

GeDiPNet Cluster 611 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:50

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Growth hormone synthesis, secretion and action	KEGG	3	GHR, GHSR, STAT5B	122	4	73.83	4.061e-6	1.381e-4
Growth hormone receptor signaling	Reactome	2	GHR, STAT5B	14	4	428.93	7.561e-6	2.316e-4
Hormone signaling	KEGG	3	GHR, GHSR, STAT5B	219	4	41.13	2.360e-5	5.981e-4
Signaling by Leptin	Reactome	1	STAT5B	2	4	1501.25	6.660e-4	8.310e-3
JAK-STAT signaling pathway	KEGG	2	GHR, STAT5B	168	4	35.74	1.146e-3	1.257e-2
Interleukin-9 signaling	Reactome	1	STAT5B	9	4	333.61	2.995e-3	2.538e-2
Interleukin-21 signaling	Reactome	1	STAT5B	10	4	300.25	3.327e-3	2.738e-2
Prolactin receptor signaling	Reactome	1	GHR	12	4	250.21	3.991e-3	3.122e-2
Interleukin-2 signaling	Reactome	1	STAT5B	12	4	250.21	3.991e-3	3.122e-2
Interleukin-15 signaling	Reactome	1	STAT5B	13	4	230.96	4.323e-3	3.305e-2
Neuroactive ligand-receptor interaction	KEGG	2	GHR, GHSR	370	4	16.23	5.450e-3	3.866e-2
Signaling by cytosolic FGFR1 fusion mutants	Reactome	1	STAT5B	18	4	166.81	5.982e-3	4.097e-2
Interleukin-3, Interleukin-5 and GM-CSF signaling	Reactome	1	STAT5B	23	4	130.54	7.639e-3	4.803e-2
Interleukin-20 family signaling	Reactome	1	STAT5B	25	4	120.10	8.301e-3	5.062e-2
Downstream signal transduction	Reactome	1	STAT5B	29	4	103.53	9.625e-3	5.562e-2