

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: 20260725T190743+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 281 mentions in open access literature.

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

Domínguez M, et al. (2025) Genomics Reveal Population Structure and Intergeneric Hybridization in an Endangered South American Bird: Implications for Management and Conservation. *Ecology and evolution*, 15(1), e70820.

Gurgul A, et al. (2025) Elucidating the transcriptomic response of adult-derived mHypoA-2/12 mouse hypothalamic neuron cell line to cannabidiol (CBD) exposure. *Journal of applied genetics*, 66(4), 1029.

Ignatov D, et al. (2025) RNA-binding protein YebC enhances translation of proline-rich amino acid stretches in bacteria. *Nature communications*, 16(1), 6262.

Van den Wyngaert S, et al. (2025) Dynamics of zoosporic parasites in summer phytoplankton communities of the Baltic Sea. *FEMS microbiology ecology*, 101(8).

Kawasaki T, et al. (2025) Meioc-Piwil1 complexes regulate rRNA transcription for differentiation of spermatogonial stem cells. *eLife*, 14.

Agrofoglio YC, et al. (2025) In vivo binding by Arabidopsis SPLICING FACTOR 1 shifts 3' splice site choice, regulating circadian rhythms and immunity in plants. *bioRxiv : the preprint server for biology*.

Oo JA, et al. (2025) Long non-coding RNAs direct the SWI/SNF complex to cell type-specific enhancers. *Nature communications*, 16(1), 131.

Xu M, et al. (2025) BASAL: a universal mapping algorithm for nucleotide base-conversion sequencing. *Nucleic acids research*, 53(2).

Flaherty JN, et al. (2025) The catalytic efficiency of METTL16 affects cellular processes by governing the intracellular S-adenosylmethionine setpoint. *Cell reports*, 44(7), 115966.

Lucero K, et al. (2025) CTCF-RNA interactions orchestrate cell-specific chromatin loop organization. *bioRxiv : the preprint server for biology*.

Fang D, et al. (2025) Investigation of TRMT61B methyltransferase activity on mRNA and its effects on translation. *bioRxiv : the preprint server for biology*.

Berdion Gabarain V, et al. (2025) Enhanced auxin signaling promotes root-hair growth at moderately low temperature in *Arabidopsis thaliana*. *Plant communications*, 6(6), 101350.

Vaknine Treidel S, et al. (2025) Maternal prenatal stress induces sex-dependent changes in tRNA fragment families and cholinergic pathways in newborns. *Molecular psychiatry*, 30(9), 4307.

Tian R, et al. (2025) Cetacean loss of the master adipose tissue regulator β -adrenergic receptor may underlie their thick blubber and an Oligocene radiation and dispersal. *Nature communications*, 16(1), 9235.

van Belle J, et al. (2025) Direct and indirect effects of multiplex genome editing of F5H and FAD2 in oil crop camelina. *Plant biotechnology journal*, 23(5), 1399.

Lucero K, et al. (2025) CTCF-RNA interactions orchestrate cell-specific chromatin loop organization. *Science advances*, 11(48), eady5507.

Chwiej J, et al. (2025) Tracing micro and nanoplastics toxicity in human pulmonary fibroblasts through integrated Raman and transcriptomic analyses. *Scientific reports*, 15(1), 39459.

Nonninger TJ, et al. (2025) A TFEB-TGF β axis systemically regulates diapause, stem cell resilience and protects against a senescence-like state. *Nature aging*, 5(7), 1340.

Maillet L, et al. (2025) Plant Genetic Bases Associated With Microbiota Descriptors Shed Light Into a Novel Holobiont Generalist Genes Theory. *Environmental microbiology*, 27(5), e70108.

Lewis CJT, et al. (2025) Quantitative profiling of human translation initiation reveals elements that potently regulate endogenous and therapeutically modified mRNAs. *Molecular cell*, 85(2), 445.