

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

MetaPSICOV

RRID:SCR_024517

Type: Tool

Proper Citation

MetaPSICOV (RRID:SCR_024517)

Resource Information

URL: <http://bioinf.cs.ucl.ac.uk/downloads/MetaPSICOV/>

Proper Citation: MetaPSICOV (RRID:SCR_024517)

Description: Software tool for accurate prediction of contacts and long range hydrogen bonding in proteins.

Resource Type: software resource, source code

Defining Citation: [PMID:25431331](#)

Keywords: accurate prediction, contacts and long range hydrogen bonding in proteins prediction,

Availability: Free, Available for download, Freely available

Resource Name: MetaPSICOV

Resource ID: SCR_024517

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260725T191441+0000

Ratings and Alerts

No rating or validation information has been found for MetaPSICOV.

No alerts have been found for MetaPSICOV.

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 [nidm-terms](#) .

Vural O, et al. (2025) Machine learning approaches for predicting protein-ligand binding sites from sequence data. Frontiers in bioinformatics, 5, 1520382.

Adhikari B, et al. (2020) A fully open-source framework for deep learning protein real-valued distances. Scientific reports, 10(1), 13374.