Resource Summary Report

Generated by RRID on Apr 11, 2025

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: software resource, data access protocol, 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: 20250410T071502+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 2 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.