

Resource Summary Report

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

Defining Citation: [PMID:24451628](#)

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

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: 20260801T190302+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 45 mentions in open access literature.

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

Lattanzi S, et al. (2025) Effectiveness and safety of adjunctive cenobamate in people with focal-onset epilepsy: Interim results after 24-week observational period from the BLESS study. *Epilepsia*, 66(7), 2239.

Hori H, et al. (2025) Assessment of minimum clinically important difference in symptoms and functionality of Japanese patients with major depressive disorder following inadequate response to antidepressants: a post hoc analysis of the long-term study of brexpiprazole augmentation therapy in Japanese patients with major depressive disorder. *Frontiers in psychiatry*, 16, 1556470.

Wenson L, et al. (2025) Precise mapping of single-stranded DNA breaks by sequence-templated erroneous DNA polymerase end-labelling. *Nature communications*, 16(1), 7130.

Xu K, et al. (2025) ChromInSight: Revealing DNA Double-Strand Breaks Through Chromatin Structural Insights With an Interpretable Graph Neural Network Framework. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(36), e04571.

Petružela J, et al. (2025) Comparative Genomic Analysis of Co-Occurring Hybrid Zones of House Mouse Parasites *Pneumocystis murina* and *Syphacia obvelata* Using Genome Polarisation. *Molecular ecology*, 34(21), e70044.

Jiang L, et al. (2025) Chromosome-level genome assembly and annotation of pawak croaker (*Pennahia pawak*). *Scientific data*, 12(1), 412.

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.

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.

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

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

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: β -Embeddings for NLP Tasks. *Entropy (Basel, Switzerland)*, 23(3).

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

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.

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.

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