Resource Summary Report

Generated by NIF on Apr 18, 2025

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

Funding:

Availability: Commercial license

Resource Name: CoNIFER

Resource ID: SCR_013213

Alternate IDs: OMICS_00330

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250410T070343+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 180 mentions in open access literature.

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

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

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

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).

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.

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).

Bakacsy L, et al. (2024) A case study on the early stage of Pinus nigra invasion and its impact on species composition and pattern in Pannonic sand grassland. Scientific reports, 14(1), 5125.

Ashbrook S, et al. (2024) American marten occupancy and activity patterns at the southern extent of their range in the eastern United States. Ecology and evolution, 14(2), e10904.

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.

Howard-Wilson S, et al. (2024) Efficacy of a Multimodal Digital Behavior Change Intervention on Lifestyle Behavior, Cardiometabolic Biomarkers, and Medical Expenditure: Protocol for a Randomized Controlled Trial. JMIR research protocols, 13, e50378.

Whiting KR, et al. (2024) Utilization of automated cilia analysis to characterize novel INPP5E

variants in patients with non-syndromic retinitis pigmentosa. European journal of human genetics : EJHG, 32(11), 1412.

Mandiracioglu B, et al. (2024) ECOLE: Learning to call copy number variants on whole exome sequencing data. Nature communications, 15(1), 132.

Tan L, et al. (2024) Clinical application value of pre-pregnancy carrier screening in Chinese Han childbearing population. Molecular genetics & genomic medicine, 12(4), e2425.

Bharadwaj T, et al. (2024) THBS1 is a new autosomal recessive non-syndromic hearing impairment gene. BMC medical genomics, 17(1), 291.

Ma Z, et al. (2024) Whole-Exome Sequencing Analysis of Idiopathic Hypogonadotropic Hypogonadism: Comparison of Varicocele and Nonobstructive Azoospermia. Reproductive sciences (Thousand Oaks, Calif.), 31(1), 222.

Demidov G, et al. (2024) Comprehensive reanalysis for CNVs in ES data from unsolved rare disease cases results in new diagnoses. NPJ genomic medicine, 9(1), 49.

Ahn JH, et al. (2024) Implementing genomic medicine in clinical practice for adults with undiagnosed rare diseases. NPJ genomic medicine, 9(1), 63.

Lee Y, et al. (2024) Central neurocytoma exhibits radial glial cell signatures with FGFR3 hypomethylation and overexpression. Experimental & molecular medicine, 56(4), 975.

Redfield SE, et al. (2024) PKHD1L1, a gene involved in the stereocilia coat, causes autosomal recessive nonsyndromic hearing loss. Human genetics, 143(3), 311.

Feng M, et al. (2024) A conserved graft formation process in Norway spruce and Arabidopsis identifies the PAT gene family as central regulators of wound healing. Nature plants, 10(1), 53.

van Tiel N, et al. (2024) Regional uniqueness of tree species composition and response to forest loss and climate change. Nature communications, 15(1), 4375.