

GeDiPNet Cluster 404 -- 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 18:29:42

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Branched-chain amino acid catabolism	Reactome	7	BCKDHA, BCKDHB, DBT, PPM1K, BCAT2, DLD, BCKDK	20	7	600.50	1.086e-20	9.519e-18
2-Oxocarboxylic acid metabolism	KEGG	5	BCKDHA, BCKDHB, DBT, BCAT2, DLD	33	7	259.96	2.386e-12	4.854e-10
Valine, leucine and isoleucine degradation	KEGG	5	BCKDHA, BCKDHB, DBT, BCAT2, DLD	48	7	178.72	1.718e-11	2.924e-9
Lipoic acid metabolism	KEGG	4	BCKDHA, BCKDHB, DBT, DLD	19	7	361.20	1.561e-10	2.169e-8
Glyoxylate metabolism and glycine degradation	Reactome	4	BCKDHA, BCKDHB, DBT, DLD	28	7	245.10	8.231e-10	9.427e-8
Propanoate metabolism	KEGG	4	BCKDHA, BCKDHB, DBT, DLD	32	7	214.46	1.444e-9	1.537e-7
Metabolic pathways	KEGG	5	BCKDHA, BCKDHB, DBT, BCAT2, DLD	1563	7	5.49	6.204e-4	9.444e-3
Valine, leucine and isoleucine biosynthesis	KEGG	1	BCAT2	4	7	428.93	2.330e-3	2.554e-2
Glycine degradation	Reactome	1	DLD	4	7	428.93	2.330e-3	2.554e-2
Biosynthesis of cofactors	KEGG	2	BCAT2, DLD	154	7	22.28	3.289e-3	3.289e-2
Lysine catabolism	Reactome	1	DLD	12	7	142.98	6.975e-3	5.451e-2
Regulation of pyruvate dehydrogenase (PDH) complex	Reactome	1	DLD	16	7	107.23	9.291e-3	6.561e-2
Pyruvate metabolism	Reactome	1	DLD	19	7	90.30	1.102e-2	7.274e-2
Pantothenate and CoA biosynthesis	KEGG	1	BCAT2	21	7	81.70	1.218e-2	7.715e-2
Signaling by Retinoic Acid	Reactome	1	DLD	21	7	81.70	1.218e-2	7.715e-2