



Full wwPDB EM Validation Report ⓘ

Jul 3, 2024 – 01:30 am BST

PDB ID : 7NT6
EMDB ID : EMD-12584
Title : CryoEM structure of the Nipah virus nucleocapsid spiral clam-shaped assembly
Authors : Ker, D.S.; Jenkins, H.T.; Greive, S.J.; Antson, A.A.
Deposited on : 2021-03-09
Resolution : 4.30 Å(reported)
Based on initial model : 7NT5

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.dev92
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) : 2.37.1

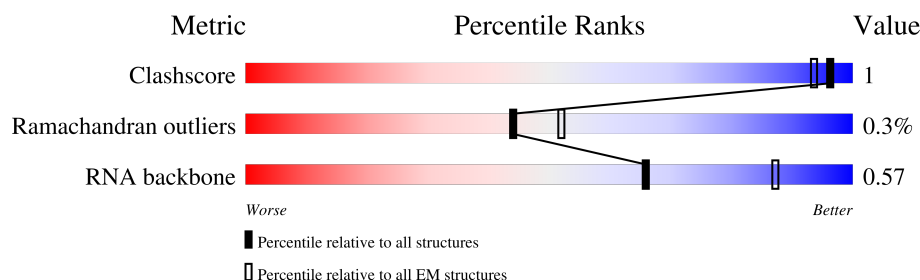
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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.





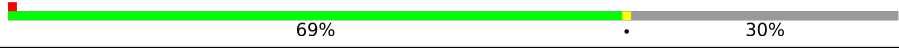



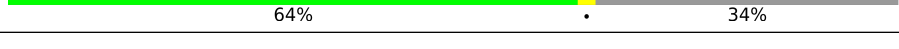
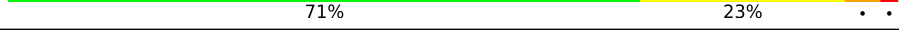
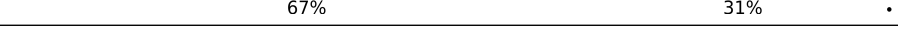
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
RNA backbone	4643	859

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	554	
1	B	554	
1	C	554	
1	D	554	
1	E	554	
1	F	554	
1	G	554	
1	H	554	

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Mol	Chain	Length	Quality of chain
1	I	554	
1	J	554	
1	K	554	
1	L	554	
1	M	554	
1	N	554	
1	O	554	
2	X	48	
3	Z	42	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24128 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 Nucleoprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	330	Total	C	N	O	0	0
			1320	660	330	330		
1	B	361	Total	C	N	O	0	0
			1444	722	361	361		
1	C	368	Total	C	N	O	0	0
			1472	736	368	368		
1	D	368	Total	C	N	O	0	0
			1472	736	368	368		
1	E	382	Total	C	N	O	0	0
			1528	764	382	382		
1	F	388	Total	C	N	O	0	0
			1552	776	388	388		
1	G	363	Total	C	N	O	0	0
			1452	726	363	363		
1	H	381	Total	C	N	O	0	0
			1524	762	381	381		
1	I	388	Total	C	N	O	0	0
			1552	776	388	388		
1	J	393	Total	C	N	O	0	0
			1572	786	393	393		
1	K	390	Total	C	N	O	0	0
			1560	780	390	390		
1	L	375	Total	C	N	O	0	0
			1500	750	375	375		
1	M	366	Total	C	N	O	0	0
			1464	732	366	366		
1	N	365	Total	C	N	O	0	0
			1460	730	365	365		
1	O	364	Total	C	N	O	0	0
			1456	728	364	364		

There are 330 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP Q9IK92
A	-20	GLY	-	expression tag	UNP Q9IK92
A	-19	SER	-	expression tag	UNP Q9IK92
A	-18	SER	-	expression tag	UNP Q9IK92
A	-17	HIS	-	expression tag	UNP Q9IK92
A	-16	HIS	-	expression tag	UNP Q9IK92
A	-15	HIS	-	expression tag	UNP Q9IK92
A	-14	HIS	-	expression tag	UNP Q9IK92
A	-13	HIS	-	expression tag	UNP Q9IK92
A	-12	HIS	-	expression tag	UNP Q9IK92
A	-11	SER	-	expression tag	UNP Q9IK92
A	-10	SER	-	expression tag	UNP Q9IK92
A	-9	GLY	-	expression tag	UNP Q9IK92
A	-8	LEU	-	expression tag	UNP Q9IK92
A	-7	GLU	-	expression tag	UNP Q9IK92
A	-6	VAL	-	expression tag	UNP Q9IK92
A	-5	LEU	-	expression tag	UNP Q9IK92
A	-4	PHE	-	expression tag	UNP Q9IK92
A	-3	GLN	-	expression tag	UNP Q9IK92
A	-2	GLY	-	expression tag	UNP Q9IK92
A	-1	PRO	-	expression tag	UNP Q9IK92
A	0	ALA	-	expression tag	UNP Q9IK92
B	-21	MET	-	initiating methionine	UNP Q9IK92
B	-20	GLY	-	expression tag	UNP Q9IK92
B	-19	SER	-	expression tag	UNP Q9IK92
B	-18	SER	-	expression tag	UNP Q9IK92
B	-17	HIS	-	expression tag	UNP Q9IK92
B	-16	HIS	-	expression tag	UNP Q9IK92
B	-15	HIS	-	expression tag	UNP Q9IK92
B	-14	HIS	-	expression tag	UNP Q9IK92
B	-13	HIS	-	expression tag	UNP Q9IK92
B	-12	HIS	-	expression tag	UNP Q9IK92
B	-11	SER	-	expression tag	UNP Q9IK92
B	-10	SER	-	expression tag	UNP Q9IK92
B	-9	GLY	-	expression tag	UNP Q9IK92
B	-8	LEU	-	expression tag	UNP Q9IK92
B	-7	GLU	-	expression tag	UNP Q9IK92
B	-6	VAL	-	expression tag	UNP Q9IK92
B	-5	LEU	-	expression tag	UNP Q9IK92
B	-4	PHE	-	expression tag	UNP Q9IK92
B	-3	GLN	-	expression tag	UNP Q9IK92
B	-2	GLY	-	expression tag	UNP Q9IK92
B	-1	PRO	-	expression tag	UNP Q9IK92

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	ALA	-	expression tag	UNP Q9IK92
C	-21	MET	-	initiating methionine	UNP Q9IK92
C	-20	GLY	-	expression tag	UNP Q9IK92
C	-19	SER	-	expression tag	UNP Q9IK92
C	-18	SER	-	expression tag	UNP Q9IK92
C	-17	HIS	-	expression tag	UNP Q9IK92
C	-16	HIS	-	expression tag	UNP Q9IK92
C	-15	HIS	-	expression tag	UNP Q9IK92
C	-14	HIS	-	expression tag	UNP Q9IK92
C	-13	HIS	-	expression tag	UNP Q9IK92
C	-12	HIS	-	expression tag	UNP Q9IK92
C	-11	SER	-	expression tag	UNP Q9IK92
C	-10	SER	-	expression tag	UNP Q9IK92
C	-9	GLY	-	expression tag	UNP Q9IK92
C	-8	LEU	-	expression tag	UNP Q9IK92
C	-7	GLU	-	expression tag	UNP Q9IK92
C	-6	VAL	-	expression tag	UNP Q9IK92
C	-5	LEU	-	expression tag	UNP Q9IK92
C	-4	PHE	-	expression tag	UNP Q9IK92
C	-3	GLN	-	expression tag	UNP Q9IK92
C	-2	GLY	-	expression tag	UNP Q9IK92
C	-1	PRO	-	expression tag	UNP Q9IK92
C	0	ALA	-	expression tag	UNP Q9IK92
D	-21	MET	-	initiating methionine	UNP Q9IK92
D	-20	GLY	-	expression tag	UNP Q9IK92
D	-19	SER	-	expression tag	UNP Q9IK92
D	-18	SER	-	expression tag	UNP Q9IK92
D	-17	HIS	-	expression tag	UNP Q9IK92
D	-16	HIS	-	expression tag	UNP Q9IK92
D	-15	HIS	-	expression tag	UNP Q9IK92
D	-14	HIS	-	expression tag	UNP Q9IK92
D	-13	HIS	-	expression tag	UNP Q9IK92
D	-12	HIS	-	expression tag	UNP Q9IK92
D	-11	SER	-	expression tag	UNP Q9IK92
D	-10	SER	-	expression tag	UNP Q9IK92
D	-9	GLY	-	expression tag	UNP Q9IK92
D	-8	LEU	-	expression tag	UNP Q9IK92
D	-7	GLU	-	expression tag	UNP Q9IK92
D	-6	VAL	-	expression tag	UNP Q9IK92
D	-5	LEU	-	expression tag	UNP Q9IK92
D	-4	PHE	-	expression tag	UNP Q9IK92
D	-3	GLN	-	expression tag	UNP Q9IK92

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	GLY	-	expression tag	UNP Q9IK92
D	-1	PRO	-	expression tag	UNP Q9IK92
D	0	ALA	-	expression tag	UNP Q9IK92
E	-21	MET	-	initiating methionine	UNP Q9IK92
E	-20	GLY	-	expression tag	UNP Q9IK92
E	-19	SER	-	expression tag	UNP Q9IK92
E	-18	SER	-	expression tag	UNP Q9IK92
E	-17	HIS	-	expression tag	UNP Q9IK92
E	-16	HIS	-	expression tag	UNP Q9IK92
E	-15	HIS	-	expression tag	UNP Q9IK92
E	-14	HIS	-	expression tag	UNP Q9IK92
E	-13	HIS	-	expression tag	UNP Q9IK92
E	-12	HIS	-	expression tag	UNP Q9IK92
E	-11	SER	-	expression tag	UNP Q9IK92
E	-10	SER	-	expression tag	UNP Q9IK92
E	-9	GLY	-	expression tag	UNP Q9IK92
E	-8	LEU	-	expression tag	UNP Q9IK92
E	-7	GLU	-	expression tag	UNP Q9IK92
E	-6	VAL	-	expression tag	UNP Q9IK92
E	-5	LEU	-	expression tag	UNP Q9IK92
E	-4	PHE	-	expression tag	UNP Q9IK92
E	-3	GLN	-	expression tag	UNP Q9IK92
E	-2	GLY	-	expression tag	UNP Q9IK92
E	-1	PRO	-	expression tag	UNP Q9IK92
E	0	ALA	-	expression tag	UNP Q9IK92
F	-21	MET	-	initiating methionine	UNP Q9IK92
F	-20	GLY	-	expression tag	UNP Q9IK92
F	-19	SER	-	expression tag	UNP Q9IK92
F	-18	SER	-	expression tag	UNP Q9IK92
F	-17	HIS	-	expression tag	UNP Q9IK92
F	-16	HIS	-	expression tag	UNP Q9IK92
F	-15	HIS	-	expression tag	UNP Q9IK92
F	-14	HIS	-	expression tag	UNP Q9IK92
F	-13	HIS	-	expression tag	UNP Q9IK92
F	-12	HIS	-	expression tag	UNP Q9IK92
F	-11	SER	-	expression tag	UNP Q9IK92
F	-10	SER	-	expression tag	UNP Q9IK92
F	-9	GLY	-	expression tag	UNP Q9IK92
F	-8	LEU	-	expression tag	UNP Q9IK92
F	-7	GLU	-	expression tag	UNP Q9IK92
F	-6	VAL	-	expression tag	UNP Q9IK92
F	-5	LEU	-	expression tag	UNP Q9IK92

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	PHE	-	expression tag	UNP Q9IK92
F	-3	GLN	-	expression tag	UNP Q9IK92
F	-2	GLY	-	expression tag	UNP Q9IK92
F	-1	PRO	-	expression tag	UNP Q9IK92
F	0	ALA	-	expression tag	UNP Q9IK92
G	-21	MET	-	initiating methionine	UNP Q9IK92
G	-20	GLY	-	expression tag	UNP Q9IK92
G	-19	SER	-	expression tag	UNP Q9IK92
G	-18	SER	-	expression tag	UNP Q9IK92
G	-17	HIS	-	expression tag	UNP Q9IK92
G	-16	HIS	-	expression tag	UNP Q9IK92
G	-15	HIS	-	expression tag	UNP Q9IK92
G	-14	HIS	-	expression tag	UNP Q9IK92
G	-13	HIS	-	expression tag	UNP Q9IK92
G	-12	HIS	-	expression tag	UNP Q9IK92
G	-11	SER	-	expression tag	UNP Q9IK92
G	-10	SER	-	expression tag	UNP Q9IK92
G	-9	GLY	-	expression tag	UNP Q9IK92
G	-8	LEU	-	expression tag	UNP Q9IK92
G	-7	GLU	-	expression tag	UNP Q9IK92
G	-6	VAL	-	expression tag	UNP Q9IK92
G	-5	LEU	-	expression tag	UNP Q9IK92
G	-4	PHE	-	expression tag	UNP Q9IK92
G	-3	GLN	-	expression tag	UNP Q9IK92
G	-2	GLY	-	expression tag	UNP Q9IK92
G	-1	PRO	-	expression tag	UNP Q9IK92
G	0	ALA	-	expression tag	UNP Q9IK92
H	-21	MET	-	initiating methionine	UNP Q9IK92
H	-20	GLY	-	expression tag	UNP Q9IK92
H	-19	SER	-	expression tag	UNP Q9IK92
H	-18	SER	-	expression tag	UNP Q9IK92
H	-17	HIS	-	expression tag	UNP Q9IK92
H	-16	HIS	-	expression tag	UNP Q9IK92
H	-15	HIS	-	expression tag	UNP Q9IK92
H	-14	HIS	-	expression tag	UNP Q9IK92
H	-13	HIS	-	expression tag	UNP Q9IK92
H	-12	HIS	-	expression tag	UNP Q9IK92
H	-11	SER	-	expression tag	UNP Q9IK92
H	-10	SER	-	expression tag	UNP Q9IK92
H	-9	GLY	-	expression tag	UNP Q9IK92
H	-8	LEU	-	expression tag	UNP Q9IK92
H	-7	GLU	-	expression tag	UNP Q9IK92

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-6	VAL	-	expression tag	UNP Q9IK92
H	-5	LEU	-	expression tag	UNP Q9IK92
H	-4	PHE	-	expression tag	UNP Q9IK92
H	-3	GLN	-	expression tag	UNP Q9IK92
H	-2	GLY	-	expression tag	UNP Q9IK92
H	-1	PRO	-	expression tag	UNP Q9IK92
H	0	ALA	-	expression tag	UNP Q9IK92
I	-21	MET	-	initiating methionine	UNP Q9IK92
I	-20	GLY	-	expression tag	UNP Q9IK92
I	-19	SER	-	expression tag	UNP Q9IK92
I	-18	SER	-	expression tag	UNP Q9IK92
I	-17	HIS	-	expression tag	UNP Q9IK92
I	-16	HIS	-	expression tag	UNP Q9IK92
I	-15	HIS	-	expression tag	UNP Q9IK92
I	-14	HIS	-	expression tag	UNP Q9IK92
I	-13	HIS	-	expression tag	UNP Q9IK92
I	-12	HIS	-	expression tag	UNP Q9IK92
I	-11	SER	-	expression tag	UNP Q9IK92
I	-10	SER	-	expression tag	UNP Q9IK92
I	-9	GLY	-	expression tag	UNP Q9IK92
I	-8	LEU	-	expression tag	UNP Q9IK92
I	-7	GLU	-	expression tag	UNP Q9IK92
I	-6	VAL	-	expression tag	UNP Q9IK92
I	-5	LEU	-	expression tag	UNP Q9IK92
I	-4	PHE	-	expression tag	UNP Q9IK92
I	-3	GLN	-	expression tag	UNP Q9IK92
I	-2	GLY	-	expression tag	UNP Q9IK92
I	-1	PRO	-	expression tag	UNP Q9IK92
I	0	ALA	-	expression tag	UNP Q9IK92
J	-21	MET	-	initiating methionine	UNP Q9IK92
J	-20	GLY	-	expression tag	UNP Q9IK92
J	-19	SER	-	expression tag	UNP Q9IK92
J	-18	SER	-	expression tag	UNP Q9IK92
J	-17	HIS	-	expression tag	UNP Q9IK92
J	-16	HIS	-	expression tag	UNP Q9IK92
J	-15	HIS	-	expression tag	UNP Q9IK92
J	-14	HIS	-	expression tag	UNP Q9IK92
J	-13	HIS	-	expression tag	UNP Q9IK92
J	-12	HIS	-	expression tag	UNP Q9IK92
J	-11	SER	-	expression tag	UNP Q9IK92
J	-10	SER	-	expression tag	UNP Q9IK92
J	-9	GLY	-	expression tag	UNP Q9IK92

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-8	LEU	-	expression tag	UNP Q9IK92
J	-7	GLU	-	expression tag	UNP Q9IK92
J	-6	VAL	-	expression tag	UNP Q9IK92
J	-5	LEU	-	expression tag	UNP Q9IK92
J	-4	PHE	-	expression tag	UNP Q9IK92
J	-3	GLN	-	expression tag	UNP Q9IK92
J	-2	GLY	-	expression tag	UNP Q9IK92
J	-1	PRO	-	expression tag	UNP Q9IK92
J	0	ALA	-	expression tag	UNP Q9IK92
K	-21	MET	-	initiating methionine	UNP Q9IK92
K	-20	GLY	-	expression tag	UNP Q9IK92
K	-19	SER	-	expression tag	UNP Q9IK92
K	-18	SER	-	expression tag	UNP Q9IK92
K	-17	HIS	-	expression tag	UNP Q9IK92
K	-16	HIS	-	expression tag	UNP Q9IK92
K	-15	HIS	-	expression tag	UNP Q9IK92
K	-14	HIS	-	expression tag	UNP Q9IK92
K	-13	HIS	-	expression tag	UNP Q9IK92
K	-12	HIS	-	expression tag	UNP Q9IK92
K	-11	SER	-	expression tag	UNP Q9IK92
K	-10	SER	-	expression tag	UNP Q9IK92
K	-9	GLY	-	expression tag	UNP Q9IK92
K	-8	LEU	-	expression tag	UNP Q9IK92
K	-7	GLU	-	expression tag	UNP Q9IK92
K	-6	VAL	-	expression tag	UNP Q9IK92
K	-5	LEU	-	expression tag	UNP Q9IK92
K	-4	PHE	-	expression tag	UNP Q9IK92
K	-3	GLN	-	expression tag	UNP Q9IK92
K	-2	GLY	-	expression tag	UNP Q9IK92
K	-1	PRO	-	expression tag	UNP Q9IK92
K	0	ALA	-	expression tag	UNP Q9IK92
L	-21	MET	-	initiating methionine	UNP Q9IK92
L	-20	GLY	-	expression tag	UNP Q9IK92
L	-19	SER	-	expression tag	UNP Q9IK92
L	-18	SER	-	expression tag	UNP Q9IK92
L	-17	HIS	-	expression tag	UNP Q9IK92
L	-16	HIS	-	expression tag	UNP Q9IK92
L	-15	HIS	-	expression tag	UNP Q9IK92
L	-14	HIS	-	expression tag	UNP Q9IK92
L	-13	HIS	-	expression tag	UNP Q9IK92
L	-12	HIS	-	expression tag	UNP Q9IK92
L	-11	SER	-	expression tag	UNP Q9IK92

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-10	SER	-	expression tag	UNP Q9IK92
L	-9	GLY	-	expression tag	UNP Q9IK92
L	-8	LEU	-	expression tag	UNP Q9IK92
L	-7	GLU	-	expression tag	UNP Q9IK92
L	-6	VAL	-	expression tag	UNP Q9IK92
L	-5	LEU	-	expression tag	UNP Q9IK92
L	-4	PHE	-	expression tag	UNP Q9IK92
L	-3	GLN	-	expression tag	UNP Q9IK92
L	-2	GLY	-	expression tag	UNP Q9IK92
L	-1	PRO	-	expression tag	UNP Q9IK92
L	0	ALA	-	expression tag	UNP Q9IK92
M	-21	MET	-	initiating methionine	UNP Q9IK92
M	-20	GLY	-	expression tag	UNP Q9IK92
M	-19	SER	-	expression tag	UNP Q9IK92
M	-18	SER	-	expression tag	UNP Q9IK92
M	-17	HIS	-	expression tag	UNP Q9IK92
M	-16	HIS	-	expression tag	UNP Q9IK92
M	-15	HIS	-	expression tag	UNP Q9IK92
M	-14	HIS	-	expression tag	UNP Q9IK92
M	-13	HIS	-	expression tag	UNP Q9IK92
M	-12	HIS	-	expression tag	UNP Q9IK92
M	-11	SER	-	expression tag	UNP Q9IK92
M	-10	SER	-	expression tag	UNP Q9IK92
M	-9	GLY	-	expression tag	UNP Q9IK92
M	-8	LEU	-	expression tag	UNP Q9IK92
M	-7	GLU	-	expression tag	UNP Q9IK92
M	-6	VAL	-	expression tag	UNP Q9IK92
M	-5	LEU	-	expression tag	UNP Q9IK92
M	-4	PHE	-	expression tag	UNP Q9IK92
M	-3	GLN	-	expression tag	UNP Q9IK92
M	-2	GLY	-	expression tag	UNP Q9IK92
M	-1	PRO	-	expression tag	UNP Q9IK92
M	0	ALA	-	expression tag	UNP Q9IK92
N	-21	MET	-	initiating methionine	UNP Q9IK92
N	-20	GLY	-	expression tag	UNP Q9IK92
N	-19	SER	-	expression tag	UNP Q9IK92
N	-18	SER	-	expression tag	UNP Q9IK92
N	-17	HIS	-	expression tag	UNP Q9IK92
N	-16	HIS	-	expression tag	UNP Q9IK92
N	-15	HIS	-	expression tag	UNP Q9IK92
N	-14	HIS	-	expression tag	UNP Q9IK92
N	-13	HIS	-	expression tag	UNP Q9IK92

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Chain	Residue	Modelled	Actual	Comment	Reference
N	-12	HIS	-	expression tag	UNP Q9IK92
N	-11	SER	-	expression tag	UNP Q9IK92
N	-10	SER	-	expression tag	UNP Q9IK92
N	-9	GLY	-	expression tag	UNP Q9IK92
N	-8	LEU	-	expression tag	UNP Q9IK92
N	-7	GLU	-	expression tag	UNP Q9IK92
N	-6	VAL	-	expression tag	UNP Q9IK92
N	-5	LEU	-	expression tag	UNP Q9IK92
N	-4	PHE	-	expression tag	UNP Q9IK92
N	-3	GLN	-	expression tag	UNP Q9IK92
N	-2	GLY	-	expression tag	UNP Q9IK92
N	-1	PRO	-	expression tag	UNP Q9IK92
N	0	ALA	-	expression tag	UNP Q9IK92
O	-21	MET	-	initiating methionine	UNP Q9IK92
O	-20	GLY	-	expression tag	UNP Q9IK92
O	-19	SER	-	expression tag	UNP Q9IK92
O	-18	SER	-	expression tag	UNP Q9IK92
O	-17	HIS	-	expression tag	UNP Q9IK92
O	-16	HIS	-	expression tag	UNP Q9IK92
O	-15	HIS	-	expression tag	UNP Q9IK92
O	-14	HIS	-	expression tag	UNP Q9IK92
O	-13	HIS	-	expression tag	UNP Q9IK92
O	-12	HIS	-	expression tag	UNP Q9IK92
O	-11	SER	-	expression tag	UNP Q9IK92
O	-10	SER	-	expression tag	UNP Q9IK92
O	-9	GLY	-	expression tag	UNP Q9IK92
O	-8	LEU	-	expression tag	UNP Q9IK92
O	-7	GLU	-	expression tag	UNP Q9IK92
O	-6	VAL	-	expression tag	UNP Q9IK92
O	-5	LEU	-	expression tag	UNP Q9IK92
O	-4	PHE	-	expression tag	UNP Q9IK92
O	-3	GLN	-	expression tag	UNP Q9IK92
O	-2	GLY	-	expression tag	UNP Q9IK92
O	-1	PRO	-	expression tag	UNP Q9IK92
O	0	ALA	-	expression tag	UNP Q9IK92

- Molecule 2 is a RNA chain called RNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	48	Total	C	N	O	P	0	0
			960	432	96	384	48		

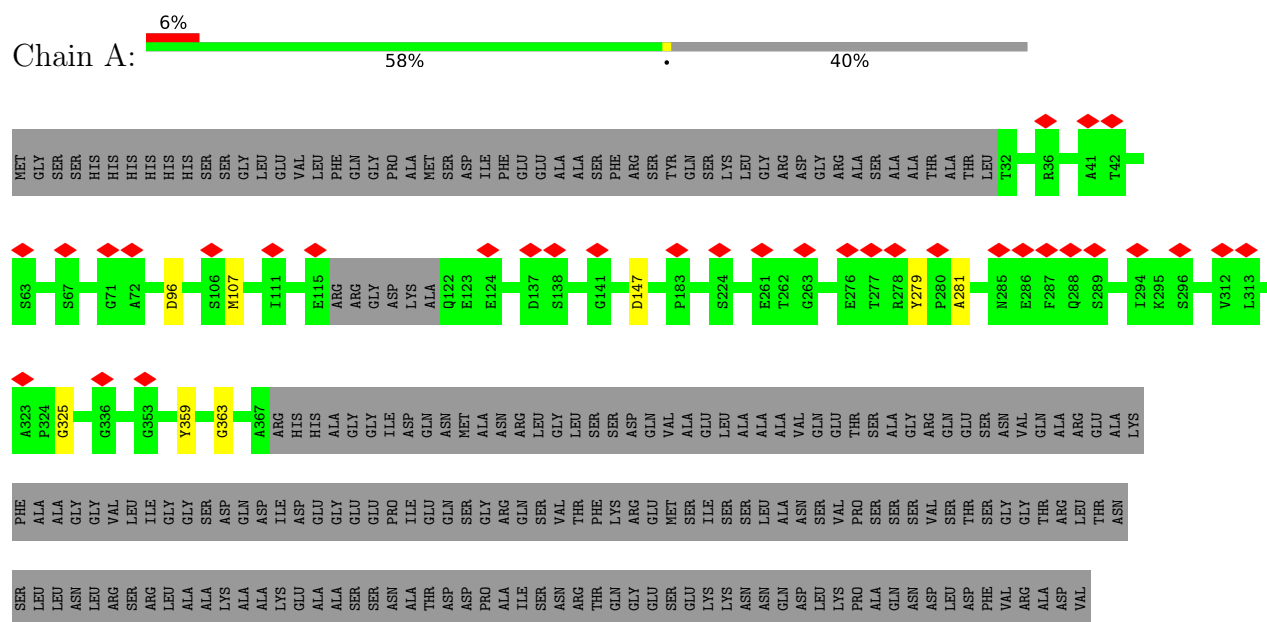
- Molecule 3 is a RNA chain called RNA (42-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z	42	Total	C	N	O	P	0	0
			840	378	84	336	42		

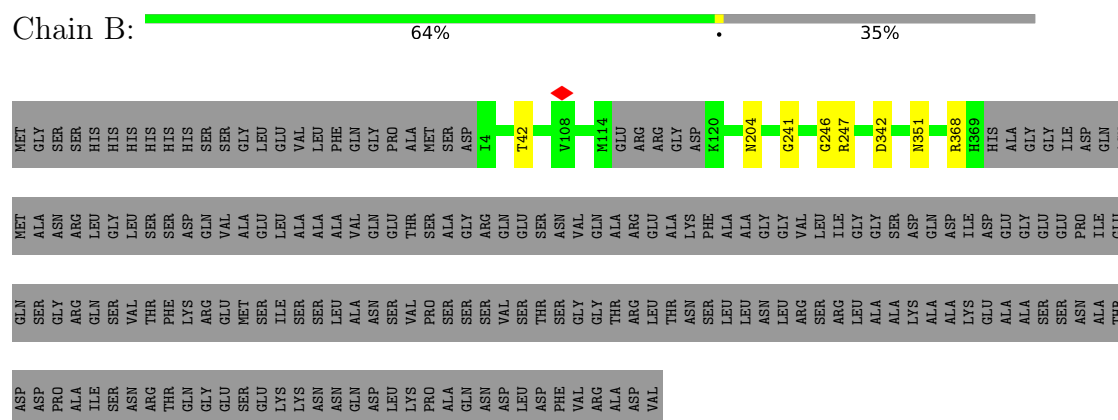
3 Residue-property plots

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: Nucleoprotein



• Molecule 1: Nucleoprotein



• Molecule 1: Nucleoprotein

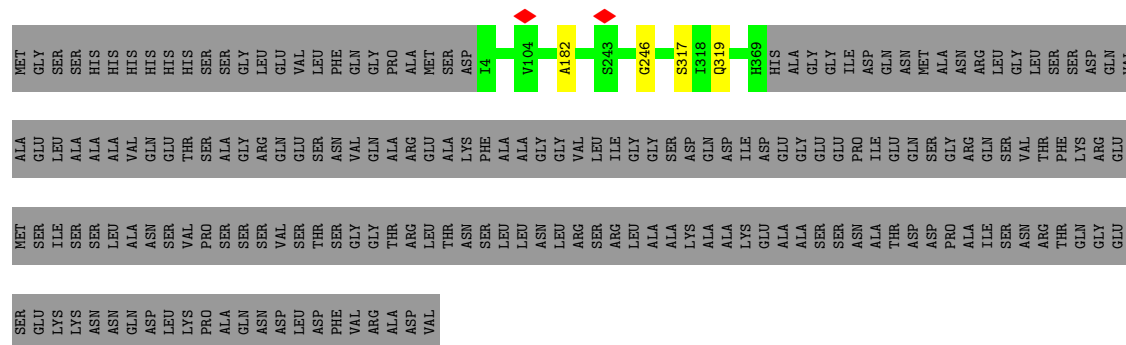


Chain J:  70% 29%

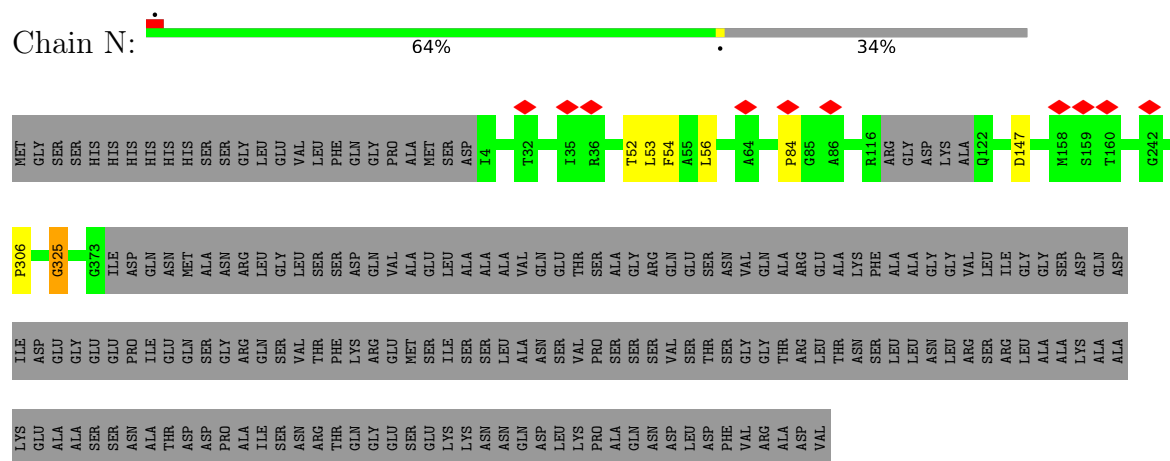
Chain K:  69% 30%

Chain L:  67% 32%

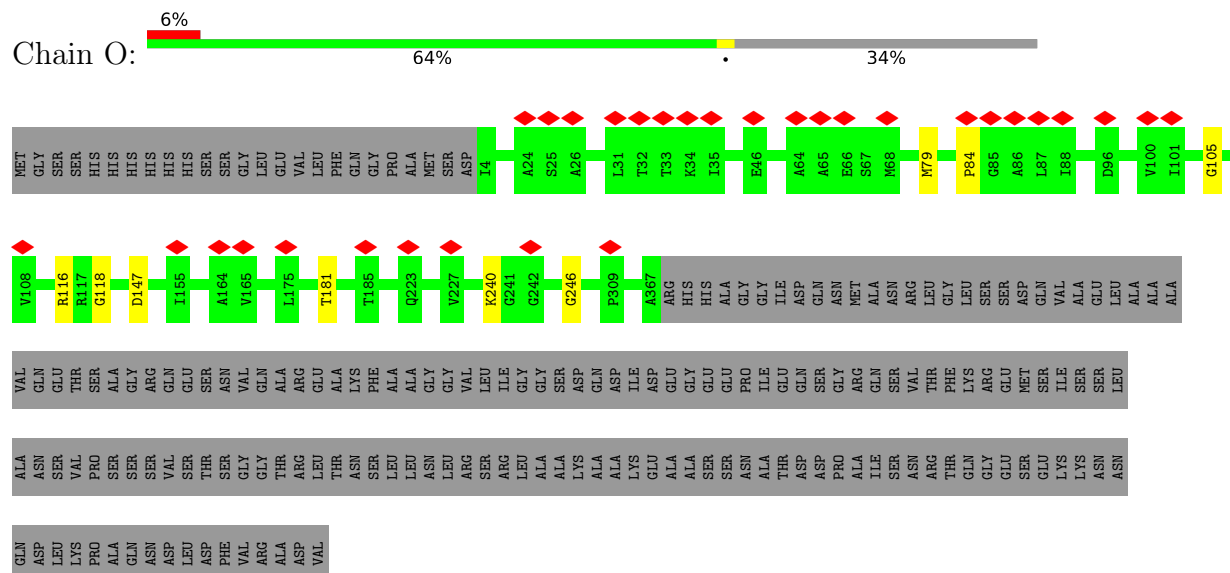
Chain M:  65% . 34%



- Molecule 1: Nucleoprotein



- Molecule 1: Nucleoprotein

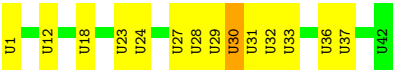


- Molecule 2: RNA (48-MER)





● Molecule 3: RNA (42-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23029	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 ($e^-/\text{\AA}^2$)	41	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.043	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.022	Depositor
Map size (Å)	314.4, 314.4, 314.4	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.572, 1.572, 1.572	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.60	0/1318	0.81	1/1644 (0.1%)
1	B	0.55	0/1442	0.79	0/1799
1	C	0.55	0/1471	0.78	0/1837
1	D	0.58	0/1471	0.84	0/1837
1	E	0.59	0/1526	0.82	0/1904
1	F	0.53	0/1550	0.78	0/1934
1	G	0.54	0/1450	0.78	0/1809
1	H	0.57	0/1521	0.80	0/1896
1	I	0.57	0/1550	0.81	0/1934
1	J	0.54	0/1571	0.82	0/1962
1	K	0.56	0/1559	0.81	0/1947
1	L	0.56	0/1498	0.80	0/1869
1	M	0.52	0/1463	0.80	0/1827
1	N	0.57	0/1458	0.80	1/1819 (0.1%)
1	O	0.62	0/1455	0.83	0/1817
2	X	0.90	0/1055	1.18	7/1628 (0.4%)
3	Z	0.86	2/923 (0.2%)	1.25	11/1424 (0.8%)
All	All	0.59	2/24281 (0.0%)	0.85	20/30887 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
1	C	0	1
1	D	0	2
1	E	0	2
1	F	0	4
1	G	0	2
1	H	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	I	0	3
1	J	0	2
1	K	0	2
1	L	0	2
1	M	0	1
1	N	0	1
1	O	0	5
All	All	0	35

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Z	1	U	P-O5'	5.31	1.65	1.59
3	Z	27	U	O3'-P	5.03	1.67	1.61

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Z	32	U	O5'-P-OP2	-10.60	96.16	105.70
2	X	36	U	C4'-C3'-O3'	-10.55	87.25	109.40
2	X	31	U	O5'-P-OP2	-9.81	96.87	105.70
3	Z	1	U	O5'-P-OP2	9.74	122.39	110.70
3	Z	24	U	O5'-P-OP1	9.42	122.00	110.70
3	Z	31	U	O5'-P-OP1	7.09	119.20	110.70
2	X	35	U	O5'-P-OP1	7.08	119.20	110.70
1	A	325	GLY	N-CA-C	-6.89	95.87	113.10
1	N	325	GLY	N-CA-C	-6.88	95.90	113.10
2	X	12	U	O5'-P-OP1	6.71	118.75	110.70
3	Z	1	U	O5'-P-OP1	6.00	117.90	110.70
3	Z	28	U	P-O5'-C5'	-5.78	111.66	120.90
3	Z	18	U	C4'-C3'-O3'	-5.50	97.85	109.40
3	Z	30	U	O5'-P-OP2	-5.43	100.81	105.70
2	X	1	U	O5'-P-OP1	-5.24	100.98	105.70
2	X	4	U	O5'-P-OP1	-5.22	101.00	105.70
2	X	35	U	O5'-P-OP2	-5.15	101.06	105.70
3	Z	23	U	O5'-P-OP1	5.12	116.85	110.70
3	Z	12	U	O5'-P-OP2	-5.11	101.10	105.70
3	Z	33	U	C5'-C4'-O4'	5.08	115.20	109.10

There are no chirality outliers.

All (35) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	147	ASP	Peptide
1	A	96	ASP	Peptide
1	B	204	ASN	Peptide
1	B	342	ASP	Peptide
1	B	368	ARG	Peptide
1	C	147	ASP	Peptide
1	D	147	ASP	Peptide
1	D	327	TYR	Peptide
1	E	147	ASP	Peptide
1	E	391	GLU	Peptide
1	F	204	ASN	Peptide
1	F	246	GLY	Peptide
1	F	327	TYR	Peptide
1	F	83	ARG	Peptide
1	G	147	ASP	Peptide
1	G	246	GLY	Peptide
1	H	147	ASP	Peptide
1	H	23	ARG	Peptide
1	H	25	SER	Peptide
1	I	147	ASP	Peptide
1	I	327	TYR	Peptide
1	I	342	ASP	Peptide
1	J	203	VAL	Peptide
1	J	204	ASN	Peptide
1	K	203	VAL	Peptide
1	K	327	TYR	Peptide
1	L	147	ASP	Peptide
1	L	246	GLY	Peptide
1	M	246	GLY	Peptide
1	N	147	ASP	Peptide
1	O	116	ARG	Peptide
1	O	118	GLY	Peptide
1	O	147	ASP	Peptide
1	O	240	LYS	Peptide
1	O	246	GLY	Peptide

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	1320	0	355	2	0
1	B	1444	0	390	2	0
1	C	1472	0	400	1	0
1	D	1472	0	400	0	0
1	E	1528	0	417	3	0
1	F	1552	0	423	1	0
1	G	1452	0	396	1	0
1	H	1524	0	411	0	0
1	I	1552	0	423	0	0
1	J	1572	0	431	2	0
1	K	1560	0	428	1	0
1	L	1500	0	406	0	0
1	M	1464	0	398	1	0
1	N	1460	0	398	2	0
1	O	1456	0	396	2	0
2	X	960	0	481	8	0
3	Z	840	0	421	1	0
All	All	24128	0	6974	24	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 (24) 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)
2:X:14:U:O2'	2:X:15:U:H5'	1.75	0.85
2:X:36:U:O2'	2:X:37:U:H5'	1.77	0.82
2:X:34:U:O2'	2:X:35:U:H5'	1.95	0.66
1:O:181:THR:CA	2:X:44:U:O2'	2.55	0.54
2:X:14:U:H2'	2:X:15:U:C6	2.47	0.49
1:A:359:TYR:O	1:A:363:GLY:N	2.39	0.49
1:E:365:LYS:O	1:E:369:HIS:N	2.45	0.48
1:F:362:LEU:O	1:F:366:SER:N	2.42	0.48
1:B:246:GLY:O	1:B:247:ARG:C	2.52	0.48
1:J:279:TYR:C	1:J:281:ALA:H	2.16	0.48
3:Z:29:U:C2'	3:Z:30:U:H5'	2.44	0.47
1:E:370:HIS:O	1:E:374:ILE:N	2.48	0.46
1:B:241:GLY:HA2	1:C:22:GLY:O	2.15	0.46
1:M:317:SER:C	1:M:319:GLN:N	2.69	0.46
1:E:364:GLN:O	1:E:367:ALA:N	2.50	0.45
1:N:54:PHE:C	1:N:56:LEU:N	2.70	0.45
1:K:45:PRO:O	1:K:46:GLU:C	2.54	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:52:THR:O	1:N:53:LEU:C	2.55	0.44
1:O:181:THR:O	2:X:44:U:O2	2.35	0.44
1:J:279:TYR:C	1:J:281:ALA:N	2.72	0.43
1:A:279:TYR:C	1:A:281:ALA:H	2.23	0.42
1:G:279:TYR:O	1:G:281:ALA:N	2.53	0.41
2:X:19:U:H2'	2:X:20:U:O4'	2.21	0.41
2:X:14:U:O2'	2:X:15:U:C5'	2.60	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	326/554 (59%)	314 (96%)	11 (3%)	1 (0%)	41	76
1	B	357/554 (64%)	342 (96%)	13 (4%)	2 (1%)	25	65
1	C	366/554 (66%)	355 (97%)	11 (3%)	0	100	100
1	D	366/554 (66%)	351 (96%)	15 (4%)	0	100	100
1	E	378/554 (68%)	358 (95%)	20 (5%)	0	100	100
1	F	384/554 (69%)	370 (96%)	14 (4%)	0	100	100
1	G	359/554 (65%)	343 (96%)	12 (3%)	4 (1%)	14	52
1	H	375/554 (68%)	360 (96%)	15 (4%)	0	100	100
1	I	384/554 (69%)	364 (95%)	19 (5%)	1 (0%)	41	76
1	J	391/554 (71%)	368 (94%)	21 (5%)	2 (0%)	29	68
1	K	388/554 (70%)	371 (96%)	16 (4%)	1 (0%)	41	76
1	L	371/554 (67%)	356 (96%)	15 (4%)	0	100	100
1	M	364/554 (66%)	347 (95%)	16 (4%)	1 (0%)	41	76
1	N	361/554 (65%)	347 (96%)	11 (3%)	3 (1%)	19	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	362/554 (65%)	345 (95%)	14 (4%)	3 (1%)	19	60
All	All	5532/8310 (67%)	5291 (96%)	223 (4%)	18 (0%)	44	76

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	112	PRO
1	J	328	PRO
1	O	84	PRO
1	G	110	GLY
1	O	105	GLY
1	B	42	THR
1	G	280	PRO
1	I	374	ILE
1	N	306	PRO
1	O	79	MET
1	A	107	MET
1	J	265	ALA
1	N	84	PRO
1	B	351	ASN
1	G	79	MET
1	N	325	GLY
1	K	306	PRO
1	M	182	ALA

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	X	47/48 (97%)	3 (6%)	1 (2%)
3	Z	41/42 (97%)	2 (4%)	0
All	All	88/90 (97%)	5 (5%)	1 (1%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	X	36	U

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Mol	Chain	Res	Type
2	X	37	U
2	X	43	U
3	Z	36	U
3	Z	37	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	X	36	U

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.

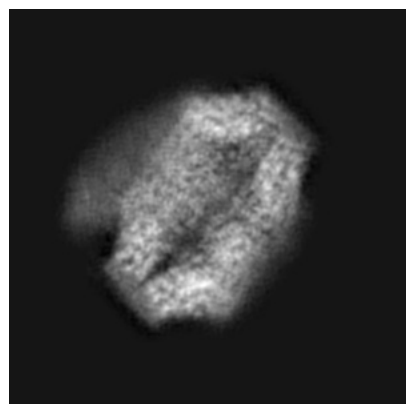
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12584. These allow visual inspection of the internal detail of the map and identification of artifacts.

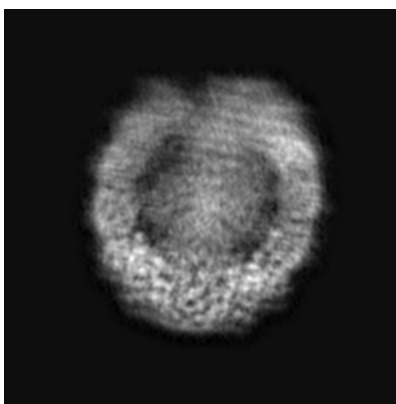
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

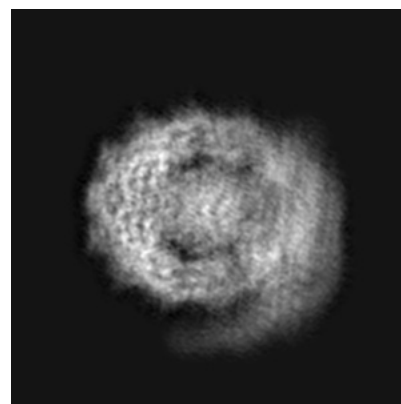
6.1.1 Primary map



X

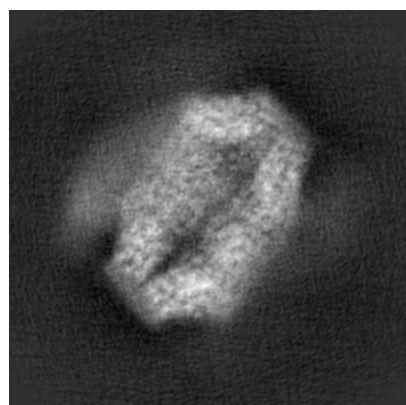


Y

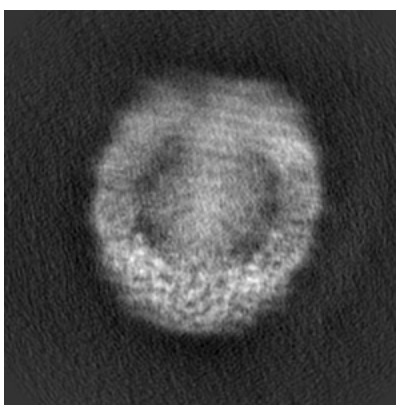


Z

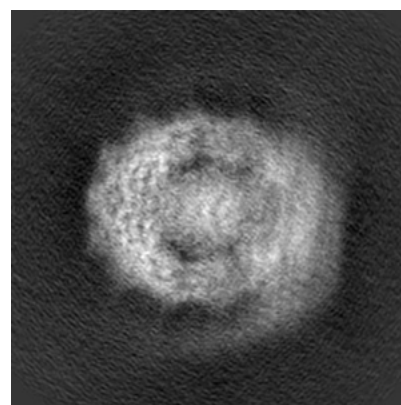
6.1.2 Raw map



X



Y

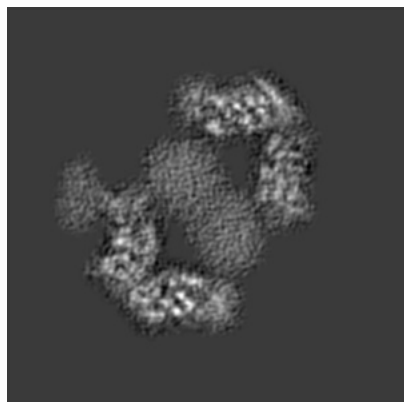


Z

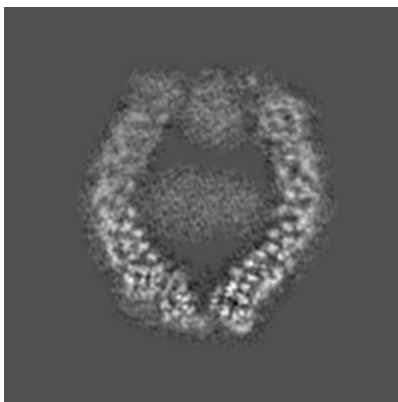
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

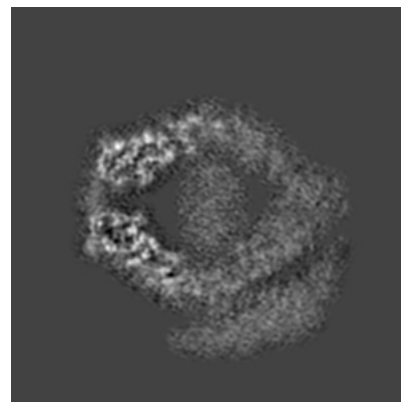
6.2.1 Primary map



X Index: 100

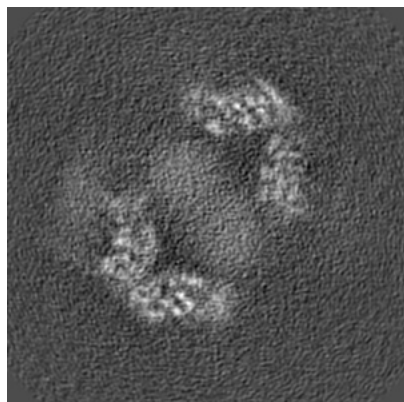


Y Index: 100

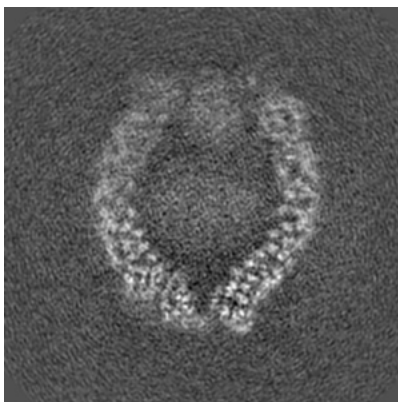


Z Index: 100

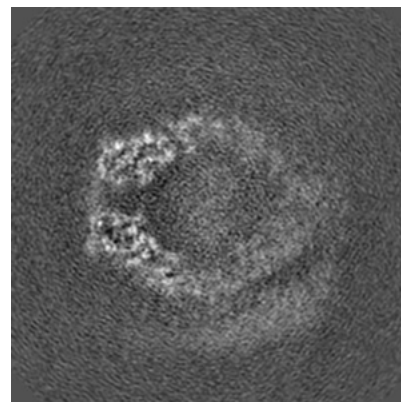
6.2.2 Raw map



X Index: 100



Y Index: 100

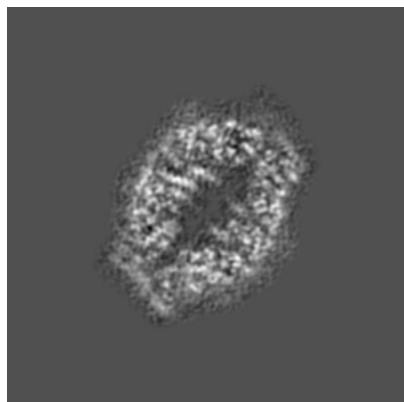


Z Index: 100

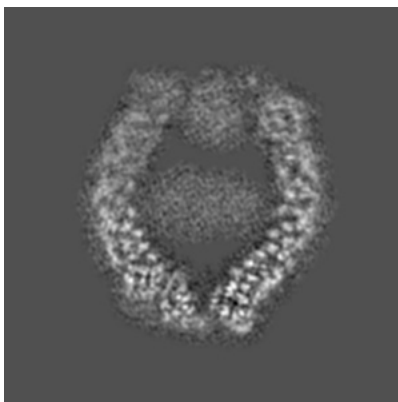
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

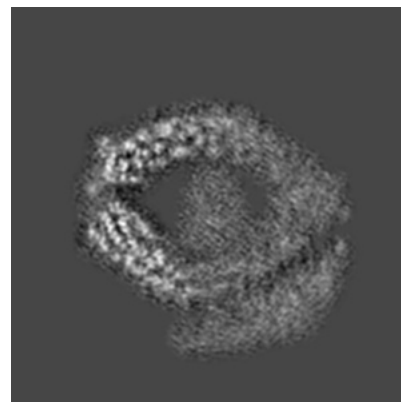
6.3.1 Primary map



X Index: 68



Y Index: 100

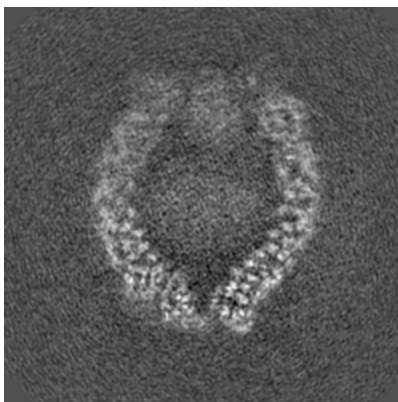


Z Index: 104

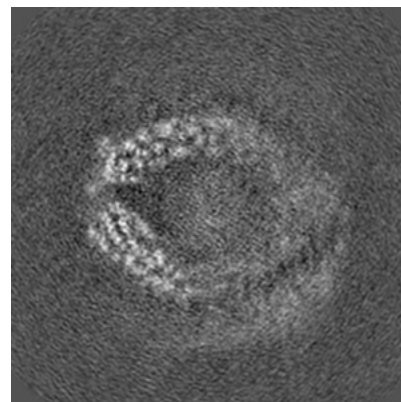
6.3.2 Raw map



X Index: 68



Y Index: 100

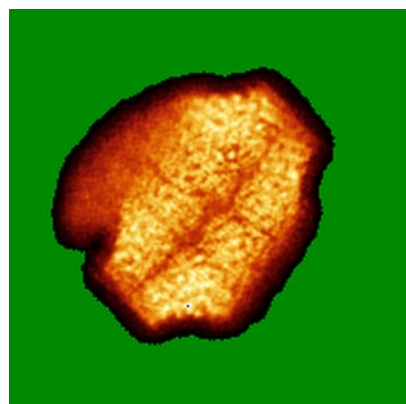


Z Index: 104

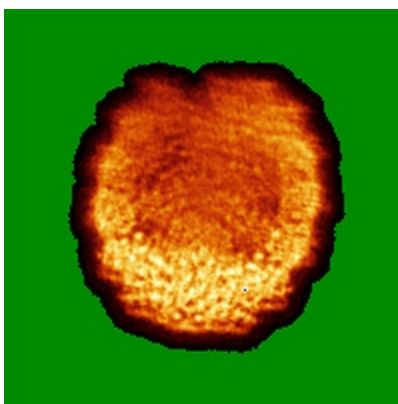
The images above show the largest variance slices of the map in three orthogonal directions.

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

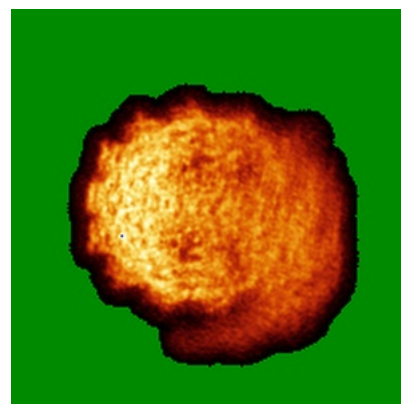
6.4.1 Primary map



X

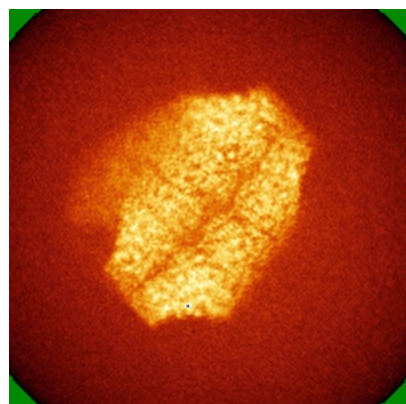


Y

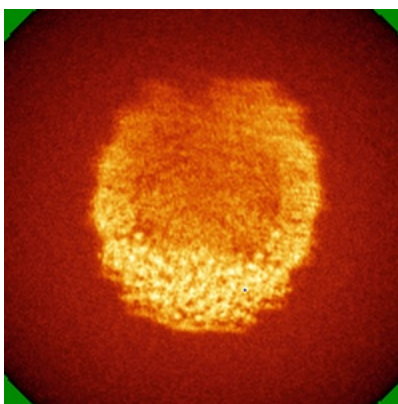


Z

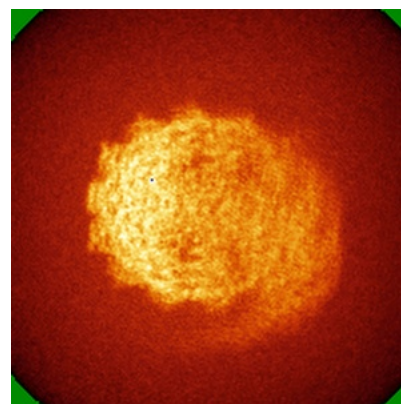
6.4.2 Raw map



X



Y

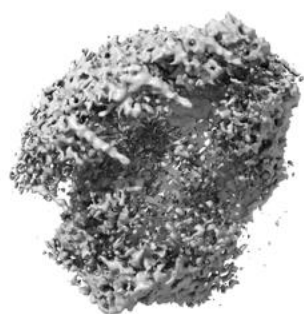


Z

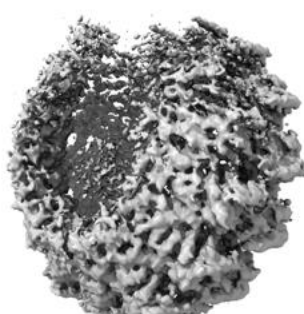
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

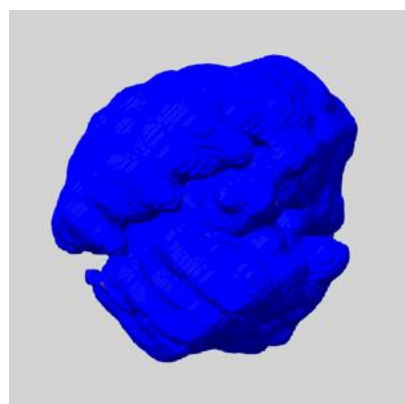
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

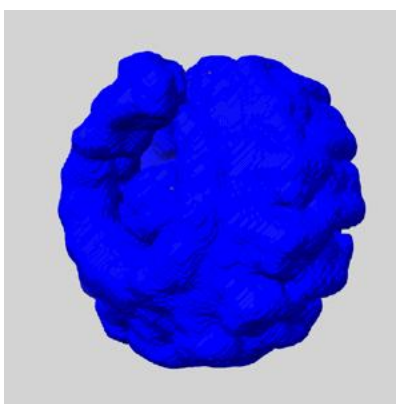
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

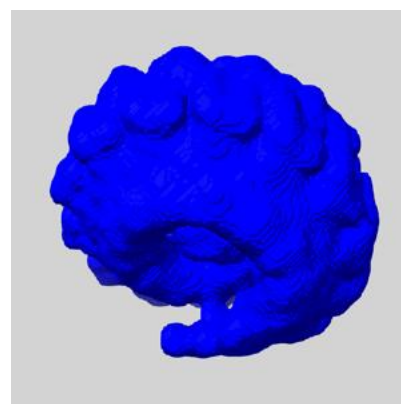
6.6.1 emd_12584_msk_1.map [i](#)



X



Y

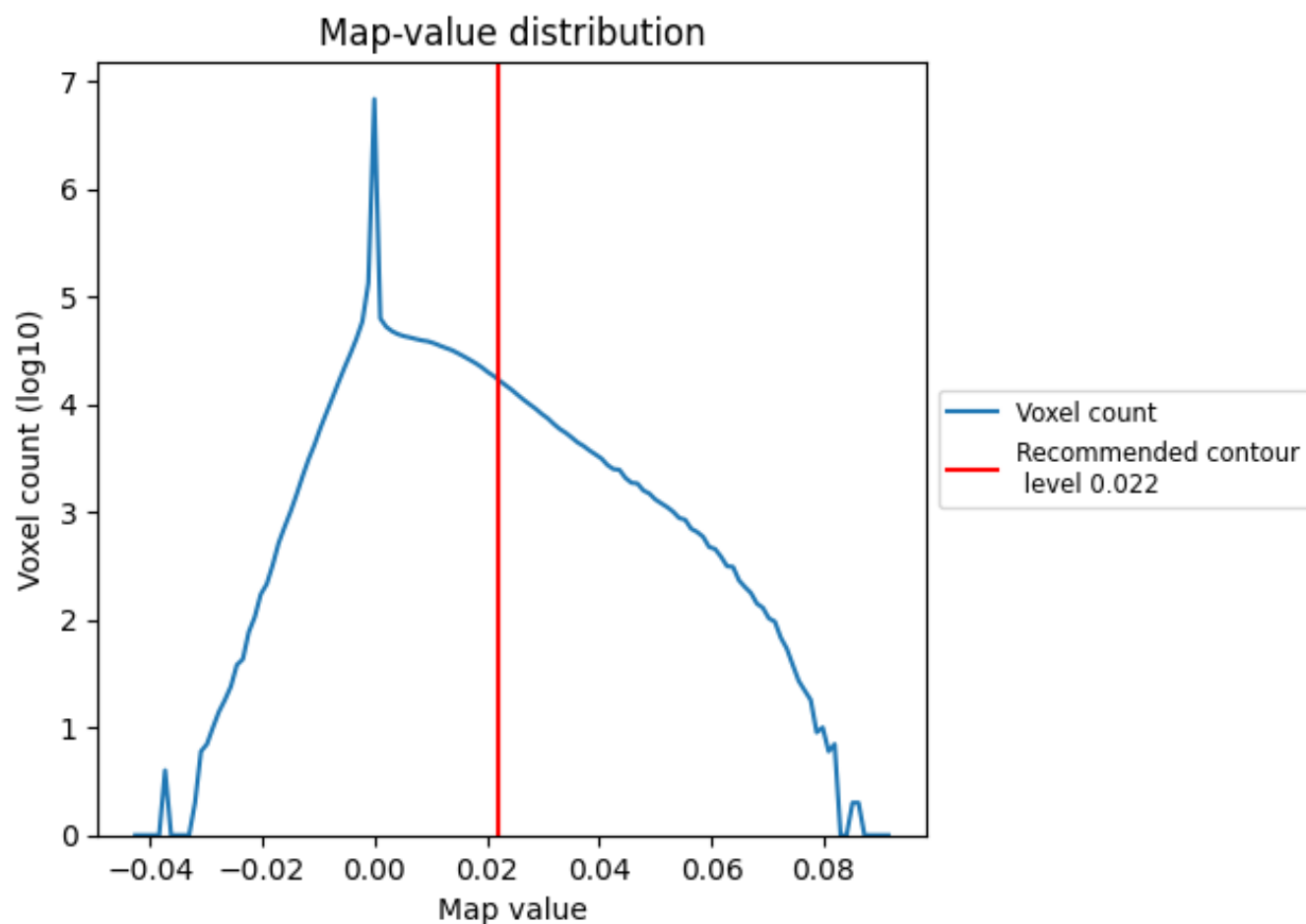


Z

7 Map analysis [i](#)

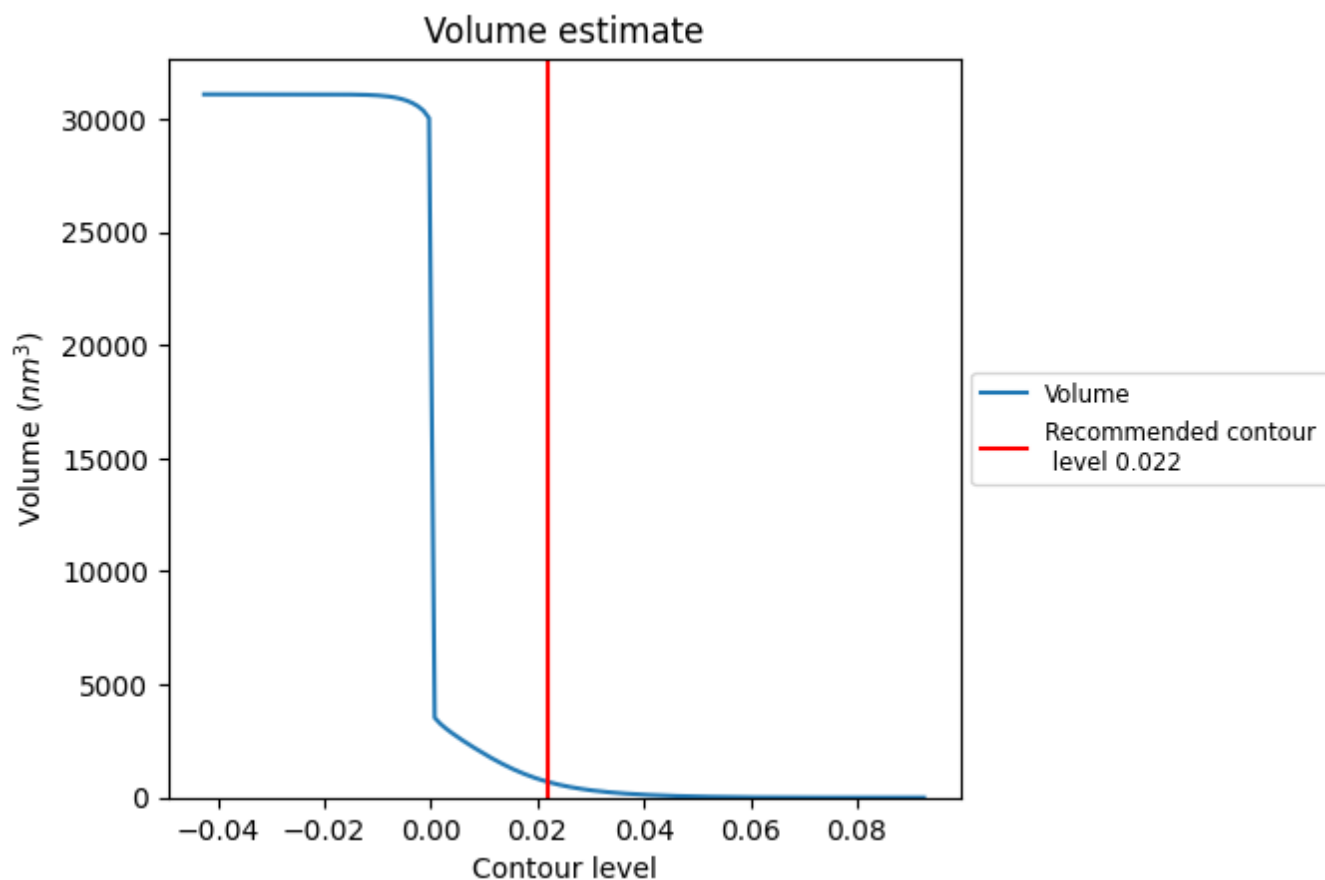
This section contains the results of statistical analysis of the map.

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.

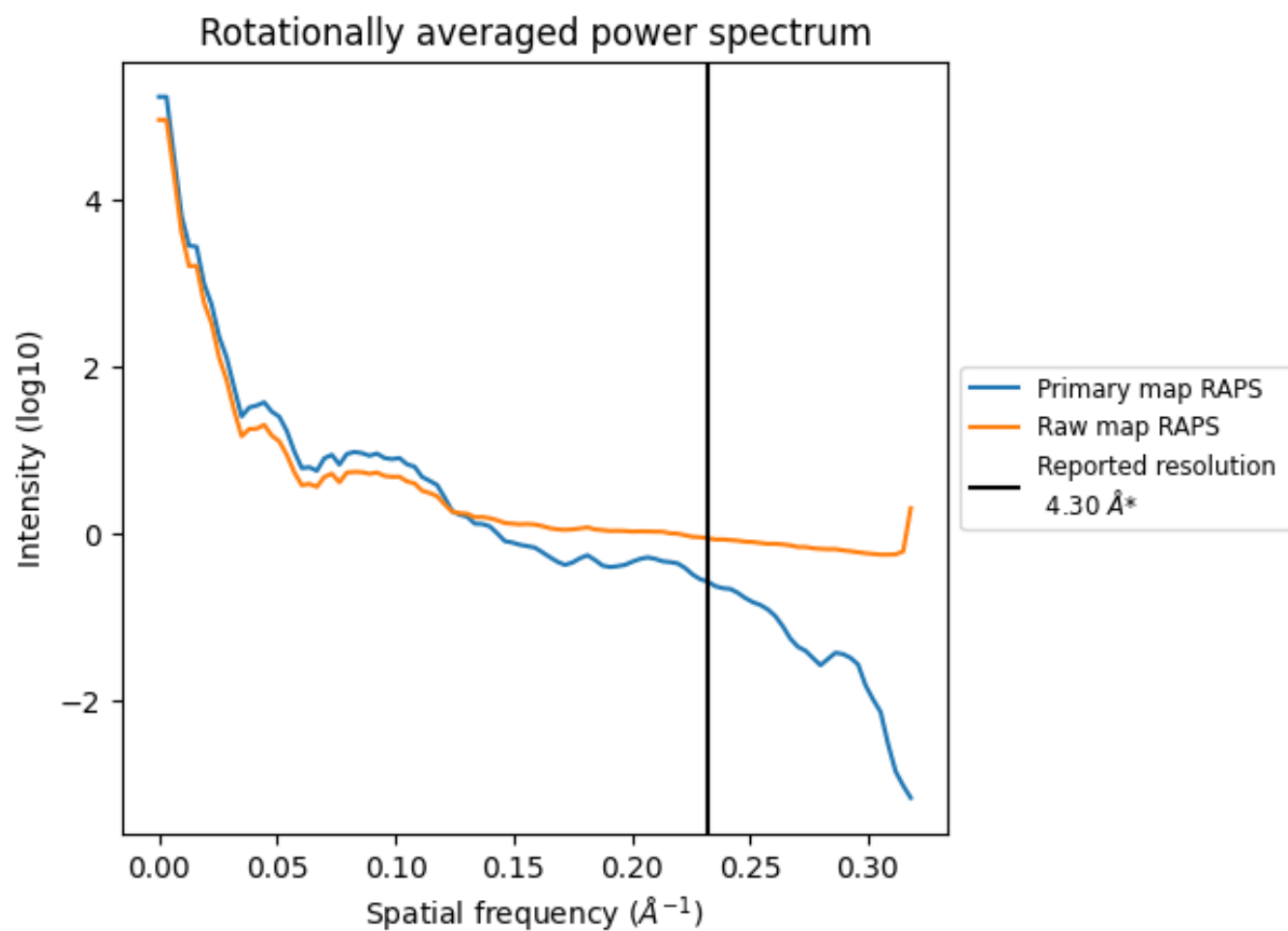
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 692 nm³; this corresponds to an approximate mass of 625 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 ⓘ

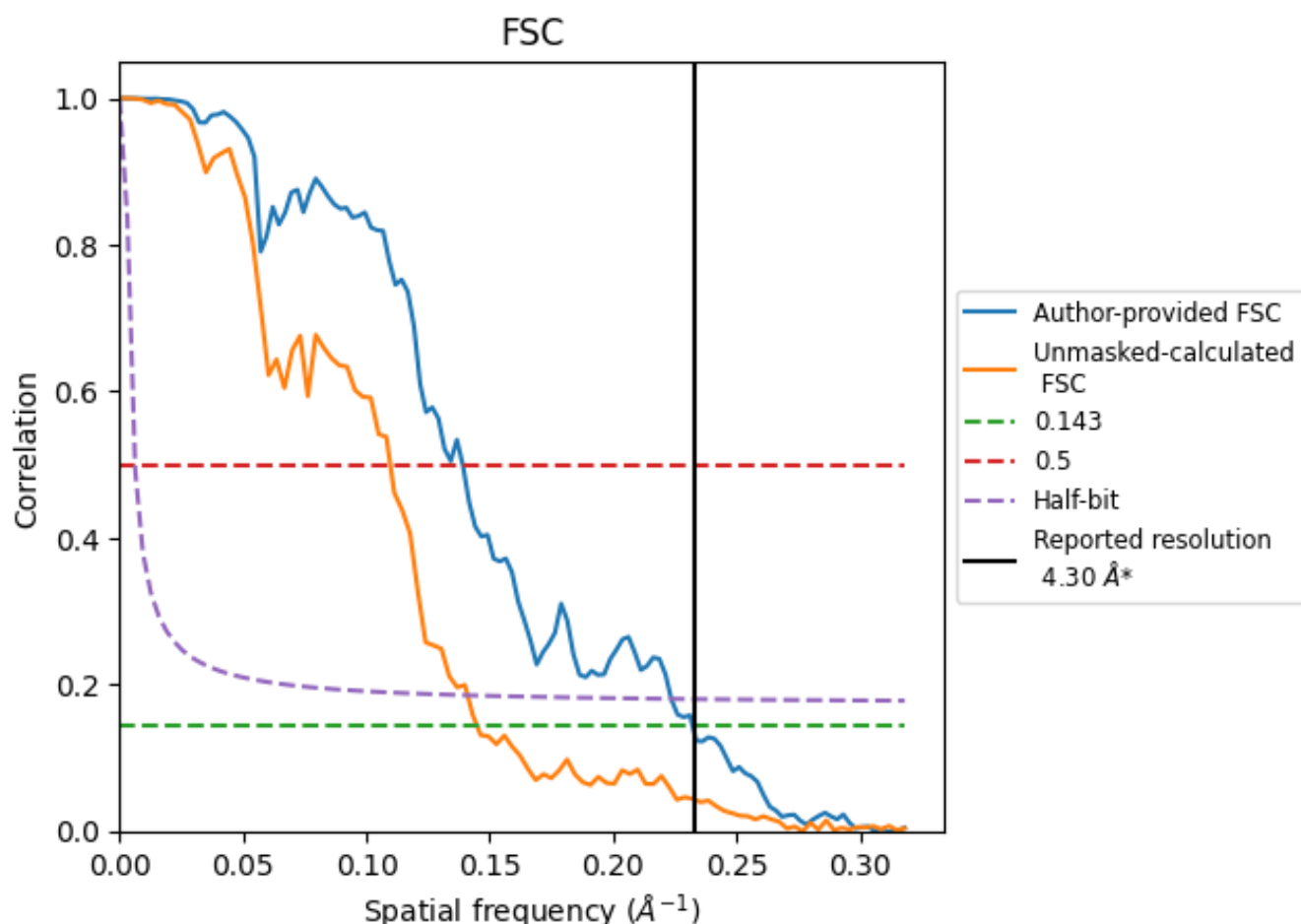


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 Å⁻¹

8.2 Resolution estimates [i](#)

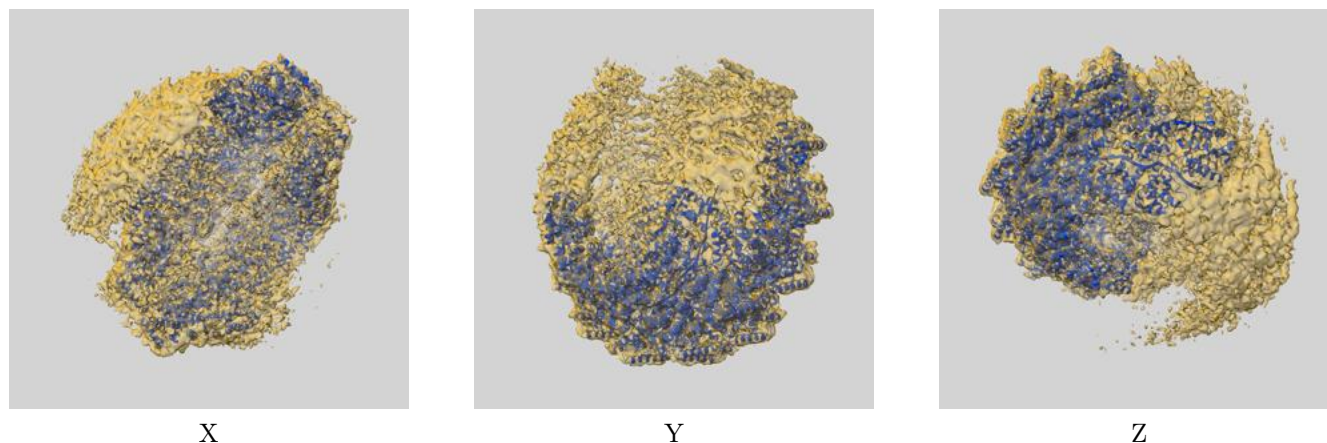
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.31	7.19	4.47
Unmasked-calculated*	6.90	9.12	7.09

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.90 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12584 and PDB model 7NT6. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



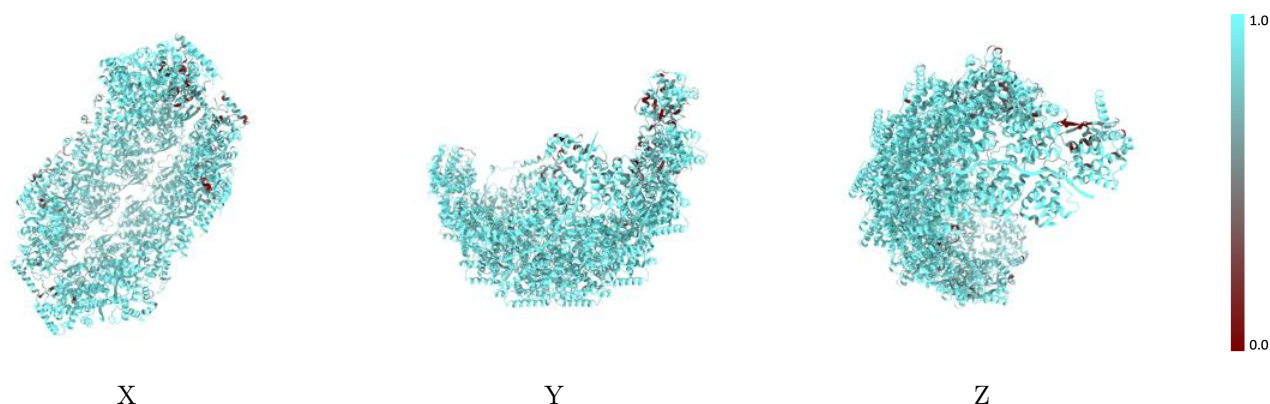
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



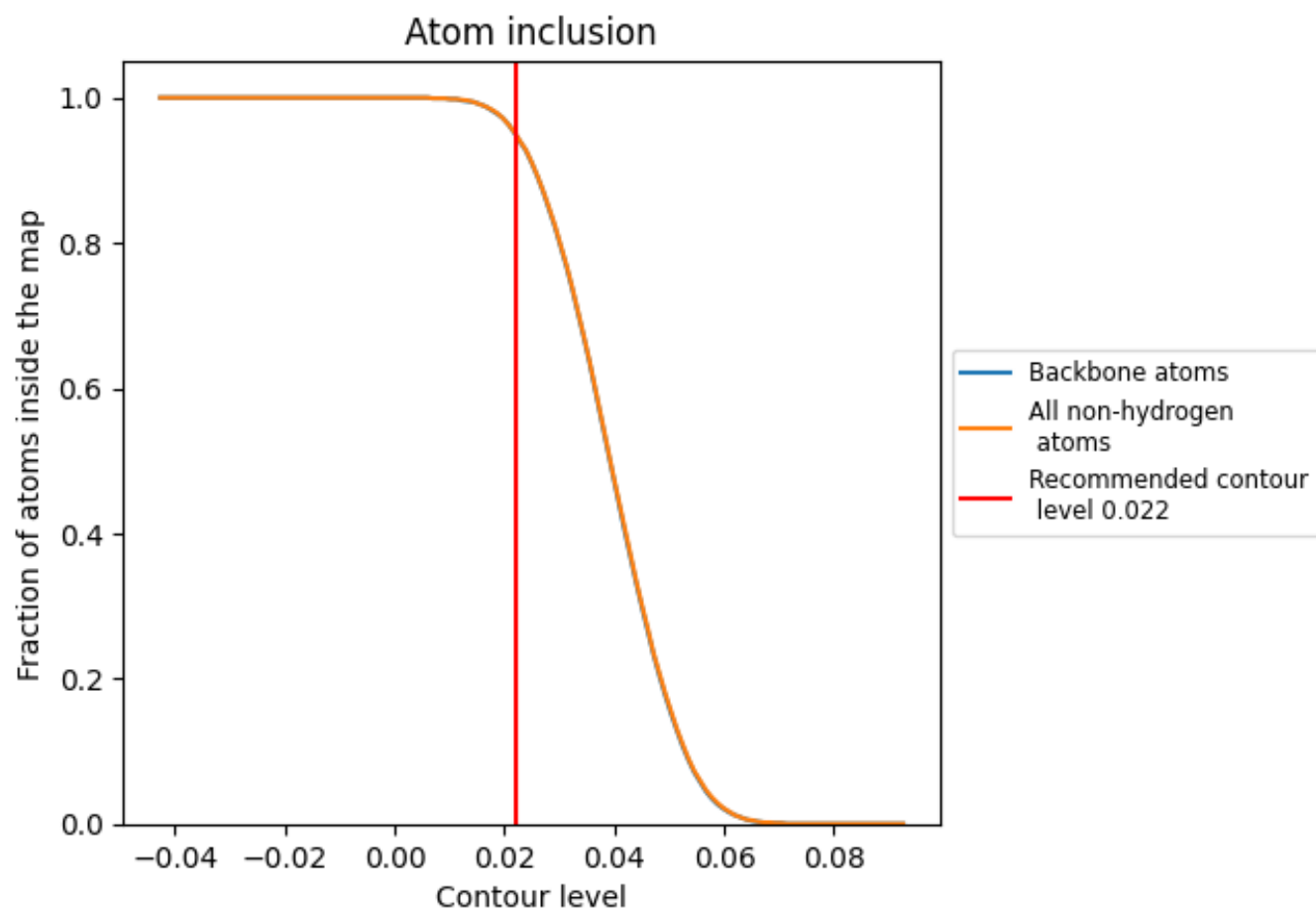
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).





































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9510	 0.3550
A	 0.8340	 0.2870
B	 0.9620	 0.3630
C	 0.9780	 0.4000
D	 0.9920	 0.3950
E	 0.9840	 0.3830
F	 0.9750	 0.3790
G	 0.9670	 0.3410
H	 0.9150	 0.3240
I	 0.9400	 0.3490
J	 0.9530	 0.3860
K	 0.9640	 0.4020
L	 0.9830	 0.4070
M	 0.9760	 0.3720
N	 0.9300	 0.3090
O	 0.8630	 0.2590
X	 0.9770	 0.3180
Z	 0.9640	 0.3290

