Resource Summary Report

Generated by NIF on May 25, 2025

NNcon

RRID:SCR_014292
Type: Tool

Proper Citation

NNcon (RRID:SCR_014292)

Resource Information

URL: http://sysbio.rnet.missouri.edu/multicom_toolbox/NNCon%201.0.html

Proper Citation: NNcon (RRID:SCR_014292)

Description: Protein contact map prediction is useful for protein folding rate prediction, model selection and 3D structure prediction. Here we describe NNcon, a fast and reliable contact map prediction server and software. NNcon was ranked among the most accurate residue contact predictors in the Eighth Critical Assessment of Techniques for Protein Structure Prediction (CASP8), 2008.

Resource Type: prediction, software tool

Defining Citation: PMID:19420062

Keywords: text mining objective, bio.tools

Funding:

Resource Name: NNcon

Resource ID: SCR_014292

Alternate IDs: biotools:nncon

Alternate URLs: https://bio.tools/nncon

Old URLs: http://casp.rnet.missouri.edu/nncon.html

Record Creation Time: 20220129T080319+0000

Record Last Update: 20250525T031339+0000

Ratings and Alerts

No rating or validation information has been found for NNcon.

No alerts have been found for NNcon.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Cheng J, et al. (2012) The MULTICOM toolbox for protein structure prediction. BMC bioinformatics, 13, 65.

Deng X, et al. (2011) MSACompro: protein multiple sequence alignment using predicted secondary structure, solvent accessibility, and residue-residue contacts. BMC bioinformatics, 12, 472.