Resource Summary Report

Generated by ASWG on Aug 2, 2026

CoNIFER

RRID:SCR_013213
Type: Tool

Proper Citation

CoNIFER (RRID:SCR_013213)

Resource Information

URL: http://sourceforge.net/projects/conifer/

Proper Citation: CoNIFER (RRID:SCR_013213)

Description: Uses exome sequencing data to find copy number variants (CNVs) and genotype the copy-number of duplicated genes.

Abbreviations: CoNIFER

Synonyms: Copy Number Inference From Exome Reads

Resource Type: software resource

Availability: Commercial license

Resource Name: CoNIFER

Resource ID: SCR_013213

Alternate IDs: OMICS_00330

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260801T190446+0000

Ratings and Alerts

No rating or validation information has been found for CoNIFER.

No alerts have been found for CoNIFER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 195 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Tesi B, et al. (2025) Validation of Guidelines for Genetic Investigation of Myeloid Neoplasms with Germline Predisposition: Results from a Prospective Cohort Study. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(14), 3062.

Podgrajsek R, et al. (2025) Genetic Testing for Monogenic Forms of Male Infertility Contributes to the Clinical Diagnosis of Men with Severe Idiopathic Male Infertility. The world journal of men's health, 43(4), 908.

Koponen L, et al. (2025) A deep intronic PHEX variant associated with X-linked hypophosphatemia in a Finnish family. JBMR plus, 9(2), ziae169.

Gridina M, et al. (2025) Combining chromosome conformation capture and exome sequencing for simultaneous detection of structural and single-nucleotide variants. Genome medicine, 17(1), 47.

Zafeer MF, et al. (2025) Human organoids for rapid validation of gene variants linked to cochlear malformations. Human genetics, 144(4), 375.

García Massini JL, et al. (2025) Jurassic Osmundaceous Landscapes in Patagonia: Exploring the Concept of Ecological Stasis in the Deseado Massif, Argentina. Plants (Basel, Switzerland), 14(2).

Mäkitie O, et al. (2025) A de novo PRPF8 Pathogenic Variant in Transient Severe Hypophosphatemia with Delayed Puberty and Growth Failure. Hormone research in paediatrics, 98(6), 677.

Ishorst N, et al. (2025) Role of ZFHX4 in orofacial clefting based on human genetic data and zebrafish models. European journal of human genetics : EJHG, 33(5), 595.

Han H, et al. (2025) Exome sequencing of 18,994 ethnically diverse patients with suspected rare Mendelian disorders. NPJ genomic medicine, 10(1), 6.

Quijada NM, et al. (2025) The food-associated resistome is shaped by processing and production environments. Nature microbiology, 10(8), 1854.

VerCauteren K, et al. (2025) Oral delivery of bovine tuberculosis vaccine to free-ranging white-tailed deer. Frontiers in veterinary science, 12, 1548627.

Zheng H, et al. (2025) Interpreting Variants of Uncertain Significance in PCD: Abnormal Splicing Caused by a Missense Variant of DNAAF3. Molecular genetics & genomic medicine, 13(1), e70036.

Sattar S, et al. (2025) A pathogenic COL7A1 variant highlights semi-dominant inheritance in dystrophic epidermolysis bullosa. BMC medical genomics, 18(1), 26.

Bharadwaj T, et al. (2025) The Diverse Genetic Landscape of Hearing Impairment in South African Families. Clinical genetics, 108(5), 511.

Potjewijd J, et al. (2025) A novel missense variant in TNFAIP3 associated with autoimmunity reveals the contribution of STAT1/mTOR pathways. Clinical and experimental immunology, 219(1).

Laurie S, et al. (2025) Genomic reanalysis of a pan-European rare-disease resource yields new diagnoses. Nature medicine, 31(2), 478.

Carlson KW, et al. (2025) Individual differences in intolerance of uncertainty is primarily linked to the structure of inferior frontal regions. Cognitive, affective & behavioral neuroscience, 25(3), 727.

Oud MS, et al. (2025) Innovative all-in-one exome sequencing strategy for diagnostic genetic testing in male infertility: Validation and 10-month experience. Andrology, 13(5), 1078.

Lu Y, et al. (2024) A frameshift mutation in the SCNN1B gene in a family with Liddle syndrome: A case report and systematic review. Molecular medicine reports, 29(2).

Perret DL, et al. (2024) A species' response to spatial climatic variation does not predict its response to climate change. Proceedings of the National Academy of Sciences of the United States of America, 121(1), e2304404120.