

GeDiPNet Cluster 8 -- 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 04:52:58

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	25	CC2D2A, CEP290, TMEM216, ALMS1, IQCB1, MKS1, NPHP1, NPHP4, RPGRIP1L, SCLT1, SDCCAG8, TMEM67	98	235	13.04	2.079e-21	2.107e-18
Hedgehog 'off' state	Reactome	20	GLI1, GLI2, IFT172, IFT57, MKS1, RPGRIP1L, WDR19, KIF7, TTC21B, DYNC2H1, OFD1, SUFU	56	235	18.25	1.264e-20	1.091e-17
BBSome-mediated cargo-targeting to cilium	Reactome	13	ARL6, BBIP1, BBS1, BBS10, BBS12, BBS2, BBS4, BBS5, BBS7, BBS9, LZTFL1, MKKS	23	235	28.89	4.256e-17	2.044e-14
Intraflagellar transport	Reactome	17	IFT172, IFT27, IFT57, IFT74, WDR19, TTC21B, DYNC2H1, IFT43, IFT81, KIF3B, TRAF3IP1, IFT80	54	235	16.09	1.255e-16	5.543e-14
Hedgehog signaling pathway	KEGG	14	GLI1, GLI2, KIF7, SUFU, EVC2, EVC, GLI3, KIF3A, MEGF8, SHH, CCND2, EFCAB7	56	235	12.78	2.294e-12	4.692e-10
Activation of SMO	Reactome	7	EVC2, EVC, KIF3A, SHH, EFCAB7, PTCH1, IQCE	18	235	19.87	2.661e-8	2.073e-6
ARL13B-mediated ciliary trafficking of INPP5E	Reactome	3	ARL13B, INPP5E, PDE6D	3	235	51.11	7.398e-6	2.606e-4
GLI proteins bind promoters of Hh responsive genes to promote transcription	Reactome	3	GLI1, GLI2, GLI3	3	235	51.11	7.398e-6	2.606e-4
Hedgehog 'on' state	Reactome	9	GLI1, GLI2, PSMD1, KIF7, SUFU, EVC2, EVC, GLI3, PTCH1	70	235	6.57	8.307e-6	2.871e-4
Basal cell carcinoma	KEGG	8	GLI1, GLI2, KIF7, SUFU, WNT9B, GLI3, SHH, PTCH1	63	235	6.49	2.922e-5	8.157e-4
Regulation of PLK1 Activity at G2/M Transition	Reactome	9	CEP290, ALMS1, SDCCAG8, CCP110, CEP164, OFD1, PPP1CB, TUBA1A, CEP41	88	235	5.23	5.379e-5	1.357e-3
Loss of Nlp from mitotic centrosomes	Reactome	8	CEP290, ALMS1, SDCCAG8, CCP110, CEP164, OFD1, TUBA1A, CEP41	70	235	5.84	6.331e-5	1.545e-3
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	8	CEP290, ALMS1, SDCCAG8, CCP110, CEP164, OFD1, TUBA1A, CEP41	70	235	5.84	6.331e-5	1.545e-3
AURKA Activation by TPX2	Reactome	8	CEP290, ALMS1, SDCCAG8, CCP110, CEP164, OFD1, TUBA1A, CEP41	73	235	5.60	8.573e-5	1.978e-3
Recruitment of mitotic centrosome proteins and complexes	Reactome	8	CEP290, ALMS1, SDCCAG8, CCP110, CEP164, OFD1, TUBA1A, CEP41	82	235	4.99	1.955e-4	3.840e-3