

GeDiPNet Cluster 499 -- 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 23:18:28

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
synaptic vesicle maturation	GO:0016188	2	ZDHHC15, STXBP1	9	8	519.08	5.765e-6	3.543e-4
conversion of seryl-tRNAsec to selenocys-tRNAsec	GO:0001717	1	SEPSECS	1	8	2335.88	4.281e-4	8.531e-3
positive regulation of vesicle docking	GO:0106022	1	STXBP1	1	8	2335.88	4.281e-4	8.531e-3
regulation of acrosomal vesicle exocytosis	GO:2000367	1	STXBP1	1	8	2335.88	4.281e-4	8.531e-3
protein localization to postsynapse	GO:0062237	1	ZDHHC15	1	8	2335.88	4.281e-4	8.531e-3
regulation of type III interferon production	GO:0034344	1	IFIH1	2	8	1167.94	8.560e-4	1.331e-2
positive regulation of glutamate secretion, neurotransmission	GO:1903296	1	STXBP1	2	8	1167.94	8.560e-4	1.331e-2
glutamate reuptake	GO:0051935	1	KCNJ10	2	8	1167.94	8.560e-4	1.331e-2
protein targeting to Golgi apparatus	GO:0140450	1	ZDHHC15	3	8	778.63	1.284e-3	1.669e-2
mitotic spindle disassembly	GO:0051228	1	SPAST	3	8	778.63	1.284e-3	1.669e-2
cytokinetic process	GO:0032506	1	SPAST	3	8	778.63	1.284e-3	1.669e-2
axon target recognition	GO:0007412	1	STXBP1	3	8	778.63	1.284e-3	1.669e-2
regulation of regulated secretory pathway	GO:1903305	1	STXBP1	3	8	778.63	1.284e-3	1.669e-2
establishment of localization in cell	GO:0051649	2	KCNJ10, STXBP1	147	8	31.78	1.668e-3	1.938e-2
detection of virus	GO:0009597	1	IFIH1	4	8	583.97	1.711e-3	1.958e-2