

GeDiPNet Cluster 575 -- 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 00:02:53

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Lysine degradation	KEGG	3	KMT2A, KMT2B, KMT2D	63	12	47.66	2.926e-5	7.099e-4
PKMTs methylate histone lysines	Reactome	3	KMT2A, KMT2B, KMT2D	71	12	42.29	4.193e-5	9.500e-4
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	Reactome	3	KMT2A, KMT2B, KMT2D	97	12	30.95	1.066e-4	1.994e-3
SUMOylation of DNA methylation proteins	Reactome	1	DNMT3B	4	12	250.21	3.991e-3	3.122e-2
ARMS-mediated activation	Reactome	1	KIDINS220	5	12	200.17	4.987e-3	3.635e-2
Cushing syndrome	KEGG	2	KMT2A, KMT2D	155	12	12.91	1.003e-2	5.687e-2
Transcriptional misregulation in cancer	KEGG	2	KDM6A, KMT2A	198	12	10.11	1.601e-2	7.548e-2
Cobalamin transport and metabolism	KEGG	1	HCFC1	18	12	55.60	1.785e-2	8.027e-2
Homologous DNA Pairing and Strand Exchange	Reactome	1	BRCA2	25	12	40.03	2.471e-2	9.672e-2
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	Reactome	1	BRCA2	26	12	38.49	2.568e-2	9.901e-2
Resolution of D-loop Structures through Holliday Junction Intermediates	Reactome	1	BRCA2	33	12	30.33	3.249e-2	1.133e-1
Presynaptic phase of homologous DNA pairing and strand exchange	Reactome	1	BRCA2	39	12	25.66	3.830e-2	1.243e-1
Homologous recombination	KEGG	1	BRCA2	41	12	24.41	4.022e-2	1.278e-1
Deactivation of the beta-catenin transactivating complex	Reactome	1	KMT2D	42	12	23.83	4.119e-2	1.295e-1
HDR through Homologous Recombination (HRR)	Reactome	1	BRCA2	48	12	20.85	4.694e-2	1.396e-1