

GeDiPNet Cluster 227 -- Pairs Within Cluster

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected across all tested pairs. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-09 03:00:12. · Rows: 12 · Generated: 2026-10-09 10:52:54

Disease A	Disease B	Similarity Score	Shared Genes	P-value	FDR Q-value
Hepatic methionine adenosyltransferase deficiency	S-adenosylhomocysteine hydrolase deficiency	0.75000	3	1.644e-12	1.924e-11
Hepatic methionine adenosyltransferase deficiency	Sulfur amino acid metabolism disorder	0.40000	2	7.592e-8	5.414e-7
S-adenosylhomocysteine hydrolase deficiency	Sulfur amino acid metabolism disorder	0.40000	2	7.592e-8	5.414e-7
Adenosine kinase deficiency	Sulfur amino acid metabolism disorder	0.25000	1	1.948e-4	5.350e-4
Glycine n-methyltransferase deficiency	S-adenosylhomocysteine hydrolase deficiency	0.25000	1	1.948e-4	5.350e-4
Glycine n-methyltransferase deficiency	Sulfur amino acid metabolism disorder	0.25000	1	1.948e-4	5.350e-4
Glycine n-methyltransferase deficiency	Hepatic methionine adenosyltransferase deficiency	0.25000	1	1.948e-4	5.350e-4
Hepatic methionine adenosyltransferase deficiency	hypermethioninemia with deficiency of S-adenosylhomocysteine hydrolase	0.25000	1	1.948e-4	5.350e-4
Hepatic methionine adenosyltransferase deficiency	methionine adenosyltransferase deficiency	0.25000	1	1.948e-4	5.350e-4
hypermethioninemia with deficiency of S-adenosylhomocysteine hydrolase	S-adenosylhomocysteine hydrolase deficiency	0.25000	1	1.948e-4	5.350e-4
hypermethioninemia with deficiency of S-adenosylhomocysteine hydrolase	Sulfur amino acid metabolism disorder	0.25000	1	1.948e-4	5.350e-4
methionine adenosyltransferase deficiency	S-adenosylhomocysteine hydrolase deficiency	0.25000	1	1.948e-4	5.350e-4