

GeDiPNet Cluster 438 -- 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: 10 · Generated: 2026-10-19 23:21:08

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Anchoring of the basal body to the plasma membrane	Reactome	3	CC2D2A, CEP290, MKS1	98	5	73.53	5.207e-6	1.700e-4
Amino acids regulate mTORC1	Reactome	1	SZT2	55	5	43.67	2.269e-2	9.200e-2
Hedgehog 'off' state	Reactome	1	MKS1	56	5	42.89	2.310e-2	9.304e-2
Loss of Nlp from mitotic centrosomes	Reactome	1	CEP290	70	5	34.31	2.881e-2	1.056e-1
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	1	CEP290	70	5	34.31	2.881e-2	1.056e-1
AURKA Activation by TPX2	Reactome	1	CEP290	73	5	32.90	3.003e-2	1.083e-1
Recruitment of mitotic centrosome proteins and complexes	Reactome	1	CEP290	82	5	29.29	3.368e-2	1.155e-1
Regulation of PLK1 Activity at G2/M Transition	Reactome	1	CEP290	88	5	27.30	3.611e-2	1.200e-1
Recruitment of NuMA to mitotic centrosomes	Reactome	1	CEP290	94	5	25.55	3.853e-2	1.248e-1
Neutrophil degranulation	Reactome	1	CEP290	480	5	5.00	1.845e-1	3.145e-1