# wwPDB Geometry-Only Validation Summary Report (i)

May 27, 2024 – 06:09 PM EDT

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|---|---|---|
| PDB ID | : | 5D97 |
| Title | : | Neutron crystal structure of H2O-solvent ribonuclease A |
| Authors | : | Chatake, T.; Fujiwara, S. |
| Deposited on | : | 2015-08-18 |
| Resolution | : | 1.80 Å(reported) |

This is a wwPDB Geometry-Only Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

| | | |
|---|---|---|
| MolProbity | : | FAILED |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36.2 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*NEUTRON DIFFRACTION*

The reported resolution of this entry is 1.80 Å.

There are no overall percentile quality scores available for this entry.

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

# 2 Model quality (i)

## 2.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

## 2.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

## 2.3 Torsion angles (i)

### 2.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

### 2.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

### 2.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

## 2.4 Non-standard residues in protein, DNA, RNA chains (i)

validation-pack failed to run properly - this section is therefore empty.

## 2.5 Carbohydrates (i)

validation-pack failed to run properly - this section is therefore empty.

## 2.6 Ligand geometry (i)

validation-pack failed to run properly - this section is therefore empty.

## 2.7 Other polymers (i)

validation-pack failed to run properly - this section is therefore empty.

## 2.8 Polymer linkage issues (i)

There are no chain breaks in this entry.