

GeDiPNet Cluster 608 -- 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: 2026-10-19 23:21:21

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Reelin signalling pathway	Reactome	1	RELN	5	3	800.67	1.249e-3	1.343e-2
Establishment of Sister Chromatid Cohesion	Reactome	1	ESCO2	11	3	363.94	2.745e-3	2.394e-2
Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	Reactome	1	CDK5	16	3	250.21	3.992e-3	3.122e-2
CRMPs in Sema3A signaling	Reactome	1	CDK5	16	3	250.21	3.992e-3	3.122e-2
DARPP-32 events	Reactome	1	CDK5	19	3	210.70	4.739e-3	3.521e-2
Cocaine addiction	KEGG	1	CDK5	49	3	81.70	1.219e-2	6.416e-2
ECM-receptor interaction	KEGG	1	RELN	89	3	44.98	2.207e-2	9.071e-2
Regulation of TP53 Activity through Phosphorylation	Reactome	1	CDK5	92	3	43.51	2.281e-2	9.234e-2
Spinocerebellar ataxia	KEGG	1	RELN	144	3	27.80	3.554e-2	1.190e-1
Cell cycle	KEGG	1	ESCO2	158	3	25.34	3.895e-2	1.256e-1
Axon guidance	KEGG	1	CDK5	183	3	21.88	4.502e-2	1.364e-1
Focal adhesion	KEGG	1	RELN	203	3	19.72	4.986e-2	1.445e-1
Human papillomavirus infection	KEGG	1	RELN	333	3	12.02	8.090e-2	1.908e-1
PI3K-Akt signaling pathway	KEGG	1	RELN	361	3	11.09	8.750e-2	1.998e-1
Alzheimer disease	KEGG	1	CDK5	388	3	10.32	9.383e-2	2.081e-1