

# Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

## KineFold

RRID:SCR\_022273

Type: Tool

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### Proper Citation

KineFold (RRID:SCR\_022273)

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### 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, web service, software resource

**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:** 20260803T040829+0000

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### Ratings and Alerts

No rating or validation information has been found for KineFold.

No alerts have been found for KineFold.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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

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.