

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: 2026-10-20 03:00:20. Filters applied: disease name contains "Cutaneous adenocystic carcinoma" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 03:43:47

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Cutaneous adenocystic carcinoma	Salivary gland carcinoma ex pleomorphic adenoma	2	0	NFIB (1), MYB (1)	0.06061	1.00000	4.136e-6	2.330e-5	
Cutaneous adenocystic carcinoma	Macrocephaly, acquired, with impaired intellectual development	1	0	NFIB (1)	0.33333	1.00000	1.291e-4	3.269e-4	
Angiocentric glioma	Cutaneous adenocystic carcinoma	1	1	MYB (2)	0.25000	0.50000	2.583e-4	5.384e-4	
Cutaneous adenocystic carcinoma	Hemoglobin e disease	1	1	MYB (2)	0.14286	0.50000	6.456e-4	1.087e-3	
Cutaneous adenocystic carcinoma	Salivary gland pleomorphic adenoma	1	0	NFIB (1)	0.06667	0.50000	1.678e-3	2.343e-3	