

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](http://FDI Lab - SciCrunch.org) on Apr 24, 2025

## Concavity

RRID:SCR\_016063

Type: Tool

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### Proper Citation

Concavity (RRID:SCR\_016063)

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### 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 toolkit, software resource, software application

**Defining Citation:** [PMID:19997483](https://pubmed.ncbi.nlm.nih.gov/19997483/), [DOI:10.1371/journal.pcbi.1000585](https://doi.org/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:** 20250424T065425+0000

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## 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 87 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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.

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

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  $\beta$ -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).