Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

SISYPHUS

RRID:SCR_007930
Type: Tool

Proper Citation

SISYPHUS (RRID:SCR_007930)

Resource Information

URL: http://sisyphus.mrc-cpe.cam.ac.uk

Proper Citation: SISYPHUS (RRID:SCR_007930)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. A collection of manually curated protein structural alignments and their interrelationships. Each multiple alignment within the SISYPHUS database consists of structurally similar regions common to a group of proteins. These regions range from oligomeric biological units, or individual domains to fragments of different size representing either internal structural repeats or motifs common to structurally distinct proteins. The SISYPHUS multiple alignments are displayed with SPICE, a browser that provides an integrated view of protein sequences, structures and their annotations.

Synonyms: SISYPHUS

Resource Type: database, data or information resource

Keywords: bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SISYPHUS

Resource ID: SCR_007930

Alternate IDs: biotools:sisyphus

Alternate URLs: https://bio.tools/sisyphus

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250412T055222+0000

Ratings and Alerts

No rating or validation information has been found for SISYPHUS.

No alerts have been found for SISYPHUS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Cretin G, et al. (2023) ICARUS: flexible protein structural alignment based on Protein Units. Bioinformatics (Oxford, England), 39(8).

Talibart H, et al. (2021) PPalign: optimal alignment of Potts models representing proteins with direct coupling information. BMC bioinformatics, 22(1), 317.

Arriagada M, et al. (2013) On the difference in quality between current heuristic and optimal solutions to the protein structure alignment problem. BioMed research international, 2013, 459248.