

GeDiPNet Cluster 196 -- 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 02:31:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cortisol synthesis and secretion	KEGG	2	GNA11, POMC	65	11	33.59	1.537e-3	1.872e-2
Defective ACTH causes Obesity and Pro-opiomelanocortinin deficiency (POMCD)	Reactome	1	POMC	2	11	545.91	1.831e-3	2.138e-2
Peptide hormone biosynthesis	Reactome	1	POMC	2	11	545.91	1.831e-3	2.138e-2
Regulation of gap junction activity	Reactome	1	GJA1	3	11	363.94	2.745e-3	2.879e-2
Opioid Signalling	Reactome	1	POMC	3	11	363.94	2.745e-3	2.879e-2
Gap junction	KEGG	2	GNA11, GJA1	89	11	24.54	2.860e-3	2.962e-2
Aldosterone synthesis and secretion	KEGG	2	GNA11, POMC	98	11	22.28	3.455e-3	3.388e-2
Parathyroid hormone synthesis, secretion and action	KEGG	2	CASR, GNA11	115	11	18.99	4.725e-3	4.212e-2
Nef Mediated CD8 Down-regulation	Reactome	1	AP2S1	7	11	155.97	6.395e-3	5.174e-2
Fatty Acids bound to GPR40 (FFAR1) regulate insulin secretion	Reactome	1	GNA11	8	11	136.48	7.306e-3	5.639e-2
Nef Mediated CD4 Down-regulation	Reactome	1	AP2S1	9	11	121.31	8.216e-3	6.112e-2
Acetylcholine regulates insulin secretion	Reactome	1	GNA11	9	11	121.31	8.216e-3	6.112e-2
Cushing syndrome	KEGG	2	GNA11, POMC	155	11	14.09	8.433e-3	6.212e-2
Glucocorticoid biosynthesis	Reactome	1	POMC	10	11	109.18	9.125e-3	6.536e-2
Retrograde neurotrophin signalling	Reactome	1	AP2S1	11	11	99.26	1.003e-2	6.930e-2