



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 05:03 PM UTC

PDB ID : 9IP4 / pdb_00009ip4
EMDB ID : EMD-60757
Title : Cryo-EM structure of the RNA-dependent RNA polymerase complex from Marburg virus
Authors : Li, G.; Du, T.; Wang, J.; Wu, S.; Ru, H.
Deposited on : 2024-07-10
Resolution : 2.84 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:

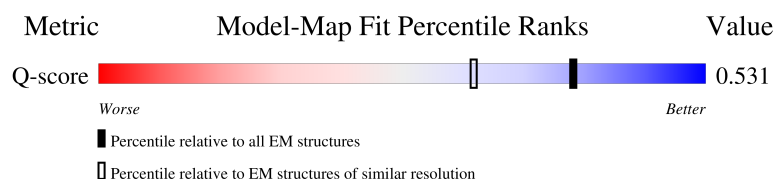
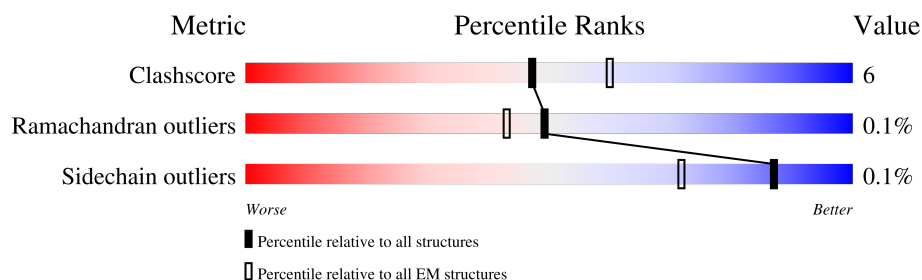
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.84 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	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11884 (2.34 - 3.34)

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	1851	
2	B	671	
2	C	671	
2	D	671	

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Mol	Chain	Length	Quality of chain
2	E	671	96%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13615 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,Maltose/maltodextrin-binding periplasmic protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1364	Total	C	N	O	S	0	0
			11049	7110	1874	2013	52		

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	489	ALA	LEU	conflict	UNP P31352
A	979	GLY	ARG	conflict	UNP P31352
A	1426	SER	-	linker	UNP P31352
A	1427	ARG	-	linker	UNP P31352
A	1428	GLU	-	linker	UNP P31352
A	1429	ASN	-	linker	UNP P31352
A	1430	LEU	-	linker	UNP P31352
A	1431	TYR	-	linker	UNP P31352
A	1432	PHE	-	linker	UNP P31352
A	1433	GLN	-	linker	UNP P31352
A	1434	GLY	-	linker	UNP P31352
A	1435	SER	-	linker	UNP P31352
A	1436	GLY	-	linker	UNP P31352
A	1437	TRP	-	linker	UNP P31352
A	1438	SER	-	linker	UNP P31352
A	1439	HIS	-	linker	UNP P31352
A	1440	PRO	-	linker	UNP P31352
A	1441	GLN	-	linker	UNP P31352
A	1442	PHE	-	linker	UNP P31352
A	1443	GLU	-	linker	UNP P31352
A	1444	LYS	-	linker	UNP P31352
A	1445	GLY	-	linker	UNP P31352
A	1446	GLY	-	linker	UNP P31352
A	1447	GLY	-	linker	UNP P31352
A	1448	SER	-	linker	UNP P31352
A	1449	GLY	-	linker	UNP P31352
A	1450	GLY	-	linker	UNP P31352

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1451	GLY	-	linker	UNP P31352
A	1452	SER	-	linker	UNP P31352
A	1453	GLY	-	linker	UNP P31352
A	1454	GLY	-	linker	UNP P31352
A	1455	SER	-	linker	UNP P31352
A	1456	ALA	-	linker	UNP P31352
A	1457	TRP	-	linker	UNP P31352
A	1458	SER	-	linker	UNP P31352
A	1459	HIS	-	linker	UNP P31352
A	1460	PRO	-	linker	UNP P31352
A	1461	GLN	-	linker	UNP P31352
A	1462	PHE	-	linker	UNP P31352
A	1463	GLU	-	linker	UNP P31352
A	1464	LYS	-	linker	UNP P31352
A	1465	GLY	-	linker	UNP P31352
A	1466	SER	-	linker	UNP P31352
A	1467	ALA	-	linker	UNP P31352
A	1468	SER	-	linker	UNP P31352
A	1469	HIS	-	linker	UNP P31352
A	1470	HIS	-	linker	UNP P31352
A	1471	HIS	-	linker	UNP P31352
A	1472	HIS	-	linker	UNP P31352
A	1473	HIS	-	linker	UNP P31352
A	1474	HIS	-	linker	UNP P31352
A	1475	GLY	-	linker	UNP P31352
A	1476	THR	-	linker	UNP P31352
A	1477	LYS	-	linker	UNP P31352
A	1478	THR	-	linker	UNP P31352
A	1843	GLY	-	expression tag	UNP P0AEX9
A	1844	ASP	-	expression tag	UNP P0AEX9
A	1845	TYR	-	expression tag	UNP P0AEX9
A	1846	LYS	-	expression tag	UNP P0AEX9
A	1847	ASP	-	expression tag	UNP P0AEX9
A	1848	ASP	-	expression tag	UNP P0AEX9
A	1849	ASP	-	expression tag	UNP P0AEX9
A	1850	ASP	-	expression tag	UNP P0AEX9
A	1851	LYS	-	expression tag	UNP P0AEX9

- Molecule 2 is a protein called Maltose/maltodextrin-binding periplasmic protein, Polymerase cofactor VP35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	217	Total 1649	C 1048	N 285	O 308	S 8	0	0
2	C	63	Total 471	C 301	N 80	O 87	S 3	0	0
2	D	32	Total 244	C 156	N 40	O 45	S 3	0	0
2	E	26	Total 201	C 128	N 34	O 36	S 3	0	0

There are 140 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-341	MET	-	initiating methionine	UNP P0AEX9
B	-340	GLY	-	expression tag	UNP P0AEX9
B	-339	SER	-	expression tag	UNP P0AEX9
B	-338	SER	-	expression tag	UNP P0AEX9
B	-337	HIS	-	expression tag	UNP P0AEX9
B	-336	HIS	-	expression tag	UNP P0AEX9
B	-335	HIS	-	expression tag	UNP P0AEX9
B	-334	HIS	-	expression tag	UNP P0AEX9
B	-333	HIS	-	expression tag	UNP P0AEX9
B	-332	HIS	-	expression tag	UNP P0AEX9
B	-331	GLY	-	expression tag	UNP P0AEX9
B	-330	THR	-	expression tag	UNP P0AEX9
B	-329	LYS	-	expression tag	UNP P0AEX9
B	-328	THR	-	expression tag	UNP P0AEX9
B	37	GLY	-	linker	UNP P0AEX9
B	38	THR	-	linker	UNP P0AEX9
B	39	ASP	-	linker	UNP P0AEX9
B	40	TYR	-	linker	UNP P0AEX9
B	41	ASP	-	linker	UNP P0AEX9
B	42	ILE	-	linker	UNP P0AEX9
B	43	PRO	-	linker	UNP P0AEX9
B	44	THR	-	linker	UNP P0AEX9
B	45	THR	-	linker	UNP P0AEX9
B	46	LEU	-	linker	UNP P0AEX9
B	47	GLU	-	linker	UNP P0AEX9
B	48	VAL	-	linker	UNP P0AEX9
B	49	LEU	-	linker	UNP P0AEX9
B	50	PHE	-	linker	UNP P0AEX9
B	51	GLN	-	linker	UNP P0AEX9
B	52	GLY	-	linker	UNP P0AEX9
B	53	PRO	-	linker	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	54	LEU	-	linker	UNP P0AEX9
B	55	GLY	-	linker	UNP P0AEX9
B	56	SER	-	linker	UNP P0AEX9
B	296	CYS	SER	conflict	UNP P35259
C	-341	MET	-	initiating methionine	UNP P0AEX9
C	-340	GLY	-	expression tag	UNP P0AEX9
C	-339	SER	-	expression tag	UNP P0AEX9
C	-338	SER	-	expression tag	UNP P0AEX9
C	-337	HIS	-	expression tag	UNP P0AEX9
C	-336	HIS	-	expression tag	UNP P0AEX9
C	-335	HIS	-	expression tag	UNP P0AEX9
C	-334	HIS	-	expression tag	UNP P0AEX9
C	-333	HIS	-	expression tag	UNP P0AEX9
C	-332	HIS	-	expression tag	UNP P0AEX9
C	-331	GLY	-	expression tag	UNP P0AEX9
C	-330	THR	-	expression tag	UNP P0AEX9
C	-329	LYS	-	expression tag	UNP P0AEX9
C	-328	THR	-	expression tag	UNP P0AEX9
C	37	GLY	-	linker	UNP P0AEX9
C	38	THR	-	linker	UNP P0AEX9
C	39	ASP	-	linker	UNP P0AEX9
C	40	TYR	-	linker	UNP P0AEX9
C	41	ASP	-	linker	UNP P0AEX9
C	42	ILE	-	linker	UNP P0AEX9
C	43	PRO	-	linker	UNP P0AEX9
C	44	THR	-	linker	UNP P0AEX9
C	45	THR	-	linker	UNP P0AEX9
C	46	LEU	-	linker	UNP P0AEX9
C	47	GLU	-	linker	UNP P0AEX9
C	48	VAL	-	linker	UNP P0AEX9
C	49	LEU	-	linker	UNP P0AEX9
C	50	PHE	-	linker	UNP P0AEX9
C	51	GLN	-	linker	UNP P0AEX9
C	52	GLY	-	linker	UNP P0AEX9
C	53	PRO	-	linker	UNP P0AEX9
C	54	LEU	-	linker	UNP P0AEX9
C	55	GLY	-	linker	UNP P0AEX9
C	56	SER	-	linker	UNP P0AEX9
C	296	CYS	SER	conflict	UNP P35259
D	-341	MET	-	initiating methionine	UNP P0AEX9
D	-340	GLY	-	expression tag	UNP P0AEX9
D	-339	SER	-	expression tag	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-338	SER	-	expression tag	UNP P0AEX9
D	-337	HIS	-	expression tag	UNP P0AEX9
D	-336	HIS	-	expression tag	UNP P0AEX9
D	-335	HIS	-	expression tag	UNP P0AEX9
D	-334	HIS	-	expression tag	UNP P0AEX9
D	-333	HIS	-	expression tag	UNP P0AEX9
D	-332	HIS	-	expression tag	UNP P0AEX9
D	-331	GLY	-	expression tag	UNP P0AEX9
D	-330	THR	-	expression tag	UNP P0AEX9
D	-329	LYS	-	expression tag	UNP P0AEX9
D	-328	THR	-	expression tag	UNP P0AEX9
D	37	GLY	-	linker	UNP P0AEX9
D	38	THR	-	linker	UNP P0AEX9
D	39	ASP	-	linker	UNP P0AEX9
D	40	TYR	-	linker	UNP P0AEX9
D	41	ASP	-	linker	UNP P0AEX9
D	42	ILE	-	linker	UNP P0AEX9
D	43	PRO	-	linker	UNP P0AEX9
D	44	THR	-	linker	UNP P0AEX9
D	45	THR	-	linker	UNP P0AEX9
D	46	LEU	-	linker	UNP P0AEX9
D	47	GLU	-	linker	UNP P0AEX9
D	48	VAL	-	linker	UNP P0AEX9
D	49	LEU	-	linker	UNP P0AEX9
D	50	PHE	-	linker	UNP P0AEX9
D	51	GLN	-	linker	UNP P0AEX9
D	52	GLY	-	linker	UNP P0AEX9
D	53	PRO	-	linker	UNP P0AEX9
D	54	LEU	-	linker	UNP P0AEX9
D	55	GLY	-	linker	UNP P0AEX9
D	56	SER	-	linker	UNP P0AEX9
D	296	CYS	SER	conflict	UNP P35259
E	-341	MET	-	initiating methionine	UNP P0AEX9
E	-340	GLY	-	expression tag	UNP P0AEX9
E	-339	SER	-	expression tag	UNP P0AEX9
E	-338	SER	-	expression tag	UNP P0AEX9
E	-337	HIS	-	expression tag	UNP P0AEX9
E	-336	HIS	-	expression tag	UNP P0AEX9
E	-335	HIS	-	expression tag	UNP P0AEX9
E	-334	HIS	-	expression tag	UNP P0AEX9
E	-333	HIS	-	expression tag	UNP P0AEX9
E	-332	HIS	-	expression tag	UNP P0AEX9

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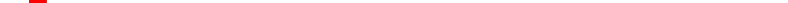
Chain	Residue	Modelled	Actual	Comment	Reference
E	-331	GLY	-	expression tag	UNP P0AEX9
E	-330	THR	-	expression tag	UNP P0AEX9
E	-329	LYS	-	expression tag	UNP P0AEX9
E	-328	THR	-	expression tag	UNP P0AEX9
E	37	GLY	-	linker	UNP P0AEX9
E	38	THR	-	linker	UNP P0AEX9
E	39	ASP	-	linker	UNP P0AEX9
E	40	TYR	-	linker	UNP P0AEX9
E	41	ASP	-	linker	UNP P0AEX9
E	42	ILE	-	linker	UNP P0AEX9
E	43	PRO	-	linker	UNP P0AEX9
E	44	THR	-	linker	UNP P0AEX9
E	45	THR	-	linker	UNP P0AEX9
E	46	LEU	-	linker	UNP P0AEX9
E	47	GLU	-	linker	UNP P0AEX9
E	48	VAL	-	linker	UNP P0AEX9
E	49	LEU	-	linker	UNP P0AEX9
E	50	PHE	-	linker	UNP P0AEX9
E	51	GLN	-	linker	UNP P0AEX9
E	52	GLY	-	linker	UNP P0AEX9
E	53	PRO	-	linker	UNP P0AEX9
E	54	LEU	-	linker	UNP P0AEX9
E	55	GLY	-	linker	UNP P0AEX9
E	56	SER	-	linker	UNP P0AEX9
E	296	CYS	SER	conflict	UNP P35259

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	

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

- Molecule 2: Maltose/maltodextrin-binding periplasmic protein, Polymerase cofactor VP35

Chain B:  30% 68%

[illegible]

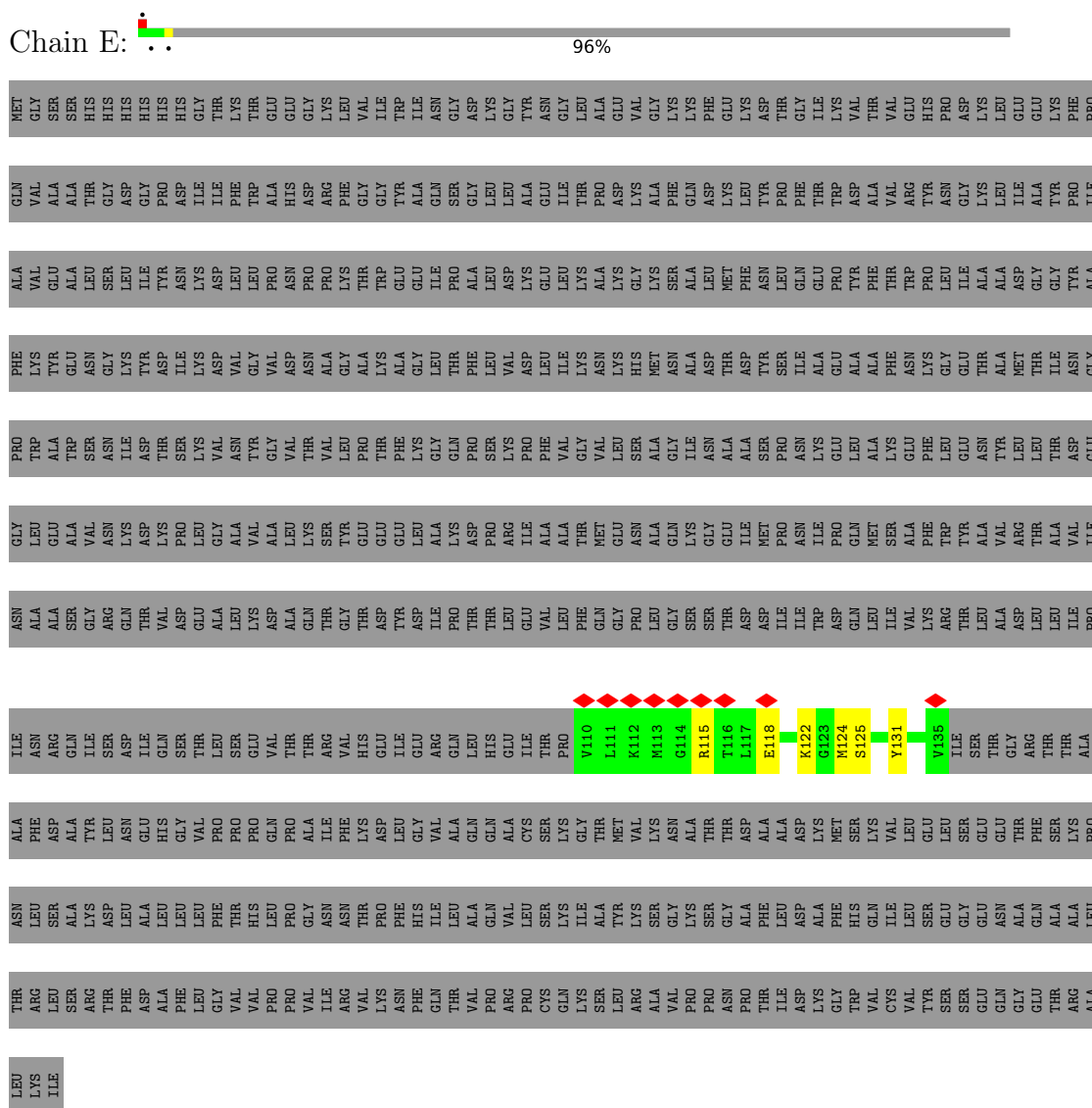
Node ID	Count	Color	Marker
R268	1	Green	
R271	1	Yellow	
D274	1	Green	Red Diamond
P281	1	Yellow	
R285	1	Green	
V286	1	Green	
K287	1	Green	Red Diamond
P304	1	Green	Red Diamond
P305	1	Green	Red Diamond
N306	1	Green	Red Diamond
W313	1	Yellow	
S318	1	Green	
S319	1	Green	
E320	1	Green	Red Diamond
Q321	1	Green	Red Diamond
G322	1	Green	Red Diamond
E323	1	Green	Red Diamond
K328	1	Green	
I329	1	Yellow	

- Molecule 2: Maltose/maltodextrin-binding periplasmic protein, Polymerase cofactor VP35

Chain C: 9% 91%



- Molecule 2: Maltose/maltodextrin-binding periplasmic protein, Polymerase cofactor VP35



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	178297	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 ($e^-/\text{\AA}^2$)	52.52	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.487	Depositor
Minimum map value	-0.913	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.135	Depositor
Map size (Å)	217.856, 217.856, 217.856	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.851, 0.851, 0.851	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.28	0/11326	0.61	15/15360 (0.1%)
2	B	0.30	1/1684 (0.1%)	0.51	0/2283
2	C	0.79	2/481 (0.4%)	0.87	3/652 (0.5%)
2	D	0.44	0/246	0.86	1/329 (0.3%)
2	E	0.25	0/202	0.57	0/267
All	All	0.32	3/13939 (0.0%)	0.62	19/18891 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	158	PRO	CA-C	12.78	1.60	1.52
2	C	159	PRO	CA-C	5.97	1.55	1.51
2	B	281	PRO	CA-C	5.95	1.55	1.51

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	158	PRO	O-C-N	13.89	127.68	121.15
1	A	892	CYS	N-CA-C	8.17	119.97	111.14
1	A	515	GLN	N-CA-C	7.97	119.75	111.14
1	A	743	MET	CG-SD-CE	7.76	117.97	100.90
1	A	794	GLU	CA-CB-CG	7.54	129.17	114.10
1	A	296	LYS	CD-CE-NZ	-7.52	87.82	111.90
1	A	478	ILE	CB-CA-C	-6.66	100.56	110.82
1	A	486	LYS	CB-CG-CD	6.62	126.53	111.30
1	A	605	LYS	CB-CG-CD	-6.54	96.26	111.30
2	D	113	MET	N-CA-CB	6.48	119.46	110.07
1	A	793	GLU	CA-CB-CG	-5.85	102.41	114.10
2	C	124	MET	CB-CG-SD	-5.80	95.28	112.70
1	A	517	LYS	N-CA-C	5.63	122.79	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	597	MET	CB-CG-SD	5.52	129.27	112.70
1	A	793	GLU	N-CA-CB	-5.49	102.03	110.16
1	A	514	PHE	N-CA-C	5.45	118.13	110.23
1	A	1306	MET	CB-CG-SD	-5.37	96.61	112.70
2	C	159	PRO	O-C-N	5.25	123.73	121.31
1	A	828	LEU	CB-CG-CD2	-5.05	95.53	110.70

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	11049	0	10953	140	0
2	B	1649	0	1679	9	0
2	C	471	0	479	3	0
2	D	244	0	264	11	0
2	E	201	0	216	4	0
3	A	1	0	0	0	0
All	All	13615	0	13591	162	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 6.

All (162) 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:1040:ARG:NH1	1:A:1246:GLU:OE1	2.07	0.88
1:A:498:ASP:OD2	1:A:694:ARG:HD2	1.82	0.79
1:A:1260:ASP:OD2	1:A:1263:LYS:NZ	2.17	0.77
1:A:743:MET:HG2	1:A:744:GLY:H	1.50	0.76
2:B:260:GLU:OE2	2:B:268:ARG:NH1	2.19	0.75
1:A:513:ARG:CZ	1:A:514:PHE:CE1	2.70	0.75
1:A:743:MET:CE	1:A:803:TYR:HB3	2.18	0.73
1:A:490:THR:OG1	1:A:517:LYS:O	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1262:GLU:O	1:A:1266:ILE:HD12	1.89	0.72
1:A:513:ARG:NH1	1:A:514:PHE:CE1	2.59	0.69
1:A:636:LEU:HD11	1:A:747:GLN:HB3	1.73	0.68
1:A:623:GLU:N	1:A:623:GLU:OE1	2.26	0.68
1:A:389:LEU:HD11	1:A:679:VAL:HG23	1.77	0.67
1:A:1269:LEU:HD11	1:A:1280:VAL:HG21	1.75	0.67
1:A:514:PHE:CZ	1:A:517:LYS:HD2	2.31	0.66
1:A:609:LEU:HD13	1:A:623:GLU:HG3	1.79	0.65
1:A:535:LEU:O	1:A:539:GLU:HG2	1.96	0.65
2:B:149:ASP:OD1	2:B:153:ASN:ND2	2.30	0.64
1:A:743:MET:HE1	1:A:803:TYR:HB3	1.78	0.64
2:D:110:VAL:HA	2:D:113:MET:SD	2.38	0.63
1:A:75:ILE:HG22	1:A:79:ILE:HG13	1.81	0.63
2:B:123:GLY:HA3	2:C:124:MET:CE	2.29	0.63
1:A:1199:VAL:HG12	1:A:1200:GLN:HG2	1.80	0.62
1:A:1191:SER:OG	1:A:1320:SER:OG	2.16	0.62
1:A:162:ILE:HG13	1:A:173:TRP:HD1	1.65	0.61
1:A:1237:PRO:O	1:A:1242:LYS:NZ	2.32	0.61
1:A:185:ILE:HG13	1:A:186:ALA:H	1.66	0.61
1:A:496:CYS:HB3	1:A:512:VAL:HG13	1.82	0.61
1:A:972:PRO:HG3	1:A:1035:ALA:HB2	1.82	0.60
1:A:39:LYS:HD2	1:A:685:PRO:HG2	1.83	0.60
1:A:1255:THR:HG22	1:A:1256:GLN:H	1.66	0.60
1:A:645:TYR:O	1:A:649:ARG:HG3	2.02	0.60
1:A:602:ARG:NH2	1:A:1312:ASN:HD22	2.01	0.59
2:D:123:GLY:HA3	2:E:124:MET:HE2	1.85	0.59
1:A:488:ARG:HB2	1:A:519:VAL:HG21	1.84	0.58
1:A:771:ASN:OD1	1:A:774:ARG:NH1	2.37	0.58
1:A:1149:LEU:HD23	1:A:1367:VAL:HG22	1.86	0.58
2:C:130:LYS:HD3	2:D:131:TYR:CZ	2.39	0.58
1:A:743:MET:HE3	1:A:803:TYR:HB3	1.86	0.57
1:A:668:MET:HE3	1:A:710:GLY:HA2	1.87	0.57
1:A:1050:LEU:O	1:A:1054:GLU:HG3	2.04	0.57
1:A:1189:TYR:HB3	1:A:1372:MET:HE2	1.87	0.57
1:A:513:ARG:NH1	1:A:514:PHE:CZ	2.73	0.56
1:A:627:VAL:HG22	1:A:754:LEU:HD23	1.86	0.56
2:C:123:GLY:HA3	2:D:124:MET:HE2	1.87	0.56
1:A:628:ARG:NH1	1:A:764:GLN:OE1	2.39	0.56
1:A:110:ASN:ND2	1:A:862:TRP:HD1	2.02	0.55
1:A:551:PHE:CZ	1:A:711:ILE:HD13	2.42	0.55
1:A:1292:ILE:H	1:A:1292:ILE:HD12	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:ARG:CZ	1:A:217:ARG:HB3	2.36	0.54
1:A:1148:ASN:HB3	1:A:1368:THR:HG22	1.90	0.54
1:A:514:PHE:CD2	1:A:514:PHE:C	2.86	0.54
1:A:903:LEU:O	1:A:907:ILE:HG12	2.08	0.53
2:B:271:ARG:HH11	2:B:271:ARG:HG3	1.74	0.53
1:A:478:ILE:HD11	1:A:481:LEU:HA	1.90	0.53
1:A:1008:PHE:HD1	1:A:1008:PHE:N	2.07	0.52
1:A:1027:ASN:HB3	1:A:1028:PRO:HD3	1.91	0.52
1:A:1262:GLU:HG2	1:A:1266:ILE:HD11	1.91	0.52
1:A:957:SER:HB2	1:A:1099:LEU:HD23	1.91	0.52
1:A:5:THR:HG21	1:A:1061:ALA:HA	1.91	0.52
1:A:1253:TRP:CH2	1:A:1292:ILE:HA	2.45	0.52
1:A:818:SER:HB2	1:A:854:THR:HB	1.93	0.51
1:A:1390:LYS:HD3	1:A:1391:PRO:HD2	1.92	0.51
1:A:157:GLN:HG3	1:A:874:LEU:HD11	1.92	0.50
1:A:743:MET:HG2	1:A:744:GLY:N	2.24	0.50
1:A:521:GLU:N	1:A:521:GLU:OE1	2.44	0.50
2:D:124:MET:HE3	2:D:128:LEU:CD2	2.42	0.50
1:A:585:ALA:HB2	1:A:717:LYS:HE2	1.92	0.50
1:A:60:THR:HA	1:A:63:GLN:HG2	1.91	0.50
1:A:743:MET:CG	1:A:744:GLY:H	2.24	0.50
1:A:1008:PHE:N	1:A:1008:PHE:CD1	2.80	0.50
1:A:503:ARG:HH11	1:A:509:ASN:HD22	1.60	0.50
1:A:1057:ARG:C	1:A:1059:LEU:H	2.21	0.49
1:A:584:LEU:HD23	1:A:717:LYS:HB2	1.94	0.49
1:A:722:ILE:O	1:A:726:GLN:HG3	2.12	0.49
1:A:814:GLN:H	1:A:1312:ASN:HD21	1.60	0.49
2:B:135:VAL:HB	2:E:131:TYR:CZ	2.47	0.49
1:A:1275:LEU:HD21	1:A:1411:LEU:HD22	1.94	0.49
1:A:841:ALA:O	1:A:845:THR:HG23	2.13	0.49
1:A:1243:GLU:OE1	1:A:1272:ARG:NH2	2.46	0.48
1:A:373:SER:OG	1:A:817:GLN:OE1	2.32	0.48
1:A:1057:ARG:HD3	1:A:1058:THR:N	2.29	0.48
2:D:124:MET:HE3	2:D:128:LEU:HD21	1.94	0.48
1:A:1362:SER:OG	1:A:1363:SER:N	2.46	0.48
1:A:1394:VAL:HG12	1:A:1396:LEU:HD12	1.95	0.48
1:A:386:ASP:OD1	1:A:387:VAL:N	2.46	0.48
1:A:530:SER:H	1:A:533:GLN:HG2	1.78	0.47
1:A:890:ILE:O	1:A:894:LYS:HA	2.14	0.47
1:A:1057:ARG:O	1:A:1058:THR:HG22	2.14	0.47
2:B:285:ARG:NH1	2:B:318:SER:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:ARG:CG	1:A:218:ASP:H	2.28	0.47
1:A:551:PHE:CD1	1:A:677:MET:HE1	2.50	0.47
1:A:514:PHE:CE2	1:A:517:LYS:HD2	2.49	0.47
1:A:1104:GLU:CD	1:A:1104:GLU:C	2.82	0.47
1:A:1236:CYS:HB2	1:A:1413:SER:OG	2.14	0.47
1:A:602:ARG:NH2	1:A:1312:ASN:ND2	2.63	0.47
1:A:1154:ARG:HH12	1:A:1161:SER:HB3	1.80	0.47
2:B:313:TRP:CZ3	2:B:328:LYS:HB2	2.49	0.47
1:A:286:ILE:HD11	1:A:351:ALA:HA	1.97	0.46
1:A:875:LEU:HA	1:A:875:LEU:HD23	1.75	0.46
1:A:551:PHE:CE1	1:A:677:MET:HE1	2.51	0.46
1:A:688:CYS:SG	1:A:698:PRO:HG2	2.55	0.46
1:A:605:LYS:HE2	1:A:605:LYS:HB3	1.65	0.46
1:A:793:GLU:H	1:A:793:GLU:HG2	1.50	0.46
1:A:4:PRO:HB3	1:A:1074:LEU:HD13	1.98	0.46
1:A:736:LEU:O	1:A:738:LEU:HD12	2.15	0.45
1:A:543:TYR:C	1:A:545:ALA:H	2.24	0.45
1:A:632:PHE:HB3	1:A:797:VAL:HG22	1.98	0.45
1:A:910:GLN:HG3	1:A:917:PHE:CZ	2.51	0.45
1:A:692:ASP:OD1	1:A:692:ASP:N	2.49	0.45
1:A:852:SER:HB2	1:A:1308:ASN:OD1	2.17	0.44
1:A:889:ASP:OD1	1:A:890:ILE:N	2.51	0.44
2:D:110:VAL:O	2:D:113:MET:SD	2.74	0.44
1:A:484:PHE:HD1	1:A:575:ASN:ND2	2.15	0.44
1:A:1231:PRO:HG2	1:A:1282:ASN:O	2.18	0.44
1:A:1400:MET:HE3	1:A:1400:MET:HB2	1.74	0.44
1:A:149:MET:HE3	1:A:149:MET:HB3	1.93	0.44
1:A:614:TRP:HD1	1:A:615:HIS:CE1	2.36	0.44
2:D:115:ARG:HA	2:D:115:ARG:HD3	1.75	0.43
1:A:737:LYS:HA	1:A:737:LYS:HD3	1.81	0.43
1:A:217:ARG:HB3	1:A:217:ARG:NH2	2.33	0.43
1:A:845:THR:O	1:A:849:ARG:HG3	2.17	0.43
1:A:1103:LEU:HD23	1:A:1103:LEU:HA	1.62	0.43
1:A:514:PHE:CD2	1:A:514:PHE:O	2.72	0.43
1:A:596:MET:HE3	1:A:596:MET:HB2	1.86	0.43
2:E:122:LYS:O	2:E:125:SER:OG	2.27	0.43
1:A:1188:ASN:OD1	1:A:1325:GLY:HA3	2.19	0.43
1:A:848:GLU:OE1	1:A:926:ARG:HG2	2.18	0.43
1:A:310:GLN:O	1:A:798:HIS:NE2	2.46	0.43
1:A:608:LEU:HD23	1:A:608:LEU:HA	1.84	0.43
1:A:1189:TYR:HB3	1:A:1372:MET:CE	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:LYS:NZ	1:A:341:LEU:HD21	2.34	0.42
1:A:403:LYS:HD2	1:A:785:TYR:CE2	2.53	0.42
1:A:513:ARG:NH2	1:A:514:PHE:CE1	2.86	0.42
1:A:711:ILE:CG2	1:A:712:GLU:H	2.32	0.42
1:A:1281:LEU:HA	1:A:1284:LEU:HD23	2.01	0.42
1:A:690:THR:H	1:A:693:ASN:HB3	1.84	0.42
1:A:1252:LEU:HD22	1:A:1261:ARG:HD3	1.99	0.42
2:B:215:LEU:HD23	2:B:215:LEU:HA	1.91	0.42
2:D:108:THR:HB	2:D:112:LYS:NZ	2.34	0.42
2:E:115:ARG:O	2:E:118:GLU:HG2	2.19	0.42
1:A:1256:GLN:HG3	1:A:1385:TYR:CE2	2.53	0.42
1:A:1129:ARG:HH12	1:A:1384:GLU:CD	2.27	0.42
1:A:482:SER:HB2	1:A:1052:TYR:CE2	2.54	0.42
1:A:626:ILE:HD11	1:A:757:ILE:HA	2.02	0.42
1:A:602:ARG:HH22	1:A:1312:ASN:ND2	2.18	0.41
1:A:602:ARG:HH22	1:A:1312:ASN:HD22	1.63	0.41
1:A:770:LEU:HD23	1:A:770:LEU:HA	1.88	0.41
1:A:959:LYS:HE3	1:A:1095:LEU:O	2.21	0.41
1:A:1251:LEU:HD22	1:A:1265:LEU:HD21	2.01	0.41
1:A:269:ASP:O	1:A:370:GLU:HG3	2.21	0.41
1:A:476:LYS:HG3	1:A:477:ILE:HD12	2.02	0.41
1:A:1295:ARG:HD3	1:A:1298:ASP:OD1	2.20	0.41
1:A:543:TYR:C	1:A:545:ALA:N	2.78	0.41
1:A:742:VAL:HG12	1:A:743:MET:O	2.21	0.41
2:B:183:ASN:O	2:B:186:THR:OG1	2.33	0.41
2:D:113:MET:HG2	2:D:114:GLY:N	2.36	0.41
2:D:122:LYS:O	2:D:125:SER:OG	2.32	0.41
1:A:1381:VAL:HG23	1:A:1381:VAL:O	2.21	0.41
1:A:293:ASP:O	1:A:296:LYS:N	2.42	0.40
1:A:339:LEU:HA	1:A:339:LEU:HD23	1.86	0.40
1:A:123:LEU:HG	1:A:1146:TRP:NE1	2.36	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	A	1352/1851 (73%)	1288 (95%)	63 (5%)	1 (0%)	48	69
2	B	215/671 (32%)	212 (99%)	3 (1%)	0	100	100
2	C	61/671 (9%)	60 (98%)	1 (2%)	0	100	100
2	D	30/671 (4%)	30 (100%)	0	0	100	100
2	E	24/671 (4%)	24 (100%)	0	0	100	100
All	All	1682/4535 (37%)	1614 (96%)	67 (4%)	1 (0%)	49	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	544	LEU

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	1226/1617 (76%)	1224 (100%)	2 (0%)	87	95
2	B	179/554 (32%)	179 (100%)	0	100	100
2	C	49/554 (9%)	49 (100%)	0	100	100
2	D	28/554 (5%)	28 (100%)	0	100	100
2	E	22/554 (4%)	22 (100%)	0	100	100
All	All	1504/3833 (39%)	1502 (100%)	2 (0%)	87	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	712	GLU
1	A	1008	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	HIS
1	A	157	GLN
1	A	360	GLN
1	A	375	GLN
1	A	377	HIS
1	A	397	GLN
1	A	426	GLN
1	A	444	GLN
1	A	449	ASN
1	A	509	ASN
1	A	575	ASN
1	A	696	ASN
1	A	811	ASN
1	A	887	ASN
1	A	938	GLN
1	A	1141	GLN
1	A	1202	HIS
1	A	1282	ASN
1	A	1287	HIS
1	A	1299	GLN
1	A	1312	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

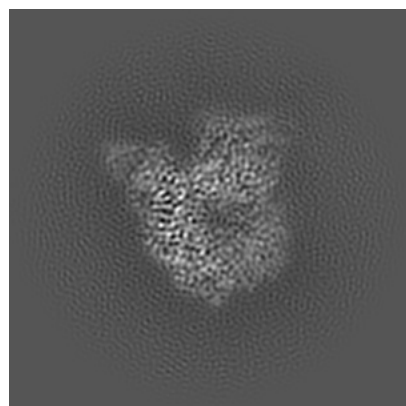
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60757. These allow visual inspection of the internal detail of the map and identification of artifacts.

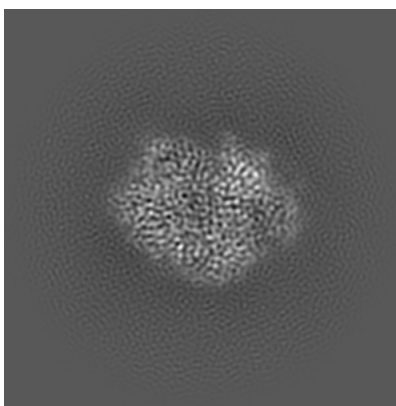
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

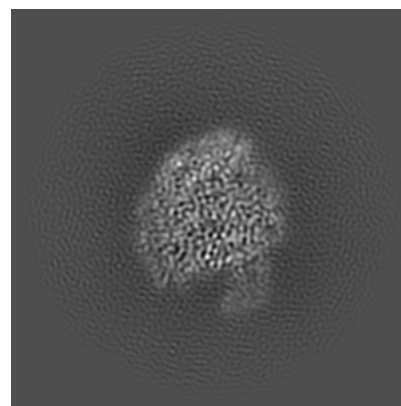
6.1.1 Primary map



X

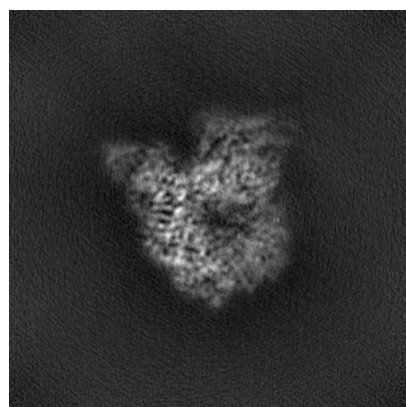


Y

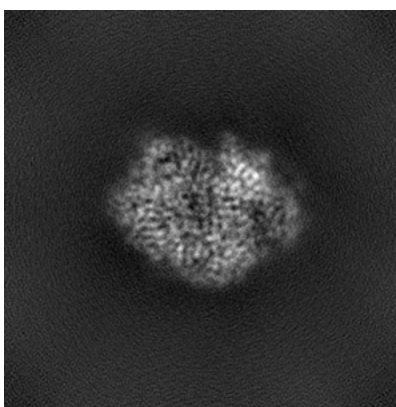


Z

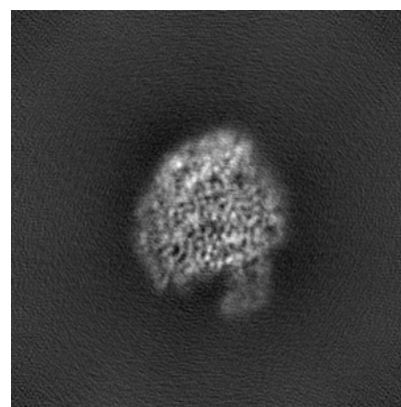
6.1.2 Raw map



X



Y

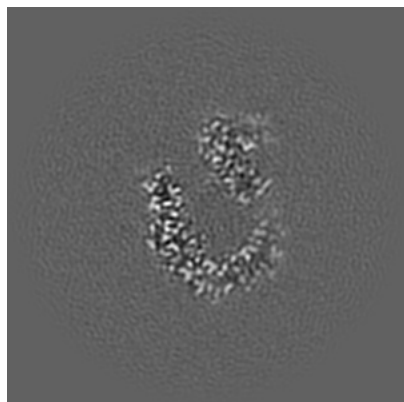


Z

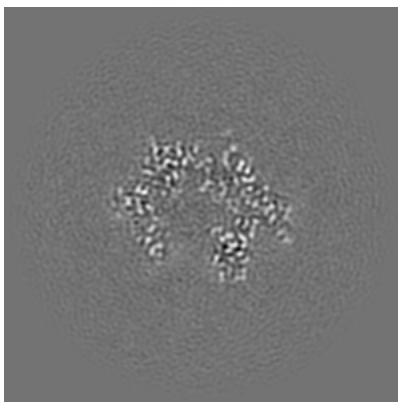
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

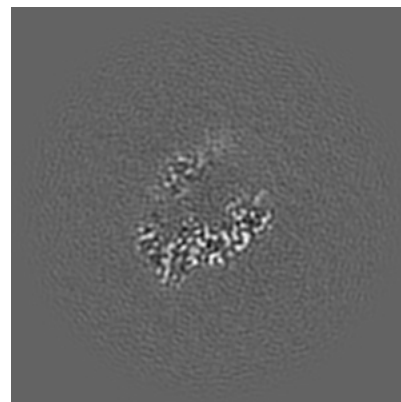
6.2.1 Primary map



X Index: 128

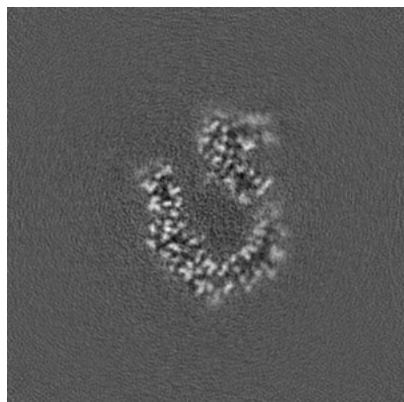


Y Index: 128

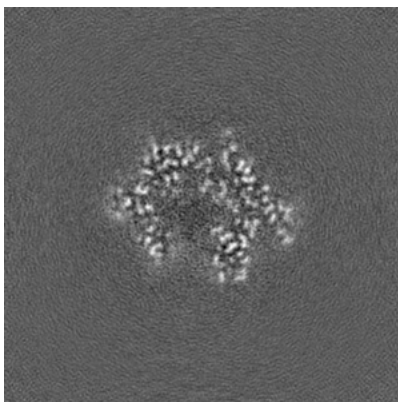


Z Index: 128

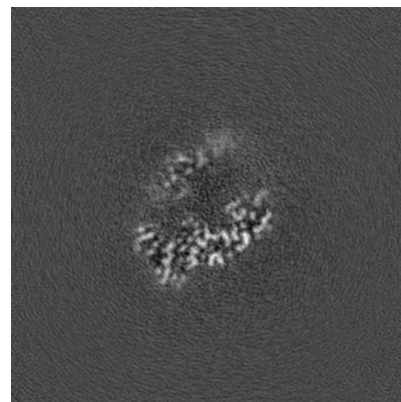
6.2.2 Raw map



X Index: 128



Y Index: 128

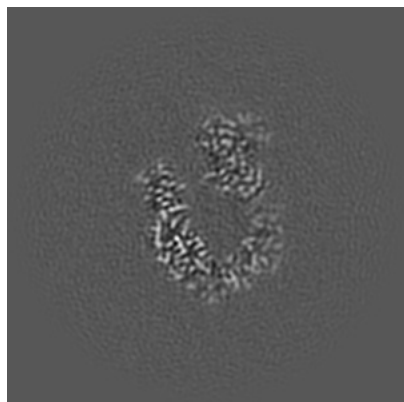


Z Index: 128

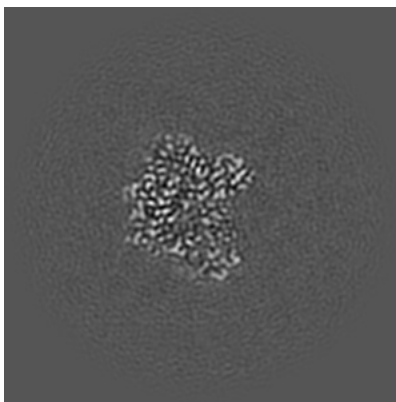
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

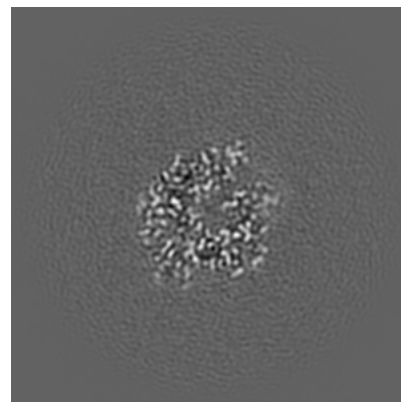
6.3.1 Primary map



X Index: 125

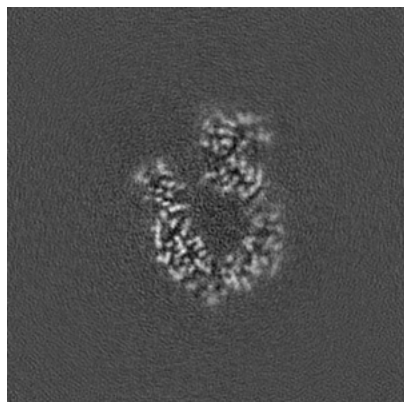


Y Index: 111

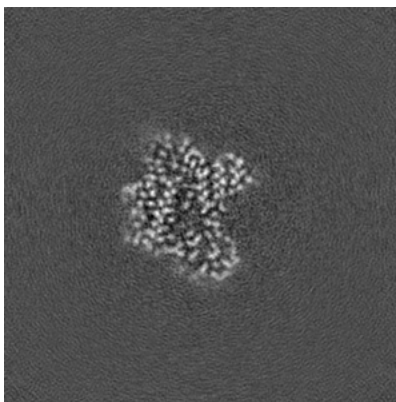


Z Index: 140

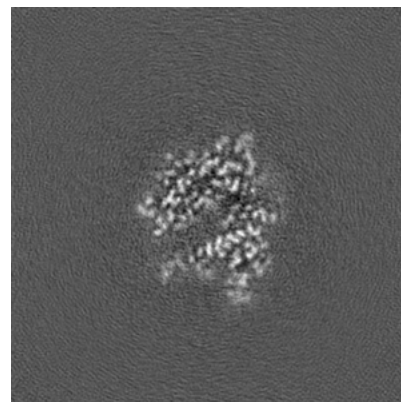
6.3.2 Raw map



X Index: 125



Y Index: 110

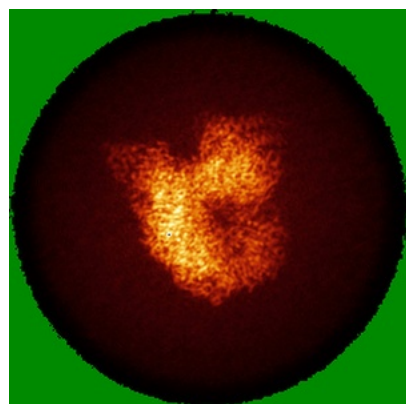


Z Index: 149

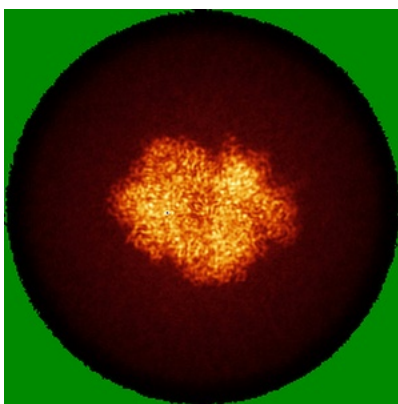
The images above show the largest variance slices of the map in three orthogonal directions.

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

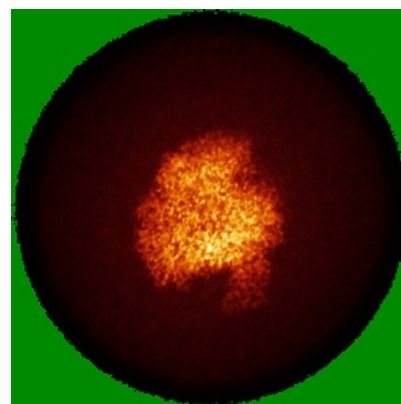
6.4.1 Primary map



X

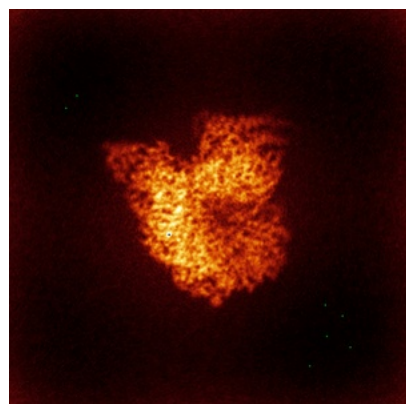


Y

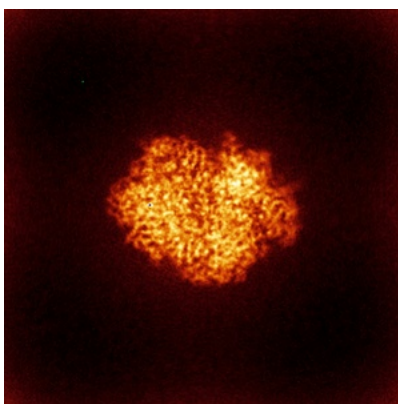


Z

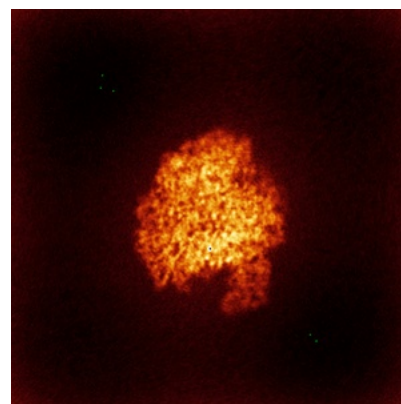
6.4.2 Raw map



X



Y

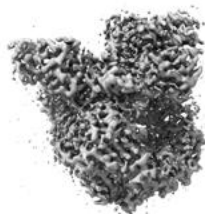


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



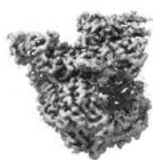
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.135. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

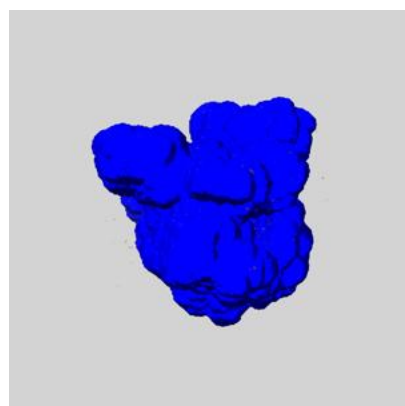
6.6 Mask visualisation [i](#)

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

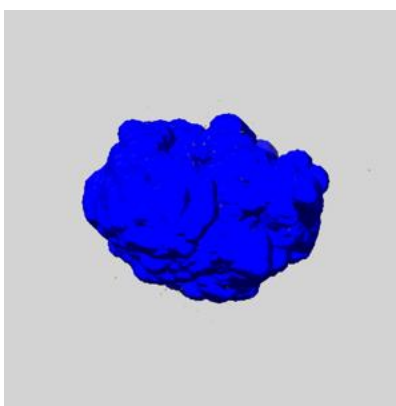
A mask typically either:

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

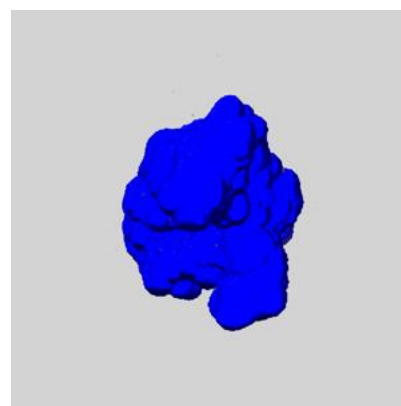
6.6.1 emd_60757_msk_1.map [i](#)



X



Y

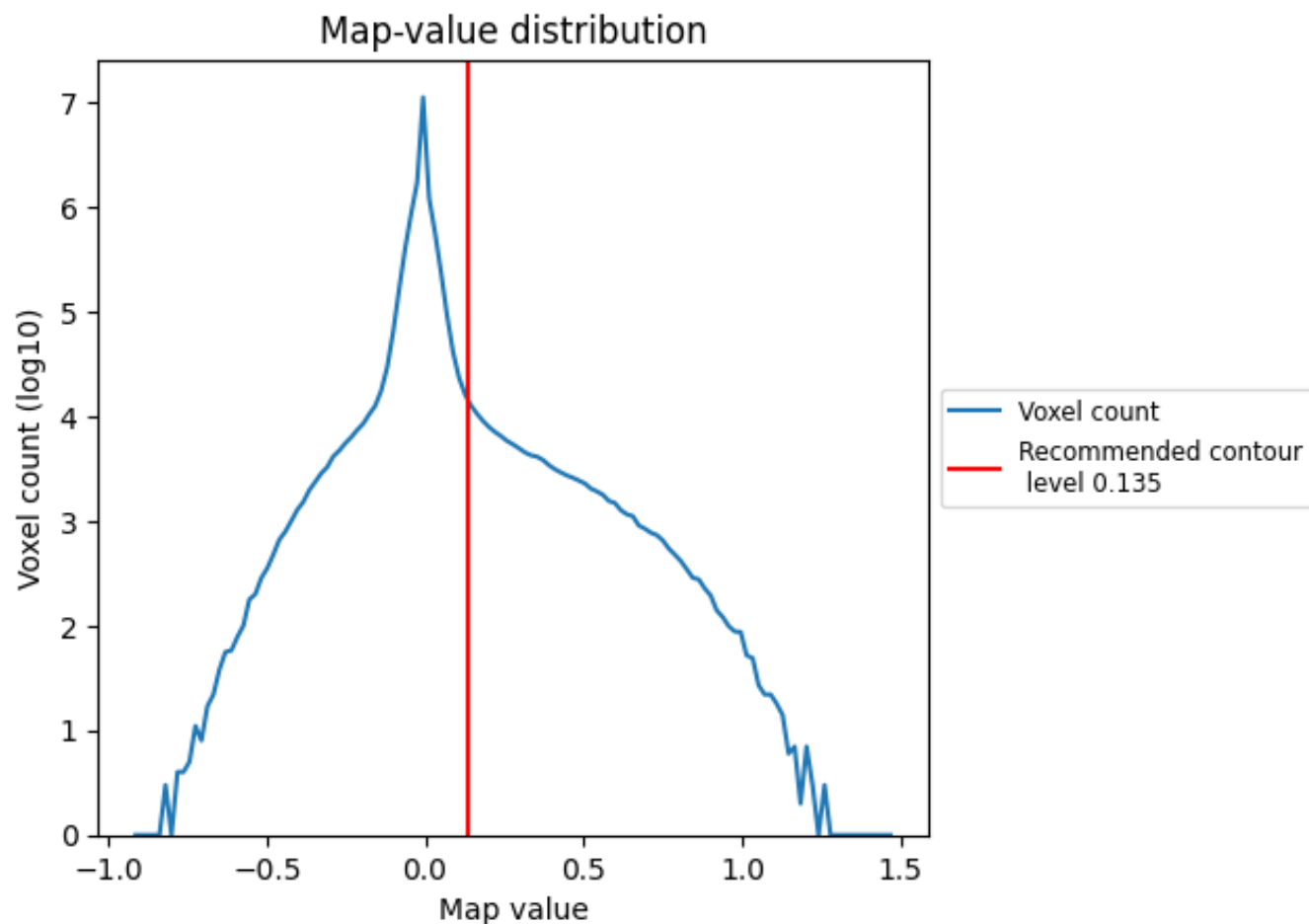


Z

7 Map analysis [i](#)

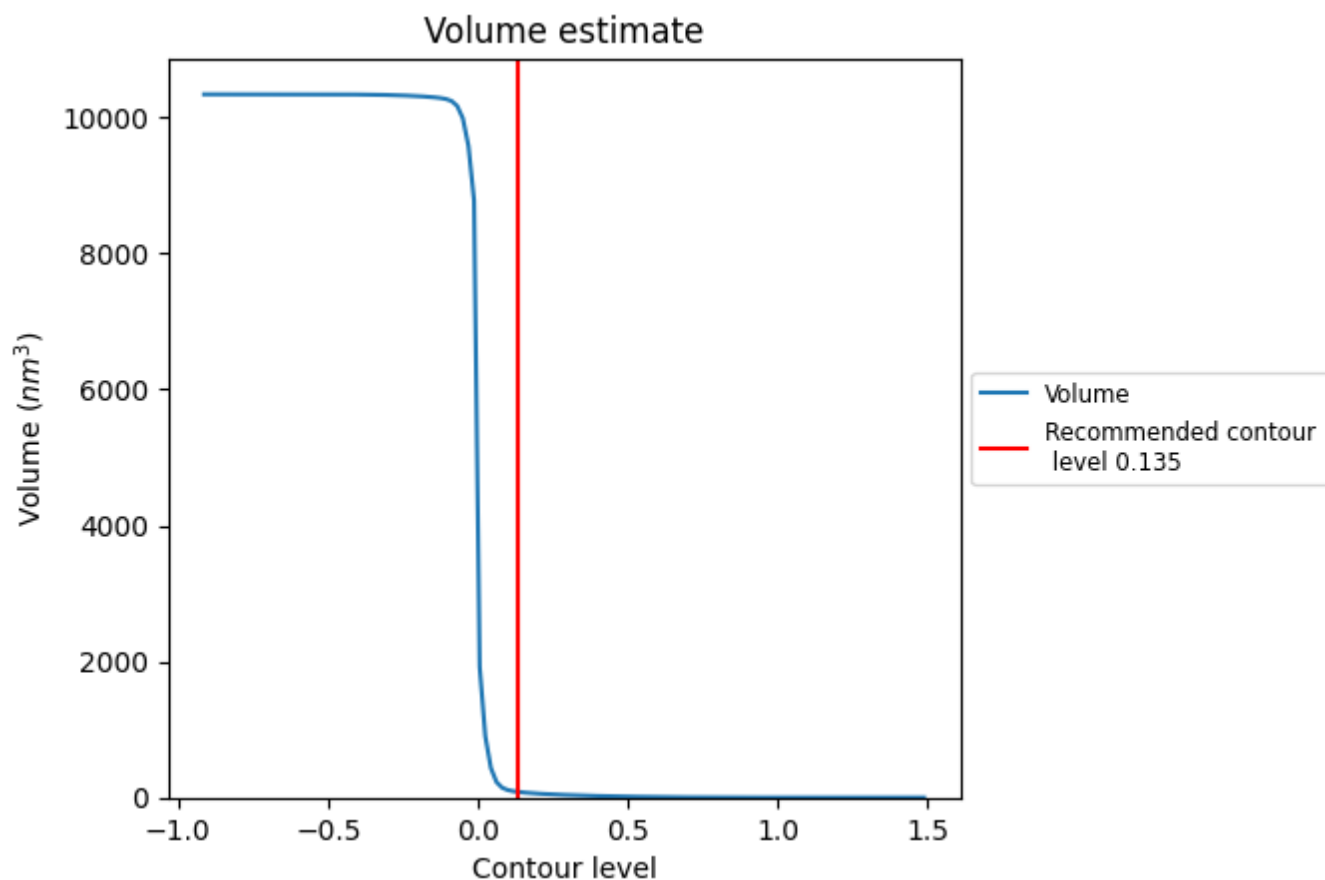
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

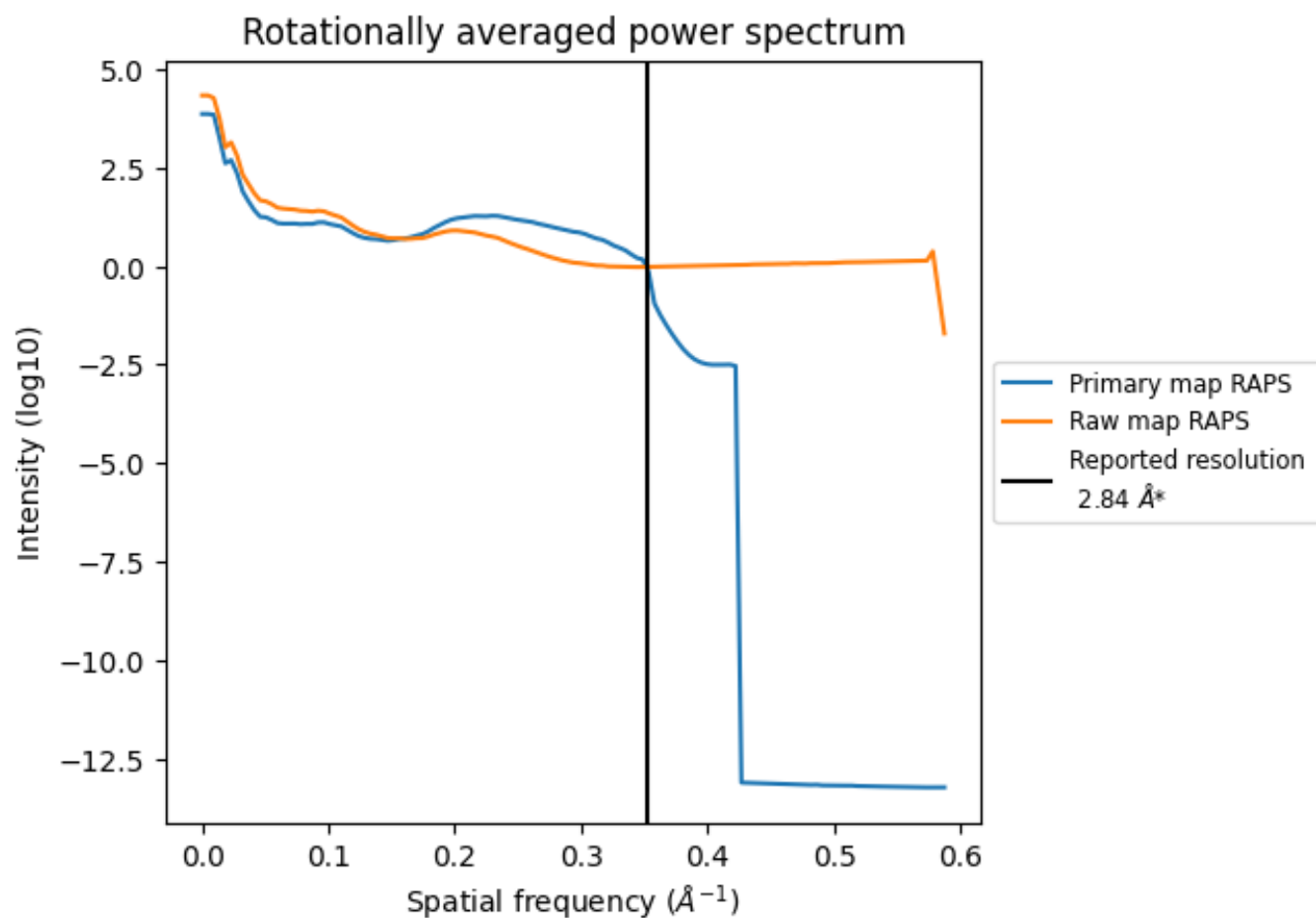
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 82 nm³; this corresponds to an approximate mass of 75 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 ⓘ

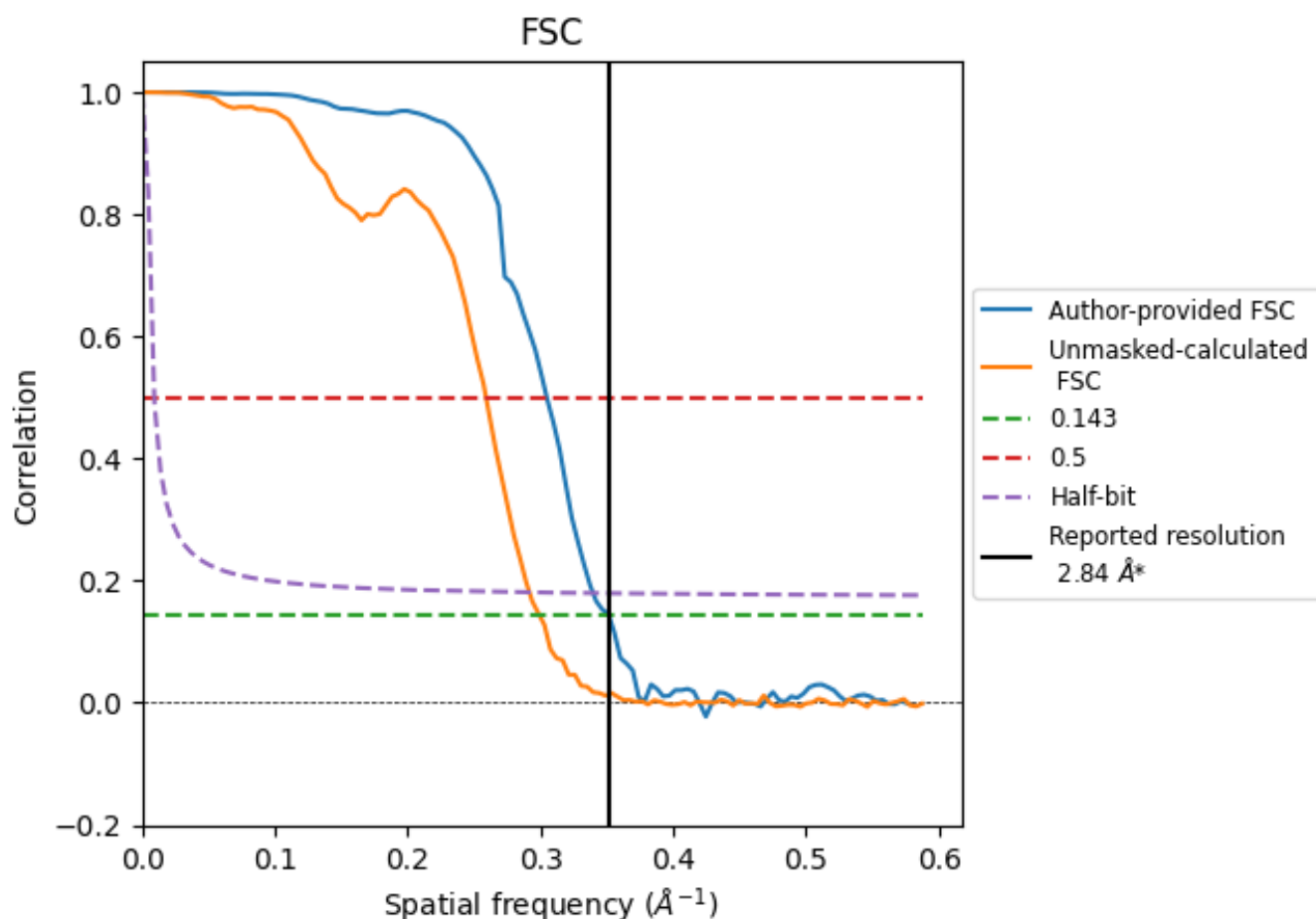


*Reported resolution corresponds to spatial frequency of 0.352 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.352 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

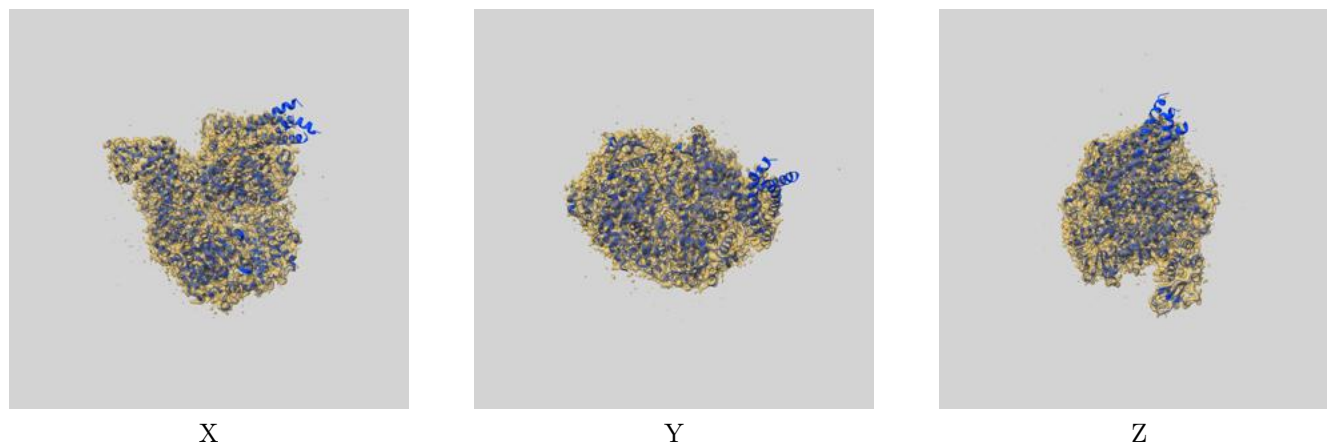
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	3.28	2.94
Unmasked-calculated*	3.34	3.86	3.43

*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 3.34 differs from the reported value 2.84 by more than 10 %

9 Map-model fit [i](#)

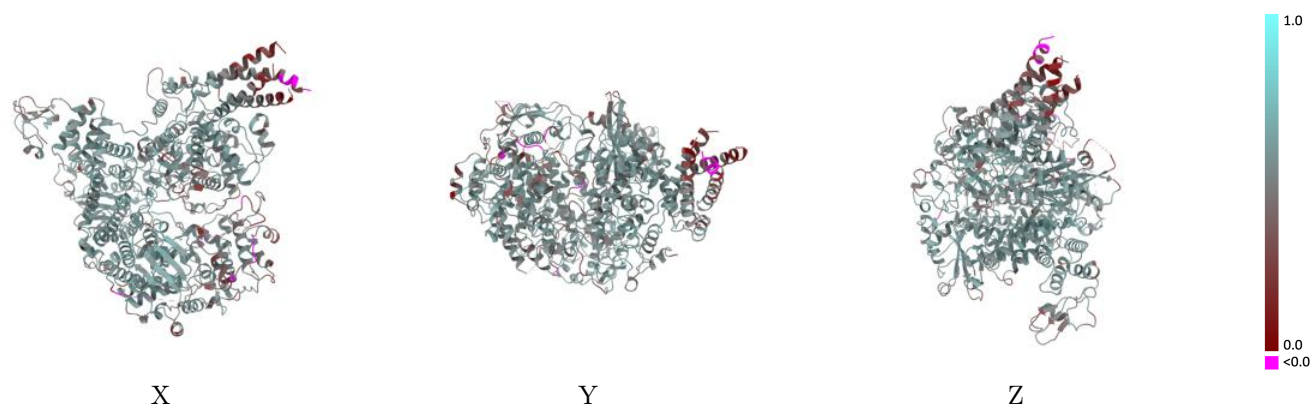
This section contains information regarding the fit between EMDB map EMD-60757 and PDB model 9IP4. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



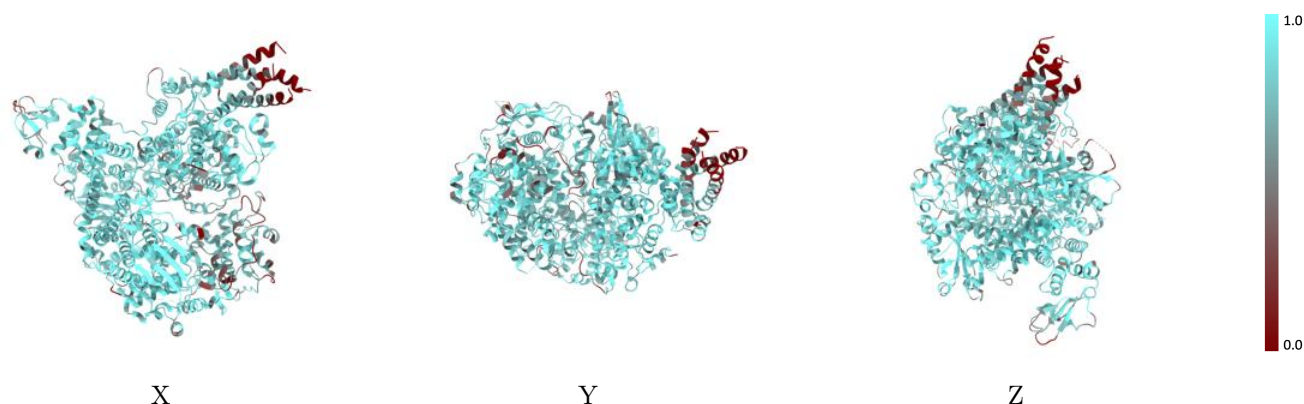
The images above show the 3D surface view of the map at the recommended contour level 0.135 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



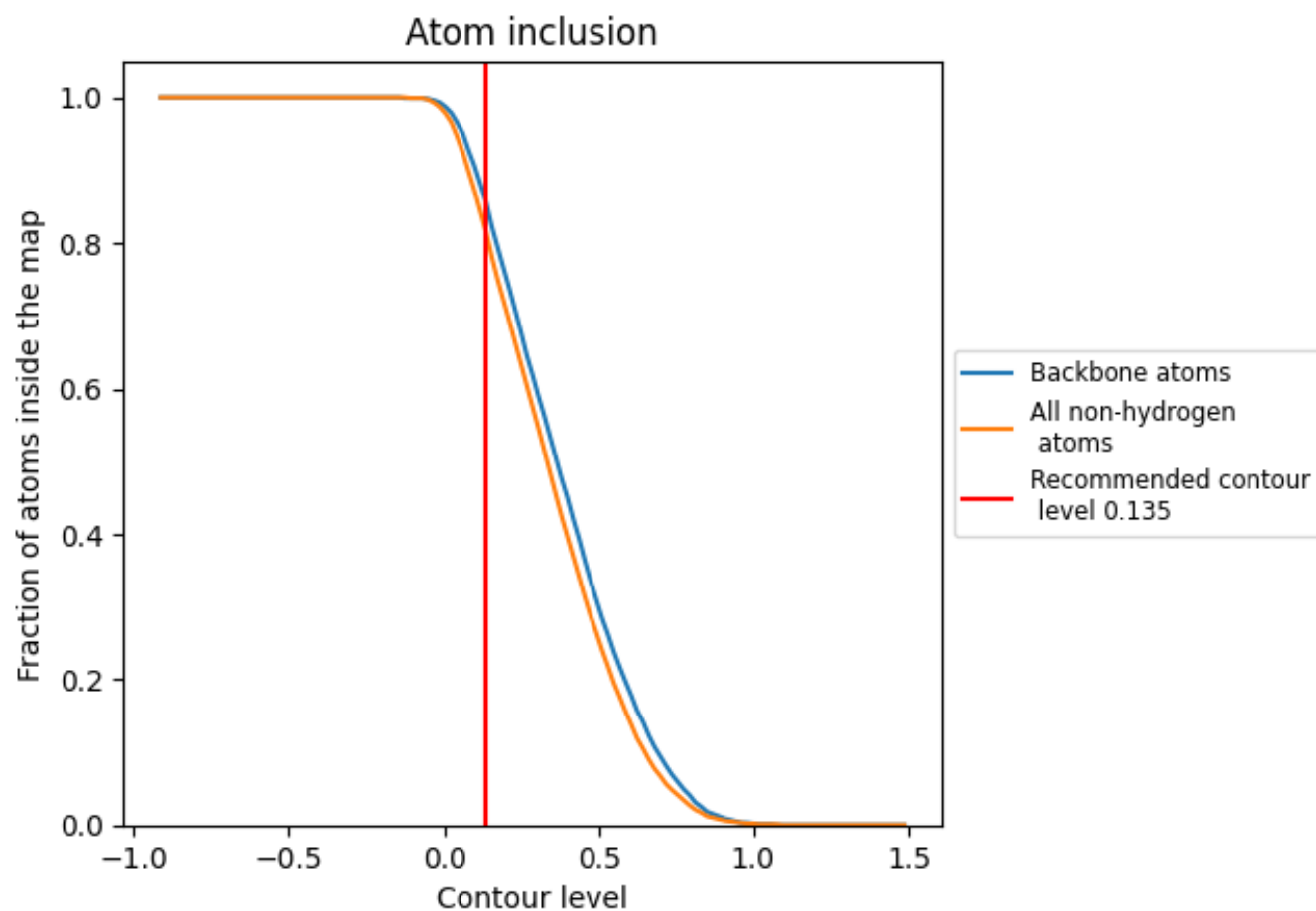
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.135).

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 (0.135) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8180	0.5310
A	0.8460	0.5440
B	0.7740	0.5150
C	0.6730	0.4680
D	0.4400	0.3360
E	0.4700	0.3660

