

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: 2026-10-20 03:00:20. Filters applied: disease name contains "Autosomal recessive nonsyndromic hearing loss 102" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 03:54:44

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Autosomal recessive nonsyndromic hearing loss 102	Deafness, autosomal recessive, 102	1	1	EPS8 (2)	0.50000	1.00000	6.457e-5	1.985e-4	
Autosomal recessive nonsyndromic hearing loss 102	Isolated sensorineural deafness	1	1	EPS8 (2)	0.00833	1.00000	7.683e-3	8.815e-3	
Autosomal recessive nonsyndromic hearing loss 102	Nonsyndromic hearing loss	1	1	EPS8 (4)	0.00833	1.00000	7.683e-3	8.815e-3	
Autosomal recessive nonsyndromic hearing loss 102	Deafness	1	1	EPS8 (4)	0.00562	1.00000	1.143e-2	1.266e-2	
Autosomal recessive nonsyndromic hearing loss 102	Hearing loss	1	1	EPS8 (2)	0.00251	1.00000	2.563e-2	2.720e-2	