



## Full wwPDB EM Validation Report ⓘ

Jul 14, 2025 – 12:37 PM EDT

PDB ID : 9COK / pdb\_00009cok  
EMDB ID : EMD-45782  
Title : Cryo-EM structure of the Nipah virus (Malaysia Strain) L:P complex  
Authors : Chen, Z.H.; Liang, B.  
Deposited on : 2024-07-16  
Resolution : 2.92 Å(reported)

This is a Full wwPDB EM Validation 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.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44



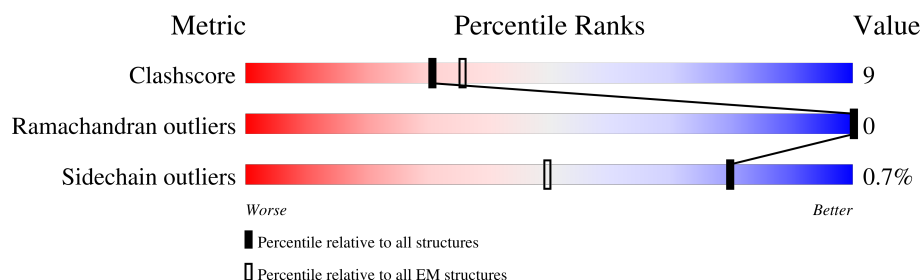
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*





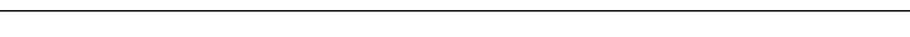
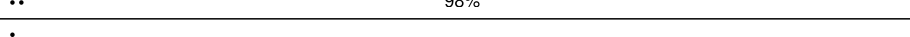
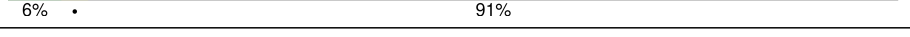
The reported resolution of this entry is 2.92 Å.

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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	B	759	 94%
1	C	759	 92%
1	D	759	 94%
1	E	759	 95%
1	F	759	 98%
1	G	759	 91%
2	A	2270	 44% 11% 45%



## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12206 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 Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	48	Total	C	N	O	S	0	0
			370	235	63	69	3		
1	D	48	Total	C	N	O	S	0	0
			380	241	66	70	3		
1	C	58	Total	C	N	O	S	0	0
			452	284	83	82	3		
1	E	41	Total	C	N	O	S	0	0
			319	203	53	60	3		
1	F	17	Total	C	N	O		0	0
			136	88	23	25			
1	G	71	Total	C	N	O	S	0	0
			573	354	96	122	1		

There are 300 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-49	MET	-	expression tag	UNP Q9IK91
B	-48	LYS	-	expression tag	UNP Q9IK91
B	-47	SER	-	expression tag	UNP Q9IK91
B	-46	SER	-	expression tag	UNP Q9IK91
B	-45	TRP	-	expression tag	UNP Q9IK91
B	-44	SER	-	expression tag	UNP Q9IK91
B	-43	HIS	-	expression tag	UNP Q9IK91
B	-42	PRO	-	expression tag	UNP Q9IK91
B	-41	GLN	-	expression tag	UNP Q9IK91
B	-40	PHE	-	expression tag	UNP Q9IK91
B	-39	GLU	-	expression tag	UNP Q9IK91
B	-38	LYS	-	expression tag	UNP Q9IK91
B	-37	GLY	-	expression tag	UNP Q9IK91
B	-36	ALA	-	expression tag	UNP Q9IK91
B	-35	MET	-	expression tag	UNP Q9IK91
B	-34	THR	-	expression tag	UNP Q9IK91
B	-33	GLY	-	expression tag	UNP Q9IK91
B	-32	TRP	-	expression tag	UNP Q9IK91

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-31	SER	-	expression tag	UNP Q9IK91
B	-30	HIS	-	expression tag	UNP Q9IK91
B	-29	PRO	-	expression tag	UNP Q9IK91
B	-28	GLN	-	expression tag	UNP Q9IK91
B	-27	PHE	-	expression tag	UNP Q9IK91
B	-26	GLU	-	expression tag	UNP Q9IK91
B	-25	LYS	-	expression tag	UNP Q9IK91
B	-24	GLY	-	expression tag	UNP Q9IK91
B	-23	SER	-	expression tag	UNP Q9IK91
B	-22	SER	-	expression tag	UNP Q9IK91
B	-21	ALA	-	expression tag	UNP Q9IK91
B	-20	SER	-	expression tag	UNP Q9IK91
B	-19	TRP	-	expression tag	UNP Q9IK91
B	-18	SER	-	expression tag	UNP Q9IK91
B	-17	HIS	-	expression tag	UNP Q9IK91
B	-16	PRO	-	expression tag	UNP Q9IK91
B	-15	GLN	-	expression tag	UNP Q9IK91
B	-14	PHE	-	expression tag	UNP Q9IK91
B	-13	GLU	-	expression tag	UNP Q9IK91
B	-12	LYS	-	expression tag	UNP Q9IK91
B	-11	GLY	-	expression tag	UNP Q9IK91
B	-10	ALA	-	expression tag	UNP Q9IK91
B	-9	GLU	-	expression tag	UNP Q9IK91
B	-8	ASN	-	expression tag	UNP Q9IK91
B	-7	LEU	-	expression tag	UNP Q9IK91
B	-6	TYR	-	expression tag	UNP Q9IK91
B	-5	PHE	-	expression tag	UNP Q9IK91
B	-4	GLN	-	expression tag	UNP Q9IK91
B	-3	SER	-	expression tag	UNP Q9IK91
B	-2	ASN	-	expression tag	UNP Q9IK91
B	-1	GLY	-	expression tag	UNP Q9IK91
B	0	SER	-	expression tag	UNP Q9IK91
D	-49	MET	-	expression tag	UNP Q9IK91
D	-48	LYS	-	expression tag	UNP Q9IK91
D	-47	SER	-	expression tag	UNP Q9IK91
D	-46	SER	-	expression tag	UNP Q9IK91
D	-45	TRP	-	expression tag	UNP Q9IK91
D	-44	SER	-	expression tag	UNP Q9IK91
D	-43	HIS	-	expression tag	UNP Q9IK91
D	-42	PRO	-	expression tag	UNP Q9IK91
D	-41	GLN	-	expression tag	UNP Q9IK91
D	-40	PHE	-	expression tag	UNP Q9IK91

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-39	GLU	-	expression tag	UNP Q9IK91
D	-38	LYS	-	expression tag	UNP Q9IK91
D	-37	GLY	-	expression tag	UNP Q9IK91
D	-36	ALA	-	expression tag	UNP Q9IK91
D	-35	MET	-	expression tag	UNP Q9IK91
D	-34	THR	-	expression tag	UNP Q9IK91
D	-33	GLY	-	expression tag	UNP Q9IK91
D	-32	TRP	-	expression tag	UNP Q9IK91
D	-31	SER	-	expression tag	UNP Q9IK91
D	-30	HIS	-	expression tag	UNP Q9IK91
D	-29	PRO	-	expression tag	UNP Q9IK91
D	-28	GLN	-	expression tag	UNP Q9IK91
D	-27	PHE	-	expression tag	UNP Q9IK91
D	-26	GLU	-	expression tag	UNP Q9IK91
D	-25	LYS	-	expression tag	UNP Q9IK91
D	-24	GLY	-	expression tag	UNP Q9IK91
D	-23	SER	-	expression tag	UNP Q9IK91
D	-22	SER	-	expression tag	UNP Q9IK91
D	-21	ALA	-	expression tag	UNP Q9IK91
D	-20	SER	-	expression tag	UNP Q9IK91
D	-19	TRP	-	expression tag	UNP Q9IK91
D	-18	SER	-	expression tag	UNP Q9IK91
D	-17	HIS	-	expression tag	UNP Q9IK91
D	-16	PRO	-	expression tag	UNP Q9IK91
D	-15	GLN	-	expression tag	UNP Q9IK91
D	-14	PHE	-	expression tag	UNP Q9IK91
D	-13	GLU	-	expression tag	UNP Q9IK91
D	-12	LYS	-	expression tag	UNP Q9IK91
D	-11	GLY	-	expression tag	UNP Q9IK91
D	-10	ALA	-	expression tag	UNP Q9IK91
D	-9	GLU	-	expression tag	UNP Q9IK91
D	-8	ASN	-	expression tag	UNP Q9IK91
D	-7	LEU	-	expression tag	UNP Q9IK91
D	-6	TYR	-	expression tag	UNP Q9IK91
D	-5	PHE	-	expression tag	UNP Q9IK91
D	-4	GLN	-	expression tag	UNP Q9IK91
D	-3	SER	-	expression tag	UNP Q9IK91
D	-2	ASN	-	expression tag	UNP Q9IK91
D	-1	GLY	-	expression tag	UNP Q9IK91
D	0	SER	-	expression tag	UNP Q9IK91
C	-49	MET	-	expression tag	UNP Q9IK91
C	-48	LYS	-	expression tag	UNP Q9IK91

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-47	SER	-	expression tag	UNP Q9IK91
C	-46	SER	-	expression tag	UNP Q9IK91
C	-45	TRP	-	expression tag	UNP Q9IK91
C	-44	SER	-	expression tag	UNP Q9IK91
C	-43	HIS	-	expression tag	UNP Q9IK91
C	-42	PRO	-	expression tag	UNP Q9IK91
C	-41	GLN	-	expression tag	UNP Q9IK91
C	-40	PHE	-	expression tag	UNP Q9IK91
C	-39	GLU	-	expression tag	UNP Q9IK91
C	-38	LYS	-	expression tag	UNP Q9IK91
C	-37	GLY	-	expression tag	UNP Q9IK91
C	-36	ALA	-	expression tag	UNP Q9IK91
C	-35	MET	-	expression tag	UNP Q9IK91
C	-34	THR	-	expression tag	UNP Q9IK91
C	-33	GLY	-	expression tag	UNP Q9IK91
C	-32	TRP	-	expression tag	UNP Q9IK91
C	-31	SER	-	expression tag	UNP Q9IK91
C	-30	HIS	-	expression tag	UNP Q9IK91
C	-29	PRO	-	expression tag	UNP Q9IK91
C	-28	GLN	-	expression tag	UNP Q9IK91
C	-27	PHE	-	expression tag	UNP Q9IK91
C	-26	GLU	-	expression tag	UNP Q9IK91
C	-25	LYS	-	expression tag	UNP Q9IK91
C	-24	GLY	-	expression tag	UNP Q9IK91
C	-23	SER	-	expression tag	UNP Q9IK91
C	-22	SER	-	expression tag	UNP Q9IK91
C	-21	ALA	-	expression tag	UNP Q9IK91
C	-20	SER	-	expression tag	UNP Q9IK91
C	-19	TRP	-	expression tag	UNP Q9IK91
C	-18	SER	-	expression tag	UNP Q9IK91
C	-17	HIS	-	expression tag	UNP Q9IK91
C	-16	PRO	-	expression tag	UNP Q9IK91
C	-15	GLN	-	expression tag	UNP Q9IK91
C	-14	PHE	-	expression tag	UNP Q9IK91
C	-13	GLU	-	expression tag	UNP Q9IK91
C	-12	LYS	-	expression tag	UNP Q9IK91
C	-11	GLY	-	expression tag	UNP Q9IK91
C	-10	ALA	-	expression tag	UNP Q9IK91
C	-9	GLU	-	expression tag	UNP Q9IK91
C	-8	ASN	-	expression tag	UNP Q9IK91
C	-7	LEU	-	expression tag	UNP Q9IK91
C	-6	TYR	-	expression tag	UNP Q9IK91

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	PHE	-	expression tag	UNP Q9IK91
C	-4	GLN	-	expression tag	UNP Q9IK91
C	-3	SER	-	expression tag	UNP Q9IK91
C	-2	ASN	-	expression tag	UNP Q9IK91
C	-1	GLY	-	expression tag	UNP Q9IK91
C	0	SER	-	expression tag	UNP Q9IK91
E	-49	MET	-	expression tag	UNP Q9IK91
E	-48	LYS	-	expression tag	UNP Q9IK91
E	-47	SER	-	expression tag	UNP Q9IK91
E	-46	SER	-	expression tag	UNP Q9IK91
E	-45	TRP	-	expression tag	UNP Q9IK91
E	-44	SER	-	expression tag	UNP Q9IK91
E	-43	HIS	-	expression tag	UNP Q9IK91
E	-42	PRO	-	expression tag	UNP Q9IK91
E	-41	GLN	-	expression tag	UNP Q9IK91
E	-40	PHE	-	expression tag	UNP Q9IK91
E	-39	GLU	-	expression tag	UNP Q9IK91
E	-38	LYS	-	expression tag	UNP Q9IK91
E	-37	GLY	-	expression tag	UNP Q9IK91
E	-36	ALA	-	expression tag	UNP Q9IK91
E	-35	MET	-	expression tag	UNP Q9IK91
E	-34	THR	-	expression tag	UNP Q9IK91
E	-33	GLY	-	expression tag	UNP Q9IK91
E	-32	TRP	-	expression tag	UNP Q9IK91
E	-31	SER	-	expression tag	UNP Q9IK91
E	-30	HIS	-	expression tag	UNP Q9IK91
E	-29	PRO	-	expression tag	UNP Q9IK91
E	-28	GLN	-	expression tag	UNP Q9IK91
E	-27	PHE	-	expression tag	UNP Q9IK91
E	-26	GLU	-	expression tag	UNP Q9IK91
E	-25	LYS	-	expression tag	UNP Q9IK91
E	-24	GLY	-	expression tag	UNP Q9IK91
E	-23	SER	-	expression tag	UNP Q9IK91
E	-22	SER	-	expression tag	UNP Q9IK91
E	-21	ALA	-	expression tag	UNP Q9IK91
E	-20	SER	-	expression tag	UNP Q9IK91
E	-19	TRP	-	expression tag	UNP Q9IK91
E	-18	SER	-	expression tag	UNP Q9IK91
E	-17	HIS	-	expression tag	UNP Q9IK91
E	-16	PRO	-	expression tag	UNP Q9IK91
E	-15	GLN	-	expression tag	UNP Q9IK91
E	-14	PHE	-	expression tag	UNP Q9IK91

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-13	GLU	-	expression tag	UNP Q9IK91
E	-12	LYS	-	expression tag	UNP Q9IK91
E	-11	GLY	-	expression tag	UNP Q9IK91
E	-10	ALA	-	expression tag	UNP Q9IK91
E	-9	GLU	-	expression tag	UNP Q9IK91
E	-8	ASN	-	expression tag	UNP Q9IK91
E	-7	LEU	-	expression tag	UNP Q9IK91
E	-6	TYR	-	expression tag	UNP Q9IK91
E	-5	PHE	-	expression tag	UNP Q9IK91
E	-4	GLN	-	expression tag	UNP Q9IK91
E	-3	SER	-	expression tag	UNP Q9IK91
E	-2	ASN	-	expression tag	UNP Q9IK91
E	-1	GLY	-	expression tag	UNP Q9IK91
E	0	SER	-	expression tag	UNP Q9IK91
F	-49	MET	-	expression tag	UNP Q9IK91
F	-48	LYS	-	expression tag	UNP Q9IK91
F	-47	SER	-	expression tag	UNP Q9IK91
F	-46	SER	-	expression tag	UNP Q9IK91
F	-45	TRP	-	expression tag	UNP Q9IK91
F	-44	SER	-	expression tag	UNP Q9IK91
F	-43	HIS	-	expression tag	UNP Q9IK91
F	-42	PRO	-	expression tag	UNP Q9IK91
F	-41	GLN	-	expression tag	UNP Q9IK91
F	-40	PHE	-	expression tag	UNP Q9IK91
F	-39	GLU	-	expression tag	UNP Q9IK91
F	-38	LYS	-	expression tag	UNP Q9IK91
F	-37	GLY	-	expression tag	UNP Q9IK91
F	-36	ALA	-	expression tag	UNP Q9IK91
F	-35	MET	-	expression tag	UNP Q9IK91
F	-34	THR	-	expression tag	UNP Q9IK91
F	-33	GLY	-	expression tag	UNP Q9IK91
F	-32	TRP	-	expression tag	UNP Q9IK91
F	-31	SER	-	expression tag	UNP Q9IK91
F	-30	HIS	-	expression tag	UNP Q9IK91
F	-29	PRO	-	expression tag	UNP Q9IK91
F	-28	GLN	-	expression tag	UNP Q9IK91
F	-27	PHE	-	expression tag	UNP Q9IK91
F	-26	GLU	-	expression tag	UNP Q9IK91
F	-25	LYS	-	expression tag	UNP Q9IK91
F	-24	GLY	-	expression tag	UNP Q9IK91
F	-23	SER	-	expression tag	UNP Q9IK91
F	-22	SER	-	expression tag	UNP Q9IK91

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-21	ALA	-	expression tag	UNP Q9IK91
F	-20	SER	-	expression tag	UNP Q9IK91
F	-19	TRP	-	expression tag	UNP Q9IK91
F	-18	SER	-	expression tag	UNP Q9IK91
F	-17	HIS	-	expression tag	UNP Q9IK91
F	-16	PRO	-	expression tag	UNP Q9IK91
F	-15	GLN	-	expression tag	UNP Q9IK91
F	-14	PHE	-	expression tag	UNP Q9IK91
F	-13	GLU	-	expression tag	UNP Q9IK91
F	-12	LYS	-	expression tag	UNP Q9IK91
F	-11	GLY	-	expression tag	UNP Q9IK91
F	-10	ALA	-	expression tag	UNP Q9IK91
F	-9	GLU	-	expression tag	UNP Q9IK91
F	-8	ASN	-	expression tag	UNP Q9IK91
F	-7	LEU	-	expression tag	UNP Q9IK91
F	-6	TYR	-	expression tag	UNP Q9IK91
F	-5	PHE	-	expression tag	UNP Q9IK91
F	-4	GLN	-	expression tag	UNP Q9IK91
F	-3	SER	-	expression tag	UNP Q9IK91
F	-2	ASN	-	expression tag	UNP Q9IK91
F	-1	GLY	-	expression tag	UNP Q9IK91
F	0	SER	-	expression tag	UNP Q9IK91
G	-49	MET	-	expression tag	UNP Q9IK91
G	-48	LYS	-	expression tag	UNP Q9IK91
G	-47	SER	-	expression tag	UNP Q9IK91
G	-46	SER	-	expression tag	UNP Q9IK91
G	-45	TRP	-	expression tag	UNP Q9IK91
G	-44	SER	-	expression tag	UNP Q9IK91
G	-43	HIS	-	expression tag	UNP Q9IK91
G	-42	PRO	-	expression tag	UNP Q9IK91
G	-41	GLN	-	expression tag	UNP Q9IK91
G	-40	PHE	-	expression tag	UNP Q9IK91
G	-39	GLU	-	expression tag	UNP Q9IK91
G	-38	LYS	-	expression tag	UNP Q9IK91
G	-37	GLY	-	expression tag	UNP Q9IK91
G	-36	ALA	-	expression tag	UNP Q9IK91
G	-35	MET	-	expression tag	UNP Q9IK91
G	-34	THR	-	expression tag	UNP Q9IK91
G	-33	GLY	-	expression tag	UNP Q9IK91
G	-32	TRP	-	expression tag	UNP Q9IK91
G	-31	SER	-	expression tag	UNP Q9IK91
G	-30	HIS	-	expression tag	UNP Q9IK91

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-29	PRO	-	expression tag	UNP Q9IK91
G	-28	GLN	-	expression tag	UNP Q9IK91
G	-27	PHE	-	expression tag	UNP Q9IK91
G	-26	GLU	-	expression tag	UNP Q9IK91
G	-25	LYS	-	expression tag	UNP Q9IK91
G	-24	GLY	-	expression tag	UNP Q9IK91
G	-23	SER	-	expression tag	UNP Q9IK91
G	-22	SER	-	expression tag	UNP Q9IK91
G	-21	ALA	-	expression tag	UNP Q9IK91
G	-20	SER	-	expression tag	UNP Q9IK91
G	-19	TRP	-	expression tag	UNP Q9IK91
G	-18	SER	-	expression tag	UNP Q9IK91
G	-17	HIS	-	expression tag	UNP Q9IK91
G	-16	PRO	-	expression tag	UNP Q9IK91
G	-15	GLN	-	expression tag	UNP Q9IK91
G	-14	PHE	-	expression tag	UNP Q9IK91
G	-13	GLU	-	expression tag	UNP Q9IK91
G	-12	LYS	-	expression tag	UNP Q9IK91
G	-11	GLY	-	expression tag	UNP Q9IK91
G	-10	ALA	-	expression tag	UNP Q9IK91
G	-9	GLU	-	expression tag	UNP Q9IK91
G	-8	ASN	-	expression tag	UNP Q9IK91
G	-7	LEU	-	expression tag	UNP Q9IK91
G	-6	TYR	-	expression tag	UNP Q9IK91
G	-5	PHE	-	expression tag	UNP Q9IK91
G	-4	GLN	-	expression tag	UNP Q9IK91
G	-3	SER	-	expression tag	UNP Q9IK91
G	-2	ASN	-	expression tag	UNP Q9IK91
G	-1	GLY	-	expression tag	UNP Q9IK91
G	0	SER	-	expression tag	UNP Q9IK91

- Molecule 2 is a protein called RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1241	Total	C	N	O	S	0	0
			9976	6360	1704	1845	67		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-25	MET	-	expression tag	UNP Q997F0
A	-24	LYS	-	expression tag	UNP Q997F0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	SER	-	expression tag	UNP Q997F0
A	-22	SER	-	expression tag	UNP Q997F0
A	-21	HIS	-	expression tag	UNP Q997F0
A	-20	HIS	-	expression tag	UNP Q997F0
A	-19	HIS	-	expression tag	UNP Q997F0
A	-18	HIS	-	expression tag	UNP Q997F0
A	-17	HIS	-	expression tag	UNP Q997F0
A	-16	HIS	-	expression tag	UNP Q997F0
A	-15	HIS	-	expression tag	UNP Q997F0
A	-14	HIS	-	expression tag	UNP Q997F0
A	-13	HIS	-	expression tag	UNP Q997F0
A	-12	HIS	-	expression tag	UNP Q997F0
A	-11	GLY	-	expression tag	UNP Q997F0
A	-10	SER	-	expression tag	UNP Q997F0
A	-9	SER	-	expression tag	UNP Q997F0
A	-8	GLU	-	expression tag	UNP Q997F0
A	-7	ASN	-	expression tag	UNP Q997F0
A	-6	LEU	-	expression tag	UNP Q997F0
A	-5	TYR	-	expression tag	UNP Q997F0
A	-4	PHE	-	expression tag	UNP Q997F0
A	-3	GLN	-	expression tag	UNP Q997F0
A	-2	SER	-	expression tag	UNP Q997F0
A	-1	GLY	-	expression tag	UNP Q997F0
A	0	SER	-	expression tag	UNP Q997F0























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



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	258905	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.546	Depositor
Minimum map value	-2.199	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.405	Depositor
Map size ( $\text{\AA}$ )	388.32, 388.32, 388.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.809, 0.809, 0.809	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	B	0.11	0/373	0.26	0/500
1	C	0.11	0/455	0.24	0/605
1	D	0.11	0/383	0.21	0/515
1	E	0.10	0/320	0.23	0/429
1	F	0.07	0/137	0.25	0/183
1	G	0.14	0/578	0.46	0/782
2	A	0.10	0/10177	0.26	0/13752
All	All	0.10	0/12423	0.27	0/16766

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	B	370	0	400	17	0
1	C	452	0	494	13	0
1	D	380	0	411	7	0
1	E	319	0	350	13	0
1	F	136	0	144	12	0
1	G	573	0	559	21	0
2	A	9976	0	9994	159	0
All	All	12206	0	12352	213	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 9.

All (213) 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:G:637:LEU:HD13	1:G:639:LEU:HG	1.67	0.77
2:A:1249:PHE:HB2	2:A:1420:TYR:HB3	1.72	0.71
2:A:121:ILE:HG21	2:A:987:ILE:HG21	1.72	0.70
2:A:909:MET:HE1	2:A:934:ILE:HD13	1.73	0.70
1:B:579:PRO:HG2	1:F:602:ILE:HD11	1.74	0.70
2:A:7:ILE:HG13	2:A:9:ASP:H	1.57	0.70
2:A:1421:HIS:HB3	2:A:1423:HIS:HE1	1.58	0.68
1:G:651:GLN:HG3	1:G:652:PHE:H	1.59	0.67
2:A:26:LEU:HD22	2:A:234:MET:HE1	1.75	0.66
2:A:983:LEU:O	2:A:987:ILE:HD12	1.95	0.66
2:A:316:ILE:HD11	2:A:342:LEU:HD11	1.78	0.66
2:A:1243:ASN:ND2	2:A:1424:VAL:O	2.27	0.65
2:A:299:GLN:NE2	2:A:307:LEU:O	2.31	0.64
2:A:755:MET:HE1	2:A:801:TYR:HB3	1.79	0.64
2:A:1391:ILE:HB	2:A:1394:GLN:HB2	1.79	0.64
2:A:305:ARG:NH2	1:G:699:ASN:OD1	2.32	0.63
2:A:1421:HIS:HB3	2:A:1423:HIS:CE1	2.34	0.63
2:A:741:ARG:NE	2:A:744:GLU:OE2	2.27	0.62
2:A:1223:GLU:O	2:A:1425:LYS:NZ	2.31	0.62
2:A:584:MET:HE1	2:A:827:ALA:HB3	1.82	0.62
2:A:103:MET:HE3	2:A:203:ASP:HB2	1.80	0.61
2:A:468:SER:HA	2:A:471:MET:HG3	1.82	0.61
2:A:1068:ILE:HG12	2:A:1162:LEU:HA	1.83	0.61
1:F:608:LEU:H	1:F:608:LEU:HD23	1.64	0.61
2:A:1414:ASP:OD2	2:A:1414:ASP:N	2.34	0.61
2:A:1290:PRO:HA	2:A:1294:LEU:HB3	1.83	0.60
1:G:690:ASN:HD21	1:G:692:GLU:HB2	1.67	0.60
2:A:719:LEU:HD11	2:A:863:PHE:HB2	1.85	0.59
2:A:1112:ARG:NH1	2:A:1438:GLN:O	2.35	0.58
2:A:244:GLY:O	2:A:248:MET:HG3	2.04	0.58
2:A:190:PRO:HA	2:A:193:ARG:HH12	1.68	0.58
2:A:993:PRO:HD2	2:A:996:ILE:HD11	1.84	0.58
2:A:987:ILE:HG23	2:A:991:LEU:HD13	1.85	0.58
1:B:557:LEU:HG	1:E:557:LEU:HD21	1.84	0.58
2:A:924:ARG:NH1	2:A:998:GLY:O	2.36	0.57
1:G:638:ILE:HG13	1:G:640:PRO:HD3	1.86	0.57
2:A:17:LEU:HD22	2:A:237:MET:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:431:LEU:HD22	2:A:436:GLU:HB3	1.85	0.57
1:B:550:LEU:HD11	1:C:550:LEU:HD22	1.86	0.57
2:A:878:LYS:HA	2:A:878:LYS:HE2	1.87	0.57
1:F:610:SER:HB3	1:G:638:ILE:HG22	1.87	0.57
2:A:1064:ASP:O	2:A:1169:GLN:NE2	2.36	0.56
2:A:842:VAL:HG21	2:A:851:LYS:HG2	1.86	0.56
1:C:583:LYS:NZ	2:A:744:GLU:OE1	2.39	0.56
2:A:973:LEU:O	2:A:977:SER:OG	2.23	0.56
1:D:532:ARG:HH11	1:C:533:LEU:HB3	1.71	0.55
2:A:1192:SER:OG	2:A:1223:GLU:OE1	2.24	0.55
2:A:1364:ASN:OD1	2:A:1367:SER:OG	2.24	0.55
2:A:36:ARG:NH2	2:A:81:LYS:O	2.40	0.55
2:A:867:ARG:HH22	1:G:644:PHE:HB2	1.72	0.55
2:A:719:LEU:HG	2:A:884:ILE:HG12	1.90	0.54
2:A:275:LEU:O	2:A:279:MET:HB2	2.08	0.53
2:A:1092:LEU:H	2:A:1092:LEU:HD23	1.73	0.53
2:A:1020:LEU:HD13	2:A:1195:LEU:HB3	1.90	0.53
2:A:384:ASP:N	2:A:384:ASP:OD1	2.39	0.53
1:G:687:LYS:HG3	1:G:688:ALA:H	1.74	0.53
2:A:22:VAL:HG12	2:A:24:GLY:H	1.74	0.53
2:A:1071:THR:O	2:A:1075:ILE:HG23	2.07	0.53
2:A:1157:LYS:O	2:A:1161:ARG:NH2	2.42	0.53
2:A:32:TYR:OH	2:A:490:GLU:O	2.26	0.52
2:A:1392:TYR:O	2:A:1396:MET:HG2	2.10	0.52
2:A:154:LEU:HD21	2:A:946:VAL:HA	1.91	0.52
2:A:758:ARG:O	2:A:758:ARG:NH1	2.42	0.52
2:A:909:MET:HE3	2:A:942:LEU:HD22	1.91	0.52
1:B:567:ILE:HD13	1:E:567:ILE:HG22	1.92	0.52
2:A:1067:SER:O	2:A:1071:THR:HG23	2.09	0.52
2:A:1380:ARG:NH1	2:A:1384:GLU:O	2.43	0.52
1:E:575:MET:HE2	1:F:596:PRO:HG3	1.92	0.52
1:F:610:SER:O	1:G:636:ASP:N	2.43	0.52
1:D:564:LEU:HD23	1:E:563:ALA:HB3	1.92	0.51
2:A:1005:SER:HB2	2:A:1012:ILE:HD12	1.91	0.51
1:E:574:MET:HG3	1:F:596:PRO:HB3	1.92	0.51
1:B:551:GLU:OE2	1:C:549:LYS:NZ	2.34	0.51
2:A:908:SER:HB2	2:A:937:ALA:HB2	1.93	0.51
2:A:827:ALA:HB2	2:A:836:ILE:HG23	1.92	0.51
2:A:898:ASP:O	2:A:1368:ARG:NH1	2.44	0.51
1:C:572:VAL:O	1:C:576:ILE:HG23	2.11	0.51
2:A:509:PHE:O	2:A:1086:ASN:ND2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:545:LYS:HA	1:E:548:ASN:HD21	1.76	0.50
2:A:487:TYR:HB2	2:A:492:LEU:HD11	1.91	0.50
2:A:286:ILE:HD12	2:A:319:MET:HE3	1.93	0.50
2:A:1112:ARG:HG3	2:A:1439:VAL:HG12	1.94	0.50
2:A:261:LEU:HD13	2:A:352:LEU:HD22	1.93	0.50
2:A:138:THR:HG23	2:A:1229:TYR:H	1.77	0.49
2:A:484:ASP:OD2	2:A:778:HIS:ND1	2.36	0.49
2:A:1246:TYR:HB3	2:A:1423:HIS:CG	2.46	0.49
1:C:545:LYS:HA	1:C:548:ASN:ND2	2.27	0.49
2:A:1294:LEU:O	2:A:1298:ILE:HG13	2.12	0.49
1:D:541:LYS:HA	1:E:539:GLN:HE22	1.77	0.49
1:B:561:ASN:OD1	1:C:560:THR:OG1	2.21	0.49
1:B:563:ALA:O	1:B:567:ILE:HG13	2.13	0.49
1:B:578:ILE:HD11	2:A:387:LEU:HD11	1.95	0.48
2:A:561:ARG:NH1	2:A:564:GLN:OE1	2.46	0.48
2:A:1246:TYR:HB3	2:A:1423:HIS:CD2	2.47	0.48
2:A:498:LYS:NZ	2:A:499:SER:O	2.39	0.48
2:A:68:LYS:HD2	2:A:196:SER:HB3	1.96	0.48
2:A:742:LEU:HD11	2:A:808:ILE:HD11	1.96	0.48
2:A:331:GLN:OE1	2:A:335:SER:OG	2.32	0.48
2:A:342:LEU:O	2:A:346:ASN:HB2	2.13	0.48
2:A:1041:MET:HE2	2:A:1186:ILE:HG12	1.96	0.48
1:G:640:PRO:HD2	1:G:641:GLU:OE2	2.13	0.48
2:A:146:ILE:HG23	2:A:256:ILE:HD12	1.94	0.47
1:B:551:GLU:O	1:B:555:ARG:HG3	2.14	0.47
2:A:250:THR:O	2:A:254:SER:OG	2.30	0.47
2:A:258:TYR:HA	2:A:352:LEU:HD21	1.96	0.47
2:A:938:ILE:HA	2:A:942:LEU:HB3	1.96	0.47
2:A:1228:ARG:HE	2:A:1237:GLN:HG2	1.80	0.47
2:A:1319:TRP:CG	2:A:1330:LEU:HG	2.49	0.47
1:G:687:LYS:HG3	1:G:688:ALA:N	2.29	0.47
2:A:755:MET:HE3	2:A:755:MET:HB2	1.81	0.47
1:B:550:LEU:HD22	1:E:550:LEU:HD11	1.97	0.47
2:A:106:LYS:NZ	2:A:964:GLU:O	2.42	0.47
2:A:489:ARG:NH1	2:A:492:LEU:O	2.48	0.47
2:A:88:TYR:OH	2:A:237:MET:SD	2.63	0.46
1:F:594:LEU:HD23	1:F:594:LEU:HA	1.82	0.46
1:B:538:GLU:HA	1:B:541:LYS:HD2	1.97	0.46
1:D:578:ILE:HD13	1:E:576:ILE:HG23	1.97	0.46
2:A:973:LEU:HD13	2:A:977:SER:OG	2.16	0.46
2:A:1230:ILE:HG13	2:A:1419:ILE:HB	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:668:ILE:HD13	1:G:681:LEU:HB3	1.98	0.46
1:G:651:GLN:C	1:G:653:VAL:H	2.24	0.46
2:A:161:MET:HE2	2:A:957:GLN:HE22	1.80	0.46
2:A:1248:TRP:CE3	2:A:1373:SER:HB3	2.50	0.45
1:E:545:LYS:HA	1:E:548:ASN:ND2	2.32	0.45
1:B:574:MET:HG3	1:B:575:MET:N	2.31	0.45
2:A:117:ALA:HB2	2:A:983:LEU:HD22	1.99	0.45
2:A:416:PRO:O	2:A:418:LEU:N	2.48	0.45
2:A:546:THR:OG1	2:A:551:ARG:NH1	2.50	0.45
2:A:346:ASN:ND2	1:G:670:THR:OG1	2.38	0.45
1:G:656:ALA:N	1:G:691:ASP:OD1	2.42	0.45
1:G:672:ILE:O	1:G:678:ARG:NH1	2.49	0.45
1:D:549:LYS:HB3	1:C:550:LEU:HD12	1.98	0.45
2:A:1327:ASN:C	2:A:1328:ILE:HD12	2.42	0.45
2:A:537:VAL:HG13	2:A:764:ILE:HG12	1.99	0.45
1:G:681:LEU:HD22	1:G:701:VAL:HG12	1.99	0.44
2:A:878:LYS:O	2:A:882:THR:OG1	2.34	0.44
2:A:1253:ARG:HH11	2:A:1253:ARG:HG3	1.81	0.44
2:A:1076:THR:O	2:A:1080:ILE:HG12	2.18	0.44
2:A:1364:ASN:ND2	2:A:1368:ARG:HB3	2.33	0.44
2:A:543:GLU:OE1	2:A:544:LYS:NZ	2.51	0.44
2:A:1311:ASN:O	2:A:1315:TRP:HB2	2.18	0.44
2:A:191:LYS:HE3	2:A:191:LYS:HB3	1.80	0.44
2:A:730:TRP:CE3	2:A:735:MET:HG2	2.53	0.44
2:A:993:PRO:HB2	2:A:1019:SER:HB3	2.00	0.44
2:A:1234:LEU:H	2:A:1234:LEU:HD23	1.83	0.44
2:A:193:ARG:HB2	2:A:193:ARG:NH1	2.33	0.43
2:A:1253:ARG:HD3	2:A:1417:ASN:OD1	2.17	0.43
2:A:211:ASN:C	2:A:211:ASN:OD1	2.61	0.43
1:G:665:LYS:HB2	1:G:665:LYS:HE3	1.80	0.43
1:C:571:LEU:O	1:C:575:MET:HG3	2.18	0.43
2:A:361:ARG:HH21	2:A:544:LYS:HE2	1.83	0.43
2:A:1041:MET:HA	2:A:1199:LEU:HD13	2.01	0.43
2:A:1432:GLU:OE1	2:A:1434:ALA:N	2.51	0.43
1:B:552:SER:O	1:B:556:VAL:HG23	2.19	0.43
2:A:891:TYR:HB3	2:A:896:HIS:CD2	2.54	0.43
2:A:1248:TRP:HE3	2:A:1373:SER:HB3	1.84	0.43
2:A:44:LYS:HB2	2:A:44:LYS:HE2	1.65	0.43
2:A:858:GLN:NE2	2:A:858:GLN:HA	2.32	0.43
2:A:107:LEU:HG	2:A:171:LEU:HD22	2.00	0.42
2:A:336:MET:HE3	2:A:336:MET:HB3	1.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:945:ASN:OD1	2:A:945:ASN:N	2.52	0.42
2:A:931:SER:HB3	2:A:1002:LEU:HB2	2.00	0.42
2:A:299:GLN:HE22	2:A:310:ALA:HB3	1.85	0.42
1:F:610:SER:N	1:G:636:ASP:O	2.27	0.42
2:A:758:ARG:HA	2:A:758:ARG:HH11	1.84	0.42
2:A:892:SER:O	2:A:892:SER:OG	2.34	0.42
1:D:579:PRO:HG3	1:F:606:GLN:HG3	2.02	0.42
2:A:823:THR:HG21	2:A:862:TYR:HB2	2.02	0.42
2:A:470:TYR:OH	2:A:517:PRO:HB3	2.20	0.42
2:A:211:ASN:OD1	2:A:213:ASN:N	2.49	0.42
2:A:1045:PRO:HB3	2:A:1203:MET:HA	2.02	0.42
2:A:1377:LEU:HD23	2:A:1377:LEU:HA	1.86	0.42
1:E:577:MET:HA	1:F:594:LEU:HB2	2.01	0.42
1:G:668:ILE:HD11	1:G:701:VAL:HG11	2.02	0.42
2:A:293:LEU:HD23	2:A:293:LEU:HA	1.90	0.42
2:A:406:GLY:C	2:A:408:ARG:H	2.28	0.42
1:D:564:LEU:HD21	1:E:564:LEU:HG	2.01	0.42
2:A:944:ARG:HB3	2:A:1007:ILE:HD12	2.02	0.42
2:A:282:ARG:NH2	2:A:322:GLU:OE2	2.43	0.41
2:A:410:ARG:HE	2:A:410:ARG:HB3	1.67	0.41
1:B:543:ILE:HG21	1:C:542:GLU:HB2	2.01	0.41
1:G:651:GLN:HB3	1:G:653:VAL:HG13	2.01	0.41
1:C:538:GLU:HA	1:C:541:LYS:HD3	2.02	0.41
2:A:1225:MET:SD	2:A:1424:VAL:HG12	2.60	0.41
2:A:559:LYS:HB2	2:A:559:LYS:HE3	1.88	0.41
2:A:100:SER:OG	2:A:203:ASP:OD2	2.37	0.41
2:A:172:PHE:O	2:A:176:ILE:HG12	2.20	0.41
2:A:960:LEU:HD23	2:A:960:LEU:HA	1.88	0.41
1:C:575:MET:HE2	1:C:575:MET:HB3	1.94	0.41
2:A:303:GLU:HB3	2:A:852:LYS:HG3	2.03	0.41
2:A:1025:ARG:HE	2:A:1025:ARG:HB2	1.74	0.41
2:A:976:THR:O	2:A:980:SER:OG	2.33	0.41
2:A:264:ARG:NH2	2:A:346:ASN:O	2.53	0.41
2:A:1253:ARG:HG3	2:A:1253:ARG:NH1	2.36	0.41
1:B:539:GLN:NE2	1:E:543:ILE:HB	2.35	0.41
1:B:580:GLY:O	1:B:581:LYS:HD3	2.21	0.41
2:A:582:ASN:OD1	2:A:582:ASN:N	2.53	0.41
2:A:784:THR:O	2:A:792:HIS:NE2	2.54	0.41
2:A:971:LEU:HD23	2:A:971:LEU:HA	1.85	0.41
2:A:1116:PRO:HG2	2:A:1216:LEU:HD11	2.02	0.41
2:A:383:ALA:O	2:A:731:ARG:NH2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1334:LYS:HE2	2:A:1334:LYS:HB2	1.80	0.41
2:A:870:LEU:HD12	2:A:877:LEU:HD13	2.02	0.40
2:A:1214:TYR:CE2	2:A:1436:VAL:HB	2.56	0.40
2:A:1124:ASP:O	2:A:1129:GLY:HA3	2.21	0.40
1:F:601:ASP:OD1	1:F:601:ASP:N	2.46	0.40
1:B:574:MET:SD	1:F:596:PRO:HB2	2.60	0.40
2:A:204:LYS:HD3	2:A:204:LYS:HA	1.92	0.40
2:A:332:LYS:O	2:A:336:MET:HG3	2.22	0.40
2:A:373:ALA:HB1	2:A:552:LEU:HD21	2.03	0.40
2:A:1191:CYS:SG	2:A:1192:SER:N	2.95	0.40
1:C:576:ILE:HD12	2:A:740:GLU:HG2	2.04	0.40
2:A:561:ARG:HA	2:A:561:ARG:HD3	1.83	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	B	46/759 (6%)	45 (98%)	1 (2%)	0	100	100
1	C	56/759 (7%)	55 (98%)	1 (2%)	0	100	100
1	D	46/759 (6%)	44 (96%)	2 (4%)	0	100	100
1	E	39/759 (5%)	39 (100%)	0	0	100	100
1	F	15/759 (2%)	14 (93%)	1 (7%)	0	100	100
1	G	69/759 (9%)	56 (81%)	13 (19%)	0	100	100
2	A	1223/2270 (54%)	1195 (98%)	28 (2%)	0	100	100
All	All	1494/6824 (22%)	1448 (97%)	46 (3%)	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	B	43/667 (6%)	43 (100%)	0	100	100
1	C	51/667 (8%)	50 (98%)	1 (2%)	50	78
1	D	45/667 (7%)	45 (100%)	0	100	100
1	E	38/667 (6%)	37 (97%)	1 (3%)	41	72
1	F	16/667 (2%)	16 (100%)	0	100	100
1	G	66/667 (10%)	66 (100%)	0	100	100
2	A	1109/2070 (54%)	1102 (99%)	7 (1%)	84	94
All	All	1368/6072 (22%)	1359 (99%)	9 (1%)	80	93

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	571	LEU
2	A	179	GLU
2	A	261	LEU
2	A	306	ILE
2	A	557	THR
2	A	853	GLU
2	A	1186	ILE
2	A	1372	ILE
1	E	578	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	55	HIS
2	A	130	GLN
2	A	1042	ASN
2	A	1086	ASN
2	A	1125	ASN
1	E	539	GLN

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Mol	Chain	Res	Type
1	G	643	ASN
1	G	690	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 oligosaccharides 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.



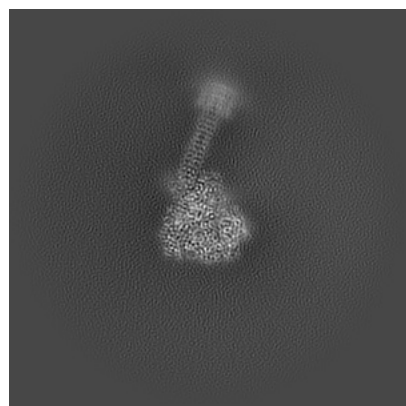
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45782. These allow visual inspection of the internal detail of the map and identification of artifacts.

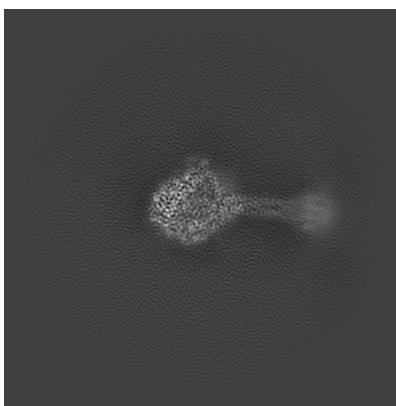
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

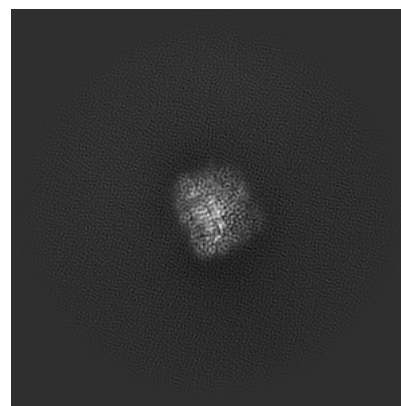
#### 6.1.1 Primary map



X

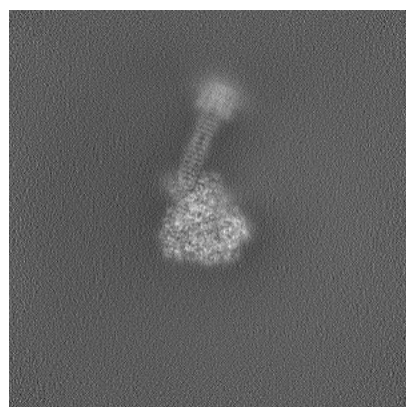


Y

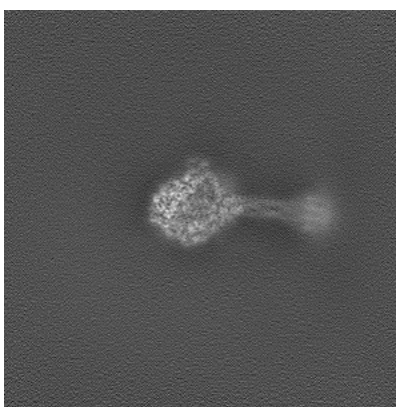


Z

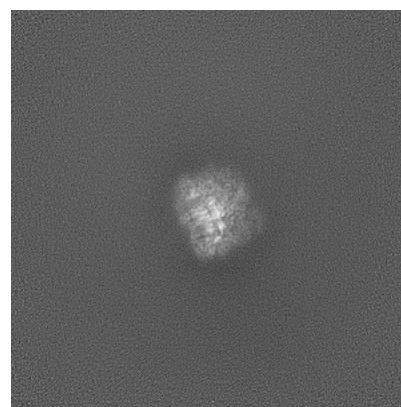
#### 6.1.2 Raw map



X



Y



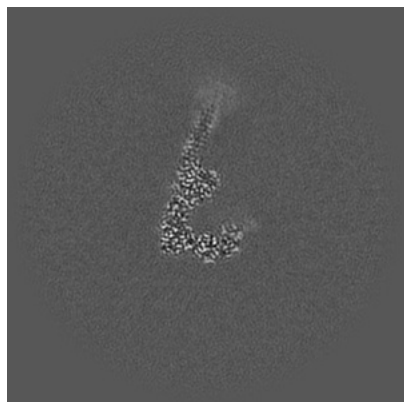
Z

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

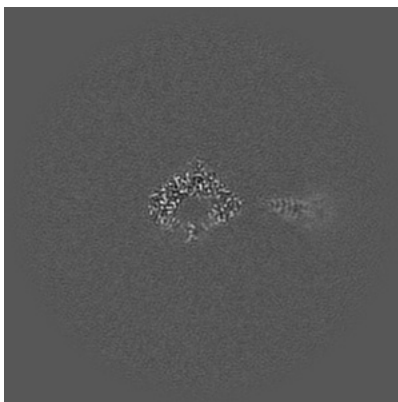


## 6.2 Central slices [i](#)

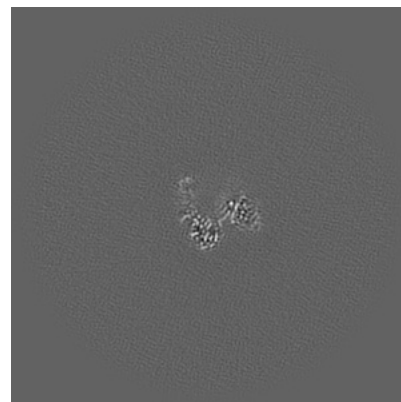
### 6.2.1 Primary map



X Index: 240

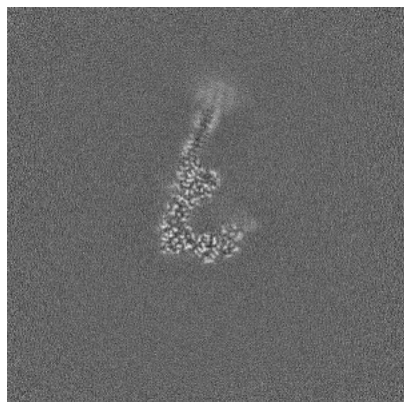


Y Index: 240

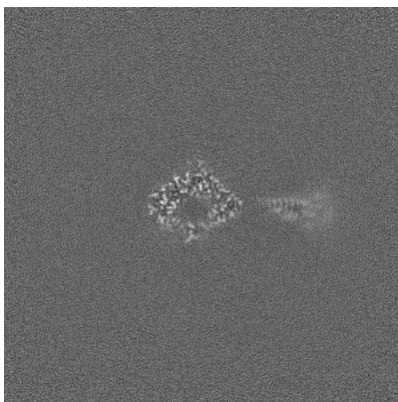


Z Index: 240

### 6.2.2 Raw map



X Index: 240



Y Index: 240



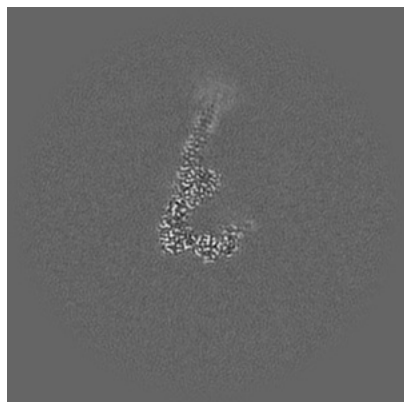
Z Index: 240

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

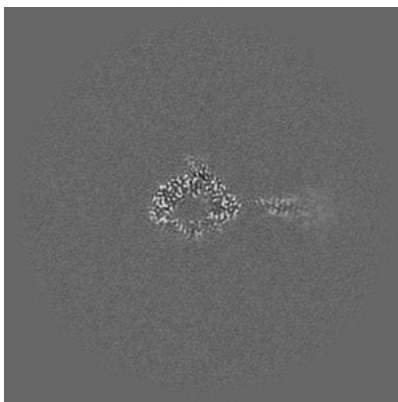


## 6.3 Largest variance slices [i](#)

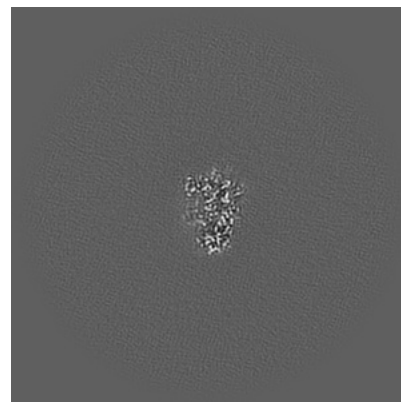
### 6.3.1 Primary map



X Index: 239

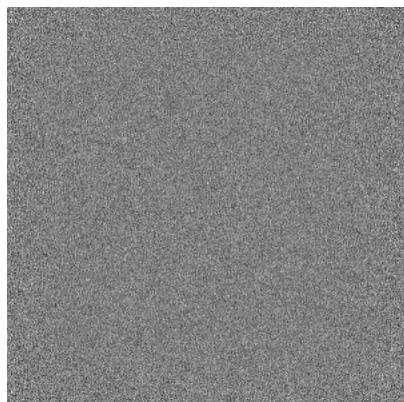


Y Index: 236

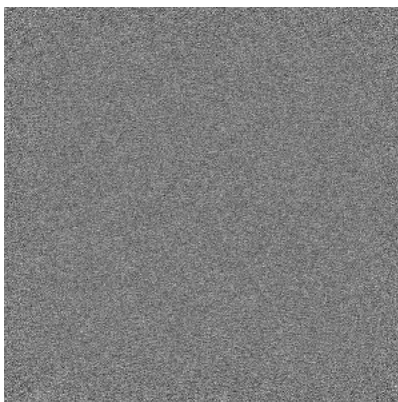


Z Index: 201

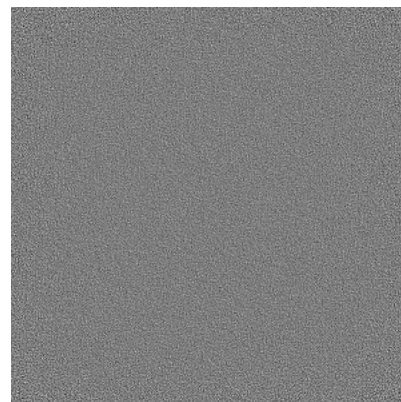
### 6.3.2 Raw map



X Index: 0



Y Index: 0



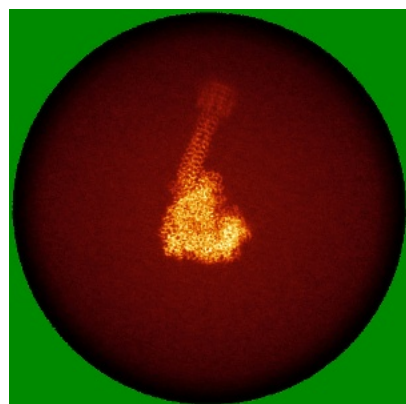
Z Index: 0

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

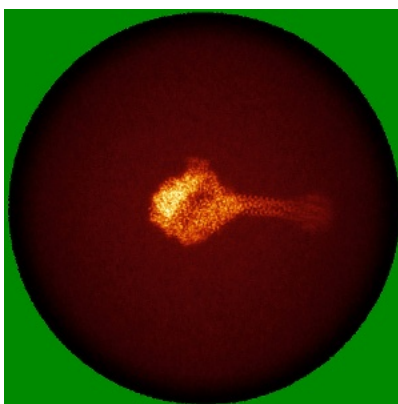


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

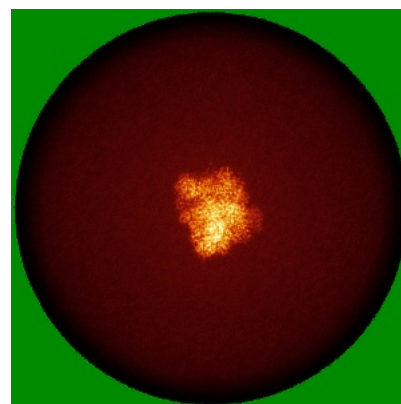
### 6.4.1 Primary map



X

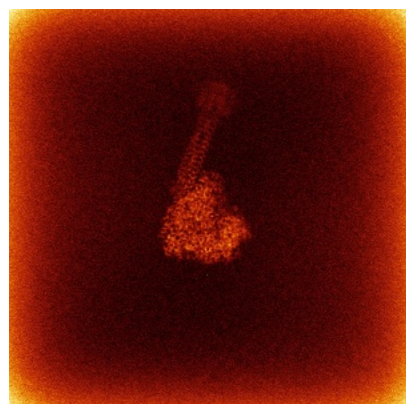


Y

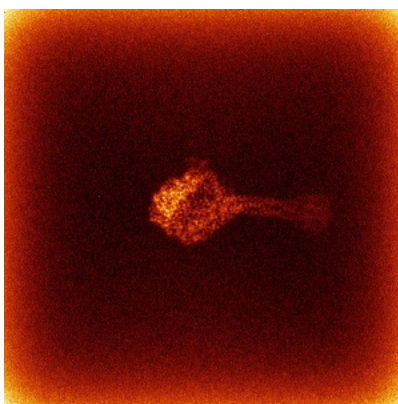


Z

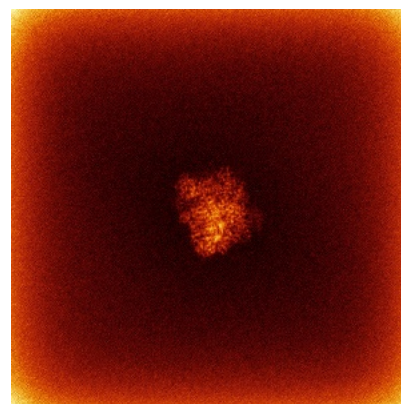
### 6.4.2 Raw map



X



Y



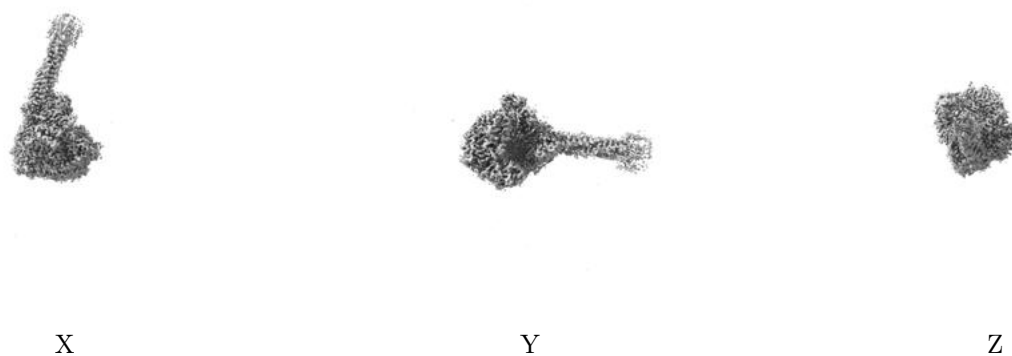
Z

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.



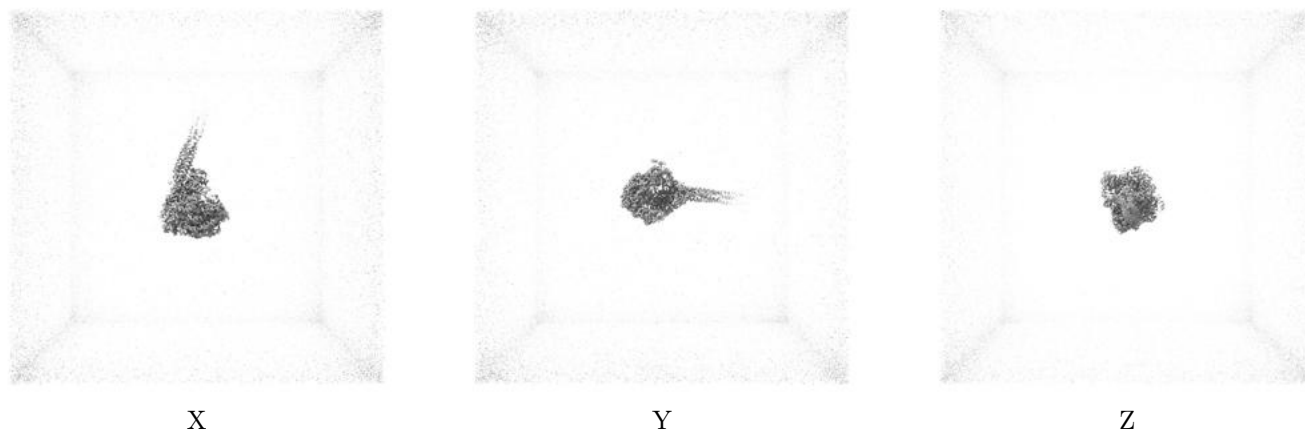
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.405. 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



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](#)

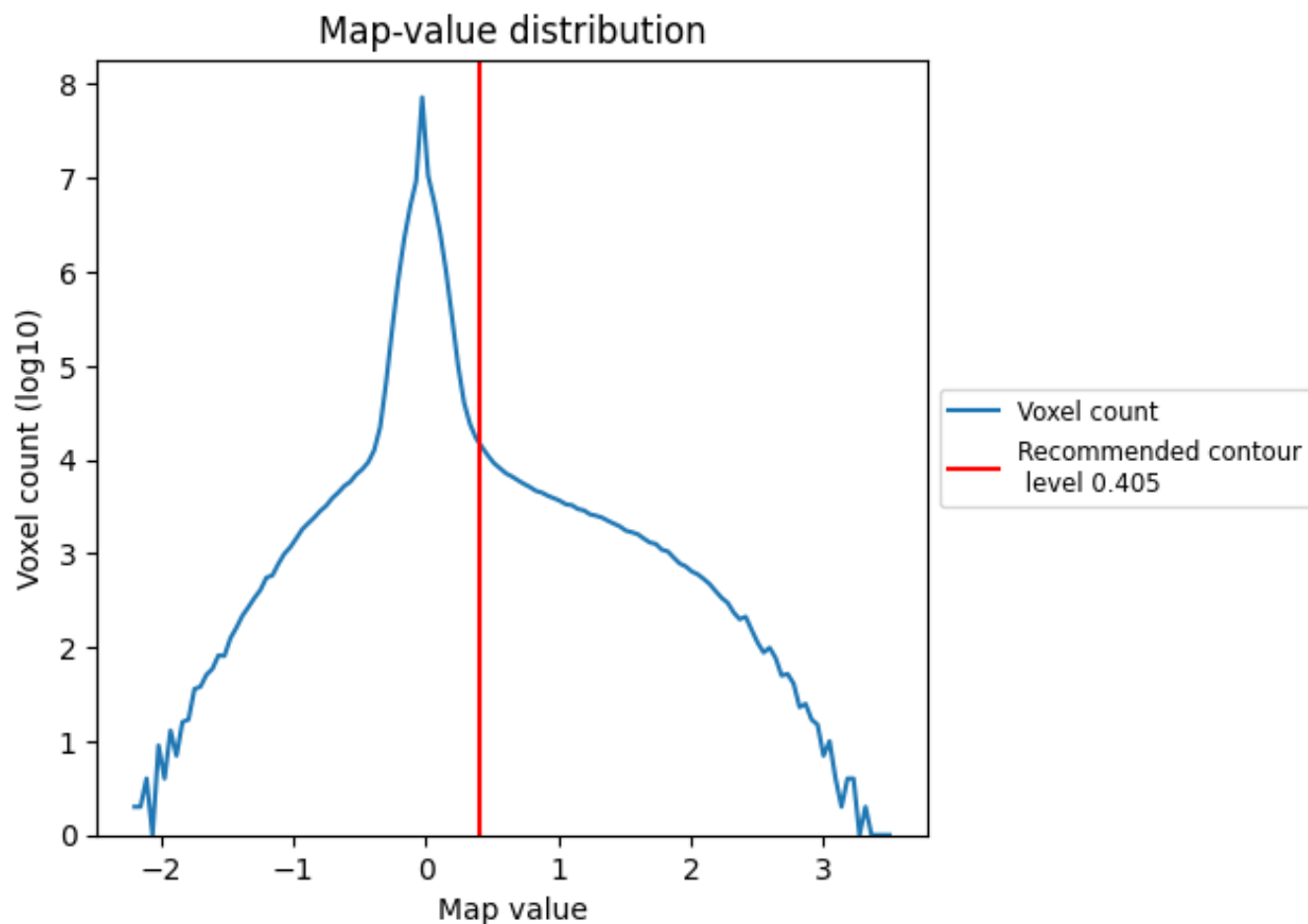
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

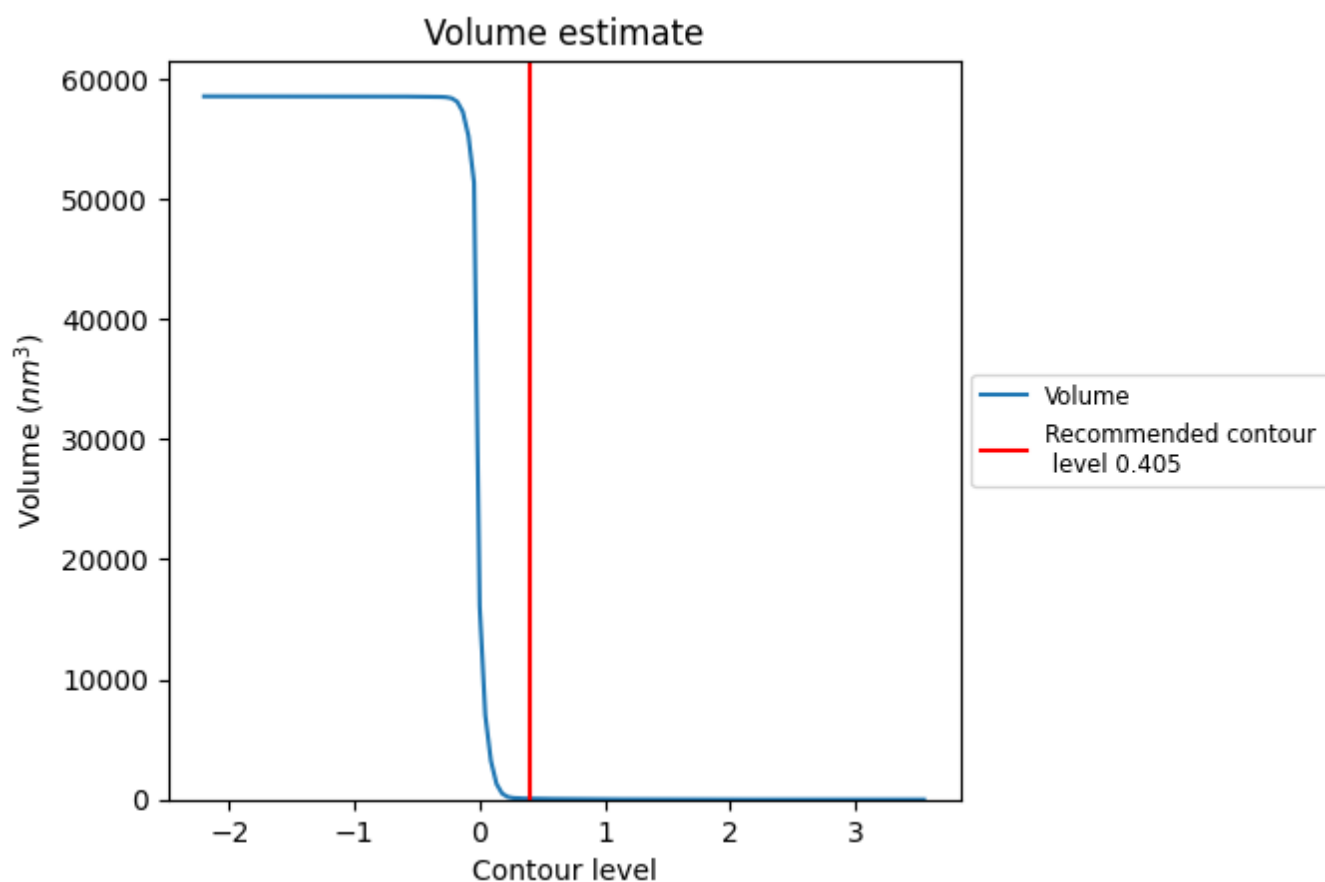
### 7.1 Map-value distribution [i](#)



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](#)

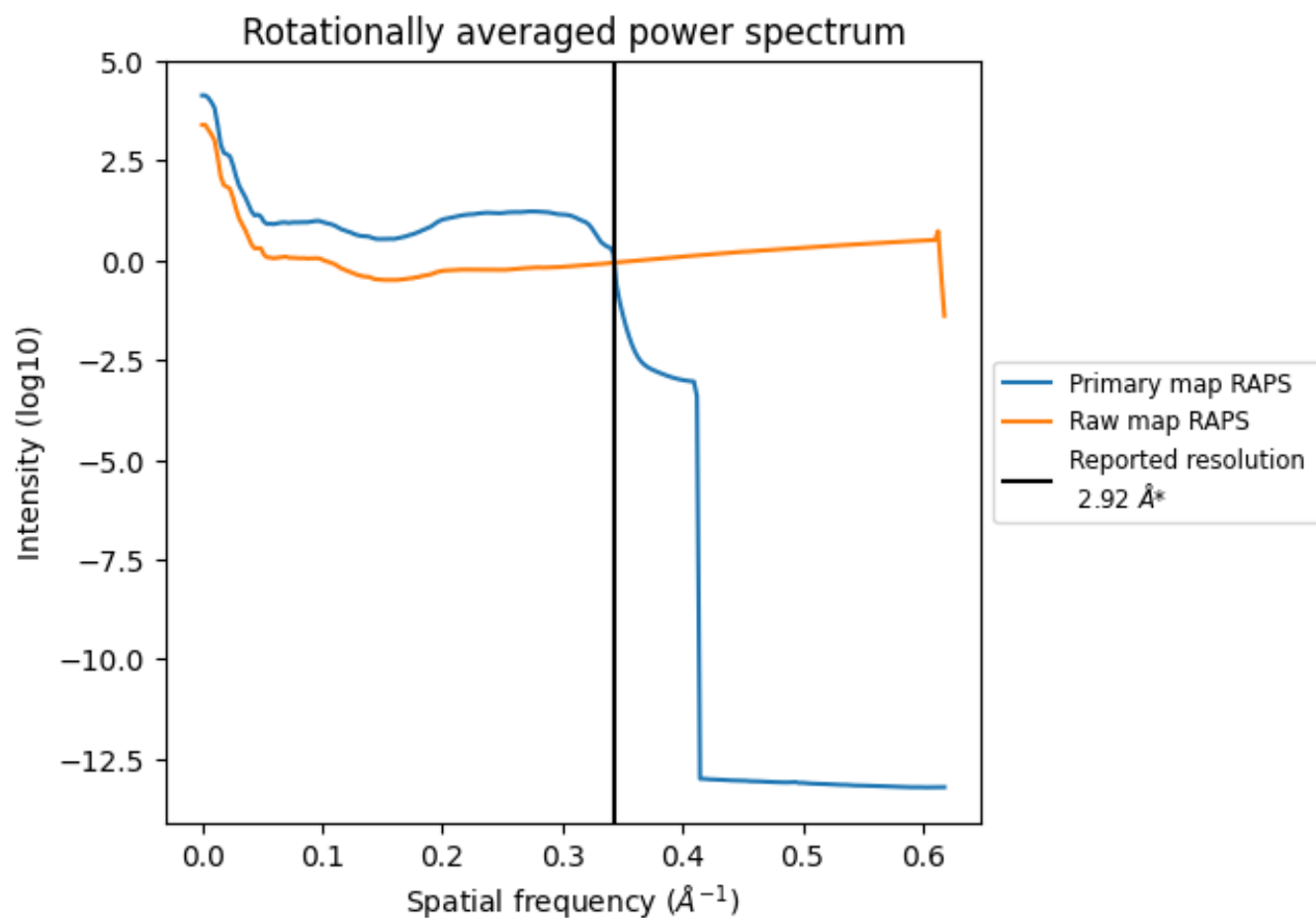


The volume at the recommended contour level is 76 nm<sup>3</sup>; this corresponds to an approximate mass of 69 kDa.

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 ⓘ



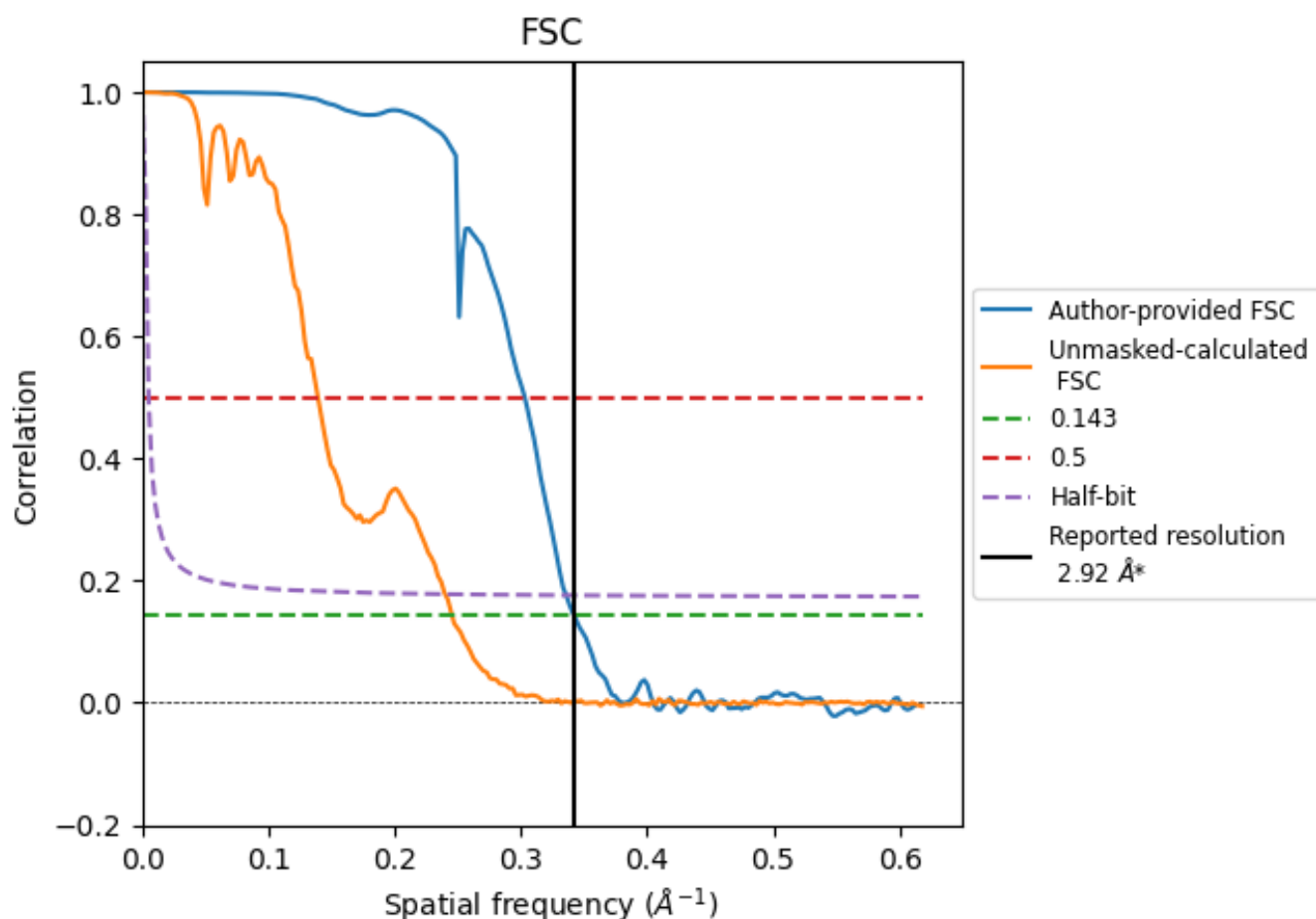
\*Reported resolution corresponds to spatial frequency of 0.342 Å<sup>-1</sup>



## 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  $0.342 \text{ \AA}^{-1}$



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.92	-	-
Author-provided FSC curve	2.92	3.30	2.98
Unmasked-calculated*	4.07	7.18	4.17

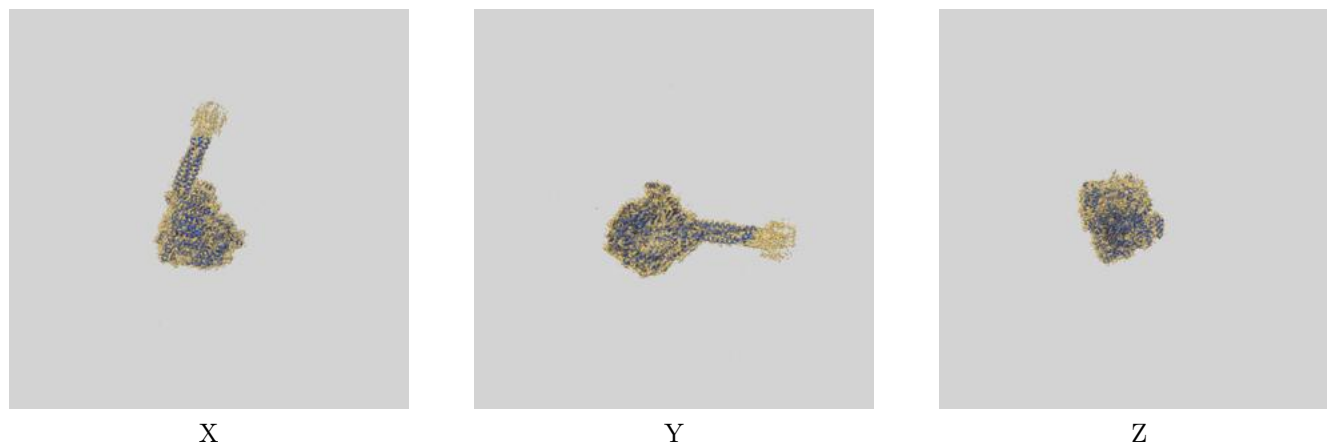
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.07 differs from the reported value 2.92 by more than 10 %



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

This section contains information regarding the fit between EMDB map EMD-45782 and PDB model 9COK. Per-residue inclusion information can be found in section [3](#) on page [12](#).

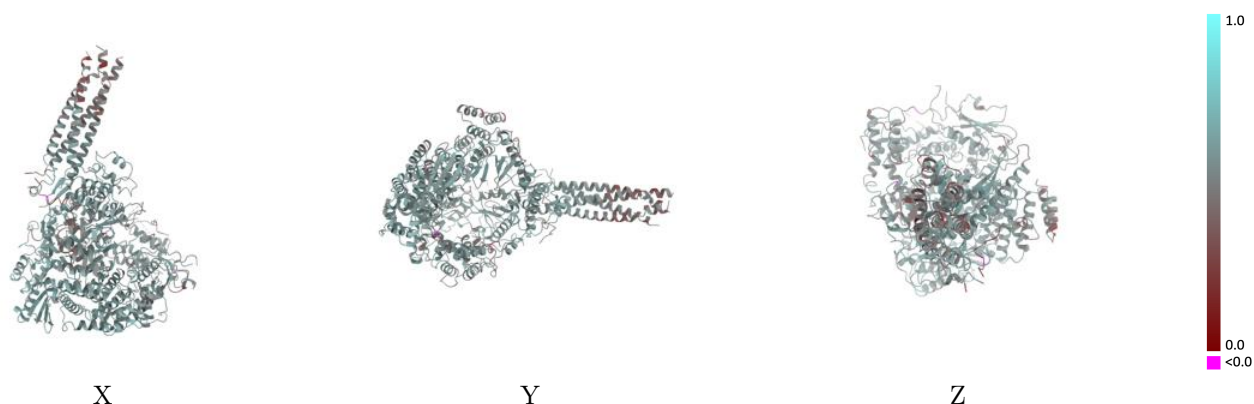
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.405 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

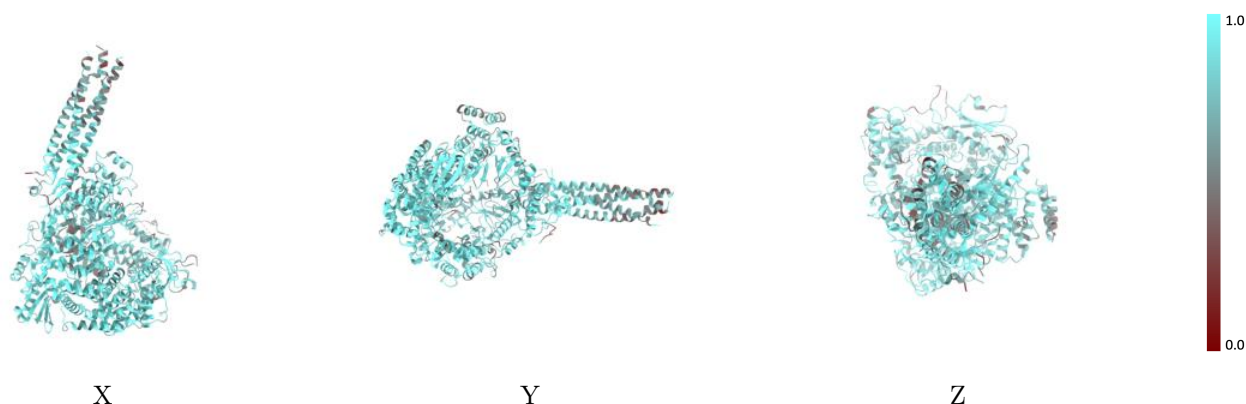


## 9.2 Q-score mapped to coordinate model [i](#)



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

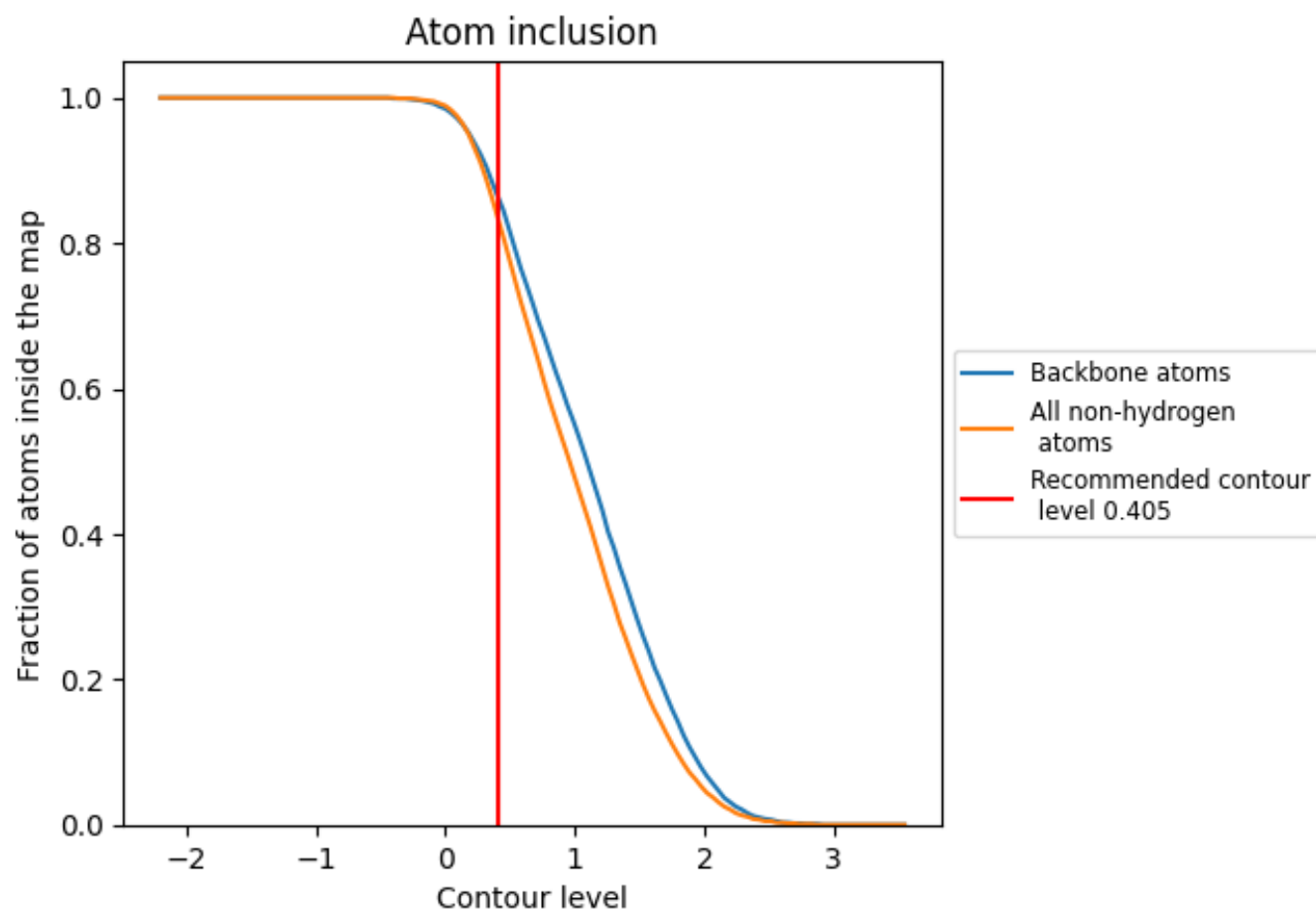
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.405).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 84% 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 (0.405) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8350	<div><div></div></div> 0.5450
A	<div><div></div></div> 0.8650	<div><div></div></div> 0.5610
B	<div><div></div></div> 0.7800	<div><div></div></div> 0.4950
C	<div><div></div></div> 0.6910	<div><div></div></div> 0.4860
D	<div><div></div></div> 0.6620	<div><div></div></div> 0.4610
E	<div><div></div></div> 0.7540	<div><div></div></div> 0.5090
F	<div><div></div></div> 0.7760	<div><div></div></div> 0.5420
G	<div><div></div></div> 0.6420	<div><div></div></div> 0.4250

1.0

0.0

<0.0