

GeDiPNet Cluster 222 -- 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: 2026-10-07 22:43:12

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
astrocyte activation involved in immune response	GO:0002265	2	APP, PSEN1	4	4	2335.88	2.062e-7	2.259e-5
positive regulation of amyloid fibril formation	GO:1905908	2	APP, PSEN1	5	4	1868.70	3.436e-7	3.449e-5
cellular response to manganese ion	GO:0071287	2	APP, LRRK2	7	4	1334.79	7.214e-7	6.417e-5
positive regulation of tumor necrosis factor production	GO:0032760	3	APP, PSEN1, LRRK2	113	4	124.03	8.574e-7	7.397e-5
neuron projection maintenance	GO:1990535	2	APP, PSEN1	13	4	718.73	2.678e-6	1.859e-4
astrocyte activation	GO:0048143	2	APP, PSEN1	17	4	549.62	4.669e-6	2.891e-4
positive regulation of glycolytic process	GO:0045821	2	APP, PSEN1	24	4	389.31	9.470e-6	5.100e-4
positive regulation of protein metabolic process	GO:0051247	2	APP, LRRK2	24	4	389.31	9.470e-6	5.100e-4
regulation of synaptic transmission, glutamatergic	GO:0051966	2	PSEN1, LRRK2	33	4	283.14	1.810e-5	8.428e-4
regulation of canonical Wnt signaling pathway	GO:0060828	2	PSEN1, LRRK2	37	4	252.53	2.283e-5	1.005e-3
regulation of gene expression	GO:0010468	3	APP, PSEN1, LRRK2	402	4	34.86	3.890e-5	1.519e-3
cellular response to amyloid-beta	GO:1904646	2	APP, PSEN1	53	4	176.29	4.718e-5	1.756e-3
learning or memory	GO:0007611	2	APP, PSEN1	72	4	129.77	8.740e-5	2.800e-3
synapse organization	GO:0050808	2	APP, PSEN1	72	4	129.77	8.740e-5	2.800e-3
positive regulation of proteasomal ubiquitin-dependent protein catabolic process	GO:0032436	2	PSEN1, LRRK2	79	4	118.27	1.053e-4	3.211e-3