

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 "Aminoglycoside-induced deafness" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 17:15:57

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Aminoglycoside-induced deafness	Infantile liver failure	1	1	TRMU (2)	0.33333	1.00000	1.299e-4	3.931e-4	
Aminoglycoside-induced deafness	Deafness, aminoglycoside-induced	1	1	TRMU (4)	0.25000	1.00000	1.948e-4	5.354e-4	
Aminoglycoside-induced deafness	Liver failure	1	1	TRMU (4)	0.01887	1.00000	3.377e-3	4.374e-3	
Aminoglycoside-induced deafness	Leigh syndrome	1	1	TRMU (3)	0.00926	1.00000	6.949e-3	8.229e-3	
Aminoglycoside-induced deafness	Mitochondrial disease	1	1	TRMU (4)	0.00412	1.00000	1.572e-2	1.733e-2	