

GeDiPNet Cluster 455 -- 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 00:02:52

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Focal adhesion	KEGG	3	BRAF, PDGFRB, PPP1CB	203	21	8.45	5.056e-3	3.673e-2
Lysine degradation	KEGG	2	KMT2D, SETD2	63	21	18.16	5.333e-3	3.805e-2
Long-term potentiation	KEGG	2	BRAF, PPP1CB	67	21	17.07	6.013e-3	4.111e-2
PKMTs methylate histone lysines	Reactome	2	KMT2D, SETD2	71	21	16.11	6.729e-3	4.425e-2
Melanoma	KEGG	2	BRAF, PDGFRB	73	21	15.67	7.102e-3	4.587e-2
Regulation of actin cytoskeleton	KEGG	3	BRAF, PDGFRB, PPP1CB	232	21	7.40	7.318e-3	4.671e-2
Glioma	KEGG	2	BRAF, PDGFRB	76	21	15.05	7.677e-3	4.818e-2
EGFR tyrosine kinase inhibitor resistance	KEGG	2	BRAF, PDGFRB	80	21	14.30	8.477e-3	5.129e-2
Regulation of PLK1 Activity at G2/M Transition	Reactome	2	PPP1CB, TUBA1A	88	21	13.00	1.018e-2	5.751e-2
Gap junction	KEGG	2	PDGFRB, TUBA1A	89	21	12.85	1.041e-2	5.837e-2
Negative feedback regulation of MAPK pathway	Reactome	1	BRAF	6	21	95.32	1.045e-2	5.837e-2
Synthesis of diphthamide-EEF2	Reactome	1	DPH1	7	21	81.70	1.218e-2	6.411e-2
Prostate cancer	KEGG	2	BRAF, PDGFRB	98	21	11.67	1.251e-2	6.520e-2
Frs2-mediated activation	Reactome	1	BRAF	12	21	47.66	2.079e-2	8.765e-2
Vascular smooth muscle contraction	KEGG	2	BRAF, PPP1CB	134	21	8.54	2.259e-2	9.181e-2