

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: 2026-10-10 03:00:13. Filters applied: disease name contains "Hearing loss with hypertrophic cardiomyopathy" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 06:51:13

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Autosomal dominant sensorineural deafness	Hearing loss with hypertrophic cardiomyopathy	1	0	MYO6 (1)	0.14286	1.00000	3.897e-4	8.665e-4	192
Hearing loss with hypertrophic cardiomyopathy	Waardenburg syndrome	1	0	MYO6 (1)	0.07143	1.00000	8.443e-4	1.499e-3	
Hearing loss with hypertrophic cardiomyopathy	Junctional epidermolysis bullosa	1	0	MYO6 (1)	0.05263	1.00000	1.169e-3	1.895e-3	
Congenital ear anomaly	Hearing loss with hypertrophic cardiomyopathy	1	0	MYO6 (1)	0.03125	1.00000	2.013e-3	2.901e-3	
Hearing loss with hypertrophic cardiomyopathy	Hereditary hearing loss	1	1	MYO6 (2)	0.01961	1.00000	3.247e-3	4.245e-3	