

GeDiPNet Cluster 317 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 17:50:07

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
PTEN Loss of Function in Cancer	Reactome	1	PTEN	1	6	2001.67	4.996e-4	7.955e-3
Switching of origins to a post-replicative state	Reactome	1	MCM7	6	6	333.61	2.994e-3	3.068e-2
Negative regulation of the PI3K/AKT network	Reactome	1	PTEN	8	6	250.21	3.991e-3	3.767e-2
Regulation of PTEN mRNA translation	Reactome	1	PTEN	9	6	222.41	4.489e-3	4.079e-2
Regulation of PTEN localization	Reactome	1	PTEN	9	6	222.41	4.489e-3	4.079e-2
SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion	Reactome	1	PLXNA4	10	6	200.17	4.986e-3	4.365e-2
Transcriptional Regulation by MECP2	Reactome	1	PTEN	10	6	200.17	4.986e-3	4.365e-2
Triglyceride biosynthesis	Reactome	1	AGMO	13	6	153.97	6.478e-3	5.190e-2
Sema3A PAK dependent Axon repulsion	Reactome	1	PLXNA4	15	6	133.44	7.472e-3	5.688e-2
Assembly of the pre-replicative complex	Reactome	1	MCM7	15	6	133.44	7.472e-3	5.688e-2
CRMPs in Sema3A signaling	Reactome	1	PLXNA4	16	6	125.10	7.968e-3	5.956e-2
Steroid biosynthesis	KEGG	1	CEL	20	6	100.08	9.952e-3	6.820e-2
Synthesis of IP3 and IP4 in the cytosol	Reactome	1	PTEN	28	6	71.49	1.391e-2	8.315e-2
Activation of the pre-replicative complex	Reactome	1	MCM7	33	6	60.66	1.638e-2	9.168e-2
DNA replication	KEGG	1	MCM7	36	6	55.60	1.785e-2	9.670e-2