

## GeDiPNet Cluster 106 -- 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 07:02:08

| GO Term                                      | GO ID      | Overlap Genes | Overlap Gene Names                  | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|----------------------------------------------|------------|---------------|-------------------------------------|-----------------|--------------------|-----------------|-----------|-------------|
| cobalamin transport                          | GO:0015889 | 6             | AMN, CUBN, TCN1, TCN2, CD320, ABCD4 | 9               | 37                 | 336.70          | 3.290e-15 | 2.325e-12   |
| cobalamin metabolic process                  | GO:0009235 | 4             | AMN, CUBN, MMAA, ABCD4              | 9               | 37                 | 224.47          | 1.627e-9  | 3.425e-7    |
| oligosaccharide biosynthetic process         | GO:0009312 | 4             | FUT1, FUT2, FUT3, FUT6              | 26              | 37                 | 77.70           | 1.884e-7  | 2.056e-5    |
| L-fucose catabolic process                   | GO:0042355 | 3             | FUT1, FUT2, FUT6                    | 10              | 37                 | 151.52          | 8.493e-7  | 7.240e-5    |
| vitamin transport                            | GO:0051180 | 3             | SLC19A2, SLC19A1, GC                | 10              | 37                 | 151.52          | 8.493e-7  | 7.240e-5    |
| fucosylation                                 | GO:0036065 | 3             | FUT1, FUT2, FUT3                    | 12              | 37                 | 126.26          | 1.553e-6  | 1.190e-4    |
| glycosphingolipid biosynthetic process       | GO:0006688 | 3             | FUT1, FUT2, FUT6                    | 25              | 37                 | 60.61           | 1.595e-5  | 7.569e-4    |
| folic acid transport                         | GO:0015884 | 2             | SLC19A2, SLC19A1                    | 8               | 37                 | 126.26          | 1.060e-4  | 3.164e-3    |
| cobalt ion transport                         | GO:0006824 | 2             | TCN1, TCN2                          | 8               | 37                 | 126.26          | 1.060e-4  | 3.164e-3    |
| regulation of endothelial cell proliferation | GO:0001936 | 2             | FUT1, FUT2                          | 9               | 37                 | 112.23          | 1.361e-4  | 3.818e-3    |
| homocysteine metabolic process               | GO:0050667 | 2             | MMUT, MTHFR                         | 10              | 37                 | 101.01          | 1.700e-4  | 4.509e-3    |
| tetrahydrofolate metabolic process           | GO:0046653 | 2             | DHFR, MTHFR                         | 11              | 37                 | 91.83           | 2.075e-4  | 5.190e-3    |
| vitamin D metabolic process                  | GO:0042359 | 2             | CYP2R1, GC                          | 12              | 37                 | 84.18           | 2.486e-4  | 5.893e-3    |
| folic acid metabolic process                 | GO:0046655 | 2             | DHFR, SLC19A1                       | 15              | 37                 | 67.34           | 3.941e-4  | 8.156e-3    |
| protein glycosylation                        | GO:0006486 | 4             | FUT1, FUT2, FUT3, FUT6              | 181             | 37                 | 11.16           | 4.380e-4  | 8.791e-3    |