

Resource Summary Report

Generated by [dkNET](#) on Sep 2, 2026

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 application, software resource, software toolkit

Defining Citation: [PMID:19997483](#), [DOI:10.1371/journal.pcbi.1000585](#)

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

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: 20260829T183110+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 94 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#).

Jibon MDK, et al. (2025) In-silico analysis of deleterious non-synonymous SNPs in the human AVPR1a gene linked to autism. BMC genomics, 26(1), 492.

Clemente-Morag??n A, et al. (2025) Pharmacogenomics and chronotherapy of drug-induced cardioprotection in acute myocardial infarction. Nature communications, 16(1), 10450.

Levingston S, et al. (2025) Assessment of the submandibular fossa depth and diameter of the mandibular canal via cone beam computed tomography: a comparative study. Maxillofacial plastic and reconstructive surgery, 47(1), 19.

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.

Sabari S, et al. (2025) Rapid ER remodeling induced by a peptide-lipid complex in dying tumor cells. Life science alliance, 8(6).

Pliushcheuskaya P, et al. (2025) Evaluation of Small-Molecule Binding Site Prediction Methods on Membrane-Embedded Protein Interfaces. Journal of chemical information and modeling, 65(13), 6949.

Dodson A, et al. (2025) A compendium of adipocyte morphologies across different breast pathologies. Adipocyte, 14(1), 2568540.

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.

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