

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 "Congenital cerebellar ataxia" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 22:27:37

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Congenital cerebellar ataxia	Status epilepticus	1	1	GRM1 (3)	0.01389	0.50000	9.072e-3	1.038e-2	
Congenital cerebellar ataxia	Differentiated thyroid carcinoma	1	1	GRM1 (2)	0.01961	0.50000	6.355e-3	7.624e-3	
Congenital cerebellar ataxia	Temporal lobe epilepsy	1	1	GRM1 (3)	0.02857	0.50000	4.282e-3	5.383e-3	
Chondromyxoid fibroma	Congenital cerebellar ataxia	1	0	GRM1 (1)	0.33333	1.00000	1.299e-4	3.931e-4	
Congenital cerebellar ataxia	Spinocerebellar ataxia	2	2	GRID2 (6), GRM1 (6)	0.01905	1.00000	4.518e-5	2.051e-4	