

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 "Smith-lemli-opitz syndrome" (7 matching pairs). · Rows: 7 · Generated: 2026-10-11 10:10:18

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Smith-lemli-opitz syndrome	Vertebral, cardiac, renal, and limb defects syndrome	1	1	NADSYN1 (4)	0.12500	0.25000	1.039e-3	1.739e-3	
Congenital vertebral-cardiac-renal anomalies syndrome	Smith-lemli-opitz syndrome	1	1	NADSYN1 (2)	0.14286	0.33333	7.792e-4	1.405e-3	
Hyperkalemic periodic paralysis	Smith-lemli-opitz syndrome	1	0	CLCN1 (1)	0.14286	0.33333	7.792e-4	1.405e-3	
Becker generalized myotonia	Smith-lemli-opitz syndrome	1	0	CLCN1 (1)	0.16667	0.50000	5.195e-4	1.061e-3	
Smith-lemli-opitz syndrome	Syndactyly of the toes	1	1	DHCR7 (7)	0.16667	0.50000	5.195e-4	1.061e-3	
Congenital myotonia	Smith-lemli-opitz syndrome	1	1	CLCN1 (2)	0.20000	1.00000	2.598e-4	6.509e-4	
Myotonia congenita	Smith-lemli-opitz syndrome	1	1	CLCN1 (3)	0.20000	1.00000	2.598e-4	6.509e-4	