

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 17, 2026

CONTRAFold

RRID:SCR_023994

Type: Tool

Proper Citation

CONTRAFold (RRID:SCR_023994)

Resource Information

URL: <http://contra.stanford.edu/contrafold/>

Proper Citation: CONTRAFold (RRID:SCR_023994)

Description: Software novel secondary structure prediction method based on conditional log-linear models, a flexible class of probabilistic models which generalize upon SCFGs by using discriminative training and feature-rich scoring. Used for sequence prediction.

Abbreviations: CONTRAFold

Synonyms: CONditional TRaining for RNA Secondary Structure Prediction, contrafold

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:16873527](#)

Keywords: sequence prediction,

Availability: Free, Available for download, Freely available

Resource Name: CONTRAFold

Resource ID: SCR_023994

Alternate IDs: OMICS_03452

Old URLs: <https://sources.debian.org/src/CONTRAFold/>

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260912T200044+0000

Ratings and Alerts

No rating or validation information has been found for CONTRAfold.

No alerts have been found for CONTRAfold.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Oleynikov M, et al. (2024) RNA tertiary structure and conformational dynamics revealed by BASH MaP. eLife, 13.

Oleynikov M, et al. (2024) RNA tertiary structure and conformational dynamics revealed by BASH MaP. bioRxiv : the preprint server for biology.