

GeDiPNet Cluster 538 -- 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 00:03:16

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Ovarian steroidogenesis	KEGG	4	ADCY8, CYP17A1, CYP19A1, FSHB	52	15	61.59	4.117e-7	1.930e-5
Hormone signaling	KEGG	4	ADCY8, CALCR, FSHB, PRL	219	15	14.62	1.254e-4	2.265e-3
ADORA2B mediated anti-inflammatory cytokines production	Reactome	3	ADCY8, CALCR, FSHB	128	15	18.77	4.899e-4	6.583e-3
G alpha (s) signalling events	Reactome	3	ADCY8, CALCR, FSHB	140	15	17.16	6.366e-4	8.055e-3
Defective CYP17A1 causes Adrenal hyperplasia 5 (AH5)	Reactome	1	CYP17A1	1	15	800.67	1.249e-3	1.343e-2
Defective CYP19A1 causes Aromatase excess syndrome (AEXS)	Reactome	1	CYP19A1	1	15	800.67	1.249e-3	1.343e-2
Cytochrome P450 - arranged by substrate type	Reactome	1	POR	1	15	800.67	1.249e-3	1.343e-2
Steroid hormone biosynthesis	KEGG	2	CYP17A1, CYP19A1	63	15	25.42	2.721e-3	2.383e-2
Cortisol synthesis and secretion	KEGG	2	ADCY8, CYP17A1	65	15	24.64	2.894e-3	2.486e-2
Prolactin signaling pathway	KEGG	2	CYP17A1, PRL	71	15	22.55	3.443e-3	2.810e-2
LDL remodeling	Reactome	1	APOB	3	15	266.89	3.743e-3	2.976e-2
Scavenging by Class H Receptors	Reactome	1	APOB	4	15	200.17	4.987e-3	3.635e-2
GnRH signaling pathway	KEGG	2	ADCY8, FSHB	93	15	17.22	5.833e-3	4.038e-2
Chylomicron clearance	Reactome	1	APOB	5	15	160.13	6.230e-3	4.212e-2
Scavenging by Class B Receptors	Reactome	1	APOB	5	15	160.13	6.230e-3	4.212e-2