

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 "Diabetic foot" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 16:11:28

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Diabetic foot	Neuropathy	3	0	LNX1 (1), TRDN (1), UNC5D (1)	0.13636	0.60000	1.590e-8	1.253e-7	
Diabetic foot	Nonobstructive azoospermia	1	1	SLC26A8 (2)	0.16667	1.00000	3.247e-4	7.709e-4	
Diabetic foot	Hepatic insufficiency	1	1	MAPK14 (2)	0.07143	0.20000	2.919e-3	3.876e-3	
Diabetic foot	Intestinal disease	1	0	MAPK14 (1)	0.05263	0.20000	4.538e-3	5.668e-3	
Diabetic foot	Polymorphic catecholaminergic ventricular tachycardia	1	1	TRDN (2)	0.05000	0.20000	4.862e-3	5.987e-3	