

GeDiPNet Cluster 387 -- 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: 2026-10-07 23:55:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Longevity regulating pathway - multiple species	KEGG	3	INS, SIRT1, SOD1	62	15	38.74	5.703e-5	1.438e-3
Synthesis, secretion, and deacylation of Ghrelin	Reactome	2	BCHE, INS	19	15	84.28	2.459e-4	4.646e-3
Defective SLC6A5 causes hyperekplexia 3 (HKPX3)	Reactome	1	SLC6A5	1	15	800.67	1.249e-3	1.645e-2
Signaling by Insulin receptor	Reactome	1	INS	2	15	400.33	2.496e-3	2.744e-2
Mineral absorption	KEGG	2	ATP7A, TRPM7	61	15	26.25	2.553e-3	2.794e-2
Neurotransmitter clearance	Reactome	1	BCHE	4	15	200.17	4.987e-3	4.437e-2
Ion influx/efflux at host-pathogen interface	Reactome	1	ATP7A	4	15	200.17	4.987e-3	4.437e-2
Longevity regulating pathway	KEGG	2	INS, SIRT1	90	15	17.79	5.473e-3	4.749e-2
IRS activation	Reactome	1	INS	5	15	160.13	6.230e-3	5.168e-2
Prostate cancer	KEGG	2	INS, PLAT	98	15	16.34	6.458e-3	5.300e-2
Insulin receptor signalling cascade	Reactome	1	INS	6	15	133.44	7.472e-3	5.806e-2
Amyloid fiber formation	Reactome	2	APP, INS	109	15	14.69	7.934e-3	6.058e-2
Highly sodium permeable postsynaptic acetylcholine nicotinic receptors	Reactome	1	CHRND	7	15	114.38	8.712e-3	6.435e-2
Regulation of FOXO transcriptional activity by acetylation	Reactome	1	SIRT1	7	15	114.38	8.712e-3	6.435e-2
Serotonergic synapse	KEGG	2	HTR1A, APP	115	15	13.92	8.798e-3	6.476e-2