

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[KineFold](#)

RRID:SCR_022273

Type: Tool

Proper Citation

KineFold (RRID:SCR_022273)

Resource Information

URL: <http://kinefold.curie.fr/>

Proper Citation: KineFold (RRID:SCR_022273)

Description: Web service for RNA/DNA folding predictions including pseudoknots and entangled helices.Used for prediction and statistics of pseudoknots in RNA structures using exactly clustered stochastic simulations.

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

Defining Citation: [PMID:14676318](#)

Keywords: RNA secondary structure, minimum free energy prediction, RNA/DNA folding predictions, pseudoknots and entangled helices, pseudoknots in RNA structures, clustered stochastic simulations

Funding: French Ministry of Higher Education

Availability: Free, Freely available

Resource Name: KineFold

Resource ID: SCR_022273

Record Creation Time: 20220511T050132+0000

Record Last Update: 20260905T133012+0000

Ratings and Alerts

No rating or validation information has been found for KineFold.

No alerts have been found for KineFold.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Kudo KI, et al. (2025) Androgen receptor contributes to radioresistance through DNA repair and autophagy in AR-positive prostate cancer cells. bioRxiv : the preprint server for biology.

Lin BC, et al. (2023) In silico methods for predicting functional synonymous variants. Genome biology, 24(1), 126.

Lam SY, et al. (2022) Capture-SELEX: Selection Strategy, Aptamer Identification, and Biosensing Application. Biosensors, 12(12).

Holcomb DD, et al. (2022) Protocol to identify host-viral protein interactions between coagulation-related proteins and their genetic variants with SARS-CoV-2 proteins. STAR protocols, 3(3), 101648.