

GeDiPNet Cluster 137 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 15:45:25

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell division	GO:0051301	27	ANKLE2, ASPM, CDK6, CENPE, CEP63, CIT, KIF14, KNL1, NCAPD3, NUP37, PDCD6IP, INO80	406	138	9.01	2.113e-18	2.668e-15
centriole replication	GO:0007099	10	CDK5RAP2, CEP135, CEP152, CEP63, SASS6, WDR62, RTTN, PLK4, CENPJ, CEP295	24	138	56.42	6.223e-16	5.070e-13
microtubule cytoskeleton organization	GO:0000226	13	CDK5RAP2, TUBA3E, KIF2A, KIFBP, TBCD, TUBA1A, TUBG1, RHO, GAPDH, TUBGCP4, TUBGCP6, NUSAP1	149	138	11.81	7.789e-11	2.278e-8
cerebral cortex development	GO:0021987	10	ASPM, KIF14, MCPH1, WDR62, FOXG1, NR2E1, SLC2A1, TUBA1A, NDE1, EOMES	88	138	15.39	9.601e-10	2.162e-7
mitotic cell cycle	GO:0000278	11	CENPE, CIT, MCPH1, TUBA3E, TBCD, TUBA1A, TUBG1, NCAPD2, TUBGCP4, TUBGCP6, KIF11	142	138	10.49	8.337e-9	1.466e-6
mitotic spindle organization	GO:0007052	8	CENPE, STIL, WDR62, DYNC1H1, KIF2A, TUBG1, KIF11, PCNT	58	138	18.68	1.013e-8	1.728e-6
positive regulation of centriole replication	GO:0046601	4	SASS6, STIL, PLK4, CENPJ	5	138	108.33	1.416e-8	2.311e-6
microtubule nucleation	GO:0007020	6	TUBG1, CENPJ, TUBGCP4, TUBGCP6, NDE1, PCNT	26	138	31.25	2.965e-8	4.348e-6
DNA damage checkpoint signaling	GO:0000077	7	CEP63, DONSON, ERCC6, TP53BP1, NBN, ATR, ATRIP	47	138	20.17	5.052e-8	6.834e-6
positive regulation of spindle assembly	GO:1905832	4	SASS6, STIL, DYNC1H1, CENPJ	8	138	67.71	1.948e-7	2.118e-5
centrosome duplication	GO:0051298	5	CEP152, SASS6, STIL, CENPJ, NDE1	19	138	35.64	2.185e-7	2.337e-5
microtubule-based movement	GO:0007018	8	CENPE, KIF14, DNAH2, RAB11A, DYNC1H1, KIF2A, KIF5C, KIF11	87	138	12.45	2.580e-7	2.685e-5
DNA damage response	GO:0006974	18	CDK6, CEP63, MCM7, INO80, PNKP, SMARCAL1, CTLA4, ERCC6, TRAIP, TP53BP1, RBBP8, WDR4	577	138	4.22	2.587e-7	2.692e-5
tRNA-type intron splice site recognition and cleavage	GO:0000379	3	TSEN2, TSEN34, TSEN54	3	138	135.41	3.941e-7	3.829e-5
spindle assembly	GO:0051225	6	CEP63, INO80, TUBGCP4, TUBGCP6, KIF11, PPP2R1A	40	138	20.31	4.541e-7	4.307e-5