



wwPDB EM Validation Summary Report ⓘ

May 13, 2024 – 07:00 pm BST

PDB ID : 6Y50
EMDB ID : EMD-10688
Title : 5'domain of human 17S U2 snRNP
Authors : Zhang, Z.; Will, C.L.; Bertram, K.; Luehrmann, R.; Stark, H.
Deposited on : 2020-02-24
Resolution : 4.10 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:

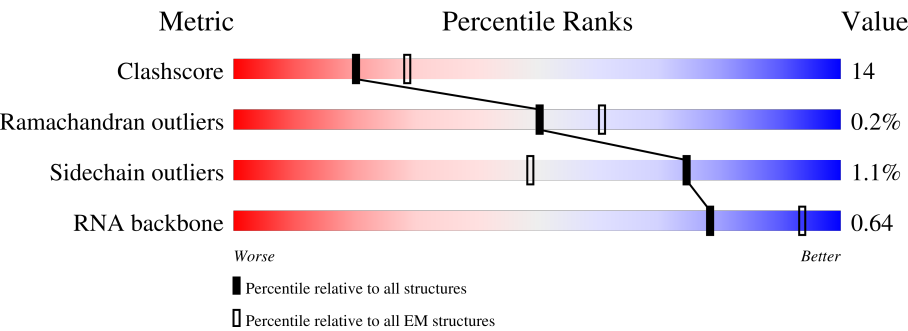
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 4.10 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	9	501	
2	y	110	
3	x	86	
4	8	895	
5	v	1217	
6	u	1304	
7	2	188	

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Mol	Chain	Length	Quality of chain
8	q	755	<div><div></div><div>6%</div><div>12%</div><div>88%</div></div>
9	p	1031	<div><div></div><div>5%</div><div>95%</div></div>

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 14916 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 Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	9	107	Total	C	N	O	0	0
			537	323	107	107		

- Molecule 2 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	y	93	Total	C	N	O	S	0	0
			554	341	112	99	2		

- Molecule 3 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	x	66	Total	C	N	O	S	0	0
			540	343	94	98	5		

- Molecule 4 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	8	107	Total	C	N	O	0	0
			552	336	109	107		

- Molecule 5 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	v	1177	Total	C	N	O	S	0	0
			6500	4042	1237	1218	3		

- Molecule 6 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	u	842	Total	C	N	O	S	0	0
			4500	2758	873	865	4		

- Molecule 7 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	2	50	Total	C	N	O	P	0	0
			1056	473	177	356	50		

- Molecule 8 is a protein called HIV Tat-specific factor 1.

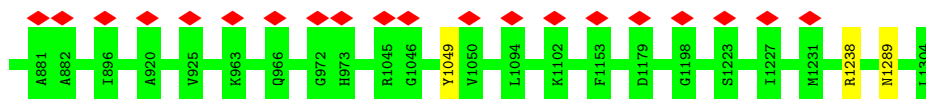
Mol	Chain	Residues	Atoms				AltConf	Trace
8	q	94	Total	C	N	O	0	0
			470	282	94	94		

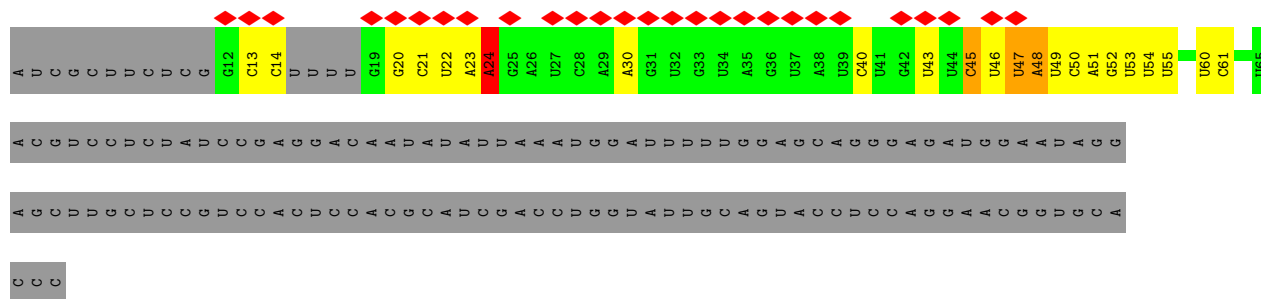
- Molecule 9 is a protein called Probable ATP-dependent RNA helicase DDX46.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	p	51	Total	C	N	O	0	0
			204	102	51	51		

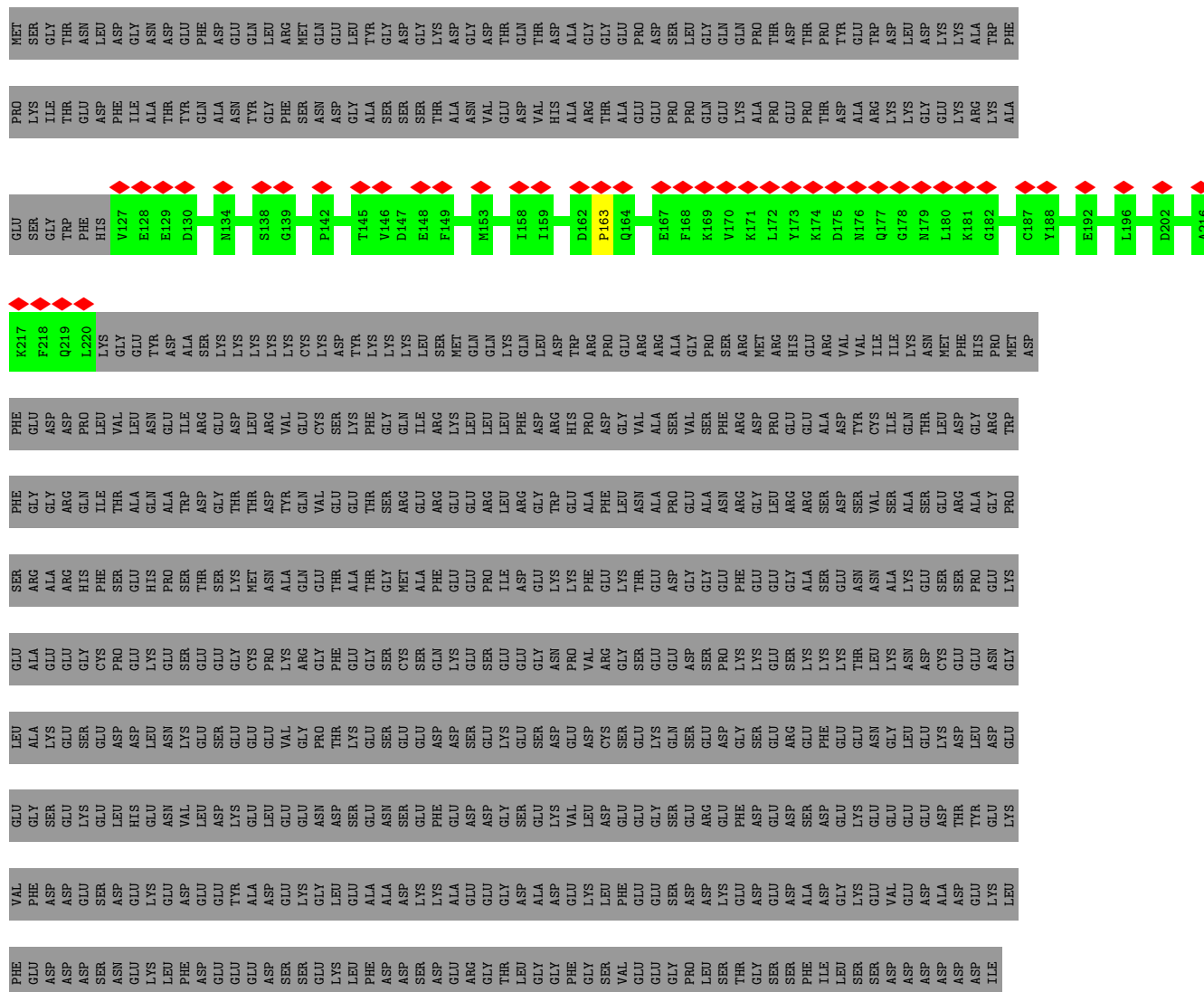
- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
10	y	3	Total	Zn	0
			3	3	





- Molecule 8: HIV Tat-specific factor 1



- Molecule 9: Probable ATP-dependent RNA helicase DDX46





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	120070	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 ($e^-/\text{\AA}^2$)	72	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.156	Depositor
Minimum map value	-0.088	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.038	Depositor
Map size (Å)	348.0, 348.0, 348.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	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

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	9	0.34	0/540	0.45	0/754
2	y	0.23	0/563	0.41	0/768
3	x	0.24	0/556	0.38	0/751
4	8	0.23	0/559	0.43	0/783
5	v	0.25	0/6605	0.45	0/9180
6	u	0.24	0/4559	0.39	0/6358
7	2	0.38	1/1177 (0.1%)	0.75	1/1827 (0.1%)
8	q	0.23	0/472	0.41	0/658
9	p	0.61	0/203	0.58	0/252
All	All	0.27	1/15234 (0.0%)	0.46	1/21331 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	2	45	C	O3'-P	-11.52	1.47	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	2	24	A	O3'-P-O5'	5.56	114.57	104.00

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	9	537	0	263	8	0
2	y	554	0	373	0	0
3	x	540	0	509	0	0
4	8	552	0	276	4	0
5	v	6500	0	3917	0	0
6	u	4500	0	2532	0	0
7	2	1056	0	533	15	0
8	q	470	0	214	0	0
9	p	204	0	56	0	0
10	y	3	0	0	0	0
All	All	14916	0	8673	24	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 14.

The worst 5 of 24 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)
1:9:405:ASN:HA	1:9:417:ARG:O	1.84	0.78
7:2:47:U:H3'	7:2:48:A:H5'	1.70	0.73
7:2:54:U:H2'	7:2:55:U:C6	2.37	0.59
7:2:20:G:H2'	7:2:21:C:C6	2.38	0.59
7:2:45:C:H5''	7:2:46:U:H5'	1.89	0.54

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	9	105/501 (21%)	91 (87%)	14 (13%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	y	91/110 (83%)	83 (91%)	8 (9%)	0	100	100
3	x	64/86 (74%)	58 (91%)	6 (9%)	0	100	100
4	8	103/895 (12%)	91 (88%)	12 (12%)	0	100	100
5	v	1165/1217 (96%)	1096 (94%)	69 (6%)	0	100	100
6	u	840/1304 (64%)	815 (97%)	24 (3%)	1 (0%)	51	84
8	q	92/755 (12%)	84 (91%)	7 (8%)	1 (1%)	14	50
9	p	49/1031 (5%)	39 (80%)	8 (16%)	2 (4%)	3	25
All	All	2509/5899 (42%)	2357 (94%)	148 (6%)	4 (0%)	50	80

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	p	185	LEU
6	u	1049	TYR
9	p	184	GLU
8	q	163	PRO

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	9	4/446 (1%)	4 (100%)	0	100	100
2	y	22/95 (23%)	22 (100%)	0	100	100
3	x	57/77 (74%)	57 (100%)	0	100	100
4	8	9/776 (1%)	9 (100%)	0	100	100
5	v	188/1051 (18%)	186 (99%)	2 (1%)	73	84
6	u	94/1104 (8%)	92 (98%)	2 (2%)	53	72
8	q	3/661 (0%)	3 (100%)	0	100	100
All	All	377/4210 (9%)	373 (99%)	4 (1%)	74	84

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

Mol	Chain	Res	Type
5	v	128	ARG
5	v	429	ARG
6	u	1238	ARG
6	u	1289	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
6	u	1289	ASN
6	u	1256	HIS
6	u	1186	GLN
5	v	1096	HIS
6	u	1213	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	2	48/188 (25%)	6 (12%)	0

5 of 6 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	2	22	U
7	2	23	A
7	2	24	A
7	2	43	U
7	2	47	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

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.

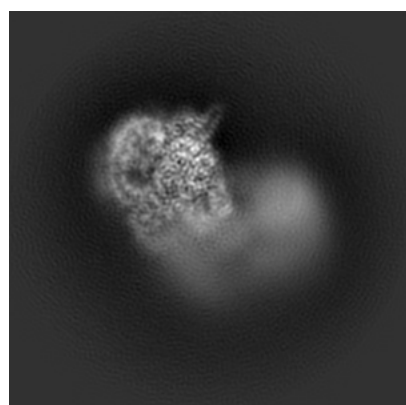
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10688. These allow visual inspection of the internal detail of the map and identification of artifacts.

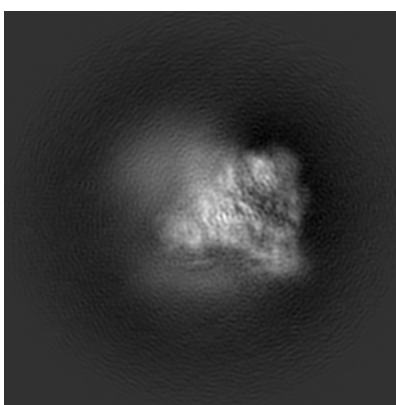
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

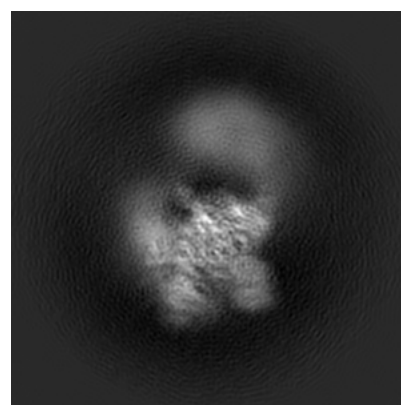
6.1.1 Primary map



X



Y

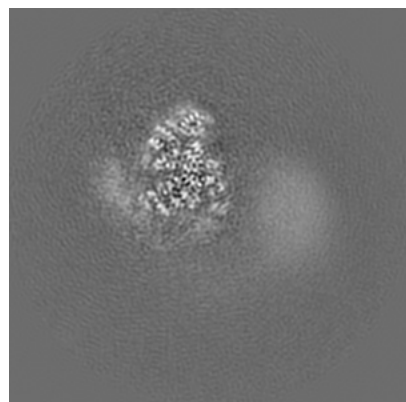


Z

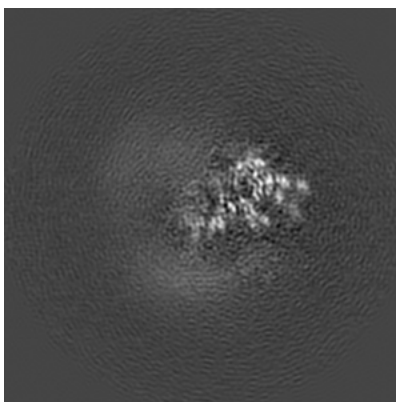
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

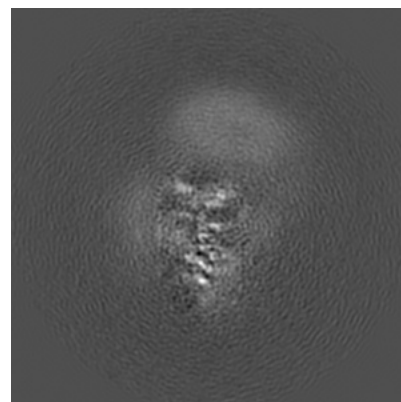
6.2.1 Primary map



X Index: 150



Y Index: 150

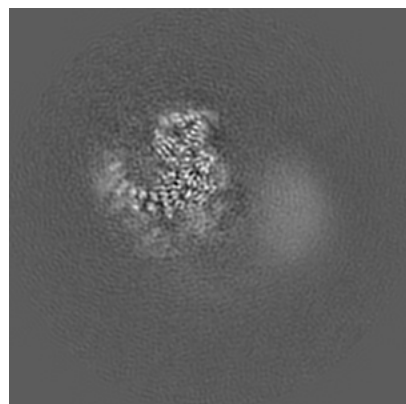


Z Index: 150

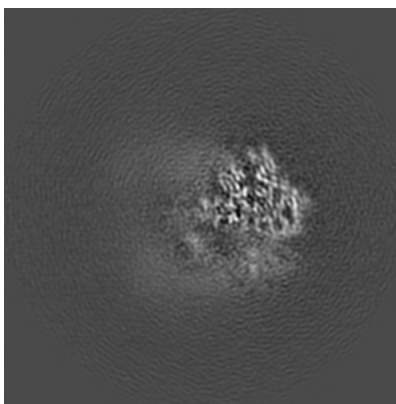
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

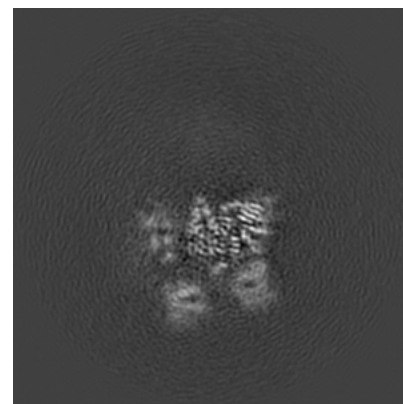
6.3.1 Primary map



X Index: 144



Y Index: 136

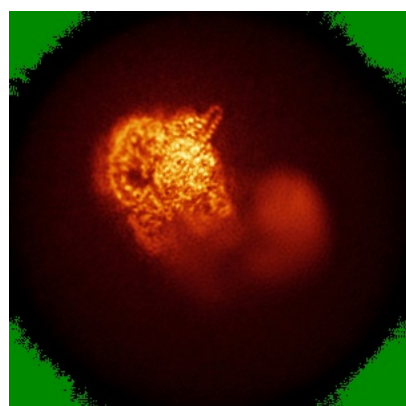


Z Index: 189

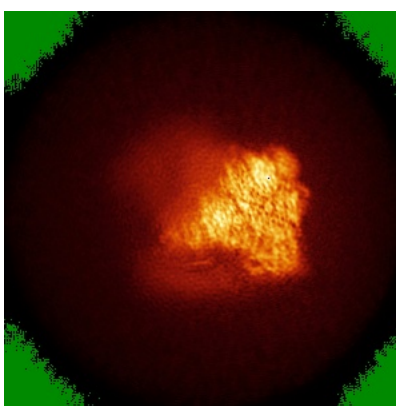
The images above show the largest variance slices of the map in three orthogonal directions.

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

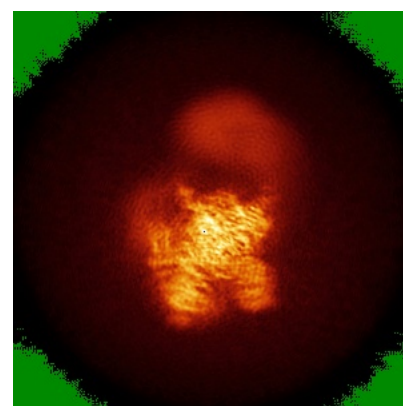
6.4.1 Primary map



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

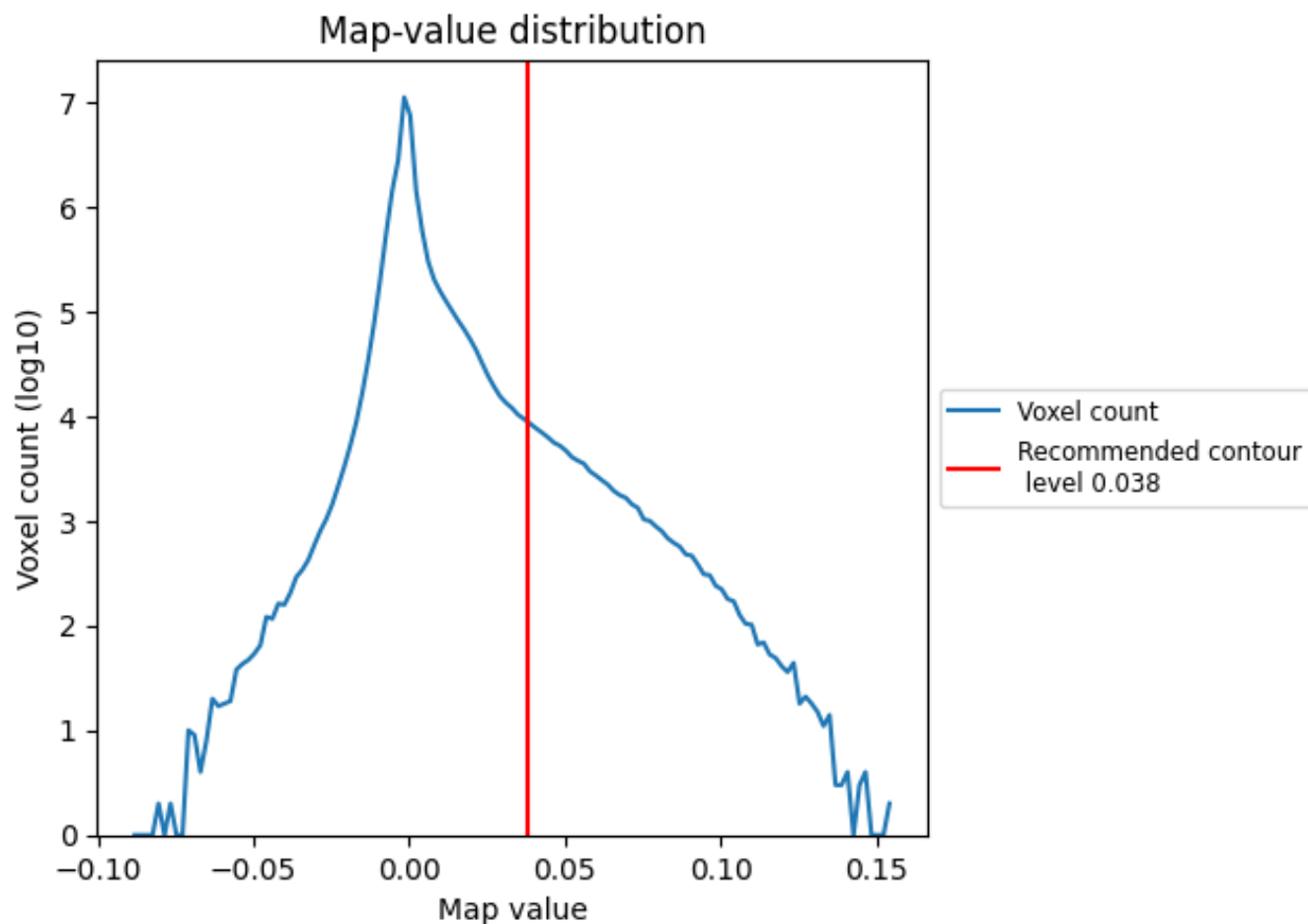
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

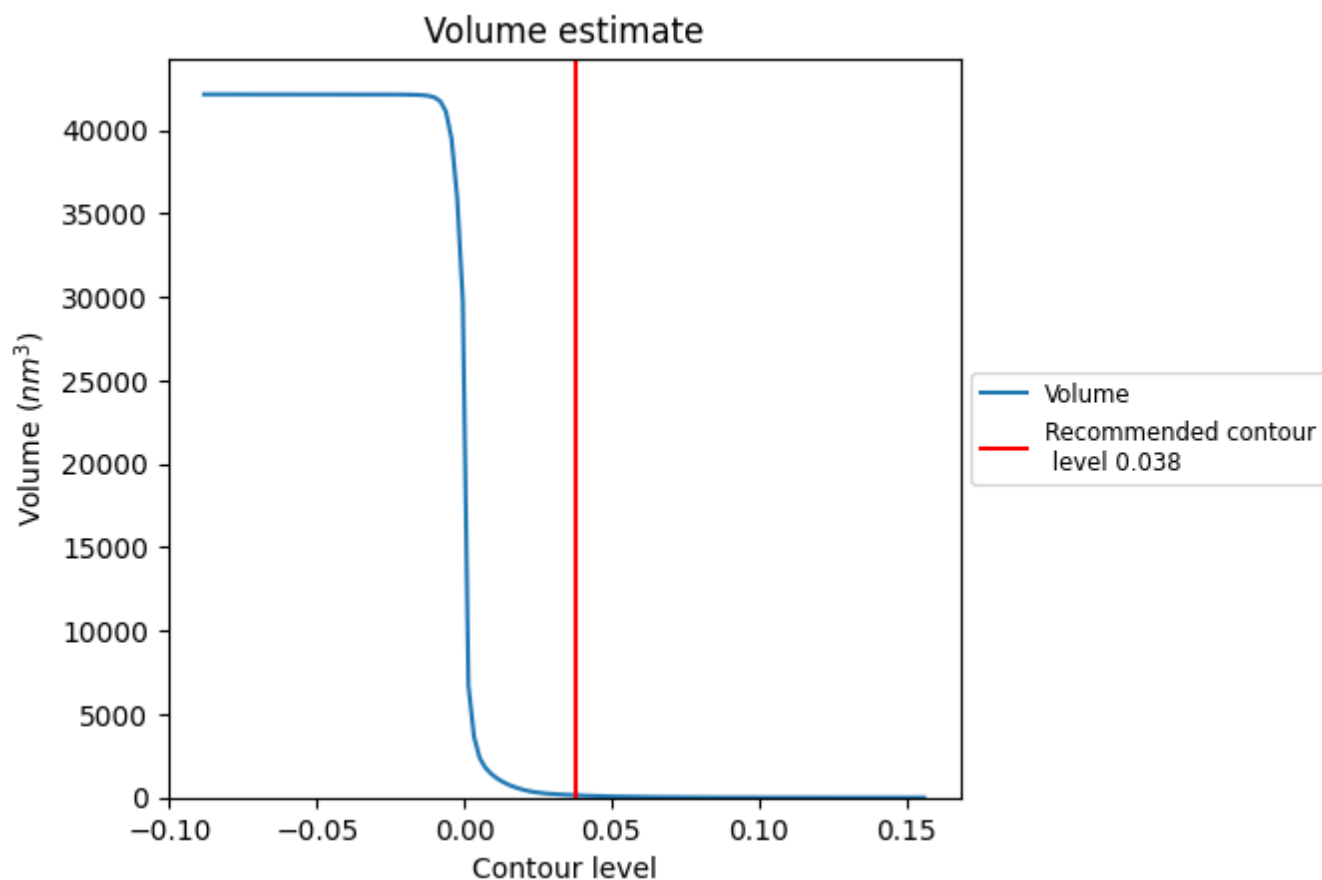
This section contains the results of statistical analysis of the map.

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.

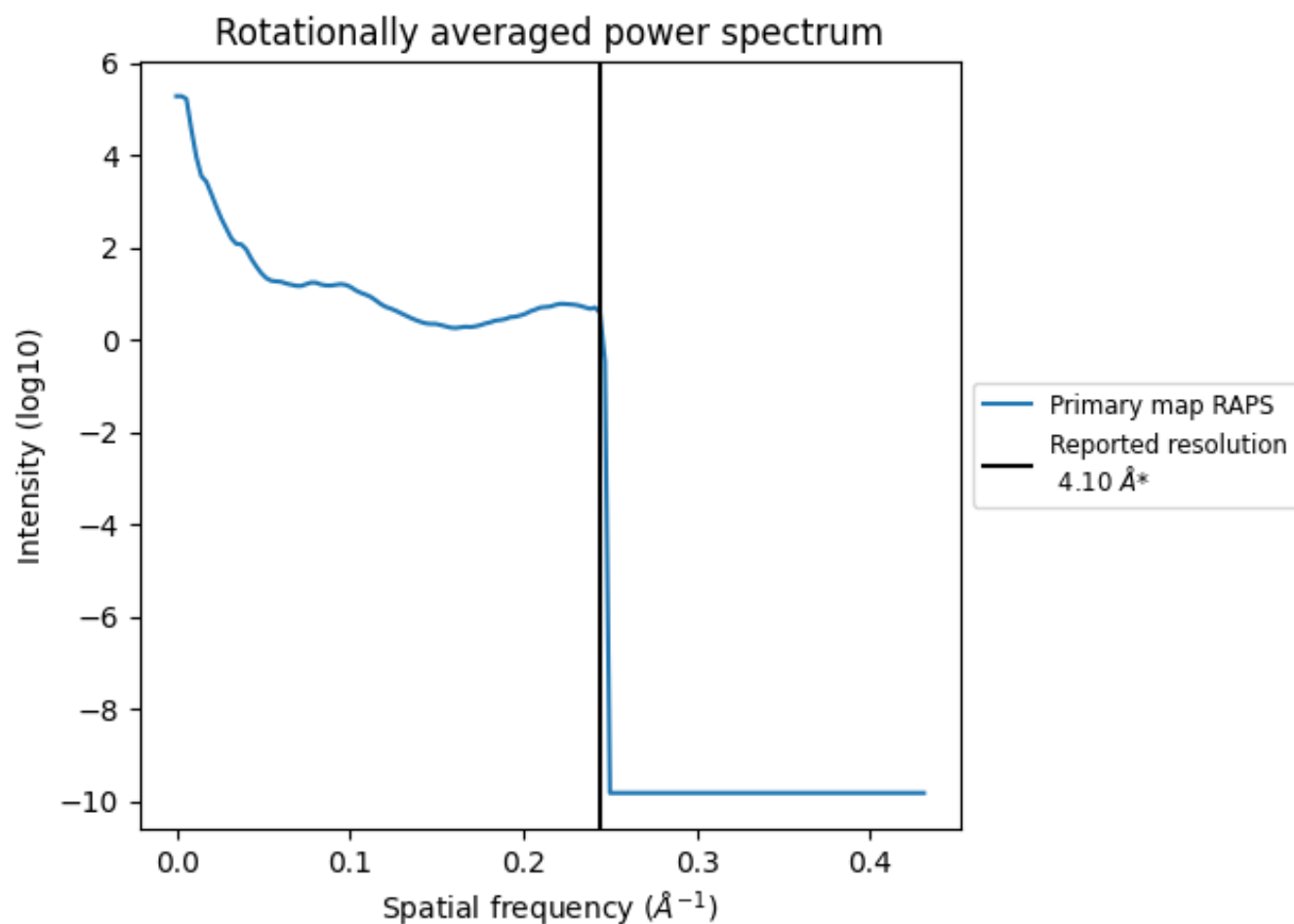
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 136 nm³; this corresponds to an approximate mass of 123 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 0.244 Å⁻¹

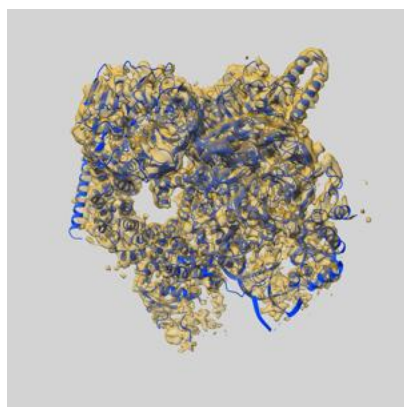
8 Fourier-Shell correlation

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

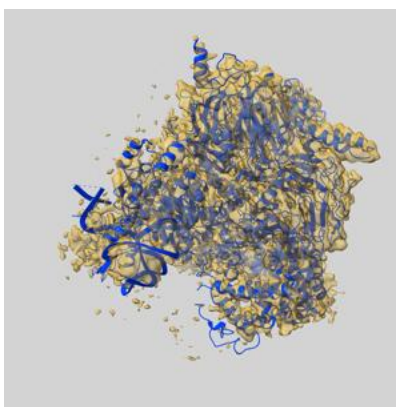
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10688 and PDB model 6Y50. Per-residue inclusion information can be found in section [3](#) on page [6](#).

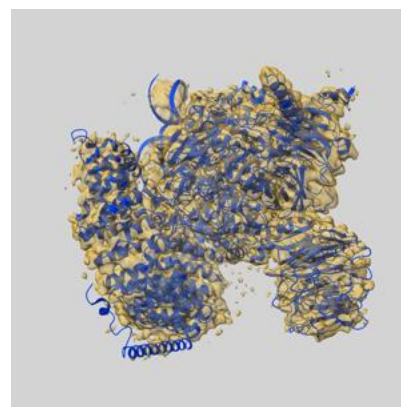
9.1 Map-model overlay [i](#)



X



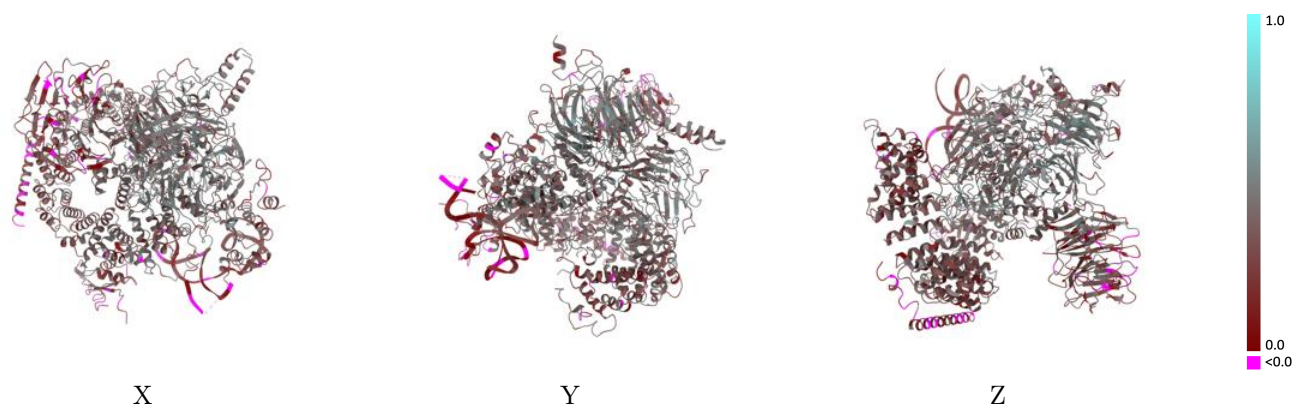
Y



Z

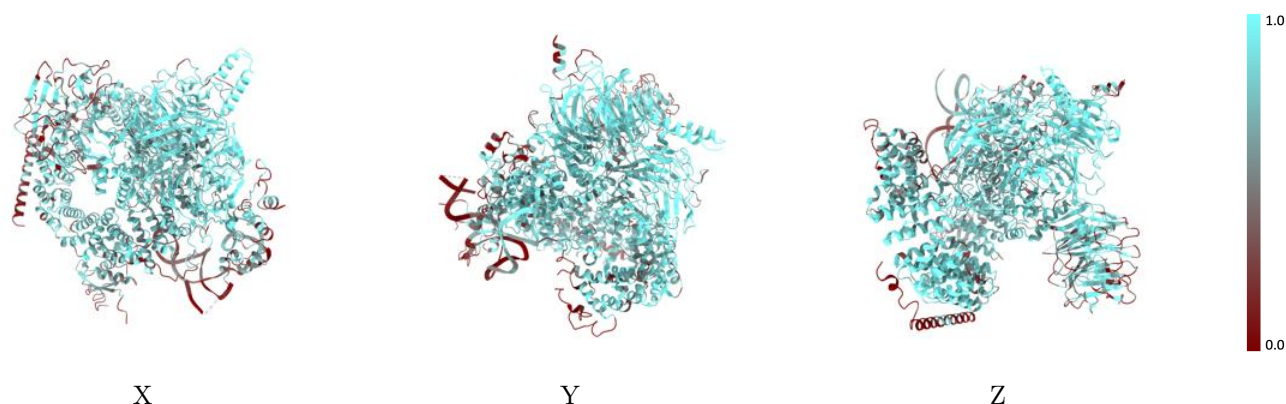
The images above show the 3D surface view of the map at the recommended contour level 0.038 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



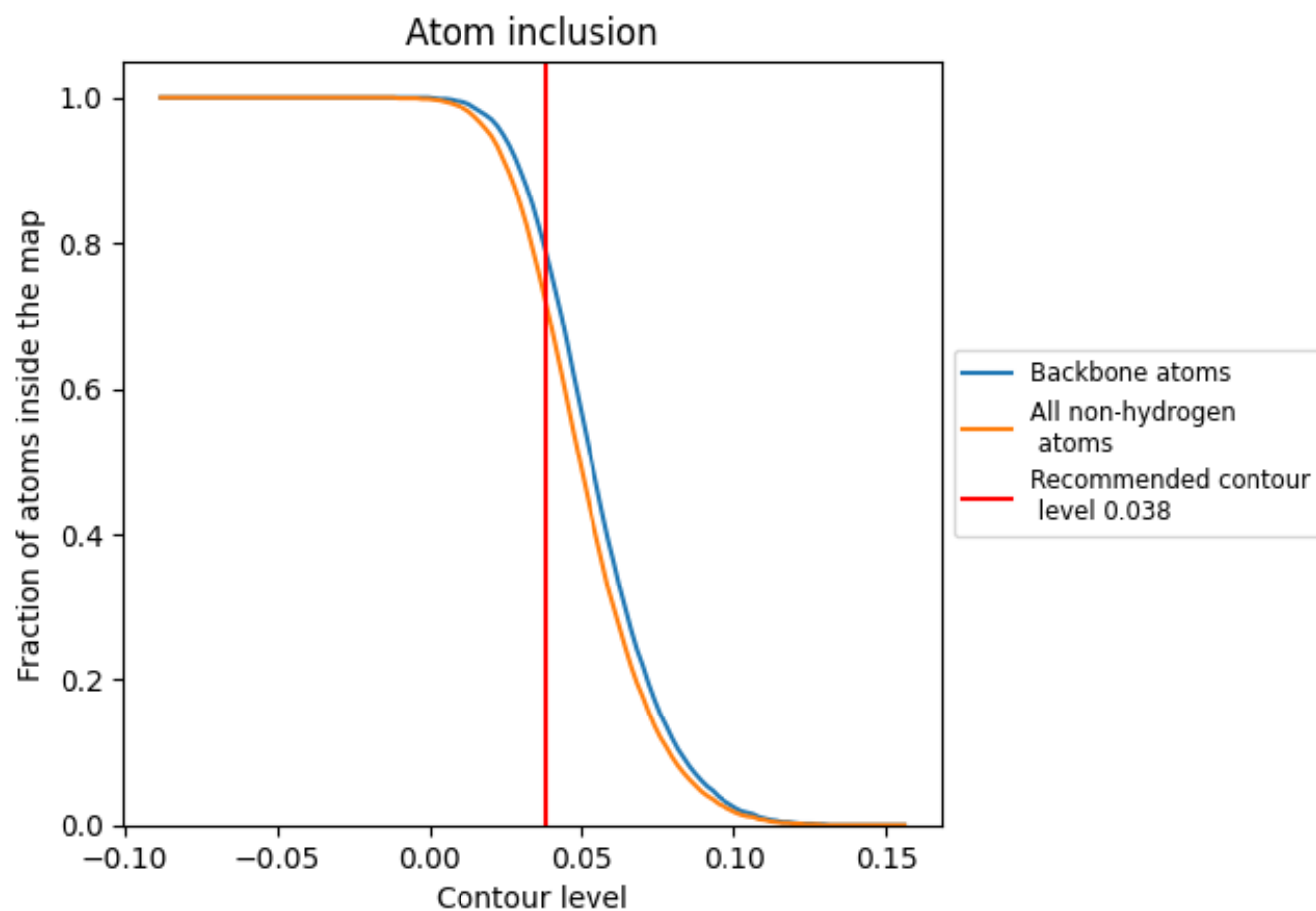
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.038).





















9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 72% 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 (0.038) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7230	 0.3510
2	 0.3610	 0.1290
8	 0.6320	 0.4010
9	 0.4920	 0.3180
p	 0.1320	 0.0800
q	 0.4910	 0.2290
u	 0.7880	 0.3480
v	 0.7990	 0.3970
x	 0.7100	 0.3830
y	 0.7400	 0.4190

