

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 "hyperinsulinism due to glucokinase deficiency" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 20:18:29

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Bone marrow failure syndromes	hyperinsulinism due to glucokinase deficiency	1	1	GCK (2)	0.10000	1.00000	5.845e-4	1.156e-3	
hyperinsulinism due to glucokinase deficiency	Prediabetes	1	1	GCK (2)	0.12500	1.00000	4.546e-4	9.726e-4	
Congenital hyperinsulinism	hyperinsulinism due to glucokinase deficiency	1	1	GCK (3)	0.14286	1.00000	3.897e-4	8.665e-4	
hyperinsulinism due to glucokinase deficiency	Intestinal disaccharide malabsorption	1	1	GCK (2)	0.20000	1.00000	2.598e-4	6.509e-4	
Congenital glucokinase-related hyperinsulinism	hyperinsulinism due to glucokinase deficiency	1	1	GCK (2)	0.50000	1.00000	6.494e-5	2.331e-4	