

GeDiPNet Cluster 441 -- 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](scripts/build_cluster_enrichment.php) on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 12 · Generated: 2026-10-20 00:02:37

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG	1	COQ4	12	7	142.98	6.975e-3	4.528e-2
Hyaluronan uptake and degradation	Reactome	1	CHP1	12	7	142.98	6.975e-3	4.528e-2
Mitochondrial tRNA aminoacylation	Reactome	1	MARS2	14	7	122.55	8.133e-3	5.006e-2
Processing of SMDT1	Reactome	1	AFG3L2	16	7	107.23	9.291e-3	5.428e-2
Selenocompound metabolism	KEGG	1	MARS2	17	7	100.92	9.869e-3	5.651e-2
Kinesins	Reactome	1	KIF1C	59	7	29.08	3.389e-2	1.159e-1
Aminoacyl-tRNA biosynthesis	KEGG	1	MARS2	66	7	26.00	3.785e-2	1.235e-1
COPI-dependent Golgi-to-ER retrograde traffic	Reactome	1	KIF1C	99	7	17.33	5.631e-2	1.550e-1
Spinocerebellar ataxia	KEGG	1	AFG3L2	144	7	11.91	8.099e-2	1.909e-1
Biosynthesis of cofactors	KEGG	1	COQ4	154	7	11.14	8.640e-2	1.982e-1
Motor proteins	KEGG	1	KIF1C	194	7	8.84	1.078e-1	2.259e-1
Metabolic pathways	KEGG	2	MARS2, COQ4	1563	7	2.20	2.285e-1	3.607e-1