

GeDiPNet Cluster 177 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-10 06:22:35

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Circadian rhythm	KEGG	4	CRY1, BHLHE40, NFIL3, RORC	34	15	94.20	7.147e-8	5.200e-6
Defective CYP17A1 causes Adrenal hyperplasia 5 (AH5)	Reactome	1	CYP17A1	1	15	800.67	1.249e-3	1.665e-2
Defective UGT1A1 causes hyperbilirubinemia	Reactome	1	UGT1A1	1	15	800.67	1.249e-3	1.665e-2
Steroid hormone biosynthesis	KEGG	2	CYP17A1, UGT1A1	63	15	25.42	2.721e-3	2.952e-2
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	Reactome	1	APOE	3	15	266.89	3.743e-3	3.693e-2
Serotonin and melatonin biosynthesis	Reactome	1	AANAT	5	15	160.13	6.230e-3	5.249e-2
Chylomicron clearance	Reactome	1	APOE	5	15	160.13	6.230e-3	5.249e-2
Zinc influx into cells by the SLC39 gene family	Reactome	1	SLC39A8	8	15	100.08	9.951e-3	7.054e-2
Chylomicron remodeling	Reactome	1	APOE	9	15	88.96	1.119e-2	7.604e-2
Chylomicron assembly	Reactome	1	APOE	9	15	88.96	1.119e-2	7.604e-2
HDL remodeling	Reactome	1	APOE	10	15	80.07	1.242e-2	8.099e-2
Glucocorticoid biosynthesis	Reactome	1	CYP17A1	10	15	80.07	1.242e-2	8.099e-2
Androgen biosynthesis	Reactome	1	CYP17A1	11	15	72.79	1.366e-2	8.548e-2
Scavenging by Class A Receptors	Reactome	1	APOE	11	15	72.79	1.366e-2	8.548e-2
Aspartate and asparagine metabolism	Reactome	1	ASPG	12	15	66.72	1.489e-2	9.000e-2