

GeDiPNet Cluster 198 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 05:42:14

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective SLC2A1 causes GLUT1 deficiency syndrome 1 (GLUT1DS1)	Reactome	1	SLC2A1	1	13	923.85	1.082e-3	1.475e-2
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	1	COMT	2	13	461.92	2.164e-3	2.467e-2
Enzymatic degradation of dopamine by COMT	Reactome	1	COMT	3	13	307.95	3.244e-3	3.296e-2
Selenocysteine synthesis	Reactome	1	SEPSECS	3	13	307.95	3.244e-3	3.296e-2
Lactose synthesis	Reactome	1	SLC2A1	3	13	307.95	3.244e-3	3.296e-2
Potassium transport channels	Reactome	1	KCNJ10	3	13	307.95	3.244e-3	3.296e-2
Insulin secretion	KEGG	2	SLC2A1, KCNMA1	86	13	21.48	3.756e-3	3.658e-2
Vitamin C (ascorbate) metabolism	Reactome	1	SLC2A1	8	13	115.48	8.629e-3	6.395e-2
Ca2+ activated K+ channels	Reactome	1	KCNMA1	9	13	102.65	9.703e-3	6.873e-2
NF-κB activation through FADD/RIP-1 pathway mediated by caspase-8 and -10	Reactome	1	IFIH1	12	13	76.99	1.292e-2	8.184e-2
GABA synthesis, release, reuptake and degradation	Reactome	1	STXBP1	13	13	71.07	1.399e-2	8.575e-2
Methylation	Reactome	1	COMT	14	13	65.99	1.506e-2	8.969e-2
TRAF3-dependent IRF activation pathway	Reactome	1	IFIH1	14	13	65.99	1.506e-2	8.969e-2
Regulation of insulin secretion	Reactome	1	SLC2A1	16	13	57.74	1.719e-2	9.741e-2
Selenocompound metabolism	KEGG	1	SEPSECS	17	13	54.34	1.825e-2	1.008e-1