

GeDiPNet Cluster 364 -- 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 08:49:26

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Thyroid cancer	KEGG	3	BAK1, BAX, BRAF	37	12	81.15	5.810e-6	2.144e-4
Release of apoptotic factors from the mitochondria	Reactome	2	BAK1, BAX	5	12	400.33	9.137e-6	3.116e-4
HDR through Homologous Recombination (HRR)	Reactome	3	ATM, MRE11, PCNA	48	12	62.55	1.285e-5	4.135e-4
Hepatitis C	KEGG	4	BAK1, BAX, BRAF, IFNG	159	12	25.18	1.348e-5	4.302e-4
Sensing of DNA Double Strand Breaks	Reactome	2	ATM, MRE11	6	12	333.61	1.370e-5	4.360e-4
Endometrial cancer	KEGG	3	BAK1, BAX, BRAF	59	12	50.89	2.401e-5	6.932e-4
RUNX1 and FOXP3 control the development of regulatory T lymphocytes (Tregs)	Reactome	2	IFNG, IL2	10	12	200.17	4.100e-5	1.088e-3
Melanoma	KEGG	3	BAK1, BAX, BRAF	73	12	41.13	4.557e-5	1.184e-3
Non-small cell lung cancer	KEGG	3	BAK1, BAX, BRAF	73	12	41.13	4.557e-5	1.184e-3
Platinum drug resistance	KEGG	3	ATM, BAK1, BAX	75	12	40.03	4.942e-5	1.266e-3
Glioma	KEGG	3	BAK1, BAX, BRAF	76	12	39.51	5.142e-5	1.309e-3
Pancreatic cancer	KEGG	3	BAK1, BAX, BRAF	77	12	38.99	5.348e-5	1.351e-3
Chronic myeloid leukemia	KEGG	3	BAK1, BAX, BRAF	77	12	38.99	5.348e-5	1.351e-3
Colorectal cancer	KEGG	3	BAK1, BAX, BRAF	87	12	34.51	7.705e-5	1.814e-3
Pathways in cancer	KEGG	5	BAK1, BAX, BRAF, IFNG, IL2	533	12	9.39	1.032e-4	2.312e-3