



Full wwPDB EM Validation Report ⓘ

Mar 11, 2024 – 01:30 AM EDT

PDB ID : 6PPE
EMDB ID : EMD-20434
Title : ClpP and ClpX IGF loop in ClpX-ClpP complex with D7 symmetry
Authors : Fei, X.; Jenni, S.; Harrison, S.C.; Sauer, R.T.
Deposited on : 2019-07-06
Resolution : 3.19 Å (reported)
Based on initial model : 3MT6

This is a Full wwPDB EM Validation 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.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

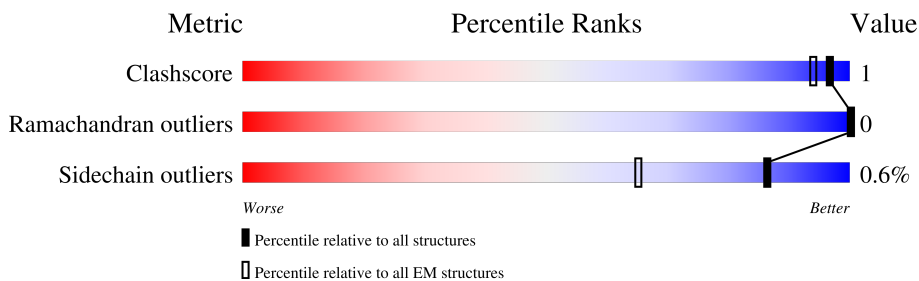
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.19 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.



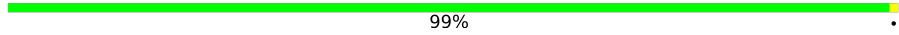
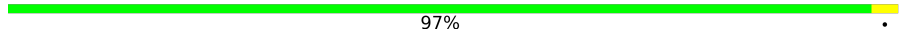
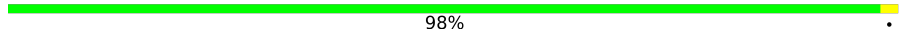
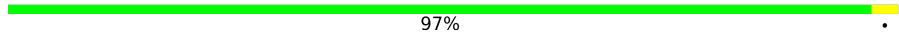
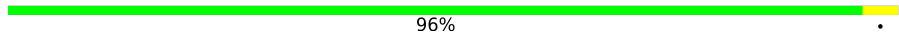
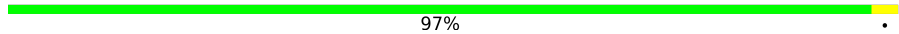
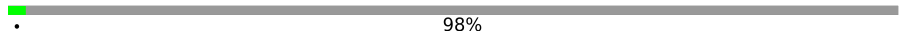
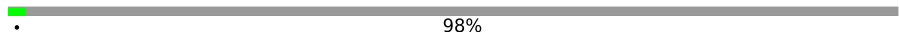
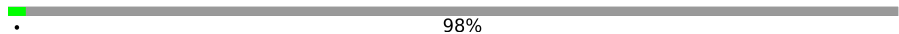
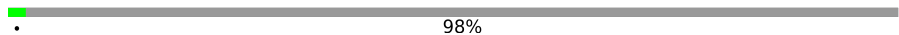
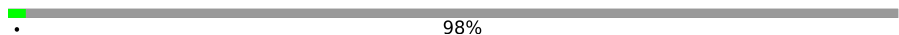
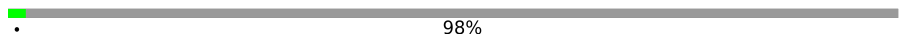

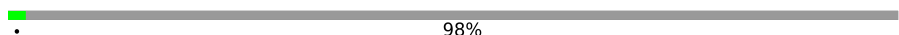
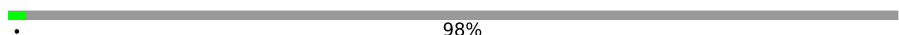
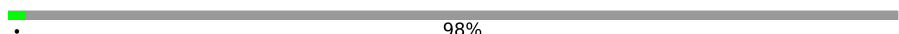
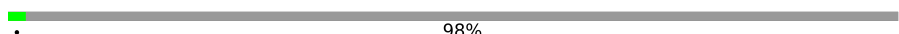
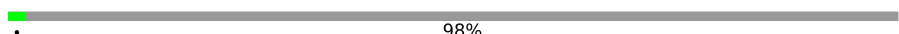
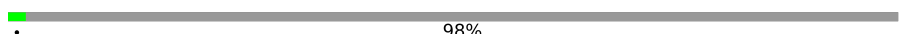
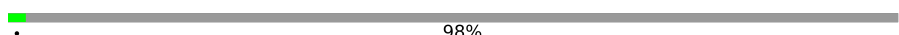
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 ≥ 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	192	97%
1	B	192	99%
1	C	192	98%
1	D	192	97%
1	E	192	98%
1	F	192	96%
1	G	192	97%
1	H	192	98%

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Mol	Chain	Length	Quality of chain
1	I	192	 99%
1	J	192	 97%
1	K	192	 98%
1	L	192	 97%
1	M	192	 96%
1	N	192	 97%
2	1	369	 98%
2	2	369	 98%
2	3	369	 98%
2	O	369	 98%
2	P	369	 98%
2	Q	369	 98%
2	R	369	 98%
2	S	369	 98%
2	T	369	 98%
2	U	369	 98%
2	V	369	 98%
2	X	369	 98%
2	Y	369	 98%
2	Z	369	 98%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 43736 atoms, of which 21896 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 ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	192	3017	947	1513	261	284	12	0	0
1	B	192	3017	947	1513	261	284	12	0	0
1	C	192	3017	947	1513	261	284	12	0	0
1	D	192	3017	947	1513	261	284	12	0	0
1	E	192	3017	947	1513	261	284	12	0	0
1	F	192	3017	947	1513	261	284	12	0	0
1	G	192	3017	947	1513	261	284	12	0	0
1	H	192	3017	947	1513	261	284	12	0	0
1	I	192	3017	947	1513	261	284	12	0	0
1	J	192	3017	947	1513	261	284	12	0	0
1	K	192	3017	947	1513	261	284	12	0	0
1	L	192	3017	947	1513	261	284	12	0	0
1	M	192	3017	947	1513	261	284	12	0	0
1	N	192	3017	947	1513	261	284	12	0	0

- Molecule 2 is a protein called ATP-dependent Clp protease ATP-binding subunit ClpX.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
2	O	9	106	36	51	9	10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	Q	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	R	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	S	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	T	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	U	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	V	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	X	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	Y	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	Z	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	1	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	2	9	Total 106	C 36	H 51	N 9	O 10	0	0
2	3	9	Total 106	C 36	H 51	N 9	O 10	0	0

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	169	SER	CYS	conflict	UNP A0A1Q9L861
O	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
O	408	GLU	LYS	conflict	UNP A0A1Q9L861
O	425	GLY	-	expression tag	UNP A0A1Q9L861
O	426	GLY	-	expression tag	UNP A0A1Q9L861
O	427	GLY	-	expression tag	UNP A0A1Q9L861
O	428	THR	-	expression tag	UNP A0A1Q9L861
O	429	SER	-	expression tag	UNP A0A1Q9L861
O	430	GLY	-	expression tag	UNP A0A1Q9L861
P	169	SER	CYS	conflict	UNP A0A1Q9L861
P	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
P	408	GLU	LYS	conflict	UNP A0A1Q9L861
P	425	GLY	-	expression tag	UNP A0A1Q9L861

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Chain	Residue	Modelled	Actual	Comment	Reference
P	426	GLY	-	expression tag	UNP A0A1Q9L861
P	427	GLY	-	expression tag	UNP A0A1Q9L861
P	428	THR	-	expression tag	UNP A0A1Q9L861
P	429	SER	-	expression tag	UNP A0A1Q9L861
P	430	GLY	-	expression tag	UNP A0A1Q9L861
Q	169	SER	CYS	conflict	UNP A0A1Q9L861
Q	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
Q	408	GLU	LYS	conflict	UNP A0A1Q9L861
Q	425	GLY	-	expression tag	UNP A0A1Q9L861
Q	426	GLY	-	expression tag	UNP A0A1Q9L861
Q	427	GLY	-	expression tag	UNP A0A1Q9L861
Q	428	THR	-	expression tag	UNP A0A1Q9L861
Q	429	SER	-	expression tag	UNP A0A1Q9L861
Q	430	GLY	-	expression tag	UNP A0A1Q9L861
R	169	SER	CYS	conflict	UNP A0A1Q9L861
R	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
R	408	GLU	LYS	conflict	UNP A0A1Q9L861
R	425	GLY	-	expression tag	UNP A0A1Q9L861
R	426	GLY	-	expression tag	UNP A0A1Q9L861
R	427	GLY	-	expression tag	UNP A0A1Q9L861
R	428	THR	-	expression tag	UNP A0A1Q9L861
R	429	SER	-	expression tag	UNP A0A1Q9L861
R	430	GLY	-	expression tag	UNP A0A1Q9L861
S	169	SER	CYS	conflict	UNP A0A1Q9L861
S	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
S	408	GLU	LYS	conflict	UNP A0A1Q9L861
S	425	GLY	-	expression tag	UNP A0A1Q9L861
S	426	GLY	-	expression tag	UNP A0A1Q9L861
S	427	GLY	-	expression tag	UNP A0A1Q9L861
S	428	THR	-	expression tag	UNP A0A1Q9L861
S	429	SER	-	expression tag	UNP A0A1Q9L861
S	430	GLY	-	expression tag	UNP A0A1Q9L861
T	169	SER	CYS	conflict	UNP A0A1Q9L861
T	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
T	408	GLU	LYS	conflict	UNP A0A1Q9L861
T	425	GLY	-	expression tag	UNP A0A1Q9L861
T	426	GLY	-	expression tag	UNP A0A1Q9L861
T	427	GLY	-	expression tag	UNP A0A1Q9L861
T	428	THR	-	expression tag	UNP A0A1Q9L861
T	429	SER	-	expression tag	UNP A0A1Q9L861
T	430	GLY	-	expression tag	UNP A0A1Q9L861
U	169	SER	CYS	conflict	UNP A0A1Q9L861

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Chain	Residue	Modelled	Actual	Comment	Reference
U	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
U	408	GLU	LYS	conflict	UNP A0A1Q9L861
U	425	GLY	-	expression tag	UNP A0A1Q9L861
U	426	GLY	-	expression tag	UNP A0A1Q9L861
U	427	GLY	-	expression tag	UNP A0A1Q9L861
U	428	THR	-	expression tag	UNP A0A1Q9L861
U	429	SER	-	expression tag	UNP A0A1Q9L861
U	430	GLY	-	expression tag	UNP A0A1Q9L861
V	169	SER	CYS	conflict	UNP A0A1Q9L861
V	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
V	408	GLU	LYS	conflict	UNP A0A1Q9L861
V	425	GLY	-	expression tag	UNP A0A1Q9L861
V	426	GLY	-	expression tag	UNP A0A1Q9L861
V	427	GLY	-	expression tag	UNP A0A1Q9L861
V	428	THR	-	expression tag	UNP A0A1Q9L861
V	429	SER	-	expression tag	UNP A0A1Q9L861
V	430	GLY	-	expression tag	UNP A0A1Q9L861
X	169	SER	CYS	conflict	UNP A0A1Q9L861
X	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
X	408	GLU	LYS	conflict	UNP A0A1Q9L861
X	425	GLY	-	expression tag	UNP A0A1Q9L861
X	426	GLY	-	expression tag	UNP A0A1Q9L861
X	427	GLY	-	expression tag	UNP A0A1Q9L861
X	428	THR	-	expression tag	UNP A0A1Q9L861
X	429	SER	-	expression tag	UNP A0A1Q9L861
X	430	GLY	-	expression tag	UNP A0A1Q9L861
Y	169	SER	CYS	conflict	UNP A0A1Q9L861
Y	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
Y	408	GLU	LYS	conflict	UNP A0A1Q9L861
Y	425	GLY	-	expression tag	UNP A0A1Q9L861
Y	426	GLY	-	expression tag	UNP A0A1Q9L861
Y	427	GLY	-	expression tag	UNP A0A1Q9L861
Y	428	THR	-	expression tag	UNP A0A1Q9L861
Y	429	SER	-	expression tag	UNP A0A1Q9L861
Y	430	GLY	-	expression tag	UNP A0A1Q9L861
Z	169	SER	CYS	conflict	UNP A0A1Q9L861
Z	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
Z	408	GLU	LYS	conflict	UNP A0A1Q9L861
Z	425	GLY	-	expression tag	UNP A0A1Q9L861
Z	426	GLY	-	expression tag	UNP A0A1Q9L861
Z	427	GLY	-	expression tag	UNP A0A1Q9L861
Z	428	THR	-	expression tag	UNP A0A1Q9L861

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	429	SER	-	expression tag	UNP A0A1Q9L861
Z	430	GLY	-	expression tag	UNP A0A1Q9L861
1	169	SER	CYS	conflict	UNP A0A1Q9L861
1	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
1	408	GLU	LYS	conflict	UNP A0A1Q9L861
1	425	GLY	-	expression tag	UNP A0A1Q9L861
1	426	GLY	-	expression tag	UNP A0A1Q9L861
1	427	GLY	-	expression tag	UNP A0A1Q9L861
1	428	THR	-	expression tag	UNP A0A1Q9L861
1	429	SER	-	expression tag	UNP A0A1Q9L861
1	430	GLY	-	expression tag	UNP A0A1Q9L861
2	169	SER	CYS	conflict	UNP A0A1Q9L861
2	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
2	408	GLU	LYS	conflict	UNP A0A1Q9L861
2	425	GLY	-	expression tag	UNP A0A1Q9L861
2	426	GLY	-	expression tag	UNP A0A1Q9L861
2	427	GLY	-	expression tag	UNP A0A1Q9L861
2	428	THR	-	expression tag	UNP A0A1Q9L861
2	429	SER	-	expression tag	UNP A0A1Q9L861
2	430	GLY	-	expression tag	UNP A0A1Q9L861
3	169	SER	CYS	conflict	UNP A0A1Q9L861
3	185	GLN	GLU	engineered mutation	UNP A0A1Q9L861
3	408	GLU	LYS	conflict	UNP A0A1Q9L861
3	425	GLY	-	expression tag	UNP A0A1Q9L861
3	426	GLY	-	expression tag	UNP A0A1Q9L861
3	427	GLY	-	expression tag	UNP A0A1Q9L861
3	428	THR	-	expression tag	UNP A0A1Q9L861
3	429	SER	-	expression tag	UNP A0A1Q9L861
3	430	GLY	-	expression tag	UNP A0A1Q9L861

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total O 1 1	0
3	B	1	Total O 1 1	0
3	C	1	Total O 1 1	0
3	D	1	Total O 1 1	0
3	E	1	Total O 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
3	F	1	Total O 1 1	0
3	G	1	Total O 1 1	0
3	H	1	Total O 1 1	0
3	I	1	Total O 1 1	0
3	J	1	Total O 1 1	0
3	K	1	Total O 1 1	0
3	L	1	Total O 1 1	0
3	M	1	Total O 1 1	0
3	N	1	Total O 1 1	0

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.

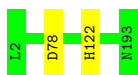
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain A:  97%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain B:  99%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain C:  98%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain D:  97%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain E:  98%



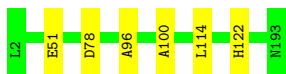
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain F:  96%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain G:  97%



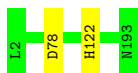
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain H:  98%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain I:  99%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain J:  97%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain K:  98%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain L:  97%



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

GLY SER
ILE ASP
GLN LYS
THR THR
LEU LEU
ALA ALA
GLU THR
THR THR
LEU LEU
ALA ALA
SER THR
ARG ARG
LYS LYS
SER ALA
ASP ARG
LEU LEU

TYR ILE
ASP ASP
GLN LYS
ILE ILE
ASP ASP
GLY LYS
ILE ILE
ALA ALA
SER THR
ARG ARG
LYS LYS
SER ALA
ASP ARG
LEU LEU

LYS ILE
LEU LEU
PHE PHE
ILE ILE
CYS CYS
GLY GLY
GLY GLY
ALA ALA
PHE PHE
SER THR
GLY GLY
LEU LEU
ASP ASP
LEU LEU
LYS LYS
VAL VAL
ILE ILE
SER SER
HIS HIS
ARG ARG
VAL VAL
GLU GLU
THR THR
GLY GLY
SER SER
G287
R275
ALA ALA
LYS LYS
SER SER
ASP ASP
LYS LYS
SER SER
GLU GLU
GLY GLY
GLU GLU
LEU LEU
LEU LEU
ALA ALA
VAL VAL
GLN GLN
PRO PRO
GLU GLU
PRO PRO
GLY GLY
LEU LEU

LEU PRO
VAL VAL
ALA ALA
THR THR
LEU LEU
ASN ASN
GLU GLU
SER SER
LEU LEU
GLU GLU
ALA ALA
LEU LEU
LEU LEU
ASP ASP
LEU LEU
ILE ILE
GLN GLN
ILE ILE
SER SER
LYS LYS
GLU GLU
ASN ASN
ALA ALA
LEU LEU
THR THR
LYS LYS
GLN GLN
TYR TYR
GLN GLN
ALA ALA
LEU LEU
PHE PHE
ASN ASN
SER SER
GLU GLU
GLY GLY
VAL VAL
PHE PHE
ASP ASP
GLU GLU
LEU LEU
LEU LEU
ILE ILE
TYR TYR
GLY GLY
LYS LYS
PRO PRO
GLU GLU
ALA ALA
ILE ILE
SER SER
GLN GLN
GLN GLN
ALA ALA
SER SER
GLY GLY
GLU GLU
GLY GLY
LYS LYS
THR THR

GLY ALA
ALA ARG
GLY GLY
LEU LEU
ARG ARG
SER SER
ILE ILE
VAL VAL
GLU GLU
ALA ALA
ALA ALA
LEU LEU
LEU LEU
ASP ASP
THR THR
MET MET
TYR TYR
ASP ASP
LEU LEU
PRO PRO
SER SER
MET MET
GLU GLU
ASP ASP
VAL VAL
GLU GLU
LYS LYS
VAL VAL
ILE ILE
ASP ASP
GLU GLU
GLN GLN
SER SER
GLU GLU
PRO PRO
LEU LEU
LEU LEU
ILE ILE
TYR TYR
GLY GLY
LYS LYS
PRO PRO
GLU GLU
ALA ALA
GLN GLN
GLN GLN
ALA ALA
SER SER
GLY GLY
GLU GLU
GLY GLY
LYS LYS
GLY GLY

THR
SER
GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D7	Depositor
Number of particles used	443717	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 ($e^-/\text{\AA}^2$)	56	Depositor
Minimum defocus (nm)	-800	Depositor
Maximum defocus (nm)	-2500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	40.065	Depositor
Minimum map value	-20.384	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.98	Depositor
Map size (\AA)	348.0, 348.0, 348.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.16, 1.16, 1.16	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	0.31	0/1528	0.53	0/2058
1	B	0.31	0/1528	0.53	0/2058
1	C	0.31	0/1528	0.53	0/2058
1	D	0.31	0/1528	0.53	0/2058
1	E	0.31	0/1528	0.53	0/2058
1	F	0.31	0/1528	0.53	0/2058
1	G	0.31	0/1528	0.53	0/2058
1	H	0.31	0/1528	0.53	0/2058
1	I	0.31	0/1528	0.53	0/2058
1	J	0.31	0/1528	0.53	0/2058
1	K	0.31	0/1528	0.53	0/2058
1	L	0.31	0/1528	0.53	0/2058
1	M	0.31	0/1528	0.53	0/2058
1	N	0.31	0/1528	0.53	0/2058
2	1	0.28	0/55	0.47	0/73
2	2	0.28	0/55	0.47	0/73
2	3	0.28	0/55	0.47	0/73
2	O	0.28	0/55	0.47	0/73
2	P	0.29	0/55	0.47	0/73
2	Q	0.28	0/55	0.47	0/73
2	R	0.28	0/55	0.47	0/73
2	S	0.28	0/55	0.47	0/73
2	T	0.28	0/55	0.47	0/73
2	U	0.28	0/55	0.47	0/73
2	V	0.28	0/55	0.47	0/73
2	X	0.28	0/55	0.47	0/73
2	Y	0.28	0/55	0.47	0/73
2	Z	0.28	0/55	0.47	0/73
All	All	0.31	0/22162	0.52	0/29834

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

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	1504	1513	1513	4	0
1	B	1504	1513	1513	1	0
1	C	1504	1513	1513	3	0
1	D	1504	1513	1513	5	0
1	E	1504	1513	1513	3	0
1	F	1504	1513	1513	5	0
1	G	1504	1513	1513	6	0
1	H	1504	1513	1513	3	0
1	I	1504	1513	1513	1	0
1	J	1504	1513	1513	4	0
1	K	1504	1513	1513	4	0
1	L	1504	1513	1513	4	0
1	M	1504	1513	1513	5	0
1	N	1504	1513	1513	6	0
2	1	55	51	51	0	0
2	2	55	51	51	0	0
2	3	55	51	51	0	0
2	O	55	51	51	0	0
2	P	55	51	51	0	0
2	Q	55	51	51	0	0
2	R	55	51	51	0	0
2	S	55	51	51	0	0
2	T	55	51	51	0	0
2	U	55	51	51	0	0
2	V	55	51	51	0	0
2	X	55	51	51	0	0
2	Y	55	51	51	0	0
2	Z	55	51	51	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
All	All	21840	21896	21896	32	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 1.

All (32) 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:M:78:ASP:HB2	1:N:114:LEU:HD23	1.95	0.49
1:F:51:GLU:OE1	1:F:83:ILE:HG22	2.13	0.49
1:F:78:ASP:HB2	1:G:114:LEU:HD23	1.95	0.49
1:H:114:LEU:HD23	1:N:78:ASP:HB2	1.95	0.48
1:A:114:LEU:HD23	1:G:78:ASP:HB2	1.96	0.47
1:H:114:LEU:HD23	1:N:78:ASP:CB	2.46	0.46
1:F:78:ASP:CB	1:G:114:LEU:HD23	2.46	0.46
1:M:78:ASP:CB	1:N:114:LEU:HD23	2.46	0.45
1:A:114:LEU:HD23	1:G:78:ASP:CB	2.47	0.45
1:J:78:ASP:HB2	1:K:114:LEU:HD23	1.98	0.44
1:C:78:ASP:HB2	1:D:114:LEU:HD23	1.98	0.44
1:J:96:ALA:O	1:J:100:ALA:N	2.46	0.43
1:D:96:ALA:O	1:D:100:ALA:N	2.46	0.43
1:M:96:ALA:O	1:M:100:ALA:N	2.46	0.43
1:G:96:ALA:O	1:G:100:ALA:N	2.46	0.43
1:K:78:ASP:CB	1:L:114:LEU:HD23	2.49	0.43
1:D:78:ASP:HB2	1:E:114:LEU:HD23	2.00	0.42
1:H:192:ARG:NE	1:N:51:GLU:OE2	2.51	0.42
1:C:78:ASP:CB	1:D:114:LEU:HD23	2.49	0.42
1:L:78:ASP:HB2	1:M:114:LEU:HD23	2.01	0.42
1:A:192:ARG:NE	1:G:51:GLU:OE2	2.53	0.42
1:D:78:ASP:CB	1:E:114:LEU:HD23	2.49	0.42
1:K:78:ASP:HB2	1:L:114:LEU:HD23	2.00	0.42
1:J:78:ASP:CB	1:K:114:LEU:HD23	2.49	0.42
1:E:78:ASP:HB2	1:F:114:LEU:HD23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:96:ALA:O	1:L:100:ALA:N	2.46	0.41
1:N:96:ALA:O	1:N:100:ALA:N	2.46	0.41
1:A:96:ALA:O	1:A:100:ALA:N	2.46	0.41
1:F:96:ALA:O	1:F:100:ALA:N	2.46	0.41
1:I:78:ASP:HB2	1:J:114:LEU:HD23	2.02	0.41
1:B:78:ASP:HB2	1:C:114:LEU:HD23	2.02	0.40
1:M:51:GLU:OE1	1:M:83:ILE:HG22	2.21	0.40

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	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	B	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	C	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	D	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	E	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	F	190/192 (99%)	188 (99%)	2 (1%)	0	100	100
1	G	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	H	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	I	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	J	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	K	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	L	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	M	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
1	N	190/192 (99%)	187 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1	7/369 (2%)	7 (100%)	0	0	100	100
2	2	7/369 (2%)	7 (100%)	0	0	100	100
2	3	7/369 (2%)	7 (100%)	0	0	100	100
2	O	7/369 (2%)	7 (100%)	0	0	100	100
2	P	7/369 (2%)	7 (100%)	0	0	100	100
2	Q	7/369 (2%)	7 (100%)	0	0	100	100
2	R	7/369 (2%)	7 (100%)	0	0	100	100
2	S	7/369 (2%)	7 (100%)	0	0	100	100
2	T	7/369 (2%)	7 (100%)	0	0	100	100
2	U	7/369 (2%)	7 (100%)	0	0	100	100
2	V	7/369 (2%)	7 (100%)	0	0	100	100
2	X	7/369 (2%)	7 (100%)	0	0	100	100
2	Y	7/369 (2%)	7 (100%)	0	0	100	100
2	Z	7/369 (2%)	7 (100%)	0	0	100	100
All	All	2758/7854 (35%)	2717 (98%)	41 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	B	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	C	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	D	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	E	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	F	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	G	163/163 (100%)	162 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	I	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	J	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	K	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	L	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	M	163/163 (100%)	162 (99%)	1 (1%)	86	94
1	N	163/163 (100%)	162 (99%)	1 (1%)	86	94
2	1	4/301 (1%)	4 (100%)	0	100	100
2	2	4/301 (1%)	4 (100%)	0	100	100
2	3	4/301 (1%)	4 (100%)	0	100	100
2	O	4/301 (1%)	4 (100%)	0	100	100
2	P	4/301 (1%)	4 (100%)	0	100	100
2	Q	4/301 (1%)	4 (100%)	0	100	100
2	R	4/301 (1%)	4 (100%)	0	100	100
2	S	4/301 (1%)	4 (100%)	0	100	100
2	T	4/301 (1%)	4 (100%)	0	100	100
2	U	4/301 (1%)	4 (100%)	0	100	100
2	V	4/301 (1%)	4 (100%)	0	100	100
2	X	4/301 (1%)	4 (100%)	0	100	100
2	Y	4/301 (1%)	4 (100%)	0	100	100
2	Z	4/301 (1%)	4 (100%)	0	100	100
All	All	2338/6496 (36%)	2324 (99%)	14 (1%)	86	94

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	HIS
1	B	122	HIS
1	C	122	HIS
1	D	122	HIS
1	E	122	HIS
1	F	122	HIS
1	G	122	HIS
1	H	122	HIS
1	I	122	HIS

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Mol	Chain	Res	Type
1	J	122	HIS
1	K	122	HIS
1	L	122	HIS
1	M	122	HIS
1	N	122	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	41	ASN
1	K	41	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.

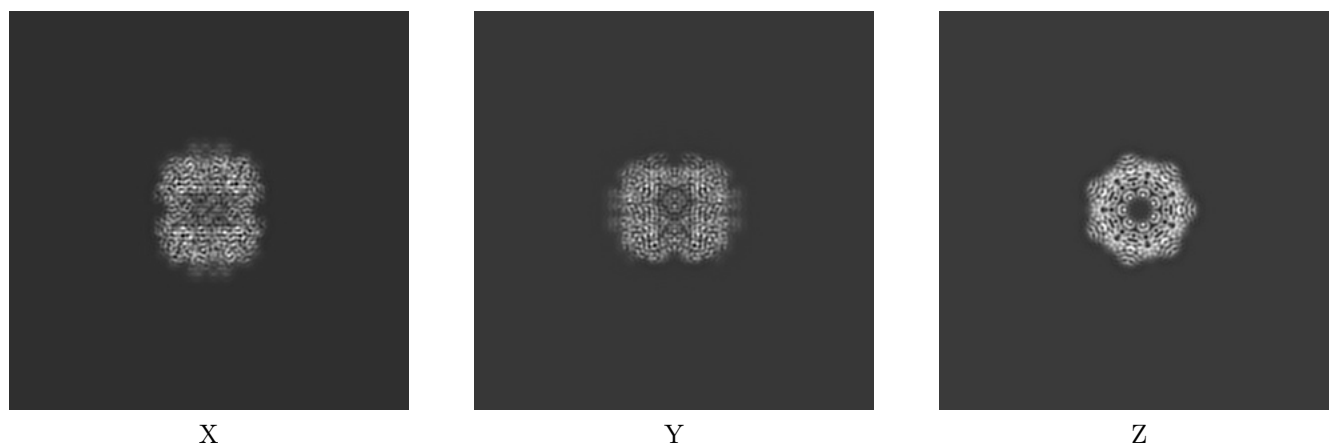
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20434. 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](#)

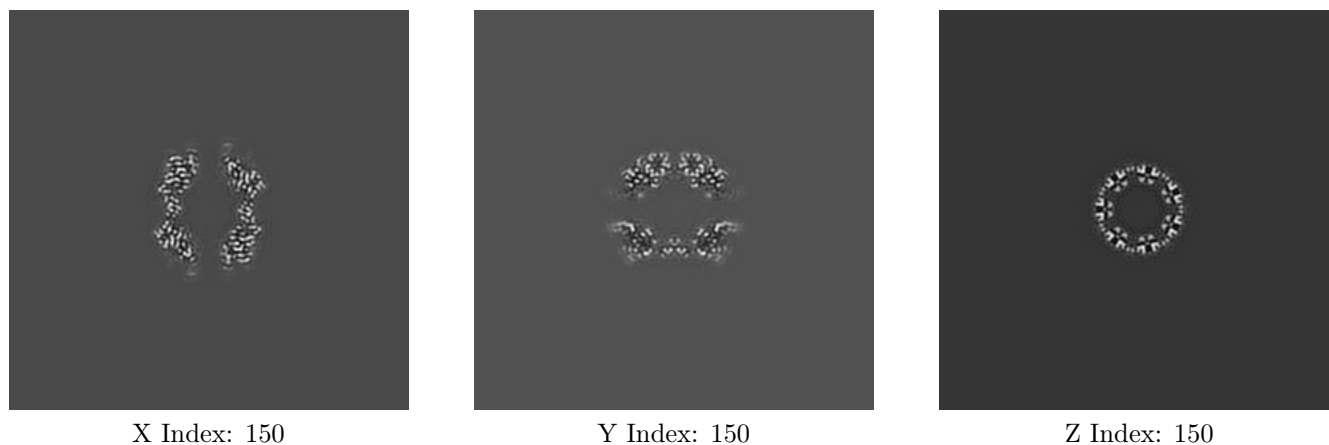
6.1.1 Primary map



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

6.2 Central slices [i](#)

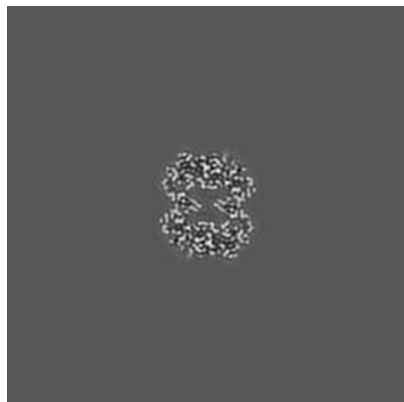
6.2.1 Primary map



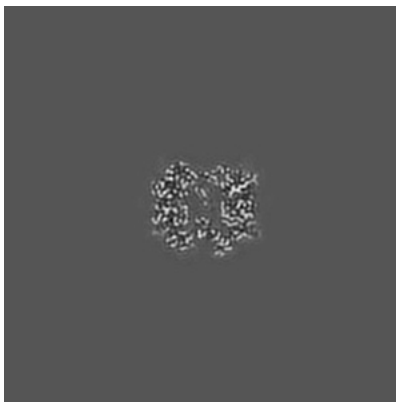
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 171



Y Index: 129

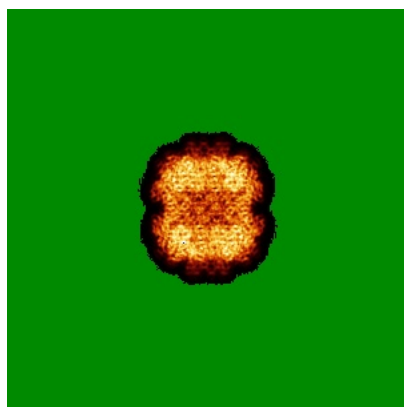


Z Index: 167

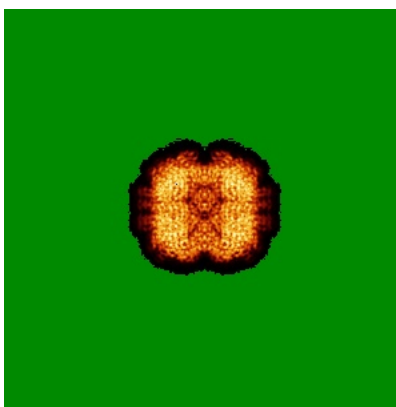
The images above show the largest variance slices of the map in three orthogonal directions.

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

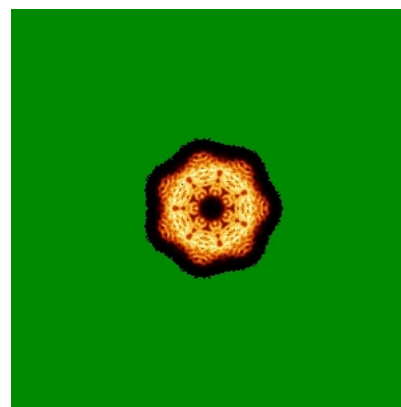
6.4.1 Primary map



X



Y

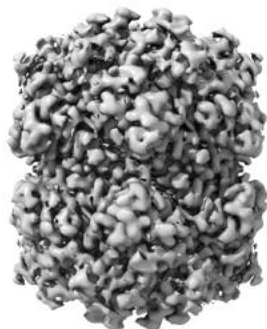


Z

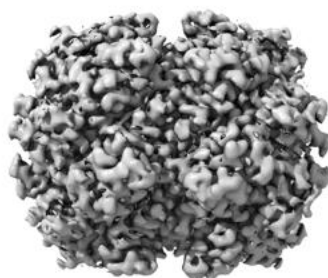
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

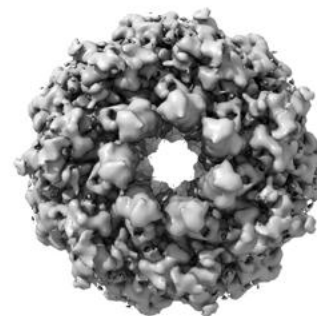
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.98. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

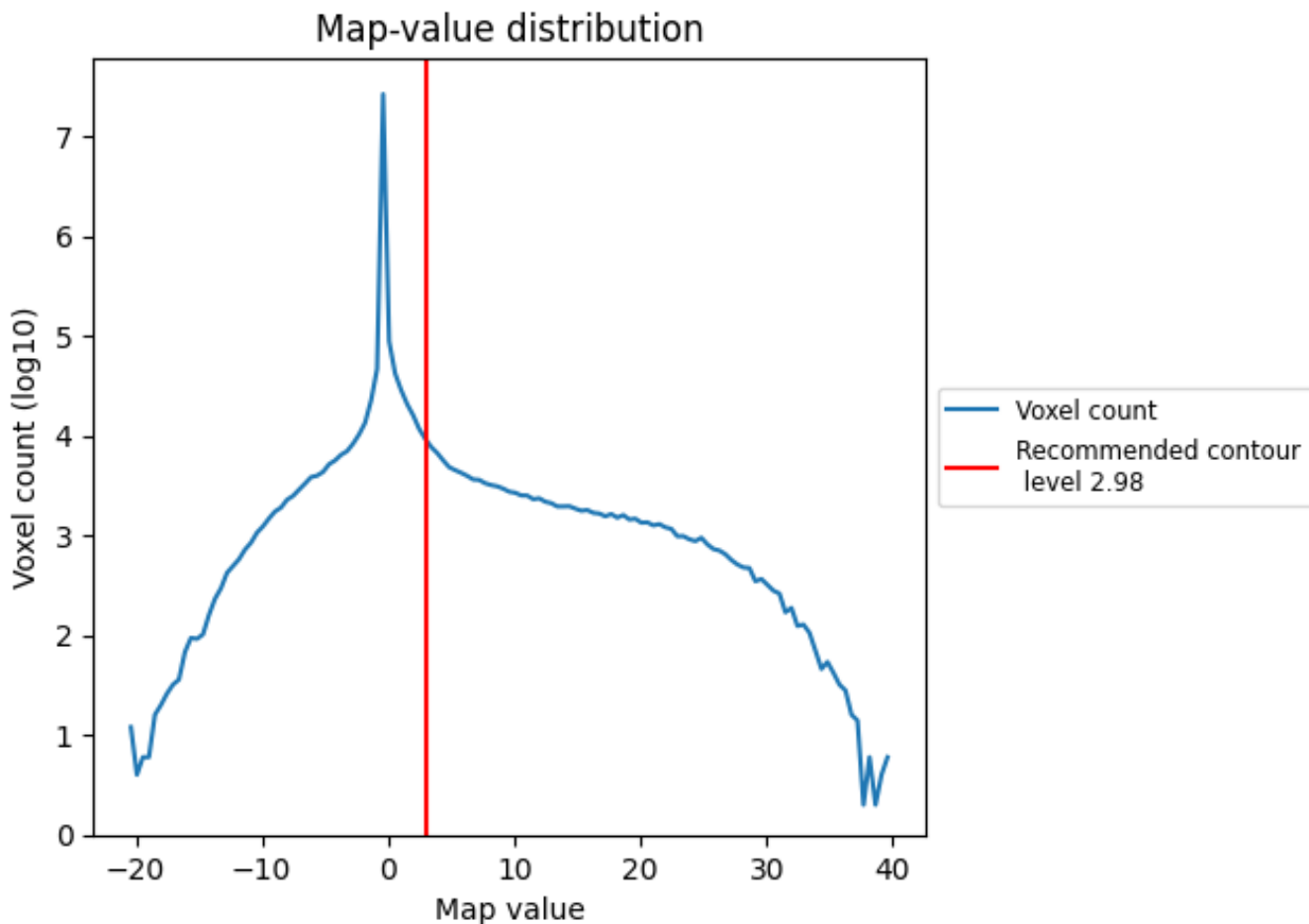
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

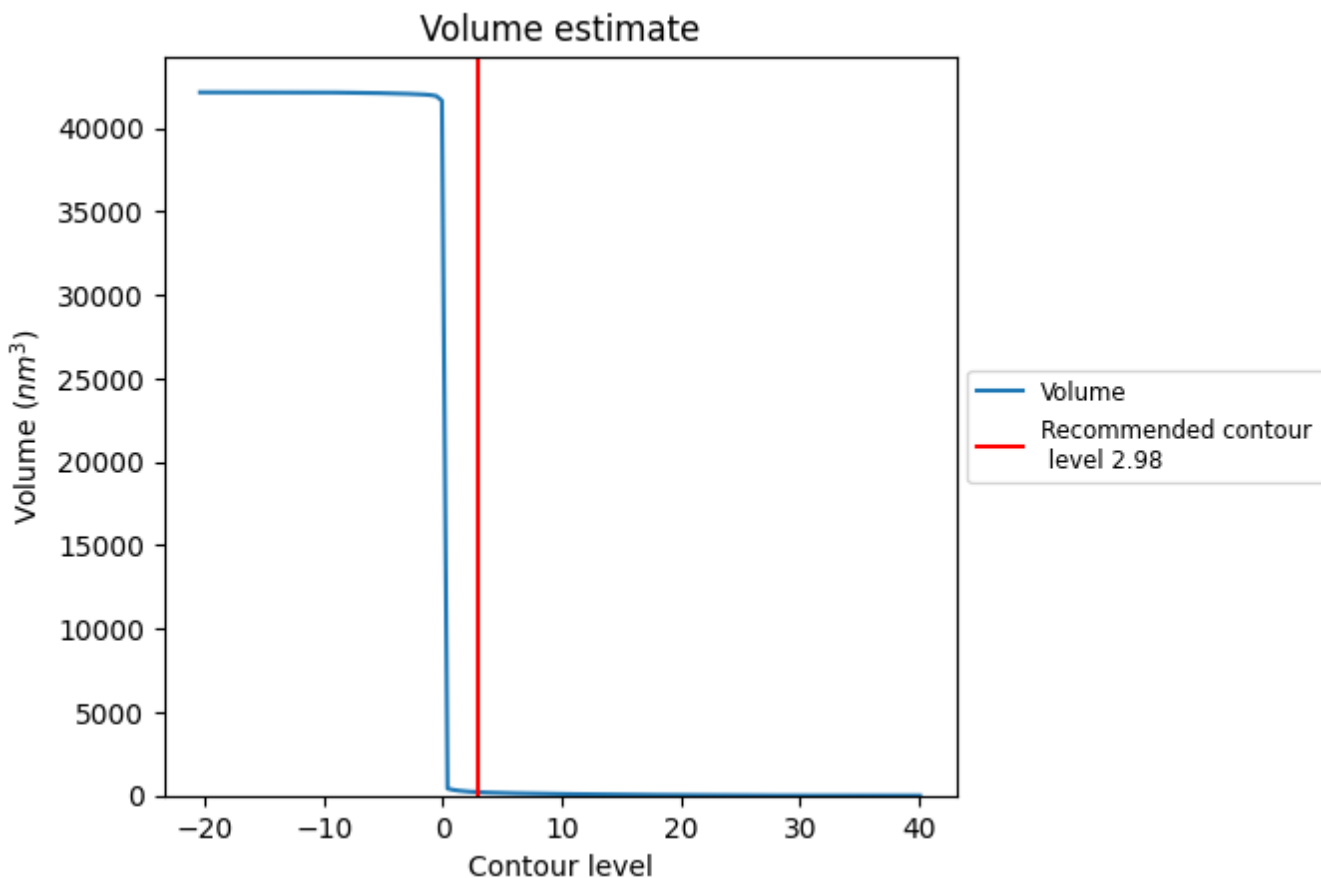
This section contains the results of statistical analysis of the map.

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.

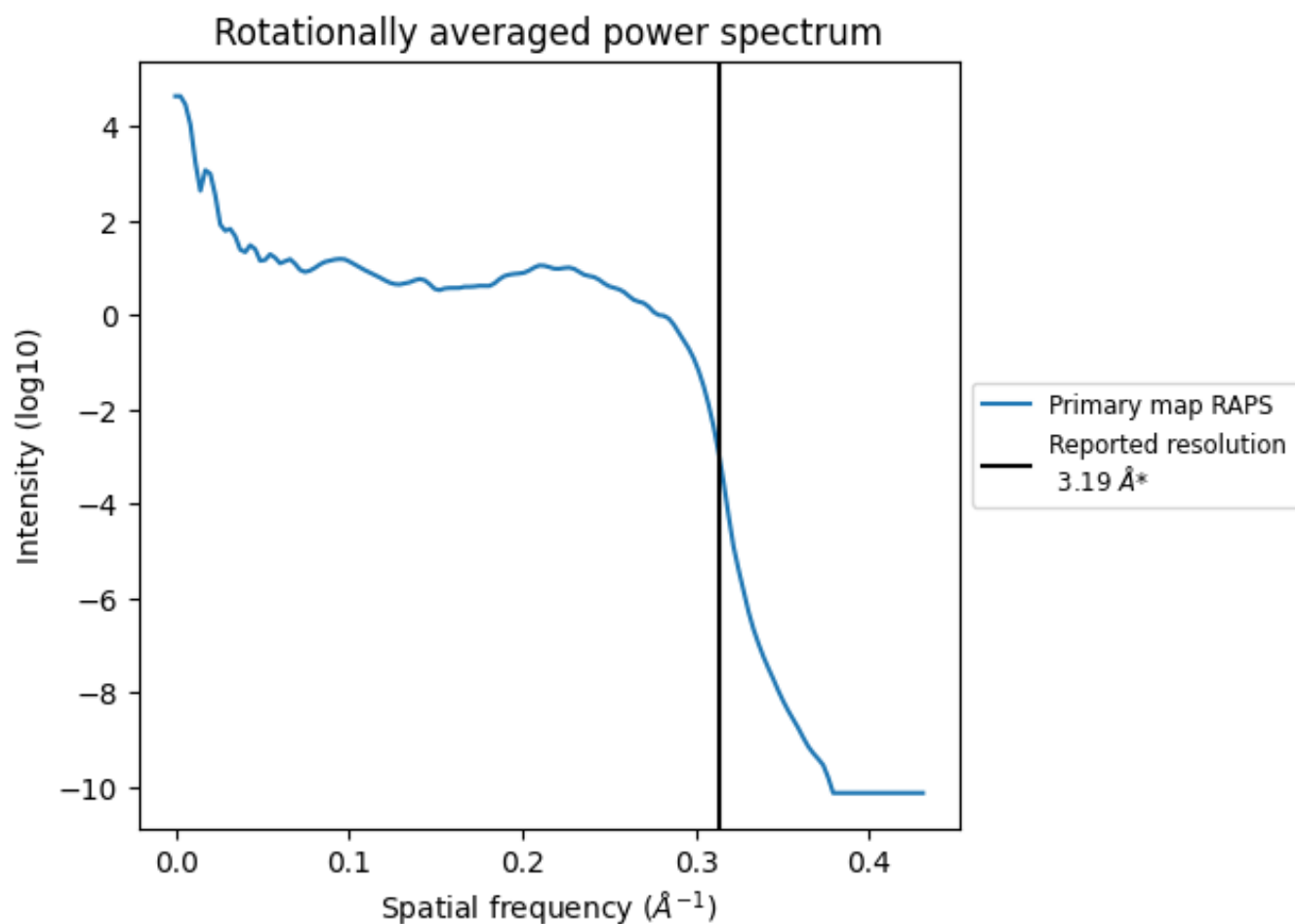
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 202 nm³; this corresponds to an approximate mass of 182 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 [\(i\)](#)

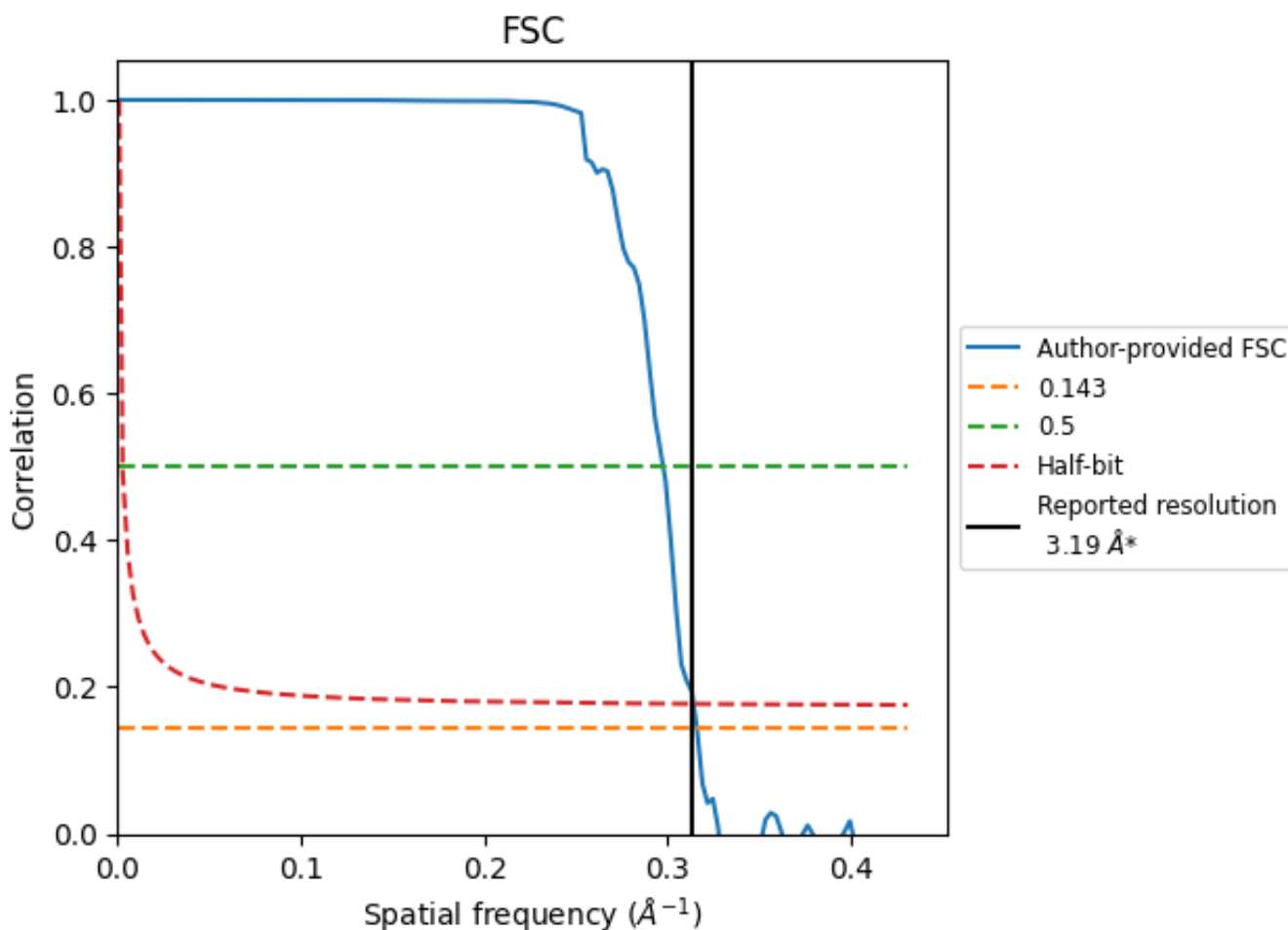


*Reported resolution corresponds to spatial frequency of 0.313 Å⁻¹

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 0.313 Å⁻¹

8.2 Resolution estimates [i](#)

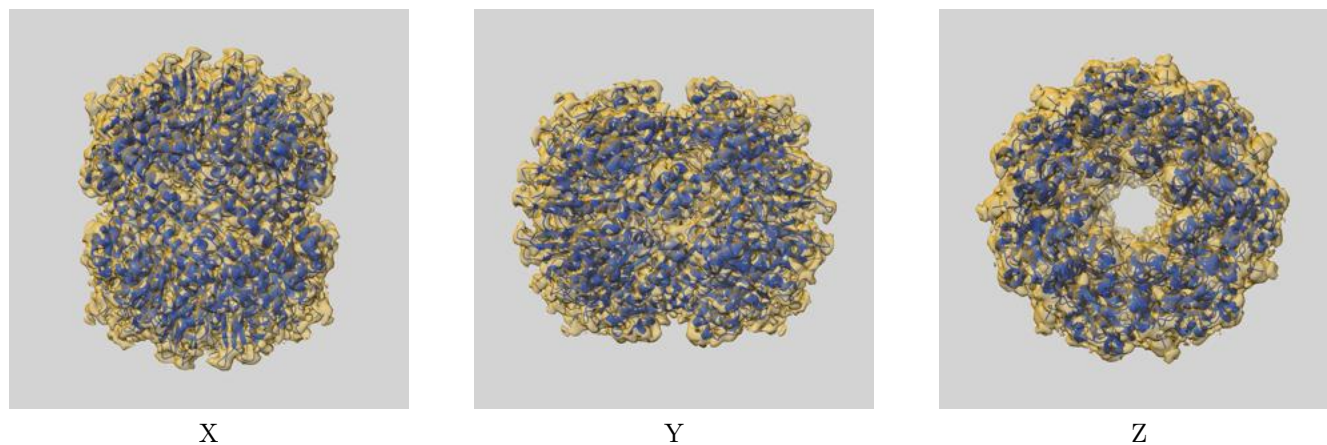
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.19	-	-
Author-provided FSC curve	3.16	3.36	3.18
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

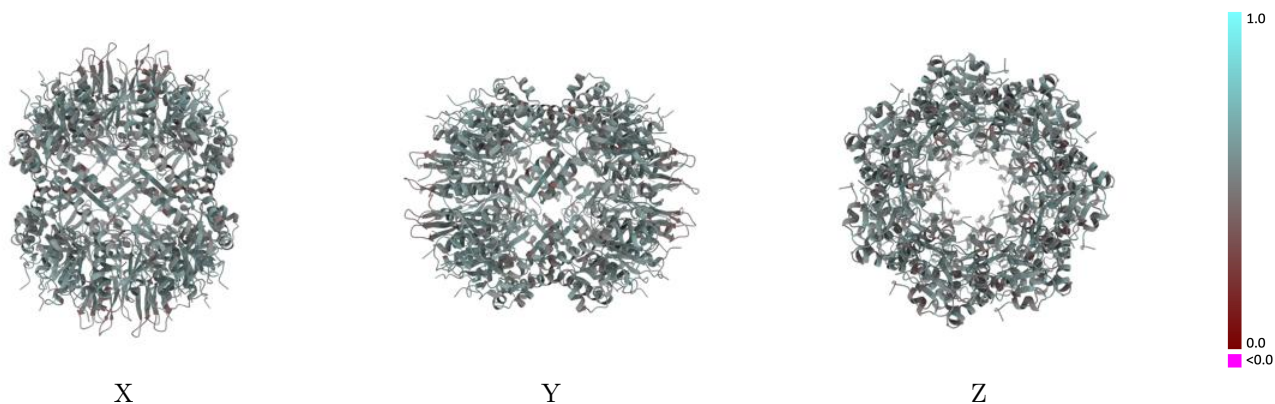
This section contains information regarding the fit between EMDB map EMD-20434 and PDB model 6PPE. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



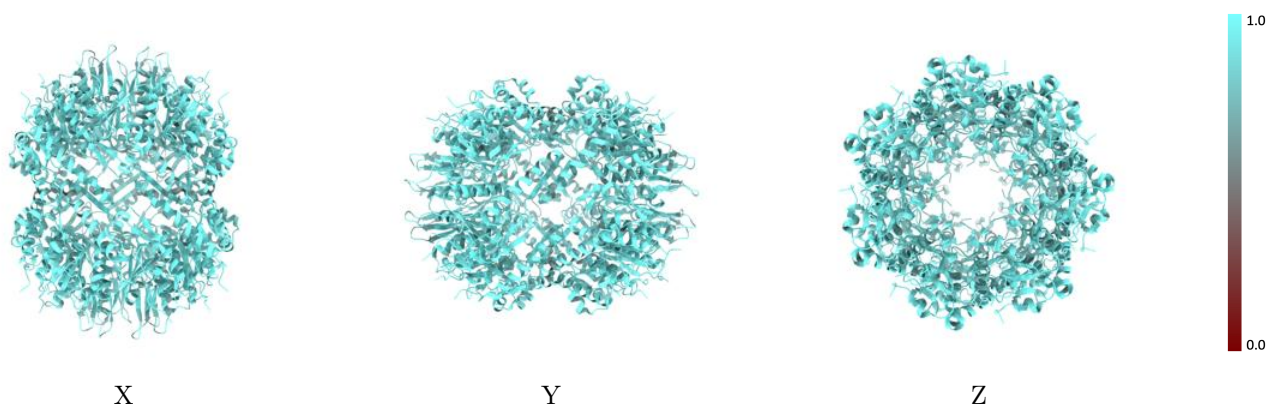
The images above show the 3D surface view of the map at the recommended contour level 2.98 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



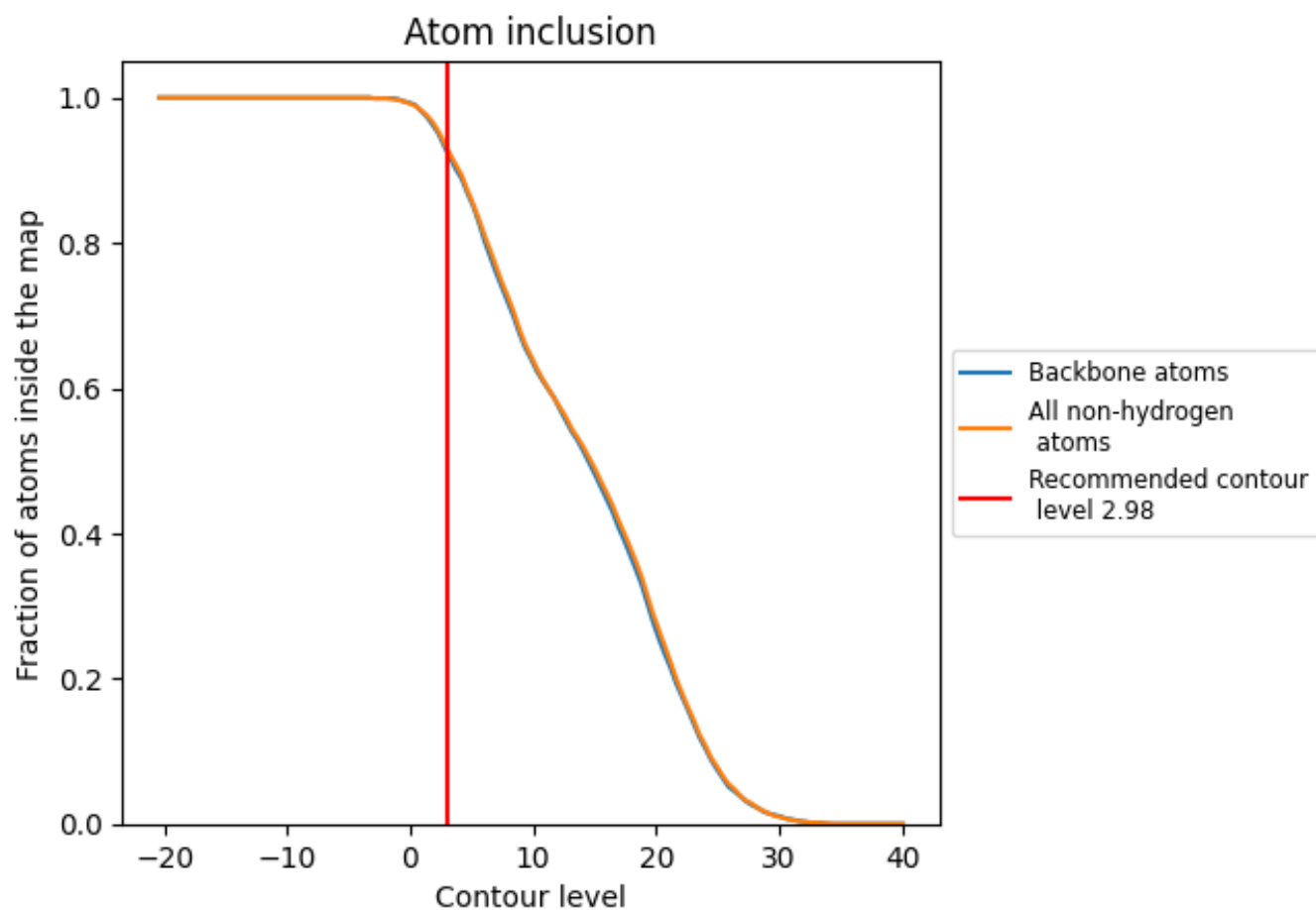
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.98).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (2.98) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.5270
1	 0.9640	 0.5320
2	 0.9460	 0.5090
3	 0.9460	 0.5130
A	 0.9350	 0.5320
B	 0.9310	 0.5300
C	 0.9350	 0.5320
D	 0.9370	 0.5350
E	 0.9350	 0.5320
F	 0.9440	 0.5310
G	 0.9410	 0.5320
H	 0.9210	 0.5200
I	 0.9270	 0.5250
J	 0.9330	 0.5290
K	 0.9350	 0.5240
L	 0.9290	 0.5170
M	 0.9270	 0.5130
N	 0.9320	 0.5200
O	 0.9460	 0.5370
P	 0.9820	 0.5410
Q	 1.0000	 0.5310
R	 0.9460	 0.5280
S	 0.9460	 0.5210
T	 0.9640	 0.5320
U	 0.9460	 0.5290
V	 0.9820	 0.5160
X	 1.0000	 0.5270
Y	 0.9820	 0.5320
Z	 0.9460	 0.5260

