

GeDiPNet Cluster 517 -- 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: 2026-10-19 23:22:10

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective CHST3 causes SEDCJD	Reactome	1	BGN	8	4	375.31	2.662e-3	2.343e-2
Defective CHST14 causes EDS, musculocontractural type	Reactome	1	BGN	8	4	375.31	2.662e-3	2.343e-2
Defective CHSY1 causes TPBS	Reactome	1	BGN	8	4	375.31	2.662e-3	2.343e-2
Dermatan sulfate biosynthesis	Reactome	1	BGN	11	4	272.95	3.659e-3	2.935e-2
CS/DS degradation	Reactome	1	BGN	14	4	214.46	4.655e-3	3.479e-2
Defective B4GALT7 causes EDS, progeroid type	Reactome	1	BGN	20	4	150.13	6.645e-3	4.390e-2
Defective B3GAT3 causes JDSSDHD	Reactome	1	BGN	20	4	150.13	6.645e-3	4.390e-2
Defective B3GALT6 causes EDSP2 and SEMDJL1	Reactome	1	BGN	20	4	150.13	6.645e-3	4.390e-2
Branched-chain amino acid catabolism	Reactome	1	HIBCH	20	4	150.13	6.645e-3	4.390e-2
Chondroitin sulfate biosynthesis	Reactome	1	BGN	20	4	150.13	6.645e-3	4.390e-2
A tetrasaccharide linker sequence is required for GAG synthesis	Reactome	1	BGN	26	4	115.48	8.632e-3	5.192e-2
beta-Alanine metabolism	KEGG	1	HIBCH	31	4	96.85	1.029e-2	5.794e-2
Propanoate metabolism	KEGG	1	HIBCH	32	4	93.83	1.062e-2	5.902e-2
TBC/RABGAPs	Reactome	1	RAB33A	46	4	65.27	1.523e-2	7.322e-2
Valine, leucine and isoleucine degradation	KEGG	1	HIBCH	48	4	62.55	1.589e-2	7.506e-2