

GeDiPNet Cluster 355 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 07:56:23

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Formation of the cornified envelope	Reactome	3	CSTA, TGM5, CDSN	130	18	15.40	8.978e-4	1.279e-2
SDK interactions	Reactome	1	SDK2	2	18	333.61	2.995e-3	3.114e-2
Negative regulation of activity of TFAP2 (AP-2) family transcription factors	Reactome	1	WWOX	9	18	74.14	1.341e-2	8.370e-2
Reactions specific to the complex N-glycan synthesis pathway	Reactome	1	CHST8	10	18	66.72	1.489e-2	8.912e-2
Activation of the TFAP2 (AP-2) family of transcription factors	Reactome	1	WWOX	12	18	55.60	1.785e-2	9.951e-2
Dissolution of Fibrin Clot	Reactome	1	SERPINB8	13	18	51.32	1.932e-2	1.040e-1
G0 and Early G1	Reactome	1	RBL2	18	18	37.07	2.666e-2	1.247e-1
TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest	Reactome	1	RBL2	18	18	37.07	2.666e-2	1.247e-1
Transcription of E2F targets under negative control by DREAM complex	Reactome	1	RBL2	18	18	37.07	2.666e-2	1.247e-1
Branched-chain amino acid catabolism	Reactome	1	ACADSB	20	18	33.36	2.958e-2	1.315e-1
Nuclear signaling by ERBB4	Reactome	1	WWOX	24	18	27.80	3.539e-2	1.450e-1
G1/S-Specific Transcription	Reactome	1	RBL2	24	18	27.80	3.539e-2	1.450e-1
Cyclin E associated events during G1/S transition	Reactome	1	RBL2	28	18	23.83	4.117e-2	1.570e-1
Cyclin A:Cdk2-associated events at S phase entry	Reactome	1	RBL2	30	18	22.24	4.405e-2	1.629e-1
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known	Reactome	1	CBX4	38	18	17.56	5.548e-2	1.839e-1