

GeDiPNet Cluster 147 -- 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 11:30:11

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycosaminoglycan degradation	KEGG	11	HYAL1, IDUA, IDS, GNS, HGSNAT, NAGLU, SGSH, GALNS, GLB1, ARSB, GUSB	19	22	316.05	2.832e-27	6.517e-24
Lysosome	KEGG	12	HYAL1, IDUA, IDS, GNS, HGSNAT, NAGLU, SGSH, GALNS, GLB1, ARSB, GUSB, GNPTAB	133	22	49.25	1.208e-18	7.990e-16
HS-GAG degradation	Reactome	7	IDUA, IDS, HGSNAT, NAGLU, SGSH, GLB1, GUSB	22	22	173.70	4.008e-15	1.388e-12
CS/DS degradation	Reactome	4	HYAL1, IDUA, IDS, ARSB	14	22	155.97	8.350e-9	7.510e-7
Metabolic pathways	KEGG	13	HYAL1, IDUA, IDS, COASY, GNS, HGSNAT, NAGLU, SGSH, GALNS, GLB1, ARSB, GUSB	1563	22	4.54	4.646e-7	2.510e-5
Keratan sulfate degradation	Reactome	3	GNS, GALNS, GLB1	13	22	125.98	1.508e-6	6.950e-5
Neutrophil degranulation	Reactome	7	GNS, HGSNAT, GALNS, GLB1, ARSB, GUSB, APRT	480	22	7.96	1.576e-5	4.911e-4
Glycosphingolipid metabolism	Reactome	3	ARSK, GLB1, ARSB	46	22	35.60	7.696e-5	1.813e-3
Multifunctional anion exchangers	Reactome	2	SLC26A1, SLC26A11	9	22	121.31	1.144e-4	2.496e-3
Hyaluronan uptake and degradation	Reactome	2	HYAL1, GUSB	12	22	90.98	2.091e-4	4.041e-3
The activation of arylsulfatases	Reactome	2	ARSK, ARSB	13	22	83.99	2.468e-4	4.600e-3
MPS IIIC - Sanfilippo syndrome C	Reactome	1	HGSNAT	1	22	545.91	1.832e-3	2.135e-2
MPS IV - Morquio syndrome A	Reactome	1	GALNS	1	22	545.91	1.832e-3	2.135e-2
MPS IV - Morquio syndrome B	Reactome	1	GLB1	1	22	545.91	1.832e-3	2.135e-2
MPS IIID - Sanfilippo syndrome D	Reactome	1	GNS	1	22	545.91	1.832e-3	2.135e-2