

GeDiPNet Cluster 484 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-20 00:01:09

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of cytoplasmic translational fidelity	GO:0140018	1	AARS1	1	6	3114.50	3.211e-4	7.044e-3
positive regulation of Toll signaling pathway	GO:0045752	1	APP	1	6	3114.50	3.211e-4	7.044e-3
regulation of response to calcium ion	GO:1905945	1	APP	1	6	3114.50	3.211e-4	7.044e-3
negative regulation of mitochondrial DNA replication	GO:0090298	1	LIG3	1	6	3114.50	3.211e-4	7.044e-3
locomotory behavior	GO:0007626	2	FIG4, APP	99	6	62.92	4.110e-4	8.341e-3
protein trimerization	GO:0070206	1	APP	2	6	1557.25	6.421e-4	1.113e-2
regulation of endoplasmic reticulum stress-induced neuron intrinsic apoptotic signaling pathway	GO:1903381	1	APP	2	6	1557.25	6.421e-4	1.113e-2
negative regulation of blood circulation	GO:1903523	1	APP	2	6	1557.25	6.421e-4	1.113e-2
positive regulation of protein import	GO:1904591	1	APP	2	6	1557.25	6.421e-4	1.113e-2
pyrimidine nucleobase metabolic process	GO:0006206	1	TYMP	2	6	1557.25	6.421e-4	1.113e-2
pyrimidine-containing compound metabolic process	GO:0072527	1	TYMP	2	6	1557.25	6.421e-4	1.113e-2
alanyl-tRNA aminoacylation	GO:0006419	1	AARS1	3	6	1038.17	9.630e-4	1.423e-2
regulation of amyloid-beta clearance	GO:1900221	1	APP	3	6	1038.17	9.630e-4	1.423e-2
regulation of amyloid fibril formation	GO:1905906	1	APP	3	6	1038.17	9.630e-4	1.423e-2
phospholipase D-activating G protein-coupled receptor signaling pathway	GO:0031583	1	APP	3	6	1038.17	9.630e-4	1.423e-2