

## GeDiPNet Cluster 437 -- 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 00:01:16

| GO Term                                                                                             | GO ID      | Overlap Genes | Overlap Gene Names | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-----------------------------------------------------------------------------------------------------|------------|---------------|--------------------|-----------------|--------------------|-----------------|----------|-------------|
| cellular response to UV-A                                                                           | GO:0071492 | 2             | MMP2, MMP9         | 11              | 7                  | 485.38          | 6.605e-6 | 3.941e-4    |
| response to amyloid-beta                                                                            | GO:1904645 | 2             | MMP2, MMP9         | 15              | 7                  | 355.94          | 1.260e-5 | 6.498e-4    |
| extracellular matrix organization                                                                   | GO:0030198 | 3             | ATP7A, MMP2, MMP9  | 145             | 7                  | 55.23           | 1.566e-5 | 7.699e-4    |
| endodermal cell differentiation                                                                     | GO:0035987 | 2             | MMP2, MMP9         | 36              | 7                  | 148.31          | 7.532e-5 | 2.505e-3    |
| collagen catabolic process                                                                          | GO:0030574 | 2             | MMP2, MMP9         | 41              | 7                  | 130.22          | 9.795e-5 | 3.042e-3    |
| extracellular matrix disassembly                                                                    | GO:0022617 | 2             | MMP2, MMP9         | 47              | 7                  | 113.60          | 1.290e-4 | 3.710e-3    |
| embryo implantation                                                                                 | GO:0007566 | 2             | MMP2, MMP9         | 48              | 7                  | 111.23          | 1.346e-4 | 3.822e-3    |
| lung alveolus development                                                                           | GO:0048286 | 2             | ATP7A, FBN1        | 49              | 7                  | 108.96          | 1.403e-4 | 3.937e-3    |
| ephrin receptor signaling pathway                                                                   | GO:0048013 | 2             | MMP2, MMP9         | 51              | 7                  | 104.69          | 1.520e-4 | 4.186e-3    |
| positive regulation of vascular associated smooth muscle cell proliferation                         | GO:1904707 | 2             | MMP2, MMP9         | 53              | 7                  | 100.74          | 1.642e-4 | 4.414e-3    |
| negative regulation of cation transmembrane transport                                               | GO:1904063 | 1             | MMP9               | 1               | 7                  | 2669.57         | 3.746e-4 | 7.813e-3    |
| negative regulation of epithelial cell differentiation involved in kidney development               | GO:2000697 | 1             | MMP9               | 1               | 7                  | 2669.57         | 3.746e-4 | 7.813e-3    |
| regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | GO:1902165 | 1             | HNRNPK             | 1               | 7                  | 2669.57         | 3.746e-4 | 7.813e-3    |
| negative regulation of apoptotic process                                                            | GO:0043066 | 3             | MMP9, HNRNPK, VHL  | 524             | 7                  | 15.28           | 7.053e-4 | 1.189e-2    |
| activation of protein kinase A activity                                                             | GO:0034199 | 1             | FBN1               | 2               | 7                  | 1334.79         | 7.491e-4 | 1.230e-2    |