

# Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

## Kinannote

RRID:SCR\_000352

Type: Tool

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### Proper Citation

Kinannote (RRID:SCR\_000352)

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### Resource Information

**URL:** <http://sourceforge.net/projects/kinannote/>

**Proper Citation:** Kinannote (RRID:SCR\_000352)

**Description:** Software that identifies and classifies protein kinases in a user-provided fasta file using an HMM derived from serine / threonine protein kinases, a position specific scoring matrix derived from the HMM, and comparison with a local version of the curated kinase database from kinase.com.

**Resource Type:** software resource

**Defining Citation:** [PMID:23904509](#)

**Keywords:** standalone software, perl

**Availability:** Free, Available for download, Freely available

**Resource Name:** Kinannote

**Resource ID:** SCR\_000352

**Alternate IDs:** OMICS\_05965

**License:** BSD License

**Record Creation Time:** 20220129T080201+0000

**Record Last Update:** 20260815T182143+0000

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### Ratings and Alerts

No rating or validation information has been found for Kinannote.

No alerts have been found for Kinannote.

## 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 [NIF](#) .

Mikhailov KV, et al. (2022) Genomic analysis reveals cryptic diversity in aphelids and sheds light on the emergence of Fungi. Current biology : CB, 32(21), 4607.

Anstead CA, et al. (2015) Lucilia cuprina genome unlocks parasitic fly biology to underpin future interventions. Nature communications, 6, 7344.