

GeDiPNet Cluster 66 -- 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: 2026-10-08 03:00:12. · Rows: 18 · Generated: 2026-10-07 22:47:42

Disease A	Disease B	Similarity Score	Shared Genes	P-value	FDR Q-value
Citrullinemia	Urea cycle disorder	0.33333	3	9.205e-11	9.200e-10
Amino acid metabolism disorder	Urea cycle disorder	0.12903	4	4.449e-10	4.190e-9
Hyperammonemia	Urea cycle disorder	0.21429	3	5.149e-9	4.364e-8
Amino acid metabolism disorder	propionic acidemia	0.07407	2	2.742e-6	1.493e-5
Citrin deficiency	Citrullinemia	0.25000	1	1.948e-4	5.325e-4
Citrullinemia	ornithine translocase deficiency	0.25000	1	1.948e-4	5.325e-4
Argininosuccinic aciduria	Urea cycle disorder	0.11111	1	5.195e-4	1.058e-3
Citrin deficiency	Urea cycle disorder	0.11111	1	5.195e-4	1.058e-3
ornithine translocase deficiency	Urea cycle disorder	0.11111	1	5.195e-4	1.058e-3
ornithine carbamoyltransferase deficiency	Urea cycle disorder	0.11111	1	5.195e-4	1.058e-3
Hyperammonemia	systemic lupus erythematosus, susceptibility to, 1	0.11111	1	5.195e-4	1.058e-3
Hyperammonemia	ornithine carbamoyltransferase deficiency	0.11111	1	5.195e-4	1.058e-3
Amino acid metabolism disorder	ornithine translocase deficiency	0.03704	1	1.689e-3	2.529e-3
Amino acid metabolism disorder	lysinuric protein intolerance	0.03704	1	1.689e-3	2.529e-3
Amino acid metabolism disorder	Cystathioninuria	0.03704	1	1.689e-3	2.529e-3
Amino acid metabolism disorder	Argininosuccinic aciduria	0.03704	1	1.689e-3	2.529e-3
Amino acid metabolism disorder	Hyperprolinemia	0.03571	1	3.374e-3	4.374e-3
Amino acid metabolism disorder	Citrullinemia	0.03448	1	5.057e-3	6.197e-3