

GeDiPNet Cluster 105 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 12:51:31

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
telencephalon regionalization	GO:0021978	2	SHH, SIX3	7	26	205.35	3.892e-5	1.519e-3
response to copper ion	GO:0046688	2	PRNP, SOD1	12	26	119.79	1.218e-4	3.569e-3
negative regulation of long-term synaptic potentiation	GO:1900272	2	PRNP, AGER	13	26	110.57	1.438e-4	4.050e-3
forebrain development	GO:0030900	3	EMX2, SEMA3A, SHH	76	26	28.37	1.571e-4	4.336e-3
cell proliferation in forebrain	GO:0021846	2	EMX2, SIX3	14	26	102.68	1.677e-4	4.541e-3
response to amyloid-beta	GO:1904645	2	PRNP, AGER	15	26	95.83	1.933e-4	5.041e-3
positive regulation of JNK cascade	GO:0046330	3	MFHAS1, SEMA3A, AGER	102	26	21.14	3.747e-4	8.017e-3
positive regulation of protein targeting to membrane	GO:0090314	2	PRNP, ANK3	27	26	53.24	6.395e-4	1.151e-2
positive regulation of p38MAPK cascade	GO:1900745	2	MFHAS1, AGER	29	26	49.57	7.385e-4	1.275e-2
thyroid gland development	GO:0030878	2	SHH, SIX3	30	26	47.92	7.906e-4	1.331e-2
regulation of developmental process	GO:0050793	2	KAT6B, SHH	32	26	44.92	8.999e-4	1.449e-2
branching involved in blood vessel morphogenesis	GO:0001569	2	COL4A1, SHH	33	26	43.56	9.571e-4	1.501e-2
neuronal action potential	GO:0019228	2	ANK3, SOD1	34	26	42.28	1.016e-3	1.554e-2
neuromuscular junction development	GO:0007528	2	COL4A1, ANK3	35	26	41.07	1.077e-3	1.610e-2
positive regulation of cell communication by electrical coupling	GO:0010650	1	ANK3	1	26	718.73	1.391e-3	1.874e-2