

GeDiPNet Cluster 265 -- 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 12:28:52

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of interleukin-1 production	GO:0032652	1	ANXA1	1	18	1038.17	9.632e-4	1.501e-2
negative regulation of aldosterone secretion	GO:2000859	1	KCNK9	1	18	1038.17	9.632e-4	1.501e-2
negative regulation of gliogenesis	GO:0014014	1	PITX3	2	18	519.08	1.926e-3	2.259e-2
response to methamphetamine hydrochloride	GO:1904313	1	PITX3	2	18	519.08	1.926e-3	2.259e-2
positive regulation of cell proliferation in midbrain	GO:1904935	1	PITX3	2	18	519.08	1.926e-3	2.259e-2
cellular response to glial cell derived neurotrophic factor	GO:1990792	1	PITX3	2	18	519.08	1.926e-3	2.259e-2
protein dephosphorylation	GO:0006470	2	PTPN4, PTPRN2	72	18	28.84	2.152e-3	2.411e-2
regulation of action potential firing rate	GO:0099605	1	KCNK9	3	18	346.06	2.887e-3	2.824e-2
myoblast migration involved in skeletal muscle regeneration	GO:0014839	1	ANXA1	4	18	259.54	3.848e-3	3.281e-2
regulation of hormone secretion	GO:0046883	1	ANXA1	4	18	259.54	3.848e-3	3.281e-2
regulation of leukocyte migration	GO:0002685	1	ANXA1	5	18	207.63	4.807e-3	3.655e-2
positive regulation of neutrophil apoptotic process	GO:0033031	1	ANXA1	5	18	207.63	4.807e-3	3.655e-2
negative regulation of T-helper 2 cell differentiation	GO:0045629	1	ANXA1	5	18	207.63	4.807e-3	3.655e-2
granulocyte chemotaxis	GO:0071621	1	ANXA1	5	18	207.63	4.807e-3	3.655e-2
positive regulation of T-helper 1 cell differentiation	GO:0045627	1	ANXA1	6	18	173.03	5.766e-3	3.993e-2