GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test (P(X>=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: 2026-10-20 03:00:20. Filters applied: disease name contains "Bcard syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 03:39:42

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Bcard syndrome	Marshall syndrome	1	1	PLOD3 (2)	0.05000	1.00000	1.227e-3	1.808e-3	
Bcard syndrome	Larsen syndrome	1	1	PLOD3 (2)	0.05556	1.00000	1.098e-3	1.651e-3	
Bcard syndrome	Contracture	1	0	PLOD3 (1)	0.06667	1.00000	9.039e-4	1.411e-3	
Bcard syndrome	Intrauterine growth restriction	1	0	PLOD3 (1)	0.20000	1.00000	2.583e-4	5.384e-4	
Bcard syndrome	Lysyl hydroxylase 3 deficiency	1	0	PLOD3 (1)	0.50000	1.00000	6.457e-5	1.985e-4	