



## wwPDB EM Validation Summary Report ⓘ

Nov 12, 2022 – 11:24 AM EST

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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

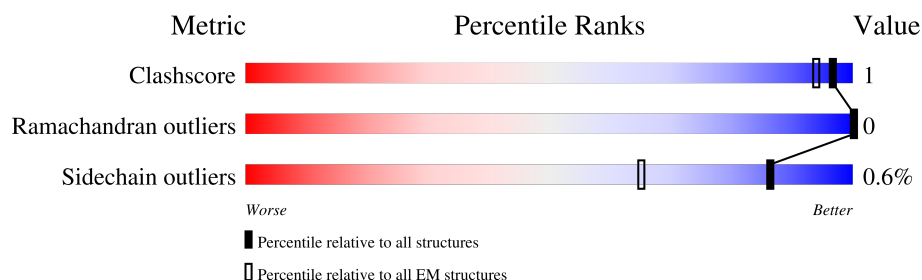
# 1 Overall quality at a glance

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.



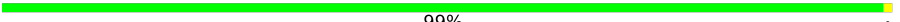
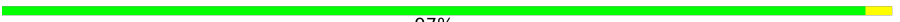
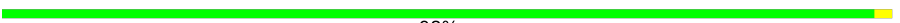












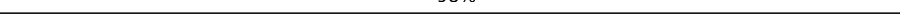
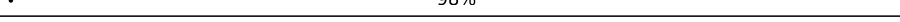
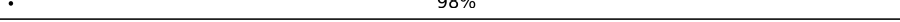
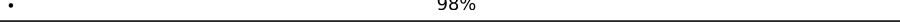
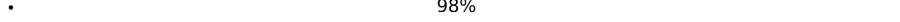
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	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

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

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

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

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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 1	O 1	0
3	G	1	Total 1	O 1	0
3	H	1	Total 1	O 1	0
3	I	1	Total 1	O 1	0
3	J	1	Total 1	O 1	0
3	K	1	Total 1	O 1	0
3	L	1	Total 1	O 1	0
3	M	1	Total 1	O 1	0
3	N	1	Total 1	O 1	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: 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%



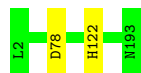
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

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%



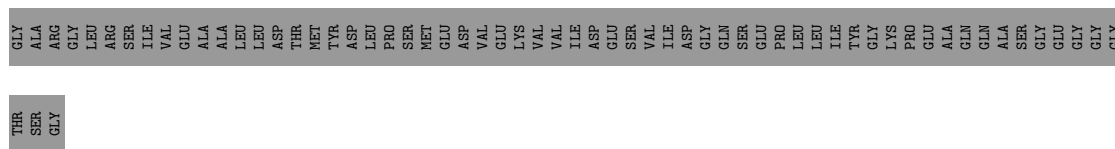
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain L:  97%



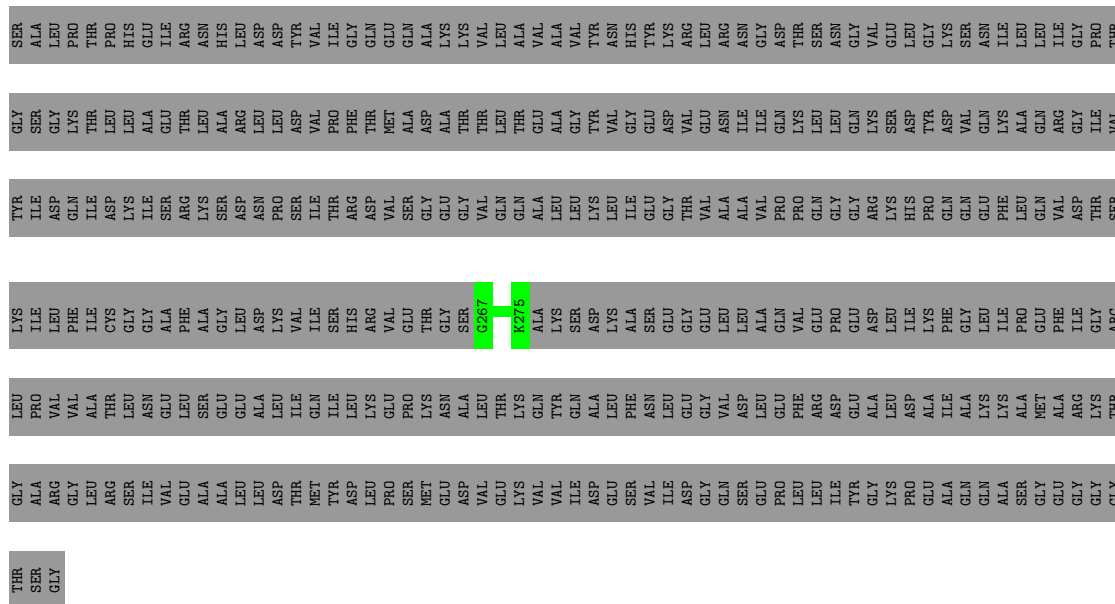
- Molecule 1: ATP-dependent Clp protease proteolytic subunit





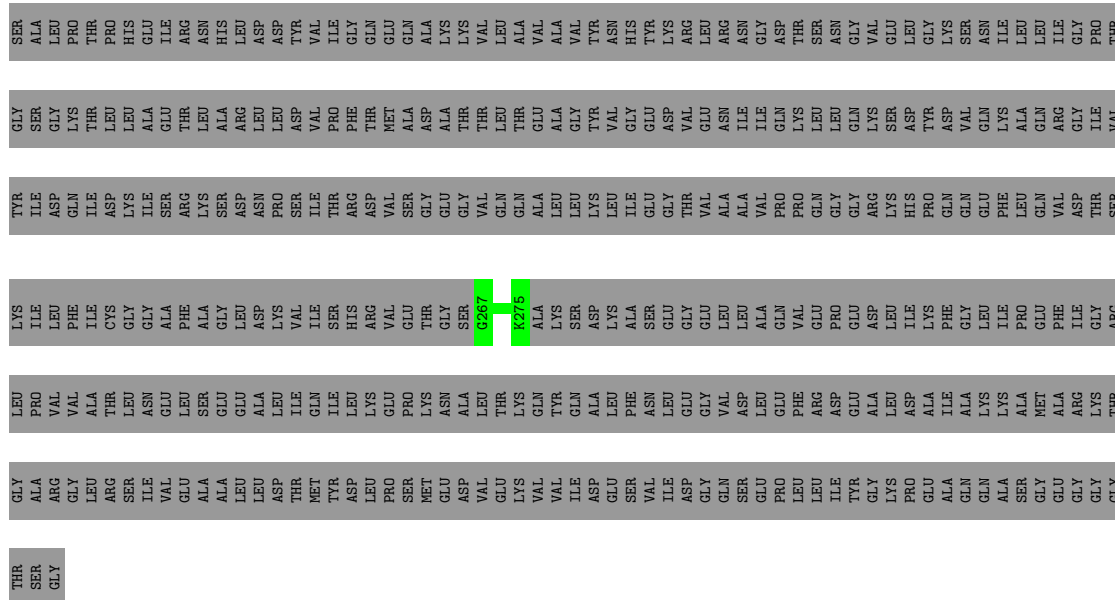
- Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

Chain Q:  98%



- Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

Chain R:  98%



- Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

98%

THR	GLY	LEU	LYS	TYR	GLY	SER
THR	ALA	PRO	ILE	ILE	SER	ALA
SER	ARG	VAL	LEU	ASP	GLY	LEU
GLY	GLY	VAL	PHE	GLN	THR	PRO
	LEU	ALA	ILE	ILE	ASP	PRO
ARG	ARG	THR	CYS	LYS	LEU	HIS
SER	SER	LEU	GLY	ASP	LEU	GLU
ILE	ILE	ASN	GLY	ILE	ALA	ILE
VAL	VAL	GLU	ALA	SER	THR	ILE
GLU	GLU	LEU	PHE	ARG	GLU	ARG
ALA	ALA	SER	GLY	LYS	LEU	ASN
LEU	LEU	GLU	GLY	ASP	ALA	HIS
ALA	LEU	GLU	LEU	ASP	ARG	LEU
LEU	LEU	ALA	ASP	ASN	LEU	ASP
ASP	ASP	LEU	LYS	PRO	ASP	ASP
THR	THR	ILE	VAL	SER	ASP	TYR
MET	MET	GLN	ILE	ILE	VAL	VAL
TYR	TYR	ILE	SER	THR	PRO	ILE
ASP	ASP	LEU	HIS	ARG	PHE	GLY
LEU	LEU	LYS	ARG	ASP	THR	GLN
PRO	PRO	GLU	VAL	VAL	MET	GLN
SER	SER	PRO	GLU	SER	ALA	GLN
MET	MET	LYS	THR	GLY	ASP	ALA
GLU	GLU	ASN	GLY	GLU	ALA	LYS
ASP	ASP	ALA	SER	GLY	THR	LYS
VAL	VAL	LEU	6267	VAL	THR	VAL
GLU	GLU	THR	6275	GLN	LEU	LEU
LYS	LYS	GLN	ALA	ALA	THR	ALA
VAL	VAL	LYS	LYS	LEU	ALA	VAL
VAL	VAL	TYR	LEU	LEU	GLY	VAL
ILE	ILE	GLN	SER	LEU	TYR	ALA
ASP	ASP	ALA	ASP	VAL	GLY	VAL
GLU	GLU	LEU	LYS	LEU	THR	ASN
SER	SER	PHE	ALA	ILE	GLY	HIS
VAL	VAL	ASN	SER	GLU	TYR	LYS
ILE	ILE	LEU	GLU	GLY	ASP	LYS
ASP	ASP	GLU	GLY	THR	VAL	ARG
GLY	GLN	VAL	LEU	VAL	GLU	LEU
SER	SER	ASP	LEU	ALA	ASN	ARG
GLU	GLU	LEU	ALA	VAL	ILE	ASN
PRO	PRO	GLU	GLN	PRO	GLN	ASP
LEU	LEU	PHE	VAL	PRO	LYS	THR
LEU	LEU	ARG	GLU	GLN	LEU	SER
ILE	ILE	ASP	PRO	GLY	LEU	ASN
TYR	TYR	GLU	GLU	ARG	GLN	GLY
ALA	LYS	LEU	ASP	LYS	SER	VAL
PRO	PRO	ASP	ILE	HIS	ASP	GLU
GLU	GLU	ALA	LYS	PRO	TYR	LEU
ALA	ALA	ILE	PHE	GLN	ASP	GLY
GLN	GLN	ALA	GLY	GLN	VAL	LYS
LYS	ALA	LYS	ILE	PHE	LYS	ILE
ALA	SER	ALA	PRO	LEU	ALA	LEU
GLY	GLY	MET	GLU	GLN	GLN	LEU
GLU	GLU	ARG	PHE	VAL	ARG	ILE
GLY	GLY	LYS	ILE	ASP	GLY	GLY
GLY	GLY	THR	ARG	SER	ILE	PRO

- Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

98%

THR	GLY	LEU	LYS	TYR	GLY	SER
SER	ALA	PRO	ILE	ILE	SER	ALA
GLY	ARG	VAL	LEU	ASP	GLN	PRO
	LEU	ALA	ILE	ILE	THR	THR
ARG	THR	THR	CYS	ASP	LEU	PRO
SER	LEU	LEU	GLY	LYS	LEU	HIS
ILE	ASN	ASN	GLY	ILE	ALA	GLU
VAL	GLU	LEU	ALA	SER	GLU	ILE
GLU	GLU	LEU	PHE	ARG	THR	ARG
ALA	ALA	SER	ALA	LYS	LEU	ASN
ALA	GLU	GLU	GLY	SER	ALA	HIS
LEU	GLU	GLU	LEU	ASP	ARG	LEU
LEU	ALA	ALA	ASP	PRO	LEU	ASP
ASP	ASP	LYS	LYS	ASN	ASP	TYR
THR	THR	ILE	VAL	SER	ASP	VAL
MET	MET	GLN	ILE	ILE	VAL	VAL
TYR	TYR	ILE	SER	THR	PRO	GLY
ASP	ASP	LEU	HIS	ARG	PHE	GLN
LEU	LEU	LYS	ARG	ASP	THR	GLY
PRO	PRO	GLU	VAL	VAL	MET	GLN
SER	SER	PRO	GLU	SER	ALA	GLN
MET	MET	LYS	THR	GLY	ASP	LYS
GLU	GLU	ASN	GLY	GLU	ALA	ALA
ASP	ASP	ALA	SER	GLY	THR	LYS
VAL	VAL	LEU	6267	VAL	THR	VAL
GLU	GLU	THR	6275	GLN	LEU	VAL
LYS	LYS	LYS	ALA	ALA	GLU	VAL
VAL	VAL	GLN	LYS	LEU	ALA	ALA
VAL	VAL	TYR	LYS	LEU	ALA	VAL
ILE	ILE	GLN	SER	LEU	GLY	VAL
ASP	ASP	ALA	ASP	LYS	TYR	VAL
GLU	GLU	LEU	LYS	ASN	VAL	ASN
SER	SER	PHE	ALA	ILE	GLY	HIS
ASN	ASN	ASN	ALA	GLU	TYR	LYS
ILE	ILE	LEU	SER	GLY	ASP	LYS
GLY	GLY	GLU	GLU	THR	VAL	ARG
SER	SER	VAL	LEU	ALA	GLU	ARG
PRO	PRO	LEU	ALA	VAL	ILE	ASN
LEU	LEU	PHE	GLN	PRO	GLN	ASP
GLY	GLY	GLY	ALA	VAL	ILE	GLY
GLY	GLY	LEU	LEU	ARG	LYS	VAL
PRO	PRO	ASP	ASP	ILE	SER	GLU
GLU	GLU	ALA	LYS	HIS	LEU	LEU
ALA	ALA	ILE	ILE	GLY	LEU	ASN
GLN	GLN	ALA	GLY	GLN	GLY	VAL
ALA	ALA	LYS	LEU	PHE	VAL	SER
SER	SER	LYS	ILE	GLU	GLN	LYS
GLY	GLY	ALA	PRO	LEU	ALA	ILE
GLY	GLY	MET	GLU	GLN	GLN	LEU
GLU	GLU	ALA	PHE	VAL	ARG	ILE
GLY	GLY	ARG	ILE	ASP	GLY	ILE
GLY	GLY	LYS	GLY	THR	ILE	PRO
		THR	ARG	SER	VAL	THR

- Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

98%

[illegible]



WORLD WIDE  
PDB  
PROTEIN DATA BANK







[illegible]

## 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 (Å)	348.0, 348.0, 348.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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.

The worst 5 of 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

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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 ⓘ

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
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



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

Mol	Chain	Res	Type
1	H	122	HIS
1	I	122	HIS
1	N	122	HIS
1	L	122	HIS
1	M	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.

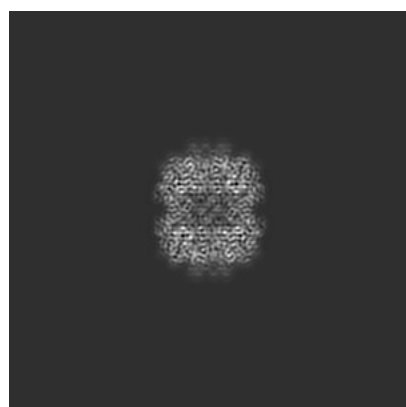
## 6 Map visualisation [i](#)

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.

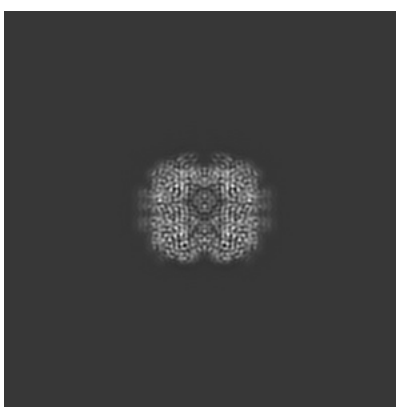
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

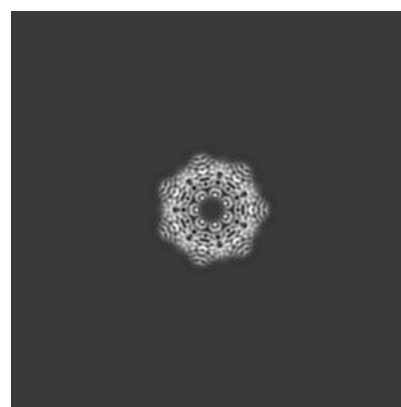
#### 6.1.1 Primary map



X



Y



Z

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

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

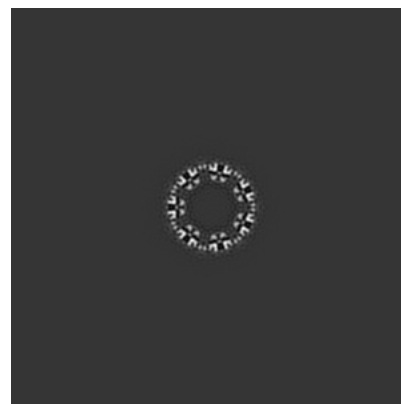
#### 6.2.1 Primary map



X Index: 150



Y Index: 150

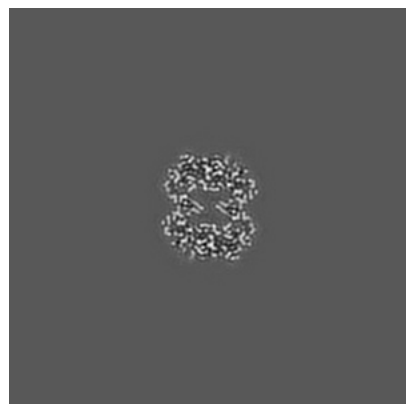


Z Index: 150

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

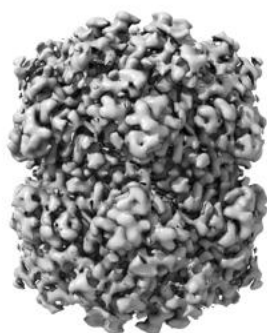


Z Index: 167

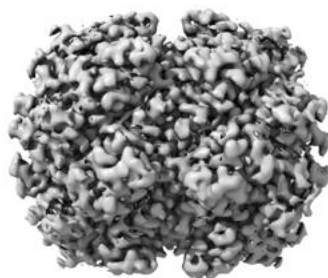
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal 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 2.98. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

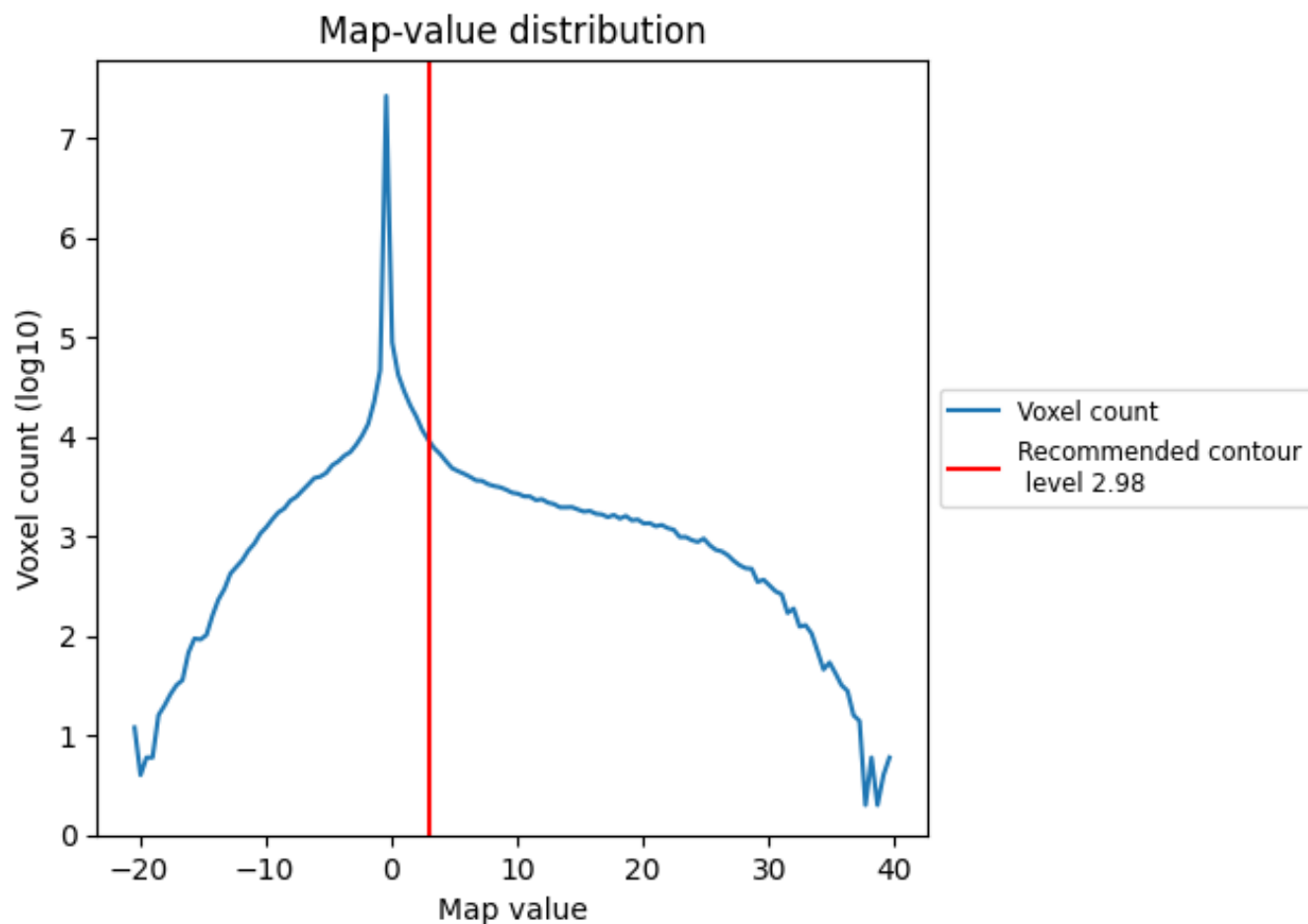
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

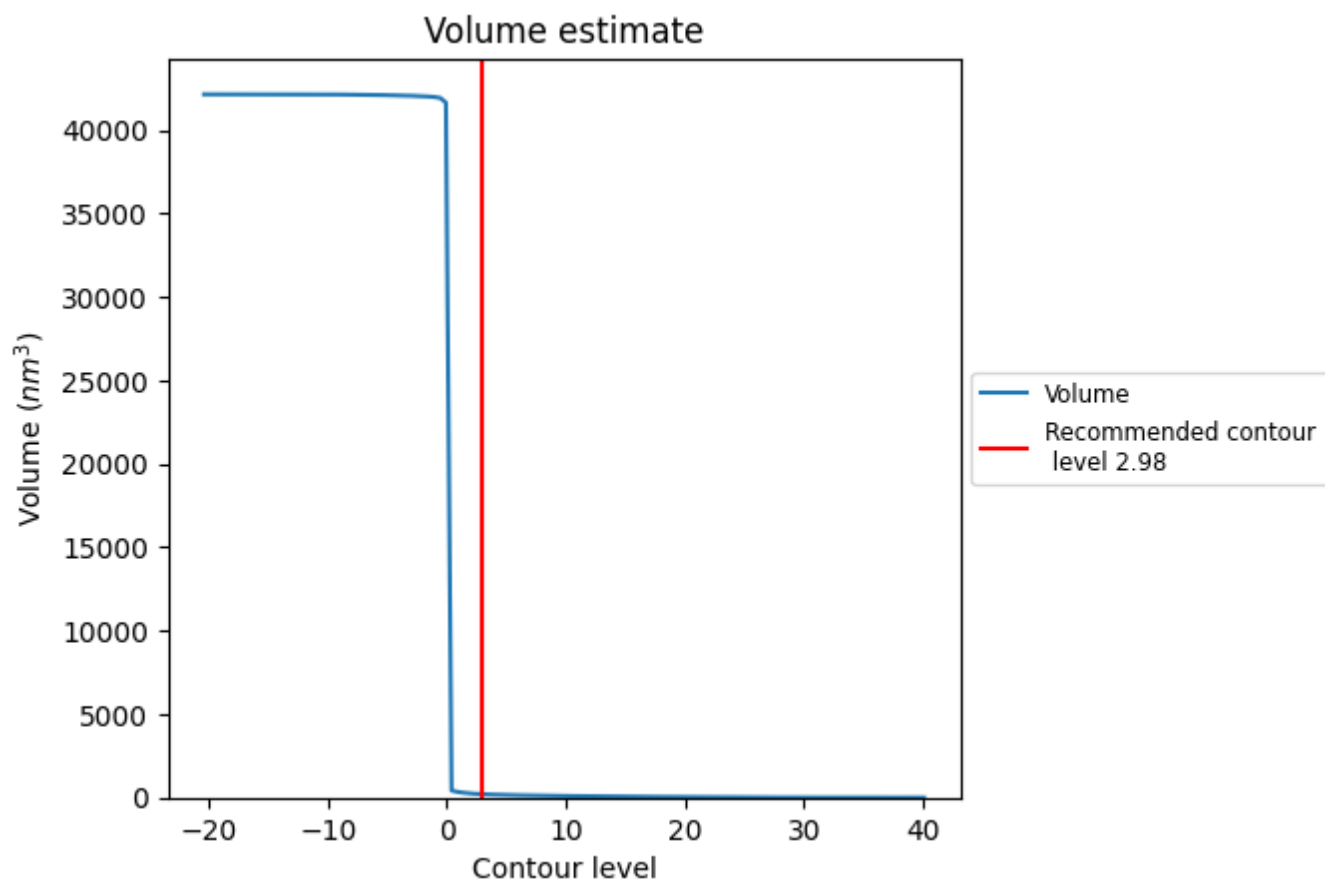
This section contains the results of statistical analysis of the map.

### 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.

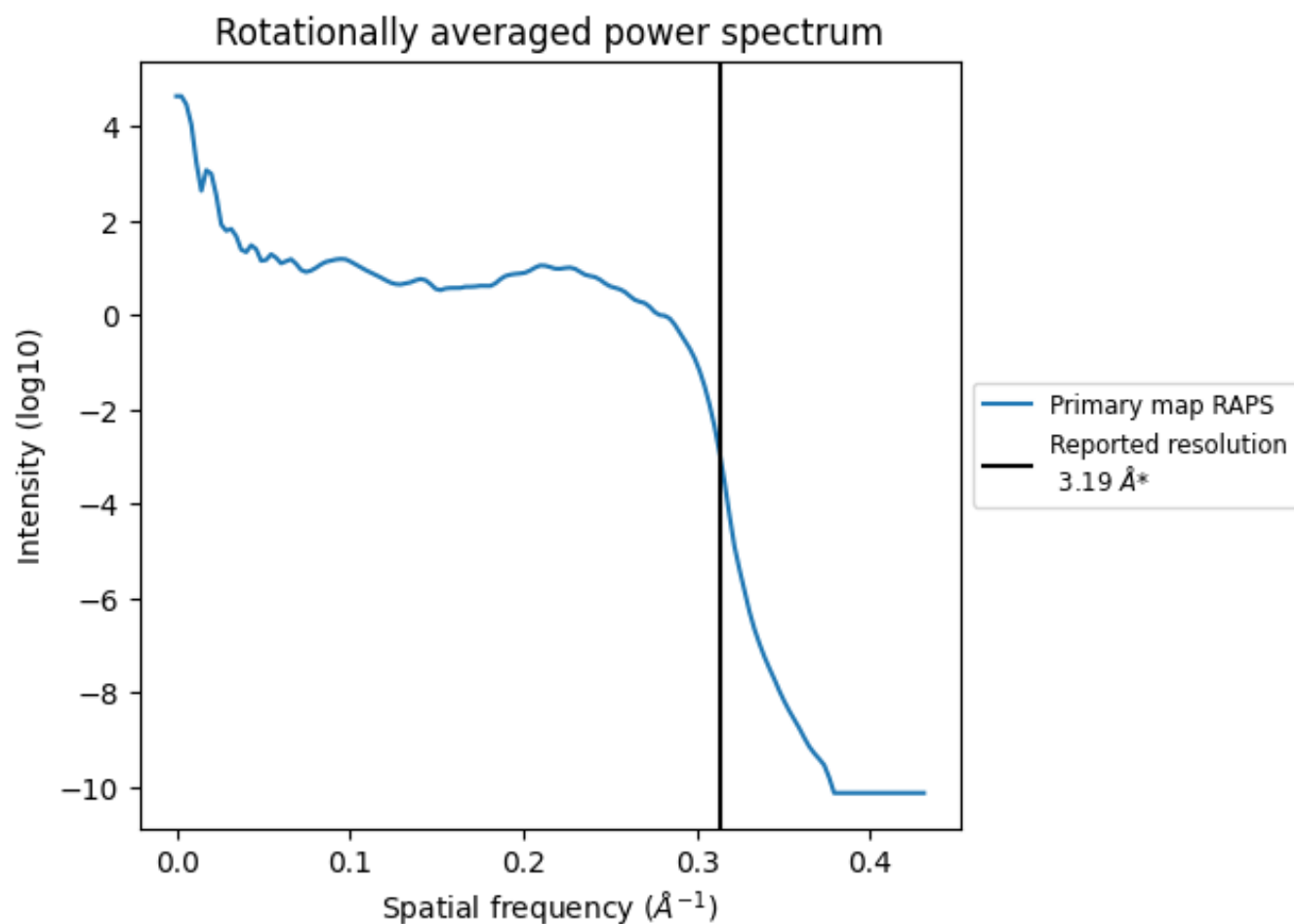
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 202 nm<sup>3</sup>; 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 ⓘ

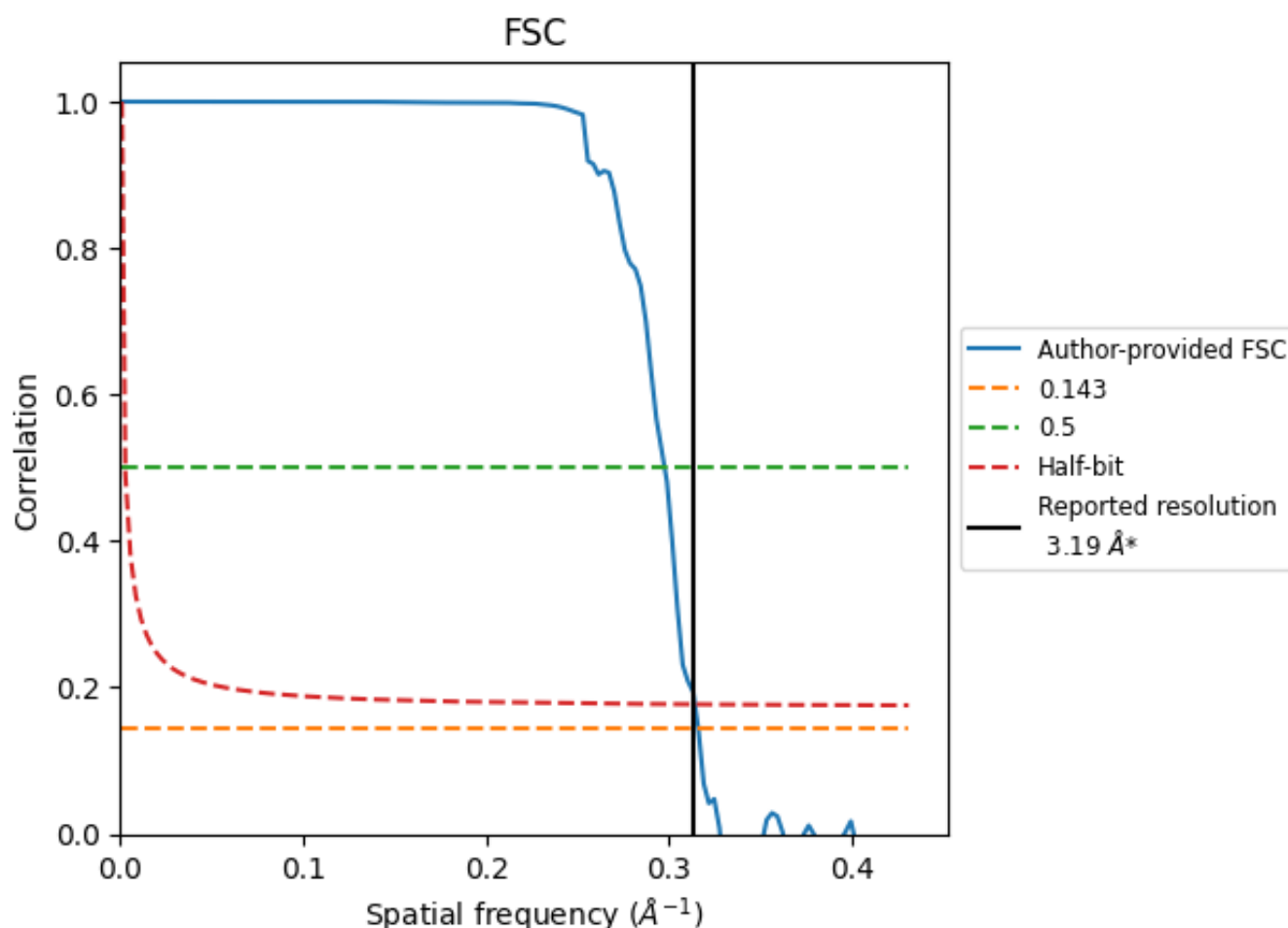


\*Reported resolution corresponds to spatial frequency of 0.313 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.313  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

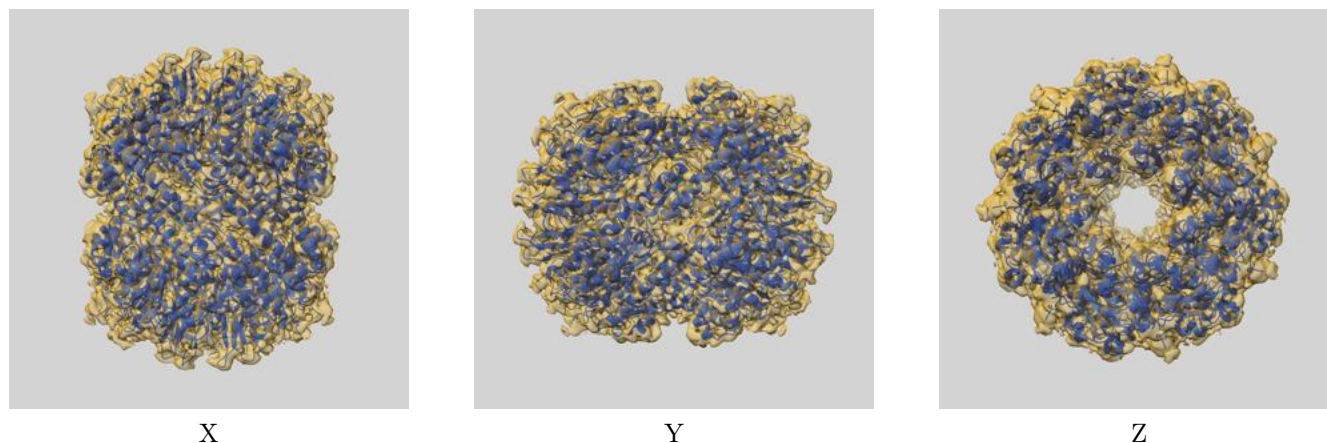
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.19	-	-
Author-provided FSC curve	3.16	3.36	3.18
Unmasked-calculated*	-	-	-

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

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

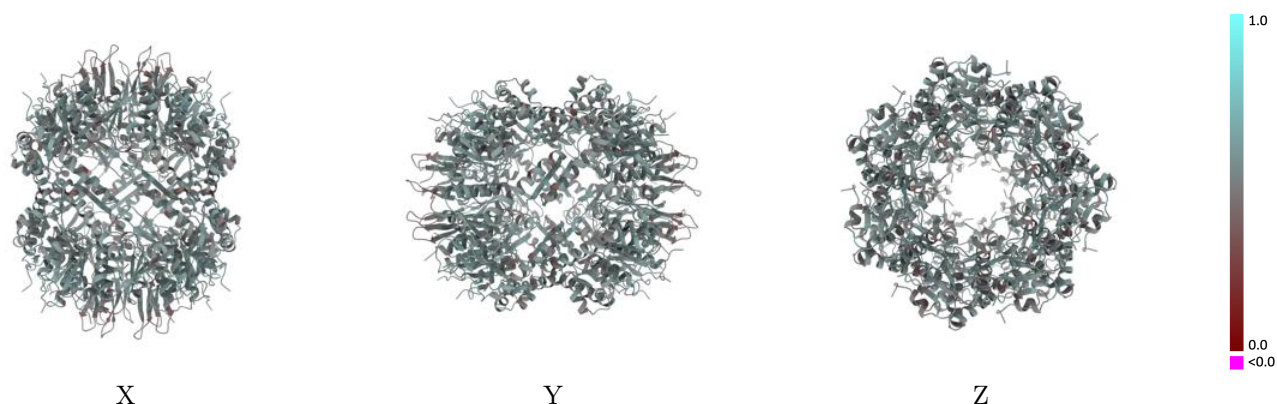
This section contains information regarding the fit between EMDB map EMD-20434 and PDB model 6PPE. Per-residue inclusion information can be found in section 3 on page 10.

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



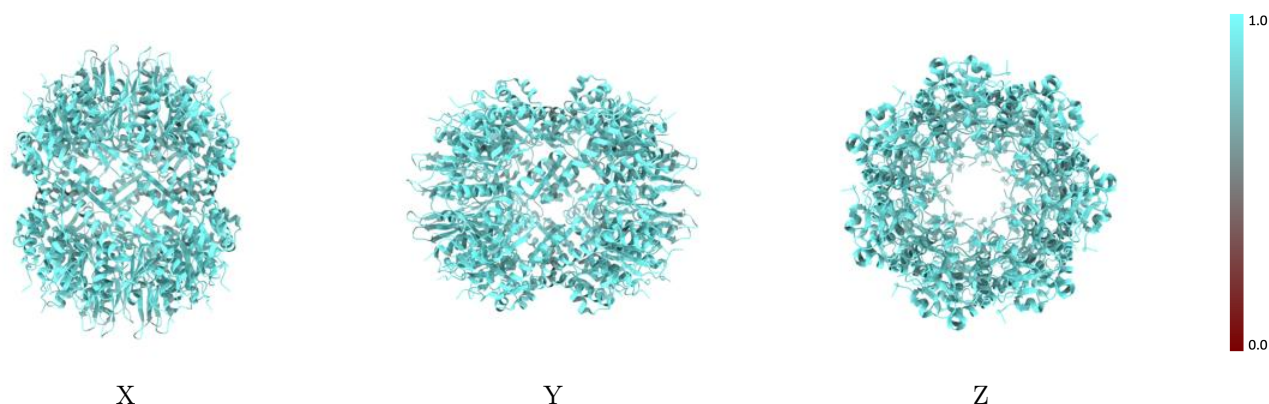
The images above show the 3D surface view of the map at the recommended contour level 2.98 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



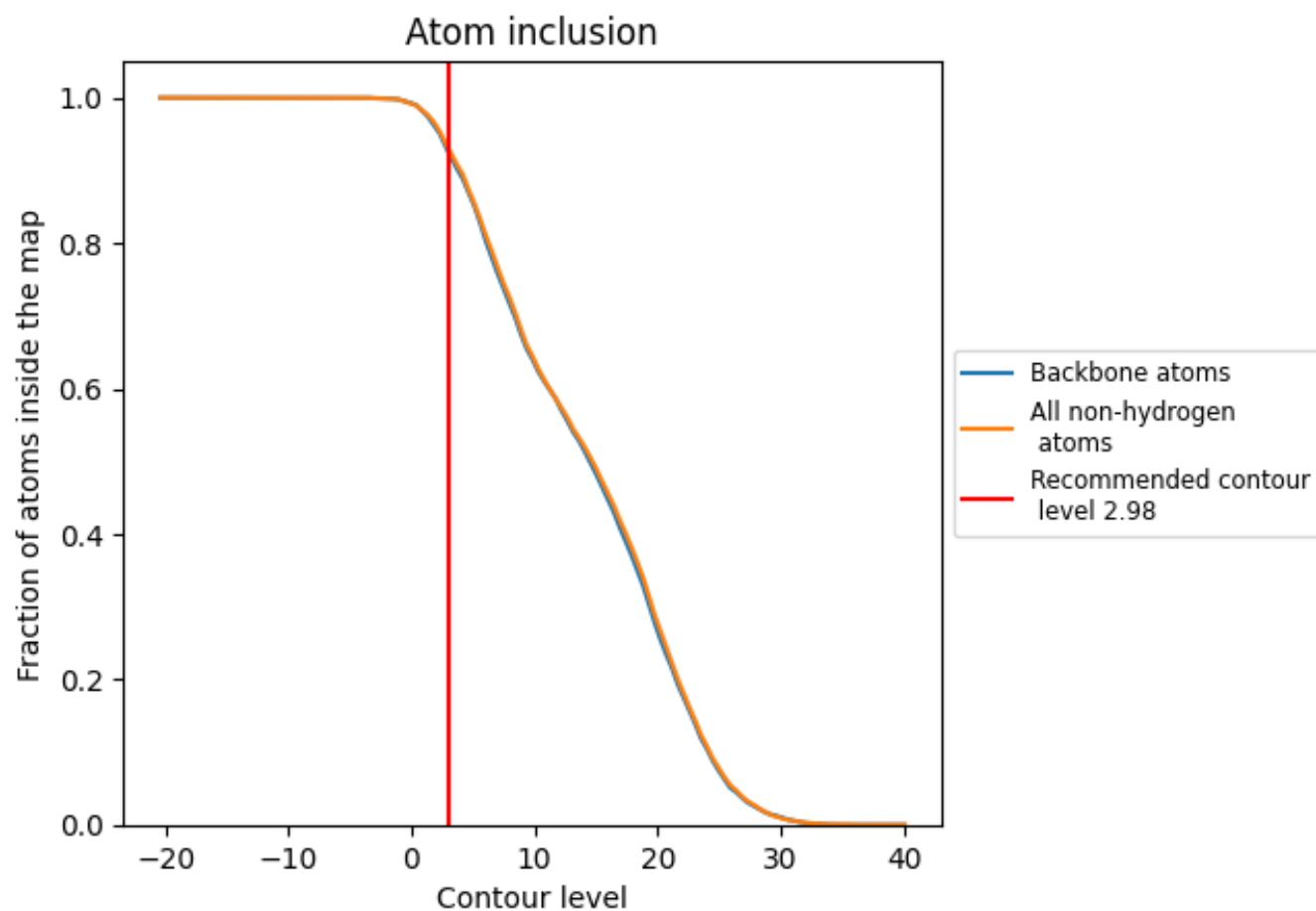
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9306	 0.5270
1	 0.9636	 0.5320
2	 0.9455	 0.5090
3	 0.9455	 0.5130
A	 0.9349	 0.5320
B	 0.9308	 0.5300
C	 0.9349	 0.5320
D	 0.9369	 0.5350
E	 0.9349	 0.5320
F	 0.9437	 0.5310
G	 0.9410	 0.5320
H	 0.9206	 0.5200
I	 0.9267	 0.5250
J	 0.9335	 0.5290
K	 0.9355	 0.5240
L	 0.9288	 0.5170
M	 0.9267	 0.5130
N	 0.9322	 0.5200
O	 0.9455	 0.5370
P	 0.9818	 0.5410
Q	 1.0000	 0.5310
R	 0.9455	 0.5280
S	 0.9455	 0.5210
T	 0.9636	 0.5320
U	 0.9455	 0.5290
V	 0.9818	 0.5170
X	 1.0000	 0.5280
Y	 0.9818	 0.5320
Z	 0.9455	 0.5260

