

# Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

## CRAC

RRID:SCR\_010652

Type: Tool

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### Proper Citation

CRAC (RRID:SCR\_010652)

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### Resource Information

**URL:** <http://crac.gforge.inria.fr/>

**Proper Citation:** CRAC (RRID:SCR\_010652)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Integrated RNA-Seq read analysis., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Abbreviations:** CRAC

**Resource Type:** software resource

**Defining Citation:** [DOI:10.1186/s12920-016-0178-5](https://doi.org/10.1186/s12920-016-0178-5)

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** CRAC

**Resource ID:** SCR\_010652

**Alternate IDs:** OMICS\_01240

**Alternate URLs:** <https://sources.debian.org/src/crac/>

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20260725T190703+0000

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### Ratings and Alerts

No rating or validation information has been found for CRAC.

No alerts have been found for CRAC.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 16 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Kelbert M, et al. (2024) The zinc-finger transcription factor Sfp1 imprints specific classes of mRNAs and links their synthesis to cytoplasmic decay. *eLife*, 12.

Shebanova A, et al. (2024) Cellular Uptake of Phase-Separating Peptide Coacervates. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(42), e2402652.

Rufflé F, et al. (2024) Effective requesting method to detect fusion transcripts in chronic myelomonocytic leukemia RNA-seq. *NAR genomics and bioinformatics*, 6(3), lqae117.

Bessi re C, et al. (2024) Transipedia.org: k-mer-based exploration of large RNA sequencing datasets and application to cancer data. *Genome biology*, 25(1), 266.

Riquier S, et al. (2021) Long non-coding RNA exploration for mesenchymal stem cell characterisation. *BMC genomics*, 22(1), 412.

Alser M, et al. (2021) Technology dictates algorithms: recent developments in read alignment. *Genome biology*, 22(1), 249.

Kim J, et al. (2020) Chromium acetate stimulates adipogenesis through regulation of gene expression and phosphorylation of adenosine monophosphate-activated protein kinase in bovine intramuscular or subcutaneous adipocytes. *Asian-Australasian journal of animal sciences*, 33(4), 651.

M Brooks R, et al. (2019) Electrospun Bimetallic NiCr Nanoparticles@Carbon Nanofibers as an Efficient Catalyst for Hydrogen Generation from Ammonia Borane. *Nanomaterials (Basel, Switzerland)*, 9(8).

Andresen L, et al. (2018) CLIP-Seq in Bacteria: Global Recognition Patterns of Bacterial RNA-Binding Proteins. *Methods in enzymology*, 612, 127.

Yeo MK, et al. (2017) Phosphorylated Protein Kinase C (Zeta/Lambda) Expression in Colorectal Adenocarcinoma and Its Correlation with Clinicopathologic Characteristics and Prognosis. *Journal of Cancer*, 8(16), 3371.

Ruff   F, et al. (2017) New chimeric RNAs in acute myeloid leukemia. *F1000Research*, 6.

Mucaki EJ, et al. (2016) A unified analytic framework for prioritization of non-coding variants of uncertain significance in heritable breast and ovarian cancer. *BMC medical genomics*, 9, 19.

Beaumeunier S, et al. (2016) On the evaluation of the fidelity of supervised classifiers in the prediction of chimeric RNAs. *BioData mining*, 9, 34.

Kowalski T, et al. (2015) Indexing Arbitrary-Length k-Mers in Sequencing Reads. *PloS one*, 10(7), e0133198.

Philippe N, et al. (2014) Combining DGE and RNA-sequencing data to identify new polyA+ non-coding transcripts in the human genome. *Nucleic acids research*, 42(5), 2820.

Philippe N, et al. (2013) CRAC: an integrated approach to the analysis of RNA-seq reads. *Genome biology*, 14(3), R30.