



## wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:05 AM UTC

PDB ID : 6TAS / pdb\_00006tas  
EMDB ID : EMD-10426  
Title : Structure of the two-fold capsomer of the dArc1 capsid  
Authors : Erlendsson, S.; Morado, D.R.; Shepherd, J.D.; Briggs, J.A.G.  
Deposited on : 2019-10-30  
Resolution : 2.75 Å (reported)  
Based on initial model : 6GSE

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)

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<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

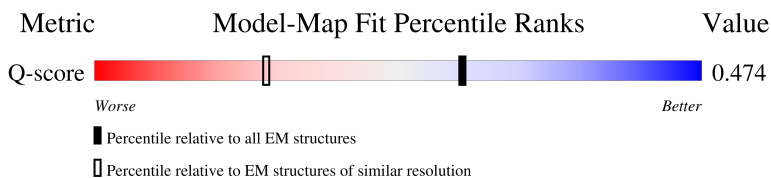
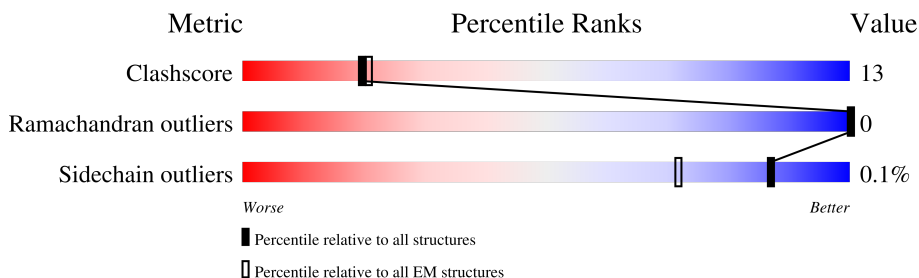
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.75 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                       | -                                                        |
| Q-score               | -                           | 25397                       | 10570 ( 2.25 - 3.25 )                                    |

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     | 254    |  |
| 1   | B     | 254    |  |
| 1   | C     | 254    |  |
| 1   | D     | 254    |  |

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| Mol | Chain | Length | Quality of chain                           |
|-----|-------|--------|--------------------------------------------|
| 1   | E     | 254    | <div><div></div><div>49%16%35%</div></div> |
| 1   | F     | 254    | <div><div></div><div>50%15%35%</div></div> |
| 1   | G     | 254    | <div><div></div><div>6%89%</div></div>     |
| 1   | H     | 254    | <div><div></div><div>6%89%</div></div>     |

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8552 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 Activity-regulated cytoskeleton associated protein 1.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 1   | A     | 164      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1339  | 852 | 233 | 251 | 3 |         |       |
| 1   | B     | 165      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1347  | 856 | 235 | 253 | 3 |         |       |
| 1   | C     | 166      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1356  | 861 | 237 | 255 | 3 |         |       |
| 1   | G     | 27       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 233   | 137 | 49  | 44  | 3 |         |       |
| 1   | D     | 164      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1339  | 852 | 233 | 251 | 3 |         |       |
| 1   | E     | 165      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1347  | 856 | 235 | 253 | 3 |         |       |
| 1   | F     | 166      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1356  | 861 | 237 | 255 | 3 |         |       |
| 1   | H     | 27       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 233   | 137 | 49  | 44  | 3 |         |       |

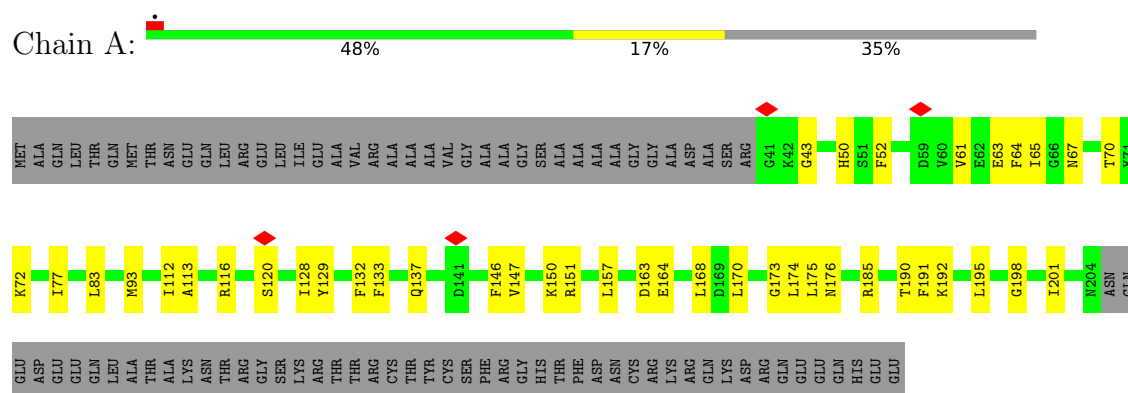
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 2   | G     | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |
| 2   | H     | 1        | Total | Zn | 0       |
|     |       |          | 1     | 1  |         |

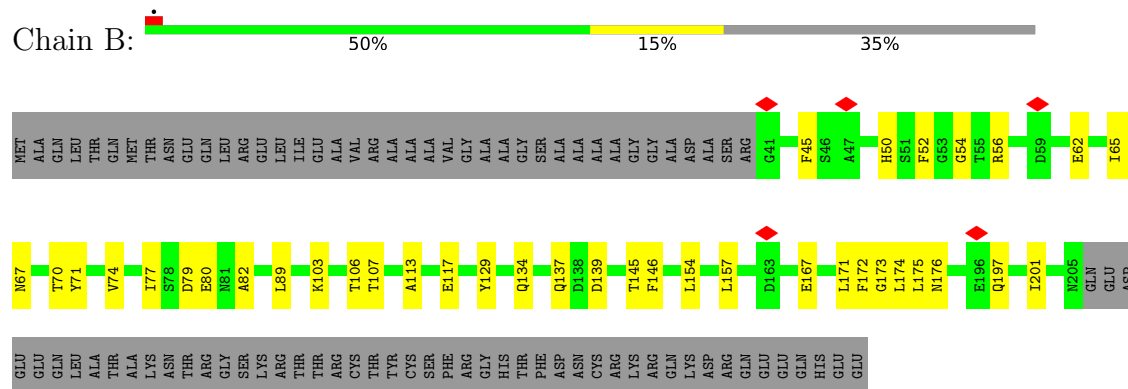
### 3 Residue-property plots

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.

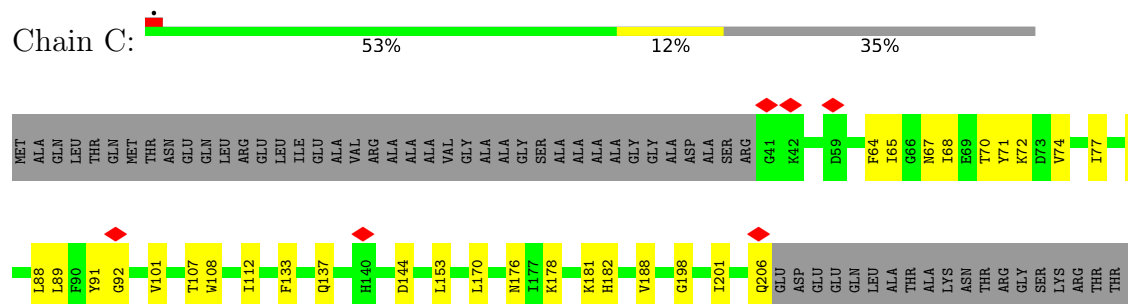
#### • Molecule 1: Activity-regulated cytoskeleton associated protein 1



#### • Molecule 1: Activity-regulated cytoskeleton associated protein 1



#### • Molecule 1: Activity-regulated cytoskeleton associated protein 1



CYS THR  
ALA TYR  
CYS CYS  
SER PHE  
ARG ARG  
GLY HIS  
THR THR  
PHE PHE  
ASN ASN  
CYS CYS  
ARG ARG  
GLN ARG  
GLN LYS  
ASP LYS  
ASP ARG  
GLN GLN  
GLU GLU  
HIS HIS  
GLU GLU

- Molecule 1: Activity-regulated cytoskeleton associated protein 1

Chain G:  6% 89%

MET ALA  
GLN LEU  
THR THR  
GLN MET  
THR THR  
ASN HIS  
GLU GLU  
GLN THR  
PHE PHE  
ARG ARG  
GLU GLU  
LEU LEU  
ILE LEU  
GLU GLU  
VAL VAL  
ARG ARG  
ASP ASP  
ASN ASN  
ALA ALA  
ALA ALA  
GLN GLN  
GLU GLU  
GLY GLY  
ALA ALA  
SER SER  
THR THR  
ALA ALA  
MET MET  
GLY GLY  
SER SER  
THR THR  
TRP TRP  
GLN GLN  
SER SER  
VAL VAL  
GLY GLY  
LYS LYS  
GLU GLU  
ASN ASN  
PHE PHE  
THR THR  
ALA ALA  
T224

VAL GLU  
GLU PHE  
ILE THR  
GLY ASN  
MET THR  
ILE THR  
HIS THR  
TYR THR  
GLU GLU  
PHE PHE  
ASP ASP  
VAL VAL  
GLU GLU  
ILE LEU  
SER SER  
ASP ASP  
GLU GLU  
VAL VAL  
HIS HIS  
ASP ASP  
PRO PRO  
ILE THR  
HIS THR  
GLN GLN  
SER SER  
PHE PHE  
VAL VAL  
GLY GLY  
ILE THR  
SER SER  
GLU GLU  
LEU LEU  
PHE PHE  
TYR THR  
MET MET  
ALA ALA  
SER SER  
THR THR  
TRP TRP  
GLN GLN  
SER SER  
VAL VAL  
GLY GLY  
LYS LYS  
GLU GLU  
ASN ASN  
PHE PHE  
THR THR  
ALA ALA  
T225

PRO THR  
LYS LYS  
PRO PRO  
ALA ALA  
TYR THR  
GLN GLN  
ILE THR  
HIS THR  
TYR THR  
GLU GLU  
PHE PHE  
ASP ASP  
VAL VAL  
GLU GLU  
ILE LEU  
SER SER  
ASP ASP  
GLU GLU  
VAL VAL  
HIS HIS  
ASP ASP  
PRO PRO  
ILE THR  
HIS THR  
GLN GLN  
SER SER  
PHE PHE  
VAL VAL  
GLY GLY  
ILE THR  
SER SER  
GLU GLU  
LEU LEU  
PHE PHE  
TYR THR  
MET MET  
ALA ALA  
SER SER  
THR THR  
TRP TRP  
GLN GLN  
SER SER  
VAL VAL  
GLY GLY  
LYS LYS  
GLU GLU  
ASN ASN  
PHE PHE  
THR THR  
ALA ALA  
T226

LYS HIS  
ILE THR  
SER SER  
ARG ARG  
HIS THR  
SER THR  
VAL THR  
HIS THR  
PHE THR  
GLN GLN  
PHE PHE  
ASP ASP  
LEU LEU  
LEU LEU  
GLU GLU  
GLN GLN  
GLY GLY  
ARG ARG  
ILE THR  
HIS THR  
GLU GLU  
HIS THR  
ASN ASN  
GLN GLN  
LEU LEU  
ALA ALA  
THR THR  
HIS THR  
LYS LYS  
ASN ASN  
THR THR  
ARG ARG  
GLY GLY  
SER SER  
LYS LYS  
HIS THR  
ASP ASP  
GLU GLU  
T227  
T228  
C230  
S231  
F232  
R233  
T236  
F237  
D238  
K242  
R243  
Q244  
K245  
D246

R247  
Q248  
E249  
E250  
GLN  
HIS  
GLU  
GLU

- Molecule 1: Activity-regulated cytoskeleton associated protein 1

Chain D:  49% 15% 35%

MET ALA  
GLN LEU  
THR THR  
GLN MET  
THR THR  
ASN THR  
GLU GLU  
GLN GLN  
LEU LEU  
ARG ARG  
GLU GLU  
LEU LEU  
ILE THR  
GLU GLU  
VAL VAL  
ALA ALA  
ARG ARG  
ALA ALA  
ALA ALA  
VAL VAL  
GLY GLY  
ALA ALA  
GLY GLY  
SER SER  
GLY GLY  
ALA ALA  
ALA ALA  
ASP ASP  
ALA ALA  
ALA ALA  
ARG ARG  
G41  
K42  
G43  
F52  
D59  
V60  
E62  
E63  
F64  
I65  
T70  
Y71  
K72  
I77

L83  
M93  
I112  
A113  
H118  
I127  
I128  
Y129  
M130  
E131  
F132  
F133  
Q137  
D141  
F146  
V147  
R151  
L157  
D163  
E164  
L168  
D169  
L170  
G173  
L174  
L175  
N176  
R185  
T190  
F191  
K192  
L195  
G198  
I201  
N204  
ASN  
GLN  
GLU  
ASP  
GLU  
GLU  
GLN

LEU ALA  
THR THR  
ALA ALA  
LEU LEU  
ASN ASN  
THR THR  
ARG ARG  
GLY GLY  
LYS LYS  
SER SER  
ARG ARG  
THR THR  
PHE PHE  
CYS CYS  
SER SER  
PHE PHE  
GLY GLY  
ALA ALA  
ASP ASP  
GLY GLY  
CYS CYS  
ARG ARG  
LYS LYS  
ARG ARG  
GLN GLN  
GLU GLU  
GLN GLN  
HIS THR  
GLU GLU

- Molecule 1: Activity-regulated cytoskeleton associated protein 1

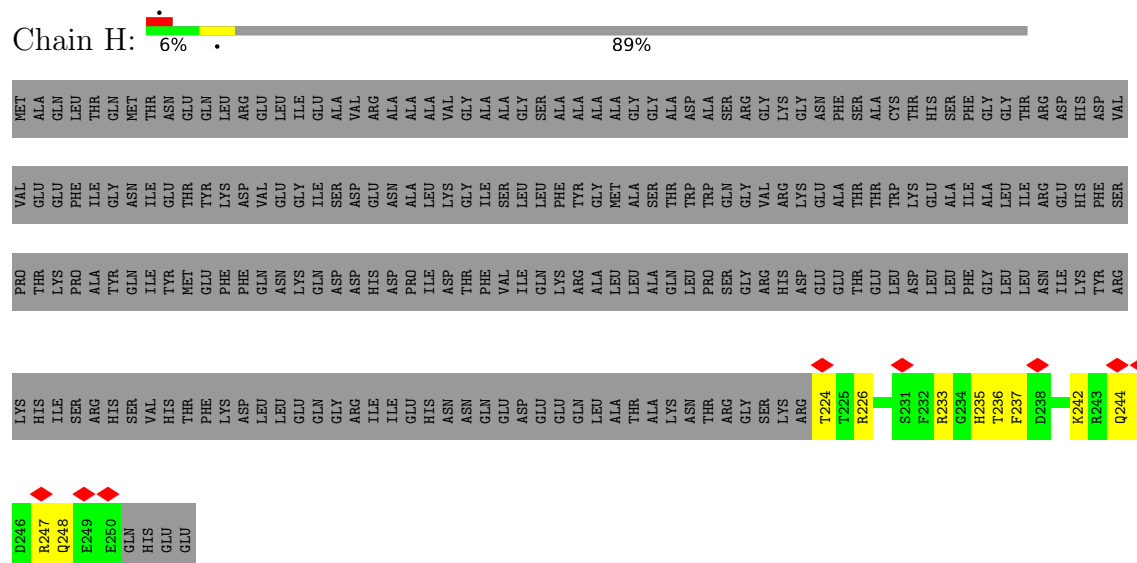
Chain E:  49% 16% 35%

MET ALA  
GLN LEU  
THR THR  
GLN MET  
THR THR  
ASN THR  
GLU GLU  
GLN GLN  
LEU LEU  
ARG ARG  
GLU GLU  
ILE THR  
GLU GLU  
VAL VAL  
ALA ALA  
ARG ARG  
ALA ALA  
ALA ALA  
VAL VAL  
GLY GLY  
ALA ALA  
ALA ALA  
GLY GLY  
SER SER  
GLY GLY  
CYS CYS  
ARG ARG  
ALA ALA  
ALA ALA  
ALA ALA  
GLY GLY  
ASP ASP  
ALA ALA  
SER SER  
GLN GLN  
HIS THR  
GLU GLU  
G41  
F45  
S46  
A47  
C48  
T49  
F52  
S53  
G54  
T55  
R56  
E62  
I65  
G66  
T70

Y71  
V74  
I77  
S78  
D79  
E80  
R81  
A82  
L89  
M93  
K103  
T106  
T107  
A113  
E117  
Y129  
Q134  
Q137  
D138  
D139  
T145  
F146  
L154  
L157  
E167  
L171  
F172  
G173  
L174  
L175  
N176  
Q197  
T201  
N205  
GLN  
GLU  
ASP  
GLU  
GLU  
GLN  
LEU

ALA THR  
ALA LYS  
ASN THR  
THR ARG  
GLY GLY  
SER SER  
LYS LYS  
ARG ARG  
THR THR  
THR THR  
ARG ARG  
CYS CYS  
THR THR  
TYR TYR  
CYS CYS  
SER SER  
PHE PHE  
ARG ARG  
GLY GLY  
HIS THR  
THR THR  
PHE PHE  
ASP ASP  
ASN ASN  
CYS CYS  
ARG ARG  
LYS LYS  
ARG ARG  
GLN GLN  
LYS LYS  
ASP ASP  
GLY GLY  
GLN GLN  
GLU GLU  
GLU GLU  
HIS THR  
GLU GLU

- Molecule 1: Activity-regulated cytoskeleton associated protein 1



## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, C1                               | Depositor |
| Number of particles used             | 1685349                                 | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | FEI TITAN KRIOS                         | Depositor |
| Voltage (kV)                         | 300                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 35                                      | Depositor |
| Minimum defocus (nm)                 | 1000                                    | Depositor |
| Maximum defocus (nm)                 | 4000                                    | Depositor |
| Magnification                        | 105000                                  | Depositor |
| Image detector                       | GATAN K2 SUMMIT (4k x 4k)               | Depositor |
| Maximum map value                    | 0.384                                   | Depositor |
| Minimum map value                    | -0.007                                  | Depositor |
| Average map value                    | 0.001                                   | Depositor |
| Map value standard deviation         | 0.013                                   | Depositor |
| Recommended contour level            | 0.04                                    | Depositor |
| Map size (Å)                         | 179.228, 179.228, 179.228               | wwPDB     |
| Map dimensions                       | 148, 148, 148                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.211, 1.211, 1.211                     | Depositor |

## 5 Model quality

### 5.1 Standard geometry

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

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     | 0.38         | 0/1372      | 0.55        | 0/1851         |
| 1   | B     | 0.32         | 0/1380      | 0.51        | 0/1862         |
| 1   | C     | 0.30         | 0/1389      | 0.52        | 0/1874         |
| 1   | D     | 0.41         | 0/1372      | 0.63        | 2/1851 (0.1%)  |
| 1   | E     | 0.28         | 0/1380      | 0.49        | 0/1862         |
| 1   | F     | 0.33         | 0/1389      | 0.56        | 1/1874 (0.1%)  |
| 1   | G     | 0.96         | 0/236       | 1.49        | 2/312 (0.6%)   |
| 1   | H     | 1.00         | 0/236       | 1.43        | 1/312 (0.3%)   |
| All | All   | 0.40         | 0/8754      | 0.63        | 6/11798 (0.1%) |

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|------|-------------|----------|
| 1   | F     | 186 | HIS  | O-C-N    | 8.03 | 130.38      | 122.03   |
| 1   | D     | 118 | HIS  | CA-CB-CG | 6.62 | 120.42      | 113.80   |
| 1   | H     | 235 | HIS  | N-CA-C   | 5.80 | 116.05      | 107.88   |
| 1   | G     | 233 | ARG  | CB-CG-CD | 5.54 | 124.03      | 111.30   |
| 1   | G     | 232 | PHE  | O-C-N    | 5.31 | 130.13      | 123.23   |

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     | 1339  | 0        | 1292     | 40      | 0            |
| 1   | B     | 1347  | 0        | 1298     | 30      | 0            |
| 1   | C     | 1356  | 0        | 1306     | 31      | 0            |
| 1   | D     | 1339  | 0        | 1292     | 29      | 0            |
| 1   | E     | 1347  | 0        | 1298     | 31      | 0            |
| 1   | F     | 1356  | 0        | 1306     | 40      | 0            |
| 1   | G     | 233   | 0        | 214      | 17      | 0            |
| 1   | H     | 233   | 0        | 214      | 19      | 0            |
| 2   | G     | 1     | 0        | 0        | 0       | 0            |
| 2   | H     | 1     | 0        | 0        | 0       | 0            |
| All | All   | 8552  | 0        | 8220     | 210     | 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 13.

The worst 5 of 210 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:F:164:GLU:OE2 | 1:F:191:PHE:HD2 | 1.45                     | 0.98              |
| 1:A:137:GLN:NE2 | 1:A:175:LEU:HA  | 1.82                     | 0.93              |
| 1:F:91:TYR:CE1  | 1:H:247:ARG:HD3 | 2.05                     | 0.91              |
| 1:F:164:GLU:OE2 | 1:F:191:PHE:CD2 | 2.23                     | 0.91              |
| 1:A:137:GLN:HB3 | 1:A:146:PHE:CE2 | 2.06                     | 0.90              |

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   | A     | 162/254 (64%) | 153 (94%) | 9 (6%)  | 0        | 100         | 100 |
| 1   | B     | 163/254 (64%) | 152 (93%) | 11 (7%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|-----------------|-----------|---------|----------|-------------|-----|
| 1   | C     | 164/254 (65%)   | 151 (92%) | 13 (8%) | 0        | 100         | 100 |
| 1   | D     | 162/254 (64%)   | 153 (94%) | 9 (6%)  | 0        | 100         | 100 |
| 1   | E     | 163/254 (64%)   | 151 (93%) | 12 (7%) | 0        | 100         | 100 |
| 1   | F     | 164/254 (65%)   | 151 (92%) | 13 (8%) | 0        | 100         | 100 |
| 1   | G     | 25/254 (10%)    | 19 (76%)  | 6 (24%) | 0        | 100         | 100 |
| 1   | H     | 25/254 (10%)    | 19 (76%)  | 6 (24%) | 0        | 100         | 100 |
| All | All   | 1028/2032 (51%) | 949 (92%) | 79 (8%) | 0        | 100         | 100 |

There are no Ramachandran outliers to report.

### 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     | 143/212 (68%)  | 143 (100%) | 0        | 100         | 100 |
| 1   | B     | 144/212 (68%)  | 144 (100%) | 0        | 100         | 100 |
| 1   | C     | 145/212 (68%)  | 144 (99%)  | 1 (1%)   | 76          | 86  |
| 1   | D     | 143/212 (68%)  | 143 (100%) | 0        | 100         | 100 |
| 1   | E     | 144/212 (68%)  | 144 (100%) | 0        | 100         | 100 |
| 1   | F     | 145/212 (68%)  | 145 (100%) | 0        | 100         | 100 |
| 1   | G     | 26/212 (12%)   | 26 (100%)  | 0        | 100         | 100 |
| 1   | H     | 26/212 (12%)   | 26 (100%)  | 0        | 100         | 100 |
| All | All   | 916/1696 (54%) | 915 (100%) | 1 (0%)   | 87          | 95  |

All (1) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | C     | 188 | VAL  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | D     | 81  | ASN  |
| 1   | D     | 162 | HIS  |
| 1   | D     | 156 | GLN  |
| 1   | E     | 50  | HIS  |
| 1   | B     | 67  | ASN  |

### 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 [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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.

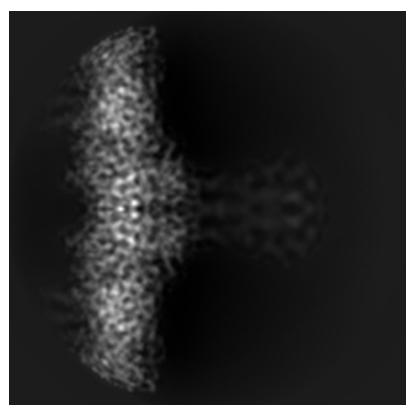
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10426. These allow visual inspection of the internal detail of the map and identification of artifacts.

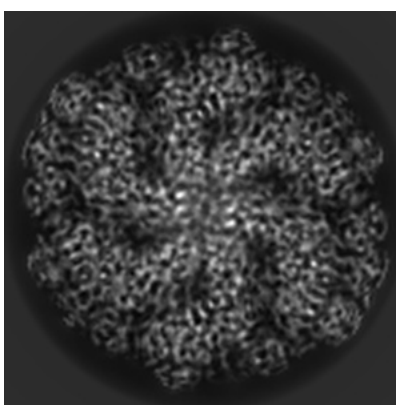
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

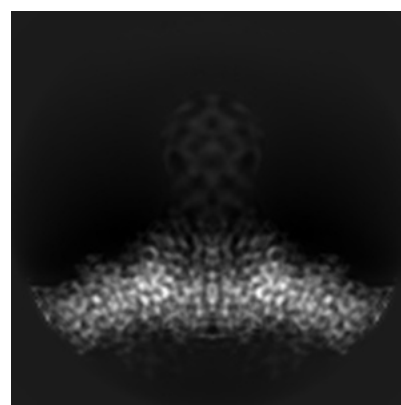
#### 6.1.1 Primary map



X



Y



Z

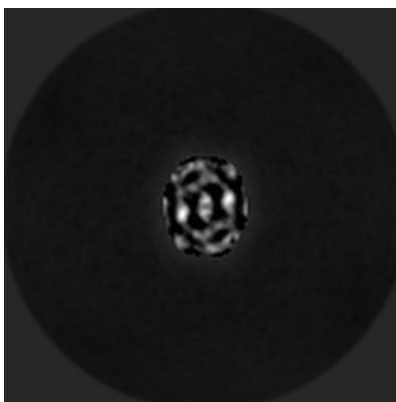
The images above show the map projected in three orthogonal directions.

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

#### 6.2.1 Primary map



X Index: 74



Y Index: 74



Z Index: 74

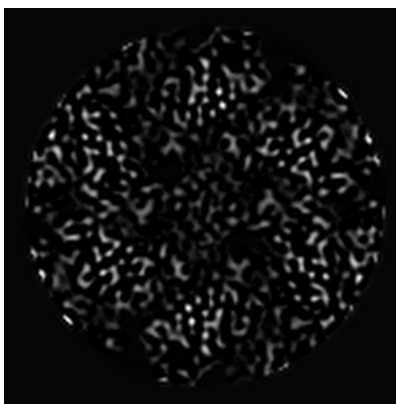
The images above show central slices of the map in three orthogonal directions.

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

### 6.3.1 Primary map



X Index: 53



Y Index: 41

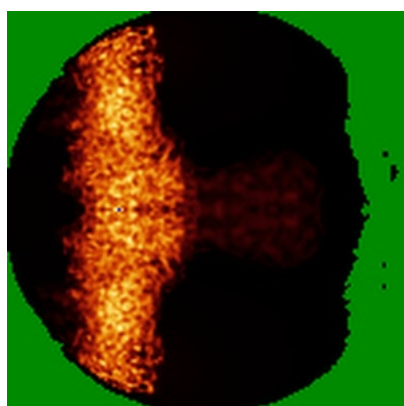


Z Index: 64

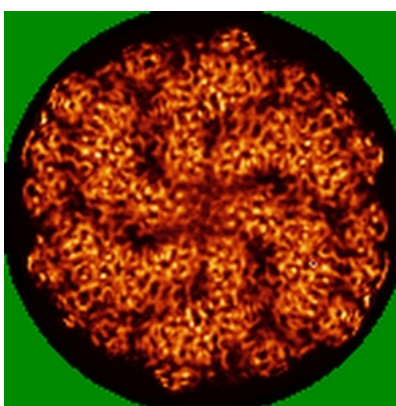
The images above show the largest variance slices of the map in three orthogonal directions.

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

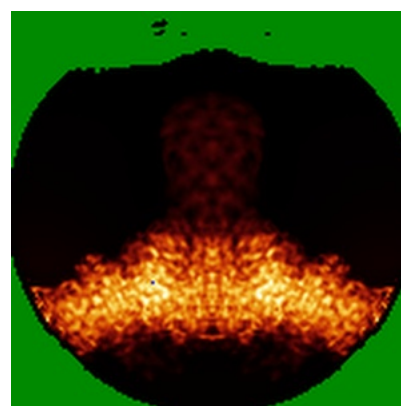
### 6.4.1 Primary map



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

This section was not generated.

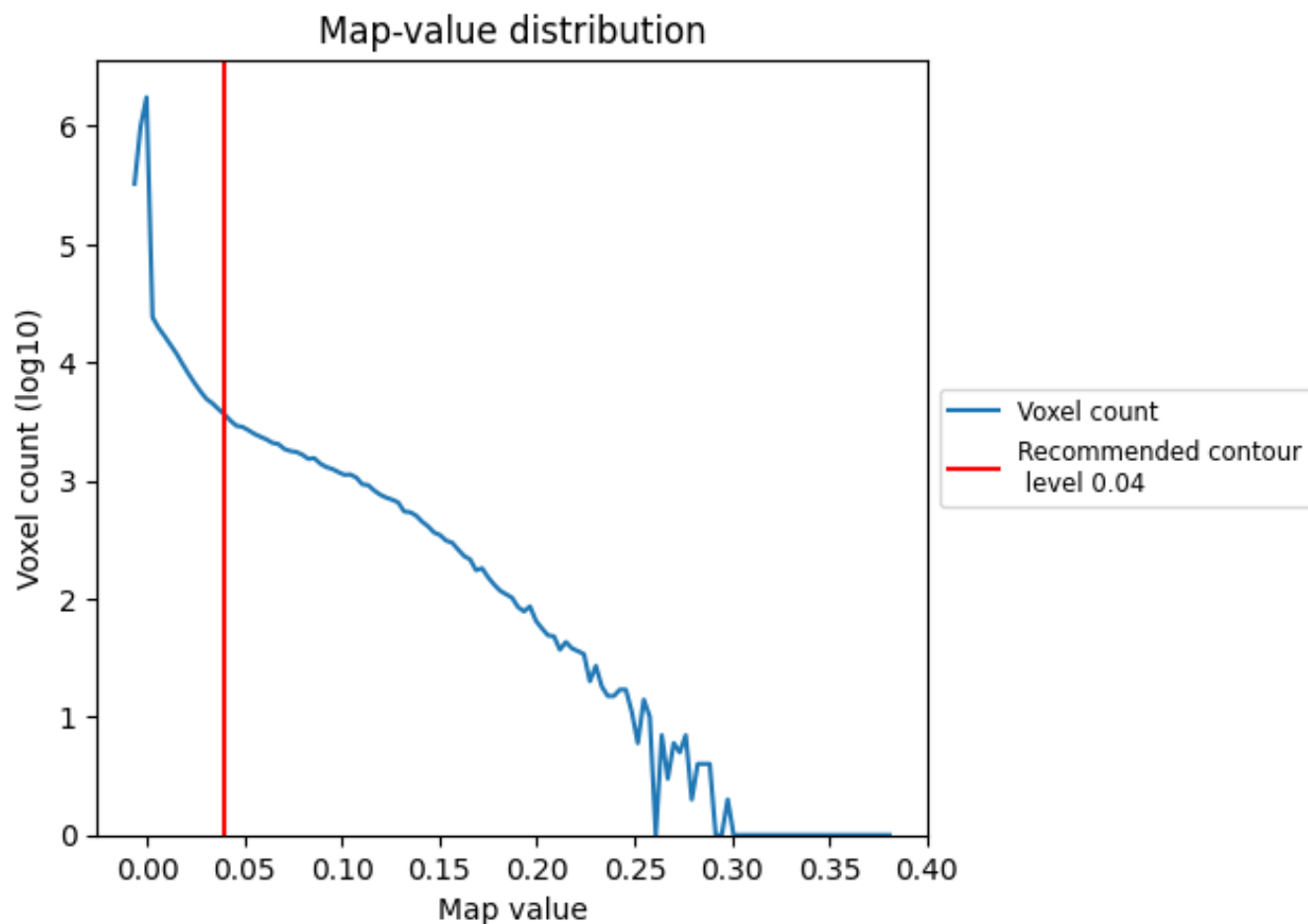
## 6.6 Mask visualisation

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

## 7 Map analysis [i](#)

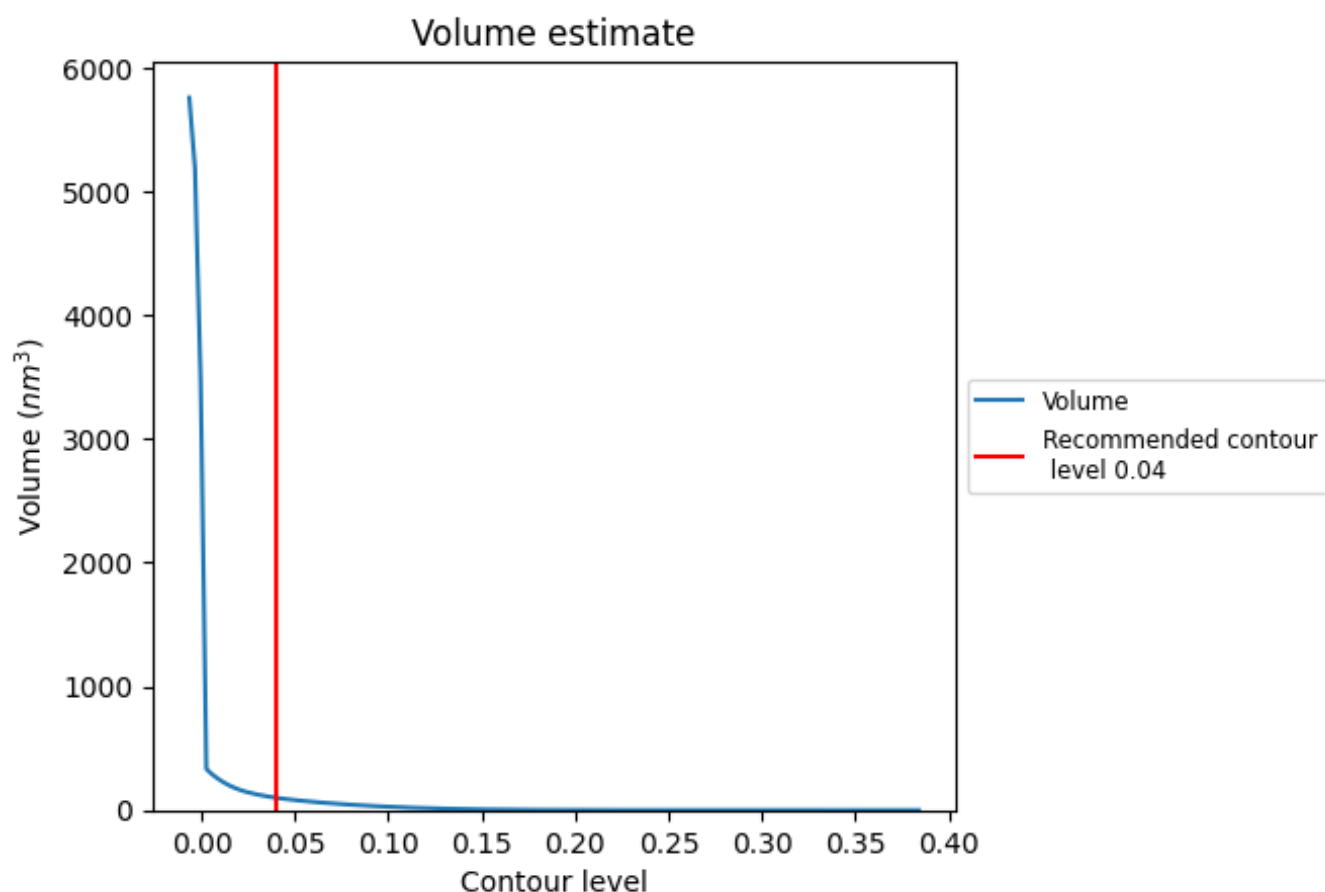
This section contains the results of statistical analysis of the map.

### 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.

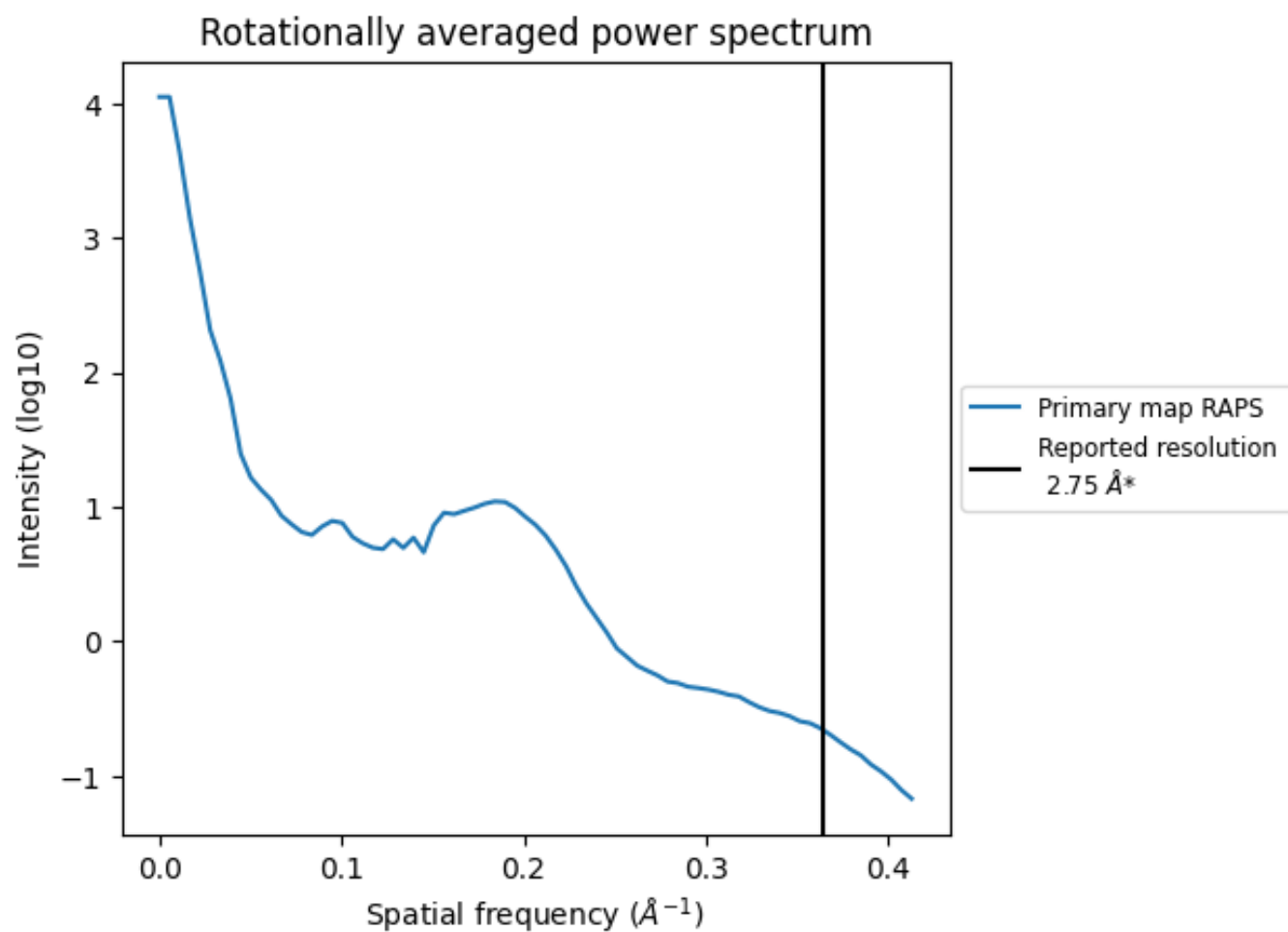
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 100 nm<sup>3</sup>; this corresponds to an approximate mass of 90 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 0.364 Å<sup>-1</sup>

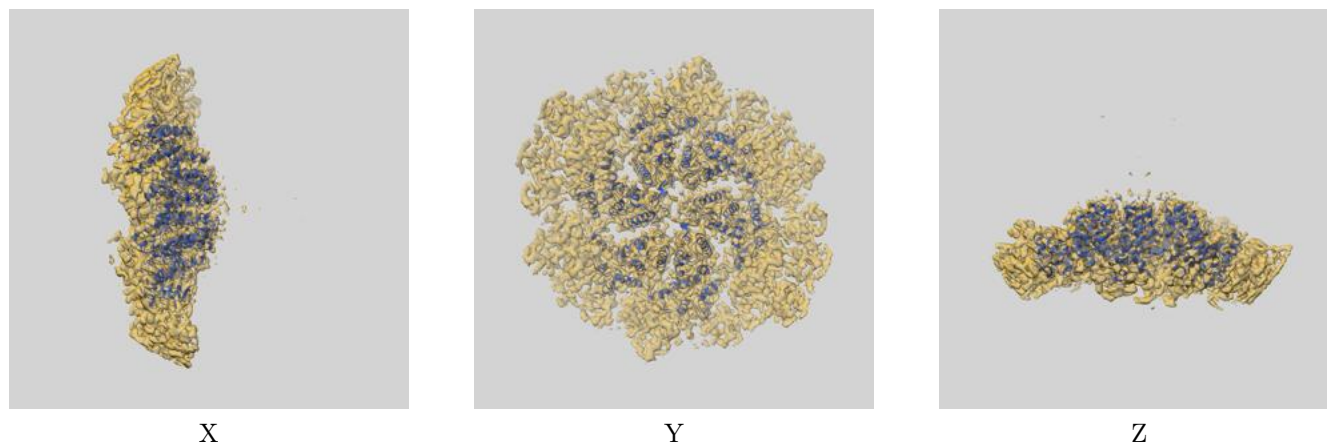
## 8 Fourier-Shell correlation

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

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

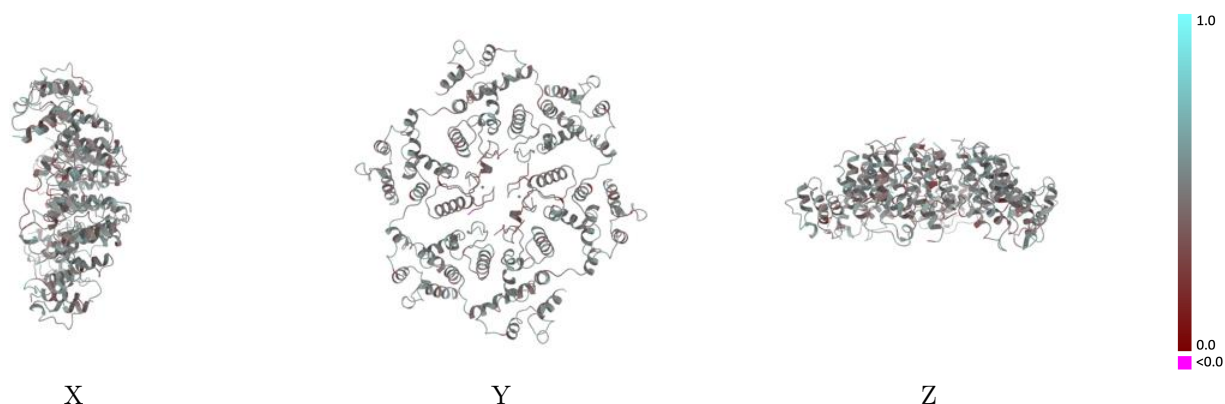
This section contains information regarding the fit between EMDB map EMD-10426 and PDB model 6TAS. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

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



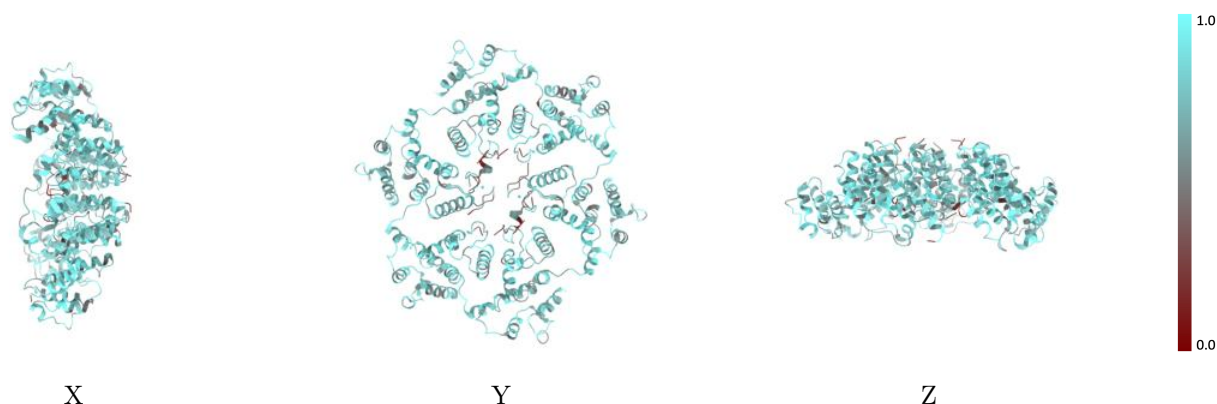
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



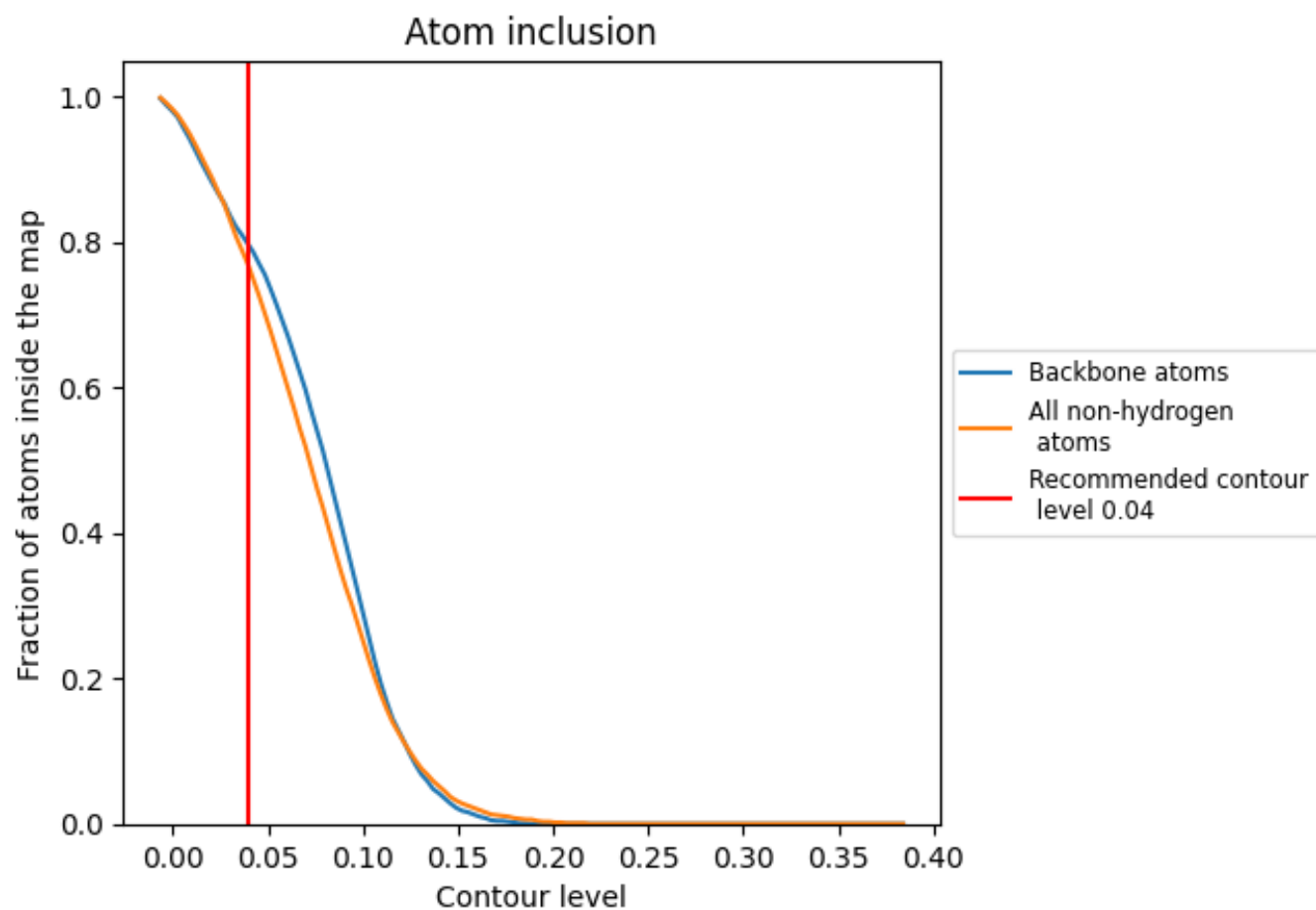
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 77% 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 (0.04) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion               | Q-score                      |
|-------|------------------------------|------------------------------|
| All   | <div><div></div>0.7660</div> | <div><div></div>0.4740</div> |
| A     | <div><div></div>0.7940</div> | <div><div></div>0.4800</div> |
| B     | <div><div></div>0.7820</div> | <div><div></div>0.4800</div> |
| C     | <div><div></div>0.7670</div> | <div><div></div>0.4790</div> |
| D     | <div><div></div>0.7870</div> | <div><div></div>0.4820</div> |
| E     | <div><div></div>0.7860</div> | <div><div></div>0.4830</div> |
| F     | <div><div></div>0.7710</div> | <div><div></div>0.4840</div> |
| G     | <div><div></div>0.4980</div> | <div><div></div>0.3430</div> |
| H     | <div><div></div>0.4750</div> | <div><div></div>0.3440</div> |

1.0

0.0

<0.0