

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: 2026-10-12 03:00:13. Filters applied: disease name contains "Congenital intrinsic factor deficiency" (3 matching pairs). · Rows: 3 · Generated: 2026-10-12 18:14:56

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Congenital intrinsic factor deficiency	Pernicious anemia	1	1	CBLIF (2)	0.11111	1.00000	5.195e-4	1.061e-3	
Bipolar disorder	Congenital intrinsic factor deficiency	1	1	CBLIF (2)	0.00082	1.00000	7.923e-2	8.034e-2	
Congenital intrinsic factor deficiency	Schizophrenia	1	1	CBLIF (3)	0.00039	1.00000	1.650e-1	1.657e-1	