

GeDiPNet Cluster 315 -- 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 14:47:45

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	4	TMEM67, CC2D2A, OFD1, RPGRIP1L	98	8	61.28	2.846e-7	1.631e-5
Hedgehog 'off' state	Reactome	2	OFD1, RPGRIP1L	56	8	53.62	5.873e-4	9.033e-3
ARL13B-mediated ciliary trafficking of INPP5E	Reactome	1	INPP5E	3	8	500.42	1.997e-3	2.278e-2
Chylomicron assembly	Reactome	1	SAR1B	9	8	166.81	5.981e-3	4.925e-2
Synthesis of PIPs at the Golgi membrane	Reactome	1	INPP5E	18	8	83.40	1.193e-2	7.605e-2
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	Reactome	1	SAR1B	25	8	60.05	1.654e-2	9.227e-2
Cargo concentration in the ER	Reactome	1	SAR1B	33	8	45.49	2.178e-2	1.080e-1
Legionellosis	KEGG	1	SAR1B	56	8	26.81	3.671e-2	1.445e-1
COPII-mediated vesicle transport	Reactome	1	SAR1B	68	8	22.08	4.442e-2	1.603e-1
Loss of Nlp from mitotic centrosomes	Reactome	1	OFD1	70	8	21.45	4.570e-2	1.632e-1
Loss of proteins required for interphase microtubule organization from the centrosome	Reactome	1	OFD1	70	8	21.45	4.570e-2	1.632e-1
Inositol phosphate metabolism	KEGG	1	INPP5E	73	8	20.57	4.762e-2	1.670e-1
AURKA Activation by TPX2	Reactome	1	OFD1	73	8	20.57	4.762e-2	1.670e-1
Recruitment of mitotic centrosome proteins and complexes	Reactome	1	OFD1	82	8	18.31	5.335e-2	1.780e-1
Regulation of PLK1 Activity at G2/M Transition	Reactome	1	OFD1	88	8	17.06	5.715e-2	1.838e-1