

GeDiPNet Cluster 337 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 13:51:03

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective ACTH causes Obesity and Pro-opiomelanocortinin deficiency (POMCD)	Reactome	2	MC2R, POMC	2	33	363.94	7.322e-6	2.583e-4
Inhibition of TSC complex formation by PKB	Reactome	2	TSC1, TSC2	3	33	242.63	2.193e-5	6.437e-4
Phase 0 - rapid depolarisation	Reactome	3	SCN1A, SCN2A, SCN8A	44	33	24.81	2.318e-4	4.394e-3
Phospholipase D signaling pathway	KEGG	4	TSC1, TSC2, DNM1, PLCB1	149	33	9.77	7.037e-4	1.041e-2
Cortisol synthesis and secretion	KEGG	3	MC2R, POMC, PLCB1	65	33	16.80	7.352e-4	1.077e-2
Cushing syndrome	KEGG	4	CRH, MC2R, POMC, PLCB1	155	33	9.39	8.159e-4	1.166e-2
Macroautophagy	Reactome	3	TSC1, TSC2, WDR45	68	33	16.06	8.388e-4	1.187e-2
Aldosterone synthesis and secretion	KEGG	3	MC2R, POMC, PLCB1	98	33	11.14	2.407e-3	2.615e-2
Energy dependent regulation of mTOR by LKB1-AMPK	Reactome	2	TSC1, TSC2	29	33	25.10	2.838e-3	2.955e-2
Hormone signaling	KEGG	4	CRH, MC2R, POMC, PLCB1	219	33	6.65	2.907e-3	3.012e-2
cAMP signaling pathway	KEGG	4	CRH, MC2R, POMC, GRIN2B	226	33	6.44	3.256e-3	3.261e-2
ADORA2B mediated anti-inflammatory cytokines production	Reactome	3	CRH, MC2R, POMC	128	33	8.53	5.109e-3	4.436e-2
Recycling pathway of L1	Reactome	2	DNM1, TUBA1A	40	33	18.20	5.350e-3	4.574e-2
Peptide hormone biosynthesis	Reactome	1	POMC	2	33	181.97	5.488e-3	4.649e-2
Dopaminergic synapse	KEGG	3	GRIN2B, PLCB1, SCN1A	132	33	8.27	5.565e-3	4.696e-2