

GeDiPNet Cluster 255 -- 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: 11 · Generated: 2026-10-07 03:54:20

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Molybdenum cofactor biosynthesis	Reactome	1	GPHN	6	8	250.21	3.991e-3	3.767e-2
Spliceosome	KEGG	2	DHX15, DHX16	162	8	18.53	4.800e-3	4.270e-2
mRNA Splicing - Major Pathway	Reactome	2	DHX15, DHX16	183	8	16.41	6.087e-3	4.984e-2
VxPx cargo-targeting to cilium	Reactome	1	PKD1	21	8	71.49	1.391e-2	8.315e-2
Folate biosynthesis	KEGG	1	GPHN	28	8	53.62	1.850e-2	9.846e-2
GABAergic synapse	KEGG	1	GPHN	89	8	16.87	5.779e-2	1.851e-1
Biosynthesis of cofactors	KEGG	1	GPHN	154	8	9.75	9.812e-2	2.454e-1
Hippo signaling pathway	KEGG	1	PALS1	157	8	9.56	9.995e-2	2.478e-1
Tight junction	KEGG	1	PALS1	170	8	8.83	1.078e-1	2.585e-1
Human papillomavirus infection	KEGG	1	PALS1	333	8	4.51	2.015e-1	3.658e-1
Metabolic pathways	KEGG	1	GPHN	1563	8	0.96	6.723e-1	7.870e-1