Resource Summary Report

Generated by kravitz2 on Jul 30, 2026

ERNE

RRID:SCR_010912
Type: Tool

Proper Citation

ERNE (RRID:SCR_010912)

Resource Information

URL: http://erne.sourceforge.net/

Proper Citation: ERNE (RRID:SCR_010912)

Description: A short string alignment package whose goal is to provide an all-inclusive set of tools to handle short (NGS-like) reads.

Abbreviations: ERNE

Resource Type: software resource

Resource Name: ERNE

Resource ID: SCR_010912

Alternate IDs: OMICS_00662

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260725T190709+0000

Ratings and Alerts

No rating or validation information has been found for ERNE.

No alerts have been found for ERNE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 46 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Bibi A, et al. (2025) Circular PVT1 promotes cardiac fibroblast activation interacting with miR-30a-5p and miR-125b-5p. Cell death & disease, 16(1), 325.

Moreno-Sanz P, et al. (2025) Investigation of mechanisms underlying seedlessness in a Sangiovese somatic variant through comparative genomic and histological analyses. BMC plant biology, 25(1), 1758.

Ferguson JN, et al. (2025) A deficient CP24 allele defines variation for dynamic nonphotochemical quenching and photosystem II efficiency in maize. The Plant cell, 37(4).

Spampinato C, et al. (2025) Improved radicchio seedling growth under CsPbI3 perovskite rooftop in a laboratory-scale greenhouse for Agrivoltaics application. Nature communications, 16(1), 2190.

Marqués-Gálvez JE, et al. (2025) Arbuscular Mycorrhiza Induce the Regulation of Ca2+, ROS, and SOS Pathways Under Salt Stress in Tomato Roots. Physiologia plantarum, 177(6), e70610.

Giovannini L, et al. (2025) Mycorrhization and chemical seed priming boost tomato stress tolerance by changing primary and defence metabolic pathways. Journal of experimental botany, 76(21), 6410.

Grigoriadou Zormpa O, et al. (2025) Genetic diversity and fine-scale spatial genetic structure of European beech populations along an elevational gradient. Heredity, 134(8), 451.

Peña-Ponton C, et al. (2024) High-resolution methylome analysis uncovers stress-responsive genomic hotspots and drought-sensitive transposable element superfamilies in the clonal Lombardy poplar. Journal of experimental botany, 75(18), 5839.

Navarini L, et al. (2024) Mozambican Coffea accessions from Ibo and Quirimba Islands: identification and geographical distribution. AoB PLANTS, 16(2), plae004.

Kareem BO, et al. (2024) Environmental and genetic regulation of Streptococcus pneumoniae galactose catabolic pathways. Nature communications, 15(1), 5171.

Tripodi P, et al. (2023) Development and application of Single Primer Enrichment Technology (SPET) SNP assay for population genomics analysis and candidate gene discovery in lettuce. Frontiers in plant science, 14, 1252777.

Rossi S, et al. (2023) C9orf72 Toxic Species Affect ArfGAP-1 Function. Cells, 12(15).

Troyee AN, et al. (2023) Herbivory induced methylation changes in the Lombardy poplar: A comparison of results obtained by epiGBS and WGBS. PloS one, 18(9), e0291202.

Allegri L, et al. (2022) Role of m6A RNA Methylation in Thyroid Cancer Cell Lines. International journal of molecular sciences, 23(19).

Mbebi AJ, et al. (2022) A comparative analysis of genomic and phenomic predictions of growth-related traits in 3-way coffee hybrids. G3 (Bethesda, Md.), 12(9).

Pontiller B, et al. (2022) Rapid bacterioplankton transcription cascades regulate organic matter utilization during phytoplankton bloom progression in a coastal upwelling system. The ISME journal, 16(10), 2360.

Miculan M, et al. (2021) A forward genetics approach integrating genome-wide association study and expression quantitative trait locus mapping to dissect leaf development in maize (Zea mays). The Plant journal : for cell and molecular biology, 107(4), 1056.

Alser M, et al. (2021) Technology dictates algorithms: recent developments in read alignment. Genome biology, 22(1), 249.

Boukail S, et al. (2021) Genome wide association study of agronomic and seed traits in a world collection of proso millet (Panicum miliaceum L.). BMC plant biology, 21(1), 330.

Allegri L, et al. (2021) Effects of Dihydrotanshinone I on Proliferation and Invasiveness of Paclitaxel-Resistant Anaplastic Thyroid Cancer Cells. International journal of molecular sciences, 22(15).