

GeDiPNet Cluster 7 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 17:43:42

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Phototransduction	KEGG	17	GUCY2D, CNGB1, PDE6A, PDE6B, RHO, GNAT2, GUCA1A, SAG, GUCA1ANB-GUCA1A, GUCA1B, CNGA1, RGS9	29	465	15.14	2.505e-17	1.252e-14
BBSome-mediated cargo-targeting to cilium	Reactome	14	ARL6, BBS2, BBS5, CCT2, TTC8, BBS10, BBS7, BBS9, MKKS, BBS1, BBS12, BBS4	23	465	15.72	8.336e-15	2.647e-12
The canonical retinoid cycle in rods (twilight vision)	Reactome	13	LRAT, RPE65, ABCA4, RBP3, RHO, RLBP1, RDH12, MYO7A, RBP1, CYP4V2, RDH11, RDH5	20	465	16.79	2.256e-14	6.522e-12
Inactivation, recovery and regulation of the phototransduction cascade	Reactome	14	GUCY2D, CNGB1, PDE6A, PDE6B, RHO, GUCA1A, SAG, GUCA1B, CNGA1, RGS9, GNAT1, PDE6G	33	465	10.96	5.846e-12	1.096e-9
Activation of the phototransduction cascade	Reactome	8	CNGB1, PDE6A, PDE6B, RHO, CNGA1, GNB1, GNAT1, PDE6G	9	465	22.96	4.143e-11	6.508e-9
Retinoid cycle disease events	Reactome	9	LRAT, ABCA4, RLBP1, OPN1MW, RDH12, RBP1, RDH5, OPN1SW, RBP4	13	465	17.88	1.129e-10	1.606e-8
Anchoring of the basal body to the plasma membrane	Reactome	21	ALMS1, CEP290, CEP78, SCLT1, AHI1, IQCB1, NPHP1, NPHP4, RPGRIP1L, TUBB4B, MKS1, TMEM67	98	465	5.53	1.136e-10	1.612e-8
Intraflagellar transport	Reactome	15	DYNC2H1, WDR19, IFT81, CLUAP1, IFT140, TUBB4B, IFT172, IFT27, IFT74, KIF3B, TUBB6, IFT80	54	465	7.17	1.135e-9	1.257e-7
Hedgehog 'off' state	Reactome	11	DYNC2H1, WDR19, IFT140, RPGRIP1L, TUBB4B, MKS1, KIF7, IFT172, TUBB6, IFT88, OFD1	56	465	5.07	8.003e-6	2.783e-4
Recruitment of NuMA to mitotic centrosomes	Reactome	14	ALMS1, CEP290, CEP78, TUBB4B, CEP250, PLK4, TUBB6, TUBGCP4, TUBGCP6, NEK2, OFD1, CEP164	94	465	3.85	1.424e-5	4.496e-4
Recruitment of mitotic centrosome proteins and complexes	Reactome	13	ALMS1, CEP290, CEP78, TUBB4B, CEP250, PLK4, TUBGCP4, TUBGCP6, NEK2, OFD1, CEP164, CEP41	82	465	4.09	1.443e-5	4.541e-4
Loss of Nlp from mitotic centrosomes	Reactome	11	ALMS1, CEP290, CEP78, TUBB4B, CEP250, PLK4, NEK2, OFD1, CEP164, CEP41, SDCCAG8	70	465	4.06	7.134e-5	1.701e-3
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	11	ALMS1, CEP290, CEP78, TUBB4B, CEP250, PLK4, NEK2, OFD1, CEP164, CEP41, SDCCAG8	70	465	4.06	7.134e-5	1.701e-3
AURKA Activation by TPX2	Reactome	11	ALMS1, CEP290, CEP78, TUBB4B, CEP250, PLK4, NEK2, OFD1, CEP164, CEP41, SDCCAG8	73	465	3.89	1.057e-4	2.355e-3
The retinoid cycle in cones (daylight vision)	Reactome	4	RBP3, RLBP1, OPN1MW, OPN1SW	8	465	12.91	1.372e-4	2.894e-3