

GeDiPNet Cluster 53 -- 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 16:51:19

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
PKMTs methylate histone lysines	Reactome	4	EED, EZH2, NSD1, SUZ12	71	15	45.11	1.457e-6	6.765e-5
Transcriptional Regulation by E2F6	Reactome	3	EED, EZH2, SUZ12	35	15	68.63	1.007e-5	3.375e-4
Regulation of PTEN gene transcription	Reactome	3	EED, EZH2, SUZ12	53	15	45.32	3.557e-5	9.619e-4
PI3K/AKT activation	Reactome	2	PIK3CA, RHOA	9	15	177.93	5.215e-5	1.324e-3
VEGFA-VEGFR2 Pathway	Reactome	3	PIK3CA, RHOA, ELMO2	62	15	38.74	5.703e-5	1.422e-3
PRC2 methylates histones and DNA	Reactome	3	EED, EZH2, SUZ12	73	15	32.90	9.302e-5	2.114e-3
Bacterial invasion of epithelial cells	KEGG	3	PIK3CA, RHOA, ELMO2	78	15	30.79	1.134e-4	2.481e-3
PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases	Reactome	2	RHOA, ELMO2	14	15	114.38	1.314e-4	2.797e-3
Polycomb repressive complex	KEGG	3	EED, EZH2, SUZ12	83	15	28.94	1.364e-4	2.880e-3
EPHA-mediated growth cone collapse	Reactome	2	RHOA, YES1	20	15	80.07	2.731e-4	4.982e-3
Regulation of signaling by CBL	Reactome	2	PIK3CA, YES1	21	15	76.25	3.016e-4	5.386e-3
Oxidative Stress Induced Senescence	Reactome	3	EED, EZH2, SUZ12	125	15	19.22	4.570e-4	7.432e-3
MicroRNAs in cancer	KEGG	4	PIK3CA, RHOA, ZFPM2, EZH2	311	15	10.30	4.803e-4	7.724e-3
HCMV Early Events	Reactome	3	EED, EZH2, SUZ12	135	15	17.79	5.725e-4	8.856e-3
Yersinia infection	KEGG	3	PIK3CA, RHOA, ELMO2	138	15	17.41	6.104e-4	9.318e-3