# wwPDB EM Validation Summary Report

Nov 10, 2026 – 06:20 PM JST

| | | |
|---|---|---|
| PDB ID | : | 27ZW / pdb_000027zw |
| EMDB ID | : | EMD-81574 |
| Title | : | Atomic structure of the ASFV virus early transcription factor in PC state |
| Authors | : | Yang, Y.G.; Xin, Y.H. |
| Deposited on | : | 2026-06-18 |
| Resolution | : | 5.00 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 ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

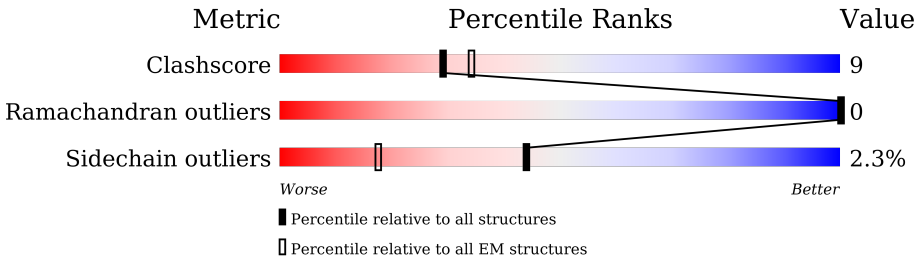
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev133 |
| MolProbity | : | 4-5-2 with Phenix2.2 |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| EM percentile statistics | : | 202505.v01 (Using data in the EMDB archive up until May 2025) |
| MapQ | : | 1.9.13 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.51 |

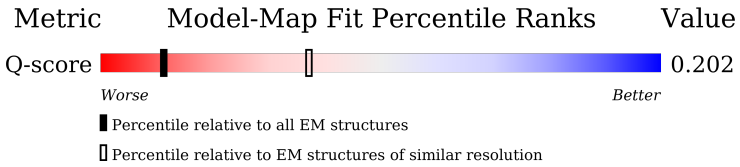
# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.00 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) | Similar EM resolution (#Entries, resolution range(Å)) |
|---|---|---|---|
| Clashscore | 229148 | 23984 | - |
| Ramachandran outliers | 224038 | 23583 | - |
| Sidechain outliers | 223484 | 23102 | - |
| Q-score | - | 25397 | 1057 ( 4.50 - 5.50 ) |

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 | 1377 | 30% 65% 18% • 17% |
| 2 | B | 1141 | 11% 49% 17% • 32% |

# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 15590 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 Early transcription factor large subunit homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 1 | A | 1148 | 9413 | 6127 | 1529 | 1731 | 26 | 0 | 0 |

There are 46 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | -28 | MET | - | initiating methionine | UNP Q65177 |
| A | -27 | TRP | - | expression tag | UNP Q65177 |
| A | -26 | SER | - | expression tag | UNP Q65177 |
| A | -25 | HIS | - | expression tag | UNP Q65177 |
| A | -24 | PRO | - | expression tag | UNP Q65177 |
| A | -23 | GLN | - | expression tag | UNP Q65177 |
| A | -22 | PHE | - | expression tag | UNP Q65177 |
| A | -21 | GLU | - | expression tag | UNP Q65177 |
| A | -20 | LYS | - | expression tag | UNP Q65177 |
| A | -19 | GLY | - | expression tag | UNP Q65177 |
| A | -18 | GLY | - | expression tag | UNP Q65177 |
| A | -17 | GLY | - | expression tag | UNP Q65177 |
| A | -16 | SER | - | expression tag | UNP Q65177 |
| A | -15 | GLY | - | expression tag | UNP Q65177 |
| A | -14 | GLY | - | expression tag | UNP Q65177 |
| A | -13 | GLY | - | expression tag | UNP Q65177 |
| A | -12 | SER | - | expression tag | UNP Q65177 |
| A | -11 | GLY | - | expression tag | UNP Q65177 |
| A | -10 | GLY | - | expression tag | UNP Q65177 |
| A | -9 | SER | - | expression tag | UNP Q65177 |
| A | -8 | ALA | - | expression tag | UNP Q65177 |
| A | -7 | TRP | - | expression tag | UNP Q65177 |
| A | -6 | SER | - | expression tag | UNP Q65177 |
| A | -5 | HIS | - | expression tag | UNP Q65177 |
| A | -4 | PRO | - | expression tag | UNP Q65177 |
| A | -3 | GLN | - | expression tag | UNP Q65177 |
| A | -2 | PHE | - | expression tag | UNP Q65177 |
| A | -1 | GLU | - | expression tag | UNP Q65177 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 0 | LYS | - | expression tag | UNP Q65177 |
| A | 20 | VAL | ALA | conflict | UNP Q65177 |
| A | 62 | GLU | LYS | conflict | UNP Q65177 |
| A | 91 | ARG | SER | conflict | UNP Q65177 |
| A | 175 | VAL | LEU | conflict | UNP Q65177 |
| A | 225 | ILE | MET | conflict | UNP Q65177 |
| A | 504 | VAL | ILE | conflict | UNP Q65177 |
| A | 552 | THR | ALA | conflict | UNP Q65177 |
| A | 906 | GLY | GLU | conflict | UNP Q65177 |
| A | 965 | ILE | VAL | conflict | UNP Q65177 |
| A | 1341 | HIS | - | expression tag | UNP Q65177 |
| A | 1342 | HIS | - | expression tag | UNP Q65177 |
| A | 1343 | HIS | - | expression tag | UNP Q65177 |
| A | 1344 | HIS | - | expression tag | UNP Q65177 |
| A | 1345 | HIS | - | expression tag | UNP Q65177 |
| A | 1346 | HIS | - | expression tag | UNP Q65177 |
| A | 1347 | HIS | - | expression tag | UNP Q65177 |
| A | 1348 | HIS | - | expression tag | UNP Q65177 |

- Molecule 2 is a protein called Early transcription factor large subunit homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 2 | B | 772 | Total | C | N | O | S | 0 | 0 |
| | | | 6177 | 3958 | 1072 | 1121 | 26 | | |

There are 9 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| B | 879 | PRO | LEU | conflict | UNP Q89525 |
| B | 1134 | HIS | - | expression tag | UNP Q89525 |
| B | 1135 | HIS | - | expression tag | UNP Q89525 |
| B | 1136 | HIS | - | expression tag | UNP Q89525 |
| B | 1137 | HIS | - | expression tag | UNP Q89525 |
| B | 1138 | HIS | - | expression tag | UNP Q89525 |
| B | 1139 | HIS | - | expression tag | UNP Q89525 |
| B | 1140 | HIS | - | expression tag | UNP Q89525 |
| B | 1141 | HIS | - | expression tag | UNP Q89525 |

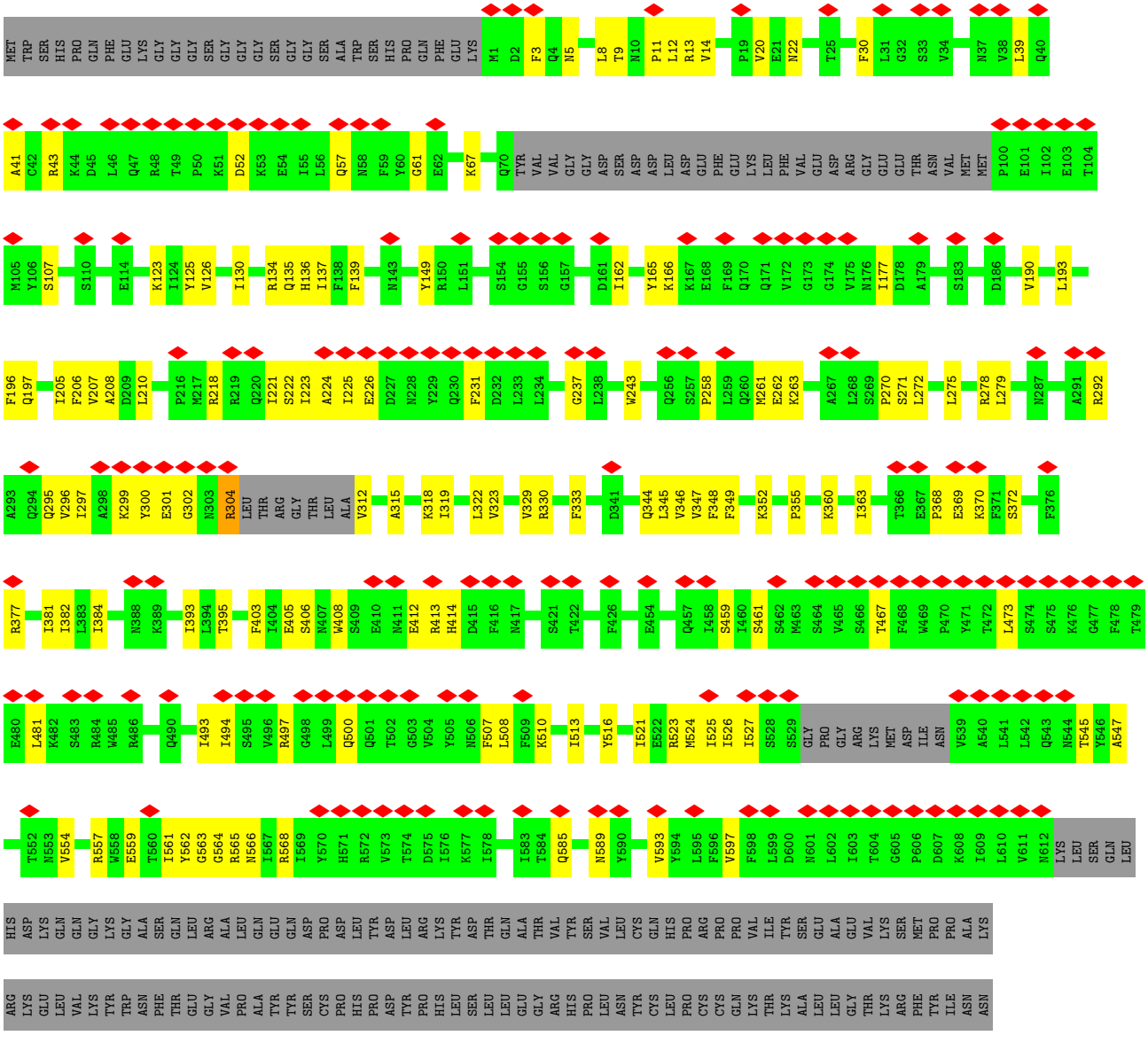
# 3 Residue-property plots (i)

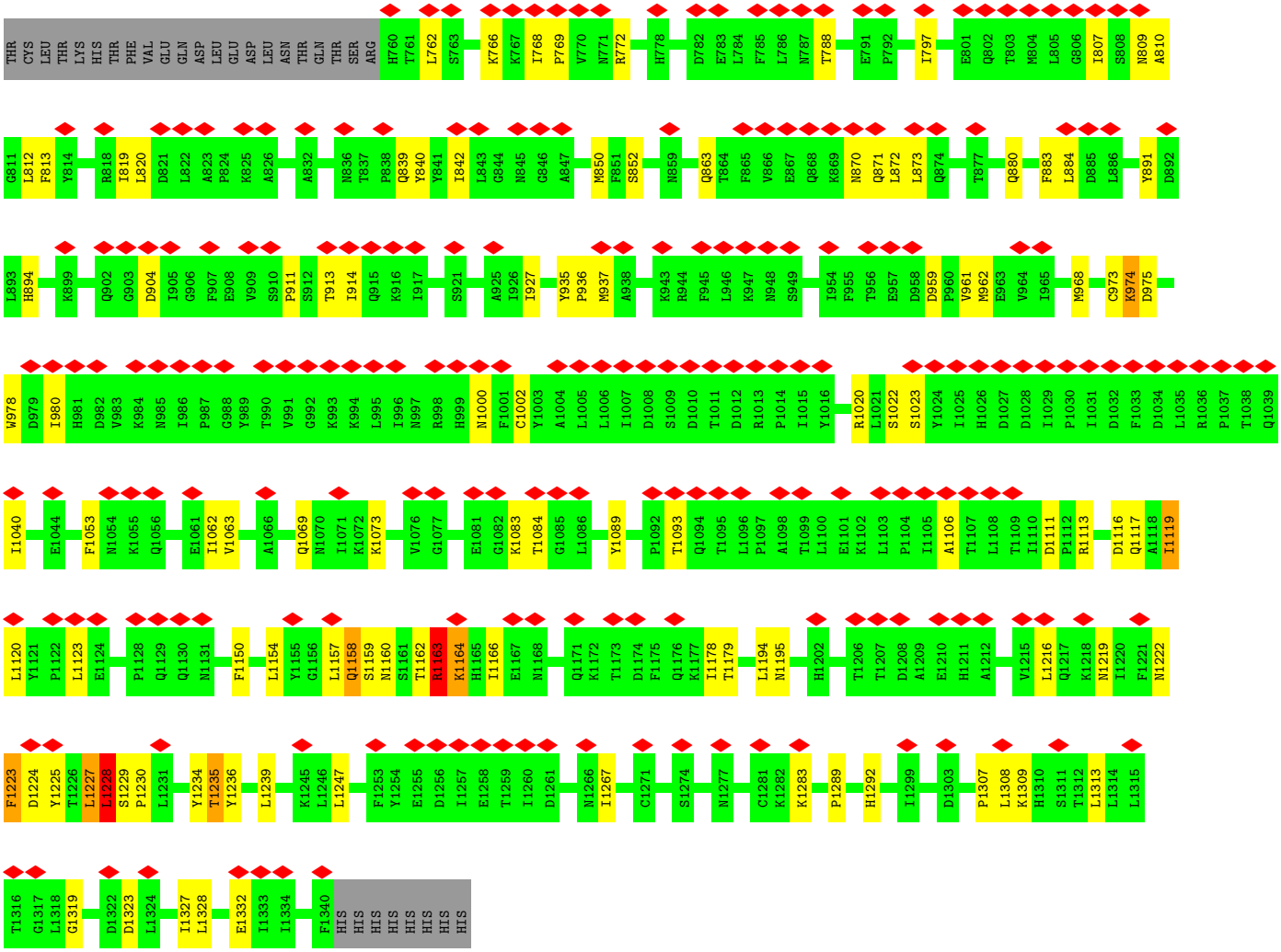
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Early transcription factor large subunit homolog

Chain A:



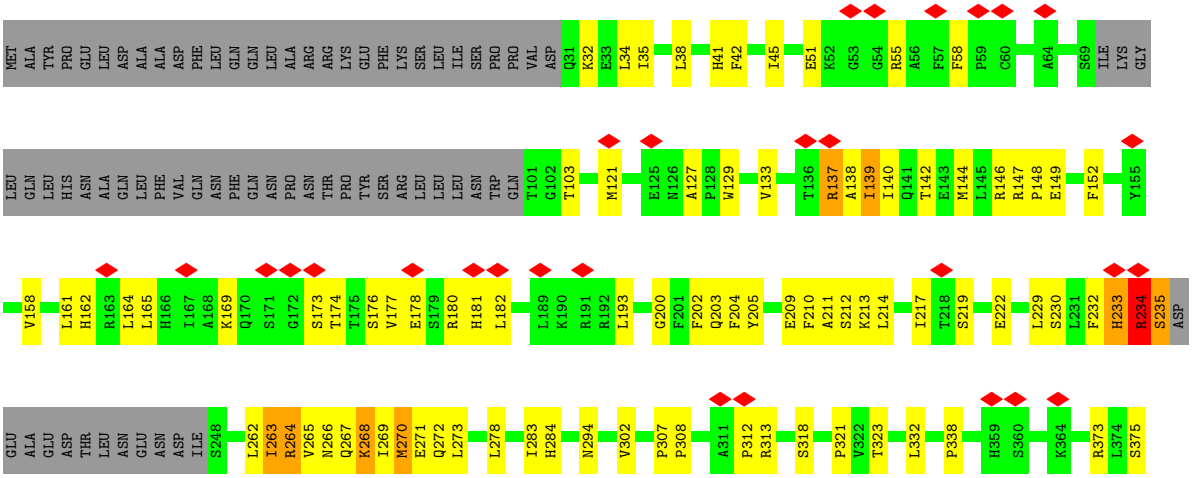



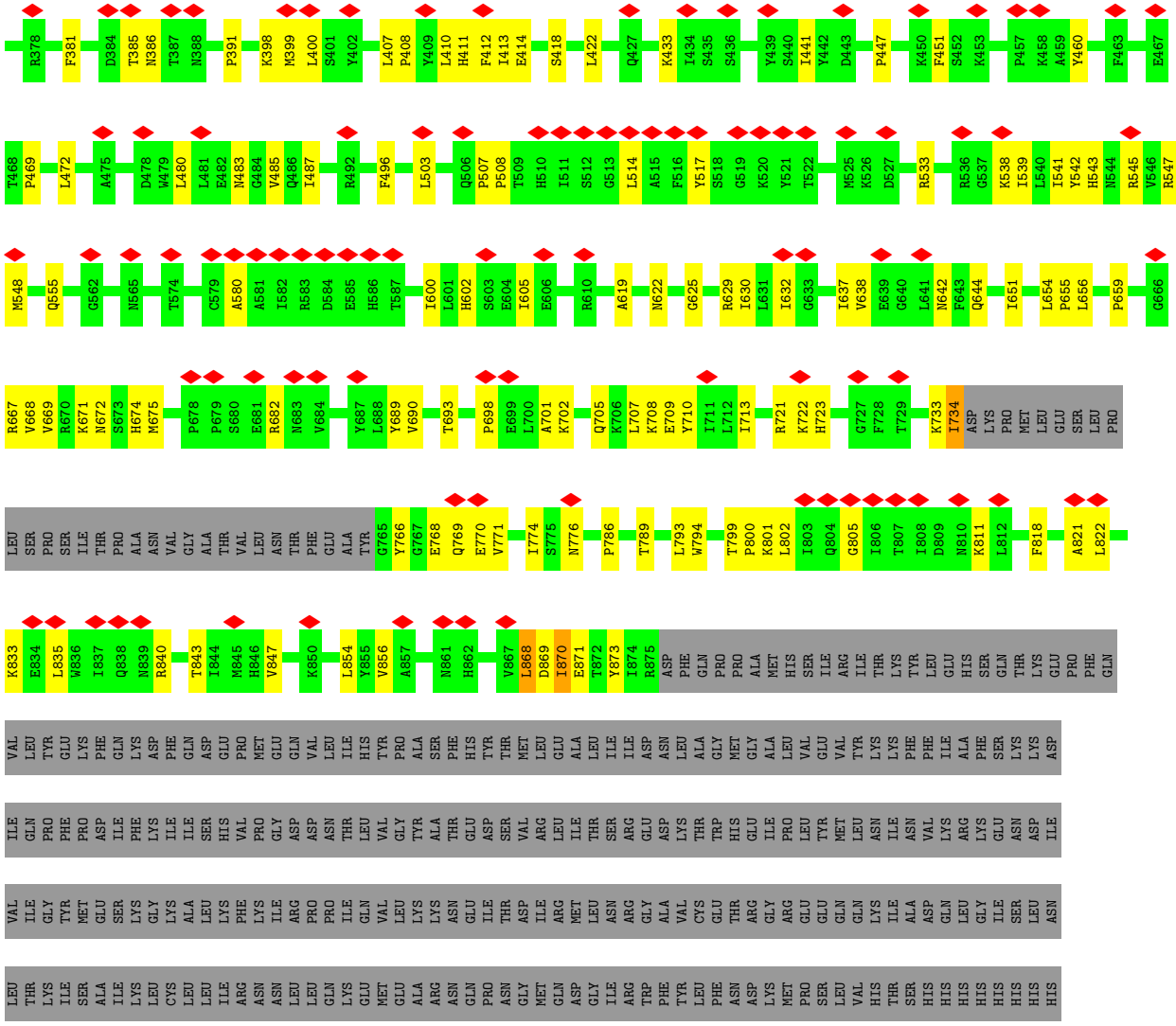


• Molecule 2: Early transcription factor large subunit homolog

Chain B:




R378 F381 D384 T385 N386 T387 N388 P391 K398 M399 L400 S401 Y402 L407 P408 Y409 L410 H411 F412 I413 E414 S418 L422 Q427 K433 I434 S435 S436 Y439 S440 I441 Y442 D443 P447 K450 F451 S452 K453 P457 K458 A459 Y460 F463 E467
T468 P469 L472 A475 D478 W479 L480 L481 E482 N483 G484 V485 Q486 I487 R492 F496 L503 Q506 P507 P508 T509 H510 I511 S512 G513 L514 A515 F516 Y517 S518 G519 K520 Y521 T522 M525 K526 D527 R533 R536 G537 K538 I539 L540 I541 Y542 H543 N544 R545 V546 R547
M548 Q555 G562 N565 T574 C579 A580 A581 I582 R583 D584 E585 H586 T587 I600 L601 H602 S603 E604 I605 E606 R610 A619 N622 G625 R629 I630 L631 I632 G633 I637 V638 E639 G640 L641 N642 F643 Q644 I651 L654 P655 L656 P659 G666
R667 V668 V669 R670 K671 N672 S673 H674 M675 P678 P679 S680 E681 R682 N683 V684 Y687 L688 Y689 V690 T693 P698 E699 L700 A701 K702 Q705 K706 L707 K708 E709 Y710 I711 L712 I713 R721 K722 H723 G727 F728 T729 K733 I734 ASP LYS PRO MET LEU GLU SER LEU PRO
LEU SER PRO SER ILE THR PRO ALA ASN VAL GLY ALA THR VAL LEU ASN THR PHE GLU ALA TYR G765 Y766 G767 E768 Q769 E770 V771 I774 S775 N776 P786 T789 L793 W794 T799 P800 K801 L802 I803 Q804 G805 I806 T807 I808 D809 N810 K811 L812 F818 A821 L822
K833 E834 L835 W836 I837 Q838 N839 R840 T843 I844 M845 H846 V847 K850 L854 Y855 V856 A857 N861 H862 V867 L868 D869 I870 E871 T872 Y873 I874 R875 ASP PHE GLN PRO PRO ALA MET HIS SER ILE ARG ILE THR LYS TYR LEU GLU HIS SER GLN THR LYS GLU PRO PHE GLN
VAL LEU TYR GLU LYS PHE GLN LYS ASP PHE GLN ASP GLU PRO MET GLU GLN VAL LEU ILE HIS TYR PRO ALA SER PHE HIS TYR THR MET LEU GLU ALA LEU ILE ILE ASP ASN LEU ALA GLY MET GLY ALA LEU VAL GLU VAL TYR LYS LYS PHE PHE ILE ALA PHE SER LYS LYS ASP
ILE GLN PRO PHE PRO ASP ILE PHE LYS ILE ILE SER HIS VAL PRO GLY ASP ASP ASN THR LEU VAL GLY TYR ALA THR GLU ASP SER VAL ARG LEU ILE THR SER ARG GLU ASP LYS THR TRP HIS GLU ILE PRO LEU TYR MET LEU ASN ILE ASN VAL LYS ARG LYS GLU ASN ASP ILE
VAL ILE GLY TYR MET GLU SER LYS GLY LYS ALA LEU LYS PHE LYS ILE ARG PRO PRO ILE GLN VAL LEU LYS LYS ASN GLU ILE THR ASP ILE ARG MET LEU ASN ARG GLY ALA VAL CYS GLU THR ARG GLY ARG GLU GLU GLN GLN LYS ILE ALA ASP GLN LEU GLY ILE SER LEU ASN
LEU THR LYS ILE SER ALA ILE LYS LEU CYS LEU LEU ILE ARG ASN ASN LEU LEU GLN LYS GLU MET GLU ALA ARG ASN GLN PRO ASN GLY MET GLN ASP GLY ILE ARG TRP PHE TYR LEU PHE ASN ASP LYS MET PRO SER LEU VAL HIS THR SER HIS HIS HIS HIS HIS HIS HIS

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 64834 | 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 ($e^-/Å^2$) | 60 | Depositor |
| Minimum defocus (nm) | 1500 | Depositor |
| Maximum defocus (nm) | 2500 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K2 QUANTUM (4k x 4k) | Depositor |
| Maximum map value | 1.157 | Depositor |
| Minimum map value | -0.750 | Depositor |
| Average map value | -0.001 | Depositor |
| Map value standard deviation | 0.019 | Depositor |
| Recommended contour level | 0.0947 | Depositor |
| Map size (Å) | 266.24, 266.24, 266.24 | wwPDB |
| Map dimensions | 256, 256, 256 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.04, 1.04, 1.04 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

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 | 0.27 | 0/9647 | 0.53 | 2/13096 (0.0%) |
| 2 | B | 0.28 | 0/6318 | 0.57 | 3/8547 (0.0%) |
| All | All | 0.28 | 0/15965 | 0.54 | 5/21643 (0.0%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 1 | A | 0 | 1 |
| 2 | B | 0 | 3 |
| All | All | 0 | 4 |

There are no bond length outliers.

All (5) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | B | 441 | ILE | N-CA-C | -6.70 | 105.95 | 111.91 |
| 1 | A | 1228 | LEU | N-CA-C | -6.30 | 106.23 | 114.04 |
| 1 | A | 1223 | PHE | N-CA-C | -6.00 | 105.67 | 112.87 |
| 2 | B | 139 | ILE | N-CA-C | -5.32 | 108.09 | 113.20 |
| 2 | B | 219 | SER | CB-CA-C | -5.01 | 110.42 | 117.23 |

There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | A | 1163 | ARG | Sidechain |
| 2 | B | 137 | ARG | Sidechain |
| 2 | B | 234 | ARG | Sidechain |
| 2 | B | 264 | ARG | Sidechain |

## 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 | 9413 | 0 | 9404 | 170 | 0 |
| 2 | B | 6177 | 0 | 6224 | 134 | 0 |
| All | All | 15590 | 0 | 15628 | 290 | 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 9.

The worst 5 of 290 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 1:A:1160:ASN:HB3 | 1:A:1227:LEU:HB3 | 1.55 | 0.88 |
| 2:B:868:LEU:O | 2:B:869:ASP:OD1 | 1.94 | 0.85 |
| 1:A:1154:LEU:HD13 | 1:A:1158:GLN:HB3 | 1.59 | 0.84 |
| 2:B:32:LYS:HD2 | 2:B:675:MET:HG3 | 1.60 | 0.81 |
| 1:A:1154:LEU:HD12 | 1:A:1227:LEU:HD21 | 1.65 | 0.79 |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | A | 1138/1377 (83%) | 1024 (90%) | 114 (10%) | 0 | 100 | 100 |
| 2 | B | 764/1141 (67%) | 684 (90%) | 80 (10%) | 0 | 100 | 100 |
| All | All | 1902/2518 (76%) | 1708 (90%) | 194 (10%) | 0 | 100 | 100 |

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 1 | A | 1051/1252 (84%) | 1030 (98%) | 21 (2%) | 48 | 66 |
| 2 | B | 681/1016 (67%) | 662 (97%) | 19 (3%) | 38 | 59 |
| All | All | 1732/2268 (76%) | 1692 (98%) | 40 (2%) | 44 | 63 |

5 of 40 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | B | 262 | LEU |
| 2 | B | 766 | TYR |
| 2 | B | 263 | ILE |
| 2 | B | 269 | ILE |
| 2 | B | 868 | LEU |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 1117 | GLN |
| 2 | B | 267 | GLN |
| 2 | B | 626 | HIS |
| 1 | A | 1232 | GLN |
| 2 | B | 294 | ASN |

### 5.3.3 RNA

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry (i)

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.

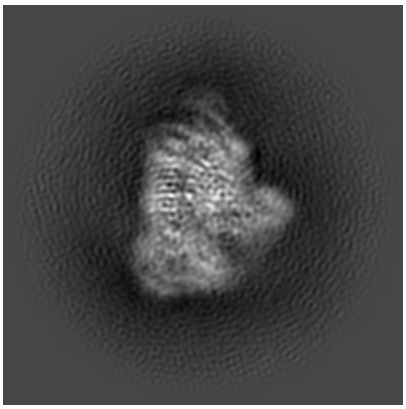
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-81574. These allow visual inspection of the internal detail of the map and identification of artifacts.

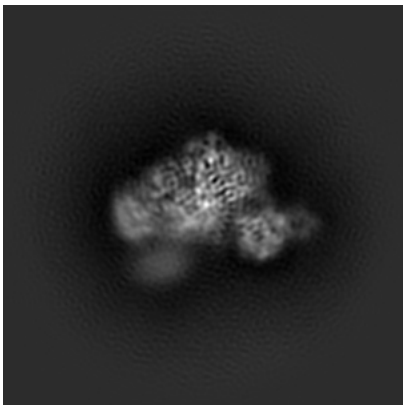
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections

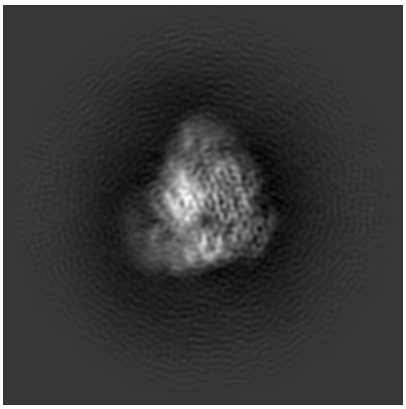
### 6.1.1 Primary map



X

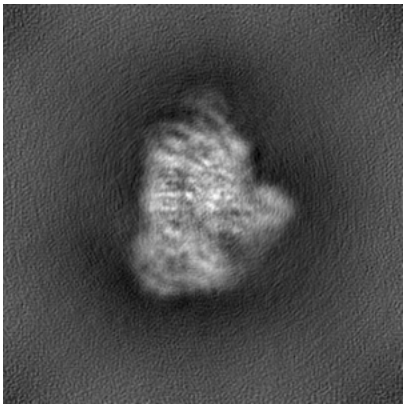


Y

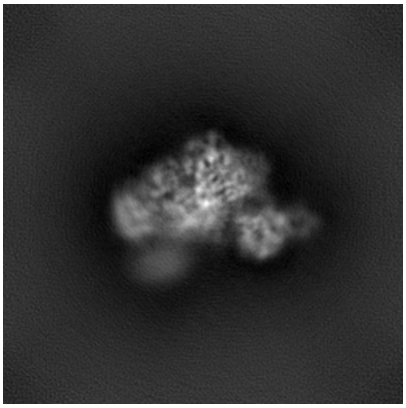


Z

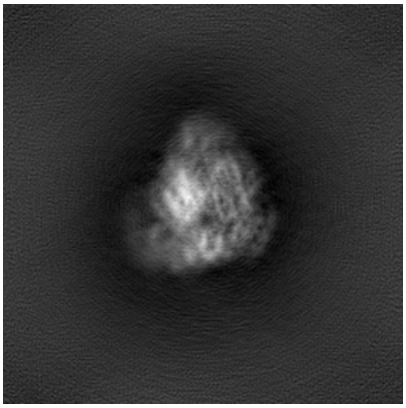
### 6.1.2 Raw map



X



Y

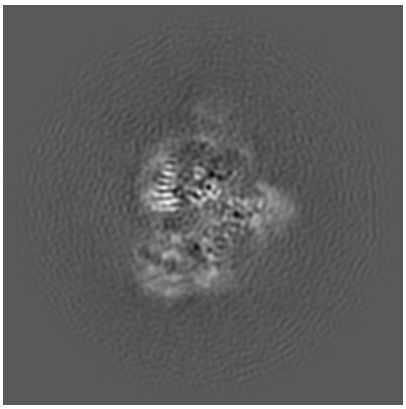


Z

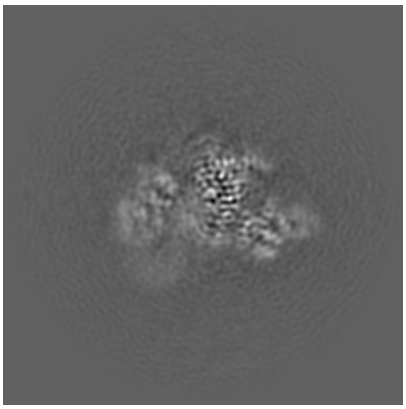
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

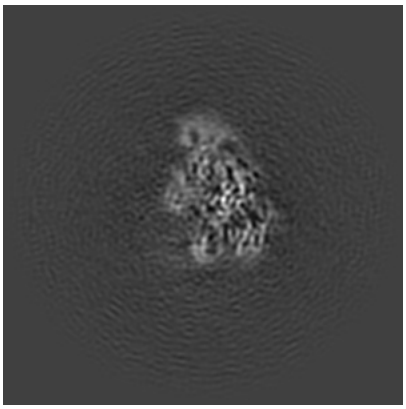
### 6.2.1 Primary map



X Index: 128

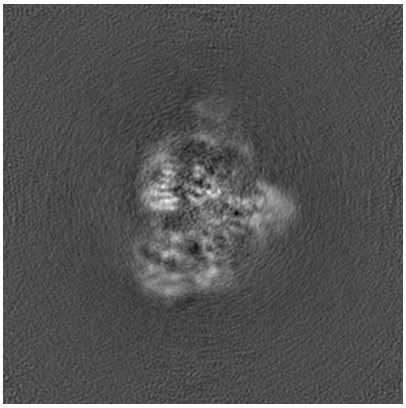


Y Index: 128

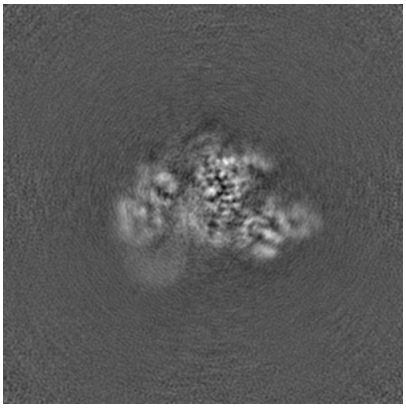


Z Index: 128

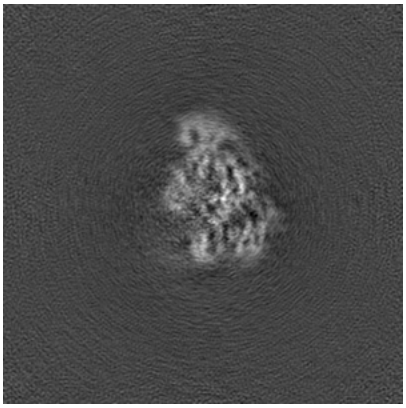
### 6.2.2 Raw map



X Index: 128



Y Index: 128

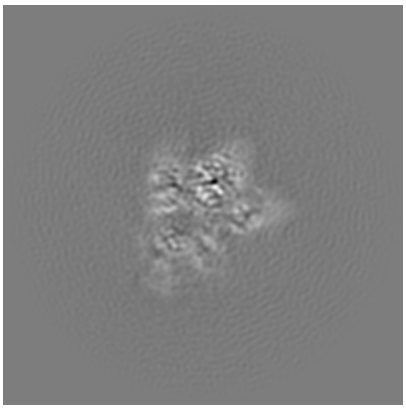


Z Index: 128

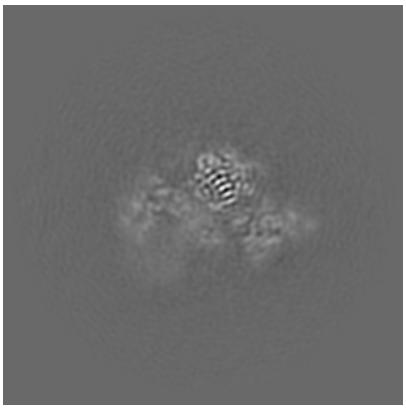
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

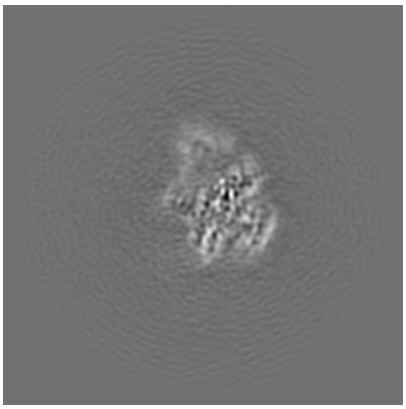
### 6.3.1 Primary map



X Index: 137

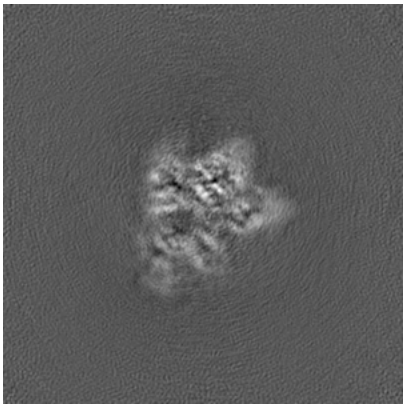


Y Index: 134

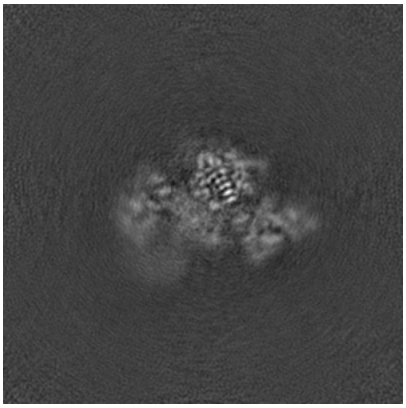


Z Index: 134

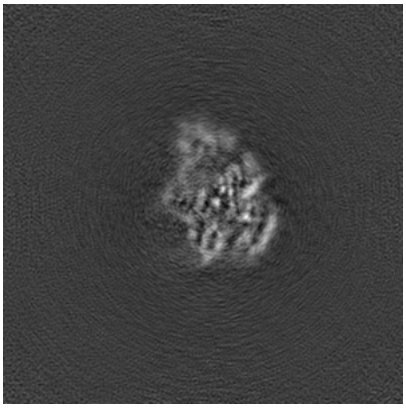
### 6.3.2 Raw map



X Index: 137



Y Index: 133

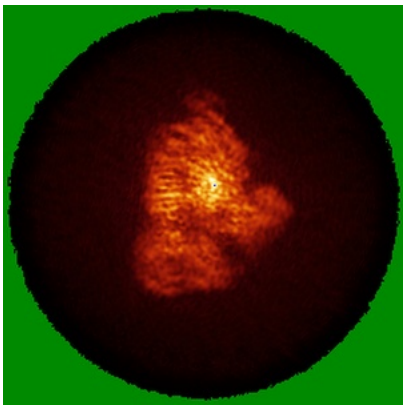


Z Index: 133

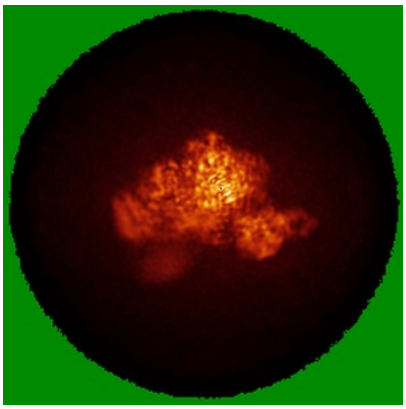
The images above show the largest variance slices of the map in three orthogonal directions.

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

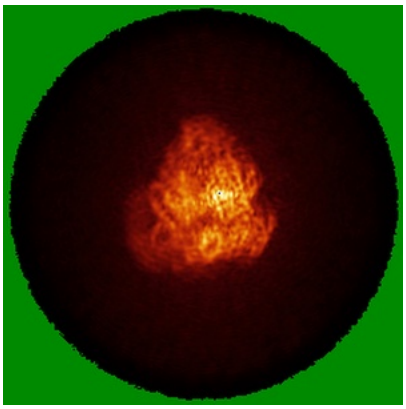
### 6.4.1 Primary map



X

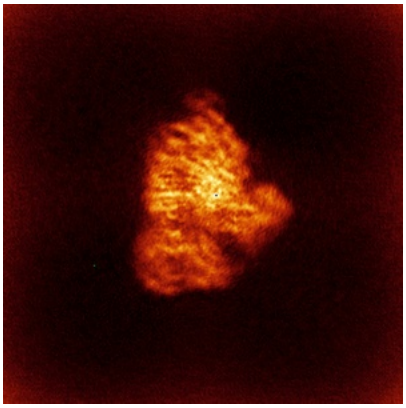


Y

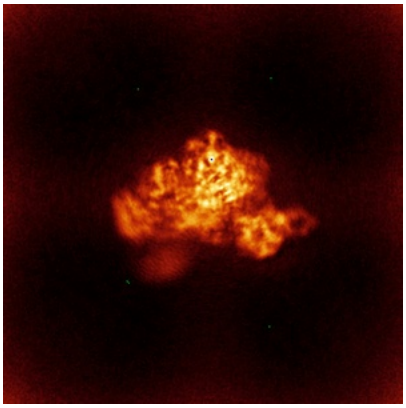


Z

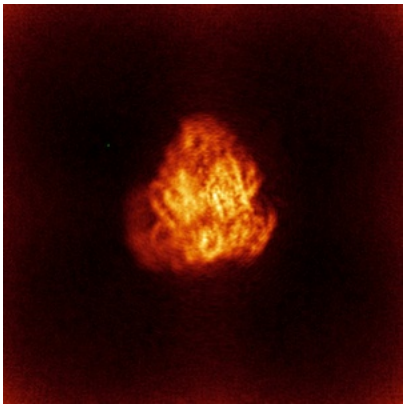
### 6.4.2 Raw map



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 0.0947. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 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.

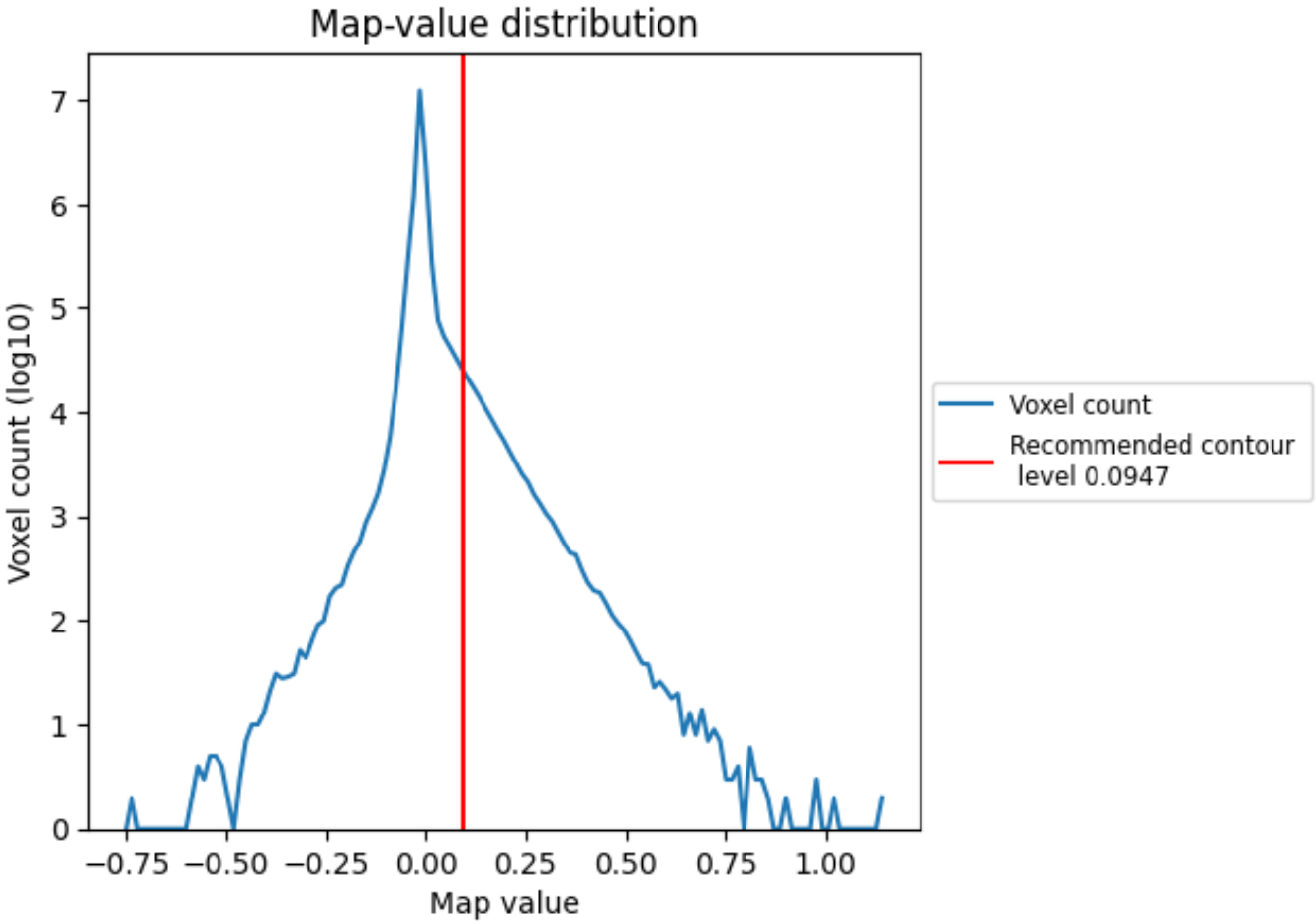
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

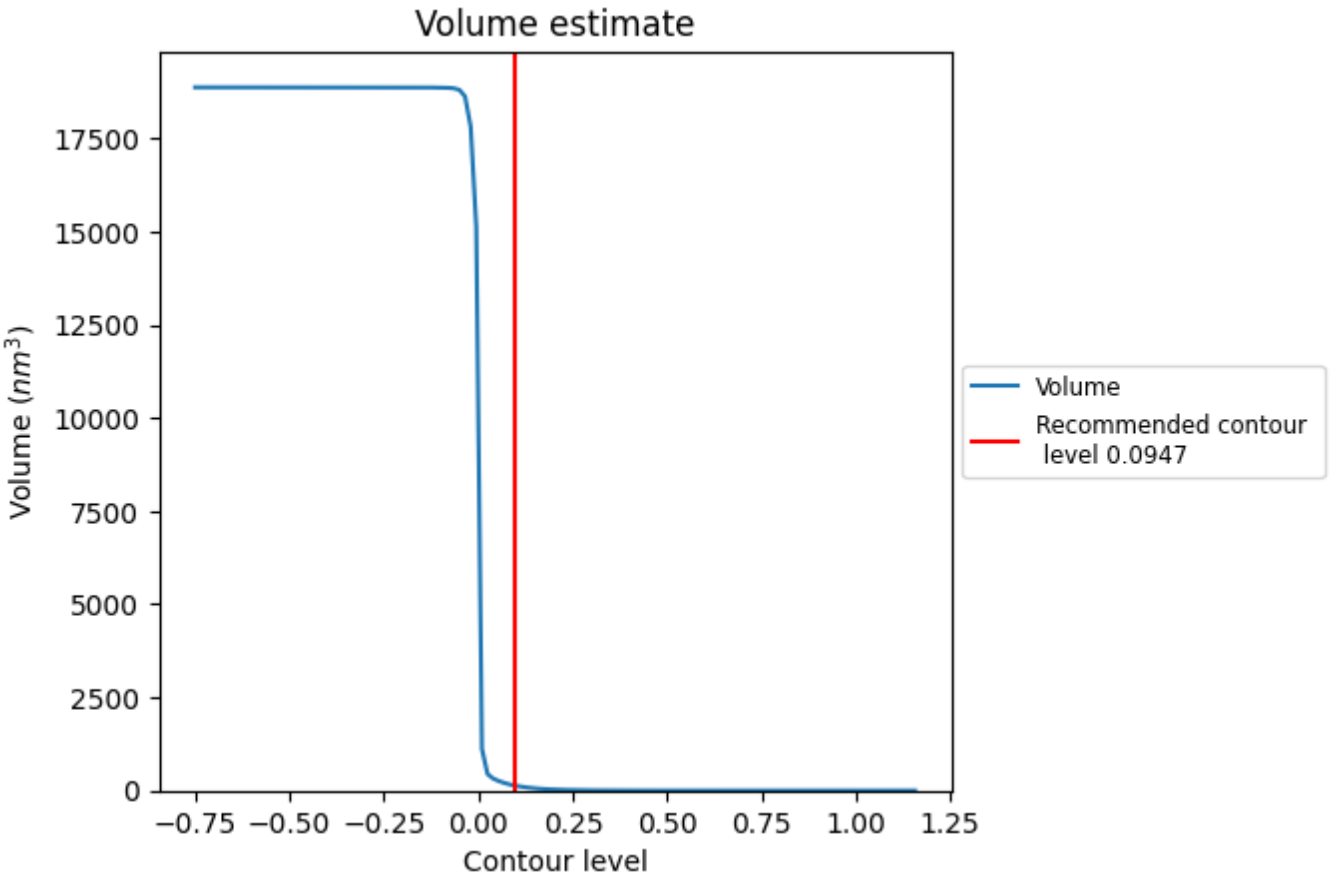
This section contains the results of statistical analysis of the map.

## 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.

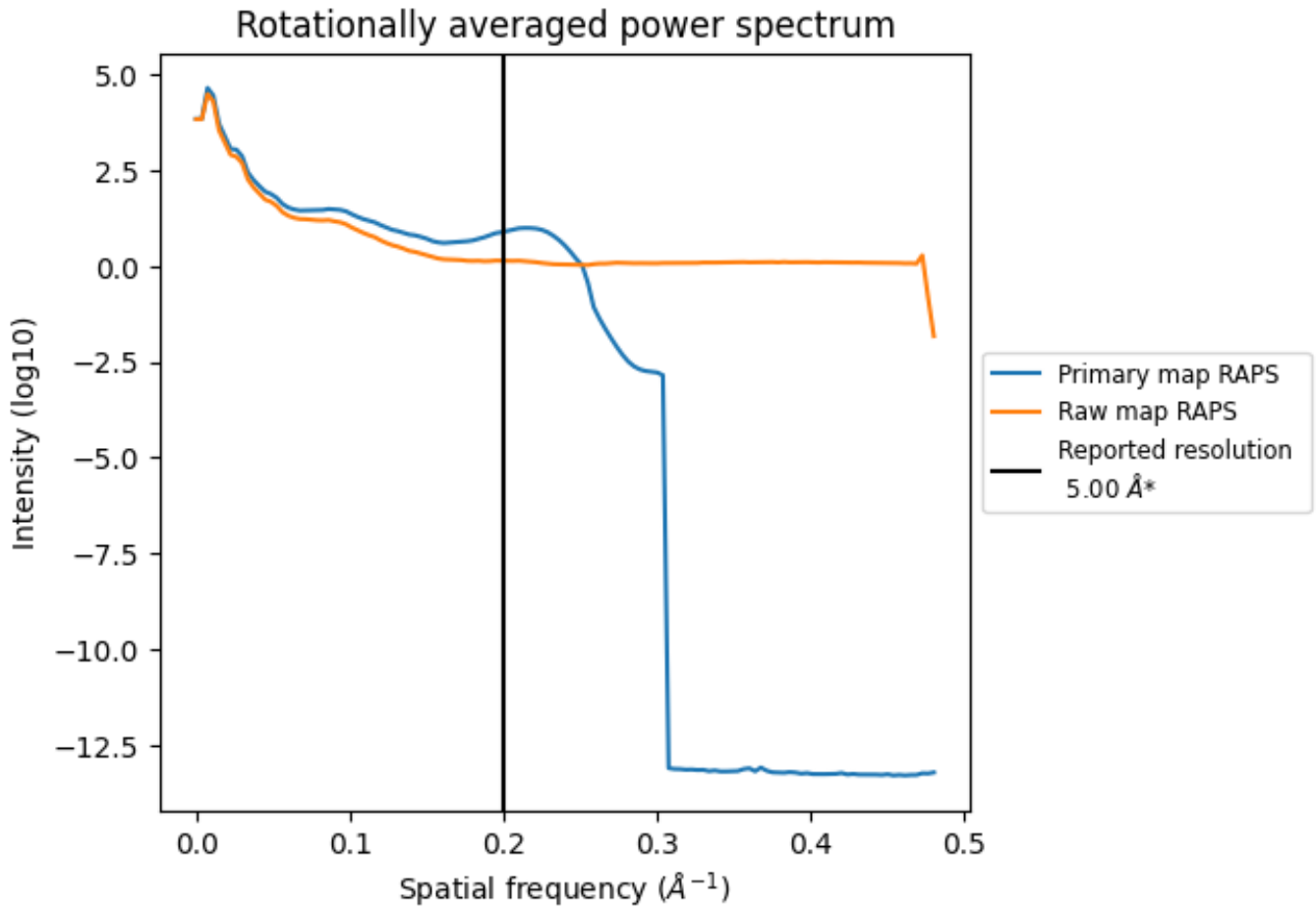
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 139 $nm^3$; this corresponds to an approximate mass of 126 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)

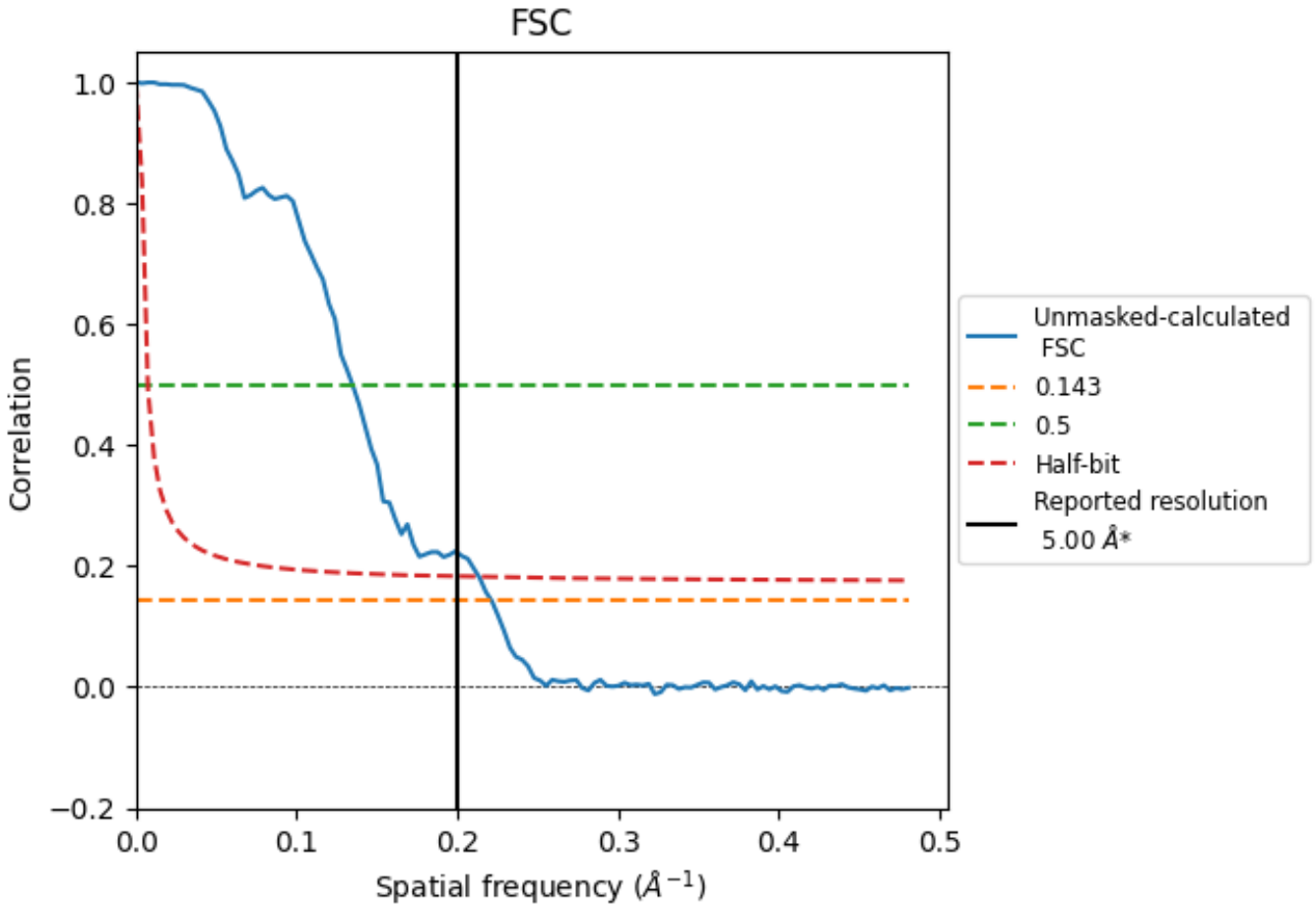



*Reported resolution corresponds to spatial frequency of 0.200 Å$^{-1}$

# 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 0.200 Å$^{-1}$

## 8.2 Resolution estimates (i)

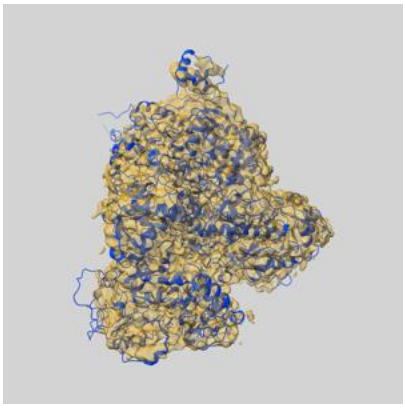
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 5.00 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 4.52 | 7.42 | 4.68 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

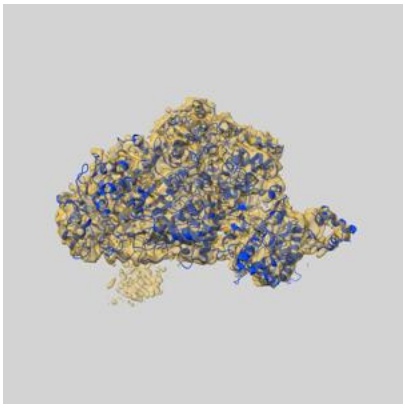
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-81574 and PDB model 27ZW. Per-residue inclusion information can be found in section 3 on page 5.

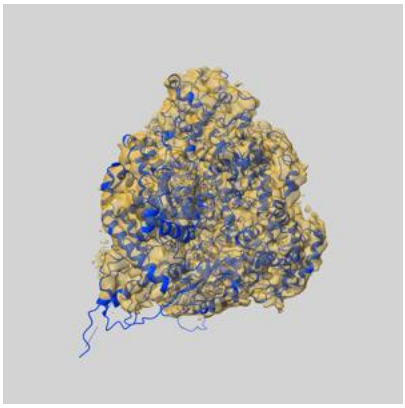
## 9.1 Map-model overlay



X



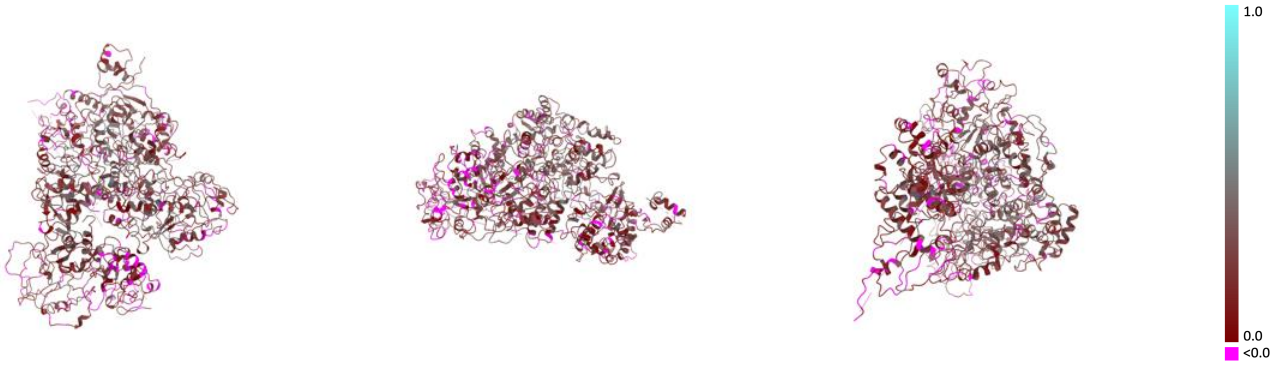
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0947 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.

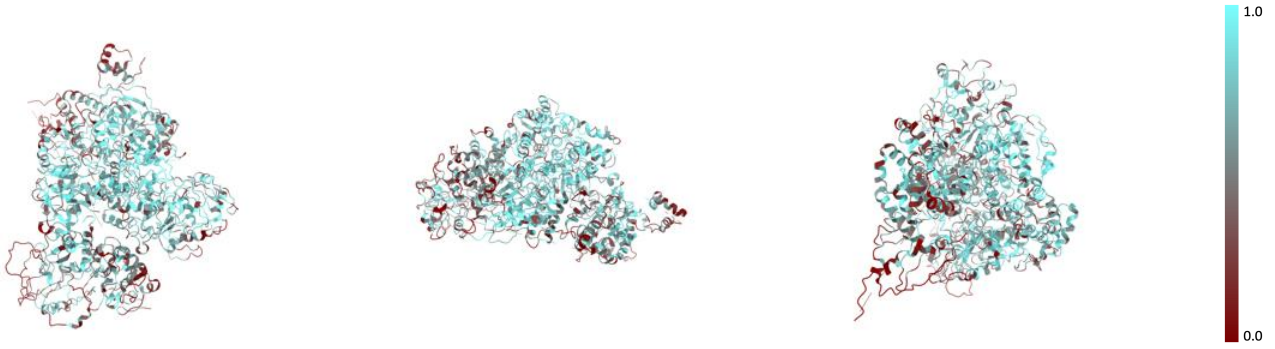
## 9.2 Q-score mapped to coordinate model




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.

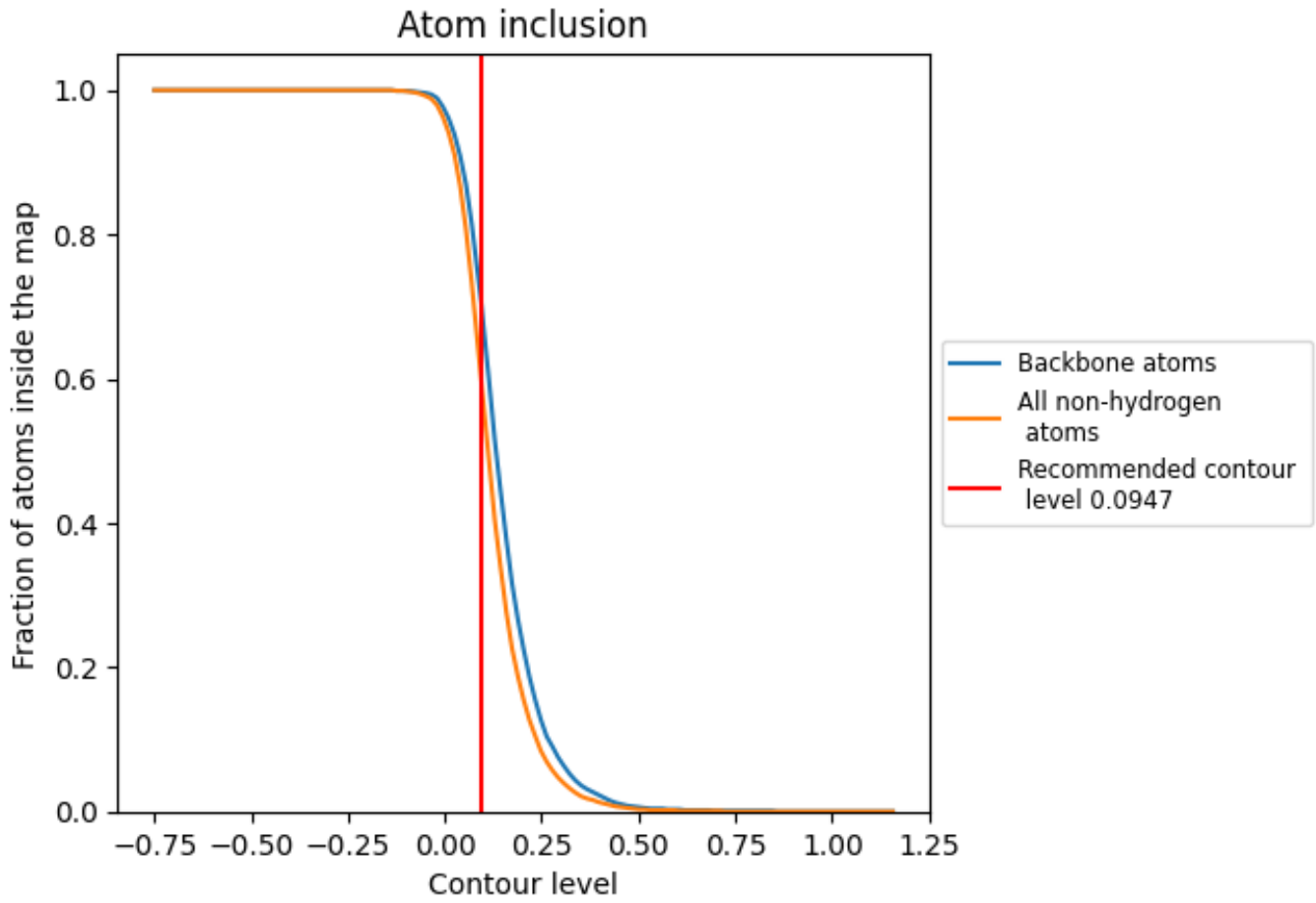
## 9.3 Atom inclusion mapped to coordinate model




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 (0.0947).

## 9.4 Atom inclusion (i)




At the recommended contour level, 70% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0947) and Q-score for the entire model and for each chain.




| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.5930 | 0.2020 |
| A | 0.5360 | 0.1810 |
| B | 0.6790 | 0.2340 |