



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:17 AM UTC

PDB ID : 6W4O / pdb_00006w4o
EMDB ID : EMD-21535
Title : CaMKII alpha-30 Cryo-EM reconstruction
Authors : Chao, L.H.; Stratton, M.M.
Deposited on : 2020-03-11
Resolution : 4.80 Å(reported)
Based on initial models : 5IG3, 3SOA

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

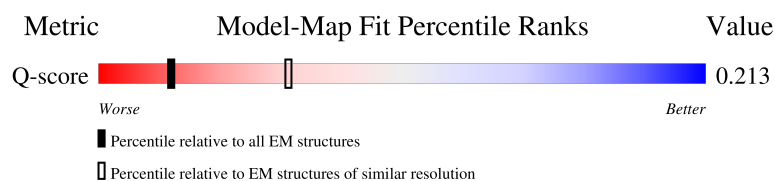
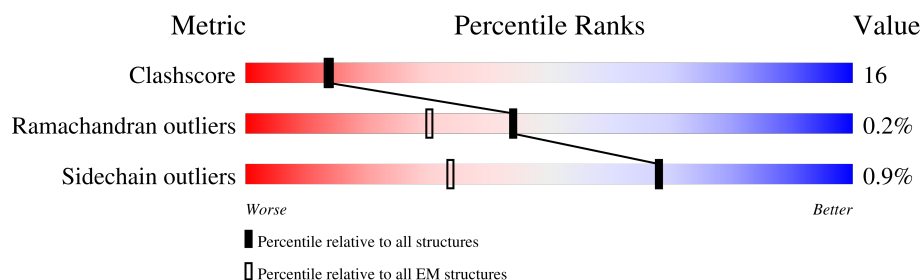
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.80 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.



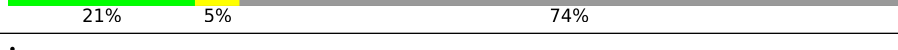
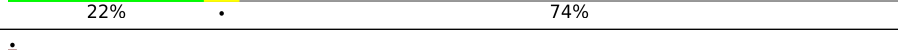
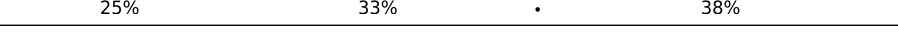
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1575 (4.30 - 5.30)

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	473	
1	B	473	
1	C	473	
1	D	473	

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Mol	Chain	Length	Quality of chain
1	E	473	
1	F	473	
1	G	473	
1	I	473	
1	J	473	
1	K	473	
1	L	473	
1	M	473	
2	O	473	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14475 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 Calcium/calmodulin-dependent protein kinase type II subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	128	Total	C	N	O	S	0	0
			1040	658	186	191	5		
1	B	126	Total	C	N	O	S	0	0
			1023	650	181	187	5		
1	C	126	Total	C	N	O	S	0	0
			1022	648	181	188	5		
1	D	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	E	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	F	122	Total	C	N	O	S	0	0
			988	625	176	182	5		
1	G	128	Total	C	N	O	S	0	0
			1041	658	187	191	5		
1	I	126	Total	C	N	O	S	0	0
			1023	650	181	187	5		
1	J	126	Total	C	N	O	S	0	0
			1022	648	181	188	5		
1	K	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	L	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	M	122	Total	C	N	O	S	0	0
			988	625	176	182	5		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-322	SER	-	expression tag	UNP Q9UQM7
B	-337	SER	-	expression tag	UNP Q9UQM7
C	-332	SER	-	expression tag	UNP Q9UQM7
D	-334	SER	-	expression tag	UNP Q9UQM7
E	-336	SER	-	expression tag	UNP Q9UQM7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-337	SER	-	expression tag	UNP Q9UQM7
G	-322	SER	-	expression tag	UNP Q9UQM7
I	-337	SER	-	expression tag	UNP Q9UQM7
J	-332	SER	-	expression tag	UNP Q9UQM7
K	-334	SER	-	expression tag	UNP Q9UQM7
L	-336	SER	-	expression tag	UNP Q9UQM7
M	-337	SER	-	expression tag	UNP Q9UQM7

- Molecule 2 is a protein called Calcium/calmodulin-dependent protein kinase type II subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	293	Total	C	N	O	S	0	0
			2352	1503	415	423	11		

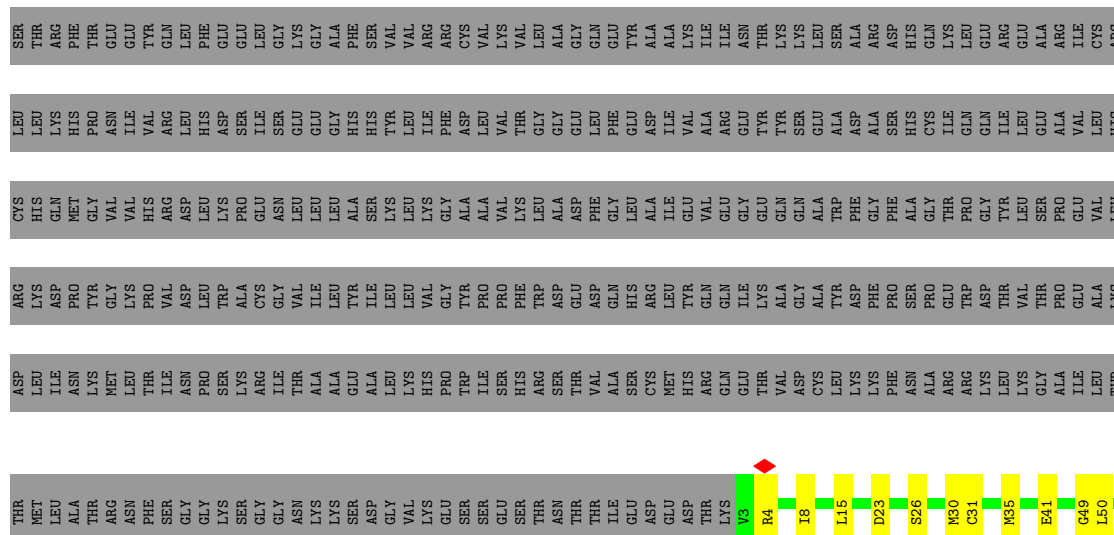
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	0	SER	-	expression tag	UNP Q9UQM7
O	34	MET	LYS	engineered mutation	UNP Q9UQM7
O	127	ASN	ASP	conflict	UNP Q9UQM7



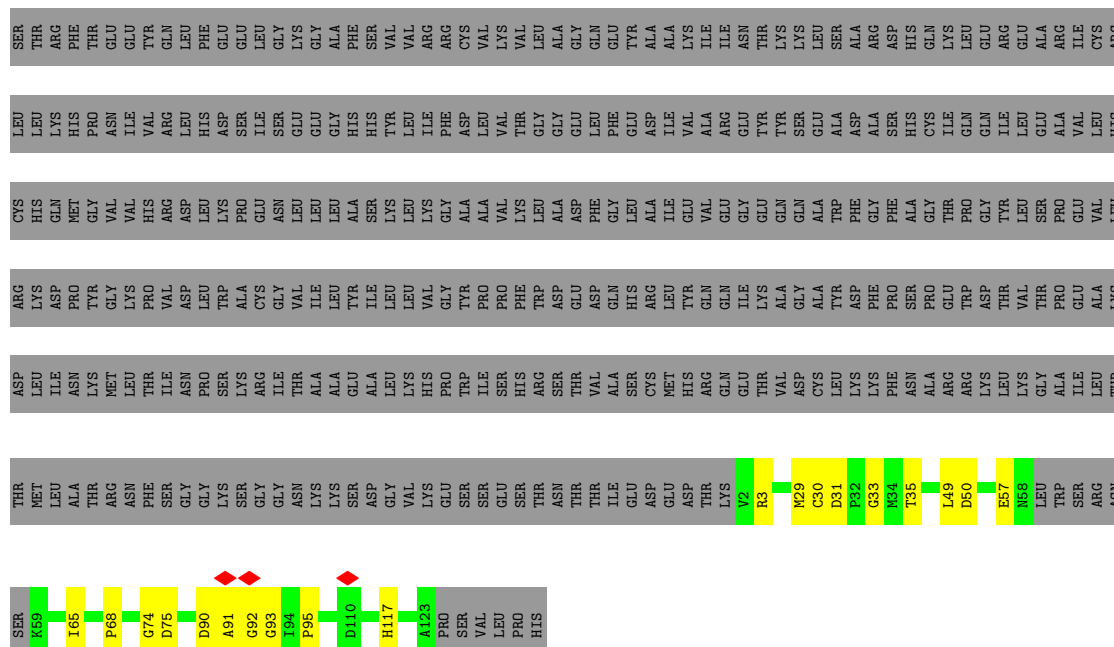
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha

Chain E: 21% 5% 74%



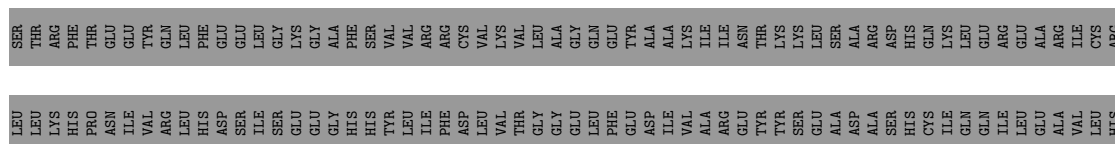
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha

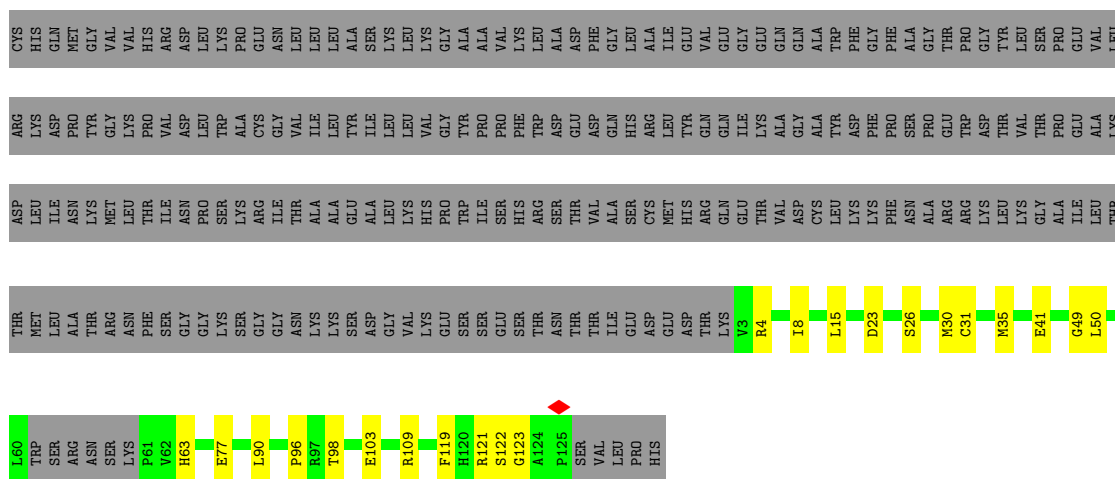
Chain F: 22% 0% 74%



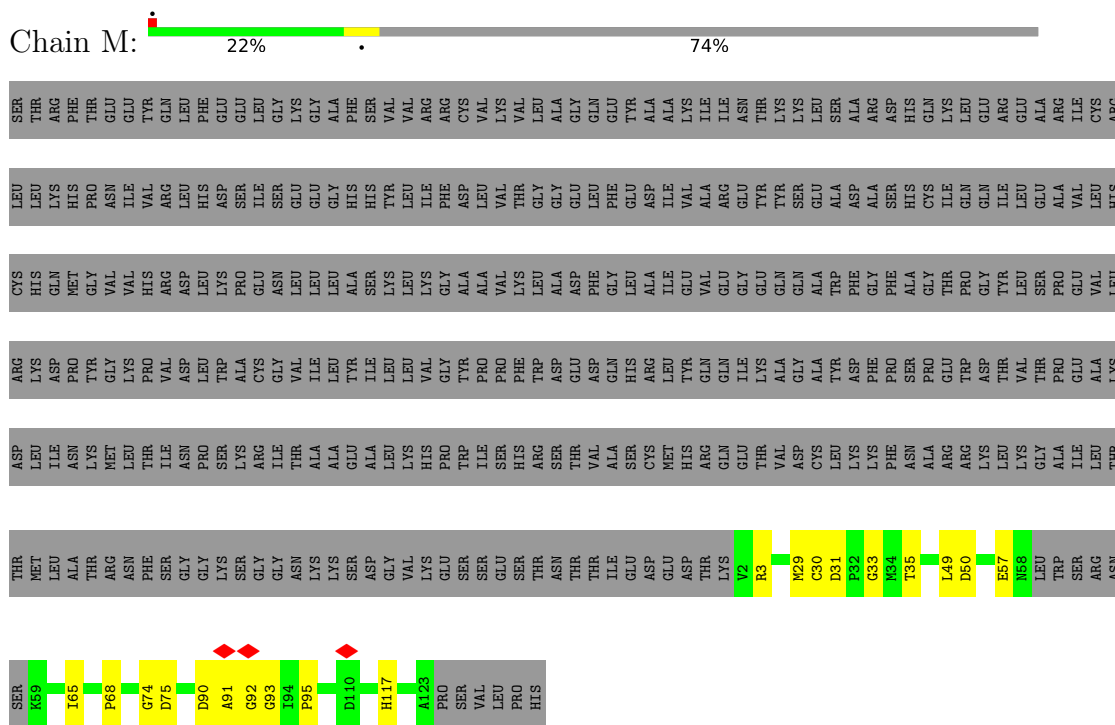
Chain G: 25% 73%



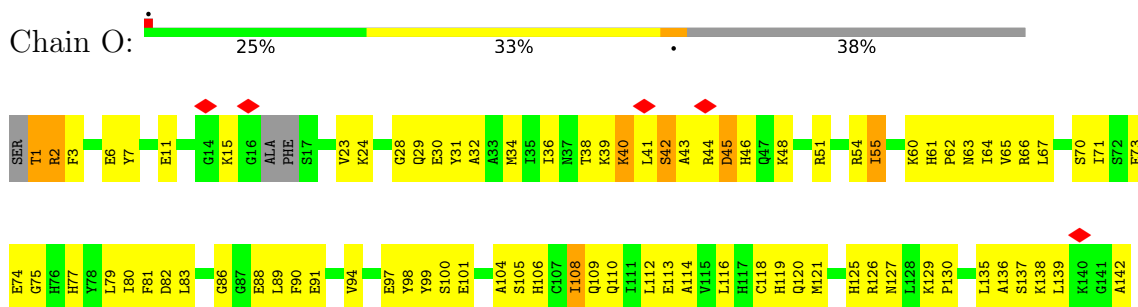




- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



- Molecule 2: Calcium/calmodulin-dependent protein kinase type II subunit alpha



HIS	LEU	ALA	K292	K145
MET	GLY	ILE	C293	L146
ASP	ASN	SER	ALA	A147
GLY	ASP	GLY	LEU	D148
GLU	ASP	THR	THR	F149
SER	PHE	THR	THR	G150
ALA	GLU	MET	THR	L151
CYS	SER	LEU	ALA	A152
ILE	TYR	ALA	S226	I153
ALA	TYR	THR	THR	E154
TYR	LYS	ARG	E228	
ILE	MET	ASN	W229	A161
ARG	CYS	PHE	D230	W162
ILE	ASP	SER	T231	F163
THR	PRO	GLY	V232	G164
GLN	GLY	GLY	T233	F165
TYR	MET	LYS	P234	A166
LEU	THR	SER	E235	G167
ASP	ALA	GLY	A236	T168
ALA	PHE	GLY		P169
GLY	GLU	ASN	L239	G170
GLY	PRO	LYS	I240	Y171
ILE	GLU	LYS		L172
PRO	ALA	SER	L244	S173
ARG	LEU	ASP		P174
THR	GLY	GLY	I252	E175
ALA	ASN	VAL	T253	V176
GLN	LEU	LYS	A254	L177
SER	VAL	GLU	A255	R178
GLU	GLY	SER		K179
GLU	GLY	SER	L258	D180
THR	LEU	GLU	K259	P181
ARG	ASP	SER	H260	Y182
VAL	PHE	THR	P261	G183
TRP	HIS	ASN	V262	K184
HIS	ARG	THR	T263	P185
ARG	PHE	THR	S264	V186
ASP	TYR	ILE	H265	D187
ASP	PHE	GLU	R266	L188
GLY	GLU	ASP	S267	W189
LYS	ASN	GLU	T268	
TRP	LEU	ASP	V269	G192
GLN	TRP	THR	A270	V193
ILE	SER	LYS	S271	I194
VAL	ARG	VAL	C272	L195
HIS	ASN	ARG	M273	Y196
PHE	SER	LYS	H274	I197
HIS	LYS	GLN	R275	L198
ARG	PRO	GLU		L199
SER	VAL	ILE	T278	V200
GLY	HIS	ILE	V279	
ALA	THR	LYS	L282	P203
PRO	THR	VAL		P204
SER	ILE	THR		F205
VAL	LEU	GLU	M286	W206
LEU	ASN	GLN		
PRO	PRO	LEU	R289	D209
HIS	HIS	ILE	K290	Q210
		GLU	L291	H211

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	160211	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	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	0.026	Depositor
Minimum map value	-0.011	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0072	Depositor
Map size ($\text{\AA}$)	364.0, 364.0, 364.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.91, 0.91, 0.91	Depositor

5 Model quality

5.1 Standard geometry

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	0.14	0/1067	0.32	0/1443
1	B	0.13	0/1050	0.35	0/1421
1	C	0.15	0/1048	0.38	0/1417
1	D	0.13	0/1019	0.34	0/1378
1	E	0.17	0/1019	0.32	0/1378
1	F	0.14	0/1012	0.34	0/1367
1	G	0.14	0/1068	0.32	0/1445
1	I	0.13	0/1050	0.35	0/1421
1	J	0.15	0/1048	0.38	0/1417
1	K	0.13	0/1019	0.34	0/1378
1	L	0.16	0/1019	0.31	0/1378
1	M	0.14	0/1012	0.35	0/1367
2	O	0.48	0/2407	1.03	12/3254 (0.4%)
All	All	0.23	0/14838	0.52	12/20064 (0.1%)

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	O	0	3

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	269	VAL	N-CA-C	14.09	126.42	112.90
2	O	262	TRP	N-CA-C	-9.51	101.60	113.01
2	O	43	ALA	N-CA-C	8.89	120.75	111.14
2	O	270	ALA	N-CA-C	7.66	122.23	110.36
2	O	267	SER	N-CA-C	-7.36	103.26	111.28

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	O	149	PHE	Peptide
2	O	150	GLY	Peptide
2	O	40	LYS	Peptide

5.2 Too-close contacts

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	1040	0	1002	9	0
1	B	1023	0	985	12	0
1	C	1022	0	983	12	0
1	D	994	0	958	11	0
1	E	994	0	958	17	0
1	F	988	0	952	11	0
1	G	1041	0	1003	8	0
1	I	1023	0	985	13	0
1	J	1022	0	982	78	0
1	K	994	0	957	54	0
1	L	994	0	958	17	0
1	M	988	0	952	12	0
2	O	2352	0	2355	324	0
All	All	14475	0	14030	451	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 16.

The worst 5 of 451 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:J:14:LYS:HD3	2:O:291:LEU:CB	1.31	1.57
1:J:14:LYS:HB2	2:O:291:LEU:CG	1.29	1.53
1:K:27:GLU:CG	2:O:164:GLY:HA2	1.17	1.50
1:J:14:LYS:CB	2:O:291:LEU:CD1	1.95	1.42
1:K:27:GLU:HG2	2:O:162:TRP:NE1	1.35	1.42

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	126/473 (27%)	123 (98%)	3 (2%)	0	100	100
1	B	122/473 (26%)	119 (98%)	3 (2%)	0	100	100
1	C	122/473 (26%)	116 (95%)	6 (5%)	0	100	100
1	D	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	E	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	F	118/473 (25%)	117 (99%)	0	1 (1%)	16	52
1	G	126/473 (27%)	123 (98%)	3 (2%)	0	100	100
1	I	122/473 (26%)	119 (98%)	3 (2%)	0	100	100
1	J	122/473 (26%)	116 (95%)	6 (5%)	0	100	100
1	K	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	L	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	M	118/473 (25%)	117 (99%)	0	1 (1%)	16	52
2	O	289/473 (61%)	270 (93%)	17 (6%)	2 (1%)	18	55
All	All	1741/6149 (28%)	1684 (97%)	53 (3%)	4 (0%)	44	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	91	ALA
1	M	91	ALA
2	O	42	SER
2	O	261	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	A	110/405 (27%)	109 (99%)	1 (1%)	70	77
1	B	109/405 (27%)	109 (100%)	0	100	100
1	C	109/405 (27%)	109 (100%)	0	100	100
1	D	106/405 (26%)	105 (99%)	1 (1%)	70	77
1	E	106/405 (26%)	106 (100%)	0	100	100
1	F	105/405 (26%)	104 (99%)	1 (1%)	68	76
1	G	111/405 (27%)	110 (99%)	1 (1%)	70	77
1	I	109/405 (27%)	109 (100%)	0	100	100
1	J	109/405 (27%)	109 (100%)	0	100	100
1	K	106/405 (26%)	105 (99%)	1 (1%)	70	77
1	L	106/405 (26%)	106 (100%)	0	100	100
1	M	105/405 (26%)	105 (100%)	0	100	100
2	O	250/405 (62%)	241 (96%)	9 (4%)	31	52
All	All	1541/5265 (29%)	1527 (99%)	14 (1%)	68	77

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	O	45	ASP
2	O	55	ILE
2	O	269	VAL
2	O	260	HIS
2	O	262	TRP

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

Mol	Chain	Res	Type
2	O	119	HIS
2	O	286	ASN

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Mol	Chain	Res	Type
1	G	59	ASN
1	G	140	HIS
1	I	13	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 [i](#)

There are no chain breaks in this entry.

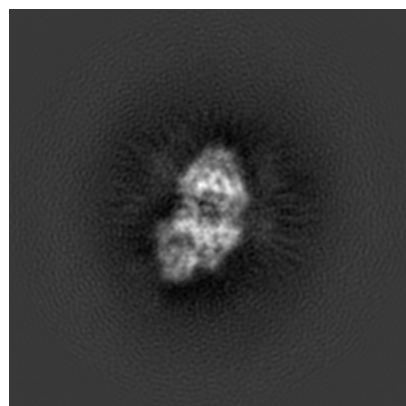
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21535. These allow visual inspection of the internal detail of the map and identification of artifacts.

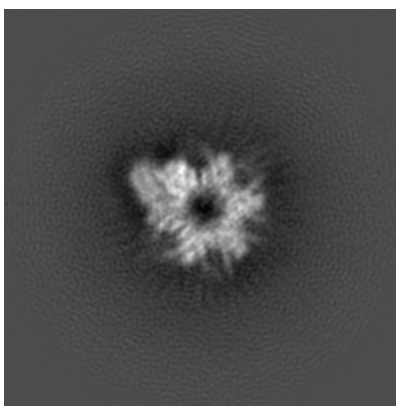
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

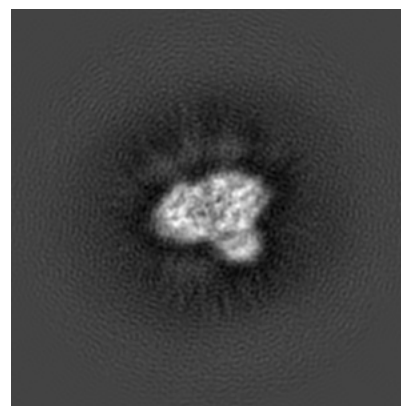
6.1.1 Primary map



X

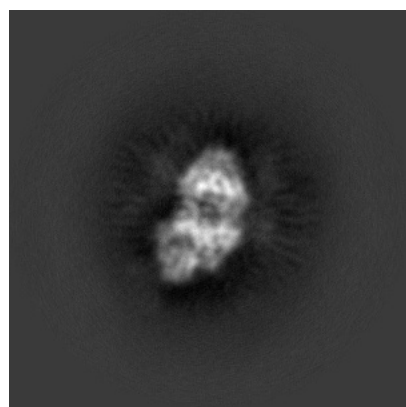


Y

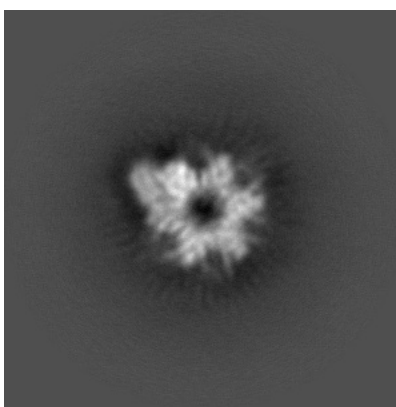


Z

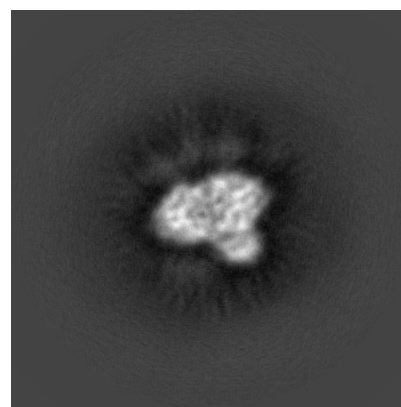
6.1.2 Raw map



X



Y

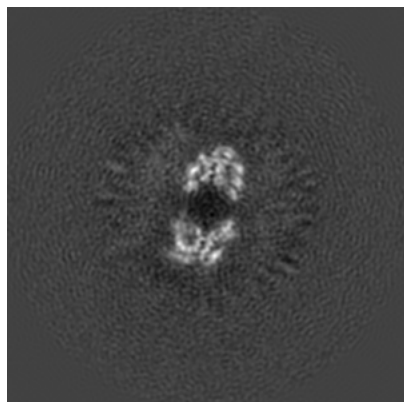


Z

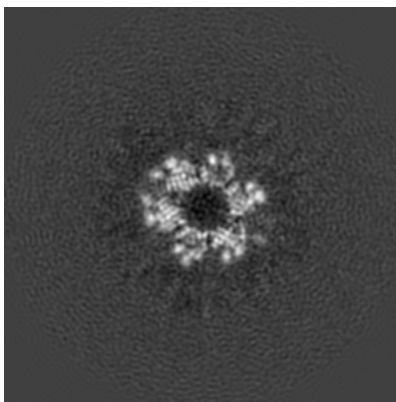
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

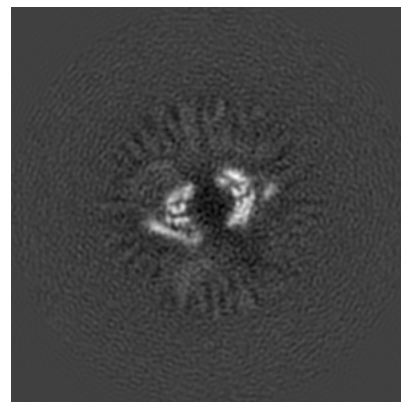
6.2.1 Primary map



X Index: 200

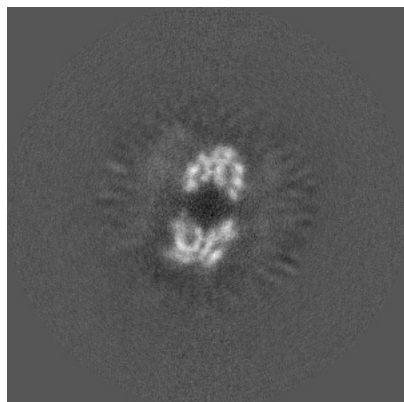


Y Index: 200

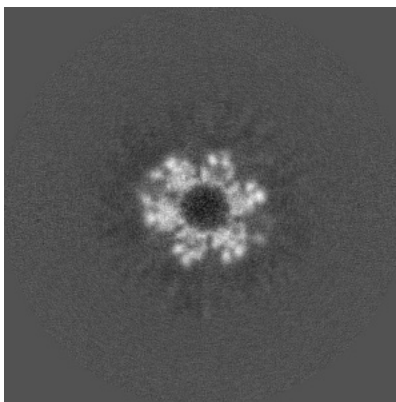


Z Index: 200

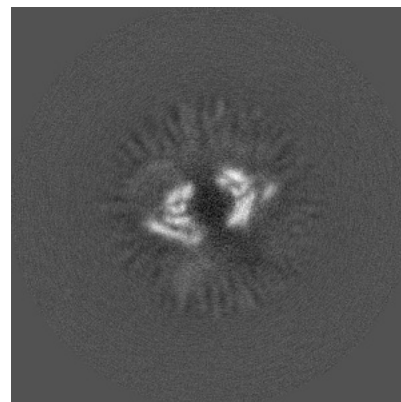
6.2.2 Raw map



X Index: 200



Y Index: 200

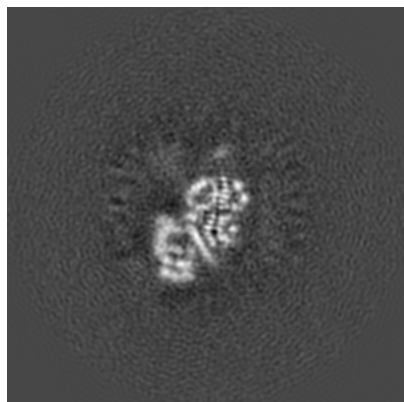


Z Index: 200

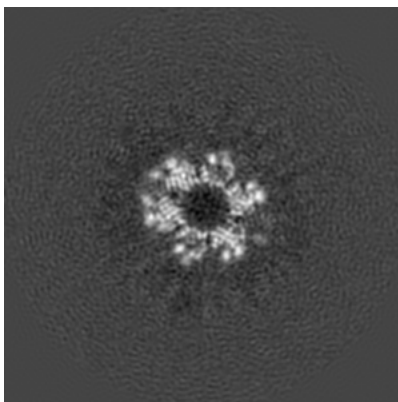
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

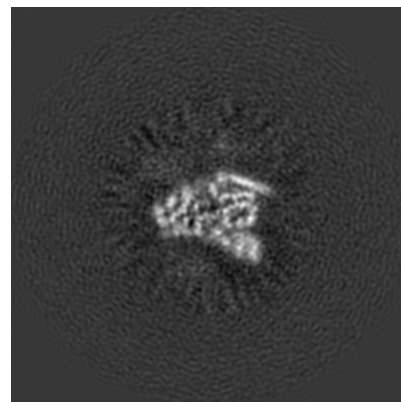
6.3.1 Primary map



X Index: 230

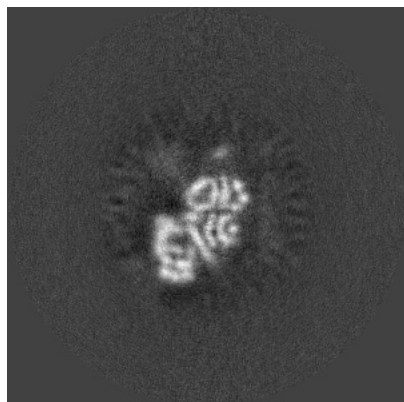


Y Index: 201

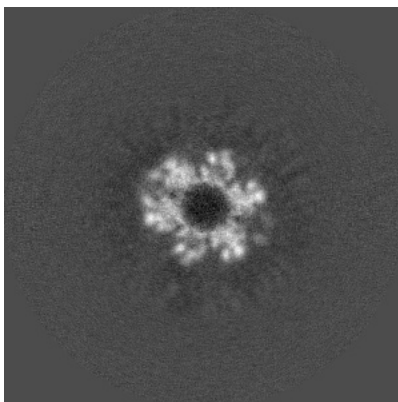


Z Index: 178

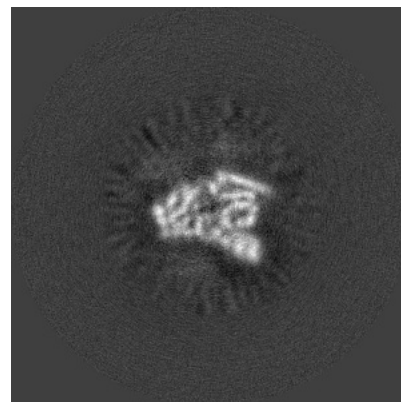
6.3.2 Raw map



X Index: 230



Y Index: 202

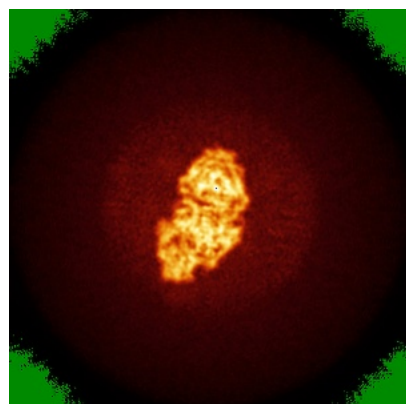


Z Index: 179

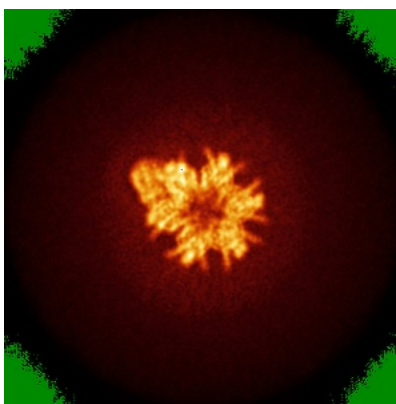
The images above show the largest variance slices of the map in three orthogonal directions.

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

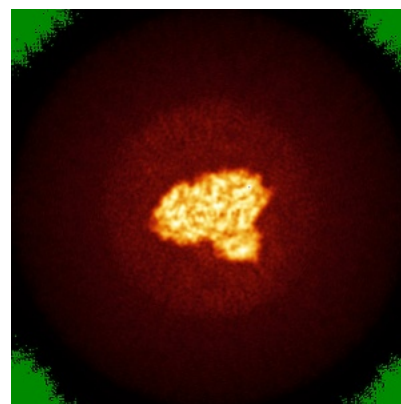
6.4.1 Primary map



X

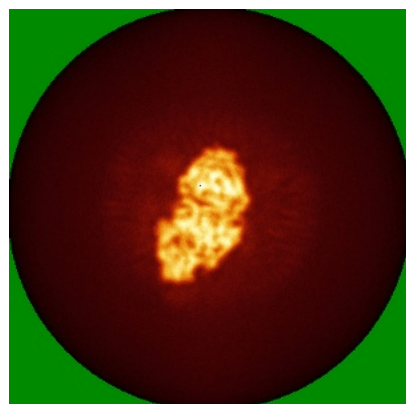


Y

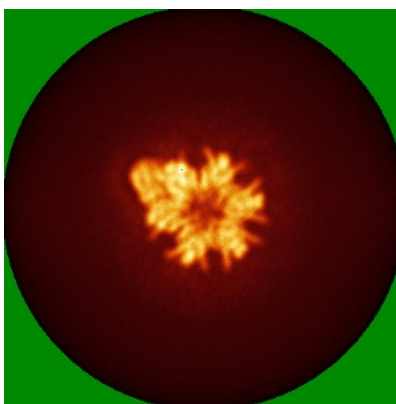


Z

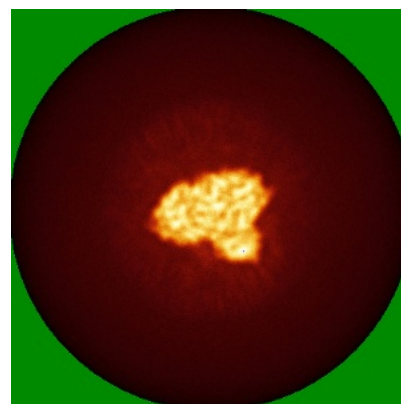
6.4.2 Raw map



X



Y

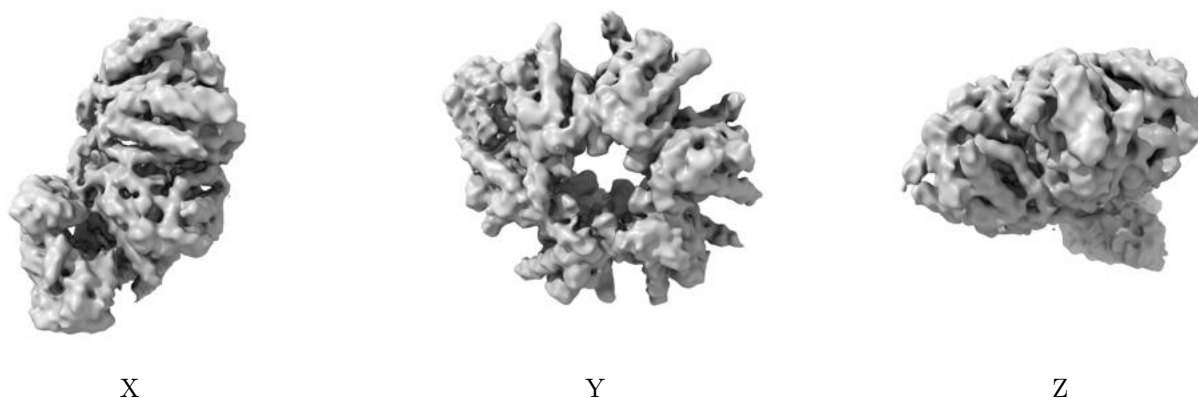


Z

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.

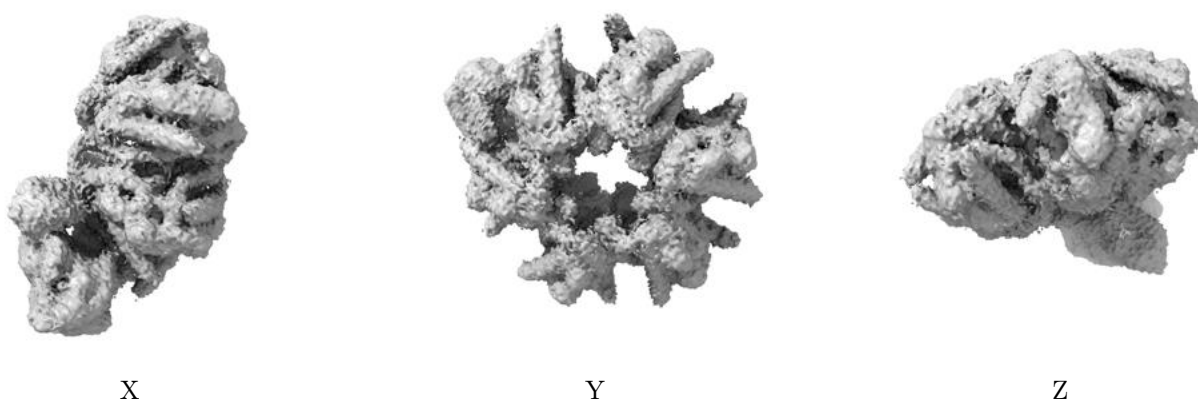
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0072. 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.

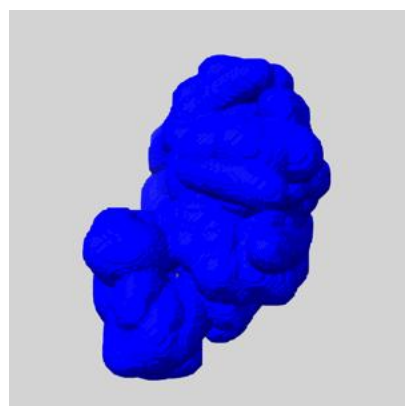
6.6 Mask visualisation [i](#)

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

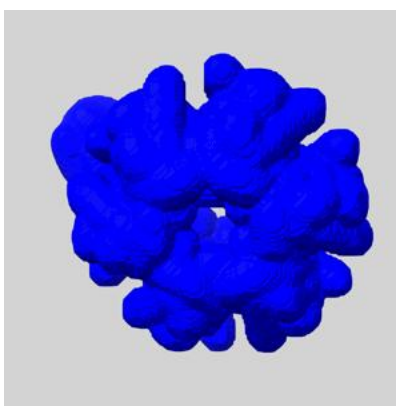
A mask typically either:

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

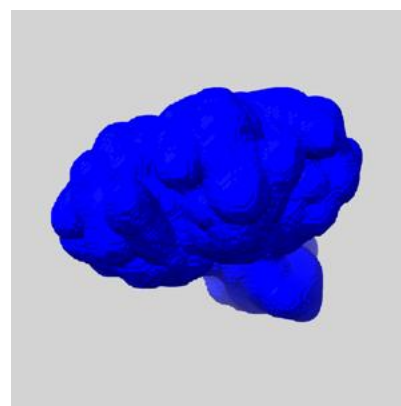
6.6.1 emd_21535_msk_1.map [i](#)



X



Y

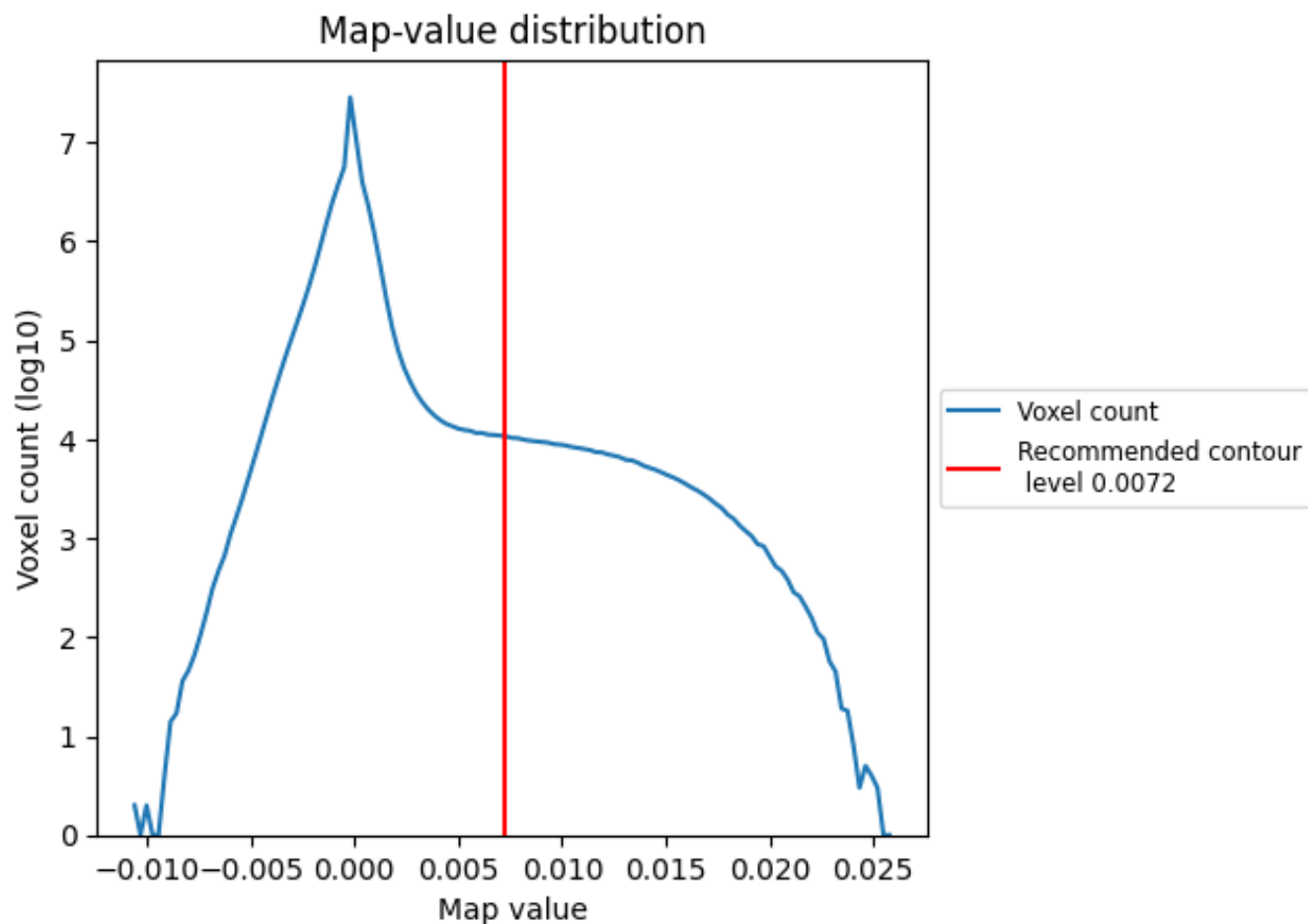


Z

7 Map analysis [i](#)

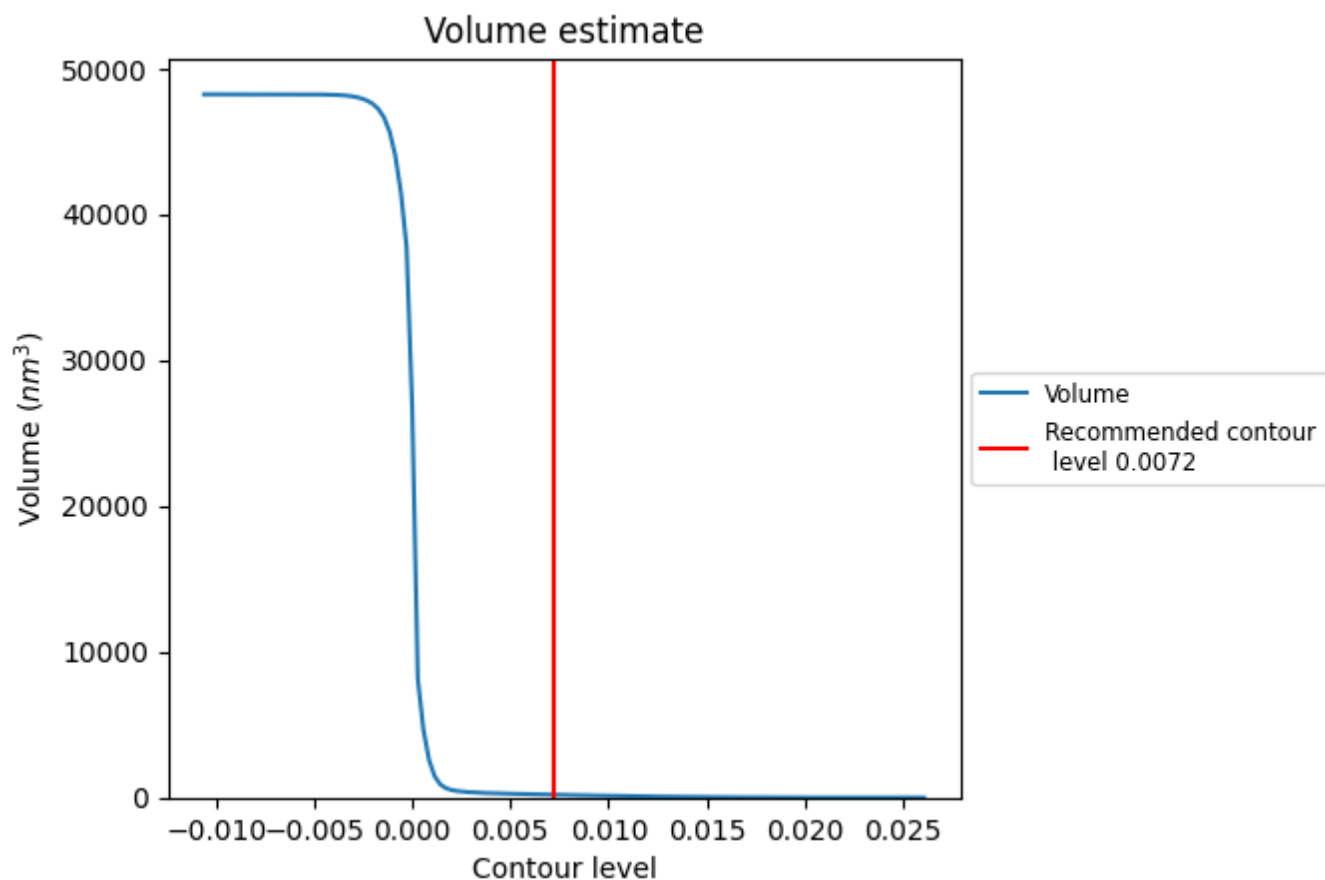
This section contains the results of statistical analysis of the map.

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.

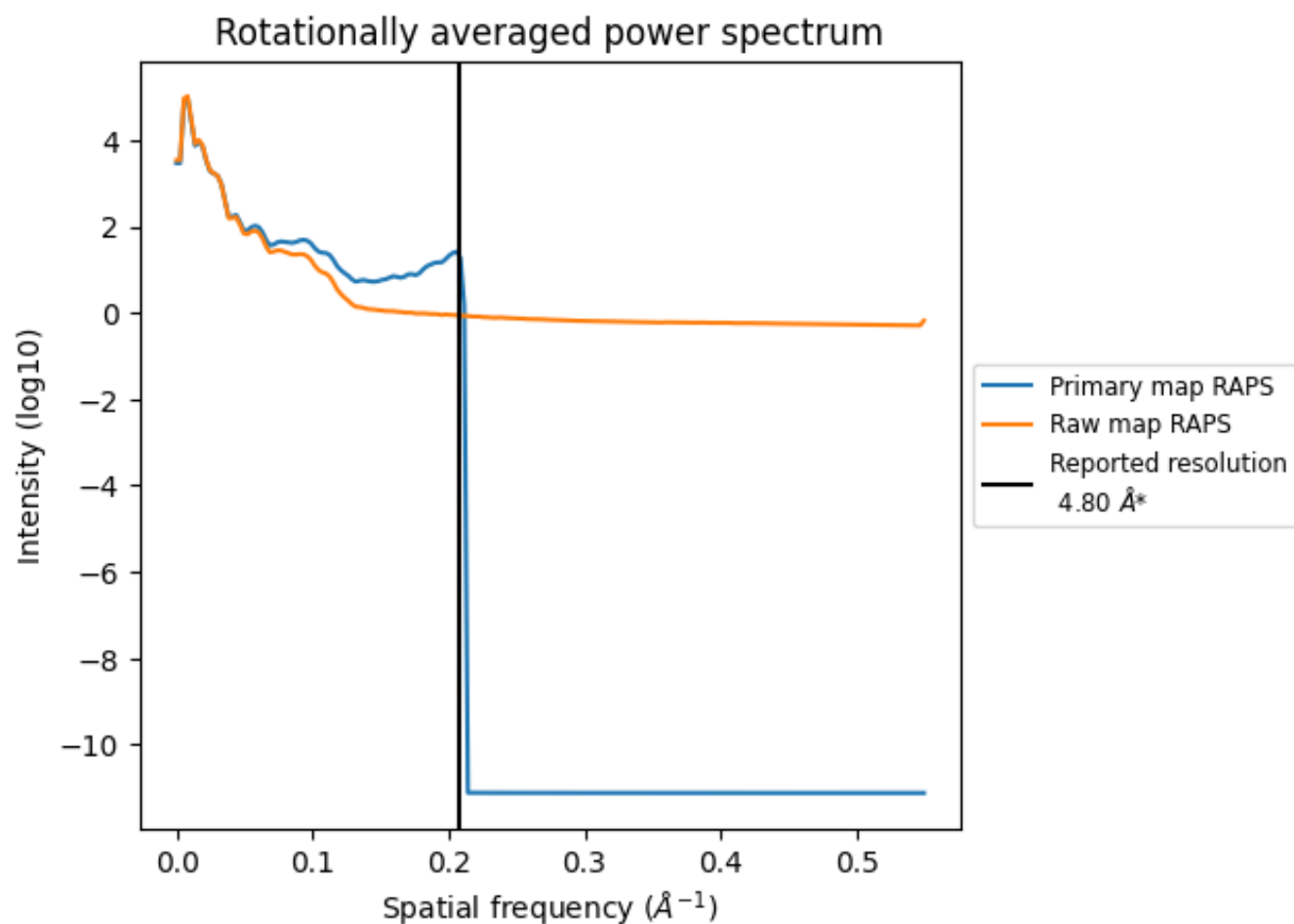
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 194 nm³; this corresponds to an approximate mass of 176 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 ⓘ

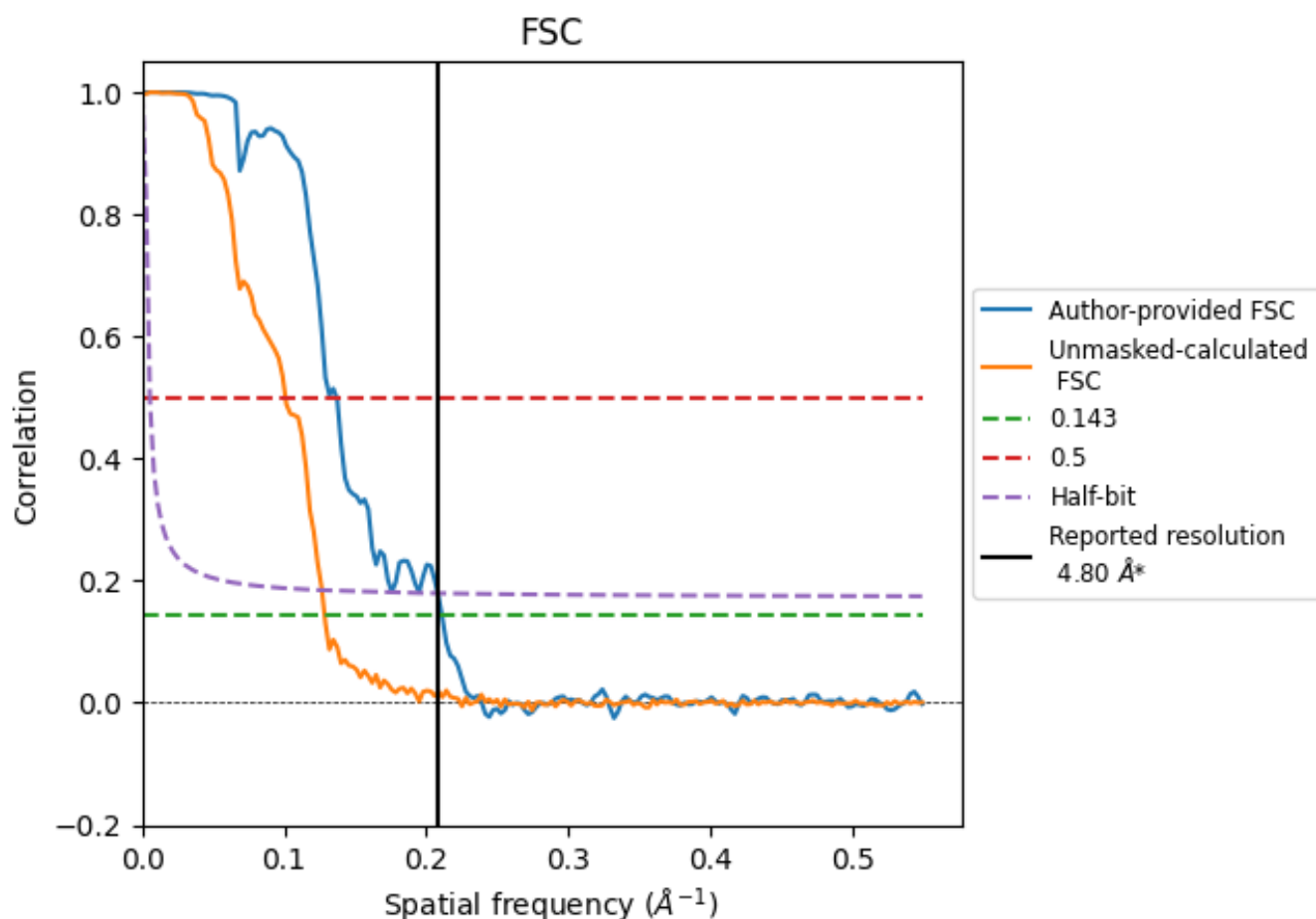


*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

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 0.208 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

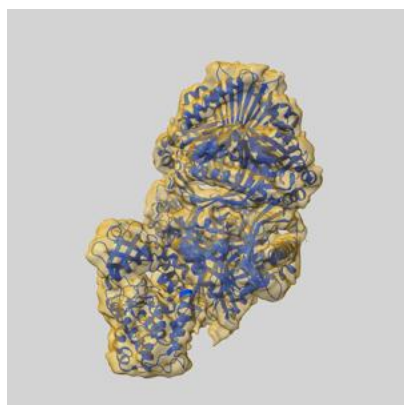
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	4.73	7.30	4.80
Unmasked-calculated*	7.78	9.90	7.90

*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 7.78 differs from the reported value 4.8 by more than 10 %

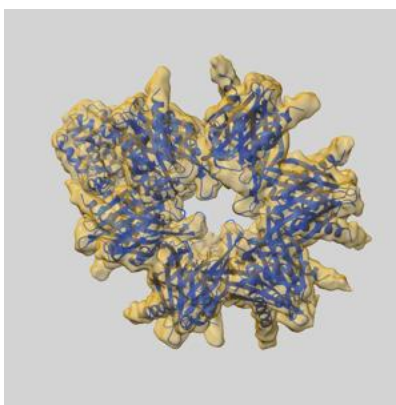
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21535 and PDB model 6W4O. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

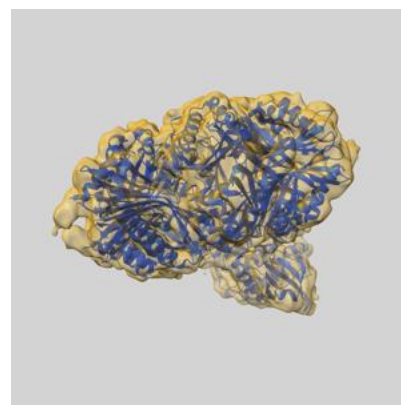
9.1 Map-model overlay [i](#)



X



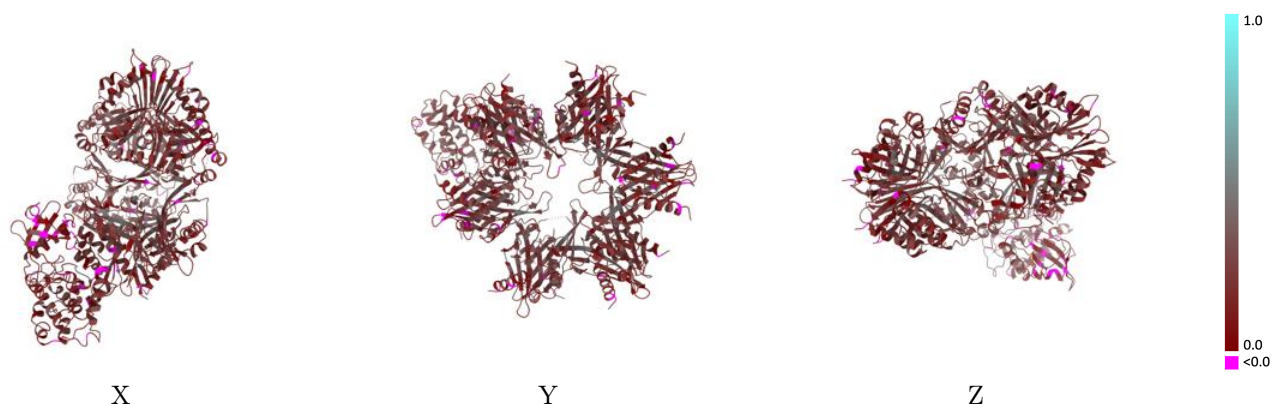
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0072 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](#)

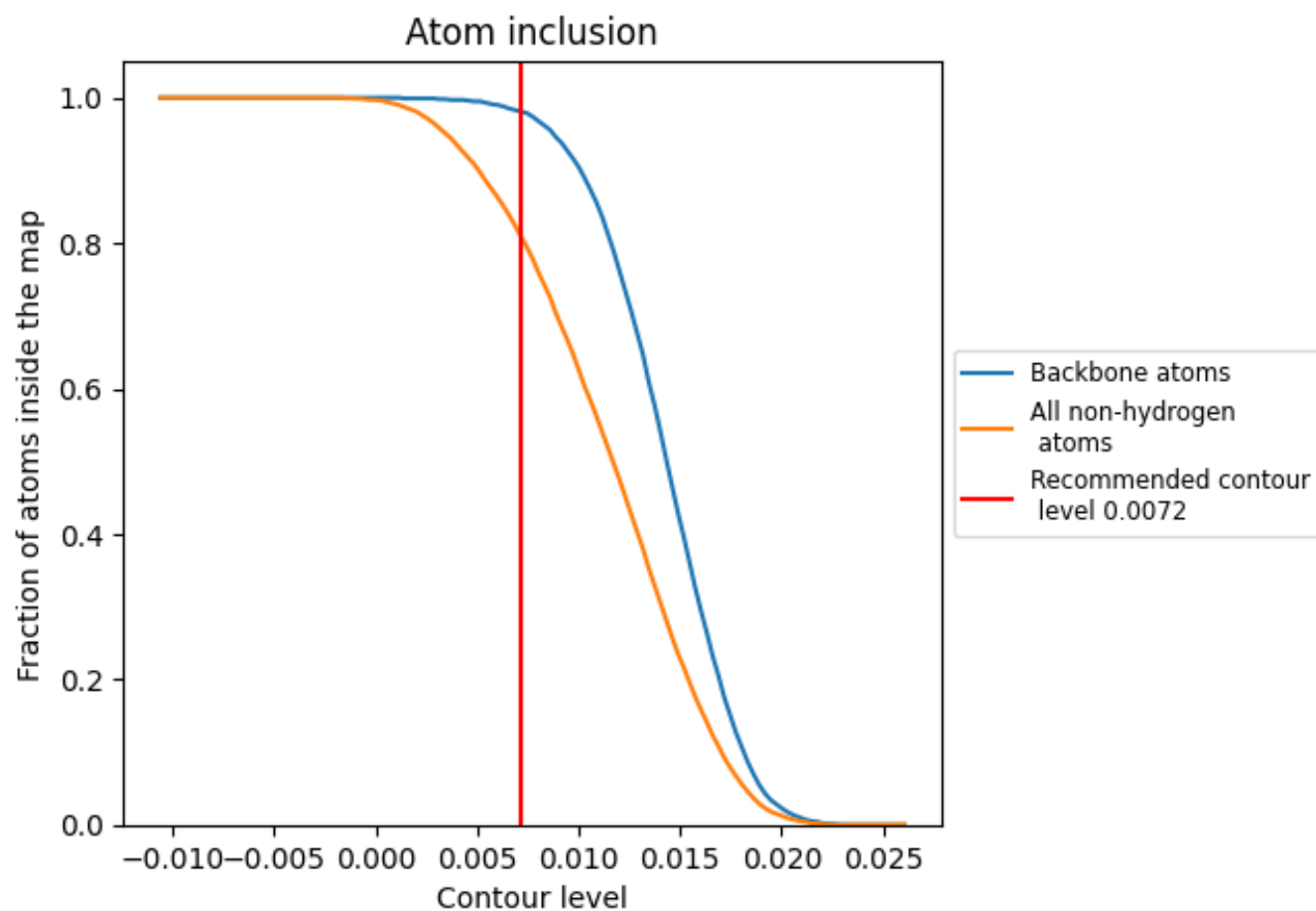


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 81% 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 (0.0072) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8070	 0.2130
A	 0.7940	 0.2140
B	 0.7890	 0.2160
C	 0.8000	 0.2260
D	 0.8120	 0.2150
E	 0.7910	 0.2130
F	 0.8130	 0.2290
G	 0.7890	 0.2170
I	 0.7880	 0.2110
J	 0.7840	 0.2360
K	 0.7960	 0.2270
L	 0.8060	 0.2180
M	 0.7910	 0.2270
O	 0.8630	 0.1750

