

GeDiPNet Cluster 409 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 07:58:22

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Motor proteins	KEGG	3	DNAH10, DNAH8, DNAH17	194	23	8.07	5.792e-3	4.832e-2
RAS signaling downstream of NF1 loss-of-function variants	Reactome	1	SPRED1	7	23	74.60	1.333e-2	8.263e-2
Activation of PUMA and translocation to mitochondria	Reactome	1	TP63	9	23	58.02	1.711e-2	9.624e-2
Peptide ligand-binding receptors	Reactome	2	PROK2, PROKR2	106	23	9.85	1.730e-2	9.692e-2
Huntington disease	KEGG	3	DNAH10, DNAH8, DNAH17	308	23	5.09	2.023e-2	1.057e-1
TP53 Regulates Transcription of Death Receptors and Ligands	Reactome	1	TP63	12	23	43.51	2.275e-2	1.128e-1
TP53 Regulates Transcription of Caspase Activators and Caspases	Reactome	1	TP63	12	23	43.51	2.275e-2	1.128e-1
FGFRL1 modulation of FGFR1 signaling	Reactome	1	SPRED1	13	23	40.17	2.462e-2	1.183e-1
Regulation of TP53 Activity through Association with Co-factors	Reactome	1	TP63	14	23	37.30	2.649e-2	1.230e-1
TP53 regulates transcription of several additional cell death genes whose specific roles in p53-dependent apoptosis remain uncertain	Reactome	1	TP63	14	23	37.30	2.649e-2	1.230e-1
Amyotrophic lateral sclerosis	KEGG	3	DNAH10, DNAH8, DNAH17	368	23	4.26	3.209e-2	1.372e-1
G0 and Early G1	Reactome	1	DYRK1A	18	23	29.01	3.394e-2	1.414e-1
TP53 Regulates Transcription of Genes Involved in Cytochrome C Release	Reactome	1	TP63	20	23	26.11	3.764e-2	1.498e-1
G alpha (q) signalling events	Reactome	2	PROK2, PROKR2	172	23	6.07	4.237e-2	1.603e-1
Pathways of neurodegeneration - multiple diseases	KEGG	3	DNAH10, DNAH8, DNAH17	480	23	3.26	6.212e-2	1.961e-1