

GeDiPNet Cluster 235 -- 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 20:43:17

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Prolactin receptor signaling	Reactome	2	GH1, PRL	12	7	285.95	1.917e-5	5.784e-4
Growth hormone receptor signaling	Reactome	2	GH1, PRL	14	7	245.10	2.641e-5	7.493e-4
Cushing syndrome	KEGG	3	AIP, GNAS, MEN1	155	7	33.21	7.104e-5	1.697e-3
Hormone signaling	KEGG	3	GH1, GNAS, PRL	219	7	23.50	1.983e-4	3.876e-3
Growth hormone synthesis, secretion and action	KEGG	2	GH1, GNAS	122	7	28.13	2.079e-3	2.349e-2
JAK-STAT signaling pathway	KEGG	2	GH1, PRL	168	7	20.43	3.901e-3	3.708e-2
Aryl hydrocarbon receptor signalling	Reactome	1	AIP	7	7	245.10	4.074e-3	3.817e-2
Chemical carcinogenesis - receptor activation	KEGG	2	AIP, GNAS	215	7	15.96	6.313e-3	5.105e-2
PKA activation in glucagon signalling	Reactome	1	GNAS	17	7	100.92	9.869e-3	6.808e-2
Prostacyclin signalling through prostacyclin receptor	Reactome	1	GNAS	19	7	90.30	1.102e-2	7.274e-2
Synthesis, secretion, and deacylation of Ghrelin	Reactome	1	GH1	19	7	90.30	1.102e-2	7.274e-2
Cytokine-cytokine receptor interaction	KEGG	2	GH1, PRL	298	7	11.51	1.187e-2	7.605e-2
Glucagon signaling in metabolic regulation	Reactome	1	GNAS	26	7	65.99	1.506e-2	8.714e-2
PI3K-Akt signaling pathway	KEGG	2	GH1, PRL	361	7	9.51	1.712e-2	9.452e-2
Neuroactive ligand-receptor interaction	KEGG	2	GH1, PRL	370	7	9.27	1.794e-2	9.705e-2