

GeDiPNet Cluster 447 -- 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](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 00:02:40

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Proteasome	KEGG	6	PSMB4, PSMB8, POMP, PSMA3, PSMB9, PSMB10	46	7	223.79	1.571e-14	4.285e-12
Cross-presentation of soluble exogenous antigens (endosomes)	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	50	7	171.57	2.125e-11	2.985e-9
Ubiquitin-dependent degradation of Cyclin D	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	51	7	168.21	2.356e-11	3.287e-9
Regulation of ornithine decarboxylase (ODC)	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	51	7	168.21	2.356e-11	3.287e-9
G2/M Checkpoints	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	51	7	168.21	2.356e-11	3.287e-9
Vpu mediated degradation of CD4	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	52	7	164.97	2.606e-11	3.609e-9
Autodegradation of the E3 ubiquitin ligase COP1	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	52	7	164.97	2.606e-11	3.609e-9
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	52	7	164.97	2.606e-11	3.609e-9
Vif-mediated degradation of APOBEC3G	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	54	7	158.86	3.170e-11	4.270e-9
FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	54	7	158.86	3.170e-11	4.270e-9
SCF-beta-TrCP mediated degradation of Emi1	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	55	7	155.97	3.487e-11	4.657e-9
Degradation of AXIN	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	55	7	155.97	3.487e-11	4.657e-9
Regulation of RUNX3 expression and activity	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	55	7	155.97	3.487e-11	4.657e-9
AUF1 (hnRNP D0) binds and destabilizes mRNA	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	56	7	153.19	3.828e-11	5.071e-9
Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	Reactome	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	56	7	153.19	3.828e-11	5.071e-9