



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 03:08 AM UTC

PDB ID : 7DSD / pdb_00007dsd
EMDB ID : EMD-30831
Title : CALHM1 close state with disordered CTH
Authors : Ren, Y.; Yang, X.; Shen, Y.Q.
Deposited on : 2020-12-30
Resolution : 2.90 Å(reported)

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

We welcome your comments at 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>.

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

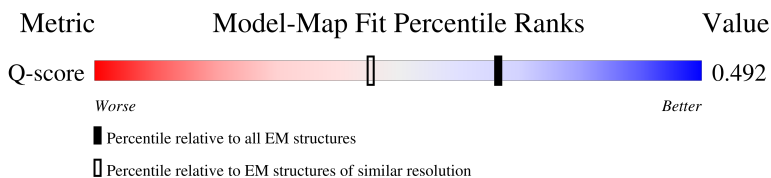
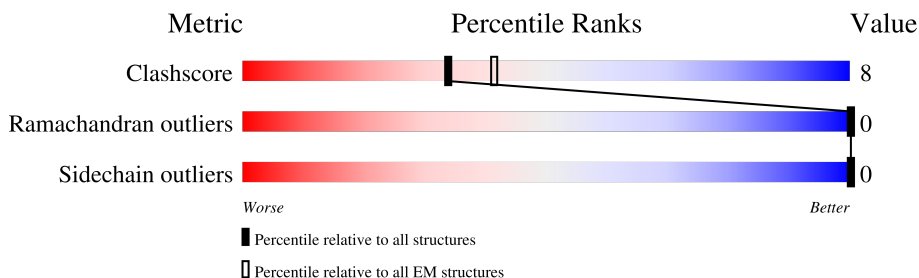
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.90 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.



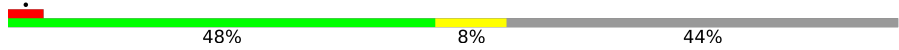
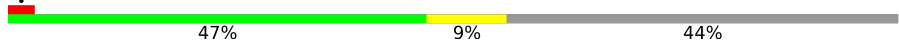
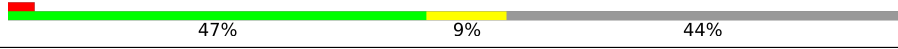
| Metric | Whole archive (#Entries) | EM structures (#Entries) | Similar EM resolution (#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|--|
| Clashscore | 229148 | 23984 | - |
| Ramachandran outliers | 224038 | 23583 | - |
| Sidechain outliers | 223484 | 23102 | - |
| Q-score | - | 25397 | 13054 (2.40 - 3.40) |

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 ≥ 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 | 346 | 47% 9% 44% |
| 1 | B | 346 | 47% 9% 44% |
| 1 | C | 346 | 47% 9% 44% |
| 1 | D | 346 | 48% 8% 44% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 1 | E | 346 |  48% 8% 44% |
| 1 | F | 346 |  47% 9% 44% |
| 1 | G | 346 |  47% 9% 44% |

2 Entry composition [i](#)

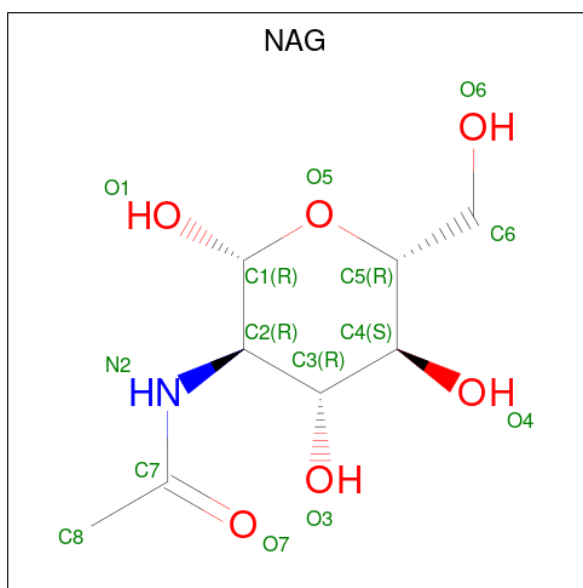
There are 2 unique types of molecules in this entry. The entry contains 10542 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Calcium homeostasis modulator 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|---------|---------|-------|
| | | | Total | C | N | O | S | | |
| 1 | A | 193 | Total 1492 | C 974 | N 241 | O 264 | S 13 | 0 | 0 |
| 1 | B | 193 | Total 1492 | C 974 | N 241 | O 264 | S 13 | 0 | 0 |
| 1 | C | 193 | Total 1492 | C 974 | N 241 | O 264 | S 13 | 0 | 0 |
| 1 | D | 193 | Total 1492 | C 974 | N 241 | O 264 | S 13 | 0 | 0 |
| 1 | E | 193 | Total 1492 | C 974 | N 241 | O 264 | S 13 | 0 | 0 |
| 1 | F | 193 | Total 1492 | C 974 | N 241 | O 264 | S 13 | 0 | 0 |
| 1 | G | 193 | Total 1492 | C 974 | N 241 | O 264 | S 13 | 0 | 0 |

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|---|---|---|---------|
| | | | Total | C | N | O | |
| 2 | A | 1 | 14 | 8 | 1 | 5 | 0 |
| 2 | B | 1 | 14 | 8 | 1 | 5 | 0 |
| 2 | C | 1 | 14 | 8 | 1 | 5 | 0 |
| 2 | D | 1 | 14 | 8 | 1 | 5 | 0 |
| 2 | E | 1 | 14 | 8 | 1 | 5 | 0 |
| 2 | F | 1 | 14 | 8 | 1 | 5 | 0 |
| 2 | G | 1 | 14 | 8 | 1 | 5 | 0 |

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

TRP HIS
HIS THR
CYS CYS
LYS ILE
PRO ILE
PRO MET
LEU LEU
LEU LEU
SER SER
LYS LYS
ARG ARG
THR THR
GLU GLU
GLU VAL
MET MET
SER SER
ASN ASN
GLN GLN
HIS HIS
ALA ALA
HIS HIS
LEU LEU
PRO PRO
ASP ASP
LYS LYS
HIS HIS
SER SER
LEU LEU
THR THR
HIS HIS
SER SER
LEU LEU
THR THR
ASP ASP
GLU GLU
LYS LYS
LYS LYS
ALA ALA
VAL VAL
TYR TYR
TYR TYR
SER SER
LYS LYS
VAL VAL

● Molecule 1: Calcium homeostasis modulator 1



MET ASP
LYS PHE
ARG ARG
ILE ILE
MET MET
V8 Q9
F10 L11
L12 Q12
A13 A13
N14 N14
Q15 Q15
E16 E16
S17 S17
F18 F18
M19 M19
ASN ASN
G21 G21
T40 T40
I57 I57
V58 V58
P59 P59
P60 P60
I61 I61
W62 W62
F63 F63
F64 F64
Y68 Y68
N71 N71
I74 I74
S75 S75
W76 W76
L77 L77
T78 T78
E79 E79
E80 E80
W81 W81
K82 K82
K87 K87
ARG ARG
SER SER
LYS LYS
D91 D91
P92 P92
M98 M98
M102 M102
W113 W113
I114 I114

A115 A115
M119 M119
D120 D120
G121 G121
K122 K122
M139 M139
E140 E140
S146 S146
E149 E149
M191 M191
T194 T194
R201 R201
R204 R204
PRO PRO
PHE PHE
THR THR
GLN GLN
ALA ALA
PHE PHE
LEU LEU
LYS LYS
LEU LEU
THR THR
ASP ASP
GLY GLY
GLU GLU
LYS LYS
SER SER
HIS HIS
TYR TYR
ILE ILE
ASP ASP
THR THR
GLU GLU
ARG ARG
LEU LEU
LYS LYS
LEU LEU
GLY GLY
ILE ILE
PHE PHE
ASP ASP
GLU GLU
THR THR
CYS CYS
LYS LYS
MET MET
GLU GLU
HIS HIS
SER SER
LYS LYS
ALA ALA
VAL VAL
SER SER
PHE PHE
ALA ALA
LYS LYS
VAL VAL

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

THR CYS
LYS LYS
PRO PRO
PRO PRO
LEU LEU
LEU LEU
SER SER
SER SER
LYS LYS
ARG ARG
THR THR
GLU GLU
GLU GLU
MET MET
ASN ASN
GLY GLY
HIS HIS
HIS HIS
ALA ALA
HIS HIS
LEU LEU
ASP ASP
THR THR
HIS HIS
SER SER
LEU LEU
THR THR
GLY GLY
ALA ALA
ASP ASP
GLU GLU
LYS LYS
HIS HIS
HIS HIS
THR THR
ASP ASP
GLY GLY
GLU GLU
LYS LYS
LYS LYS
ALA ALA
VAL VAL
VAL VAL
TYR TYR
TYR TYR
SER SER
LYS LYS
VAL VAL

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---------------------------|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 56801 | 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) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 1.390 | Depositor |
| Minimum map value | -0.580 | Depositor |
| Average map value | -0.001 | Depositor |
| Map value standard deviation | 0.045 | Depositor |
| Recommended contour level | 0.154 | Depositor |
| Map size (\AA) | 263.64, 263.64, 263.64 | wwPDB |
| Map dimensions | 260, 260, 260 | wwPDB |
| Map angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (\AA) | 1.014, 1.014, 1.014 | Depositor |

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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 | 0.18 | 0/1526 | 0.38 | 0/2072 |
| 1 | B | 0.18 | 0/1526 | 0.38 | 0/2072 |
| 1 | C | 0.18 | 0/1526 | 0.38 | 0/2072 |
| 1 | D | 0.18 | 0/1526 | 0.38 | 0/2072 |
| 1 | E | 0.18 | 0/1526 | 0.38 | 0/2072 |
| 1 | F | 0.18 | 0/1526 | 0.38 | 0/2072 |
| 1 | G | 0.18 | 0/1526 | 0.38 | 0/2072 |
| All | All | 0.18 | 0/10682 | 0.38 | 0/14504 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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 | A | 1492 | 0 | 1467 | 28 | 0 |
| 1 | B | 1492 | 0 | 1467 | 26 | 0 |
| 1 | C | 1492 | 0 | 1467 | 27 | 0 |
| 1 | D | 1492 | 0 | 1467 | 25 | 0 |
| 1 | E | 1492 | 0 | 1467 | 25 | 0 |
| 1 | F | 1492 | 0 | 1467 | 27 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | G | 1492 | 0 | 1467 | 28 | 0 |
| 2 | A | 14 | 0 | 13 | 0 | 0 |
| 2 | B | 14 | 0 | 13 | 0 | 0 |
| 2 | C | 14 | 0 | 13 | 0 | 0 |
| 2 | D | 14 | 0 | 13 | 0 | 0 |
| 2 | E | 14 | 0 | 13 | 0 | 0 |
| 2 | F | 14 | 0 | 13 | 0 | 0 |
| 2 | G | 14 | 0 | 13 | 0 | 0 |
| All | All | 10542 | 0 | 10360 | 171 | 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 8.

The worst 5 of 171 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:C:91:ASP:HB3 | 1:C:92:PRO:CD | 1.83 | 1.09 |
| 1:B:91:ASP:HB3 | 1:B:92:PRO:CD | 1.83 | 1.09 |
| 1:D:91:ASP:HB3 | 1:D:92:PRO:CD | 1.83 | 1.09 |
| 1:E:91:ASP:HB3 | 1:E:92:PRO:CD | 1.82 | 1.08 |
| 1:A:91:ASP:HB3 | 1:A:92:PRO:CD | 1.83 | 1.08 |

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 | 187/346 (54%) | 182 (97%) | 5 (3%) | 0 | 100 100 |
| 1 | B | 187/346 (54%) | 182 (97%) | 5 (3%) | 0 | 100 100 |
| 1 | C | 187/346 (54%) | 182 (97%) | 5 (3%) | 0 | 100 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|---------|----------|-------------|-----|
| 1 | D | 187/346 (54%) | 182 (97%) | 5 (3%) | 0 | 100 | 100 |
| 1 | E | 187/346 (54%) | 182 (97%) | 5 (3%) | 0 | 100 | 100 |
| 1 | F | 187/346 (54%) | 182 (97%) | 5 (3%) | 0 | 100 | 100 |
| 1 | G | 187/346 (54%) | 182 (97%) | 5 (3%) | 0 | 100 | 100 |
| All | All | 1309/2422 (54%) | 1274 (97%) | 35 (3%) | 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 | 155/306 (51%) | 155 (100%) | 0 | 100 | 100 |
| 1 | B | 155/306 (51%) | 155 (100%) | 0 | 100 | 100 |
| 1 | C | 155/306 (51%) | 155 (100%) | 0 | 100 | 100 |
| 1 | D | 155/306 (51%) | 155 (100%) | 0 | 100 | 100 |
| 1 | E | 155/306 (51%) | 155 (100%) | 0 | 100 | 100 |
| 1 | F | 155/306 (51%) | 155 (100%) | 0 | 100 | 100 |
| 1 | G | 155/306 (51%) | 155 (100%) | 0 | 100 | 100 |
| All | All | 1085/2142 (51%) | 1085 (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. 5 of 7 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | D | 71 | ASN |
| 1 | E | 71 | ASN |
| 1 | G | 71 | ASN |
| 1 | F | 71 | ASN |
| 1 | C | 71 | 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](#)

7 ligands are modelled in this entry.

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

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 2 | NAG | E | 1001 | 1 | 14,14,15 | 0.30 | 0 | 17,19,21 | 0.53 | 0 |
| 2 | NAG | A | 1001 | 1 | 14,14,15 | 0.29 | 0 | 17,19,21 | 0.52 | 0 |
| 2 | NAG | G | 1001 | 1 | 14,14,15 | 0.29 | 0 | 17,19,21 | 0.52 | 0 |
| 2 | NAG | C | 1001 | 1 | 14,14,15 | 0.30 | 0 | 17,19,21 | 0.52 | 0 |
| 2 | NAG | B | 1001 | 1 | 14,14,15 | 0.30 | 0 | 17,19,21 | 0.52 | 0 |
| 2 | NAG | F | 1001 | 1 | 14,14,15 | 0.31 | 0 | 17,19,21 | 0.52 | 0 |
| 2 | NAG | D | 1001 | 1 | 14,14,15 | 0.29 | 0 | 17,19,21 | 0.53 | 0 |

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

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|------|---------|-----------|---------|
| 2 | NAG | E | 1001 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 2 | NAG | A | 1001 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 2 | NAG | G | 1001 | 1 | - | 0/6/23/26 | 0/1/1/1 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|------|---------|-----------|---------|
| 2 | NAG | C | 1001 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 2 | NAG | B | 1001 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 2 | NAG | F | 1001 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 2 | NAG | D | 1001 | 1 | - | 0/6/23/26 | 0/1/1/1 |

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.

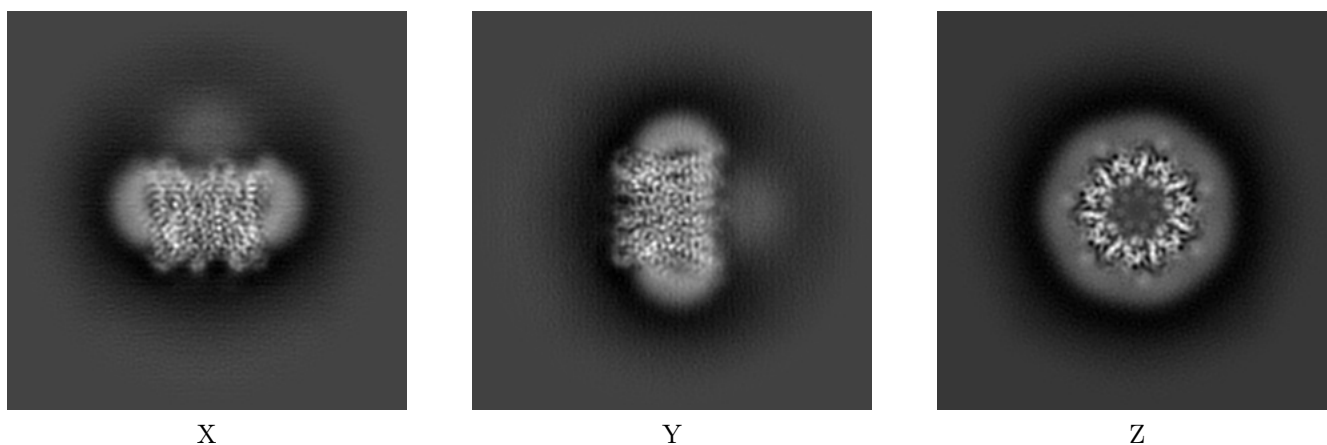
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30831. 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](#)

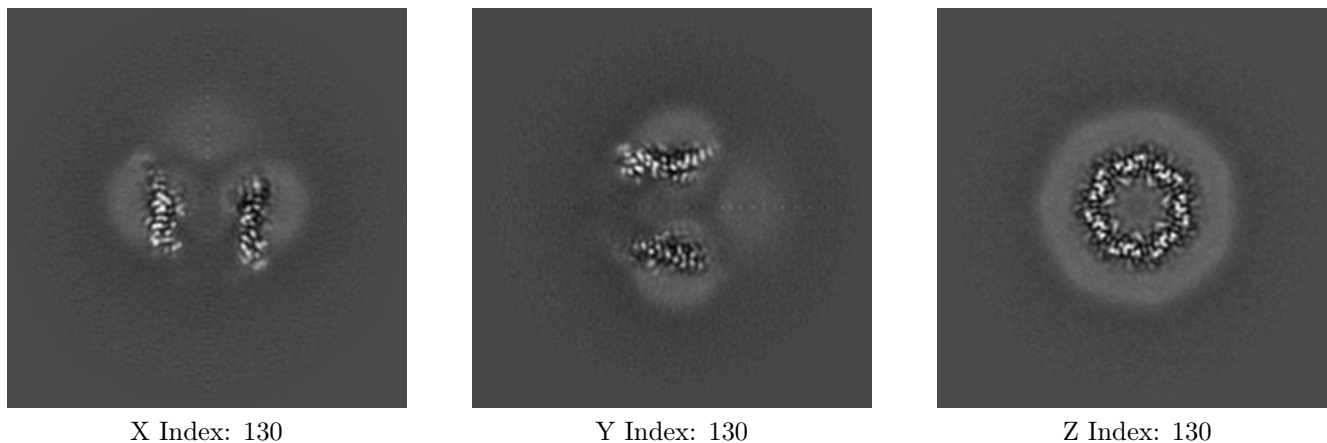
6.1.1 Primary map



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

6.2 Central slices [i](#)

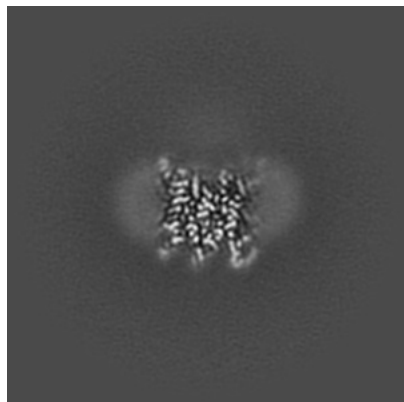
6.2.1 Primary map



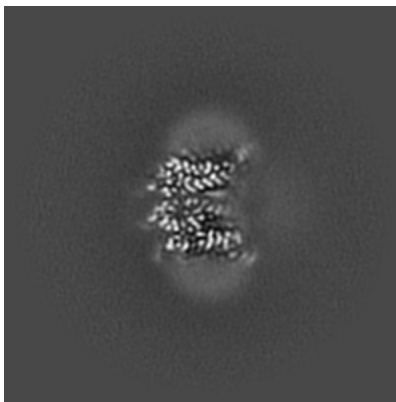
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

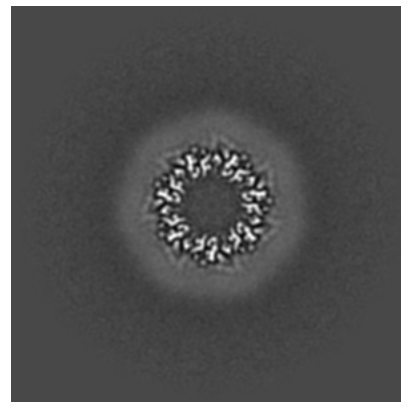
6.3.1 Primary map



X Index: 156



Y Index: 109

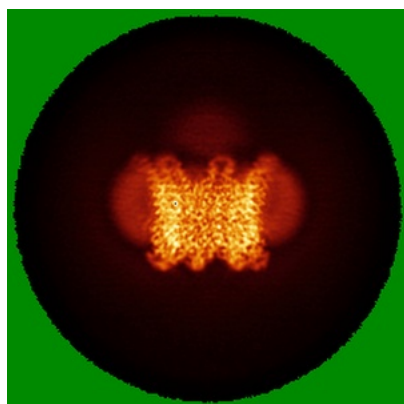


Z Index: 118

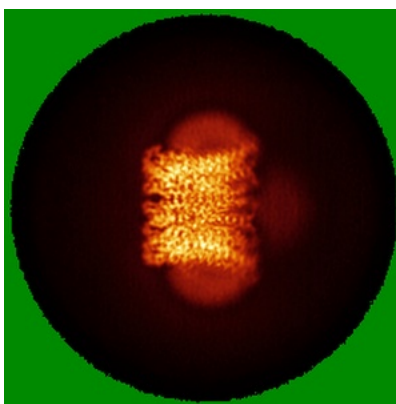
The images above show the largest variance slices of the map in three orthogonal directions.

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

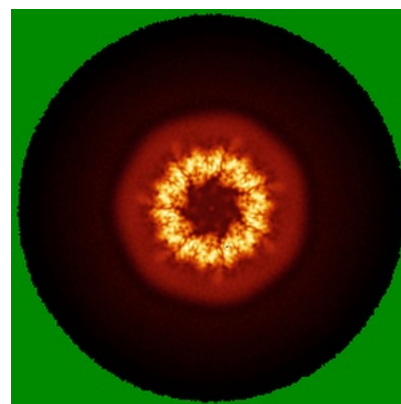
6.4.1 Primary map



X



Y

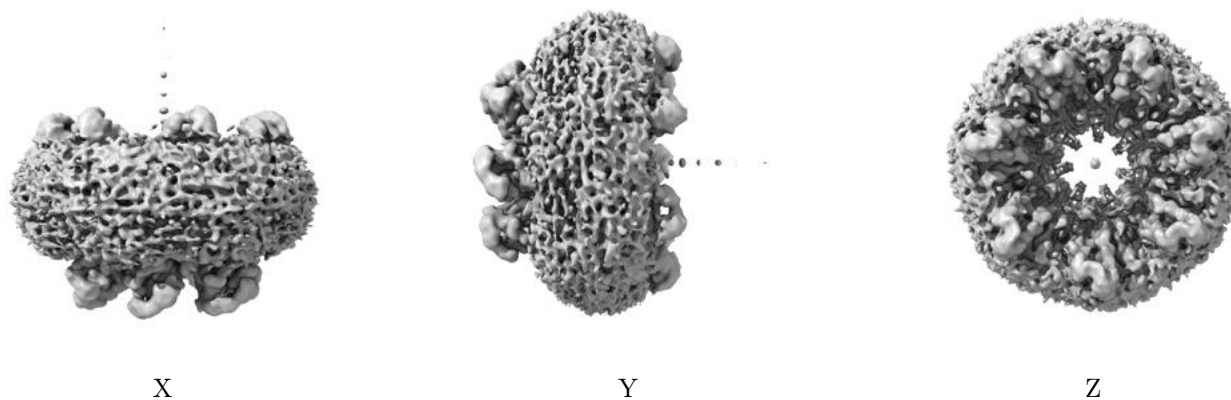


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.154. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

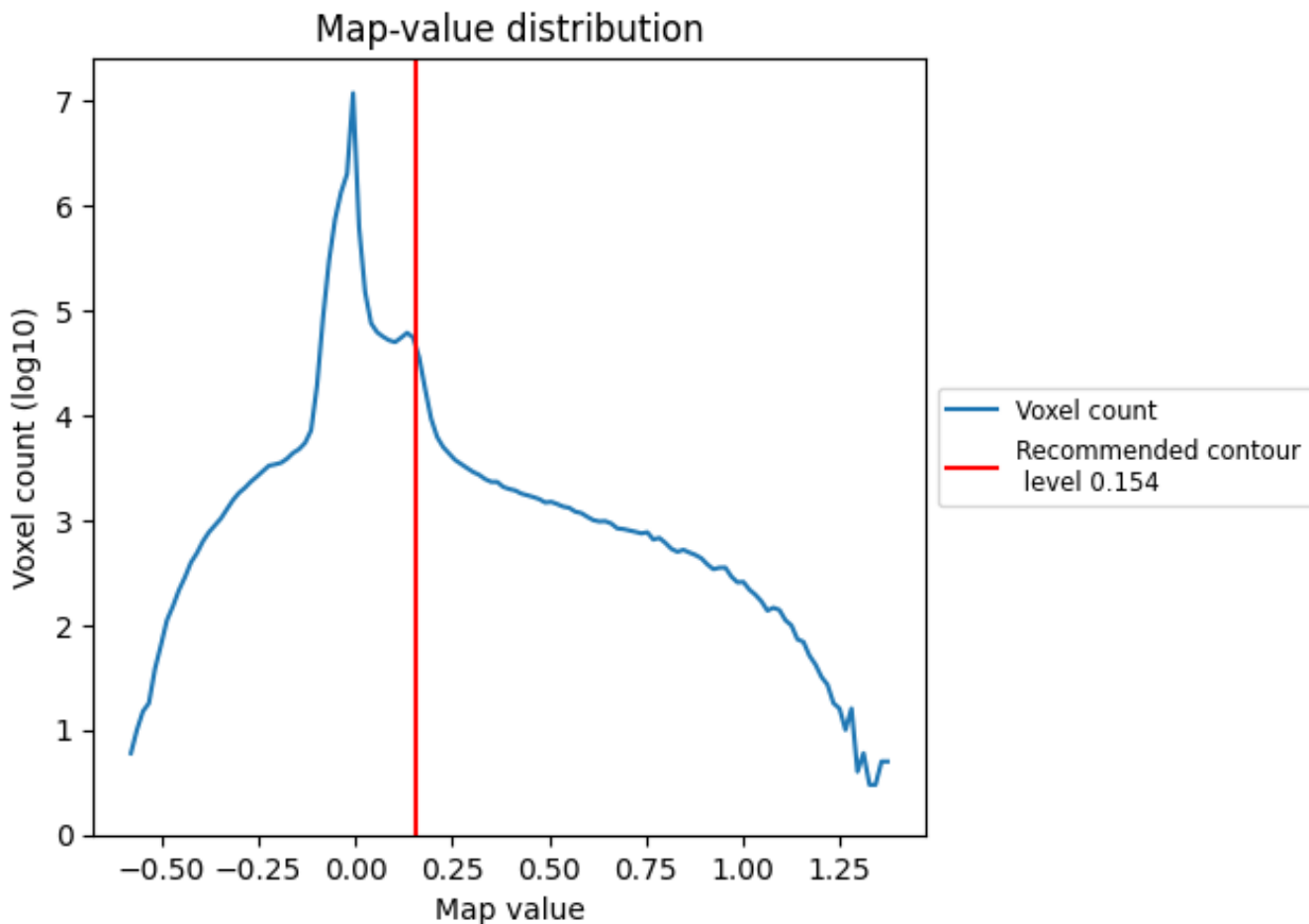
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

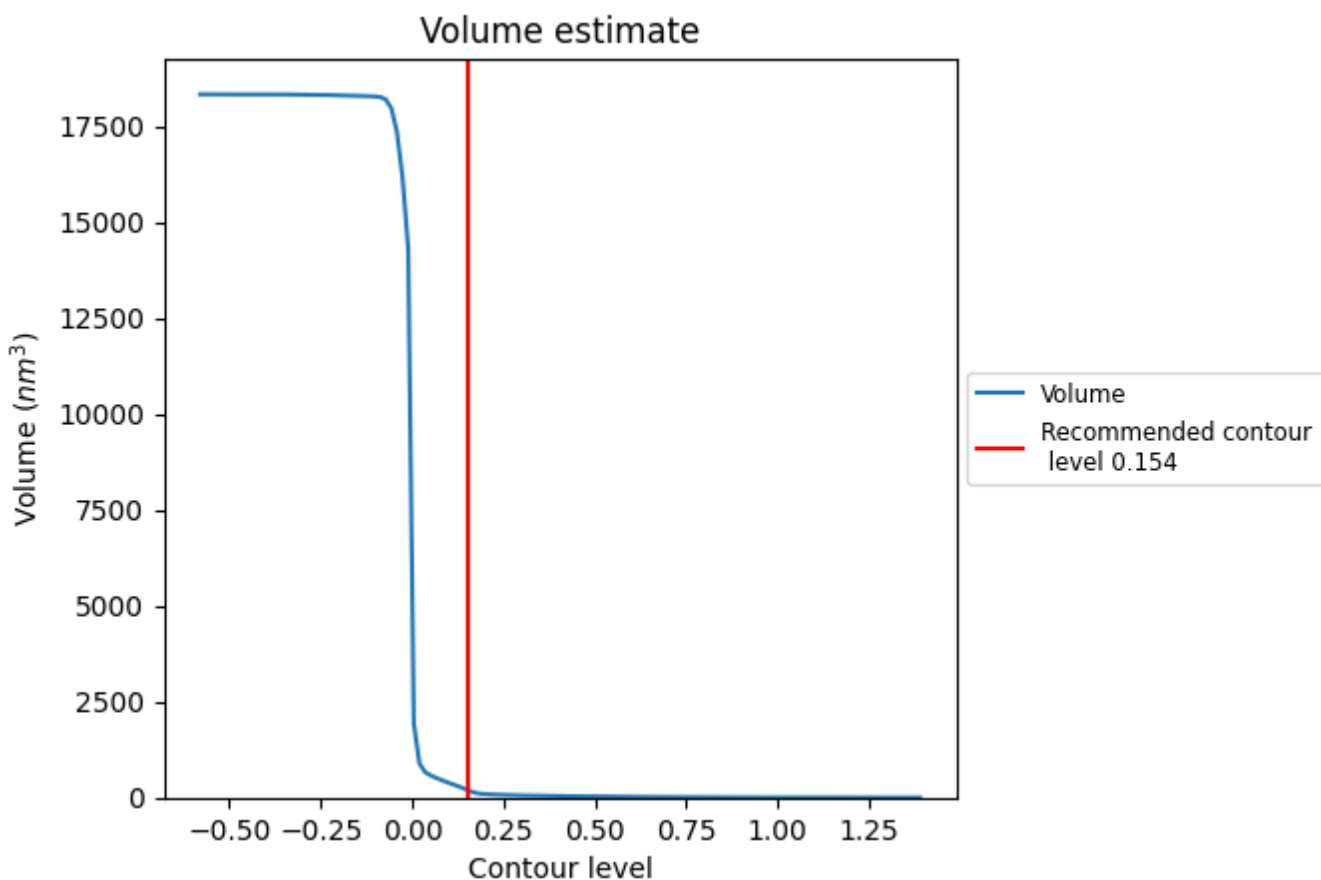
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

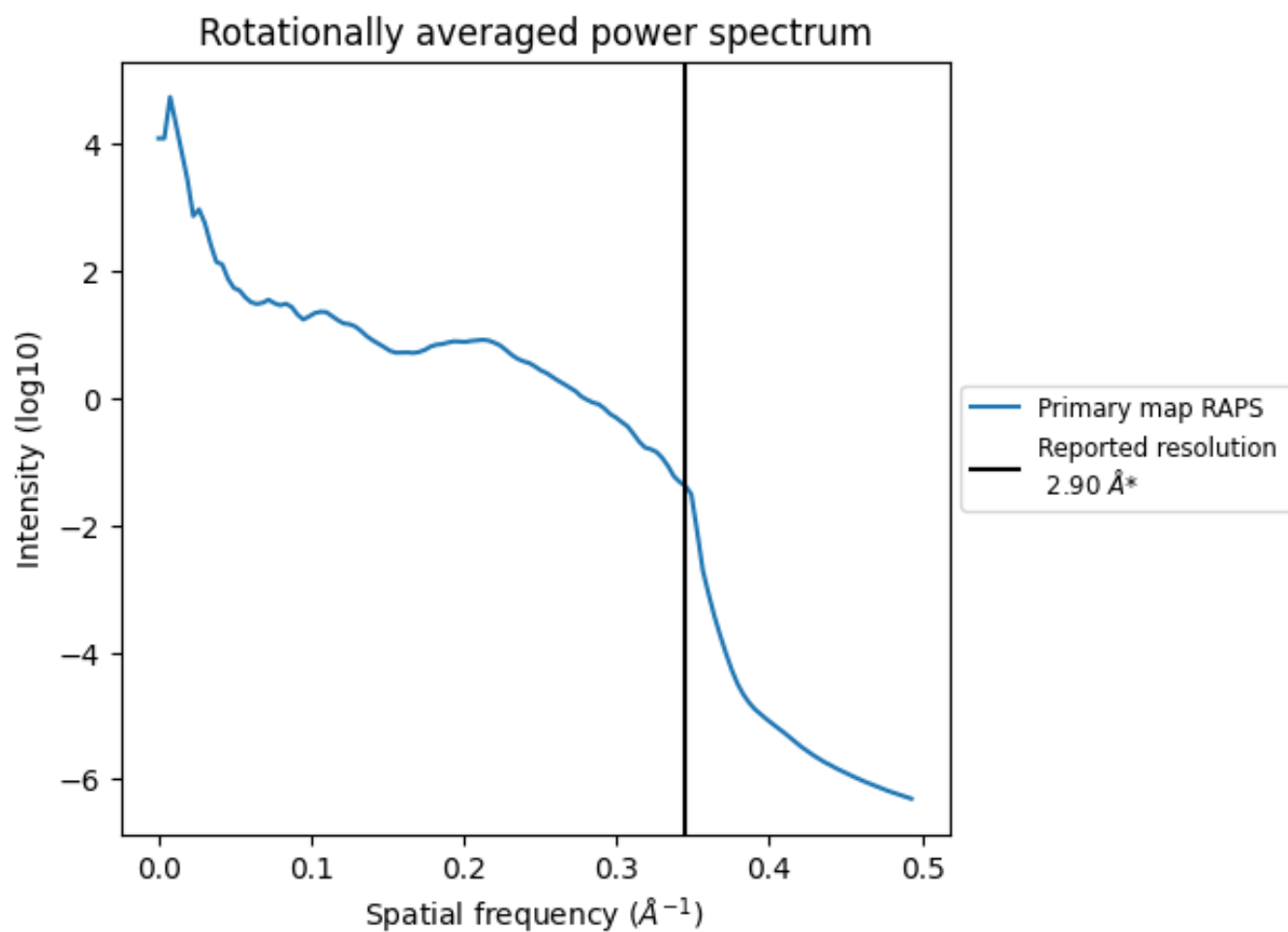
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 185 nm³; this corresponds to an approximate mass of 167 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 0.345\AA^{-1}

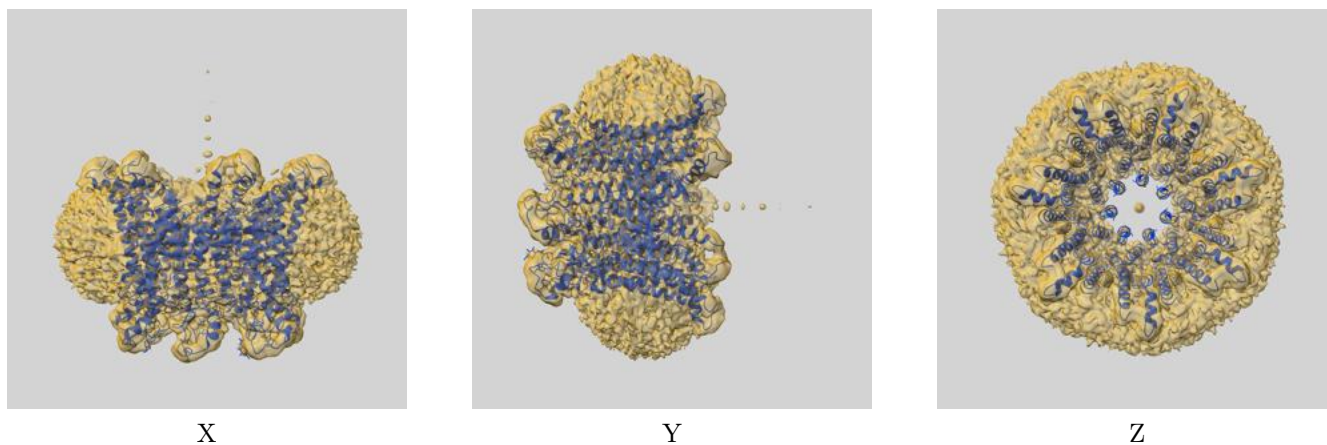
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

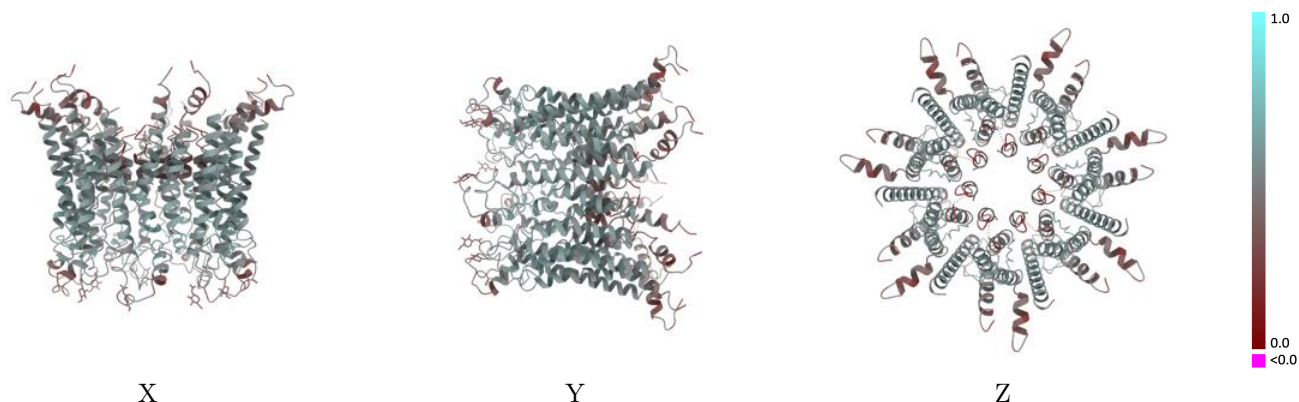
This section contains information regarding the fit between EMDB map EMD-30831 and PDB model 7DSD. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



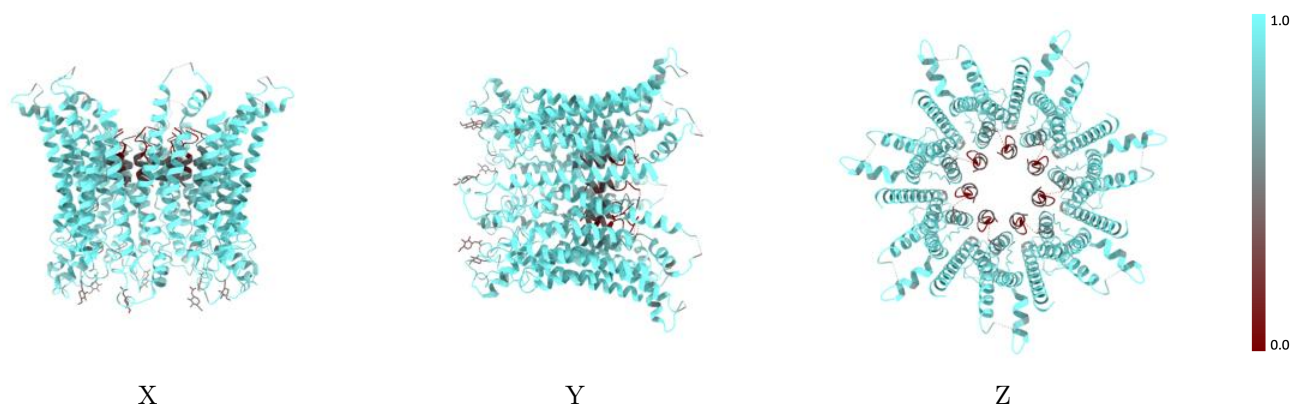
The images above show the 3D surface view of the map at the recommended contour level 0.154 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



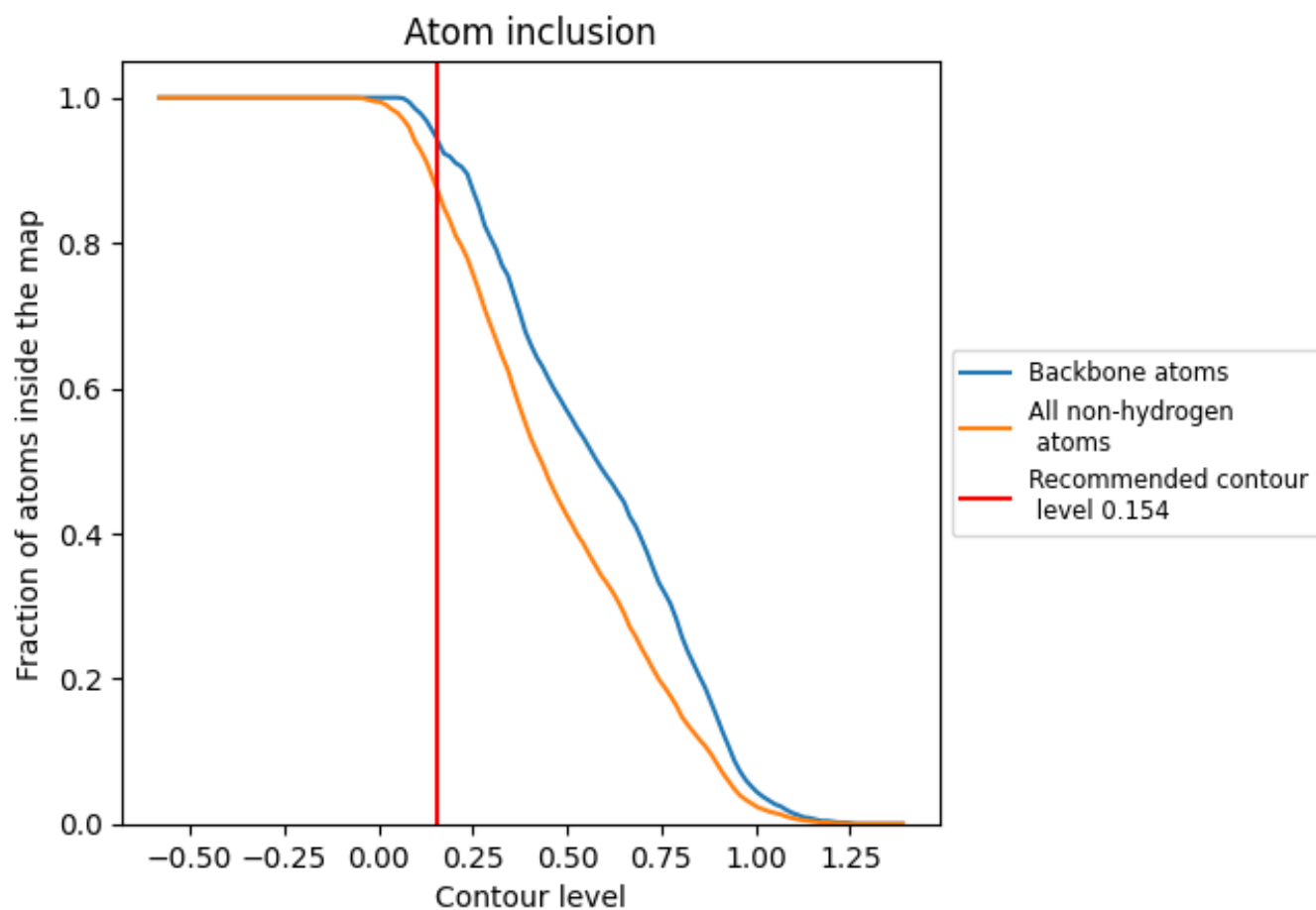
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.154).

















9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.154) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.8760 |  0.4920 |
| A |  0.8750 |  0.4920 |
| B |  0.8760 |  0.4920 |
| C |  0.8760 |  0.4910 |
| D |  0.8750 |  0.4920 |
| E |  0.8760 |  0.4920 |
| F |  0.8750 |  0.4920 |
| G |  0.8780 |  0.4930 |

