

GeDiPNet Cluster 463 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-19 22:49:36

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective SLCO1B1 causes hyperbilirubinemia, Rotor type (HBLRR)	Reactome	1	SLCO1B1	1	102	117.75	8.493e-3	5.136e-2
Reversal of alkylation damage by DNA dioxygenases	Reactome	1	FTO	2	102	58.87	1.691e-2	7.786e-2
Activation and oligomerization of BAK protein	Reactome	1	BAK1	2	102	58.87	1.691e-2	7.786e-2
Clathrin-mediated endocytosis	Reactome	4	SYT9, ARRB1, GAPVD1, PACSIN1	130	102	3.62	2.469e-2	9.672e-2
Tandem of pore domain in a weak inwardly rectifying K+ channels (TWIK)	Reactome	1	KCNK1	3	102	39.25	2.527e-2	9.801e-2
TCF7L2 mutants don't bind CTBP	Reactome	1	TCF7L2	3	102	39.25	2.527e-2	9.801e-2
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	Reactome	1	APOE	3	102	39.25	2.527e-2	9.801e-2
Adherens junctions interactions	Reactome	2	CADM2, CDH4	32	102	7.36	3.003e-2	1.083e-1
Neurophilin interactions with VEGF and VEGFR	Reactome	1	NRP1	4	102	29.44	3.355e-2	1.151e-1
Thyroid cancer	KEGG	2	BAK1, TCF7L2	37	102	6.36	3.923e-2	1.260e-1
GRB7 events in ERBB2 signaling	Reactome	1	NRG1	5	102	23.55	4.176e-2	1.306e-1
Chylomicron clearance	Reactome	1	APOE	5	102	23.55	4.176e-2	1.306e-1
Release of apoptotic factors from the mitochondria	Reactome	1	BAK1	5	102	23.55	4.176e-2	1.306e-1
Beta defensins	Reactome	2	DEFB127, DEFB128	40	102	5.89	4.521e-2	1.367e-1
Defensins	Reactome	2	DEFB127, DEFB128	42	102	5.61	4.936e-2	1.438e-1