

GeDiPNet Cluster 589 -- 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 00:03:17

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Thyroid cancer	KEGG	2	HRAS, CTNNB1	37	3	216.40	2.765e-5	6.787e-4
Endometrial cancer	KEGG	2	HRAS, CTNNB1	59	3	135.71	7.095e-5	1.442e-3
Colorectal cancer	KEGG	2	HRAS, CTNNB1	87	3	92.03	1.549e-4	2.682e-3
Prostate cancer	KEGG	2	HRAS, CTNNB1	98	3	81.70	1.967e-4	3.238e-3
Melanogenesis	KEGG	2	HRAS, CTNNB1	101	3	79.27	2.089e-4	3.399e-3
C-type lectin receptor signaling pathway	KEGG	2	CYLD, HRAS	105	3	76.25	2.258e-4	3.618e-3
Thyroid hormone signaling pathway	KEGG	2	HRAS, CTNNB1	122	3	65.63	3.050e-4	4.565e-3
Signaling pathways regulating pluripotency of stem cells	KEGG	2	HRAS, CTNNB1	144	3	55.60	4.249e-4	5.893e-3
Breast cancer	KEGG	2	HRAS, CTNNB1	148	3	54.10	4.489e-4	6.137e-3
Gastric cancer	KEGG	2	HRAS, CTNNB1	150	3	53.38	4.611e-4	6.276e-3
Hepatitis C	KEGG	2	HRAS, CTNNB1	159	3	50.36	5.180e-4	6.853e-3
Hepatocellular carcinoma	KEGG	2	HRAS, CTNNB1	170	3	47.10	5.920e-4	7.605e-3
RAS GTPase cycle mutants	Reactome	1	HRAS	3	3	1334.44	7.493e-4	9.089e-3
Kaposi sarcoma-associated herpesvirus infection	KEGG	2	HRAS, CTNNB1	196	3	40.85	7.864e-4	9.431e-3
Focal adhesion	KEGG	2	HRAS, CTNNB1	203	3	39.44	8.434e-4	9.945e-3