GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test (P(X>=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 "Spinocerebellar ataxia, autosomal recessive, 15" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 04:46:11

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Psychiatric disorders	Spinocerebellar ataxia, autosomal recessive, 15	1	1	RUBCN (2)	0.00452	1.00000	1.420e-2	1.561e-2	
Cerebellar ataxia	Spinocerebellar ataxia, autosomal recessive, 15	1	1	RUBCN (3)	0.00820	1.00000	7.813e-3	8.931e-3	
Spinocerebellar ataxia	Spinocerebellar ataxia, autosomal recessive, 15	1	1	RUBCN (6)	0.00943	1.00000	6.779e-3	7.882e-3	
Nystagmus	Spinocerebellar ataxia, autosomal recessive, 15	1	1	RUBCN (2)	0.02128	1.00000	2.970e-3	3.788e-3	
Spinocerebellar ataxia, autosomal recessive, 15	Syndromic intellectual disability with ataxia, dysarthria and epilepsy	1	0	RUBCN (1)	0.50000	1.00000	6.457e-5	1.985e-4	