

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 "Bruck syndrome" (6 matching pairs). · Rows: 6 · Generated: 2026-10-11 22:36:22

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Bruck syndrome	Osteogenesis imperfecta	3	3	PLOD2 (6), FKBP10 (6), COL1A2 (7)	0.07500	1.00000	1.502e-8	1.186e-7	
Bruck syndrome	ehlers-danlos syndrome, cardiac valvular type	1	1	COL1A2 (2)	0.25000	1.00000	1.948e-4	5.354e-4	
Bruck syndrome	COL1A2-related Ehlers-Danlos syndrome	1	1	COL1A2 (2)	0.25000	1.00000	1.948e-4	5.354e-4	
Bruck syndrome	COL1A2-related osteogenesis imperfecta	1	1	COL1A2 (2)	0.25000	1.00000	1.948e-4	5.354e-4	
Bowed long bones	Bruck syndrome	1	1	PLOD2 (6)	0.20000	0.50000	3.896e-4	8.665e-4	
Bruck syndrome	Buruli ulcer	1	1	PLOD2 (6)	0.20000	0.50000	3.896e-4	8.665e-4	