GeDiPNet Cluster 653 -- 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: 2026-10-21 12:16:30. · Rows: 15 · Generated: 2026-10-21 08:36:22

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	4.757e-2
GABA synthesis, release, reuptake and degradation	Reactome	1	HSPA8	13	12	76.99	1.292e-2	6.414e-2
Attenuation phase	Reactome	1	HSPA8	14	12	71.49	1.391e-2	6.723e-2
Protein methylation	Reactome	1	HSPA8	19	12	52.68	1.883e-2	8.057e-2
HSF1-dependent transactivation	Reactome	1	HSPA8	19	12	52.68	1.883e-2	8.057e-2
Lysosome Vesicle Biogenesis	Reactome	1	HSPA8	35	12	28.60	3.443e-2	1.149e-1
NRAGE signals death through JNK	Reactome	1	ARHGEF10L	55	12	18.20	5.361e-2	1.483e-1
HSP90 chaperone cycle for steroid hormone receptors (SHR)	Reactome	1	HSPA8	55	12	18.20	5.361e-2	1.483e-1
Legionellosis	KEGG	1	HSPA8	56	12	17.87	5.456e-2	1.499e-1
Golgi Associated Vesicle Biogenesis	Reactome	1	HSPA8	56	12	17.87	5.456e-2	1.499e-1
AUF1 (hnRNP D0) binds and destabilizes mRNA	Reactome	1	HSPA8	56	12	17.87	5.456e-2	1.499e-1
Longevity regulating pathway - multiple species	KEGG	1	HSPA8	62	12	16.14	6.025e-2	1.586e-1
Regulation of HSF1-mediated heat shock response	Reactome	1	HSPA8	69	12	14.50	6.683e-2	1.684e-1
RUNX1 regulates transcription of genes involved in differentiation of HSCs	Reactome	1	LMO2	69	12	14.50	6.683e-2	1.684e-1
Viral myocarditis	KEGG	1	EIF4G3	70	12	14.30	6.777e-2	1.698e-1