

Resource Summary Report

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Flexbar

RRID:SCR_013001

Type: Tool

Proper Citation

Flexbar (RRID:SCR_013001)

Resource Information

URL: <http://sourceforge.net/projects/flexbar/>

Proper Citation: Flexbar (RRID:SCR_013001)

Description: Flexible barcode and adapter removal for sequencing platforms.

Abbreviations: Flexbar

Resource Type: software resource

Defining Citation: [DOI:10.3390/biology1030895](https://doi.org/10.3390/biology1030895)

Keywords: bio.tools

Resource Name: Flexbar

Resource ID: SCR_013001

Alternate IDs: biotools:flexbar

Alternate URLs: <https://bio.tools/flexbar>, <https://sources.debian.org/src/flexbar/>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260815T182435+0000

Ratings and Alerts

No rating or validation information has been found for Flexbar.

No alerts have been found for Flexbar.

Data and Source Information

Usage and Citation Metrics

We found 307 mentions in open access literature.

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

Szmato?a T, et al. (2026) Genomic diversity and structure in arabian horses revealed by whole-genome sequencing: establishment of an allele frequency database of common genetic variation. BMC genomics, 27(1).

Mikhaylova Y, et al. (2026) Short-Term Within-Host Genomic Diversity and Clone Turnover of Carbapenem-Resistant Klebsiella pneumoniae in an Intensive Care Unit Patient. Antibiotics (Basel, Switzerland), 15(6).

Rostami MR, et al. (2026) Smoking-induced dysregulation of transposable elements in the small airway epithelium. Respiratory research, 27(1).

Pereirinha J, et al. (2026) SLBP-independent control of maternal histone mRNA. bioRxiv : the preprint server for biology.

Kleiber N, et al. (2026) 2'-O-methylation-dependent installation of N2-methylguanosine in the U6 internal stem loop facilitates efficient spliceosome assembly. Nature communications, 17(1).

Zhuang J, et al. (2026) Molecular diagnosis of rare biallelic CDC45 gene variants causing Meier-Gorlin syndrome-7 using whole exome sequencing. Human genomics, 20(1).

Azouzi C, et al. (2026) Ribosomal RNA synthesis by RNA polymerase I is subject to premature termination of transcription. eLife, 14.

Meijer J, et al. (2026) Eco-evolutionary dynamics of massive, parallel bacteriophage outbreaks in compost communities. Science advances, 12(22), eaeb8246.

Cañas-Duarte SJ, et al. (2026) An integrative multi-omics approach points to membrane composition as a key factor in E. coli persistence. PloS one, 21(6), e0351161.

Thomé CC, et al. (2026) Distinct steps of nuclear maturation of human pre-60S complexes require the activity of GTPases including GNL3L. Nucleic acids research, 54(5).

Fang D, et al. (2026) Investigation of TRMT61B methyltransferase activity on mRNA and its effects on translation. Nucleic acids research, 54(8).

Wan F, et al. (2026) Intravenous administration of an engineered AAV9-gene-silencing vector suppresses human SOD1 and extends survival in an ALS mouse model. Nature communications, 17(1).

Paulson AR, et al. (2026) Functional Genomic Evidence for Candidate Small Viral RNA-Mediated Epigenetic Interference in SARS-CoV-1 and SARS-CoV-2. Computational and structural biotechnology journal, 35(1), 0148.

Broglia L, et al. (2026) SAM68 is a multifunctional post-transcriptional regulator of cardiomyocyte differentiation. *Nucleic acids research*, 54(10).

Liu J, et al. (2026) Epstein-Barr Virus Expressed Long Non-Coding RNA (lncBARTs) Regulate EBV Latent Genome Replication. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(8), e07286.

Zhao X, et al. (2026) m6AConquer: a consistently quantified and orthogonally validated database for the N6-methyladenosine (m6A) epitranscriptome. *Nucleic acids research*, 54(D1), D204.

Clever F, et al. (2026) Dietary resilience of coral reef fishes to habitat degradation. *The Journal of animal ecology*, 95(3), 397.

Campbell S, et al. (2026) Negative regulation of TH17-mediated inflammation by the nuclear receptor REV-ERB?. *bioRxiv : the preprint server for biology*.

Jaworska J, et al. (2026) Comparative analysis of the transcriptome and methylome in distinct trophoblast populations at the time of embryo implantation in mares. *BMC genomics*, 27(1).

Tretow K, et al. (2026) RNA G-quadruplexes mediate cooperativity in HNRNPH binding and splicing regulation. *bioRxiv : the preprint server for biology*.