

GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test ($P(X \geq k)$), Benjamini-Hochberg FDR-corrected across all tested pairs. Corroborated Shared Genes: count of shared genes backed by ≥ 2 distinct disease_gdp.main_source values combined across both diseases (e.g. GWAS-backed for one, ClinVar-backed for the other still counts); Shared Gene Names lists each gene's own source count in parentheses. Overlap Coefficient: shared genes / MIN(each disease's own total gene count) -- complements the Jaccard-based Similarity Score by showing how much of the SMALLER disease's entire known gene-set is covered by this pair, which Jaccard (dividing by the union) can understate. Shared Cluster: cluster id if both diseases fall in the same label-propagation cluster (scripts/build_disease_clusters.php), blank otherwise. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-09 03:00:13. Filters applied: disease name contains "hyperlysinemia" (3 matching pairs). · Rows: 3 · Generated: 2026-10-09 17:25:05

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Color vision deficiency	hyperlysinemia	1	1	AASS (2)	0.00103	1.00000	6.274e-2	6.418e-2	
Hyperlipidemia	hyperlysinemia	1	1	AASS (7)	0.00704	1.00000	9.157e-3	1.046e-2	
hyperlysinemia	Saccharopinuria	1	1	AASS (3)	0.50000	1.00000	6.494e-5	2.329e-4	