

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 "C1q deficiency" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 04:09:46

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
C1q deficiency	Ovarian cysts	1	1	C1QB (6)	0.02632	0.33333	6.804e-3	8.082e-3	
C1q deficiency	Exanthema	1	1	C1QA (5)	0.11111	0.33333	1.169e-3	1.895e-3	
C1q deficiency	systemic lupus erythematosus related to C1QA	1	1	C1QA (6)	0.25000	1.00000	1.948e-4	5.354e-4	
C1q deficiency	Stevens-johnson syndrome	2	2	C1QA (5), C1QC (5)	0.02500	0.66667	7.575e-5	2.710e-4	
C1q deficiency	Complement pathway abnormality	3	3	C1QA (5), C1QB (5), C1QC (4)	0.33333	1.00000	9.205e-11	9.154e-10	