



## Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 07:38 PM UTC

PDB ID : 7KZQ / pdb\_00007kzq  
EMDB ID : EMD-23086  
Title : Structure of the human Fanconi anaemia Core-ID complex  
Authors : Wang, S.L.; Pavletich, N.P.  
Deposited on : 2020-12-10  
Resolution : 4.30 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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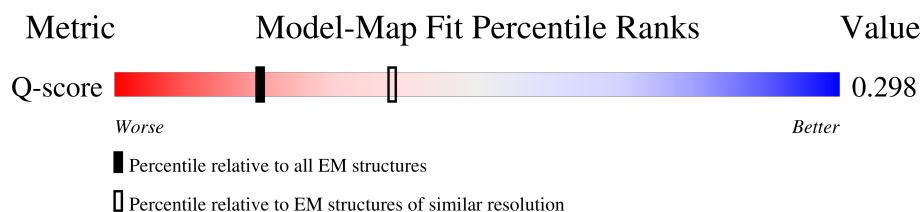
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132  
MolProbity : **FAILED**  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

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ELECTRON MICROSCOPY

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric  | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|---------|-----------------------------|----------------------------------------------------------|
| Q-score | 25397                       | 4585 ( 3.80 - 4.80 )                                     |

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 172709 atoms, of which 87163 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Fanconi anemia group A protein.

| Mol | Chain | Residues | Atoms |      |       |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|-------|------|------|----|---------|-------|
| 1   | A     | 1186     | Total | C    | H     | N    | O    | S  | 0       | 0     |
|     |       |          | 18889 | 6001 | 9487  | 1650 | 1692 | 59 |         |       |
| 1   | S     | 1250     | Total | C    | H     | N    | O    | S  | 0       | 0     |
|     |       |          | 19961 | 6345 | 10028 | 1747 | 1780 | 61 |         |       |

There are 44 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| A     | 1456    | ALA      | -      | expression tag | UNP O15360 |
| A     | 1457    | ALA      | -      | expression tag | UNP O15360 |
| A     | 1458    | ALA      | -      | expression tag | UNP O15360 |
| A     | 1459    | LYS      | -      | expression tag | UNP O15360 |
| A     | 1460    | LEU      | -      | expression tag | UNP O15360 |
| A     | 1461    | VAL      | -      | expression tag | UNP O15360 |
| A     | 1462    | ASP      | -      | expression tag | UNP O15360 |
| A     | 1463    | GLU      | -      | expression tag | UNP O15360 |
| A     | 1464    | ASP      | -      | expression tag | UNP O15360 |
| A     | 1465    | LEU      | -      | expression tag | UNP O15360 |
| A     | 1466    | TYR      | -      | expression tag | UNP O15360 |
| A     | 1467    | PHE      | -      | expression tag | UNP O15360 |
| A     | 1468    | GLN      | -      | expression tag | UNP O15360 |
| A     | 1469    | SER      | -      | expression tag | UNP O15360 |
| A     | 1470    | ASP      | -      | expression tag | UNP O15360 |
| A     | 1471    | TYR      | -      | expression tag | UNP O15360 |
| A     | 1472    | LYS      | -      | expression tag | UNP O15360 |
| A     | 1473    | ASP      | -      | expression tag | UNP O15360 |
| A     | 1474    | ASP      | -      | expression tag | UNP O15360 |
| A     | 1475    | ASP      | -      | expression tag | UNP O15360 |
| A     | 1476    | ASP      | -      | expression tag | UNP O15360 |
| A     | 1477    | LYS      | -      | expression tag | UNP O15360 |
| S     | 1456    | ALA      | -      | expression tag | UNP O15360 |
| S     | 1457    | ALA      | -      | expression tag | UNP O15360 |
| S     | 1458    | ALA      | -      | expression tag | UNP O15360 |
| S     | 1459    | LYS      | -      | expression tag | UNP O15360 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| S     | 1460    | LEU      | -      | expression tag | UNP O15360 |
| S     | 1461    | VAL      | -      | expression tag | UNP O15360 |
| S     | 1462    | ASP      | -      | expression tag | UNP O15360 |
| S     | 1463    | GLU      | -      | expression tag | UNP O15360 |
| S     | 1464    | ASP      | -      | expression tag | UNP O15360 |
| S     | 1465    | LEU      | -      | expression tag | UNP O15360 |
| S     | 1466    | TYR      | -      | expression tag | UNP O15360 |
| S     | 1467    | PHE      | -      | expression tag | UNP O15360 |
| S     | 1468    | GLN      | -      | expression tag | UNP O15360 |
| S     | 1469    | SER      | -      | expression tag | UNP O15360 |
| S     | 1470    | ASP      | -      | expression tag | UNP O15360 |
| S     | 1471    | TYR      | -      | expression tag | UNP O15360 |
| S     | 1472    | LYS      | -      | expression tag | UNP O15360 |
| S     | 1473    | ASP      | -      | expression tag | UNP O15360 |
| S     | 1474    | ASP      | -      | expression tag | UNP O15360 |
| S     | 1475    | ASP      | -      | expression tag | UNP O15360 |
| S     | 1476    | ASP      | -      | expression tag | UNP O15360 |
| S     | 1477    | LYS      | -      | expression tag | UNP O15360 |

- Molecule 2 is a protein called Fanconi anemia group B protein.

| Mol | Chain | Residues | Atoms |      |      |     |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|------|----|---------|-------|
| 2   | B     | 701      | Total | C    | H    | N   | O    | S  | 0       | 0     |
|     |       |          | 11395 | 3619 | 5790 | 934 | 1013 | 39 |         |       |
| 2   | O     | 699      | Total | C    | H    | N   | O    | S  | 0       | 0     |
|     |       |          | 11353 | 3622 | 5759 | 926 | 1010 | 36 |         |       |

There are 50 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| B     | -24     | MET      | -      | initiating methionine | UNP Q8NB91 |
| B     | -23     | ASP      | -      | expression tag        | UNP Q8NB91 |
| B     | -22     | TYR      | -      | expression tag        | UNP Q8NB91 |
| B     | -21     | LYS      | -      | expression tag        | UNP Q8NB91 |
| B     | -20     | ASP      | -      | expression tag        | UNP Q8NB91 |
| B     | -19     | ASP      | -      | expression tag        | UNP Q8NB91 |
| B     | -18     | ASP      | -      | expression tag        | UNP Q8NB91 |
| B     | -17     | ASP      | -      | expression tag        | UNP Q8NB91 |
| B     | -16     | LYS      | -      | expression tag        | UNP Q8NB91 |
| B     | -15     | GLU      | -      | expression tag        | UNP Q8NB91 |
| B     | -14     | ASN      | -      | expression tag        | UNP Q8NB91 |
| B     | -13     | LEU      | -      | expression tag        | UNP Q8NB91 |

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| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| B     | -12     | TYR      | -      | expression tag        | UNP Q8NB91 |
| B     | -11     | PHE      | -      | expression tag        | UNP Q8NB91 |
| B     | -10     | GLN      | -      | expression tag        | UNP Q8NB91 |
| B     | -9      | GLY      | -      | expression tag        | UNP Q8NB91 |
| B     | -8      | GLY      | -      | expression tag        | UNP Q8NB91 |
| B     | -7      | GLY      | -      | expression tag        | UNP Q8NB91 |
| B     | -6      | ARG      | -      | expression tag        | UNP Q8NB91 |
| B     | -5      | LYS      | -      | expression tag        | UNP Q8NB91 |
| B     | -4      | LEU      | -      | expression tag        | UNP Q8NB91 |
| B     | -3      | GLY      | -      | expression tag        | UNP Q8NB91 |
| B     | -2      | THR      | -      | expression tag        | UNP Q8NB91 |
| B     | -1      | GLY      | -      | expression tag        | UNP Q8NB91 |
| B     | 0       | SER      | -      | expression tag        | UNP Q8NB91 |
| O     | -24     | MET      | -      | initiating methionine | UNP Q8NB91 |
| O     | -23     | ASP      | -      | expression tag        | UNP Q8NB91 |
| O     | -22     | TYR      | -      | expression tag        | UNP Q8NB91 |
| O     | -21     | LYS      | -      | expression tag        | UNP Q8NB91 |
| O     | -20     | ASP      | -      | expression tag        | UNP Q8NB91 |
| O     | -19     | ASP      | -      | expression tag        | UNP Q8NB91 |
| O     | -18     | ASP      | -      | expression tag        | UNP Q8NB91 |
| O     | -17     | ASP      | -      | expression tag        | UNP Q8NB91 |
| O     | -16     | LYS      | -      | expression tag        | UNP Q8NB91 |
| O     | -15     | GLU      | -      | expression tag        | UNP Q8NB91 |
| O     | -14     | ASN      | -      | expression tag        | UNP Q8NB91 |
| O     | -13     | LEU      | -      | expression tag        | UNP Q8NB91 |
| O     | -12     | TYR      | -      | expression tag        | UNP Q8NB91 |
| O     | -11     | PHE      | -      | expression tag        | UNP Q8NB91 |
| O     | -10     | GLN      | -      | expression tag        | UNP Q8NB91 |
| O     | -9      | GLY      | -      | expression tag        | UNP Q8NB91 |
| O     | -8      | GLY      | -      | expression tag        | UNP Q8NB91 |
| O     | -7      | GLY      | -      | expression tag        | UNP Q8NB91 |
| O     | -6      | ARG      | -      | expression tag        | UNP Q8NB91 |
| O     | -5      | LYS      | -      | expression tag        | UNP Q8NB91 |
| O     | -4      | LEU      | -      | expression tag        | UNP Q8NB91 |
| O     | -3      | GLY      | -      | expression tag        | UNP Q8NB91 |
| O     | -2      | THR      | -      | expression tag        | UNP Q8NB91 |
| O     | -1      | GLY      | -      | expression tag        | UNP Q8NB91 |
| O     | 0       | SER      | -      | expression tag        | UNP Q8NB91 |

- Molecule 3 is a protein called Fanconi anemia group C protein.

| Mol | Chain | Residues | Atoms |      |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 3   | C     | 550      | Total | C    | H    | N   | O   | S  | 0       | 0     |
|     |       |          | 8838  | 2826 | 4442 | 749 | 791 | 30 |         |       |

There are 25 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| C     | -24     | MET      | -      | initiating methionine | UNP Q00597 |
| C     | -23     | ASP      | -      | expression tag        | UNP Q00597 |
| C     | -22     | TYR      | -      | expression tag        | UNP Q00597 |
| C     | -21     | LYS      | -      | expression tag        | UNP Q00597 |
| C     | -20     | ASP      | -      | expression tag        | UNP Q00597 |
| C     | -19     | ASP      | -      | expression tag        | UNP Q00597 |
| C     | -18     | ASP      | -      | expression tag        | UNP Q00597 |
| C     | -17     | ASP      | -      | expression tag        | UNP Q00597 |
| C     | -16     | LYS      | -      | expression tag        | UNP Q00597 |
| C     | -15     | GLU      | -      | expression tag        | UNP Q00597 |
| C     | -14     | ASN      | -      | expression tag        | UNP Q00597 |
| C     | -13     | LEU      | -      | expression tag        | UNP Q00597 |
| C     | -12     | TYR      | -      | expression tag        | UNP Q00597 |
| C     | -11     | PHE      | -      | expression tag        | UNP Q00597 |
| C     | -10     | GLN      | -      | expression tag        | UNP Q00597 |
| C     | -9      | GLY      | -      | expression tag        | UNP Q00597 |
| C     | -8      | GLY      | -      | expression tag        | UNP Q00597 |
| C     | -7      | GLY      | -      | expression tag        | UNP Q00597 |
| C     | -6      | ARG      | -      | expression tag        | UNP Q00597 |
| C     | -5      | LYS      | -      | expression tag        | UNP Q00597 |
| C     | -4      | LEU      | -      | expression tag        | UNP Q00597 |
| C     | -3      | GLY      | -      | expression tag        | UNP Q00597 |
| C     | -2      | THR      | -      | expression tag        | UNP Q00597 |
| C     | -1      | GLY      | -      | expression tag        | UNP Q00597 |
| C     | 0       | SER      | -      | expression tag        | UNP Q00597 |

- Molecule 4 is a protein called Fanconi anemia group E protein.

| Mol | Chain | Residues | Atoms |      |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 4   | E     | 419      | Total | C    | H    | N   | O   | S  | 0       | 0     |
|     |       |          | 6614  | 2048 | 3390 | 560 | 592 | 24 |         |       |

There are 19 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| E     | -18     | MET      | -      | initiating methionine | UNP Q9HB96 |
| E     | -17     | ASP      | -      | expression tag        | UNP Q9HB96 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| E     | -16     | TYR      | -      | expression tag | UNP Q9HB96 |
| E     | -15     | LYS      | -      | expression tag | UNP Q9HB96 |
| E     | -14     | ASP      | -      | expression tag | UNP Q9HB96 |
| E     | -13     | ASP      | -      | expression tag | UNP Q9HB96 |
| E     | -12     | ASP      | -      | expression tag | UNP Q9HB96 |
| E     | -11     | ASP      | -      | expression tag | UNP Q9HB96 |
| E     | -10     | LYS      | -      | expression tag | UNP Q9HB96 |
| E     | -9      | GLU      | -      | expression tag | UNP Q9HB96 |
| E     | -8      | ASN      | -      | expression tag | UNP Q9HB96 |
| E     | -7      | LEU      | -      | expression tag | UNP Q9HB96 |
| E     | -6      | TYR      | -      | expression tag | UNP Q9HB96 |
| E     | -5      | PHE      | -      | expression tag | UNP Q9HB96 |
| E     | -4      | GLN      | -      | expression tag | UNP Q9HB96 |
| E     | -3      | GLY      | -      | expression tag | UNP Q9HB96 |
| E     | -2      | GLY      | -      | expression tag | UNP Q9HB96 |
| E     | -1      | GLY      | -      | expression tag | UNP Q9HB96 |
| E     | 0       | ARG      | -      | expression tag | UNP Q9HB96 |

- Molecule 5 is a protein called Fanconi anemia group F protein.

| Mol | Chain | Residues | Atoms |      |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 5   | F     | 340      | Total | C    | H    | N   | O   | S | 0       | 0     |
|     |       |          | 5466  | 1730 | 2740 | 506 | 483 | 7 |         |       |

There are 25 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| F     | -24     | MET      | -      | initiating methionine | UNP Q9NPI8 |
| F     | -23     | ASP      | -      | expression tag        | UNP Q9NPI8 |
| F     | -22     | TYR      | -      | expression tag        | UNP Q9NPI8 |
| F     | -21     | LYS      | -      | expression tag        | UNP Q9NPI8 |
| F     | -20     | ASP      | -      | expression tag        | UNP Q9NPI8 |
| F     | -19     | ASP      | -      | expression tag        | UNP Q9NPI8 |
| F     | -18     | ASP      | -      | expression tag        | UNP Q9NPI8 |
| F     | -17     | ASP      | -      | expression tag        | UNP Q9NPI8 |
| F     | -16     | LYS      | -      | expression tag        | UNP Q9NPI8 |
| F     | -15     | GLU      | -      | expression tag        | UNP Q9NPI8 |
| F     | -14     | ASN      | -      | expression tag        | UNP Q9NPI8 |
| F     | -13     | LEU      | -      | expression tag        | UNP Q9NPI8 |
| F     | -12     | TYR      | -      | expression tag        | UNP Q9NPI8 |
| F     | -11     | PHE      | -      | expression tag        | UNP Q9NPI8 |
| F     | -10     | GLN      | -      | expression tag        | UNP Q9NPI8 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| F     | -9      | GLY      | -      | expression tag | UNP Q9NPI8 |
| F     | -8      | GLY      | -      | expression tag | UNP Q9NPI8 |
| F     | -7      | GLY      | -      | expression tag | UNP Q9NPI8 |
| F     | -6      | ARG      | -      | expression tag | UNP Q9NPI8 |
| F     | -5      | LYS      | -      | expression tag | UNP Q9NPI8 |
| F     | -4      | LEU      | -      | expression tag | UNP Q9NPI8 |
| F     | -3      | GLY      | -      | expression tag | UNP Q9NPI8 |
| F     | -2      | THR      | -      | expression tag | UNP Q9NPI8 |
| F     | -1      | GLY      | -      | expression tag | UNP Q9NPI8 |
| F     | 0       | SER      | -      | expression tag | UNP Q9NPI8 |

- Molecule 6 is a protein called Fanconi anemia group G protein.

| Mol | Chain | Residues | Atoms |      |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 6   | G     | 577      | Total | C    | H    | N   | O   | S  | 0       | 0     |
|     |       |          | 9020  | 2843 | 4537 | 778 | 844 | 18 |         |       |
| 6   | H     | 544      | Total | C    | H    | N   | O   | S  | 0       | 0     |
|     |       |          | 8504  | 2676 | 4288 | 734 | 790 | 16 |         |       |

There are 38 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| G     | -18     | MET      | -      | initiating methionine | UNP O15287 |
| G     | -17     | ASP      | -      | expression tag        | UNP O15287 |
| G     | -16     | TYR      | -      | expression tag        | UNP O15287 |
| G     | -15     | LYS      | -      | expression tag        | UNP O15287 |
| G     | -14     | ASP      | -      | expression tag        | UNP O15287 |
| G     | -13     | ASP      | -      | expression tag        | UNP O15287 |
| G     | -12     | ASP      | -      | expression tag        | UNP O15287 |
| G     | -11     | ASP      | -      | expression tag        | UNP O15287 |
| G     | -10     | LYS      | -      | expression tag        | UNP O15287 |
| G     | -9      | GLU      | -      | expression tag        | UNP O15287 |
| G     | -8      | ASN      | -      | expression tag        | UNP O15287 |
| G     | -7      | LEU      | -      | expression tag        | UNP O15287 |
| G     | -6      | TYR      | -      | expression tag        | UNP O15287 |
| G     | -5      | PHE      | -      | expression tag        | UNP O15287 |
| G     | -4      | GLN      | -      | expression tag        | UNP O15287 |
| G     | -3      | GLY      | -      | expression tag        | UNP O15287 |
| G     | -2      | GLY      | -      | expression tag        | UNP O15287 |
| G     | -1      | GLY      | -      | expression tag        | UNP O15287 |
| G     | 0       | ARG      | -      | expression tag        | UNP O15287 |
| H     | -18     | MET      | -      | initiating methionine | UNP O15287 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| H     | -17     | ASP      | -      | expression tag | UNP O15287 |
| H     | -16     | TYR      | -      | expression tag | UNP O15287 |
| H     | -15     | LYS      | -      | expression tag | UNP O15287 |
| H     | -14     | ASP      | -      | expression tag | UNP O15287 |
| H     | -13     | ASP      | -      | expression tag | UNP O15287 |
| H     | -12     | ASP      | -      | expression tag | UNP O15287 |
| H     | -11     | ASP      | -      | expression tag | UNP O15287 |
| H     | -10     | LYS      | -      | expression tag | UNP O15287 |
| H     | -9      | GLU      | -      | expression tag | UNP O15287 |
| H     | -8      | ASN      | -      | expression tag | UNP O15287 |
| H     | -7      | LEU      | -      | expression tag | UNP O15287 |
| H     | -6      | TYR      | -      | expression tag | UNP O15287 |
| H     | -5      | PHE      | -      | expression tag | UNP O15287 |
| H     | -4      | GLN      | -      | expression tag | UNP O15287 |
| H     | -3      | GLY      | -      | expression tag | UNP O15287 |
| H     | -2      | GLY      | -      | expression tag | UNP O15287 |
| H     | -1      | GLY      | -      | expression tag | UNP O15287 |
| H     | 0       | ARG      | -      | expression tag | UNP O15287 |

- Molecule 7 is a protein called E3 ubiquitin-protein ligase FANCL.

| Mol | Chain | Residues | Atoms |      |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 7   | L     | 370      | Total | C    | H    | N   | O   | S  | 0       | 0     |
|     |       |          | 5951  | 1914 | 2977 | 496 | 542 | 22 |         |       |
| 7   | M     | 370      | Total | C    | H    | N   | O   | S  | 0       | 0     |
|     |       |          | 5951  | 1914 | 2977 | 496 | 542 | 22 |         |       |

There are 38 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| L     | -18     | MET      | -      | initiating methionine | UNP Q9NW38 |
| L     | -17     | ASP      | -      | expression tag        | UNP Q9NW38 |
| L     | -16     | TYR      | -      | expression tag        | UNP Q9NW38 |
| L     | -15     | LYS      | -      | expression tag        | UNP Q9NW38 |
| L     | -14     | ASP      | -      | expression tag        | UNP Q9NW38 |
| L     | -13     | ASP      | -      | expression tag        | UNP Q9NW38 |
| L     | -12     | ASP      | -      | expression tag        | UNP Q9NW38 |
| L     | -11     | ASP      | -      | expression tag        | UNP Q9NW38 |
| L     | -10     | LYS      | -      | expression tag        | UNP Q9NW38 |
| L     | -9      | GLU      | -      | expression tag        | UNP Q9NW38 |
| L     | -8      | ASN      | -      | expression tag        | UNP Q9NW38 |
| L     | -7      | LEU      | -      | expression tag        | UNP Q9NW38 |

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| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| L     | -6      | TYR      | -      | expression tag        | UNP Q9NW38 |
| L     | -5      | PHE      | -      | expression tag        | UNP Q9NW38 |
| L     | -4      | GLN      | -      | expression tag        | UNP Q9NW38 |
| L     | -3      | GLY      | -      | expression tag        | UNP Q9NW38 |
| L     | -2      | GLY      | -      | expression tag        | UNP Q9NW38 |
| L     | -1      | GLY      | -      | expression tag        | UNP Q9NW38 |
| L     | 0       | ARG      | -      | expression tag        | UNP Q9NW38 |
| M     | -18     | MET      | -      | initiating methionine | UNP Q9NW38 |
| M     | -17     | ASP      | -      | expression tag        | UNP Q9NW38 |
| M     | -16     | TYR      | -      | expression tag        | UNP Q9NW38 |
| M     | -15     | LYS      | -      | expression tag        | UNP Q9NW38 |
| M     | -14     | ASP      | -      | expression tag        | UNP Q9NW38 |
| M     | -13     | ASP      | -      | expression tag        | UNP Q9NW38 |
| M     | -12     | ASP      | -      | expression tag        | UNP Q9NW38 |
| M     | -11     | ASP      | -      | expression tag        | UNP Q9NW38 |
| M     | -10     | LYS      | -      | expression tag        | UNP Q9NW38 |
| M     | -9      | GLU      | -      | expression tag        | UNP Q9NW38 |
| M     | -8      | ASN      | -      | expression tag        | UNP Q9NW38 |
| M     | -7      | LEU      | -      | expression tag        | UNP Q9NW38 |
| M     | -6      | TYR      | -      | expression tag        | UNP Q9NW38 |
| M     | -5      | PHE      | -      | expression tag        | UNP Q9NW38 |
| M     | -4      | GLN      | -      | expression tag        | UNP Q9NW38 |
| M     | -3      | GLY      | -      | expression tag        | UNP Q9NW38 |
| M     | -2      | GLY      | -      | expression tag        | UNP Q9NW38 |
| M     | -1      | GLY      | -      | expression tag        | UNP Q9NW38 |
| M     | 0       | ARG      | -      | expression tag        | UNP Q9NW38 |

- Molecule 8 is a protein called Fanconi anemia core complex-associated protein 100.

| Mol | Chain | Residues | Atoms |      |      |     |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|------|----|---------|-------|
| 8   | P     | 748      | Total | C    | H    | N   | O    | S  | 0       | 0     |
|     |       |          | 11279 | 3520 | 5681 | 972 | 1058 | 48 |         |       |
| 8   | Q     | 754      | Total | C    | H    | N   | O    | S  | 0       | 0     |
|     |       |          | 11355 | 3548 | 5724 | 978 | 1058 | 47 |         |       |

There are 50 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| P     | -24     | MET      | -      | initiating methionine | UNP Q0VG06 |
| P     | -23     | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -22     | TYR      | -      | expression tag        | UNP Q0VG06 |
| P     | -21     | LYS      | -      | expression tag        | UNP Q0VG06 |

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| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| P     | -20     | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -19     | HIS      | -      | expression tag        | UNP Q0VG06 |
| P     | -18     | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -17     | GLY      | -      | expression tag        | UNP Q0VG06 |
| P     | -16     | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -15     | TYR      | -      | expression tag        | UNP Q0VG06 |
| P     | -14     | LYS      | -      | expression tag        | UNP Q0VG06 |
| P     | -13     | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -12     | HIS      | -      | expression tag        | UNP Q0VG06 |
| P     | -11     | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -10     | ILE      | -      | expression tag        | UNP Q0VG06 |
| P     | -9      | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -8      | TYR      | -      | expression tag        | UNP Q0VG06 |
| P     | -7      | LYS      | -      | expression tag        | UNP Q0VG06 |
| P     | -6      | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -5      | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -4      | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -3      | ASP      | -      | expression tag        | UNP Q0VG06 |
| P     | -2      | LYS      | -      | expression tag        | UNP Q0VG06 |
| P     | -1      | GLY      | -      | expression tag        | UNP Q0VG06 |
| P     | 0       | SER      | -      | expression tag        | UNP Q0VG06 |
| Q     | -24     | MET      | -      | initiating methionine | UNP Q0VG06 |
| Q     | -23     | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -22     | TYR      | -      | expression tag        | UNP Q0VG06 |
| Q     | -21     | LYS      | -      | expression tag        | UNP Q0VG06 |
| Q     | -20     | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -19     | HIS      | -      | expression tag        | UNP Q0VG06 |
| Q     | -18     | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -17     | GLY      | -      | expression tag        | UNP Q0VG06 |
| Q     | -16     | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -15     | TYR      | -      | expression tag        | UNP Q0VG06 |
| Q     | -14     | LYS      | -      | expression tag        | UNP Q0VG06 |
| Q     | -13     | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -12     | HIS      | -      | expression tag        | UNP Q0VG06 |
| Q     | -11     | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -10     | ILE      | -      | expression tag        | UNP Q0VG06 |
| Q     | -9      | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -8      | TYR      | -      | expression tag        | UNP Q0VG06 |
| Q     | -7      | LYS      | -      | expression tag        | UNP Q0VG06 |
| Q     | -6      | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -5      | ASP      | -      | expression tag        | UNP Q0VG06 |
| Q     | -4      | ASP      | -      | expression tag        | UNP Q0VG06 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| Q     | -3      | ASP      | -      | expression tag | UNP Q0VG06 |
| Q     | -2      | LYS      | -      | expression tag | UNP Q0VG06 |
| Q     | -1      | GLY      | -      | expression tag | UNP Q0VG06 |
| Q     | 0       | SER      | -      | expression tag | UNP Q0VG06 |

- Molecule 9 is a protein called Fanconi anemia core complex-associated protein 20.

| Mol | Chain | Residues | Atoms |     |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| 9   | W     | 39       | Total | C   | H   | N  | O  | 0       | 0     |
|     |       |          | 513   | 179 | 242 | 42 | 50 |         |       |

- Molecule 10 is a protein called Fanconi anemia, complementation group I.

| Mol | Chain | Residues | Atoms |      |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|----|---------|-------|
| 10  | U     | 1168     | Total | C    | H    | N    | O    | S  | 0       | 0     |
|     |       |          | 18882 | 5933 | 9626 | 1549 | 1720 | 54 |         |       |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| U     | 877     | LEU      | ILE    | conflict | UNP B7ZMF2 |
| U     | 1235    | VAL      | ALA    | conflict | UNP B7ZMF2 |
| U     | 1274    | SER      | ASN    | conflict | UNP B7ZMF2 |

- Molecule 11 is a protein called Fanconi anemia group D2 protein.

| Mol | Chain | Residues | Atoms |      |      |      |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|------|----|---------|-------|
| 11  | V     | 1153     | Total | C    | H    | N    | O    | S  | 0       | 0     |
|     |       |          | 18733 | 5970 | 9475 | 1527 | 1709 | 52 |         |       |

- Molecule 12 is ZINC ION (CCD ID: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 12  | G     | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |
| 12  | L     | 2        | Total | Zn | 0       |
|     |       |          | 2     | 2  |         |
| 12  | M     | 2        | Total | Zn | 0       |
|     |       |          | 2     | 2  |         |

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

### 3 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 76111                                   | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | FEI TITAN KRIOS                         | Depositor |
| Voltage (kV)                         | 300                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 65                                      | Depositor |
| Minimum defocus (nm)                 | Not provided                            |           |
| Maximum defocus (nm)                 | Not provided                            |           |
| Magnification                        | Not provided                            |           |
| Image detector                       | GATAN K2 SUMMIT (4k x 4k)               | Depositor |
| Maximum map value                    | 0.071                                   | Depositor |
| Minimum map value                    | -0.039                                  | Depositor |
| Average map value                    | 0.000                                   | Depositor |
| Map value standard deviation         | 0.001                                   | Depositor |
| Recommended contour level            | 0.0055                                  | Depositor |
| Map size (Å)                         | 487.63455, 487.63455, 487.63455         | wwPDB     |
| Map dimensions                       | 448, 448, 448                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.08847, 1.08847, 1.08847               | Depositor |

## 4 Model quality [i](#)

### 4.1 Standard geometry [i](#)

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

### 4.2 Too-close contacts [i](#)

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

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

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

#### 4.3.2 Protein sidechains [i](#)

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

#### 4.3.3 RNA [i](#)

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

### 4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 4.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 4.7 Other polymers [i](#)

There are no such residues in this entry.

## 4.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 9   | W     | 2                |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1     | W     | 9:UNK     | C      | 73:GLU    | N      | 36.69        |
| 1     | W     | 95:TRP    | C      | 101:UNK   | N      | 7.00         |

## 5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23086. These allow visual inspection of the internal detail of the map and identification of artifacts.

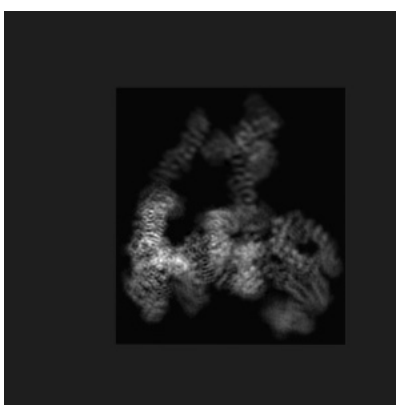
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 5.1 Orthogonal projections [i](#)

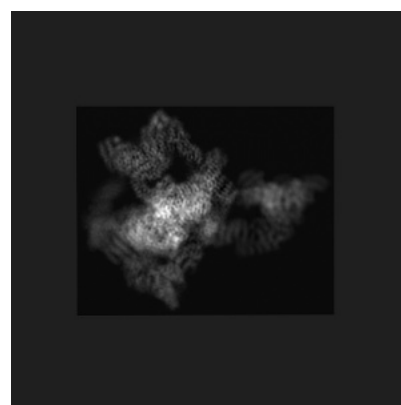
#### 5.1.1 Primary map



X



Y

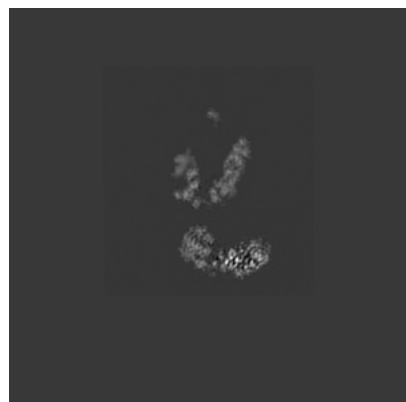


Z

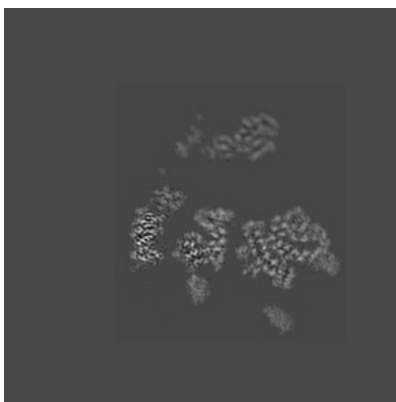
The images above show the map projected in three orthogonal directions.

### 5.2 Central slices [i](#)

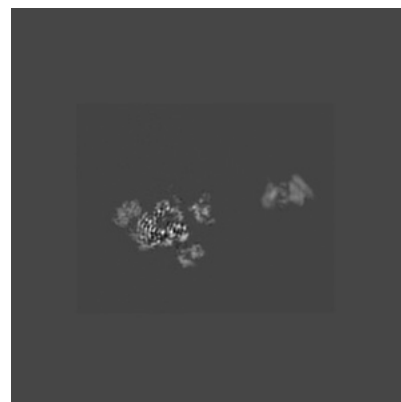
#### 5.2.1 Primary map



X Index: 224



Y Index: 224



Z Index: 224



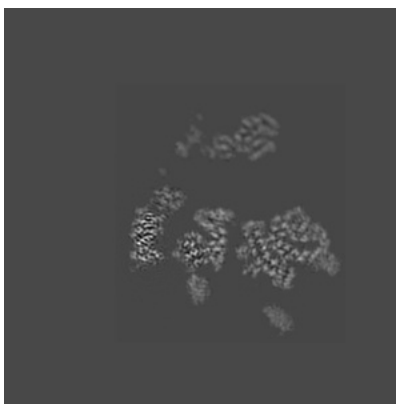
The images above show central slices of the map in three orthogonal directions.

## 5.3 Largest variance slices [i](#)

### 5.3.1 Primary map



X Index: 168



Y Index: 224

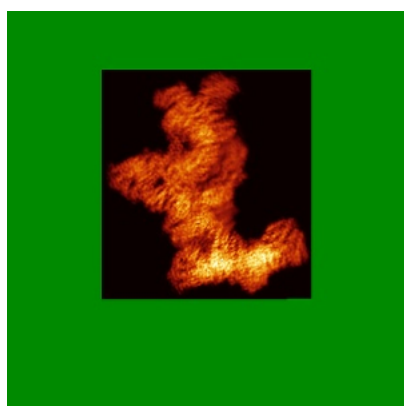


Z Index: 168

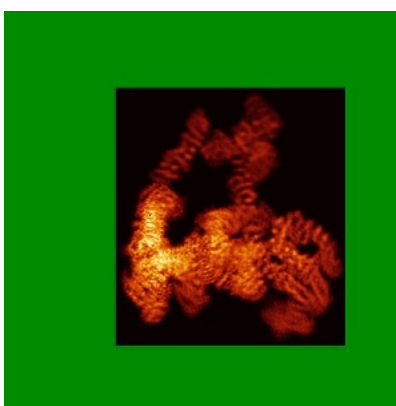
The images above show the largest variance slices of the map in three orthogonal directions.

## 5.4 Orthogonal standard-deviation projections (False-color) [i](#)

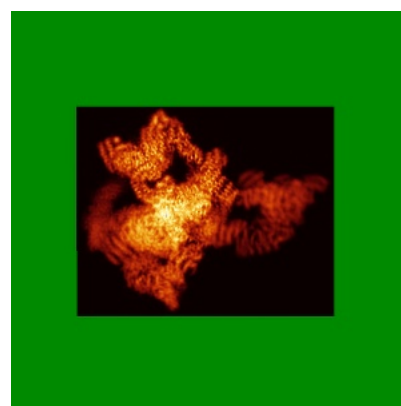
### 5.4.1 Primary map



X



Y

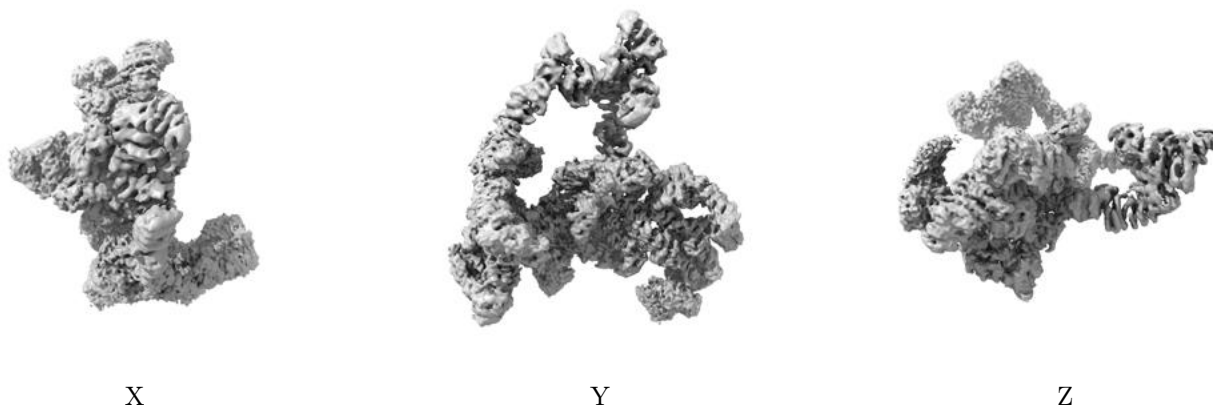


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 5.5 Orthogonal surface views [i](#)

### 5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

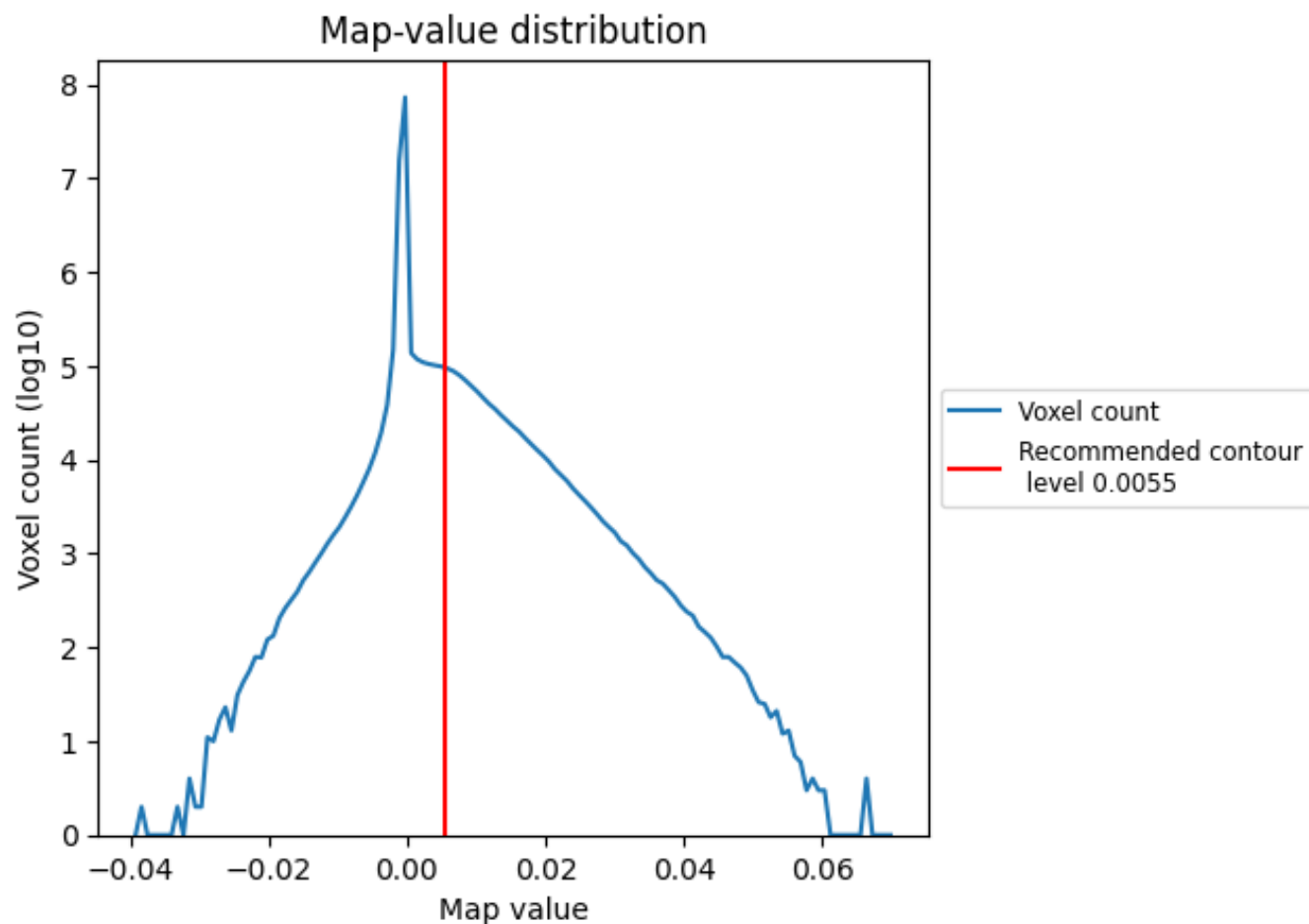
## 5.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 6 Map analysis [i](#)

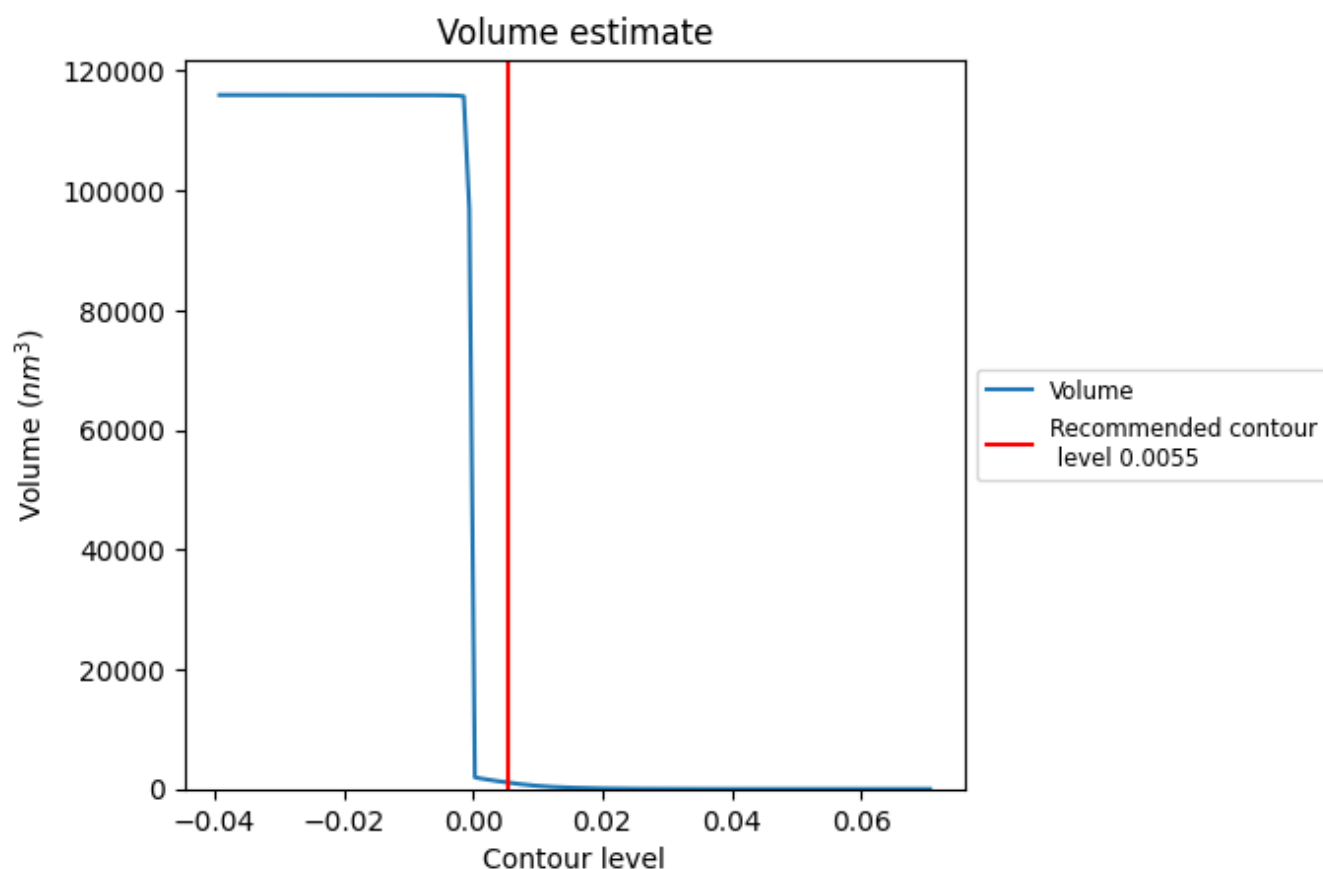
This section contains the results of statistical analysis of the map.

### 6.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

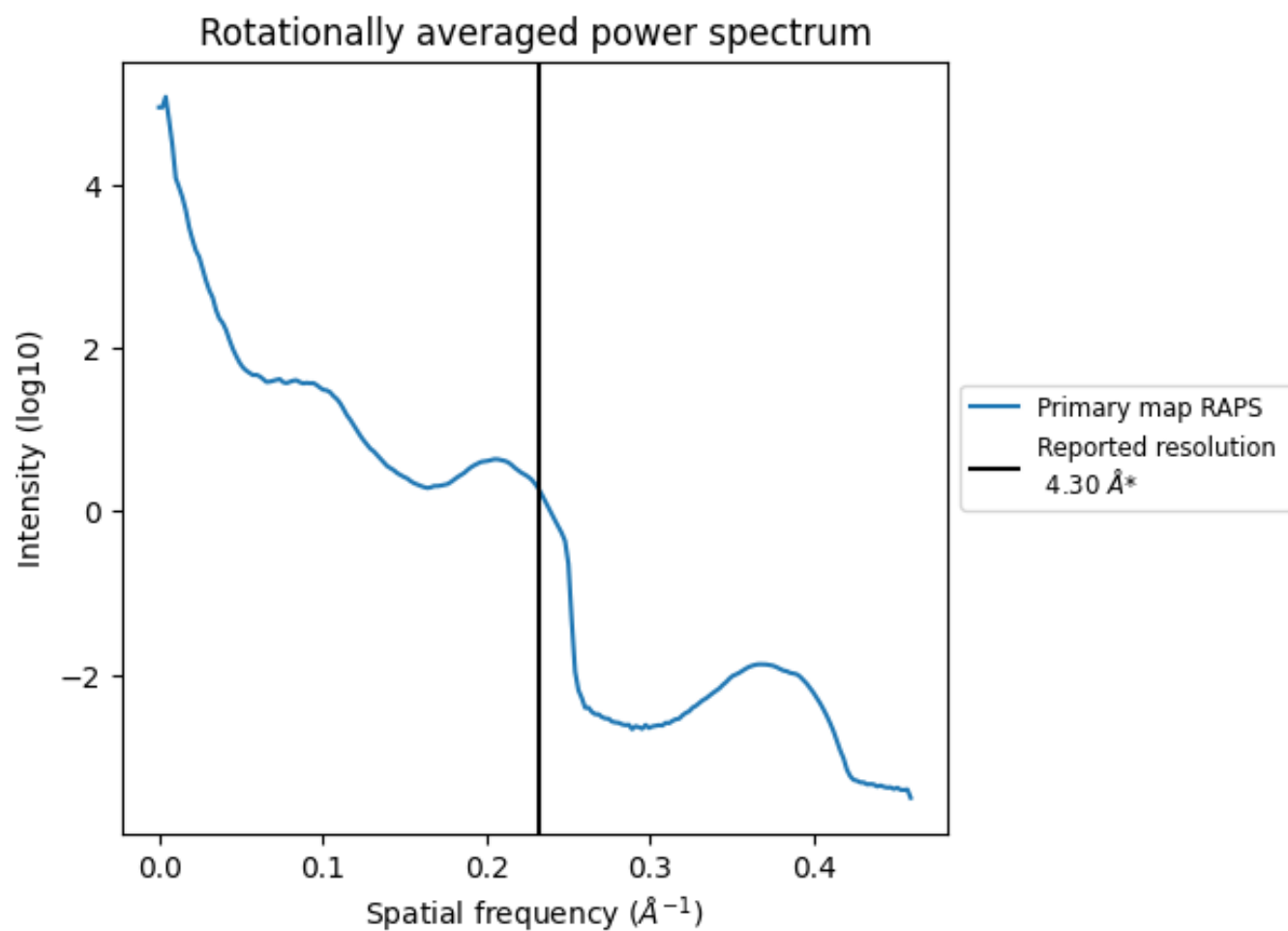
## 6.2 Volume estimate [i](#)



The volume at the recommended contour level is 1056 nm<sup>3</sup>; this corresponds to an approximate mass of 954 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 6.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.233 Å<sup>-1</sup>

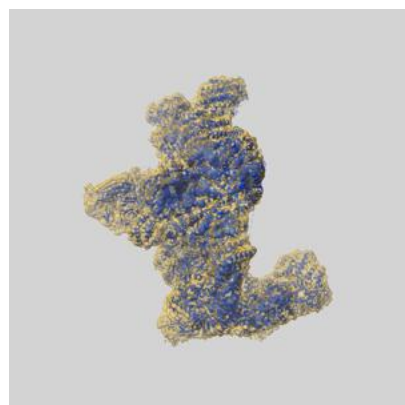
## 7 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

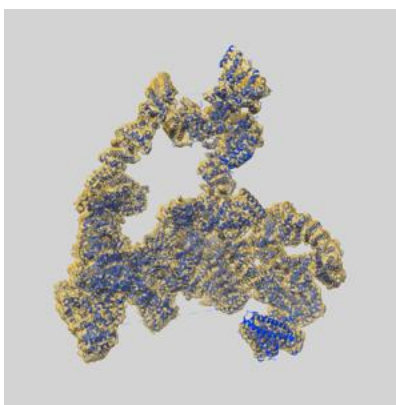
## 8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23086 and PDB model 7KZQ. Per-residue inclusion information can be found in section ?? on page ??.

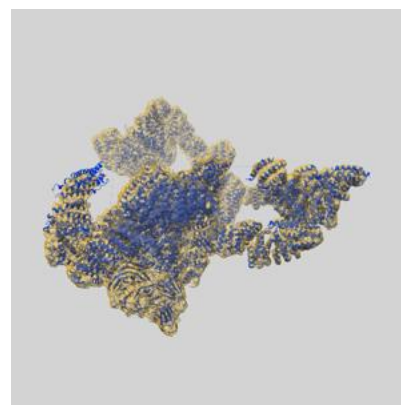
### 8.1 Map-model overlay [i](#)



X



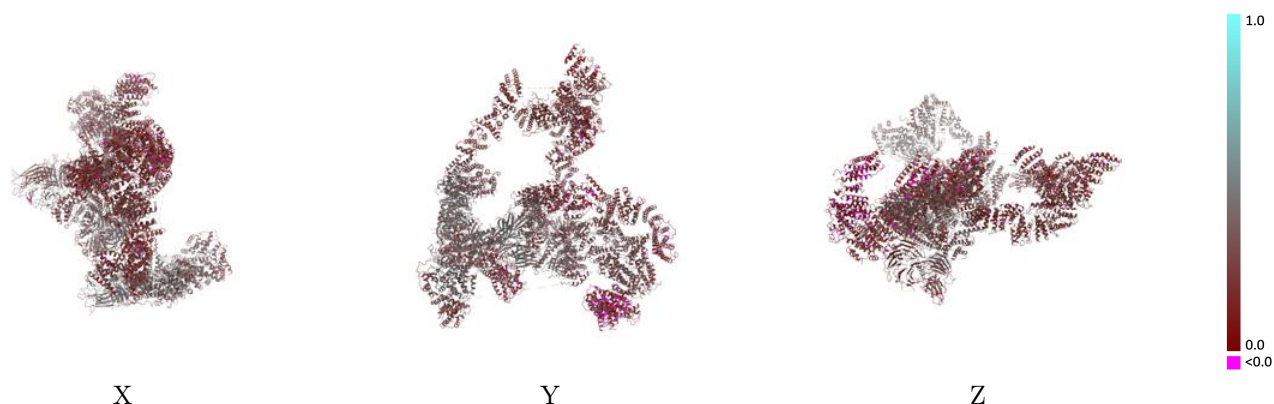
Y



Z

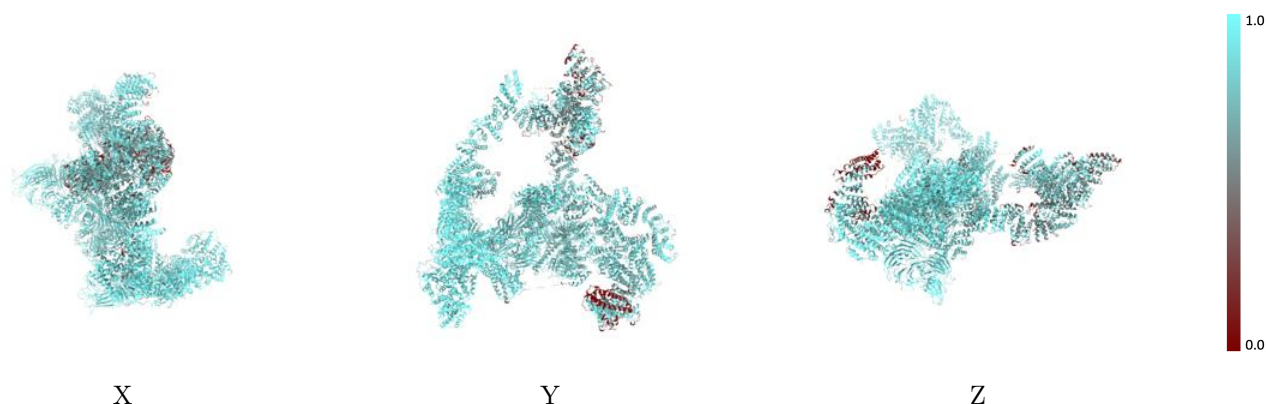
The images above show the 3D surface view of the map at the recommended contour level 0.0055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 8.2 Q-score mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

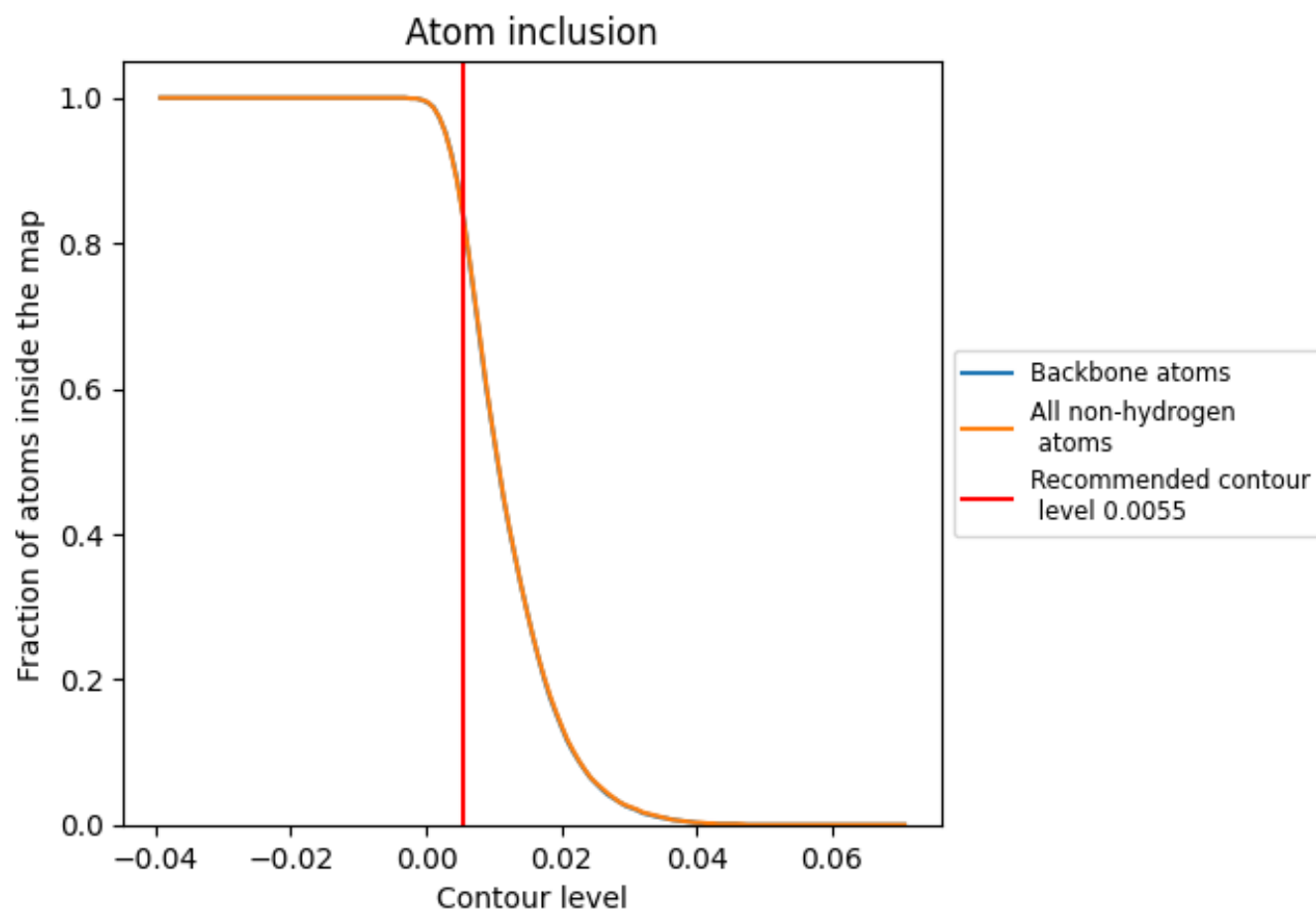
## 8.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0055).



## 8.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

## 8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0055) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.8360   |  0.2980   |
| A     |  0.7390   |  0.2360   |
| B     |  0.9210   |  0.3940   |
| C     |  0.9510   |  0.3710   |
| E     |  0.8730   |  0.3550   |
| F     |  0.9480   |  0.3640   |
| G     |  0.8810   |  0.3380   |
| H     |  0.8480   |  0.2740   |
| L     |  0.9370   |  0.3810   |
| M     |  0.9010   |  0.3080   |
| O     |  0.9100   |  0.3130   |
| P     |  0.9400   |  0.4100   |
| Q     |  0.9050   |  0.2980   |
| S     |  0.7160   |  0.2390   |
| U     |  0.8690  |  0.2570  |
| V     |  0.7190 |  0.2130 |
| W     |  0.7360 |  0.2920 |

