



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:50 PM UTC

PDB ID : 7LTO / pdb_00007lto
EMDB ID : EMD-23517
Title : Nse5-6 complex
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Deposited on : 2021-02-19
Resolution : 3.20 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.dev132
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) : 2.49

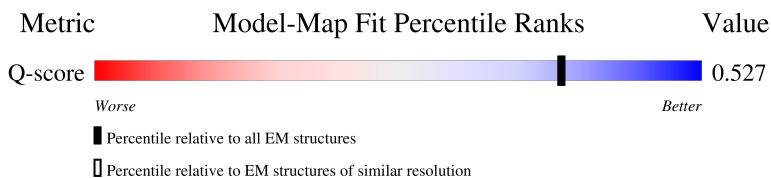
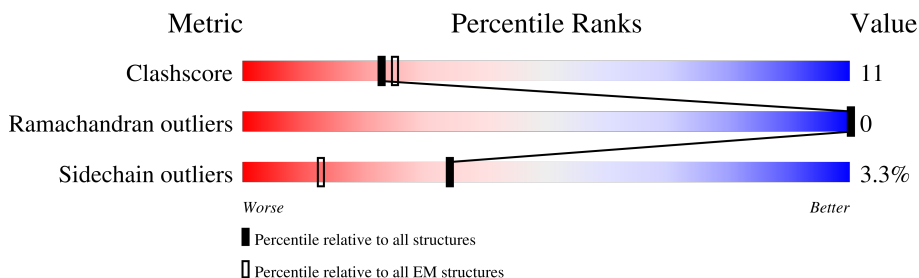
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	567	 50% 14% 35%
2	B	586	 31% 10% 59%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4754 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 Non-structural maintenance of chromosome element 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	367	Total	C	N	O	S	0	0
			2876	1865	467	530	14		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	expression tag	UNP Q03718
A	-9	ALA	-	expression tag	UNP Q03718
A	-8	ASP	-	expression tag	UNP Q03718
A	-7	LEU	-	expression tag	UNP Q03718
A	-6	ASN	-	expression tag	UNP Q03718
A	-5	TRP	-	expression tag	UNP Q03718
A	-4	ILE	-	expression tag	UNP Q03718
A	-3	SER	-	expression tag	UNP Q03718
A	-2	ALA	-	expression tag	UNP Q03718
A	-1	GLY	-	expression tag	UNP Q03718
A	0	HIS	-	expression tag	UNP Q03718

- Molecule 2 is a protein called Ubiquitin-like protein SMT3,DNA repair protein KRE29 chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	238	Total	C	N	O	S	0	0
			1878	1249	309	308	12		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-121	MET	-	expression tag	UNP Q12306
B	-120	GLY	-	expression tag	UNP Q12306
B	-119	SER	-	expression tag	UNP Q12306
B	-118	SER	-	expression tag	UNP Q12306
B	-117	HIS	-	expression tag	UNP Q12306

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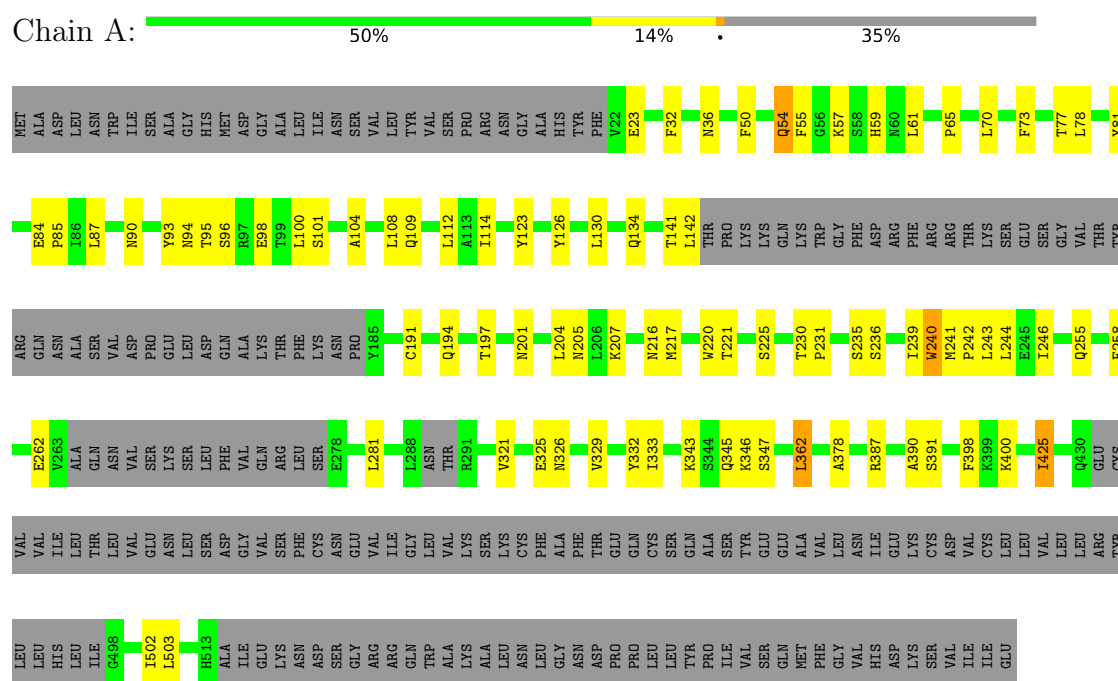
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-116	HIS	-	expression tag	UNP Q12306
B	-115	HIS	-	expression tag	UNP Q12306
B	-114	HIS	-	expression tag	UNP Q12306
B	-113	HIS	-	expression tag	UNP Q12306
B	-112	HIS	-	expression tag	UNP Q12306
B	-111	SER	-	expression tag	UNP Q12306
B	-110	SER	-	expression tag	UNP Q12306
B	-109	GLY	-	expression tag	UNP Q12306
B	-108	LEU	-	expression tag	UNP Q12306
B	-107	VAL	-	expression tag	UNP Q12306
B	-106	PRO	-	expression tag	UNP Q12306
B	-105	ARG	-	expression tag	UNP Q12306
B	-104	GLY	-	expression tag	UNP Q12306
B	-103	SER	-	expression tag	UNP Q12306
B	-102	HIS	-	expression tag	UNP Q12306
B	-101	MET	-	expression tag	UNP Q12306
B	-100	ALA	-	expression tag	UNP Q12306
B	-99	SER	-	expression tag	UNP Q12306
B	0	SER	-	linker	UNP Q12306

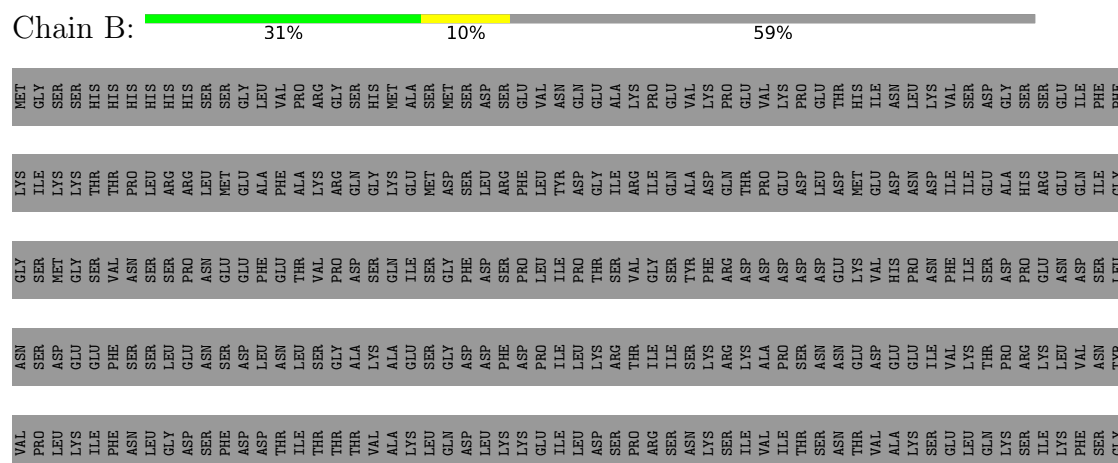
3 Residue-property plots

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: Non-structural maintenance of chromosome element 5



- Molecule 2: Ubiquitin-like protein SMT3,DNA repair protein KRE29 chimera



SER	ILE	PRO	GLU	ILE	TYR	LEU	ASP	VAL	VAL	THR	LYS	GLU	THR	ILE	SER	D195	W200	N206	Q211	D219	Y222	L225	PHE	GLY	SER	SER	ARG	SER	GLN	GLY	LYS	VAL	PRO	E237	F238	V239	K242	N248	V251	I252	F253	G254	V255	K259	CYS	ASN	SER	L263	K264
I265	N266	Y267	K270	E271	N272	T280	I281	V284	N285	M292	L308	I312	G313	L314	I315	I316	D317	A323	M324	L330	V334	L337	F338	N339	E340	A341	H342	F348	E349	I350	D355	H359	Y360	R361	Q364	L369	Q370	S379	GLU	LYS	GLN	GLY	ARG						
THR	GLU	I387	E395	F396	N397	E398	F399	K406	L413	T414	M415	Y416	K426	CYS	GLN	VAL	THR	E431	Y432	F433	S441	ASN	GLU	THR	THR	ASN	ASP	V448	E449	I456	I463	ARG																	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	188986	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	47262	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.193	Depositor
Minimum map value	-0.111	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	297.92, 297.92, 297.92	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	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	A	0.20	0/2933	0.48	2/3980 (0.1%)
2	B	0.18	0/1920	0.43	0/2583
All	All	0.19	0/4853	0.46	2/6563 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	194	GLN	N-CA-C	5.80	119.12	112.57
1	A	240	TRP	N-CA-C	5.53	119.19	112.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2876	0	2800	69	0
2	B	1878	0	1789	37	0
All	All	4754	0	4589	105	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 11.

The worst 5 of 105 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:78:LEU:CD1	1:A:87:LEU:HD11	1.66	1.24
1:A:225:SER:CB	1:A:241:MET:HE1	1.70	1.22
1:A:78:LEU:HD13	1:A:87:LEU:HD11	1.27	1.09
1:A:236:SER:O	1:A:241:MET:HB2	1.54	1.07
1:A:225:SER:HB2	1:A:241:MET:CE	1.83	1.06

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	357/567 (63%)	326 (91%)	31 (9%)	0	100	100
2	B	226/586 (39%)	204 (90%)	22 (10%)	0	100	100
All	All	583/1153 (51%)	530 (91%)	53 (9%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	307/520 (59%)	300 (98%)	7 (2%)	44	70
2	B	185/548 (34%)	176 (95%)	9 (5%)	22	55
All	All	492/1068 (46%)	476 (97%)	16 (3%)	34	65

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	395	GLU
2	B	324	MET
2	B	239	VAL
2	B	315	ILE
2	B	225	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	201	HIS
2	B	206	ASN
2	B	407	ASN
2	B	211	GLN
1	A	134	GLN

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](#)

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.

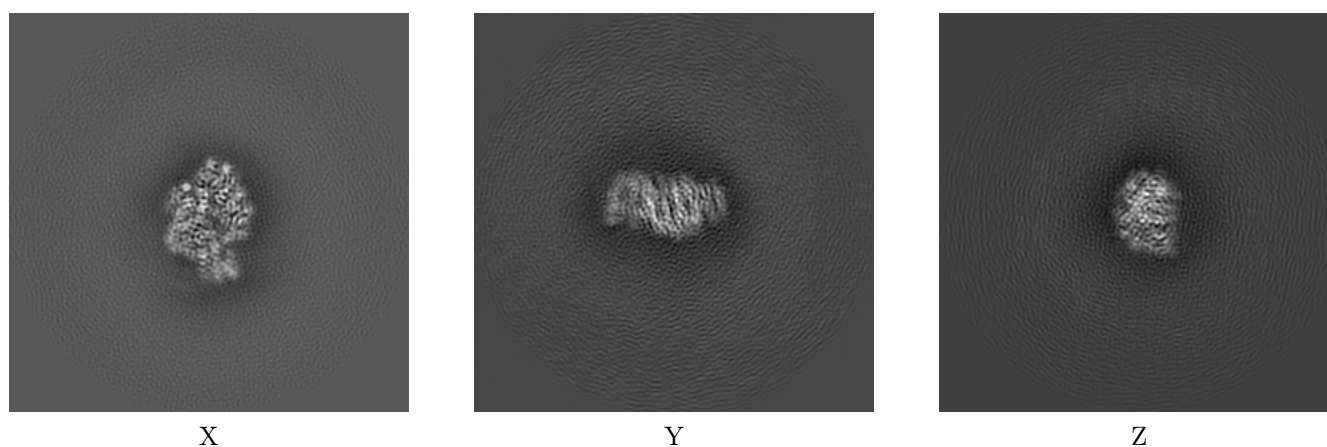
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23517. 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](#)

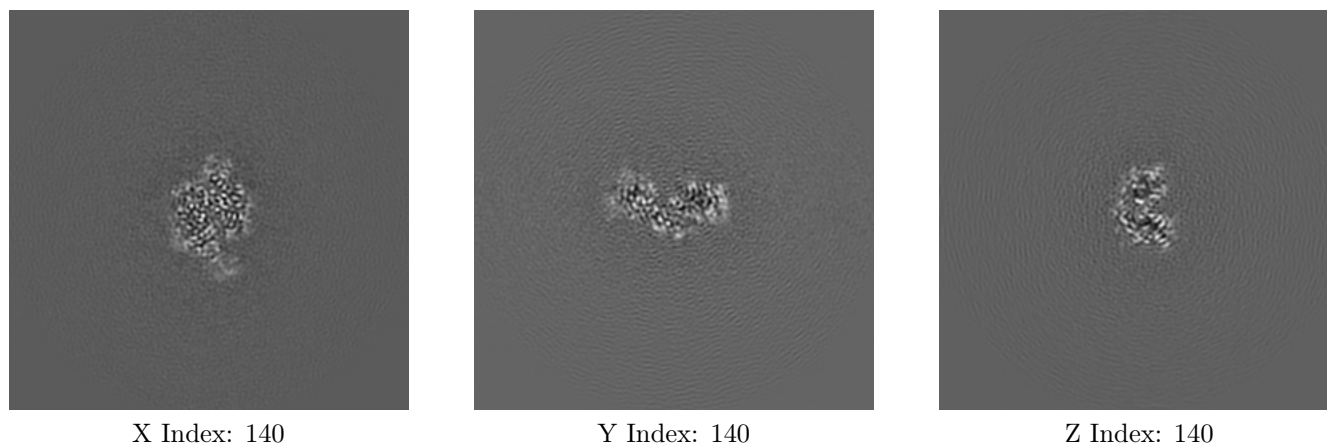
6.1.1 Primary map



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

6.2 Central slices [i](#)

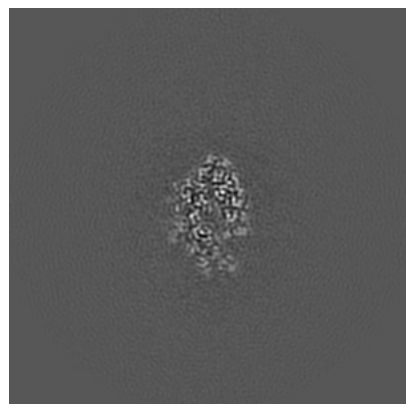
6.2.1 Primary map



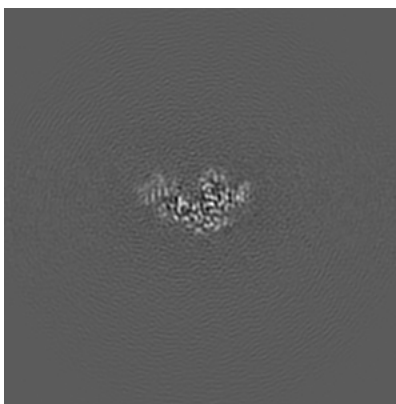
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

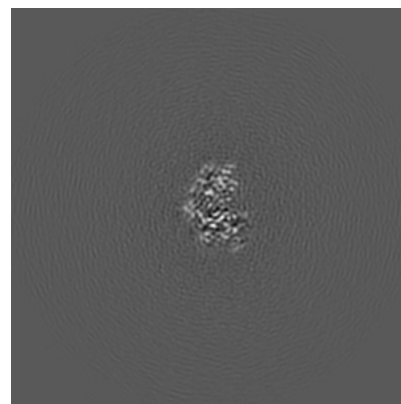
6.3.1 Primary map



X Index: 146



Y Index: 134

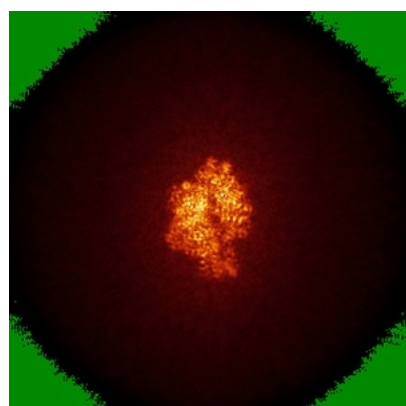


Z Index: 142

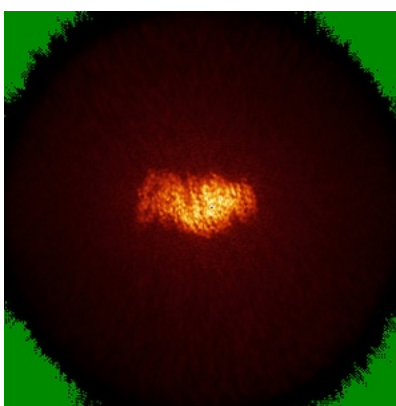
The images above show the largest variance slices of the map in three orthogonal directions.

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

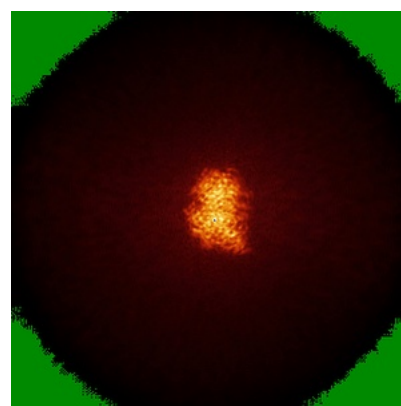
6.4.1 Primary map



X



Y

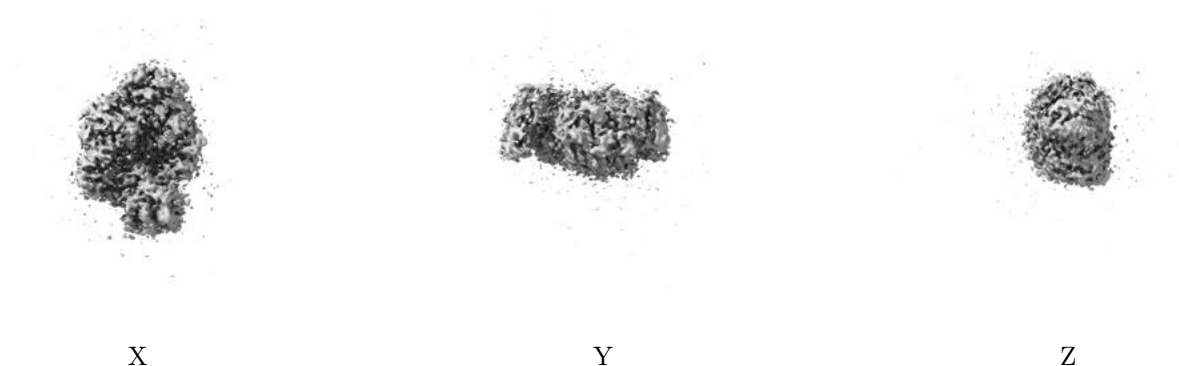


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

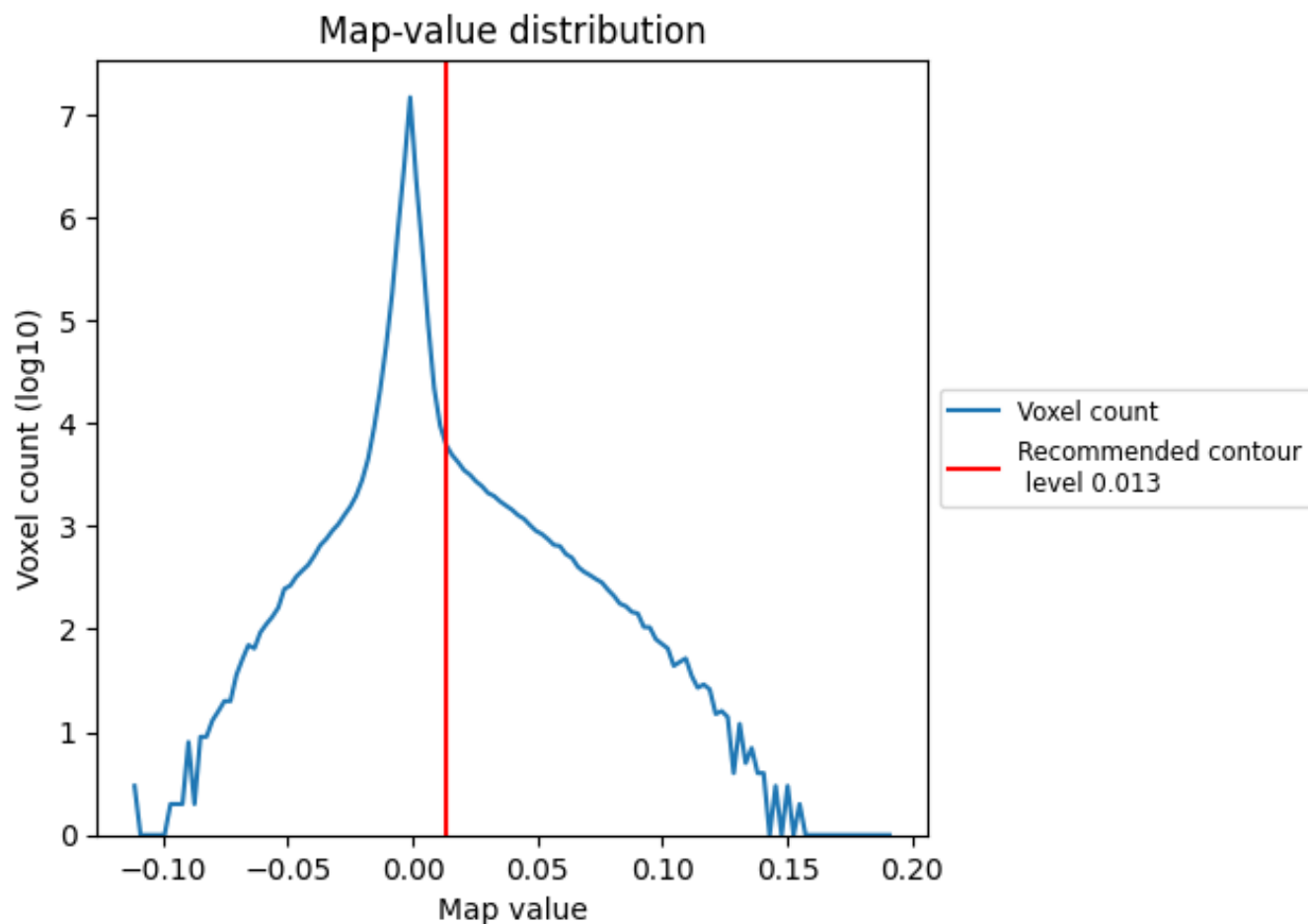
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

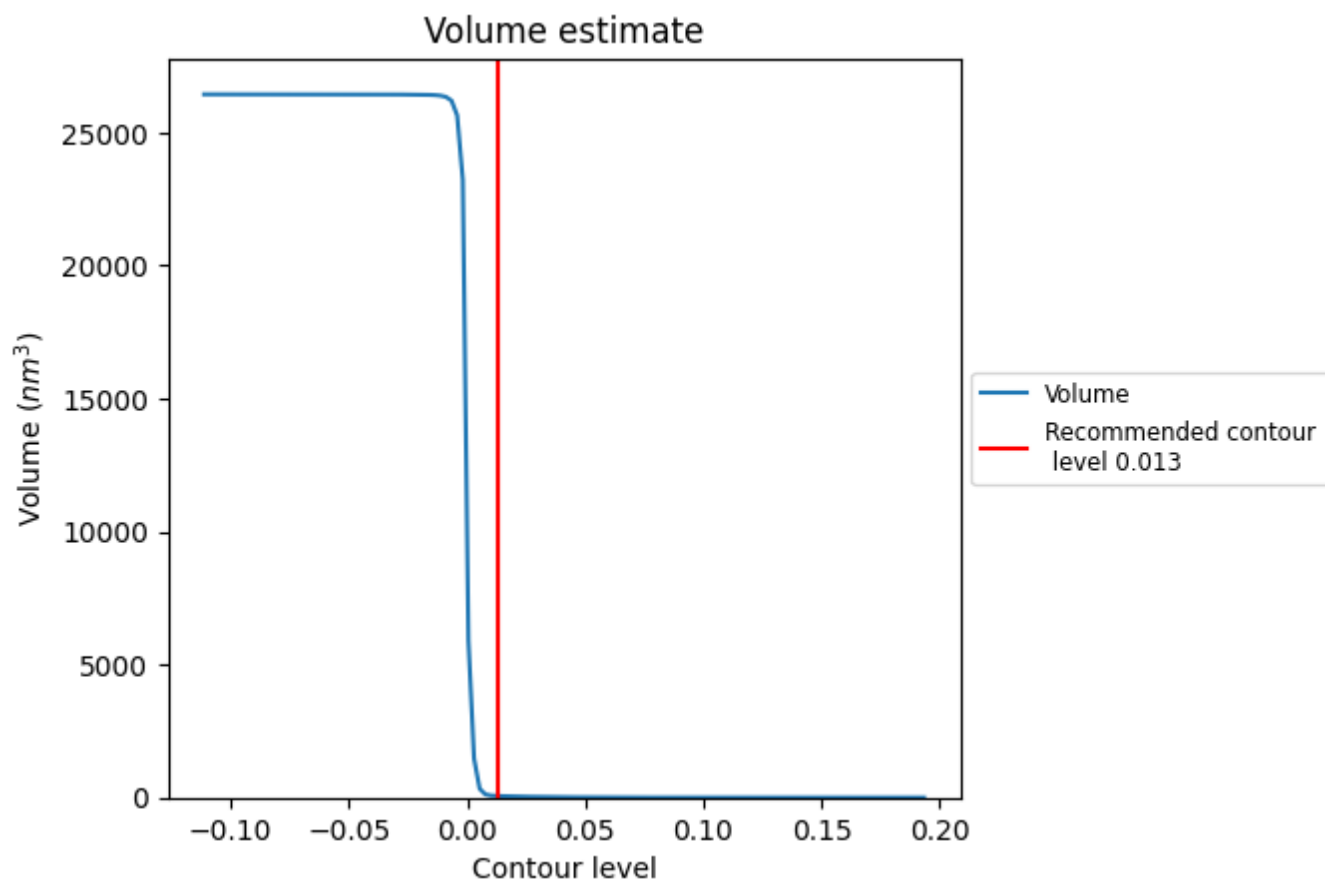
This section contains the results of statistical analysis of the map.

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.

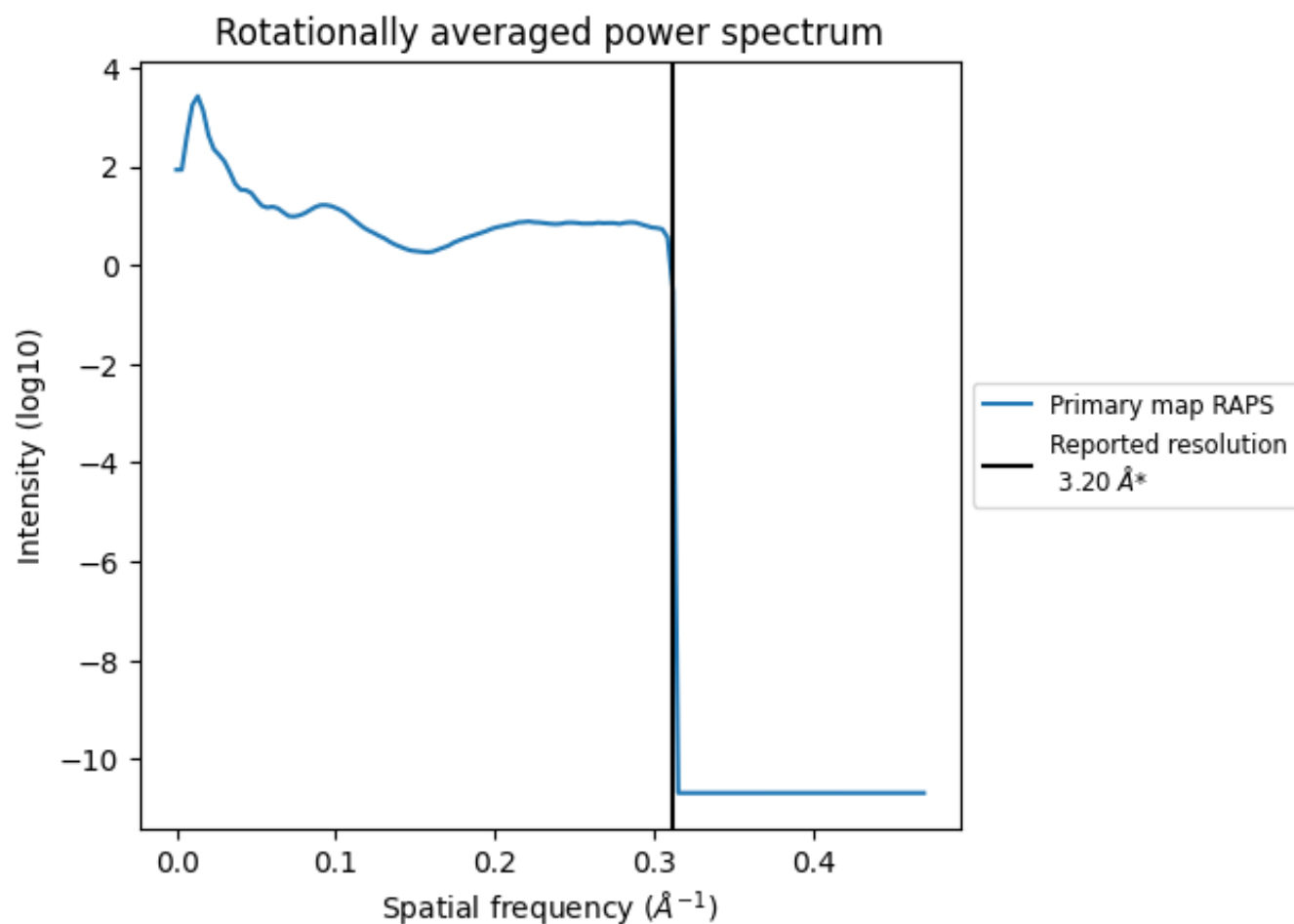
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 60 nm^3 ; this corresponds to an approximate mass of 54 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 0.312 $\text{\AA}^{-1}$

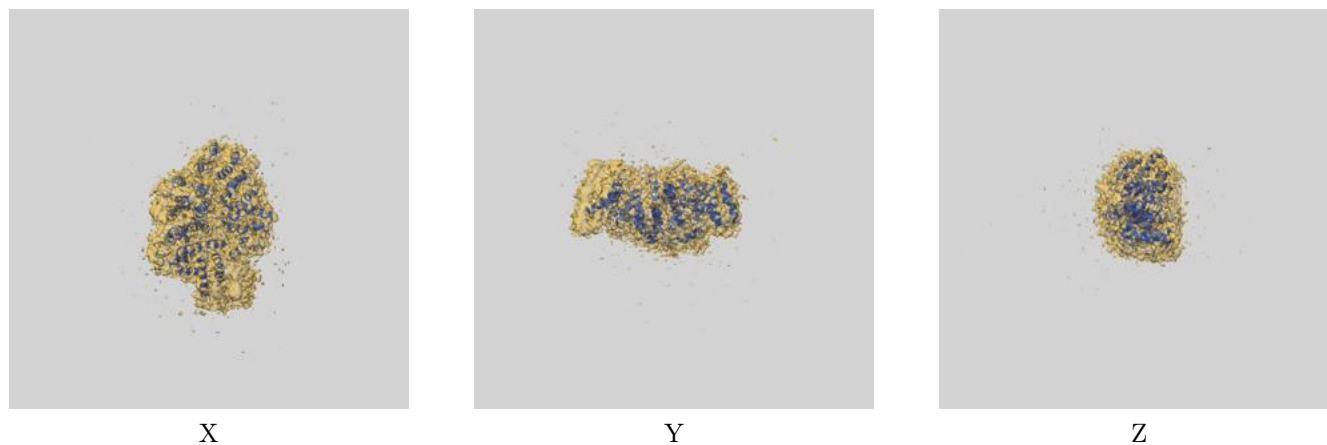
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

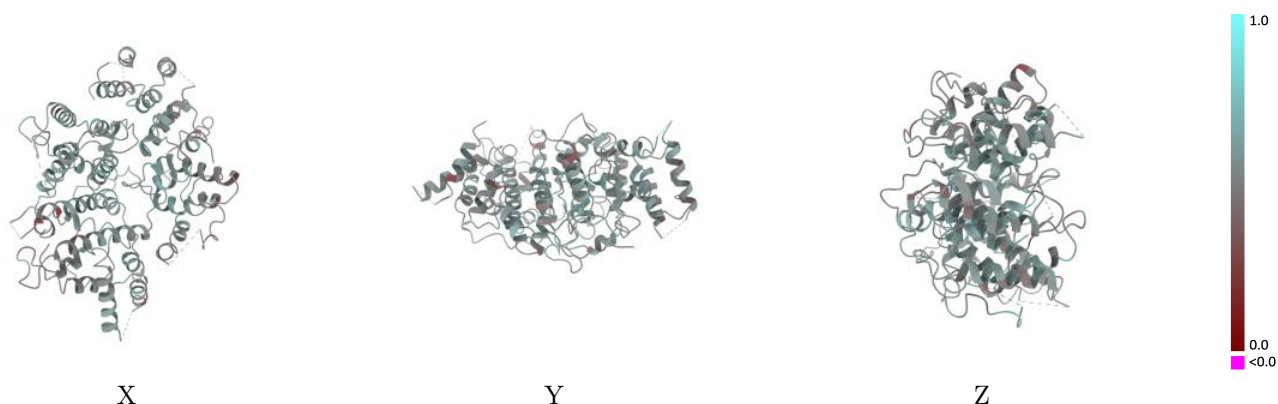
This section contains information regarding the fit between EMDB map EMD-23517 and PDB model 7LTO. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



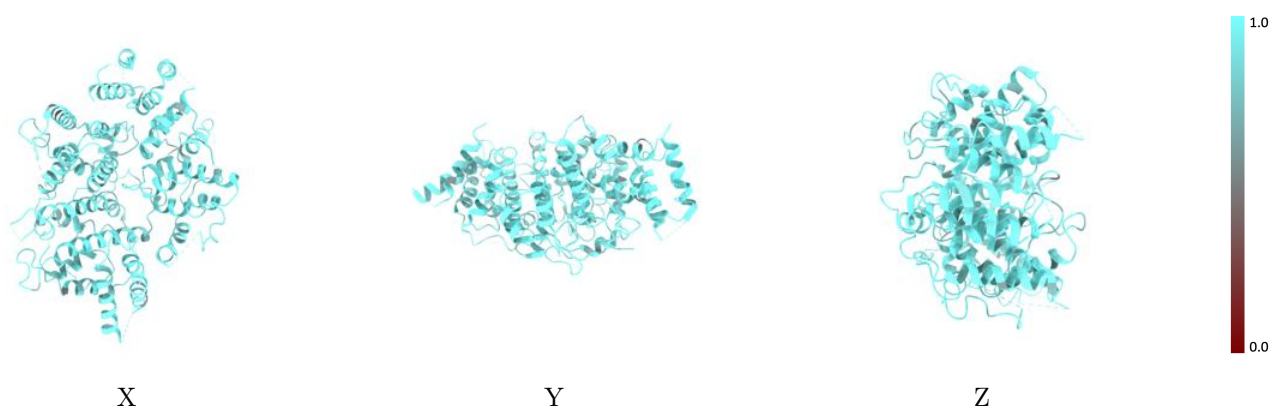
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



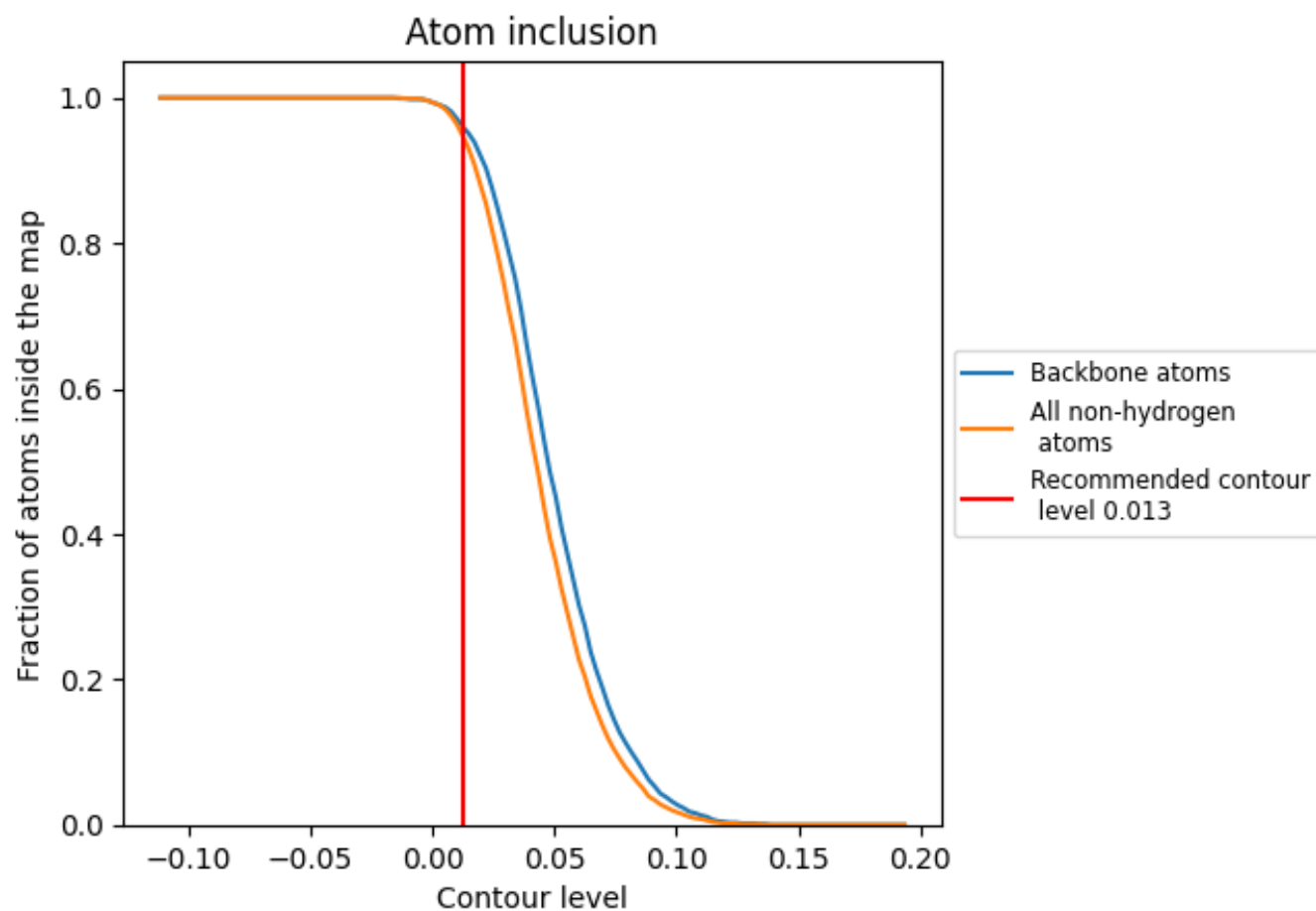
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9440	0.5270
A	0.9390	0.5290
B	0.9530	0.5250

