

Resource Summary Report

Generated by T1D on Aug 9, 2026

FRED - Fast exhaustive docking

RRID:SCR_014885

Type: Tool

Proper Citation

FRED - Fast exhaustive docking (RRID:SCR_014885)

Resource Information

URL: <http://www.eyesopen.com/oedocking>

Proper Citation: FRED - Fast exhaustive docking (RRID:SCR_014885)

Description: Complementary OEDocking tool for virtual screening, it performs a systematic and non-stochastic examination of all possible protein-ligand poses. The software also filters for shape complementarity and chemical feature alignment before selecting and optimizing protein-ligand poses.

Abbreviations: FRED

Synonyms: Fast exhaustive docking (FRED), Fast exhaustive docking

Resource Type: software resource

Keywords: docking, protein ligand, protein-ligand, protein ligand interaction, protein-ligand interaction, protein ligand pose, protein-ligand pose, ultra high throughput, compliment

Resource Name: FRED - Fast exhaustive docking

Resource ID: SCR_014885

Alternate URLs: <http://docs.eyesopen.com/oedocking/fred.html>

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260808T190031+0000

Ratings and Alerts

No rating or validation information has been found for FRED - Fast exhaustive docking.

No alerts have been found for FRED - Fast exhaustive docking.

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 [T1D](#) .

Poleboyina SM, et al. (2023) Homology Modeling, Screening, and Identification of Potential FOXO6 Inhibitors Curtail Gastric Cancer Progression: an In Silico Drug Repurposing Approach. Applied biochemistry and biotechnology.