

Resource Summary Report

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CentroidFold

RRID:SCR_017253

Type: Tool

Proper Citation

CentroidFold (RRID:SCR_017253)

Resource Information

URL: <http://rtools.cbrc.jp/centroidfold/>

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Description: Web server for RNA secondary structure prediction. Predicts RNA secondary structure from RNA sequence. Based on generalized centroid estimator.

Resource Type: data access protocol, simulation software, software resource, web service, software application

Defining Citation: [PMID:19435882](#)

Keywords: RNA, secondary, structure, prediction, centroid, estimator, sequecne, data, alignment, bio.tools

Funding: New Energy and Industrial Technology Development Organization of Japan ;
Ministry of Education ;
Culture ;
Sports ;
Science and Technology of Japan ;
Internal fund of Computational Biology Research Center

Availability: Free, Freely available

Resource Name: CentroidFold

Resource ID: SCR_017253

Alternate IDs: biotools:centroidfold, OMICS_03449

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

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260731T043018+0000

Ratings and Alerts

No rating or validation information has been found for CentroidFold.

No alerts have been found for CentroidFold.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Kobayashi D, et al. (2025) Deglycosylation and truncation in the neuraminidase stalk are functionally equivalent in enhancing the pathogenicity of a high pathogenicity avian influenza virus in chickens. *Journal of virology*, 99(3), e0147824.

Izumikawa K, et al. (2025) Molecular basis of the autoregulatory mechanism of motor neuron-related splicing factor 30. *The Journal of biological chemistry*, 301(9), 110522.

Shimizu T, et al. (2024) A cytidine deaminase regulates axon regeneration by modulating the functions of the *Caenorhabditis elegans* HGF/plasminogen family protein SVH-1. *PLoS genetics*, 20(7), e1011367.

Kida Y, et al. (2021) Structural Requirements in the Hemagglutinin Cleavage Site-Coding RNA Region for the Generation of Highly Pathogenic Avian Influenza Virus. *Pathogens (Basel, Switzerland)*, 10(12).

Kuwano Y, et al. (2021) Overexpression of the transcribed ultraconserved region Uc.138 accelerates colon cancer progression. *Scientific reports*, 11(1), 8667.

Amano R, et al. (2021) Specific inhibition of FGF5-induced cell proliferation by RNA aptamers. *Scientific reports*, 11(1), 2976.

Takahashi M, et al. (2021) Nucleic acid ligands act as a PAM and agonist depending on the intrinsic ligand binding state of P2RY2. *Proceedings of the National Academy of Sciences of the United States of America*, 118(18).

Monshi FI, et al. (2020) Structure and diversity of 13S globulin zero-repeat subunit, the trypsin-resistant storage protein of common buckwheat (*Fagopyrum esculentum* M.) seeds. *Breeding science*, 70(1), 118.

Wakida H, et al. (2020) Stability of RNA sequences derived from the coronavirus genome in human cells. *Biochemical and biophysical research communications*, 527(4), 993.

Ohmori S, et al. (2020) RNA Aptamers for a tRNA-Binding Protein from *Aeropyrum pernix* with Homologous Counterparts Distributed Throughout Evolution. *Life (Basel,*

Switzerland), 10(2).

Nakata M, et al. (2020) Thermosensitive pilus production by FCT type 3 *Streptococcus pyogenes* controlled by Nra regulator translational efficiency. *Molecular microbiology*, 113(1), 173.

Abaeva IS, et al. (2020) The Halastavi ϕ rva Virus Intergenic Region IRES Promotes Translation by the Simplest Possible Initiation Mechanism. *Cell reports*, 33(10), 108476.

Shim SH, et al. (2019) Loss of Function of Rice Plastidic Glycolate/Glycerate Translocator 1 Impairs Photorespiration and Plant Growth. *Frontiers in plant science*, 10, 1726.

Wang F, et al. (2019) TabZIP74 Acts as a Positive Regulator in Wheat Stripe Rust Resistance and Involves Root Development by mRNA Splicing. *Frontiers in plant science*, 10, 1551.

Hamada M, et al. (2011) CentroidHomfold-LAST: accurate prediction of RNA secondary structure using automatically collected homologous sequences. *Nucleic acids research*, 39(Web Server issue), W100.