

GeDiPNet Cluster 232 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 02:54:40

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Formation of the cornified envelope	Reactome	7	TGM1, KRT1, ST14, LIPN, CASP14, FLG, KRT2	130	25	25.87	6.049e-9	5.657e-7
Synthesis of 12-eicosatetraenoic acid derivatives	Reactome	2	ALOX12B, ALOXE3	7	25	137.26	8.681e-5	2.001e-3
Defective SLC27A4 causes ichthyosis prematurity syndrome (IPS)	Reactome	1	SLC27A4	1	25	480.40	2.082e-3	2.349e-2
Defective CYP4F22 causes Ichthyosis, congenital, autosomal recessive 5 (ARCI5)	Reactome	1	CYP4F22	1	25	480.40	2.082e-3	2.349e-2
Defective ABCA12 causes autosomal recessive congenital ichthyosis type 4B	Reactome	1	ABCA12	1	25	480.40	2.082e-3	2.349e-2
Transport of connexons to the plasma membrane	Reactome	1	GJB2	1	25	480.40	2.082e-3	2.349e-2
Sphingolipid metabolism	KEGG	2	CERS3, UGCG	54	25	17.79	5.571e-3	4.701e-2
Arachidonic acid metabolism	KEGG	2	ALOX12B, ALOXE3	63	25	15.25	7.517e-3	5.709e-2
Transport of fatty acids	Reactome	1	SLC27A4	8	25	60.05	1.654e-2	9.227e-2
Eicosanoids	Reactome	1	CYP4F22	12	25	40.03	2.471e-2	1.156e-1
Miscellaneous substrates	Reactome	1	CYP4F22	12	25	40.03	2.471e-2	1.156e-1
Interleukin-2 signaling	Reactome	1	IL2RB	12	25	40.03	2.471e-2	1.156e-1
Interleukin-15 signaling	Reactome	1	IL2RB	13	25	36.95	2.674e-2	1.209e-1
Fatty acids	Reactome	1	CYP4F22	15	25	32.03	3.079e-2	1.308e-1
Extracellular matrix organization	Reactome	1	COL7A1	15	25	32.03	3.079e-2	1.308e-1