Concavity

RRID:SCR_016063
Type: Tool

Proper Citation

Concavity (RRID:SCR_016063)

Resource Information

URL: http://compbio.cs.princeton.edu/concavity/

Description: Software for predicting protein ligand binding sites that integrate evolutionary sequence conservation estimates with structure-based methods for identifying protein surface cavities. Used in predicting catalytic sites and drug binding pockets.

Resource Name: Concavity

Proper Citation: Concavity (RRID:SCR_016063)

Resource Type: Resource, software resource, software toolkit, software application

Keywords: predict, protein, ligand, binding, site, catalytic, drug, algorithm

Resource ID: SCR_016063

Related resources: Princeton University; New Jersey; USA

References: PMID:19997483

Availability: Free, Available for download

Website Status: Last checked up

Alternate URLs: http://manpages.ubuntu.com/manpages/bionic/man1/concavity.1.html

Mentions Count: 46

Ratings and Alerts
No rating or validation information has been found for Concavity.

No alerts have been found for Concavity.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 46 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure.](https://fdilab.scicrunch.org/)


Asamitsu K, et al. (2017) MD simulation of the Tat/Cyclin T1/CDK9 complex revealing the hidden catalytic cavity within the CDK9 molecule upon Tat binding. PloS one, 12(2), e0171727.


Cao C, et al. (2016) Improving the performance of the PLB index for ligand-binding site prediction using dihedral angles and the solvent-accessible surface area. Scientific reports, 6, 33232.

