

GeDiPNet Cluster 108 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 08:02:41

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
SDK interactions	Reactome	1	SDK1	2	37	162.30	6.152e-3	5.035e-2
TWIK-related acid-sensitive K+ channel (TASK)	Reactome	1	KCNK9	2	37	162.30	6.152e-3	5.035e-2
Type I diabetes mellitus	KEGG	2	PTPRN2, HLA-DQB1	44	37	14.75	8.054e-3	6.028e-2
MECP2 regulates neuronal receptors and channels	Reactome	1	PTPN4	4	37	81.15	1.227e-2	7.878e-2
Formyl peptide receptors bind formyl peptides and many other ligands	Reactome	1	ANXA1	8	37	40.57	2.439e-2	1.177e-1
Synthesis, secretion, and inactivation of Glucagon-like Peptide-1 (GLP-1)	Reactome	1	GCG	14	37	23.19	4.230e-2	1.601e-1
Selenocompound metabolism	KEGG	1	SEPHS1	17	37	19.09	5.114e-2	1.773e-1
Signaling by cytosolic FGFR1 fusion mutants	Reactome	1	ZMYM2	18	37	18.03	5.406e-2	1.829e-1
Toll Like Receptor 4 (TLR4) Cascade	Reactome	1	PTPN4	19	37	17.08	5.698e-2	1.879e-1
Phase 4 - resting membrane potential	Reactome	1	KCNK9	19	37	17.08	5.698e-2	1.879e-1
Synthesis, secretion, and deacylation of Ghrelin	Reactome	1	GCG	19	37	17.08	5.698e-2	1.879e-1
Translocation of ZAP-70 to Immunological synapse	Reactome	1	HLA-DQB1	19	37	17.08	5.698e-2	1.879e-1
Interleukin-37 signaling	Reactome	1	PTPN4	21	37	15.46	6.279e-2	1.973e-1
Phosphorylation of CD3 and TCR zeta chains	Reactome	1	HLA-DQB1	22	37	14.75	6.568e-2	2.025e-1
Regulation of TP53 Activity through Acetylation	Reactome	1	BRPF1	23	37	14.11	6.857e-2	2.067e-1