

GeDiPNet Cluster 479 -- 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: 15 · Generated: 2026-10-20 00:03:19

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Kinesins	Reactome	2	KIF23, RACGAP1	59	11	37.01	1.268e-3	1.359e-2
Mitotic Telophase/Cytokinesis	Reactome	1	KIF23	3	11	363.94	2.745e-3	2.394e-2
COPI-dependent Golgi-to-ER retrograde traffic	Reactome	2	KIF23, RACGAP1	99	11	22.06	3.525e-3	2.846e-2
IRAK4 deficiency (TLR5)	Reactome	1	IRAK4	4	11	272.95	3.659e-3	2.935e-2
MHC class II antigen presentation	Reactome	2	KIF23, RACGAP1	123	11	17.75	5.387e-3	3.834e-2
Alcoholic liver disease	KEGG	2	IRAK4, LPIN2	144	11	15.16	7.315e-3	4.669e-2
MyD88 dependent cascade initiated on endosome	Reactome	1	IRAK4	8	11	136.48	7.306e-3	4.669e-2
MyD88 cascade initiated on plasma membrane	Reactome	1	IRAK4	9	11	121.31	8.216e-3	5.037e-2
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	Reactome	1	IRAK4	10	11	109.18	9.125e-3	5.370e-2
IRAK4 deficiency (TLR2/4)	Reactome	1	IRAK4	11	11	99.26	1.003e-2	5.687e-2
Lysine catabolism	Reactome	1	GCDH	12	11	90.98	1.094e-2	6.008e-2
Synthesis of PE	Reactome	1	LPIN2	12	11	90.98	1.094e-2	6.008e-2
Triglyceride biosynthesis	Reactome	1	LPIN2	13	11	83.99	1.185e-2	6.307e-2
Depolymerisation of the Nuclear Lamina	Reactome	1	LPIN2	15	11	72.79	1.366e-2	6.870e-2
TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling	Reactome	1	IRAK4	15	11	72.79	1.366e-2	6.870e-2