



# wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 02:50 pm GMT

PDB ID : 7O01  
EMDB ID : EMD-12672  
Title : Dimeric Photosystem I of a temperature sensitive mutant *Chlamydomonas reinhardtii*  
Authors : Caspy, I.; Nelson, N.  
Deposited on : 2021-03-25  
Resolution : 17.10 Å(reported)  
Based on initial model : 6JO5

This is a wwPDB EM Validation Summary 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.dev113  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

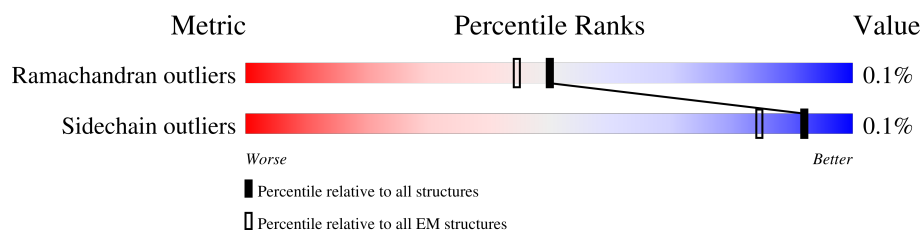
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 17.10 Å.

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.



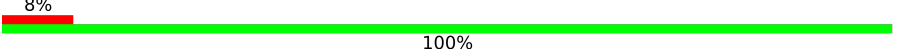
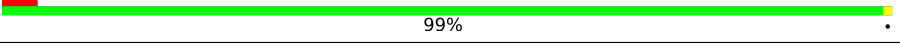
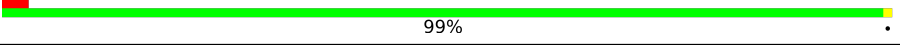


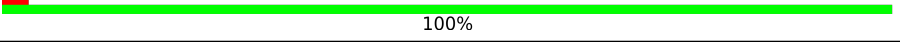
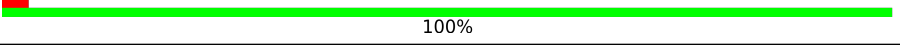
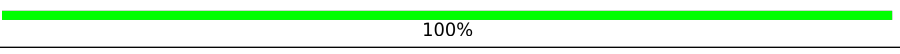
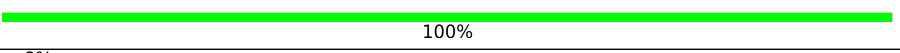
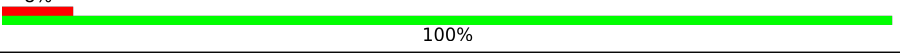
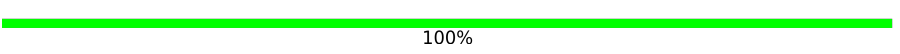


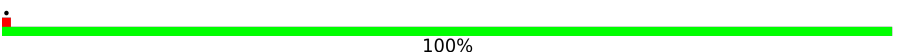

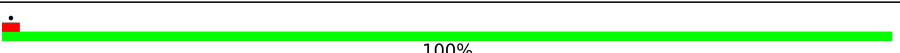
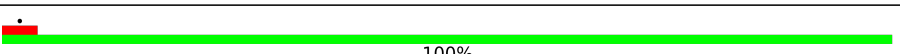
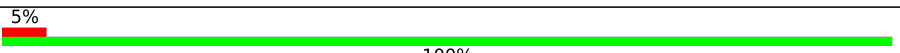
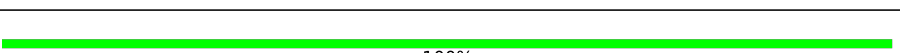
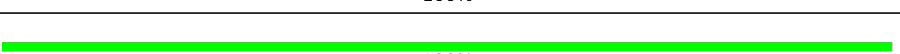
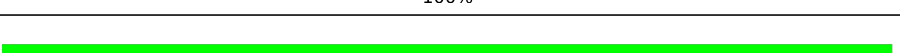
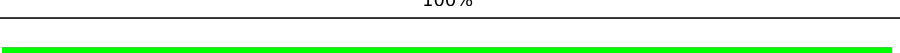
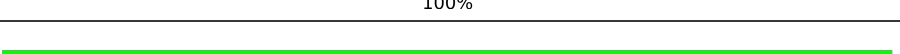
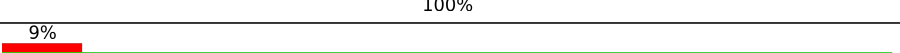
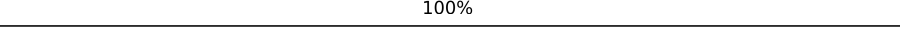
| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Ramachandran outliers | 207382                      | 16835                       |
| Sidechain outliers    | 206894                      | 16415                       |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | A     | 741    | 100%             |
| 1   | a     | 741    | 100%             |
| 2   | B     | 733    | 100%             |
| 2   | b     | 733    | 100%             |
| 3   | C     | 80     | 100%             |
| 3   | c     | 80     | 100%             |
| 4   | D     | 144    | 99% .            |
| 4   | d     | 144    | 99% .            |
| 5   | E     | 63     | 100%             |

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| Mol | Chain | Length | Quality of chain   |
|-----|-------|--------|--|
| 5   | e     | 63     |    |
| 6   | F     | 165    |    |
| 6   | f     | 165    |    |
| 7   | G     | 91     |    |
| 7   | g     | 91     |    |
| 8   | I     | 37     |    |
| 8   | i     | 37     |    |
| 9   | J     | 39     |    |
| 9   | j     | 39     |    |
| 10  | K     | 84     |    |
| 10  | k     | 84     |    |
| 11  | L     | 138    |   |
| 11  | l     | 138    |  |
| 12  | 1     | 194    |  |
| 12  | Z     | 194    |  |
| 12  | p     | 194    |  |
| 12  | z     | 194    |  |
| 13  | 3     | 219    |  |
| 13  | q     | 219    |  |
| 14  | 7     | 213    |  |
| 14  | r     | 213    |  |
| 15  | 8     | 217    |  |
| 15  | s     | 217    |  |
| 16  | 4     | 210    |  |
| 16  | t     | 210    |  |

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| Mol | Chain | Length | Quality of chain  |
|-----|-------|--------|---|
| 17  | 5     | 227    |  100% |
| 17  | u     | 227    |  100% |
| 18  | 6     | 229    |  100% |
| 18  | v     | 229    |  100% |
| 19  | 2     | 198    |  99%  |
| 20  | 9     | 183    |  99%  |

## 2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 64554 atoms, of which 0 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 Photosystem I P700 chlorophyll a apoprotein A1.

| Mol | Chain | Residues | Atoms |      |     |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|----|---------|-------|
| 1   | A     | 741      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5820  | 3805 | 993 | 1000 | 22 |         |       |
| 1   | a     | 741      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5820  | 3805 | 993 | 1000 | 22 |         |       |

- Molecule 2 is a protein called Photosystem I P700 chlorophyll a apoprotein A2.

| Mol | Chain | Residues | Atoms |      |     |      |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|----|---------|-------|
| 2   | B     | 733      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5825  | 3825 | 977 | 1005 | 18 |         |       |
| 2   | b     | 733      | Total | C    | N   | O    | S  | 0       | 0     |
|     |       |          | 5825  | 3825 | 977 | 1005 | 18 |         |       |

- Molecule 3 is a protein called Photosystem I iron-sulfur center.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 3   | C     | 80       | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 601   | 369 | 103 | 117 | 12 |         |       |
| 3   | c     | 80       | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 601   | 369 | 103 | 117 | 12 |         |       |

- Molecule 4 is a protein called Photosystem I reaction center subunit II, chloroplastic.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | D     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1135  | 725 | 201 | 202 | 7 |         |       |
| 4   | d     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1135  | 725 | 201 | 202 | 7 |         |       |

- Molecule 5 is a protein called Photosystem I reaction center subunit IV, chloroplastic.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 5   | E     | 63       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 497   | 316 | 87 | 94 |         |       |
| 5   | e     | 63       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 497   | 316 | 87 | 94 |         |       |

- Molecule 6 is a protein called Photosystem I reaction center subunit III, chloroplastic.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 6   | F     | 165      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1266  | 817 | 213 | 233 | 3 |         |       |
| 6   | f     | 165      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1266  | 817 | 213 | 233 | 3 |         |       |

- Molecule 7 is a protein called Photosystem I reaction center subunit V, chloroplastic.

| Mol | Chain | Residues | Atoms |     |    |     | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---------|-------|
| 7   | G     | 74       | Total | C   | N  | O   | 0       | 0     |
|     |       |          | 550   | 354 | 94 | 102 |         |       |
| 7   | g     | 74       | Total | C   | N  | O   | 0       | 0     |
|     |       |          | 550   | 354 | 94 | 102 |         |       |

- Molecule 8 is a protein called Photosystem I reaction center subunit VIII.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 8   | I     | 37       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 282   | 195 | 39 | 47 | 1 |         |       |
| 8   | i     | 37       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 282   | 195 | 39 | 47 | 1 |         |       |

- Molecule 9 is a protein called Photosystem I reaction center subunit IX.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 9   | J     | 39       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 321   | 219 | 45 | 56 | 1 |         |       |
| 9   | j     | 39       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 321   | 219 | 45 | 56 | 1 |         |       |

- Molecule 10 is a protein called Photosystem I reaction center subunit psaK, chloroplastic.

| Mol | Chain | Residues | Atoms |     |    |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---|---------|-------|
| 10  | K     | 84       | Total | C   | N  | O   | S | 0       | 0     |
|     |       |          | 571   | 362 | 98 | 109 | 2 |         |       |

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| Mol | Chain | Residues | Atoms |     |    |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---|---------|-------|
| 10  | k     | 84       | Total | C   | N  | O   | S | 0       | 0     |
|     |       |          | 571   | 362 | 98 | 109 | 2 |         |       |

- Molecule 11 is a protein called PSI subunit V.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11  | L     | 126      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 914   | 595 | 148 | 168 | 3 |         |       |
| 11  | l     | 126      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 914   | 595 | 148 | 168 | 3 |         |       |

- Molecule 12 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | 1     | 194      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1445  | 941 | 240 | 261 | 3 |         |       |
| 12  | Z     | 194      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1445  | 941 | 240 | 261 | 3 |         |       |
| 12  | p     | 194      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1445  | 941 | 240 | 261 | 3 |         |       |
| 12  | z     | 194      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1445  | 941 | 240 | 261 | 3 |         |       |

- Molecule 13 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 13  | 3     | 219      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1674  | 1092 | 270 | 304 | 8 |         |       |
| 13  | q     | 219      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1674  | 1092 | 270 | 304 | 8 |         |       |

- Molecule 14 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 14  | 7     | 213      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1650  | 1072 | 274 | 298 | 6 |         |       |
| 14  | r     | 213      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1650  | 1072 | 274 | 298 | 6 |         |       |

- Molecule 15 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 15  | 8     | 217      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1650  | 1073 | 280 | 293 | 4 |         |       |
| 15  | s     | 217      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1650  | 1073 | 280 | 293 | 4 |         |       |

- Molecule 16 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 16  | 4     | 210      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1628  | 1068 | 262 | 293 | 5 |         |       |
| 16  | t     | 210      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1628  | 1068 | 262 | 293 | 5 |         |       |

- Molecule 17 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 17  | 5     | 227      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1775  | 1154 | 297 | 316 | 8 |         |       |
| 17  | u     | 227      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1775  | 1154 | 297 | 316 | 8 |         |       |

- Molecule 18 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 18  | 6     | 229      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1766  | 1164 | 292 | 304 | 6 |         |       |
| 18  | v     | 229      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1766  | 1164 | 292 | 304 | 6 |         |       |

- Molecule 19 is a protein called Chlorophyll a-b binding protein, chloroplastic.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 19  | 2     | 198      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 1518  | 983 | 249 | 276 | 10 |         |       |

- Molecule 20 is a protein called Chlorophyll a-b binding protein, chloroplastic.

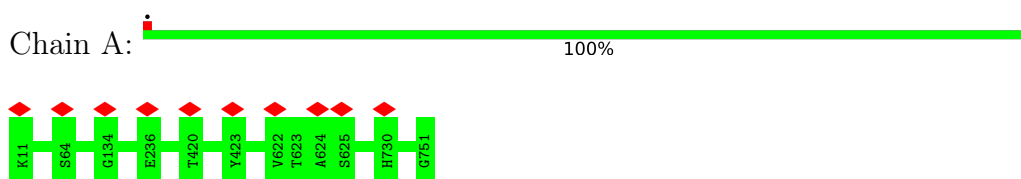
| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20  | 9     | 183      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1406  | 910 | 235 | 254 | 7 |         |       |



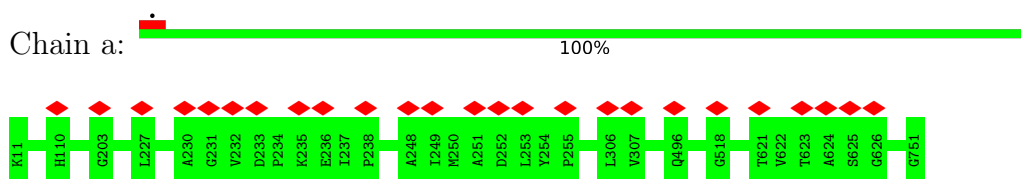
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

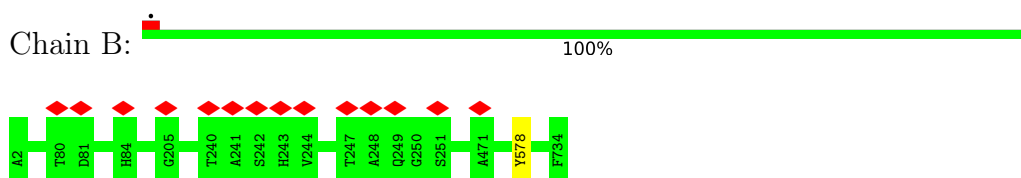
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



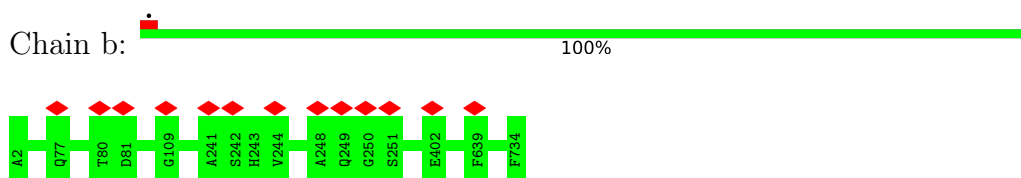
- Molecule 1: Photosystem I P700 chlorophyll a apoprotein A1



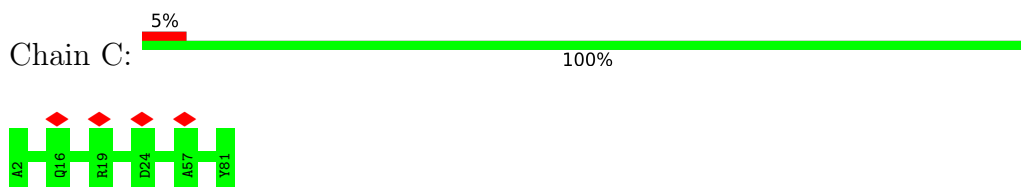
- Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2



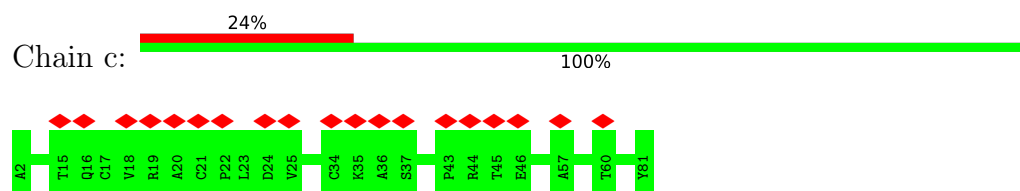
- Molecule 2: Photosystem I P700 chlorophyll a apoprotein A2



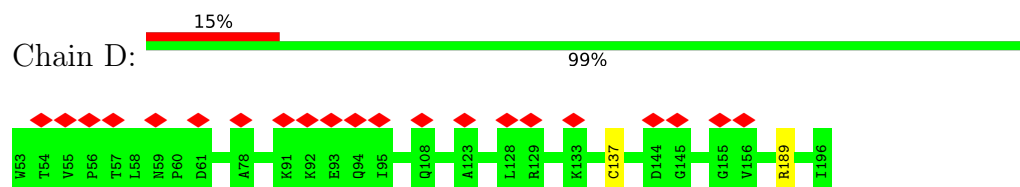
- Molecule 3: Photosystem I iron-sulfur center



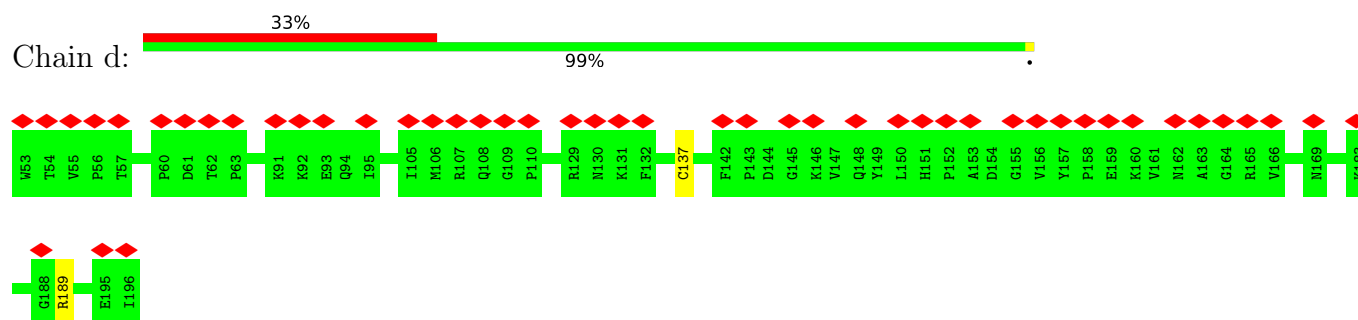
- Molecule 3: Photosystem I iron-sulfur center



- Molecule 4: Photosystem I reaction center subunit II, chloroplastic



- Molecule 4: Photosystem I reaction center subunit II, chloroplastic

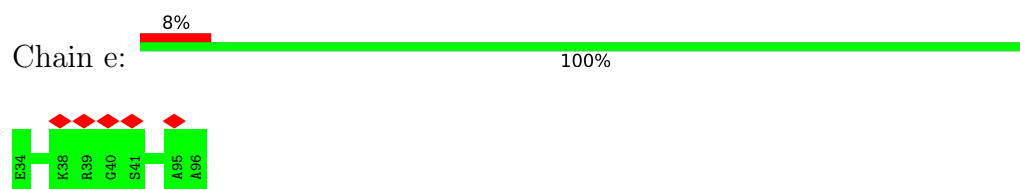


- Molecule 5: Photosystem I reaction center subunit IV, chloroplastic

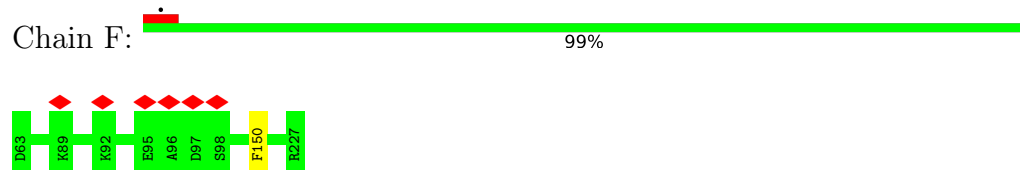


There are no outlier residues recorded for this chain.

- Molecule 5: Photosystem I reaction center subunit IV, chloroplastic

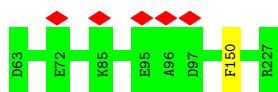


- Molecule 6: Photosystem I reaction center subunit III, chloroplastic



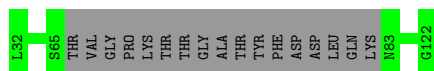
- Molecule 6: Photosystem I reaction center subunit III, chloroplastic





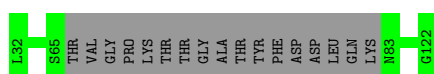
- Molecule 7: Photosystem I reaction center subunit V, chloroplastic

Chain G: 81% 19%



- Molecule 7: Photosystem I reaction center subunit V, chloroplastic

Chain g: 81% 19%



- Molecule 8: Photosystem I reaction center subunit VIII

Chain I: 100%



- Molecule 8: Photosystem I reaction center subunit VIII

Chain i: 100%



- Molecule 9: Photosystem I reaction center subunit IX

Chain J: 100%

There are no outlier residues recorded for this chain.

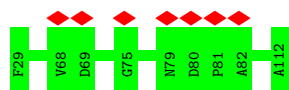
- Molecule 9: Photosystem I reaction center subunit IX

Chain j: 100%

There are no outlier residues recorded for this chain.

- Molecule 10: Photosystem I reaction center subunit psaK, chloroplastic

Chain K: 8% 100%



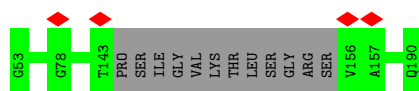
- Molecule 10: Photosystem I reaction center subunit psaK, chloroplastic

Chain k: 100%

There are no outlier residues recorded for this chain.

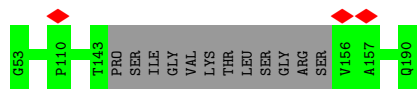
- Molecule 11: PSI subunit V

Chain L: 91% 9%



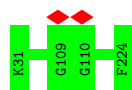
- Molecule 11: PSI subunit V

Chain l: 91% 9%



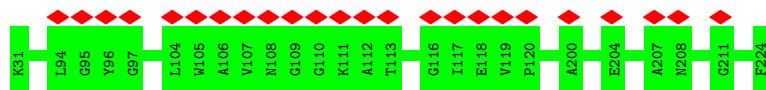
- Molecule 12: Chlorophyll a-b binding protein, chloroplastic

Chain 1: 100%



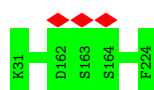
- Molecule 12: Chlorophyll a-b binding protein, chloroplastic

Chain Z: 12% 100%



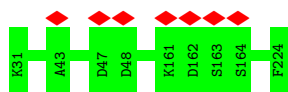
- Molecule 12: Chlorophyll a-b binding protein, chloroplastic

Chain p: 100%

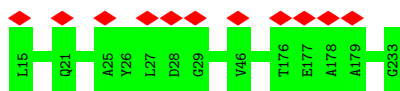


- Molecule 12: Chlorophyll a-b binding protein, chloroplastic

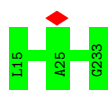
Chain z: 100%



- Molecule 13: Chlorophyll a-b binding protein, chloroplastic



- Molecule 13: Chlorophyll a-b binding protein, chloroplastic



- Molecule 14: Chlorophyll a-b binding protein, chloroplastic



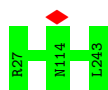
There are no outlier residues recorded for this chain.

- Molecule 14: Chlorophyll a-b binding protein, chloroplastic

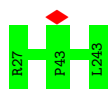


There are no outlier residues recorded for this chain.

- Molecule 15: Chlorophyll a-b binding protein, chloroplastic

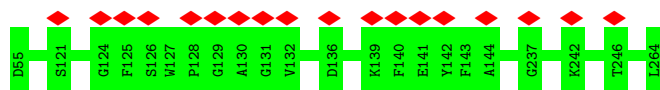


- Molecule 15: Chlorophyll a-b binding protein, chloroplastic



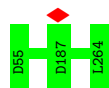
- Molecule 16: Chlorophyll a-b binding protein, chloroplastic





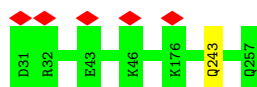
- Molecule 16: Chlorophyll a-b binding protein, chloroplastic

Chain t: 100%



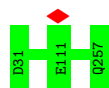
- Molecule 17: Chlorophyll a-b binding protein, chloroplastic

Chain 5: 100%



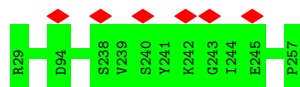
- Molecule 17: Chlorophyll a-b binding protein, chloroplastic

Chain u: 100%



- Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 6: 100%



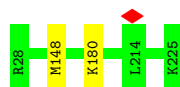
- Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain v: 100%

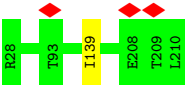


- Molecule 19: Chlorophyll a-b binding protein, chloroplastic

Chain 2: 99%



- Molecule 20: Chlorophyll a-b binding protein, chloroplastic



## 4 Experimental information

| Property                             | Value                           | Source    |
|--------------------------------------|---------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                 | Depositor |
| Imposed symmetry                     | POINT, Not provided             |           |
| Number of particles used             | 5707                            | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF               | Depositor |
| CTF correction method                | NONE                            | Depositor |
| Microscope                           | FEI TITAN KRIOS                 | Depositor |
| Voltage (kV)                         | 300                             | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 46.8                            | Depositor |
| Minimum defocus (nm)                 | Not provided                    |           |
| Maximum defocus (nm)                 | Not provided                    |           |
| Magnification                        | 165000                          | Depositor |
| Image detector                       | GATAN K3 BIOQUANTUM (6k x 4k)   | Depositor |
| Maximum map value                    | 0.094                           | Depositor |
| Minimum map value                    | -0.034                          | Depositor |
| Average map value                    | 0.001                           | Depositor |
| Map value standard deviation         | 0.008                           | Depositor |
| Recommended contour level            | 0.011                           | Depositor |
| Map size ( $\text{\AA}$ )            | 496.19998, 496.19998, 496.19998 | wwPDB     |
| Map dimensions                       | 200, 200, 200                   | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0                | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 2.481, 2.481, 2.481             | Depositor |



## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: SNC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths |               | Bond angles |             |
|-----|-------|--------------|---------------|-------------|-------------|
|     |       | RMSZ         | $\# Z  > 5$   | RMSZ        | $\# Z  > 5$ |
| 1   | A     | 0.31         | 0/6016        | 0.51        | 0/8201      |
| 1   | a     | 0.32         | 0/6016        | 0.52        | 0/8201      |
| 2   | B     | 0.33         | 1/6037 (0.0%) | 0.53        | 0/8242      |
| 2   | b     | 0.32         | 0/6037        | 0.53        | 0/8242      |
| 3   | C     | 0.27         | 0/611         | 0.56        | 0/826       |
| 3   | c     | 0.29         | 0/611         | 0.59        | 0/826       |
| 4   | D     | 0.28         | 0/1154        | 0.56        | 0/1556      |
| 4   | d     | 0.31         | 0/1154        | 0.57        | 0/1556      |
| 5   | E     | 0.28         | 0/507         | 0.50        | 0/689       |
| 5   | e     | 0.31         | 0/507         | 0.52        | 0/689       |
| 6   | F     | 0.29         | 0/1292        | 0.51        | 0/1747      |
| 6   | f     | 0.32         | 0/1292        | 0.54        | 0/1747      |
| 7   | G     | 0.28         | 0/561         | 0.48        | 0/760       |
| 7   | g     | 0.28         | 0/561         | 0.48        | 0/760       |
| 8   | I     | 0.33         | 0/294         | 0.55        | 0/406       |
| 8   | i     | 0.31         | 0/294         | 0.52        | 0/406       |
| 9   | J     | 0.29         | 0/332         | 0.46        | 0/454       |
| 9   | j     | 0.34         | 0/332         | 0.52        | 0/454       |
| 10  | K     | 0.26         | 0/576         | 0.46        | 0/779       |
| 10  | k     | 0.29         | 0/576         | 0.50        | 0/779       |
| 11  | L     | 0.29         | 0/935         | 0.50        | 0/1277      |
| 11  | l     | 0.29         | 0/935         | 0.50        | 0/1277      |
| 12  | 1     | 0.28         | 0/1491        | 0.45        | 0/2028      |
| 12  | Z     | 0.27         | 0/1491        | 0.44        | 0/2028      |
| 12  | p     | 0.30         | 0/1491        | 0.48        | 0/2028      |
| 12  | z     | 0.28         | 0/1491        | 0.46        | 0/2028      |
| 13  | 3     | 0.31         | 0/1722        | 0.51        | 0/2336      |
| 13  | q     | 0.32         | 0/1722        | 0.51        | 0/2336      |
| 14  | 7     | 0.29         | 0/1702        | 0.49        | 0/2310      |
| 14  | r     | 0.31         | 0/1702        | 0.48        | 0/2310      |
| 15  | 8     | 0.28         | 0/1701        | 0.45        | 0/2315      |
| 15  | s     | 0.30         | 0/1701        | 0.47        | 0/2315      |

| Mol | Chain | Bond lengths |                | Bond angles |         |
|-----|-------|--------------|----------------|-------------|---------|
|     |       | RMSZ         | # Z  >5        | RMSZ        | # Z  >5 |
| 16  | 4     | 0.28         | 0/1683         | 0.48        | 0/2296  |
| 16  | t     | 0.30         | 0/1683         | 0.50        | 0/2296  |
| 17  | 5     | 0.28         | 0/1830         | 0.47        | 0/2492  |
| 17  | u     | 0.30         | 0/1830         | 0.49        | 0/2492  |
| 18  | 6     | 0.27         | 0/1828         | 0.48        | 0/2497  |
| 18  | v     | 0.30         | 0/1828         | 0.50        | 0/2497  |
| 19  | 2     | 0.28         | 0/1556         | 0.53        | 0/2109  |
| 20  | 9     | 0.30         | 0/1447         | 0.54        | 0/1967  |
| All | All   | 0.30         | 1/66529 (0.0%) | 0.51        | 0/90554 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms   | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 2   | B     | 578 | TYR  | CD1-CE1 | -5.09 | 1.31        | 1.39     |

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

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

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed       | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|----------------|-----------|---------|----------|-------------|-----|
| 1   | A     | 739/741 (100%) | 720 (97%) | 19 (3%) | 0        | 100         | 100 |
| 1   | a     | 739/741 (100%) | 717 (97%) | 22 (3%) | 0        | 100         | 100 |
| 2   | B     | 731/733 (100%) | 707 (97%) | 24 (3%) | 0        | 100         | 100 |
| 2   | b     | 731/733 (100%) | 706 (97%) | 25 (3%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 3   | C     | 78/80 (98%)   | 75 (96%)  | 3 (4%)  | 0        | 100         | 100 |
| 3   | c     | 78/80 (98%)   | 76 (97%)  | 2 (3%)  | 0        | 100         | 100 |
| 4   | D     | 141/144 (98%) | 135 (96%) | 6 (4%)  | 0        | 100         | 100 |
| 4   | d     | 141/144 (98%) | 136 (96%) | 5 (4%)  | 0        | 100         | 100 |
| 5   | E     | 61/63 (97%)   | 57 (93%)  | 4 (7%)  | 0        | 100         | 100 |
| 5   | e     | 61/63 (97%)   | 57 (93%)  | 4 (7%)  | 0        | 100         | 100 |
| 6   | F     | 163/165 (99%) | 158 (97%) | 4 (2%)  | 1 (1%)   | 22          | 60  |
| 6   | f     | 163/165 (99%) | 157 (96%) | 5 (3%)  | 1 (1%)   | 22          | 60  |
| 7   | G     | 70/91 (77%)   | 70 (100%) | 0       | 0        | 100         | 100 |
| 7   | g     | 70/91 (77%)   | 70 (100%) | 0       | 0        | 100         | 100 |
| 8   | I     | 35/37 (95%)   | 34 (97%)  | 1 (3%)  | 0        | 100         | 100 |
| 8   | i     | 35/37 (95%)   | 34 (97%)  | 1 (3%)  | 0        | 100         | 100 |
| 9   | J     | 37/39 (95%)   | 36 (97%)  | 1 (3%)  | 0        | 100         | 100 |
| 9   | j     | 37/39 (95%)   | 36 (97%)  | 1 (3%)  | 0        | 100         | 100 |
| 10  | K     | 82/84 (98%)   | 81 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 10  | k     | 82/84 (98%)   | 80 (98%)  | 2 (2%)  | 0        | 100         | 100 |
| 11  | L     | 122/138 (88%) | 119 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 11  | l     | 122/138 (88%) | 119 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 12  | 1     | 192/194 (99%) | 185 (96%) | 7 (4%)  | 0        | 100         | 100 |
| 12  | Z     | 192/194 (99%) | 187 (97%) | 5 (3%)  | 0        | 100         | 100 |
| 12  | p     | 192/194 (99%) | 182 (95%) | 10 (5%) | 0        | 100         | 100 |
| 12  | z     | 192/194 (99%) | 189 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 13  | 3     | 217/219 (99%) | 209 (96%) | 8 (4%)  | 0        | 100         | 100 |
| 13  | q     | 217/219 (99%) | 209 (96%) | 8 (4%)  | 0        | 100         | 100 |
| 14  | 7     | 211/213 (99%) | 203 (96%) | 8 (4%)  | 0        | 100         | 100 |
| 14  | r     | 211/213 (99%) | 205 (97%) | 6 (3%)  | 0        | 100         | 100 |
| 15  | 8     | 215/217 (99%) | 210 (98%) | 5 (2%)  | 0        | 100         | 100 |
| 15  | s     | 215/217 (99%) | 208 (97%) | 7 (3%)  | 0        | 100         | 100 |
| 16  | 4     | 208/210 (99%) | 199 (96%) | 9 (4%)  | 0        | 100         | 100 |
| 16  | t     | 208/210 (99%) | 198 (95%) | 10 (5%) | 0        | 100         | 100 |
| 17  | 5     | 225/227 (99%) | 221 (98%) | 3 (1%)  | 1 (0%)   | 30          | 68  |

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| Mol | Chain | Analysed        | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 17  | u     | 225/227 (99%)   | 221 (98%)  | 4 (2%)   | 0        | 100         | 100 |
| 18  | 6     | 227/229 (99%)   | 223 (98%)  | 4 (2%)   | 0        | 100         | 100 |
| 18  | v     | 227/229 (99%)   | 222 (98%)  | 5 (2%)   | 0        | 100         | 100 |
| 19  | 2     | 196/198 (99%)   | 187 (95%)  | 8 (4%)   | 1 (0%)   | 25          | 64  |
| 20  | 9     | 181/183 (99%)   | 170 (94%)  | 10 (6%)  | 1 (1%)   | 22          | 60  |
| All | All   | 8269/8417 (98%) | 8008 (97%) | 256 (3%) | 5 (0%)   | 50          | 83  |

All (5) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6   | F     | 150 | PHE  |
| 6   | f     | 150 | PHE  |
| 17  | 5     | 243 | GLN  |
| 19  | 2     | 180 | LYS  |
| 20  | 9     | 139 | ILE  |

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed       | Rotameric  | Outliers | Percentiles |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 1   | A     | 601/601 (100%) | 601 (100%) | 0        | 100         | 100 |
| 1   | a     | 601/601 (100%) | 601 (100%) | 0        | 100         | 100 |
| 2   | B     | 596/596 (100%) | 596 (100%) | 0        | 100         | 100 |
| 2   | b     | 596/596 (100%) | 596 (100%) | 0        | 100         | 100 |
| 3   | C     | 69/69 (100%)   | 69 (100%)  | 0        | 100         | 100 |
| 3   | c     | 69/69 (100%)   | 69 (100%)  | 0        | 100         | 100 |
| 4   | D     | 120/120 (100%) | 119 (99%)  | 1 (1%)   | 79          | 85  |
| 4   | d     | 120/120 (100%) | 119 (99%)  | 1 (1%)   | 79          | 85  |
| 5   | E     | 54/54 (100%)   | 54 (100%)  | 0        | 100         | 100 |
| 5   | e     | 54/54 (100%)   | 54 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Rotameric   | Outliers | Percentiles |     |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 6   | F     | 127/127 (100%)  | 127 (100%)  | 0        | 100         | 100 |
| 6   | f     | 127/127 (100%)  | 127 (100%)  | 0        | 100         | 100 |
| 7   | G     | 54/68 (79%)     | 54 (100%)   | 0        | 100         | 100 |
| 7   | g     | 54/68 (79%)     | 54 (100%)   | 0        | 100         | 100 |
| 8   | I     | 31/31 (100%)    | 31 (100%)   | 0        | 100         | 100 |
| 8   | i     | 31/31 (100%)    | 31 (100%)   | 0        | 100         | 100 |
| 9   | J     | 35/35 (100%)    | 35 (100%)   | 0        | 100         | 100 |
| 9   | j     | 35/35 (100%)    | 35 (100%)   | 0        | 100         | 100 |
| 10  | K     | 58/58 (100%)    | 58 (100%)   | 0        | 100         | 100 |
| 10  | k     | 58/58 (100%)    | 58 (100%)   | 0        | 100         | 100 |
| 11  | L     | 92/102 (90%)    | 92 (100%)   | 0        | 100         | 100 |
| 11  | l     | 92/102 (90%)    | 92 (100%)   | 0        | 100         | 100 |
| 12  | 1     | 137/137 (100%)  | 137 (100%)  | 0        | 100         | 100 |
| 12  | Z     | 137/137 (100%)  | 137 (100%)  | 0        | 100         | 100 |
| 12  | p     | 137/137 (100%)  | 137 (100%)  | 0        | 100         | 100 |
| 12  | z     | 137/137 (100%)  | 137 (100%)  | 0        | 100         | 100 |
| 13  | 3     | 167/167 (100%)  | 167 (100%)  | 0        | 100         | 100 |
| 13  | q     | 167/167 (100%)  | 167 (100%)  | 0        | 100         | 100 |
| 14  | 7     | 164/164 (100%)  | 164 (100%)  | 0        | 100         | 100 |
| 14  | r     | 164/164 (100%)  | 164 (100%)  | 0        | 100         | 100 |
| 15  | 8     | 163/163 (100%)  | 163 (100%)  | 0        | 100         | 100 |
| 15  | s     | 163/163 (100%)  | 163 (100%)  | 0        | 100         | 100 |
| 16  | 4     | 164/165 (99%)   | 164 (100%)  | 0        | 100         | 100 |
| 16  | t     | 164/165 (99%)   | 164 (100%)  | 0        | 100         | 100 |
| 17  | 5     | 184/184 (100%)  | 184 (100%)  | 0        | 100         | 100 |
| 17  | u     | 184/184 (100%)  | 184 (100%)  | 0        | 100         | 100 |
| 18  | 6     | 183/183 (100%)  | 183 (100%)  | 0        | 100         | 100 |
| 18  | v     | 183/183 (100%)  | 182 (100%)  | 1 (0%)   | 86          | 89  |
| 19  | 2     | 154/156 (99%)   | 153 (99%)   | 1 (1%)   | 84          | 88  |
| 20  | 9     | 141/141 (100%)  | 141 (100%)  | 0        | 100         | 100 |
| All | All   | 6567/6619 (99%) | 6563 (100%) | 4 (0%)   | 92          | 95  |

All (4) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 4   | D     | 189 | ARG  |
| 19  | 2     | 148 | MET  |
| 4   | d     | 189 | ARG  |
| 18  | v     | 133 | ARG  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | B     | 453 | GLN  |
| 1   | a     | 539 | HIS  |
| 12  | p     | 52  | ASN  |

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths |      |             | Bond angles |      |             |
|-----|------|-------|-----|------|--------------|------|-------------|-------------|------|-------------|
|     |      |       |     |      | Counts       | RMSZ | $\# Z  > 2$ | Counts      | RMSZ | $\# Z  > 2$ |
| 4   | SNC  | D     | 137 | 4    | 4,7,8        | 1.07 | 0           | 1,7,9       | 3.62 | 1 (100%)    |
| 4   | SNC  | d     | 137 | 4    | 4,7,8        | 1.00 | 0           | 1,7,9       | 3.26 | 1 (100%)    |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------|-------|
| 4   | SNC  | D     | 137 | 4    | -       | 0/0/6/8  | -     |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------|-------|
| 4   | SNC  | d     | 137 | 4    | -       | 0/0/6/8  | -     |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 4   | D     | 137 | SNC  | CA-CB-SG | -3.62 | 105.24      | 112.76   |
| 4   | d     | 137 | SNC  | CA-CB-SG | -3.26 | 105.97      | 112.76   |

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

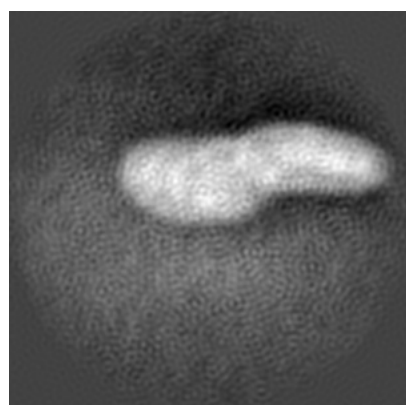
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12672. These allow visual inspection of the internal detail of the map and identification of artifacts.

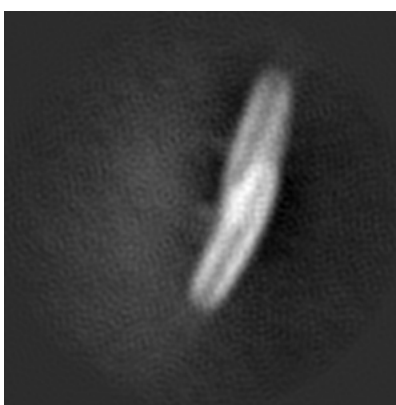
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

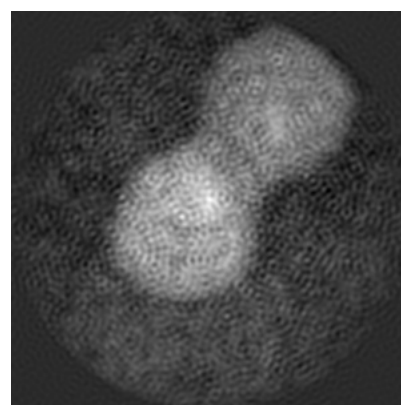
#### 6.1.1 Primary map



X



Y

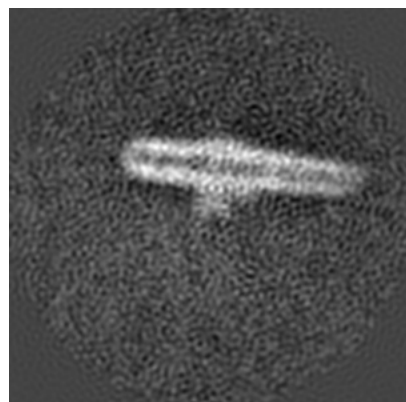


Z

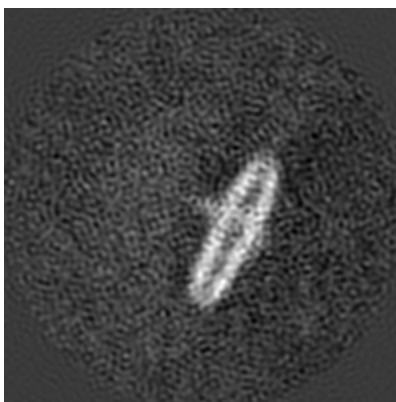
The images above show the map projected in three orthogonal directions.

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

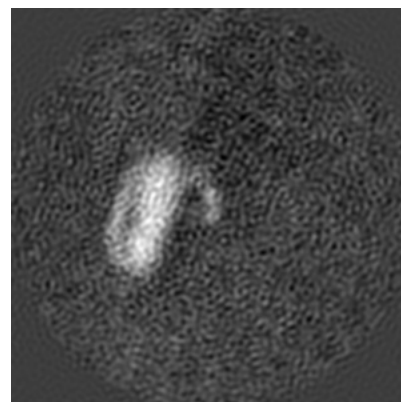
#### 6.2.1 Primary map



X Index: 100



Y Index: 100



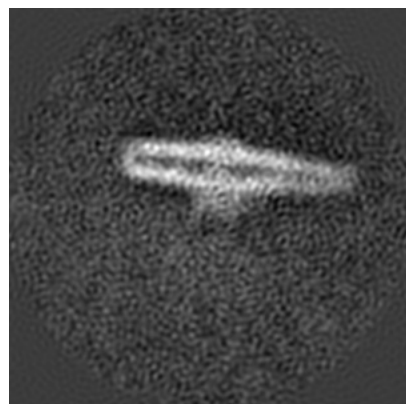
Z Index: 100



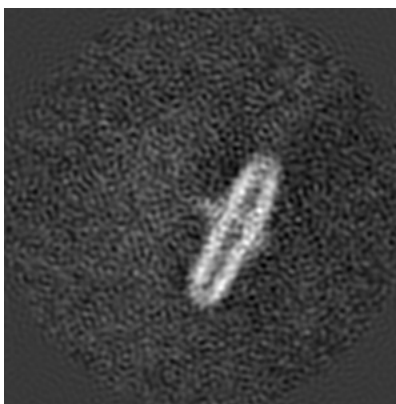
The images above show central slices of the map in three orthogonal directions.

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

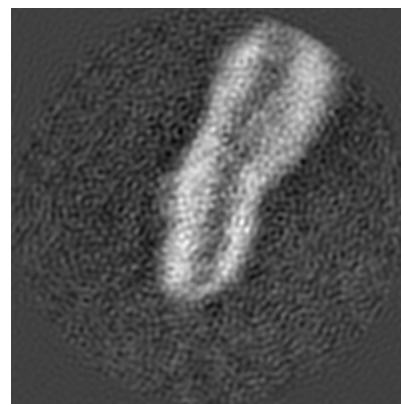
### 6.3.1 Primary map



X Index: 98



Y Index: 99

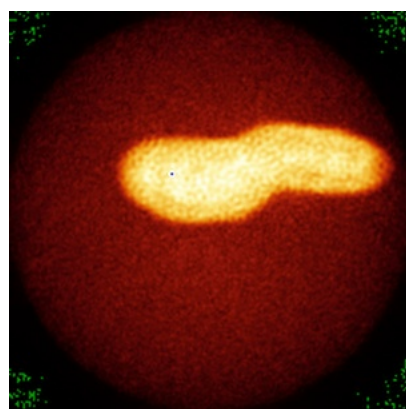


Z Index: 123

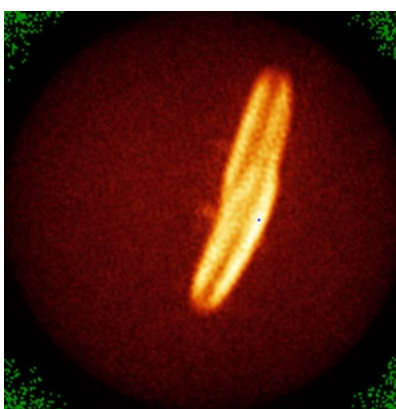
The images above show the largest variance slices of the map in three orthogonal directions.

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

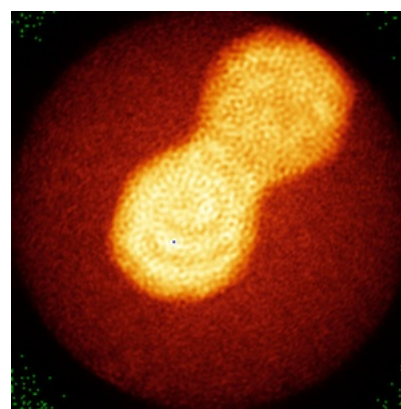
### 6.4.1 Primary map



X



Y

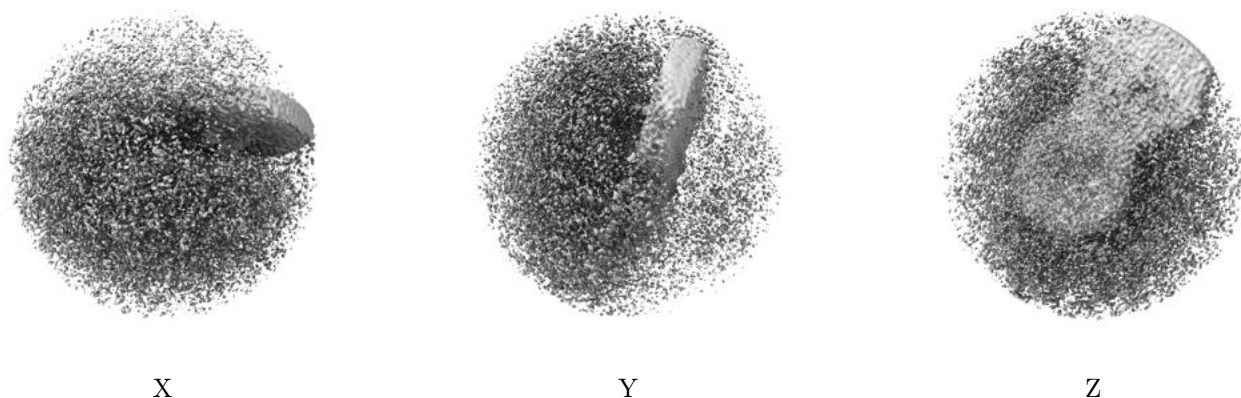


Z

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.

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

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

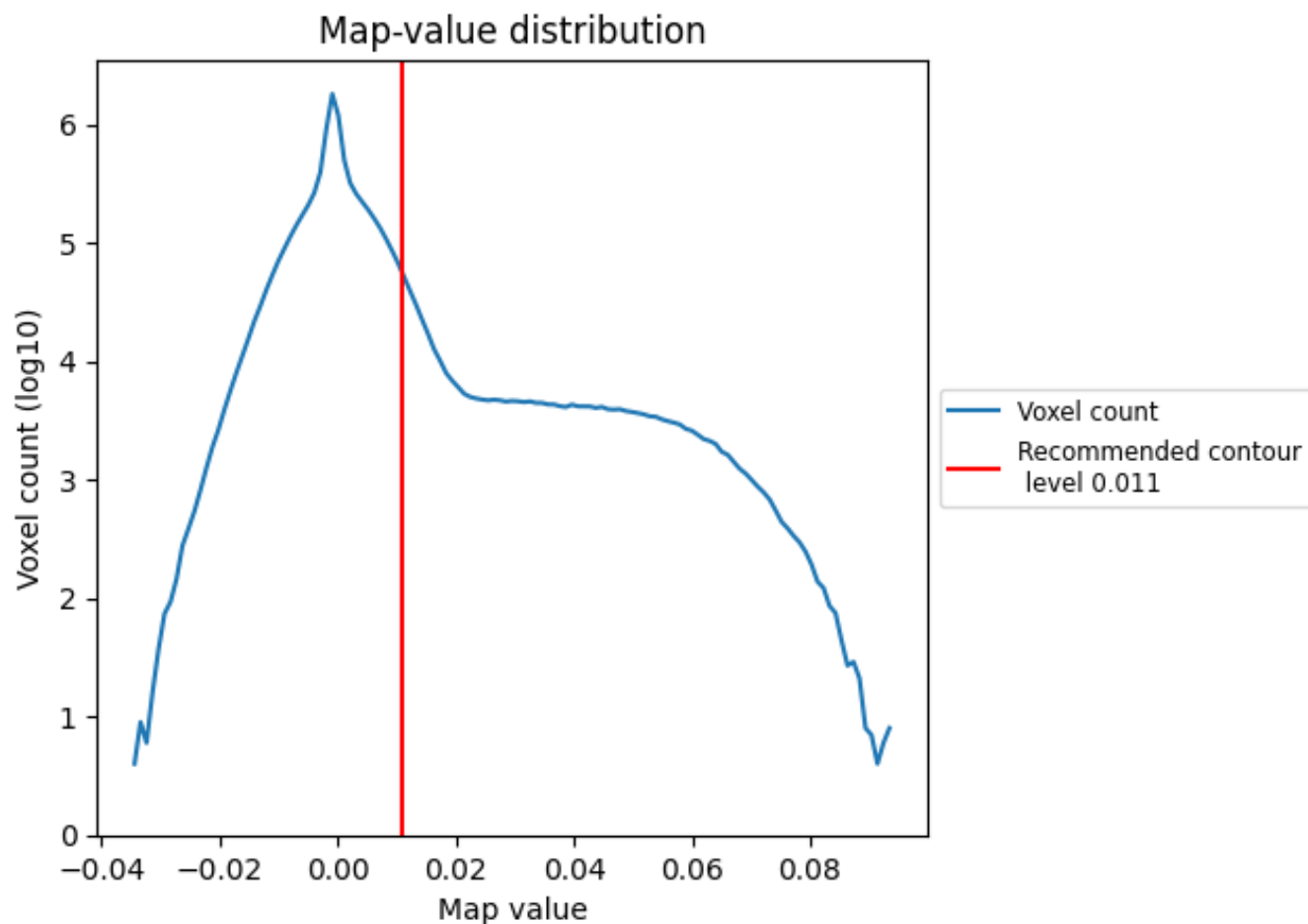
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

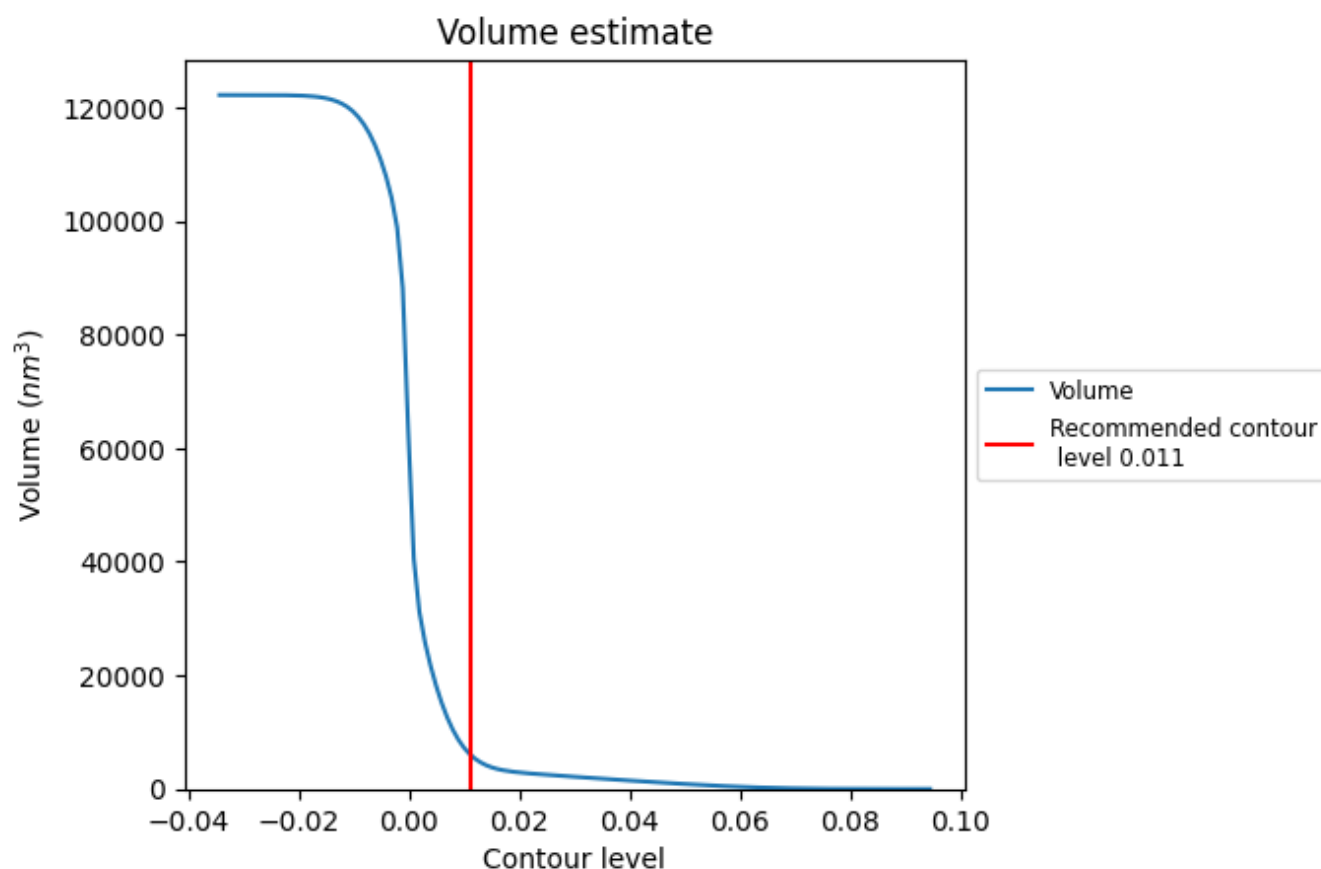
This section contains the results of statistical analysis of the map.

### 7.1 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.

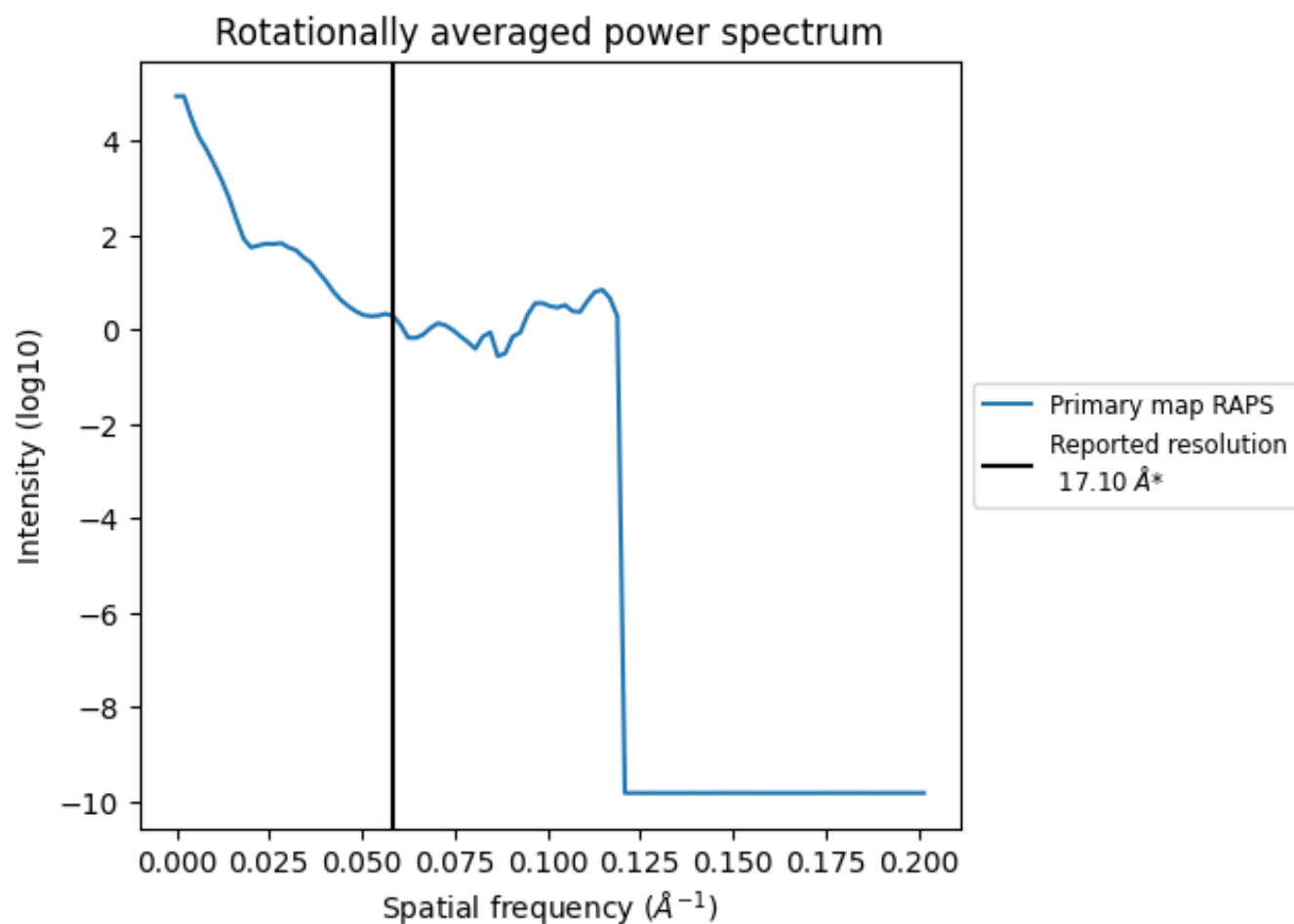
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6120  $\text{nm}^3$ ; this corresponds to an approximate mass of 5529 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.

### 7.3 Rotationally averaged power spectrum ⓘ

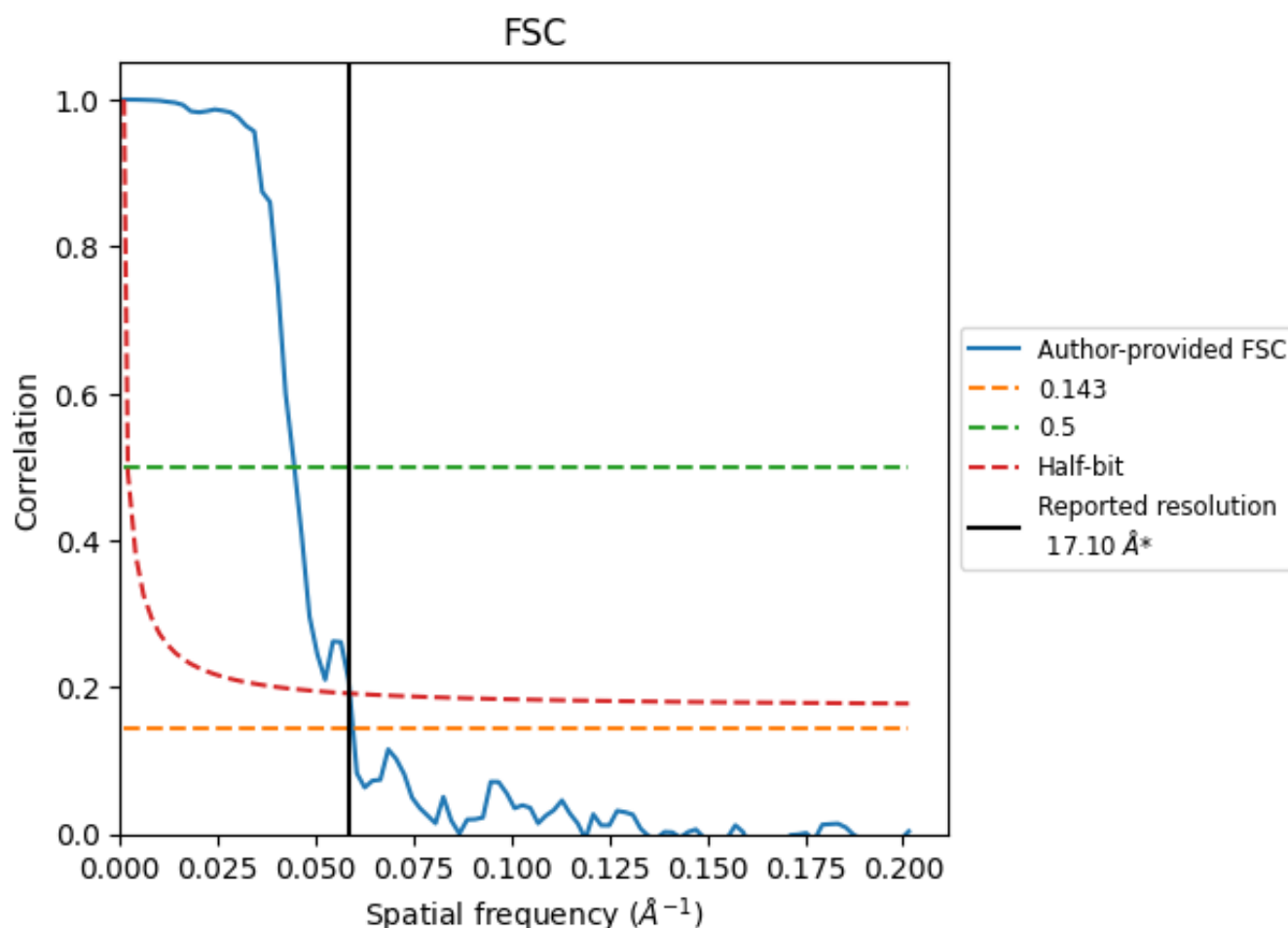


\*Reported resolution corresponds to spatial frequency of 0.058 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.058 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

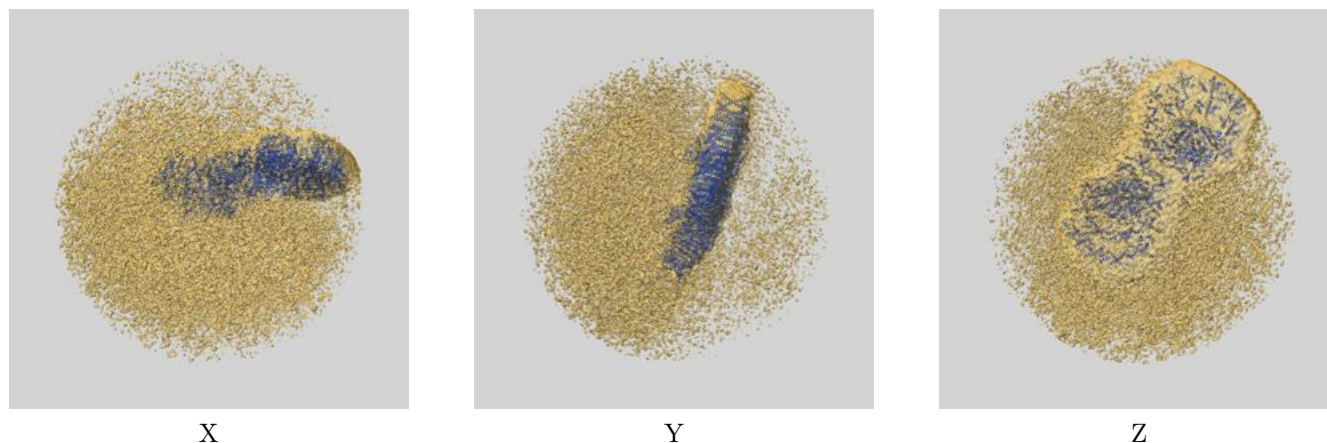
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |       |          |
|---------------------------|------------------------------------|-------|----------|
|                           | 0.143                              | 0.5   | Half-bit |
| Reported by author        | 17.10                              | -     | -        |
| Author-provided FSC curve | 16.81                              | 22.47 | 17.04    |
| Unmasked-calculated*      | -                                  | -     | -        |

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

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

This section contains information regarding the fit between EMDB map EMD-12672 and PDB model 7O01. Per-residue inclusion information can be found in section [3](#) on page [9](#).

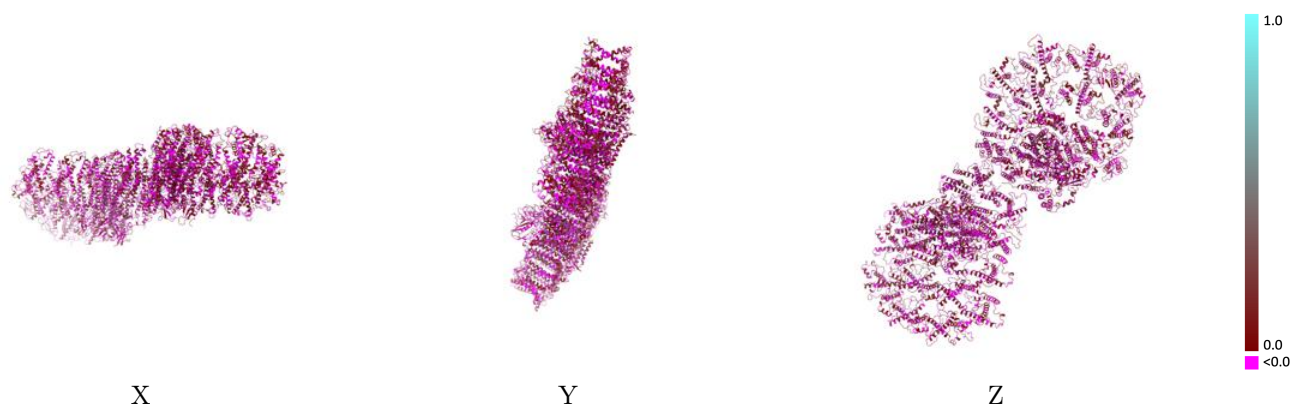
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.011 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.

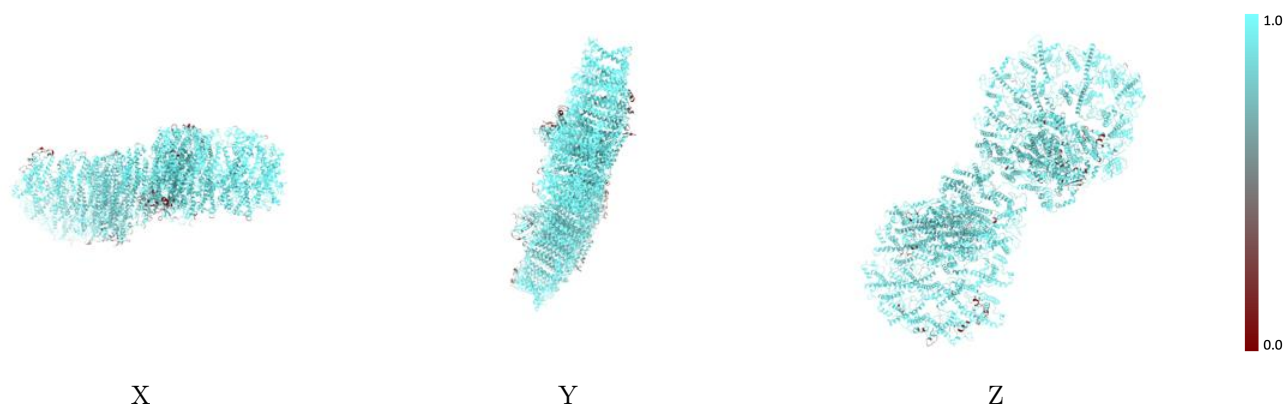


## 9.2 Q-score mapped to coordinate model [i](#)



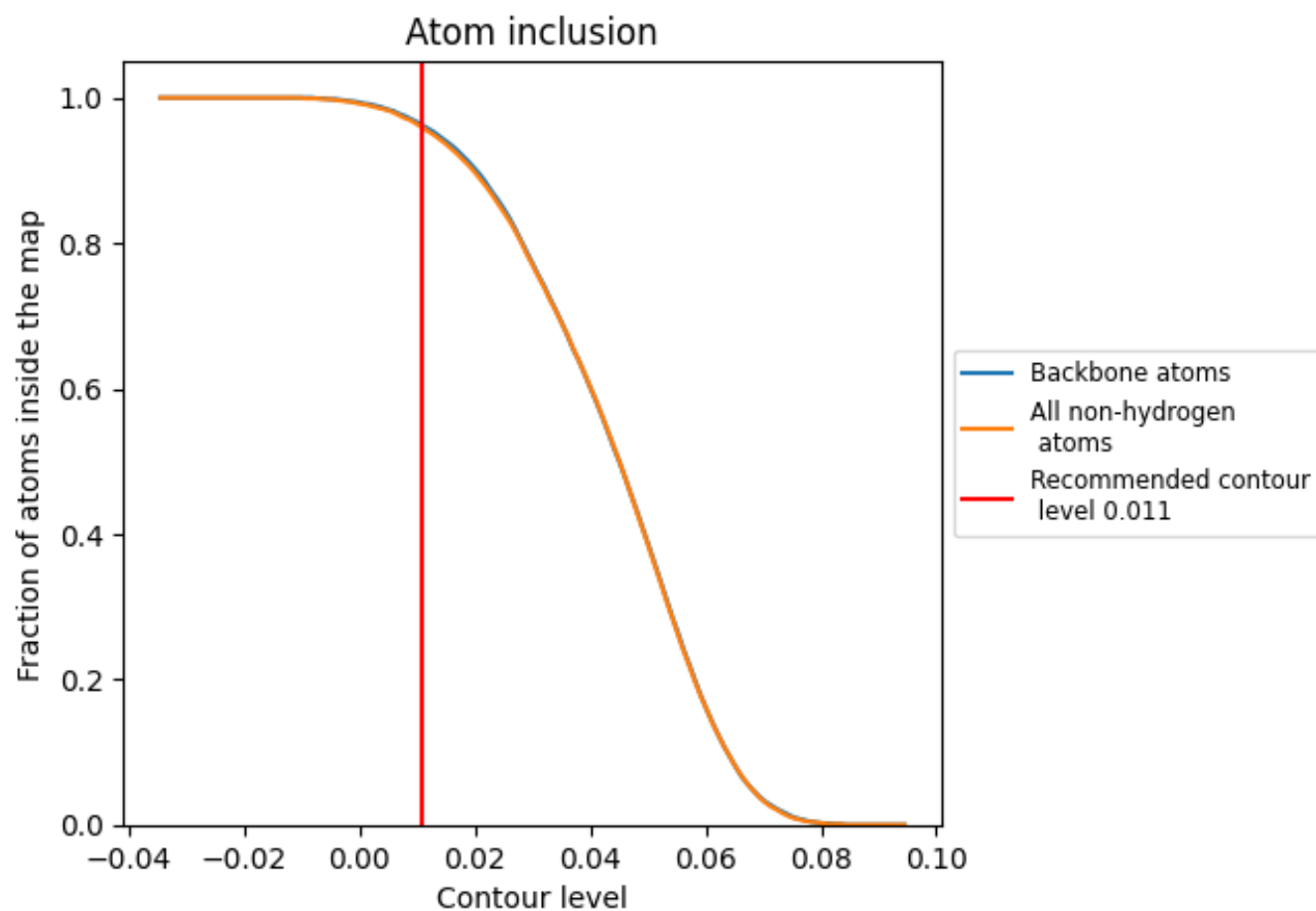
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

## 9.3 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 (0.011).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ













The table lists the average atom inclusion at the recommended contour level (0.011) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion   | Q-score   |
|-------|--|---|
| All   |  0.9590   |  0.0360      |
| 1     |  0.9860   |  0.0350      |
| 2     |  0.9870   |  0.0500      |
| 3     |  0.9470   |  0.0180      |
| 4     |  0.9060   |  0.0240      |
| 5     |  0.9710   |  0.0460      |
| 6     |  0.9670   |  0.0370      |
| 7     |  0.9960   |  0.0500      |
| 8     |  0.9830   |  0.0320      |
| 9     |  0.9740   |  0.0380      |
| A     |  0.9800   |  0.0340      |
| B     |  0.9770   |  0.0230      |
| C     |  0.9050   |  -0.0090   |
| D     |  0.7990   |  0.0210      |
| E     |  0.9810  |  0.0240     |
| F     |  0.9390 |  0.0300    |
| G     |  0.9960 |  0.0270    |
| I     |  0.9820 |  0.0380    |
| J     |  1.0000 |  0.0610    |
| K     |  0.8820 |  -0.0110 |
| L     |  0.9610 |  0.0090    |
| Z     |  0.8740 |  0.0260    |
| a     |  0.9600 |  0.0400    |
| b     |  0.9780 |  0.0280    |
| c     |  0.7210 |  -0.0380 |
| d     |  0.6350 |  0.0210    |
| e     |  0.8970 |  0.0470    |
| f     |  0.9480 |  0.0410    |
| g     |  1.0000 |  0.0370    |
| i     |  0.9710 |  0.0500    |
| j     |  1.0000 |  0.0550    |
| k     |  0.9950 |  0.0290    |
| l     |  0.9690 |  0.0440    |
| p     |  0.9830 |  0.0690    |
| q     |  0.9950 |  0.0620    |



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| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| r     |  0.9890 |  0.0490 |
| s     |  0.9930 |  0.0550 |
| t     |  0.9890 |  0.0590 |
| u     |  0.9770 |  0.0510 |
| v     |  0.9930 |  0.0450 |
| z     |  0.9620 |  0.0580 |