

## GeDiPNet Cluster 366 -- 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 00:25:52

| GO Term                                                                                   | GO ID      | Overlap Genes | Overlap Gene Names                                                            | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|-------------------------------------------------------------------------------------------|------------|---------------|-------------------------------------------------------------------------------|-----------------|--------------------|-----------------|-----------|-------------|
| negative regulation of gene expression                                                    | GO:0010629 | 18            | APP, IFNG, TBK1, TGFB1, AGT, APOE, CRH, GSK3B, MAPT, NR0B2, PINK1, PSEN1      | 339             | 111                | 8.94            | 1.490e-12 | 6.581e-10   |
| response to ethanol                                                                       | GO:0045471 | 10            | TGFB1, TH, CRH, DRD2, DRD3, FOSB, NR0B2, SETD7, CSF3, FGF2                    | 110             | 111                | 15.30           | 1.034e-9  | 2.304e-7    |
| memory                                                                                    | GO:0007613 | 9             | APP, SLC1A1, TH, COMT, HTR2A, MAPT, PSEN1, SLC6A4, TAFA2                      | 87              | 111                | 17.42           | 2.309e-9  | 4.685e-7    |
| positive regulation of glycolytic process                                                 | GO:0045821 | 6             | APP, IFNG, HTR2A, PSEN1, HIF1A, INS                                           | 24              | 111                | 42.09           | 4.728e-9  | 8.872e-7    |
| positive regulation of amyloid fibril formation                                           | GO:1905908 | 4             | APP, APOE, PSEN1, CLU                                                         | 5               | 111                | 134.68          | 5.868e-9  | 1.076e-6    |
| learning or memory                                                                        | GO:0007611 | 8             | APP, SLC1A1, COMT, CRH, DRD3, MAPT, PSEN1, PICALM                             | 72              | 111                | 18.71           | 1.048e-8  | 1.780e-6    |
| synaptic transmission, dopaminergic                                                       | GO:0001963 | 5             | TH, COMT, CRH, DRD2, DRD3                                                     | 15              | 111                | 56.12           | 1.934e-8  | 3.028e-6    |
| behavioral response to cocaine                                                            | GO:0048148 | 5             | DRD2, DRD3, FOSB, HTR2A, SLC6A4                                               | 17              | 111                | 49.52           | 3.948e-8  | 5.552e-6    |
| positive regulation of gene expression                                                    | GO:0010628 | 16            | APP, IFNG, TGFB1, TICAM1, CRH, GSK3B, NR0B2, PSEN1, SLC6A4, SMAD4, CLU, HIF1A | 504             | 111                | 5.34            | 4.772e-8  | 6.530e-6    |
| intracellular copper ion homeostasis                                                      | GO:0006878 | 5             | APP, CP, SCO1, SCO2, MT2A                                                     | 18              | 111                | 46.76           | 5.440e-8  | 7.274e-6    |
| positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction | GO:0051897 | 11            | APP, TBK1, TGFB1, AGT, GSK3B, IGF2, PINK1, VEGFA, CSF3, FGF2, INS             | 217             | 111                | 8.53            | 6.883e-8  | 8.872e-6    |
| response to hypoxia                                                                       | GO:0001666 | 10            | TGFB1, TH, CAPN2, COMT, DRD2, EPO, SLC6A4, SMAD4, HIF1A, VEGFA                | 176             | 111                | 9.57            | 9.647e-8  | 1.169e-5    |
| positive regulation of cell population proliferation                                      | GO:0008284 | 16            | CXCR2, IFNG, STAMBP, TGFB1, CRH, EPO, HTR2A, IGF2, LEPR, VIP, CR1, HDAC4      | 532             | 111                | 5.06            | 1.001e-7  | 1.208e-5    |
| positive regulation of nitric oxide biosynthetic process                                  | GO:0045429 | 6             | APP, IFNG, TICAM1, APOE, PTGS2, CLU                                           | 42              | 111                | 24.05           | 1.689e-7  | 1.879e-5    |
| regulation of amyloid-beta clearance                                                      | GO:1900221 | 3             | APP, APOE, CLU                                                                | 3               | 111                | 168.35          | 2.040e-7  | 2.207e-5    |