

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: 2026-10-11 03:00:14. Filters applied: disease name contains "cardiomyopathy, dilated, 2d" (4 matching pairs). · Rows: 4 · Generated: 2026-10-11 20:10:06

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Cardioembolic stroke	cardiomyopathy, dilated, 2d	1	1	RPL3L (2)	0.00980	1.00000	6.559e-3	7.816e-3	
Cardiomyopathy	cardiomyopathy, dilated, 2d	1	1	RPL3L (2)	0.00408	1.00000	1.585e-2	1.746e-2	
cardiomyopathy, dilated, 2d	Dilated cardiomyopathy	1	1	RPL3L (6)	0.00365	1.00000	1.773e-2	1.940e-2	
Atrial fibrillation	cardiomyopathy, dilated, 2d	1	1	RPL3L (4)	0.00116	1.00000	5.605e-2	5.765e-2	