

GeDiPNet Cluster 271 -- 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 05:04:02

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Pyrimidine biosynthesis	Reactome	3	CAD, DHODH, UMPS	3	39	307.95	3.166e-8	2.403e-6
Interaction between L1 and Ankyrins	Reactome	3	SPTB, SPTA1, ANK1	13	39	71.07	8.854e-6	3.037e-4
COPI-mediated anterograde transport	Reactome	4	SPTB, CAPZA3, SPTA1, ANK1	101	39	12.20	3.091e-4	5.495e-3
Pyrimidine metabolism	KEGG	3	CAD, DHODH, UMPS	58	39	15.93	8.634e-4	1.213e-2
NCAM signaling for neurite out-growth	Reactome	2	SPTB, SPTA1	20	39	30.79	1.881e-3	2.179e-2
Defective SLCO1B1 causes hyperbilirubinemia, Rotor type (HBLRR)	Reactome	1	SLCO1B1	1	39	307.95	3.247e-3	3.258e-2
Defective SLC4A1 causes hereditary spherocytosis type 4 (HSP4), distal renal tubular acidosis (dRTA) and dRTA with hemolytic anemia (dRTA-HA)	Reactome	1	SLC4A1	1	39	307.95	3.247e-3	3.258e-2
Activation and oligomerization of BAK protein	Reactome	1	BAK1	2	39	153.97	6.484e-3	5.191e-2
RAF/MAP kinase cascade	Reactome	3	SPTB, NRG1, SPTA1	124	39	7.45	7.488e-3	5.693e-2
Neurofascin interactions	Reactome	1	ANK1	4	39	76.99	1.293e-2	7.946e-2
Biosynthesis of cofactors	KEGG	3	CAD, DHODH, UMPS	154	39	6.00	1.348e-2	8.161e-2
GRB7 events in ERBB2 signaling	Reactome	1	NRG1	5	39	61.59	1.613e-2	9.107e-2
Release of apoptotic factors from the mitochondria	Reactome	1	BAK1	5	39	61.59	1.613e-2	9.107e-2
Melanoma	KEGG	2	BAK1, MITF	73	39	8.44	2.336e-2	1.123e-1
Hydrolysis of LPC	Reactome	1	PLA2G4F	9	39	34.22	2.886e-2	1.262e-1