Concavity

RRID:SCR_016063
Type: Tool

Proper Citation

Concavity (RRID:SCR_016063)

Resource Information

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

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

**References:** PMID:19997483

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

**Related resources:** Princeton University; New Jersey; USA

**Availability:** Free, Available for download

**Website Status:** Last checked down

**Resource Name:** Concavity

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

Ratings and Alerts

No rating or validation information has been found for Concavity.
No alerts have been found for Concavity.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 53 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - 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.


