

# Resource Summary Report

Generated by ASWG on Aug 26, 2026

## F2DockClient

RRID:SCR\_000185

Type: Tool

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### Proper Citation

F2DockClient (RRID:SCR\_000185)

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### Resource Information

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

**Proper Citation:** F2DockClient (RRID:SCR\_000185)

**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:** Free, Available for download, Freely available

**Resource Name:** F2DockClient

**Resource ID:** SCR\_000185

**Alternate IDs:** OMICS\_01599

**Record Creation Time:** 20220129T080200+0000

**Record Last Update:** 20260815T182141+0000

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### Ratings and Alerts

No rating or validation information has been found for F2DockClient.

No alerts have been found for F2DockClient.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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