

GeDiPNet Cluster 471 -- 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: 15 · Generated: 2026-10-20 00:03:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
VEGF binds to VEGFR leading to receptor dimerization	Reactome	2	FLT4, KDR	8	12	250.21	2.554e-5	6.377e-4
Lysosome	KEGG	3	NEU1, LIPA, ASAH1	133	12	22.58	2.715e-4	4.176e-3
Glycosphingolipid metabolism	Reactome	2	NEU1, ASAH1	46	12	43.51	9.244e-4	1.068e-2
Defective AHCY causes Hypermethioninemia with S-adenosylhomocysteine hydrolase deficiency (HMAHCHD)	Reactome	1	AHCY	1	12	1000.83	9.992e-4	1.132e-2
Sphingolipid metabolism	KEGG	2	NEU1, ASAH1	54	12	37.07	1.272e-3	1.363e-2
Defective NEU1 causes sialidosis	Reactome	1	NEU1	3	12	333.61	2.995e-3	2.538e-2
Neurophilin interactions with VEGF and VEGFR	Reactome	1	KDR	4	12	250.21	3.991e-3	3.122e-2
Signaling by membrane-tethered fusions of PDGFRA or PDGFRB	Reactome	1	KDR	5	12	200.17	4.987e-3	3.635e-2
Sulfur amino acid metabolism	Reactome	1	AHCY	6	12	166.81	5.981e-3	4.097e-2
RUNX1 regulates transcription of genes involved in WNT signaling	Reactome	1	FOXP3	6	12	166.81	5.981e-3	4.097e-2
RUNX1 and FOXP3 control the development of regulatory T lymphocytes (Tregs)	Reactome	1	FOXP3	10	12	100.08	9.951e-3	5.666e-2
Uptake and function of anthrax toxins	Reactome	1	ANTXR1	13	12	76.99	1.292e-2	6.623e-2
Methylation	Reactome	1	AHCY	14	12	71.49	1.391e-2	6.943e-2
VEGFR2 mediated cell proliferation	Reactome	1	KDR	14	12	71.49	1.391e-2	6.943e-2
Focal adhesion	KEGG	2	FLT4, KDR	203	12	9.86	1.678e-2	7.755e-2