

GeDiPNet Cluster 134 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 08:03:10

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Metabolism of Angiotensinogen to Angiotensins	Reactome	2	REN, AGT	17	13	108.69	1.458e-4	2.959e-3
Renin-angiotensin system	KEGG	2	REN, AGT	23	13	80.33	2.702e-4	4.829e-3
Protein export	KEGG	2	SEC61A1, SEC63	31	13	59.60	4.941e-4	7.811e-3
Fat digestion and absorption	KEGG	2	APOA4, ABCG5	43	13	42.97	9.526e-4	1.292e-2
Defective CYP17A1 causes Adrenal hyperplasia 5 (AH5)	Reactome	1	CYP17A1	1	13	923.85	1.082e-3	1.426e-2
Cholesterol metabolism	KEGG	2	APOA4, ABCG5	51	13	36.23	1.338e-3	1.680e-2
Cortisol synthesis and secretion	KEGG	2	AGT, CYP17A1	65	13	28.43	2.165e-3	2.412e-2
Defective ABCG8 causes gallbladder disease 4 and sitosterolemia	Reactome	1	ABCG5	2	13	461.92	2.164e-3	2.412e-2
Defective ABCG5 causes sitosterolemia	Reactome	1	ABCG5	2	13	461.92	2.164e-3	2.412e-2
Renin secretion	KEGG	2	REN, AGT	69	13	26.78	2.436e-3	2.636e-2
Insulin-like Growth Factor-2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs) bind RNA	Reactome	1	IGF2BP2	3	13	307.95	3.244e-3	3.239e-2
Glucocorticoid biosynthesis	Reactome	1	CYP17A1	10	13	92.38	1.078e-2	7.275e-2
Cushing syndrome	KEGG	2	AGT, CYP17A1	155	13	11.92	1.176e-2	7.667e-2
Androgen biosynthesis	Reactome	1	CYP17A1	11	13	83.99	1.185e-2	7.709e-2
Asparagine N-linked glycosylation	Reactome	1	UMOD	11	13	83.99	1.185e-2	7.709e-2