# wwPDB EM Validation Summary Report

Oct 26, 2026 – 04:30 PM EDT

| | | |
|---|---|---|
| PDB ID | : | 37XO / pdb_000037xo |
| EMDB ID | : | EMD-78603 |
| Title | : | Polynucleotide kinase phosphatase bound to a nucleosome containing a nick with a 3'-phosphate and 5'-OH at SHL-3 (catalytic-FHA, composite) |
| Authors | : | Boesch, D.J.; Evans, J.J.; Weaver, T.M. |
| Deposited on | : | 2026-08-12 |
| Resolution | : | 3.10 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.

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

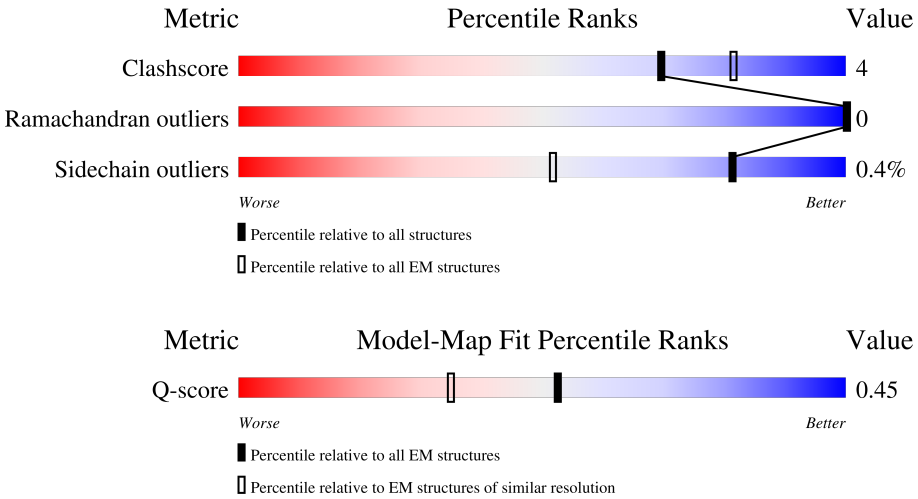
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev133 |
| Mogul | : | 2022.3.0, CSD as543be (2022) |
| MolProbity | : | 4-5-2 with Phenix2.2 |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| EM percentile statistics | : | 202505.v01 (Using 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) | : | 2.51 |

# 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 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.







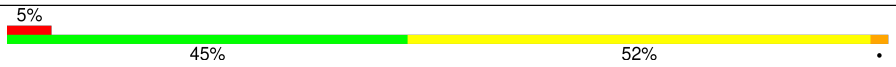
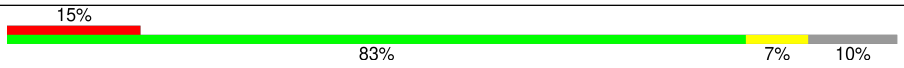
| Metric | Whole archive (#Entries) | EM structures (#Entries) | Similar EM resolution (#Entries, resolution range(Å)) |
|---|---|---|---|
| Clashscore | 229148 | 23984 | - |
| Ramachandran outliers | 224038 | 23583 | - |
| Sidechain outliers | 223484 | 23102 | - |
| Q-score | - | 25397 | 14724 ( 2.60 - 3.60 ) |

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 <=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 | 135 | 60% 11% 29% |
| 1 | E | 135 | 67% 5% 28% |
| 2 | B | 102 | 75% 5% 21% |
| 2 | F | 102 | 76% 5% 19% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 3 | C | 129 |   |
| 3 | G | 129 |   |
| 4 | D | 125 |   |
| 4 | H | 125 |   |
| 5 | I | 147 |   |
| 6 | J | 44 |   |
| 7 | K | 103 |   |
| 8 | L | 528 |   |

# 2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 15651 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Histone H3.2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 789 | 499 | 151 | 137 | 2 | | |
| 1 | E | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 800 | 505 | 155 | 138 | 2 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 110 | ALA | CYS | engineered mutation | UNP Q71DI3 |
| E | 110 | ALA | CYS | engineered mutation | UNP Q71DI3 |

- Molecule 2 is a protein called Histone H4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 2 | B | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 648 | 410 | 126 | 111 | 1 | | |
| 2 | F | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 668 | 422 | 132 | 113 | 1 | | |

- Molecule 3 is a protein called Histone H2A type 1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| 3 | C | 108 | Total | C | N | O | 0 | 0 |
| | | | 832 | 526 | 163 | 143 | | |
| 3 | G | 107 | Total | C | N | O | 0 | 0 |
| | | | 823 | 520 | 161 | 142 | | |

- Molecule 4 is a protein called Histone H2B type 1-C/E/F/G/I.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 4 | D | 92 | Total | C | N | O | S | 0 | 0 |
| | | | 719 | 452 | 129 | 136 | 2 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 4 | H | 92 | Total | C | N | O | S | 0 | 0 |
| | | | 719 | 452 | 129 | 136 | 2 | | |

- Molecule 5 is a DNA chain called 601 I strand (non-damaged strand).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 5 | I | 147 | Total | C | N | O | P | 0 | 0 |
| | | | 2996 | 1423 | 545 | 881 | 147 | | |

- Molecule 6 is a DNA chain called 601 J strand (damaged strand).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 6 | J | 44 | Total | C | N | O | P | 0 | 0 |
| | | | 916 | 433 | 173 | 265 | 45 | | |

- Molecule 7 is a DNA chain called 601 K strand (damaged strand).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | K | 103 | Total | C | N | O | P | 0 | 0 |
| | | | 2116 | 1002 | 393 | 619 | 102 | | |

- Molecule 8 is a protein called Bifunctional polynucleotide phosphatase/kinase.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | L | 475 | Total | C | N | O | S | 0 | 0 |
| | | | 3625 | 2314 | 644 | 653 | 14 | | |

There are 9 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| L | -6 | MET | - | initiating methionine | UNP Q96T60 |
| L | -5 | HIS | - | expression tag | UNP Q96T60 |
| L | -4 | HIS | - | expression tag | UNP Q96T60 |
| L | -3 | HIS | - | expression tag | UNP Q96T60 |
| L | -2 | HIS | - | expression tag | UNP Q96T60 |
| L | -1 | HIS | - | expression tag | UNP Q96T60 |
| L | 0 | HIS | - | expression tag | UNP Q96T60 |
| L | 1 | GLY | - | expression tag | UNP Q96T60 |
| L | 171 | ALA | ASP | engineered mutation | UNP Q96T60 |

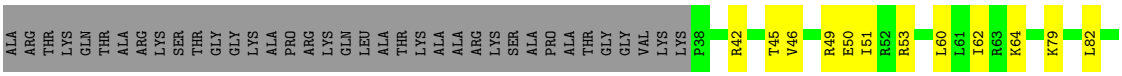
# 3 Residue-property plots (i)

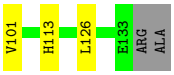
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Histone H3.2

Chain A:



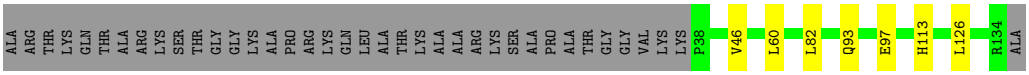




- Molecule 1: Histone H3.2

Chain E:

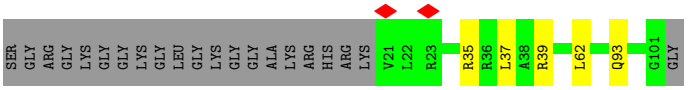



- Molecule 2: Histone H4

Chain B:

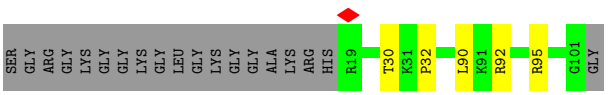



- Molecule 2: Histone H4

Chain F:

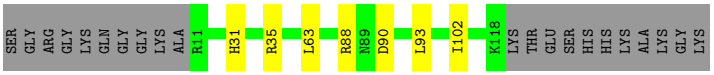



- Molecule 3: Histone H2A type 1

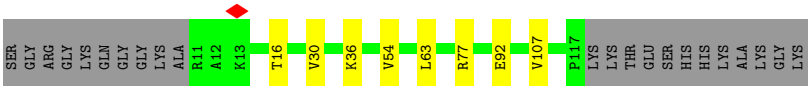
Chain C:






• Molecule 3: Histone H2A type 1




• Molecule 4: Histone H2B type 1-C/E/F/G/I

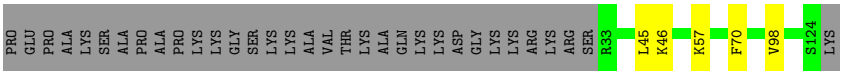






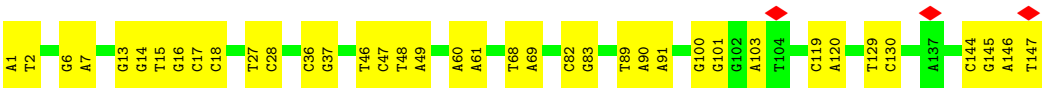
• Molecule 4: Histone H2B type 1-C/E/F/G/I



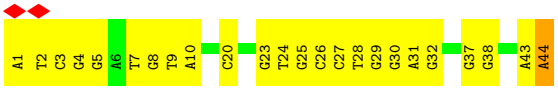

• Molecule 5: 601 I strand (non-damaged strand)



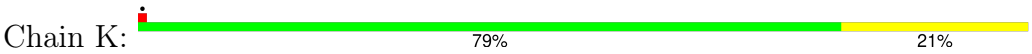



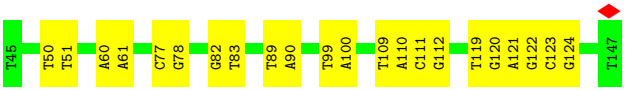

• Molecule 6: 601 J strand (damaged strand)



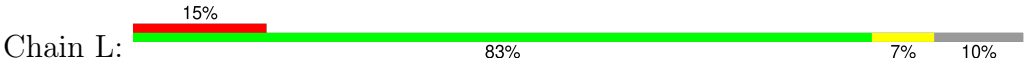

• Molecule 7: 601 K strand (damaged strand)

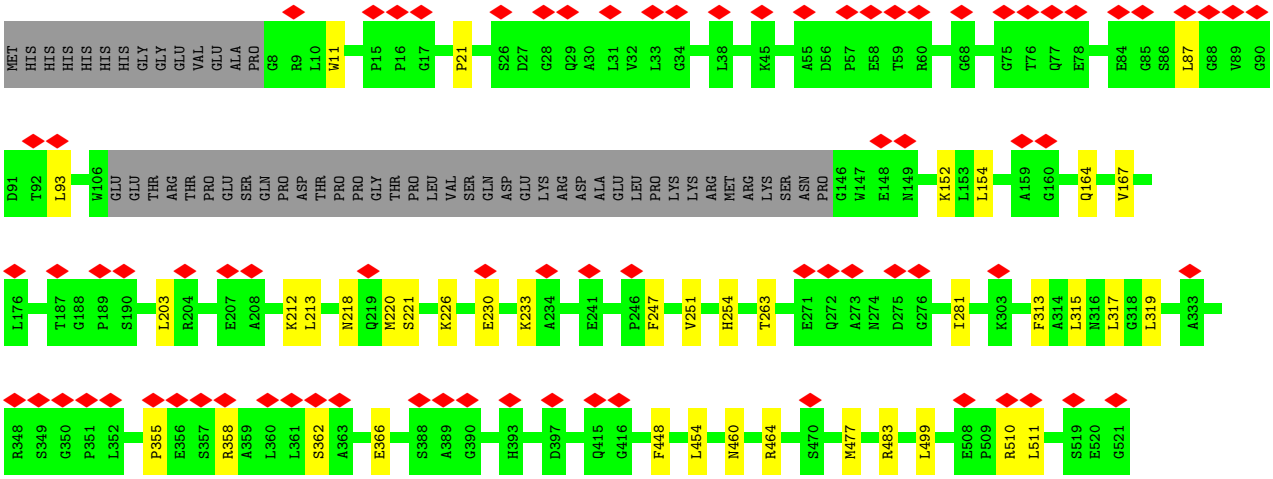



• Molecule 8: Bifunctional polynucleotide phosphatase/kinase

Chain L:


15%
83%
7%
10%


MET HIS HIS HIS HIS HIS HIS GLY GLY GLU VAL GLU ALA PRO G8 R9 L10 W11 P15 P16 G17 P21 S26 D27 G28 Q29 A30 L31 V32 L33 G34 L38 K45 A55 D56 P57 E58 T59 R60 G68 G75 T76 Q77 E78 E84 G85 S86 L87 G88 V89 G90
D91 T92 L93 W106 GLU GLU THR ARG THR PRO GLU SER GLN PRO ASP THR PRO PRO GLY THR PRO LEU VAL SER GLN ASP GLU LYS ARG ASP ALA GLU LEU PRO LYS LYS ARG MET ARG LYS SER ASN PRO G146 W147 E148 N149 K152 L153 L154 A159 G160 Q164 V167
L176 T187 G188 P189 S190 L203 R204 E207 A208 K212 L213 N218 Q219 M220 S221 K226 E230 K233 A234 E241 P246 F247 V251 H254 T263 E271 Q272 A273 N274 D275 G276 I281 K303 F313 A314 L315 N316 L317 G318 L319 A333
R348 S349 G350 P351 L352 P355 E356 S357 R358 A359 L360 L361 S362 A363 E366 S388 A389 G390 H393 D397 Q415 G416 F448 L454 N460 R464 S470 M477 R483 L499 E508 P509 R510 L511 S519 E520 G521

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 24323 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | TFS KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 50 | Depositor |
| Minimum defocus (nm) | 1200 | Depositor |
| Maximum defocus (nm) | 1800 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 29.199 | Depositor |
| Minimum map value | -12.840 | Depositor |
| Average map value | 0.003 | Depositor |
| Map value standard deviation | 1.017 | Depositor |
| Recommended contour level | 5 | Depositor |
| Map size (Å) | 260.80002, 260.80002, 260.80002 | wwPDB |
| Map dimensions | 400, 400, 400 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 0.65200007, 0.65200007, 0.65200007 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AD2

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 | 0.22 | 0/801 | 0.34 | 0/1075 |
| 1 | E | 0.19 | 0/812 | 0.31 | 0/1089 |
| 2 | B | 0.20 | 0/655 | 0.33 | 0/878 |
| 2 | F | 0.19 | 0/675 | 0.35 | 0/903 |
| 3 | C | 0.19 | 0/842 | 0.29 | 0/1135 |
| 3 | G | 0.16 | 0/833 | 0.27 | 0/1124 |
| 4 | D | 0.18 | 0/730 | 0.29 | 0/982 |
| 4 | H | 0.18 | 0/730 | 0.27 | 0/982 |
| 5 | I | 0.73 | 0/3357 | 0.90 | 0/5174 |
| 6 | J | 0.70 | 0/1001 | 0.88 | 0/1545 |
| 7 | K | 0.74 | 0/2374 | 0.86 | 0/3665 |
| 8 | L | 0.12 | 0/3717 | 0.29 | 0/5054 |
| All | All | 0.48 | 0/16527 | 0.63 | 0/23606 |

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

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 | 789 | 0 | 826 | 12 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | E | 800 | 0 | 839 | 6 | 0 |
| 2 | B | 648 | 0 | 693 | 4 | 0 |
| 2 | F | 668 | 0 | 719 | 2 | 0 |
| 3 | C | 832 | 0 | 897 | 5 | 0 |
| 3 | G | 823 | 0 | 884 | 7 | 0 |
| 4 | D | 719 | 0 | 738 | 2 | 0 |
| 4 | H | 719 | 0 | 738 | 4 | 0 |
| 5 | I | 2996 | 0 | 1650 | 25 | 0 |
| 6 | J | 916 | 0 | 495 | 18 | 0 |
| 7 | K | 2116 | 0 | 1157 | 14 | 0 |
| 8 | L | 3625 | 0 | 3612 | 25 | 0 |
| All | All | 15651 | 0 | 13248 | 105 | 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 4.

The worst 5 of 105 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:I:119:DC:H2" | 5:I:120:DA:C8 | 2.30 | 0.67 |
| 8:L:281:ILE:HG23 | 8:L:319:LEU:HD22 | 1.84 | 0.60 |
| 8:L:510:ARG:HG3 | 8:L:511:LEU:HG | 1.84 | 0.59 |
| 6:J:24:DT:H2' | 6:J:25:DG:C8 | 2.37 | 0.59 |
| 5:I:90:DA:H1' | 5:I:91:DA:N7 | 2.18 | 0.58 |

There are no symmetry-related clashes.

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | A | 94/135 (70%) | 91 (97%) | 3 (3%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | E | 95/135 (70%) | 95 (100%) | 0 | 0 | 100 | 100 |
| 2 | B | 79/102 (78%) | 78 (99%) | 1 (1%) | 0 | 100 | 100 |
| 2 | F | 81/102 (79%) | 78 (96%) | 3 (4%) | 0 | 100 | 100 |
| 3 | C | 106/129 (82%) | 105 (99%) | 1 (1%) | 0 | 100 | 100 |
| 3 | G | 105/129 (81%) | 104 (99%) | 1 (1%) | 0 | 100 | 100 |
| 4 | D | 90/125 (72%) | 88 (98%) | 2 (2%) | 0 | 100 | 100 |
| 4 | H | 90/125 (72%) | 89 (99%) | 1 (1%) | 0 | 100 | 100 |
| 8 | L | 471/528 (89%) | 465 (99%) | 6 (1%) | 0 | 100 | 100 |
| All | All | 1211/1510 (80%) | 1193 (98%) | 18 (2%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains (i)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 1 | A | 83/109 (76%) | 83 (100%) | 0 | 100 | 100 |
| 1 | E | 84/109 (77%) | 84 (100%) | 0 | 100 | 100 |
| 2 | B | 67/78 (86%) | 66 (98%) | 1 (2%) | 57 | 75 |
| 2 | F | 69/78 (88%) | 68 (99%) | 1 (1%) | 59 | 76 |
| 3 | C | 84/98 (86%) | 84 (100%) | 0 | 100 | 100 |
| 3 | G | 83/98 (85%) | 82 (99%) | 1 (1%) | 63 | 78 |
| 4 | D | 79/105 (75%) | 79 (100%) | 0 | 100 | 100 |
| 4 | H | 79/105 (75%) | 78 (99%) | 1 (1%) | 61 | 77 |
| 8 | L | 377/435 (87%) | 377 (100%) | 0 | 100 | 100 |
| All | All | 1005/1215 (83%) | 1001 (100%) | 4 (0%) | 81 | 86 |

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

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | B | 93 | GLN |
| 2 | F | 92 | ARG |
| 3 | G | 92 | GLU |
| 4 | H | 57 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 4 | H | 67 | ASN |
| 4 | H | 82 | HIS |
| 8 | L | 456 | GLN |
| 8 | L | 385 | HIS |
| 8 | L | 415 | GLN |

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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 | $\#\|Z\| > 2$ |
| 6 | AD2 | J | 44 | 6 | 24,27,28 | 0.50 | 0 | 35,40,43 | 1.16 | 4 (11%) |

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 |
|---|---|---|---|---|---|---|---|
| 6 | AD2 | J | 44 | 6 | - | 3/12/26/27 | 0/3/3/3 |

There are no bond length outliers.

All (4) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 6 | J | 44 | AD2 | O4'-C4'-C3' | 3.14 | 111.21 | 105.28 |
| 6 | J | 44 | AD2 | O6P-P2-O5P | 3.11 | 119.46 | 107.80 |
| 6 | J | 44 | AD2 | O3'-P2-O4P | -2.85 | 99.17 | 109.33 |
| 6 | J | 44 | AD2 | P2-O3'-C3' | -2.19 | 117.66 | 123.54 |

There are no chirality outliers.

All (3) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 6 | J | 44 | AD2 | O4'-C4'-C5'-O5' |
| 6 | J | 44 | AD2 | C3'-C4'-C5'-O5' |
| 6 | J | 44 | AD2 | C4'-C5'-O5'-P1 |

There are no ring outliers.

1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 6 | J | 44 | AD2 | 1 | 0 |

## 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.

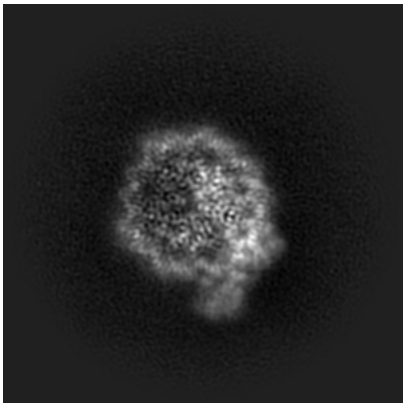
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-78603. These allow visual inspection of the internal detail of the map and identification of artifacts.

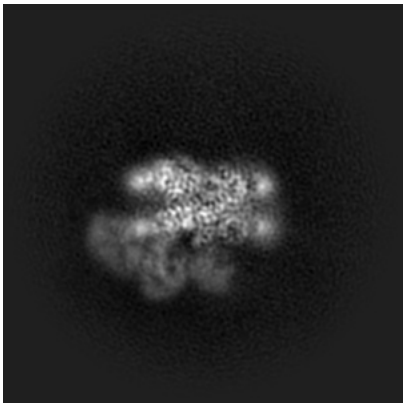
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

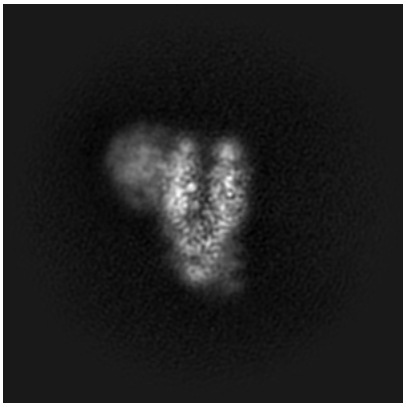
### 6.1.1 Primary map



X



Y

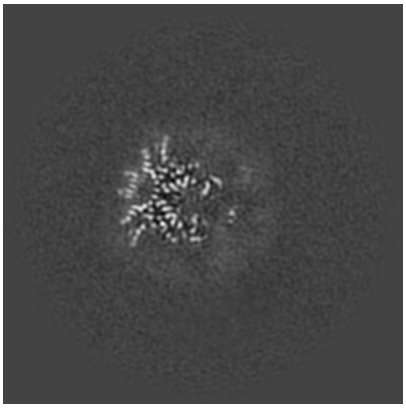


Z

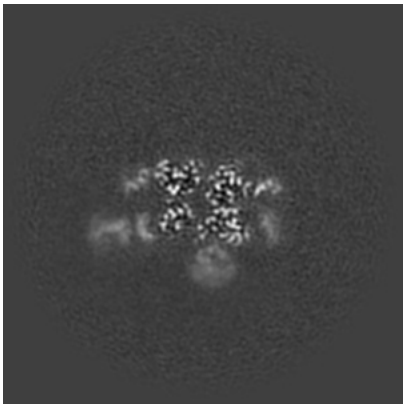
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices

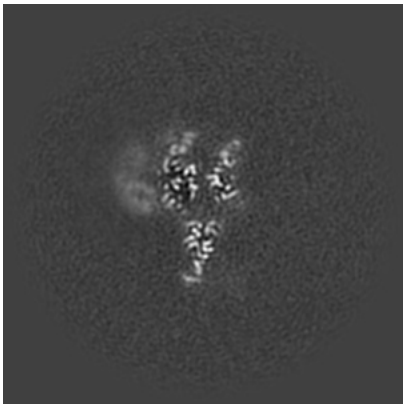
### 6.2.1 Primary map



X Index: 200



Y Index: 200

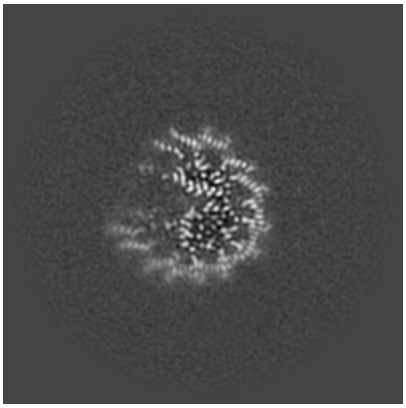


Z Index: 200

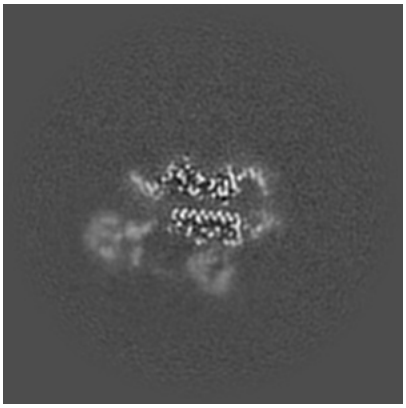
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

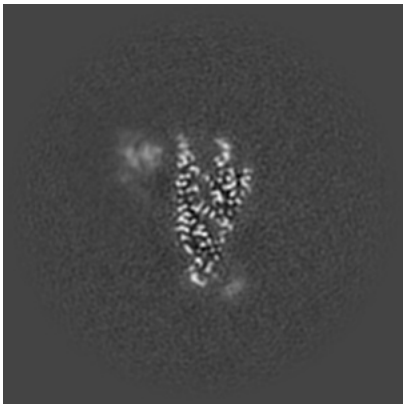
### 6.3.1 Primary map



X Index: 221



Y Index: 215

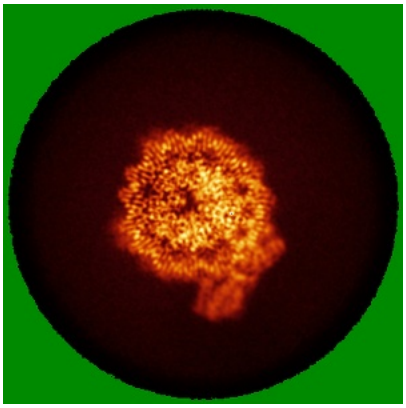


Z Index: 181

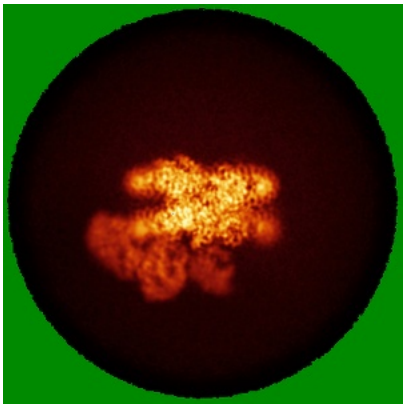
The images above show the largest variance slices of the map in three orthogonal directions.

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

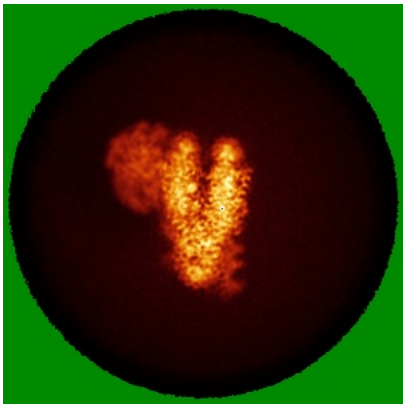
### 6.4.1 Primary map



X



Y

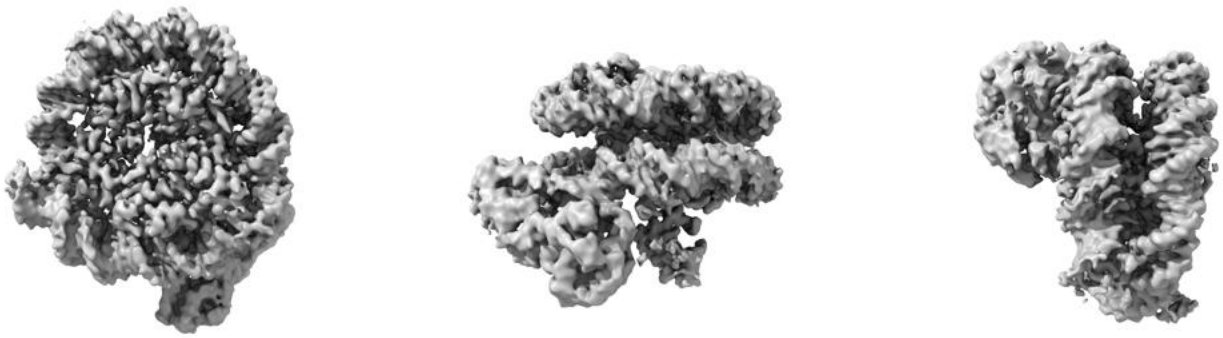


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

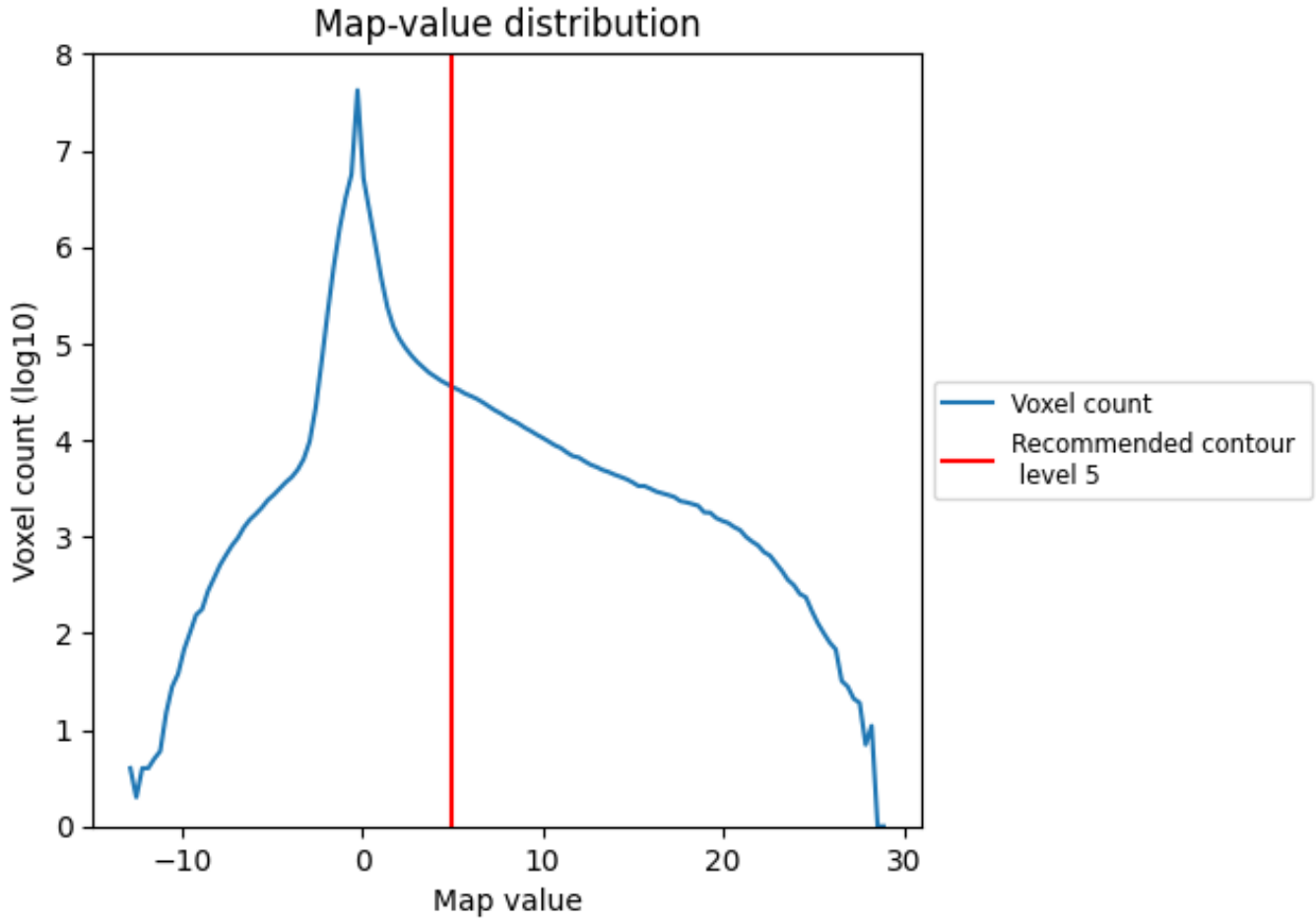
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

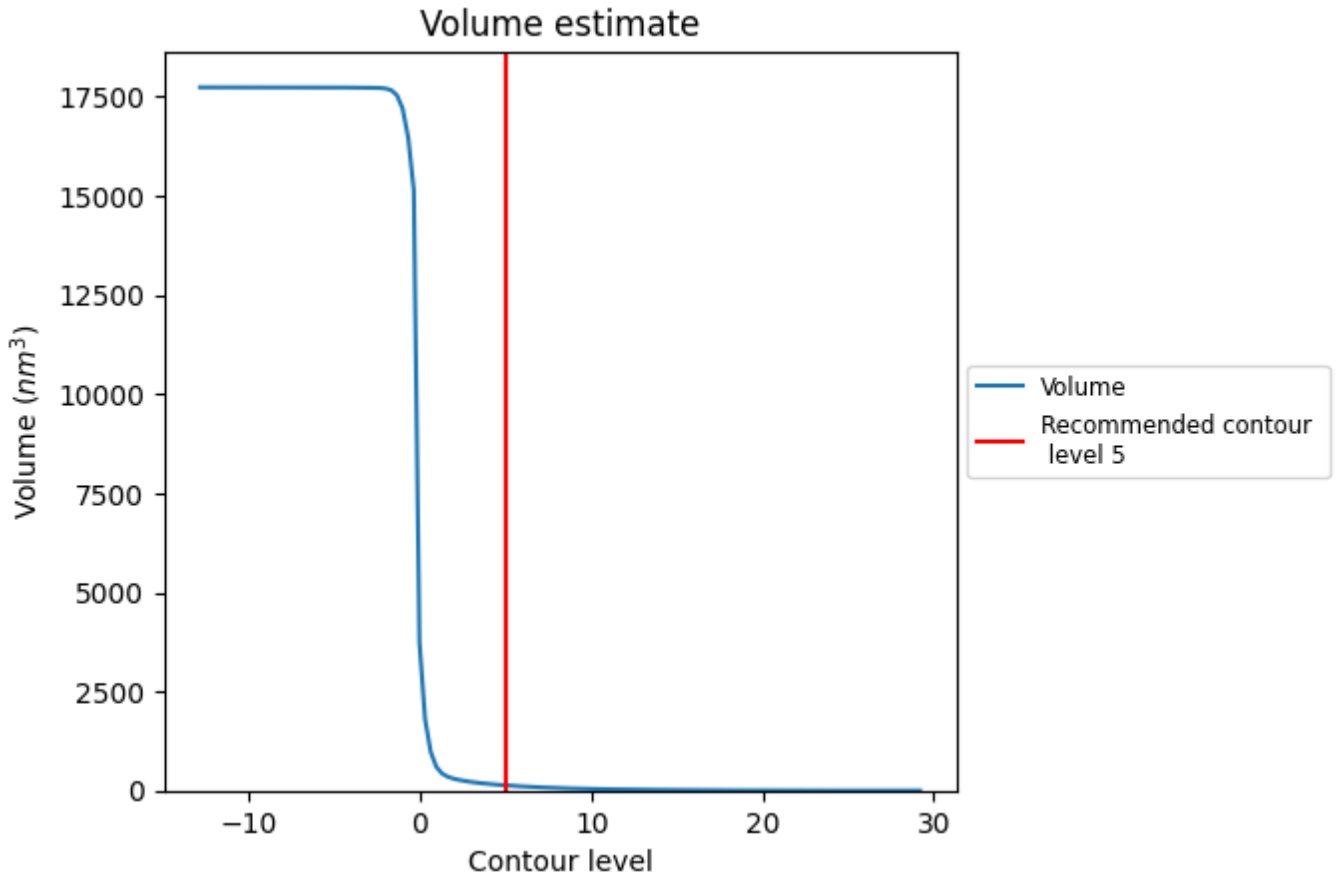
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution




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.

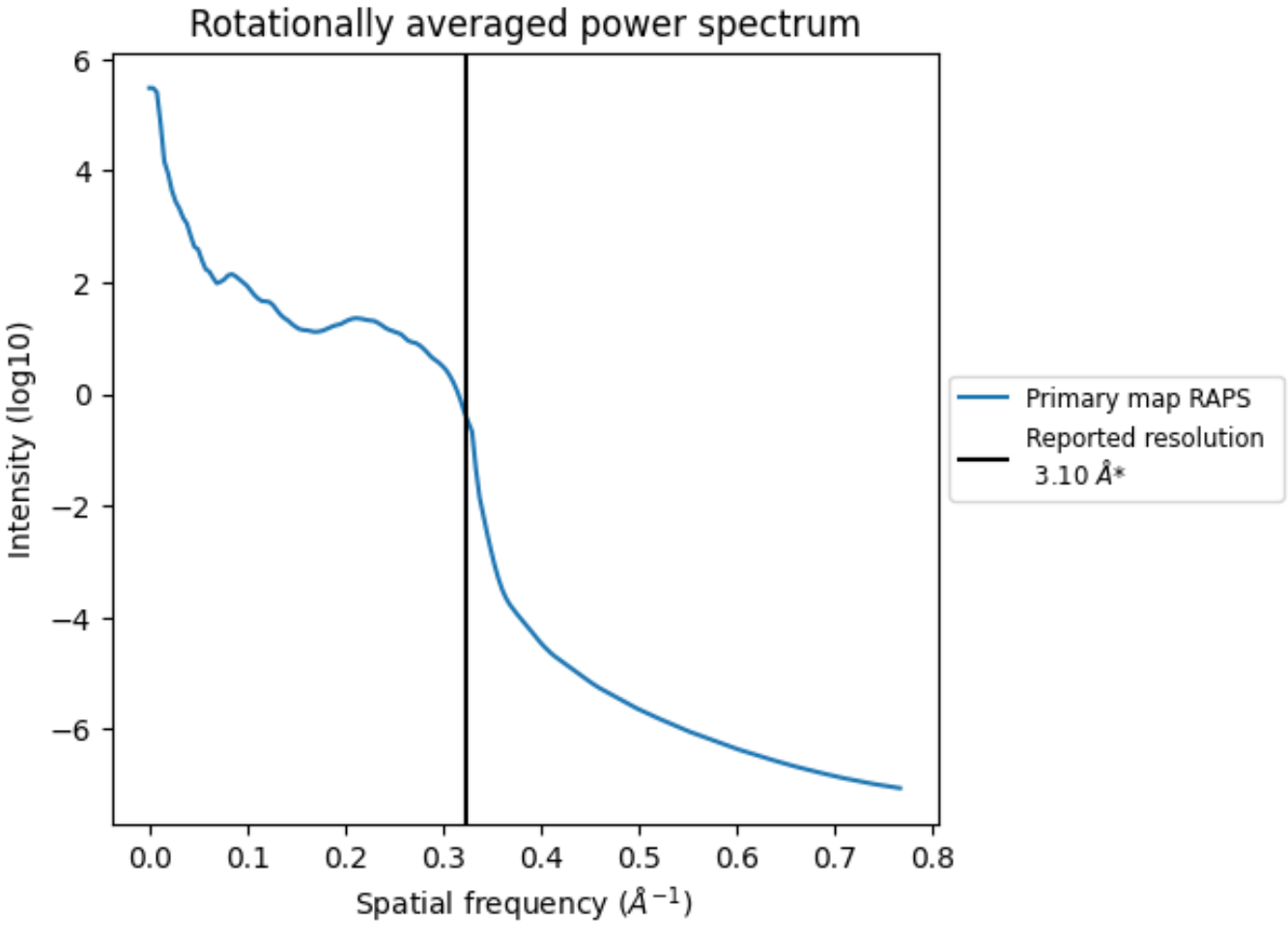
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 132 $nm^3$; this corresponds to an approximate mass of 119 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 0.323 Å$^{-1}$

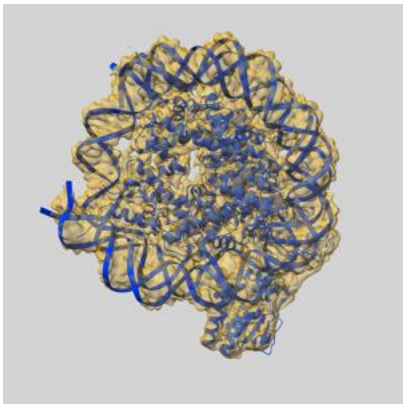
# 8 Fourier-Shell correlation (i)

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

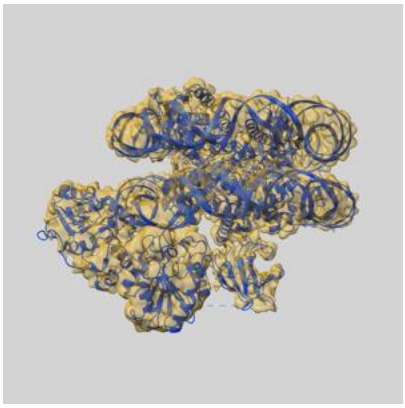
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-78603 and PDB model 37XO. Per-residue inclusion information can be found in section 3 on page 6.

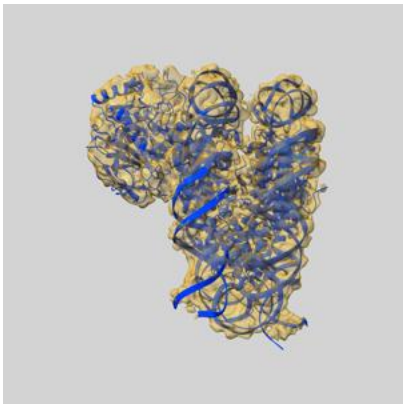
## 9.1 Map-model overlay



X



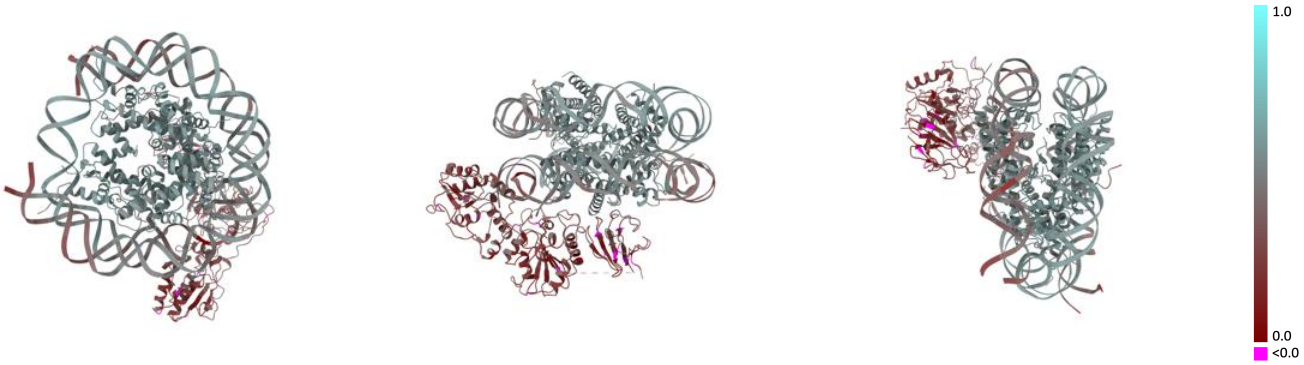
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0 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.

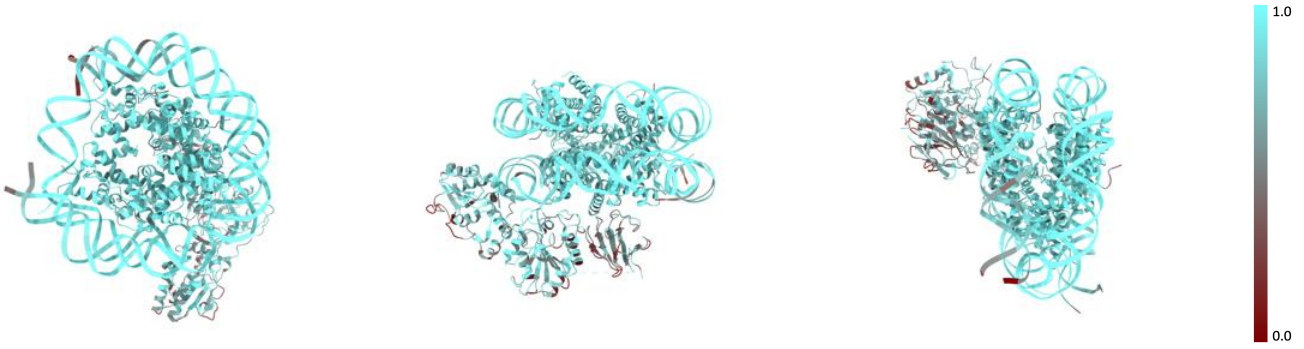
## 9.2 Q-score mapped to coordinate model (i)




X Y Z

The images above show the model with each residue coloured according 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.

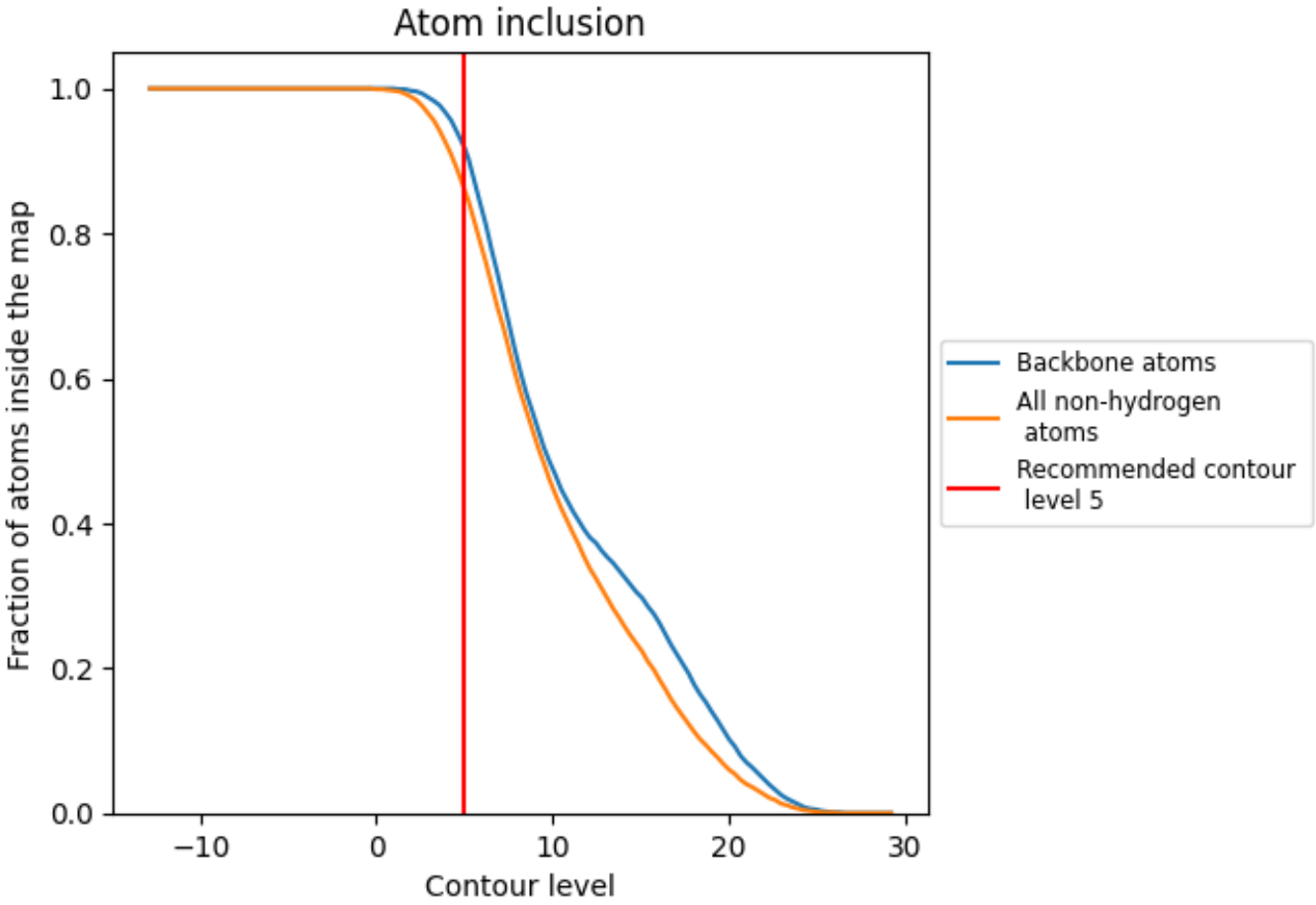
## 9.3 Atom inclusion mapped to coordinate model (i)




X Y Z

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 (5).

## 9.4 Atom inclusion (i)




At the recommended contour level, 92% of all backbone atoms, 86% 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 (5) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.8600 | 0.4500 |
| A | 0.9180 | 0.5590 |
| B | 0.9320 | 0.5650 |
| C | 0.9140 | 0.5510 |
| D | 0.9320 | 0.5490 |
| E | 0.9300 | 0.5550 |
| F | 0.9200 | 0.5600 |
| G | 0.8920 | 0.5490 |
| H | 0.9020 | 0.5430 |
| I | 0.9190 | 0.4780 |
| J | 0.8440 | 0.4140 |
| K | 0.9630 | 0.5020 |
| L | 0.6590 | 0.2350 |

