

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 "Jak3 deficiency" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 04:19:21

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Jak3 deficiency	Lung adenoma	1	0	JAK3 (1)	0.05882	1.00000	1.033e-3	1.574e-3	
Jak3 deficiency	Malignant struma ovarii	1	0	JAK3 (1)	0.14286	1.00000	3.874e-4	7.329e-4	
Dysplasia of larynx	Jak3 deficiency	1	0	JAK3 (1)	0.20000	1.00000	2.583e-4	5.384e-4	
Calcifying epithelial odontogenic tumor	Jak3 deficiency	1	0	JAK3 (1)	0.20000	1.00000	2.583e-4	5.384e-4	
Jak3 deficiency	severe combined immunodeficiency, autosomal recessive, t-negative/b-positive type	1	0	JAK3 (1)	0.50000	1.00000	6.457e-5	1.985e-4	