# wwPDB EM Validation Summary Report

Aug 26, 2021 – 06:36 am BST

| | | |
|---|---|---|
| PDB ID | : | 7OL0 |
| EMDB ID | : | EMD-12974 |
| Title | : | Structure of active transcription elongation complex Pol II-DSIF (SPT5-KOW5) |
| Authors | : | Chen, Y.; Vos, S.M.; Dienemann, C.; Ninov, M.; Urlaub, H.; Cramer, P. |
| Deposited on | : | 2021-05-18 |
| Resolution | : | 3.00 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

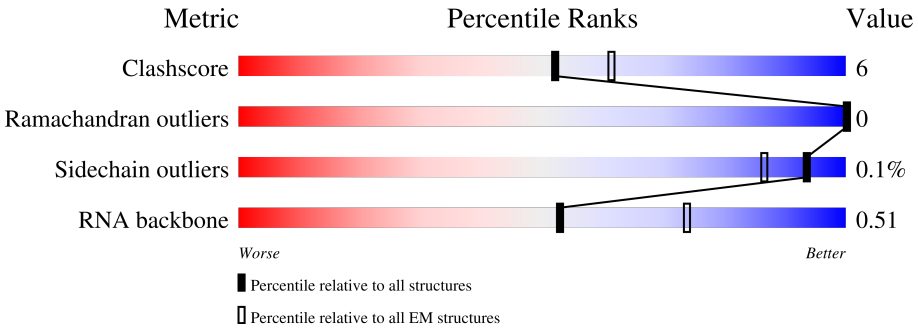
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.0.dev97 |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.23.1 |

# 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 3.00 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.



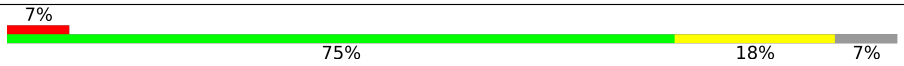
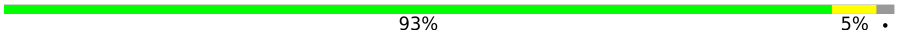
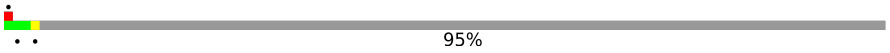
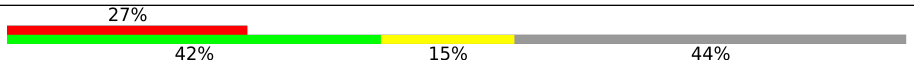
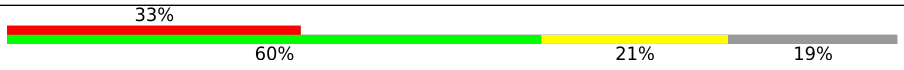

| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|---|---|---|
| Clashscore | 158937 | 4297 |
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

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 | 1970 | 60% 11% 29% |
| 2 | B | 1251 | 77% 14% 10% |
| 3 | C | 275 | 78% 16% 6% |
| 4 | D | 184 | 59% 50% 14% 36% |
| 5 | E | 210 | 87% 12% |
| 6 | F | 127 | 54% 8% 39% |
| 7 | G | 172 | 65% 81% 18% |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 8 | H | 150 |   |
| 9 | I | 125 |   |
| 10 | J | 67 |   |
| 11 | K | 117 |   |
| 12 | L | 58 |   |
| 13 | Z | 1087 |   |
| 14 | P | 47 |   |
| 15 | N | 48 |   |
| 16 | T | 48 |   |

# 2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 32892 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 DNA-directed RNA polymerase II subunit RPB1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 1407 | Total | C | N | O | S | 0 | 0 |
| | | | 11149 | 7018 | 1998 | 2062 | 71 | | |

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 2 | B | 1131 | Total | C | N | O | S | 0 | 0 |
| | | | 9047 | 5721 | 1592 | 1670 | 64 | | |

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 3 | C | 258 | Total | C | N | O | S | 0 | 0 |
| | | | 2068 | 1298 | 356 | 408 | 6 | | |

- Molecule 4 is a protein called RNA polymerase II subunit D.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 4 | D | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 967 | 608 | 167 | 188 | 4 | | |

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit E.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 5 | E | 209 | Total | C | N | O | S | 0 | 0 |
| | | | 1721 | 1089 | 300 | 324 | 8 | | |

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit F.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 6 | F | 78 | Total | C | N | O | S | 0 | 0 |
| | | | 626 | 401 | 106 | 114 | 5 | | |

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | G | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1347 | 872 | 218 | 249 | 8 | | |

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | H | 148 | Total | C | N | O | S | 0 | 0 |
| | | | 1186 | 750 | 194 | 237 | 5 | | |

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 9 | I | 116 | Total | C | N | O | S | 0 | 0 |
| | | | 926 | 574 | 162 | 179 | 11 | | |

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 10 | J | 66 | Total | C | N | O | S | 0 | 0 |
| | | | 524 | 339 | 88 | 91 | 6 | | |

- Molecule 11 is a protein called RNA_pol_L_2 domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | K | 115 | Total | C | N | O | S | 0 | 0 |
| | | | 920 | 593 | 152 | 173 | 2 | | |

- Molecule 12 is a protein called RNA polymerase II subunit K.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 12 | L | 44 | Total | C | N | O | S | 0 | 0 |
| | | | 373 | 231 | 72 | 64 | 6 | | |

- Molecule 13 is a protein called Transcription elongation factor SPT5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 13 | Z | 51 | Total | C | N | O | S | 0 | 0 |
| | | | 393 | 241 | 72 | 79 | 1 | | |

- Molecule 14 is a RNA chain called RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 14 | P | 13 | Total | C | N | O | P | 0 | 0 |
| | | | 279 | 125 | 54 | 87 | 13 | | |

- Molecule 15 is a DNA chain called Non-template DNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 15 | N | 27 | Total | C | N | O | P | 0 | 0 |
| | | | 549 | 264 | 96 | 162 | 27 | | |

- Molecule 16 is a DNA chain called Template DNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 16 | T | 39 | Total | C | N | O | P | 0 | 0 |
| | | | 808 | 385 | 149 | 235 | 39 | | |

- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 17 | A | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 18 is ZINC ION (three-letter code: ZN) (formula: Zn).

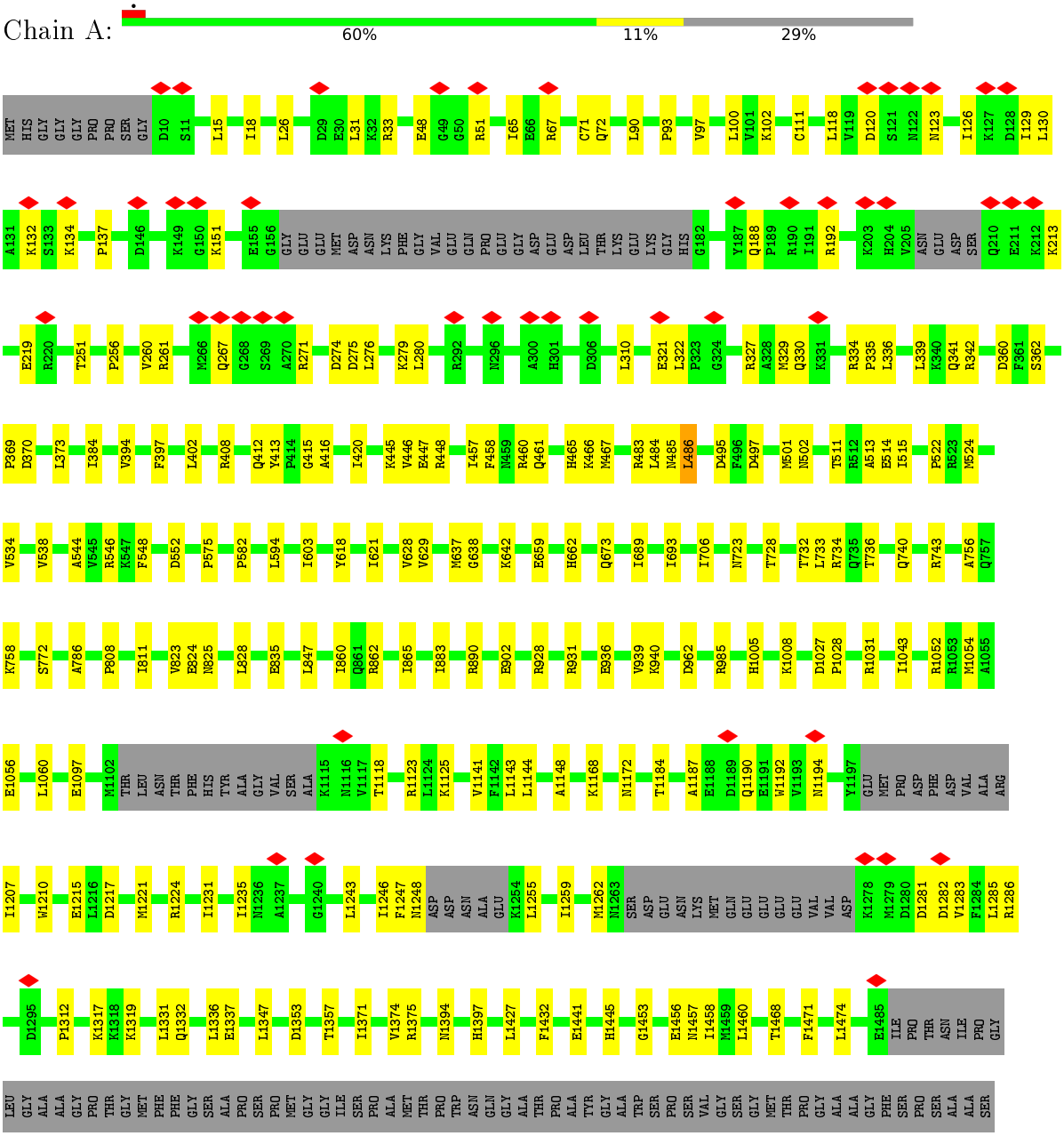
| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 18 | A | 2 | Total | Zn | 0 |
| | | | 2 | 2 | |
| 18 | B | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 18 | C | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 18 | I | 2 | Total | Zn | 0 |
| | | | 2 | 2 | |
| 18 | J | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 18 | L | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |

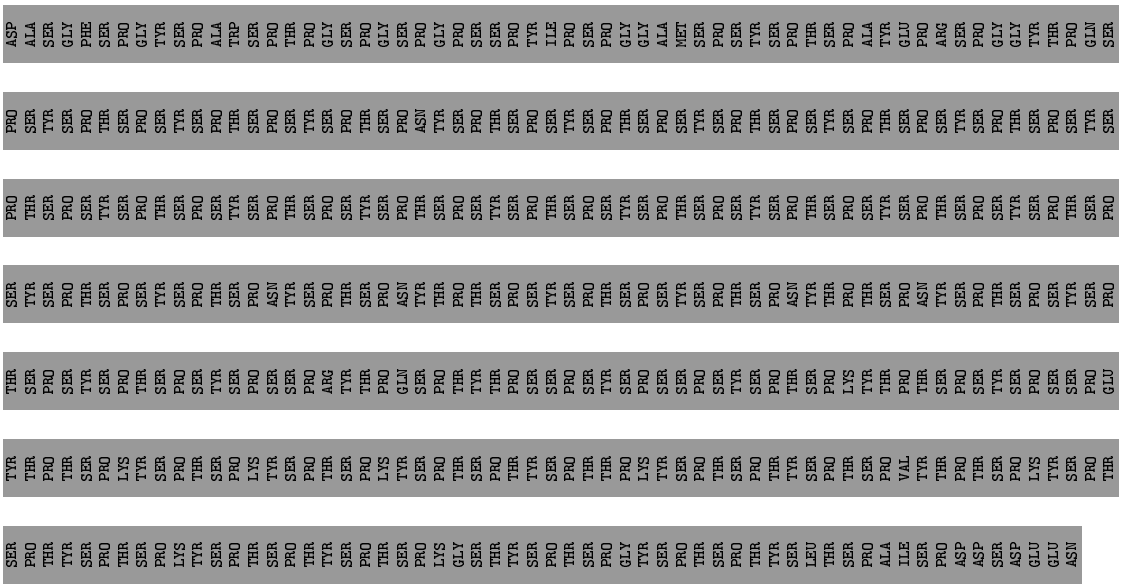
# 3 Residue-property plots (i)

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.

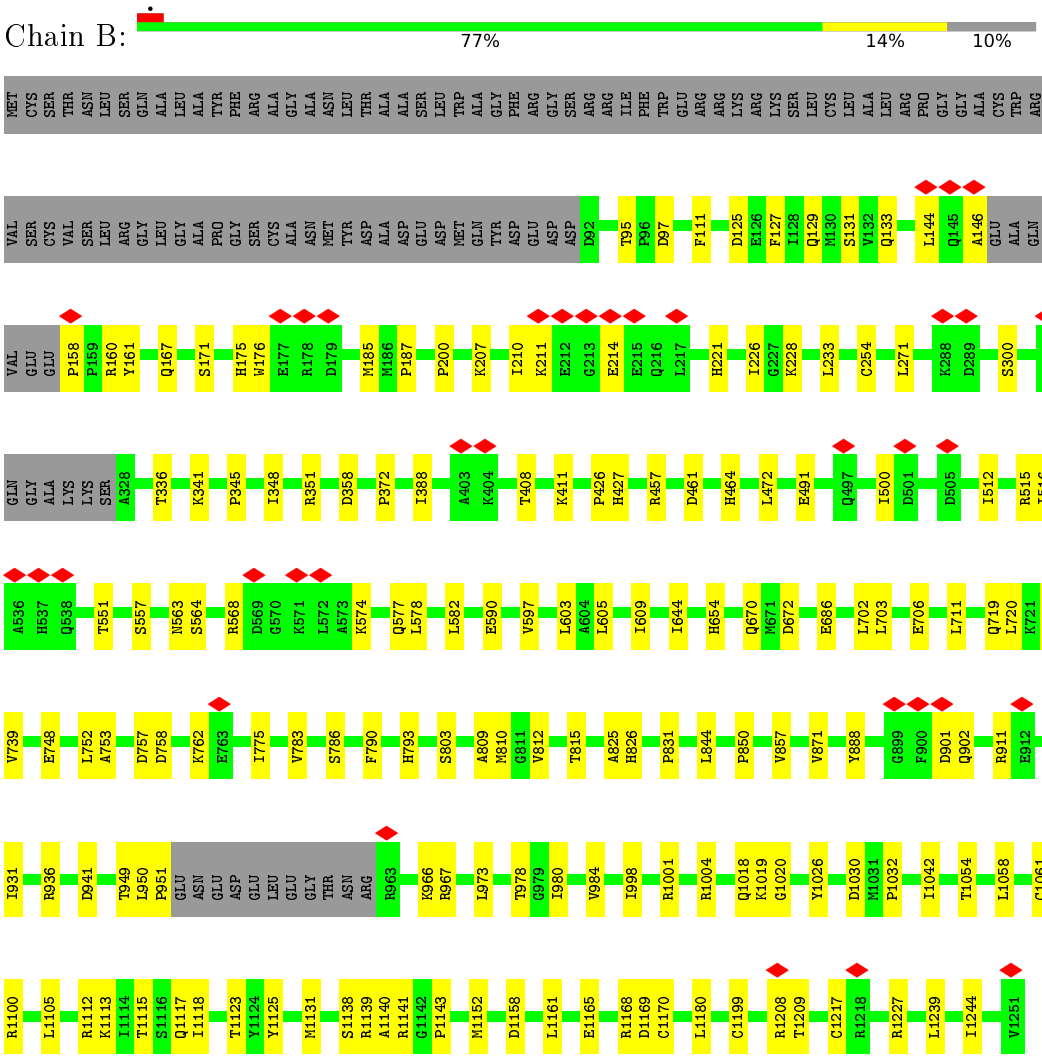
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1

Chain A:



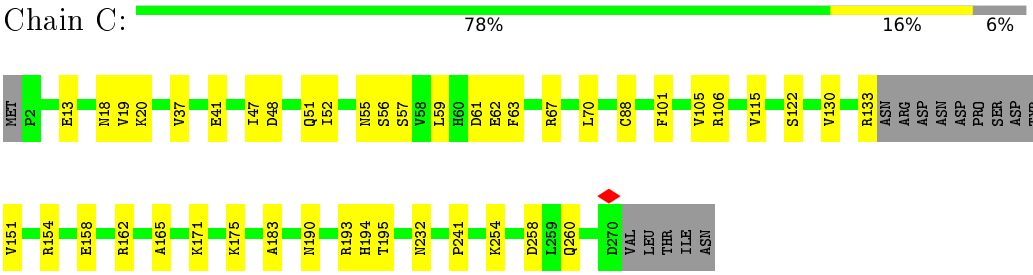


• Molecule 2: DNA-directed RNA polymerase subunit beta



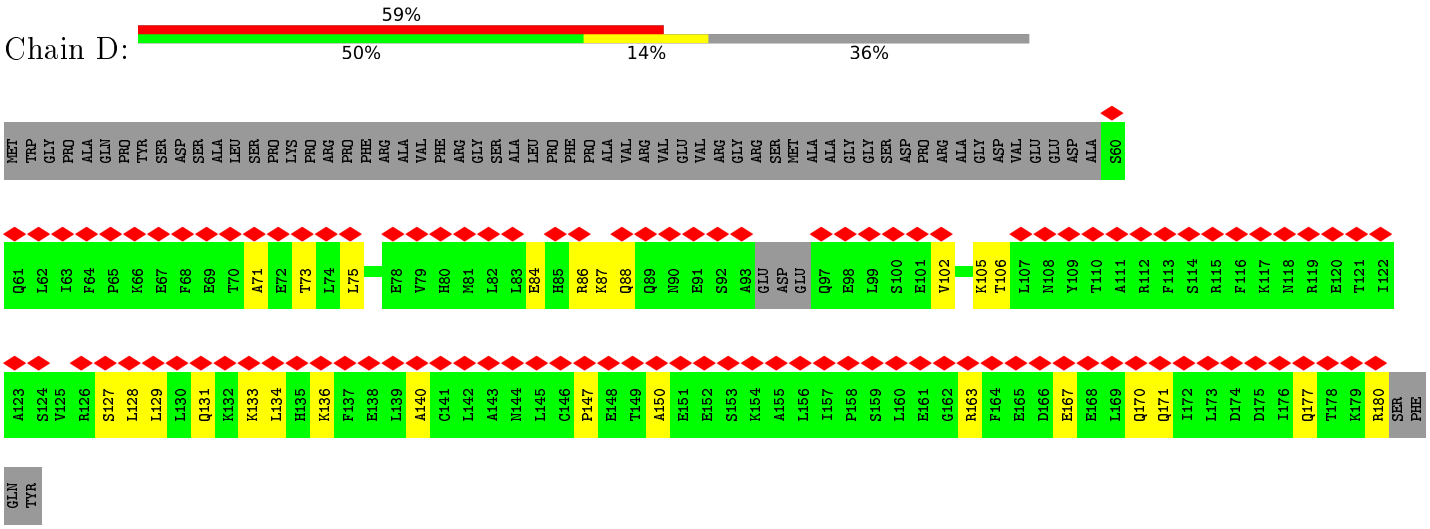

• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

Chain C:



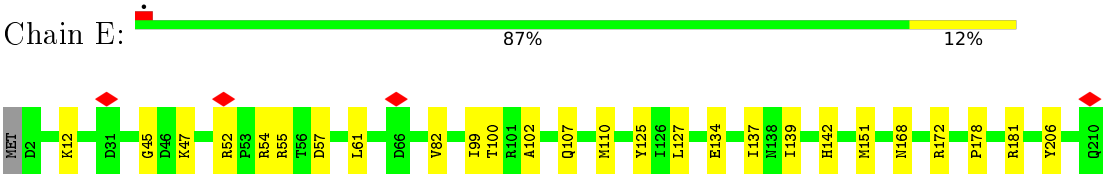

• Molecule 4: RNA polymerase II subunit D

Chain D:



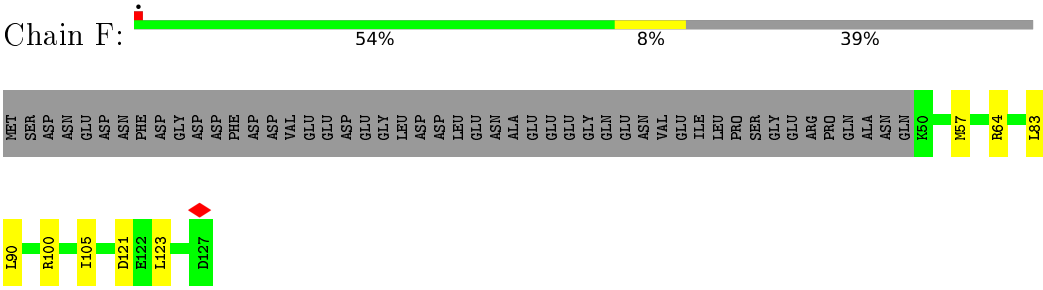

• Molecule 5: DNA-directed RNA polymerase II subunit E

Chain E:



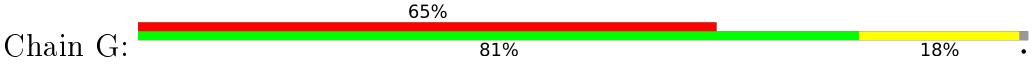

• Molecule 6: DNA-directed RNA polymerase II subunit F

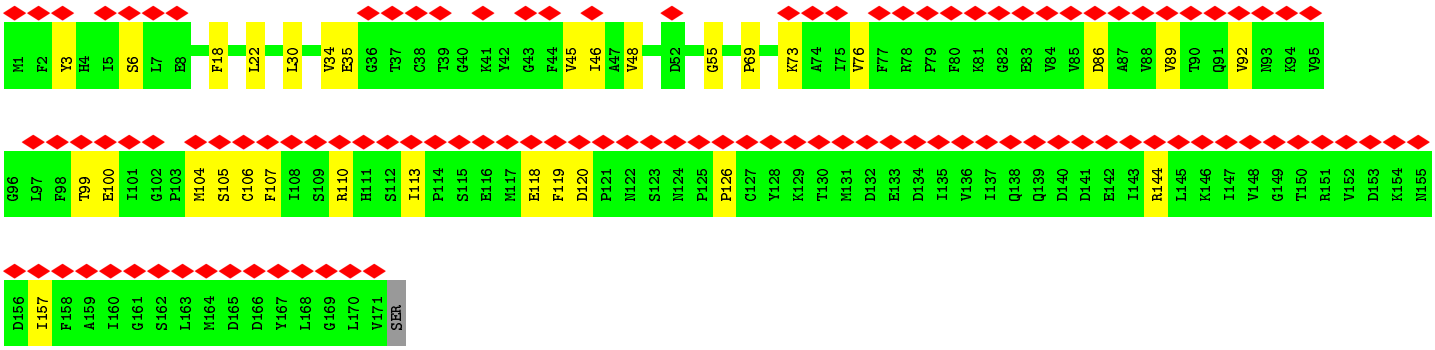
Chain F:




• Molecule 7: DNA-directed RNA polymerase II subunit RPB7

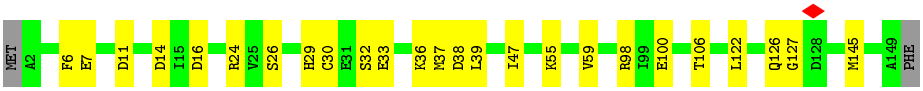
Chain G:





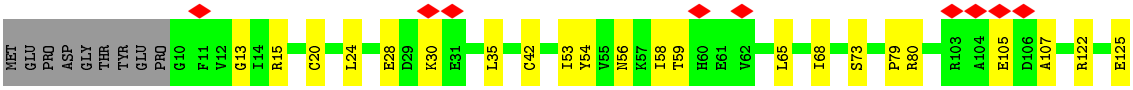

- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:

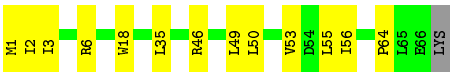

- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

Chain I:

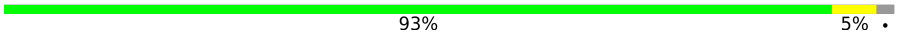

- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

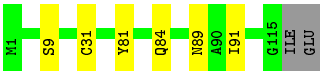
Chain J:


- Molecule 11: RNA_pol_L_2 domain-containing protein

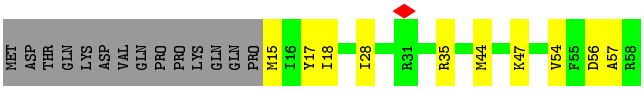
Chain K:



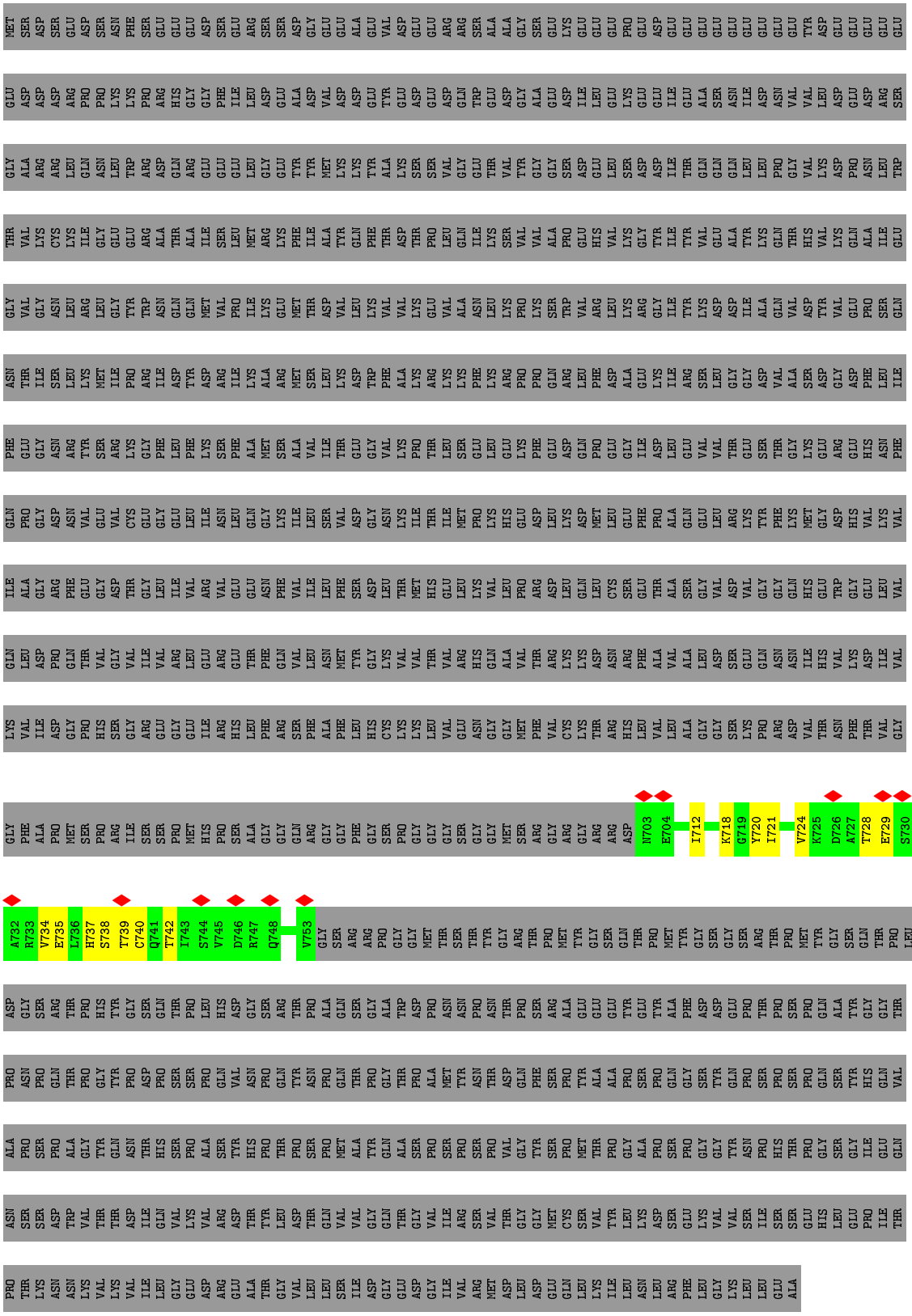

- Molecule 12: RNA polymerase II subunit K

Chain L:

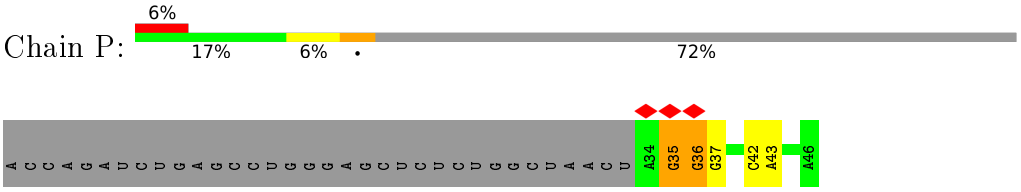




- Molecule 13: Transcription elongation factor SPT5

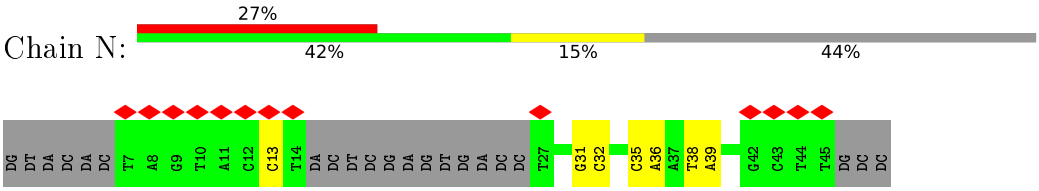
Chain Z:

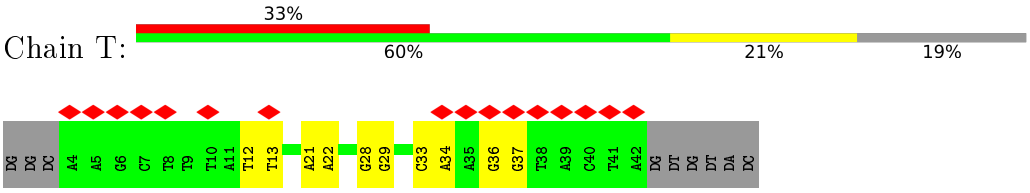

- Molecule 14: RNA




- Molecule 15: Non-template DNA




- Molecule 16: Template DNA



# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 194785 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 43.21 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum map value | 0.160 | Depositor |
| Minimum map value | -0.089 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.005 | Depositor |
| Recommended contour level | 0.018 | Depositor |
| Map size (Å) | 315.0, 315.0, 315.0 | wwPDB |
| Map dimensions | 300, 300, 300 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.05, 1.05, 1.05 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

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

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 | 0.43 | 0/11350 | 0.55 | 2/15314 (0.0%) |
| 2 | B | 0.50 | 0/9227 | 0.57 | 1/12454 (0.0%) |
| 3 | C | 0.53 | 0/2111 | 0.52 | 0/2868 |
| 4 | D | 0.26 | 0/979 | 0.54 | 0/1312 |
| 5 | E | 0.41 | 0/1752 | 0.52 | 0/2366 |
| 6 | F | 0.50 | 0/636 | 0.57 | 0/859 |
| 7 | G | 0.35 | 0/1378 | 0.55 | 0/1870 |
| 8 | H | 0.51 | 0/1207 | 0.57 | 0/1628 |
| 9 | I | 0.46 | 0/948 | 0.57 | 0/1286 |
| 10 | J | 0.56 | 0/533 | 0.55 | 0/719 |
| 11 | K | 0.48 | 0/939 | 0.57 | 0/1271 |
| 12 | L | 0.49 | 0/378 | 0.64 | 0/500 |
| 13 | Z | 0.29 | 0/396 | 0.52 | 0/536 |
| 14 | P | 0.49 | 0/312 | 0.84 | 0/484 |
| 15 | N | 0.57 | 0/613 | 0.94 | 0/940 |
| 16 | T | 0.71 | 0/907 | 0.94 | 0/1400 |
| All | All | 0.47 | 0/33666 | 0.58 | 3/45807 (0.0%) |

There are no bond length outliers.

All (3) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 486 | LEU | CA-CB-CG | -6.32 | 100.77 | 115.30 |
| 1 | A | 883 | ILE | CG1-CB-CG2 | -5.11 | 100.16 | 111.40 |
| 2 | B | 973 | LEU | CA-CB-CG | 5.03 | 126.88 | 115.30 |

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 | 11149 | 0 | 11300 | 144 | 0 |
| 2 | B | 9047 | 0 | 9080 | 114 | 0 |
| 3 | C | 2068 | 0 | 2015 | 32 | 0 |
| 4 | D | 967 | 0 | 973 | 20 | 0 |
| 5 | E | 1721 | 0 | 1737 | 17 | 0 |
| 6 | F | 626 | 0 | 657 | 8 | 0 |
| 7 | G | 1347 | 0 | 1347 | 21 | 0 |
| 8 | H | 1186 | 0 | 1147 | 19 | 0 |
| 9 | I | 926 | 0 | 845 | 14 | 0 |
| 10 | J | 524 | 0 | 540 | 9 | 0 |
| 11 | K | 920 | 0 | 942 | 4 | 0 |
| 12 | L | 373 | 0 | 378 | 7 | 0 |
| 13 | Z | 393 | 0 | 400 | 10 | 0 |
| 14 | P | 279 | 0 | 142 | 3 | 0 |
| 15 | N | 549 | 0 | 308 | 4 | 0 |
| 16 | T | 808 | 0 | 442 | 7 | 0 |
| 17 | A | 1 | 0 | 0 | 0 | 0 |
| 18 | A | 2 | 0 | 0 | 0 | 0 |
| 18 | B | 1 | 0 | 0 | 0 | 0 |
| 18 | C | 1 | 0 | 0 | 0 | 0 |
| 18 | I | 2 | 0 | 0 | 0 | 0 |
| 18 | J | 1 | 0 | 0 | 0 | 0 |
| 18 | L | 1 | 0 | 0 | 0 | 0 |
| All | All | 32892 | 0 | 32253 | 372 | 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 6.

The worst 5 of 372 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:E:168:ASN:HA | 5:E:172:ARG:HH21 | 1.29 | 0.95 |
| 2:B:300:SER:HG | 2:B:427:HIS:HD1 | 1.22 | 0.86 |
| 1:A:1192:TRP:HB2 | 1:A:1248:ASN:HD22 | 1.48 | 0.79 |
| 1:A:1247:PHE:O | 1:A:1248:ASN:OD1 | 2.07 | 0.72 |

*Continued on next page...*

*Continued from previous page...*

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 9:I:68:ILE:O | 9:I:122:ARG:NH1 | 2.23 | 0.71 |

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 | 1393/1970 (71%) | 1357 (97%) | 36 (3%) | 0 | 100 | 100 |
| 2 | B | 1123/1251 (90%) | 1094 (97%) | 29 (3%) | 0 | 100 | 100 |
| 3 | C | 254/275 (92%) | 250 (98%) | 4 (2%) | 0 | 100 | 100 |
| 4 | D | 114/184 (62%) | 105 (92%) | 9 (8%) | 0 | 100 | 100 |
| 5 | E | 207/210 (99%) | 203 (98%) | 4 (2%) | 0 | 100 | 100 |
| 6 | F | 76/127 (60%) | 74 (97%) | 2 (3%) | 0 | 100 | 100 |
| 7 | G | 169/172 (98%) | 156 (92%) | 13 (8%) | 0 | 100 | 100 |
| 8 | H | 146/150 (97%) | 141 (97%) | 5 (3%) | 0 | 100 | 100 |
| 9 | I | 114/125 (91%) | 107 (94%) | 7 (6%) | 0 | 100 | 100 |
| 10 | J | 64/67 (96%) | 63 (98%) | 1 (2%) | 0 | 100 | 100 |
| 11 | K | 113/117 (97%) | 109 (96%) | 4 (4%) | 0 | 100 | 100 |
| 12 | L | 42/58 (72%) | 41 (98%) | 1 (2%) | 0 | 100 | 100 |
| 13 | Z | 49/1087 (4%) | 49 (100%) | 0 | 0 | 100 | 100 |
| All | All | 3864/5793 (67%) | 3749 (97%) | 115 (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 | 1239/1749 (71%) | 1236 (100%) | 3 (0%) | 93 98 |
| 2 | B | 991/1084 (91%) | 991 (100%) | 0 | 100 100 |
| 3 | C | 234/252 (93%) | 234 (100%) | 0 | 100 100 |
| 4 | D | 109/160 (68%) | 109 (100%) | 0 | 100 100 |
| 5 | E | 191/192 (100%) | 191 (100%) | 0 | 100 100 |
| 6 | F | 68/111 (61%) | 68 (100%) | 0 | 100 100 |
| 7 | G | 151/153 (99%) | 151 (100%) | 0 | 100 100 |
| 8 | H | 129/131 (98%) | 129 (100%) | 0 | 100 100 |
| 9 | I | 101/112 (90%) | 101 (100%) | 0 | 100 100 |
| 10 | J | 55/56 (98%) | 55 (100%) | 0 | 100 100 |
| 11 | K | 104/106 (98%) | 104 (100%) | 0 | 100 100 |
| 12 | L | 41/55 (74%) | 41 (100%) | 0 | 100 100 |
| 13 | Z | 45/940 (5%) | 45 (100%) | 0 | 100 100 |
| All | All | 3458/5101 (68%) | 3455 (100%) | 3 (0%) | 93 98 |

All (3) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 33 | ARG |
| 1 | A | 538 | VAL |
| 1 | A | 1375 | ARG |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 143 | HIS |
| 1 | A | 1248 | ASN |
| 2 | B | 726 | ASN |
| 2 | B | 1102 | ASN |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|---|---|---|---|
| 11 | K | 84 | GLN |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 14 | P | 12/47 (25%) | 3 (25%) | 0 |

All (3) RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 14 | P | 35 | G |
| 14 | P | 36 | G |
| 14 | P | 37 | G |

There are no RNA pucker outliers to report.

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

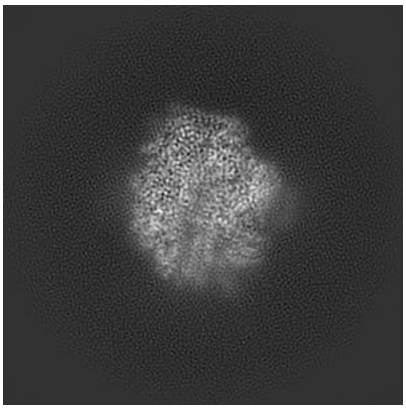
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12974. These allow visual inspection of the internal detail of the map and identification of artifacts.

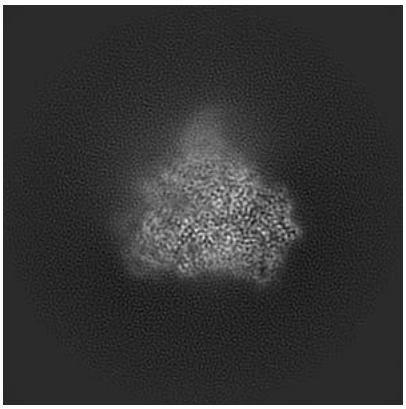
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections

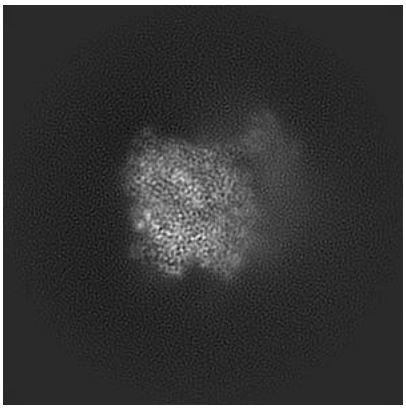
### 6.1.1 Primary map



X

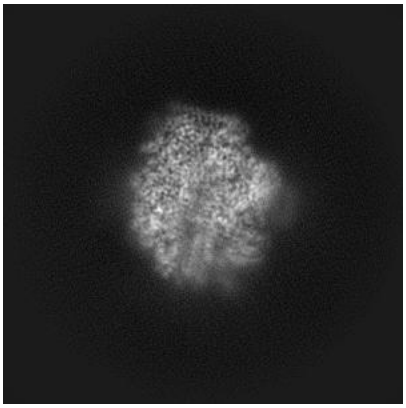


Y

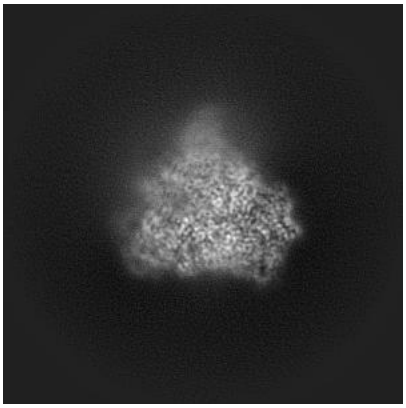


Z

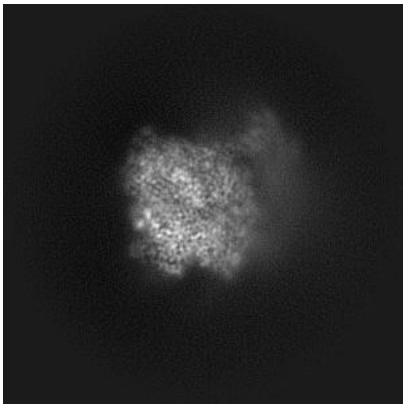
### 6.1.2 Raw map



X



Y

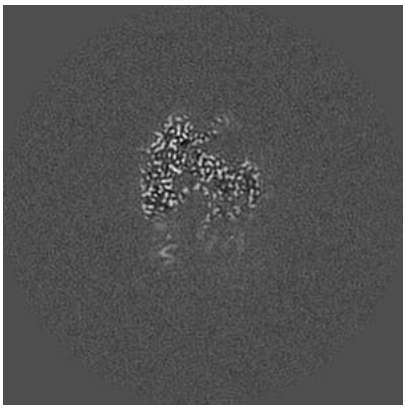


Z

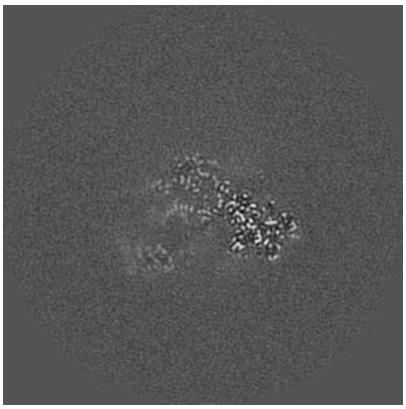
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

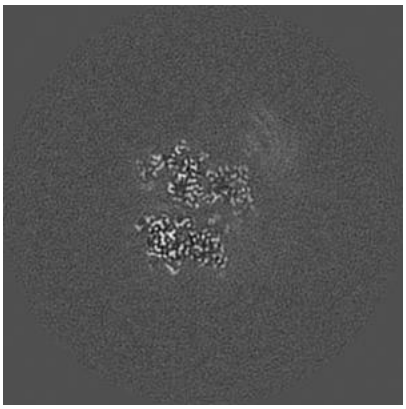
### 6.2.1 Primary map



X Index: 150

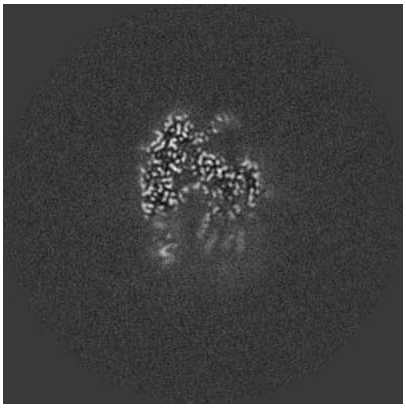


Y Index: 150

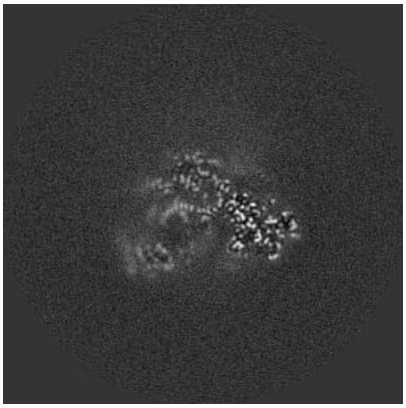


Z Index: 150

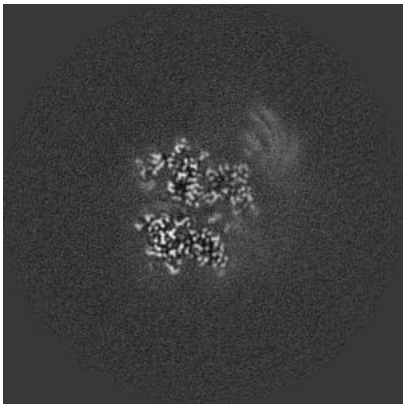
### 6.2.2 Raw map



X Index: 150



Y Index: 150

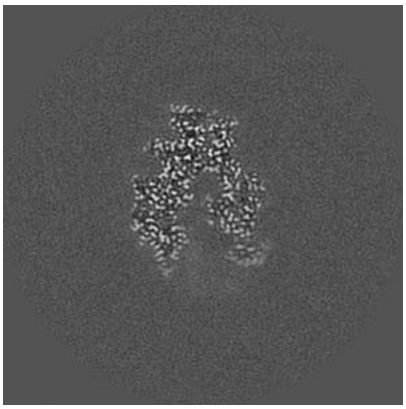


Z Index: 150

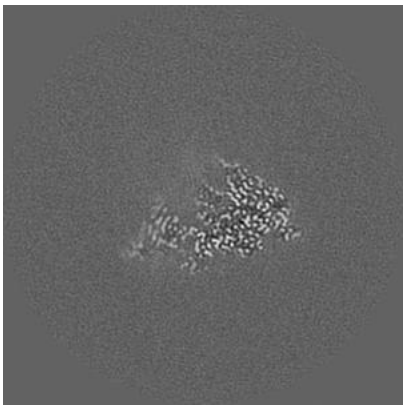
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

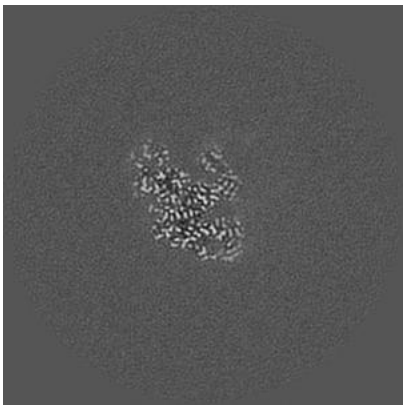
### 6.3.1 Primary map



X Index: 129

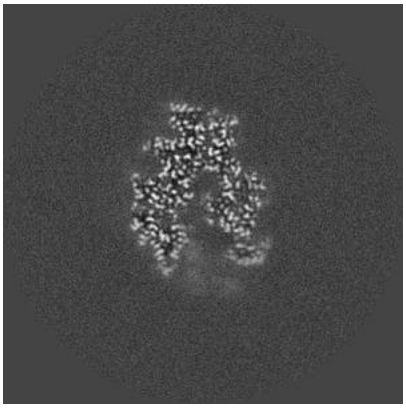


Y Index: 129

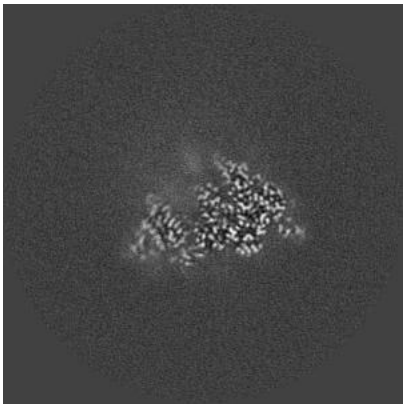


Z Index: 181

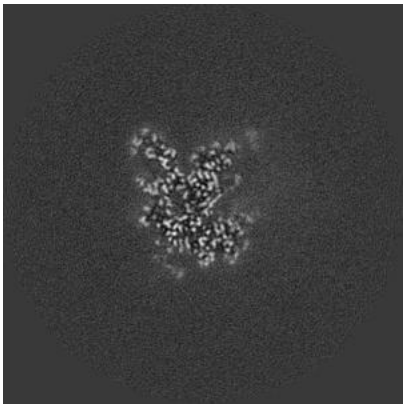
### 6.3.2 Raw map



X Index: 129



Y Index: 127



Z Index: 173

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

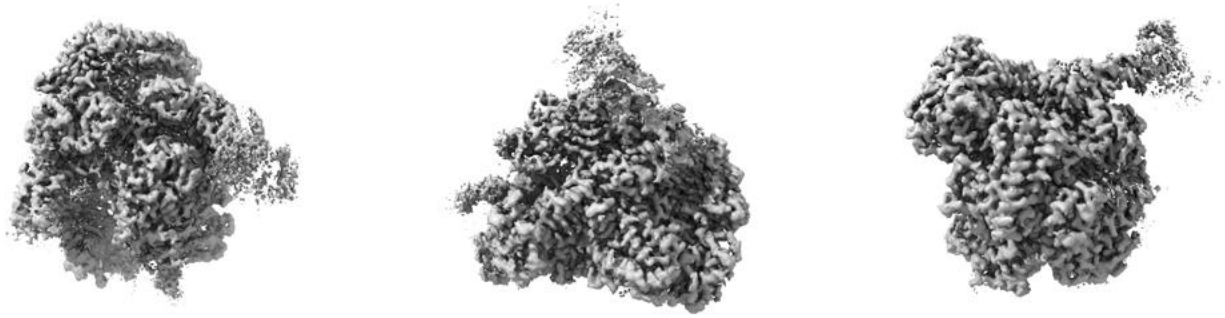
## 6.4 Orthogonal surface views (i)

### 6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

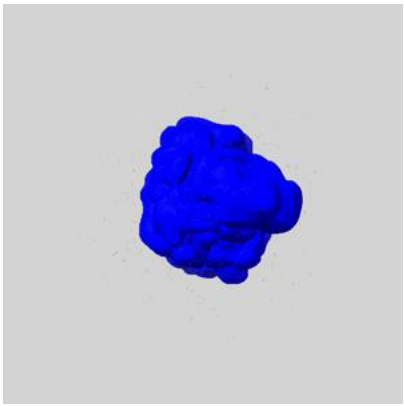
## 6.5 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

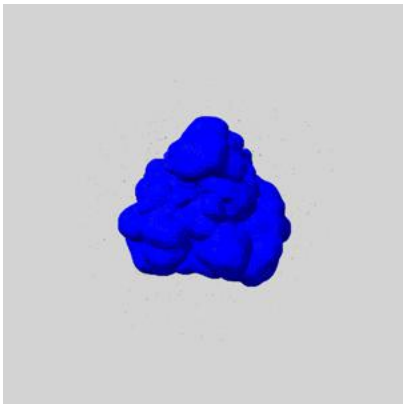
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

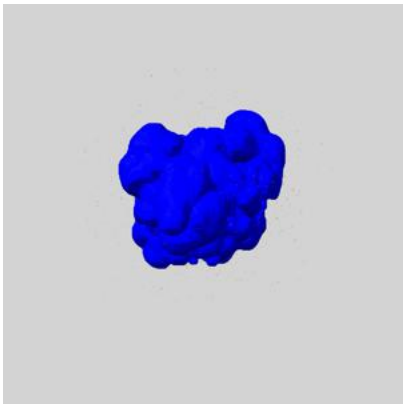
### 6.5.1 emd_12974_msk_1.map



X



Y

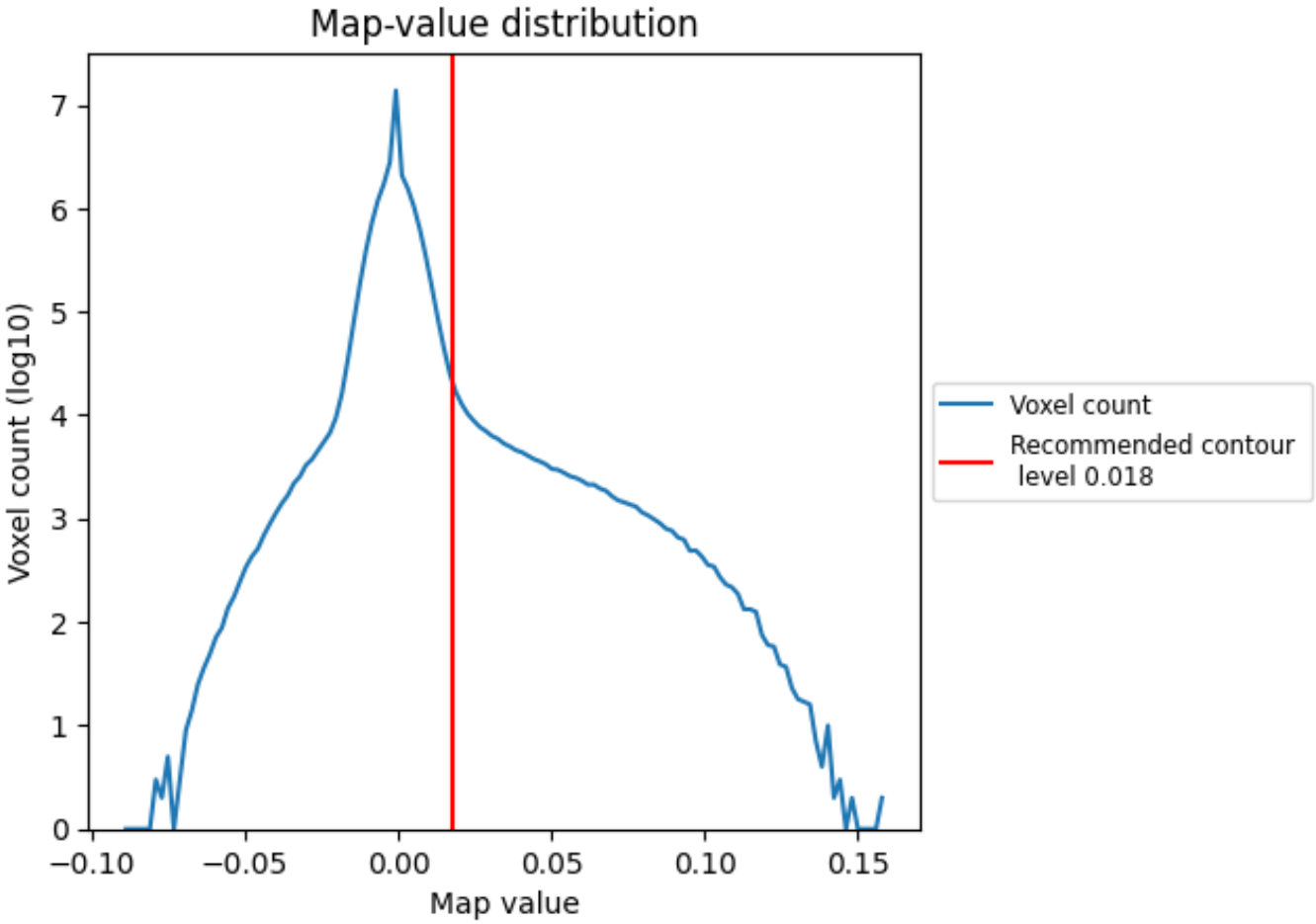


Z

# 7 Map analysis

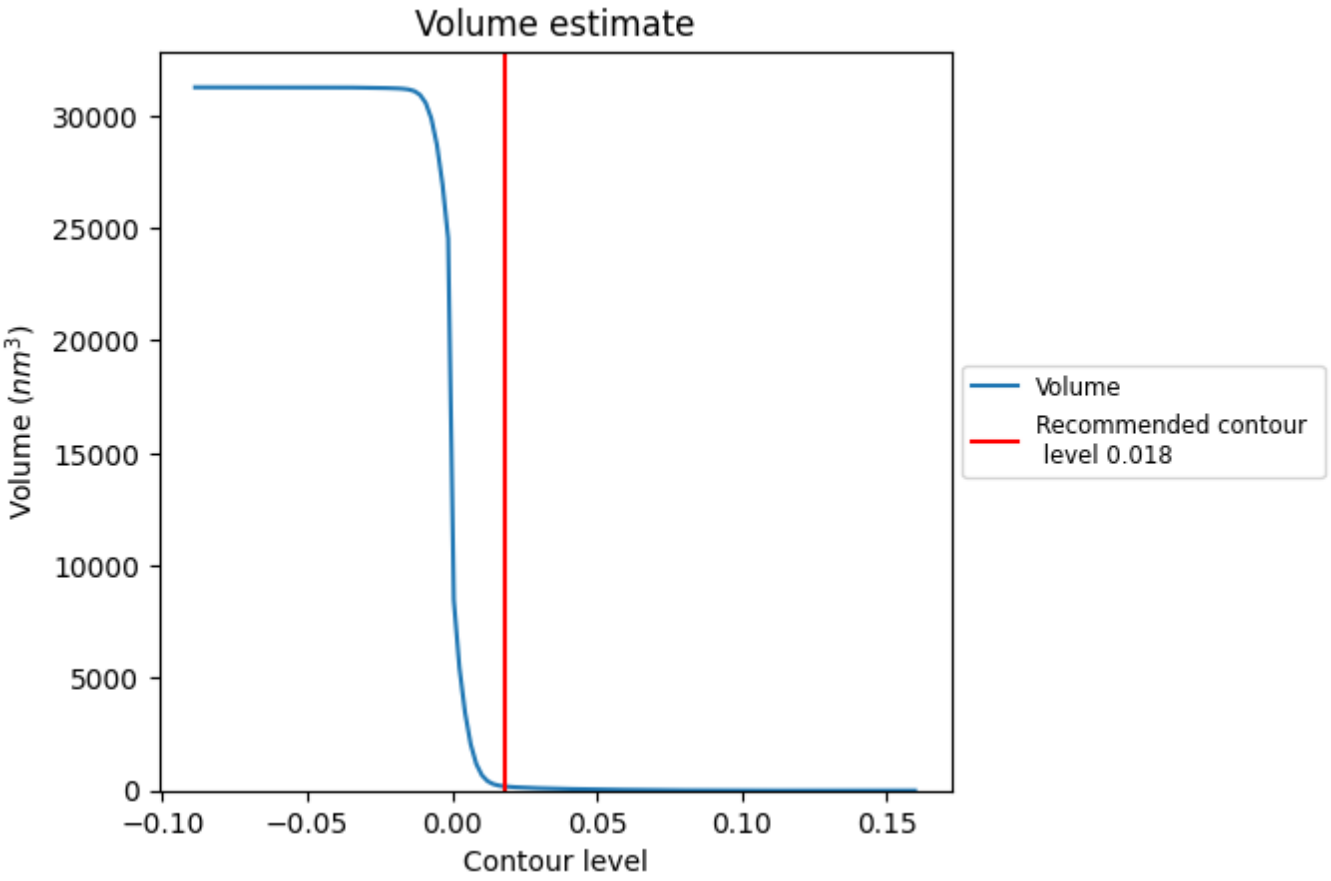
This section contains the results of statistical analysis of the map.

## 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.

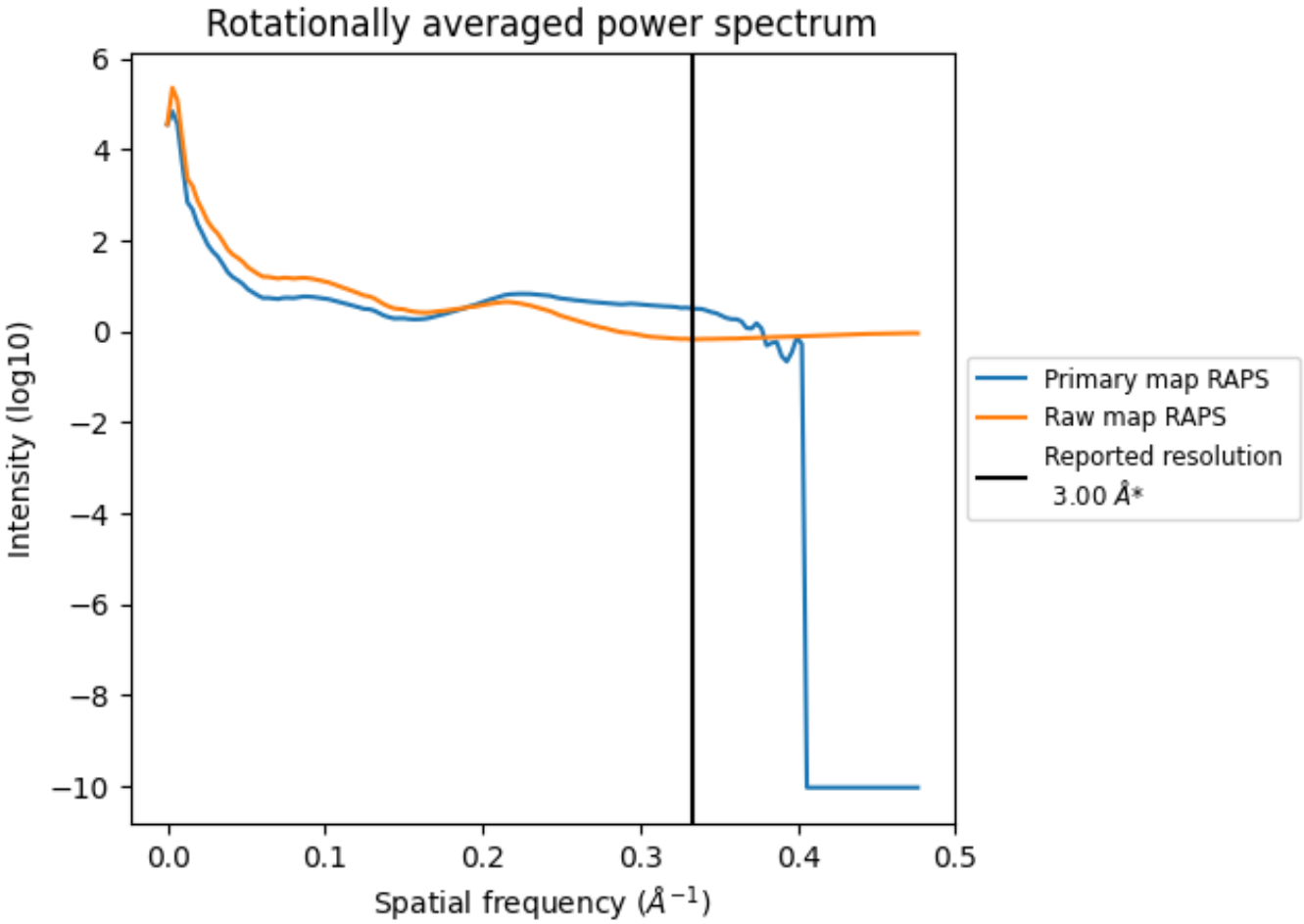
## 7.2 Volume estimate




The volume at the recommended contour level is 187 $nm^3$; this corresponds to an approximate mass of 169 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)

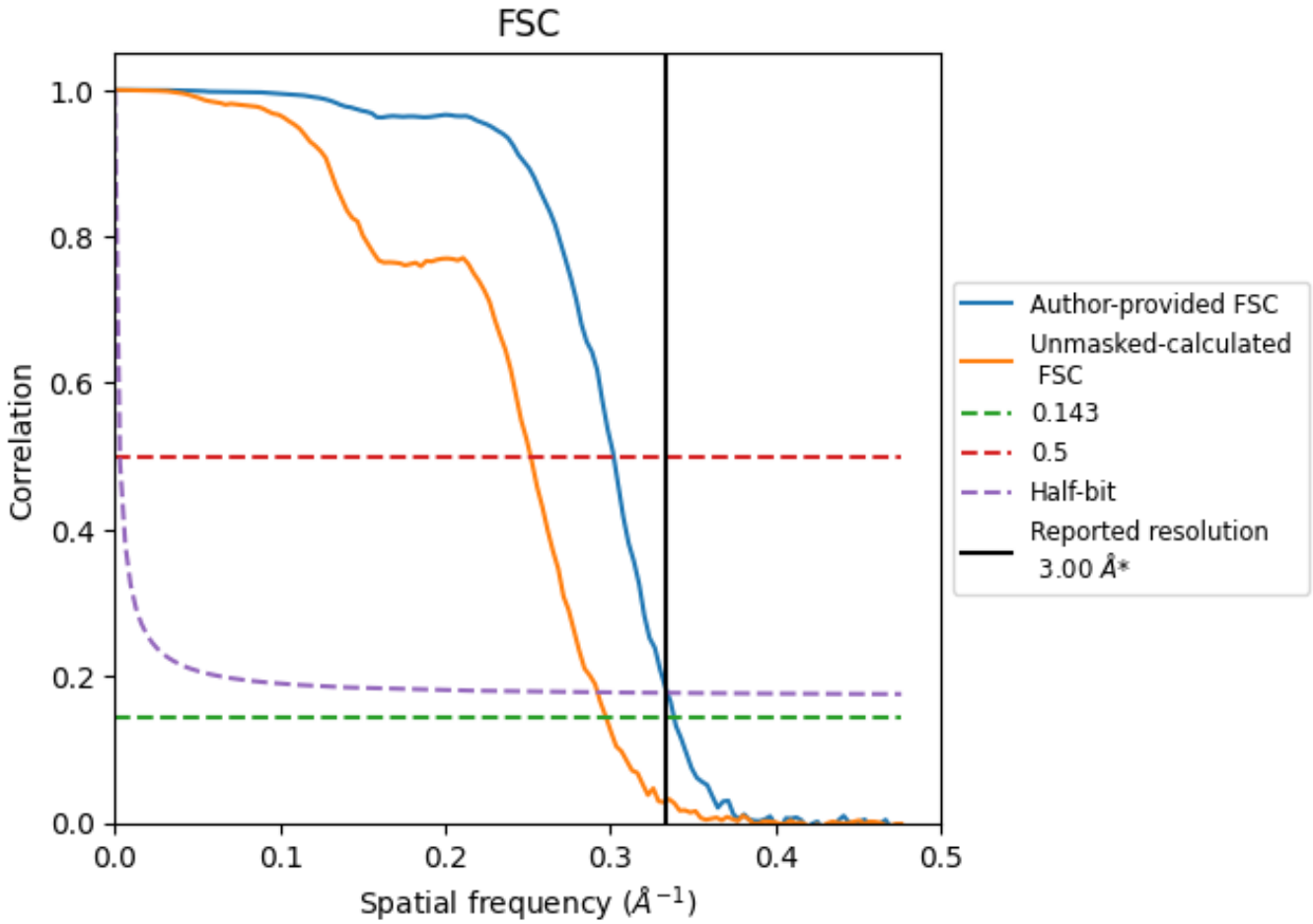



*Reported resolution corresponds to spatial frequency of 0.333 $Å^{-1}$

# 8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

## 8.1 FSC




*Reported resolution corresponds to spatial frequency of 0.333 $Å^{-1}$

## 8.2 Resolution estimates (i)

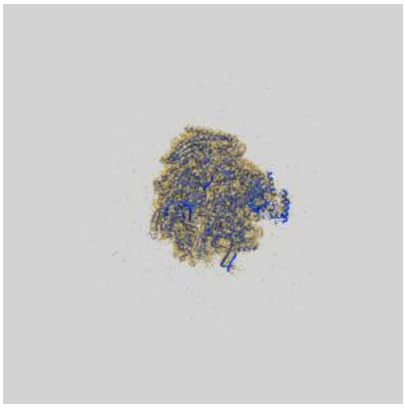
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.00 | - | - |
| Author-provided FSC curve | 2.95 | 3.31 | 2.99 |
| Unmasked-calculated* | 3.36 | 3.97 | 3.42 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.36 differs from the reported value 3.0 by more than 10 %

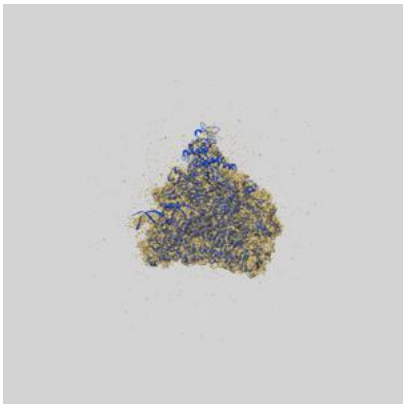
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12974 and PDB model 7OL0. Per-residue inclusion information can be found in section 3 on page 7.

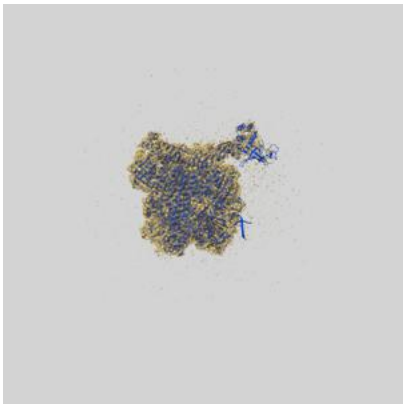
## 9.1 Map-model overlay



X



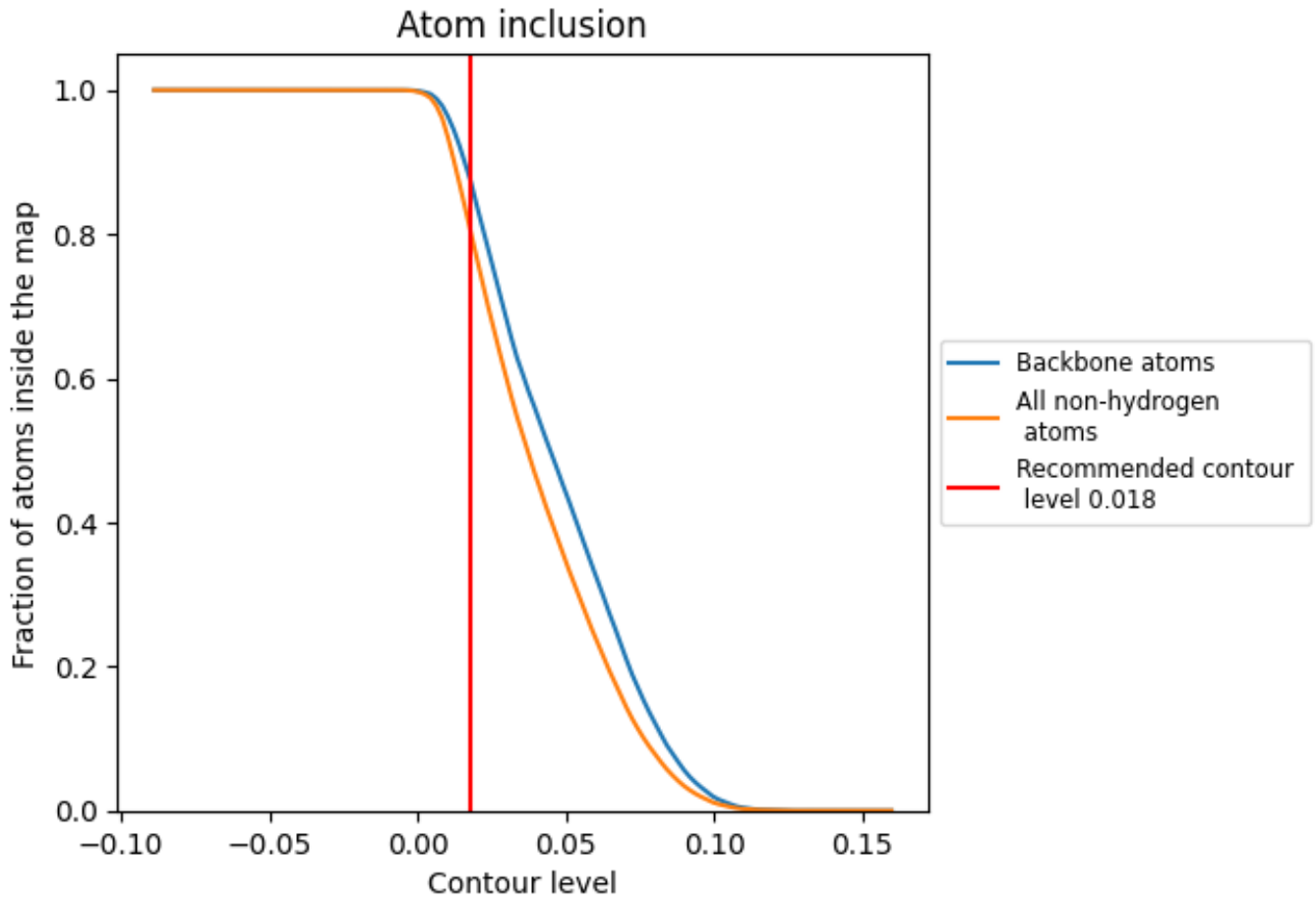
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018 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 Atom inclusion (i)




At the recommended contour level, 87% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.