

GeDiPNet Cluster 559 -- 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: 8 · Generated: 2026-10-20 00:03:17

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, TMEM216	98	7	52.52	1.801e-5	4.772e-4
Loss of Nlp from mitotic centrosomes	Reactome	1	CEP290	70	7	24.51	4.010e-2	1.276e-1
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	1	CEP290	70	7	24.51	4.010e-2	1.276e-1
AURKA Activation by TPX2	Reactome	1	CEP290	73	7	23.50	4.179e-2	1.307e-1
Recruitment of mitotic centrosome proteins and complexes	Reactome	1	CEP290	82	7	20.92	4.684e-2	1.394e-1
Regulation of PLK1 Activity at G2/M Transition	Reactome	1	CEP290	88	7	19.50	5.019e-2	1.451e-1
Recruitment of NuMA to mitotic centrosomes	Reactome	1	CEP290	94	7	18.25	5.353e-2	1.503e-1
Neutrophil degranulation	Reactome	1	CEP290	480	7	3.57	2.484e-1	3.809e-1