

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 "Complement pathway abnormality" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 13:29:48

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Complement pathway abnormality	systemic lupus erythematosus related to C1QA	1	1	C1QA (2)	0.11111	1.00000	5.195e-4	1.061e-3	
C1 esterase inhibitor deficiency	Complement pathway abnormality	2	0	C2 (1), C4B (1)	0.15385	0.33333	3.539e-6	1.886e-5	
Complement pathway abnormality	Periodontal ehlers-danlos syndrome	2	2	C1S (2), C1R (2)	0.22222	1.00000	2.362e-7	1.551e-6	
C1q deficiency	Complement pathway abnormality	3	3	C1QA (5), C1QB (5), C1QC (4)	0.33333	1.00000	9.205e-11	9.154e-10	
Complement component deficiency	Complement pathway abnormality	4	4	C1S (5), C2 (5), C4B (5), C4A (5)	0.18182	0.50000	7.096e-11	7.166e-10	