

GeDiPNet Cluster 625 -- 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 00:03:13

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Vitamin D (calciferol) metabolism	Reactome	3	CYP27B1, CYP2R1, VDR	11	7	467.92	1.997e-8	1.362e-6
Vitamins	Reactome	2	CYP27B1, CYP2R1	6	7	571.90	4.363e-6	1.469e-4
Steroid biosynthesis	KEGG	2	CYP27B1, CYP2R1	20	7	171.57	5.505e-5	1.177e-3
Defective CYP2R1 causes Rickets vitamin D-dependent 1B (VDDR1B)	Reactome	1	CYP2R1	1	7	1715.71	5.828e-4	7.518e-3
Defective CYP27B1 causes Rickets vitamin D-dependent 1A (VDDR1A)	Reactome	1	CYP27B1	1	7	1715.71	5.828e-4	7.518e-3
PDE3B signalling	Reactome	1	PDE3B	1	7	1715.71	5.828e-4	7.518e-3
Parathyroid hormone synthesis, secretion and action	KEGG	2	CYP27B1, VDR	115	7	29.84	1.850e-3	1.796e-2
Biosynthesis of maresin-like SPMs	Reactome	1	CYP3A4	6	7	285.95	3.493e-3	2.829e-2
Tuberculosis	KEGG	2	CYP27B1, VDR	181	7	18.96	4.513e-3	3.406e-2
Chemical carcinogenesis - receptor activation	KEGG	2	VDR, CYP3A4	215	7	15.96	6.313e-3	4.251e-2
Metabolic pathways	KEGG	4	CYP27B1, CYP2R1, PDE3B, CYP3A4	1563	7	4.39	7.213e-3	4.637e-2
Aflatoxin activation and detoxification	Reactome	1	CYP3A4	19	7	90.30	1.102e-2	6.031e-2
Cobalamin (Cbl, vitamin B12) transport and metabolism	Reactome	1	PRSS1	21	7	81.70	1.218e-2	6.411e-2
Xenobiotics	Reactome	1	CYP3A4	24	7	71.49	1.391e-2	6.943e-2
SUMOylation of intracellular receptors	Reactome	1	VDR	27	7	63.54	1.564e-2	7.438e-2