

GeDiPNet Cluster 569 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:54

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
RHO GTPases activate CIT	Reactome	1	DLG4	8	3	500.42	1.997e-3	1.898e-2
Activation of Ca-permeable Kainate Receptor	Reactome	1	DLG4	12	3	333.61	2.995e-3	2.538e-2
LGI-ADAM interactions	Reactome	1	DLG4	14	3	285.95	3.493e-3	2.829e-2
Trafficking of AMPA receptors	Reactome	1	DLG4	17	3	235.49	4.241e-3	3.256e-2
Apoptotic cleavage of cellular proteins	Reactome	1	SATB1	18	3	222.41	4.490e-3	3.394e-2
Synaptic adhesion-like molecules	Reactome	1	DLG4	21	3	190.63	5.237e-3	3.760e-2
Unblocking of NMDA receptors, glutamate binding and activation	Reactome	1	DLG4	22	3	181.97	5.486e-3	3.872e-2
Neurexins and neuroligins	Reactome	1	DLG4	32	3	125.10	7.973e-3	4.940e-2
Cocaine addiction	KEGG	1	DLG4	49	3	81.70	1.219e-2	6.416e-2
SUMOylation of chromatin organization proteins	Reactome	1	SATB1	70	3	57.19	1.739e-2	7.887e-2
Glutamatergic synapse	KEGG	1	DLG4	116	3	34.51	2.870e-2	1.055e-1
RAF/MAP kinase cascade	Reactome	1	DLG4	124	3	32.28	3.066e-2	1.098e-1
Hippo signaling pathway	KEGG	1	DLG4	157	3	25.50	3.871e-2	1.252e-1
Huntington disease	KEGG	1	DLG4	308	3	13.00	7.499e-2	1.830e-1
Pathways of neurodegeneration - multiple diseases	KEGG	1	DLG4	480	3	8.34	1.152e-1	2.351e-1