



## wwPDB EM Validation Summary Report ⓘ

Jun 25, 2025 – 10:01 PM JST

PDB ID : 8WFZ / pdb\_00008wfz  
EMDB ID : EMD-37500  
Title : AtGORK Full length 2  
Authors : Chen, Y.H.; Li, Q.Y.; Qin, L.; Tang, L.H.; zhang, C.R.  
Deposited on : 2023-09-20  
Resolution : 4.30 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](mailto: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>.

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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) : 2.44

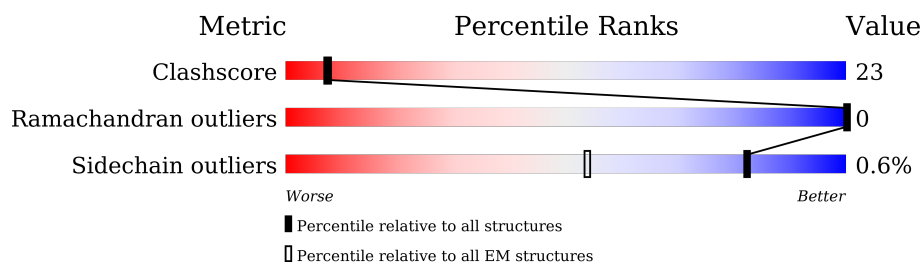
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.30 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  $\geq 3$ , 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	820	<div> <div>14%</div> <div>45%</div> <div>35%</div> <div>20%</div> </div>
1	B	820	<div> <div>15%</div> <div>45%</div> <div>35%</div> <div>20%</div> </div>
1	C	820	<div> <div>16%</div> <div>44%</div> <div>36%</div> <div>20%</div> </div>
1	D	820	<div> <div>13%</div> <div>48%</div> <div>32%</div> <div>20%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 21266 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.

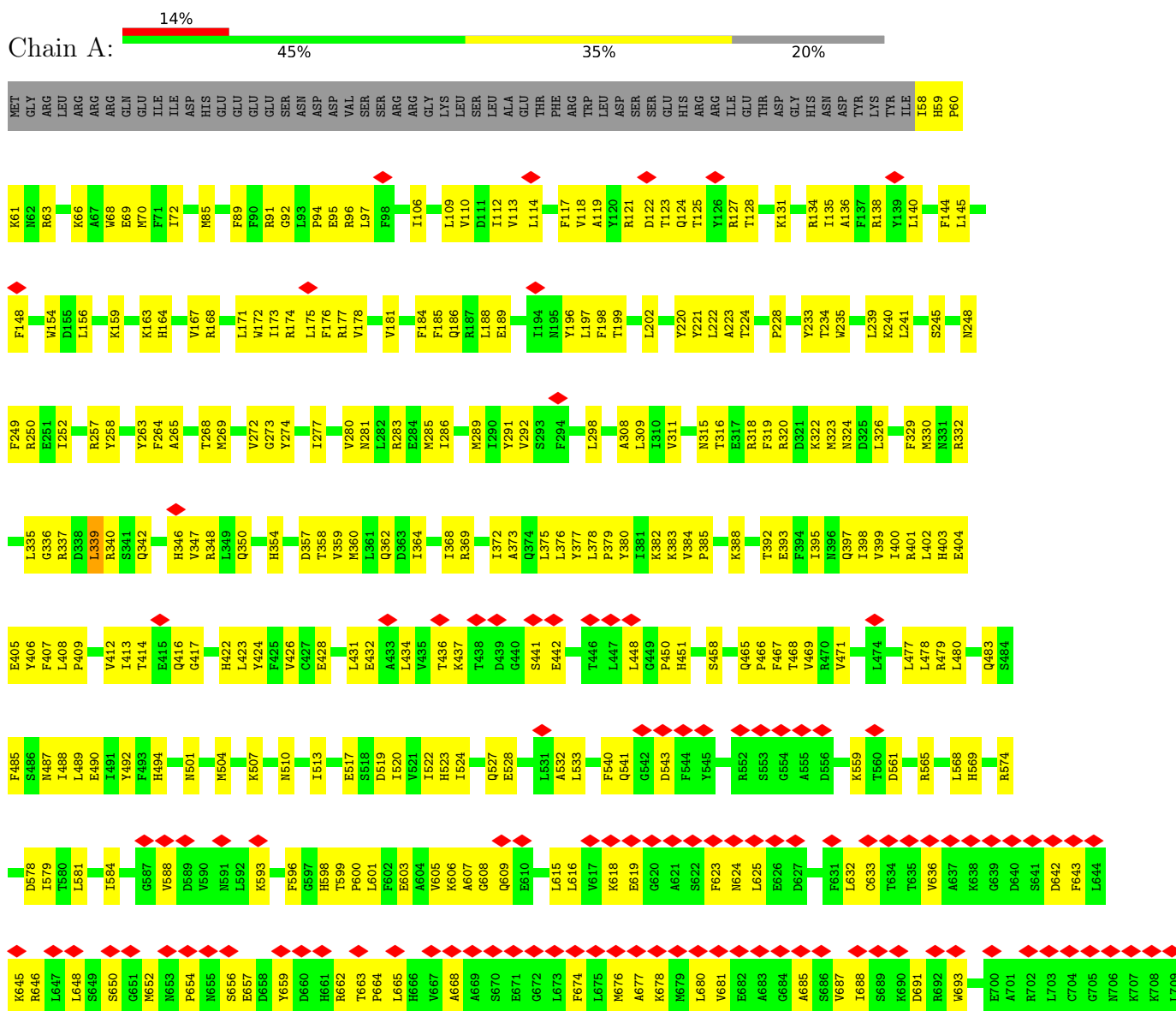
- Molecule 1 is a protein called Potassium channel GORK.

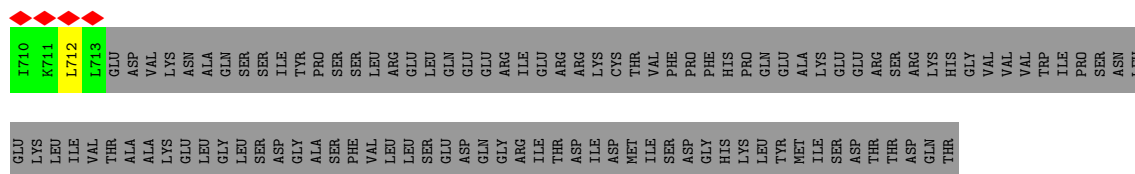
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	656	Total	C	N	O	S	0	0
			5315	3452	885	953	25		
1	B	656	Total	C	N	O	S	0	0
			5315	3452	885	953	25		
1	C	656	Total	C	N	O	S	0	0
			5321	3455	887	954	25		
1	D	656	Total	C	N	O	S	0	0
			5315	3452	885	953	25		

### 3 Residue-property plots

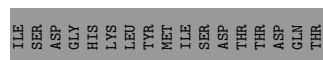
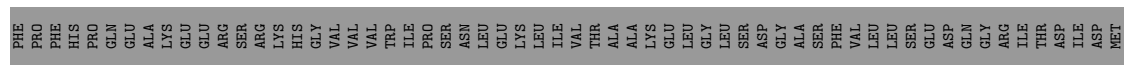
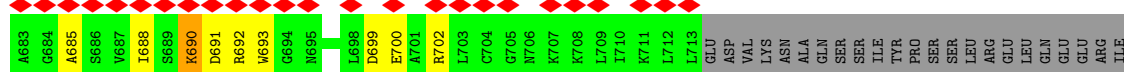
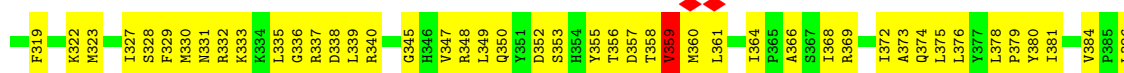
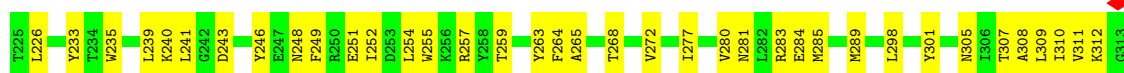
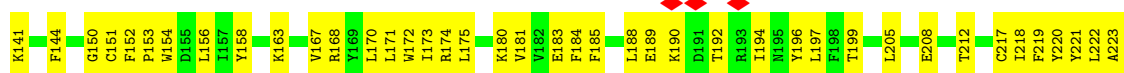
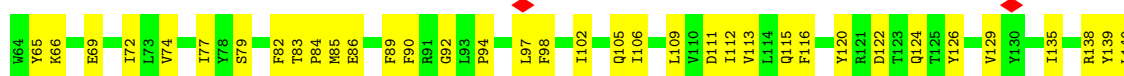
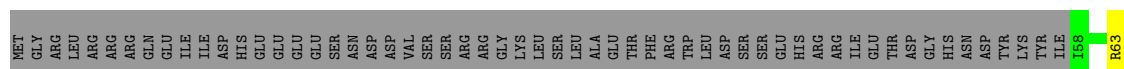
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

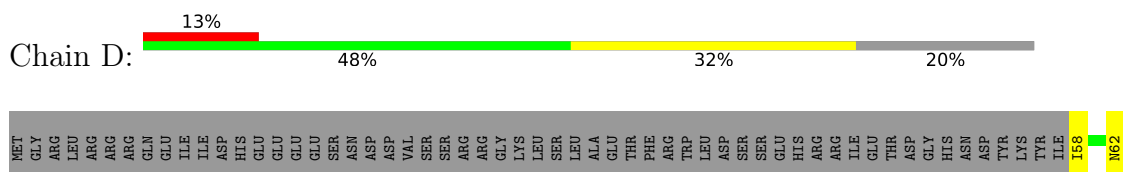
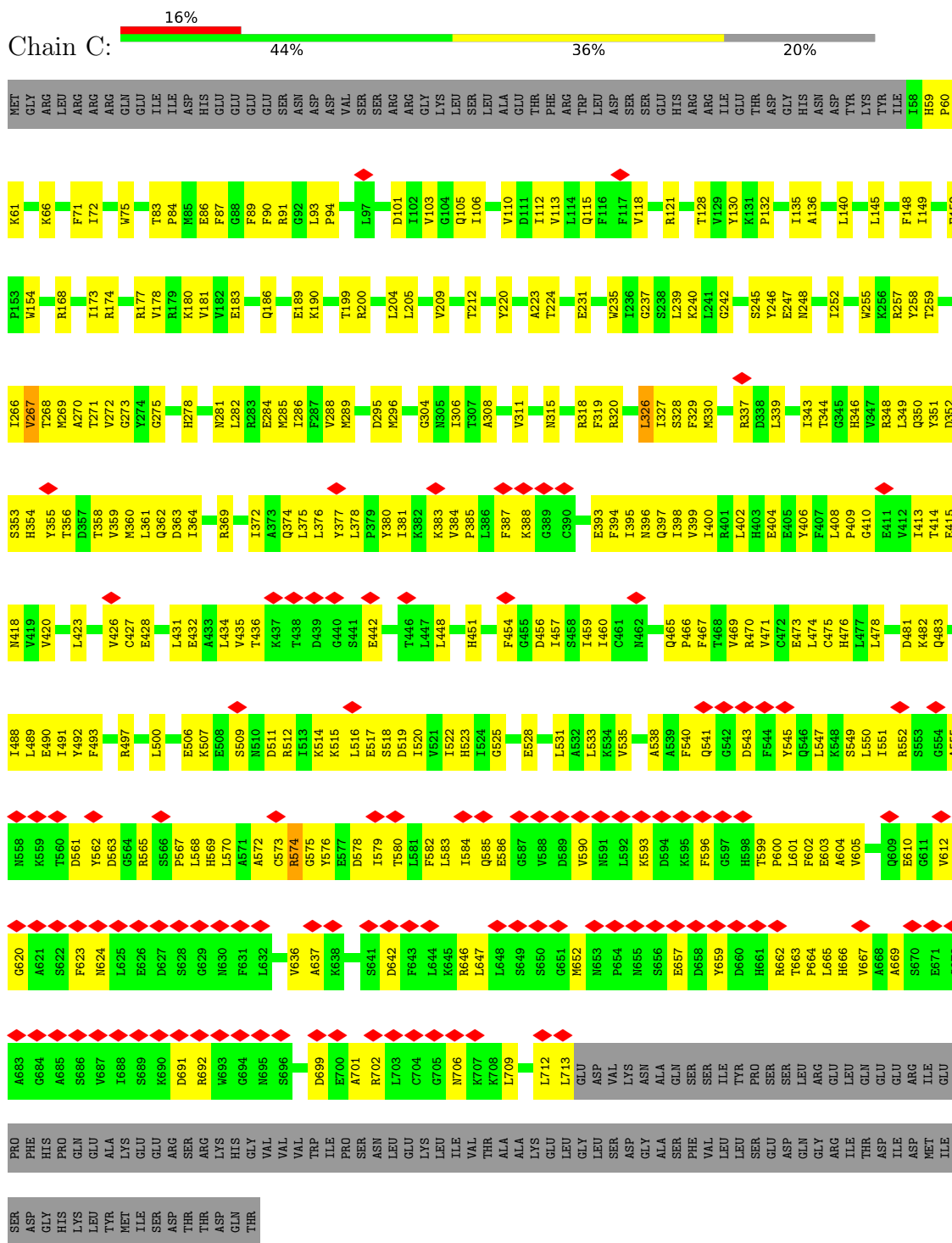
#### • Molecule 1: Potassium channel GORK





### ● Molecule 1: Potassium channel GORK





ALA	D658	L592	S509	L431	I343	L252	L140	R63
GLN	Y659	K593	RS10	L434	V347	D253	K141	W64
SER	D660	D594	RS11	V435	R348	R257	S142	Y65
LEU	K595	K596	RS12	T436	L349	Y258	H143	K66
ILE	F596	F597	IS13	K437	Q350	T259	I149	A67
TYR	G597	G598	K514	T438	T356	L262	W154	W68
PRO	H598	T599	D519	D439	T357	Y263	D155	E69
SER	P600	P600	Q527	G440	F264	F264	D155	W70
SER	L601	L601	Q527	G441	T358	A265	Y158	I72
LEU	F602	F602	E530	S441	L361	L266	K159	L73
ARG	E603	E603	L533	E442	Q362	Y267		
LEU	A607	A607	K534	V445	D363	T268	K163	I77
LEU	S670	S670	V535	T446	I364	M269	L81	Y78
SER	E671	G608	F544	L447	P365	V272	V167	L81
GLU	G672	Q609	Y545	L448	A366	G273	F92	F92
ARG	G673	E610	Q548	L448	A366	Y274	Y169	T83
GLY	L673	G611	S549	S453	R369	Y275	L170	P84
ARG	F674	V612	D543	S458	Q374	D276	L171	W85
ARG	L675	L615	F544	I459	Q374	I277	R174	E86
ASP	M676	L615	Y545	S458	Q374	I277	R174	F87
THR	A677	L615	Q546	I459	Q374	I277	R174	G88
ILE	K678	K618	L547	C461	L378	N281	R177	F89
VAL	M679	E619	L547	C461	L378	L282	V178	F90
PHE	M679	E620	K548	N462	K382	R283	R179	R91
PRO	L680	G520	S549	N463	K382	E284	K180	G92
PHE	V681	A621	L550	I463	F387	M285	V181	L93
HIS	E682	S622	IS51	F467	K388	D295	V182	P94
GLN	A683	F623	R552	T468	G389	I303	E183	E95
GLY	G684	N624	G554	V469	G389	T307	F184	
LEU	G684	L625	A555	R470	E393	A308	F185	F98
ALA	A685	E626	Q555	V471	F394	L309	Q186	G104
LYS	S686	D627	D556	C472	Q397	I310	R187	Q105
GLU	V687	S628	P557	L474	I398	V311	E189	I106
ILE	I688	G629	N558	H476	I399	F319	K190	A107
SER	S689	N630	T560	L477	I400	E208	D191	F108
ARG	K690	F631	D561	L478	R401	Y220	T192	L109
LYS	D691	L632	Y562	K482	L402	K322	E208	I112
GLY	R692	L632	G564	F485	H403	M323	Y220	V113
VAL	W693	V636	R565	S486	E404	L326	L226	L114
VAL	G694	A637	H569	N487	E405	I327	L226	Q115
VAL	N695	A637	L570	I488	Y406	S328	E231	R121
TRP	S696	K638	A571	L489	F407	F329	E231	Y126
ILE	P697	G639	G572	E490	P409	M330	T234	R127
PRO	L698	D640	A572	E490	G410	N331	W235	T128
SER	D699	S641	G575	D495	E411	R332	I236	V129
ASN	E700	D642	G575	G496	V420	K333	Y130	Y130
LEU	A701	F643	I579	R497	D421	K334	K131	K131
GLU	R702	L644	L579	L500	Y424	L335	L239	R134
LYS	L703	K645	I584	L500	F425	G336	K240	I136
VAL	C704	R646	Q585	I503	V426	R337	Y246	A136
THR	G705	L647	E586	M504	C427	D338	E247	F137
ALA	N706	L648	G587	E505	G429	L339	R250	R138
ALA	K707	S649	V588	E506	G429	R340	E251	Y139
LYS	K708	S650	D589	K507	G429			
	L709	G651	V590	E508	L430			
	I710	M652	N591					
	K711	N653						
	L712	P654						
	L713	N655						
	GLU	S656						
	ASP	E657						
	VAL							
	VAL							
	LYS							
	ASN							
GLU								
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GLY								
LEU								
LEU								
ALA								
LYS								
THR								
THR								
ASP								
GLN								
THR								

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39551	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.363	Depositor
Minimum map value	-0.173	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.085	Depositor
Map size ( $\text{\AA}$ )	305.27997, 305.27997, 305.27997	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.06, 1.06, 1.06	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	0.27	0/5438	0.52	3/7356 (0.0%)
1	B	0.35	0/5438	0.62	5/7356 (0.1%)
1	C	0.30	0/5445	0.56	5/7365 (0.1%)
1	D	0.37	0/5438	0.63	8/7356 (0.1%)
All	All	0.33	0/21759	0.59	21/29433 (0.1%)

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	393	GLU	N-CA-C	-9.32	101.10	111.07
1	D	186	GLN	N-CA-C	-7.88	102.69	111.28
1	B	359	VAL	N-CA-C	7.12	117.89	110.62
1	D	95	GLU	N-CA-C	-7.01	103.68	111.82
1	C	326	LEU	N-CA-C	-6.92	103.73	111.28

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	5315	0	5344	257	0
1	B	5315	0	5344	271	0
1	C	5321	0	5352	268	0
1	D	5315	0	5344	251	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	21266	0	21384	977	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 23.

The worst 5 of 977 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:339:LEU:CD1	1:A:340:ARG:HG2	1.52	1.36
1:C:271:THR:HA	1:D:272:VAL:CG2	1.63	1.25
1:C:356:THR:HG22	1:C:360:MET:CE	1.68	1.23
1:C:271:THR:CA	1:D:272:VAL:HG22	1.73	1.18
1:A:265:ALA:O	1:A:268:THR:HG22	1.41	1.17

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	654/820 (80%)	634 (97%)	20 (3%)	0	100	100
1	B	654/820 (80%)	637 (97%)	17 (3%)	0	100	100
1	C	654/820 (80%)	640 (98%)	14 (2%)	0	100	100
1	D	654/820 (80%)	642 (98%)	12 (2%)	0	100	100
All	All	2616/3280 (80%)	2553 (98%)	63 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	577/729 (79%)	575 (100%)	2 (0%)	91	92
1	B	577/729 (79%)	572 (99%)	5 (1%)	75	83
1	C	579/729 (79%)	576 (100%)	3 (0%)	86	90
1	D	577/729 (79%)	574 (100%)	3 (0%)	86	90
All	All	2310/2916 (79%)	2297 (99%)	13 (1%)	82	88

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	267	VAL
1	C	326	LEU
1	D	267	VAL
1	D	247	GLU
1	D	253	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	350	GLN
1	C	523	HIS
1	D	655	ASN
1	C	487	ASN
1	C	630	ASN

### 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 [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.

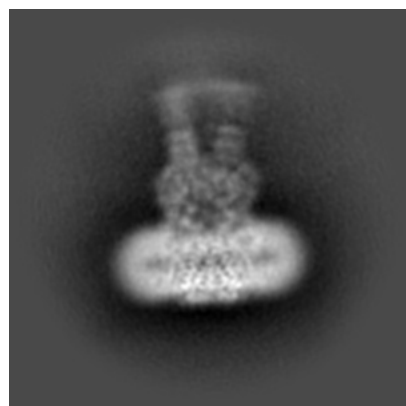
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37500. These allow visual inspection of the internal detail of the map and identification of artifacts.

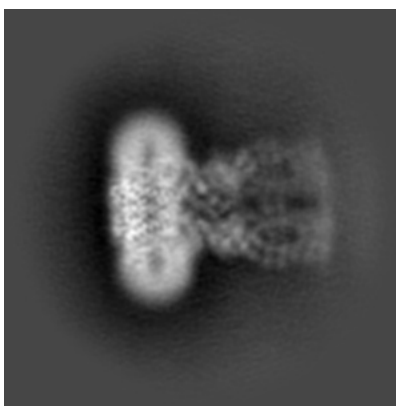
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

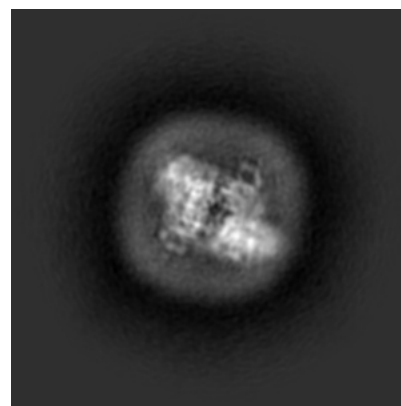
#### 6.1.1 Primary map



X

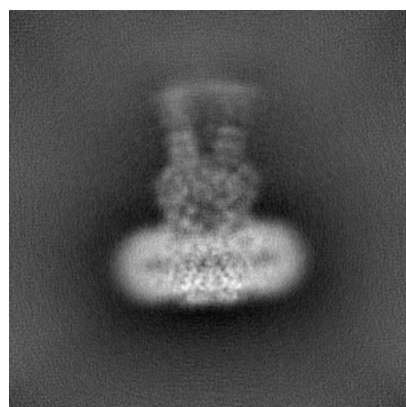


Y

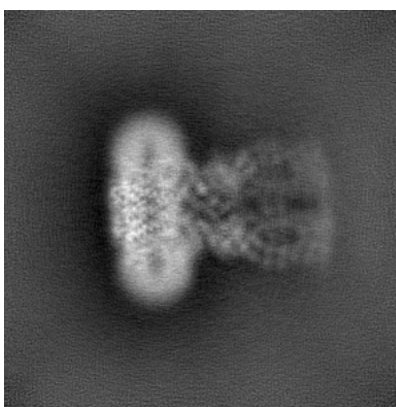


Z

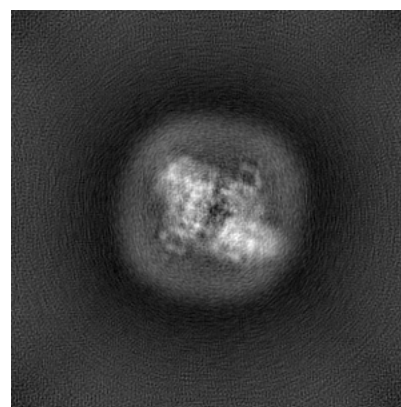
#### 6.1.2 Raw map



X



Y



Z

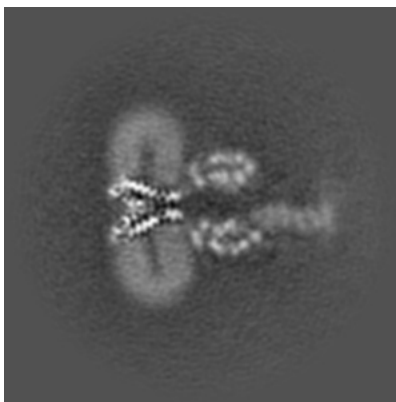
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

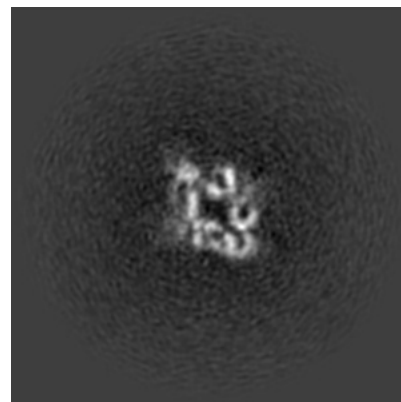
### 6.2.1 Primary map



X Index: 144

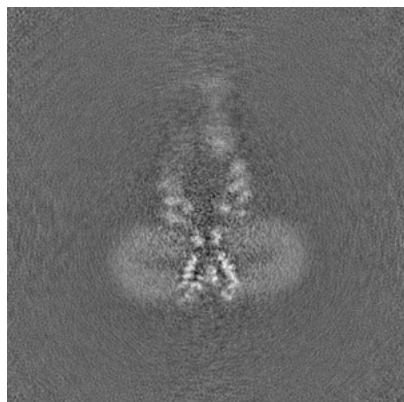


Y Index: 144

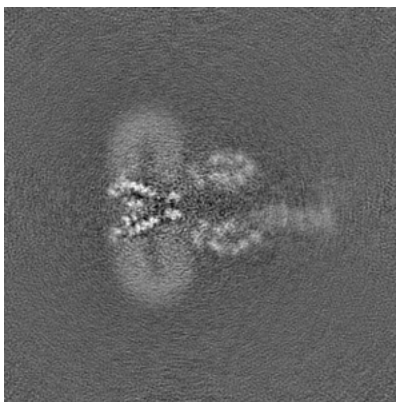


Z Index: 144

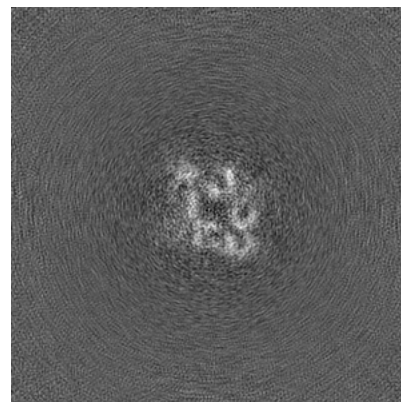
### 6.2.2 Raw map



X Index: 144



Y Index: 144

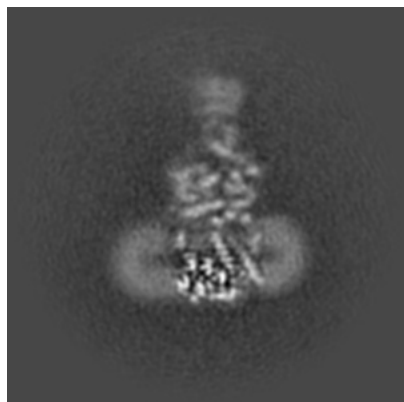


Z Index: 144

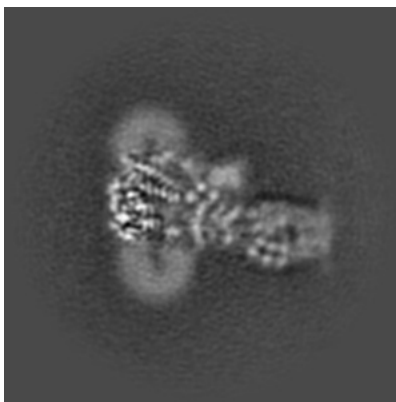
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

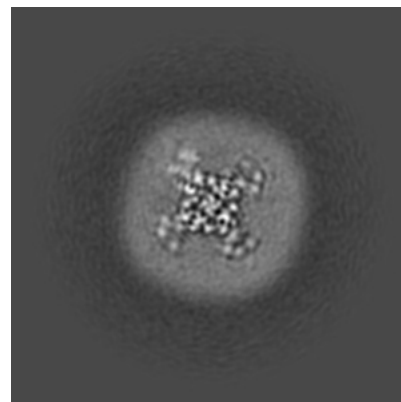
### 6.3.1 Primary map



X Index: 130

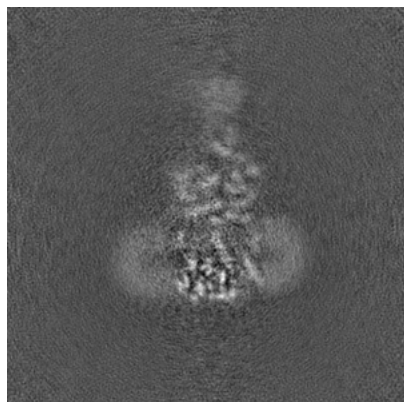


Y Index: 159

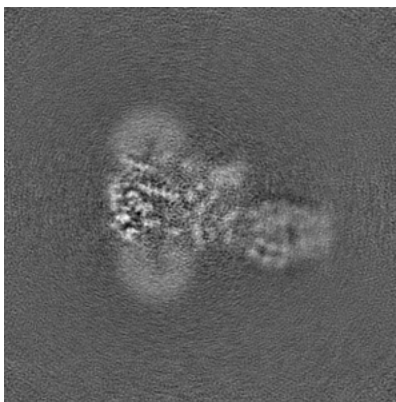


Z Index: 92

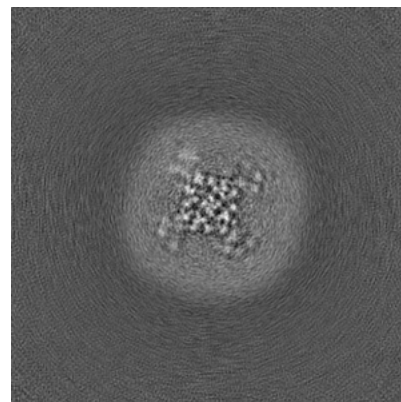
### 6.3.2 Raw map



X Index: 130



Y Index: 158

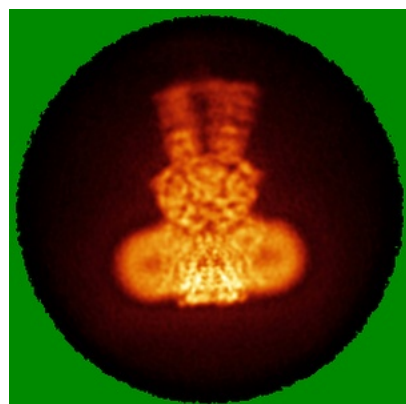


Z Index: 92

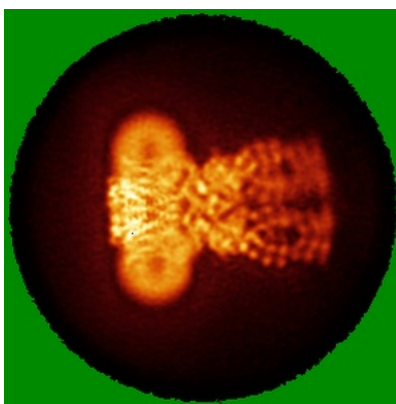
The images above show the largest variance slices of the map in three orthogonal directions.

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

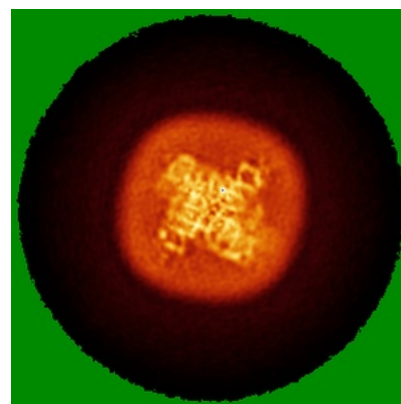
### 6.4.1 Primary map



X

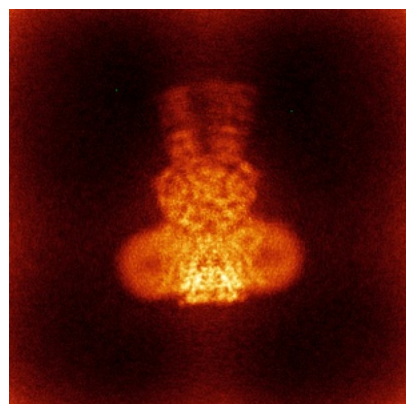


Y

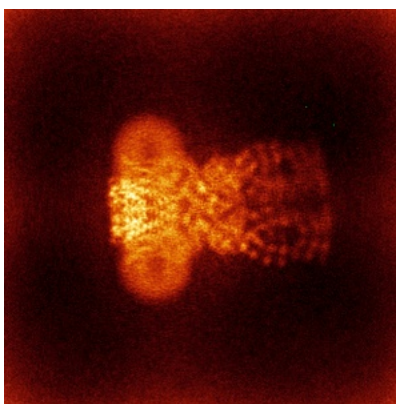


Z

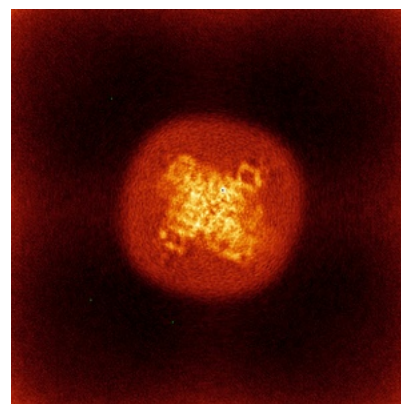
### 6.4.2 Raw map



X



Y

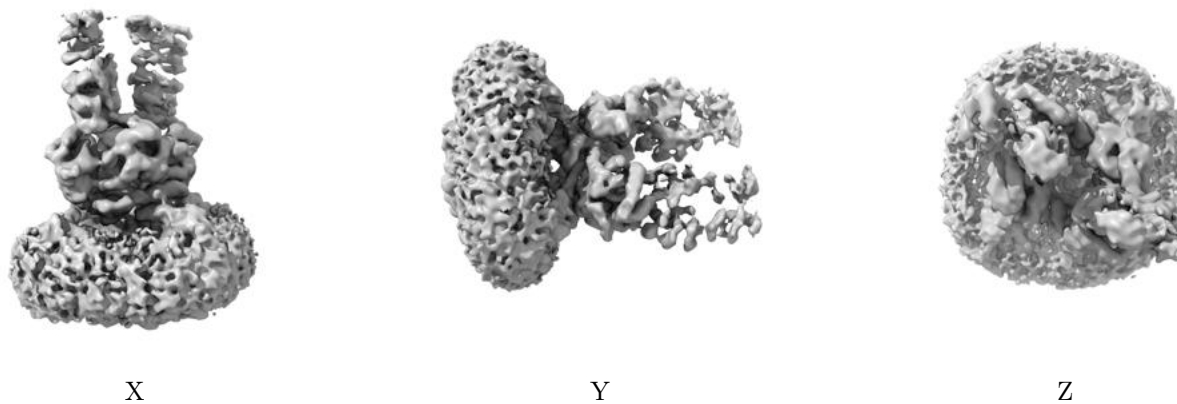


Z

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.

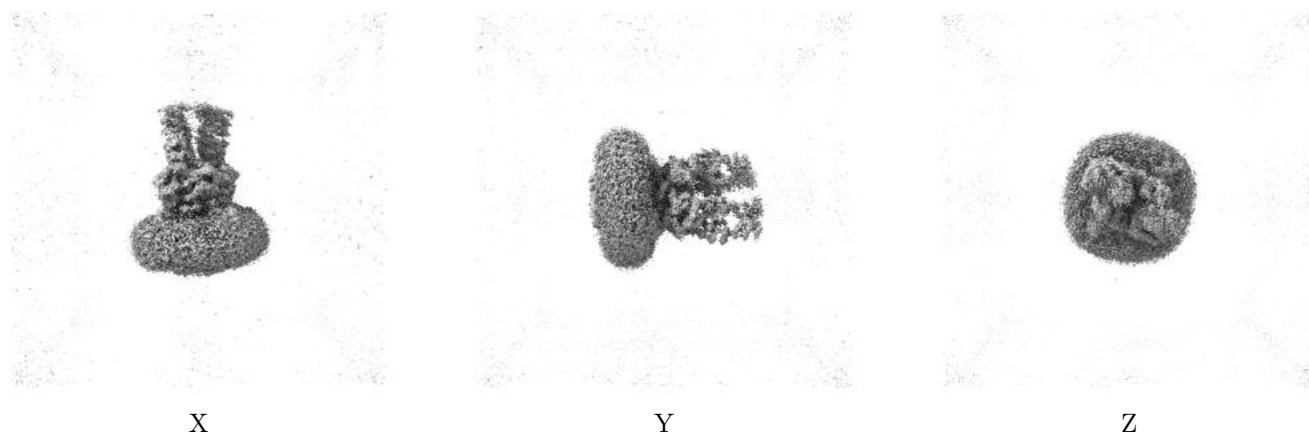
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.085. 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.

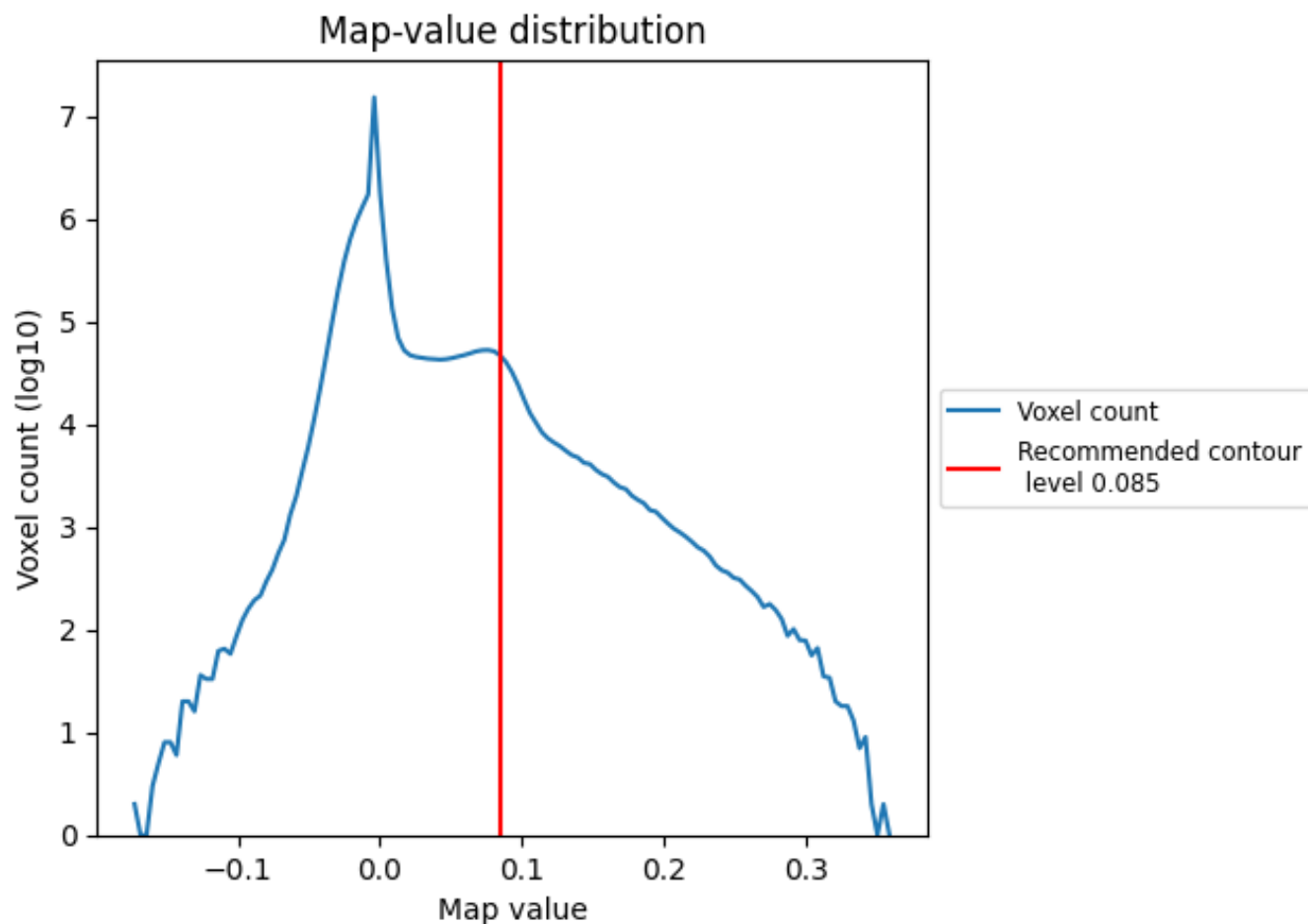
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

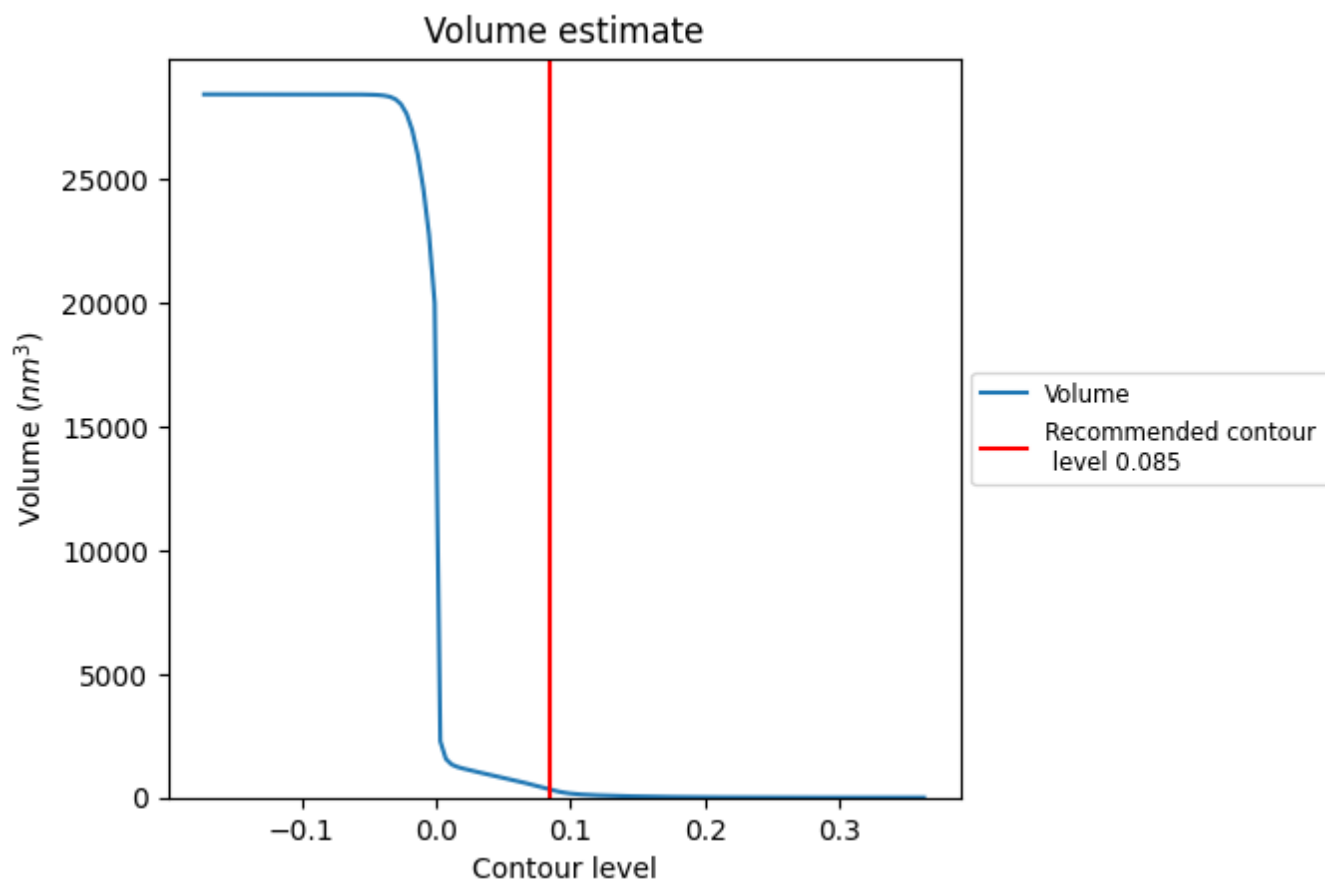
This section contains the results of statistical analysis of the map.

### 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.

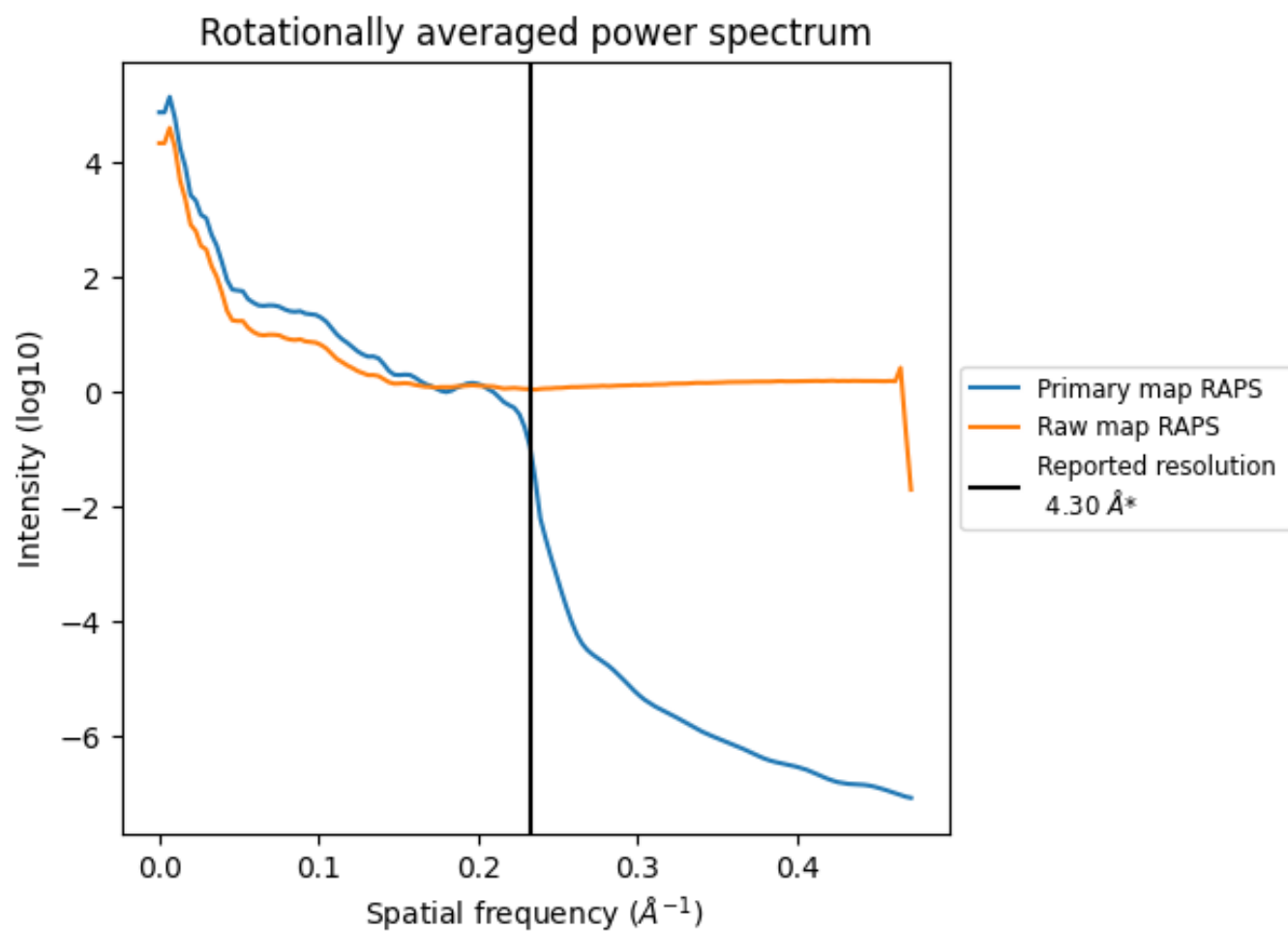
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 321 nm<sup>3</sup>; this corresponds to an approximate mass of 290 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 ⓘ

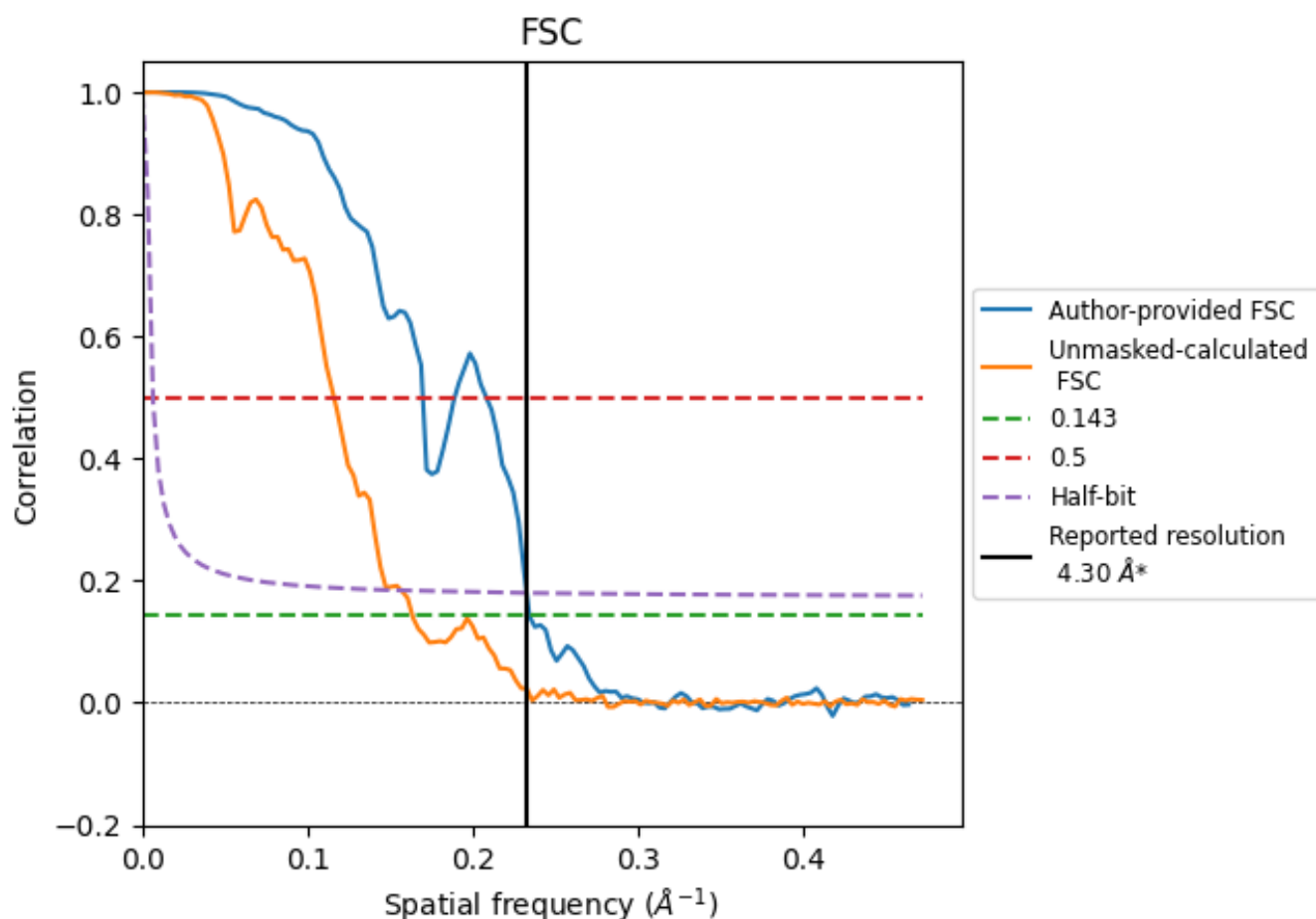


\*Reported resolution corresponds to spatial frequency of 0.233 Å<sup>-1</sup>

## 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  $0.233 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

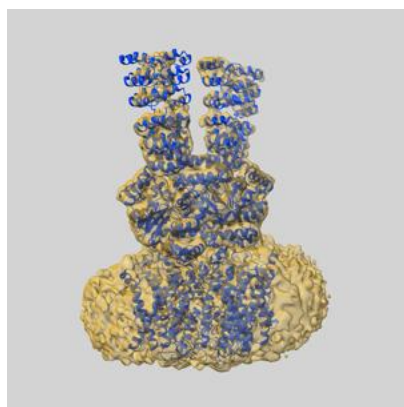
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.27	5.89	4.30
Unmasked-calculated*	6.12	8.62	6.38

\*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 6.12 differs from the reported value 4.3 by more than 10 %

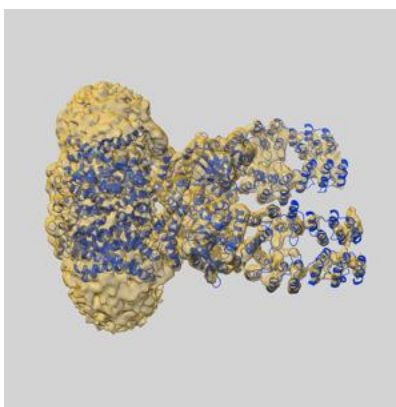
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37500 and PDB model 8WFZ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

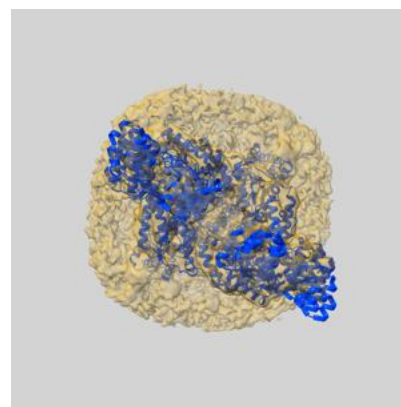
### 9.1 Map-model overlay [i](#)



X



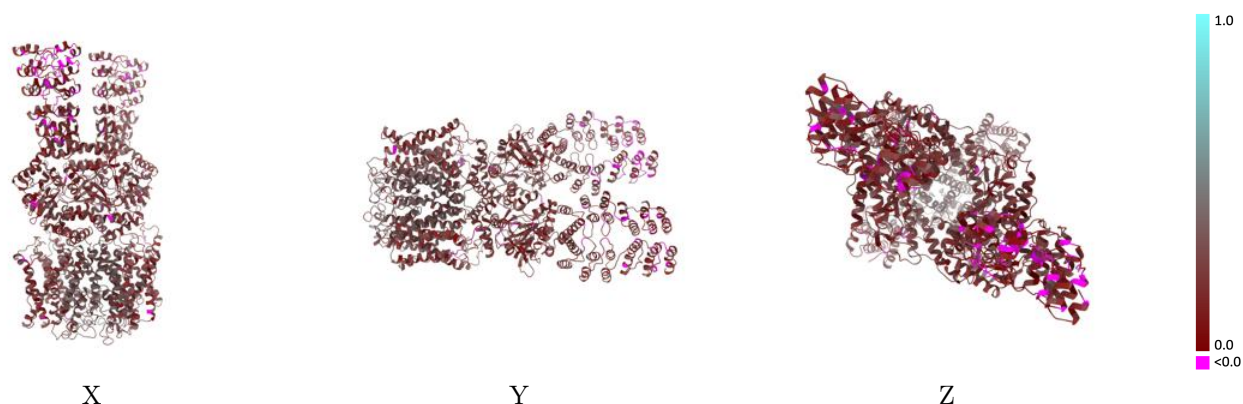
Y



Z

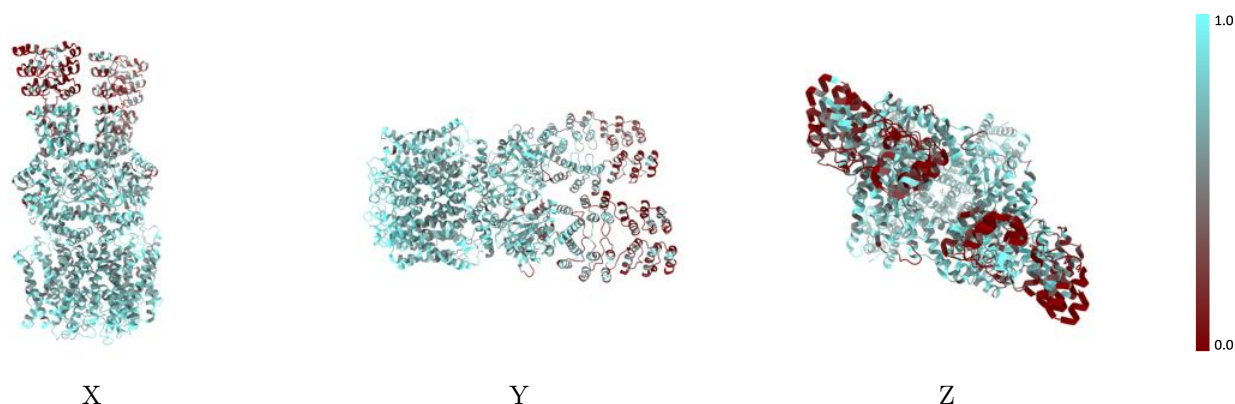
The images above show the 3D surface view of the map at the recommended contour level 0.085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



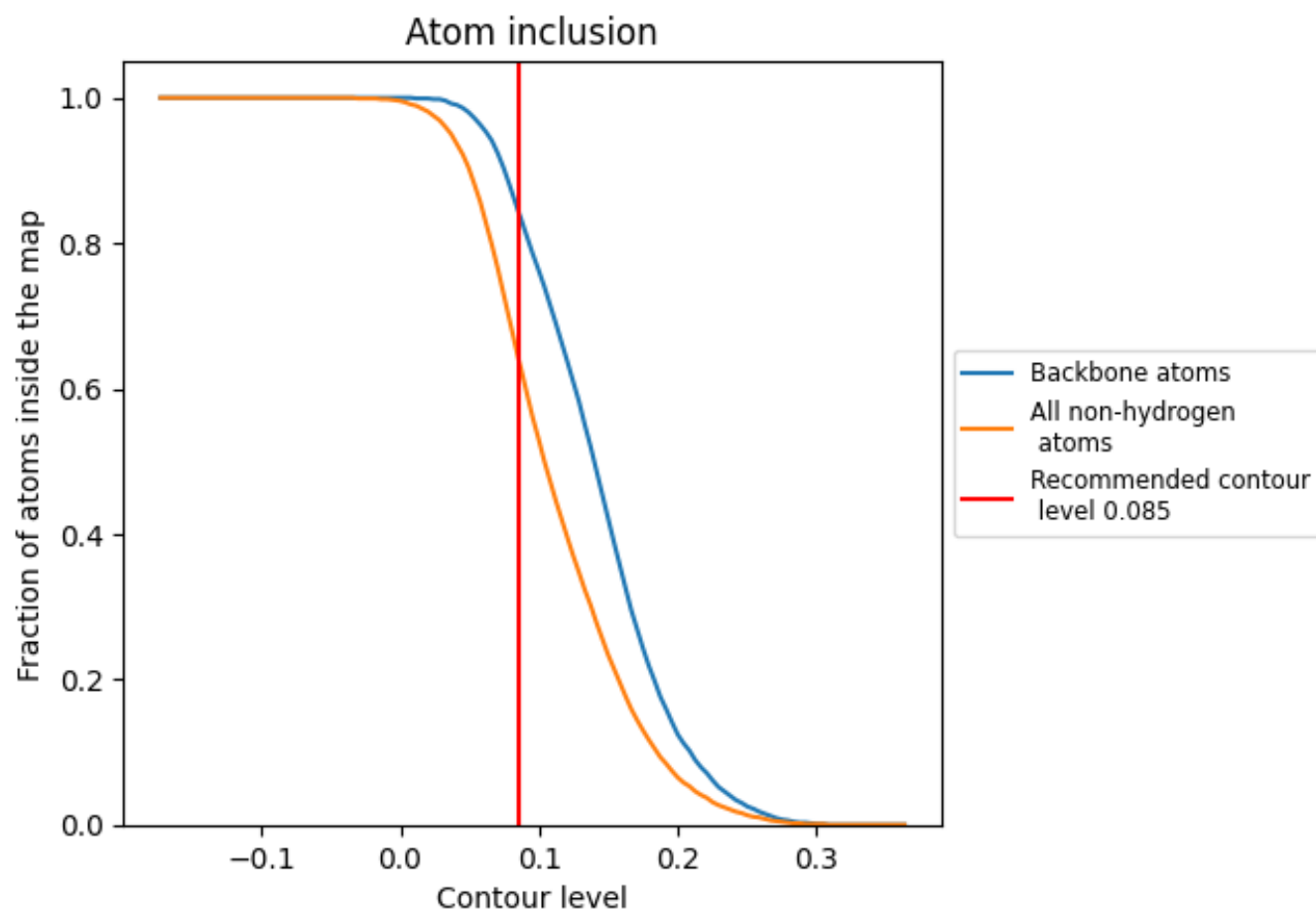
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.085).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 64% 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 (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6420	<div></div> 0.2330
A	<div></div> 0.6580	<div></div> 0.2300
B	<div></div> 0.6370	<div></div> 0.2330
C	<div></div> 0.6230	<div></div> 0.2430
D	<div></div> 0.6480	<div></div> 0.2280

