

GeDiPNet Cluster 287 -- 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 16:26:51

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
brain development	GO:0007420	5	ADGRG1, DMBX1, FOXG1, NF1, PTPN11	244	34	11.26	7.439e-5	2.428e-3
dendrite extension	GO:0097484	2	CYFIP1, SLC9A6	10	34	109.92	1.433e-4	3.959e-3
histone mRNA catabolic process	GO:0071044	2	LSM1, UPF1	14	34	78.52	2.884e-4	6.529e-3
cerebral cortex development	GO:0021987	3	FOXG1, NF1, SLC2A1	88	34	18.74	5.433e-4	1.008e-2
nuclear-transcribed mRNA catabolic process	GO:0000956	2	LSM1, UPF1	24	34	45.80	8.649e-4	1.368e-2
Rac protein signal transduction	GO:0016601	2	CYFIP1, NF1	26	34	42.28	1.016e-3	1.522e-2
positive regulation of signal transduction	GO:0009967	2	ADGRG1, PTPN11	29	34	37.90	1.265e-3	1.747e-2
neurotransmitter secretion	GO:0007269	2	NF1, STXBP1	29	34	37.90	1.265e-3	1.747e-2
regulation of macrophage colony-stimulating factor production	GO:1901256	1	FOXP1	1	34	549.62	1.819e-3	2.147e-2
positive regulation of mast cell apoptotic process	GO:0033027	1	NF1	1	34	549.62	1.819e-3	2.147e-2
regulation of glial cell differentiation	GO:0045685	1	NF1	1	34	549.62	1.819e-3	2.147e-2
observational learning	GO:0098597	1	NF1	1	34	549.62	1.819e-3	2.147e-2
beta-catenin-TCF complex assembly	GO:1904837	1	KMT2D	1	34	549.62	1.819e-3	2.147e-2
protein heterotrimerization	GO:0070208	1	COL1A2	1	34	549.62	1.819e-3	2.147e-2
negative regulation of cortisol secretion	GO:0051463	1	PTPN11	1	34	549.62	1.819e-3	2.147e-2