

GeDiPNet Cluster 460 -- 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 00:02:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycosphingolipid metabolism	Reactome	3	HEXA, GM2A, HEXB	46	4	195.82	2.098e-7	1.069e-5
Sphingolipid metabolism	KEGG	3	HEXA, GM2A, HEXB	54	4	166.81	3.426e-7	1.643e-5
Lysosome	KEGG	3	HEXA, GM2A, HEXB	133	4	67.73	5.269e-6	1.715e-4
Hyaluronan uptake and degradation	Reactome	2	HEXA, HEXB	12	4	500.42	5.485e-6	1.772e-4
Keratan sulfate degradation	Reactome	2	HEXA, HEXB	13	4	461.92	6.482e-6	2.036e-4
CS/DS degradation	Reactome	2	HEXA, HEXB	14	4	428.93	7.561e-6	2.316e-4
Glycosphingolipid biosynthesis - ganglio series	KEGG	2	HEXA, HEXB	15	4	400.33	8.724e-6	2.604e-4
Glycosphingolipid biosynthesis - globo and isoglobo series	KEGG	2	HEXA, HEXB	16	4	375.31	9.969e-6	2.906e-4
Other glycan degradation	KEGG	2	HEXA, HEXB	18	4	333.61	1.271e-5	3.553e-4
Glycosaminoglycan degradation	KEGG	2	HEXA, HEXB	19	4	316.05	1.420e-5	3.897e-4
Amino sugar and nucleotide sugar metabolism	KEGG	2	HEXA, HEXB	38	4	158.03	5.826e-5	1.232e-3
Various types of N-glycan biosynthesis	KEGG	2	HEXA, HEXB	43	4	139.65	7.479e-5	1.505e-3
Defective HEXA causes GM2G1	Reactome	1	HEXA	1	4	3002.50	3.331e-4	4.876e-3
Defective HEXB causes GM2G2	Reactome	1	HEXB	1	4	3002.50	3.331e-4	4.876e-3
Neutrophil degranulation	Reactome	2	GM2A, HEXB	480	4	12.51	9.065e-3	5.360e-2