

Resource Summary Report

Generated by [RRID](#) on Apr 28, 2025

[ea-utils](#)

RRID:SCR_005553

Type: Tool

Proper Citation

ea-utils (RRID:SCR_005553)

Resource Information

URL: <http://code.google.com/p/ea-utils/>

Proper Citation: ea-utils (RRID:SCR_005553)

Description: Command-line software tools for processing biological sequencing data. Barcode demultiplexing, adapter trimming, etc. Primarily written to support an Illumina based pipeline - but should work with any FASTQs.

Abbreviations: ea-utils

Synonyms: ea-utils: FASTQ processing utilities

Resource Type: software resource

Defining Citation: [DOI:10.2174/1875036201307010001](https://doi.org/10.2174/1875036201307010001)

Keywords: bio.tools

Funding:

Availability: MIT License

Resource Name: ea-utils

Resource ID: SCR_005553

Alternate IDs: OMICS_01041, biotools:ea-utils

Alternate URLs: <https://bio.tools/ea-utils>, <https://sources.debian.org/src/ea-utils/>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20250420T014255+0000

Ratings and Alerts

No rating or validation information has been found for ea-utils.

No alerts have been found for ea-utils.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 271 mentions in open access literature.

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

Nguyen GT, et al. (2024) CRISPR-Cas12a exhibits metal-dependent specificity switching. Nucleic acids research, 52(16), 9343.

Rachubinski AL, et al. (2024) JAK inhibition decreases the autoimmune burden in Down syndrome. medRxiv : the preprint server for health sciences.

Wang J, et al. (2024) ATM and 53BP1 regulate alternative end joining-mediated V(D)J recombination. Science advances, 10(31), eadn4682.

Cameirão C, et al. (2024) Diversity, Composition, and Specificity of the *Philaenus spumarius* Bacteriome. Microorganisms, 12(2).

Rachubinski AL, et al. (2024) JAK inhibition decreases the autoimmune burden in Down syndrome. eLife, 13.

Wei H, et al. (2024) Proteolytic activation of fatty acid synthase signals pan-stress resolution. Nature metabolism, 6(1), 113.

Kink JA, et al. (2024) Large-scale bioreactor production of extracellular vesicles from mesenchymal stromal cells for treatment of acute radiation syndrome. Stem cell research & therapy, 15(1), 72.

Donovan MG, et al. (2024) Variegated overexpression of chromosome 21 genes reveals molecular and immune subtypes of Down syndrome. Nature communications, 15(1), 5473.

Pinchart PE, et al. (2024) The genus *Limnospira* contains only two species both unable to

produce microcystins: *L. maxima* and *L. platensis* comb. nov. *iScience*, 27(9), 110845.

Bravo González-Blas C, et al. (2024) Single-cell spatial multi-omics and deep learning dissect enhancer-driven gene regulatory networks in liver zonation. *Nature cell biology*, 26(1), 153.

Donovan MG, et al. (2024) Multimodal analysis of dysregulated heme metabolism, hypoxic signaling, and stress erythropoiesis in Down syndrome. *Cell reports*, 43(8), 114599.

Wang J, et al. (2024) DNA-PKcs suppresses illegitimate chromosome rearrangements. *Nucleic acids research*, 52(9), 5048.

Sweatt AJ, et al. (2024) Proteome-wide copy-number estimation from transcriptomics. *Molecular systems biology*, 20(11), 1230.

Merberg D, et al. (2024) Combined miRNA transcriptome and proteome analysis of extracellular vesicles in urine and blood from the Pompe mouse model. *Annals of medicine*, 56(1), 2402503.

Takase HM, et al. (2024) Transcriptomic signatures of WNT-driven pathways and granulosa cell-oocyte interactions during primordial follicle activation. *PLoS one*, 19(10), e0311978.

Meyer I, et al. (2024) RNase-mediated reprogramming of *Yersinia* virulence. *PLoS pathogens*, 20(8), e1011965.

Arrones A, et al. (2024) Irregular green netting of eggplant fruit peel: a domestication trait controlled by SmGLK2 with potential for fruit colour diversification. *Journal of experimental botany*, 75(22), 7066.

Edwards KR, et al. (2023) Multiple environmental factors, but not nutrient addition, directly affect wet grassland soil microbial community structure: a mesocosm study. *FEMS microbiology ecology*, 99(7).

Luláková P, et al. (2023) Mineral substrate quality determines the initial soil microbial development in front of the Nordenskiöldbreen, Svalbard. *FEMS microbiology ecology*, 99(10).

Tatavosian R, et al. (2023) Cell differentiation modifies the p53 transcriptional program through a combination of gene silencing and constitutive transactivation. *Cell death and differentiation*, 30(4), 952.