

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: 2026-10-08 03:00:13. Filters applied: disease name contains "Acid-base disorder" (5 matching pairs). · Rows: 5 · Generated: 2026-10-08 09:42:07

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Acid-base disorder	Wernicke-korsakoff syndrome	1	1	ADH1B (2)	0.25000	0.50000	2.598e-4	6.484e-4	359
Acid-base disorder	Respiratory system neoplasm	1	0	ADH1B (1)	0.14286	0.50000	6.494e-4	1.239e-3	359
Acid-base disorder	Laryngeal neoplasms	1	1	ADH1B (2)	0.12500	0.50000	7.792e-4	1.404e-3	
Acid-base disorder	Oral cavity carcinoma	1	0	ADH1B (1)	0.03333	0.50000	3.634e-3	4.667e-3	
Acid-base disorder	Genetic predisposition to disease	1	1	ADH1B (2)	0.02000	0.50000	6.225e-3	7.480e-3	