

Resource Summary Report

Generated by T1D on Aug 2, 2026

Kinannote

RRID:SCR_000352

Type: Tool

Proper Citation

Kinannote (RRID:SCR_000352)

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](https://pubmed.ncbi.nlm.nih.gov/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: 20260801T190118+0000

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](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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.