

GeDiPNet Cluster 317 -- 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 17:15:58

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
synapse assembly	GO:0007416	2	PTEN, PLXNA4	78	6	79.86	2.552e-4	5.995e-3
negative regulation of cell communication	GO:0010648	1	PTEN	1	6	3114.50	3.211e-4	7.027e-3
negative regulation of synaptic vesicle clustering	GO:2000808	1	PTEN	1	6	3114.50	3.211e-4	7.027e-3
chemorepulsion of branchiomotor axon	GO:0021793	1	PLXNA4	1	6	3114.50	3.211e-4	7.027e-3
regulation of negative chemotaxis	GO:0050923	1	PLXNA4	1	6	3114.50	3.211e-4	7.027e-3
trigeminal nerve morphogenesis	GO:0021636	1	PLXNA4	2	6	1557.25	6.421e-4	1.127e-2
negative regulation of keratinocyte migration	GO:0051548	1	PTEN	2	6	1557.25	6.421e-4	1.127e-2
postganglionic parasympathetic fiber development	GO:0021784	1	PLXNA4	2	6	1557.25	6.421e-4	1.127e-2
cranial nerve morphogenesis	GO:0021602	1	PLXNA4	2	6	1557.25	6.421e-4	1.127e-2
vagus nerve morphogenesis	GO:0021644	1	PLXNA4	2	6	1557.25	6.421e-4	1.127e-2
membrane lipid metabolic process	GO:0006643	1	AGMO	2	6	1557.25	6.421e-4	1.127e-2
facial nerve morphogenesis	GO:0021610	1	PLXNA4	3	6	1038.17	9.630e-4	1.467e-2
negative regulation of signaling	GO:0023057	1	PTEN	3	6	1038.17	9.630e-4	1.467e-2
rhythmic synaptic transmission	GO:0060024	1	PTEN	3	6	1038.17	9.630e-4	1.467e-2
regulation of axon extension involved in axon guidance	GO:0048841	1	PLXNA4	4	6	778.63	1.284e-3	1.747e-2