

# Resource Summary Report

Generated by [ASWG](#) on Aug 5, 2026

## MoRDa

RRID:SCR\_017278

Type: Tool

### Proper Citation

MoRDa (RRID:SCR\_017278)

### Resource Information

**URL:** <http://www.biomexsolutions.co.uk/morda>

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**Description:** Software package for molecular replacement protein structure solution using X-ray data. Includes database and set of programs for structure solution. Automatic molecular replacement pipeline.

**Synonyms:** Automatic Molecular Replacement Pipeline

**Resource Type:** data processing software, data analysis software, software resource, software application, software toolkit, database, data or information resource

**Defining Citation:** [DOI:10.1107/S2053273315099672](https://doi.org/10.1107/S2053273315099672)

**Keywords:** molecular, replacement, protein, structure, data, Xray, crystallography

**Availability:** Restricted

**Resource Name:** MoRDa

**Resource ID:** SCR\_017278

**Alternate URLs:** <https://ccp4serv7.rc-harwell.ac.uk/ccp4online/>

**Record Creation Time:** 20220129T080334+0000

**Record Last Update:** 20260805T044408+0000

### Ratings and Alerts

No rating or validation information has been found for MoRDa.

No alerts have been found for MoRDa.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Schmidt J, et al. (2021) Prediction of neo-epitope immunogenicity reveals TCR recognition determinants and provides insight into immunoediting. Cell reports. Medicine, 2(2), 100194.

Shi C, et al. (2021) Structural insights revealed by crystal structures of CYP76AH1 and CYP76AH1 in complex with its natural substrate. Biochemical and biophysical research communications, 582, 125.

Pak JS, et al. (2020) NELL2-Robo3 complex structure reveals mechanisms of receptor activation for axon guidance. Nature communications, 11(1), 1489.

Gu M, et al. (2019) Crystal structure of CYP76AH1 in 4-PI-bound state from Salvia miltiorrhiza. Biochemical and biophysical research communications, 511(4), 813.

Zak KM, et al. (2019) Crystal Structure of Kluyveromyces lactis Glucokinase (KlGlc1). International journal of molecular sciences, 20(19).

Kim YS, et al. (2018) Crystal structure of the natural anion-conducting channelrhodopsin GtACR1. Nature, 561(7723), 343.