Resource Summary Report

Generated by dkNET on Apr 29, 2025

F2DockClient

RRID:SCR_000185
Type: Tool

Proper Citation

F2DockClient (RRID:SCR_000185)

Resource Information

URL: http://www.cs.utexas.edu/~bajaj/cvc/software/f2dockclient.shtml

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Description: A collection of user interfaces packaged into TexMol that allows a user to interactively submit protein-protein docking jobs to a remote computing cluster, monitor the status of the jobs and retrieve and visually display/compare the results.

Abbreviations: F2DockClient

Resource Type: software resource

Defining Citation: PMID:23483883

Keywords: user interface, protein-protein docking, computing cluster, analysis,

Funding: National Science Foundation ;
National Institutes of Health

Availability: Open Source

Resource Name: F2DockClient

Resource ID: SCR_000185

Alternate IDs: OMICS_01599

Record Creation Time: 20220129T080200+0000

Record Last Update: 20250420T013933+0000

Ratings and Alerts

No rating or validation information has been found for F2DockClient.

No alerts have been found for F2DockClient.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Chowdhury R, et al. (2013) Protein-protein docking with F(2)Dock 2.0 and GB-rerank. PloS one, 8(3), e51307.