

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 "RP1-related dominant retinopathy" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 01:00:55

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Leber congenital amaurosis	RP1-related dominant retinopathy	1	1	RP1 (2)	0.01370	1.00000	4.676e-3	5.787e-3	
Retinopathy	RP1-related dominant retinopathy	1	1	RP1 (2)	0.01887	1.00000	3.377e-3	4.374e-3	
Biliary atresia	RP1-related dominant retinopathy	1	1	RP1 (2)	0.03125	1.00000	2.013e-3	2.901e-3	
Leber hereditary optic neuropathy	RP1-related dominant retinopathy	1	1	RP1 (2)	0.03448	1.00000	1.818e-3	2.677e-3	
RP1-related dominant retinopathy	RP1-related recessive retinopathy	1	0	RP1 (1)	0.50000	1.00000	6.494e-5	2.331e-4	