Resource Summary Report

Generated by dkNET on Apr 29, 2025

FlexX

RRID:SCR_000186
Type: Tool

Proper Citation

FlexX (RRID:SCR_000186)

Resource Information

URL: http://www.biosolveit.de/flexx/index.html?ct=1

Proper Citation: FlexX (RRID:SCR_000186)

Description: A software with two main applications: predicting the binding mode of three-dimensional proteins and virtual high-throughput screening (vHTS) which allows screening of compounds at rapid speeds.

Abbreviations: FlexX

Resource Type: software resource

Defining Citation: PMID:15382244

Keywords: protein binding, analysis, ligand, prediction, compounds, screening, protein-ligand docking,

Funding:

Availability: Public, Open Source

Resource Name: FlexX

Resource ID: SCR_000186

Alternate IDs: OMICS_01600

Record Creation Time: 20220129T080200+0000

Record Last Update: 20250420T013933+0000

Ratings and Alerts

No rating or validation information has been found for FlexX.

No alerts have been found for FlexX.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Star?evi? Š, et al. (2011) Discovery of highly potent, nonsteroidal 17?-hydroxysteroid dehydrogenase type 1 inhibitors by virtual high-throughput screening. The Journal of steroid biochemistry and molecular biology, 127(3-5), 255.

Chen HM, et al. (2007) SODOCK: swarm optimization for highly flexible protein-ligand docking. Journal of computational chemistry, 28(2), 612.

Schellhammer I, et al. (2004) FlexX-Scan: fast, structure-based virtual screening. Proteins, 57(3), 504.

Kramer B, et al. (1999) Evaluation of the FLEXX incremental construction algorithm for protein-ligand docking. Proteins, 37(2), 228.

Rarey M, et al. (1999) Docking of hydrophobic ligands with interaction-based matching algorithms. Bioinformatics (Oxford, England), 15(3), 243.