

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

pKiss

RRID:SCR_017256

Type: Tool

Proper Citation

pKiss (RRID:SCR_017256)

Resource Information

URL: <https://bibiserv.cebitec.uni-bielefeld.de/pkiss>

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Description: Software tool for folding RNA secondary structures, including two limited classes of pseudoknots. Performs abstract shape analysis for structures holding pseudoknots up to complexity of kissing hairpin motifs. Successor of pknotsRG. Used for secondary structure prediction including kissing hairpin motifs.

Synonyms: pKISS

Resource Type: data analysis software, software application, software resource, sequence analysis software, data processing software

Defining Citation: [PMID:25273103](#)

Keywords: folding, RNA, secondary, structure, pseudoknot, abstract, shape, analysis, hairpin, motif

Availability: Free, Available for download, Freely available

Resource Name: pKiss

Resource ID: SCR_017256

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260801T042806+0000

Ratings and Alerts

No rating or validation information has been found for pKiss.

No alerts have been found for pKiss.

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 [PRECISE-TBI](#) .

Wang LL, et al. (2024) Xinyang flavivirus, from Haemaphysalis flava ticks in Henan Province, China, defines a basal, likely tick-only Orthoflavivirus clade. The Journal of general virology, 105(5).

Gosavi D, et al. (2022) Insights into the secondary and tertiary structure of the Bovine Viral Diarrhea Virus Internal Ribosome Entry Site. RNA biology, 19(1), 496.

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

Singh J, et al. (2019) RNA secondary structure prediction using an ensemble of two-dimensional deep neural networks and transfer learning. Nature communications, 10(1), 5407.