

GeDiPNet Cluster 339 -- 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 21:08:36

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Myoclonic epilepsy of Lafora	Reactome	2	NHLRC1, EPM2A	9	25	106.76	1.484e-4	3.086e-3
Amino acids regulate mTORC1	Reactome	3	DEPDC5, NPRL2, NPRL3	55	25	26.20	1.946e-4	3.826e-3
Glycogen synthesis	Reactome	2	NHLRC1, EPM2A	16	25	60.05	4.904e-4	7.856e-3
mTOR signaling pathway	KEGG	3	DEPDC5, NPRL2, NPRL3	158	25	9.12	4.154e-3	3.874e-2
Defective DHDDS causes retinitis pigmentosa 59	Reactome	1	NUS1	2	25	240.20	4.159e-3	3.874e-2
Synthesis of Dolichyl-phosphate	Reactome	1	NUS1	6	25	80.07	1.243e-2	7.776e-2
Lysosome	KEGG	2	SCARB2, CLN3	133	25	7.22	3.092e-2	1.311e-1
Terpenoid backbone biosynthesis	KEGG	1	NUS1	23	25	20.89	4.684e-2	1.653e-1
Wnt signaling pathway	KEGG	2	PRICKLE1, PRICKLE2	174	25	5.52	5.036e-2	1.722e-1
SNARE interactions in vesicular transport	KEGG	1	GOSR2	33	25	14.56	6.654e-2	1.990e-1
Cargo concentration in the ER	Reactome	1	GOSR2	33	25	14.56	6.654e-2	1.990e-1
Sphingolipid de novo biosynthesis	Reactome	1	CERS1	43	25	11.17	8.585e-2	2.279e-1
Voltage gated Potassium channels	Reactome	1	KCNC1	43	25	11.17	8.585e-2	2.279e-1
Base excision repair	KEGG	1	POLG	44	25	10.92	8.776e-2	2.308e-1
Intra-Golgi traffic	Reactome	1	GOSR2	44	25	10.92	8.776e-2	2.308e-1