



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:42 PM UTC

PDB ID : 7RK8 / pdb_00007rk8
EMDB ID : EMD-24494
Title : Cryo-EM Structure of Adeno-Associated Virus Serotype 9 with Engineered Peptide Domain PHP.B (AAV9-PHP.B)
Authors : Fluck, E.C.; Pumroy, R.A.; Moiseenkova-Bell, V.Y.
Deposited on : 2021-07-22
Resolution : 2.27 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 ⓘ 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.dev132
MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

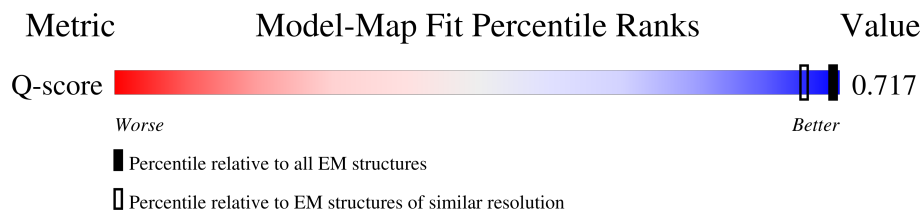
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.27 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	3593 (1.77 - 2.77)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 246720 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	B	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	C	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	D	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	E	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	F	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	G	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	H	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	I	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	J	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	K	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	L	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	M	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	N	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	O	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	P	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	Q	517	Total 4112	C 2601	N 714	O 783	S 14	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	S	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	T	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	V	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	W	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	X	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	Y	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	Z	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	AA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	BA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	CA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	DA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	EA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	FA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	GA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	HA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	IA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	JA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	KA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	LA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	MA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	NA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	OA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	PA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	QA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	RA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	SA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	TA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	UA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	VA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	WA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	XA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	YA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	ZA	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	AB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	BB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	CB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	DB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	EB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	FB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	GB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0
1	HB	517	Total 4112	C 2601	N 714	O 783	S 14	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	IB	517	Total	C	N	O	S	0	0
			4112	2601	714	783	14		

There are 420 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	589	THR	-	insertion	UNP Q6JC40
A	590	LEU	-	insertion	UNP Q6JC40
A	591	ALA	-	insertion	UNP Q6JC40
A	592	VAL	-	insertion	UNP Q6JC40
A	593	PRO	-	insertion	UNP Q6JC40
A	594	PHE	-	insertion	UNP Q6JC40
A	595	LYS	-	insertion	UNP Q6JC40
B	589	THR	-	insertion	UNP Q6JC40
B	590	LEU	-	insertion	UNP Q6JC40
B	591	ALA	-	insertion	UNP Q6JC40
B	592	VAL	-	insertion	UNP Q6JC40
B	593	PRO	-	insertion	UNP Q6JC40
B	594	PHE	-	insertion	UNP Q6JC40
B	595	LYS	-	insertion	UNP Q6JC40
C	589	THR	-	insertion	UNP Q6JC40
C	590	LEU	-	insertion	UNP Q6JC40
C	591	ALA	-	insertion	UNP Q6JC40
C	592	VAL	-	insertion	UNP Q6JC40
C	593	PRO	-	insertion	UNP Q6JC40
C	594	PHE	-	insertion	UNP Q6JC40
C	595	LYS	-	insertion	UNP Q6JC40
D	589	THR	-	insertion	UNP Q6JC40
D	590	LEU	-	insertion	UNP Q6JC40
D	591	ALA	-	insertion	UNP Q6JC40
D	592	VAL	-	insertion	UNP Q6JC40
D	593	PRO	-	insertion	UNP Q6JC40
D	594	PHE	-	insertion	UNP Q6JC40
D	595	LYS	-	insertion	UNP Q6JC40
E	589	THR	-	insertion	UNP Q6JC40
E	590	LEU	-	insertion	UNP Q6JC40
E	591	ALA	-	insertion	UNP Q6JC40
E	592	VAL	-	insertion	UNP Q6JC40
E	593	PRO	-	insertion	UNP Q6JC40
E	594	PHE	-	insertion	UNP Q6JC40
E	595	LYS	-	insertion	UNP Q6JC40
F	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	590	LEU	-	insertion	UNP Q6JC40
F	591	ALA	-	insertion	UNP Q6JC40
F	592	VAL	-	insertion	UNP Q6JC40
F	593	PRO	-	insertion	UNP Q6JC40
F	594	PHE	-	insertion	UNP Q6JC40
F	595	LYS	-	insertion	UNP Q6JC40
G	589	THR	-	insertion	UNP Q6JC40
G	590	LEU	-	insertion	UNP Q6JC40
G	591	ALA	-	insertion	UNP Q6JC40
G	592	VAL	-	insertion	UNP Q6JC40
G	593	PRO	-	insertion	UNP Q6JC40
G	594	PHE	-	insertion	UNP Q6JC40
G	595	LYS	-	insertion	UNP Q6JC40
H	589	THR	-	insertion	UNP Q6JC40
H	590	LEU	-	insertion	UNP Q6JC40
H	591	ALA	-	insertion	UNP Q6JC40
H	592	VAL	-	insertion	UNP Q6JC40
H	593	PRO	-	insertion	UNP Q6JC40
H	594	PHE	-	insertion	UNP Q6JC40
H	595	LYS	-	insertion	UNP Q6JC40
I	589	THR	-	insertion	UNP Q6JC40
I	590	LEU	-	insertion	UNP Q6JC40
I	591	ALA	-	insertion	UNP Q6JC40
I	592	VAL	-	insertion	UNP Q6JC40
I	593	PRO	-	insertion	UNP Q6JC40
I	594	PHE	-	insertion	UNP Q6JC40
I	595	LYS	-	insertion	UNP Q6JC40
J	589	THR	-	insertion	UNP Q6JC40
J	590	LEU	-	insertion	UNP Q6JC40
J	591	ALA	-	insertion	UNP Q6JC40
J	592	VAL	-	insertion	UNP Q6JC40
J	593	PRO	-	insertion	UNP Q6JC40
J	594	PHE	-	insertion	UNP Q6JC40
J	595	LYS	-	insertion	UNP Q6JC40
K	589	THR	-	insertion	UNP Q6JC40
K	590	LEU	-	insertion	UNP Q6JC40
K	591	ALA	-	insertion	UNP Q6JC40
K	592	VAL	-	insertion	UNP Q6JC40
K	593	PRO	-	insertion	UNP Q6JC40
K	594	PHE	-	insertion	UNP Q6JC40
K	595	LYS	-	insertion	UNP Q6JC40
L	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	590	LEU	-	insertion	UNP Q6JC40
L	591	ALA	-	insertion	UNP Q6JC40
L	592	VAL	-	insertion	UNP Q6JC40
L	593	PRO	-	insertion	UNP Q6JC40
L	594	PHE	-	insertion	UNP Q6JC40
L	595	LYS	-	insertion	UNP Q6JC40
M	589	THR	-	insertion	UNP Q6JC40
M	590	LEU	-	insertion	UNP Q6JC40
M	591	ALA	-	insertion	UNP Q6JC40
M	592	VAL	-	insertion	UNP Q6JC40
M	593	PRO	-	insertion	UNP Q6JC40
M	594	PHE	-	insertion	UNP Q6JC40
M	595	LYS	-	insertion	UNP Q6JC40
N	589	THR	-	insertion	UNP Q6JC40
N	590	LEU	-	insertion	UNP Q6JC40
N	591	ALA	-	insertion	UNP Q6JC40
N	592	VAL	-	insertion	UNP Q6JC40
N	593	PRO	-	insertion	UNP Q6JC40
N	594	PHE	-	insertion	UNP Q6JC40
N	595	LYS	-	insertion	UNP Q6JC40
O	589	THR	-	insertion	UNP Q6JC40
O	590	LEU	-	insertion	UNP Q6JC40
O	591	ALA	-	insertion	UNP Q6JC40
O	592	VAL	-	insertion	UNP Q6JC40
O	593	PRO	-	insertion	UNP Q6JC40
O	594	PHE	-	insertion	UNP Q6JC40
O	595	LYS	-	insertion	UNP Q6JC40
P	589	THR	-	insertion	UNP Q6JC40
P	590	LEU	-	insertion	UNP Q6JC40
P	591	ALA	-	insertion	UNP Q6JC40
P	592	VAL	-	insertion	UNP Q6JC40
P	593	PRO	-	insertion	UNP Q6JC40
P	594	PHE	-	insertion	UNP Q6JC40
P	595	LYS	-	insertion	UNP Q6JC40
Q	589	THR	-	insertion	UNP Q6JC40
Q	590	LEU	-	insertion	UNP Q6JC40
Q	591	ALA	-	insertion	UNP Q6JC40
Q	592	VAL	-	insertion	UNP Q6JC40
Q	593	PRO	-	insertion	UNP Q6JC40
Q	594	PHE	-	insertion	UNP Q6JC40
Q	595	LYS	-	insertion	UNP Q6JC40
R	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
R	590	LEU	-	insertion	UNP Q6JC40
R	591	ALA	-	insertion	UNP Q6JC40
R	592	VAL	-	insertion	UNP Q6JC40
R	593	PRO	-	insertion	UNP Q6JC40
R	594	PHE	-	insertion	UNP Q6JC40
R	595	LYS	-	insertion	UNP Q6JC40
S	589	THR	-	insertion	UNP Q6JC40
S	590	LEU	-	insertion	UNP Q6JC40
S	591	ALA	-	insertion	UNP Q6JC40
S	592	VAL	-	insertion	UNP Q6JC40
S	593	PRO	-	insertion	UNP Q6JC40
S	594	PHE	-	insertion	UNP Q6JC40
S	595	LYS	-	insertion	UNP Q6JC40
T	589	THR	-	insertion	UNP Q6JC40
T	590	LEU	-	insertion	UNP Q6JC40
T	591	ALA	-	insertion	UNP Q6JC40
T	592	VAL	-	insertion	UNP Q6JC40
T	593	PRO	-	insertion	UNP Q6JC40
T	594	PHE	-	insertion	UNP Q6JC40
T	595	LYS	-	insertion	UNP Q6JC40
V	589	THR	-	insertion	UNP Q6JC40
V	590	LEU	-	insertion	UNP Q6JC40
V	591	ALA	-	insertion	UNP Q6JC40
V	592	VAL	-	insertion	UNP Q6JC40
V	593	PRO	-	insertion	UNP Q6JC40
V	594	PHE	-	insertion	UNP Q6JC40
V	595	LYS	-	insertion	UNP Q6JC40
W	589	THR	-	insertion	UNP Q6JC40
W	590	LEU	-	insertion	UNP Q6JC40
W	591	ALA	-	insertion	UNP Q6JC40
W	592	VAL	-	insertion	UNP Q6JC40
W	593	PRO	-	insertion	UNP Q6JC40
W	594	PHE	-	insertion	UNP Q6JC40
W	595	LYS	-	insertion	UNP Q6JC40
X	589	THR	-	insertion	UNP Q6JC40
X	590	LEU	-	insertion	UNP Q6JC40
X	591	ALA	-	insertion	UNP Q6JC40
X	592	VAL	-	insertion	UNP Q6JC40
X	593	PRO	-	insertion	UNP Q6JC40
X	594	PHE	-	insertion	UNP Q6JC40
X	595	LYS	-	insertion	UNP Q6JC40
Y	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Y	590	LEU	-	insertion	UNP Q6JC40
Y	591	ALA	-	insertion	UNP Q6JC40
Y	592	VAL	-	insertion	UNP Q6JC40
Y	593	PRO	-	insertion	UNP Q6JC40
Y	594	PHE	-	insertion	UNP Q6JC40
Y	595	LYS	-	insertion	UNP Q6JC40
Z	589	THR	-	insertion	UNP Q6JC40
Z	590	LEU	-	insertion	UNP Q6JC40
Z	591	ALA	-	insertion	UNP Q6JC40
Z	592	VAL	-	insertion	UNP Q6JC40
Z	593	PRO	-	insertion	UNP Q6JC40
Z	594	PHE	-	insertion	UNP Q6JC40
Z	595	LYS	-	insertion	UNP Q6JC40
AA	589	THR	-	insertion	UNP Q6JC40
AA	590	LEU	-	insertion	UNP Q6JC40
AA	591	ALA	-	insertion	UNP Q6JC40
AA	592	VAL	-	insertion	UNP Q6JC40
AA	593	PRO	-	insertion	UNP Q6JC40
AA	594	PHE	-	insertion	UNP Q6JC40
AA	595	LYS	-	insertion	UNP Q6JC40
BA	589	THR	-	insertion	UNP Q6JC40
BA	590	LEU	-	insertion	UNP Q6JC40
BA	591	ALA	-	insertion	UNP Q6JC40
BA	592	VAL	-	insertion	UNP Q6JC40
BA	593	PRO	-	insertion	UNP Q6JC40
BA	594	PHE	-	insertion	UNP Q6JC40
BA	595	LYS	-	insertion	UNP Q6JC40
CA	589	THR	-	insertion	UNP Q6JC40
CA	590	LEU	-	insertion	UNP Q6JC40
CA	591	ALA	-	insertion	UNP Q6JC40
CA	592	VAL	-	insertion	UNP Q6JC40
CA	593	PRO	-	insertion	UNP Q6JC40
CA	594	PHE	-	insertion	UNP Q6JC40
CA	595	LYS	-	insertion	UNP Q6JC40
DA	589	THR	-	insertion	UNP Q6JC40
DA	590	LEU	-	insertion	UNP Q6JC40
DA	591	ALA	-	insertion	UNP Q6JC40
DA	592	VAL	-	insertion	UNP Q6JC40
DA	593	PRO	-	insertion	UNP Q6JC40
DA	594	PHE	-	insertion	UNP Q6JC40
DA	595	LYS	-	insertion	UNP Q6JC40
EA	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
EA	590	LEU	-	insertion	UNP Q6JC40
EA	591	ALA	-	insertion	UNP Q6JC40
EA	592	VAL	-	insertion	UNP Q6JC40
EA	593	PRO	-	insertion	UNP Q6JC40
EA	594	PHE	-	insertion	UNP Q6JC40
EA	595	LYS	-	insertion	UNP Q6JC40
FA	589	THR	-	insertion	UNP Q6JC40
FA	590	LEU	-	insertion	UNP Q6JC40
FA	591	ALA	-	insertion	UNP Q6JC40
FA	592	VAL	-	insertion	UNP Q6JC40
FA	593	PRO	-	insertion	UNP Q6JC40
FA	594	PHE	-	insertion	UNP Q6JC40
FA	595	LYS	-	insertion	UNP Q6JC40
GA	589	THR	-	insertion	UNP Q6JC40
GA	590	LEU	-	insertion	UNP Q6JC40
GA	591	ALA	-	insertion	UNP Q6JC40
GA	592	VAL	-	insertion	UNP Q6JC40
GA	593	PRO	-	insertion	UNP Q6JC40
GA	594	PHE	-	insertion	UNP Q6JC40
GA	595	LYS	-	insertion	UNP Q6JC40
HA	589	THR	-	insertion	UNP Q6JC40
HA	590	LEU	-	insertion	UNP Q6JC40
HA	591	ALA	-	insertion	UNP Q6JC40
HA	592	VAL	-	insertion	UNP Q6JC40
HA	593	PRO	-	insertion	UNP Q6JC40
HA	594	PHE	-	insertion	UNP Q6JC40
HA	595	LYS	-	insertion	UNP Q6JC40
IA	589	THR	-	insertion	UNP Q6JC40
IA	590	LEU	-	insertion	UNP Q6JC40
IA	591	ALA	-	insertion	UNP Q6JC40
IA	592	VAL	-	insertion	UNP Q6JC40
IA	593	PRO	-	insertion	UNP Q6JC40
IA	594	PHE	-	insertion	UNP Q6JC40
IA	595	LYS	-	insertion	UNP Q6JC40
JA	589	THR	-	insertion	UNP Q6JC40
JA	590	LEU	-	insertion	UNP Q6JC40
JA	591	ALA	-	insertion	UNP Q6JC40
JA	592	VAL	-	insertion	UNP Q6JC40
JA	593	PRO	-	insertion	UNP Q6JC40
JA	594	PHE	-	insertion	UNP Q6JC40
JA	595	LYS	-	insertion	UNP Q6JC40
KA	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
KA	590	LEU	-	insertion	UNP Q6JC40
KA	591	ALA	-	insertion	UNP Q6JC40
KA	592	VAL	-	insertion	UNP Q6JC40
KA	593	PRO	-	insertion	UNP Q6JC40
KA	594	PHE	-	insertion	UNP Q6JC40
KA	595	LYS	-	insertion	UNP Q6JC40
LA	589	THR	-	insertion	UNP Q6JC40
LA	590	LEU	-	insertion	UNP Q6JC40
LA	591	ALA	-	insertion	UNP Q6JC40
LA	592	VAL	-	insertion	UNP Q6JC40
LA	593	PRO	-	insertion	UNP Q6JC40
LA	594	PHE	-	insertion	UNP Q6JC40
LA	595	LYS	-	insertion	UNP Q6JC40
MA	589	THR	-	insertion	UNP Q6JC40
MA	590	LEU	-	insertion	UNP Q6JC40
MA	591	ALA	-	insertion	UNP Q6JC40
MA	592	VAL	-	insertion	UNP Q6JC40
MA	593	PRO	-	insertion	UNP Q6JC40
MA	594	PHE	-	insertion	UNP Q6JC40
MA	595	LYS	-	insertion	UNP Q6JC40
NA	589	THR	-	insertion	UNP Q6JC40
NA	590	LEU	-	insertion	UNP Q6JC40
NA	591	ALA	-	insertion	UNP Q6JC40
NA	592	VAL	-	insertion	UNP Q6JC40
NA	593	PRO	-	insertion	UNP Q6JC40
NA	594	PHE	-	insertion	UNP Q6JC40
NA	595	LYS	-	insertion	UNP Q6JC40
OA	589	THR	-	insertion	UNP Q6JC40
OA	590	LEU	-	insertion	UNP Q6JC40
OA	591	ALA	-	insertion	UNP Q6JC40
OA	592	VAL	-	insertion	UNP Q6JC40
OA	593	PRO	-	insertion	UNP Q6JC40
OA	594	PHE	-	insertion	UNP Q6JC40
OA	595	LYS	-	insertion	UNP Q6JC40
PA	589	THR	-	insertion	UNP Q6JC40
PA	590	LEU	-	insertion	UNP Q6JC40
PA	591	ALA	-	insertion	UNP Q6JC40
PA	592	VAL	-	insertion	UNP Q6JC40
PA	593	PRO	-	insertion	UNP Q6JC40
PA	594	PHE	-	insertion	UNP Q6JC40
PA	595	LYS	-	insertion	UNP Q6JC40
QA	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
QA	590	LEU	-	insertion	UNP Q6JC40
QA	591	ALA	-	insertion	UNP Q6JC40
QA	592	VAL	-	insertion	UNP Q6JC40
QA	593	PRO	-	insertion	UNP Q6JC40
QA	594	PHE	-	insertion	UNP Q6JC40
QA	595	LYS	-	insertion	UNP Q6JC40
RA	589	THR	-	insertion	UNP Q6JC40
RA	590	LEU	-	insertion	UNP Q6JC40
RA	591	ALA	-	insertion	UNP Q6JC40
RA	592	VAL	-	insertion	UNP Q6JC40
RA	593	PRO	-	insertion	UNP Q6JC40
RA	594	PHE	-	insertion	UNP Q6JC40
RA	595	LYS	-	insertion	UNP Q6JC40
SA	589	THR	-	insertion	UNP Q6JC40
SA	590	LEU	-	insertion	UNP Q6JC40
SA	591	ALA	-	insertion	UNP Q6JC40
SA	592	VAL	-	insertion	UNP Q6JC40
SA	593	PRO	-	insertion	UNP Q6JC40
SA	594	PHE	-	insertion	UNP Q6JC40
SA	595	LYS	-	insertion	UNP Q6JC40
TA	589	THR	-	insertion	UNP Q6JC40
TA	590	LEU	-	insertion	UNP Q6JC40
TA	591	ALA	-	insertion	UNP Q6JC40
TA	592	VAL	-	insertion	UNP Q6JC40
TA	593	PRO	-	insertion	UNP Q6JC40
TA	594	PHE	-	insertion	UNP Q6JC40
TA	595	LYS	-	insertion	UNP Q6JC40
UA	589	THR	-	insertion	UNP Q6JC40
UA	590	LEU	-	insertion	UNP Q6JC40
UA	591	ALA	-	insertion	UNP Q6JC40
UA	592	VAL	-	insertion	UNP Q6JC40
UA	593	PRO	-	insertion	UNP Q6JC40
UA	594	PHE	-	insertion	UNP Q6JC40
UA	595	LYS	-	insertion	UNP Q6JC40
VA	589	THR	-	insertion	UNP Q6JC40
VA	590	LEU	-	insertion	UNP Q6JC40
VA	591	ALA	-	insertion	UNP Q6JC40
VA	592	VAL	-	insertion	UNP Q6JC40
VA	593	PRO	-	insertion	UNP Q6JC40
VA	594	PHE	-	insertion	UNP Q6JC40
VA	595	LYS	-	insertion	UNP Q6JC40
WA	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
WA	590	LEU	-	insertion	UNP Q6JC40
WA	591	ALA	-	insertion	UNP Q6JC40
WA	592	VAL	-	insertion	UNP Q6JC40
WA	593	PRO	-	insertion	UNP Q6JC40
WA	594	PHE	-	insertion	UNP Q6JC40
WA	595	LYS	-	insertion	UNP Q6JC40
XA	589	THR	-	insertion	UNP Q6JC40
XA	590	LEU	-	insertion	UNP Q6JC40
XA	591	ALA	-	insertion	UNP Q6JC40
XA	592	VAL	-	insertion	UNP Q6JC40
XA	593	PRO	-	insertion	UNP Q6JC40
XA	594	PHE	-	insertion	UNP Q6JC40
XA	595	LYS	-	insertion	UNP Q6JC40
YA	589	THR	-	insertion	UNP Q6JC40
YA	590	LEU	-	insertion	UNP Q6JC40
YA	591	ALA	-	insertion	UNP Q6JC40
YA	592	VAL	-	insertion	UNP Q6JC40
YA	593	PRO	-	insertion	UNP Q6JC40
YA	594	PHE	-	insertion	UNP Q6JC40
YA	595	LYS	-	insertion	UNP Q6JC40
ZA	589	THR	-	insertion	UNP Q6JC40
ZA	590	LEU	-	insertion	UNP Q6JC40
ZA	591	ALA	-	insertion	UNP Q6JC40
ZA	592	VAL	-	insertion	UNP Q6JC40
ZA	593	PRO	-	insertion	UNP Q6JC40
ZA	594	PHE	-	insertion	UNP Q6JC40
ZA	595	LYS	-	insertion	UNP Q6JC40
AB	589	THR	-	insertion	UNP Q6JC40
AB	590	LEU	-	insertion	UNP Q6JC40
AB	591	ALA	-	insertion	UNP Q6JC40
AB	592	VAL	-	insertion	UNP Q6JC40
AB	593	PRO	-	insertion	UNP Q6JC40
AB	594	PHE	-	insertion	UNP Q6JC40
AB	595	LYS	-	insertion	UNP Q6JC40
BB	589	THR	-	insertion	UNP Q6JC40
BB	590	LEU	-	insertion	UNP Q6JC40
BB	591	ALA	-	insertion	UNP Q6JC40
BB	592	VAL	-	insertion	UNP Q6JC40
BB	593	PRO	-	insertion	UNP Q6JC40
BB	594	PHE	-	insertion	UNP Q6JC40
BB	595	LYS	-	insertion	UNP Q6JC40
CB	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
CB	590	LEU	-	insertion	UNP Q6JC40
CB	591	ALA	-	insertion	UNP Q6JC40
CB	592	VAL	-	insertion	UNP Q6JC40
CB	593	PRO	-	insertion	UNP Q6JC40
CB	594	PHE	-	insertion	UNP Q6JC40
CB	595	LYS	-	insertion	UNP Q6JC40
DB	589	THR	-	insertion	UNP Q6JC40
DB	590	LEU	-	insertion	UNP Q6JC40
DB	591	ALA	-	insertion	UNP Q6JC40
DB	592	VAL	-	insertion	UNP Q6JC40
DB	593	PRO	-	insertion	UNP Q6JC40
DB	594	PHE	-	insertion	UNP Q6JC40
DB	595	LYS	-	insertion	UNP Q6JC40
EB	589	THR	-	insertion	UNP Q6JC40
EB	590	LEU	-	insertion	UNP Q6JC40
EB	591	ALA	-	insertion	UNP Q6JC40
EB	592	VAL	-	insertion	UNP Q6JC40
EB	593	PRO	-	insertion	UNP Q6JC40
EB	594	PHE	-	insertion	UNP Q6JC40
EB	595	LYS	-	insertion	UNP Q6JC40
FB	589	THR	-	insertion	UNP Q6JC40
FB	590	LEU	-	insertion	UNP Q6JC40
FB	591	ALA	-	insertion	UNP Q6JC40
FB	592	VAL	-	insertion	UNP Q6JC40
FB	593	PRO	-	insertion	UNP Q6JC40
FB	594	PHE	-	insertion	UNP Q6JC40
FB	595	LYS	-	insertion	UNP Q6JC40
GB	589	THR	-	insertion	UNP Q6JC40
GB	590	LEU	-	insertion	UNP Q6JC40
GB	591	ALA	-	insertion	UNP Q6JC40
GB	592	VAL	-	insertion	UNP Q6JC40
GB	593	PRO	-	insertion	UNP Q6JC40
GB	594	PHE	-	insertion	UNP Q6JC40
GB	595	LYS	-	insertion	UNP Q6JC40
HB	589	THR	-	insertion	UNP Q6JC40
HB	590	LEU	-	insertion	UNP Q6JC40
HB	591	ALA	-	insertion	UNP Q6JC40
HB	592	VAL	-	insertion	UNP Q6JC40
HB	593	PRO	-	insertion	UNP Q6JC40
HB	594	PHE	-	insertion	UNP Q6JC40
HB	595	LYS	-	insertion	UNP Q6JC40
IB	589	THR	-	insertion	UNP Q6JC40

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
IB	590	LEU	-	insertion	UNP Q6JC40
IB	591	ALA	-	insertion	UNP Q6JC40
IB	592	VAL	-	insertion	UNP Q6JC40
IB	593	PRO	-	insertion	UNP Q6JC40
IB	594	PHE	-	insertion	UNP Q6JC40
IB	595	LYS	-	insertion	UNP Q6JC40

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	42570	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.211	Depositor
Minimum map value	-0.115	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	457.91998, 457.91998, 457.91998	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues

There are no chain breaks in this entry.

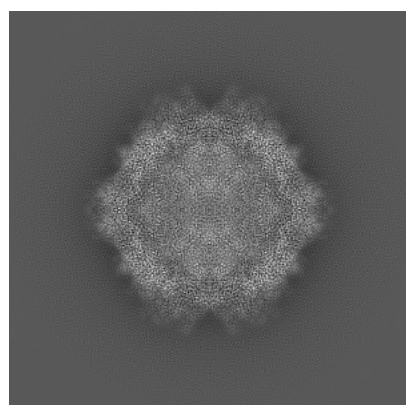
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24494. These allow visual inspection of the internal detail of the map and identification of artifacts.

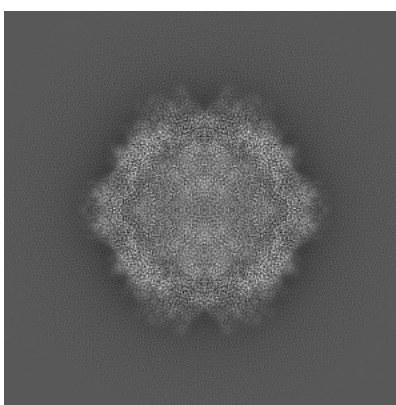
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

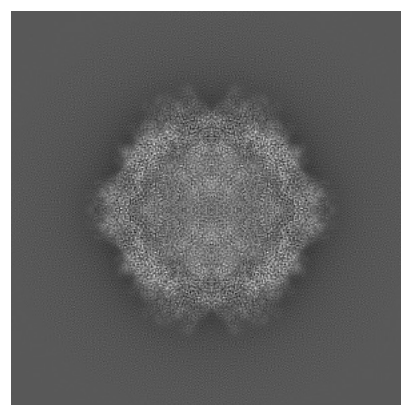
5.1.1 Primary map



X



Y

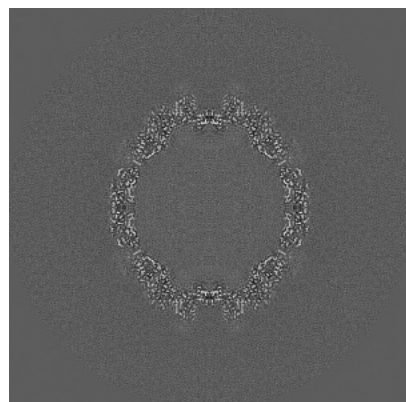


Z

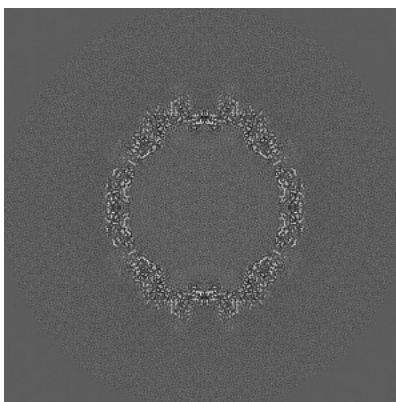
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

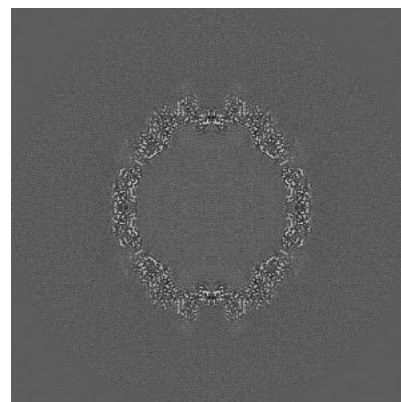
5.2.1 Primary map



X Index: 216



Y Index: 216

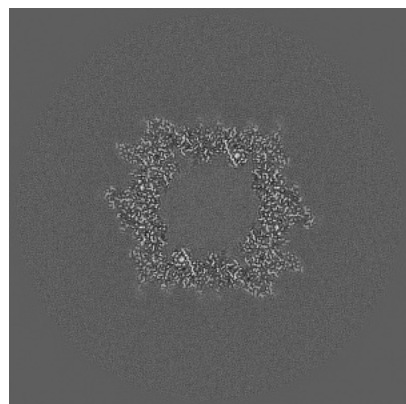


Z Index: 216

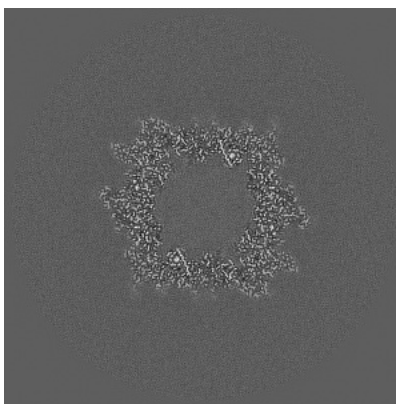
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

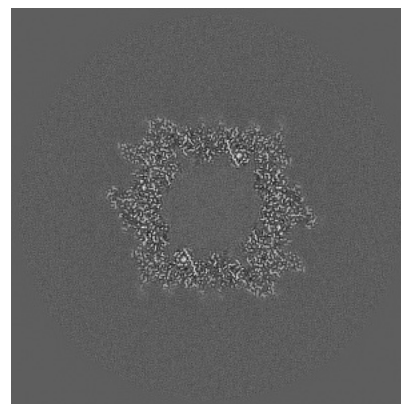
5.3.1 Primary map



X Index: 278



Y Index: 278

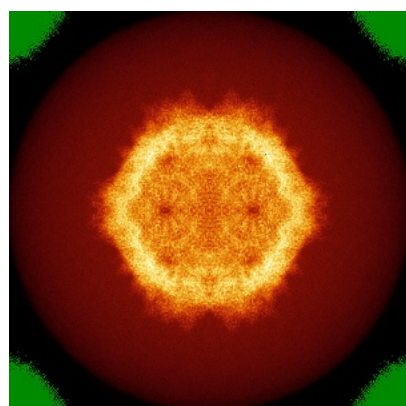


Z Index: 278

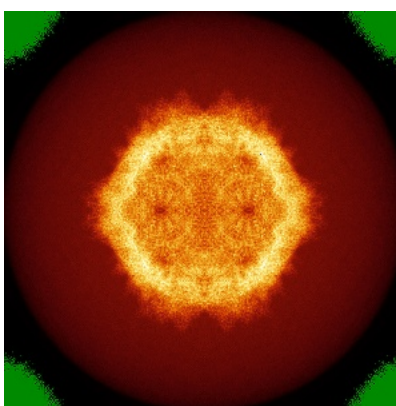
The images above show the largest variance slices of the map in three orthogonal directions.

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

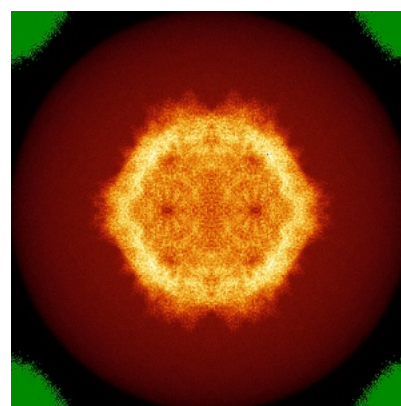
5.4.1 Primary map



X



Y

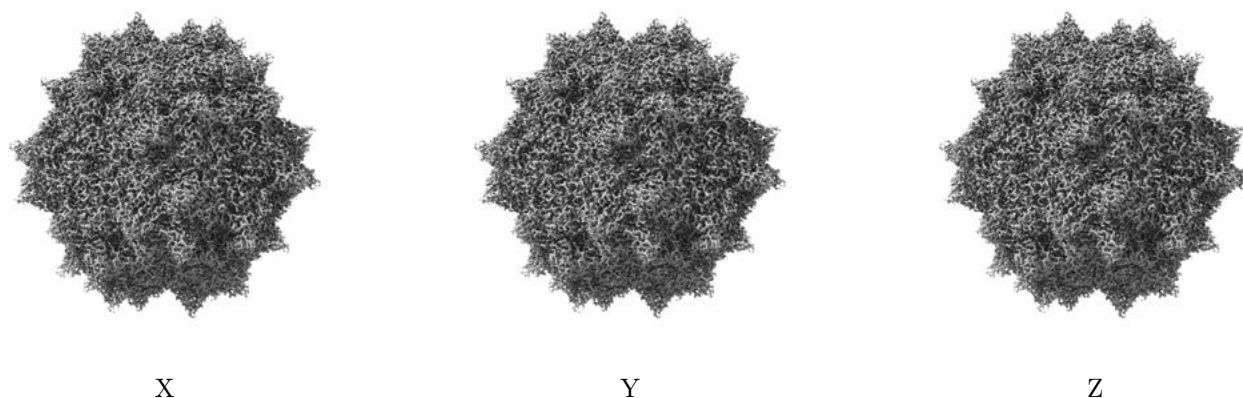


Z

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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

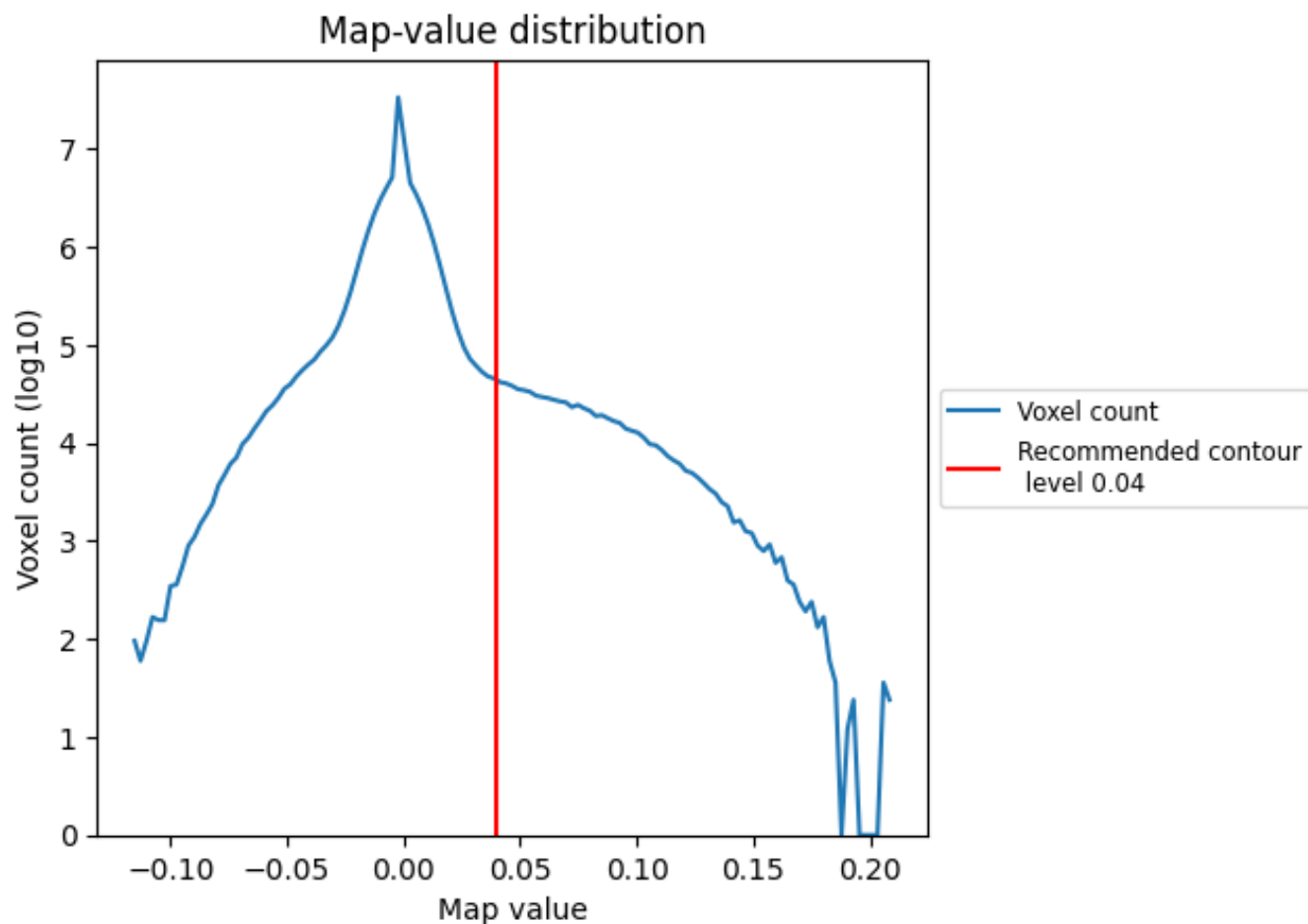
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

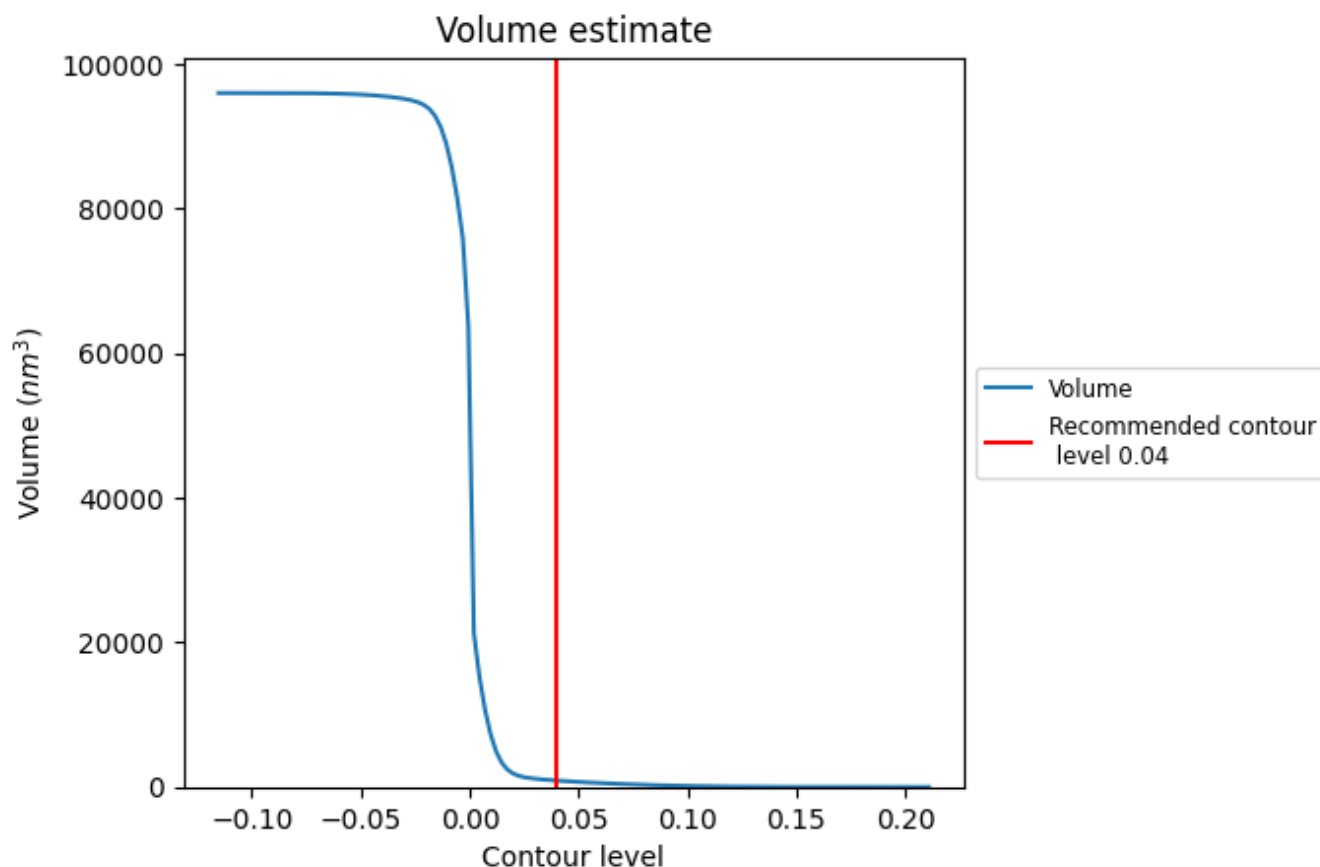
This section contains the results of statistical analysis of the map.

6.1 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.

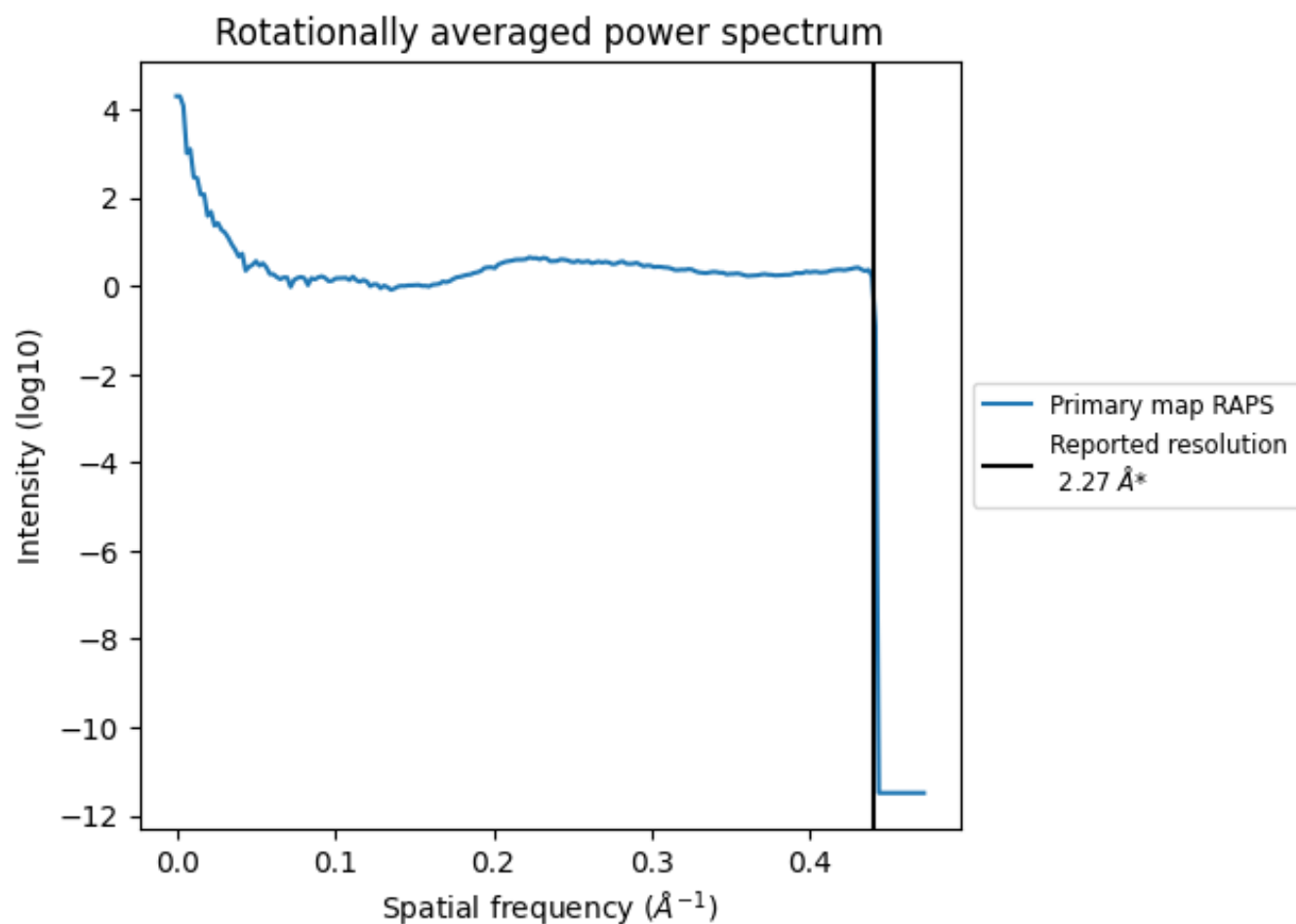
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 882 nm³; this corresponds to an approximate mass of 796 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.

6.3 Rotationally averaged power spectrum ⓘ

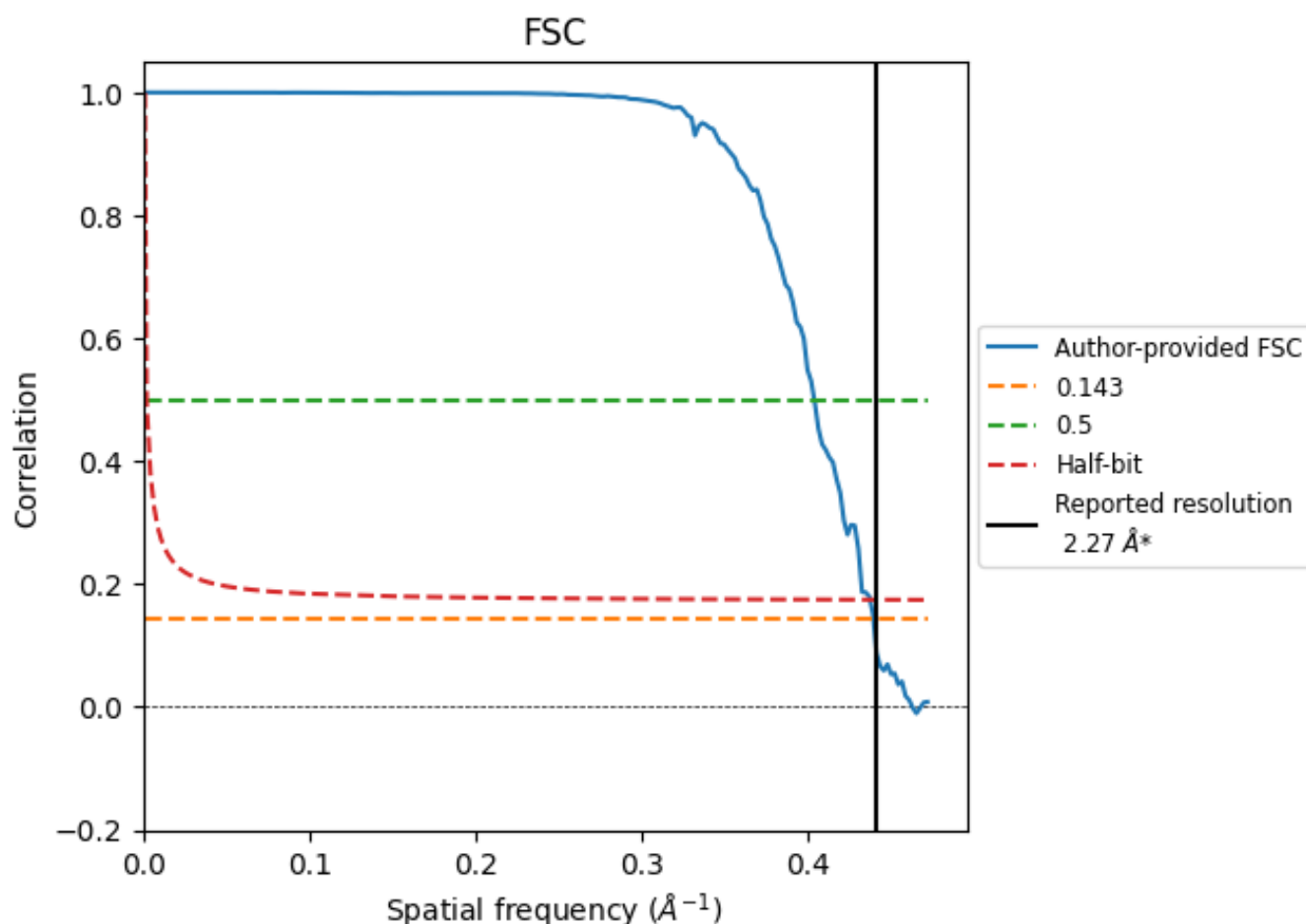


*Reported resolution corresponds to spatial frequency of 0.441 Å⁻¹

7 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.

7.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.441 Å⁻¹

7.2 Resolution estimates [i](#)

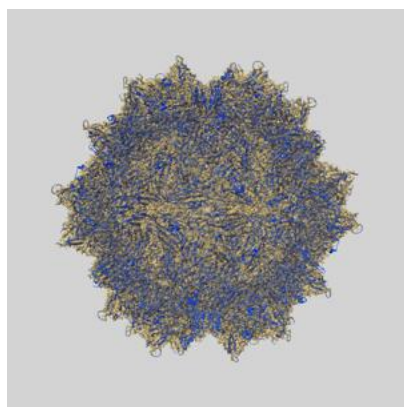
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.27	-	-
Author-provided FSC curve	2.28	2.48	2.29
Unmasked-calculated*	-	-	-

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

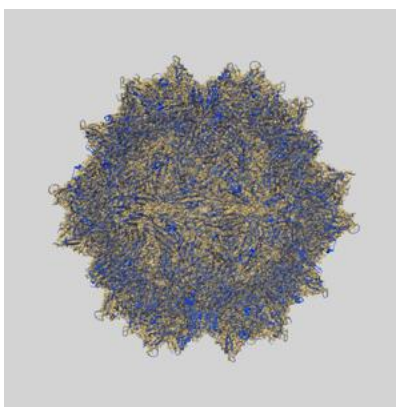
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24494 and PDB model 7RK8. Per-residue inclusion information can be found in section ?? on page ??.

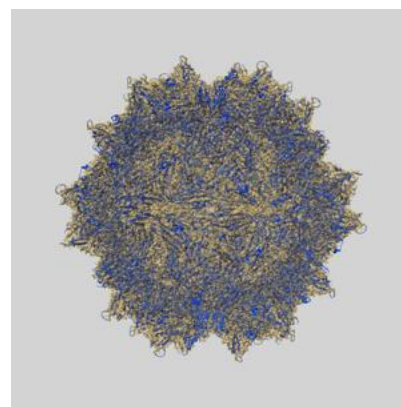
8.1 Map-model overlay [i](#)



X



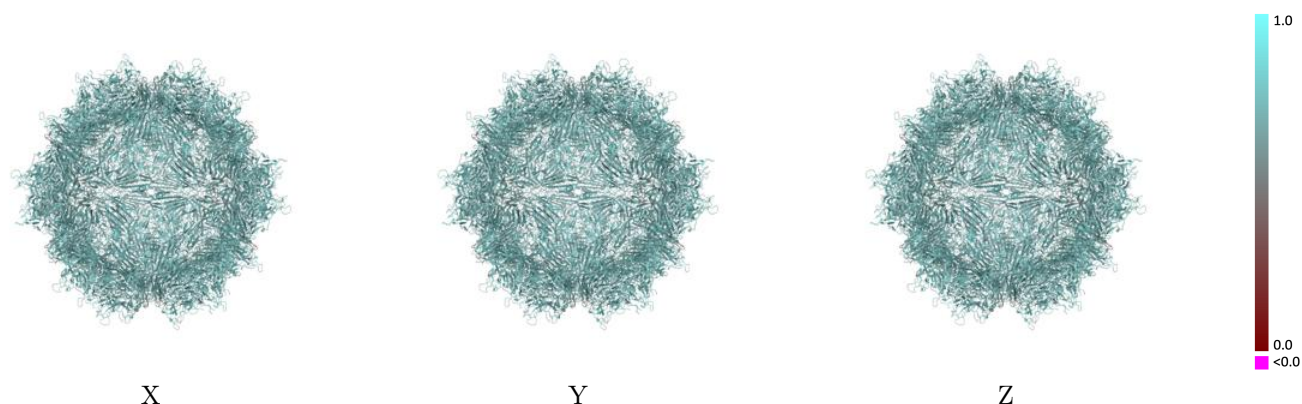
Y



Z

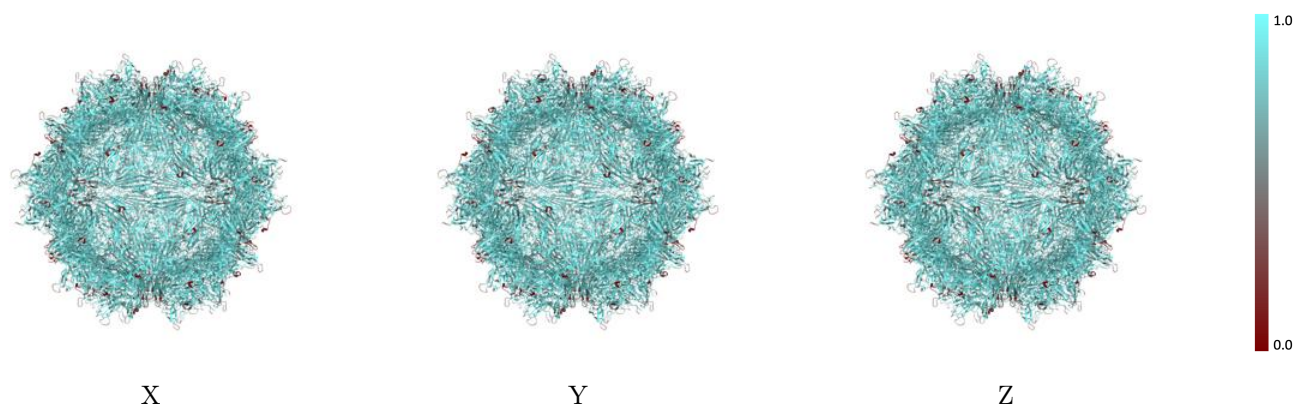
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



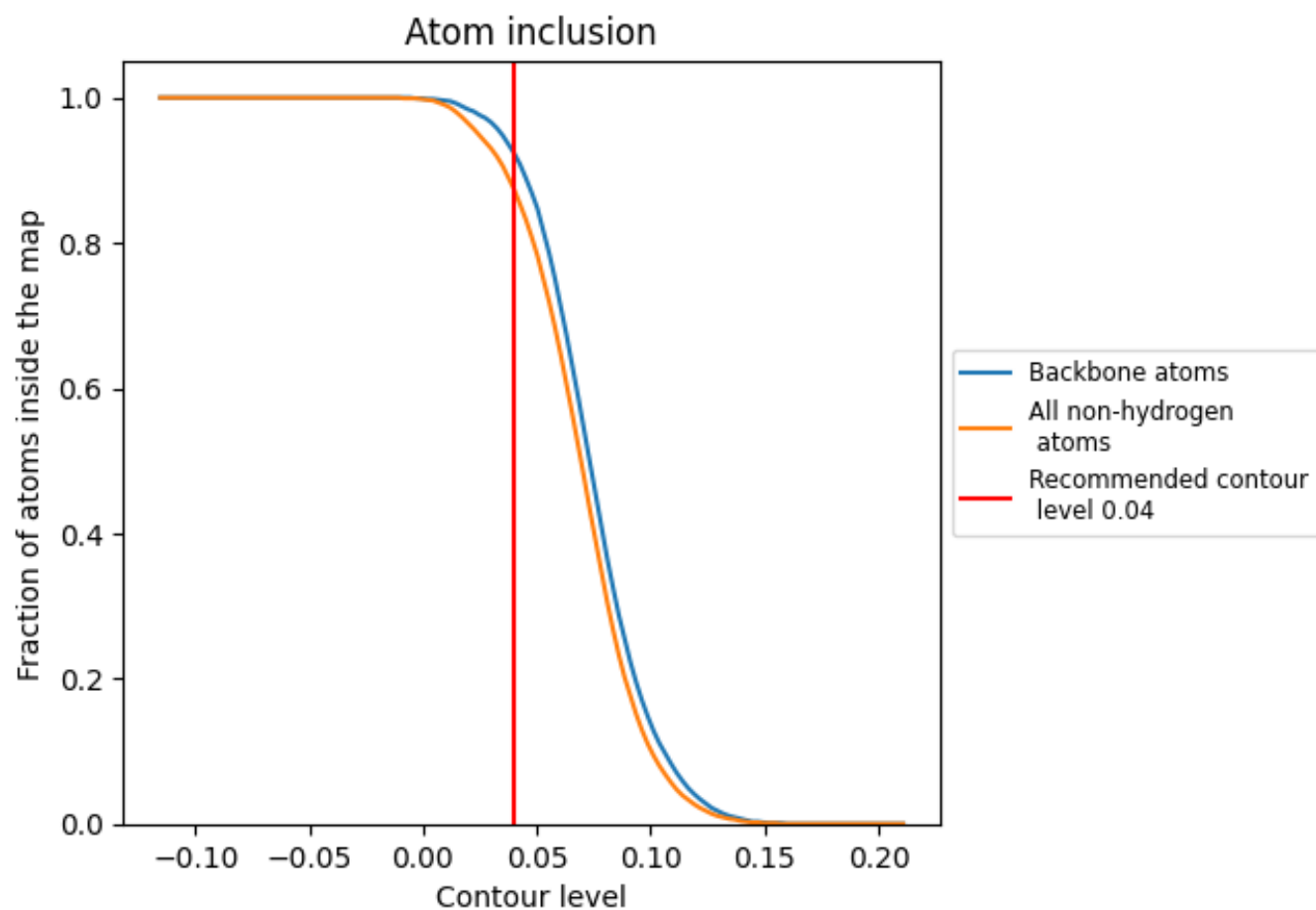
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 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 (0.04).

8.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.7170
A	 0.8740	 0.7180
AA	 0.8710	 0.7160
AB	 0.8750	 0.7160
B	 0.8760	 0.7190
BA	 0.8750	 0.7180
BB	 0.8740	 0.7150
C	 0.8710	 0.7160
CA	 0.8760	 0.7170
CB	 0.8750	 0.7160
D	 0.8780	 0.7180
DA	 0.8760	 0.7180
DB	 0.8760	 0.7160
E	 0.8740	 0.7180
EA	 0.8760	 0.7190
EB	 0.8760	 0.7170
F	 0.8760	 0.7190
FA	 0.8740	 0.7160
FB	 0.8760	 0.7180
G	 0.8710	 0.7160
GA	 0.8730	 0.7170
GB	 0.8700	 0.7150
H	 0.8750	 0.7160
HA	 0.8760	 0.7170
HB	 0.8730	 0.7180
I	 0.8710	 0.7160
IA	 0.8740	 0.7180
IB	 0.8710	 0.7170
J	 0.8760	 0.7180
JA	 0.8750	 0.7160
K	 0.8760	 0.7170
KA	 0.8750	 0.7170
L	 0.8740	 0.7180
LA	 0.8750	 0.7180
M	 0.8750	 0.7170



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
MA	 0.8750	 0.7170
N	 0.8750	 0.7160
NA	 0.8710	 0.7160
O	 0.8740	 0.7180
OA	 0.8750	 0.7160
P	 0.8750	 0.7170
PA	 0.8750	 0.7160
Q	 0.8750	 0.7180
QA	 0.8750	 0.7160
R	 0.8710	 0.7150
RA	 0.8740	 0.7180
S	 0.8750	 0.7160
SA	 0.8750	 0.7180
T	 0.8740	 0.7170
TA	 0.8700	 0.7160
UA	 0.8750	 0.7170
V	 0.8740	 0.7170
VA	 0.8720	 0.7150
W	 0.8760	 0.7190
WA	 0.8720	 0.7170
X	 0.8760	 0.7180
XA	 0.8770	 0.7190
Y	 0.8720	 0.7160
YA	 0.8700	 0.7160
Z	 0.8750	 0.7160
ZA	 0.8750	 0.7150