GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test (P(X>=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: 2026-10-22 03:00:19. Filters applied: disease name contains "Aromatase excess syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-22 05:06:49

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Aromatase excess syndrome	Bladder neck obstruction	1	1	CYP19A1 (2)	0.25000	0.50000	2.583e-4	5.385e-4	
Aromatase excess syndrome	Ovarian diseases	1	1	CYP19A1 (3)	0.20000	0.50000	3.874e-4	7.329e-4	
Aromatase excess syndrome	Uterine cancer	1	1	CYP19A1 (2)	0.16667	0.50000	5.165e-4	9.127e-4	
Aromatase excess syndrome	Congenital esophageal anomaly	1	1	CGNL1 (2)	0.09091	0.50000	1.162e-3	1.729e-3	
Aromatase excess syndrome	Bone resorption	1	1	CYP19A1 (2)	0.08333	0.50000	1.291e-3	1.889e-3	