

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 "Acral peeling skin syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 04:59:32

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Acral peeling skin syndrome	Lung cancer	1	1	TGM5 (2)	0.00154	0.50000	8.252e-2	8.366e-2	
Acral peeling skin syndrome	Glioblastoma	1	1	CSTA (2)	0.00164	0.50000	7.729e-2	7.858e-2	
Acral peeling skin syndrome	Nasopharyngeal carcinoma	1	1	CSTA (2)	0.04167	0.50000	2.856e-3	3.806e-3	
Acral peeling skin syndrome	Junctional epidermolysis bullosa	1	1	CSTA (3)	0.05000	0.50000	2.337e-3	3.243e-3	
Acral peeling skin syndrome	Peeling skin syndrome	2	2	CSTA (4), TGM5 (4)	0.25000	1.00000	1.772e-7	1.182e-6	