

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 "Brown-vialetto-van laere syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 19:04:38

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Brown-vialetto-van laere syndrome	Esophageal squamous cell carcinoma	1	1	SLC52A3 (6)	0.00763	0.50000	1.669e-2	1.833e-2	
Brown-vialetto-van laere syndrome	Obstructive sleep apnea syndrome	1	1	SLC52A3 (6)	0.01205	0.50000	1.049e-2	1.186e-2	
Brown-vialetto-van laere syndrome	Bulbar palsy	1	1	SLC52A3 (6)	0.20000	0.50000	3.896e-4	8.665e-4	
Auditory neuropathy	Brown-vialetto-van laere syndrome	2	2	SLC52A3 (6), SLC52A2 (6)	0.06250	1.00000	3.923e-6	2.071e-5	
Brown-vialetto-van laere syndrome	Riboflavin transporter deficiency	2	2	SLC52A3 (7), SLC52A2 (6)	0.50000	1.00000	2.531e-8	1.927e-7	