



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 12:13 AM EST

PDB ID : 7TRC  
EMDB ID : EMD-26085  
Title : Human telomerase H/ACA RNP at 3.3 Angstrom  
Authors : Liu, B.; He, Y.; Wang, Y.; Song, H.; Zhou, Z.H.; Feigon, J.  
Deposited on : 2022-01-28  
Resolution : 3.30 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

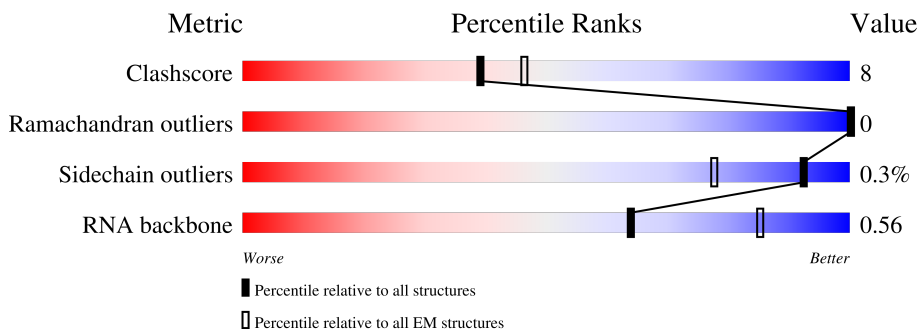
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 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  $\geq 3$ , 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  $\leq 5\%$ . 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	K	548	
2	C	514	
2	G	514	
3	F	64	
3	J	64	
4	B	451	
5	D	217	

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Mol	Chain	Length	Quality of chain
5	H	217	<div><div><div></div><div></div><div></div></div><div><div>33%</div><div>9%</div><div>57%</div></div></div>
6	E	153	<div><div><div></div><div></div><div></div></div><div><div>14%</div><div>67%</div><div>17%</div><div>16%</div></div></div>
6	I	153	<div><div><div></div><div></div><div></div></div><div><div>73%</div><div>12%</div><div>16%</div></div></div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14747 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 Telomerase Cajal body protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	K	330	Total	C	N	O	S	0	0
			2572	1630	445	482	15		

- Molecule 2 is a protein called H/ACA ribonucleoprotein complex subunit DKC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	341	Total	C	N	O	S	0	0
			2703	1710	490	484	19		
2	C	357	Total	C	N	O	S	0	0
			2830	1793	510	508	19		

- Molecule 3 is a protein called H/ACA ribonucleoprotein complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	64	Total	C	N	O	S	0	0
			541	346	99	92	4		
3	F	64	Total	C	N	O	S	0	0
			541	346	99	92	4		

- Molecule 4 is a RNA chain called Telomerase RNA, partial sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	92	Total	C	N	O	P	0	0
			1973	878	365	638	92		

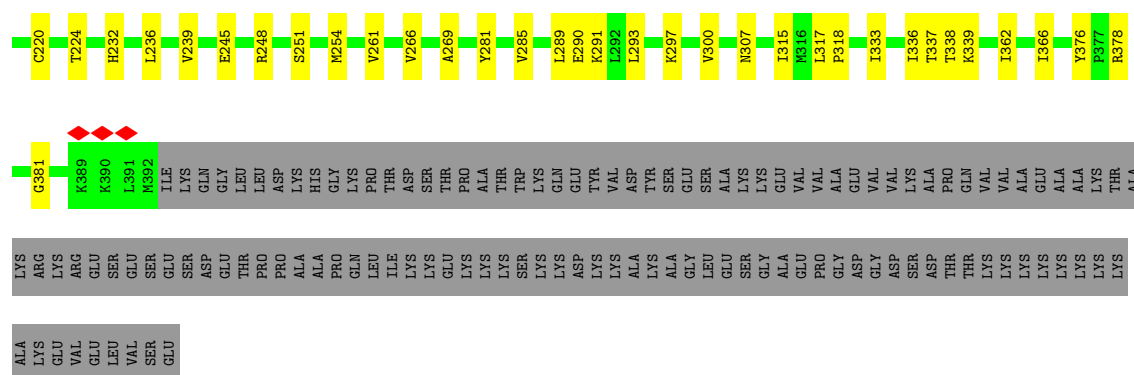
- Molecule 5 is a protein called H/ACA ribonucleoprotein complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	94	Total	C	N	O	S	0	0
			780	512	123	141	4		
5	D	91	Total	C	N	O	S	0	0
			759	497	120	138	4		

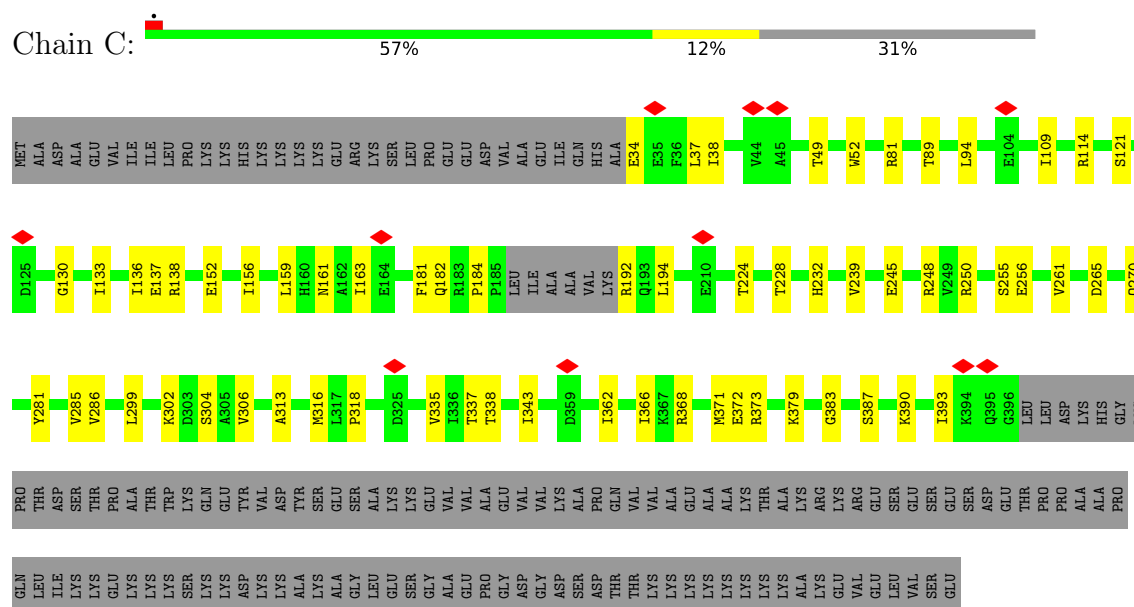
- Molecule 6 is a protein called H/ACA ribonucleoprotein complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	129	Total	C	N	O	S	0	0
			1024	652	179	185	8		
6	E	129	Total	C	N	O	S	0	0
			1024	652	179	185	8		

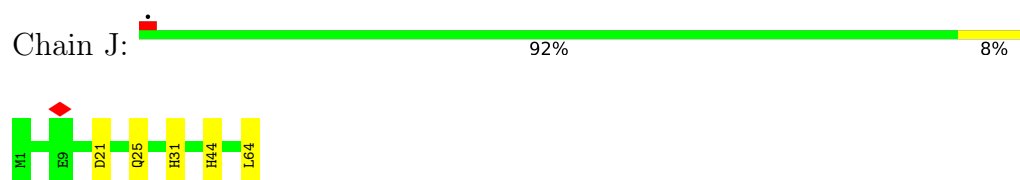




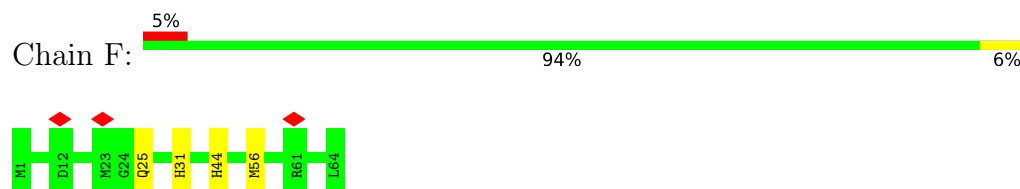
• Molecule 2: H/ACA ribonucleoprotein complex subunit DKC1



• Molecule 3: H/ACA ribonucleoprotein complex subunit 3

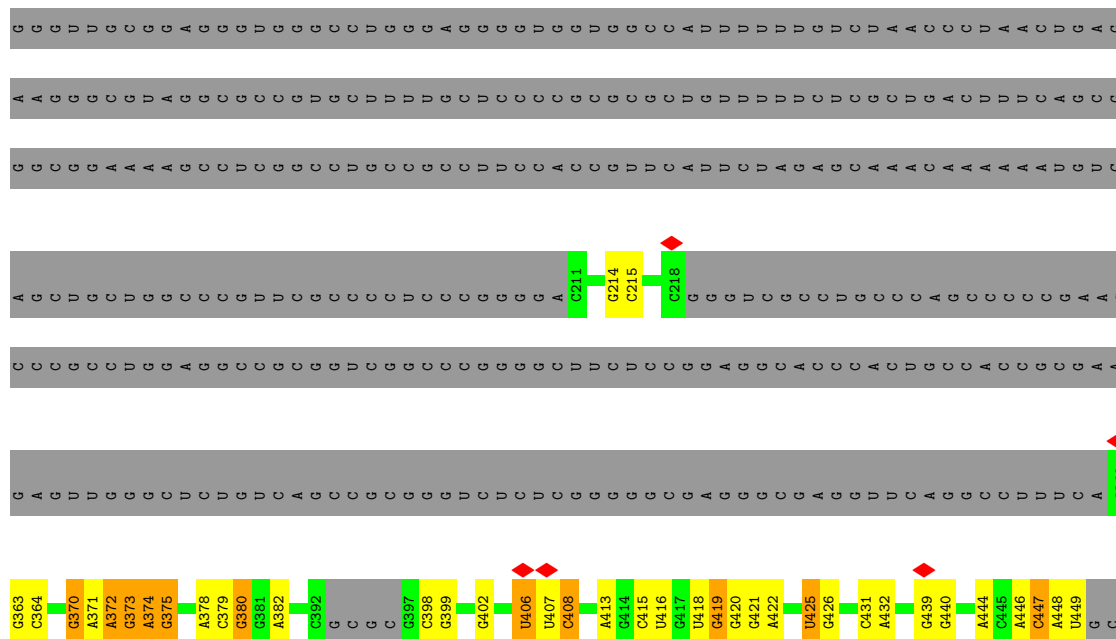


• Molecule 3: H/ACA ribonucleoprotein complex subunit 3

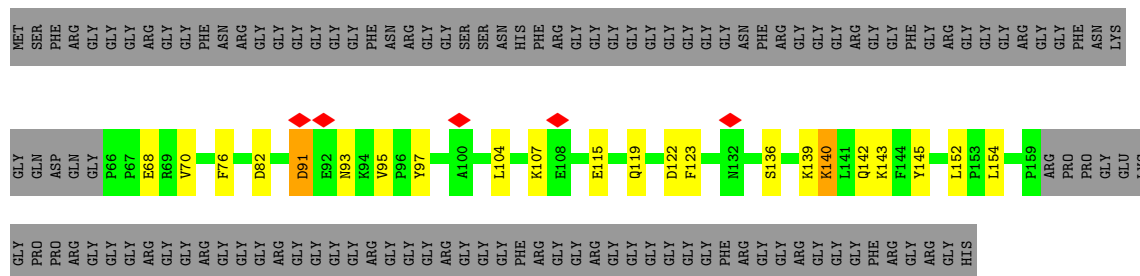
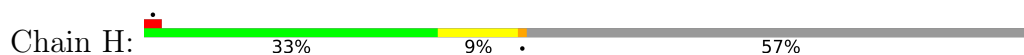


• Molecule 4: Telomerase RNA, partial sequence

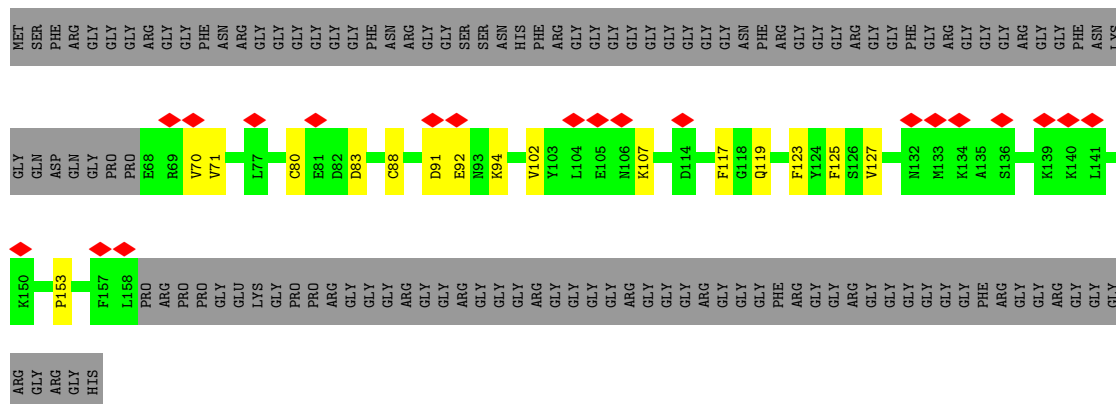
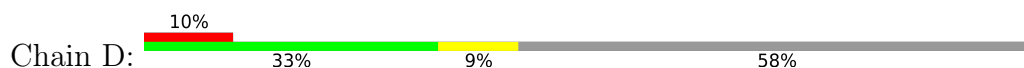




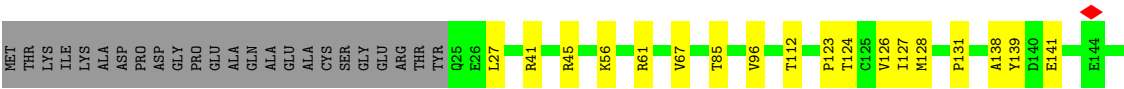
• Molecule 5: H/ACA ribonucleoprotein complex subunit 1



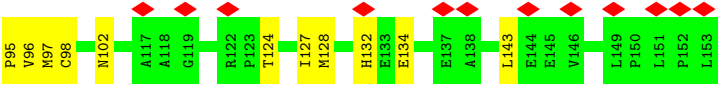
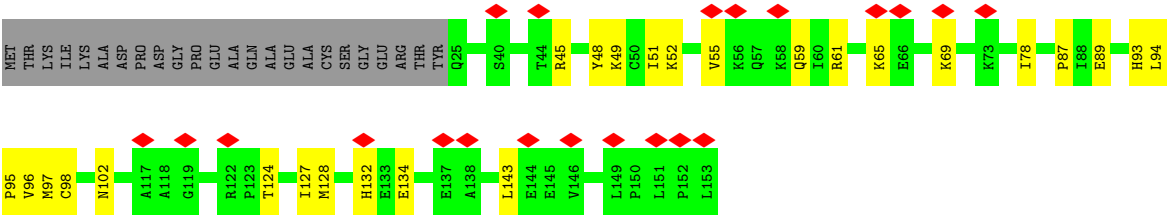
• Molecule 5: H/ACA ribonucleoprotein complex subunit 1



• Molecule 6: H/ACA ribonucleoprotein complex subunit 2



● Molecule 6: H/ACA ribonucleoprotein complex subunit 2



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	256859	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 ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.182	Depositor
Minimum map value	-0.111	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.025	Depositor
Map size ( $\text{\AA}$ )	352.0, 352.0, 352.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	K	0.25	0/2644	0.53	0/3594
2	C	0.25	0/2879	0.51	0/3884
2	G	0.25	0/2750	0.54	0/3712
3	F	0.26	0/555	0.50	0/745
3	J	0.26	0/555	0.51	0/745
4	B	0.21	0/2204	0.71	0/3432
5	D	0.26	0/777	0.53	0/1046
5	H	0.26	0/801	0.54	0/1081
6	E	0.26	0/1042	0.51	0/1407
6	I	0.27	0/1042	0.51	0/1407
All	All	0.25	0/15249	0.56	0/21053

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [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	K	2572	0	2457	52	0
2	C	2830	0	2939	40	0
2	G	2703	0	2803	54	0
3	F	541	0	550	4	0
3	J	541	0	550	5	0
4	B	1973	0	1004	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	759	0	760	11	0
5	H	780	0	782	22	0
6	E	1024	0	1073	16	0
6	I	1024	0	1073	12	0
All	All	14747	0	13991	219	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 8.

The worst 5 of 219 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:H:140:LYS:O	5:H:140:LYS:HD3	1.82	0.80
5:H:142:GLN:HG3	5:H:143:LYS:H	1.47	0.79
5:H:142:GLN:HG3	5:H:143:LYS:N	1.99	0.77
6:E:61:ARG:HB2	6:E:128:MET:HB3	1.68	0.74
4:B:371:A:H5''	4:B:372:A:H5'	1.70	0.74

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	K	322/548 (59%)	305 (95%)	17 (5%)	0	100	100
2	C	353/514 (69%)	342 (97%)	11 (3%)	0	100	100
2	G	337/514 (66%)	324 (96%)	13 (4%)	0	100	100
3	F	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
3	J	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
5	D	89/217 (41%)	83 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	H	92/217 (42%)	89 (97%)	3 (3%)	0	100	100
6	E	127/153 (83%)	121 (95%)	6 (5%)	0	100	100
6	I	127/153 (83%)	122 (96%)	5 (4%)	0	100	100
All	All	1571/2444 (64%)	1505 (96%)	66 (4%)	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	K	281/457 (62%)	280 (100%)	1 (0%)	91	95
2	C	312/444 (70%)	312 (100%)	0	100	100
2	G	298/444 (67%)	298 (100%)	0	100	100
3	F	60/60 (100%)	60 (100%)	0	100	100
3	J	60/60 (100%)	60 (100%)	0	100	100
5	D	86/142 (61%)	86 (100%)	0	100	100
5	H	89/142 (63%)	86 (97%)	3 (3%)	37	65
6	E	115/133 (86%)	115 (100%)	0	100	100
6	I	115/133 (86%)	115 (100%)	0	100	100
All	All	1416/2015 (70%)	1412 (100%)	4 (0%)	92	96

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

Mol	Chain	Res	Type
1	K	381	ARG
5	H	91	ASP
5	H	136	SER
5	H	140	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	K	470	HIS
5	H	142	GLN
6	E	68	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	B	89/451 (19%)	23 (25%)	1 (1%)

5 of 23 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	B	370	G
4	B	372	A
4	B	373	G
4	B	374	A
4	B	375	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	B	374	A

## 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](#)

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 ⓘ

There are no chain breaks in this entry.

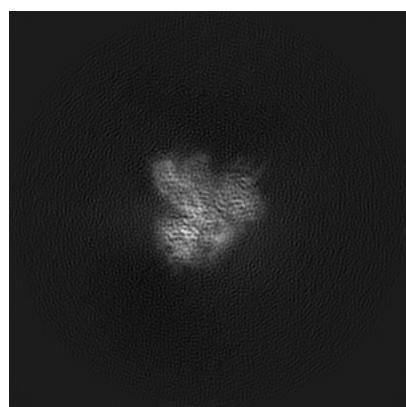
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26085. These allow visual inspection of the internal detail of the map and identification of artifacts.

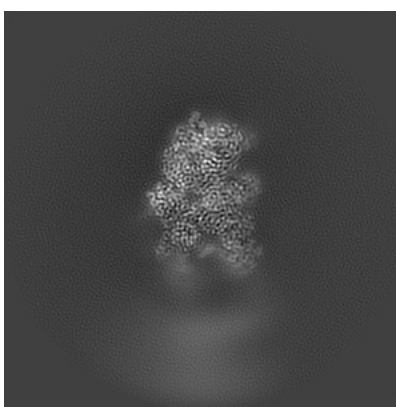
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

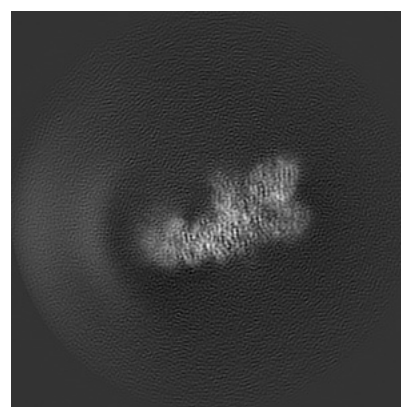
#### 6.1.1 Primary map



X



Y

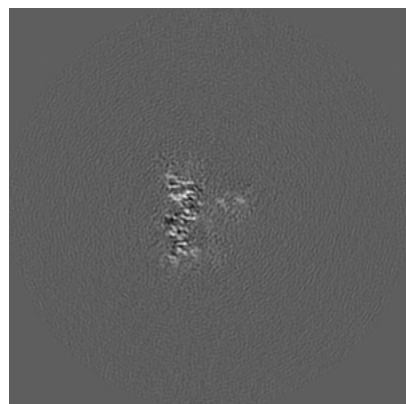


Z

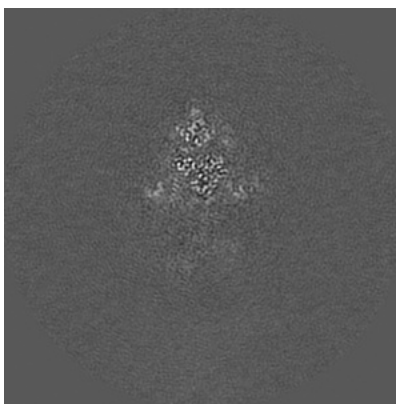
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

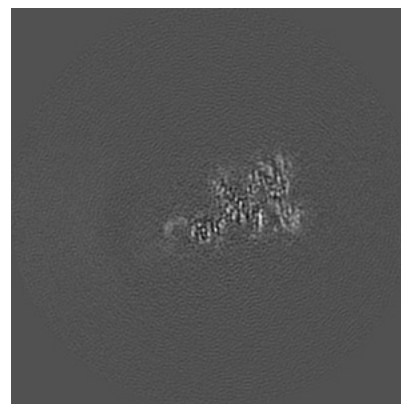
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

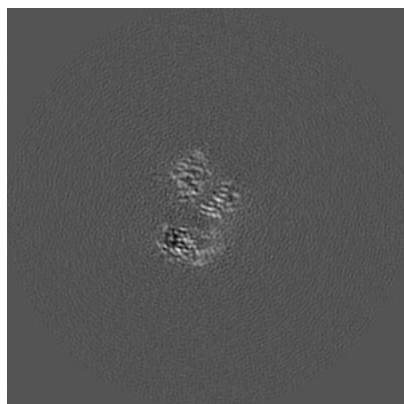


Z Index: 160

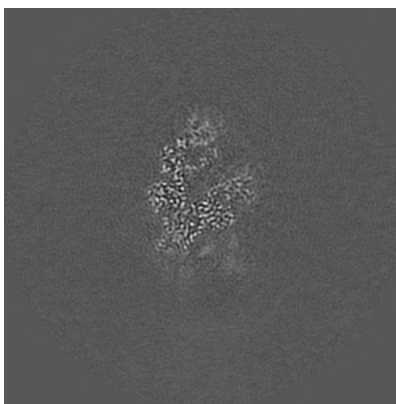
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

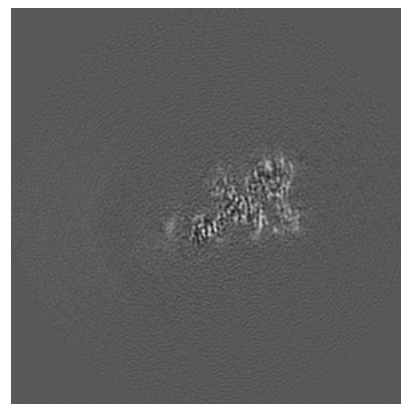
### 6.3.1 Primary map



X Index: 174



Y Index: 142



Z Index: 161

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

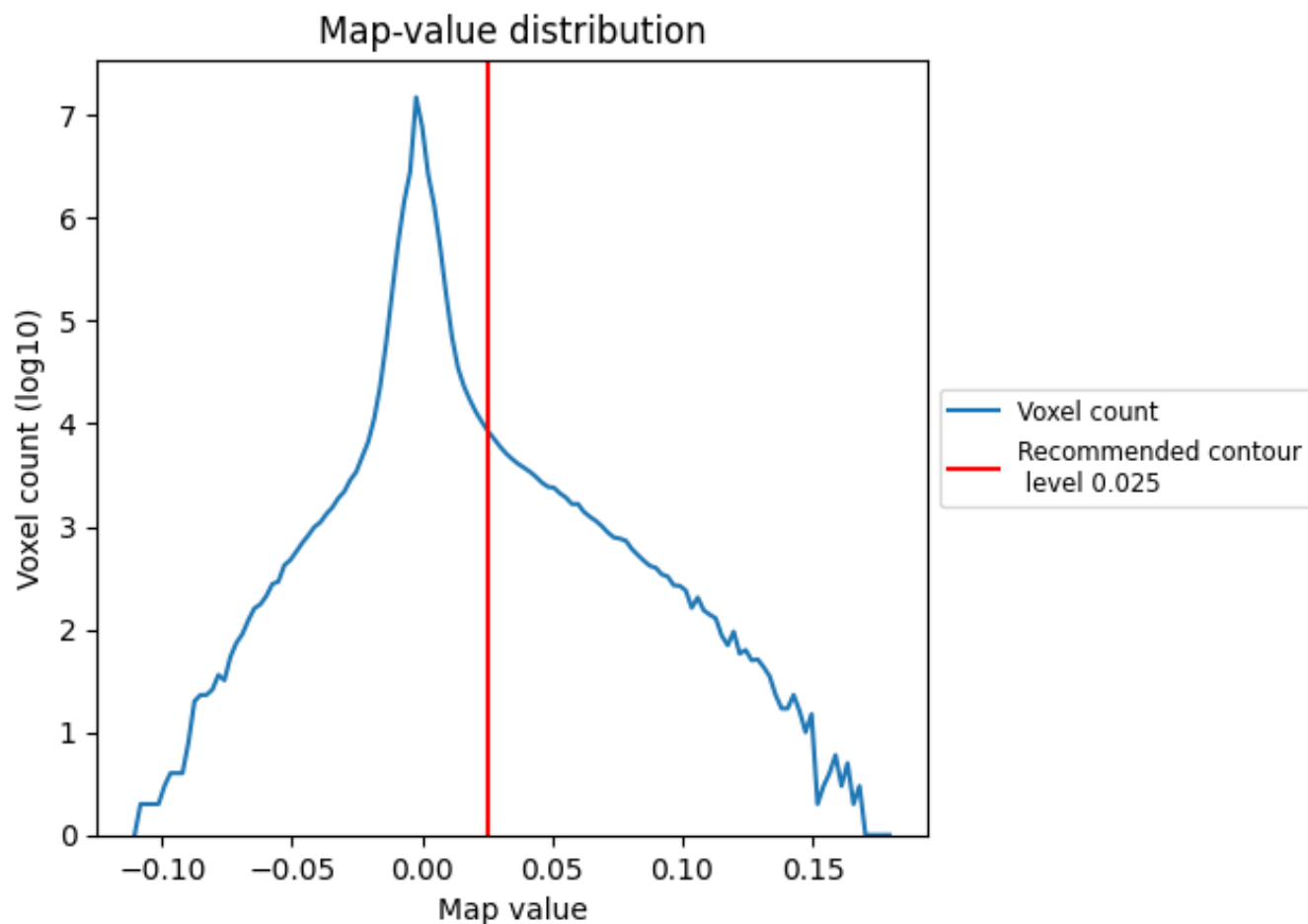
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

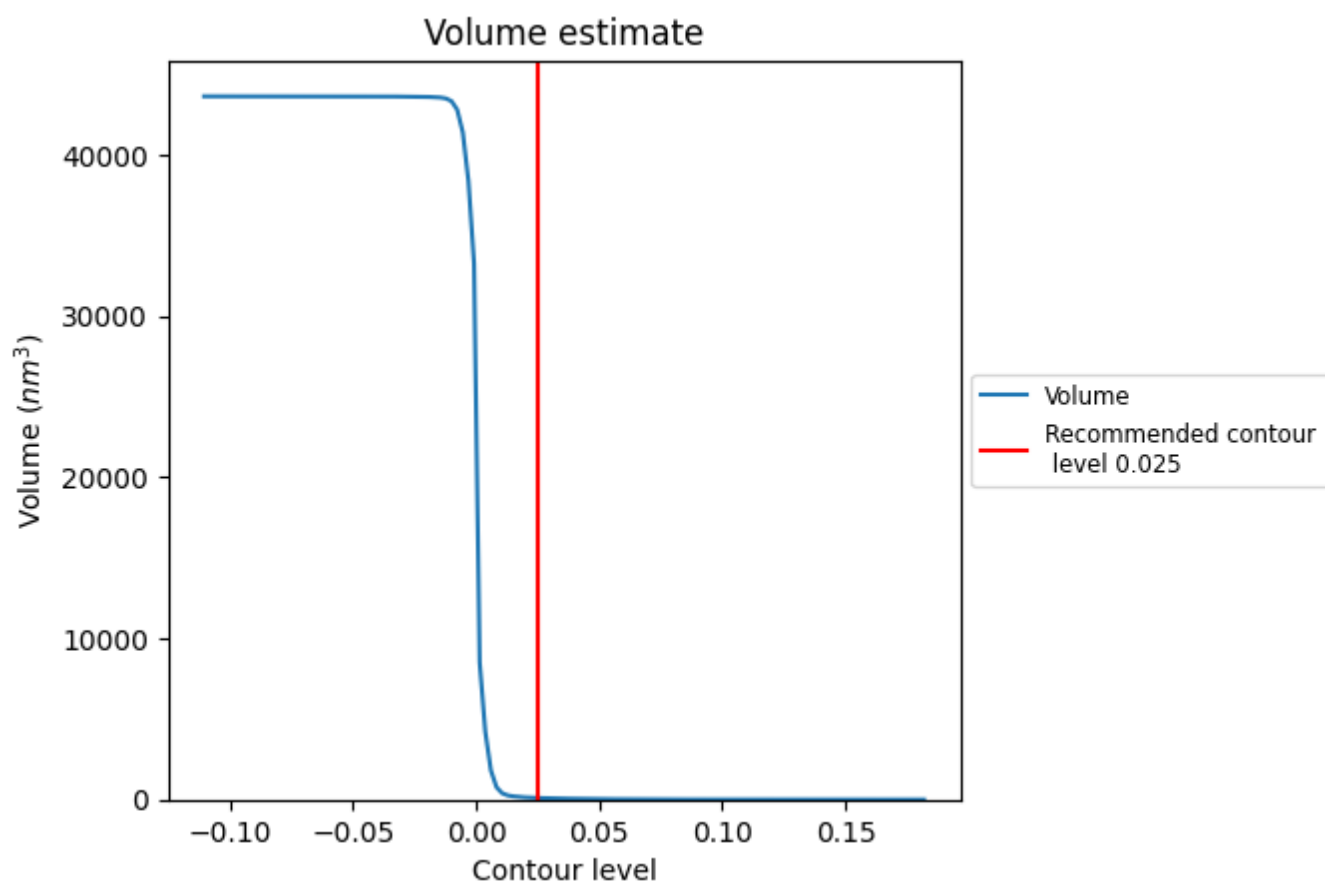
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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.

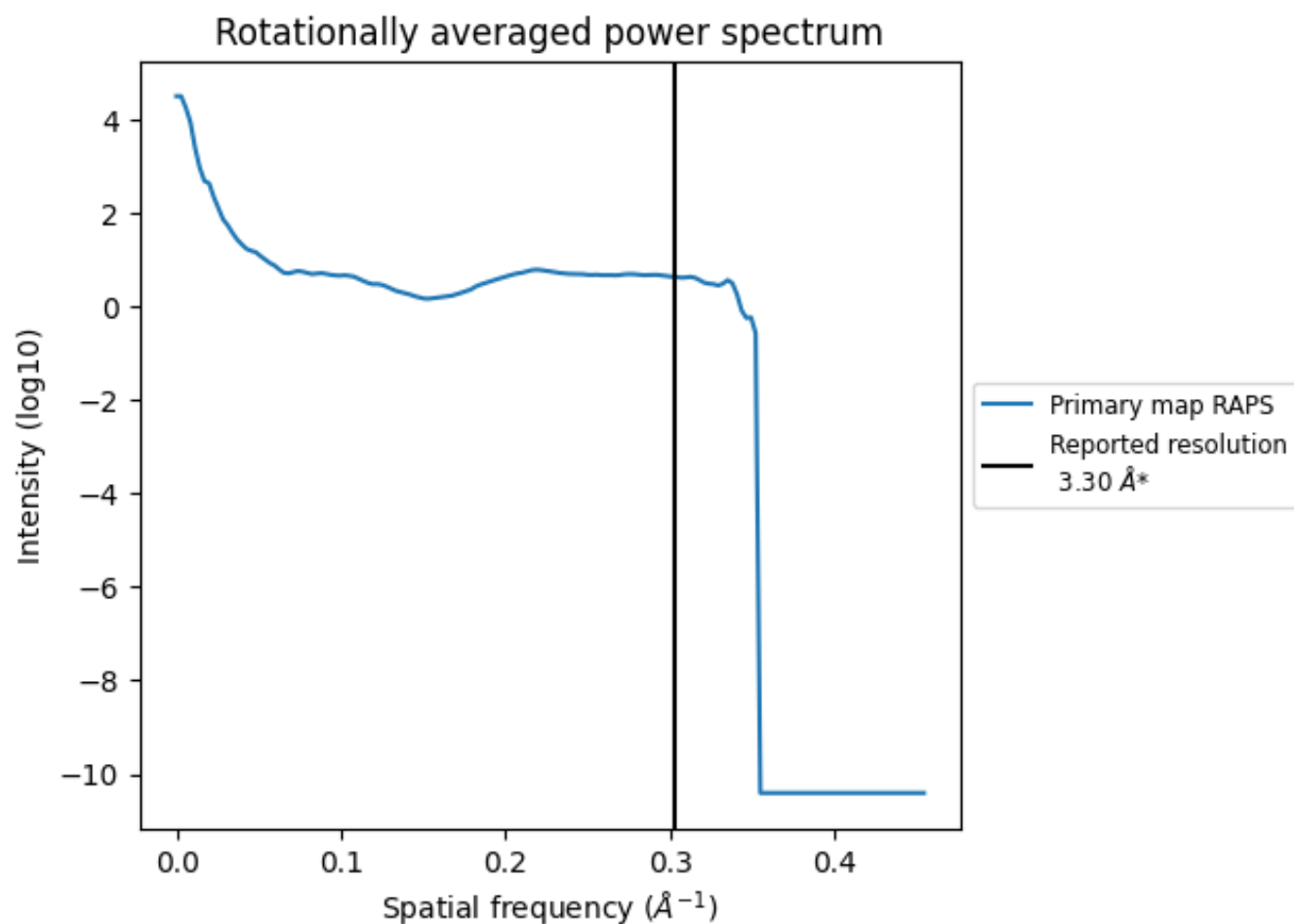
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 100 nm<sup>3</sup>; this corresponds to an approximate mass of 90 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 ⓘ



\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

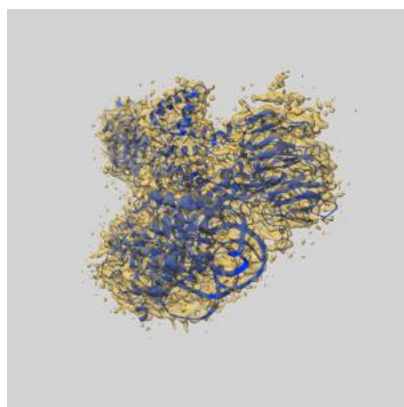
## 8 Fourier-Shell correlation

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

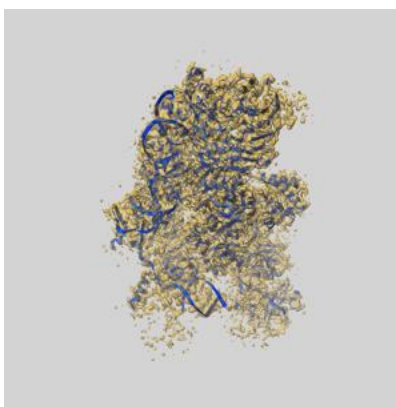
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26085 and PDB model 7TRC. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

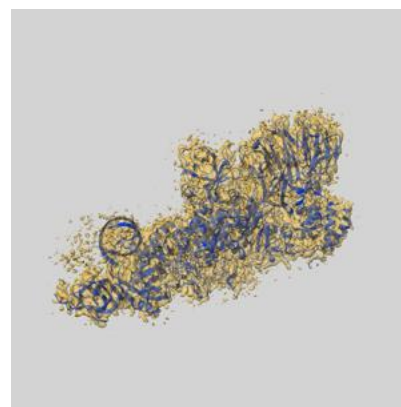
### 9.1 Map-model overlay [i](#)



X



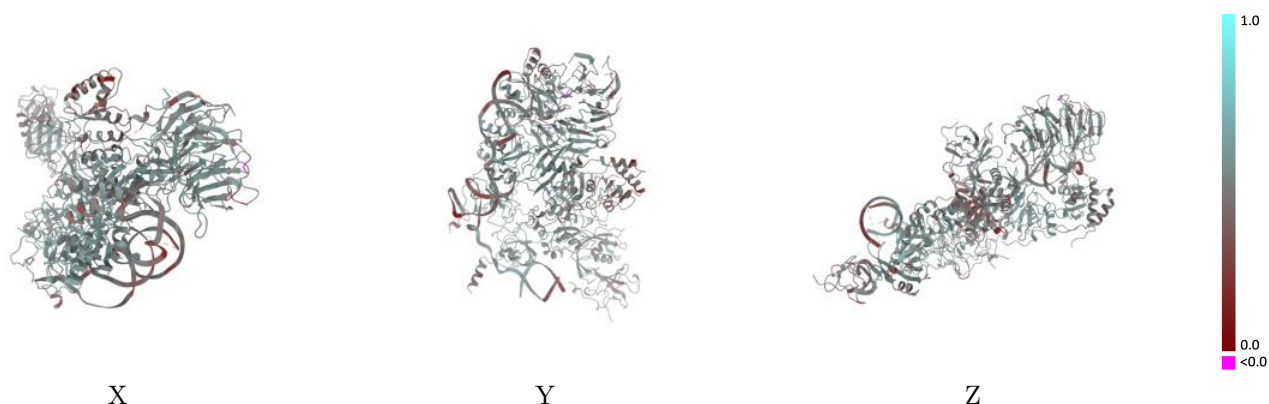
Y



Z

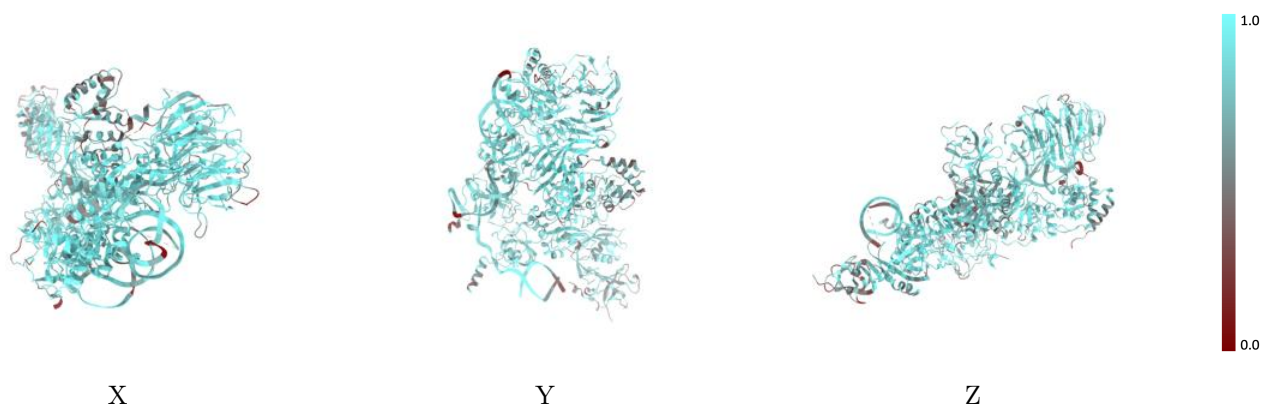
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



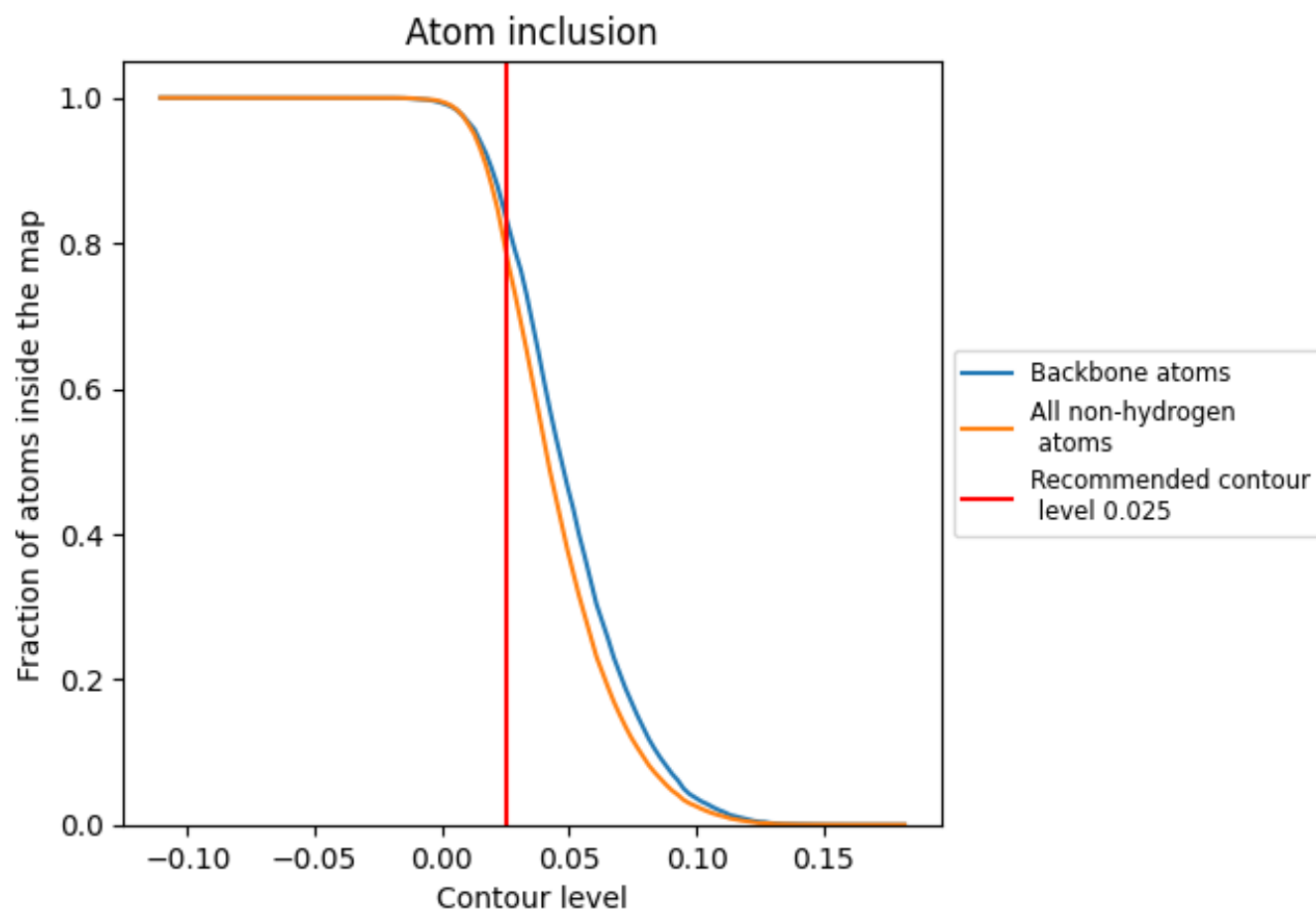
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.025).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 79% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.7938	<div><div></div></div> 0.4980
B	<div><div></div></div> 0.7704	<div><div></div></div> 0.4480
C	<div><div></div></div> 0.8278	<div><div></div></div> 0.5210
D	<div><div></div></div> 0.5869	<div><div></div></div> 0.4290
E	<div><div></div></div> 0.6554	<div><div></div></div> 0.4240
F	<div><div></div></div> 0.7829	<div><div></div></div> 0.4990
G	<div><div></div></div> 0.8708	<div><div></div></div> 0.5440
H	<div><div></div></div> 0.7555	<div><div></div></div> 0.4930
I	<div><div></div></div> 0.7998	<div><div></div></div> 0.4980
J	<div><div></div></div> 0.8667	<div><div></div></div> 0.5430
K	<div><div></div></div> 0.8074	<div><div></div></div> 0.5060

1.0

0.0

<0.0