

# Resource Summary Report

Generated by [ASWG](#) on Aug 3, 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:** source code, software resource

**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:** 20260801T191301+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 [ASWG](#) .

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.