

GeDiPNet Cluster 20 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 21:01:31

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cohesin Loading onto Chromatin	Reactome	2	WAPL, NIPBL	10	50	48.04	7.483e-4	1.115e-2
Synthesis of Prostaglandins (PG) and Thromboxanes (TX)	Reactome	2	PTGES, PTGS2	12	50	40.03	1.092e-3	1.484e-2
Retinoid cycle disease events	Reactome	2	LRAT, RBP4	13	50	36.95	1.287e-3	1.683e-2
Aminoacyl-tRNA biosynthesis	KEGG	3	AARS1, DARS2, AARS2	66	50	10.92	2.584e-3	2.819e-2
The canonical retinoid cycle in rods (twilight vision)	Reactome	2	LRAT, RBP4	20	50	24.02	3.077e-3	3.176e-2
Mtb iron assimilation by chelation	Reactome	1	LTF	1	50	240.20	4.163e-3	3.932e-2
Biosynthesis of EPA-derived SPMs	Reactome	1	PTGS2	1	50	240.20	4.163e-3	3.932e-2
Biosynthesis of DPAn-3 SPMs	Reactome	1	PTGS2	1	50	240.20	4.163e-3	3.932e-2
Retinoid metabolism disease events	Reactome	1	RBP4	1	50	240.20	4.163e-3	3.932e-2
Biosynthesis of electrophilic 1%-3 PUFA oxo-derivatives	Reactome	1	PTGS2	2	50	120.10	8.309e-3	6.229e-2
ARL13B-mediated ciliary trafficking of INPP5E	Reactome	1	INPP5E	3	50	80.07	1.244e-2	8.001e-2
Biosynthesis of DHA-derived SPMs	Reactome	1	PTGS2	3	50	80.07	1.244e-2	8.001e-2
Retinoid metabolism and transport	Reactome	2	LRAT, RBP4	41	50	11.72	1.256e-2	8.066e-2
Biosynthesis of protectins	Reactome	1	CYP1A1	4	50	60.05	1.655e-2	9.503e-2
Ovarian steroidogenesis	KEGG	2	CYP1A1, PTGS2	52	50	9.24	1.973e-2	1.052e-1