

GeDiPNet Cluster 33 -- 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 02:13:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
response to copper ion	GO:0046688	3	LOXL2, PRNP, SOD1	12	89	52.49	2.227e-5	9.764e-4
cardiac myofibril assembly	GO:0055003	3	PDGFRB, TTN, MYL2	13	89	48.45	2.885e-5	1.186e-3
heart contraction	GO:0060047	3	ACE, MYL2, SOD1	23	89	27.39	1.726e-4	4.545e-3
menaquinone catabolic process	GO:0042361	2	CYP4F3, CYP4F8	5	89	83.99	2.222e-4	5.431e-3
negative regulation of dendritic spine maintenance	GO:1902951	2	GRIN2B, PRNP	6	89	69.99	3.323e-4	7.201e-3
regulation of viral entry into host cell	GO:0046596	2	NECTIN2, TRIM5	6	89	69.99	3.323e-4	7.201e-3
phyloquinone catabolic process	GO:0042376	2	CYP4F3, CYP4F8	6	89	69.99	3.323e-4	7.201e-3
peripheral nervous system myelin maintenance	GO:0032287	2	PALS1, SOD1	9	89	46.66	7.901e-4	1.297e-2
cerebral cortex cell migration	GO:0021795	2	EGFR, DAB1	11	89	38.18	1.200e-3	1.688e-2
telomere maintenance via recombination	GO:0000722	2	BRCA2, TEP1	11	89	38.18	1.200e-3	1.688e-2
icosanoid metabolic process	GO:0006690	2	CYP4F3, CYP4F8	11	89	38.18	1.200e-3	1.688e-2
microtubule-based process	GO:0007017	3	HTT, TUBA1A, TUBB4A	46	89	13.69	1.367e-3	1.824e-2
collagen-activated tyrosine kinase receptor signaling pathway	GO:0038063	2	COL4A1, COL4A2	12	89	34.99	1.435e-3	1.871e-2
calcium ion transport into cytosol	GO:0060402	2	CACNA1C, JPH3	14	89	30.00	1.966e-3	2.238e-2
response to amyloid-beta	GO:1904645	2	CACNA1A, PRNP	15	89	28.00	2.262e-3	2.423e-2