

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: 2026-10-07 17:17:47. Filters applied: disease name contains "Terminal complement component deficiency" (5 matching pairs). · Rows: 5 · Generated: 2026-10-07 20:22:50

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Complement component deficiency	Terminal complement component deficiency	6	6	C8B (4), C5 (5), C9 (4), C8A (4), C6 (5), C7 (5)	0.31579	0.85714	4.681e-18	8.120e-17	
C1 esterase inhibitor deficiency	Terminal complement component deficiency	3	0	C8B (1), C9 (1), C8A (1)	0.27273	0.50000	1.150e-9	1.041e-8	
C9 deficiency	Terminal complement component deficiency	1	1	C9 (2)	0.12500	1.00000	4.546e-4	9.697e-4	
Cold paroxysmal hemoglobinuria	Terminal complement component deficiency	1	0	C5 (1)	0.07692	0.16667	2.725e-3	3.664e-3	
Hemoglobinuria paroxysmal	Terminal complement component deficiency	1	0	C5 (1)	0.07692	0.16667	2.725e-3	3.664e-3	