

GeDiPNet Cluster 382 -- 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 03:58:28

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Longevity regulating pathway	KEGG	4	IGF1, SIRT1, TP53, INS	90	15	35.59	3.779e-6	1.511e-4
Longevity regulating pathway - multiple species	KEGG	3	IGF1, SIRT1, INS	62	15	38.74	5.703e-5	1.422e-3
Prostate cancer	KEGG	3	IGF1, TP53, INS	98	15	24.51	2.233e-4	4.271e-3
Synthesis, secretion, and deacylation of Ghrelin	Reactome	2	IGF1, INS	19	15	84.28	2.459e-4	4.590e-3
EGR2 and SOX10-mediated initiation of Schwann cell myelination	Reactome	2	MBP, PMP22	20	15	80.07	2.731e-4	4.982e-3
MAPK signaling pathway	KEGG	4	MYC, IGF1, TP53, INS	299	15	10.71	4.137e-4	6.882e-3
AMPK signaling pathway	KEGG	3	IGF1, SIRT1, INS	122	15	19.69	4.256e-4	7.028e-3
FoxO signaling pathway	KEGG	3	IGF1, SIRT1, INS	133	15	18.06	5.480e-4	8.541e-3
Breast cancer	KEGG	3	MYC, IGF1, TP53	148	15	16.23	7.484e-4	1.092e-2
PI3K-Akt signaling pathway	KEGG	4	MYC, IGF1, TP53, INS	361	15	8.87	8.424e-4	1.191e-2
Cellular senescence	KEGG	3	MYC, SIRT1, TP53	157	15	15.30	8.885e-4	1.241e-2
Thyroid cancer	KEGG	2	MYC, TP53	37	15	43.28	9.455e-4	1.301e-2
Aldosterone-regulated sodium reabsorption	KEGG	2	IGF1, INS	38	15	42.14	9.973e-4	1.354e-2
Bladder cancer	KEGG	2	MYC, TP53	41	15	39.06	1.161e-3	1.518e-2
Wnt signaling pathway	KEGG	3	MYC, SIRT1, TP53	174	15	13.80	1.196e-3	1.549e-2