

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 II deficiency" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 16:54:52

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
MHC class II deficiency	Oligoarticular juvenile idiopathic arthritis	1	1	CIITA (2)	0.00575	0.25000	4.344e-2	4.523e-2	
MHC class II deficiency	Nasopharyngeal neoplasms	1	1	CIITA (2)	0.02128	0.25000	1.112e-2	1.252e-2	
Gastro-entero-pancreatic neuroendocrine tumor	MHC class II deficiency	1	1	CIITA (2)	0.05263	0.25000	3.891e-3	4.941e-3	
MHC class II deficiency	Severe combined immunodeficiency	2	2	RFX5 (2), RFXANK (2)	0.03704	0.50000	6.426e-5	2.331e-4	
Bare lymphocyte syndrome	MHC class II deficiency	4	4	CIITA (3), RFX5 (2), RFXANK (2), RFXAP (2)	0.44444	1.00000	2.990e-14	4.025e-13	