

GeDiPNet Cluster 82 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 17:25:44

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Opioid Signalling	Reactome	2	OPRM1, POMC	3	26	307.95	1.350e-5	4.383e-4
Necroptosis	KEGG	5	TRPM7, IFNA2, IFNG, TNF, TNFRSF10A	159	26	14.53	2.006e-5	6.119e-4
Interleukin-4 and Interleukin-13 signaling	Reactome	4	OPRM1, POMC, TNF, HMOX1	108	26	17.11	7.938e-5	1.878e-3
Natural killer cell mediated cytotoxicity	KEGG	4	IFNA2, IFNG, TNF, TNFRSF10A	133	26	13.89	1.779e-4	3.598e-3
Hepatitis C	KEGG	4	EIF2AK4, IFNA2, IFNG, TNF	159	26	11.62	3.523e-4	6.192e-3
Cytokine-cytokine receptor interaction	KEGG	5	IFNA2, IFNG, TNF, TNFRSF10A, LEPR	298	26	7.75	3.898e-4	6.700e-3
Heme degradation	Reactome	2	ALB, HMOX1	14	26	65.99	4.036e-4	6.895e-3
Adipocytokine signaling pathway	KEGG	3	POMC, TNF, LEPR	70	26	19.80	4.478e-4	7.478e-3
Influenza A	KEGG	4	IFNA2, IFNG, TNF, TNFRSF10A	173	26	10.68	4.853e-4	7.948e-3
Herpes simplex virus 1 infection	KEGG	4	EIF2AK4, IFNA2, IFNG, TNF	182	26	10.15	5.876e-4	9.213e-3
Class A/1 (Rhodopsin-like receptors)	Reactome	2	CNR2, GPBAR1	19	26	48.62	7.534e-4	1.120e-2
Neuroactive ligand-receptor interaction	KEGG	5	CNR2, GCG, OPRM1, POMC, LEPR	370	26	6.24	1.041e-3	1.432e-2
Lipid and atherosclerosis	KEGG	4	IFNA2, TNF, TNFRSF10A, AGER	216	26	8.55	1.115e-3	1.507e-2
Hormone signaling	KEGG	4	GCG, OPRM1, POMC, LEPR	219	26	8.44	1.173e-3	1.568e-2
Amoebiasis	KEGG	3	ARG1, IFNG, TNF	103	26	13.45	1.380e-3	1.776e-2