

GeDiPNet Cluster 461 -- 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 00:02:24

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Peptide chain elongation	Reactome	1	EEF2	1	13	923.85	1.082e-3	1.201e-2
Uptake and function of diphtheria toxin	Reactome	1	EEF2	6	13	153.97	6.478e-3	4.320e-2
Synthesis of diphthamide-EEF2	Reactome	1	EEF2	7	13	131.98	7.554e-3	4.766e-2
Tight junction interactions	Reactome	1	PRKCI	8	13	115.48	8.629e-3	5.192e-2
Presynaptic depolarization and calcium channel opening	Reactome	1	CACNA1E	12	13	76.99	1.292e-2	6.623e-2
p75NTR recruits signalling complexes	Reactome	1	PRKCI	13	13	71.07	1.399e-2	6.967e-2
Regulation of insulin secretion	Reactome	1	CACNA1E	16	13	57.74	1.719e-2	7.864e-2
Protein methylation	Reactome	1	EEF2	19	13	48.62	2.038e-2	8.671e-2
Regulation of TP53 Activity through Acetylation	Reactome	1	CHD3	23	13	40.17	2.462e-2	9.668e-2
SUMOylation of intracellular receptors	Reactome	1	THRA	27	13	34.22	2.885e-2	1.057e-1
Pre-NOTCH Transcription and Translation	Reactome	1	PRKCI	31	13	29.80	3.306e-2	1.144e-1
RNA Polymerase I Transcription Initiation	Reactome	1	CHD3	45	13	20.53	4.765e-2	1.409e-1
Type II diabetes mellitus	KEGG	1	CACNA1E	47	13	19.66	4.972e-2	1.444e-1
Nuclear Receptor transcription pathway	Reactome	1	THRA	52	13	17.77	5.487e-2	1.525e-1
Regulation of PTEN gene transcription	Reactome	1	CHD3	53	13	17.43	5.590e-2	1.544e-1