



## wwPDB EM Validation Summary Report ⓘ

Nov 15, 2022 – 07:24 PM EST

PDB ID : 6XJV  
EMDB ID : EMD-22215  
Title : MCU holocomplex in High-calcium state  
Authors : Wang, Y.; Jiang, Y.  
Deposited on : 2020-06-24  
Resolution : 4.17 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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

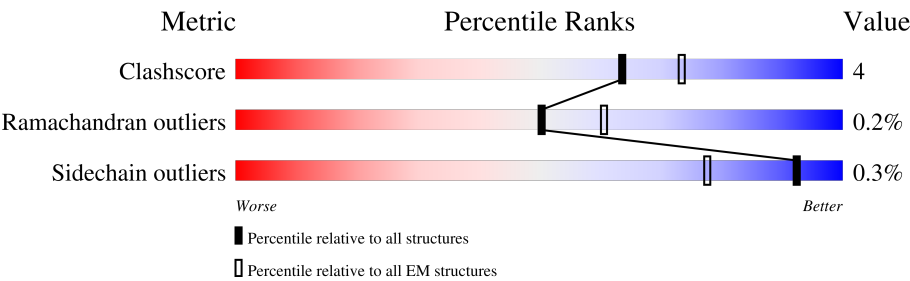
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 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 4.17 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.





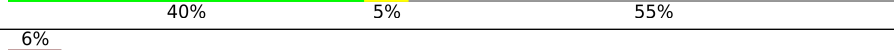
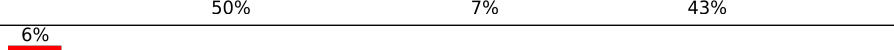
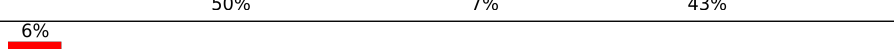

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	351	<div><div></div><div>68%9%22%</div></div>
1	C	351	<div><div></div><div>66%10%24%</div></div>
1	E	351	<div><div></div><div>67%9%23%</div></div>
1	G	351	<div><div></div><div>62%10%29%</div></div>
1	I	351	<div><div></div><div>67%10%22%</div></div>
1	K	351	<div><div></div><div>67%9%24%</div></div>
1	M	351	<div><div></div><div>66%11%23%</div></div>
1	O	351	<div><div></div><div>62%9%29%</div></div>

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
2	B	107	
2	D	107	
2	F	107	
2	H	107	
2	J	107	
2	L	107	
2	N	107	
2	P	107	
3	Q	476	
3	S	476	
4	R	434	
4	T	434	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 29921 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 uniporter protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	273	Total	C	N	O	S	0	0
			2254	1444	393	409	8		
1	C	268	Total	C	N	O	S	0	0
			2211	1416	384	403	8		
1	E	270	Total	C	N	O	S	0	0
			2226	1427	386	405	8		
1	G	250	Total	C	N	O	S	0	0
			2069	1329	357	375	8		
1	I	273	Total	C	N	O	S	0	0
			2254	1444	393	409	8		
1	K	268	Total	C	N	O	S	0	0
			2211	1416	384	403	8		
1	M	270	Total	C	N	O	S	0	0
			2226	1427	386	405	8		
1	O	250	Total	C	N	O	S	0	0
			2069	1329	357	375	8		

- Molecule 2 is a protein called Essential MCU regulator, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	53	Total	C	N	O	S	0	0
			416	281	65	69	1		
2	D	49	Total	C	N	O	S	0	0
			381	256	61	63	1		
2	F	53	Total	C	N	O	S	0	0
			414	281	65	67	1		
2	H	48	Total	C	N	O	S	0	0
			373	252	60	60	1		
2	J	53	Total	C	N	O	S	0	0
			416	281	65	69	1		
2	L	49	Total	C	N	O	S	0	0
			381	256	61	63	1		
2	N	53	Total	C	N	O	S	0	0
			414	281	65	67	1		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	48	Total	C	N	O	S	0	0
			373	252	60	60	1		

- Molecule 3 is a protein called Calcium uptake protein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	269	Total	C	N	O	S	0	0
			2189	1404	365	407	13		
3	S	270	Total	C	N	O	S	0	0
			2198	1410	367	408	13		

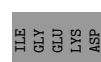
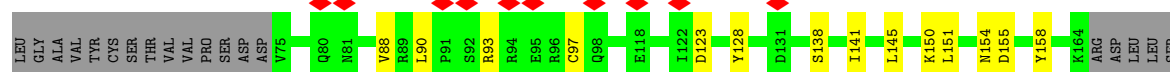
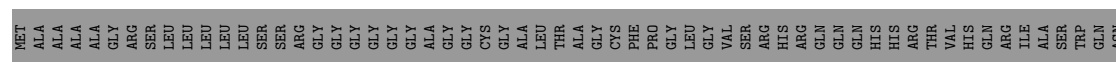
- Molecule 4 is a protein called Calcium uptake protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	291	Total	C	N	O	S	0	0
			2423	1558	409	440	16		
4	T	291	Total	C	N	O	S	0	0
			2423	1558	409	440	16		

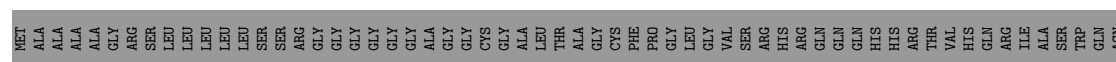




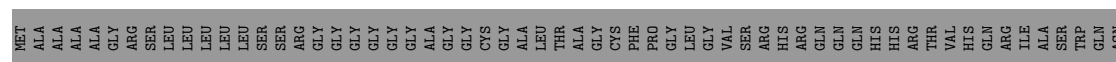
- Molecule 1: Calcium uniporter protein, mitochondrial



- Molecule 1: Calcium uniporter protein, mitochondrial



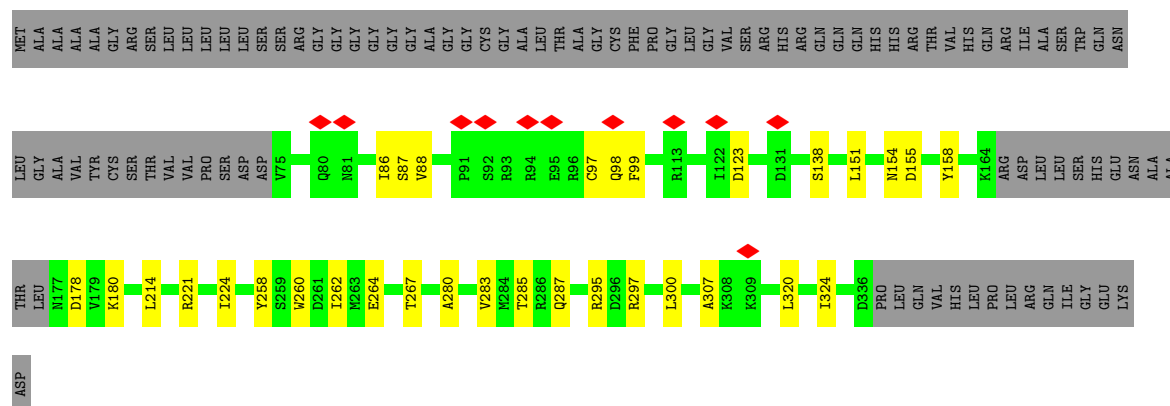
- Molecule 1: Calcium uniporter protein, mitochondrial



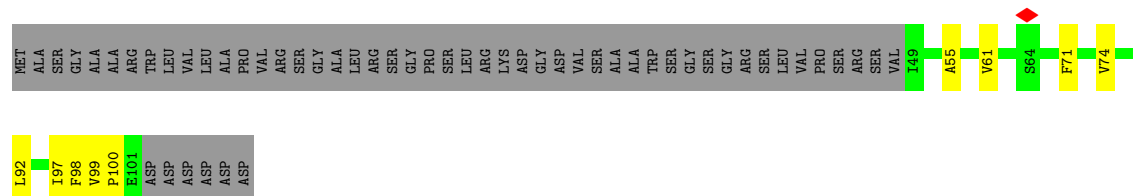
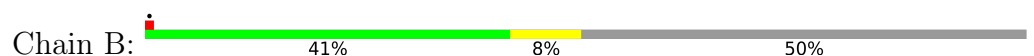
- Molecule 1: Calcium uniporter protein, mitochondrial



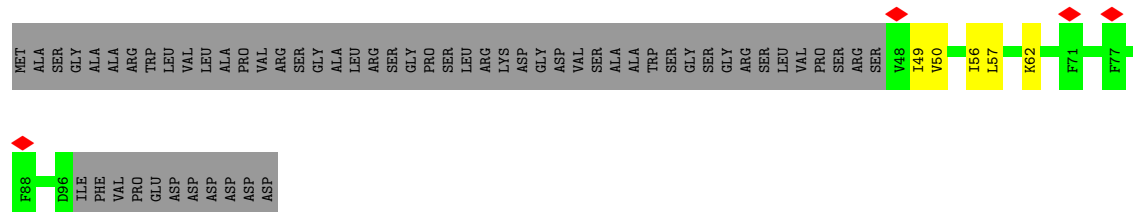
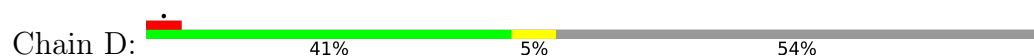
- Molecule 1: Calcium uniporter protein, mitochondrial



- Molecule 2: Essential MCU regulator, mitochondrial



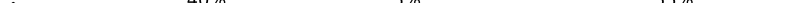
- Molecule 2: Essential MCU regulator, mitochondrial

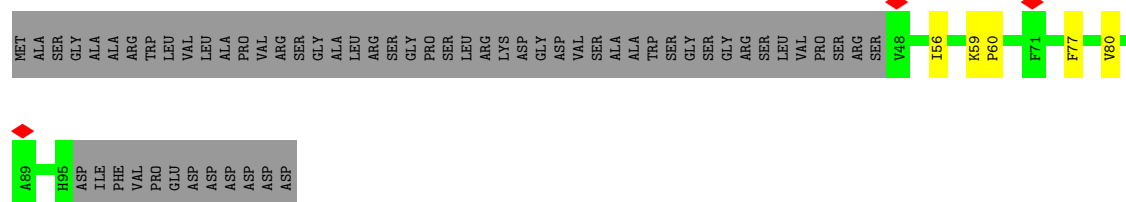


- Molecule 2: Essential MCU regulator, mitochondrial



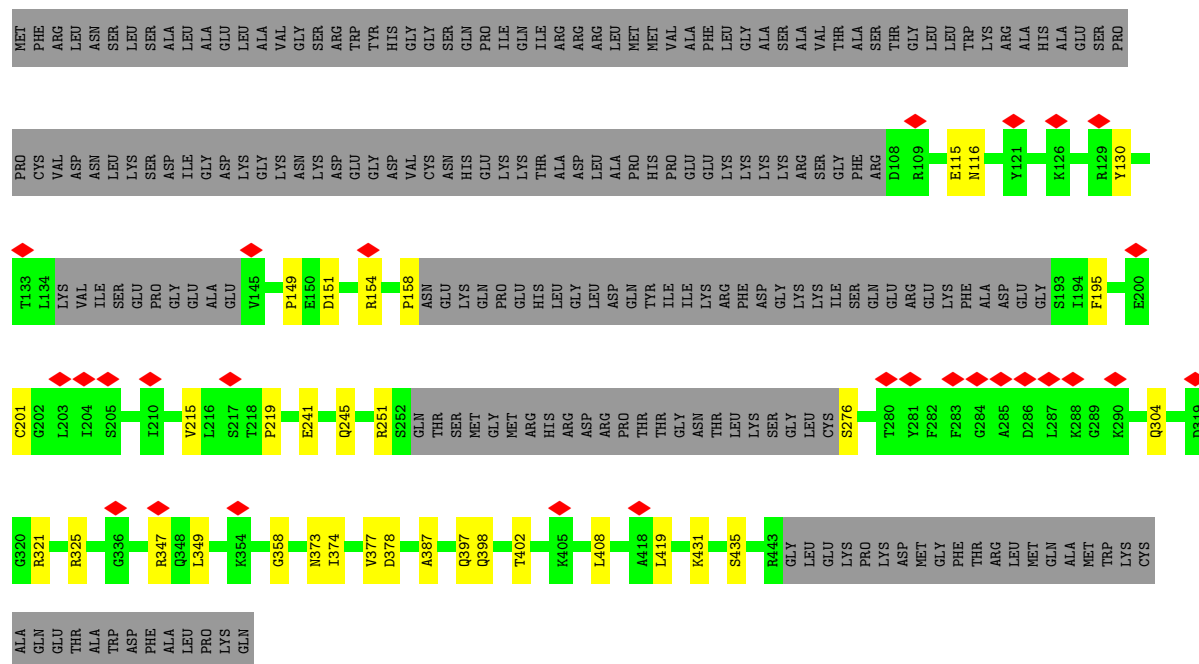


Chain P: 



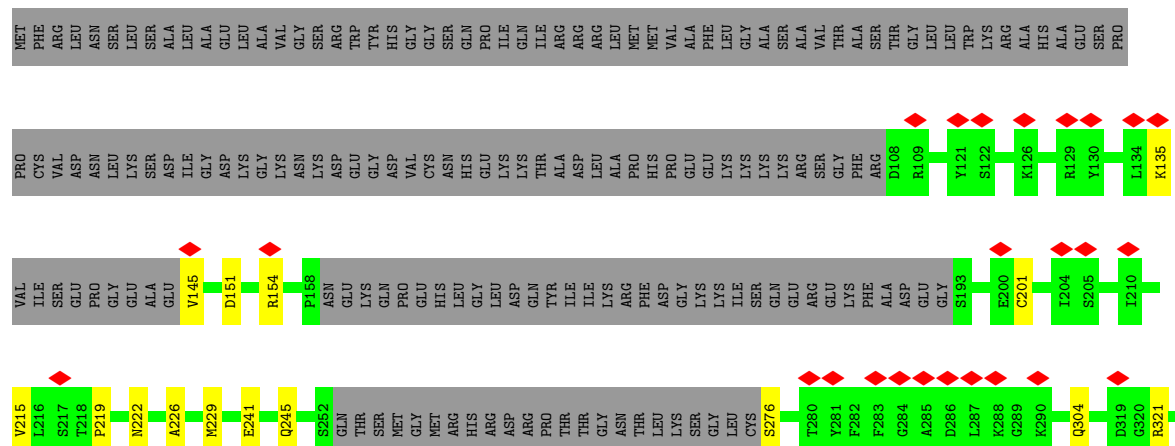
- Molecule 3: Calcium uptake protein 1, mitochondrial

Chain Q: 

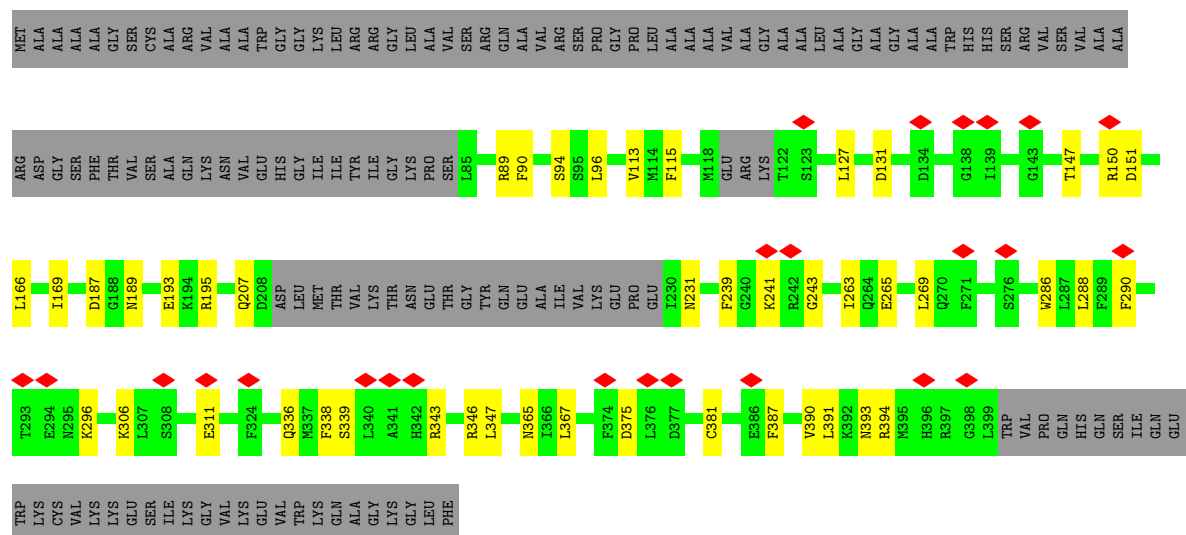


- Molecule 3: Calcium uptake protein 1, mitochondrial

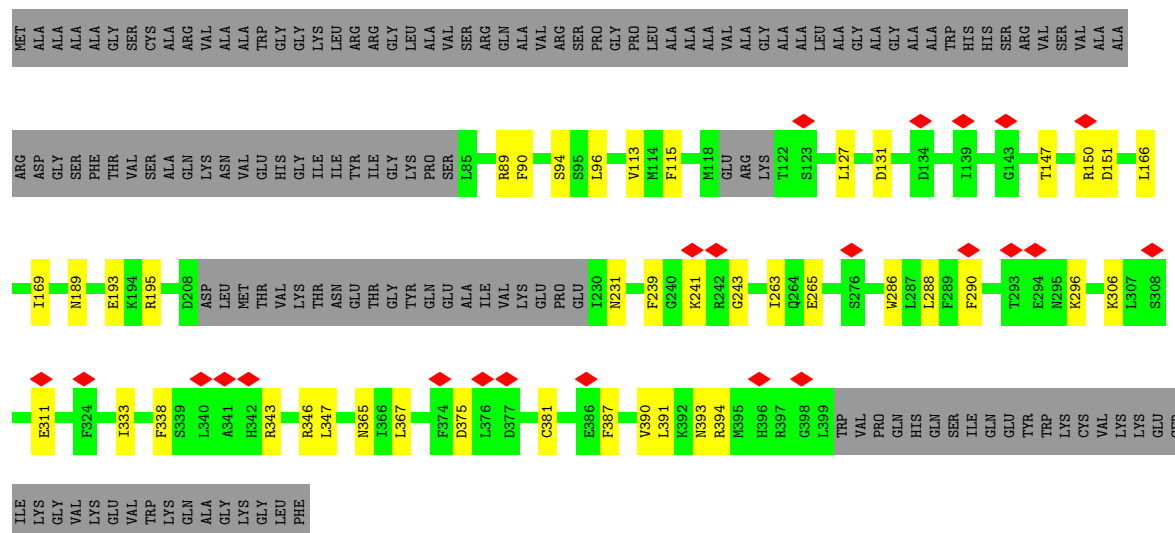
Chain S:  6% 50% 7% 43%



- Molecule 4: Calcium uptake protein 2, mitochondrial



- Molecule 4: Calcium uptake protein 2, mitochondrial



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19924	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size ( $\text{\AA}$ )	299.88, 299.88, 299.88	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.833, 0.833, 0.833	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	0.35	0/2300	0.59	0/3114
1	C	0.37	0/2256	0.62	0/3054
1	E	0.36	0/2272	0.62	2/3077 (0.1%)
1	G	0.34	0/2110	0.59	0/2852
1	I	0.35	0/2300	0.59	0/3114
1	K	0.36	0/2256	0.59	0/3054
1	M	0.36	0/2272	0.61	2/3077 (0.1%)
1	O	0.34	0/2110	0.59	0/2852
2	B	0.34	0/426	0.60	0/578
2	D	0.34	0/389	0.61	0/527
2	F	0.33	0/424	0.61	0/576
2	H	0.32	0/381	0.64	0/516
2	J	0.43	1/426 (0.2%)	0.70	2/578 (0.3%)
2	L	0.35	0/389	0.60	0/527
2	N	0.32	0/424	0.63	0/576
2	P	0.32	0/381	0.63	0/516
3	Q	0.31	0/2229	0.52	0/2989
3	S	0.31	0/2238	0.51	0/3000
4	R	0.31	0/2473	0.48	0/3302
4	T	0.32	0/2473	0.48	0/3302
All	All	0.34	1/30529 (0.0%)	0.57	6/41181 (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
1	E	0	1
1	I	0	1
1	K	0	1
2	B	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	99	VAL	C-N	5.05	1.43	1.34

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	96	ASP	CB-CG-OD1	6.51	124.16	118.30
1	E	153	ILE	CG1-CB-CG2	-6.11	97.95	111.40
1	M	153	ILE	CG1-CB-CG2	-6.04	98.12	111.40
1	E	155	ASP	CB-CG-OD1	5.64	123.38	118.30
1	M	155	ASP	CB-CG-OD1	5.59	123.33	118.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	91	PRO	Peptide
2	B	99	VAL	Peptide
1	E	339	GLN	Peptide
1	I	91	PRO	Peptide
1	K	161	ARG	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	2254	0	2287	25	0
1	C	2211	0	2237	26	0
1	E	2226	0	2255	24	0
1	G	2069	0	2099	24	0
1	I	2254	0	2287	27	0
1	K	2211	0	2237	26	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	M	2226	0	2255	27	0
1	O	2069	0	2099	22	0
2	B	416	0	445	5	0
2	D	381	0	412	4	0
2	F	414	0	448	3	0
2	H	373	0	408	4	0
2	J	416	0	445	4	0
2	L	381	0	412	6	0
2	N	414	0	448	3	0
2	P	373	0	408	4	0
3	Q	2189	0	2168	19	0
3	S	2198	0	2181	16	0
4	R	2423	0	2398	26	0
4	T	2423	0	2398	23	0
All	All	29921	0	30327	260	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 4.

The worst 5 of 260 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)
3:S:201:CYS:HG	3:S:276:SER:N	1.57	1.00
3:Q:201:CYS:HG	3:Q:276:SER:N	1.72	0.86
1:C:94:ARG:HE	1:K:94:ARG:HE	1.39	0.68
1:M:259:SER:H	1:M:262:ILE:HD12	1.60	0.66
1:C:290:VAL:HG12	1:C:292:PRO:HD2	1.77	0.66

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	271/351 (77%)	256 (94%)	13 (5%)	2 (1%)	22	62
1	C	266/351 (76%)	251 (94%)	15 (6%)	0	100	100
1	E	268/351 (76%)	251 (94%)	16 (6%)	1 (0%)	34	71
1	G	246/351 (70%)	238 (97%)	8 (3%)	0	100	100
1	I	271/351 (77%)	258 (95%)	11 (4%)	2 (1%)	22	62
1	K	266/351 (76%)	250 (94%)	16 (6%)	0	100	100
1	M	268/351 (76%)	254 (95%)	13 (5%)	1 (0%)	34	71
1	O	246/351 (70%)	239 (97%)	7 (3%)	0	100	100
2	B	51/107 (48%)	43 (84%)	8 (16%)	0	100	100
2	D	47/107 (44%)	46 (98%)	1 (2%)	0	100	100
2	F	51/107 (48%)	48 (94%)	3 (6%)	0	100	100
2	H	46/107 (43%)	44 (96%)	2 (4%)	0	100	100
2	J	51/107 (48%)	44 (86%)	7 (14%)	0	100	100
2	L	47/107 (44%)	46 (98%)	1 (2%)	0	100	100
2	N	51/107 (48%)	48 (94%)	3 (6%)	0	100	100
2	P	46/107 (43%)	44 (96%)	2 (4%)	0	100	100
3	Q	261/476 (55%)	248 (95%)	13 (5%)	0	100	100
3	S	262/476 (55%)	249 (95%)	13 (5%)	0	100	100
4	R	285/434 (66%)	272 (95%)	13 (5%)	0	100	100
4	T	285/434 (66%)	272 (95%)	13 (5%)	0	100	100
All	All	3585/5484 (65%)	3401 (95%)	178 (5%)	6 (0%)	50	80

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	92	SER
1	E	155	ASP
1	I	92	SER
1	M	155	ASP
1	A	91	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	245/299 (82%)	244 (100%)	1 (0%)	91	94
1	C	240/299 (80%)	238 (99%)	2 (1%)	81	89
1	E	242/299 (81%)	242 (100%)	0	100	100
1	G	224/299 (75%)	224 (100%)	0	100	100
1	I	245/299 (82%)	244 (100%)	1 (0%)	91	94
1	K	240/299 (80%)	238 (99%)	2 (1%)	81	89
1	M	242/299 (81%)	242 (100%)	0	100	100
1	O	224/299 (75%)	224 (100%)	0	100	100
2	B	47/88 (53%)	47 (100%)	0	100	100
2	D	43/88 (49%)	43 (100%)	0	100	100
2	F	47/88 (53%)	47 (100%)	0	100	100
2	H	42/88 (48%)	42 (100%)	0	100	100
2	J	47/88 (53%)	47 (100%)	0	100	100
2	L	43/88 (49%)	43 (100%)	0	100	100
2	N	47/88 (53%)	47 (100%)	0	100	100
2	P	42/88 (48%)	42 (100%)	0	100	100
3	Q	241/413 (58%)	240 (100%)	1 (0%)	91	94
3	S	242/413 (59%)	240 (99%)	2 (1%)	81	89
4	R	265/369 (72%)	265 (100%)	0	100	100
4	T	265/369 (72%)	265 (100%)	0	100	100
All	All	3273/4660 (70%)	3264 (100%)	9 (0%)	92	95

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	S	375	ASN
3	S	393	LYS
3	Q	251	ARG
1	I	246	GLN
1	K	120	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
3	S	247	GLN
4	T	302	ASN
4	T	393	ASN
4	T	323	HIS
3	S	375	ASN

### 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 monosaccharides 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.

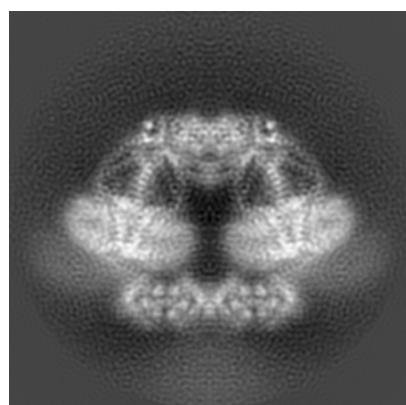
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22215. These allow visual inspection of the internal detail of the map and identification of artifacts.

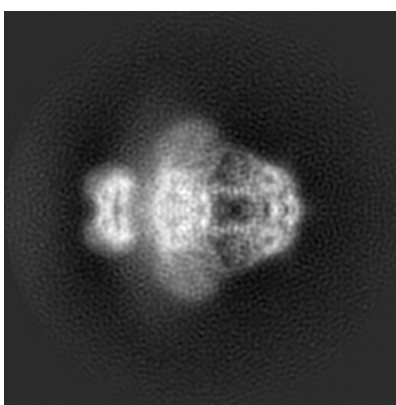
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

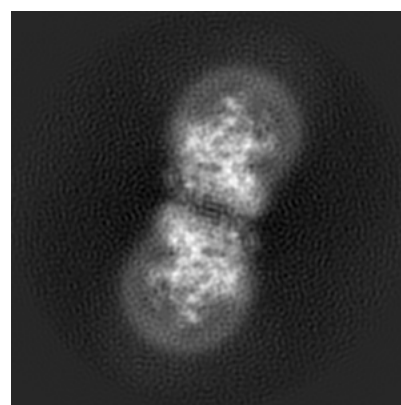
#### 6.1.1 Primary map



X



Y

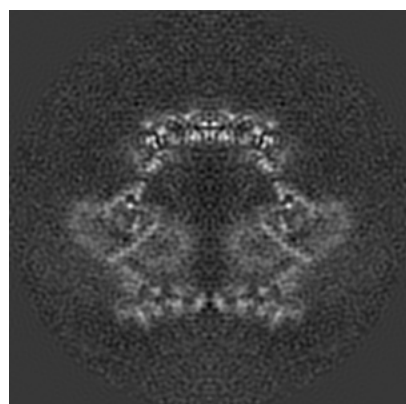


Z

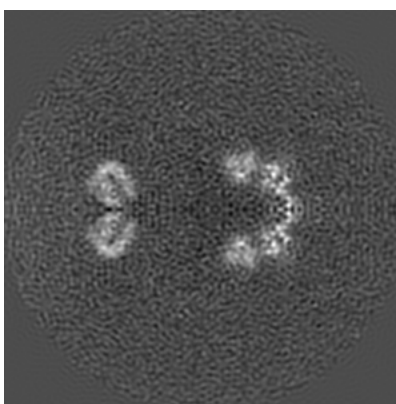
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

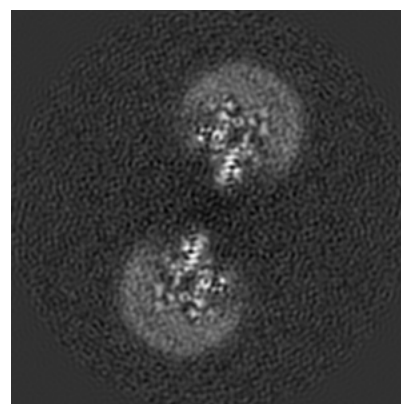
#### 6.2.1 Primary map



X Index: 180



Y Index: 180

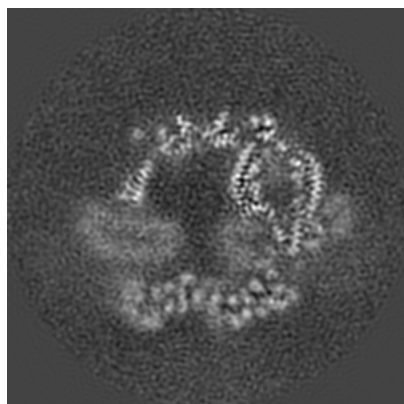


Z Index: 180

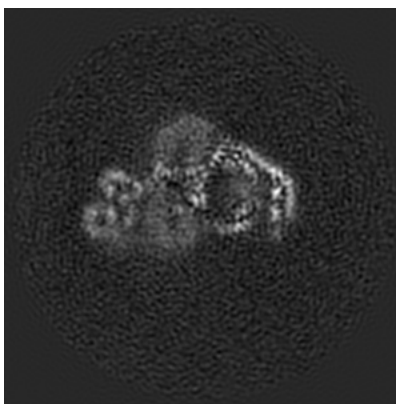
The images above show central slices of the map in three orthogonal directions.

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

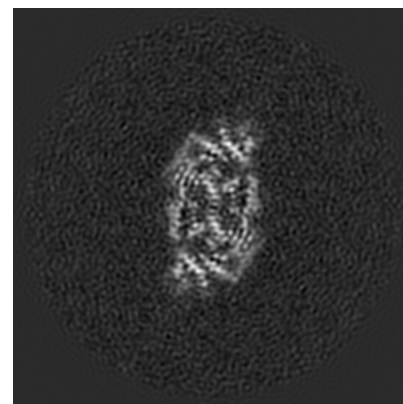
### 6.3.1 Primary map



X Index: 197



Y Index: 237



Z Index: 244

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

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

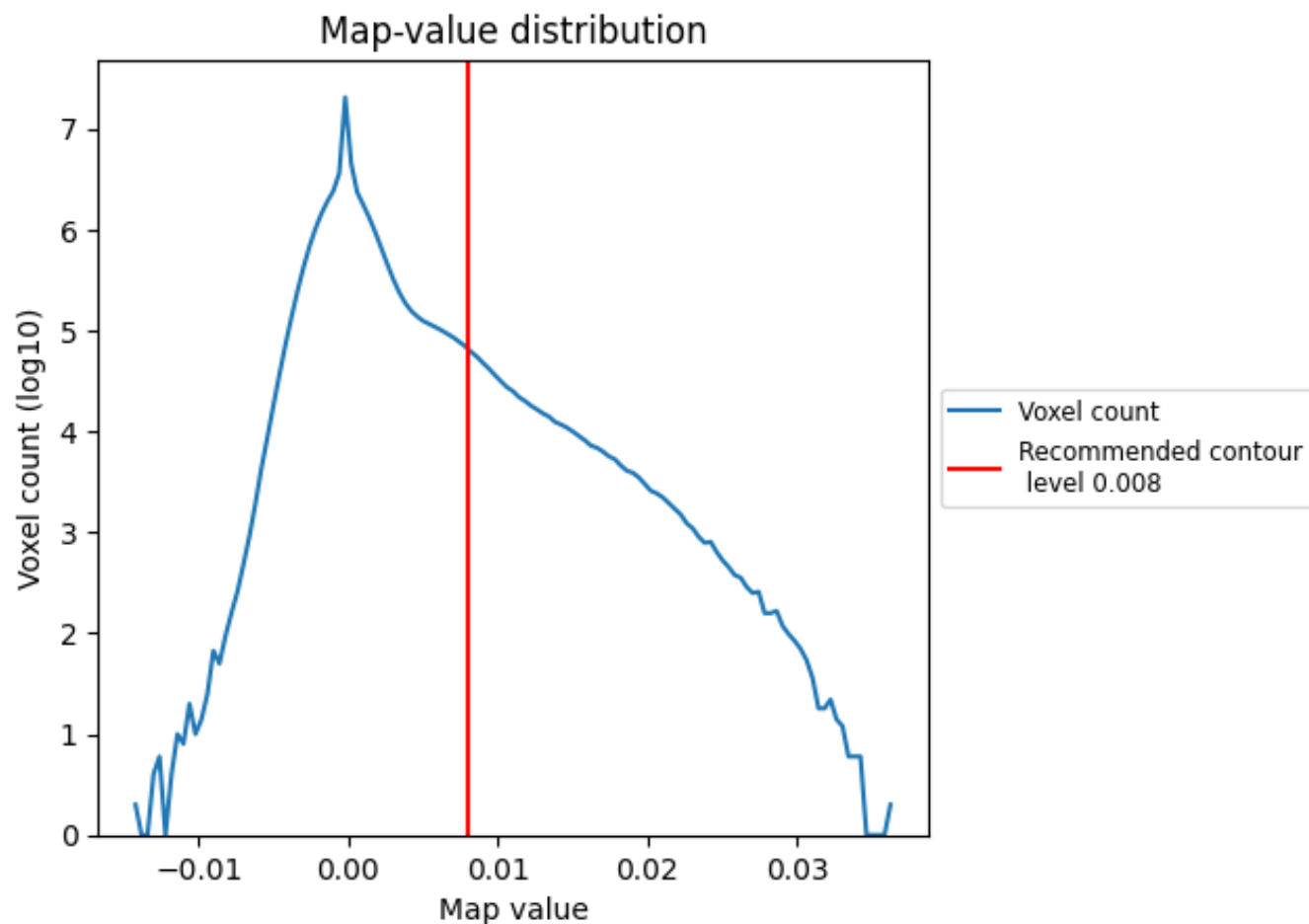
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

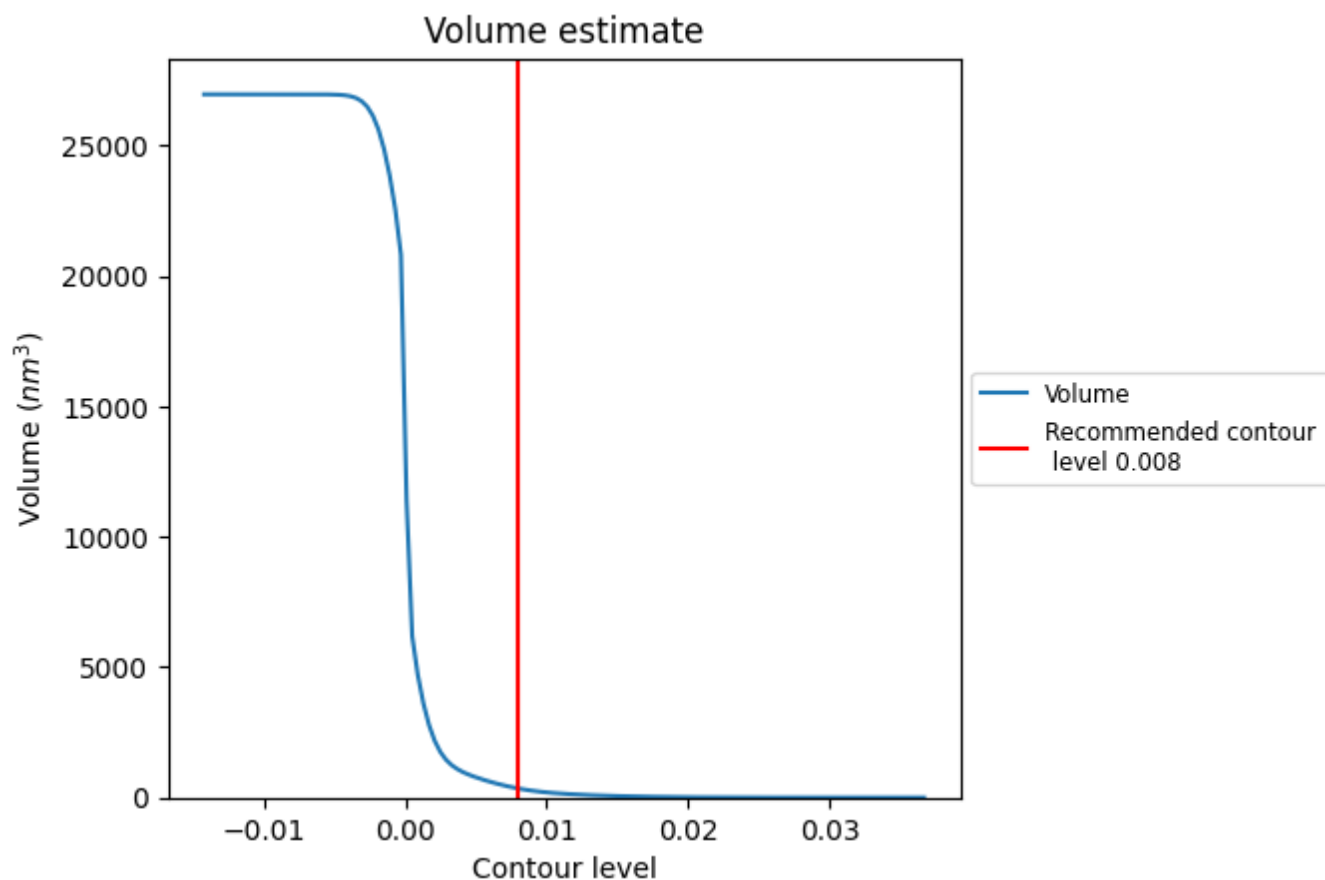
This section contains the results of statistical analysis of the map.

### 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.

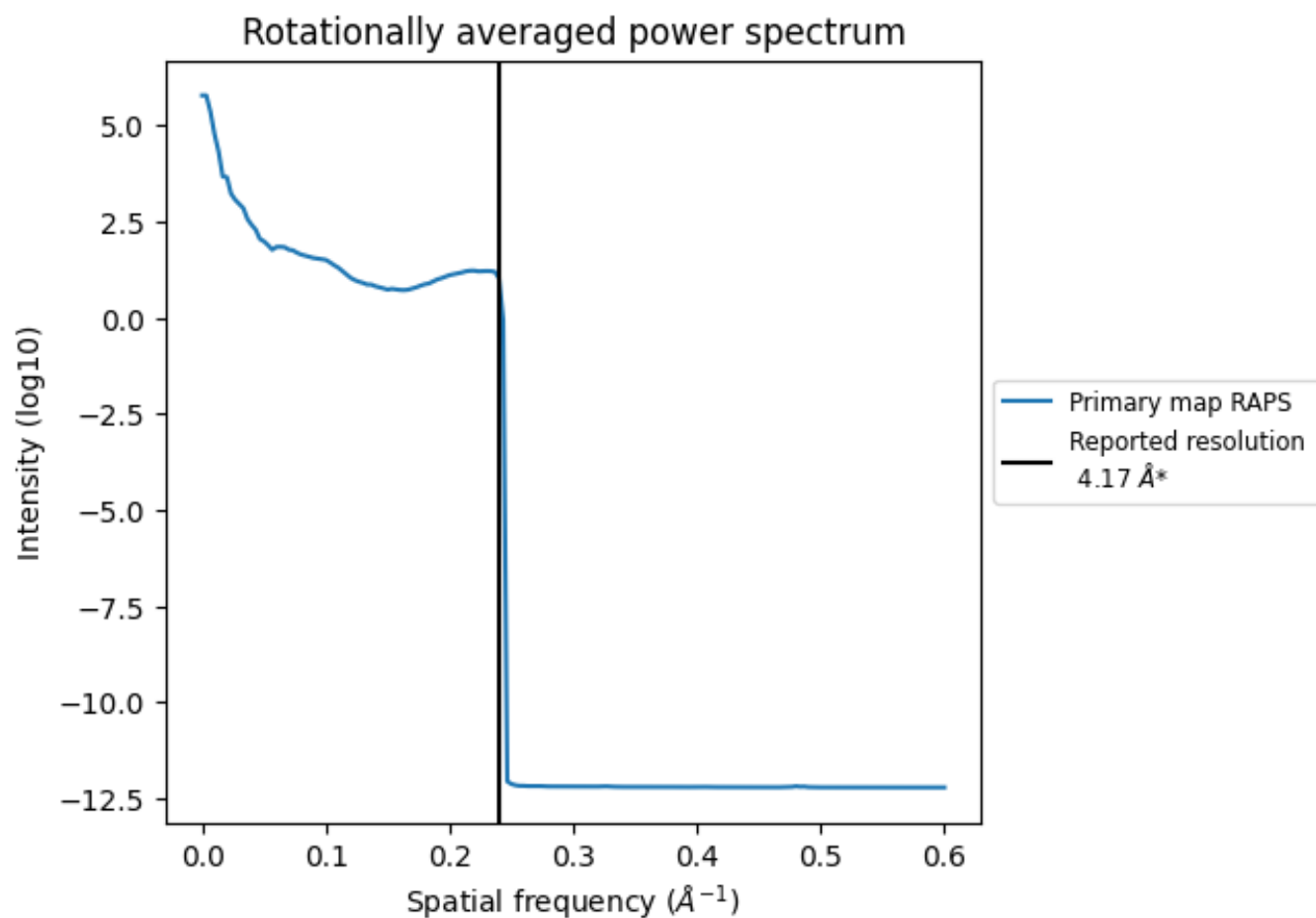
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 349 nm<sup>3</sup>; this corresponds to an approximate mass of 315 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 0.240  $\text{\AA}^{-1}$



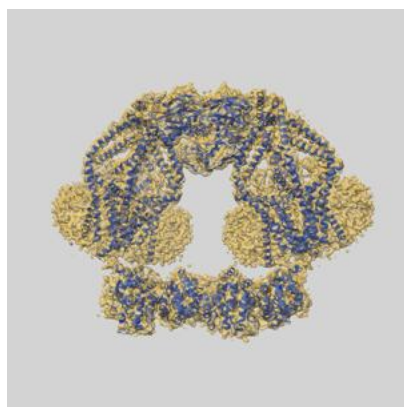
## 8 Fourier-Shell correlation

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

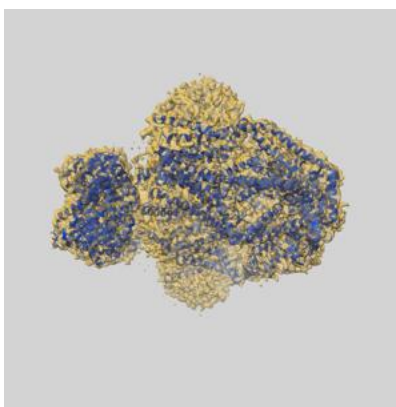
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22215 and PDB model 6XJV. Per-residue inclusion information can be found in section [3](#) on page [6](#).

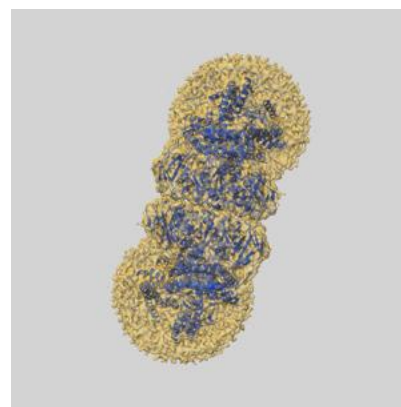
### 9.1 Map-model overlay [i](#)



X



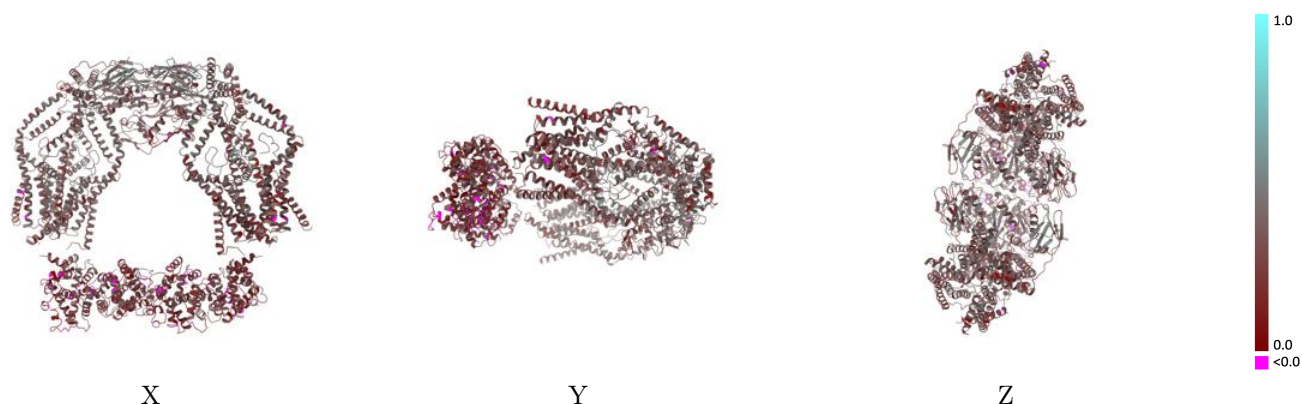
Y



Z

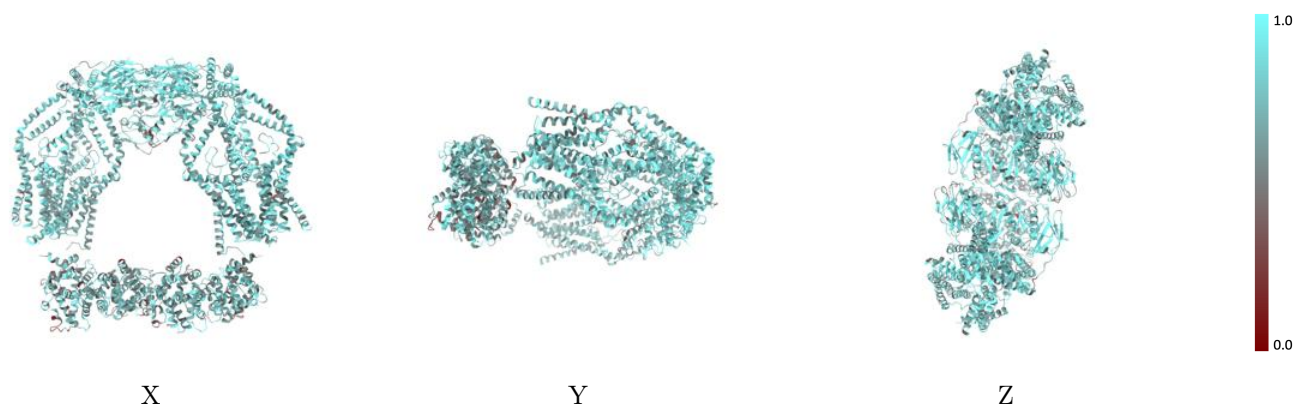
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



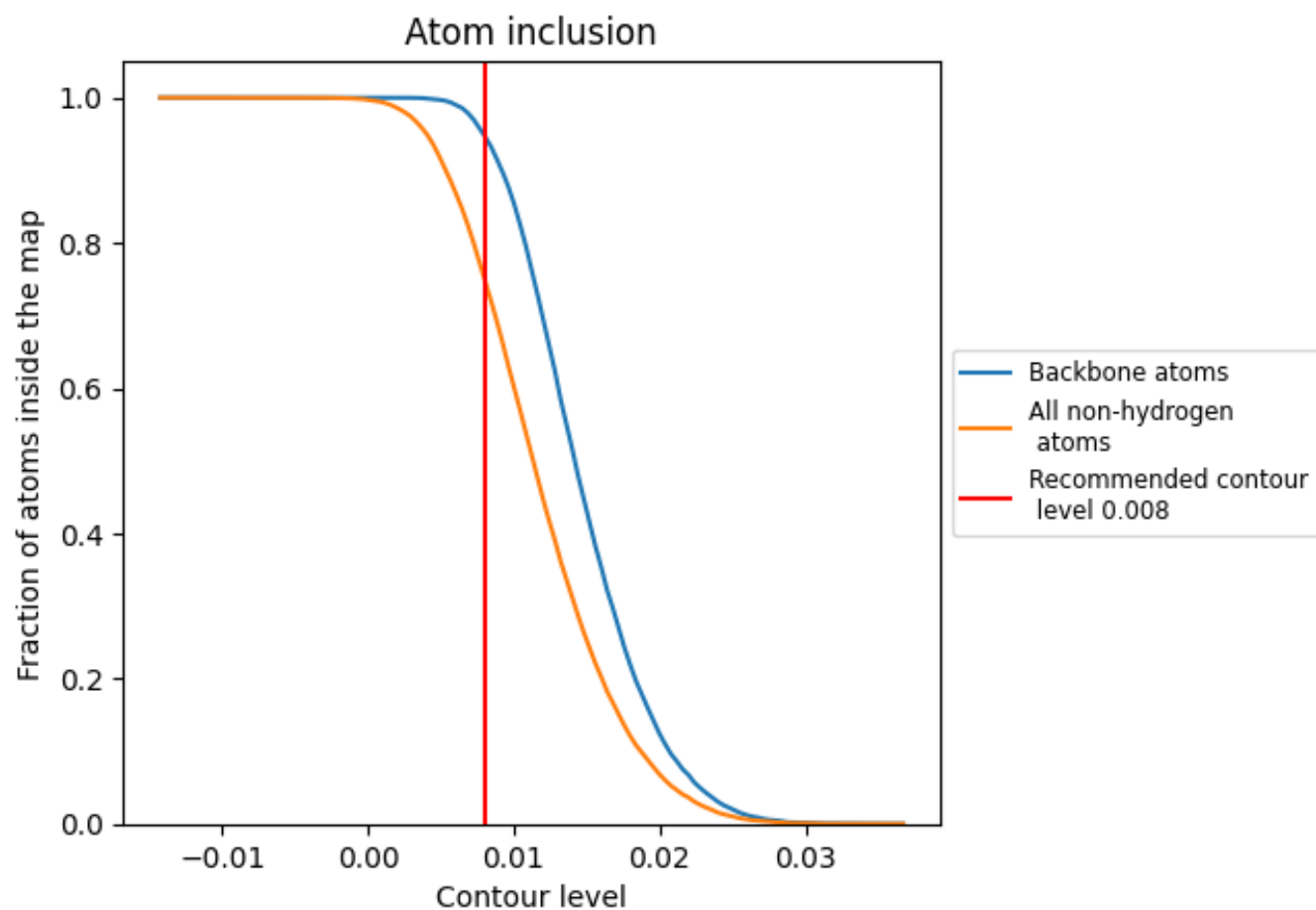
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).











































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 75% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7502	 0.3100
A	 0.8005	 0.3600
B	 0.6934	 0.3210
C	 0.8027	 0.3530
D	 0.7074	 0.2850
E	 0.8175	 0.3690
F	 0.7262	 0.3440
G	 0.7740	 0.3200
H	 0.7283	 0.3020
I	 0.8005	 0.3600
J	 0.6813	 0.3190
K	 0.8060	 0.3560
L	 0.7128	 0.2940
M	 0.8124	 0.3710
N	 0.7237	 0.3390
O	 0.7775	 0.3250
P	 0.7310	 0.3030
Q	 0.6616	 0.2160
R	 0.6791	 0.2370
S	 0.6620	 0.2180
T	 0.6800	 0.2360

