

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 "KCNH1 associated disorder" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 09:12:54

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Intellectual disability	KCNH1 associated disorder	1	1	KCNH1 (2)	0.01299	1.00000	4.936e-3	6.053e-3	
KCNH1 associated disorder	Osteosarcoma	1	1	KCNH1 (2)	0.01724	1.00000	3.702e-3	4.735e-3	
KCNH1 associated disorder	Smooth surface dental caries	1	1	KCNH1 (2)	0.02703	1.00000	2.338e-3	3.243e-3	
KCNH1 associated disorder	Zimmermann-laband syndrome	1	1	KCNH1 (4)	0.25000	1.00000	1.948e-4	5.354e-4	
KCNH1 associated disorder	Temple-baraitser syndrome	1	1	KCNH1 (6)	0.50000	1.00000	6.494e-5	2.331e-4	