ACFIS

A free web server for Auto Core Fragment in silico Screening (ACFIS) to accelerate Fragment-Based Drug Discovery (FBDD).

https://academic.oup.com/nar/article/51/W1/W25/7157533

Overview

ACFIS (Auto Core Fragment in silico Screening) is a powerful and free web server designed as a one-stop platform for Fragment-Based Drug Discovery (FBDD). Developed by researchers primarily from Central China Normal University, the tool streamlines the entire FBDD workflow from core fragment identification to lead compound generation. The most recent version, ACFIS 2.0, was published in 2023, offering significant improvements over its predecessor.

Key Features and Capabilities

ACFIS operates through two main computational modules: **CORE_GEN** and **CAND_GEN**, providing a comprehensive, integral workflow for drug lead identification.

Core Fragment Generation (CORE_GEN): This module performs fragment deconstruction analysis on an active molecule to derive the core fragment structure. It calculates the binding free energy (ΔG) and Ligand Efficiency (LE) for each fragment to identify the most efficient core.

Candidate Generation (CAND_GEN): This module is responsible for fragment-to-lead optimization. It links new fragments to the identified core fragment to generate novel candidate compounds.

Dynamic Fragment Growing Strategy: ACFIS 2.0 incorporates a dynamic growing method that considers the influence of protein flexibility, which significantly improves the accuracy of predicting protein-fragment binding modes.

Enhanced Prediction Accuracy: ACFIS 2.0 achieved an accuracy of 88.5% in identifying hit compounds on a validated test set, representing an increase of over 10% compared to the previous version.

Comprehensive Molecular Property Prediction: The output interface integrates functionality for predicting molecular properties, including binding affinity, physicochemical properties (e.g., LogP, MW), drug-likeness (using rules like Lipinski's and QED), pesticide-likeness, and synthetic accessibility.

3D Molecular Visualization: The server utilizes JSmol, an interactive molecular viewer applet, to enable users to view the binding mode of top-ranking molecules in 3D.

Target Users and Use Cases

ACFIS is primarily targeted at computational chemists, pharmaceutical researchers, and academic scientists involved in early-stage drug discovery and design. It is particularly useful for accelerating the FBDD process in a cost-efficient and time-saving manner. Successful use cases include the discovery of drug leads for treating Parkinson's disease, cancer, and major depressive disorder.

Key Features

- Fragment-Based Drug Discovery (FBDD) Workflow
- Core Fragment Identification (CORE_GEN)
- Fragment-to-Lead Optimization (CAND_GEN)
- Dynamic Fragment Growing Strategy (Protein Flexibility)
- Molecular Property Prediction (Drug-likeness, Synthetic Accessibility)
- 3D Molecular Visualization (JSmol)

Pricing

Model: free

ACFIS is a free and open-to-all web server for academic and non-commercial research, developed by Central China Normal University.

Target Company Size: startup, small, medium, enterprise

Integrations

JSmol, AutoDock Tools, CHIMERA, PYMOL