



Full wwPDB EM Validation Report ⓘ

Oct 27, 2025 – 04:56 PM EDT

PDB ID : 9MUW / pdb_00009muw
EMDB ID : EMD-48649
Title : Cryo-EM structure of a truncated Nipah virus (Malaysia Strain) L:P complex
Authors : Chen, Z.H.; Liang, B.
Deposited on : 2025-01-14
Resolution : 2.99 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

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:

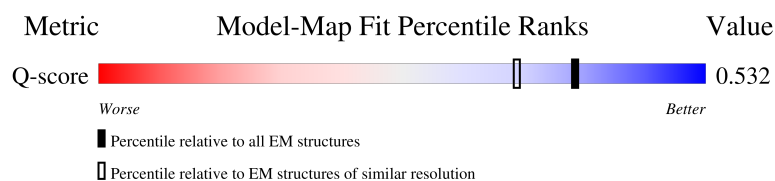
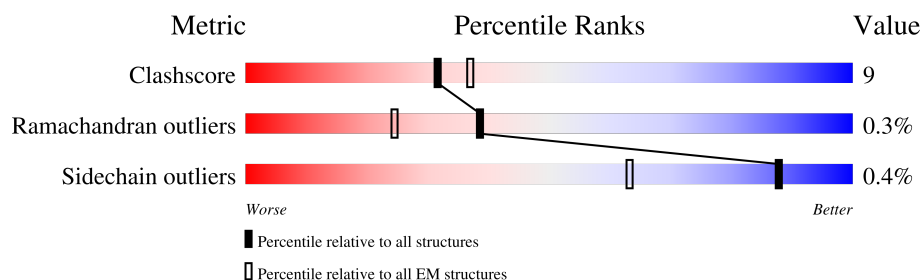
EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 2.99 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	13287 (2.49 - 3.49)

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	1489	
2	B	759	
2	C	759	
2	D	759	

Continued on next page...

Mol	Chain	Length	Quality of chain
2	E	759	 95%
2	F	759	 98%
2	G	759	 91%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11978 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1208	Total	C	N	O	S	0	0
			9748	6220	1665	1797	66		

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
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

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	48	Total	C	N	O	S	0	0
			370	235	63	69	3		
2	C	58	Total	C	N	O	S	0	0
			452	284	83	82	3		
2	D	48	Total	C	N	O	S	0	0
			380	241	66	70	3		
2	E	41	Total	C	N	O	S	0	0
			319	203	53	60	3		
2	F	17	Total	C	N	O		0	0
			136	88	23	25			
2	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
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
C	-49	MET	-	expression tag	UNP Q9IK91
C	-48	LYS	-	expression tag	UNP Q9IK91
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
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
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
D	-39	GLU	-	expression tag	UNP Q9IK91
D	-38	LYS	-	expression tag	UNP Q9IK91

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
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

Continued on next page...

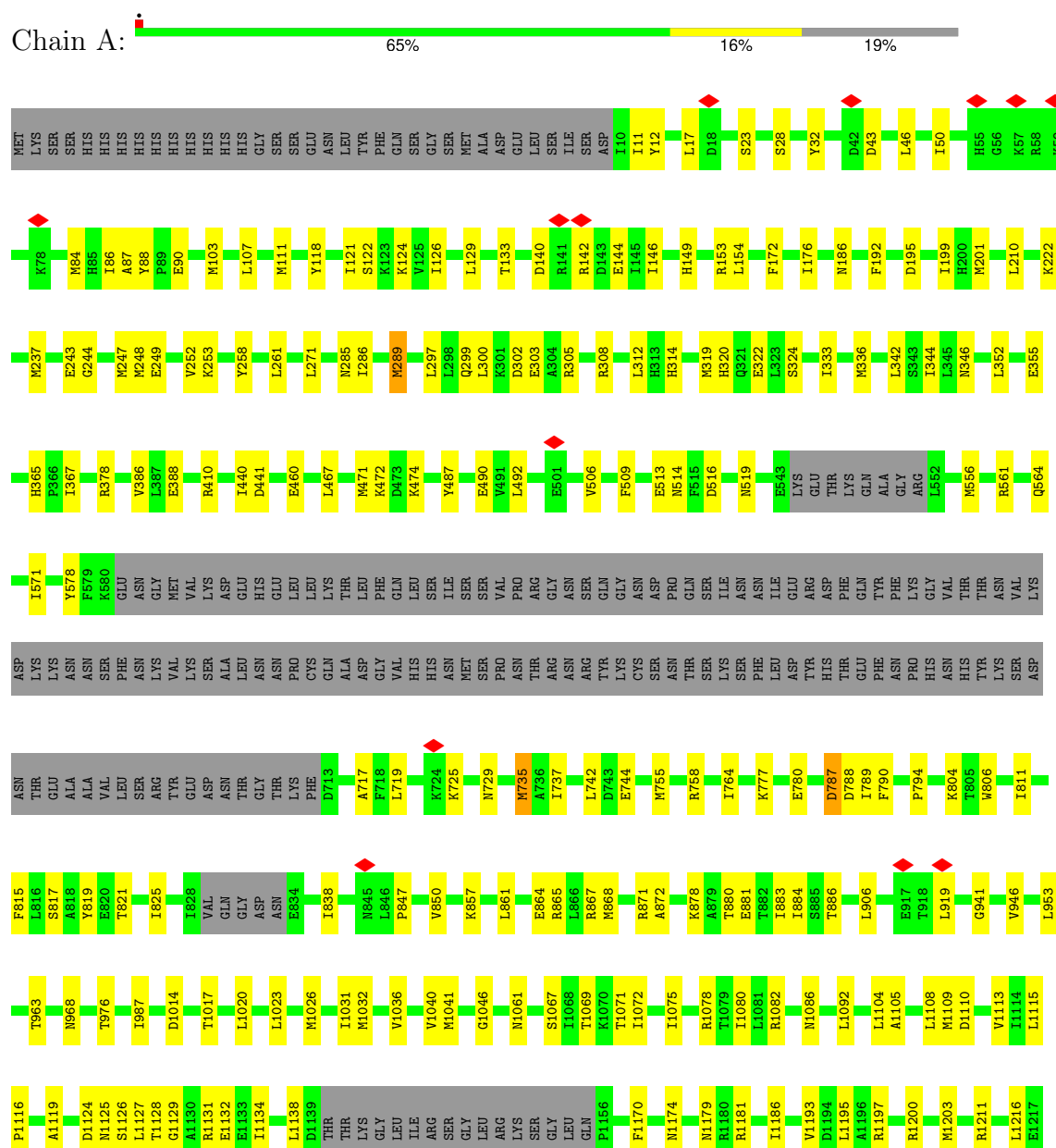
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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

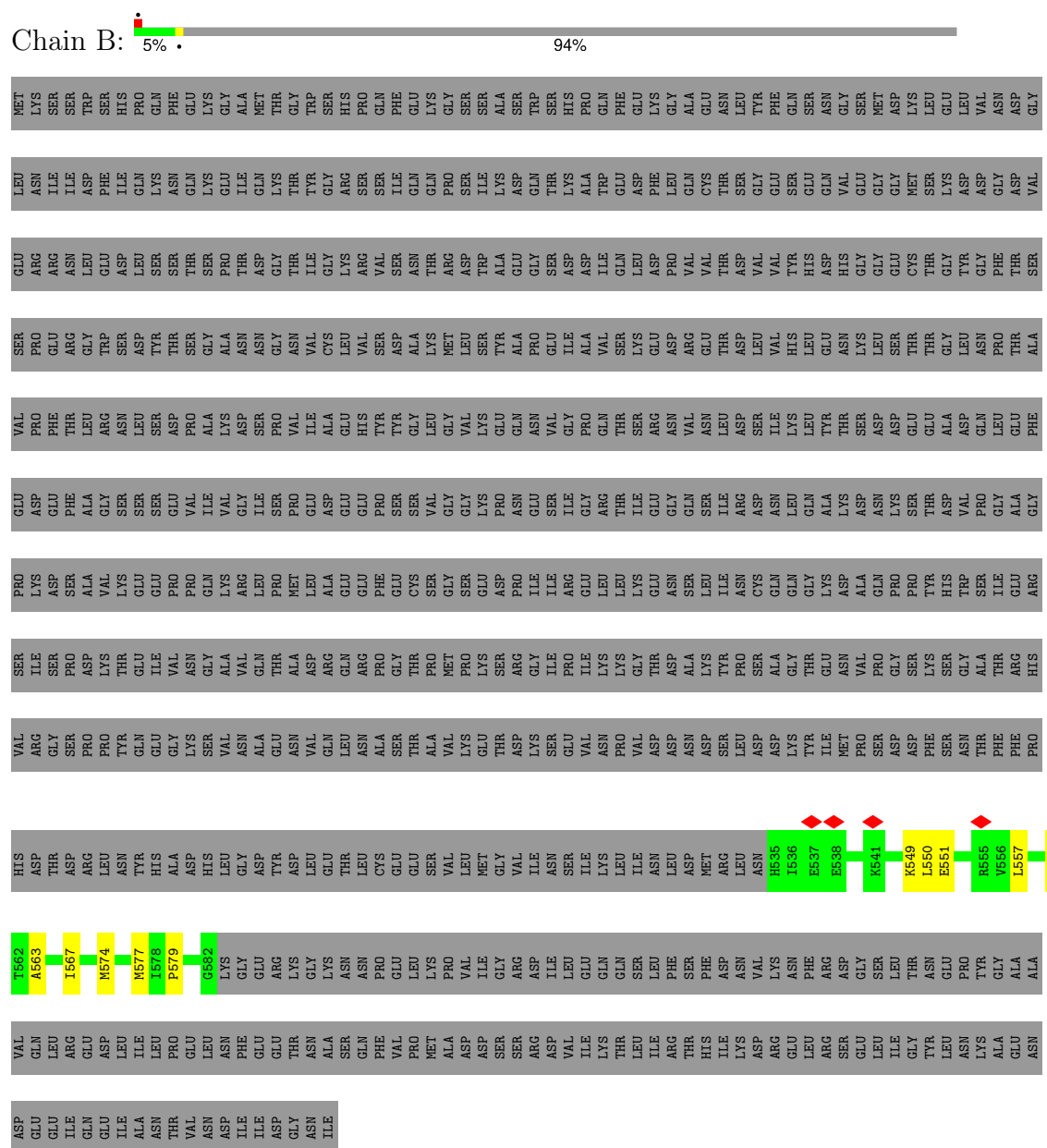
3 Residue-property plots

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.

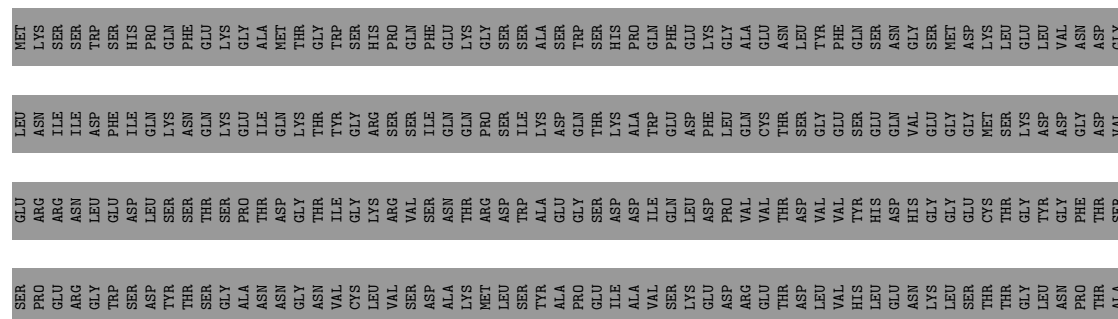
• Molecule 1: RNA-directed RNA polymerase L



- Molecule 2: Phosphoprotein



- Molecule 2: Phosphoprotein



[illegible]

Category	Value	Color
R555	1578	Red
V556	1577	Yellow
L557	1575	Green
E568	1572	Yellow
V572	1571	Yellow
M575	1570	Green
L578	1569	Green
P579	1568	Red
GLY	1567	Grey
LYS	1566	Grey
GLY	1565	Grey
LYS	1564	Grey
GLY	1563	Grey
GLU	1562	Grey
ARG	1561	Grey
LYS	1560	Grey
GLY	1559	Grey
LYS	1558	Grey
ASN	1557	Grey
ASN	1556	Grey
PRO	1555	Grey
GLU	1554	Grey
LEU	1553	Grey
LYS	1552	Grey
PRO	1551	Grey
VAL	1550	Grey
ILE	1549	Grey
GLY	1548	Grey
ARG	1547	Grey
ASP	1546	Grey
ILE	1545	Grey
LEU	1544	Grey
GLU	1543	Grey
GLN	1542	Grey
GLN	1541	Grey
SER	1540	Grey
LEU	1539	Grey
PHE	1538	Grey
SER	1537	Grey
PHE	1536	Grey
ASP	1535	Grey
ASN	1534	Grey
VAL	1533	Grey
LYS	1532	Grey
ASN	1531	Grey
PHE	1530	Grey
ARG	1529	Grey
ASP	1528	Grey
GLY	1527	Grey
SER	1526	Grey
LEU	1525	Grey
THR	1524	Grey
ASN	1523	Grey
GLU	1522	Grey
PRO	1521	Grey
TYR	1520	Grey

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

ALA
GLU
ASN
ASP
GLU
GLU
ILE
GLN
GLU
ILE
ALA
ASN
THR
VAL
ASN
ASP
ILE
ILE
ASP
GLY
ASN
ILE

- Molecule 2: Phosphoprotein

Chain E:  95%

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

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

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

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

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

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

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

[illegible]

AL	RG	ER	RO	PRO	YR	LN	LY	YS	ER	AL	SN	LA	LU	SN	AL	EU	SN	ER	HR	LA	AL	YS	SP	SP	ER	AL	LU	SN	RO	RO	AL	SP	SP	SP	SP	EU	SP	SP	YS	YR	LE	TET	PRO	ER	SP	SP	HE	ER	SN	HR	HE	HE	PRO
----	----	----	----	-----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	----	----	----	----	----	----	----	----	----	-----

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	173715	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	1.657	Depositor
Minimum map value	-1.128	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	355.968, 355.968, 355.968	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.927, 0.927, 0.927	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.11	0/9948	0.30	0/13443
2	B	0.14	0/373	0.33	0/500
2	C	0.12	0/455	0.28	0/605
2	D	0.20	0/383	0.45	0/515
2	E	0.12	0/320	0.30	0/429
2	F	0.12	0/137	0.34	0/183
2	G	0.21	0/578	0.48	0/782
All	All	0.12	0/12194	0.31	0/16457

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9748	0	9783	159	0
2	B	370	0	400	11	0
2	C	452	0	494	12	0
2	D	380	0	411	10	0
2	E	319	0	350	13	0
2	F	136	0	144	6	0
2	G	573	0	559	19	0
All	All	11978	0	12141	206	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 (206) 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:A:1105:ALA:O	1:A:1109:MET:HB2	1.70	0.91
1:A:755:MET:HE1	1:A:806:TRP:HZ2	1.45	0.81
1:A:1388:THR:HG22	1:A:1390:LEU:H	1.52	0.73
1:A:1124:ASP:HA	1:A:1129:GLY:HA3	1.70	0.73
1:A:1092:LEU:O	1:A:1131:ARG:NH2	2.21	0.72
1:A:142:ARG:O	1:A:146:ILE:HD12	1.93	0.68
1:A:1116:PRO:HG2	1:A:1216:LEU:HD11	1.76	0.66
1:A:737:ILE:HD12	2:C:576:ILE:HD11	1.77	0.65
2:D:541:LYS:HE2	2:D:541:LYS:HA	1.77	0.65
2:F:610:SER:N	2:G:636:ASP:O	2.30	0.65
1:A:248:MET:HE3	1:A:906:LEU:HB3	1.79	0.64
1:A:744:GLU:OE2	2:C:583:LYS:NZ	2.30	0.64
2:B:551:GLU:OE2	2:C:549:LYS:NZ	2.29	0.64
1:A:12:TYR:OH	1:A:968:ASN:ND2	2.31	0.63
1:A:868:MET:SD	1:A:871:ARG:NH2	2.72	0.63
1:A:1248:TRP:HB3	1:A:1373:SER:HB3	1.80	0.63
1:A:299:GLN:NE2	1:A:884:ILE:O	2.32	0.62
1:A:410:ARG:HD2	1:A:578:TYR:HE1	1.64	0.62
1:A:244:GLY:O	1:A:248:MET:HG3	2.00	0.62
1:A:561:ARG:NH1	1:A:564:GLN:OE1	2.33	0.61
2:B:550:LEU:HD12	2:E:550:LEU:HD11	1.83	0.60
1:A:149:HIS:O	1:A:153:ARG:HG3	2.02	0.59
2:B:549:LYS:HB3	2:E:550:LEU:HD12	1.86	0.58
2:D:553:ILE:O	2:D:557:LEU:HD22	2.03	0.58
1:A:308:ARG:NH2	2:G:706:ASP:OD1	2.36	0.58
1:A:312:LEU:HD11	1:A:342:LEU:HD21	1.85	0.58
2:B:561:ASN:OD1	2:C:560:THR:OG1	2.14	0.58
1:A:140:ASP:N	1:A:140:ASP:OD1	2.35	0.58
1:A:1193:VAL:O	1:A:1197:ARG:HG3	2.04	0.57
1:A:122:SER:O	1:A:126:ILE:HD12	2.04	0.57
1:A:1296:SER:O	1:A:1300:ILE:HG13	2.03	0.57
1:A:1243:ASN:ND2	1:A:1424:VAL:O	2.34	0.57
1:A:124:LYS:HB3	1:A:1031:ILE:HG12	1.86	0.56
1:A:346:ASN:OD1	2:G:670:THR:OG1	2.15	0.56
1:A:878:LYS:HB2	1:A:881:GLU:HB3	1.87	0.56
1:A:1105:ALA:O	1:A:1109:MET:CB	2.51	0.56
2:G:697:ILE:O	2:G:701:VAL:HG12	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:568:GLU:O	2:D:572:VAL:HG12	2.04	0.56
2:C:533:LEU:HB3	2:D:532:ARG:HH11	1.71	0.56
1:A:472:LYS:HB3	1:A:474:LYS:HE2	1.88	0.56
1:A:378:ARG:NH2	1:A:787:ASP:O	2.39	0.55
1:A:286:ILE:HG13	1:A:319:MET:HE3	1.88	0.55
1:A:1127:LEU:HD12	1:A:1324:GLN:HB2	1.88	0.55
2:C:550:LEU:HD12	2:D:549:LYS:HB3	1.88	0.55
2:D:536:ILE:O	2:D:540:VAL:HG12	2.07	0.55
1:A:825:ILE:HG22	1:A:838:ILE:HG13	1.89	0.54
2:G:637:LEU:HD11	2:G:642:LEU:HD21	1.88	0.54
2:G:638:ILE:HG13	2:G:640:PRO:HD2	1.88	0.54
1:A:386:VAL:HG22	2:B:577:MET:HG2	1.89	0.54
1:A:1432:GLU:O	1:A:1434:ALA:N	2.29	0.54
2:B:563:ALA:HB3	2:E:564:LEU:HD13	1.90	0.54
1:A:867:ARG:NH2	2:G:643:ASN:OD1	2.41	0.53
1:A:1372:ILE:HG22	1:A:1396:MET:HE3	1.90	0.53
1:A:17:LEU:HD22	1:A:237:MET:HB2	1.89	0.53
2:F:601:ASP:OD1	2:F:601:ASP:N	2.41	0.53
1:A:195:ASP:OD1	1:A:195:ASP:N	2.40	0.53
1:A:1365:ARG:NH1	1:A:1407:PHE:O	2.42	0.52
1:A:963:THR:HB	1:A:976:THR:HG23	1.90	0.52
1:A:1032:MET:HE3	1:A:1036:VAL:HG11	1.91	0.52
1:A:1080:ILE:HD11	1:A:1138:LEU:HD21	1.90	0.52
1:A:857:LYS:O	1:A:861:LEU:HD13	2.09	0.52
1:A:1041:MET:HG3	1:A:1186:ILE:HG21	1.92	0.52
1:A:285:ASN:ND2	1:A:322:GLU:OE2	2.42	0.51
1:A:121:ILE:HD13	1:A:987:ILE:HG23	1.92	0.51
1:A:719:LEU:HD13	1:A:838:ILE:HD13	1.91	0.51
1:A:388:GLU:HB2	1:A:872:ALA:HB1	1.91	0.51
1:A:300:LEU:HD11	1:A:312:LEU:HD22	1.93	0.51
1:A:1129:GLY:HA2	1:A:1132:GLU:HG2	1.92	0.51
2:F:610:SER:O	2:G:636:ASP:N	2.44	0.51
1:A:154:LEU:HD21	1:A:946:VAL:HA	1.93	0.51
1:A:1014:ASP:HB3	1:A:1017:THR:HG22	1.92	0.51
2:E:545:LYS:HA	2:E:548:ASN:HD21	1.74	0.51
1:A:249:GLU:O	1:A:253:LYS:HG3	2.10	0.50
1:A:146:ILE:HG12	1:A:1409:LEU:HD12	1.93	0.50
1:A:1046:GLY:O	1:A:1061:ASN:ND2	2.45	0.50
1:A:556:MET:HB2	1:A:561:ARG:HG2	1.94	0.50
1:A:1128:THR:HA	1:A:1131:ARG:HD2	1.93	0.50
1:A:1110:ASP:HB3	1:A:1443:LEU:HD21	1.93	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:LEU:O	1:A:50:ILE:HG13	2.13	0.49
1:A:764:ILE:HG13	1:A:794:PRO:HG3	1.93	0.49
1:A:1023:LEU:HA	1:A:1026:MET:HE2	1.95	0.49
1:A:243:GLU:O	1:A:247:MET:HG2	2.13	0.49
1:A:1067:SER:O	1:A:1071:THR:HG23	2.13	0.49
2:C:572:VAL:O	2:C:576:ILE:HG23	2.12	0.49
1:A:509:PHE:O	1:A:1086:ASN:ND2	2.46	0.48
1:A:941:GLY:O	1:A:1408:ARG:NH1	2.45	0.48
2:F:603:LEU:HD12	2:F:603:LEU:H	1.78	0.48
1:A:1126:SER:O	1:A:1128:THR:N	2.46	0.48
1:A:471:MET:HA	1:A:506:VAL:HG12	1.94	0.48
1:A:252:VAL:HG12	1:A:258:TYR:HB3	1.96	0.48
1:A:847:PRO:HG2	1:A:850:VAL:HG23	1.94	0.48
1:A:513:GLU:HG2	1:A:514:ASN:ND2	2.28	0.48
1:A:788:ASP:O	1:A:790:PHE:N	2.47	0.47
2:D:532:ARG:O	2:D:536:ILE:HG22	2.13	0.47
1:A:43:ASP:HB3	1:A:46:LEU:HB3	1.96	0.47
1:A:342:LEU:HD23	2:G:666:THR:HG21	1.95	0.47
1:A:1108:LEU:HD11	1:A:1119:ALA:HA	1.96	0.47
1:A:314:HIS:HB2	1:A:880:THR:HB	1.95	0.47
1:A:460:GLU:OE1	1:A:460:GLU:N	2.42	0.47
1:A:1041:MET:HE1	1:A:1195:LEU:HB3	1.95	0.47
1:A:571:ILE:HD11	1:A:742:LEU:HD13	1.96	0.47
1:A:864:GLU:HG3	1:A:865:ARG:N	2.29	0.47
1:A:1128:THR:O	1:A:1128:THR:HG23	2.15	0.47
1:A:1237:GLN:HG3	1:A:1237:GLN:O	2.14	0.47
1:A:755:MET:HE1	1:A:806:TRP:CZ2	2.36	0.46
1:A:513:GLU:HG2	1:A:514:ASN:HD22	1.80	0.46
1:A:32:TYR:OH	1:A:490:GLU:O	2.26	0.46
1:A:1126:SER:C	1:A:1128:THR:H	2.23	0.46
2:E:557:LEU:O	2:E:560:THR:HG22	2.15	0.46
1:A:88:TYR:OH	1:A:365:HIS:O	2.27	0.46
2:B:574:MET:HG2	2:C:574:MET:HE2	1.98	0.46
1:A:140:ASP:O	1:A:144:GLU:HG2	2.16	0.46
1:A:258:TYR:OH	1:A:355:GLU:OE2	2.31	0.46
1:A:305:ARG:HG3	2:G:702:ASN:HD22	1.81	0.46
1:A:1071:THR:O	1:A:1075:ILE:HD13	2.15	0.46
1:A:1170:PHE:O	1:A:1174:ASN:ND2	2.48	0.46
2:C:586:ARG:HA	2:C:586:ARG:HD2	1.74	0.46
1:A:87:ALA:HB3	1:A:90:GLU:HG2	1.97	0.46
1:A:725:LYS:O	1:A:729:ASN:ND2	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1302:THR:O	1:A:1306:TRP:HB2	2.16	0.45
1:A:1014:ASP:CG	1:A:1200:ARG:HH22	2.24	0.45
1:A:571:ILE:HG21	1:A:804:LYS:HB3	1.97	0.45
2:C:545:LYS:HA	2:C:548:ASN:ND2	2.31	0.45
1:A:333:ILE:HA	1:A:336:MET:HG2	1.99	0.45
1:A:88:TYR:OH	1:A:237:MET:SD	2.75	0.45
1:A:441:ASP:OD1	1:A:819:TYR:OH	2.28	0.45
1:A:1179:ASN:HD22	1:A:1181:ARG:NH2	2.14	0.45
2:D:545:LYS:HE3	2:D:545:LYS:HB3	1.62	0.45
1:A:103:MET:HE2	1:A:201:MET:HB2	1.99	0.44
1:A:129:LEU:O	1:A:133:THR:HG23	2.16	0.44
1:A:286:ILE:HA	1:A:289:MET:HE2	1.98	0.44
2:E:545:LYS:HA	2:E:548:ASN:ND2	2.32	0.44
1:A:320:HIS:O	1:A:324:SER:OG	2.29	0.44
2:B:579:PRO:HG2	2:F:602:ILE:HD11	1.99	0.44
2:B:567:ILE:HD13	2:E:567:ILE:HG22	1.99	0.44
1:A:297:LEU:HD23	1:A:300:LEU:HD12	2.00	0.44
1:A:1256:GLN:HB2	1:A:1260:VAL:HG13	1.98	0.44
1:A:487:TYR:HB2	1:A:492:LEU:HD11	1.99	0.44
1:A:788:ASP:C	1:A:790:PHE:H	2.26	0.44
1:A:84:MET:HE2	1:A:86:ILE:HD13	1.99	0.44
1:A:107:LEU:HD11	1:A:111:MET:HE3	1.99	0.44
1:A:302:ASP:OD1	1:A:303:GLU:N	2.51	0.44
2:B:563:ALA:O	2:B:567:ILE:HG13	2.18	0.44
2:E:577:MET:N	2:G:636:ASP:OD2	2.46	0.44
1:A:319:MET:HE2	1:A:319:MET:HB3	1.95	0.43
1:A:1298:ILE:O	1:A:1302:THR:HG22	2.18	0.43
2:G:658:ASP:OD1	2:G:658:ASP:N	2.51	0.43
1:A:11:ILE:HD11	1:A:919:LEU:HD22	2.00	0.43
1:A:1364:ASN:O	1:A:1368:ARG:HG2	2.18	0.43
2:E:564:LEU:HD23	2:E:564:LEU:HA	1.79	0.43
2:G:660:SER:O	2:G:664:ILE:HG13	2.18	0.43
1:A:1125:ASN:O	1:A:1300:ILE:HD11	2.19	0.43
1:A:758:ARG:HA	1:A:758:ARG:HH11	1.83	0.43
1:A:118:TYR:HB2	1:A:953:LEU:HD13	2.01	0.43
2:C:545:LYS:HA	2:C:548:ASN:HD21	1.82	0.43
1:A:1078:ARG:O	1:A:1082:ARG:HG2	2.19	0.43
2:E:571:LEU:HD12	2:E:571:LEU:HA	1.89	0.43
1:A:467:LEU:HD11	1:A:1134:ILE:HG12	2.00	0.43
1:A:1069:THR:HA	1:A:1072:ILE:HG22	2.00	0.43
2:F:608:LEU:H	2:F:608:LEU:HD23	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:SER:HA	1:A:50:ILE:CD1	2.49	0.43
1:A:305:ARG:HG3	2:G:702:ASN:ND2	2.34	0.43
1:A:440:ILE:HD12	1:A:440:ILE:HA	1.87	0.43
1:A:1203:MET:HE3	1:A:1203:MET:HB3	1.89	0.43
1:A:1431:LYS:HD3	1:A:1431:LYS:HA	1.76	0.43
1:A:23:SER:HA	1:A:367:ILE:HD11	2.01	0.42
1:A:516:ASP:HB3	1:A:519:ASN:HB3	2.00	0.42
1:A:1017:THR:HG21	1:A:1218:VAL:O	2.20	0.42
1:A:811:ILE:HG23	1:A:815:PHE:HE2	1.84	0.42
1:A:1020:LEU:HD11	1:A:1041:MET:HE2	2.02	0.42
1:A:1104:LEU:O	1:A:1108:LEU:HD23	2.19	0.42
1:A:735:MET:HB3	1:A:735:MET:HE3	1.87	0.42
1:A:1375:ASP:OD1	1:A:1375:ASP:C	2.62	0.42
1:A:172:PHE:O	1:A:176:ILE:HG12	2.19	0.42
1:A:1020:LEU:HD13	1:A:1020:LEU:HA	1.91	0.42
1:A:780:GLU:OE1	1:A:780:GLU:N	2.51	0.42
1:A:1109:MET:HE1	1:A:1116:PRO:HA	2.01	0.42
1:A:1113:VAL:HB	1:A:1439:VAL:HG11	2.02	0.42
1:A:1374:ASN:OD1	1:A:1377:LEU:HB3	2.20	0.42
2:B:557:LEU:HG	2:E:557:LEU:HD21	2.00	0.42
2:E:549:LYS:O	2:E:553:ILE:HG12	2.19	0.42
1:A:199:ILE:HG13	1:A:210:LEU:HB2	2.01	0.42
2:G:643:ASN:HB3	2:G:644:PHE:H	1.59	0.42
1:A:222:LYS:HA	1:A:222:LYS:HD2	1.90	0.42
1:A:248:MET:O	1:A:252:VAL:HG22	2.19	0.41
1:A:817:SER:O	1:A:821:THR:HG23	2.19	0.41
1:A:1398:LEU:HD23	1:A:1422:LEU:HD21	2.01	0.41
2:D:578:ILE:HD13	2:E:576:ILE:HG23	2.02	0.41
1:A:186:ASN:O	1:A:192:PHE:HB2	2.20	0.41
2:C:564:LEU:HD12	2:C:564:LEU:HA	1.91	0.41
1:A:1301:ALA:O	1:A:1305:THR:HG23	2.21	0.41
1:A:1115:LEU:HD13	1:A:1307:ALA:HB1	2.02	0.41
1:A:1036:VAL:O	1:A:1040:VAL:HG13	2.20	0.41
2:D:572:VAL:O	2:D:575:MET:HG2	2.20	0.41
1:A:271:LEU:HD22	1:A:344:ILE:HD12	2.01	0.41
1:A:253:LYS:HE2	1:A:253:LYS:HB3	1.88	0.41
1:A:261:LEU:HD11	1:A:352:LEU:HB3	2.03	0.41
1:A:1110:ASP:OD1	1:A:1211:ARG:NH1	2.49	0.41
2:G:700:THR:HA	2:G:703:ASP:OD2	2.21	0.41
1:A:717:ALA:HA	1:A:886:THR:HA	2.02	0.40
1:A:28:SER:HA	1:A:50:ILE:HD11	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:777:LYS:HA	1:A:777:LYS:HD2	1.62	0.40
2:G:638:ILE:H	2:G:638:ILE:HG12	1.68	0.40
2:G:687:LYS:HE2	2:G:687:LYS:HB2	1.84	0.40
2:G:687:LYS:NZ	2:G:688:ALA:H	2.20	0.40
1:A:1236:CYS:O	1:A:1237:GLN:HB3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1190/1489 (80%)	1163 (98%)	25 (2%)	2 (0%)	44	77
2	B	46/759 (6%)	44 (96%)	2 (4%)	0	100	100
2	C	56/759 (7%)	54 (96%)	2 (4%)	0	100	100
2	D	46/759 (6%)	41 (89%)	5 (11%)	0	100	100
2	E	39/759 (5%)	39 (100%)	0	0	100	100
2	F	15/759 (2%)	14 (93%)	1 (7%)	0	100	100
2	G	69/759 (9%)	59 (86%)	8 (12%)	2 (3%)	3	20
All	All	1461/6043 (24%)	1414 (97%)	43 (3%)	4 (0%)	38	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	789	ILE
2	G	639	LEU
2	G	643	ASN
1	A	1433	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1086/1341 (81%)	1081 (100%)	5 (0%)	86	94
2	B	43/667 (6%)	43 (100%)	0	100	100
2	C	51/667 (8%)	51 (100%)	0	100	100
2	D	45/667 (7%)	45 (100%)	0	100	100
2	E	38/667 (6%)	38 (100%)	0	100	100
2	F	16/667 (2%)	16 (100%)	0	100	100
2	G	66/667 (10%)	66 (100%)	0	100	100
All	All	1345/5343 (25%)	1340 (100%)	5 (0%)	88	95

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	289	MET
1	A	735	MET
1	A	787	ASP
1	A	883	ILE
1	A	1291	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	A	433	ASN
1	A	454	GLN
1	A	514	ASN
1	A	951	ASN
1	A	968	ASN
1	A	1029	HIS
1	A	1125	ASN
1	A	1179	ASN
1	A	1259	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	C	539	GLN
2	C	561	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.

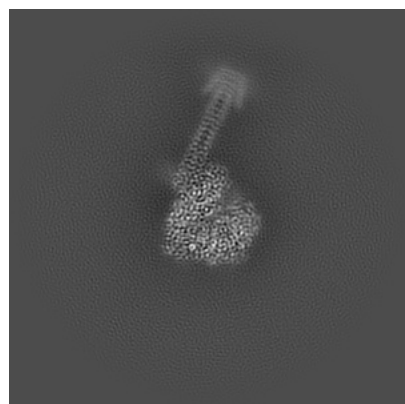
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48649. These allow visual inspection of the internal detail of the map and identification of artifacts.

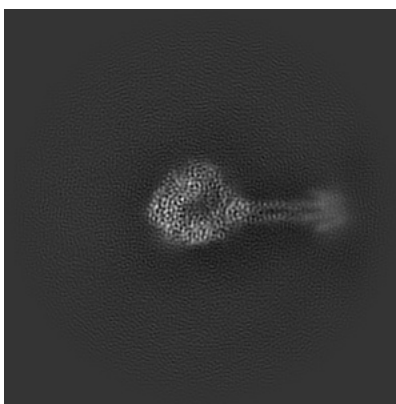
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

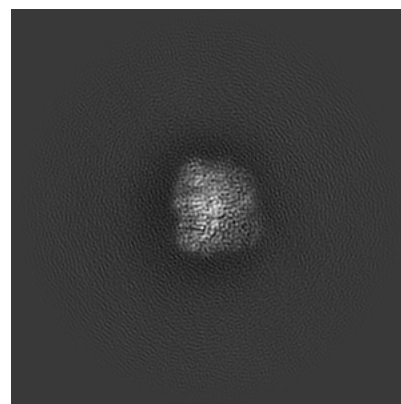
6.1.1 Primary map



X

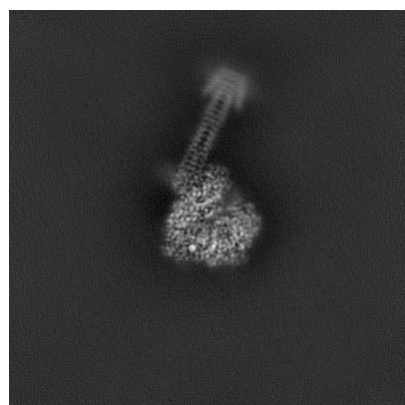


Y

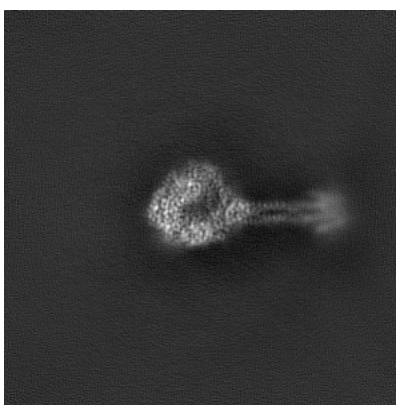


Z

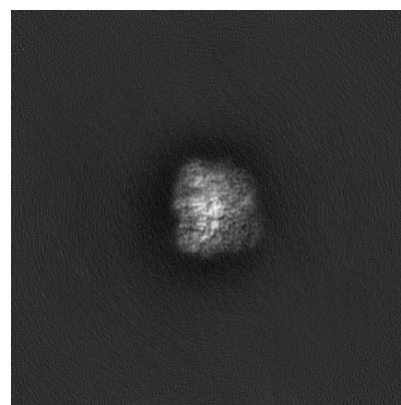
6.1.2 Raw map



X



Y

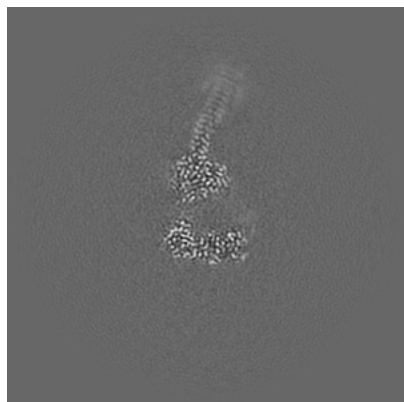


Z

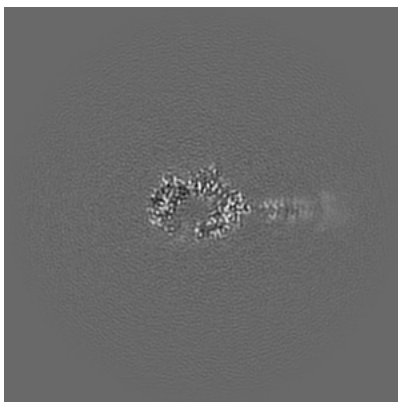
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

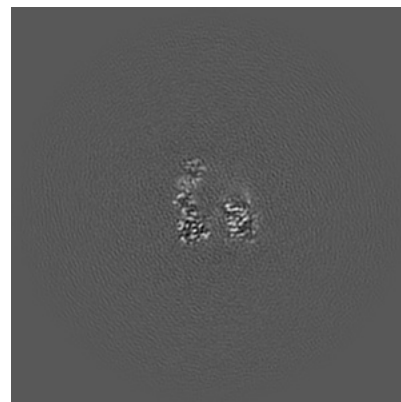
6.2.1 Primary map



X Index: 192

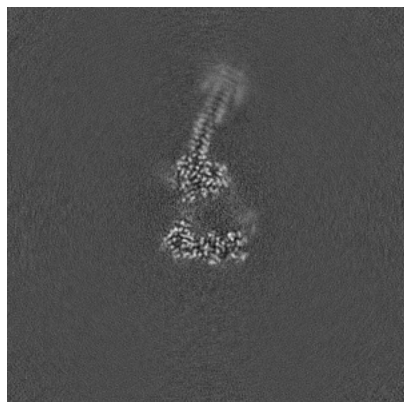


Y Index: 192

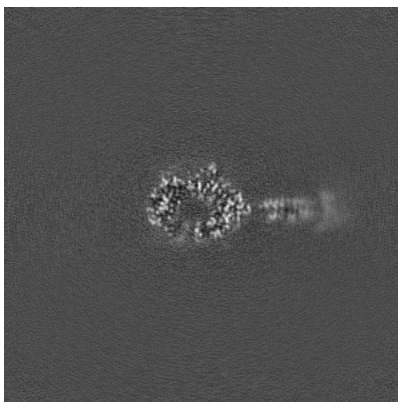


Z Index: 192

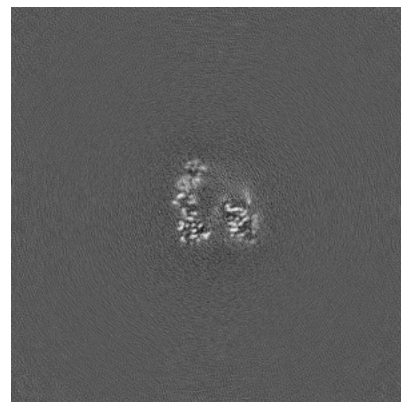
6.2.2 Raw map



X Index: 192



Y Index: 192

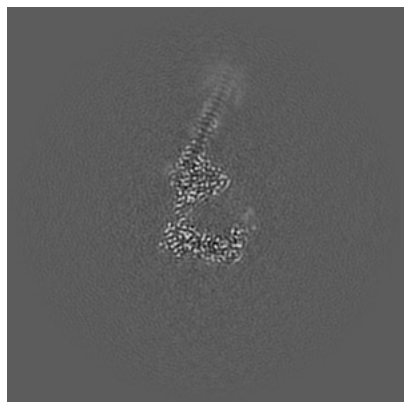


Z Index: 192

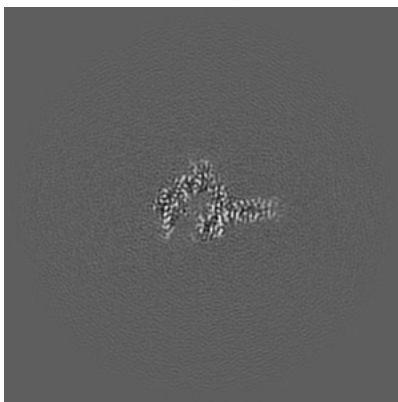
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

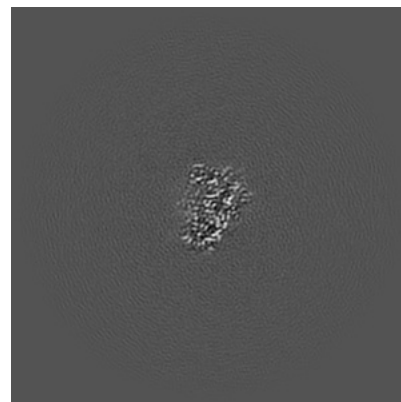
6.3.1 Primary map



X Index: 188

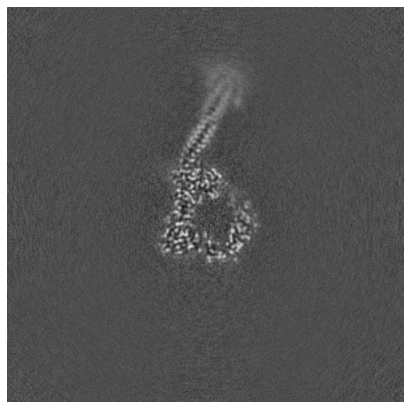


Y Index: 178

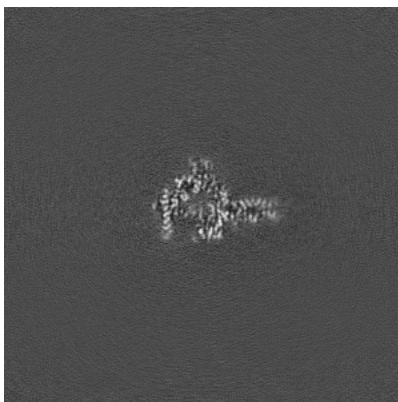


Z Index: 161

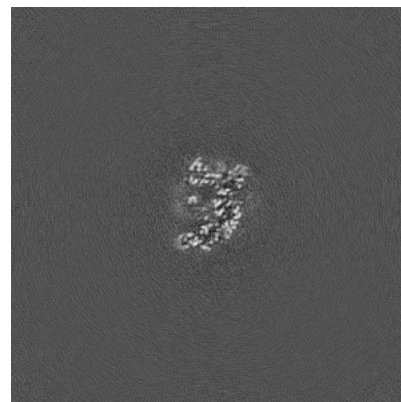
6.3.2 Raw map



X Index: 183



Y Index: 177

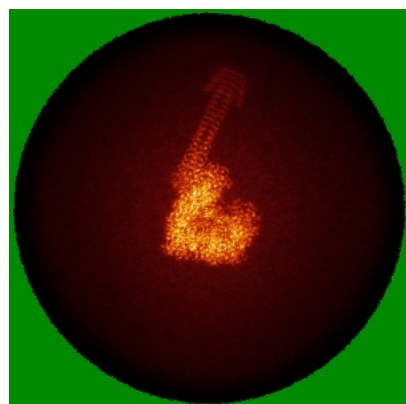


Z Index: 167

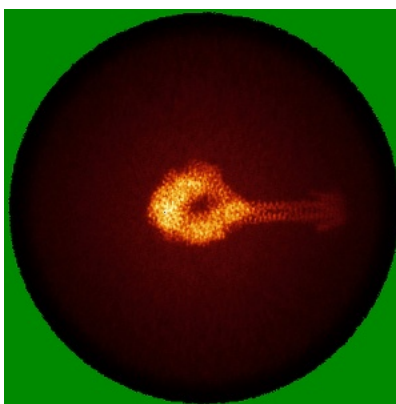
The images above show the largest variance slices of the map in three orthogonal directions.

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

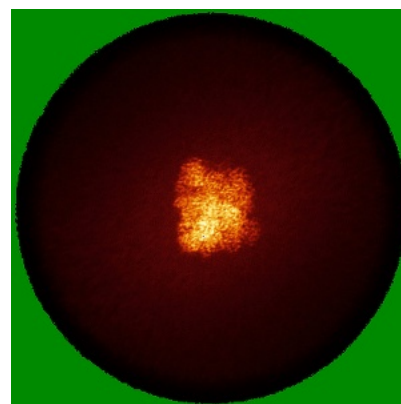
6.4.1 Primary map



X

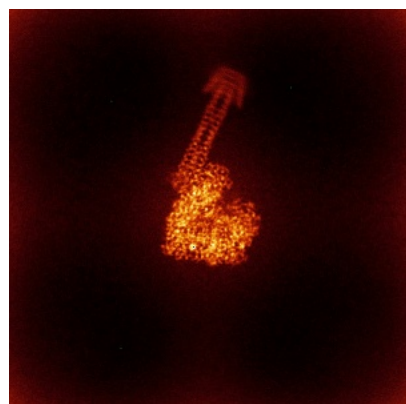


Y

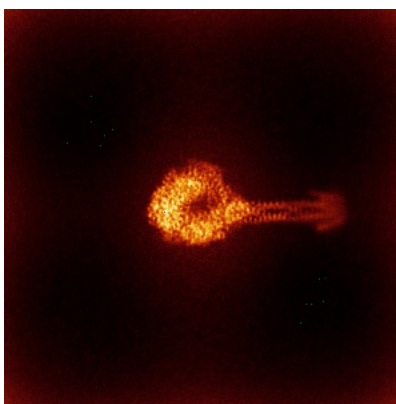


Z

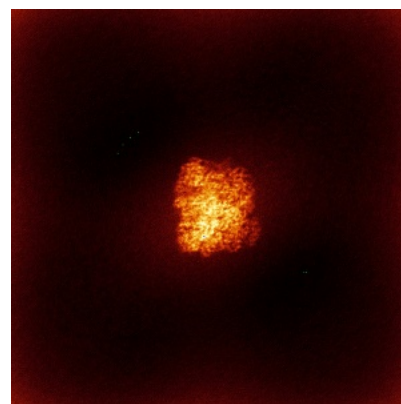
6.4.2 Raw map



X



Y

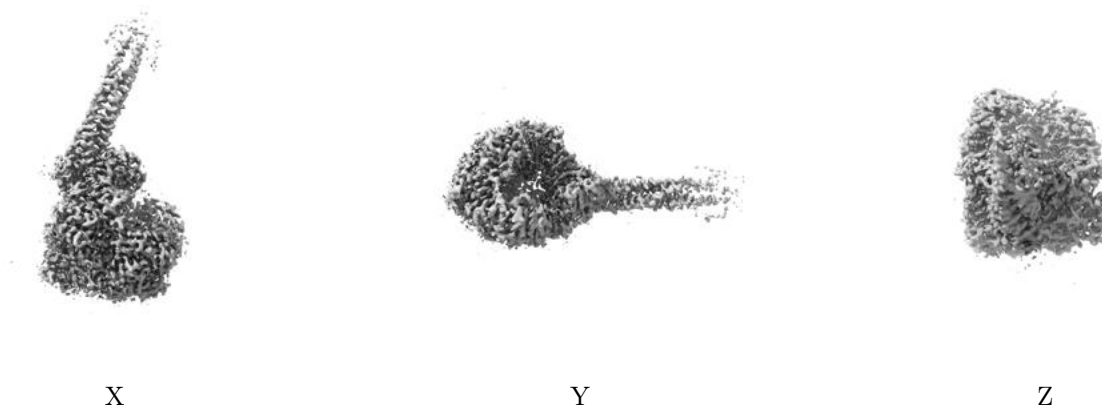


Z

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 0.2. 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.

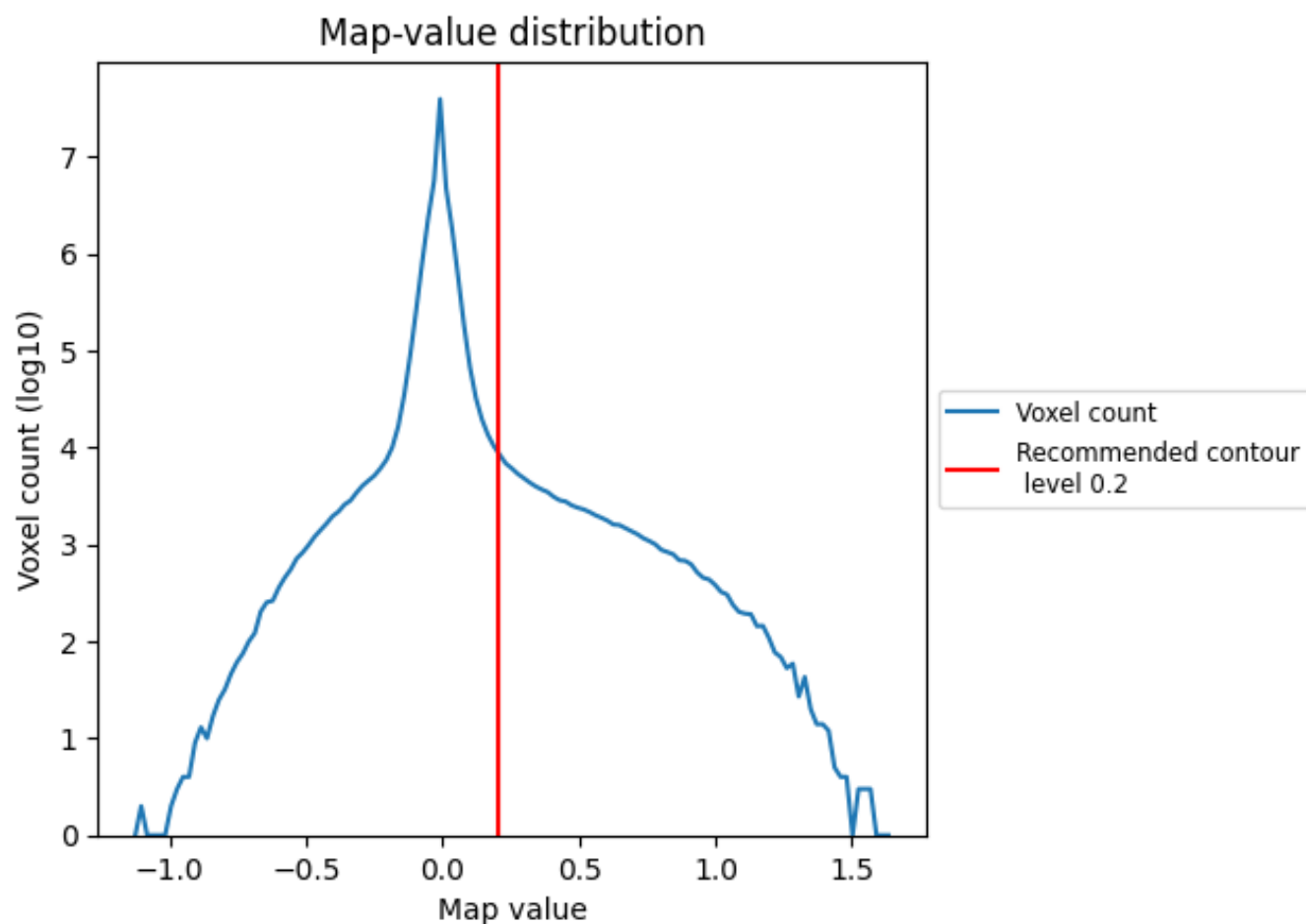
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

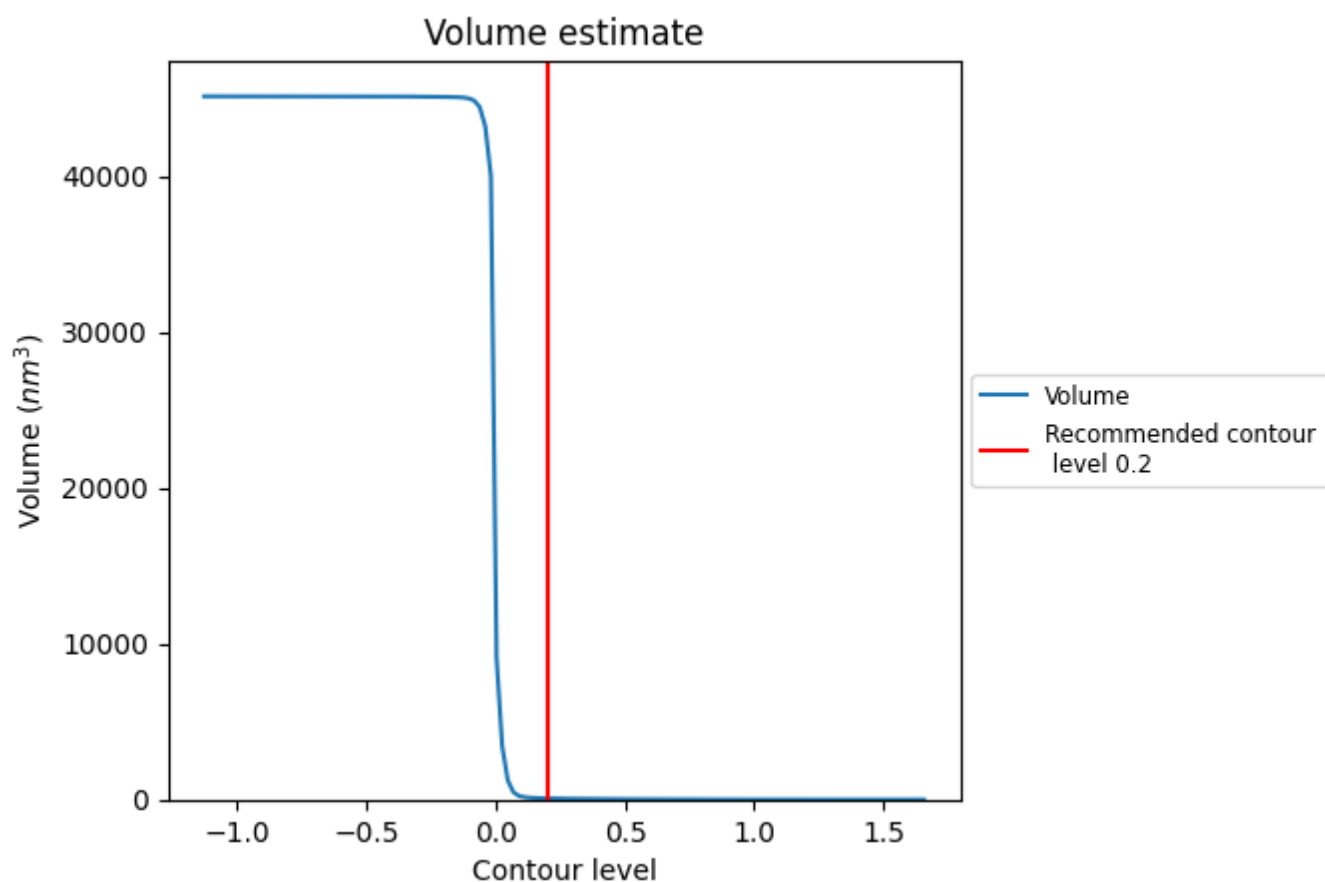
This section contains the results of statistical analysis of the map.

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.

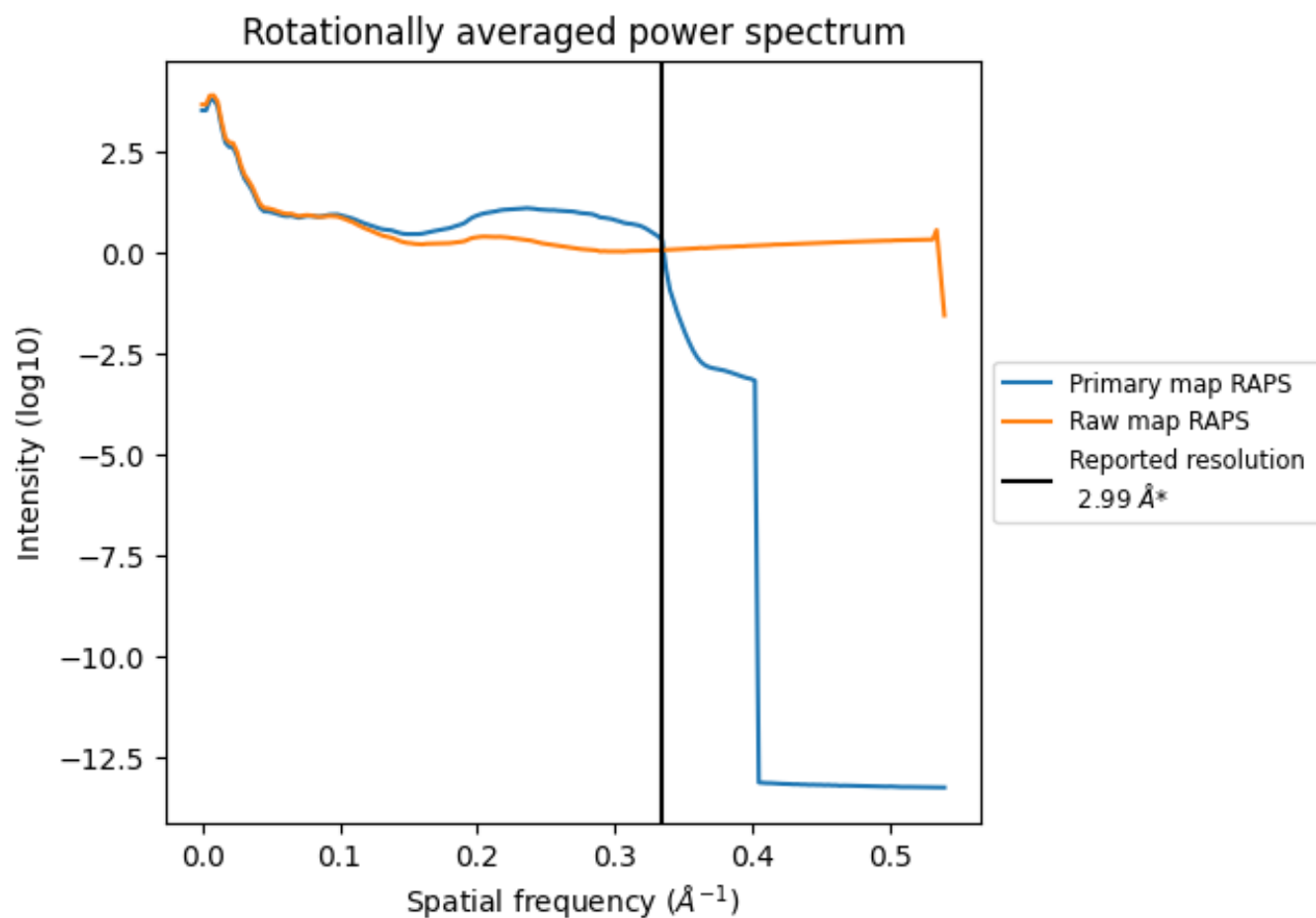
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 75 nm³; this corresponds to an approximate mass of 68 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

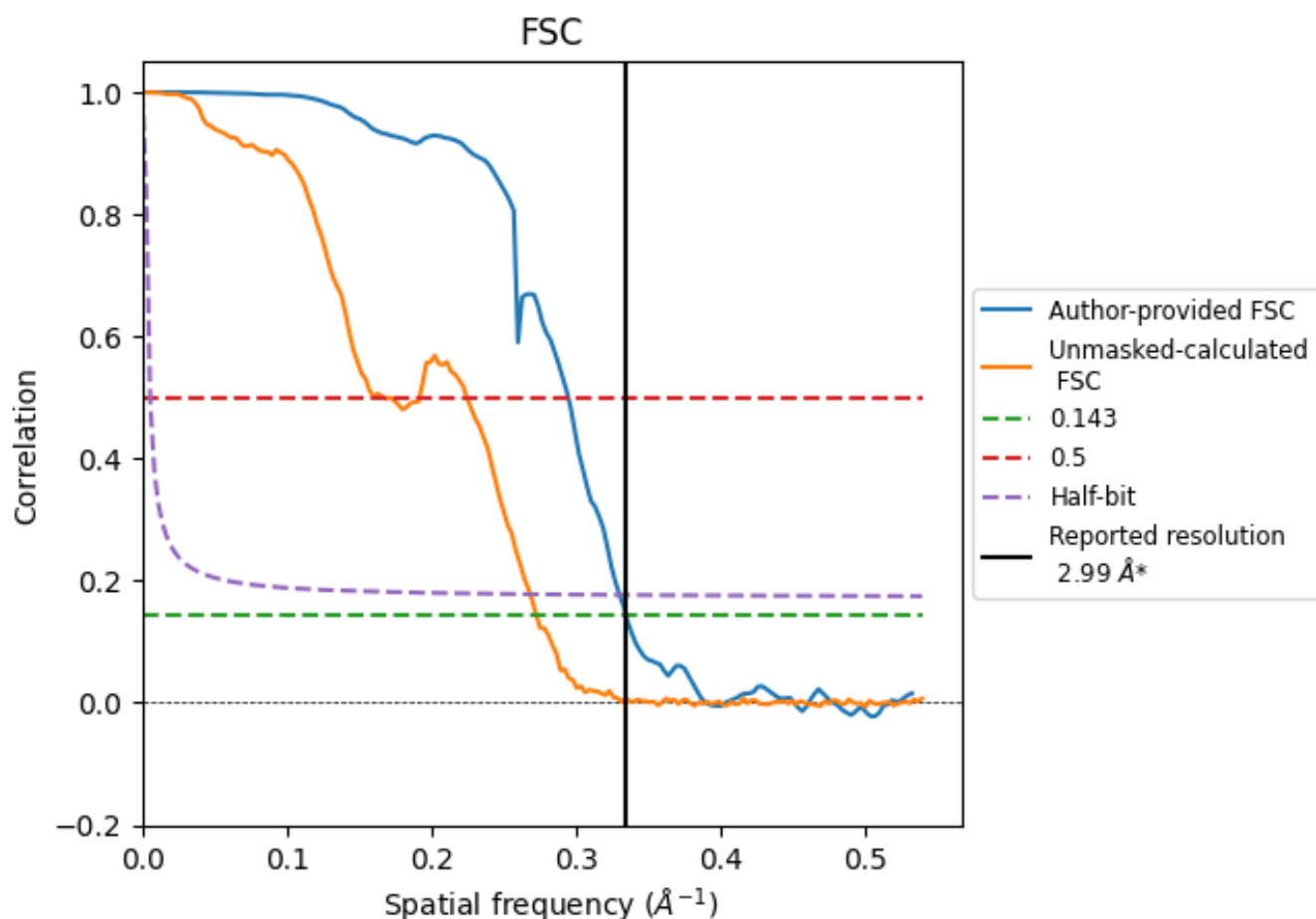


*Reported resolution corresponds to spatial frequency of 0.334 \AA^{-1}

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 0.334 \AA^{-1}

8.2 Resolution estimates [i](#)

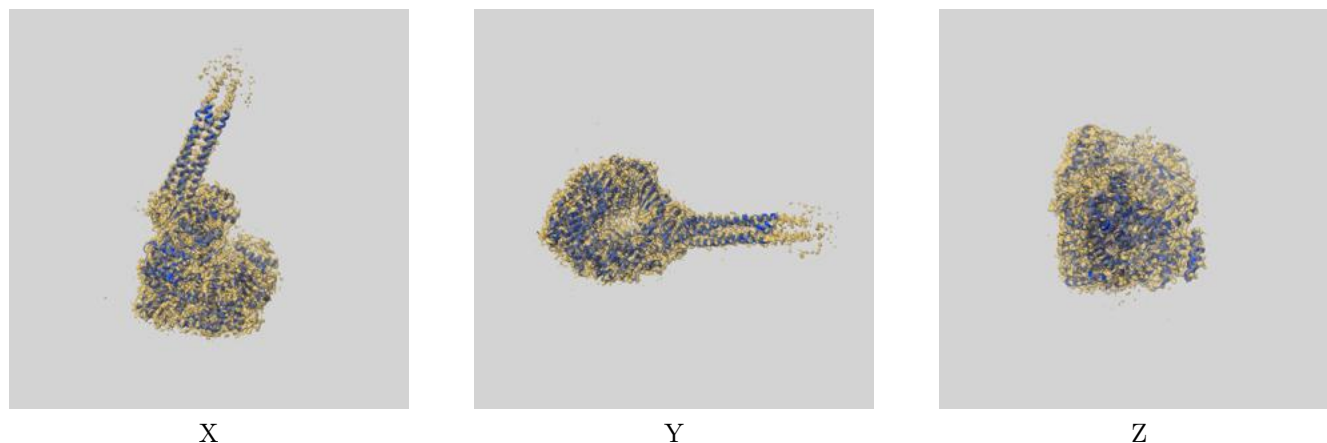
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.99	-	-
Author-provided FSC curve	2.99	3.39	3.03
Unmasked-calculated*	3.67	5.98	3.73

*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 3.67 differs from the reported value 2.99 by more than 10 %

9 Map-model fit [i](#)

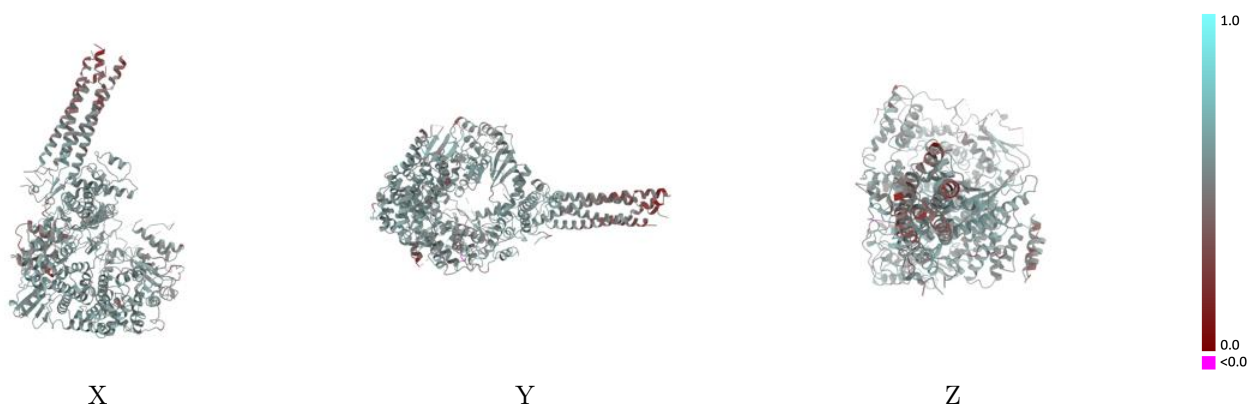
This section contains information regarding the fit between EMDB map EMD-48649 and PDB model 9MUW. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



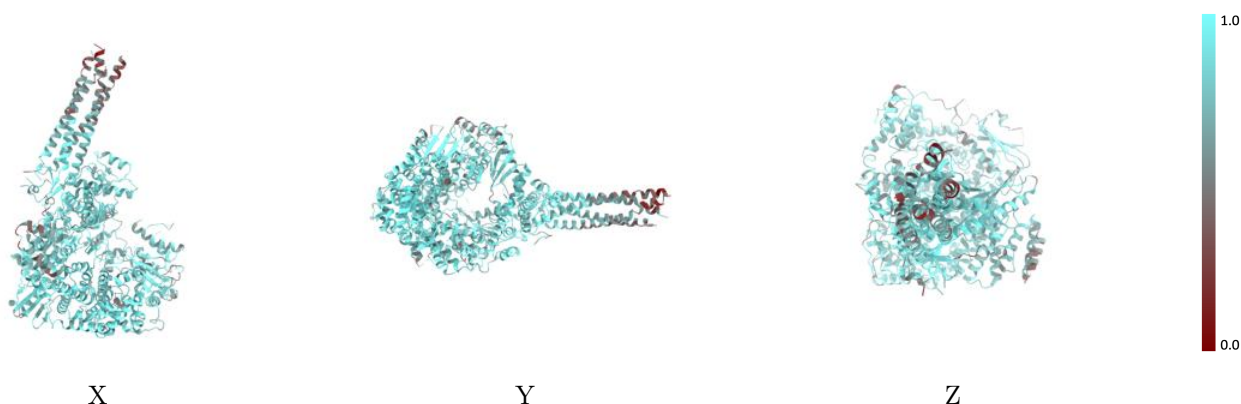
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



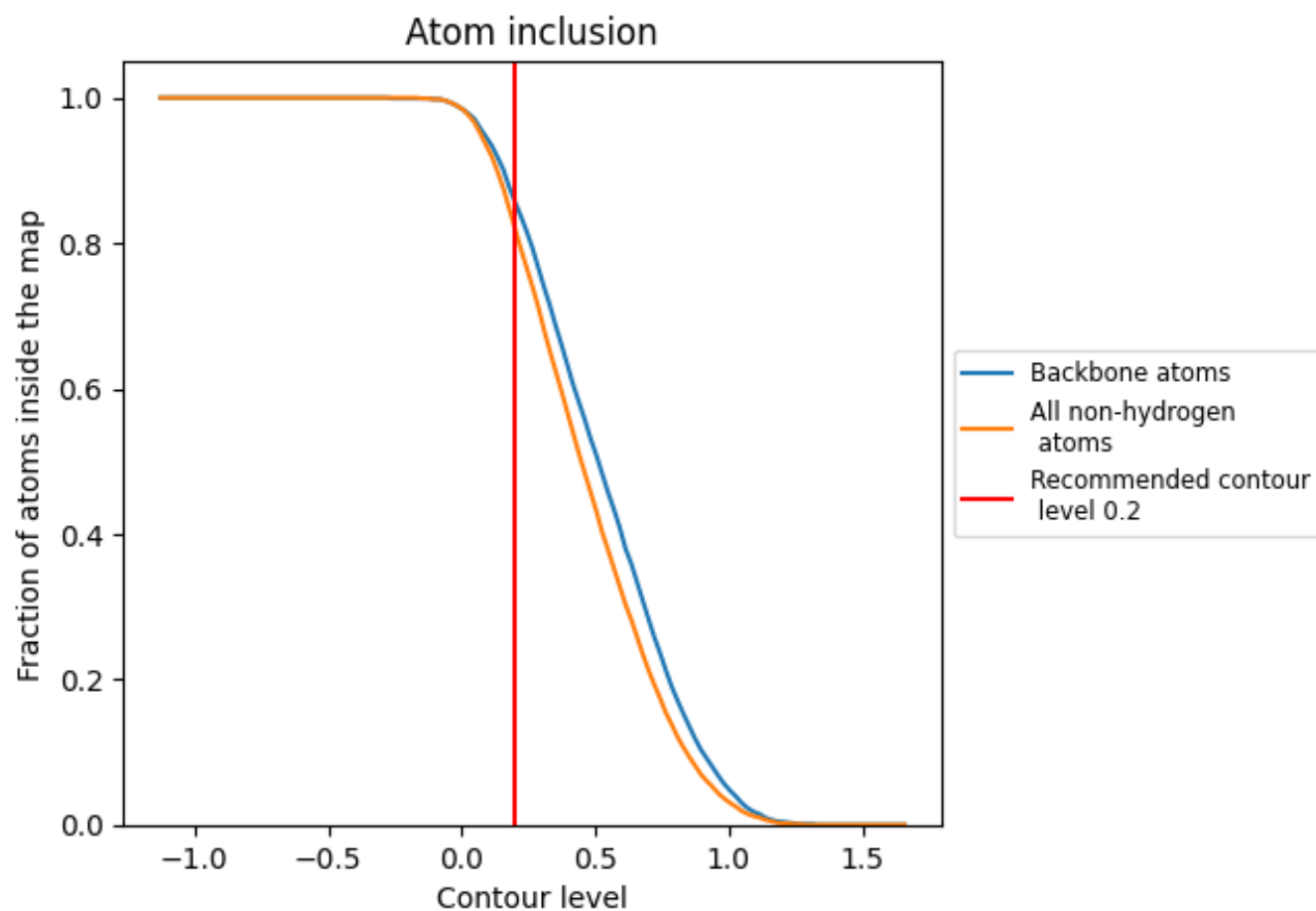
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8190</div>	<div><div></div>0.5320</div>
A	<div><div></div>0.8580</div>	<div><div></div>0.5490</div>
B	<div><div></div>0.7170</div>	<div><div></div>0.4610</div>
C	<div><div></div>0.6500</div>	<div><div></div>0.4440</div>
D	<div><div></div>0.5960</div>	<div><div></div>0.4380</div>
E	<div><div></div>0.6750</div>	<div><div></div>0.4560</div>
F	<div><div></div>0.7460</div>	<div><div></div>0.5340</div>
G	<div><div></div>0.6220</div>	<div><div></div>0.4560</div>

1.0

0.0

<0.0