

GeDiPNet Cluster 310 -- 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 18:17:58

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Synthesis of PIPs at the late endosome membrane	Reactome	2	FIG4, VAC14	10	5	480.40	6.232e-6	2.313e-4
Synthesis of PIPs at the early endosome membrane	Reactome	2	FIG4, VAC14	15	5	320.27	1.453e-5	4.649e-4
Synthesis of PIPs at the Golgi membrane	Reactome	2	FIG4, VAC14	18	5	266.89	2.116e-5	6.401e-4
Androgen biosynthesis	Reactome	1	SRD5A2	11	5	218.36	4.572e-3	4.188e-2
FGFR1c ligand binding and activation	Reactome	1	ANOS1	12	5	200.17	4.987e-3	4.437e-2
BBSome-mediated cargo-targeting to cilium	Reactome	1	BBIP1	23	5	104.43	9.540e-3	6.798e-2
Negative regulation of FGFR1 signaling	Reactome	1	ANOS1	26	5	92.38	1.078e-2	7.350e-2
Steroid hormone biosynthesis	KEGG	1	SRD5A2	63	5	38.13	2.596e-2	1.231e-1
Inositol phosphate metabolism	KEGG	1	FIG4	73	5	32.90	3.003e-2	1.326e-1
Prostate cancer	KEGG	1	SRD5A2	98	5	24.51	4.015e-2	1.548e-1
Viral carcinogenesis	KEGG	1	VAC14	205	5	11.72	8.249e-2	2.270e-1
Human T-cell leukemia virus 1 infection	KEGG	1	VAC14	224	5	10.72	8.986e-2	2.368e-1
Metabolic pathways	KEGG	2	FIG4, SRD5A2	1563	5	3.07	1.294e-1	2.876e-1
Amyotrophic lateral sclerosis	KEGG	1	FIG4	368	5	6.53	1.441e-1	3.055e-1
Pathways of neurodegeneration - multiple diseases	KEGG	1	FIG4	480	5	5.00	1.845e-1	3.507e-1