

GeDiPNet Cluster 550 -- 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 00:02:38

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cysteine formation from homocysteine	Reactome	1	CBS	3	6	667.22	1.498e-3	1.536e-2
Negative feedback regulation of MAPK pathway	Reactome	1	BRAF	6	6	333.61	2.994e-3	2.538e-2
cAMP signaling pathway	KEGG	2	BRAF, RYR2	226	6	17.71	5.031e-3	3.658e-2
Frs2-mediated activation	Reactome	1	BRAF	12	6	166.81	5.981e-3	4.097e-2
Spry regulation of FGF signaling	Reactome	1	BRAF	16	6	125.10	7.968e-3	4.940e-2
VxPx cargo-targeting to cilium	Reactome	1	PKD1	21	6	95.32	1.045e-2	5.837e-2
RAF activation	Reactome	1	BRAF	32	6	62.55	1.588e-2	7.505e-2
Signaling by high-kinase activity BRAF mutants	Reactome	1	BRAF	36	6	55.60	1.785e-2	8.027e-2
Thyroid cancer	KEGG	1	BRAF	37	6	54.10	1.835e-2	8.162e-2
One carbon pool by folate	KEGG	1	CBS	38	6	52.68	1.884e-2	8.276e-2
Negative regulation of MAPK pathway	Reactome	1	BRAF	38	6	52.68	1.884e-2	8.276e-2
Glycine, serine and threonine metabolism	KEGG	1	CBS	40	6	50.04	1.982e-2	8.517e-2
MAP2K and MAPK activation	Reactome	1	BRAF	40	6	50.04	1.982e-2	8.517e-2
Bladder cancer	KEGG	1	BRAF	41	6	48.82	2.031e-2	8.650e-2
Pathways of neurodegeneration - multiple diseases	KEGG	2	BRAF, RYR2	480	6	8.34	2.148e-2	8.927e-2