

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: 2026-10-12 03:00:13. Filters applied: disease name contains "Cochlear diseases" (5 matching pairs). · Rows: 5 · Generated: 2026-10-12 01:23:38

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Cochlear diseases	Navajo neurohepatopathy	1	1	MPV17 (3)	0.20000	0.50000	3.896e-4	8.665e-4	
Cochlear diseases	Retinitis pigmentosa-deafness syndrome	1	1	PCDH15 (2)	0.07692	0.50000	1.428e-3	2.226e-3	
Cochlear diseases	Male reproductive organ cancer	1	1	PCDH15 (3)	0.05263	0.50000	2.207e-3	3.113e-3	
Cochlear diseases	Mitochondrial dna depletion syndrome	1	1	MPV17 (4)	0.03226	0.50000	3.763e-3	4.809e-3	
Cochlear diseases	Congenital ear anomaly	1	1	PCDH15 (2)	0.03030	0.50000	4.023e-3	5.086e-3	