

GeDiPNet Cluster 407 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 10:05:57

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of neuronal synaptic plasticity	GO:0048168	2	CAMK2D, JPH3	26	50	28.75	2.189e-3	2.410e-2
regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	GO:0010880	2	CAMK2D, JPH3	28	50	26.70	2.537e-3	2.635e-2
dADP biosynthetic process	GO:0006173	1	AK5	1	50	373.74	2.676e-3	2.702e-2
ERBB3 signaling pathway	GO:0038129	1	NRG1	1	50	373.74	2.676e-3	2.702e-2
positive regulation of peptidyl-tyrosine autophosphorylation	GO:1900086	1	NRG1	1	50	373.74	2.676e-3	2.702e-2
chemical synaptic transmission	GO:0007268	4	AMPH, CACNB2, DLG2, GRIK4	236	50	6.33	3.623e-3	3.176e-2
blood vessel diameter maintenance	GO:0097746	2	KNG1, NTS	37	50	20.20	4.402e-3	3.482e-2
mammary gland development	GO:0030879	2	NRG1, PTCH1	37	50	20.20	4.402e-3	3.482e-2
retrograde axonal protein transport	GO:0099642	1	DLG2	2	50	186.87	5.344e-3	3.860e-2
negative regulation of Kit signaling pathway	GO:1900235	1	SH2B3	2	50	186.87	5.344e-3	3.860e-2
positive regulation of protein modification process	GO:0031401	1	ATG7	2	50	186.87	5.344e-3	3.860e-2
ultradian rhythm	GO:0007624	1	ENOX1	2	50	186.87	5.344e-3	3.860e-2
phosphatidylglycerol catabolic process	GO:0034478	1	PLA2G4A	2	50	186.87	5.344e-3	3.860e-2
regulation of relaxation of cardiac muscle	GO:1901897	1	CAMK2D	2	50	186.87	5.344e-3	3.860e-2
response to chlorate	GO:0010157	1	PTCH1	2	50	186.87	5.344e-3	3.860e-2