

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: 2026-10-22 03:00:19. Filters applied: disease name contains "Autosomal recessive cerebellar ataxia" (5 matching pairs). · Rows: 5 · Generated: 2026-10-22 01:13:30

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 cerebellar ataxia	Nonalcoholic fatty liver disease	1	1	CWF19L1 (3)	0.00315	1.00000	2.040e-2	2.189e-2	
Autosomal recessive cerebellar ataxia	Upper aerodigestive tract neoplasm	1	1	CWF19L1 (3)	0.00621	1.00000	1.033e-2	1.151e-2	
Autosomal recessive cerebellar ataxia	Cerebellar ataxia	1	1	CWF19L1 (5)	0.00820	1.00000	7.813e-3	8.932e-3	
Autosomal recessive cerebellar ataxia	Spinocerebellar ataxia	1	1	CWF19L1 (7)	0.00943	1.00000	6.779e-3	7.883e-3	
Autosomal recessive cerebellar ataxia	Developmental delay with epilepsy, progressive ataxia and cerebellar atrophy	1	1	CWF19L1 (2)	0.50000	1.00000	6.457e-5	1.985e-4	