

GeDiPNet Cluster 536 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:17

| GO Term                                                           | GO ID      | Overlap Genes | Overlap Gene Names | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-------------------------------------------------------------------|------------|---------------|--------------------|-----------------|--------------------|-----------------|----------|-------------|
| metanephric glomerular basement membrane development              | GO:0072274 | 1             | LAMB2              | 1               | 3                  | 6229.00         | 1.605e-4 | 4.340e-3    |
| Golgi calcium ion homeostasis                                     | GO:0032468 | 1             | ATP2C1             | 2               | 3                  | 3114.50         | 3.211e-4 | 7.044e-3    |
| Golgi calcium ion transport                                       | GO:0032472 | 1             | ATP2C1             | 2               | 3                  | 3114.50         | 3.211e-4 | 7.044e-3    |
| trans-Golgi network membrane organization                         | GO:0098629 | 1             | ATP2C1             | 2               | 3                  | 3114.50         | 3.211e-4 | 7.044e-3    |
| metanephric podocyte development                                  | GO:0072249 | 1             | LAMB2              | 2               | 3                  | 3114.50         | 3.211e-4 | 7.044e-3    |
| axon extension involved in regeneration                           | GO:0048677 | 1             | LAMB2              | 3               | 3                  | 2076.33         | 4.816e-4 | 9.241e-3    |
| intracellular manganese ion homeostasis                           | GO:0030026 | 1             | ATP2C1             | 5               | 3                  | 1245.80         | 8.025e-4 | 1.283e-2    |
| positive regulation of Golgi to plasma membrane protein transport | GO:0042998 | 1             | ATP2C1             | 6               | 3                  | 1038.17         | 9.630e-4 | 1.423e-2    |
| regulation of basement membrane organization                      | GO:0110011 | 1             | LAMB2              | 6               | 3                  | 1038.17         | 9.630e-4 | 1.423e-2    |
| manganese ion transport                                           | GO:0006828 | 1             | ATP2C1             | 9               | 3                  | 692.11          | 1.444e-3 | 1.794e-2    |
| manganese ion transmembrane transport                             | GO:0071421 | 1             | ATP2C1             | 9               | 3                  | 692.11          | 1.444e-3 | 1.794e-2    |
| glomerular basement membrane development                          | GO:0032836 | 1             | COL4A4             | 10              | 3                  | 622.90          | 1.605e-3 | 1.885e-2    |
| positive regulation of integrin-mediated signaling pathway        | GO:2001046 | 1             | LAMB2              | 13              | 3                  | 479.15          | 2.086e-3 | 2.170e-2    |
| astrocyte development                                             | GO:0014002 | 1             | LAMB2              | 15              | 3                  | 415.27          | 2.406e-3 | 2.324e-2    |
| positive regulation of muscle cell differentiation                | GO:0051149 | 1             | LAMB2              | 16              | 3                  | 389.31          | 2.567e-3 | 2.402e-2    |