

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 "Hydatidiform mole" (6 matching pairs). · Rows: 6 · Generated: 2026-10-10 21:33:37

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Breast cancer	Hydatidiform mole	1	1	TOP6BL (5)	0.00093	0.16667	3.496e-1	3.497e-1	
Atrial fibrillation	Hydatidiform mole	1	1	MEI1 (6)	0.00115	0.16667	2.926e-1	2.927e-1	
Gout	Hydatidiform mole	1	1	TOP6BL (5)	0.00121	0.16667	2.796e-1	2.798e-1	
Alzheimer disease	Partial hydatidiform mole	1	1	NLRP7 (2)	0.00045	0.50000	2.673e-1	2.675e-1	
Hydatidiform mole	Keratoconus	1	0	KIR3DL1 (1)	0.00855	0.16667	4.249e-2	4.429e-2	
Hydatidiform mole	Partial hydatidiform mole	2	2	NLRP7 (6), KHDC3L (6)	0.28571	1.00000	1.265e-7	8.712e-7	