

GeDiPNet Cluster 85 -- 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 00:42:07

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Presynaptic depolarization and calcium channel opening	Reactome	2	CACNA2D2, CACNA1B	12	17	117.75	1.234e-4	2.656e-3
Regulation of insulin secretion	Reactome	2	CACNA2D2, SLC2A1	16	17	88.31	2.237e-4	4.278e-3
Defective SLC2A1 causes GLUT1 deficiency syndrome 1 (GLUT1DS1)	Reactome	1	SLC2A1	1	17	706.47	1.415e-3	1.763e-2
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	1	COMT	2	17	353.24	2.829e-3	2.950e-2
Enzymatic degradation of dopamine by COMT	Reactome	1	COMT	3	17	235.49	4.241e-3	3.926e-2
Lactose synthesis	Reactome	1	SLC2A1	3	17	235.49	4.241e-3	3.926e-2
Potassium transport channels	Reactome	1	KCNJ10	3	17	235.49	4.241e-3	3.926e-2
Insulin secretion	KEGG	2	KCNMA1, SLC2A1	86	17	16.43	6.428e-3	5.166e-2
Pancreatic secretion	KEGG	2	KCNMA1, RAB11A	102	17	13.85	8.939e-3	6.417e-2
Vitamin C (ascorbate) metabolism	Reactome	1	SLC2A1	8	17	88.31	1.127e-2	7.364e-2
Ca2+ activated K+ channels	Reactome	1	KCNMA1	9	17	78.50	1.267e-2	7.872e-2
Dopaminergic synapse	KEGG	2	COMT, CACNA1B	132	17	10.70	1.464e-2	8.581e-2
Methylation	Reactome	1	COMT	14	17	50.46	1.965e-2	1.020e-1
VxPx cargo-targeting to cilium	Reactome	1	RAB11A	21	17	33.64	2.933e-2	1.274e-1
Cellular hexose transport	Reactome	1	SLC2A1	21	17	33.64	2.933e-2	1.274e-1