# wwPDB EM Validation Summary Report

Oct 26, 2026 – 06:39 PM EDT

| | | |
|---|---|---|
| PDB ID | : | 37XQ / pdb_000037xq |
| EMDB ID | : | EMD-78605 |
| Title | : | Polynucleotide kinase phosphatase bound to a nucleosome containing a nick with a 3'-phosphate and 5'-OH at SHL-4 (catalytic, composite) |
| Authors | : | Boesch, D.J.; Evans, J.J.; Weaver, T.M. |
| Deposited on | : | 2026-08-12 |
| Resolution | : | 3.50 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:

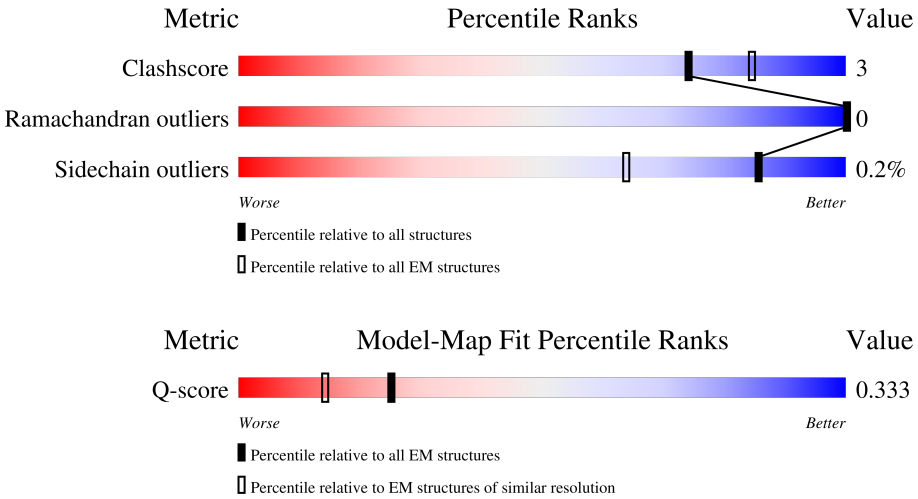
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev133 |
| Mogul | : | 2022.3.0, CSD as543be (2022) |
| MolProbity | : | 4-5-2 with Phenix2.2 |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| EM percentile statistics | : | 202505.v01 (Using 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 3.50 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.







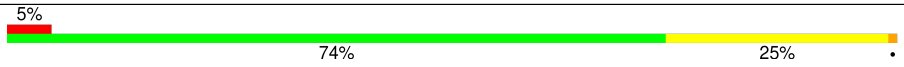
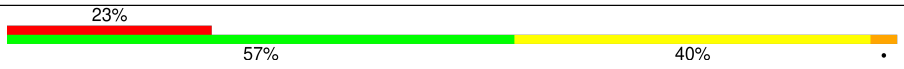
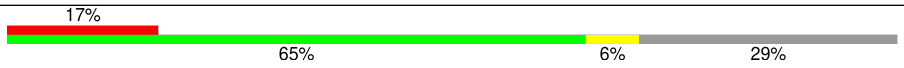
| Metric | Whole archive (#Entries) | EM structures (#Entries) | Similar EM resolution (#Entries, resolution range(Å)) |
|---|---|---|---|
| Clashscore | 229148 | 23984 | - |
| Ramachandran outliers | 224038 | 23583 | - |
| Sidechain outliers | 223484 | 23102 | - |
| Q-score | - | 25397 | 13950 ( 3.00 - 4.00 ) |

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 | 67% · 29% |
| 1 | E | 135 | 67% 5% 28% |
| 2 | B | 102 | 77% · 21% |
| 2 | F | 102 | 75% 5% 21% |

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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 | 35 |   |
| 7 | K | 112 |   |
| 8 | L | 528 |   |

# 2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 14892 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 | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 648 | 410 | 126 | 111 | 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 | 103 | Total | C | N | O | 0 | 0 |
| | | | 793 | 502 | 153 | 138 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 4 | D | 94 | Total | C | N | O | S | 0 | 0 |
| | | | 736 | 461 | 134 | 139 | 2 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 4 | H | 93 | Total | C | N | O | S | 0 | 0 |
| | | | 725 | 455 | 130 | 138 | 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 | 35 | Total | C | N | O | P | 0 | 0 |
| | | | 724 | 343 | 131 | 214 | 36 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | K | 112 | Total | C | N | O | P | 0 | 0 |
| | | | 2308 | 1092 | 435 | 670 | 111 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | L | 376 | Total | C | N | O | S | 0 | 0 |
| | | | 2893 | 1850 | 513 | 517 | 13 | | |

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 |

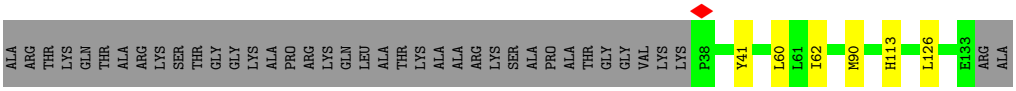
# 3 Residue-property plots (i)

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:

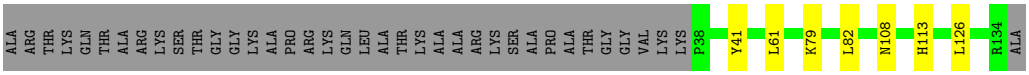



- Molecule 1: Histone H3.2

Chain E:

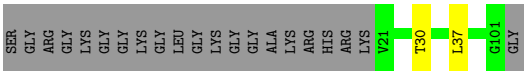



- Molecule 2: Histone H4

Chain B:




- Molecule 2: Histone H4

Chain F:



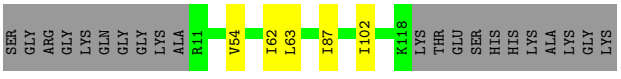




- Molecule 3: Histone H2A type 1

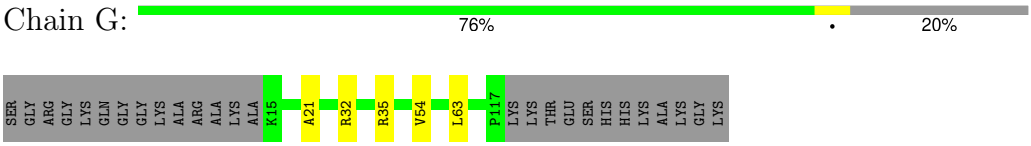
Chain C:



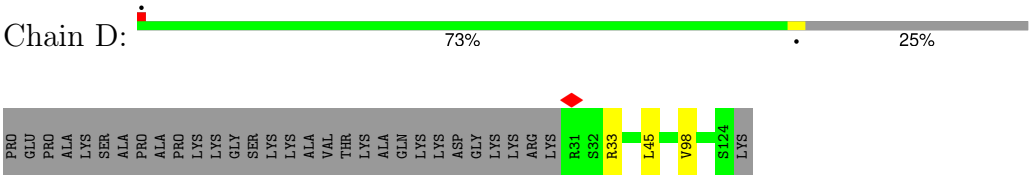

- Molecule 3: Histone H2A type 1

Chain G:



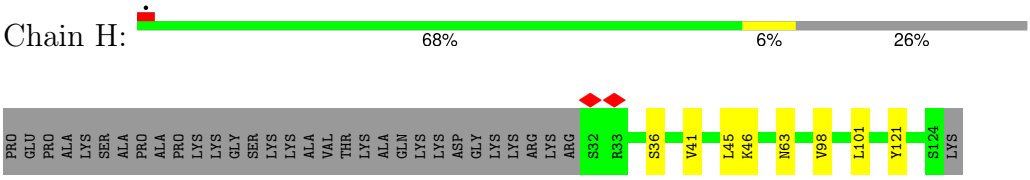

• Molecule 4: Histone H2B type 1-C/E/F/G/I

Chain D:



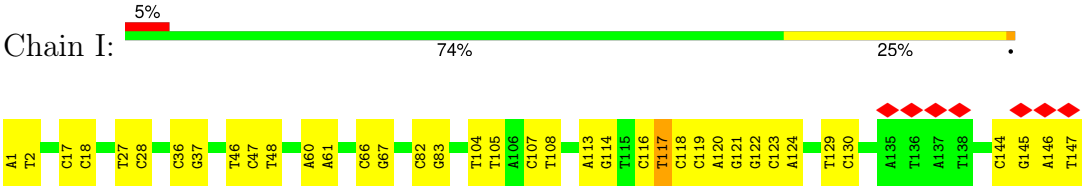

• Molecule 4: Histone H2B type 1-C/E/F/G/I

Chain H:



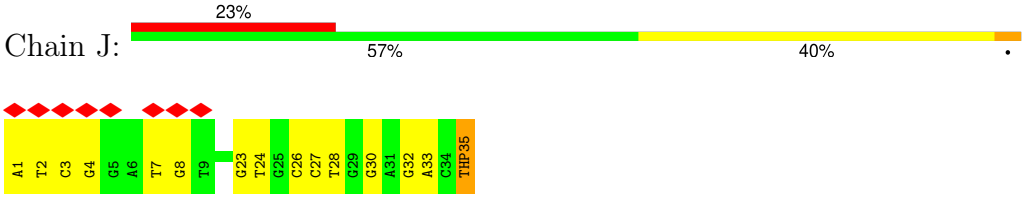

• Molecule 5: 601 I strand (non-damaged strand)

Chain I:



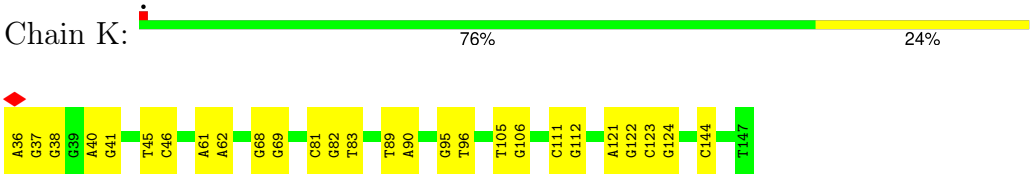

• Molecule 6: 601 J strand (damaged strand)

Chain J:



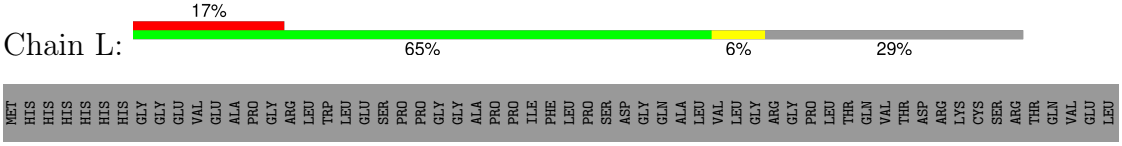

• Molecule 7: 601 K strand (damaged strand)

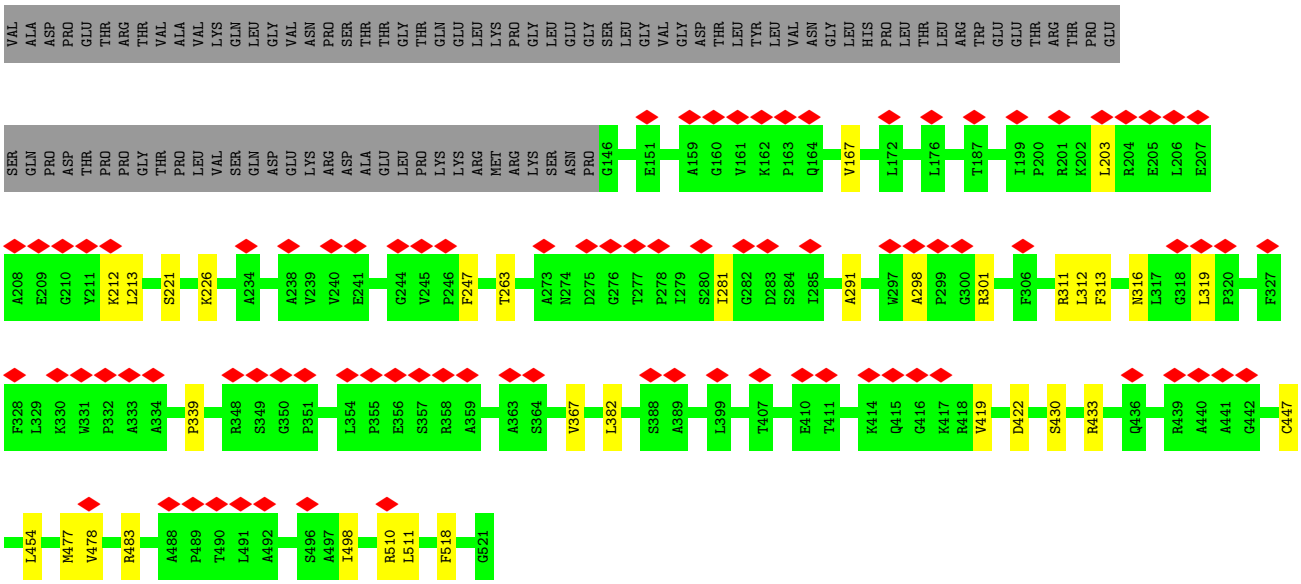
Chain K:




• Molecule 8: Bifunctional polynucleotide phosphatase/kinase

Chain L:




VAL ALA ASP PRO GLU THR ARG THR VAL ALA VAL LYS GLN LEU GLY VAL ASN PRO SER THR THR GLY THR GLN GLU LEU LYS PRO GLY LEU GLU GLY SER LEU GLY VAL GLY ASP THR LEU TYR LEU VAL ASN GLY LEU HIS PRO LEU THR LEU ARG TRP 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 E151 A159 G160 V161 K162 P163 Q164 V167 L172 L176 T187 I199 P200 R201 K202 L203 R204 E205 L206 E207
A208 E209 G210 Y211 K212 L213 S221 K226 A234 A238 V239 V240 E241 G244 V245 P246 F247 T263 A273 N274 D275 G276 T277 P278 I279 S280 I281 G282 D283 S284 I285 A291 W297 A298 P299 G300 R301 F306 R311 L312 F313 N316 L317 G318 L319 P320 F327
F328 L329 K330 W331 P332 A333 A334 P339 R348 S349 G350 P351 L354 P355 E356 S357 R358 A359 A363 S364 V367 L382 S388 A389 L399 T407 E410 T411 K414 Q415 G416 K417 R418 V419 D422 S430 R433 Q436 R439 A440 A441 G442 C447
L454 M477 V478 R483 A488 P489 T490 L491 A492 S496 A497 I498 R510 L511 F518 G521

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 23237 | 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 | 27.545 | Depositor |
| Minimum map value | -11.758 | Depositor |
| Average map value | 0.003 | Depositor |
| Map value standard deviation | 1.012 | Depositor |
| Recommended contour level | 4.5 | 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: THP

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 | 0.13 | 0/801 | 0.27 | 0/1075 |
| 1 | E | 0.13 | 0/812 | 0.25 | 0/1089 |
| 2 | B | 0.13 | 0/655 | 0.28 | 0/878 |
| 2 | F | 0.16 | 0/655 | 0.28 | 0/878 |
| 3 | C | 0.15 | 0/842 | 0.29 | 0/1135 |
| 3 | G | 0.11 | 0/803 | 0.24 | 0/1085 |
| 4 | D | 0.12 | 0/747 | 0.24 | 0/1004 |
| 4 | H | 0.11 | 0/736 | 0.26 | 0/990 |
| 5 | I | 0.73 | 0/3357 | 0.92 | 1/5174 (0.0%) |
| 6 | J | 0.67 | 0/785 | 0.86 | 0/1210 |
| 7 | K | 0.73 | 0/2592 | 0.89 | 0/4003 |
| 8 | L | 0.09 | 0/2969 | 0.24 | 0/4030 |
| All | All | 0.48 | 0/15754 | 0.64 | 1/22551 (0.0%) |

There are no bond length outliers.

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 5 | I | 117 | DT | N3-C4-O4 | 5.11 | 122.97 | 119.90 |

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 | 5 | 0 |
| 1 | E | 800 | 0 | 839 | 6 | 0 |
| 2 | B | 648 | 0 | 693 | 2 | 0 |
| 2 | F | 648 | 0 | 693 | 5 | 0 |
| 3 | C | 832 | 0 | 897 | 3 | 0 |
| 3 | G | 793 | 0 | 848 | 5 | 0 |
| 4 | D | 736 | 0 | 756 | 3 | 0 |
| 4 | H | 725 | 0 | 743 | 7 | 0 |
| 5 | I | 2996 | 0 | 1650 | 25 | 0 |
| 6 | J | 724 | 0 | 395 | 10 | 0 |
| 7 | K | 2308 | 0 | 1257 | 18 | 0 |
| 8 | L | 2893 | 0 | 2862 | 17 | 0 |
| All | All | 14892 | 0 | 12459 | 87 | 0 |

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

The worst 5 of 87 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:113:DA:H1' | 5:I:114:DG:H5' | 1.70 | 0.73 |
| 7:K:36:DA:H1' | 8:L:478:VAL:HG11 | 1.74 | 0.69 |
| 2:F:30:THR:HG21 | 7:K:61:DA:H5" | 1.79 | 0.65 |
| 7:K:37:DG:H2" | 7:K:38:DG:C8 | 2.35 | 0.61 |
| 3:G:32:ARG:HD3 | 3:G:35:ARG:HH12 | 1.66 | 0.60 |

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%) | 93 (99%) | 1 (1%) | 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%) | 77 (98%) | 2 (2%) | 0 | 100 | 100 |
| 2 | F | 79/102 (78%) | 77 (98%) | 2 (2%) | 0 | 100 | 100 |
| 3 | C | 106/129 (82%) | 105 (99%) | 1 (1%) | 0 | 100 | 100 |
| 3 | G | 101/129 (78%) | 101 (100%) | 0 | 0 | 100 | 100 |
| 4 | D | 92/125 (74%) | 92 (100%) | 0 | 0 | 100 | 100 |
| 4 | H | 91/125 (73%) | 89 (98%) | 2 (2%) | 0 | 100 | 100 |
| 8 | L | 374/528 (71%) | 369 (99%) | 5 (1%) | 0 | 100 | 100 |
| All | All | 1111/1510 (74%) | 1098 (99%) | 13 (1%) | 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%) | 67 (100%) | 0 | 100 | 100 |
| 2 | F | 67/78 (86%) | 67 (100%) | 0 | 100 | 100 |
| 3 | C | 84/98 (86%) | 83 (99%) | 1 (1%) | 63 | 73 |
| 3 | G | 81/98 (83%) | 81 (100%) | 0 | 100 | 100 |
| 4 | D | 81/105 (77%) | 81 (100%) | 0 | 100 | 100 |
| 4 | H | 80/105 (76%) | 80 (100%) | 0 | 100 | 100 |
| 8 | L | 297/435 (68%) | 296 (100%) | 1 (0%) | 86 | 83 |
| All | All | 924/1215 (76%) | 922 (100%) | 2 (0%) | 85 | 85 |

All (2) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | C | 62 | ILE |
| 8 | L | 477 | MET |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 8 | L | 270 | GLN |
| 8 | L | 296 | ASN |
| 4 | H | 63 | ASN |
| 4 | H | 84 | ASN |
| 8 | L | 218 | 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)

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 | THP | J | 35 | 6 | 22,25,26 | 0.76 | 0 | 32,37,40 | 0.87 | 2 (6%) |

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 | THP | J | 35 | 6 | - | 7/12/26/27 | 0/2/2/2 |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 6 | J | 35 | THP | O4-C4-C5 | -2.13 | 122.48 | 124.92 |
| 6 | J | 35 | THP | O2P-P1-O1P | 2.05 | 118.81 | 110.83 |

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 6 | J | 35 | THP | O4'-C1'-N1-C2 |
| 6 | J | 35 | THP | O4'-C1'-N1-C6 |
| 6 | J | 35 | THP | C3'-C4'-C5'-O5' |
| 6 | J | 35 | THP | O4'-C4'-C5'-O5' |
| 6 | J | 35 | THP | C2'-C1'-N1-C6 |

There are no ring outliers.

1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 6 | J | 35 | THP | 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.

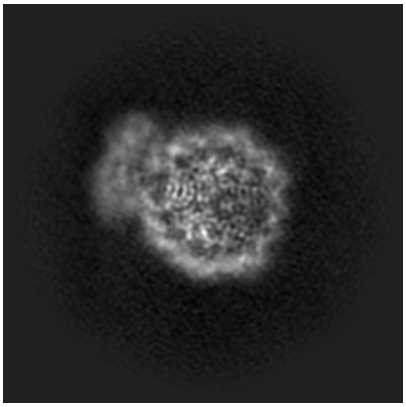
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-78605. These allow visual inspection of the internal detail of the map and identification of artifacts.

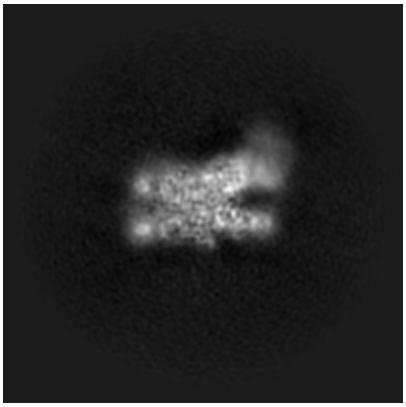
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

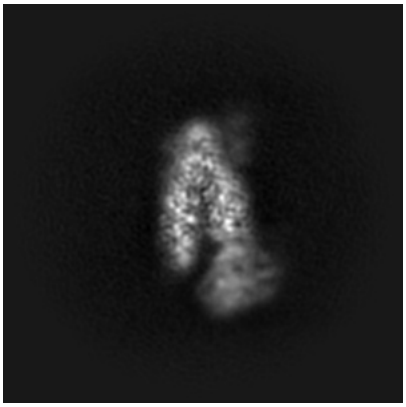
### 6.1.1 Primary map



X



Y

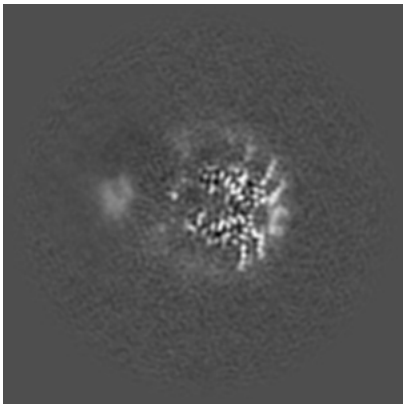


Z

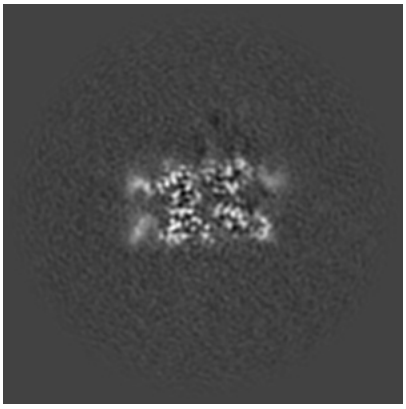
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices

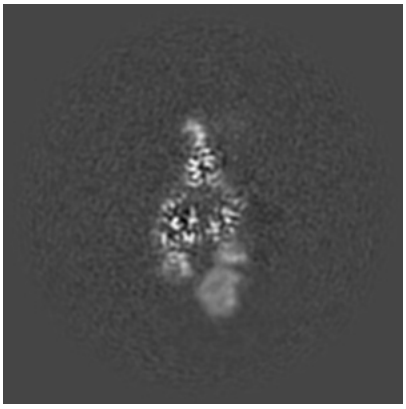
### 6.2.1 Primary map



X Index: 200



Y Index: 200

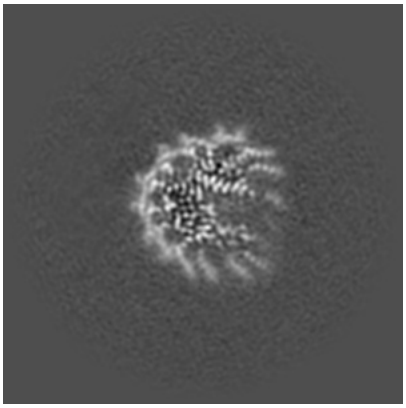


Z Index: 200

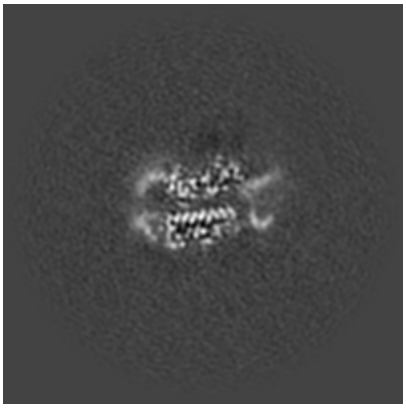
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

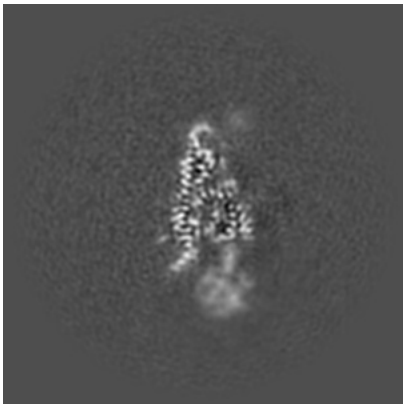
### 6.3.1 Primary map



X Index: 181



Y Index: 184

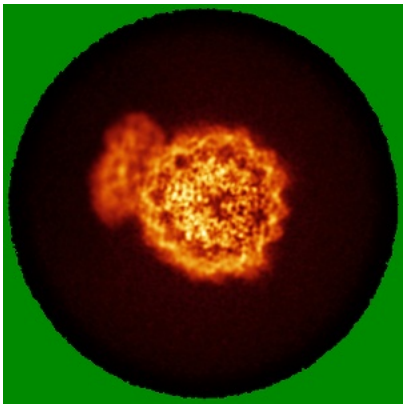


Z Index: 215

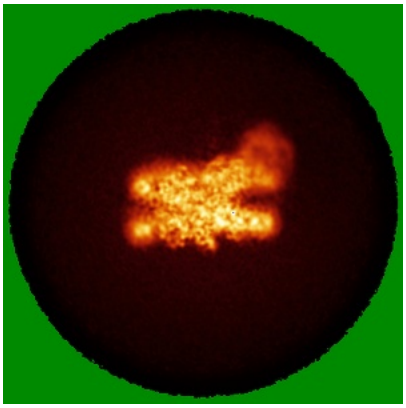
The images above show the largest variance slices of the map in three orthogonal directions.

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

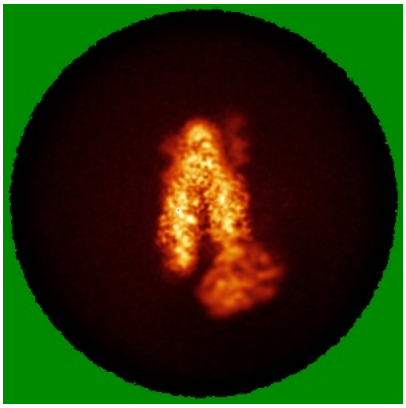
### 6.4.1 Primary map



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 4.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

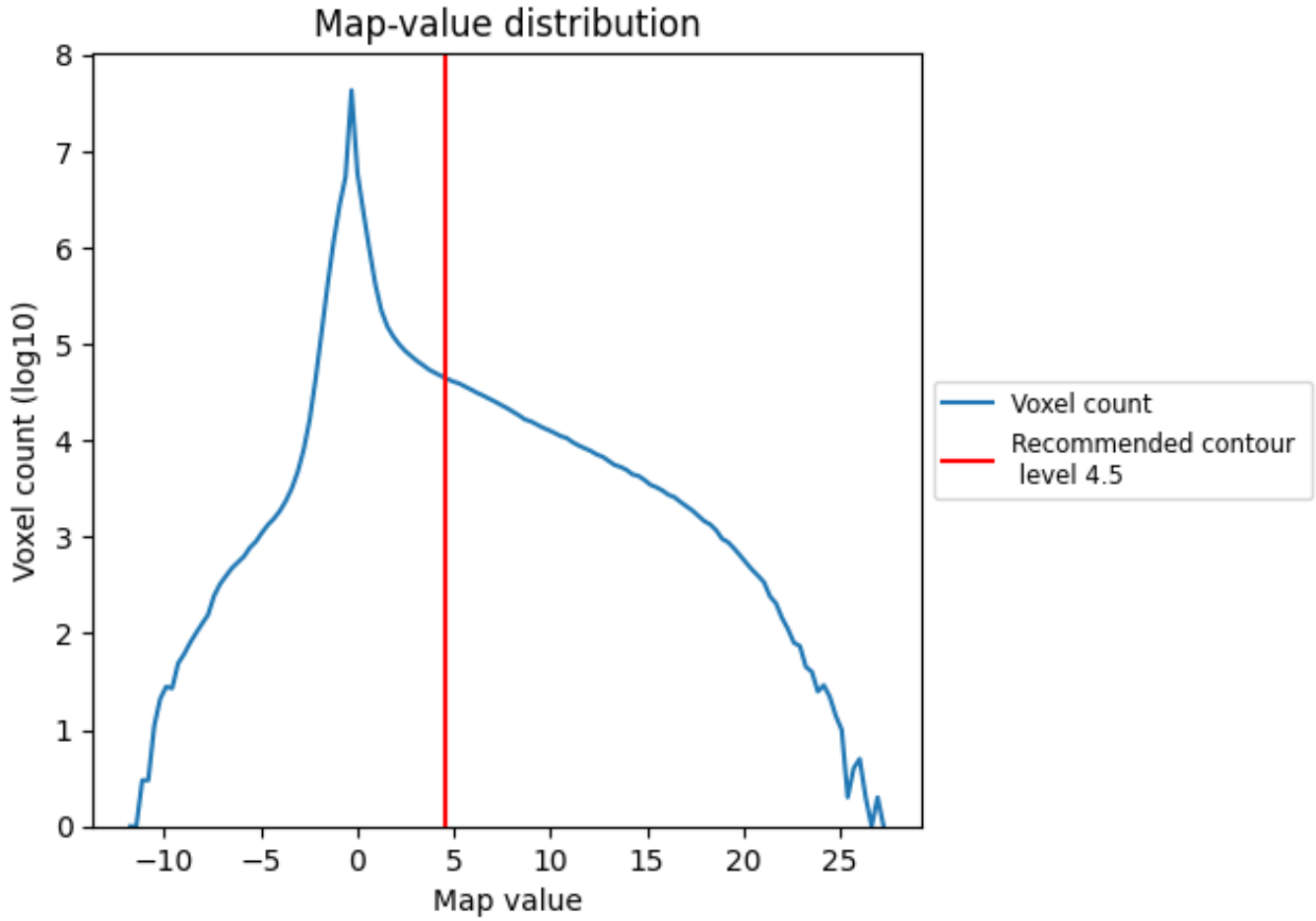
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

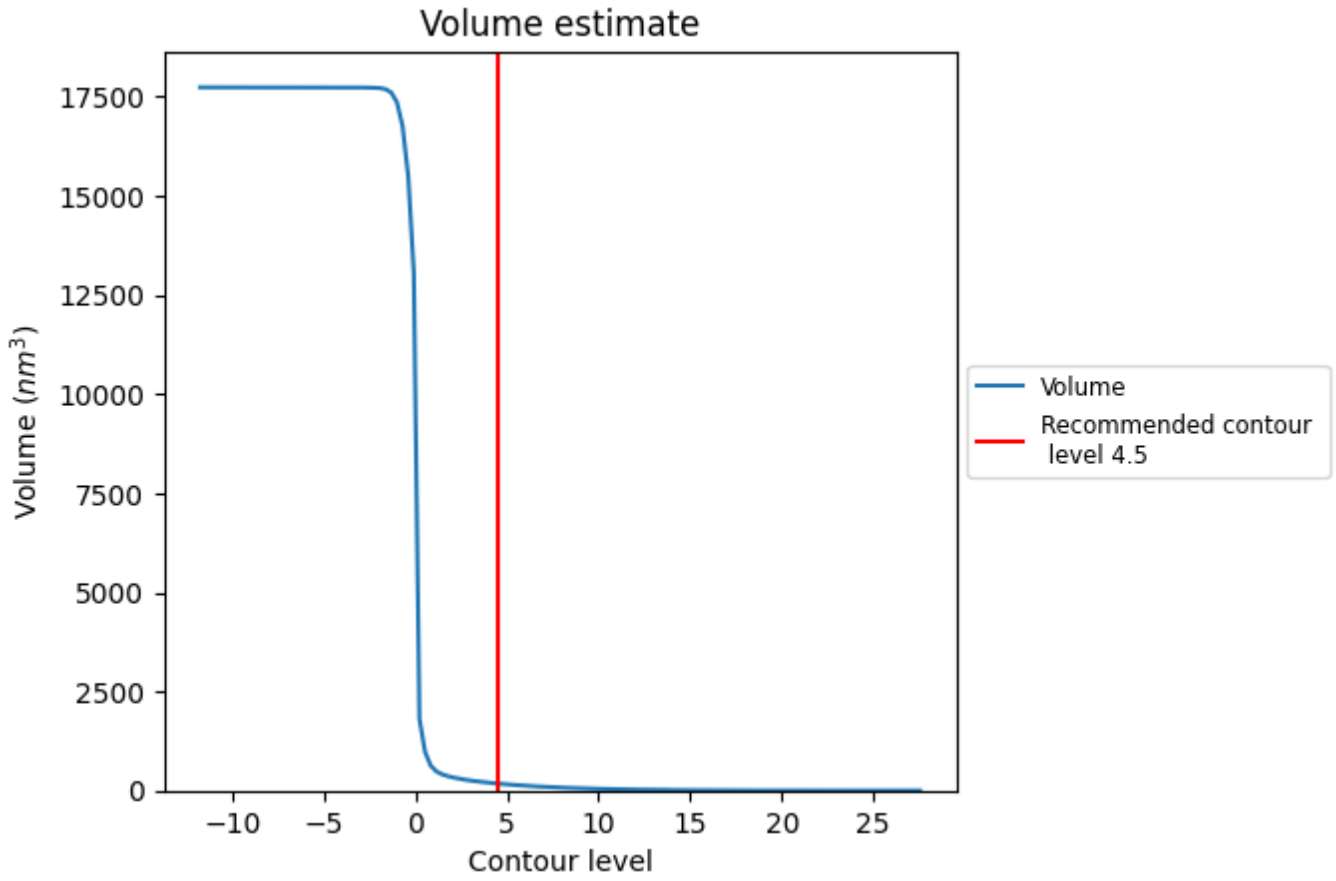
This section contains the results of statistical analysis of the map.

## 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.

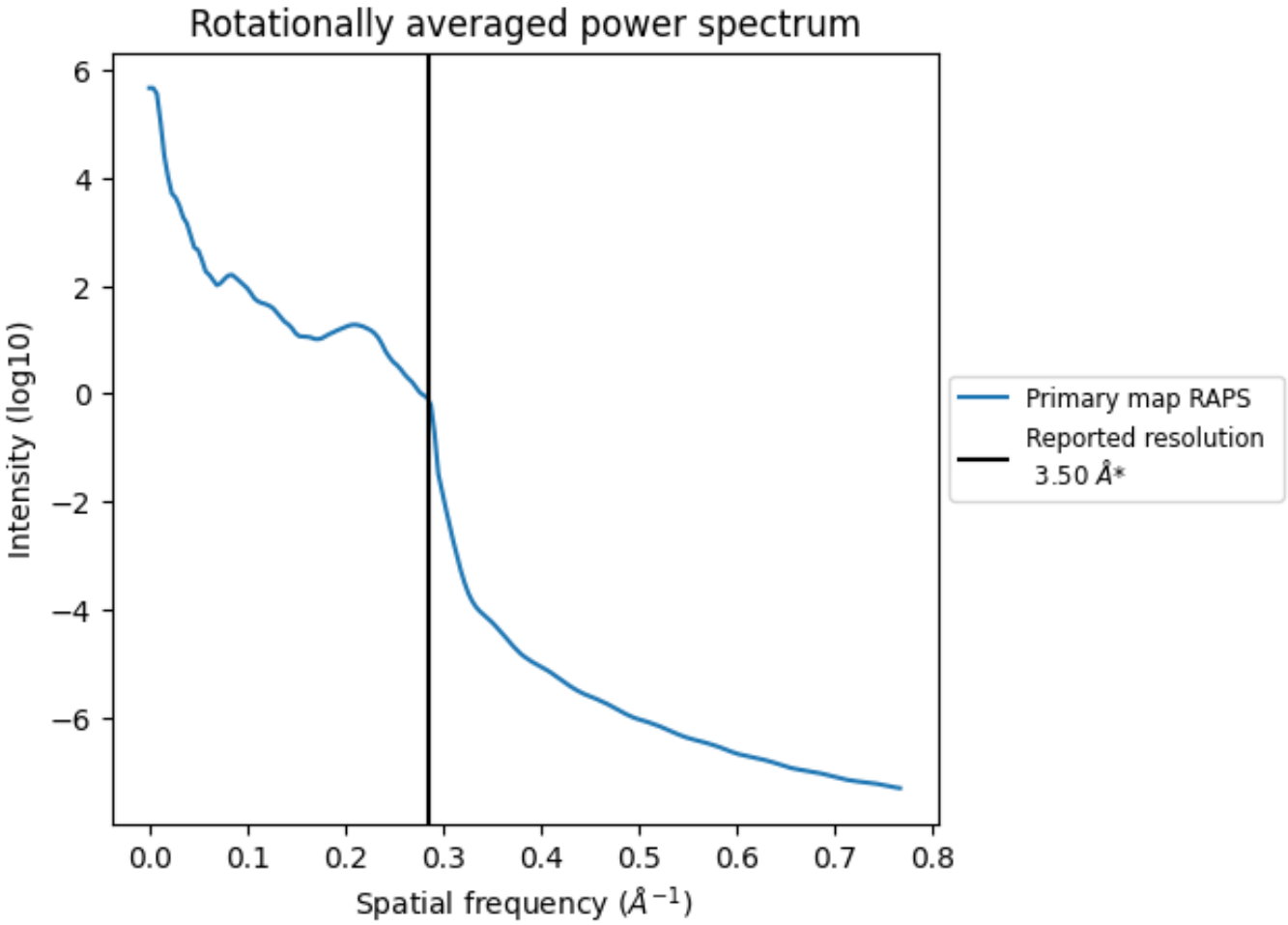
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 176 $nm^3$; this corresponds to an approximate mass of 159 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 0.286 Å$^{-1}$

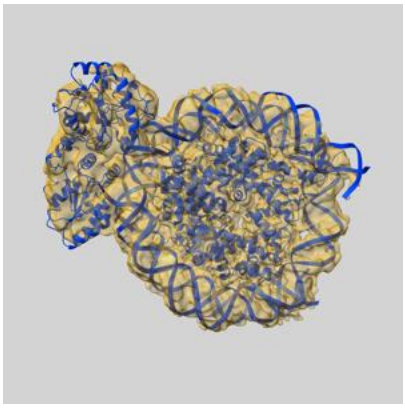
# 8 Fourier-Shell correlation (i)

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

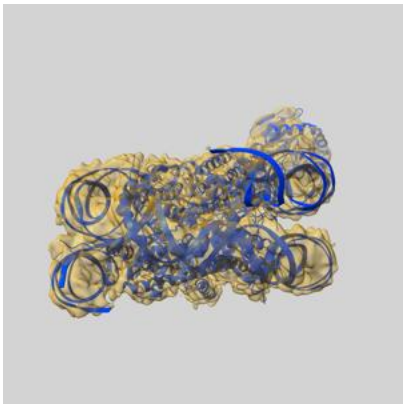
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-78605 and PDB model 37XQ. Per-residue inclusion information can be found in section 3 on page 6.

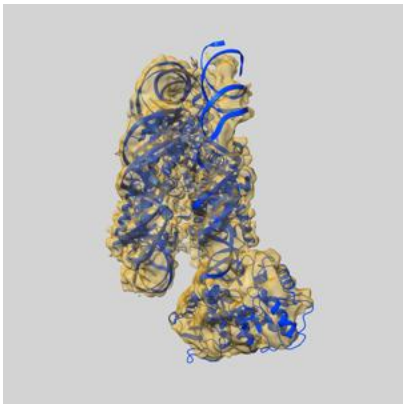
## 9.1 Map-model overlay



X



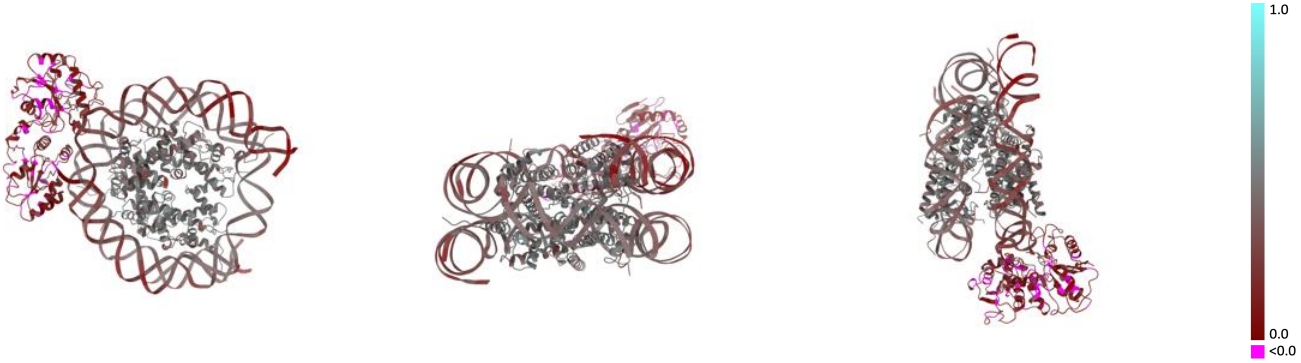
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.5 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.

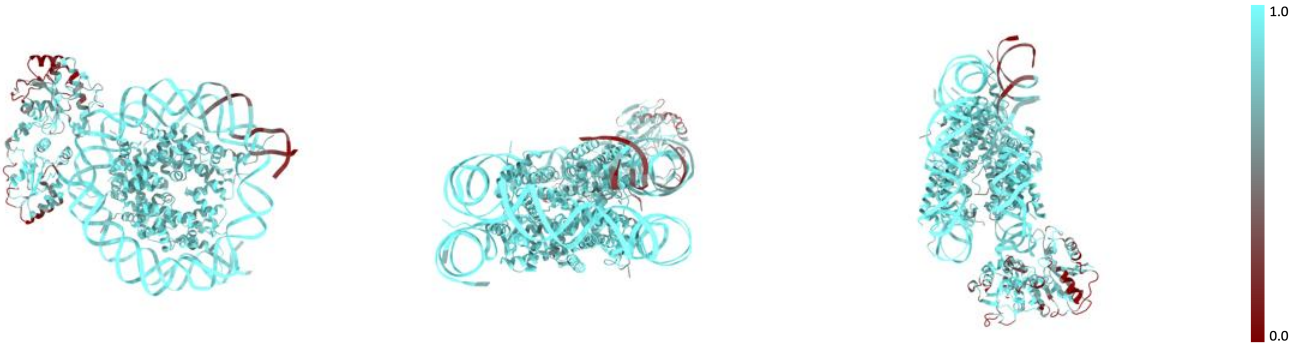
## 9.2 Q-score mapped to coordinate model (i)




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.

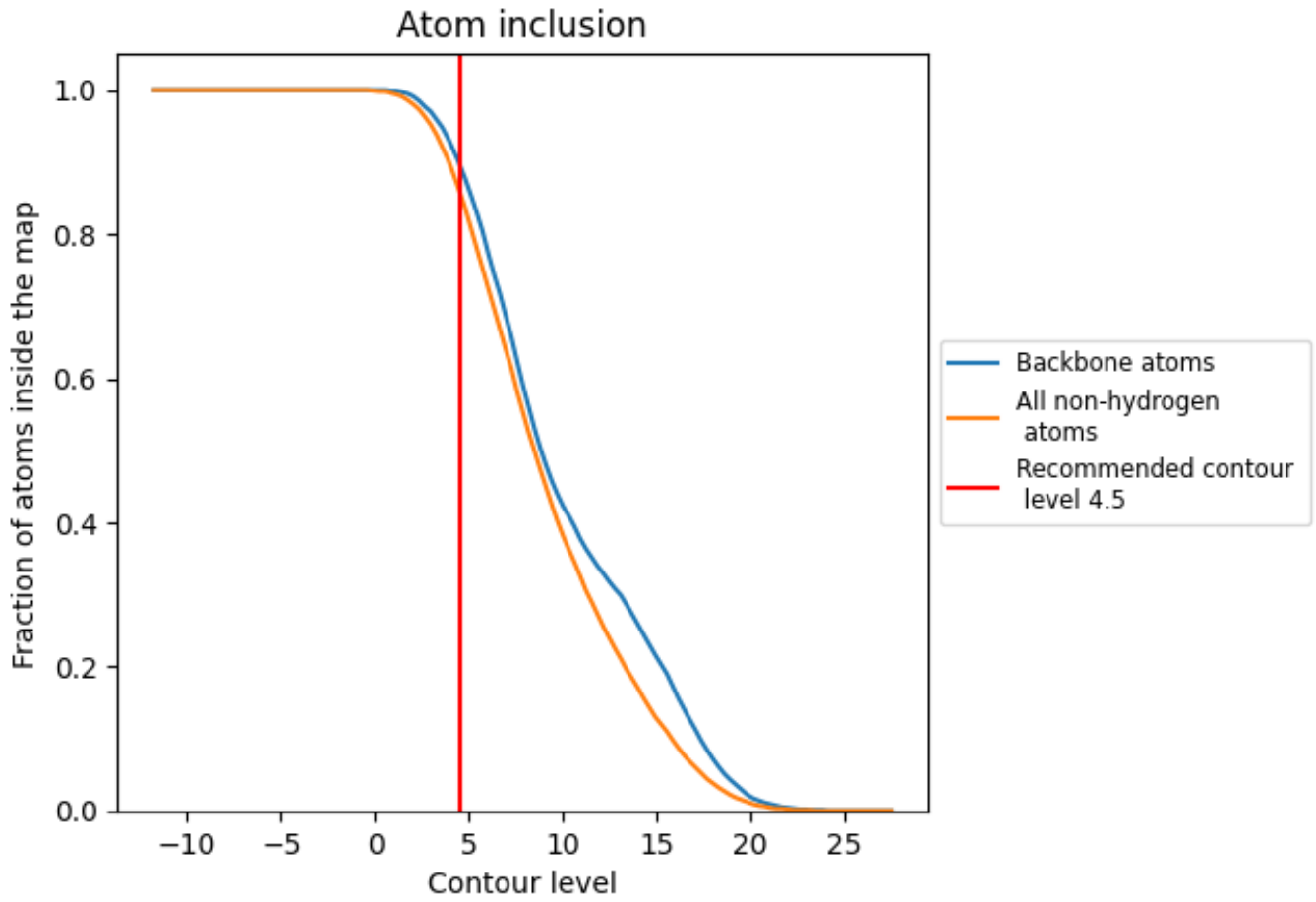
## 9.3 Atom inclusion mapped to coordinate model (i)




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 (4.5).

## 9.4 Atom inclusion (i)




At the recommended contour level, 90% 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 (4.5) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.8620 | 0.3330 |
| A | 0.8930 | 0.4580 |
| B | 0.9130 | 0.4610 |
| C | 0.9180 | 0.4560 |
| D | 0.9130 | 0.4460 |
| E | 0.9280 | 0.4680 |
| F | 0.9310 | 0.4730 |
| G | 0.8780 | 0.4320 |
| H | 0.8830 | 0.4230 |
| I | 0.9050 | 0.3180 |
| J | 0.6950 | 0.2380 |
| K | 0.9670 | 0.3380 |
| L | 0.6800 | 0.1220 |

