

Resource Summary Report

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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: 20260815T182437+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

Usage and Citation Metrics

We found 200 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Aslam F, et al. (2026) Molecular characterization of recessively inherited ataxic and neuropathic disorders in consanguineous Pakistani families. *Scientific reports*, 16(1), 6529.

Zhang Y, et al. (2026) Dynamic heterogeneity towards drug resistance in AML cells is primarily driven by epigenomic mechanism unveiled by multi-omics analysis. *Journal of advanced research*, 80, 487.

Othman AA, et al. (2026) Genotypic and phenotypic features of 23 Egyptian patients with tuberous sclerosis complex. *BMC pediatrics*, 26(1).

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.

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.

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.

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.

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

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.

Zhang Q, et al. (2025) Haploinsufficiency of brain-specific kinase BRSK1 causes epilepsy and neurodevelopmental disorders. *Epilepsia*, 66(12), 5033.

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).

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

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

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

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.

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.

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).