wwPDB EM Validation Summary Report

Aug 5, 2026 – 09:28 AM EDT

PDB ID	:	8FOC / pdb_00008foc
EMDB ID	:	EMD-29345
Title	:	Cryo-EM structure of S. cerevisiae DNA polymerase alpha-primase in Apo state conformation I
Authors	:	Yuan, Z.; Georgescu, R.; Li, H.; O'Donnell, M.
Deposited on	:	2022-12-30
Resolution	:	3.70 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:

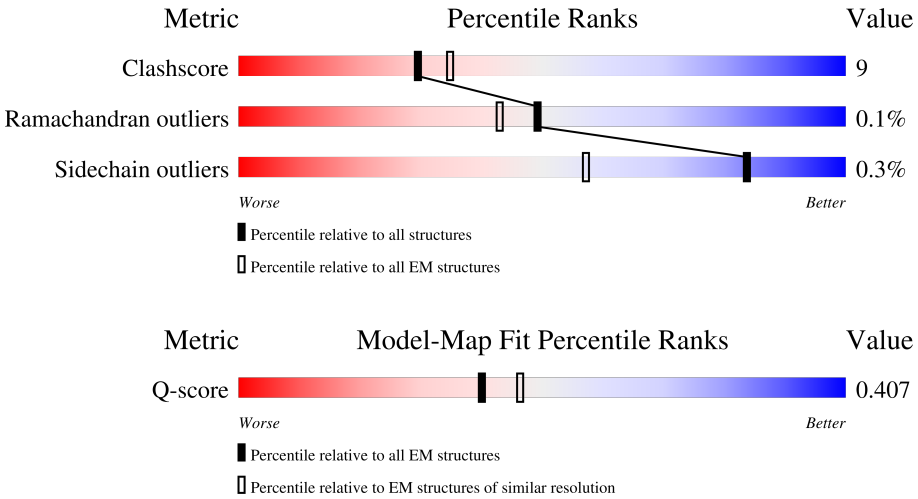
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

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 3.70 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	11569 (3.20 - 4.20)

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	B	528	69% 16% 15%
2	A	409	28% 78% 19%
3	C	705	49% 12% 39%
4	1	1468	53% 15% 31%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 18382 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 primase large subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	450	3676	2343	631	690	12	0	0

- Molecule 2 is a protein called DNA primase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	397	3257	2073	567	601	16	0	0

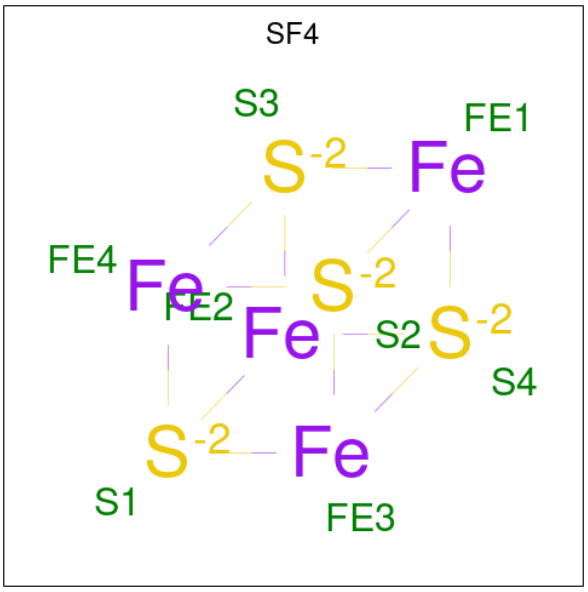
- Molecule 3 is a protein called DNA polymerase alpha subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	433	3412	2171	582	649	10	3	0

- Molecule 4 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	1	1007	8029	5072	1376	1526	55	7	0

- Molecule 5 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
5	B	1	8	4	4	0

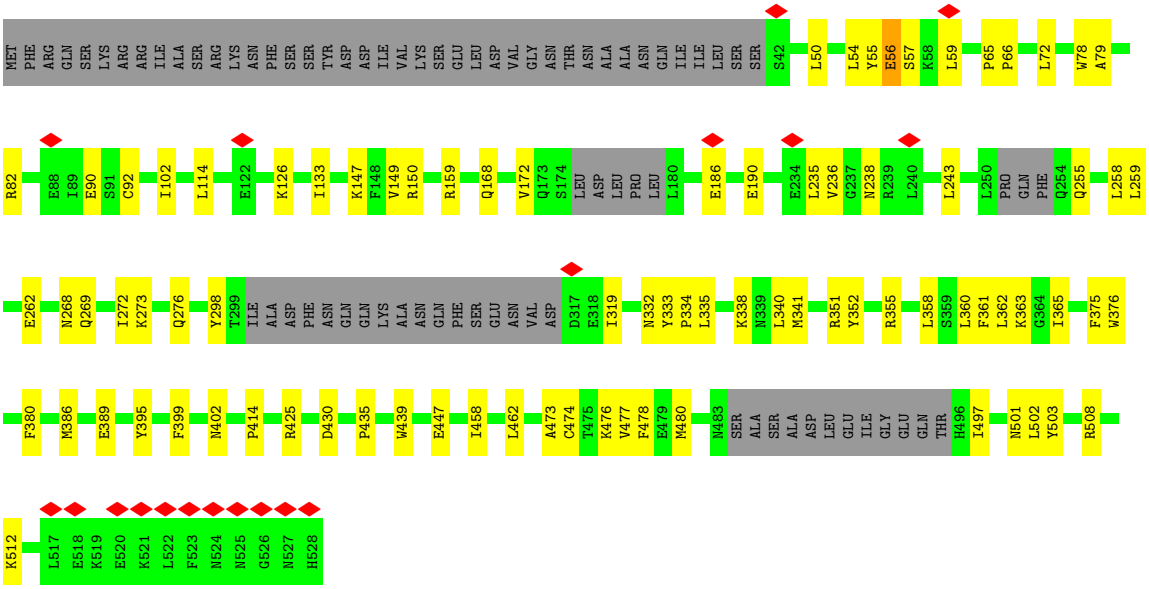
3 Residue-property plots (i)

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 primase large subunit

Chain B:

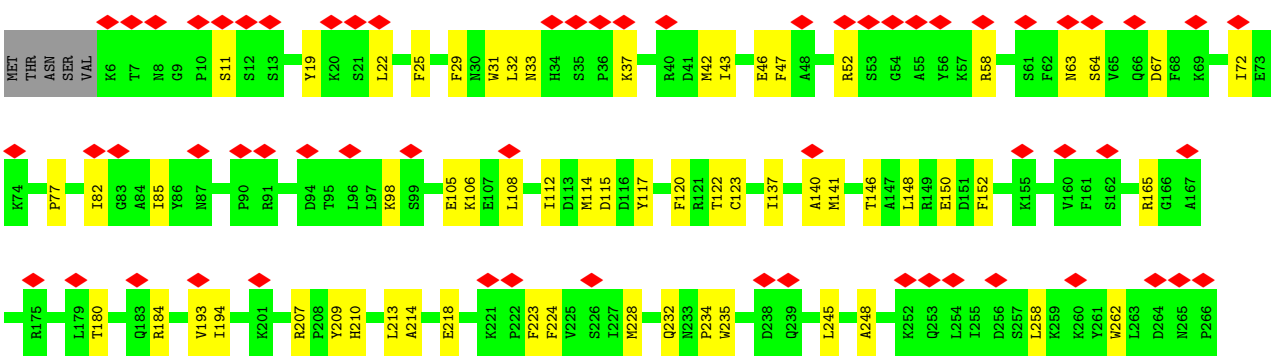


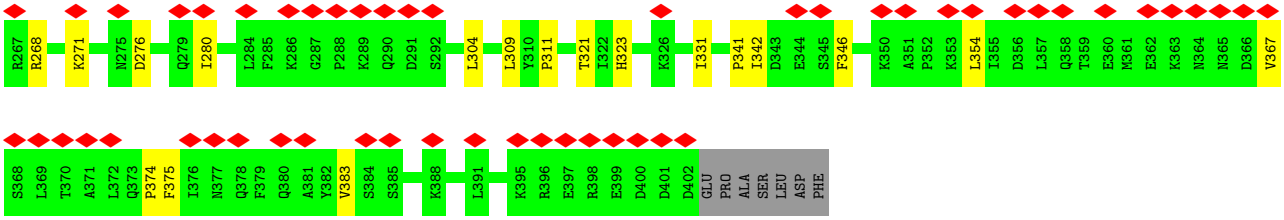


• Molecule 2: DNA primase

Chain A:



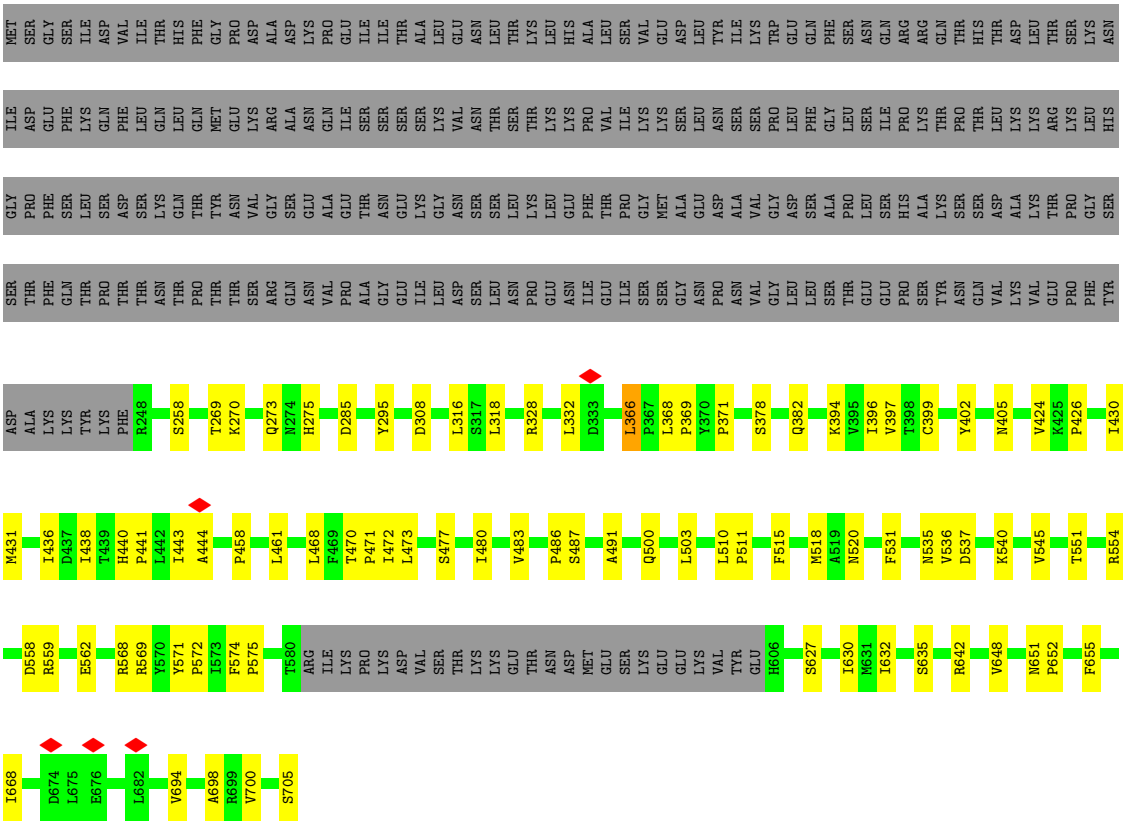




• Molecule 3: DNA polymerase alpha subunit B

Chain C:



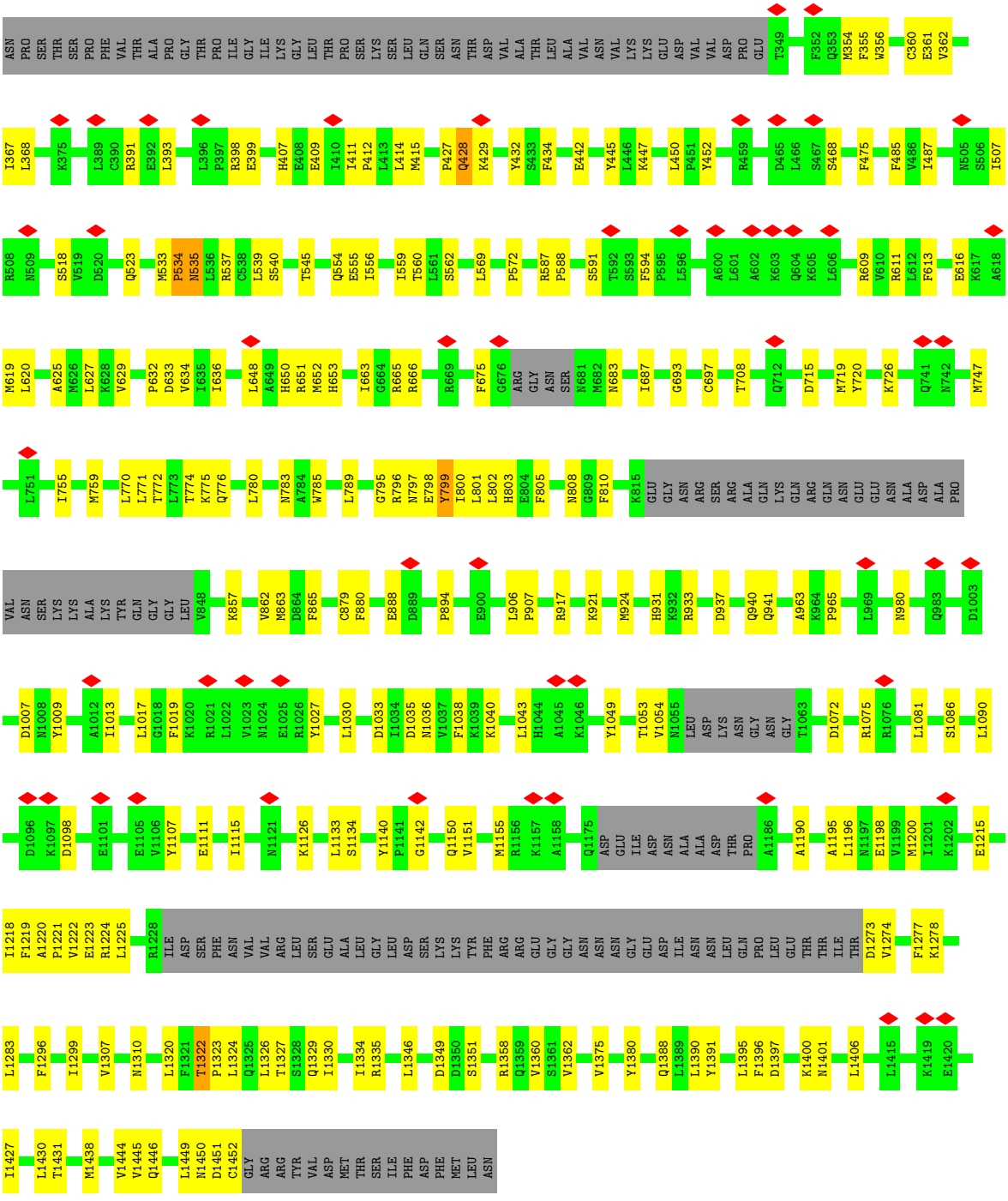


• Molecule 4: DNA polymerase

Chain 1:






ASN PRO SER THR SER PRO PHE VAL THR ALA PRO GLY THR PRO ILE GLY ILE LYS GLY LEU THR PRO SER LYS SER LEU GLN SER ASN THR ASP VAL ALA THR LEU ALA VAL ASN VAL LYS LYS GLU ASP VAL VAL ASP PRO GLU T349 F352 Q353 M354 F355 W356 C360 E361 V362
I367 L368 K375 L389 C390 R391 E392 L393 L396 P397 R398 E399 H407 E408 E409 I410 T411 P412 L413 L414 M415 P427 Q428 K429 Y432 S433 F434 E442 Y445 L446 K447 L450 P451 Y452 R459 D465 L466 S467 S468 F475 F485 V486 I487 N505 S506 I507
R508 M509 S518 V519 D520 Q523 M533 P534 N535 L536 R537 G538 L539 S540 T545 Q554 E555 I556 I559 T560 L561 S562 L569 P572 R587 P588 S591 T592 S593 P594 P595 L596 A600 L601 A602 K603 Q604 K605 L606 R609 V610 R611 L612 F613 E616 K617 A618
M619 L620 A625 M626 L627 K628 V629 P632 D633 V634 I635 I636 L648 A649 H650 R651 M652 H653 I663 G664 R665 R666 R669 F675 G676 ARG GLY ASN SER N681 M682 N683 I687 G693 C697 T708 Q712 D715 M719 Y720 K726 Q741 N742 M747
L751 I755 M759 L770 L771 T772 L773 T774 K775 Q776 L780 N783 A784 W785 L789 G795 R796 N797 E798 Y799 I800 L801 L802 H803 E804 F805 N808 G809 F810 K815 GLU GLY ASN ARG SER ARG ALA GLN LYS GLN ARG GLN ASN GLU GLU ASN ALA ASP ALA PRO
VAL ASN SER LYS LYS ALA LYS TYR GLN GLY GLY LEU V848 K857 V862 M863 D864 F865 C879 F880 E888 D889 P894 E900 L906 P907 R917 K921 M924 H931 K932 R933 D937 Q940 Q941 A963 K964 P965 L969 N980 Q983 D1003
D1007 N1008 Y1009 A1012 I1013 L1017 G1018 F1019 K1020 R1021 L1022 V1023 N1024 E1025 R1026 Y1027 L1030 D1033 I1034 D1035 N1036 V1037 F1038 K1039 K1040 L1043 H1044 A1045 K1046 Y1049 T1063 V1054 N1055 LEU ASP LYS ASN GLY GLY T1063 D1072 R1075 R1076 L1081 S1086 L1090
D1096 K1097 D1098 E1101 E1105 V1106 Y1107 E1111 I1115 N1121 K1126 L1133 S1134 Y1140 P1141 G1142 Q1150 V1151 M1155 R1156 K1157 A1158 Q1175 ASP GLU ILE ASP ASN ALA ALA ASP THR PRO A1186 A1190 A1195 L1196 N1197 E1198 V1199 M1200 I1201 K1202 E1215
I1218 F1219 A1220 P1221 V1222 E1223 R1224 L1225 R1228 ILE ASP SER PHE ASN VAL VAL ARG LEU SER GLU ALA LEU GLY LEU ASP SER LYS LYS TYR PHE ARG ARG GLU GLY GLY ASN ASN ASN GLY GLU ASP ILE ASN ASN LEU GLN PRO LEU GLU THR THR ILE THR D1273 V1274 F1277 K1278
L1283 F1296 I1299 V1307 N1310 L1320 F1321 T1322 P1323 L1324 Q1325 L1326 T1327 S1328 Q1329 I1330 I1334 R1335 L1346 D1349 D1350 S1351 R1358 Q1359 V1360 S1361 V1362 V1375 Y1380 Q1388 L1389 L1390 Y1391 L1395 F1396 D1397 K1400 N1401 L1406 L1415 K1419 E1420
I1427 L1430 T1431 M1438 V1444 V1445 Q1446 L1449 N1450 D1451 C1452 GLY ARG ARG TYR VAL ASP MET THR SER ILE PHE ASP PHE MET LEU ASN

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	263795	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.218	Depositor
Minimum map value	-0.120	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.021	Depositor
Map size (Å)	211.968, 211.968, 211.968	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4

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	B	0.28	1/3754 (0.0%)	0.42	2/5052 (0.0%)
2	A	0.17	0/3335	0.37	3/4506 (0.1%)
3	C	0.23	0/3490	0.40	0/4743
4	1	0.26	0/8185	0.42	1/11087 (0.0%)
All	All	0.25	1/18764 (0.0%)	0.41	6/25388 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	334	PRO	N-CD	-5.25	1.40	1.47

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	374	PRO	N-CD-CG	-6.35	93.68	103.20
2	A	374	PRO	CA-CB-CG	-6.01	93.08	104.50
4	1	534	PRO	CA-N-CD	-5.48	104.33	112.00
2	A	374	PRO	CA-N-CD	-5.15	104.79	112.00
1	B	332	ASN	CA-C-N	-5.02	113.89	121.92

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	B	3676	0	3529	54	0
2	A	3257	0	3221	54	0
3	C	3412	0	3335	63	0
4	1	8029	0	7932	172	0
5	B	8	0	0	1	0
All	All	18382	0	18017	335	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 335 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)
3:C:371:PRO:HG2	3:C:627:SER:HB2	1.71	0.71
2:A:85:ILE:HD12	2:A:105:GLU:HB3	1.73	0.70
2:A:137:ILE:O	2:A:141:MET:HG3	1.91	0.69
4:1:863:MET:HE2	4:1:1019:PHE:HD2	1.57	0.68
1:B:258:LEU:O	1:B:262:GLU:HG3	1.94	0.68

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	B	440/528 (83%)	434 (99%)	4 (1%)	2 (0%)	24 56
2	A	395/409 (97%)	389 (98%)	6 (2%)	0	100 100
3	C	432/705 (61%)	423 (98%)	9 (2%)	0	100 100
4	1	1002/1468 (68%)	987 (98%)	15 (2%)	0	100 100
All	All	2269/3110 (73%)	2233 (98%)	34 (2%)	2 (0%)	49 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	425	ARG
1	B	56	GLU

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	B	393/488 (80%)	393 (100%)	0	100	100
2	A	359/373 (96%)	359 (100%)	0	100	100
3	C	380/637 (60%)	378 (100%)	2 (0%)	81	80
4	1	900/1334 (68%)	895 (99%)	5 (1%)	78	79
All	All	2032/2832 (72%)	2025 (100%)	7 (0%)	84	83

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	1	535	ASN
4	1	799	TYR
4	1	1322	THR
4	1	801	LEU
4	1	428	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
4	1	776	GLN
4	1	1359	GLN
4	1	1446	GLN
4	1	1388	GLN
4	1	1024	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand 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	$\#\|Z\| > 2$
5	SF4	B	601	1	0,12,12	-	-	-		

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
5	SF4	B	601	1	-	-	0/6/5/5

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	601	SF4	1	0

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.

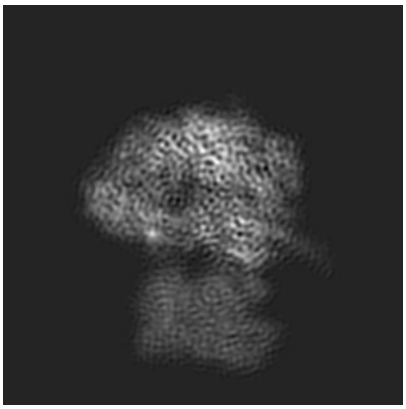
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-29345. These allow visual inspection of the internal detail of the map and identification of artifacts.

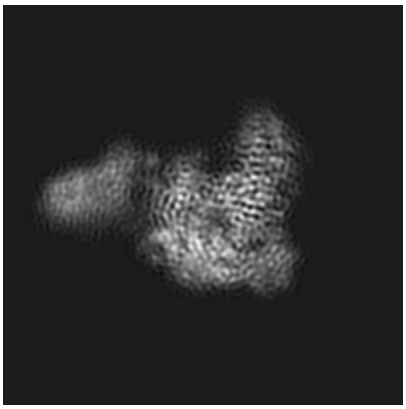
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

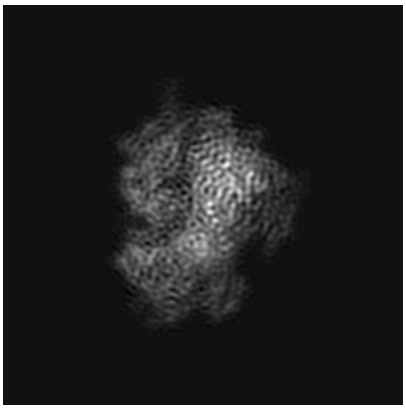
6.1.1 Primary map



X

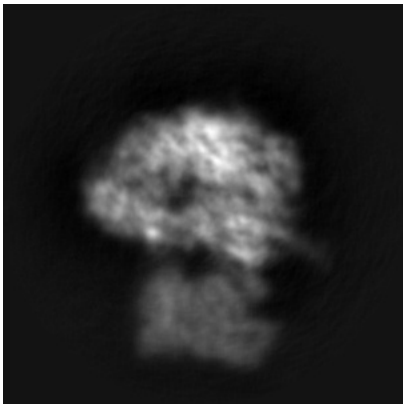


Y

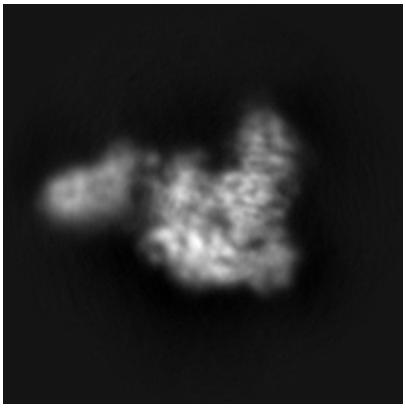


Z

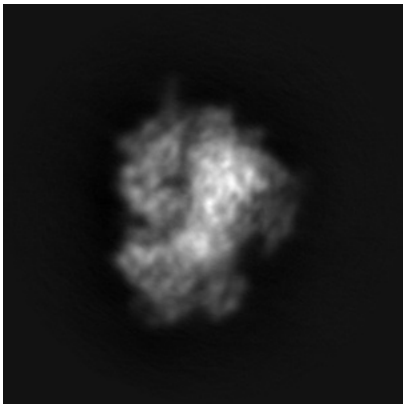
6.1.2 Raw map



X



Y

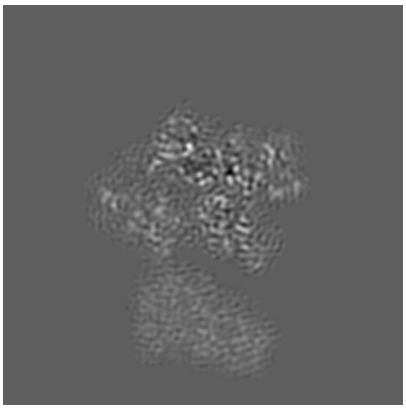


Z

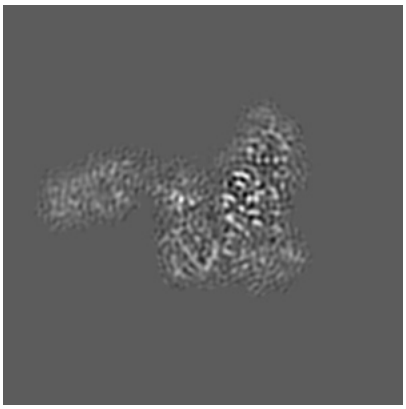
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

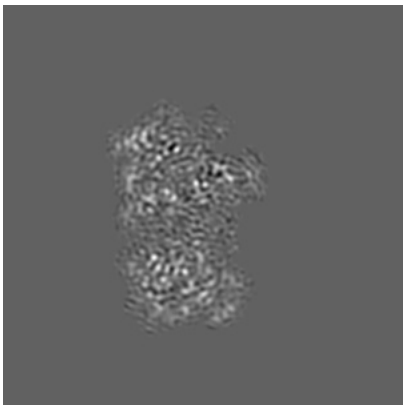
6.2.1 Primary map



X Index: 128

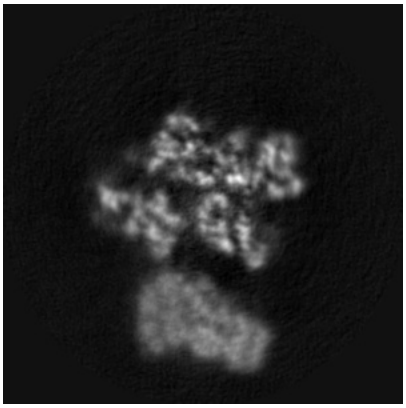


Y Index: 128

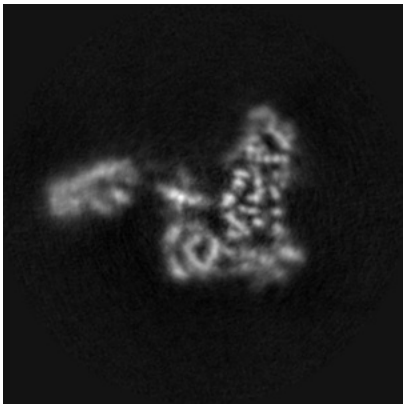


Z Index: 128

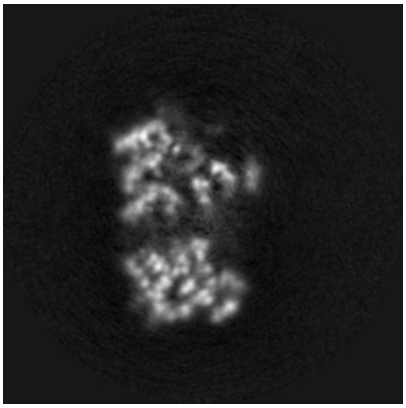
6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

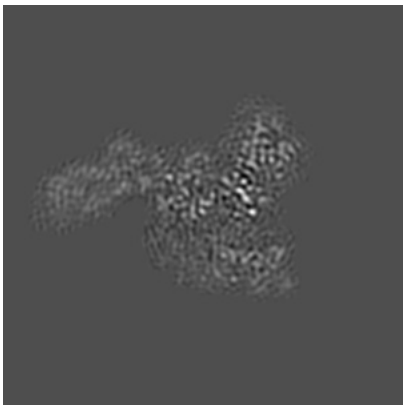
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

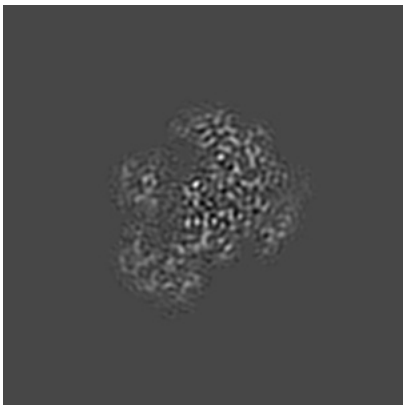
6.3.1 Primary map



X Index: 132

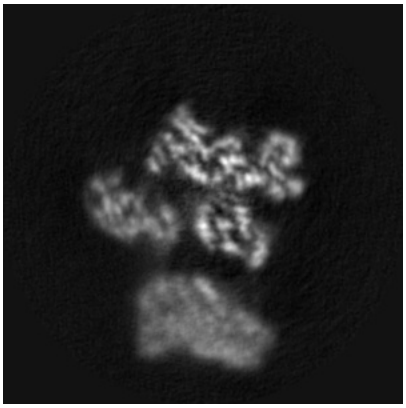


Y Index: 141

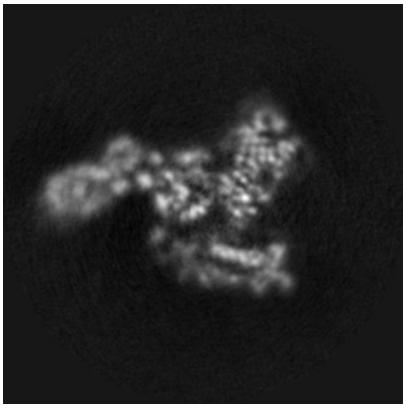


Z Index: 159

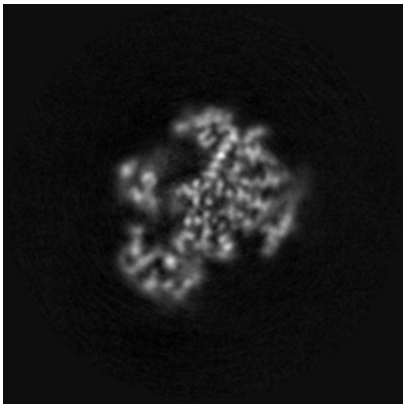
6.3.2 Raw map



X Index: 132



Y Index: 142

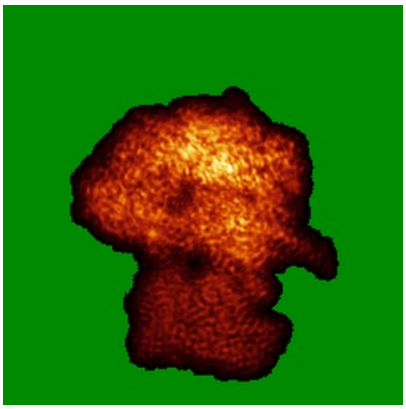


Z Index: 158

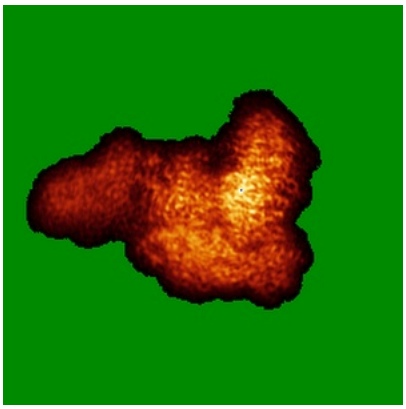
The images above show the largest variance slices of the map in three orthogonal directions.

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

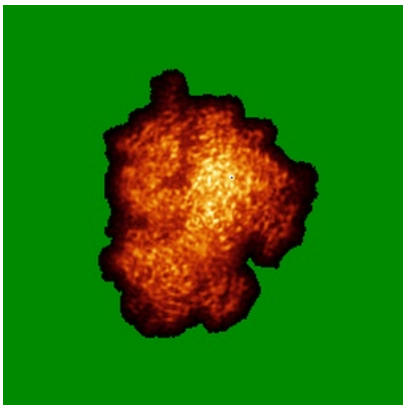
6.4.1 Primary map



X

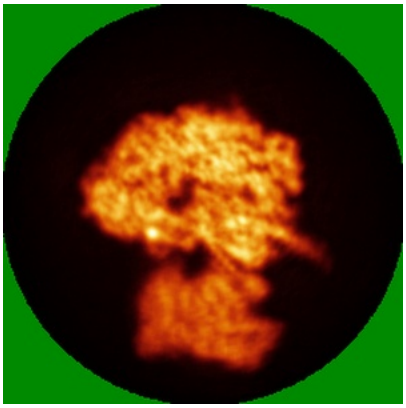


Y



Z

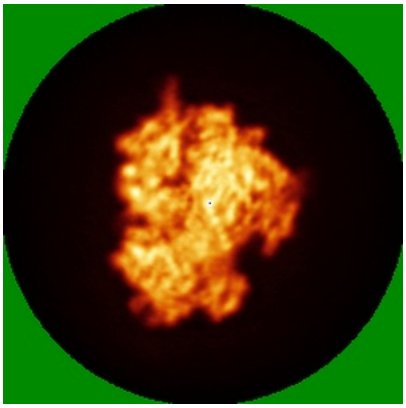
6.4.2 Raw map



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)

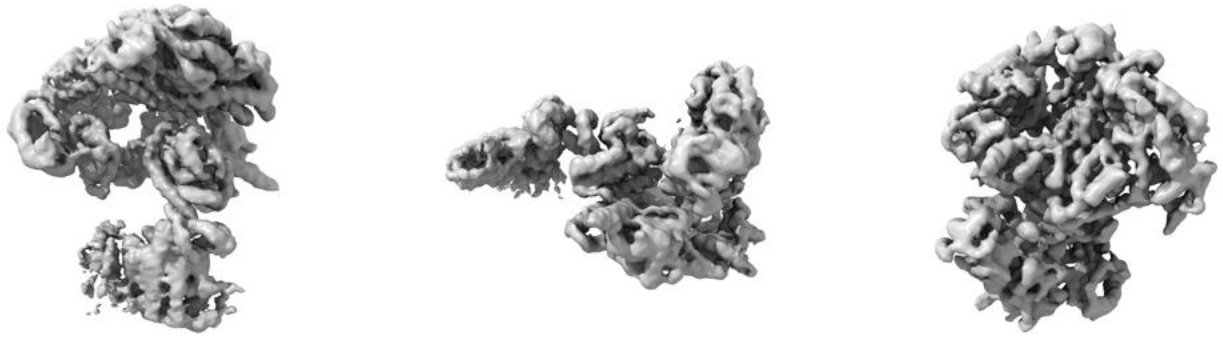
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.021. 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.

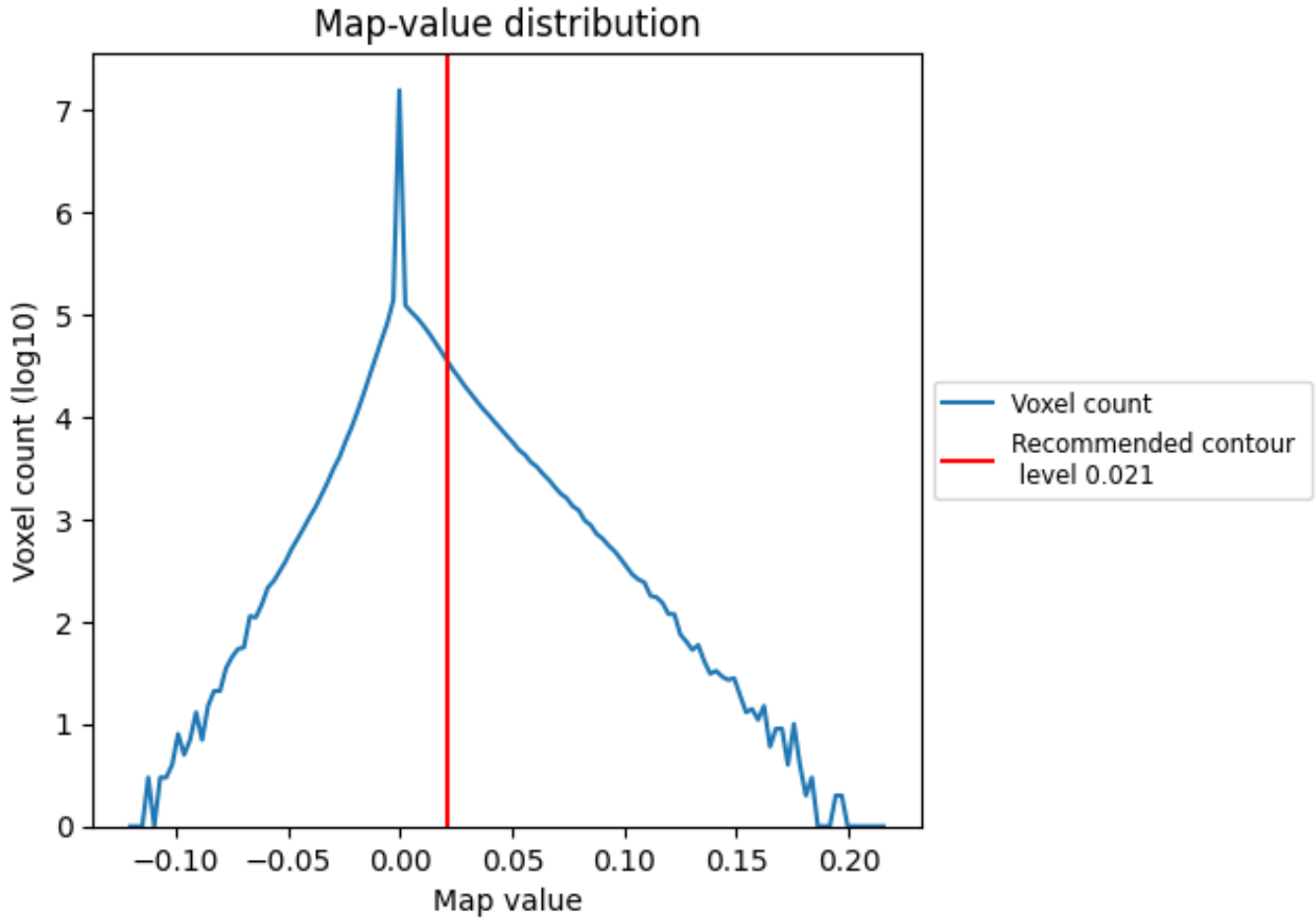
6.6 Mask visualisation (i)

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

7 Map analysis

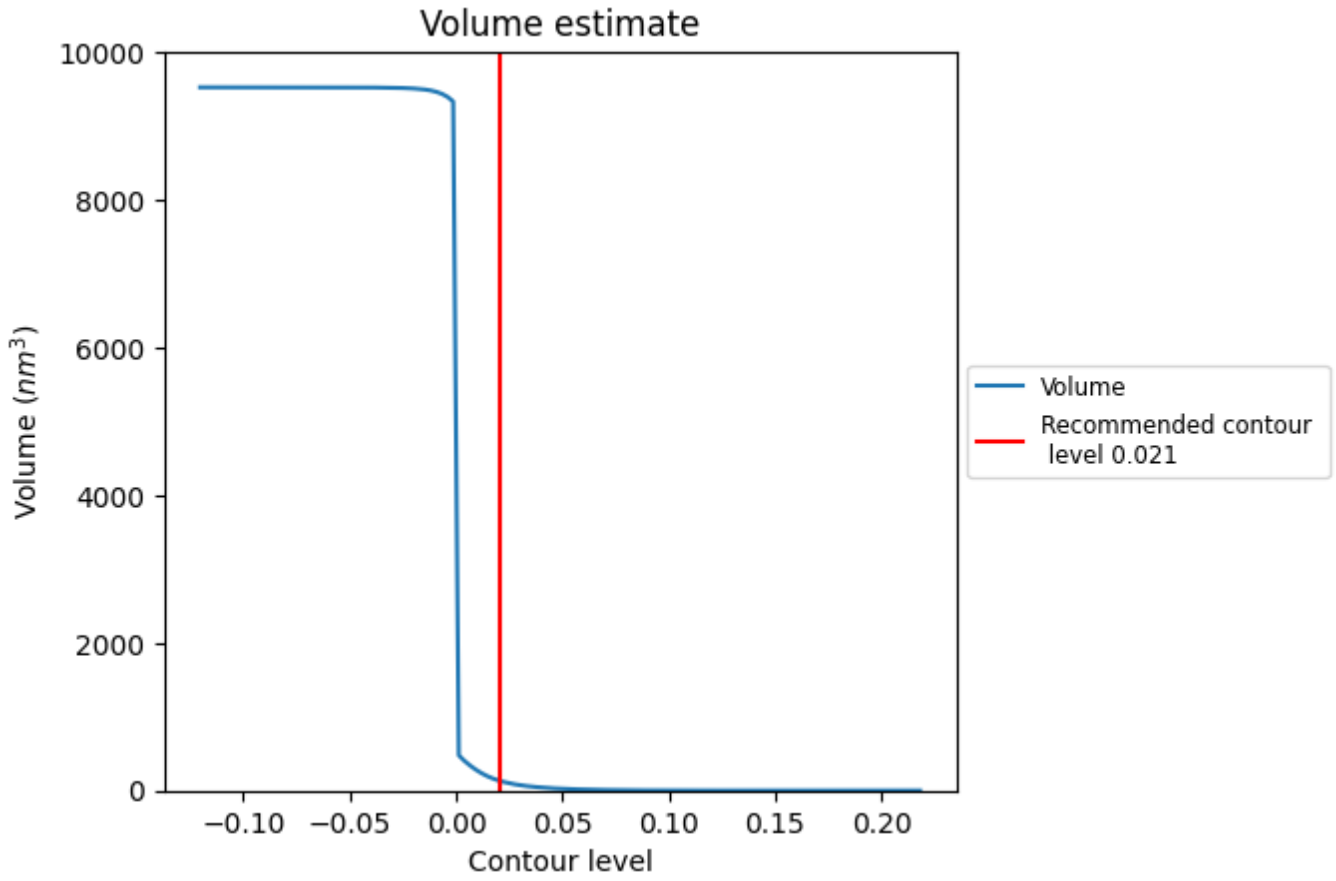
This section contains the results of statistical analysis of the map.

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.

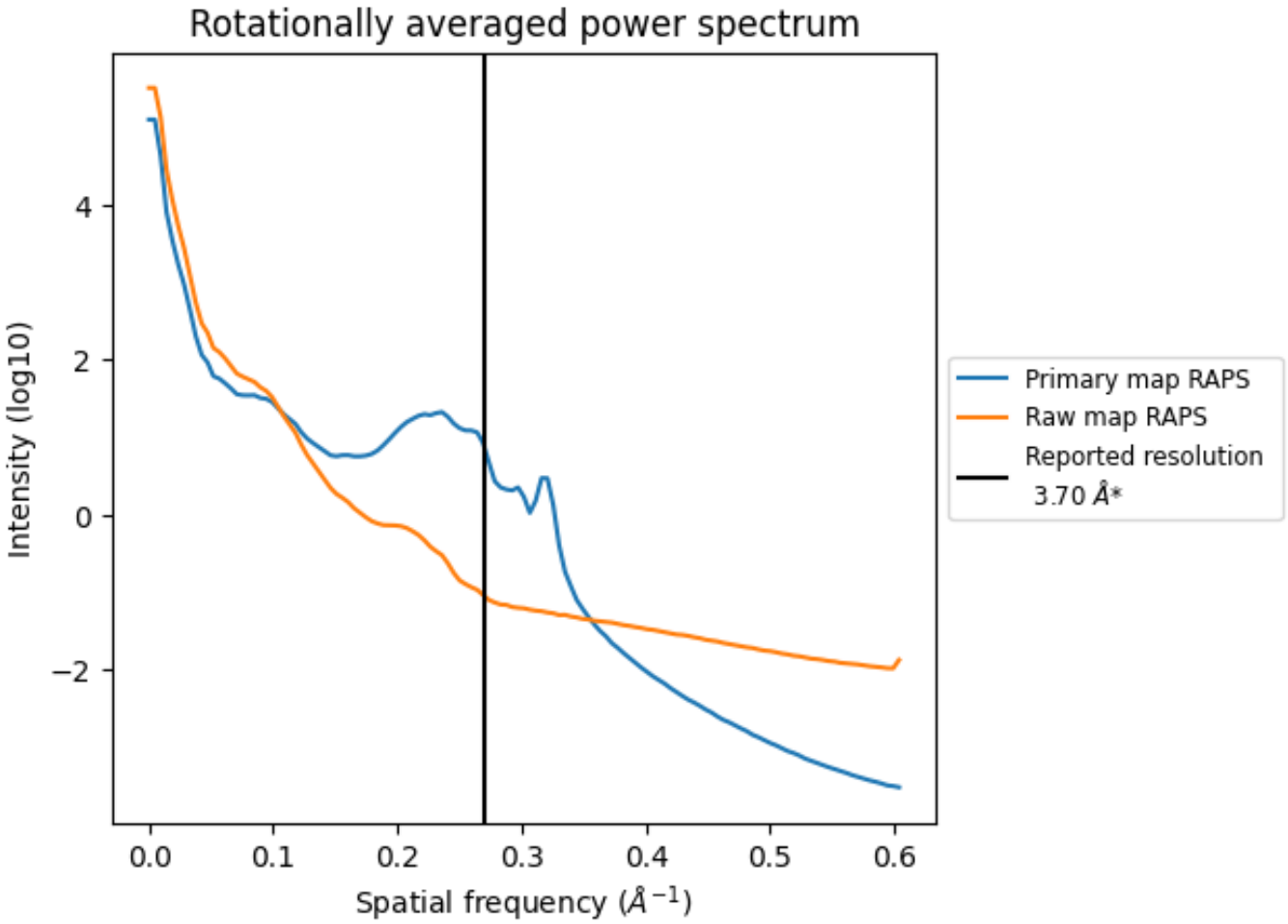
7.2 Volume estimate (i)



The volume at the recommended contour level is 129 nm^3; this corresponds to an approximate mass of 116 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)

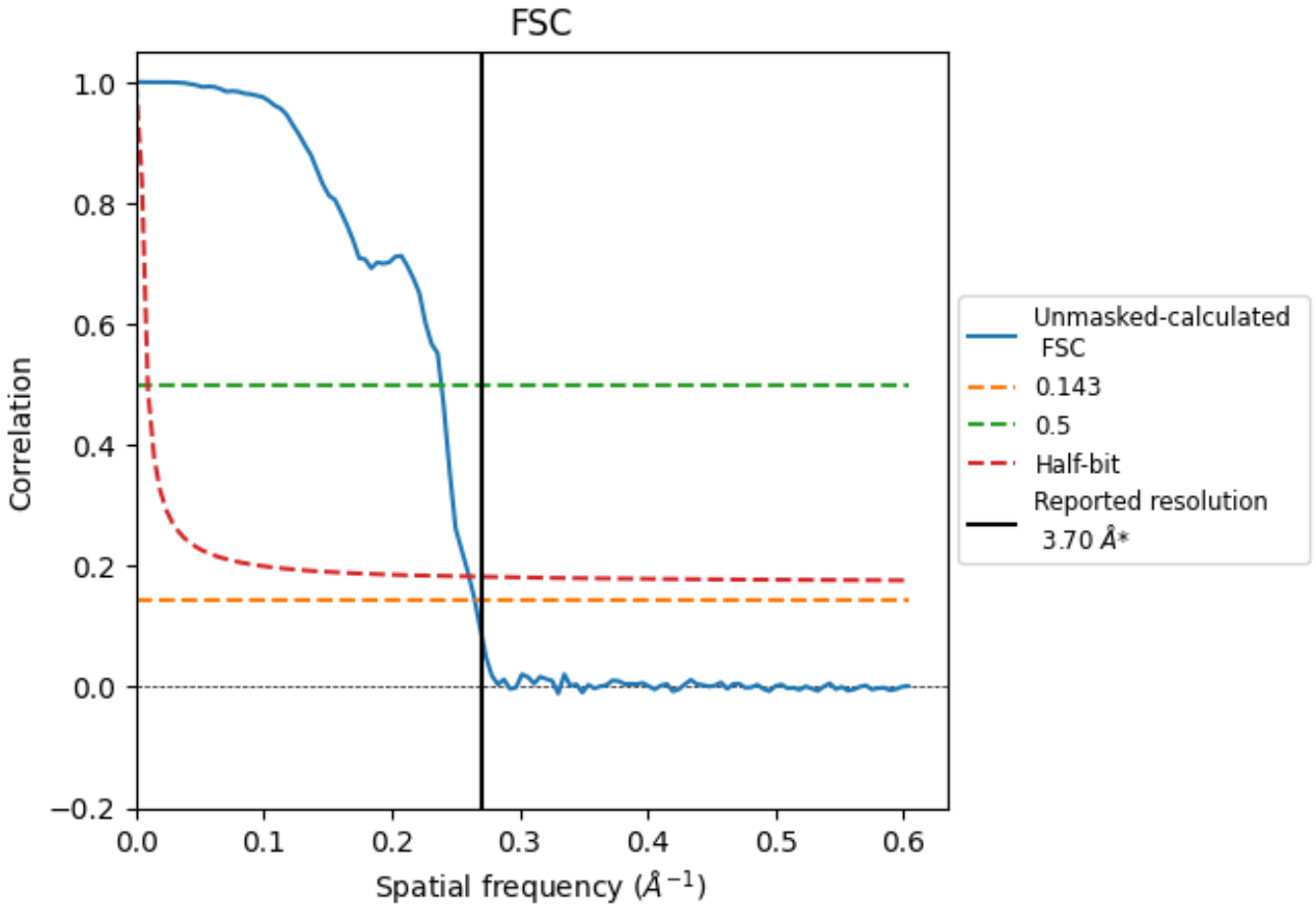


*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

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 0.270 Å^{-1}

8.2 Resolution estimates (i)

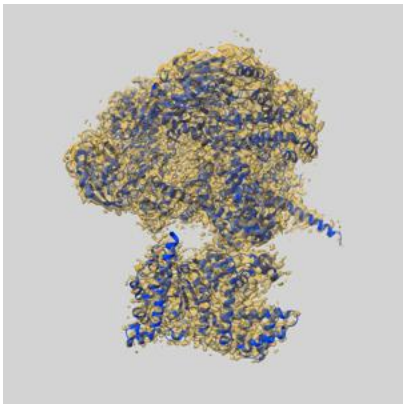
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.78	4.19	3.84

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

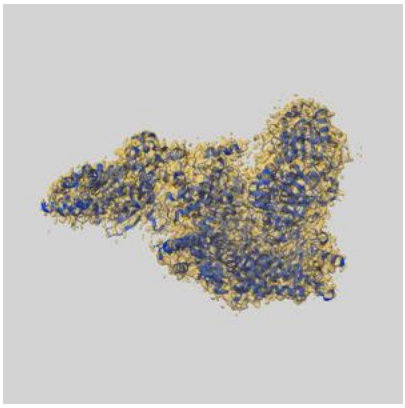
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-29345 and PDB model 8FOC. Per-residue inclusion information can be found in section 3 on page 5.

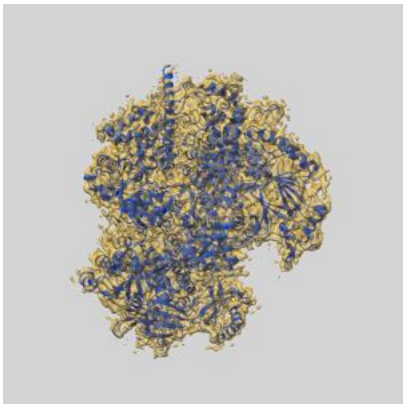
9.1 Map-model overlay



X



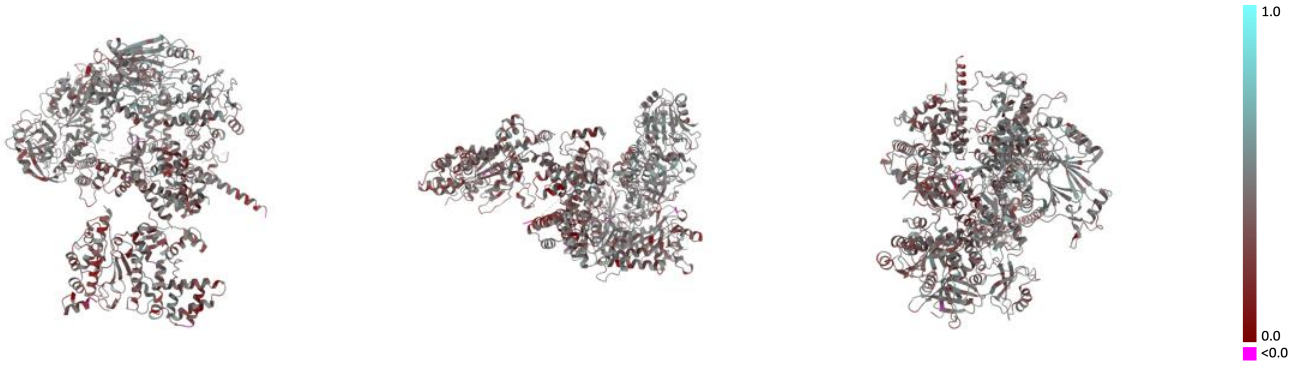
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.021 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.

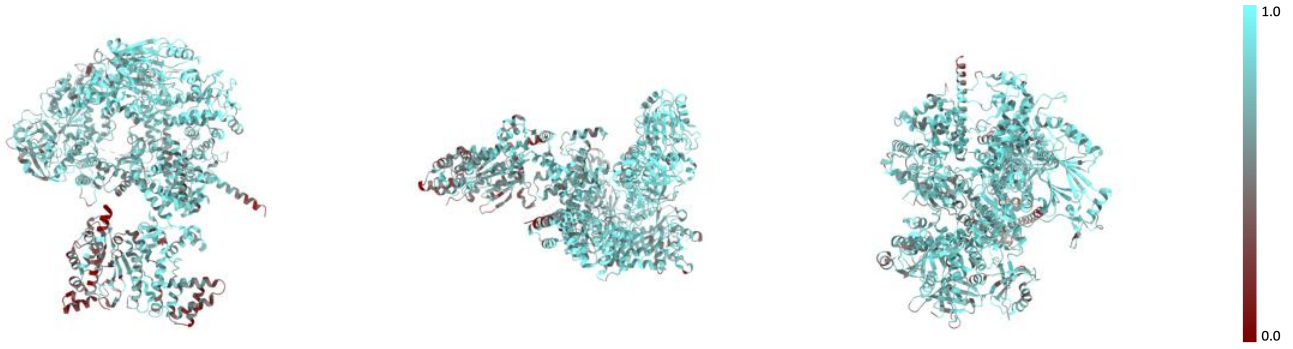
9.2 Q-score mapped to coordinate model (i)



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.

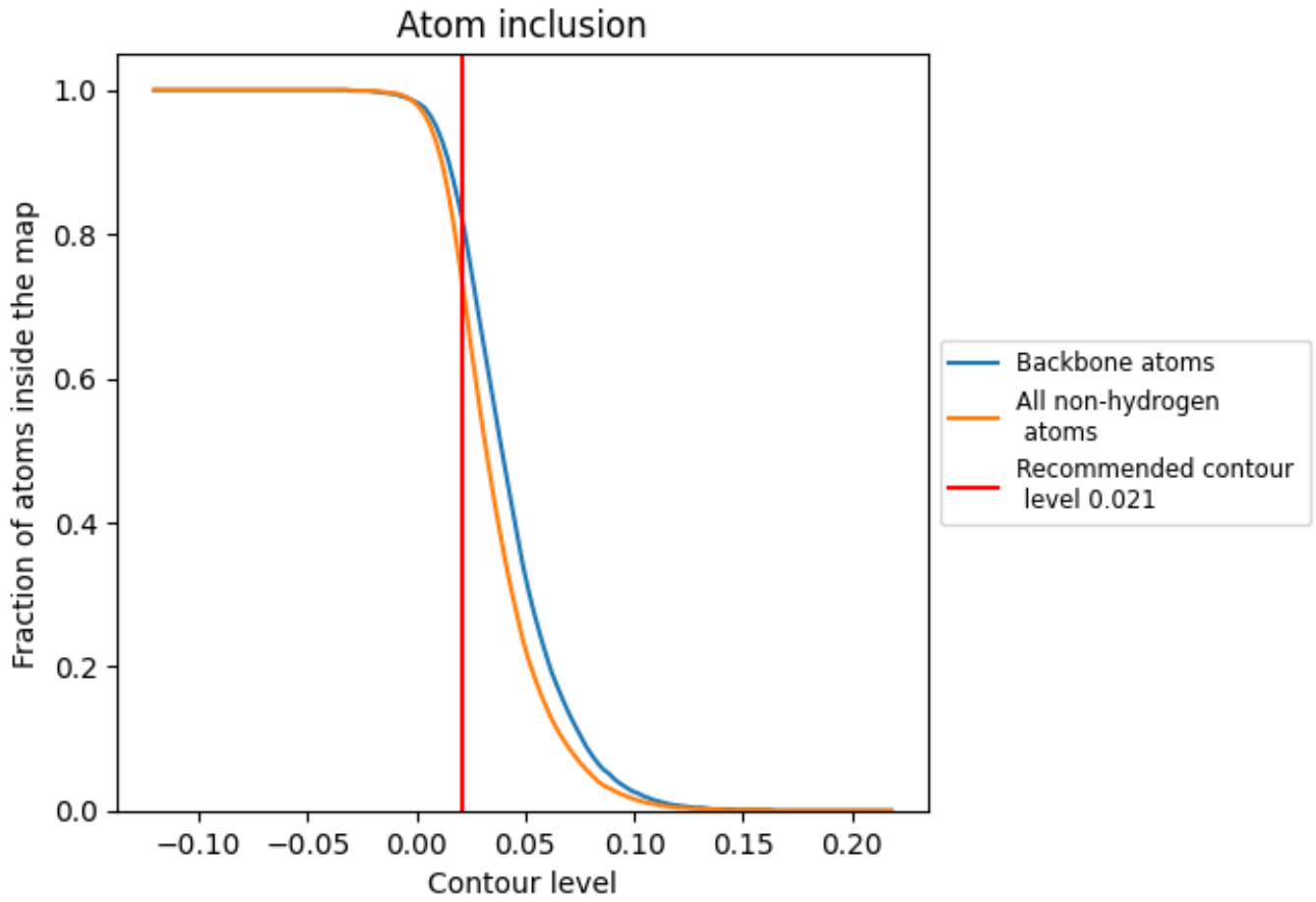
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.021).

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 74% 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 (0.021) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.7370	0.4070
1	0.7570	0.4080
A	0.5680	0.3580
B	0.7670	0.3990
C	0.8210	0.4600