

GeDiPNet Cluster 9 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 00:38:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Motor proteins	KEGG	13	DNAH11, DNAI1, DNAH5, DNAL1, DNAH1, DNAH9, DNAH6, DNAH7, DNAI2, DNAH10, DNAH8, TNNT3	194	102	7.89	9.064e-9	8.015e-7
Huntington disease	KEGG	13	DNAH11, DNAI1, DNAH5, DNAL1, CREBBP, DNAH1, DNAH9, DNAH6, DNAH7, DNAI2, DNAH10, DNAH8	308	102	4.97	1.944e-6	8.584e-5
Pathways of neurodegeneration - multiple diseases	KEGG	14	DNAH11, DNAI1, DNAH5, DNAL1, NFKB1, DNAH1, DNAH9, DNAH6, DNAH7, DNAI2, CYBB, DNAH10	480	102	3.43	5.175e-5	1.316e-3
Amyotrophic lateral sclerosis	KEGG	12	DNAH11, DNAI1, DNAH5, DNAL1, DNAH1, DNAH9, DNAH6, DNAH7, DNAI2, DNAH10, DNAH8, DNAH14	368	102	3.84	6.456e-5	1.570e-3
Hedgehog 'off' state	Reactome	4	PRKAR1B, IFT122, OFD1, RPGRIP1L	56	102	8.41	1.284e-3	1.635e-2
TP53 Regulates Transcription of Genes Involved in Cytochrome C Release	Reactome	2	CREBBP, TP73	20	102	11.77	1.228e-2	7.746e-2
CD209 (DC-SIGN) signaling	Reactome	2	CREBBP, NFKB1	21	102	11.21	1.350e-2	8.168e-2
Glycogen storage disease type II (GAA)	Reactome	1	GAA	2	102	58.87	1.691e-2	9.378e-2
ARL13B-mediated ciliary trafficking of INPP5E	Reactome	1	INPP5E	3	102	39.25	2.527e-2	1.171e-1
Antifolate resistance	KEGG	2	ABCC5, NFKB1	30	102	7.85	2.662e-2	1.207e-1
Hyaluronan biosynthesis and export	Reactome	1	ABCC5	5	102	23.55	4.176e-2	1.552e-1
LRR FLII-interacting protein 1 (LRRFIP1) activates type I IFN production	Reactome	1	CREBBP	5	102	23.55	4.176e-2	1.552e-1
CLEC7A/inflammasome pathway	Reactome	1	NFKB1	6	102	19.62	4.990e-2	1.712e-1
IκBA variant leads to EDA-ID	Reactome	1	NFKB1	7	102	16.82	5.797e-2	1.852e-1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	Reactome	1	CREBBP	7	102	16.82	5.797e-2	1.852e-1