

GeDiPNet Cluster 567 -- 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: 2026-10-20 00:01:23

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	3	CDK5RAP2, PTPN11, NF2	244	8	28.72	1.173e-4	3.471e-3
positive regulation of stress fiber assembly	GO:0051496	2	BRAF, NF2	53	8	88.15	2.186e-4	5.402e-3
epidermal growth factor receptor signaling pathway	GO:0007173	2	BRAF, PTPN11	64	8	73.00	3.190e-4	7.044e-3
negative regulation of cortisol secretion	GO:0051463	1	PTPN11	1	8	2335.88	4.281e-4	8.531e-3
negative regulation of growth hormone secretion	GO:0060125	1	PTPN11	1	8	2335.88	4.281e-4	8.531e-3
intestinal epithelial cell migration	GO:0061582	1	PTPN11	1	8	2335.88	4.281e-4	8.531e-3
single stranded viral RNA replication via double stranded DNA intermediate	GO:0039692	1	SMARCB1	1	8	2335.88	4.281e-4	8.531e-3
Ras protein signal transduction	GO:0007265	2	RIT1, SOS2	79	8	59.14	4.860e-4	9.301e-3
positive regulation of cell differentiation	GO:0045597	2	SMARCB1, NF2	83	8	56.29	5.364e-4	9.902e-3
microvillus organization	GO:0032528	1	PTPN11	2	8	1167.94	8.560e-4	1.331e-2
regulation of gliogenesis	GO:0014013	1	NF2	2	8	1167.94	8.560e-4	1.331e-2
positive T cell selection	GO:0043368	1	BRAF	3	8	778.63	1.284e-3	1.669e-2
CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	GO:0043369	1	BRAF	3	8	778.63	1.284e-3	1.669e-2
Schwann cell proliferation	GO:0014010	1	NF2	3	8	778.63	1.284e-3	1.669e-2
positive regulation of glucose mediated signaling pathway	GO:1902661	1	SMARCB1	3	8	778.63	1.284e-3	1.669e-2