

GeDiPNet Cluster 613 -- 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: 13 · Generated: 2026-10-19 23:20:31

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Intestinal infectious diseases	Reactome	1	GUCY2C	2	6	1000.83	9.990e-4	1.132e-2
Digestion	Reactome	1	GUCY2C	5	6	400.33	2.496e-3	2.231e-2
Acyl chain remodeling of DAG and TAG	Reactome	1	DGAT1	7	6	285.95	3.493e-3	2.829e-2
Triglyceride biosynthesis	Reactome	1	DGAT1	13	6	153.97	6.478e-3	4.320e-2
Fat digestion and absorption	KEGG	1	DGAT1	43	6	46.55	2.130e-2	8.893e-2
Virion - Hepatitis viruses	KEGG	1	EPCAM	48	6	41.70	2.375e-2	9.458e-2
Glycerolipid metabolism	KEGG	1	DGAT1	64	6	31.28	3.156e-2	1.114e-1
Retinol metabolism	KEGG	1	DGAT1	68	6	29.44	3.350e-2	1.150e-1
Cell surface interactions at the vascular wall	Reactome	1	EPCAM	84	6	23.83	4.125e-2	1.296e-1
Purine metabolism	KEGG	1	GUCY2C	128	6	15.64	6.228e-2	1.641e-1
Hormone signaling	KEGG	1	GUCY2C	219	6	9.14	1.046e-1	2.221e-1
Metabolic pathways	KEGG	2	DGAT1, GUCY2C	1563	6	2.56	1.779e-1	3.074e-1
Neutrophil degranulation	Reactome	1	DGAT1	480	6	4.17	2.171e-1	3.486e-1