



## Full wwPDB EM Validation Report ⓘ

May 12, 2025 – 11:41 PM EDT

PDB ID : 8UW1 / pdb\_00008uw1  
EMDB ID : EMD-42636  
Title : Cryo-EM structure of DNMT3A1 UDR in complex with H2AK119Ub-nucleosome  
Authors : Gretarsson, K.; Abini-Agbomson, S.; Armache, K.-J.; Lu, C.  
Deposited on : 2023-11-05  
Resolution : 2.88 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.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
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) : 2.43.1

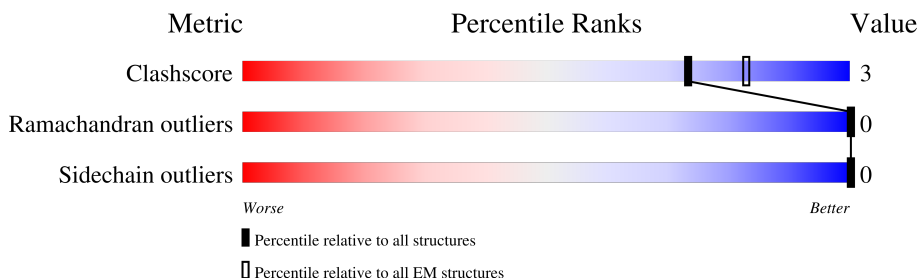
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*









The reported resolution of this entry is 2.88 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) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore            | 210492                      | 15764                       |
| 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     | 136    |  |
| 1   | E     | 136    |  |
| 2   | B     | 103    |  |
| 2   | F     | 103    |  |
| 3   | C     | 130    |  |
| 3   | G     | 130    |  |
| 4   | D     | 126    |  |
| 4   | H     | 126    |  |

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| Mol | Chain | Length | Quality of chain                           |
|-----|-------|--------|--|
| 5   | K     | 76     | <div><div></div><div>33%11%57%</div></div> |
| 6   | I     | 146    | <div><div></div><div>73%27%</div></div>    |
| 7   | J     | 146    | <div><div></div><div>78%21%</div></div>    |

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12164 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 Histone H3.2.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 1   | A     | 96       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 790   | 497 | 152 | 138 | 3 |         |       |
| 1   | E     | 91       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 745   | 469 | 141 | 132 | 3 |         |       |

- Molecule 2 is a protein called Histone H4.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 2   | B     | 79       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 627   | 395 | 121 | 110 | 1 |         |       |
| 2   | F     | 82       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 653   | 412 | 127 | 113 | 1 |         |       |

- Molecule 3 is a protein called Histone H2A.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 3   | C     | 106      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 814   | 513 | 159 | 142 |         |       |
| 3   | G     | 108      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 824   | 519 | 161 | 144 |         |       |

- Molecule 4 is a protein called Histone H2B 1.1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | D     | 93       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 729   | 459 | 131 | 137 | 2 |         |       |
| 4   | H     | 95       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 745   | 469 | 134 | 140 | 2 |         |       |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| D     | 29      | THR      | SER    | conflict | UNP P02281 |

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| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| H     | 29      | THR      | SER    | conflict | UNP P02281 |

- Molecule 5 is a protein called DNA (cytosine-5)-methyltransferase 3A.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 5   | K     | 33       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 251   | 153 | 54 | 43 | 1 |         |       |

There are 6 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| K     | 153     | HIS      | -      | expression tag | UNP Q9Y6K1 |
| K     | 154     | HIS      | -      | expression tag | UNP Q9Y6K1 |
| K     | 155     | HIS      | -      | expression tag | UNP Q9Y6K1 |
| K     | 156     | HIS      | -      | expression tag | UNP Q9Y6K1 |
| K     | 157     | HIS      | -      | expression tag | UNP Q9Y6K1 |
| K     | 158     | HIS      | -      | expression tag | UNP Q9Y6K1 |


- Molecule 6 is a DNA chain called DNA (146-MER).

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 6   | I     | 146      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2975  | 1414 | 539 | 876 | 146 |         |       |

- Molecule 7 is a DNA chain called DNA (146-MER).

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 7   | J     | 146      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 3011  | 1426 | 563 | 876 | 146 |         |       |



Chain G:  82% 17%

MET SER GLY ARG GLY LYS GLN GLY LYS THR ARG A12 D90 L108 K119 THR GLU SER SER SER LYS SER ALA LYS SER LYS

- Molecule 4: Histone H2B 1.1

Chain D:  73% 26%

MET PRO GLU PRO PRO LYS SER ALA PRO PRO PRO LYS GLY SER LYS LYS ALA VAL THR LYS THR GLN LYS LYS ASP GLY LYS ARG ARG LYS THR R30 K122

- Molecule 4: Histone H2B 1.1

Chain H:  71% 25%

MET PRO GLU PRO ALA LYS SER ALA PRO PRO LYS LYS GLY SER LYS LYS ALA VAL THR LYS THR GLN LYS LYS ASP GLY LYS ARG ARG V28 K54 I58 E73 R76 R83 K122

- Molecule 5: DNA (cytosine-5)-methyltransferase 3A

Chain K:  33% 11% 57%


HIS HIS HIS HIS HIS GLU SER MET MET MET GLU G165 S166 R167 G168 R169 L174 E177 R181 R187 L188 Y196 Y197 ILE SER LYS ARG LYS LYS ARG ASP GLU TRP LEU ALA ARG TRP LYS ARG GLU ALA GLU LYS LYS LYS ALA VAL ILE ALA GLY MET ASN ALA VAL GLU

- Molecule 6: DNA (146-MER)

Chain I:  73% 27%

T2 C3 G4 C17 C18 T27 C28 G40 A41 T46 C47 T48 A49 G67 T68 C78 C79 C80 C81 C82 G83 T89 A90 G101 G102 C109 C110 A113 G114 G121 G122 C123 T129 C130 T134 A135 T136 A137 T138 A139 G145 A146 T147

- Molecule 7: DNA (146-MER)

Chain J:  78% 21%

A1 T2 C3 G4 G5 T11 A12 T13 A14 T15 C16 C20 A21 G38 G39 C48 C49 T50 G70 A71 G72 A73 C81 C82 T99 A100 A110 C111 C123 G124 G125 C126 C127 A139 T140 A146

## 4 Experimental information

| Property                             | Value               | Source    |
|--------------------------------------|---------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE     | Depositor |
| Imposed symmetry                     | POINT, Not provided |           |
| Number of particles used             | 55652               | 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 ( $e^-/\text{\AA}^2$ ) | 50                  | Depositor |
| Minimum defocus (nm)                 | 1300                | Depositor |
| Maximum defocus (nm)                 | 2000                | Depositor |
| Magnification                        | Not provided        |           |
| Image detector                       | GATAN K3 (6k x 4k)  | Depositor |
| Maximum map value                    | 0.708               | Depositor |
| Minimum map value                    | 0.000               | Depositor |
| Average map value                    | 0.005               | Depositor |
| Map value standard deviation         | 0.022               | Depositor |
| Recommended contour level            | 0.0946              | Depositor |
| Map size ( $\text{\AA}$ )            | 272.0, 272.0, 272.0 | wwPDB     |
| Map dimensions                       | 320, 320, 320       | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0    | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 0.85, 0.85, 0.85    | Depositor |



## 5 Model quality

### 5.1 Standard geometry

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     | 0.34         | 0/800   | 0.39        | 0/1071         |
| 1   | E     | 0.34         | 0/753   | 0.42        | 0/1008         |
| 2   | B     | 0.34         | 0/634   | 0.43        | 0/848          |
| 2   | F     | 0.34         | 0/660   | 0.44        | 0/883          |
| 3   | C     | 0.30         | 0/824   | 0.45        | 0/1113         |
| 3   | G     | 0.32         | 0/834   | 0.39        | 0/1127         |
| 4   | D     | 0.28         | 0/740   | 0.37        | 0/994          |
| 4   | H     | 0.31         | 0/756   | 0.38        | 0/1015         |
| 5   | K     | 0.44         | 0/256   | 0.67        | 0/342          |
| 6   | I     | 0.33         | 0/3333  | 0.46        | 0/5137         |
| 7   | J     | 0.34         | 0/3381  | 0.48        | 3/5221 (0.1%)  |
| All | All   | 0.33         | 0/12971 | 0.45        | 3/18759 (0.0%) |

There are no bond length outliers.

All (3) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms     | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 7   | J     | 73  | DA   | P-O3'-C3' | -6.80 | 109.99      | 120.20   |
| 7   | J     | 72  | DG   | P-O3'-C3' | -6.59 | 110.32      | 120.20   |
| 7   | J     | 71  | DA   | P-O3'-C3' | -6.54 | 110.39      | 120.20   |

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | A     | 790   | 0        | 829      | 2       | 0            |
| 1   | E     | 745   | 0        | 784      | 3       | 0            |
| 2   | B     | 627   | 0        | 663      | 1       | 0            |
| 2   | F     | 653   | 0        | 696      | 7       | 0            |
| 3   | C     | 814   | 0        | 869      | 4       | 0            |
| 3   | G     | 824   | 0        | 873      | 2       | 0            |
| 4   | D     | 729   | 0        | 753      | 1       | 0            |
| 4   | H     | 745   | 0        | 773      | 3       | 0            |
| 5   | K     | 251   | 0        | 245      | 6       | 0            |
| 6   | I     | 2975  | 0        | 1640     | 25      | 0            |
| 7   | J     | 3011  | 0        | 1640     | 19      | 0            |
| All | All   | 12164 | 0        | 9765     | 67      | 0            |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1          | Atom-2          | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|-----------------|--------------------------|-------------------|
| 1:A:106:ASP:OD2 | 1:A:131:ARG:NH2 | 2.27                     | 0.68              |
| 2:F:22:LEU:HB3  | 2:F:25:ASN:HD21 | 1.62                     | 0.65              |
| 7:J:139:DA:H2"  | 7:J:140:DT:H5"  | 1.78                     | 0.64              |
| 1:E:125:GLN:OE1 | 1:E:134:ARG:NH1 | 2.32                     | 0.63              |
| 6:I:113:DA:H2"  | 6:I:114:DG:H5"  | 1.86                     | 0.58              |
| 1:A:121:PRO:HB3 | 2:B:53:GLU:HG3  | 1.86                     | 0.58              |
| 6:I:48:DT:H2"   | 6:I:49:DA:C8    | 2.41                     | 0.56              |
| 3:G:90:ASP:OD1  | 5:K:181:ARG:NH2 | 2.39                     | 0.55              |
| 6:I:101:DG:H2"  | 6:I:102:DG:C8   | 2.41                     | 0.55              |
| 3:C:15:LYS:HZ3  | 3:C:20:ARG:HD2  | 1.71                     | 0.54              |
| 1:E:97:GLU:HG3  | 2:F:37:LEU:HD21 | 1.89                     | 0.54              |
| 5:K:167:ARG:NH1 | 5:K:181:ARG:O   | 2.41                     | 0.53              |
| 6:I:109:DC:H2"  | 6:I:110:DC:C5   | 2.43                     | 0.52              |
| 3:C:15:LYS:HZ1  | 4:D:122:LYS:HD2 | 1.76                     | 0.50              |
| 7:J:20:DC:H2"   | 7:J:21:DA:C8    | 2.47                     | 0.49              |
| 7:J:123:DC:H2"  | 7:J:124:DG:C8   | 2.48                     | 0.49              |
| 6:I:27:DT:H2"   | 6:I:28:DC:C5    | 2.48                     | 0.49              |
| 6:I:129:DT:H2"  | 6:I:130:DC:C5   | 2.49                     | 0.48              |
| 2:F:84:MET:HE1  | 2:F:102:GLY:HA2 | 1.96                     | 0.48              |
| 6:I:123:DC:H5"  | 6:I:123:DC:H6   | 1.78                     | 0.48              |
| 6:I:113:DA:H5"  | 6:I:113:DA:H8   | 1.78                     | 0.48              |
| 6:I:3:DC:H2"    | 6:I:4:DG:C8     | 2.49                     | 0.47              |
| 6:I:17:DC:H2"   | 6:I:18:DC:C5    | 2.49                     | 0.47              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 4:H:83:ARG:HA    | 4:H:83:ARG:HD3   | 1.73                     | 0.47              |
| 2:F:22:LEU:HB3   | 2:F:25:ASN:ND2   | 2.30                     | 0.46              |
| 3:C:15:LYS:NZ    | 3:C:20:ARG:HD2   | 2.30                     | 0.46              |
| 7:J:99:DT:H2''   | 7:J:100:DA:C8    | 2.51                     | 0.46              |
| 4:H:73:GLU:OE1   | 4:H:76:ARG:NH2   | 2.44                     | 0.46              |
| 7:J:4:DG:H2''    | 7:J:5:DG:H2'     | 1.97                     | 0.46              |
| 5:K:196:TYR:O    | 5:K:197:TYR:C    | 2.60                     | 0.45              |
| 7:J:126:DC:H1'   | 7:J:127:DC:H5''  | 1.99                     | 0.44              |
| 6:I:47:DC:H2''   | 6:I:48:DT:H71    | 1.99                     | 0.44              |
| 7:J:3:DC:H2''    | 7:J:4:DG:C8      | 2.53                     | 0.44              |
| 5:K:169:ARG:HA   | 5:K:177:GLU:OE1  | 2.17                     | 0.44              |
| 7:J:12:DA:H2'    | 7:J:13:DT:C6     | 2.52                     | 0.44              |
| 3:G:108:LEU:HD12 | 5:K:187:ARG:HH21 | 1.81                     | 0.44              |
| 6:I:82:DC:H2''   | 6:I:83:DG:C8     | 2.52                     | 0.44              |
| 6:I:121:DG:H2''  | 6:I:122:DG:C8    | 2.52                     | 0.44              |
| 6:I:135:DA:H2''  | 6:I:136:DT:H5'   | 2.00                     | 0.43              |
| 7:J:81:DC:H2''   | 7:J:82:DG:C8     | 2.53                     | 0.43              |
| 7:J:100:DA:C8    | 7:J:100:DA:H5''  | 2.53                     | 0.43              |
| 7:J:70:DG:H2''   | 7:J:71:DA:C8     | 2.53                     | 0.43              |
| 5:K:188:LEU:H    | 5:K:188:LEU:HD23 | 1.82                     | 0.43              |
| 6:I:78:DC:H2''   | 6:I:79:DC:C5     | 2.54                     | 0.43              |
| 1:E:121:PRO:HB3  | 2:F:53:GLU:HG3   | 2.01                     | 0.42              |
| 7:J:49:DC:H2''   | 7:J:50:DT:H72    | 2.01                     | 0.42              |
| 6:I:40:DG:H2''   | 6:I:41:DA:C8     | 2.54                     | 0.42              |
| 6:I:67:DG:H2''   | 6:I:68:DT:H71    | 2.01                     | 0.42              |
| 6:I:135:DA:H2'   | 6:I:136:DT:H71   | 2.00                     | 0.42              |
| 7:J:38:DG:H2''   | 7:J:39:DG:N7     | 2.34                     | 0.42              |
| 6:I:46:DT:H2''   | 6:I:47:DC:C6     | 2.54                     | 0.42              |
| 6:I:27:DT:H2''   | 6:I:28:DC:C6     | 2.55                     | 0.42              |
| 7:J:100:DA:H5''  | 7:J:100:DA:H8    | 1.85                     | 0.42              |
| 6:I:79:DC:H2''   | 6:I:80:DC:C5     | 2.55                     | 0.41              |
| 6:I:134:DT:H2''  | 6:I:135:DA:H8    | 1.85                     | 0.41              |
| 2:F:52:GLU:OE2   | 2:F:55:ARG:NH1   | 2.53                     | 0.41              |
| 6:I:138:DT:H2''  | 6:I:139:DA:C8    | 2.55                     | 0.41              |
| 7:J:14:DA:C8     | 7:J:14:DA:H5'    | 2.55                     | 0.41              |
| 7:J:11:DT:H2'    | 7:J:12:DA:C8     | 2.55                     | 0.41              |
| 7:J:15:DT:H4'    | 7:J:16:DC:OP1    | 2.19                     | 0.41              |
| 3:C:63:LEU:HD23  | 3:C:63:LEU:HA    | 1.87                     | 0.41              |
| 4:H:54:LYS:O     | 4:H:58:ILE:HG12  | 2.21                     | 0.41              |
| 6:I:89:DT:H2''   | 6:I:90:DA:C8     | 2.56                     | 0.41              |
| 7:J:48:DC:H2''   | 7:J:49:DC:C6     | 2.56                     | 0.41              |

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| Atom-1          | Atom-2         | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|----------------|--------------------------|-------------------|
| 2:F:26:ILE:HD12 | 2:F:26:ILE:HA  | 1.96                     | 0.40              |
| 7:J:110:DA:H4'  | 7:J:111:DC:OP1 | 2.21                     | 0.40              |
| 6:I:145:DG:H2'' | 6:I:146:DA:H8  | 1.85                     | 0.40              |

There are no symmetry-related clashes.

## 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     | 94/136 (69%)   | 93 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 1   | E     | 89/136 (65%)   | 87 (98%)  | 2 (2%)  | 0        | 100         | 100 |
| 2   | B     | 77/103 (75%)   | 76 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 2   | F     | 80/103 (78%)   | 78 (98%)  | 2 (2%)  | 0        | 100         | 100 |
| 3   | C     | 104/130 (80%)  | 101 (97%) | 3 (3%)  | 0        | 100         | 100 |
| 3   | G     | 106/130 (82%)  | 104 (98%) | 2 (2%)  | 0        | 100         | 100 |
| 4   | D     | 91/126 (72%)   | 90 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 4   | H     | 93/126 (74%)   | 92 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 5   | K     | 31/76 (41%)    | 26 (84%)  | 5 (16%) | 0        | 100         | 100 |
| All | All   | 765/1066 (72%) | 747 (98%) | 18 (2%) | 0        | 100         | 100 |

There are no Ramachandran outliers to report.

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

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     | 83/111 (75%)  | 83 (100%)  | 0        | 100         | 100 |
| 1   | E     | 79/111 (71%)  | 79 (100%)  | 0        | 100         | 100 |
| 2   | B     | 64/79 (81%)   | 64 (100%)  | 0        | 100         | 100 |
| 2   | F     | 67/79 (85%)   | 67 (100%)  | 0        | 100         | 100 |
| 3   | C     | 83/102 (81%)  | 83 (100%)  | 0        | 100         | 100 |
| 3   | G     | 83/102 (81%)  | 83 (100%)  | 0        | 100         | 100 |
| 4   | D     | 79/106 (74%)  | 79 (100%)  | 0        | 100         | 100 |
| 4   | H     | 81/106 (76%)  | 81 (100%)  | 0        | 100         | 100 |
| 5   | K     | 24/63 (38%)   | 24 (100%)  | 0        | 100         | 100 |
| All | All   | 643/859 (75%) | 643 (100%) | 0        | 100         | 100 |

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | B     | 75  | HIS  |
| 4   | D     | 81  | ASN  |
| 3   | G     | 73  | ASN  |
| 3   | G     | 84  | GLN  |
| 3   | G     | 104 | GLN  |

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

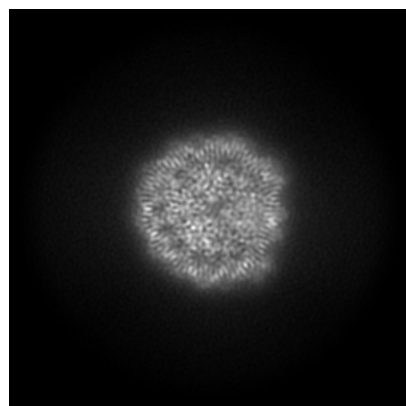
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42636. These allow visual inspection of the internal detail of the map and identification of artifacts.

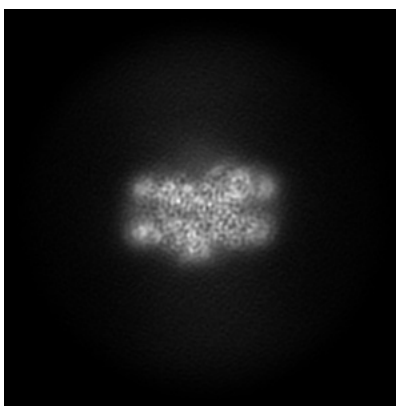
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

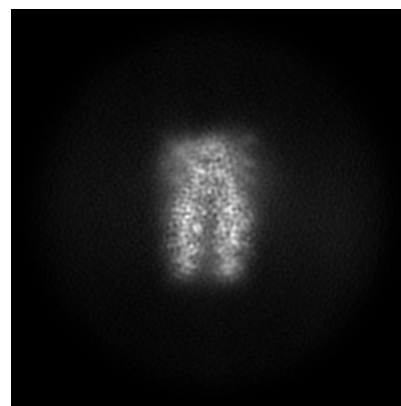
#### 6.1.1 Primary map



X

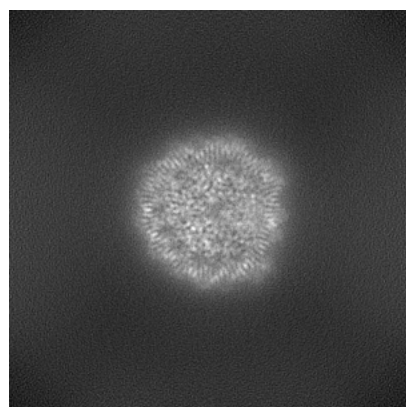


Y

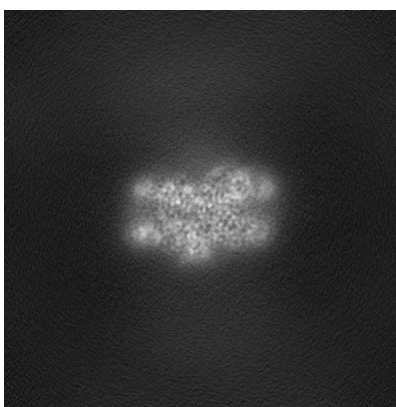


Z

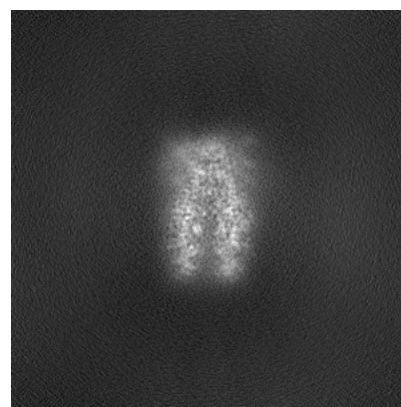
#### 6.1.2 Raw map



X



Y

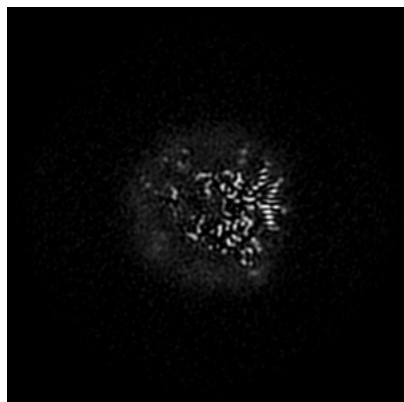


Z

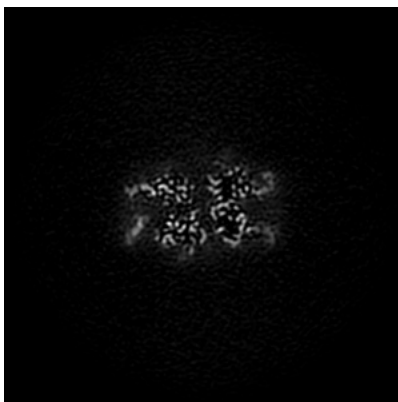
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

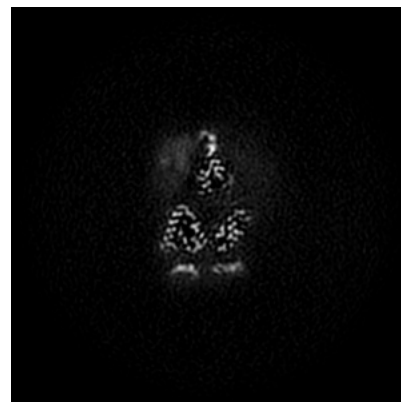
### 6.2.1 Primary map



X Index: 160

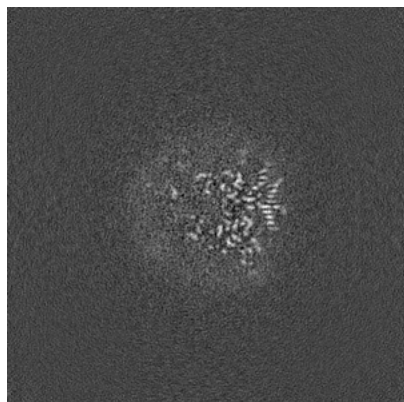


Y Index: 160

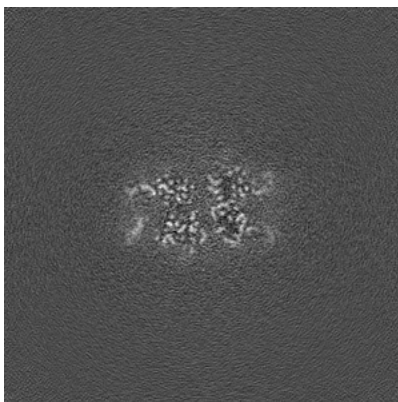


Z Index: 160

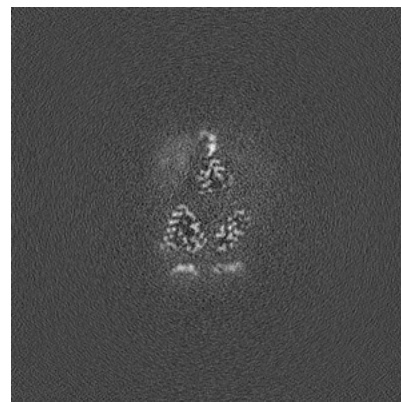
### 6.2.2 Raw map



X Index: 160



Y Index: 160



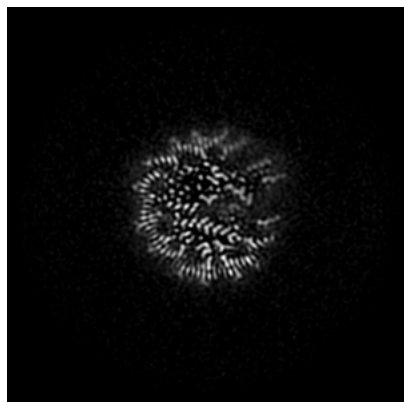
Z Index: 160

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

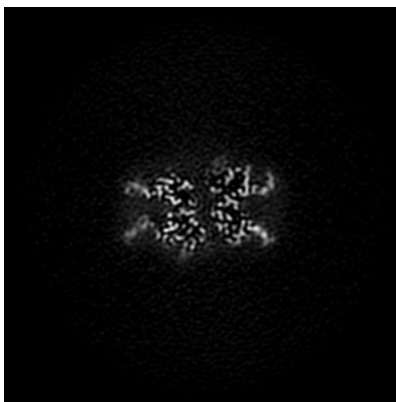


## 6.3 Largest variance slices [i](#)

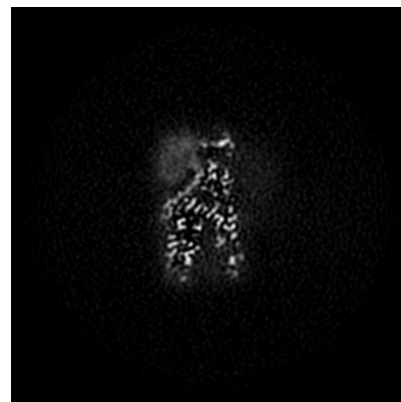
### 6.3.1 Primary map



X Index: 175

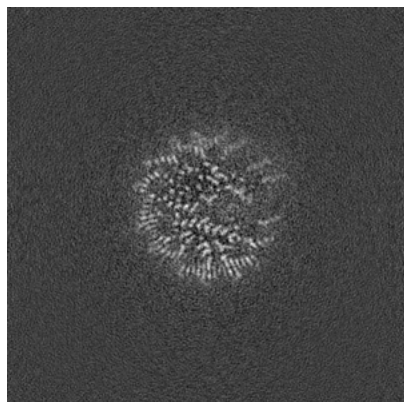


Y Index: 158

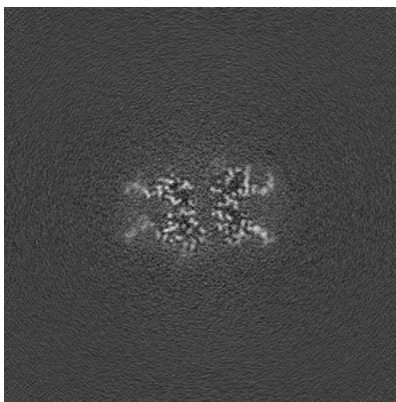


Z Index: 149

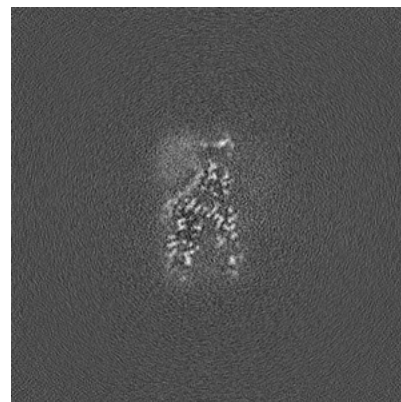
### 6.3.2 Raw map



X Index: 175



Y Index: 158

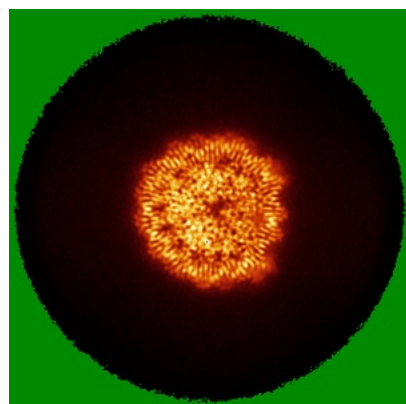


Z Index: 149

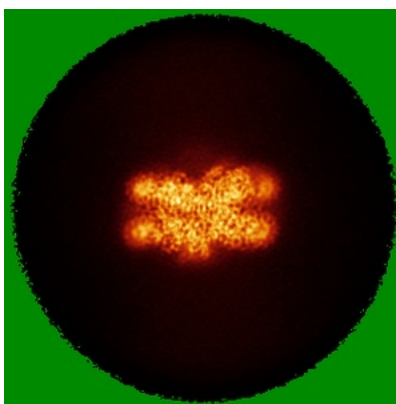
The images above show the largest variance slices of the map in three orthogonal directions.

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

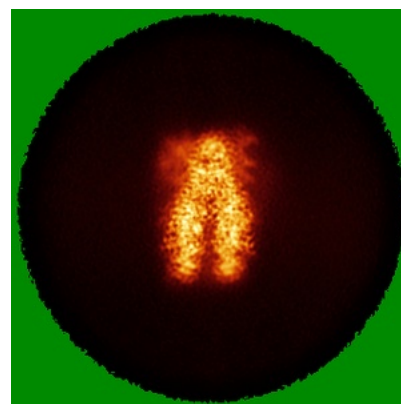
### 6.4.1 Primary map



X

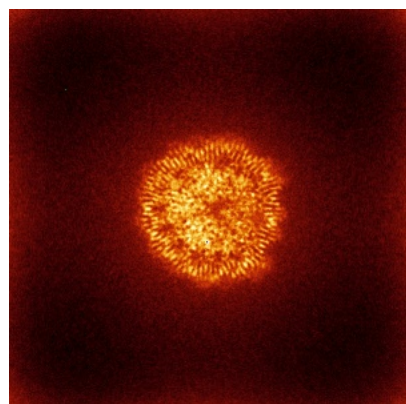


Y

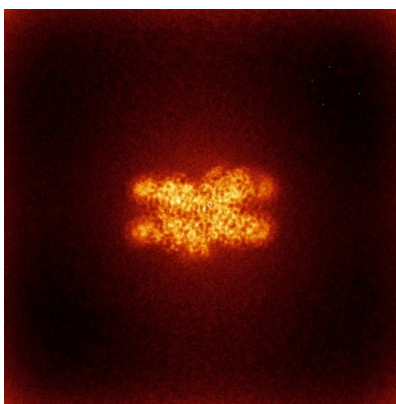


Z

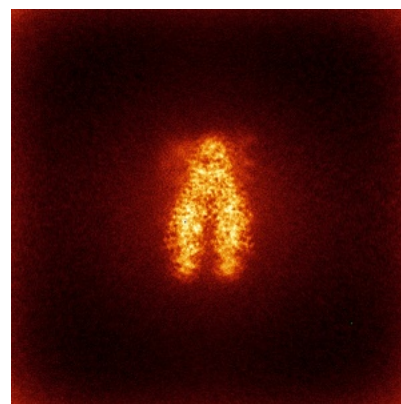
### 6.4.2 Raw map



X



Y

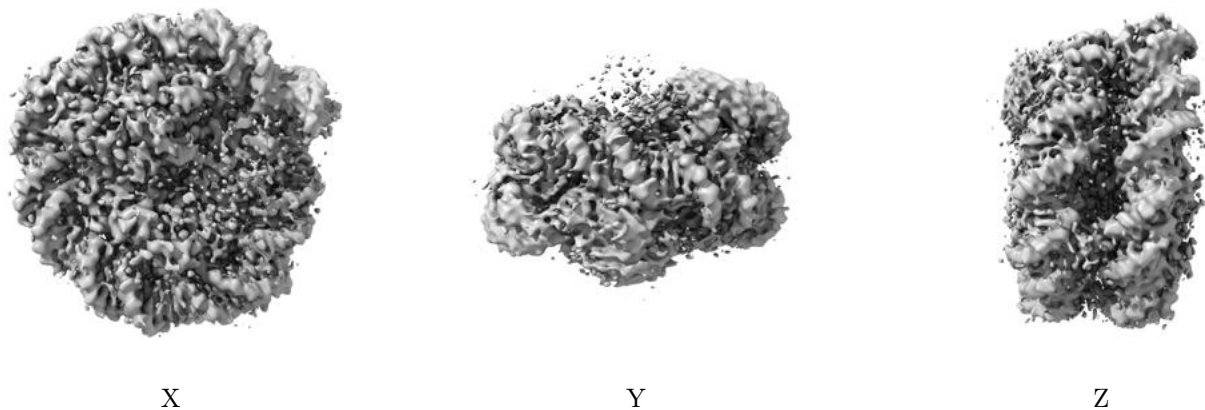


Z

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.

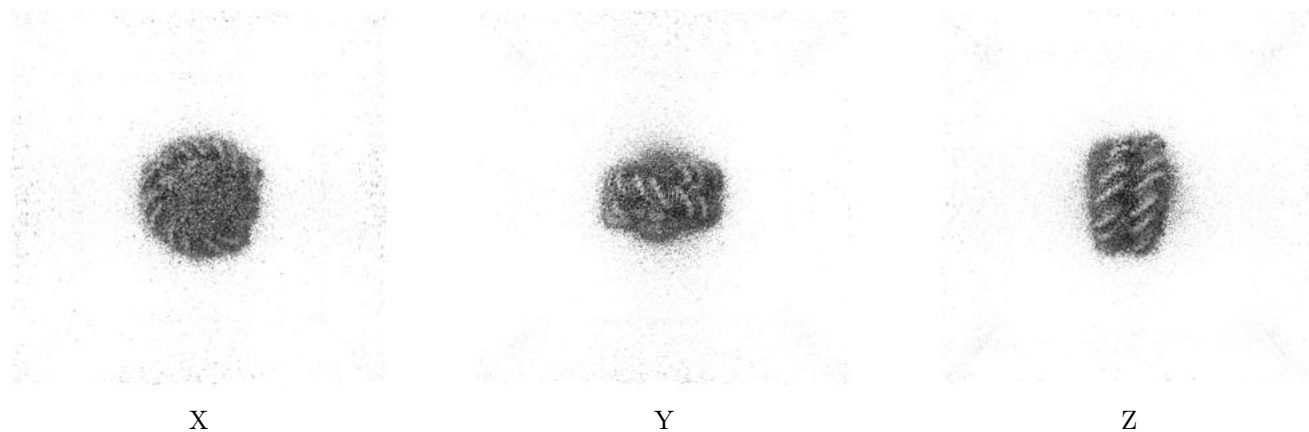
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0946. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

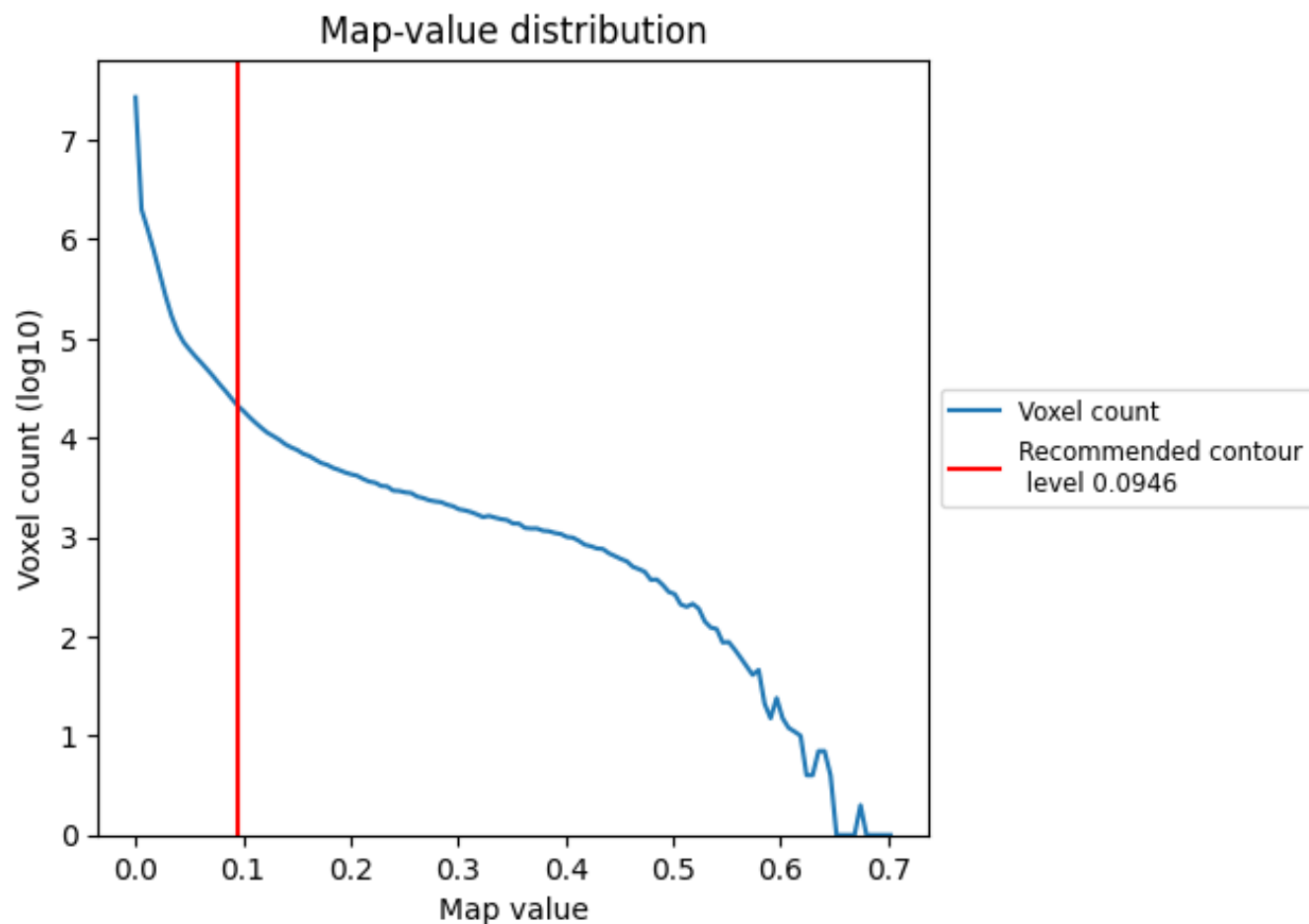
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

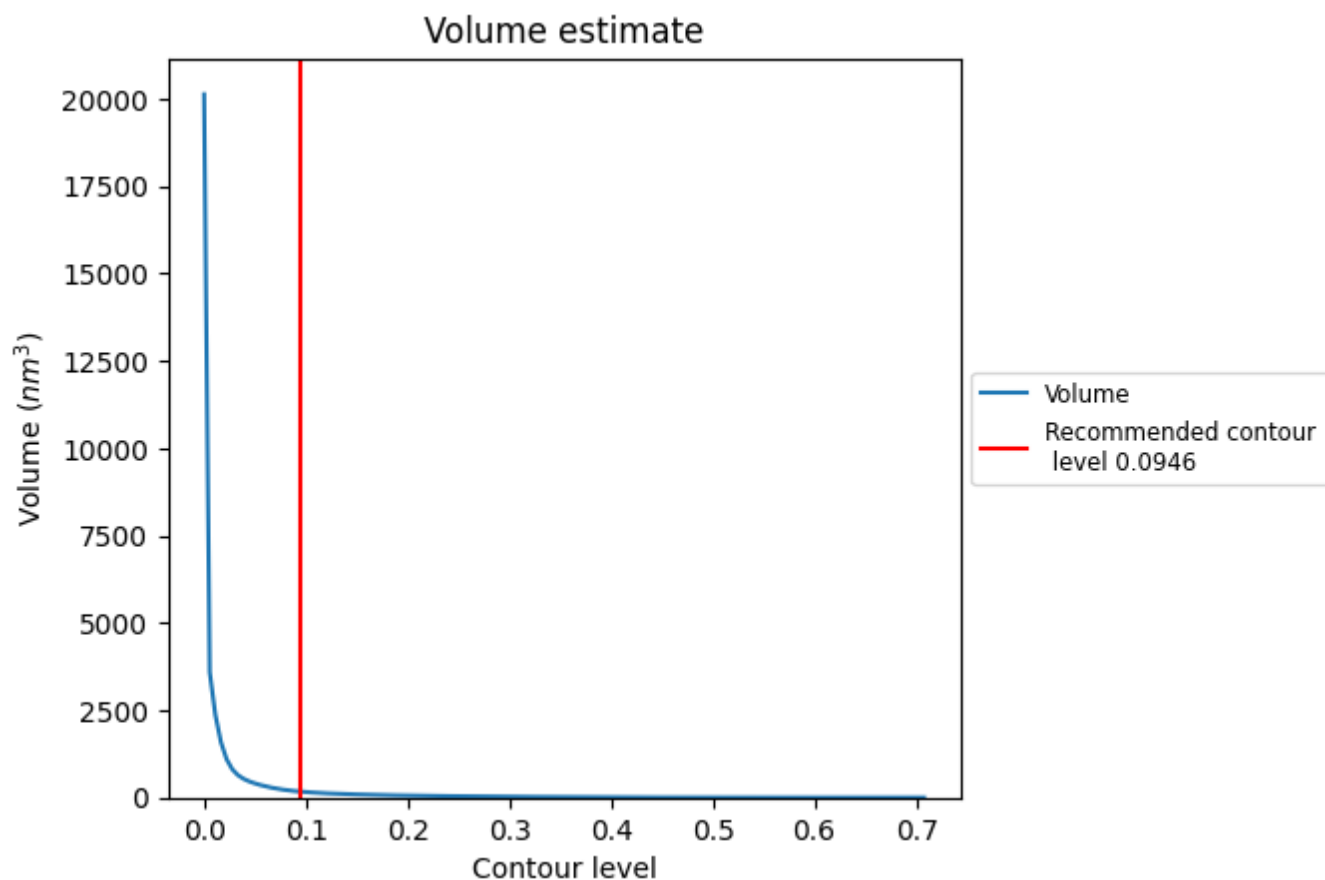
This section contains the results of statistical analysis of the map.

### 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.

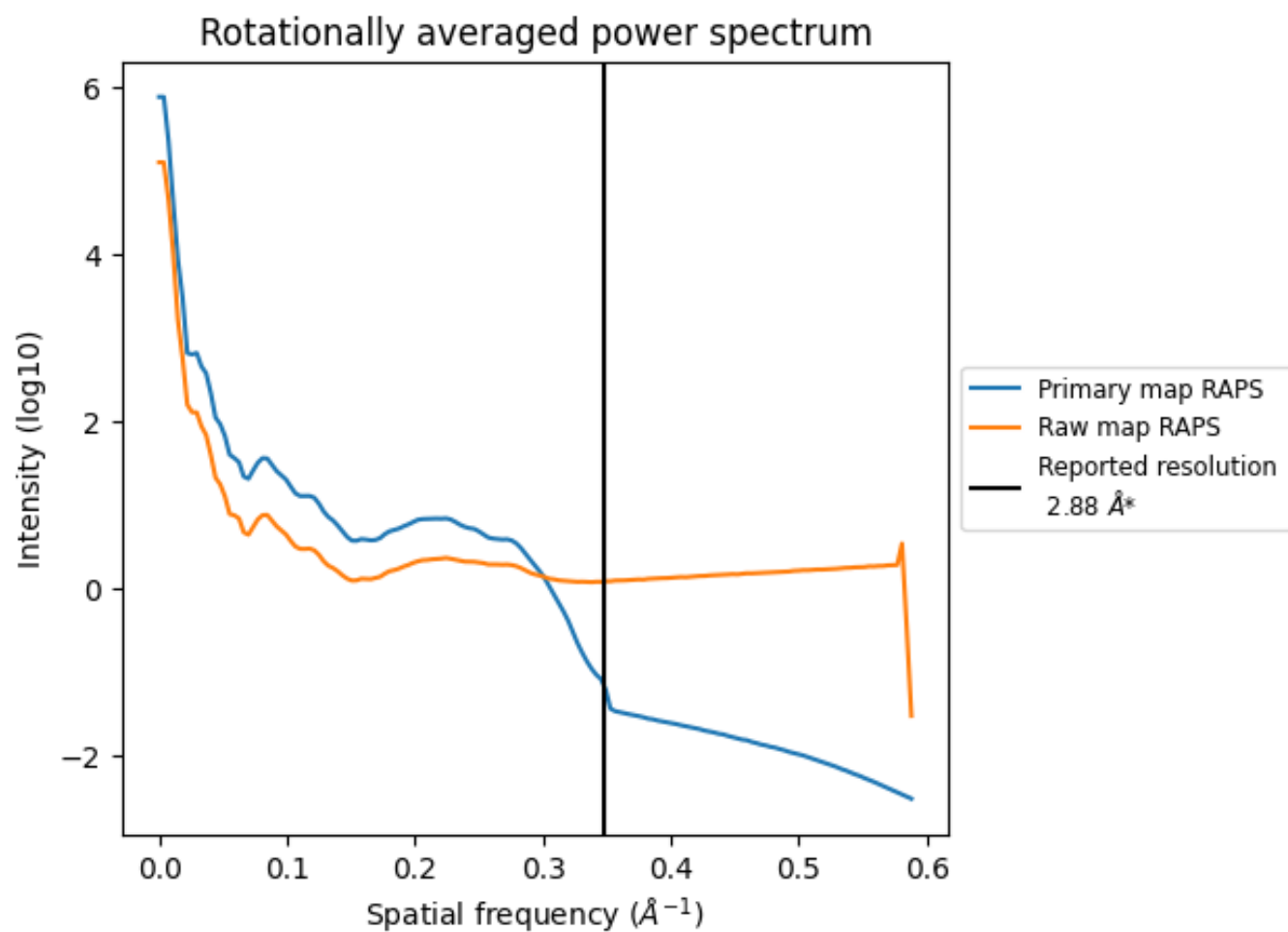
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 170 nm<sup>3</sup>; this corresponds to an approximate mass of 154 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 [i](#)

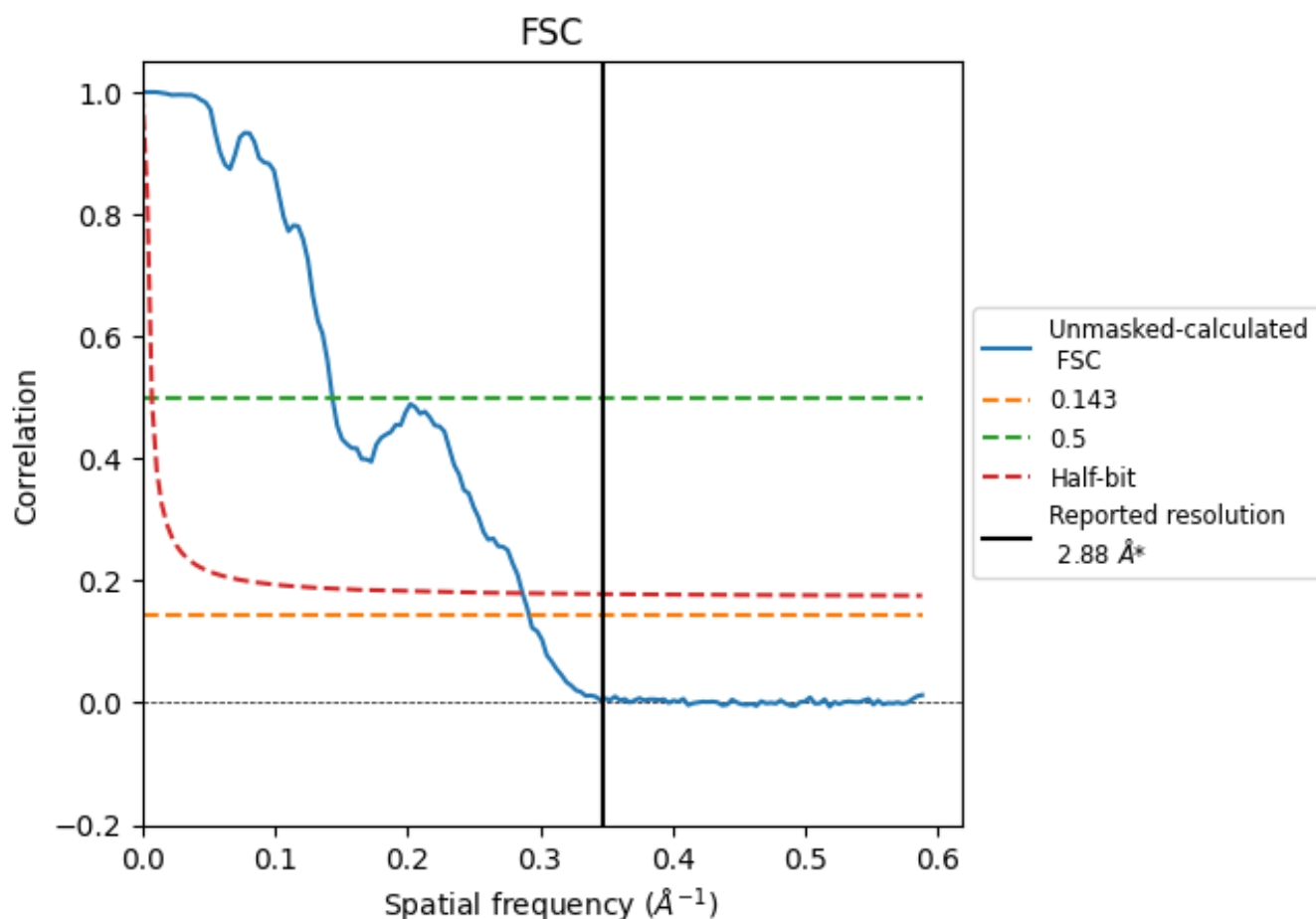


\*Reported resolution corresponds to spatial frequency of 0.347  $\text{\AA}^{-1}$

## 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 0.347  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 2.88                               | -    | -        |
| Author-provided FSC curve | -                                  | -    | -        |
| Unmasked-calculated*      | 3.43                               | 6.98 | 3.49     |

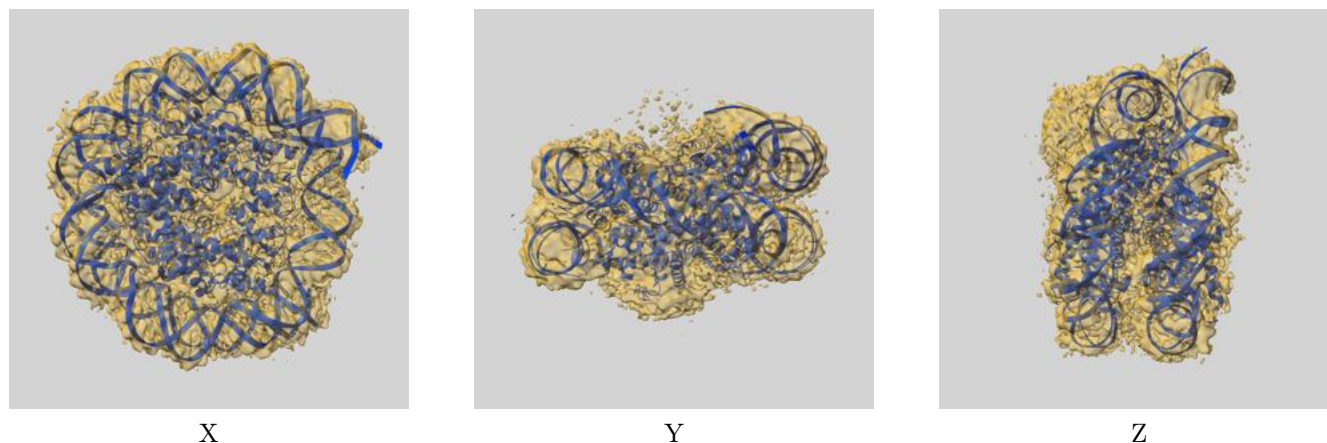
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.43 differs from the reported value 2.88 by more than 10 %



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

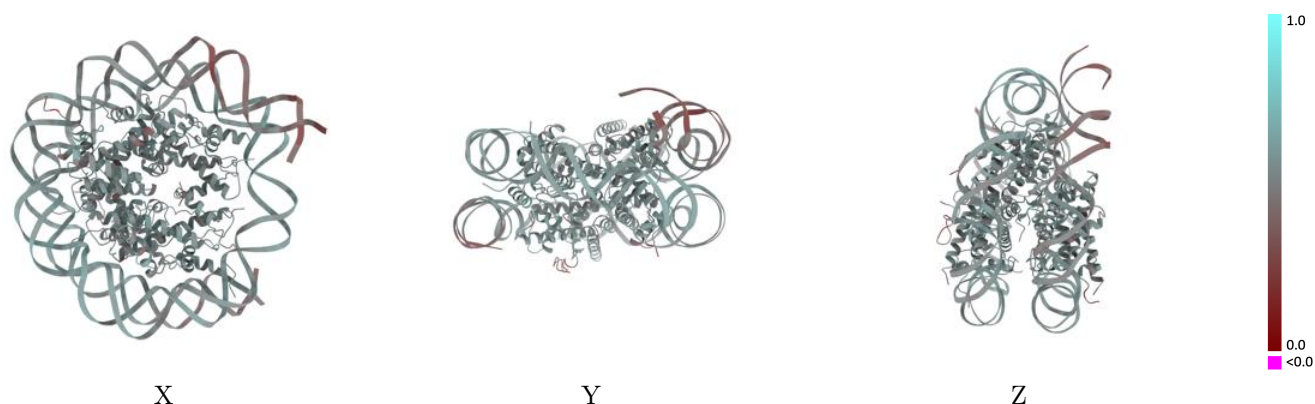
This section contains information regarding the fit between EMDB map EMD-42636 and PDB model 8UW1. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

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



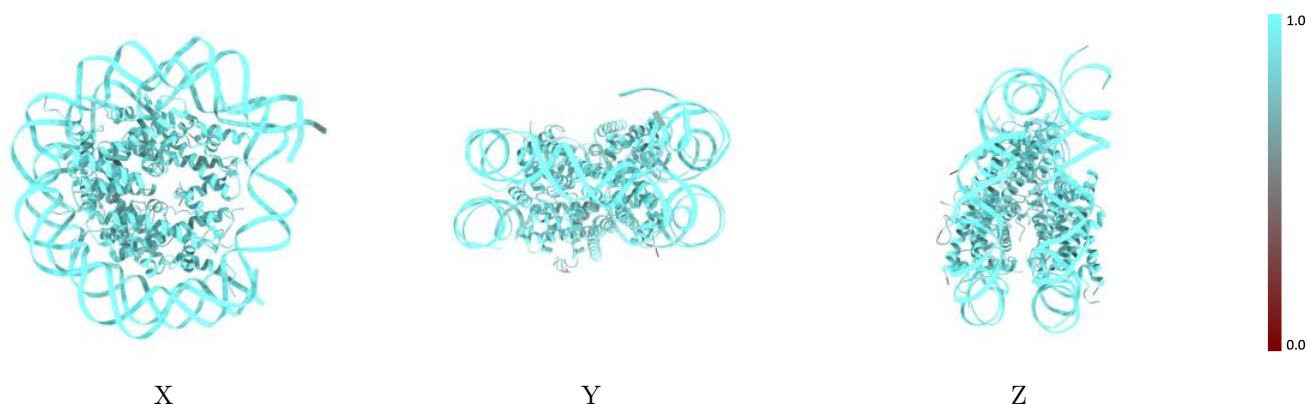
The images above show the 3D surface view of the map at the recommended contour level 0.0946 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



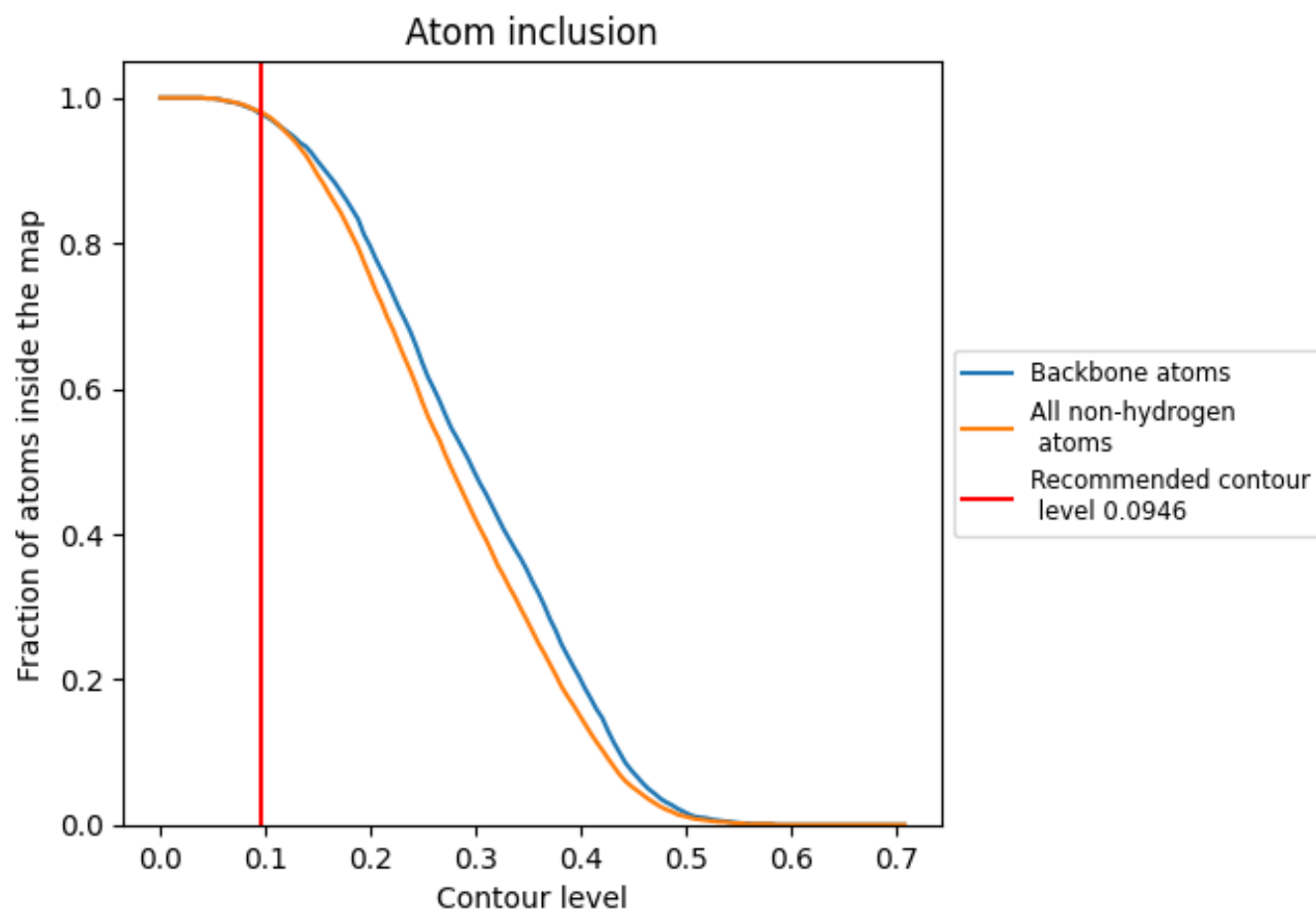
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0946).

## 9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.0946) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion     | Q-score            |
|-------|--------------------|--------------------|
| All   | <div></div> 0.9810 | <div></div> 0.5270 |
| A     | <div></div> 0.9680 | <div></div> 0.5420 |
| B     | <div></div> 0.9870 | <div></div> 0.5540 |
| C     | <div></div> 0.9680 | <div></div> 0.5250 |
| D     | <div></div> 0.9680 | <div></div> 0.5290 |
| E     | <div></div> 0.9750 | <div></div> 0.5290 |
| F     | <div></div> 0.9630 | <div></div> 0.5310 |
| G     | <div></div> 0.9780 | <div></div> 0.5520 |
| H     | <div></div> 0.9640 | <div></div> 0.5410 |
| I     | <div></div> 0.9940 | <div></div> 0.5230 |
| J     | <div></div> 0.9940 | <div></div> 0.5190 |
| K     | <div></div> 0.8780 | <div></div> 0.4270 |

1.0

0.0

<0.0