

GeDiPNet Cluster 340 -- 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 06:23:08

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Calcium signaling pathway	KEGG	4	OXTR, CASQ1, ORAI1, STIM1	254	9	21.01	2.265e-5	6.757e-4
Ion homeostasis	Reactome	2	CASQ1, STIM1	54	9	49.42	7.001e-4	1.058e-2
Defective DPAGT1 causes DPAGT1-CDG (CDG-1j) and CMSTA2	Reactome	1	DPAGT1	1	9	1334.44	7.494e-4	1.115e-2
Platelet activation	KEGG	2	ORAI1, STIM1	126	9	21.18	3.746e-3	3.651e-2
Vasopressin-like receptors	Reactome	1	OXTR	6	9	222.41	4.489e-3	4.138e-2
Biosynthesis of the N-glycan precursor (dolichol lipid-linked oligosaccharide, LLO) and transfer to a nascent protein	Reactome	1	DPAGT1	11	9	121.31	8.216e-3	6.202e-2
cAMP signaling pathway	KEGG	2	OXTR, ORAI1	226	9	11.81	1.163e-2	7.667e-2
Cholesterol biosynthesis	Reactome	1	GGPS1	21	9	63.54	1.563e-2	9.212e-2
Terpenoid backbone biosynthesis	KEGG	1	GGPS1	23	9	58.02	1.711e-2	9.715e-2
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	Reactome	1	STIM1	23	9	58.02	1.711e-2	9.715e-2
Smooth Muscle Contraction	Reactome	1	CAV3	34	9	39.25	2.520e-2	1.209e-1
Primary immunodeficiency	KEGG	1	ORAI1	38	9	35.12	2.813e-2	1.280e-1
Activation of gene expression by SREBF (SREBP)	Reactome	1	GGPS1	42	9	31.77	3.105e-2	1.350e-1
N-Glycan biosynthesis	KEGG	1	DPAGT1	55	9	24.26	4.048e-2	1.554e-1
Cortisol synthesis and secretion	KEGG	1	ORAI1	65	9	20.53	4.768e-2	1.703e-1