Resource Summary Report

Generated by RRID on Apr 14, 2025

Kinomer

RRID:SCR_007707
Type: Tool

Proper Citation

Kinomer (RRID:SCR_007707)

Resource Information

URL: http://www.compbio.dundee.ac.uk/kinomer

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Description: Kinomer is a multilevel HMM library that models these protein kinase groups. It allows accurate identification of protein kinases and classification to the appropriate kinase group. Profile hidden Markov models (HMMs) are statistical descriptions of sequence conservation from multiple sequence alignments, and have been shown to outperform standard pairwise sequence comparison methods, both in terms of sensitivity and specificity. HMMs form the basis of protein family and domain description libraries such as SUPERFAMILY and Pfam.

Synonyms: Kinomer

Resource Type: database, data or information resource

Funding:

Resource Name: Kinomer

Resource ID: SCR_007707

Alternate IDs: nif-0000-03072

Record Creation Time: 20220129T080243+0000

Record Last Update: 20250412T055208+0000

Ratings and Alerts

No rating or validation information has been found for Kinomer.

No alerts have been found for Kinomer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

van Rhijn N, et al. (2024) Functional analysis of the Aspergillus fumigatus kinome identifies a druggable DYRK kinase that regulates septal plugging. Nature communications, 15(1), 4984.

Das S, et al. (2022) An insight into the role of protein kinases as virulent factors, regulating pathogenic attributes in Candida albicans. Microbial pathogenesis, 164, 105418.

Wang D, et al. (2021) Functional Genomics and Comparative Lineage-Specific Region Analyses Reveal Novel Insights into Race Divergence in Verticillium dahliae. Microbiology spectrum, 9(3), e0111821.

Lee KT, et al. (2016) Systematic functional analysis of kinases in the fungal pathogen Cryptococcus neoformans. Nature communications, 7, 12766.

Tang YT, et al. (2014) Genome of the human hookworm Necator americanus. Nature genetics, 46(3), 261.

Li Z, et al. (2014) Genome-wide identification and comprehensive analyses of the kinomes in four pathogenic microsporidia species. PloS one, 9(12), e115890.

Rosenblum JS, et al. (2013) Functional interrogation of kinases and other nucleotide-binding proteins. FEBS letters, 587(13), 1870.