

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 "long qt syndrome 5" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 17:28:46

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Jervell and lange-nielsen syndrome	long qt syndrome 5	1	1	KCNE1 (7)	0.33333	1.00000	1.299e-4	3.931e-4	
long qt syndrome 5	Long qt syndrome, digenic	1	1	KCNE1 (2)	0.16667	1.00000	3.247e-4	7.709e-4	
Congenital hearing disorder	long qt syndrome 5	1	1	KCNE1 (2)	0.14286	1.00000	3.897e-4	8.665e-4	
Hereditary atrial fibrillation	long qt syndrome 5	1	1	KCNE1 (2)	0.04000	1.00000	1.559e-3	2.376e-3	
Arrhythmogenic right ventricular cardiomyopathy	long qt syndrome 5	1	1	KCNE1 (2)	0.01887	1.00000	3.377e-3	4.374e-3	