

Resource Summary Report

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TRAL

RRID:SCR_018979

Type: Tool

Proper Citation

TRAL (RRID:SCR_018979)

Resource Information

URL: <https://github.com/acg-team/tral>

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Description: Software tool to make annotation of tandem repeats in amino acid and nucleic data simple. Includes modules for detecting tandem repeats with both de novo software and sequence profile HMMs. Used for statistical significance analysis of putative tandem repeats, and filtering of redundant predictions.

Abbreviations: TRAL

Synonyms: Tandem Repeat Annotation Library

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

Defining Citation: [DOI:10.1093/bioinformatics/btv306](https://doi.org/10.1093/bioinformatics/btv306)

Keywords: Annotation, tandem repeats annotation, amino acid repeats, nucleic data, statistical analysis, redundant predictions filtering, redundant annotation clustering, overlapping annotations clustering, false positive annotation filtering, bio.tools

Funding: Swiss State Secretariat for Education ;
Research ;
and Innovation

Availability: Free, Freely available

Resource Name: TRAL

Resource ID: SCR_018979

Alternate IDs: biotools:tral

Alternate URLs: <https://bio.tools/tral>

License: GPL-2.0

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260731T043042+0000

Ratings and Alerts

No rating or validation information has been found for TRAL.

No alerts have been found for TRAL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.