

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 "Bare lymphocyte syndrome" (7 matching pairs). · Rows: 7 · Generated: 2026-10-11 13:05:17

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
amyloidosis, hereditary systemic 6	Bare lymphocyte syndrome	1	1	B2M (2)	0.11111	1.00000	5.195e-4	1.061e-3	
Bare lymphocyte syndrome	Beta2-microglobulinic amyloidosis	1	0	B2M (1)	0.11111	1.00000	5.195e-4	1.061e-3	
Bare lymphocyte syndrome	Hypergammaglobulinemia	1	1	B2M (2)	0.11111	1.00000	5.195e-4	1.061e-3	
Bare lymphocyte syndrome	hypoproteinemia, hypercatabolic	1	1	B2M (2)	0.11111	1.00000	5.195e-4	1.061e-3	
Bare lymphocyte syndrome	Severe combined immunodeficiency	3	0	RFX5 (1), RFXANK (1), TAPBP (1)	0.05263	0.37500	1.895e-6	1.061e-5	
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	
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	