

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, autosomal recessive 116" (4 matching pairs). · Rows: 4 · Generated: 2026-10-10 12:36:22

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
hearing loss, autosomal recessive 116	Pendred syndrome	1	1	CLDN9 (2)	0.12500	1.00000	4.546e-4	9.726e-4	
Deafness	hearing loss, autosomal recessive 116	1	1	CLDN9 (3)	0.00578	1.00000	1.117e-2	1.256e-2	
Hearing loss	hearing loss, autosomal recessive 116	1	1	CLDN9 (4)	0.00258	1.00000	2.513e-2	2.687e-2	
hearing loss, autosomal recessive 116	Prostatic neoplasms	1	1	CLDN9 (2)	0.00159	1.00000	4.072e-2	4.256e-2	