

GeDiPNet Cluster 593 -- 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 00:02:24

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Lectin pathway of complement activation	Reactome	1	MBL2	8	5	300.25	3.327e-3	2.738e-2
TNFR1-induced proapoptotic signaling	Reactome	1	USP21	13	5	184.77	5.401e-3	3.839e-2
Glycosaminoglycan biosynthesis - keratan sulfate	KEGG	1	B4GALT3	14	5	171.57	5.816e-3	4.033e-2
Heme biosynthesis	Reactome	1	PPOX	14	5	171.57	5.816e-3	4.033e-2
N-Glycan antennae elongation	Reactome	1	B4GALT3	15	5	160.13	6.230e-3	4.212e-2
Initial triggering of complement	Reactome	1	MBL2	17	5	141.29	7.059e-3	4.563e-2
Mannose type O-glycan biosynthesis	KEGG	1	B4GALT3	23	5	104.43	9.540e-3	5.527e-2
Glycosphingolipid biosynthesis - lacto and neolacto series	KEGG	1	B4GALT3	28	5	85.79	1.160e-2	6.220e-2
Keratan sulfate biosynthesis	Reactome	1	B4GALT3	28	5	85.79	1.160e-2	6.220e-2
TNFR1-induced NFkappaB signaling pathway	Reactome	1	USP21	30	5	80.07	1.243e-2	6.493e-2
Transferrin endocytosis and recycling	Reactome	1	HFE	31	5	77.48	1.284e-2	6.602e-2
Regulation of TNFR1 signaling	Reactome	1	USP21	33	5	72.79	1.367e-2	6.870e-2
Various types of N-glycan biosynthesis	KEGG	1	B4GALT3	43	5	55.86	1.778e-2	8.022e-2
Porphyrin metabolism	KEGG	1	PPOX	46	5	52.22	1.901e-2	8.322e-2
Other types of O-glycan biosynthesis	KEGG	1	B4GALT3	47	5	51.11	1.942e-2	8.427e-2