

GeDiPNet Cluster 122 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-10 06:22:49

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective SLC9A9 causes autism 16 (AUTS16)	Reactome	1	SLC9A9	1	27	444.81	2.248e-3	2.580e-2
Defective ACTH causes Obesity and Pro-opiomelanocortinin deficiency (POMCD)	Reactome	1	POMC	2	27	222.41	4.491e-3	4.207e-2
Peptide hormone biosynthesis	Reactome	1	POMC	2	27	222.41	4.491e-3	4.207e-2
ARL13B-mediated ciliary trafficking of INPP5E	Reactome	1	INPP5E	3	27	148.27	6.730e-3	5.511e-2
Intracellular metabolism of fatty acids regulates insulin secretion	Reactome	1	ACSL4	3	27	148.27	6.730e-3	5.511e-2
Opioid Signalling	Reactome	1	POMC	3	27	148.27	6.730e-3	5.511e-2
Localization of the PINCH-ILK-PARVIN complex to focal adhesions	Reactome	1	ILK	4	27	111.20	8.963e-3	6.622e-2
Adipocytokine signaling pathway	KEGG	2	POMC, ACSL4	70	27	12.71	1.070e-2	7.403e-2
PPAR signaling pathway	KEGG	2	ILK, ACSL4	76	27	11.71	1.252e-2	8.148e-2
Sodium/Proton exchangers	Reactome	1	SLC9A9	9	27	49.42	2.006e-2	1.070e-1
Glucocorticoid biosynthesis	Reactome	1	POMC	10	27	44.48	2.226e-2	1.135e-1
Androgen biosynthesis	Reactome	1	POMC	11	27	40.44	2.446e-2	1.202e-1
Cell-extracellular matrix interactions	Reactome	1	ILK	12	27	37.07	2.666e-2	1.260e-1
Activation of Ca-permeable Kainate Receptor	Reactome	1	DLG3	12	27	37.07	2.666e-2	1.260e-1
Trafficking of GluR2-containing AMPA receptors	Reactome	1	TSPAN7	17	27	26.17	3.756e-2	1.512e-1