



wwPDB EM Validation Summary Report ⓘ

Jun 9, 2025 – 12:34 PM JST

PDB ID : 9JNZ / pdb_00009jnz
EMDB ID : EMD-61632
Title : Structure of isw1-nucleosome complex in Apo state
Authors : Sia, Y.; Pan, H.; Chen, Z.
Deposited on : 2024-09-24
Resolution : 3.00 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

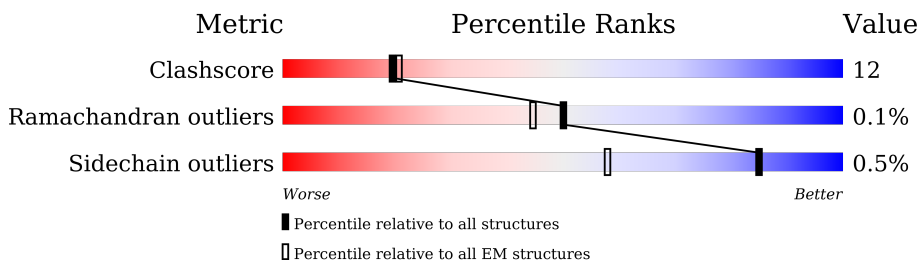
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.




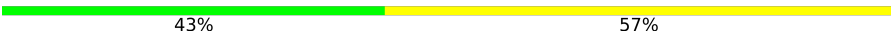

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	135	
1	E	135	
2	B	102	
2	F	102	
3	C	129	
3	G	129	
4	D	122	
4	H	122	

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Mol	Chain	Length	Quality of chain
5	I	146	 43% 57%
6	J	146	 43% 57%
7	K	1061	 11% 30% 19% 51%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 16323 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 Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	98	Total	C	N	O	S	0	0
			801	506	153	139	3		
1	E	95	Total	C	N	O	S	0	0
			779	492	148	136	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	F	86	Total	C	N	O	S	0	0
			672	424	130	117	1		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	107	Total	C	N	O	0	0
			811	510	158	143		
3	G	107	Total	C	N	O	0	0
			815	513	159	143		

- Molecule 4 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	93	Total	C	N	O	S	0	0
			718	451	128	137	2		
4	H	93	Total	C	N	O	S	0	0
			726	457	130	137	2		

- Molecule 5 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		

- Molecule 6 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		

- Molecule 7 is a protein called ISWI chromatin-remodeling complex ATPase ISW1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	525	Total	C	N	O	S	0	0
			4311	2760	741	797	13		

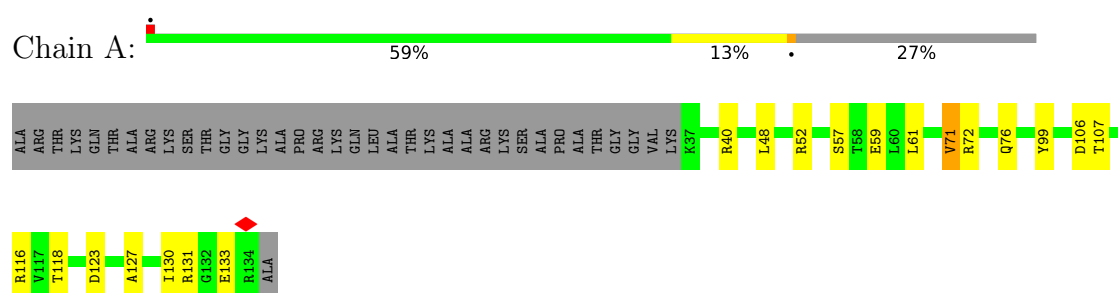
- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
8	K	1	Total	Cl	0
			1	1	

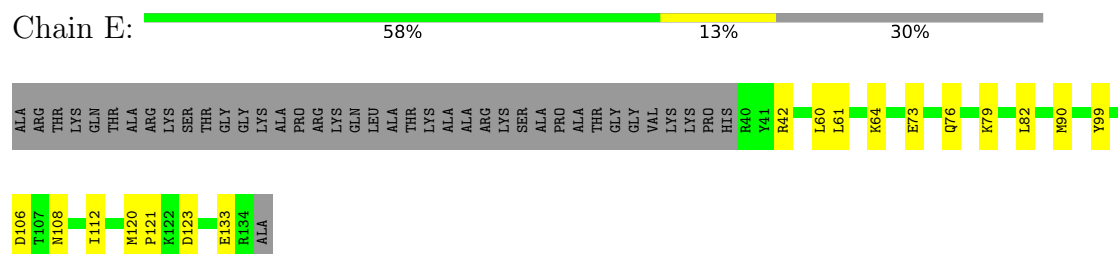
3 Residue-property plots [i](#)

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.

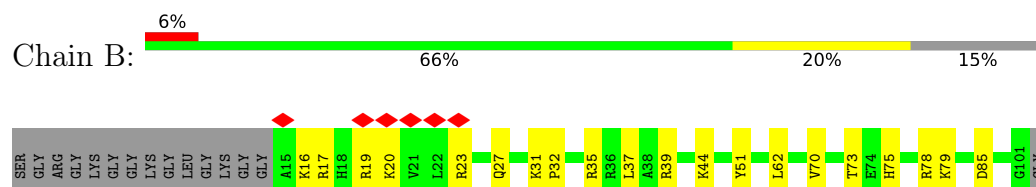
• Molecule 1: Histone H3



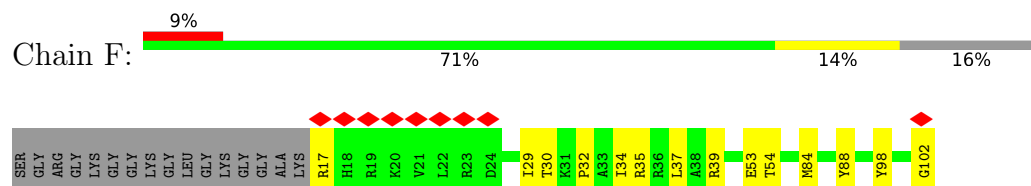
• Molecule 1: Histone H3



• Molecule 2: Histone H4



• Molecule 2: Histone H4



• Molecule 3: Histone H2A

Chain C:  73% 10% 17%

SER GLY ARG GLY LYS GLN GLY LYS THR ARG A12 K13 A14 K15 T16 S19 R20 Y39 T59 L63 R88 E91 E92 V100 T101 T102 K118 LYS THR GLU SER SER LYS SER ALA LYS LYS

• Molecule 3: Histone H2A

Chain G:  74% 9% 17%

SER GLY ARG GLY LYS GLN GLY LYS THR ARG A12 K15 S19 V30 H31 R35 R42 A47 L68 I62 L63 N73 K74 K75 K118 LYS THR GLU SER SER LYS SER ALA LYS LYS

• Molecule 4: Histone H2B

Chain D:  63% 13% 24%

ALA LYS SER ALA PRO ALA PRO LYS LYS GLY SER LYS LYS LYS ALA VAL THR THR THR GLN LYS ASP GLY LYS LYS ARG ARG LYS T29 S33 L42 K43 D48 K54 T58 M59 N60 N64 D65 E68 E69 V108 S109 E110 G111 T112 K113 A121 LYS

• Molecule 4: Histone H2B

Chain H:  60% 16% 24%

ALA LYS SER ALA PRO ALA PRO LYS LYS GLY SER LYS LYS LYS ALA VAL THR THR THR GLN LYS ASP GLY LYS LYS ARG ARG LYS T29 R30 A35 I36 Y37 V38 Y39 K40 V41 L42 K43 S53 M56 M59 N64 D65 V66 F67 E68 R69 I70 T85 I86 T87 S88 V95 A121 LYS

• Molecule 5: DNA (146-MER)

Chain I:  43% 57%

T2 G6 A7 G12 G13 G14 T15 G16 G17 C18 G19 A20 T27 C28 A39 C40 T46 C47 T48 A49 A52 C53 A59 A60 A61 C62 A65 C66 C67 T68 A69 C70 G71 C72 G73 G76 T77 C78 C79 C80 C83 T89 A90 C93 C94 C95 G99 G100 G101 A102 T104 A106 A107 T108 G109 C110 C111 T112 A113 G114 T115 C116 T117 G118 C119 A120 G121 G122 C123 A124 T127 G128 T129 C130 A131 T134 A135 T136 A137 T138 A139 C140 A141 T142 C143 A146 T147

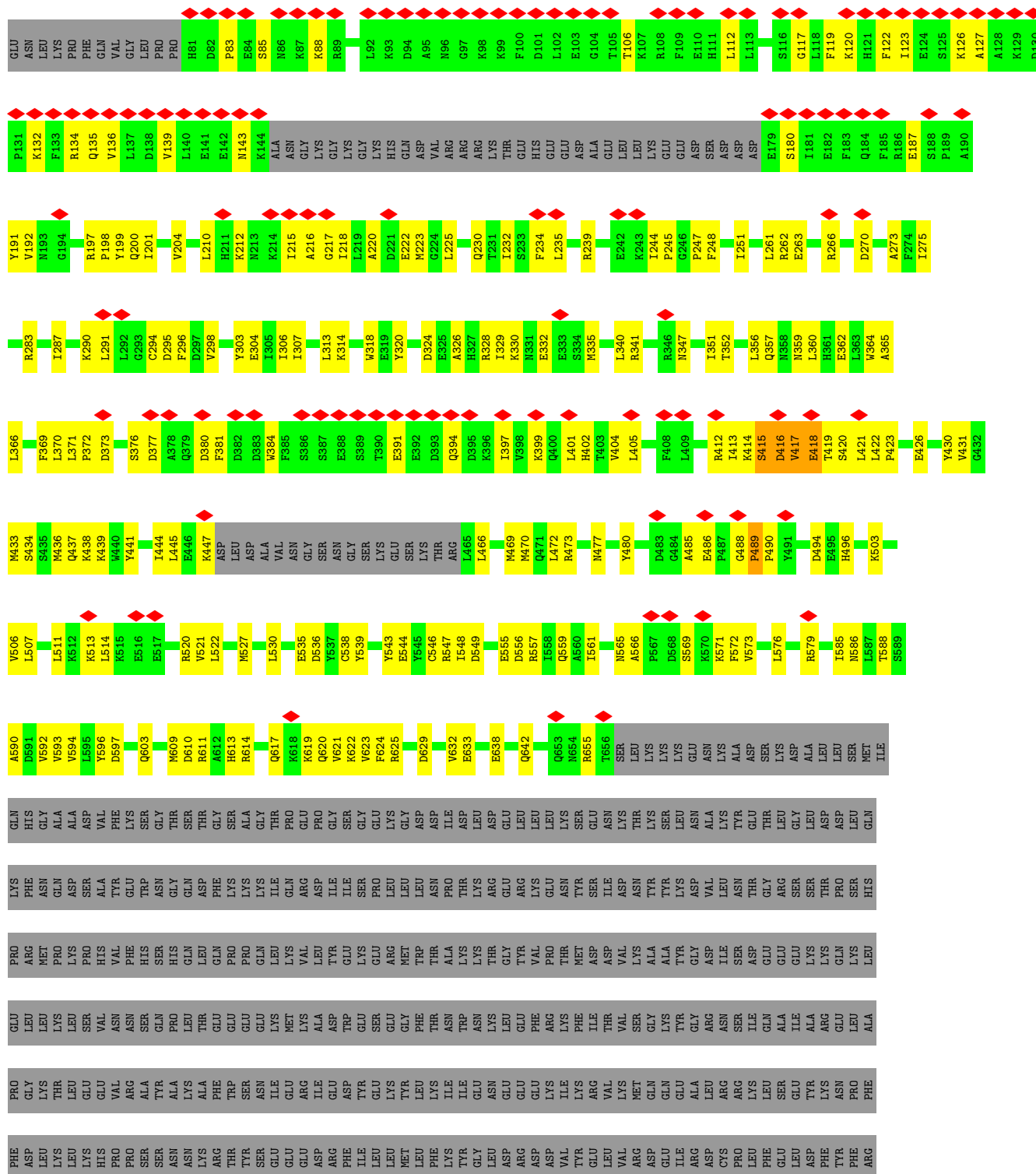
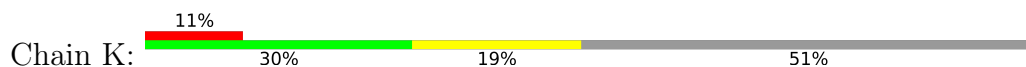
• Molecule 6: DNA (146-MER)

Chain J:  43% 57%

A1 T7 C8 T9 A10 T11 A12 T15 C16 C17 T17 T28 G29 C30 A31 G32 A33 C34 T35 A36 C37 G38 C39 A40 G41 T42 A43 T50 T51 G52 C53 C54 C55 G56 T57 T58 A59 A60 A61 C65 C66 C67 C68 C69 G70 A71 C72 G78 T79 A80 C81 C82 T83 G84 C85



● Molecule 7: ISWI chromatin-remodeling complex ATPase ISW1



VAL	ASP	GLY	VAL	GLU	SER	LYS	LYS	ALA	ARG	ILE	GLU	ASP	THR	SER	ASN	VAL	VAL	GLY	THR	GLU	GLU	GLN	LEU	LEU	VAL	VAL	GLY	THR	GLU	GLY	THR	THR	THR	HIS																																
SER	ARG	THR	PRO	VAL	GLU	LEU	LEU	ALA	ARG	GLY	ASN	THR	LEU	LEU	GLN	CYS	CYS	LEU	GLU	LYS	LYS	GLU	GLU	LEU	LEU	ALA	GLY	ILE	VAL	VAL	LEU	ASP	ASP	ALA	THR	THR	LYS	ASP	ARG	MET	LYS	LYS	GLY	GLU	ASP	ASP	GLU	ASN	GLY	ILE	ARG	ARG	GLU	GLU	PHE	ASN	ALA	GLN	THR	ALA	ASN	GLU	LYS	LYS	GLU	ASP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59121	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.300	Depositor
Minimum map value	-0.113	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.061	Depositor
Map size (\AA)	277.12, 277.12, 277.12	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0825, 1.0825, 1.0825	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.24	0/813	0.41	0/1093
1	E	0.24	0/789	0.41	0/1059
2	B	0.25	0/711	0.44	0/950
2	F	0.26	0/680	0.45	0/912
3	C	0.23	0/821	0.39	0/1112
3	G	0.22	0/825	0.33	0/1116
4	D	0.23	0/729	0.43	0/985
4	H	0.23	0/737	0.37	0/993
5	I	0.26	0/3333	0.43	0/5137
6	J	0.26	0/3381	0.40	0/5221
7	K	0.28	2/4395 (0.0%)	0.45	1/5927 (0.0%)
All	All	0.26	2/17214 (0.0%)	0.42	1/24505 (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
1	A	0	1
7	K	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	416	ASP	CA-C	-5.13	1.45	1.52
7	K	415	SER	CA-C	-5.12	1.46	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	K	415	SER	N-CA-C	-5.46	99.18	110.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	71	VAL	Peptide
7	K	489	PRO	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	801	0	831	16	0
1	E	779	0	815	12	0
2	B	703	0	757	18	0
2	F	672	0	698	13	0
3	C	811	0	849	11	0
3	G	815	0	860	11	0
4	D	718	0	725	14	0
4	H	726	0	747	17	0
5	I	2975	0	1639	67	0
6	J	3011	0	1639	70	0
7	K	4311	0	4366	167	0
8	K	1	0	0	0	0
All	All	16323	0	13926	371	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 12.

The worst 5 of 371 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)
7:K:225:LEU:HD13	7:K:417:VAL:HG11	1.54	0.88
5:I:113:DA:H2'	5:I:114:DG:C8	2.13	0.83
1:A:106:ASP:OD2	1:A:131:ARG:NH2	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:417:VAL:HG13	7:K:418:GLU:H	1.50	0.76
7:K:547:ARG:NH2	7:K:549:ASP:OD2	2.20	0.74

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	96/135 (71%)	93 (97%)	3 (3%)	0	100	100
1	E	93/135 (69%)	92 (99%)	1 (1%)	0	100	100
2	B	85/102 (83%)	83 (98%)	2 (2%)	0	100	100
2	F	84/102 (82%)	81 (96%)	3 (4%)	0	100	100
3	C	105/129 (81%)	101 (96%)	4 (4%)	0	100	100
3	G	105/129 (81%)	103 (98%)	2 (2%)	0	100	100
4	D	91/122 (75%)	89 (98%)	2 (2%)	0	100	100
4	H	91/122 (75%)	88 (97%)	3 (3%)	0	100	100
7	K	519/1061 (49%)	472 (91%)	46 (9%)	1 (0%)	44	77
All	All	1269/2037 (62%)	1202 (95%)	66 (5%)	1 (0%)	50	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	K	423	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	
1	A	84/110 (76%)	84 (100%)	0	100	100
1	E	82/110 (74%)	82 (100%)	0	100	100
2	B	72/78 (92%)	72 (100%)	0	100	100
2	F	67/78 (86%)	67 (100%)	0	100	100
3	C	81/101 (80%)	81 (100%)	0	100	100
3	G	82/101 (81%)	82 (100%)	0	100	100
4	D	77/102 (76%)	77 (100%)	0	100	100
4	H	79/102 (78%)	79 (100%)	0	100	100
7	K	478/958 (50%)	472 (99%)	6 (1%)	65	85
All	All	1102/1740 (63%)	1096 (100%)	6 (0%)	85	94

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	K	418	GLU
7	K	422	LEU
7	K	565	ASN
7	K	416	ASP
7	K	415	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
7	K	648	GLN
7	K	654	ASN
4	H	60	ASN
7	K	500	ASN
7	K	554	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is 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.

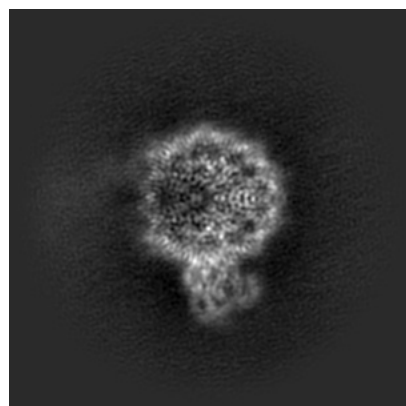
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61632. These allow visual inspection of the internal detail of the map and identification of artifacts.

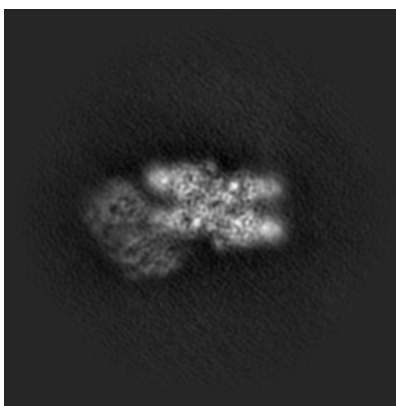
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

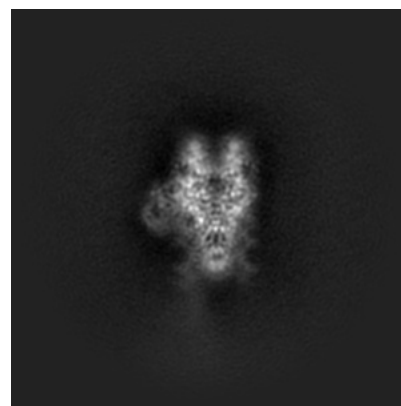
6.1.1 Primary map



X

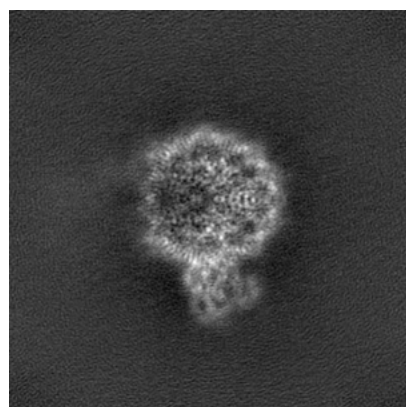


Y

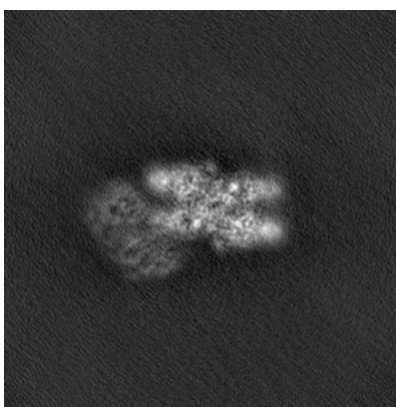


Z

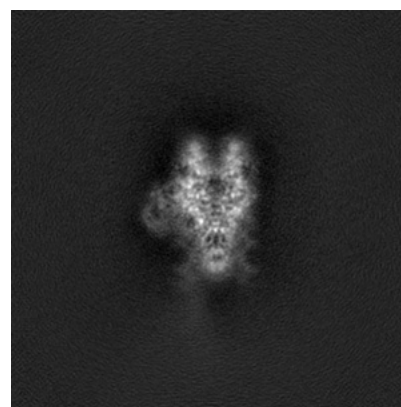
6.1.2 Raw map



X



Y

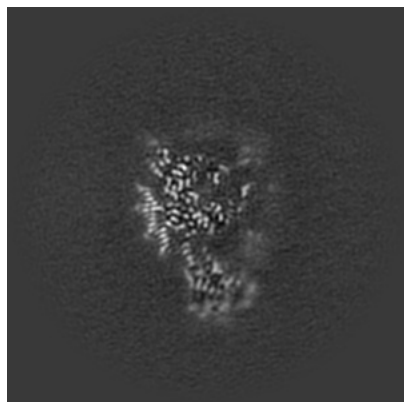


Z

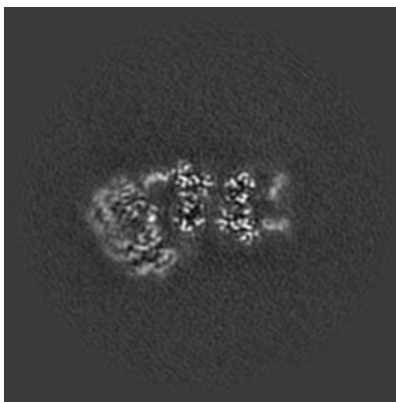
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

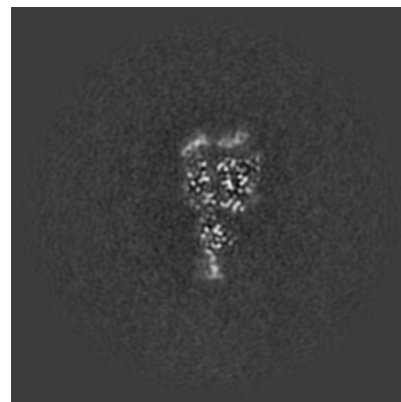
6.2.1 Primary map



X Index: 128

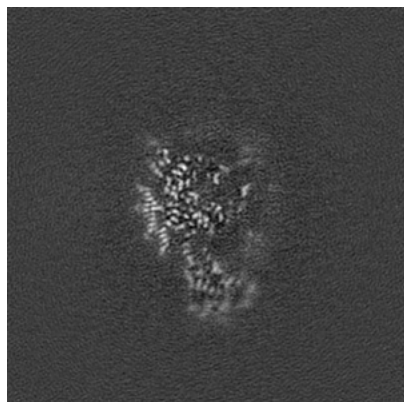


Y Index: 128

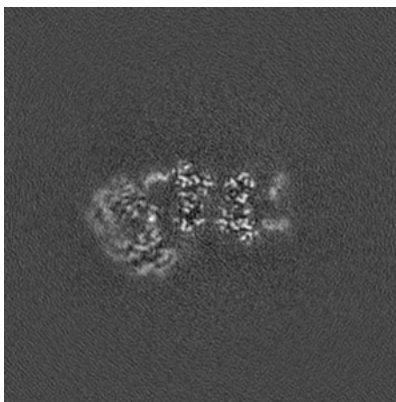


Z Index: 128

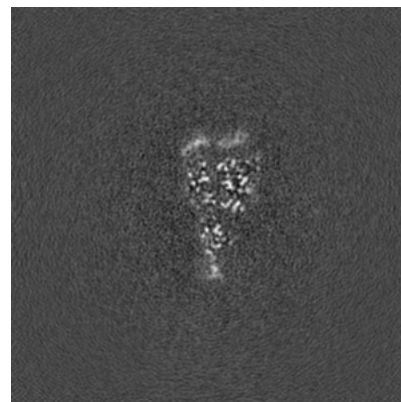
6.2.2 Raw map



X Index: 128



Y Index: 128

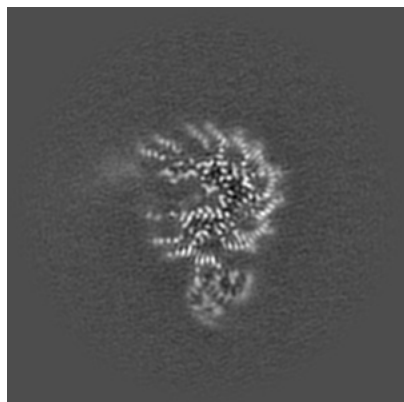


Z Index: 128

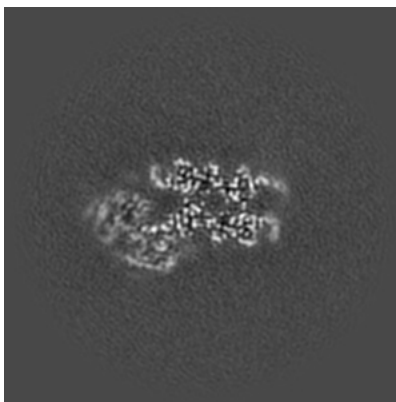
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

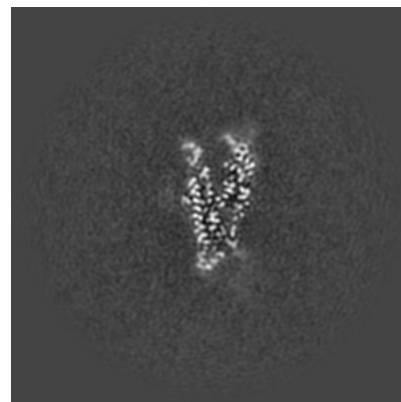
6.3.1 Primary map



X Index: 119

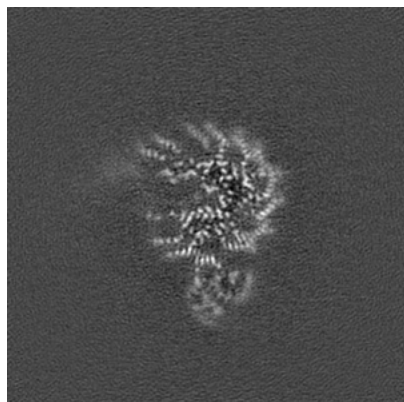


Y Index: 137

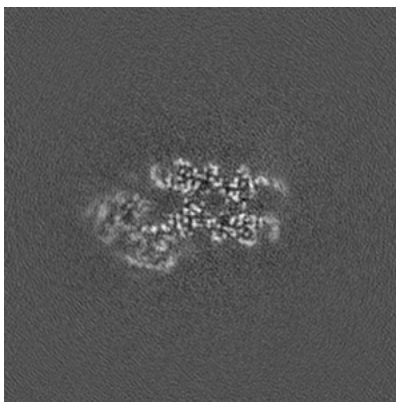


Z Index: 122

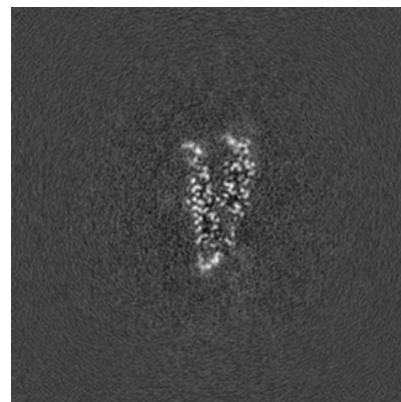
6.3.2 Raw map



X Index: 119



Y Index: 137

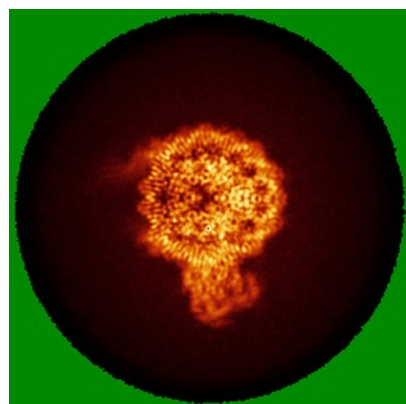


Z Index: 123

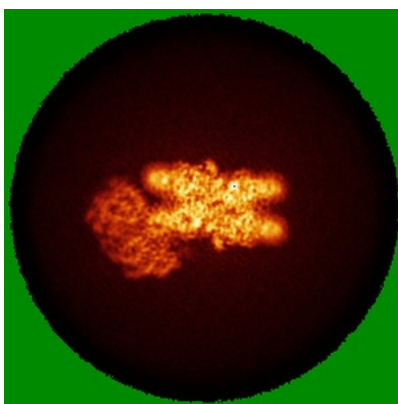
The images above show the largest variance slices of the map in three orthogonal directions.

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

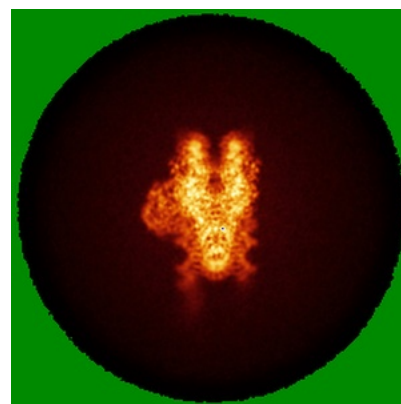
6.4.1 Primary map



X

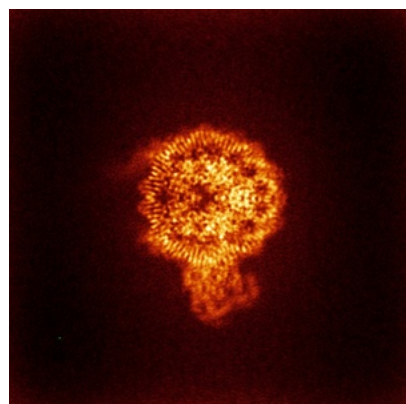


Y

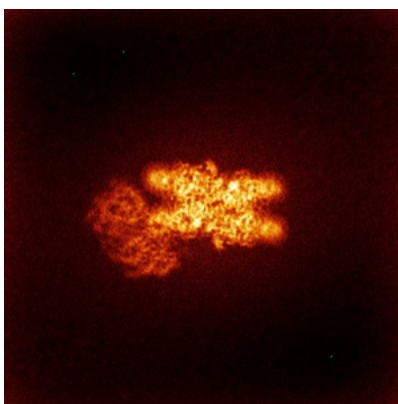


Z

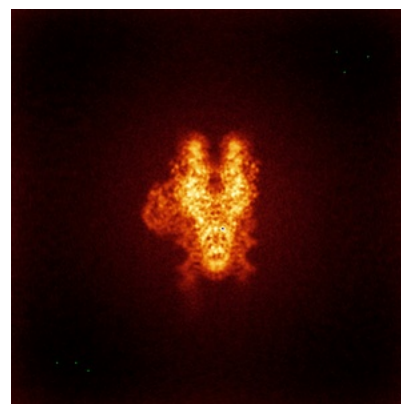
6.4.2 Raw map



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.

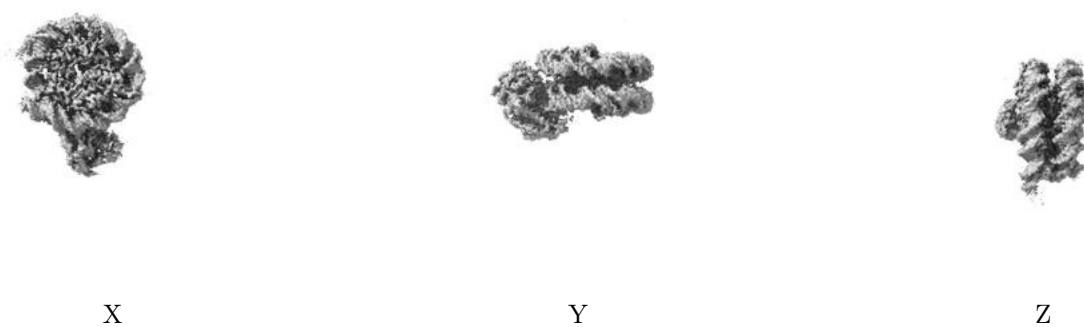
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.061. 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



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.

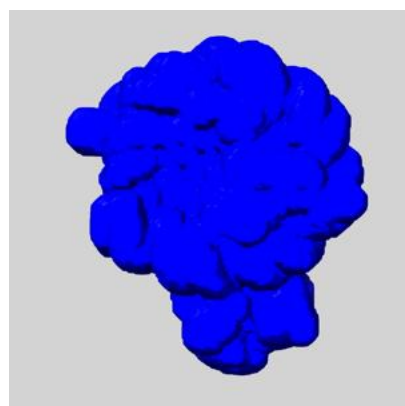
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

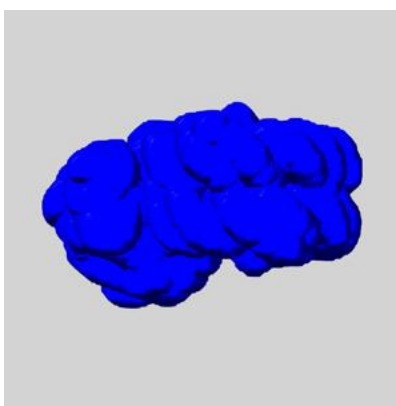
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

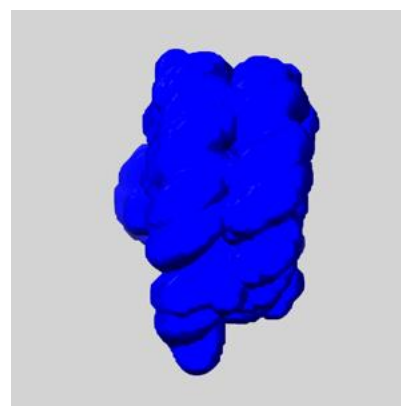
6.6.1 emd_61632_msk_1.map [i](#)



X



Y

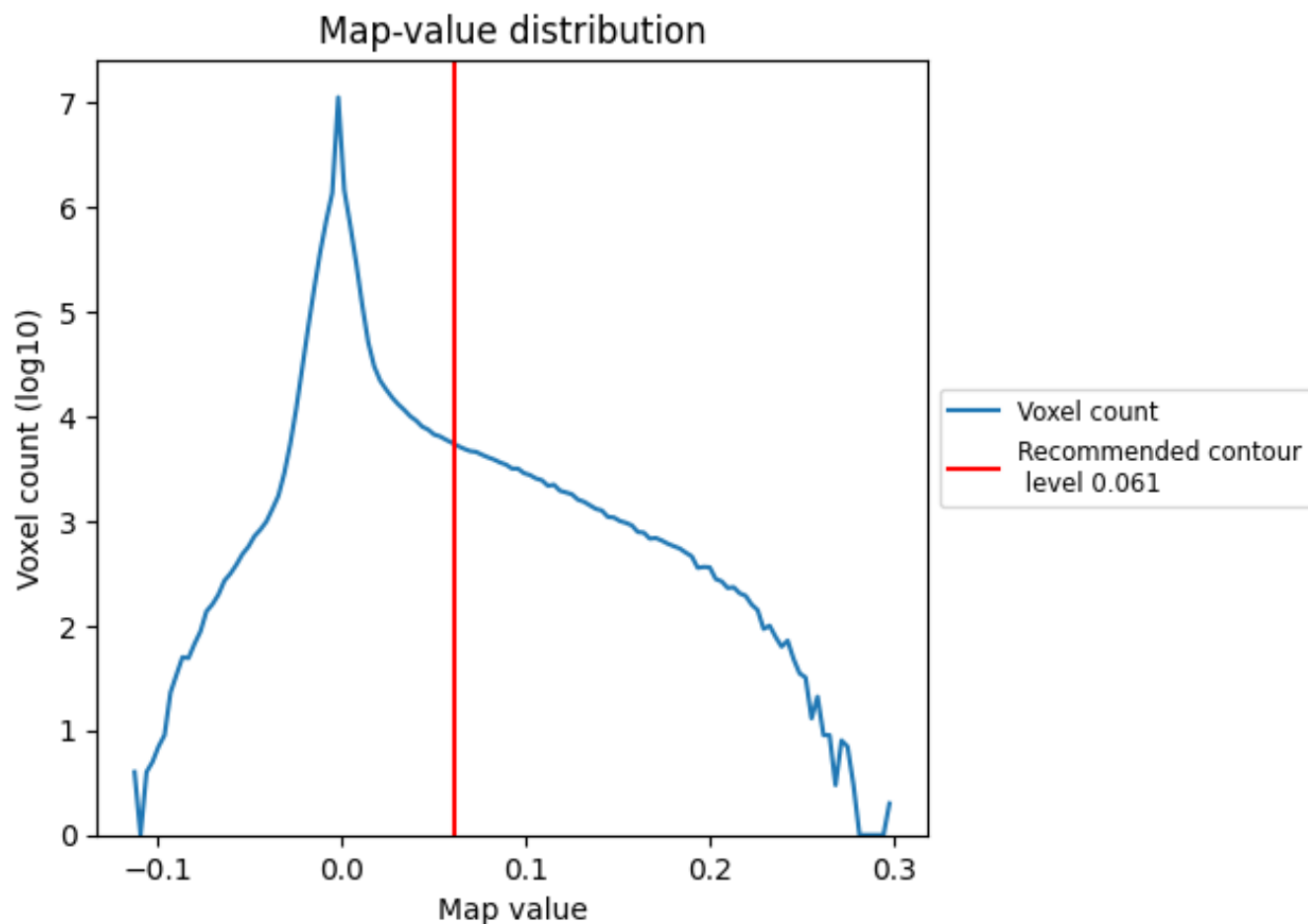


Z

7 Map analysis [i](#)

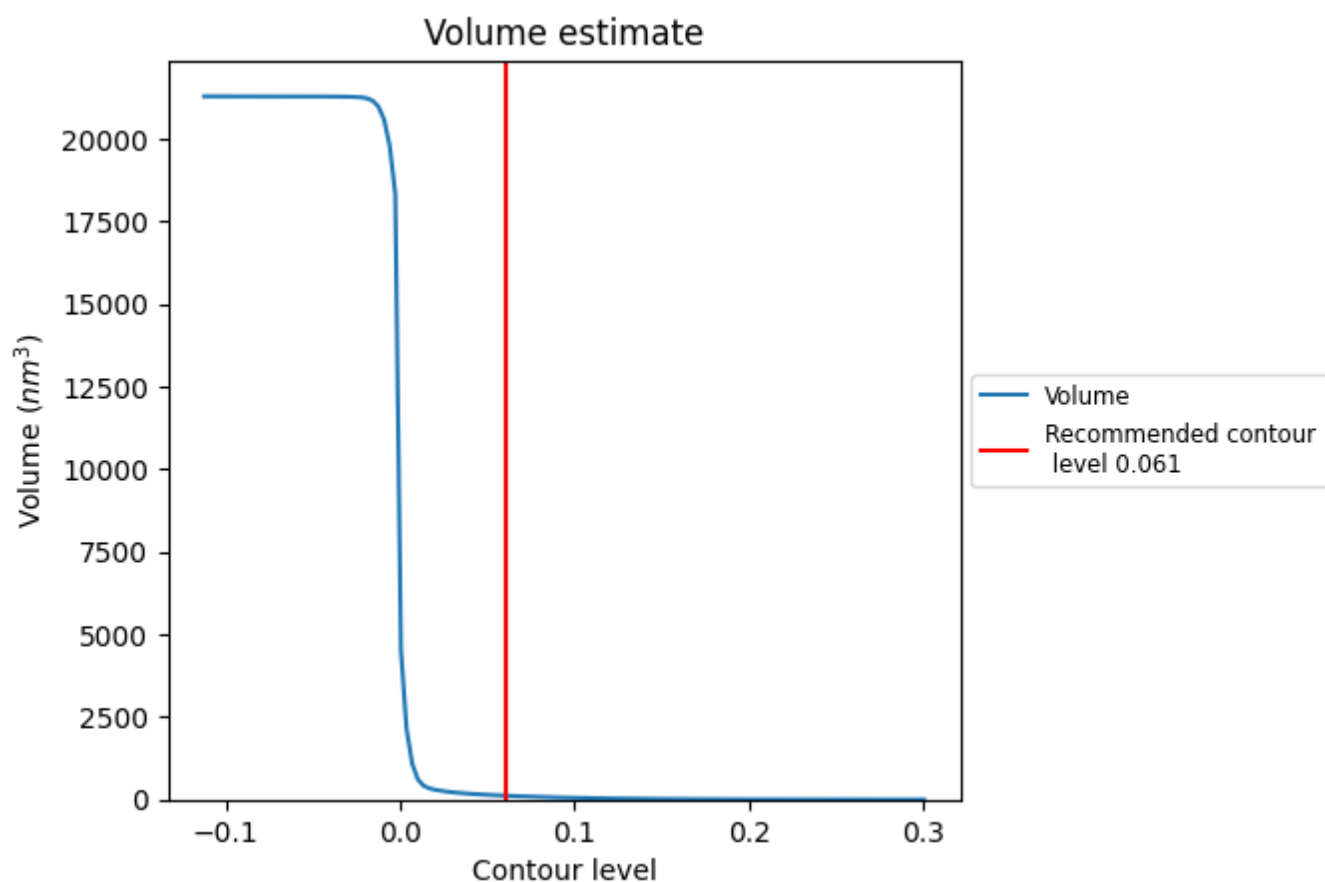
This section contains the results of statistical analysis of the map.

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.

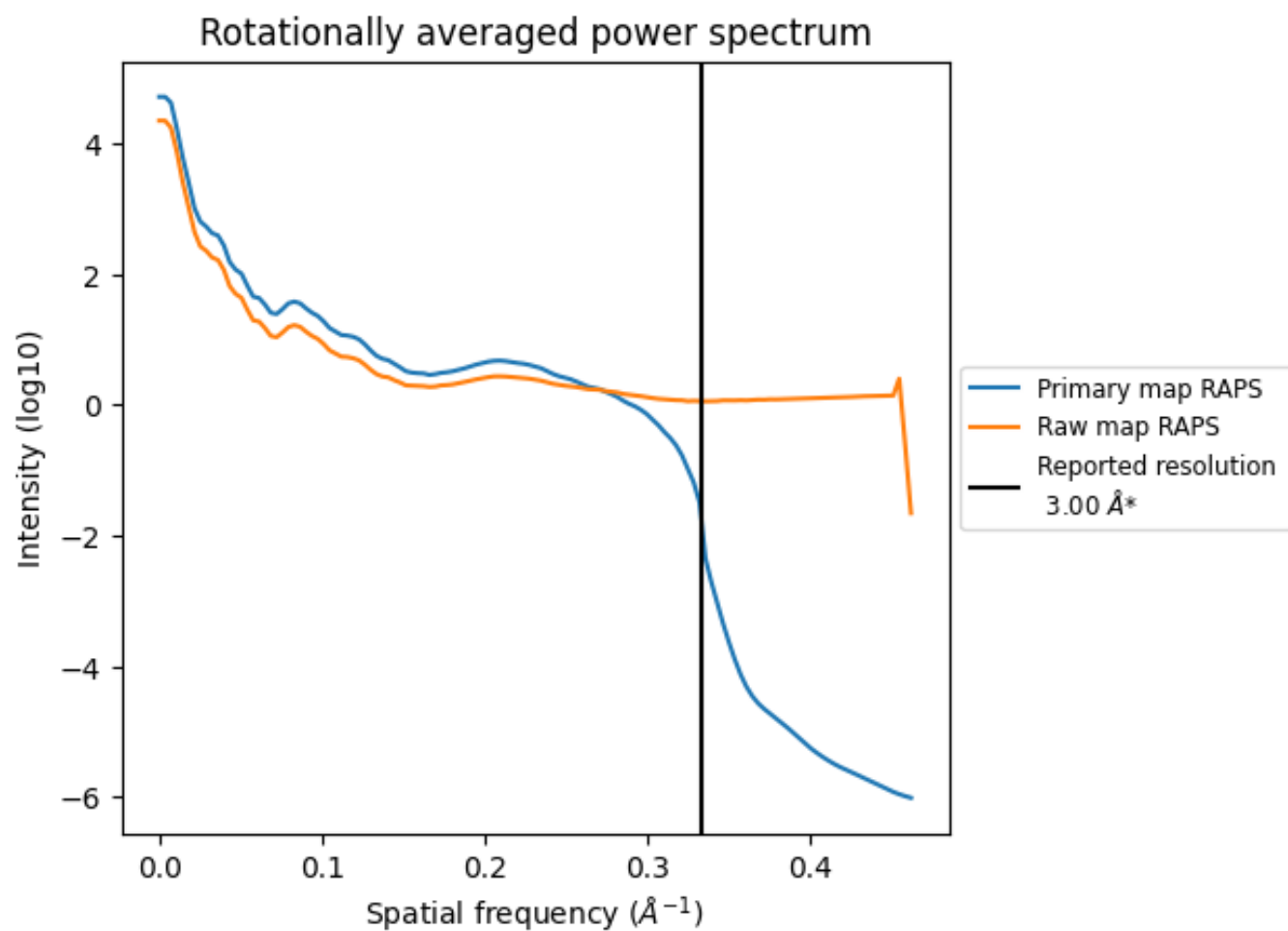
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 115 nm³; this corresponds to an approximate mass of 104 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 ⓘ

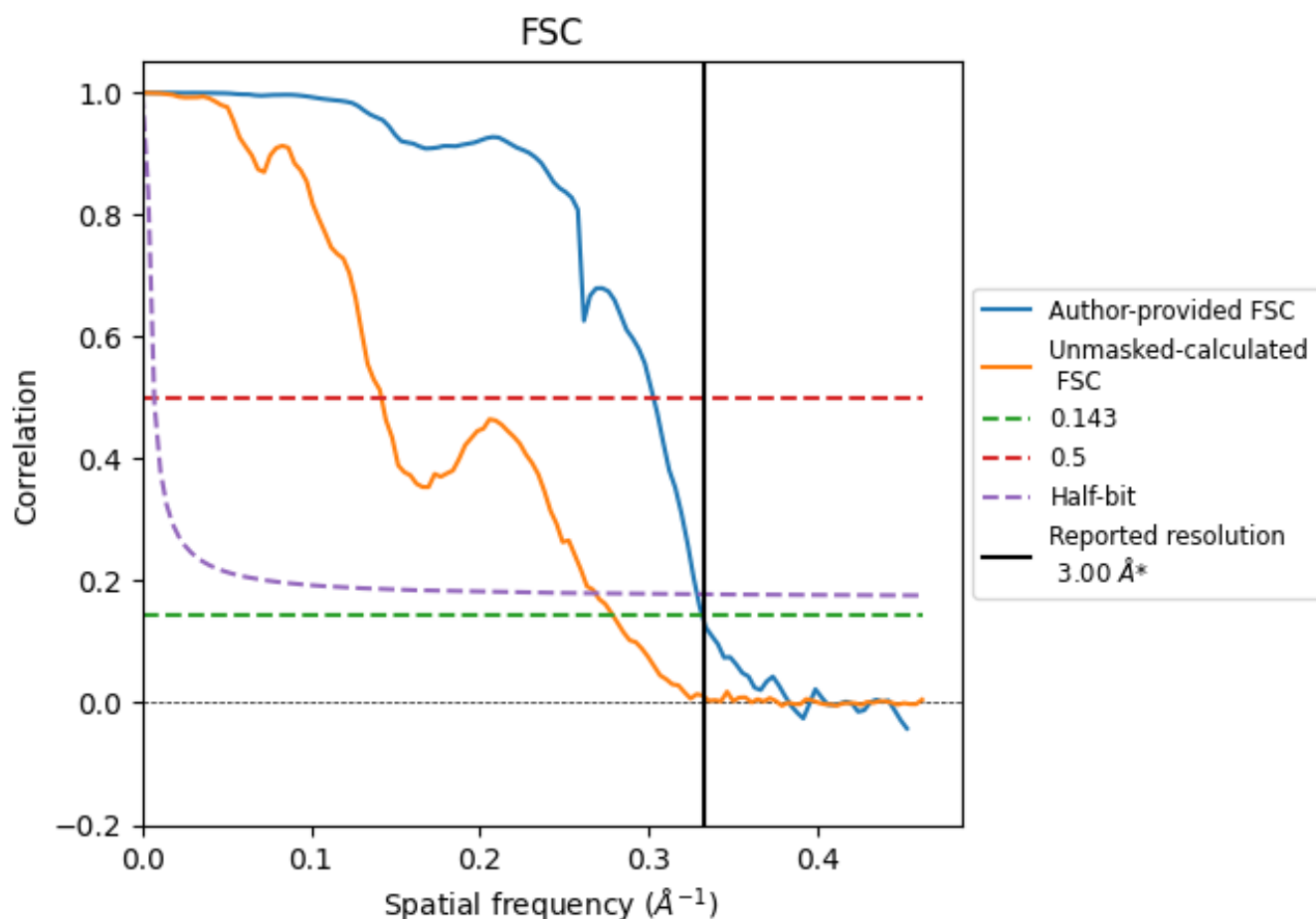


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

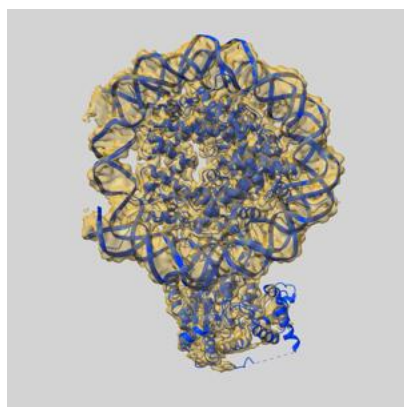
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.01	3.30	3.04
Unmasked-calculated*	3.59	7.06	3.73

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.59 differs from the reported value 3.0 by more than 10 %

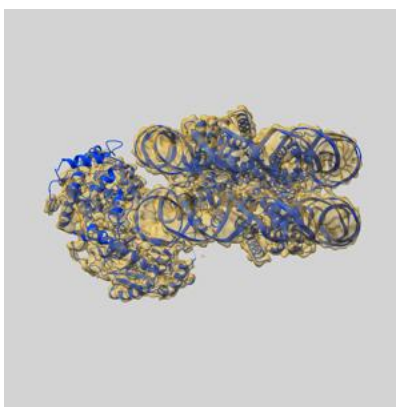
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61632 and PDB model 9JNZ. Per-residue inclusion information can be found in section [3](#) on page [6](#).

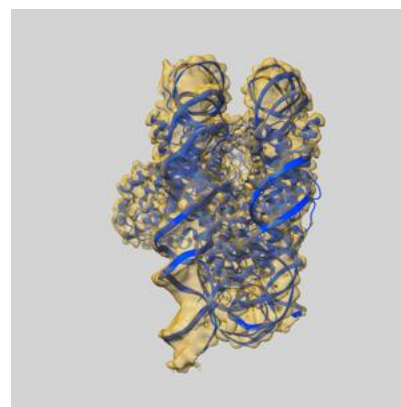
9.1 Map-model overlay [i](#)



X



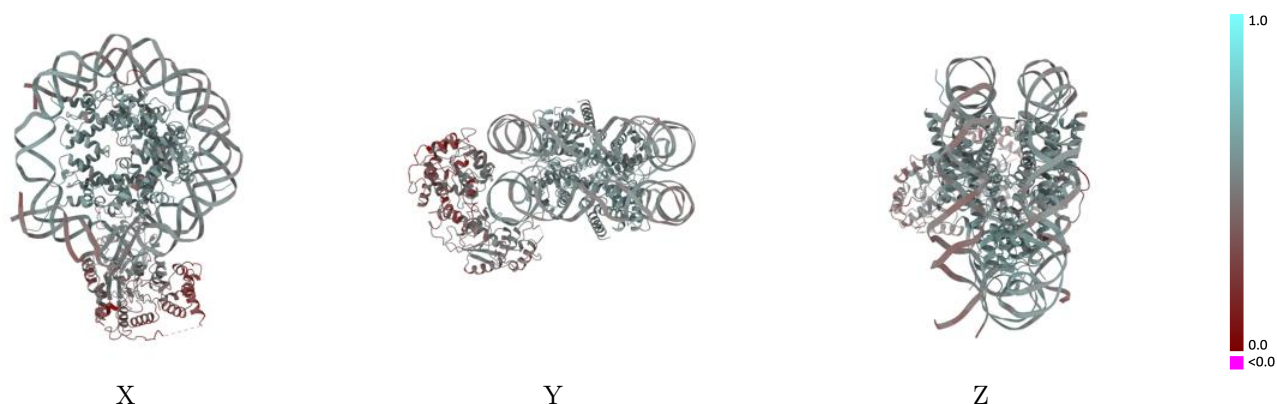
Y



Z

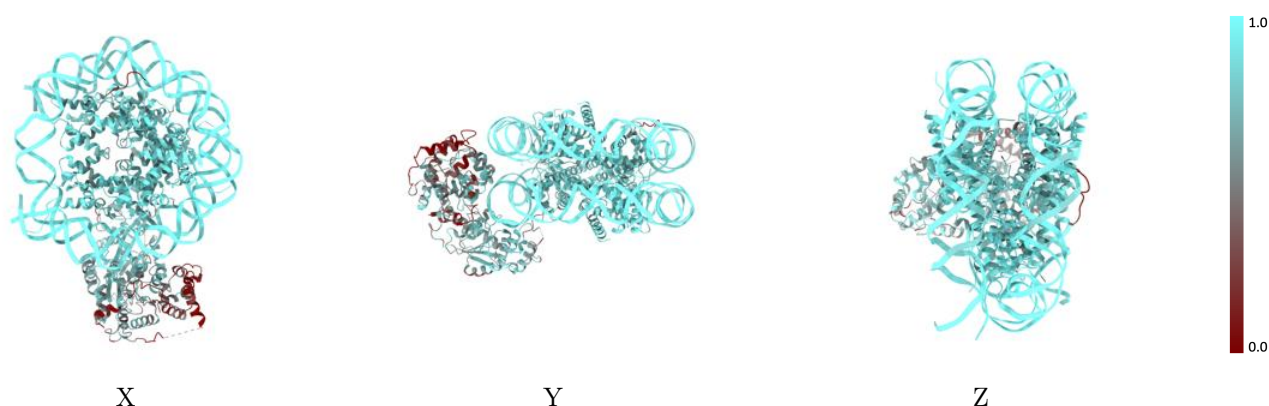
The images above show the 3D surface view of the map at the recommended contour level 0.061 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



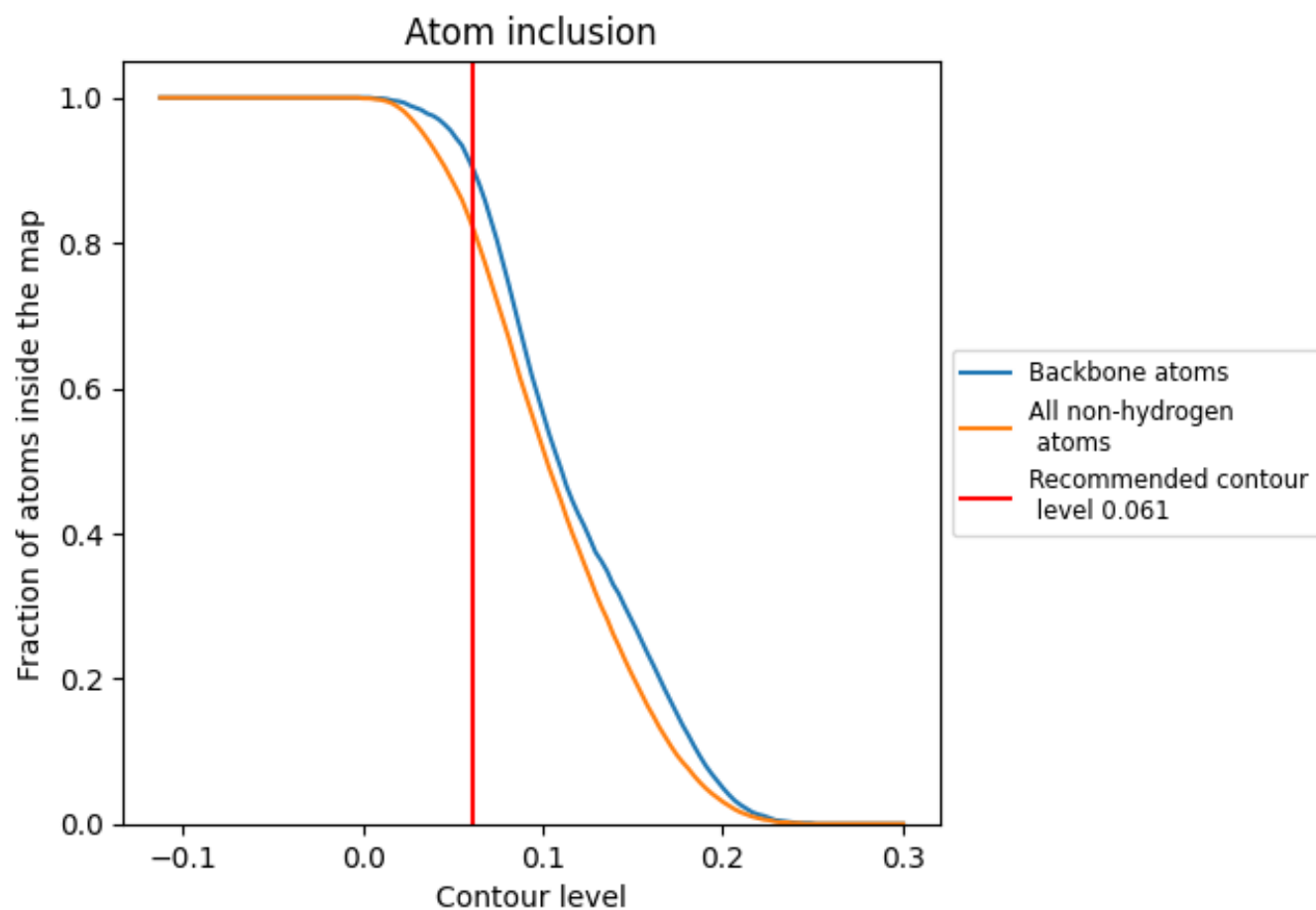
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.061).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 82% 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 (0.061) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8220</div>	<div><div></div>0.4930</div>
A	<div><div></div>0.8730</div>	<div><div></div>0.5580</div>
B	<div><div></div>0.8510</div>	<div><div></div>0.5490</div>
C	<div><div></div>0.9010</div>	<div><div></div>0.5630</div>
D	<div><div></div>0.8860</div>	<div><div></div>0.5470</div>
E	<div><div></div>0.8630</div>	<div><div></div>0.5680</div>
F	<div><div></div>0.8270</div>	<div><div></div>0.5480</div>
G	<div><div></div>0.8730</div>	<div><div></div>0.5560</div>
H	<div><div></div>0.8860</div>	<div><div></div>0.5520</div>
I	<div><div></div>0.9470</div>	<div><div></div>0.5000</div>
J	<div><div></div>0.9510</div>	<div><div></div>0.5020</div>
K	<div><div></div>0.5750</div>	<div><div></div>0.3960</div>

1.0

0.0

<0.0