

# wwPDB EM Validation Summary Report (i)

Dec 18, 2022 – 07:44 am GMT

PDB ID	:	7A6B
EMDB ID	:	EMD-11669
Title	:	1.33 A structure of human apoferritin obtained from Titan Mono- BCOR mi-
		croscope
Authors	:	Yip, K.M.; Fischer, N.; Chari, A.; Stark, H.
Deposited on	:	2020-08-25
Resolution	:	1.33 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 (i) 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 (i)) were used in the production of this report:

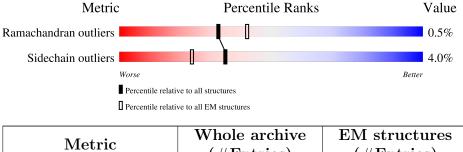
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as $541$ be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

# 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 1.33 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	(# Entries)	(#Entries)
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 >=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 <=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	1	183	<b>•</b> 91%	• 5%
1	2	183	91%	• 5%
1	4	183	91%	• 5%
1	6	183	91%	• 5%
1	А	183	<b>•</b> 91%	• 5%
1	В	183	91%	• 5%
1	Е	183	91%	• 5%
1	F	183	91%	• 5%
1	G	183	• 91%	• 5%



Mol	Chain	Length	Quality of chain	
1	Н	183	91%	• 5%
1	Ι	183	91%	• 5%
1	K	183	91%	• 5%
1	М	183	91%	• 5%
1	О	183	91%	• 5%
1	Р	183	91%	• 5%
1	Q	183	91%	• 5%
1	S	183	91%	• 5%
1	U	183	91%	• 5%
1	W	183	91%	• 5%
1	Х	183	91%	• 5%
1	Y	183	91%	• 5%
1	a	183	91%	• 5%
1	е	183	91%	• 5%
1	r	183	91%	• 5%

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# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 41494 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.

$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	Mol	Chain	Residues		At	oms			AltConf	Trace							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	٨	179	Total	С	Ν	0	S	10	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	175	1567	980	278	304	5	10	0							
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	1	179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	1	173	1567	980	278	304	5	18	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	I/	179	Total	С	Ν	Ο	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	ĸ	173	1567	980	278	304	5	18	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	_	179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	а	173	1567	980	278	304	5	18	0							
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	D	179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	173	1567	980	278	304	5	18	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	Б	179	Total	С	Ν	0	S	10	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	E	173	1567	980	278	304	5	18	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1		179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	е	173	1567	980	278	304	5	18	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1		179	Total	С	Ν	0	S	10	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	r	173	1567	980	278	304	5	18								
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	C	C	C	C	C	C	C	C	179	Total	С	Ν	0	S	10	0
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	G	173	1567	980	278	304	5	10	U							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	т	179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	1	173	1567	980	278	304	5	10	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	м	179	Total	С	Ν	Ο	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	IVI	173	1567	980	278	304	5	18	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	0	179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	0	173	1567	980	278	304	5	18	0							
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	1	0	179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	Q	173	1567	980	278	304	5	18	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	C	179	Total	С	Ν	0	S	10	0							
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	S	175	1567	980	278	304	5	10	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	TT	179	Total	С	Ν	0	S	10	0							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$		U	113	1567	980	278	304	5	18	U							
1         Y         173         Total         C         N         O         S         18         0	1	117	179	Total	С	Ν	0	S	10	0							
		VV	1/3	1567	980	278	304	5	18	U							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	V	179	Total	С	Ν	0	S	10	0							
		х	1/3	1567	980	278	304	5	18								

• Molecule 1 is a protein called Ferritin heavy chain.



Mol	Chain	Residues	Atoms				AltConf	Trace		
1	2	173	Total	С	Ν	0	S	18	0	
	Δ	175	1567	980	278	304	5	10	0	
1	4	173	Total	С	Ν	0	S	18	0	
	4	175	1567	980	278	304	5	10	0	
1	F	173	Total	С	Ν	0	S	18	0	
	Г	175	1567	980	278	304	5	10	0	
1	Н	173	Total	С	Ν	0	S	18	0	
	11	11	175	1567	980	278	304	5	10	0
1	Р	173	Total	С	Ν	0	S	18	0	
	1	175	1567	980	278	304	5	10	0	
1	Х	179	Total	С	Ν	0	S	18	0	
		173	1567	980	278	304	5	10	0	
1	1 6	172	Total	С	Ν	0	S	18	0	
	U	6 173	1567	980	278	304	5	10	U	

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There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	86	GLN	LYS	conflict	UNP P02794
1	86	GLN	LYS	conflict	UNP P02794
К	86	GLN	LYS	conflict	UNP P02794
a	86	GLN	LYS	conflict	UNP P02794
В	86	GLN	LYS	conflict	UNP P02794
Е	86	GLN	LYS	conflict	UNP P02794
e	86	GLN	LYS	conflict	UNP P02794
r	86	GLN	LYS	conflict	UNP P02794
G	86	GLN	LYS	conflict	UNP P02794
Ι	86	GLN	LYS	conflict	UNP P02794
М	86	GLN	LYS	conflict	UNP P02794
0	86	GLN	LYS	conflict	UNP P02794
Q	86	GLN	LYS	conflict	UNP P02794
S	86	GLN	LYS	conflict	UNP P02794
U	86	GLN	LYS	conflict	UNP P02794
W	86	GLN	LYS	conflict	UNP P02794
Y	86	GLN	LYS	conflict	UNP P02794
2	86	GLN	LYS	conflict	UNP P02794
4	86	GLN	LYS	conflict	UNP P02794
F	86	GLN	LYS	conflict	UNP P02794
Н	86	GLN	LYS	conflict	UNP P02794
Р	86	GLN	LYS	conflict	UNP P02794
Х	86	GLN	LYS	conflict	UNP P02794
6	86	GLN	LYS	conflict	UNP P02794



• Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	AltConf
2	А	2	Total Na 2 2	0
2	1	2	Total Na 2 2	0
2	K	1	Total Na 1 1	0
2	a	1	Total Na 1 1	0
2	В	2	Total Na 2 2	0
2	Е	1	Total Na 1 1	0
2	е	1	Total Na 1 1	0
2	r	1	Total Na 1 1	0
2	G	1	Total Na 1 1	0
2	Ι	1	Total Na 1 1	0
2	М	2	Total Na 2 2	0
2	0	1	Total Na 1 1	0
2	Q	1	Total Na 1 1	0
2	S	1	Total Na 1 1	0
2	U	1	Total Na 1 1	0
2	W	1	Total Na 1 1	0
2	Y	1	Total Na 1 1	0
2	2	2	Total Na 2 2	0
2	4	2	Total Na 2 2	0
2	F	1	Total Na 1 1	0
2	Н	2	Total Na 2 2	0



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Mol	Chain	Residues	Atoms	AltConf
2	Р	1	Total Na 1 1	0
2	Х	1	Total Na 1 1	0
2	6	2	Total Na 2 2	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	AltConf
3	٨	169	Total O	0
3	А	162	162 162	0
3	1	160	Total O	0
3	1	100	160 160	0
3	K	162	Total O	0
5	Т	102	162  162	0
3	a	161	Total O	0
0	a	101	161 161	0
3	В	160	Total O	0
0	D	100	160 160	0
3	Е	161	Total O	0
0	Ľ	101	161 161	0
3	е	160	Total O	0
0	C	100	160 160	0
3	r	160	Total O	0
0	1	100	160 160	0
3	G	161	Total O	0
0	<u> </u>	101	161 161	0
3	Ι	161	Total O	0
	1	101	161 161	0
3	М	160	Total O	0
		100	160 160	Ŭ
3	Ο	162	Total O	0
0		102	162 162	Ŭ
3	Q	161	Total O	0
	<u>ب</u> ې	101	161 161	Ŭ
3	S	160	Total O	0
		100	160 160	
3	U	160	Total O	0
		100	160 160	
3	W	161	Total O	0
	* *	101	161  161	



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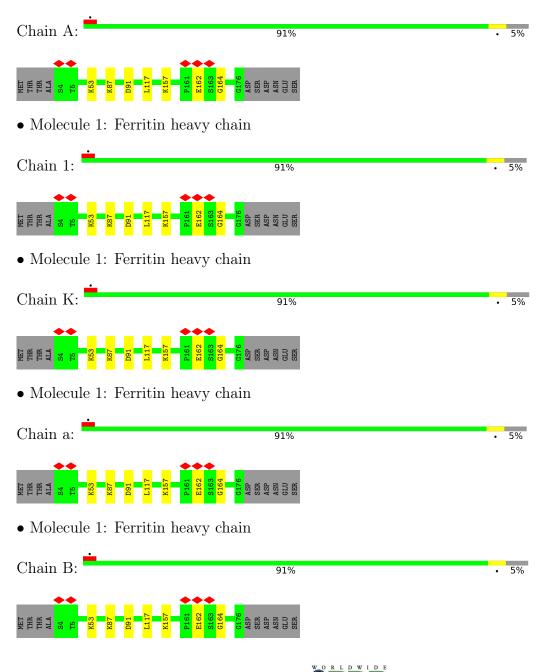
Mol	Chain	Residues	Atoms	AltConf
3	Y	161	Total O 161 161	0
3	2	160	Total O 160 160	0
3	4	161	Total O 161 161	0
3	F	160	Total O 160 160	0
3	Н	160	Total O 160 160	0
3	Р	160	Total O 160 160	0
3	Х	160	Total O 160 160	0
3	6	160	Total O 160 160	0



# 3 Residue-property plots (i)

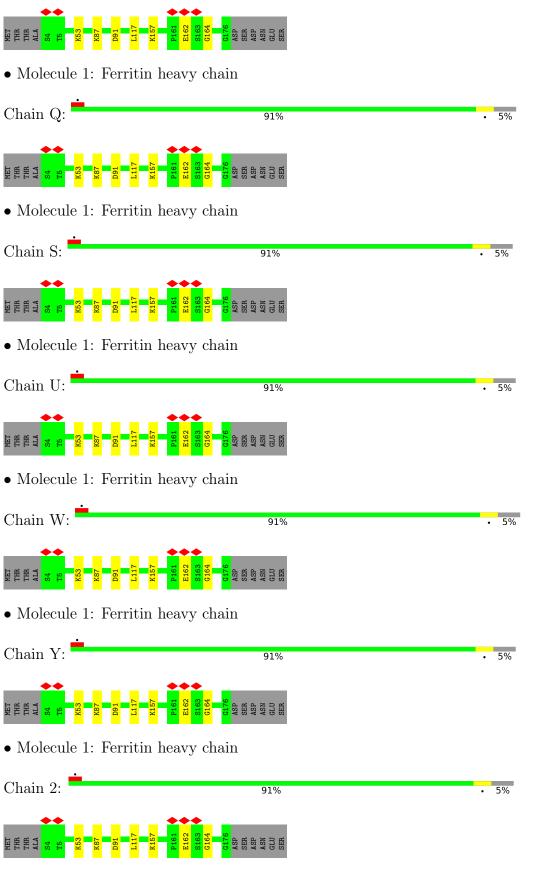
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



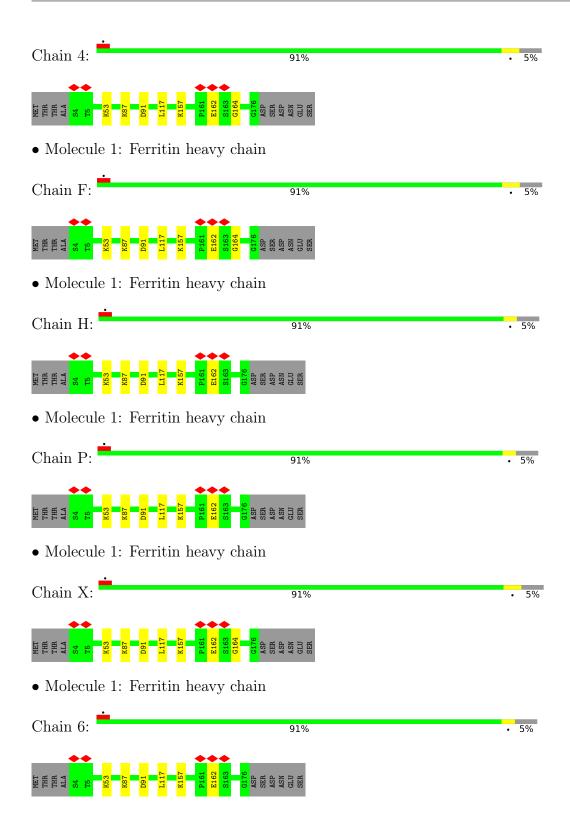
• Molecule 1: Ferritin	heavy chain	
Chain E:	91%	• 5%
MET THR THR ALA ALA K53 K53 K67 D91 L117 C53 K53 K53 K53 K53 K53 K53 K53 K53 K53 K	P161           P161           E162           S163           G176           SER           ASP           ASP           ASP           ASP           ASP           SER	
• Molecule 1: Ferritin	heavy chain	
Chain e:	91%	• 5%
MET THR ALA ALA ALA ALA K53 K53 K53 K53 D91 D91	P161 P161 E162 C176 C176 C176 C176 ASP SER ASP G10 G1U SER	
• Molecule 1: Ferritin	heavy chain	
Chain r:	91%	• 5%
MET THR THR ALA ALA ALA KG3 KG3 KG3 KG3 KG3 L1117 C01	P1 61 E1 62 S1 63 A1 76 A1 76 A17 A1 A1 76 A17 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1 A1	
• Molecule 1: Ferritin	heavy chain	
Chain G:	91%	• 5%
MET THR THR ALA ALA S4 K63 K63 K87 K87 L117	P161 P162 B162 B164 C164 C176 ASP ASP ASP ASP ASP ASP SER SER	
• Molecule 1: Ferritin	heavy chain	
Chain I:	91%	• 5%
MET THR ALA ALA ALA ALA K63 K63 K67 D91 D91	PIE1 E162 C176 C176 C176 C176 ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	
• Molecule 1: Ferritin	heavy chain	
Chain M:	91%	• 5%
MET THR ALA ALA K5 K6 K6 K6 K6 K6 K6 K6 K6 K6 K6 K6 K6 K6	P161 E162 S163 S163 ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	
• Molecule 1: Ferritin	heavy chain	
Chain O:	91%	• 5%





• Molecule 1: Ferritin heavy chain







# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1074000	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 $(e^-/\text{\AA}^2)$	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.549	Depositor
Minimum map value	-0.197	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	236.16, 236.16, 236.16	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.492,  0.492,  0.492	Depositor



# 5 Model quality (i)

## 5.1 Standard geometry (i)

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

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		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	1	0.68	0/1588	0.80	0/2132	
1	2	0.69	0/1588	0.80	0/2132	
1	4	0.69	0/1588	0.80	0/2132	
1	6	0.69	0/1588	0.80	0/2132	
1	А	0.68	0/1588	0.80	0/2132	
1	В	0.68	0/1588	0.80	0/2132	
1	Е	0.68	0/1588	0.80	0/2132	
1	F	0.69	0/1588	0.80	0/2132	
1	G	0.68	0/1588	0.80	0/2132	
1	Н	0.68	0/1588	0.80	0/2132	
1	Ι	0.68	0/1588	0.80	0/2132	
1	Κ	0.68	0/1588	0.80	0/2132	
1	М	0.68	0/1588	0.80	0/2132	
1	0	0.68	0/1588	0.80	0/2132	
1	Р	0.68	0/1588	0.80	0/2132	
1	Q	0.69	0/1588	0.80	0/2132	
1	S	0.69	0/1588	0.80	0/2132	
1	U	0.68	0/1588	0.80	0/2132	
1	W	0.69	0/1588	0.80	0/2132	
1	Х	0.69	0/1588	0.80	0/2132	
1	Y	0.68	0/1588	0.80	0/2132	
1	a	0.68	0/1588	0.80	0/2132	
1	е	0.68	0/1588	0.80	0/2132	
1	r	0.68	0/1588	0.80	0/2132	
All	All	0.68	0/38112	0.80	0/51168	

There are no bond length outliers. There are no bond angle outliers. There are no chirality outliers. There are no planarity outliers.



#### 5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

#### 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	1	188/183~(103%)	183~(97%)	3(2%)	2(1%)	14 1
1	2	188/183~(103%)	183~(97%)	3 (2%)	2(1%)	14 1
1	4	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	6	188/183~(103%)	183 (97%)	5 (3%)	0	100 100
1	А	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	В	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	Е	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	F	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	G	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	Н	188/183~(103%)	183 (97%)	5 (3%)	0	100 100
1	Ι	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	K	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	М	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	Ο	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	Р	188/183~(103%)	183 (97%)	5 (3%)	0	100 100
1	Q	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	S	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	U	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	W	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	Х	188/183~(103%)	183 (97%)	3 (2%)	2 (1%)	14 1
1	Y	188/183~(103%)	183~(97%)	3 (2%)	2 (1%)	14 1



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	a	188/183~(103%)	183~(97%)	3~(2%)	2(1%)	14 1
1	е	188/183~(103%)	183~(97%)	3~(2%)	2(1%)	14 1
1	r	188/183~(103%)	183 (97%)	3~(2%)	2(1%)	14 1
All	All	4512/4392~(103%)	4392 (97%)	78 (2%)	42 (1%)	32 3

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5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	U	164[A]	GLY
1	U	164[B]	GLY
1	W	164[A]	GLY
1	W	164[B]	GLY
1	Y	164[A]	GLY

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	1	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	2	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	4	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	6	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	А	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	В	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	Ε	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	F	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	G	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	Н	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	Ι	168/162~(104%)	159 (95%)	9~(5%)	22 2		
1	К	168/162~(104%)	159 (95%)	9~(5%)	22 2		
1	М	168/162~(104%)	159~(95%)	9~(5%)	22 2		



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	Ο	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	Р	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	$\mathbf{Q}$	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	S	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	U	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	W	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	Х	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	Υ	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	a	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	е	168/162~(104%)	159~(95%)	9~(5%)	22 2		
1	r	168/162~(104%)	159~(95%)	9~(5%)	22 2		
All	All	4032/3888~(104%)	3816~(95%)	216 (5%)	35 2		

Continued from previous page...

5 of 216 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	Q	162[A]	GLU
1	W	162[B]	GLU
1	Х	53[B]	LYS
1	S	87[A]	LYS
1	U	91	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
1	U	98	ASN
1	2	136	HIS
1	U	136	HIS
1	Y	98	ASN
1	4	136	HIS

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

24 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal	Trune	Chain	Dec	Tinle	B	ond leng	gths	B	ond ang	gles
Mol	Type	Chain	Res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	CSX	Х	90	1	3,6,7	0.72	0	$1,\!6,\!8$	1.14	0
1	CSX	А	90	1	3,6,7	0.71	0	$1,\!6,\!8$	1.15	0
1	CSX	1	90	1	3,6,7	0.73	0	$1,\!6,\!8$	1.15	0
1	CSX	Q	90	1	3,6,7	0.74	0	$1,\!6,\!8$	1.15	0
1	CSX	Н	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.15	0
1	CSX	G	90	1	3,6,7	0.72	0	$1,\!6,\!8$	1.15	0
1	CSX	Ε	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.13	0
1	CSX	Р	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.14	0
1	CSX	4	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.16	0
1	CSX	6	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.15	0
1	CSX	В	90	1	$3,\!6,\!7$	0.72	0	$1,\!6,\!8$	1.15	0
1	CSX	a	90	1	$3,\!6,\!7$	0.72	0	$1,\!6,\!8$	1.15	0
1	CSX	Ι	90	1	$3,\!6,\!7$	0.72	0	$1,\!6,\!8$	1.15	0
1	CSX	U	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.15	0
1	CSX	F	90	1	$3,\!6,\!7$	0.74	0	$1,\!6,\!8$	1.16	0
1	CSX	r	90	1	$3,\!6,\!7$	0.72	0	$1,\!6,\!8$	1.15	0
1	CSX	М	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.15	0
1	CSX	е	90	1	$3,\!6,\!7$	0.72	0	$1,\!6,\!8$	1.15	0
1	CSX	S	90	1	$3,\!6,\!7$	0.73	0	$1,\!6,\!8$	1.15	0
1	CSX	2	90	1	3,6,7	0.74	0	$1,\!6,\!8$	1.15	0
1	CSX	0	90	1	3,6,7	0.72	0	$1,\!6,\!8$	1.16	0
1	CSX	Y	90	1	$3,\!6,\!7$	0.74	0	$1,\!6,\!8$	1.15	0
1	CSX	K	90	1	3,6,7	0.72	0	$1,\!6,\!8$	1.16	0
1	CSX	W	90	1	$3,\!6,\!7$	0.74	0	$1,\!6,\!8$	1.17	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSX	Х	90	1	-	0/1/5/7	-
					Conti	nued on nex	t page

Mol	Type	m previoi	Res	Link	Chirals	Torsions	Rings
1	CSX	А	90	1	_	0/1/5/7	-
1	CSX	1	90	1	-	0/1/5/7	-
1	CSX	Q	90	1	-	0/1/5/7	-
1	CSX	Н	90	1	-	0/1/5/7	-
1	CSX	G	90	1	-	0/1/5/7	-
1	CSX	Е	90	1	-	0/1/5/7	-
1	CSX	Р	90	1	-	0/1/5/7	-
1	CSX	4	90	1	-	0/1/5/7	-
1	CSX	6	90	1	-	0/1/5/7	-
1	CSX	В	90	1	-	0/1/5/7	-
1	CSX	a	90	1	-	0/1/5/7	-
1	CSX	Ι	90	1	-	0/1/5/7	-
1	CSX	U	90	1	-	0/1/5/7	-
1	CSX	F	90	1	-	0/1/5/7	-
1	CSX	r	90	1	-	0/1/5/7	-
1	CSX	М	90	1	-	0/1/5/7	-
1	CSX	е	90	1	-	0/1/5/7	-
1	CSX	S	90	1	-	0/1/5/7	-
1	CSX	2	90	1	-	0/1/5/7	-
1	CSX	0	90	1	-	0/1/5/7	-
1	CSX	Y	90	1	-	0/1/5/7	_
1	CSX	K	90	1	-	0/1/5/7	-
1	CSX	W	90	1	-	0/1/5/7	-

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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.

#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 32 ligands modelled in this entry, 32 are monoatomic - leaving 0 for Mogul analysis. There are no bond length outliers.



There are no bond angle outliers. There are no chirality outliers. There are no torsion outliers. There are no ring outliers. No monomer is involved in short contacts.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



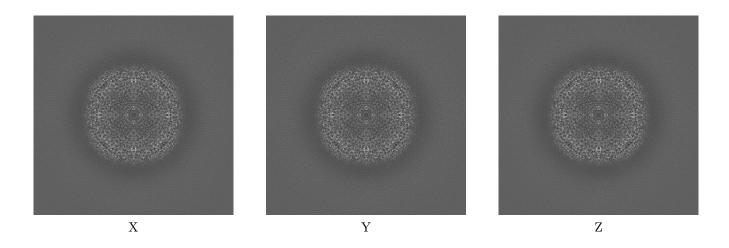
# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-11669. 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)

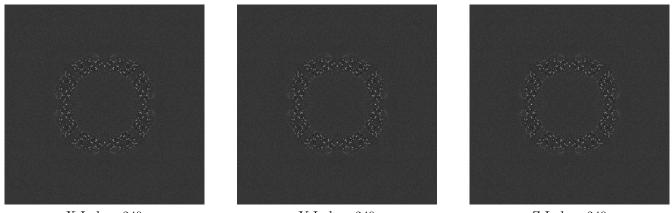
#### 6.1.1 Primary map



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

#### 6.2 Central slices (i)

#### 6.2.1 Primary map



X Index: 240

Y Index: 240

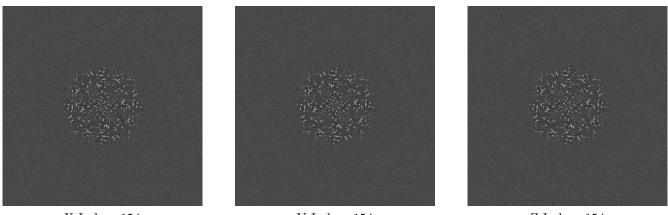




The images above show central slices of the map in three orthogonal directions.

#### 6.3 Largest variance slices (i)

#### 6.3.1 Primary map



X Index: 154

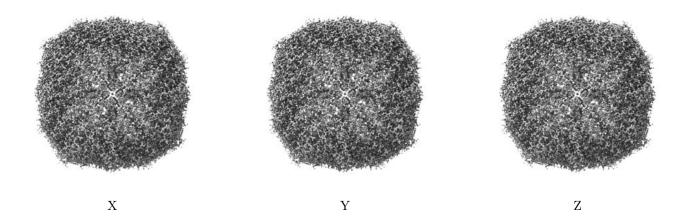
Y Index: 154

Z Index: 154

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



The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



## 6.5 Mask visualisation (i)

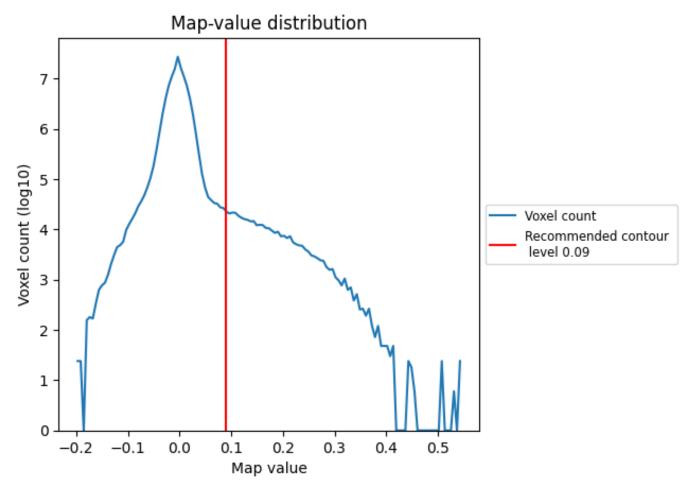
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis (i)

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

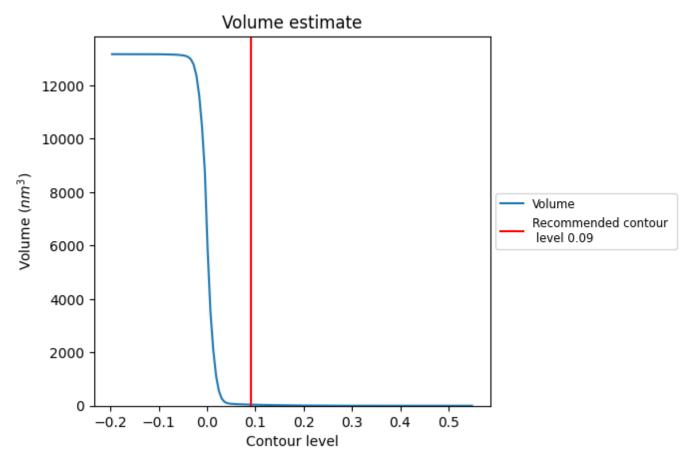
## 7.1 Map-value distribution (i)



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)

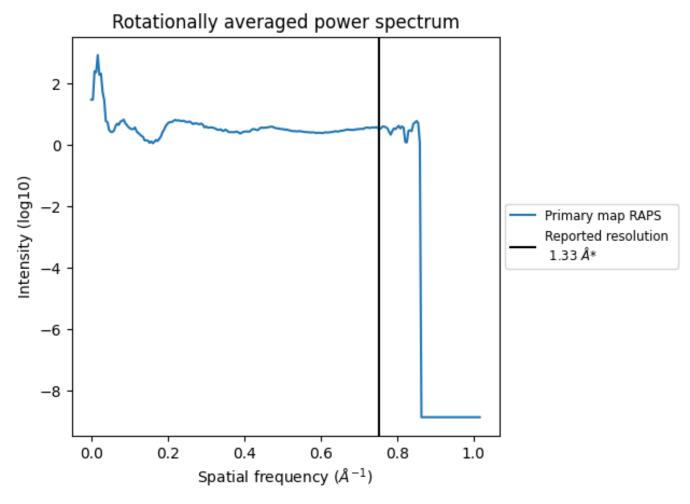


The volume at the recommended contour level is  $42 \text{ nm}^3$ ; this corresponds to an approximate mass of 38 kDa.

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 (i)



\*Reported resolution corresponds to spatial frequency of 0.752  $\mathrm{\AA^{-1}}$ 



# 8 Fourier-Shell correlation (i)

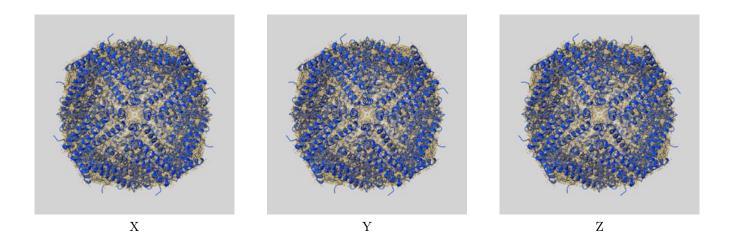
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-11669 and PDB model 7A6B. Per-residue inclusion information can be found in section 3 on page 9.

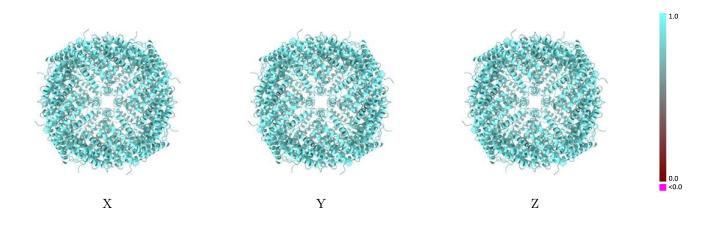
## 9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.09 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.

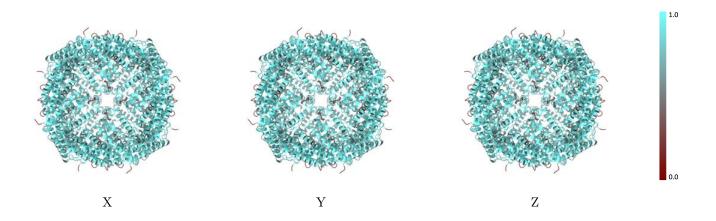


#### 9.2 Q-score mapped to coordinate model (i)



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.

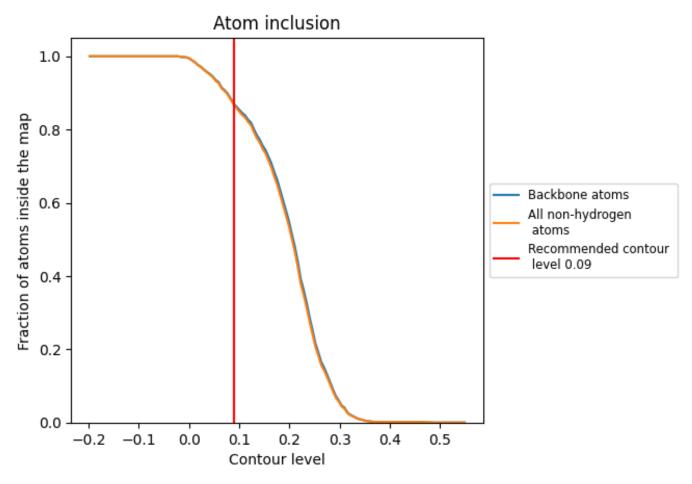
#### 9.3 Atom inclusion mapped to coordinate model (i)



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 (0.09).



#### 9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

### 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8658	0.9150
1	0.8660	0.9150
2	0.8660	0.9150
4	0.8660	0.9160
6	0.8660	0.9160
А	0.8660	0.9160
В	0.8660	0.9150
Е	0.8667	0.9150
F	0.8667	0.9150
G	0.8667	0.9160
Н	0.8660	0.9160
Ι	0.8667	0.9160
К	0.8667	0.9150
М	0.8660	0.9150
0	0.8667	0.9160
Р	0.8667	0.9160
Q	0.8667	0.9160
S	0.8667	0.9160
U	0.8667	0.9150
W	0.8667	0.9150
Х	0.8667	0.9160
Y	0.8667	0.9150
a	0.8667	0.9150
е	0.8667	0.9150
r	0.8667	0.9150

