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 "Spastic paraplegia 23, autosomal recessive" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 03:14:09

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Hereditary spastic paraplegia	Spastic paraplegia 23, autosomal recessive	1	1	DSTYK (2)	0.00943	1.00000	6.779e-3	7.882e-3	
Dupuytren contracture	Spastic paraplegia 23, autosomal recessive	1	1	DSTYK (2)	0.01111	1.00000	5.746e-3	6.781e-3	
Congenital anomalies of the kidney and urinary tract	Spastic paraplegia 23, autosomal recessive	1	1	DSTYK (4)	0.01471	1.00000	4.326e-3	5.276e-3	
Complex hereditary spastic paraplegia	Spastic paraplegia 23, autosomal recessive	1	1	DSTYK (2)	0.11111	1.00000	5.165e-4	9.125e-4	
Complicated spastic paraparesis	Spastic paraplegia 23, autosomal recessive	1	0	DSTYK (1)	0.50000	1.00000	6.457e-5	1.985e-4	