

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 "fanconi anemia complementation group g" (3 matching pairs). · Rows: 3 · Generated: 2026-10-10 19:10:44

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
fanconi anemia complementation group g	Mouth disease	1	1	FANCG (3)	0.05000	1.00000	1.234e-3	1.986e-3	
fanconi anemia complementation group g	Pituitary stalk interruption syndrome	1	1	FANCG (2)	0.03125	1.00000	2.013e-3	2.901e-3	
Fanconi anemia	fanconi anemia complementation group g	1	1	FANCG (6)	0.02500	1.00000	2.533e-3	3.446e-3	