Resource Summary Report

Generated by NIF on Apr 19, 2025

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

Keywords: standalone software, perl

Funding:

Availability: BSD License

Resource Name: Kinannote

Resource ID: SCR_000352

Alternate IDs: OMICS_05965

Record Creation Time: 20220129T080201+0000

Record Last Update: 20250410T064549+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 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.