

GeDiPNet Cluster 535 -- 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 00:01:26

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
renal tubule morphogenesis	GO:0061333	1	COL4A1	4	4	1167.94	8.560e-4	1.331e-2
retinal blood vessel morphogenesis	GO:0061304	1	COL4A1	6	4	778.63	1.284e-3	1.669e-2
chorionic trophoblast cell differentiation	GO:0060718	1	HTRA1	6	4	778.63	1.284e-3	1.669e-2
collagen-activated tyrosine kinase receptor signaling pathway	GO:0038063	1	COL4A1	12	4	389.31	2.566e-3	2.402e-2
basement membrane organization	GO:0071711	1	COL4A1	29	4	161.09	6.194e-3	3.697e-2
negative regulation of osteoclast differentiation	GO:0045671	1	TMEM178A	30	4	155.73	6.407e-3	3.733e-2
branching involved in blood vessel morphogenesis	GO:0001569	1	COL4A1	33	4	141.57	7.046e-3	3.929e-2
blood vessel morphogenesis	GO:0048514	1	COL4A1	34	4	137.40	7.259e-3	3.989e-2
neuromuscular junction development	GO:0007528	1	COL4A1	35	4	133.48	7.471e-3	4.045e-2
regulation of cytosolic calcium ion concentration	GO:0051480	1	TMEM178A	39	4	119.79	8.323e-3	4.251e-2
programmed cell death	GO:0012501	1	HTRA1	42	4	111.23	8.961e-3	4.406e-2
placenta development	GO:0001890	1	HTRA1	48	4	97.33	1.024e-2	4.689e-2
cellular response to amino acid stimulus	GO:0071230	1	COL4A1	64	4	73.00	1.363e-2	5.401e-2
negative regulation of BMP signaling pathway	GO:0030514	1	HTRA1	75	4	62.29	1.596e-2	5.836e-2
epithelial cell differentiation	GO:0030855	1	COL4A1	110	4	42.47	2.334e-2	7.077e-2