

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: 2026-10-10 03:00:13. Filters applied: disease name contains "Complex regional pain syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 19:08:28

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Complex regional pain syndrome	primary ciliary dyskinesia 28	1	1	SPAG1 (2)	0.11111	1.00000	5.195e-4	1.061e-3	
Complex regional pain syndrome	Nocturnal frontal lobe epilepsy	1	1	SPAG1 (2)	0.05882	0.12500	4.667e-3	5.787e-3	
Complex regional pain syndrome	Secondary malignant neoplasm	1	0	KIF2B (1)	0.03704	0.12500	9.831e-3	1.116e-2	
Complex regional pain syndrome	Sezary syndrome	1	1	RPS6KA1 (2)	0.02857	0.12500	1.395e-2	1.552e-2	
Complex regional pain syndrome	Congenital nasopharyngeal atresia	1	1	SPAG1 (2)	0.02632	0.12500	1.548e-2	1.710e-2	