

GeDiPNet Cluster 572 -- 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: 2026-10-19 23:19:29

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
pituitary gland development	GO:0021983	2	SOX2, LHX3	30	10	124.58	1.112e-4	3.335e-3
brain development	GO:0007420	3	SOX2, PLXNB2, STXBP3	244	10	22.98	2.466e-4	5.894e-3
inner ear development	GO:0048839	2	SOX2, LHX3	54	10	69.21	3.634e-4	7.686e-3
regulation of interleukin-18 production	GO:0032661	1	NLRP12	1	10	1868.70	5.351e-4	9.880e-3
regulation of glial cell migration	GO:1903975	1	NTN1	1	10	1868.70	5.351e-4	9.880e-3
positive regulation of cell differentiation	GO:0045597	2	SMARCA4, SOX2	83	10	45.03	8.570e-4	1.331e-2
prolactin secreting cell differentiation	GO:0060127	1	LHX3	2	10	934.35	1.070e-3	1.514e-2
regulation of myofibroblast cell apoptotic process	GO:1904520	1	SOX2	2	10	934.35	1.070e-3	1.514e-2
medial motor column neuron differentiation	GO:0021526	1	LHX3	2	10	934.35	1.070e-3	1.514e-2
negative regulation of Toll signaling pathway	GO:0045751	1	NLRP12	2	10	934.35	1.070e-3	1.514e-2
positive regulation of glucose mediated signaling pathway	GO:1902661	1	SMARCA4	3	10	622.90	1.605e-3	1.885e-2
glial cell fate commitment	GO:0021781	1	SOX2	3	10	622.90	1.605e-3	1.885e-2
chemorepulsion of axon	GO:0061643	1	NTN1	3	10	622.90	1.605e-3	1.885e-2
Cdc42 protein signal transduction	GO:0032488	1	NTN1	3	10	622.90	1.605e-3	1.885e-2
regulation of cell migration	GO:0030334	2	NTN1, PLXNB2	122	10	30.63	1.838e-3	2.040e-2