

GeDiPNet Cluster 513 -- 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 00:03:12

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Proteasome	KEGG	1	PSMD12	46	2	130.54	7.646e-3	4.806e-2
Cross-presentation of soluble exogenous antigens (endosomes)	Reactome	1	PSMD12	50	2	120.10	8.309e-3	5.066e-2
Ubiquitin-dependent degradation of Cyclin D	Reactome	1	PSMD12	51	2	117.75	8.475e-3	5.129e-2
Regulation of ornithine decarboxylase (ODC)	Reactome	1	PSMD12	51	2	117.75	8.475e-3	5.129e-2
G2/M Checkpoints	Reactome	1	PSMD12	51	2	117.75	8.475e-3	5.129e-2
Vpu mediated degradation of CD4	Reactome	1	PSMD12	52	2	115.48	8.641e-3	5.196e-2
Autodegradation of the E3 ubiquitin ligase COP1	Reactome	1	PSMD12	52	2	115.48	8.641e-3	5.196e-2
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	Reactome	1	PSMD12	52	2	115.48	8.641e-3	5.196e-2
Vif-mediated degradation of APOBEC3G	Reactome	1	PSMD12	54	2	111.20	8.973e-3	5.313e-2
FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	Reactome	1	PSMD12	54	2	111.20	8.973e-3	5.313e-2
SCF-beta-TrCP mediated degradation of Emi1	Reactome	1	PSMD12	55	2	109.18	9.138e-3	5.373e-2
Degradation of AXIN	Reactome	1	PSMD12	55	2	109.18	9.138e-3	5.373e-2
Regulation of RUNX3 expression and activity	Reactome	1	PSMD12	55	2	109.18	9.138e-3	5.373e-2
AUF1 (hnRNP D0) binds and destabilizes mRNA	Reactome	1	PSMD12	56	2	107.23	9.304e-3	5.433e-2
Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	Reactome	1	PSMD12	56	2	107.23	9.304e-3	5.433e-2