process                     | GO:0006145 | 1             | DPYD               | 1               | 7                  | 2669.57         | 3.746e-4 | 7.813e-3    |
| thymidine catabolic process                             | GO:0006214 | 1             | DPYD               | 1               | 7                  | 2669.57         | 3.746e-4 | 7.813e-3    |
| beta-alanine biosynthetic process                       | GO:0019483 | 1             | DPYD               | 2               | 7                  | 1334.79         | 7.491e-4 | 1.251e-2    |
| regulation of fever generation                          | GO:0031620 | 1             | PTGES              | 2               | 7                  | 1334.79         | 7.491e-4 | 1.251e-2    |
| negative regulation of RNA splicing                     | GO:0033119 | 1             | PTBP2              | 6               | 7                  | 444.93          | 2.246e-3 | 2.412e-2    |
| positive regulation of protein tyrosine kinase activity | GO:0061098 | 1             | GPRC5B             | 9               | 7                  | 296.62          | 3.367e-3 | 3.005e-2    |
| positive regulation of prostaglandin secretion          | GO:0032308 | 1             | PTGES              | 9               | 7                  | 296.62          | 3.367e-3 | 3.005e-2    |
| regulation of neural precursor cell proliferation       | GO:2000177 | 1             | PTBP2              | 11              | 7                  | 242.69          | 4.114e-3 | 3.324e-2    |