Resource Summary Report

Generated by dkNET on May 19, 2025

BLESS

RRID:SCR_005963
Type: Tool

Proper Citation

BLESS (RRID:SCR_005963)

Resource Information

URL: http://sourceforge.net/projects/bless-ec/

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Description: Software tool for Bloom-filter-based error correction for next-generation sequencing (NGS) reads. The algorithm produces accurate correction results with much less memory.

Abbreviations: BLESS

Synonyms: BLoom-filter-based Error correction Solution for high-throughput Sequencing reads, BLESS - Bloom-filter-based Error Correction Tool for NGS reads

Resource Type: software application, data analysis software, data processing software, sequence analysis software, algorithm resource, software resource

Defining Citation: PMID:24451628

Keywords: c++, next-generation sequencing, bloom-filter, error correction, ngs, bio.tools

Funding:

Availability: GNU General Public License v3

Resource Name: BLESS

Resource ID: SCR_005963

Alternate IDs: OMICS_02246, biotools:bless

Alternate URLs: https://bio.tools/bless

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250519T203427+0000

Ratings and Alerts

No rating or validation information has been found for BLESS.

No alerts have been found for BLESS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Menacher A, et al. (2024) Bayesian Lesion Estimation with a Structured Spike-and-Slab Prior. Journal of the American Statistical Association, 119(545), 66.

Long Q, et al. (2024) Tetrameric INTS6-SOSS1 complex facilitates DNA:RNA hybrid autoregulation at double-strand breaks. Nucleic acids research, 52(21), 13036.

Zheng Y, et al. (2024) Electrochemically coupled CH4 and CO2 consumption driven by microbial processes. Nature communications, 15(1), 3097.

Gardiner K, et al. (2024) BLESS: bagged logistic regression for biomarker identification. Frontiers in genetics, 15, 1336891.

Kato M, et al. (2024) A Multicenter, Open-Label Study to Evaluate the Long-term Safety and Efficacy of Adjunctive Brexpiprazole 2 mg Daily in Japanese Patients with Major Depressive Disorder. CNS drugs, 38(12), 1003.

Han J, et al. (2023) Long Term Effects of a Social Capital-Based Exercise Adherence Intervention for Breast Cancer Survivors With Moderate Fatigue: A Randomized Controlled Trial. Integrative cancer therapies, 22, 15347354231209440.

Liu K, et al. (2023) Bilineage embryo-like structure from EPS cells can produce live mice with tetraploid trophectoderm. Protein & cell, 14(4), 262.

Chatzinikolaou G, et al. (2023) XPF interacts with TOP2B for R-loop processing and DNA

looping on actively transcribed genes. Science advances, 9(45), eadi2095.

Volpi R, et al. (2021) Changing the Geometry of Representations: ?-Embeddings for NLP Tasks. Entropy (Basel, Switzerland), 23(3).

Bulut-Karslioglu A, et al. (2021) Chd1 protects genome integrity at promoters to sustain hypertranscription in embryonic stem cells. Nature communications, 12(1), 4859.

Alsuhaibani M, et al. (2021) Fine-Tuning Word Embeddings for Hierarchical Representation of Data Using a Corpus and a Knowledge Base for Various Machine Learning Applications. Computational and mathematical methods in medicine, 2021, 9761163.

Akimova E, et al. (2021) SAMHD1 restrains aberrant nucleotide insertions at repair junctions generated by DNA end joining. Nucleic acids research, 49(5), 2598.

Manghwar H, et al. (2020) CRISPR/Cas Systems in Genome Editing: Methodologies and Tools for sgRNA Design, Off-Target Evaluation, and Strategies to Mitigate Off-Target Effects. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 7(6), 1902312.

Saha C, et al. (2020) Guide-free Cas9 from pathogenic Campylobacter jejuni bacteria causes severe damage to DNA. Science advances, 6(25), eaaz4849.

Naeem M, et al. (2020) Latest Developed Strategies to Minimize the Off-Target Effects in CRISPR-Cas-Mediated Genome Editing. Cells, 9(7).

Pascoal S, et al. (2020) Field cricket genome reveals the footprint of recent, abrupt adaptation in the wild. Evolution letters, 4(1), 19.

Zhu Y, et al. (2019) qDSB-Seq is a general method for genome-wide quantification of DNA double-strand breaks using sequencing. Nature communications, 10(1), 2313.

Schwager S, et al. (2019) Evaluation of "Healthy Learning. Together", an Easily Applicable Mental Health Promotion Tool for Students Aged 9 to 18 Years. International journal of environmental research and public health, 16(3).

Cao H, et al. (2019) Novel approach reveals genomic landscapes of single-strand DNA breaks with nucleotide resolution in human cells. Nature communications, 10(1), 5799.

Ballinger TJ, et al. (2019) Modeling double strand break susceptibility to interrogate structural variation in cancer. Genome biology, 20(1), 28.