Resource Summary Report

Generated by RRID on May 22, 2025

Concavity

RRID:SCR_016063
Type: Tool

Proper Citation

Concavity (RRID:SCR_016063)

Resource Information

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

Proper Citation: Concavity (RRID:SCR_016063)

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: software resource, software toolkit, software application

Defining Citation: PMID:19997483, DOI:10.1371/journal.pcbi.1000585

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

Funding:

Availability: Free, Available for download

Resource Name: Concavity

Resource ID: SCR_016063

Alternate IDs: OMICS_04161

Alternate URLs: http://manpages.ubuntu.com/manpages/bionic/man1/concavity.1.html, https://sources.debian.org/src/concavity/

License: GNU General Public License (GPL)

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250521T061638+0000

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 87 mentions in open access literature.

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

Abdelazim AA, et al. (2025) In-silico screening and analysis of missense SNPs in human CYP3A4/5 affecting drug-enzyme interactions of FDA-approved COVID-19 antiviral drugs. Scientific reports, 15(1), 2153.

Sweatt AJ, et al. (2024) Proteome-wide copy-number estimation from transcriptomics. Molecular systems biology, 20(11), 1230.

James R, et al. (2024) In-silico analysis predicts disruption of normal angiogenesis as a causative factor in osteoporosis pathogenesis. BMC genomic data, 25(1), 85.

Selim MS, et al. (2024) Characterization, modeling, and anticancer activity of L.arginase production from marine Bacillus licheniformis OF2. BMC biotechnology, 24(1), 6.

Hansen E, et al. (2024) Emerin deficiency drives MCF7 cells to an invasive phenotype. bioRxiv : the preprint server for biology.

Zaylaa AJ, et al. (2024) Advancing Breast Cancer Diagnosis through Breast Mass Images, Machine Learning, and Regression Models. Sensors (Basel, Switzerland), 24(7).

Liu YX, et al. (2024) Site differentiation strategy for selective strontium uptake and elution within an all-inorganic polyoxoniobate framework. Nature communications, 15(1), 8896.

Ogun OJ, et al. (2023) Molecular Structural Analysis of Porcine CMAH-Native Ligand Complex and High Throughput Virtual Screening to Identify Novel Inhibitors. Pathogens (Basel, Switzerland), 12(5).

Liu C, et al. (2023) An Outstandingly Rare Occurrence of Mycoviruses in Soil Strains of the Plant-Beneficial Fungi from the Genus Trichoderma and a Novel Polymycoviridae Isolate.

Microbiology spectrum, 11(3), e0522822.

Sweatt AJ, et al. (2023) Proteome-wide copy-number estimation from transcriptomics. bioRxiv : the preprint server for biology.

Mitchell SM, et al. (2023) An investigation of binding interactions of tumor-targeted peptide conjugated polyphenols with the kinase domain of ephrin B4 and B2 receptors. Molecular diversity, 1.

Paz-Linares D, et al. (2023) Identifying oscillatory brain networks with hidden Gaussian graphical spectral models of MEEG. Scientific reports, 13(1), 11466.

Iyengar SM, et al. (2022) Identification and characterization of alternative sites and molecular probes for SARS-CoV-2 target proteins. Frontiers in chemistry, 10, 1017394.

Ozcan I, et al. (2022) Comparison of Classification Success Rates of Different Machine Learning Algorithms in the Diagnosis of Breast Cancer. Asian Pacific journal of cancer prevention : APJCP, 23(10), 3287.

Rodrigues CHM, et al. (2022) Structural landscapes of PPI interfaces. Briefings in bioinformatics, 23(4).

Anwaar MU, et al. (2022) Combined deep learning and molecular docking simulations approach identifies potentially effective FDA approved drugs for repurposing against SARS-CoV-2. Computers in biology and medicine, 141, 105049.

Rocha GD, et al. (2022) Impact of polymorphisms in blaZ, blaR1 and blaI genes and their relationship with ?-lactam resistance in S. aureus strains isolated from bovine mastitis. Microbial pathogenesis, 165, 105453.

Khedr M, et al. (2022) Molecular docking and nucleotide sequencing of successive expressed recombinant fungal peroxidase gene in E.coli. Journal, genetic engineering & biotechnology, 20(1), 94.

Jiang X, et al. (2022) Study on Spatial Geometric Similarity Based on Conformal Geometric Algebra. International journal of environmental research and public health, 19(17).

Panchangam SS, et al. (2022) BabyBoom: 3-Dimensional Structure-Based Ligand and Protein Interaction Prediction by Molecular Docking. Biomolecules, 12(11).