

GeDiPNet Cluster 619 -- 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: 2026-10-20 00:03:15

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycosphingolipid metabolism	Reactome	2	B4GALNT1, GBA2	46	8	65.27	3.960e-4	5.582e-3
Sphingolipid metabolism	KEGG	2	B4GALNT1, GBA2	54	8	55.60	5.461e-4	7.147e-3
Pyrimidine metabolism	KEGG	2	ENTPD1, NT5C2	58	8	51.77	6.299e-4	7.991e-3
Nucleotide metabolism	KEGG	2	ENTPD1, NT5C2	85	8	35.32	1.348e-3	1.420e-2
Signaling by plasma membrane FGFR1 fusions	Reactome	1	ERLIN2	3	8	500.42	1.997e-3	1.898e-2
Abacavir metabolism	Reactome	1	NT5C2	3	8	500.42	1.997e-3	1.898e-2
Purine metabolism	KEGG	2	ENTPD1, NT5C2	128	8	23.46	3.026e-3	2.557e-2
Phosphate bond hydrolysis by NTPDase proteins	Reactome	1	ENTPD1	8	8	187.66	5.318e-3	3.801e-2
Axonal growth inhibition (RHOA activation)	Reactome	1	MAG	9	8	166.81	5.981e-3	4.097e-2
Purine catabolism	Reactome	1	NT5C2	12	8	125.10	7.968e-3	4.940e-2
Membrane binding and targetting of GAG proteins	Reactome	1	VPS37A	14	8	107.23	9.290e-3	5.428e-2
Glycosphingolipid biosynthesis - ganglio series	KEGG	1	B4GALNT1	15	8	100.08	9.951e-3	5.666e-2
Other glycan degradation	KEGG	1	GBA2	18	8	83.40	1.193e-2	6.320e-2
Metabolic pathways	KEGG	4	B4GALNT1, ENTDP1, NT5C2, GBA2	1563	8	3.84	1.295e-2	6.631e-2
Purinergic signaling in leishmaniasis infection	Reactome	1	ENTPD1	24	8	62.55	1.588e-2	7.505e-2