



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:42 PM UTC

PDB ID : 9GC0 / pdb\_00009gc0  
EMDB ID : EMD-51226  
Title : 3'-lobe of the substrate-bound U11 snRNP  
Authors : Zhao, J.; Galej, W.P.  
Deposited on : 2024-07-31  
Resolution : 3.20 Å (reported)  
Based on initial models : ., 4PJO

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:

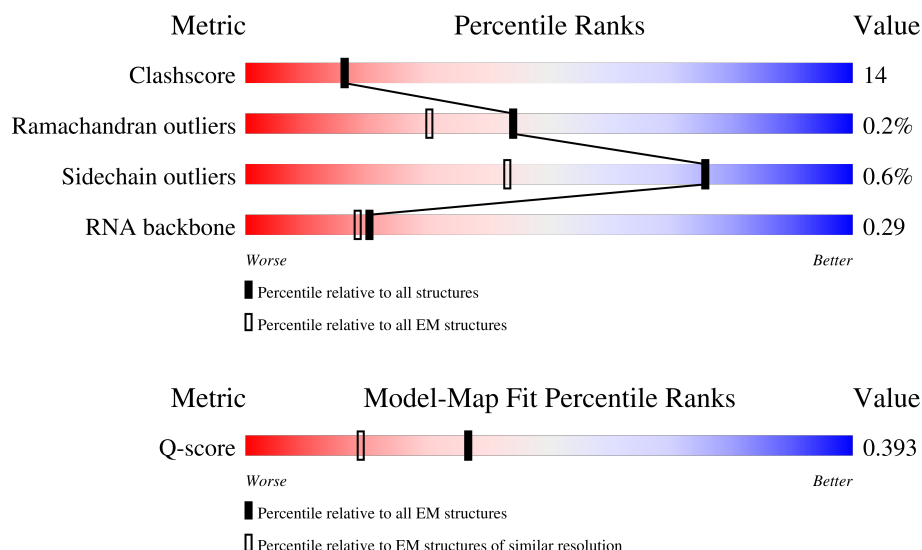
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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.



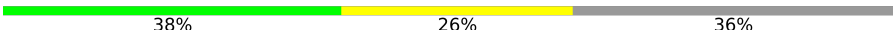
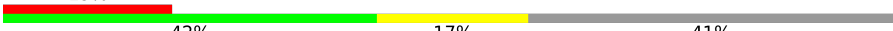
| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 15020 ( 2.70 - 3.70 )                                    |

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   | E     | 170    | <div> <div>8%</div> <div>19%</div> <div>76%</div> </div>                |
| 2   | D     | 485    | <div> <div>15%</div> <div>15%</div> <div>9%</div> <div>76%</div> </div> |
| 3   | h     | 119    | <div> <div>44%</div> <div>24%</div> <div>32%</div> </div>               |

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| Mol | Chain | Length | Quality of chain                                                                   |
|-----|-------|--------|------------------------------------------------------------------------------------|
| 4   | j     | 126    |  |
| 5   | k     | 240    |  |
| 6   | l     | 92     |  |
| 7   | m     | 86     |  |
| 8   | n     | 76     |  |
| 9   | Q     | 135    |  |
| 10  | F     | 339    |  |
| 11  | i     | 118    |  |

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 8297 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 Zinc finger matrin-type protein 5.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 1   | E     | 40       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 358   | 227 | 69 | 59 | 3 |         |       |

- Molecule 2 is a protein called Programmed cell death protein 7.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 2   | D     | 116      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 965   | 587 | 209 | 168 | 1 |         |       |

- Molecule 3 is a protein called Small nuclear ribonucleoprotein Sm D1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 3   | h     | 81       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 641   | 408 | 112 | 118 | 3 |         |       |

- Molecule 4 is a protein called Small nuclear ribonucleoprotein Sm D3.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | j     | 81       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 637   | 400 | 112 | 119 | 6 |         |       |

- Molecule 5 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 5   | k     | 86       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 692   | 435 | 126 | 124 | 7 |         |       |

- Molecule 6 is a protein called Small nuclear ribonucleoprotein E.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 6   | l     | 77       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 638   | 405 | 113 | 115 | 5 |         |       |

- Molecule 7 is a protein called Small nuclear ribonucleoprotein F.

| Mol | Chain | Residues | Atoms |     |    |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---|---------|-------|
| 7   | m     | 74       | Total | C   | N  | O   | S | 0       | 0     |
|     |       |          | 576   | 373 | 95 | 103 | 5 |         |       |

- Molecule 8 is a protein called Small nuclear ribonucleoprotein G.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8   | n     | 73       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 568   | 358 | 102 | 102 | 6 |         |       |

- Molecule 9 is a RNA chain called U11 snRNA.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 9   | Q     | 39       | Total | C   | N   | O   | P  | 0       | 0     |
|     |       |          | 823   | 367 | 135 | 282 | 39 |         |       |

- Molecule 10 is a protein called U11/U12 small nuclear ribonucleoprotein 48 kDa protein.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 10  | F     | 200      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1635  | 1016 | 278 | 330 | 11 |         |       |

- Molecule 11 is a protein called Small nuclear ribonucleoprotein Sm D2.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11  | i     | 94       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 764   | 478 | 139 | 141 | 6 |         |       |



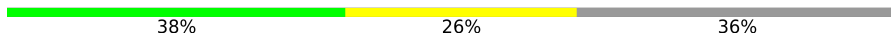
ARG GLN TYR TYR LEU LEU ALA ALA GLU HIS SER SER LEU PRO PRO ALA LEU ILE ILE ILE ARG HIS ASP TRP ASP ASP GLN TYR TYR VAL VAL PRO PRO GLN GLY TRP VAL LEU PRO PRO LEU PRO PRO SER SER ASP ASP TRP TRP THR THR ALA VAL VAL LYS LEU HIS

• Molecule 3: Small nuclear ribonucleoprotein Sm D1

Chain h:  44% 24% 32%

MET F2 L3 V4 R5 F6 L7 M8 R9 L10 L11 I17 K20 R21 R22 L23 V25 T29 V32 V33 T38 H39 L40 R41 A42 V43 K44 M45 K48 E51 Q54 L55 E56 T57 L58 R61 G62 N63 N64 I65 F68 I69 D77 T78 L79 D82 VAL GLU PRO LYS

• Molecule 4: Small nuclear ribonucleoprotein Sm D3

Chain j:  38% 26% 36%

MET SER I3 G4 V5 F6 V9 L10 H11 I17 Y18 T19 E20 E21 T22 R23 T24 G30 K31 L32 I33 D37 F38 M39 N40 C41 Q42 M45 Y50 R51 Q57 L58 E59 Q60 R64 G65 S66 I72 D75 M76 N79 A80 R81 M82 L83 LYS SER MET LYS

• Molecule 5: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain k:  8% 25% 11% 64%

MET THR VAL GLY LYS S6 S7 K8 M9 L10 H11 Q12 I13 D14 Y15 R16 M17 Q22 R25 Q29 D35 M38 I41 E47 K52 P53 K54 N55 S56 K57 Q58 A59 E60 R61 E62 E63 R64 R65 R73 L77 V78 S79 M80 T81 G84 P85 P86 P87 K88

• Molecule 6: Small nuclear ribonucleoprotein E

Chain l:  53% 29% 16%

MET ALA TYR ARG GLN GLY GLN VAL VAL M14 P17 I18 F22 R23 Y24 R28 S29 R30 I31 Q38 I47 I48 D51 L56 V57 D60 K69 L74 I77 M78 L79 K80 G81 D82 N83 L86 L87 Q88 S89 V90 SER ASN

• Molecule 7: Small nuclear ribonucleoprotein F

Chain m:  67% 19% 14%





## 4 Experimental information

| Property                             | Value                   | Source    |
|--------------------------------------|-------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE         | Depositor |
| Imposed symmetry                     | POINT, Not provided     |           |
| Number of particles used             | 52290                   | 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 ( $e^-/\text{\AA}^2$ ) | 41.73                   | Depositor |
| Minimum defocus (nm)                 | 700                     | Depositor |
| Maximum defocus (nm)                 | 1500                    | Depositor |
| Magnification                        | 165000                  | Depositor |
| Image detector                       | FEI FALCON IV (4k x 4k) | Depositor |
| Maximum map value                    | 0.171                   | Depositor |
| Minimum map value                    | -0.105                  | Depositor |
| Average map value                    | 0.000                   | Depositor |
| Map value standard deviation         | 0.003                   | Depositor |
| Recommended contour level            | 0.024                   | Depositor |
| Map size ( $\text{\AA}$ )            | 321.2, 321.2, 321.2     | wwPDB     |
| Map dimensions                       | 440, 440, 440           | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0        | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 0.73, 0.73, 0.73        | 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   | E     | 0.14         | 0/368   | 0.43        | 0/490   |
| 2   | D     | 0.16         | 0/972   | 0.45        | 0/1301  |
| 3   | h     | 0.16         | 0/649   | 0.52        | 0/878   |
| 4   | j     | 0.17         | 0/645   | 0.55        | 0/870   |
| 5   | k     | 0.16         | 0/702   | 0.45        | 0/936   |
| 6   | l     | 0.16         | 0/646   | 0.46        | 0/867   |
| 7   | m     | 0.16         | 0/588   | 0.42        | 0/795   |
| 8   | n     | 0.21         | 0/575   | 0.65        | 0/768   |
| 9   | Q     | 0.13         | 0/915   | 0.34        | 0/1420  |
| 10  | F     | 0.16         | 0/1667  | 0.46        | 0/2251  |
| 11  | i     | 0.18         | 0/773   | 0.54        | 0/1039  |
| All | All   | 0.16         | 0/8500  | 0.48        | 0/11615 |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 3   | h     | 0                   | 1                   |
| 4   | j     | 0                   | 1                   |
| 8   | n     | 0                   | 1                   |
| All | All   | 0                   | 3                   |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group   |
|-----|-------|-----|------|---------|
| 3   | h     | 41  | LYS  | Peptide |

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| Mol | Chain | Res | Type | Group   |
|-----|-------|-----|------|---------|
| 4   | j     | 59  | GLU  | Peptide |
| 8   | n     | 43  | ASP  | Peptide |

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

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   | E     | 358   | 0        | 340      | 6       | 0            |
| 2   | D     | 965   | 0        | 1007     | 34      | 0            |
| 3   | h     | 641   | 0        | 681      | 26      | 0            |
| 4   | j     | 637   | 0        | 652      | 24      | 0            |
| 5   | k     | 692   | 0        | 717      | 22      | 0            |
| 6   | l     | 638   | 0        | 657      | 24      | 0            |
| 7   | m     | 576   | 0        | 589      | 15      | 0            |
| 8   | n     | 568   | 0        | 590      | 26      | 0            |
| 9   | Q     | 823   | 0        | 417      | 23      | 0            |
| 10  | F     | 1635  | 0        | 1561     | 50      | 0            |
| 11  | i     | 764   | 0        | 783      | 26      | 0            |
| All | All   | 8297  | 0        | 7994     | 230     | 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 14.

The worst 5 of 230 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) |
|------------------|------------------|--------------------------|-------------------|
| 5:k:12:HIS:HB3   | 5:k:17:MET:HE1   | 1.51                     | 0.92              |
| 2:D:276:ARG:HH21 | 2:D:277:TRP:HD1  | 1.34                     | 0.76              |
| 10:F:78:CYS:SG   | 10:F:82:LYS:NZ   | 2.59                     | 0.76              |
| 6:l:21:ILE:HD11  | 8:n:61:VAL:HG11  | 1.68                     | 0.75              |
| 3:h:69:ILE:HG12  | 11:i:96:ILE:HD11 | 1.69                     | 0.74              |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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   | E     | 38/170 (22%)   | 38 (100%) | 0        | 0        | 100         | 100 |
| 2   | D     | 114/485 (24%)  | 107 (94%) | 7 (6%)   | 0        | 100         | 100 |
| 3   | h     | 79/119 (66%)   | 75 (95%)  | 4 (5%)   | 0        | 100         | 100 |
| 4   | j     | 79/126 (63%)   | 71 (90%)  | 8 (10%)  | 0        | 100         | 100 |
| 5   | k     | 84/240 (35%)   | 82 (98%)  | 2 (2%)   | 0        | 100         | 100 |
| 6   | l     | 75/92 (82%)    | 72 (96%)  | 3 (4%)   | 0        | 100         | 100 |
| 7   | m     | 72/86 (84%)    | 71 (99%)  | 1 (1%)   | 0        | 100         | 100 |
| 8   | n     | 71/76 (93%)    | 59 (83%)  | 12 (17%) | 0        | 100         | 100 |
| 10  | F     | 196/339 (58%)  | 186 (95%) | 9 (5%)   | 1 (0%)   | 24          | 59  |
| 11  | i     | 90/118 (76%)   | 85 (94%)  | 4 (4%)   | 1 (1%)   | 11          | 43  |
| All | All   | 898/1851 (48%) | 846 (94%) | 50 (6%)  | 2 (0%)   | 44          | 73  |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11  | i     | 14  | GLU  |
| 10  | F     | 53  | ASP  |

### 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   | E     | 38/151 (25%) | 38 (100%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed       | Rotameric  | Outliers | Percentiles |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 2   | D     | 93/401 (23%)   | 93 (100%)  | 0        | 100         | 100 |
| 3   | h     | 76/101 (75%)   | 76 (100%)  | 0        | 100         | 100 |
| 4   | j     | 71/101 (70%)   | 71 (100%)  | 0        | 100         | 100 |
| 5   | k     | 78/177 (44%)   | 77 (99%)   | 1 (1%)   | 61          | 78  |
| 6   | l     | 72/84 (86%)    | 70 (97%)   | 2 (3%)   | 38          | 68  |
| 7   | m     | 63/74 (85%)    | 63 (100%)  | 0        | 100         | 100 |
| 8   | n     | 63/66 (96%)    | 63 (100%)  | 0        | 100         | 100 |
| 10  | F     | 185/313 (59%)  | 184 (100%) | 1 (0%)   | 81          | 85  |
| 11  | i     | 89/110 (81%)   | 88 (99%)   | 1 (1%)   | 65          | 79  |
| All | All   | 828/1578 (52%) | 823 (99%)  | 5 (1%)   | 76          | 84  |

All (5) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 5   | k     | 80  | MET  |
| 6   | l     | 83  | ASN  |
| 6   | l     | 89  | SER  |
| 10  | F     | 1   | MET  |
| 11  | i     | 31  | VAL  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 10  | F     | 135 | GLN  |
| 10  | F     | 121 | GLN  |
| 8   | n     | 53  | GLN  |
| 6   | l     | 38  | GLN  |
| 10  | F     | 15  | GLN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed     | Backbone Outliers | Pucker Outliers |
|-----|-------|--------------|-------------------|-----------------|
| 9   | Q     | 37/135 (27%) | 14 (37%)          | 2 (5%)          |

5 of 14 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 9   | Q     | 86  | U    |
| 9   | Q     | 90  | U    |
| 9   | Q     | 94  | U    |
| 9   | Q     | 96  | G    |
| 9   | Q     | 97  | U    |

All (2) RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 9   | Q     | 95  | G    |
| 9   | Q     | 106 | A    |

## 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 [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.

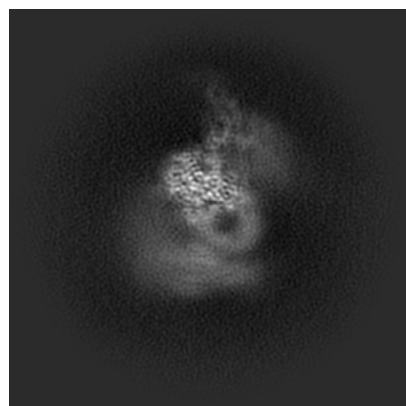
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51226. These allow visual inspection of the internal detail of the map and identification of artifacts.

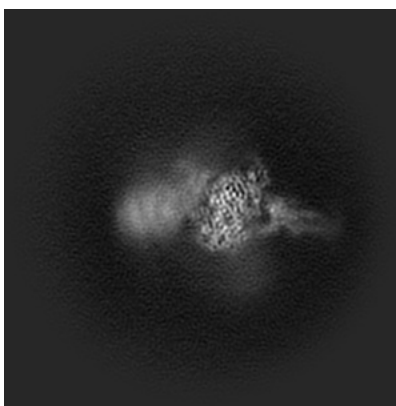
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

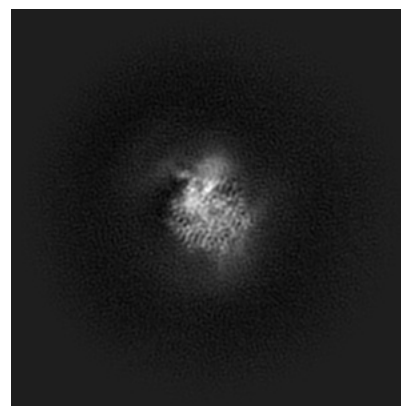
#### 6.1.1 Primary map



X

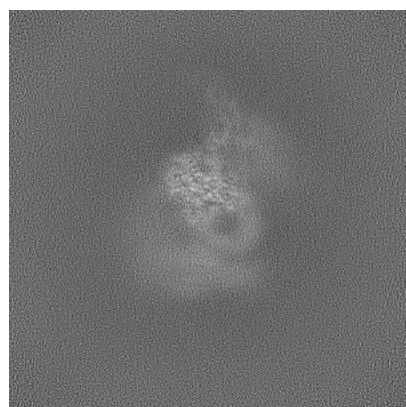


Y

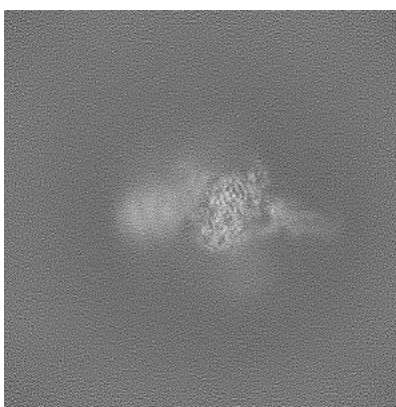


Z

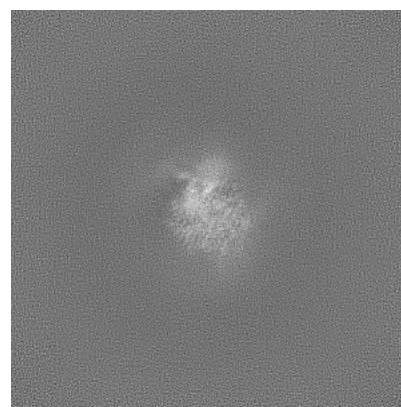
#### 6.1.2 Raw map



X



Y

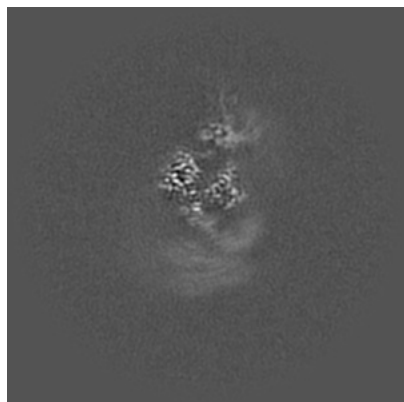


Z

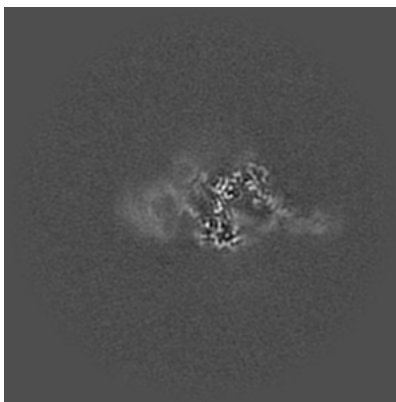
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

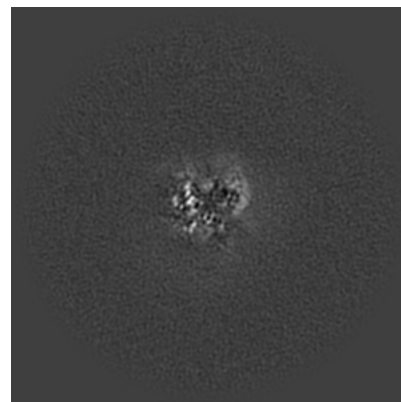
### 6.2.1 Primary map



X Index: 220

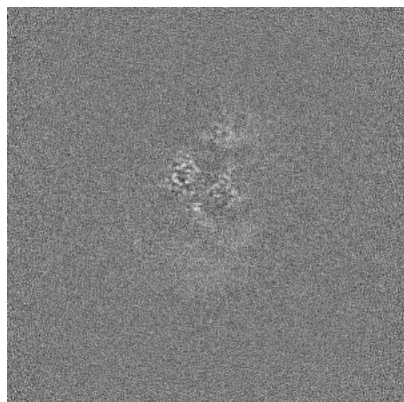


Y Index: 220

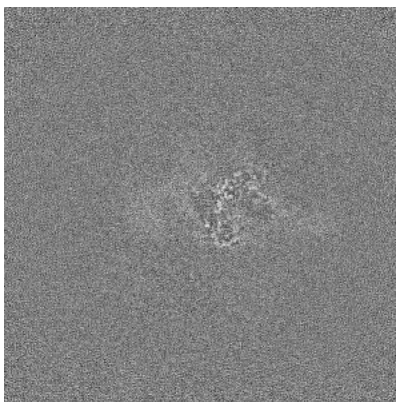


Z Index: 220

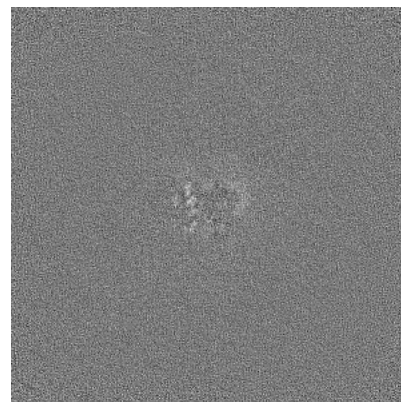
### 6.2.2 Raw map



X Index: 220



Y Index: 220

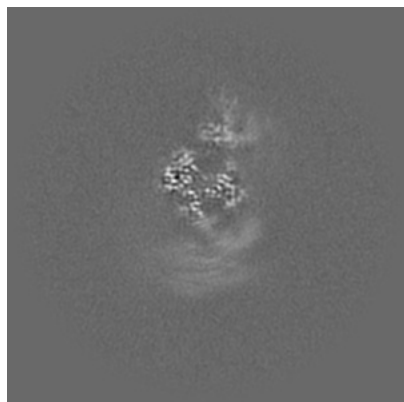


Z Index: 220

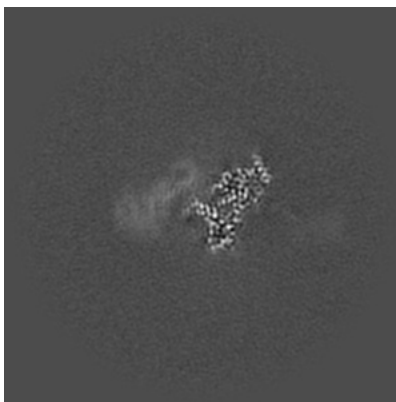
The images above show central slices of the map in three orthogonal directions.

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

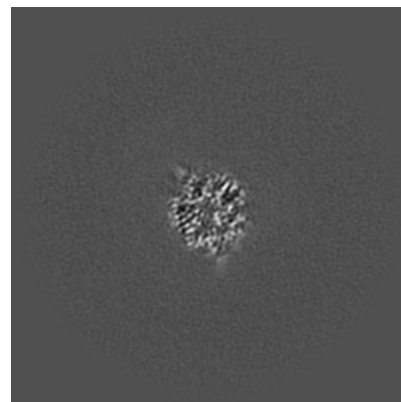
### 6.3.1 Primary map



X Index: 218

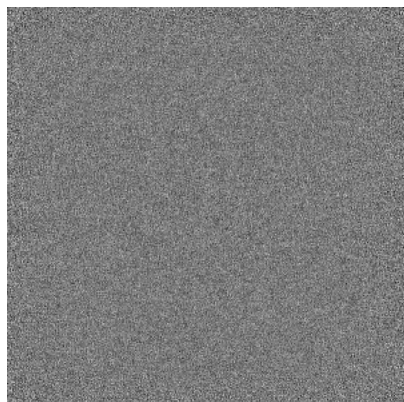


Y Index: 208

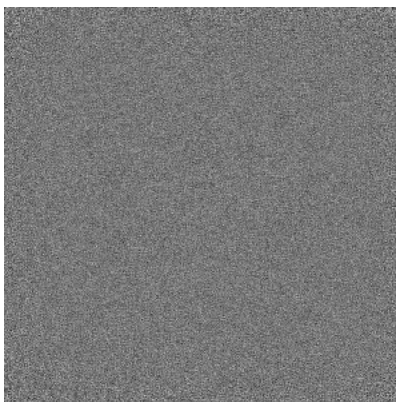


Z Index: 241

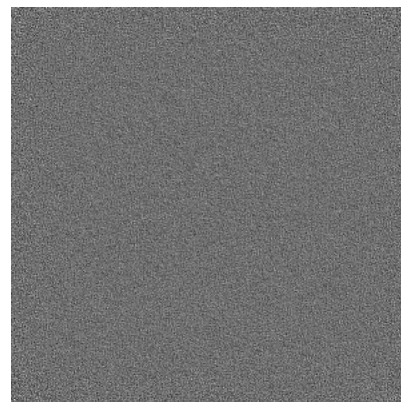
### 6.3.2 Raw map



X Index: 0



Y Index: 0

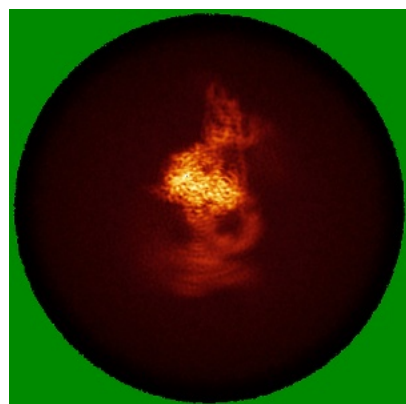


Z Index: 0

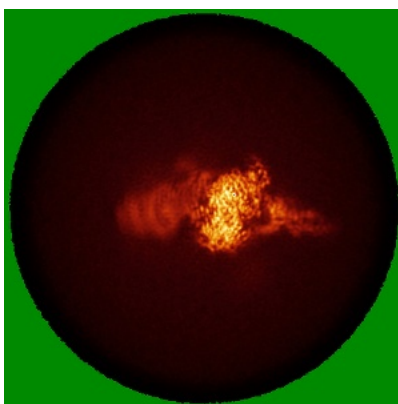
The images above show the largest variance slices of the map in three orthogonal directions.

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

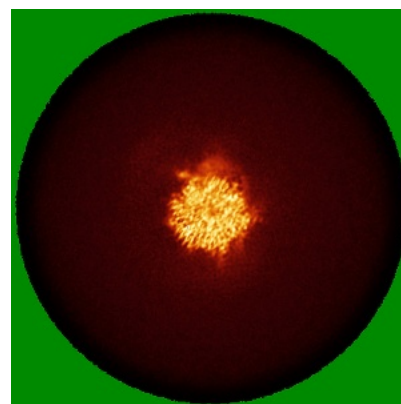
### 6.4.1 Primary map



X

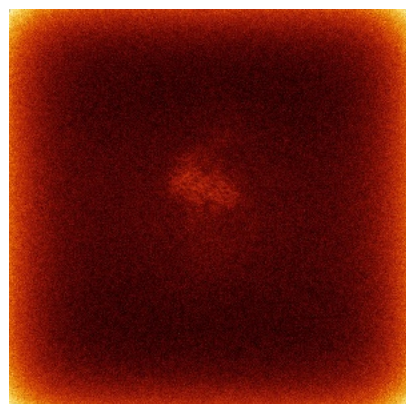


Y

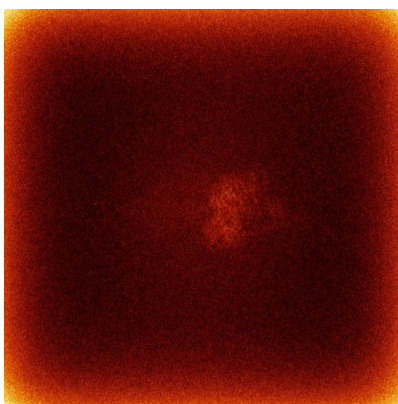


Z

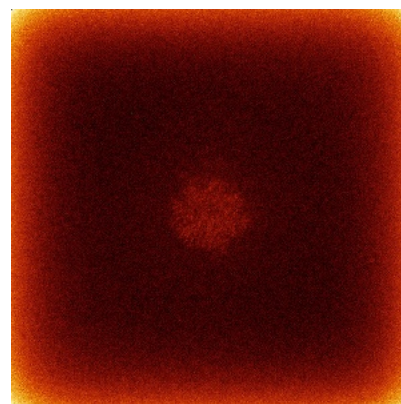
### 6.4.2 Raw map



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.

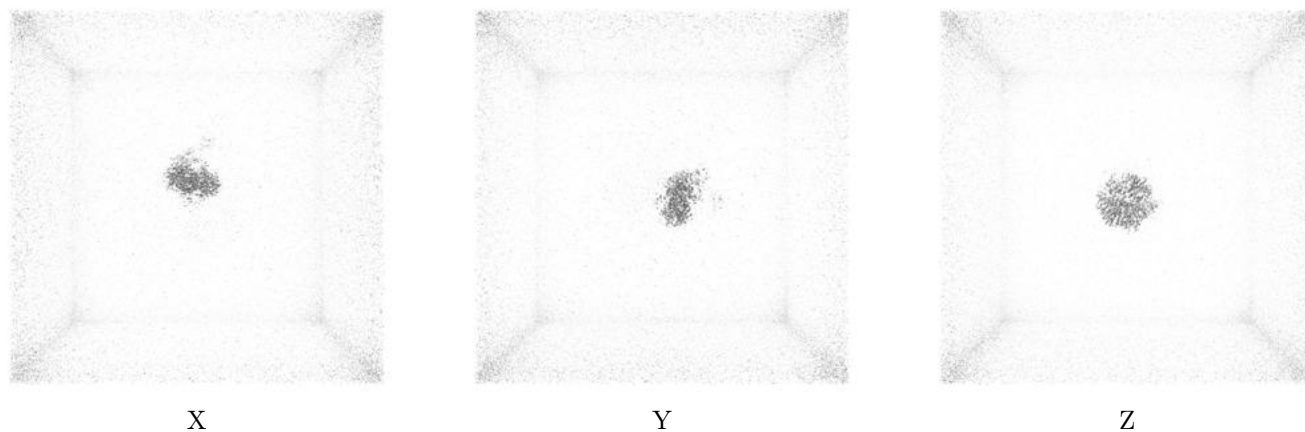
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.024. 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.

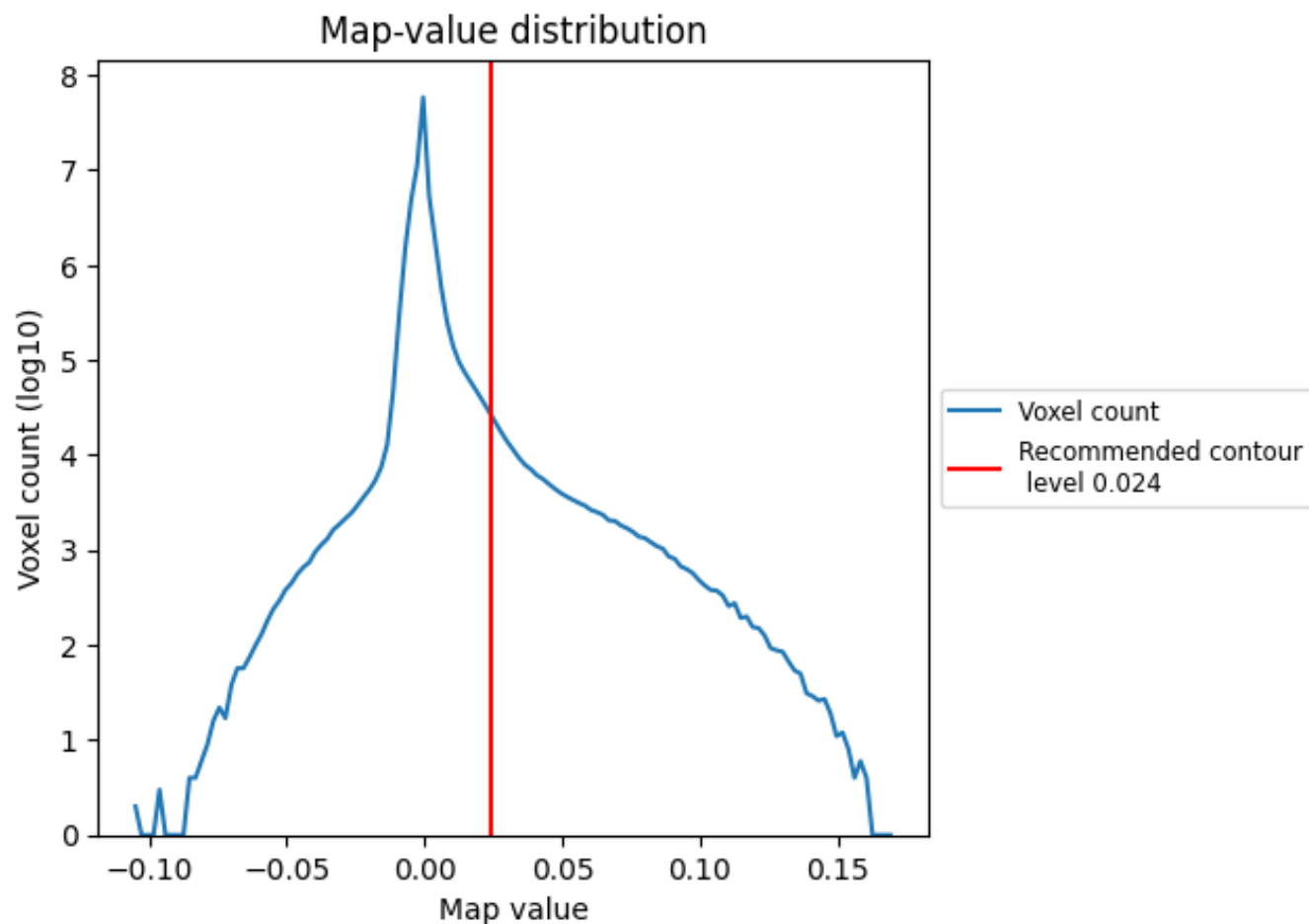
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

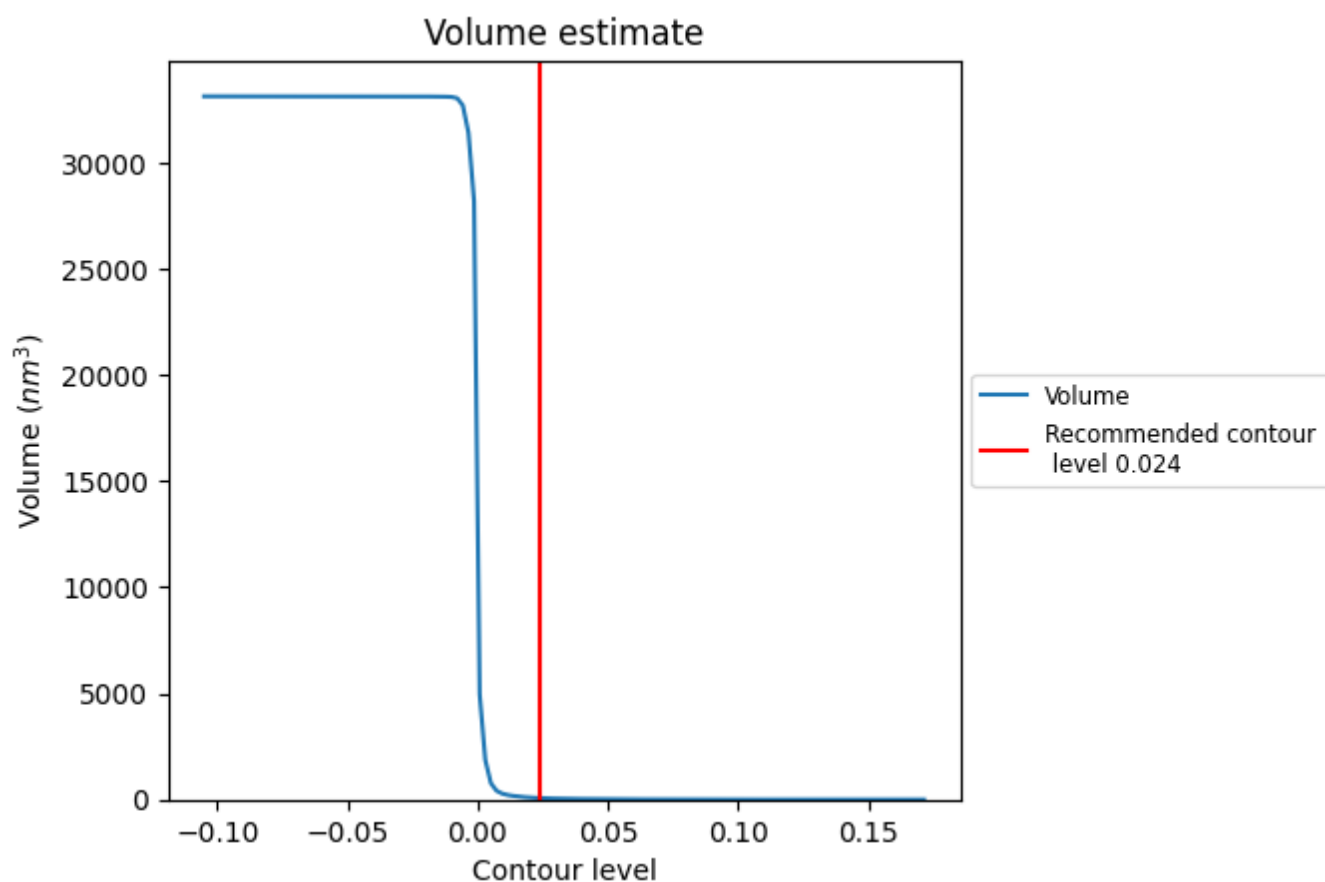
This section contains the results of statistical analysis of the map.

### 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.

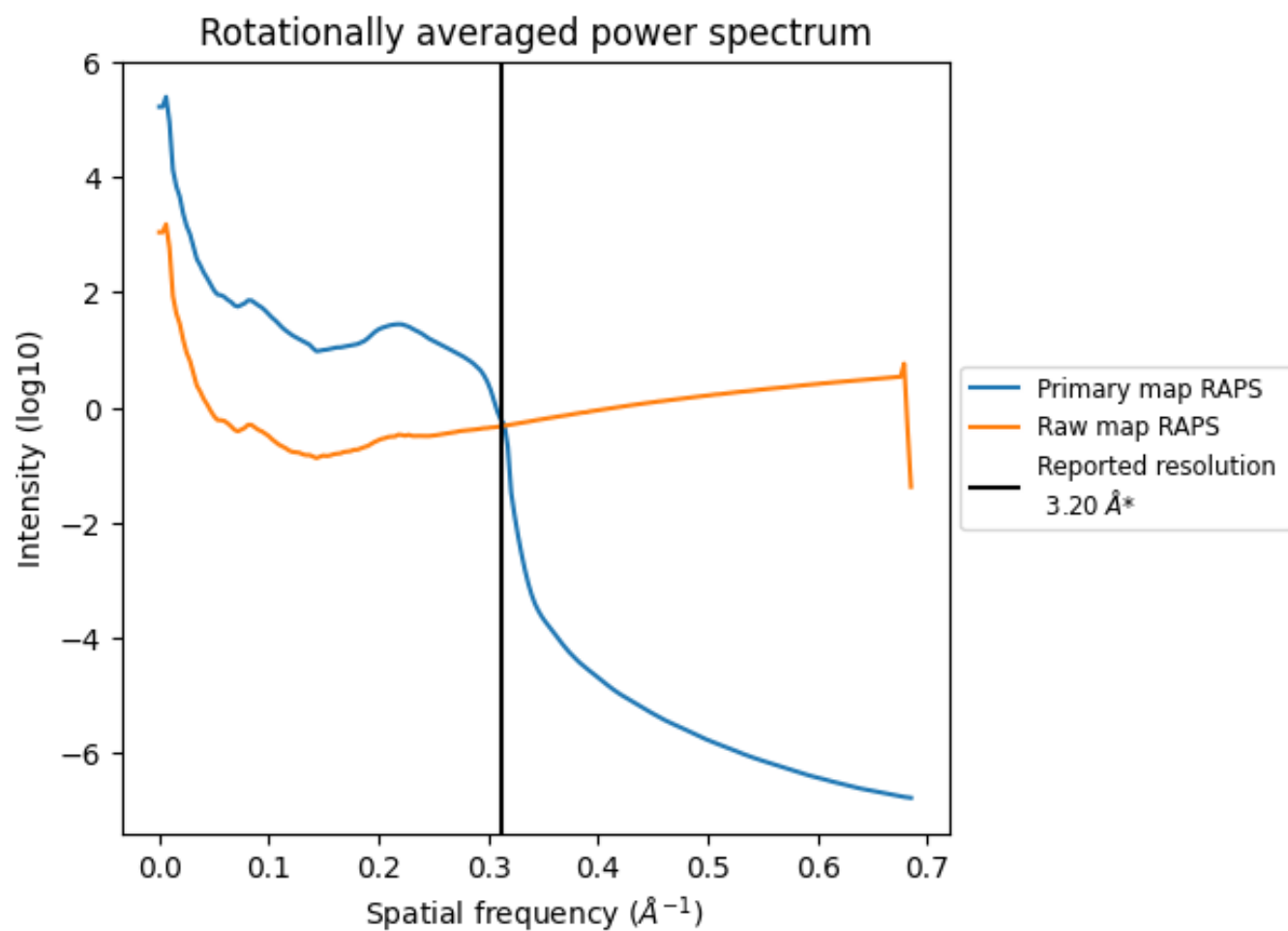
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm<sup>3</sup>; this corresponds to an approximate mass of 63 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 ⓘ

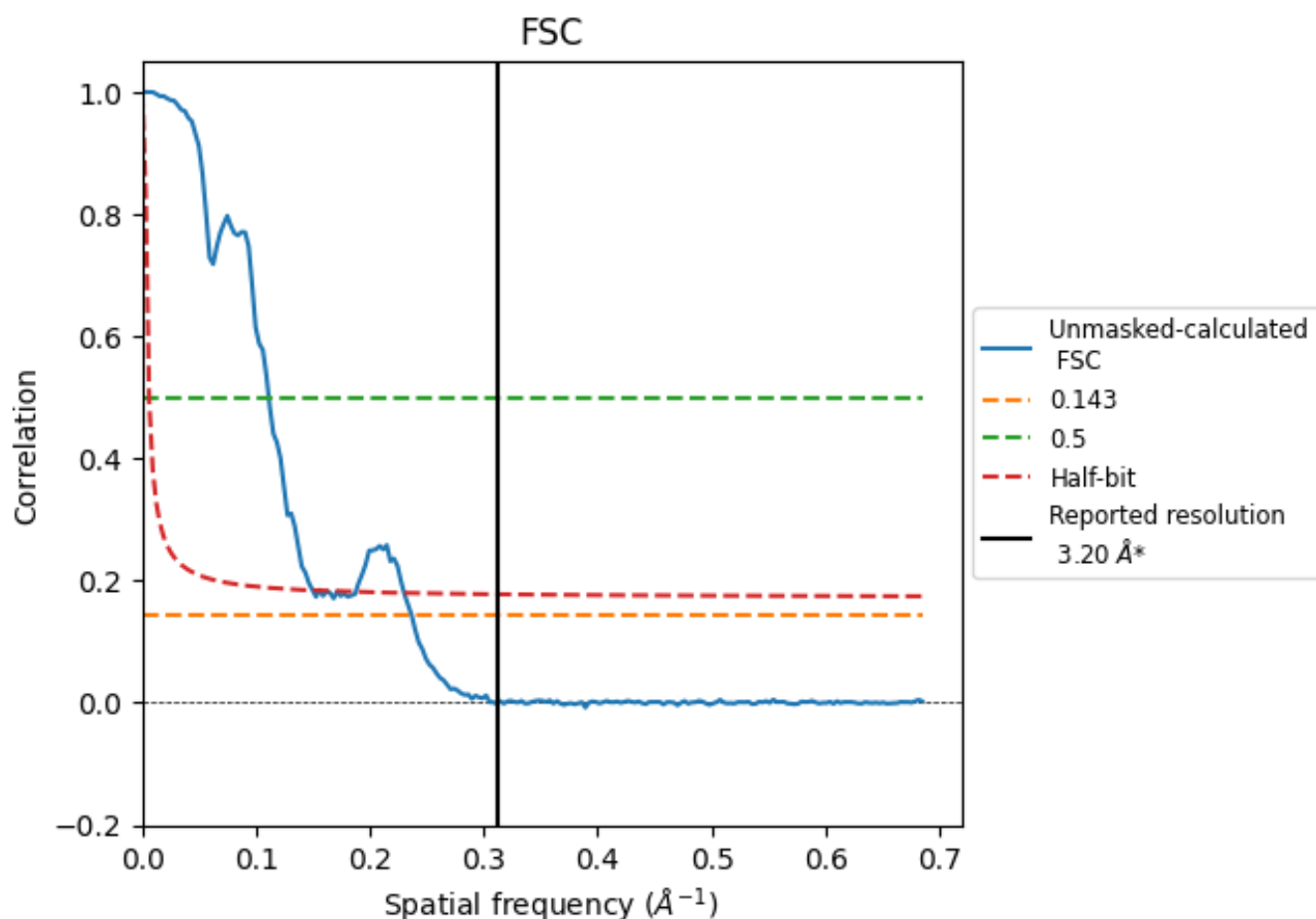


\*Reported resolution corresponds to spatial frequency of 0.312  $\text{\AA}^{-1}$

## 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 0.312 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

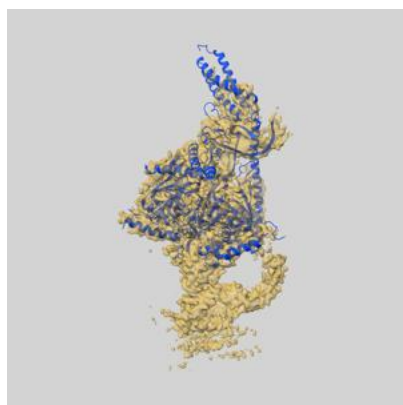
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 3.20                               | -    | -        |
| Author-provided FSC curve | -                                  | -    | -        |
| Unmasked-calculated*      | 4.23                               | 9.00 | 6.68     |

\*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 4.23 differs from the reported value 3.2 by more than 10 %

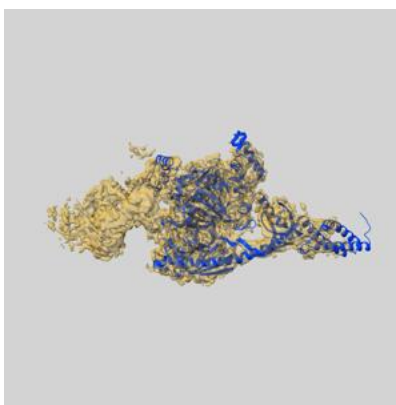
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51226 and PDB model 9GC0. Per-residue inclusion information can be found in section [3](#) on page [6](#).

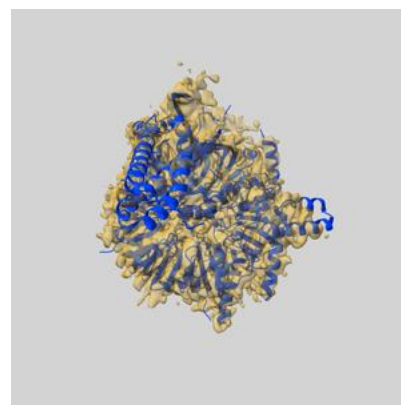
### 9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.024 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](#)

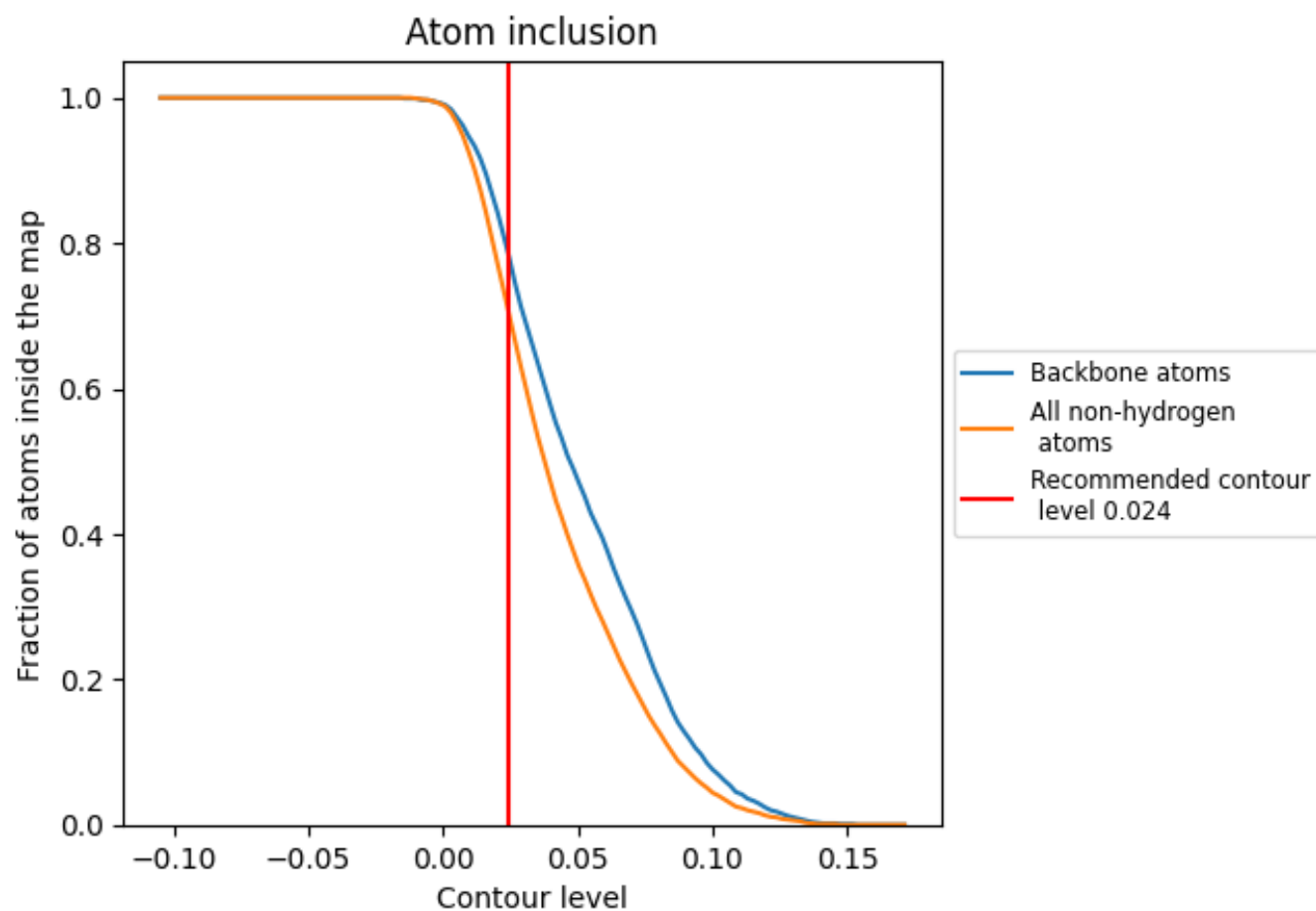


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 71% 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 (0.024) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion     | Q-score            |
|-------|--------------------|--------------------|
| All   | <div></div> 0.7100 | <div></div> 0.3930 |
| D     | <div></div> 0.3470 | <div></div> 0.1760 |
| E     | <div></div> 0.5290 | <div></div> 0.3260 |
| F     | <div></div> 0.5690 | <div></div> 0.3300 |
| Q     | <div></div> 0.7490 | <div></div> 0.3170 |
| h     | <div></div> 0.8450 | <div></div> 0.4880 |
| i     | <div></div> 0.8260 | <div></div> 0.4620 |
| j     | <div></div> 0.8690 | <div></div> 0.4990 |
| k     | <div></div> 0.6840 | <div></div> 0.4100 |
| l     | <div></div> 0.9160 | <div></div> 0.5110 |
| m     | <div></div> 0.9010 | <div></div> 0.5160 |
| n     | <div></div> 0.8860 | <div></div> 0.5030 |

1.0

0.0

<0.0