

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 "Combined deficiency of factor v and factor viii" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 01:43:49

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Combined deficiency of factor v and factor viii	Hemophilia a	1	1	LMAN1 (3)	0.05556	0.50000	2.077e-3	2.969e-3	
Combined deficiency of factor v and factor viii	Combined immunodeficiency, enteropathy spectrum	1	1	MCFD2 (3)	0.20000	0.50000	3.896e-4	8.665e-4	
Combined deficiency of factor v and factor viii	Gastrointestinal defects and immunodeficiency syndrome	1	1	MCFD2 (3)	0.20000	0.50000	3.896e-4	8.665e-4	
Combined deficiency of factor v and factor viii	Factor v deficiency	1	1	LMAN1 (3)	0.25000	0.50000	2.598e-4	6.509e-4	
Combined deficiency of factor v and factor viii	Combined factor v and factor viii deficiency	2	2	LMAN1 (8), MCFD2 (7)	0.66667	1.00000	8.436e-9	6.818e-8	