

GeDiPNet Cluster 367 -- 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: 10 · Generated: 2026-10-07 19:12:37

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	1	HIBCH	20	3	200.17	4.988e-3	4.365e-2
beta-Alanine metabolism	KEGG	1	HIBCH	31	3	129.14	7.724e-3	5.831e-2
Propanoate metabolism	KEGG	1	HIBCH	32	3	125.10	7.973e-3	5.956e-2
TBC/RABGAPs	Reactome	1	RAB33A	46	3	87.03	1.145e-2	7.440e-2
Valine, leucine and isoleucine degradation	KEGG	1	HIBCH	48	3	83.40	1.194e-2	7.605e-2
RAB geranylgeranylation	Reactome	1	RAB33A	65	3	61.59	1.615e-2	9.112e-2
Carbon metabolism	KEGG	1	HIBCH	115	3	34.81	2.845e-2	1.253e-1
Apoptosis	KEGG	1	AIFM1	137	3	29.22	3.384e-2	1.382e-1
Necroptosis	KEGG	1	AIFM1	159	3	25.18	3.920e-2	1.500e-1
Metabolic pathways	KEGG	1	HIBCH	1563	3	2.56	3.418e-1	5.012e-1