

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 "MHC class I deficiency" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 13:33:07

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Bare lymphocyte syndrome	MHC class I deficiency	3	3	TAP2 (2), TAP1 (3), TAPBP (2)	0.33333	1.00000	9.205e-11	9.154e-10	
Diffuse cutaneous systemic sclerosis	MHC class I deficiency	2	2	TAP2 (2), TAP1 (2)	0.08000	0.66667	6.397e-6	3.254e-5	
Extrinsic allergic alveolitis	MHC class I deficiency	1	1	TAP1 (2)	0.14286	0.33333	7.792e-4	1.405e-3	
Lymphoproliferative syndrome	MHC class I deficiency	1	1	TAP2 (2)	0.05882	0.33333	2.725e-3	3.665e-3	
Bronchiectasis	MHC class I deficiency	1	1	TAP1 (2)	0.05000	0.33333	3.309e-3	4.310e-3	