

GeDiPNet Cluster 641 -- 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 00:02:19

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Negative regulation of the PI3K/AKT network	Reactome	1	PHLPP2	8	12	125.10	7.968e-3	4.940e-2
GABA synthesis, release, reuptake and degradation	Reactome	1	HSPA8	13	12	76.99	1.292e-2	6.623e-2
Attenuation phase	Reactome	1	HSPA8	14	12	71.49	1.391e-2	6.943e-2
Protein methylation	Reactome	1	HSPA8	19	12	52.68	1.883e-2	8.276e-2
HSF1-dependent transactivation	Reactome	1	HSPA8	19	12	52.68	1.883e-2	8.276e-2
Lysosome Vesicle Biogenesis	Reactome	1	HSPA8	35	12	28.60	3.443e-2	1.168e-1
NRAGE signals death through JNK	Reactome	1	ARHGEF10L	55	12	18.20	5.361e-2	1.503e-1
HSP90 chaperone cycle for steroid hormone receptors (SHR)	Reactome	1	HSPA8	55	12	18.20	5.361e-2	1.503e-1
Legionellosis	KEGG	1	HSPA8	56	12	17.87	5.456e-2	1.520e-1
Golgi Associated Vesicle Biogenesis	Reactome	1	HSPA8	56	12	17.87	5.456e-2	1.520e-1
AUF1 (hnRNP D0) binds and destabilizes mRNA	Reactome	1	HSPA8	56	12	17.87	5.456e-2	1.520e-1
Longevity regulating pathway - multiple species	KEGG	1	HSPA8	62	12	16.14	6.025e-2	1.608e-1
Regulation of HSF1-mediated heat shock response	Reactome	1	HSPA8	69	12	14.50	6.683e-2	1.707e-1
RUNX1 regulates transcription of genes involved in differentiation of HSCs	Reactome	1	LMO2	69	12	14.50	6.683e-2	1.707e-1
Viral myocarditis	KEGG	1	EIF4G3	70	12	14.30	6.777e-2	1.721e-1