



wwPDB EM Validation Summary Report ⓘ

Nov 9, 2022 – 02:46 AM JST

PDB ID : 6AH3
EMDB ID : EMD-9622
Title : Cryo-EM structure of yeast Ribonuclease P with pre-tRNA substrate
Authors : Lan, P.; Tan, M.; Wu, J.; Lei, M.
Deposited on : 2018-08-16
Resolution : 3.48 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:

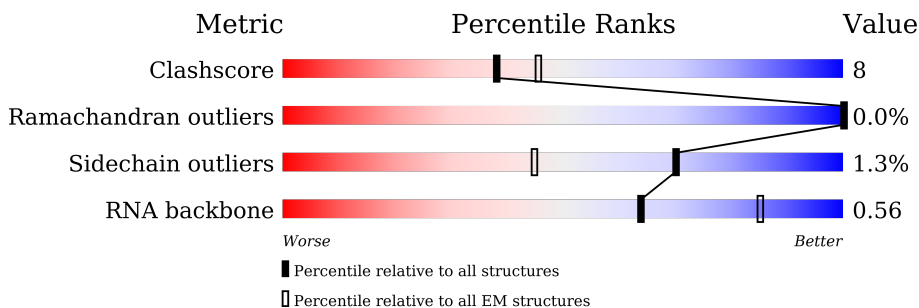
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.48 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.



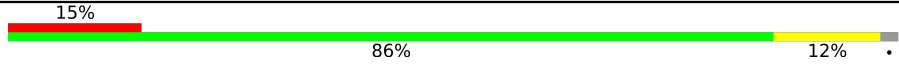
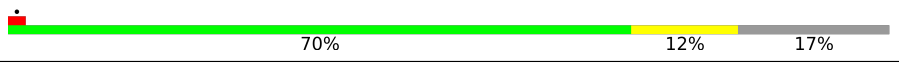
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. 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	A	369	
2	B	875	
3	C	195	
4	D	279	
5	E	173	
6	F	158	
7	G	140	

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Mol	Chain	Length	Quality of chain
8	H	133	
9	I	293	
9	J	293	
10	K	144	
11	T	80	

2 Entry composition i

There are 13 unique types of molecules in this entry. The entry contains 28703 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 RNA chain called Ribonuclease P RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	369	7861	3509	1387	2596	369	0	0

- Molecule 2 is a protein called Ribonucleases P/MRP protein subunit POP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	784	6389	4046	1161	1146	36	0	0

- Molecule 3 is a protein called Ribonucleases P/MRP protein subunit POP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	175	1435	935	241	250	9	0	0

- Molecule 4 is a protein called RNases MRP/P 32.9 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	203	1685	1087	285	305	8	0	0

- Molecule 5 is a protein called Ribonuclease P/MRP protein subunit POP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	146	1141	719	202	212	8	0	0

- Molecule 6 is a protein called Ribonucleases P/MRP protein subunit POP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	157	1272	804	222	242	4	0	0

- Molecule 7 is a protein called Ribonucleases P/MRP protein subunit POP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	121	961	609	167	183	2	0	0

- Molecule 8 is a protein called Ribonucleases P/MRP protein subunit POP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	131	1079	683	177	215	4	0	0

- Molecule 9 is a protein called Ribonuclease P/MRP protein subunit RPP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	242	1881	1188	339	345	9	0	0
9	J	293	2260	1415	413	422	10	0	0

- Molecule 10 is a protein called Ribonuclease P protein subunit RPR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	128	1024	642	193	183	6	0	0

- Molecule 11 is a RNA chain called pre-tRNA.

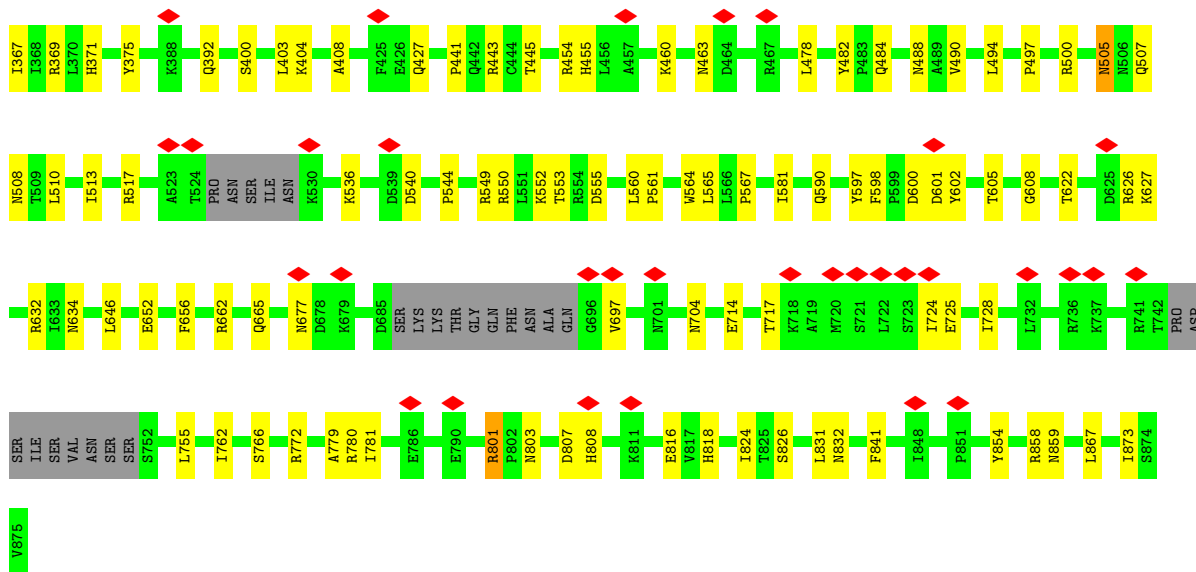
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	T	80	1712	764	308	560	80	0	0

- Molecule 12 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

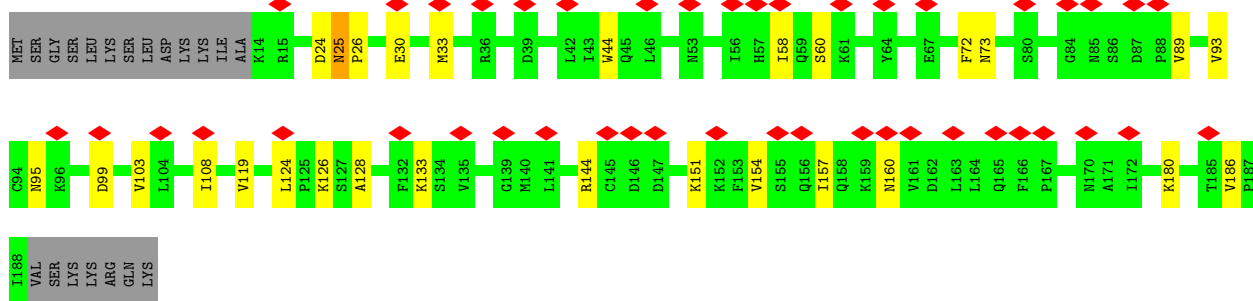
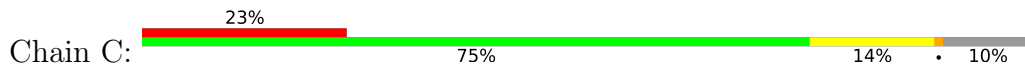
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
12	A	2	2	2	0

- Molecule 13 is ZINC ION (three-letter code: ZN) (formula: Zn).

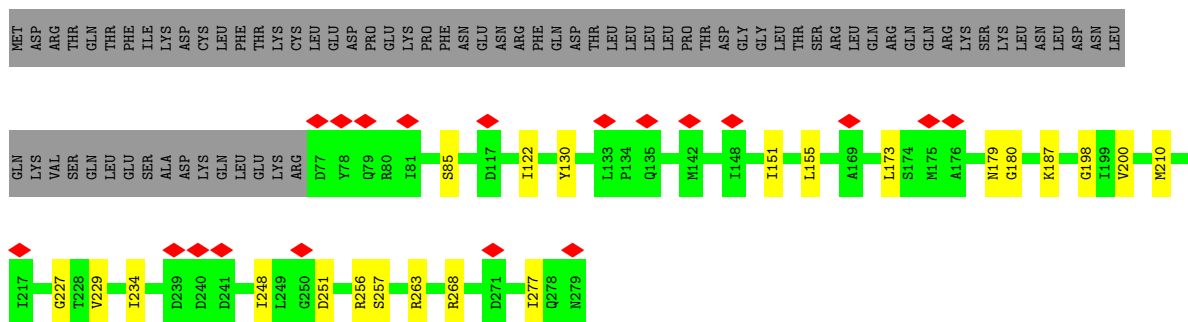
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
13	K	1	1	1	0



• Molecule 3: Ribonucleases P/MRP protein subunit POP3

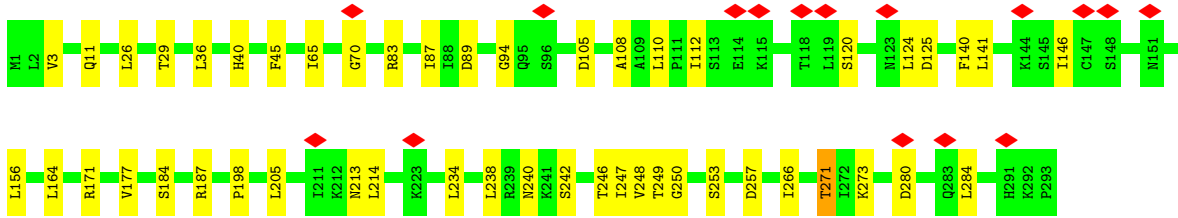


• Molecule 4: RNases MRP/P 32.9 kDa subunit

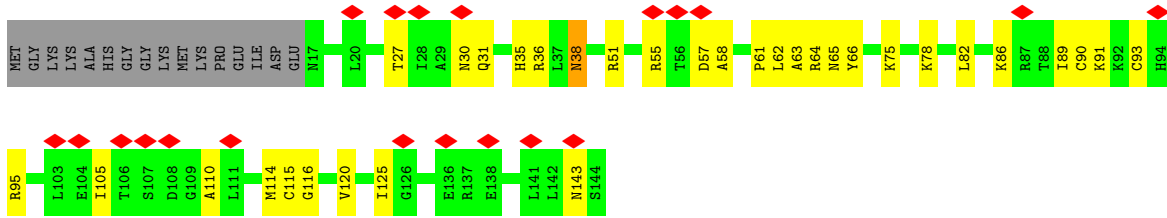


• Molecule 5: Ribonuclease P/MRP protein subunit POP5

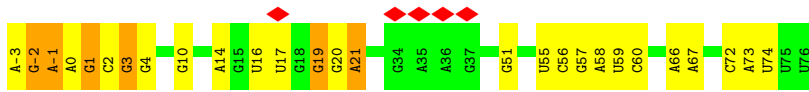




• Molecule 10: Ribonuclease P protein subunit RPR2



• Molecule 11: pre-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	176896	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 ($e^-/\text{\AA}^2$)	1.5625	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.308	Depositor
Minimum map value	-0.194	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	337.92, 337.92, 337.92	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

5 Model quality i

5.1 Standard geometry i

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	0.22	0/8786	0.86	14/13692 (0.1%)
2	B	0.27	0/6527	0.51	0/8792
3	C	0.28	0/1473	0.52	0/2005
4	D	0.25	0/1716	0.48	0/2304
5	E	0.25	0/1154	0.50	0/1550
6	F	0.26	0/1290	0.48	0/1733
7	G	0.24	0/973	0.48	0/1305
8	H	0.26	0/1101	0.53	1/1488 (0.1%)
9	I	0.25	0/1908	0.51	0/2577
9	J	0.25	0/2291	0.53	1/3092 (0.0%)
10	K	0.29	0/1044	0.54	0/1410
11	T	0.27	1/1915 (0.1%)	0.75	0/2984
All	All	0.25	1/30178 (0.0%)	0.66	16/42932 (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
2	B	0	1
9	J	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	T	4	G	O3'-P	-8.62	1.50	1.61

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	135	C	N1-C2-O2	7.26	123.26	118.90
1	A	182	C	N1-C2-O2	7.05	123.13	118.90
1	A	266	U	P-O3'-C3'	6.43	127.41	119.70
8	H	90	LEU	CA-CB-CG	5.96	129.01	115.30
1	A	367	A	P-O3'-C3'	5.92	126.81	119.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	363	LYS	Peptide
9	J	271	THR	Peptide

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	7861	0	3964	176	0
2	B	6389	0	6463	91	0
3	C	1435	0	1478	16	0
4	D	1685	0	1739	14	0
5	E	1141	0	1204	19	0
6	F	1272	0	1305	11	0
7	G	961	0	1005	11	0
8	H	1079	0	1037	9	0
9	I	1881	0	1975	23	0
9	J	2260	0	2351	41	0
10	K	1024	0	1058	23	0
11	T	1712	0	860	56	0
12	A	2	0	0	0	0
13	K	1	0	0	0	0
All	All	28703	0	24439	415	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 415 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:311:U:O2	1:A:344:A:C5	1.72	1.40
1:A:309:A:N6	1:A:343:G:C2	2.02	1.27
1:A:311:U:H1'	1:A:344:A:N6	1.48	1.26
1:A:309:A:N6	1:A:343:G:N3	1.88	1.20
1:A:311:U:C2	1:A:344:A:C5	2.35	1.14

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	
2	B	774/875 (88%)	716 (92%)	58 (8%)	0	100	100
3	C	173/195 (89%)	158 (91%)	15 (9%)	0	100	100
4	D	201/279 (72%)	200 (100%)	1 (0%)	0	100	100
5	E	144/173 (83%)	140 (97%)	4 (3%)	0	100	100
6	F	155/158 (98%)	153 (99%)	2 (1%)	0	100	100
7	G	117/140 (84%)	115 (98%)	2 (2%)	0	100	100
8	H	129/133 (97%)	122 (95%)	7 (5%)	0	100	100
9	I	240/293 (82%)	224 (93%)	15 (6%)	1 (0%)	34	70
9	J	291/293 (99%)	268 (92%)	23 (8%)	0	100	100
10	K	126/144 (88%)	111 (88%)	15 (12%)	0	100	100
All	All	2350/2683 (88%)	2207 (94%)	142 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	I	138	PRO

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	
2	B	708/785 (90%)	697 (98%)	11 (2%)	62	82
3	C	167/185 (90%)	163 (98%)	4 (2%)	49	75
4	D	188/261 (72%)	187 (100%)	1 (0%)	88	95
5	E	134/160 (84%)	133 (99%)	1 (1%)	84	93
6	F	148/149 (99%)	144 (97%)	4 (3%)	44	72
7	G	110/127 (87%)	109 (99%)	1 (1%)	78	91
8	H	122/123 (99%)	121 (99%)	1 (1%)	81	92
9	I	216/258 (84%)	213 (99%)	3 (1%)	67	85
9	J	258/258 (100%)	257 (100%)	1 (0%)	91	96
10	K	114/126 (90%)	112 (98%)	2 (2%)	59	81
All	All	2165/2432 (89%)	2136 (99%)	29 (1%)	70	86

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	144	ARG
10	K	38	ASN
6	F	8	ASN
9	I	79	LYS
5	E	3	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
6	F	54	ASN
9	I	34	HIS
6	F	76	GLN
8	H	27	HIS
9	I	151	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	368/369 (99%)	101 (27%)	10 (2%)
11	T	79/80 (98%)	13 (16%)	0
All	All	447/449 (99%)	114 (25%)	10 (2%)

5 of 114 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	16	U
1	A	17	U
1	A	24	A
1	A	25	U
1	A	26	U

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	303	C
1	A	305	G
1	A	367	A
1	A	191	A
1	A	195	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](#)

Of 3 ligands modelled in this entry, 3 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

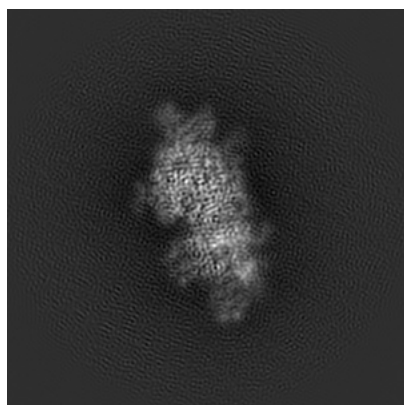
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9622. These allow visual inspection of the internal detail of the map and identification of artifacts.

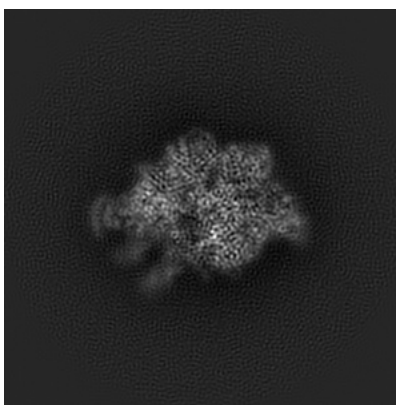
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

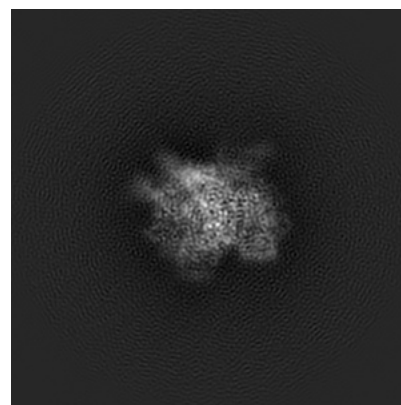
6.1.1 Primary map



X



Y

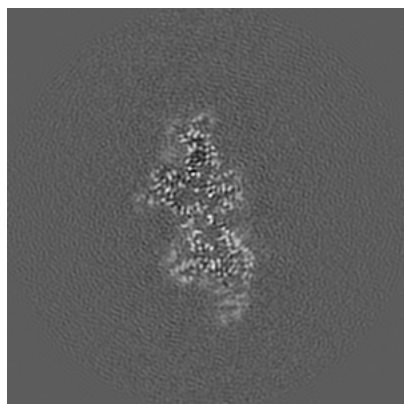


Z

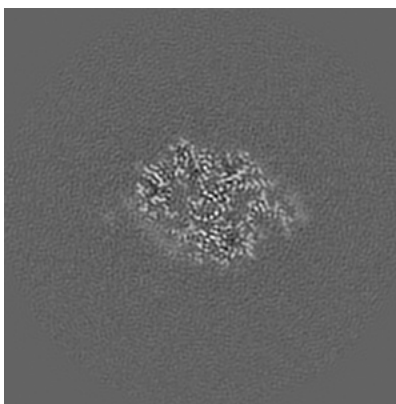
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

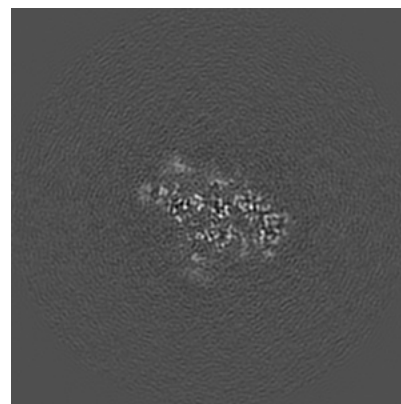
6.2.1 Primary map



X Index: 128



Y Index: 128

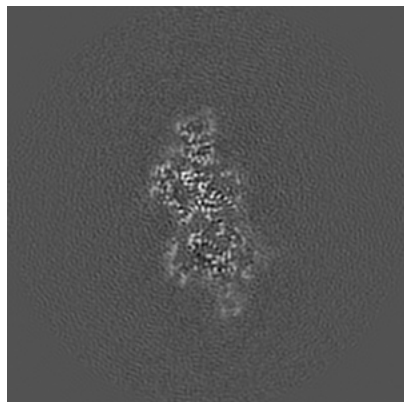


Z Index: 128

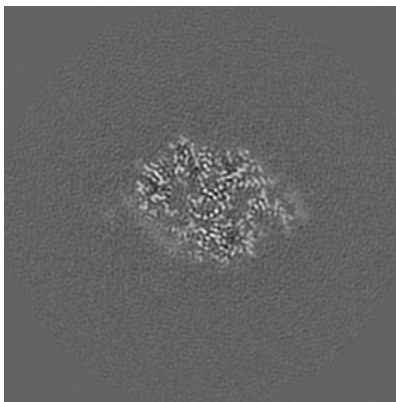
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

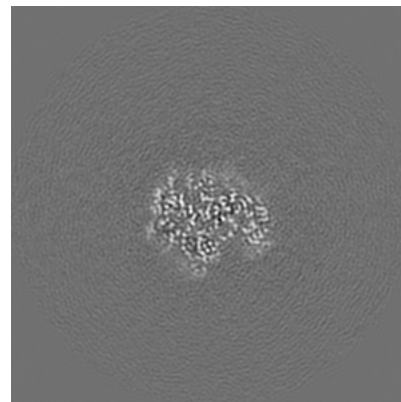
6.3.1 Primary map



X Index: 131



Y Index: 128



Z Index: 141

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.

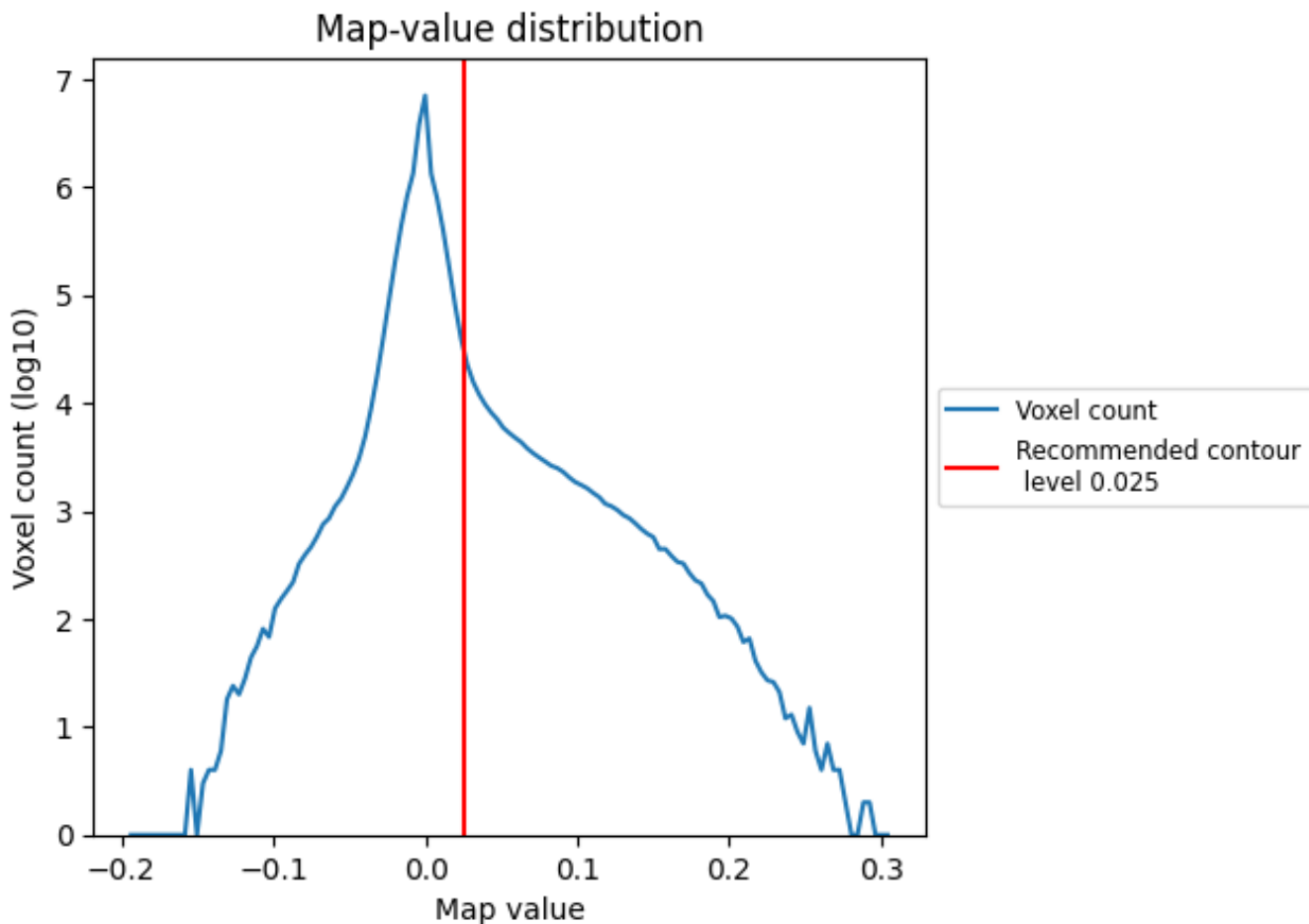
6.5 Mask visualisation

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

7 Map analysis [i](#)

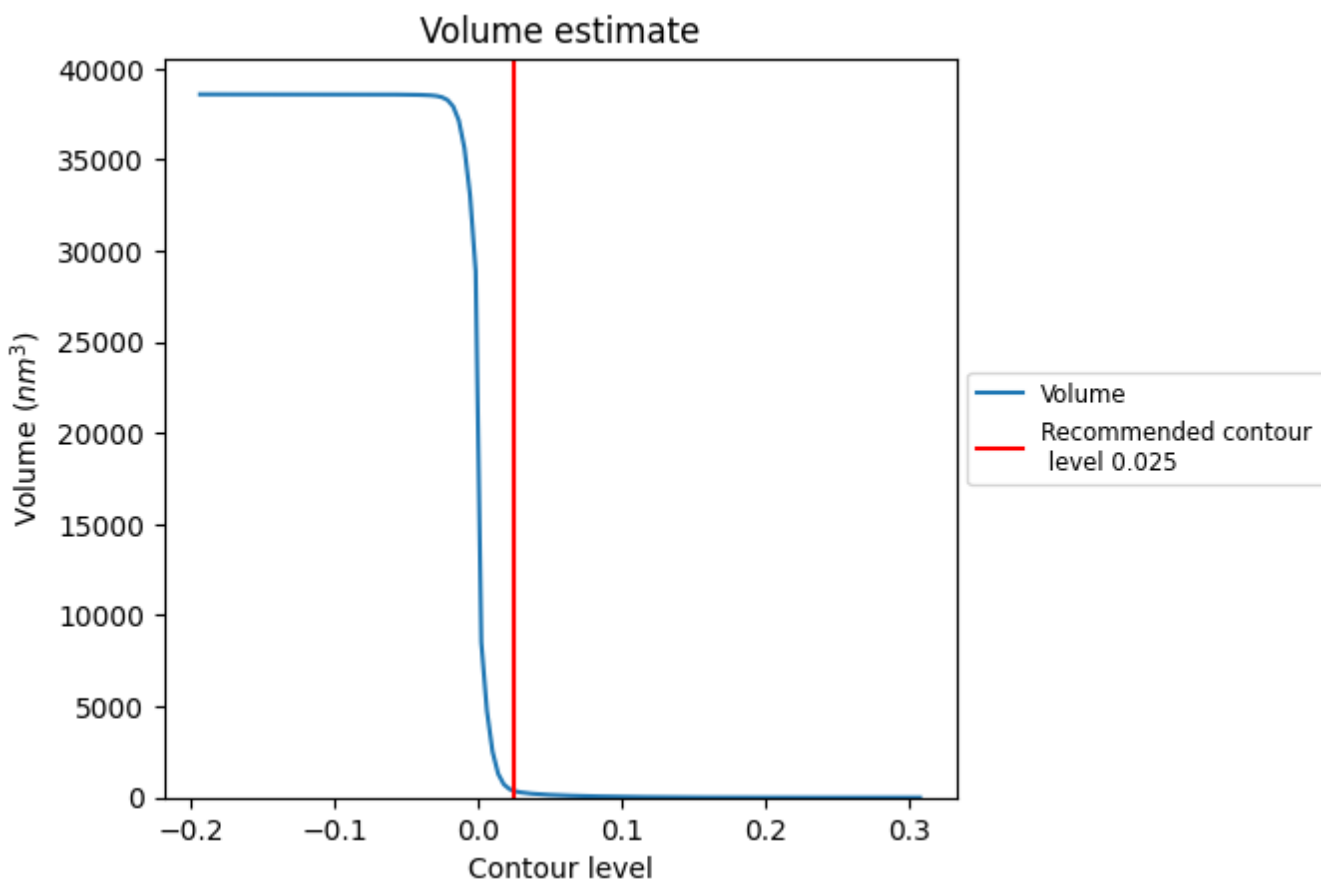
This section contains the results of statistical analysis of the map.

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.

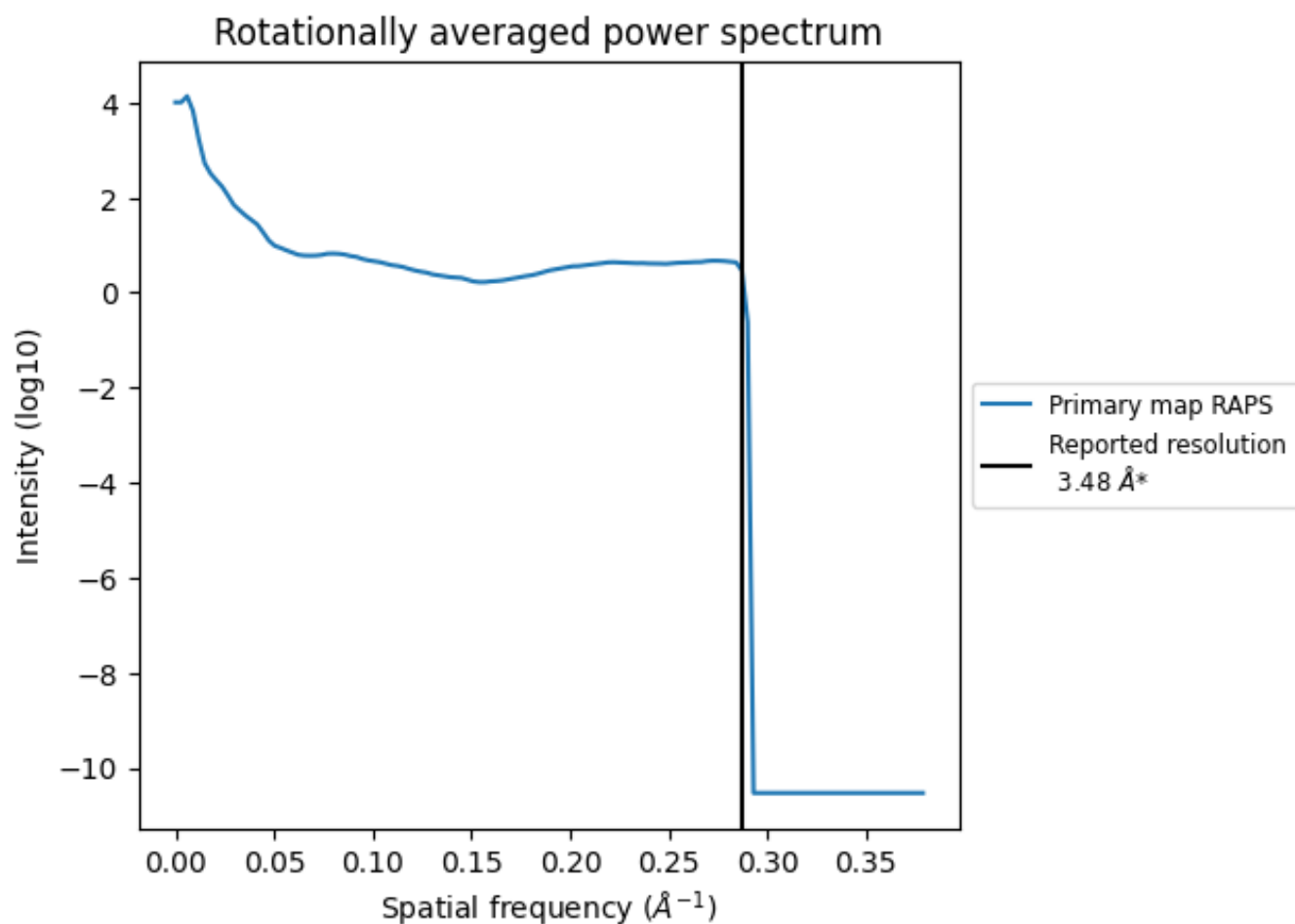
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 373 nm³; this corresponds to an approximate mass of 337 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 0.287 Å⁻¹

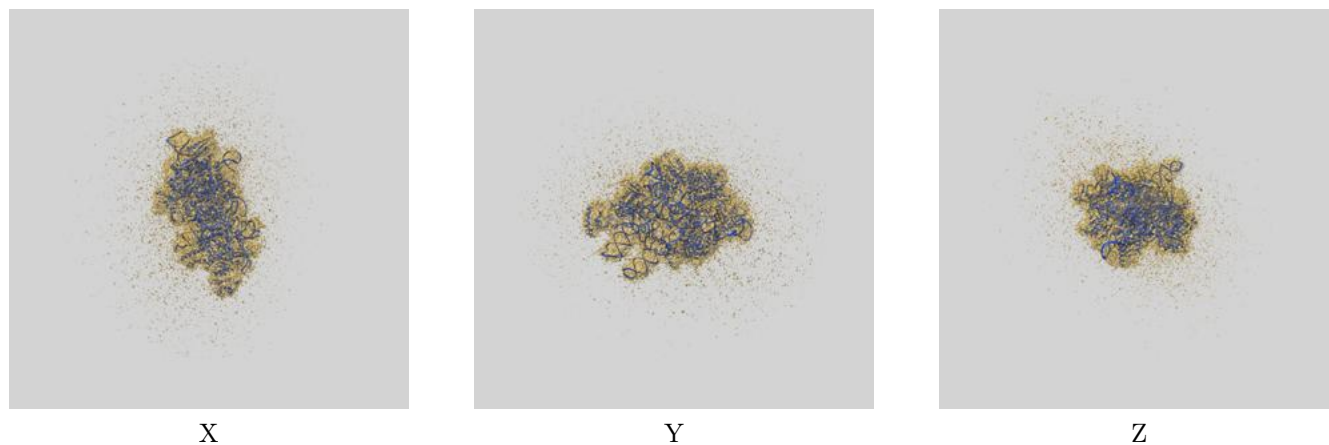
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

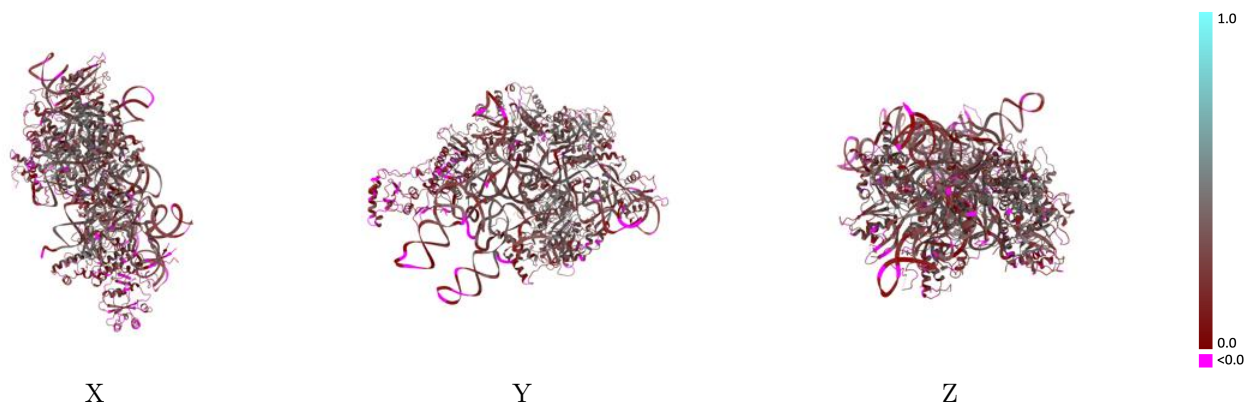
This section contains information regarding the fit between EMDB map EMD-9622 and PDB model 6AH3. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



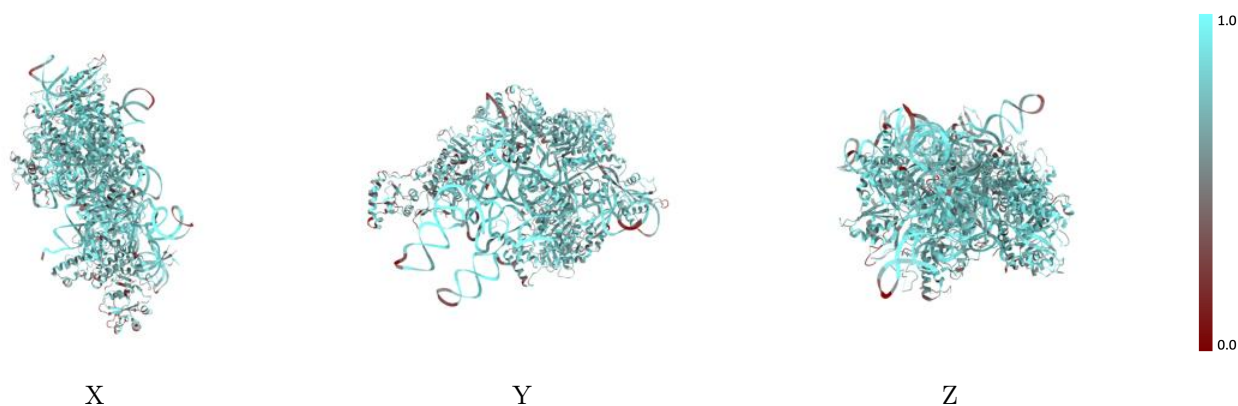
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



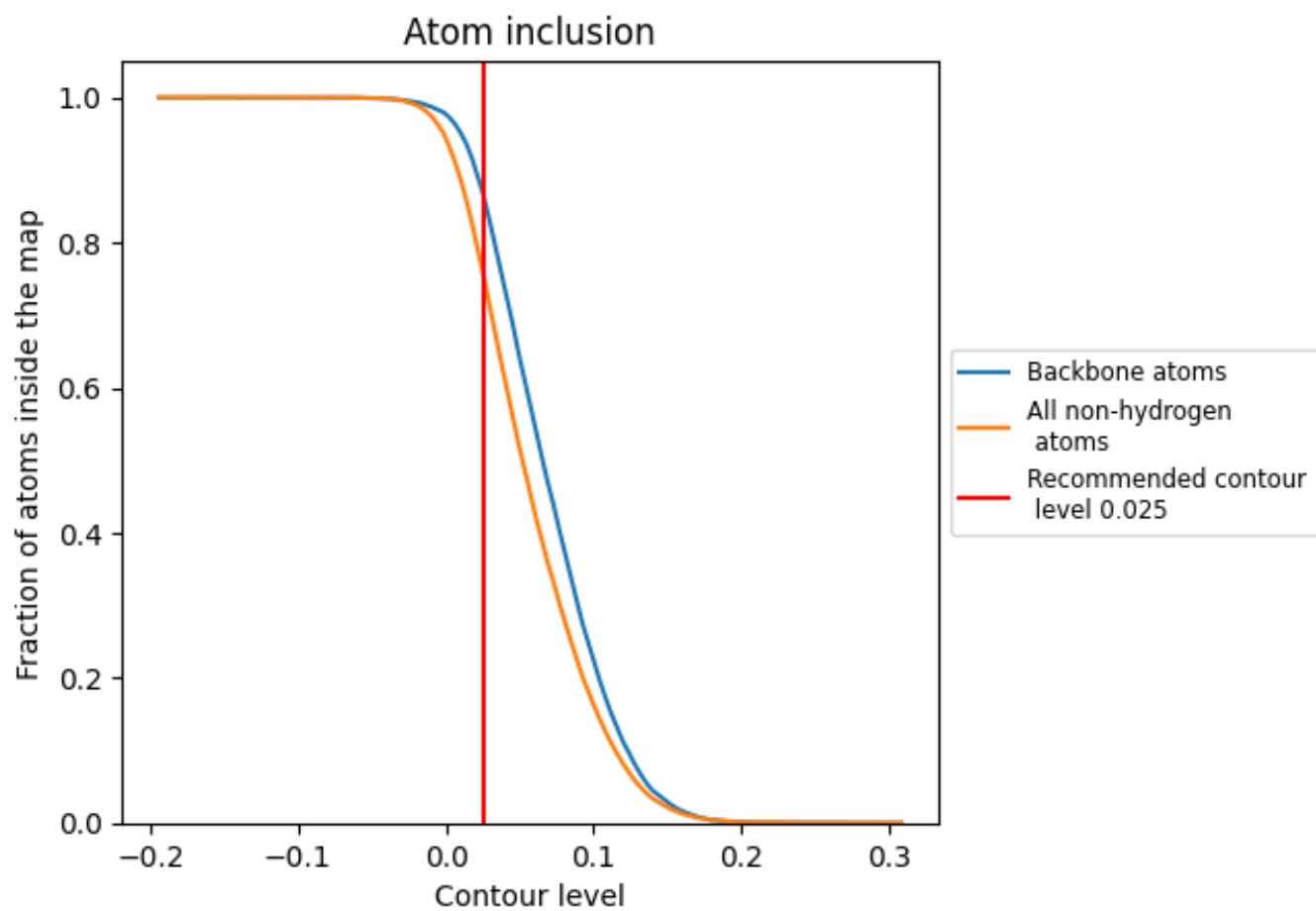
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 87% of all backbone atoms, 76% 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	 0.7594	 0.2590
A	 0.8292	 0.2620
B	 0.7472	 0.2850
C	 0.6084	 0.1040
D	 0.7048	 0.2440
E	 0.7821	 0.3160
F	 0.7127	 0.2220
G	 0.7777	 0.3120
H	 0.6616	 0.2050
I	 0.7772	 0.3020
J	 0.7485	 0.2920
K	 0.6717	 0.1620
T	 0.7769	 0.2590

