

GeDiPNet Cluster 159 -- 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 06:23:38

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Protein export	KEGG	3	SRP54, SRPRA, SRP19	31	16	72.64	8.524e-6	3.125e-4
Ribosome biogenesis in eukaryotes	KEGG	3	SBDS, EFL1, EIF6	125	16	18.02	5.583e-4	9.008e-3
SRP-dependent cotranslational protein targeting to membrane	Reactome	2	SRP54, SRP19	93	16	16.14	6.633e-3	5.473e-2
FGFRL1 modulation of FGFR1 signaling	Reactome	1	FGFRL1	13	16	57.74	1.719e-2	9.836e-2
Synthesis of glycosylphosphatidylinositol (GPI)	Reactome	1	PIGG	17	16	44.15	2.242e-2	1.141e-1
Formation of HIV-1 elongation complex containing HIV-1 Tat	Reactome	1	NELFA	23	16	32.64	3.022e-2	1.347e-1
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	KEGG	1	PIGG	30	16	25.02	3.925e-2	1.550e-1
Formation of the Early Elongation Complex	Reactome	1	NELFA	33	16	22.75	4.310e-2	1.631e-1
Molecules associated with elastic fibres	Reactome	1	LTBP3	38	16	19.75	4.947e-2	1.757e-1
XBP1(S) activates chaperone genes	Reactome	1	SRPRA	50	16	15.01	6.461e-2	2.022e-1
RNA Polymerase II Transcription Elongation	Reactome	1	NELFA	59	16	12.72	7.582e-2	2.203e-1
Formation of RNA Pol II elongation complex	Reactome	1	NELFA	61	16	12.31	7.829e-2	2.240e-1
Lysine degradation	KEGG	1	NSD2	63	16	11.91	8.076e-2	2.279e-1
Viral life cycle - HIV-1	KEGG	1	NELFA	64	16	11.73	8.199e-2	2.295e-1
TP53 Regulates Transcription of DNA Repair Genes	Reactome	1	NELFA	65	16	11.55	8.322e-2	2.311e-1