



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 04:22 PM UTC

PDB ID : 6YSZ / pdb_00006ysz
EMDB ID : EMD-10911
Title : Cryo-EM structure of T7 bacteriophage DNA translocation gp15 core protein intermediate assembly
Authors : Perez-Ruiz, M.; Pulido-Cid, M.; Luque-Ortega, J.R.; Cuervo, A.; Carrascosa, J.L.
Deposited on : 2020-04-23
Resolution : 3.60 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:

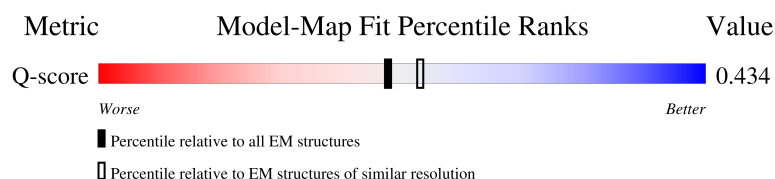
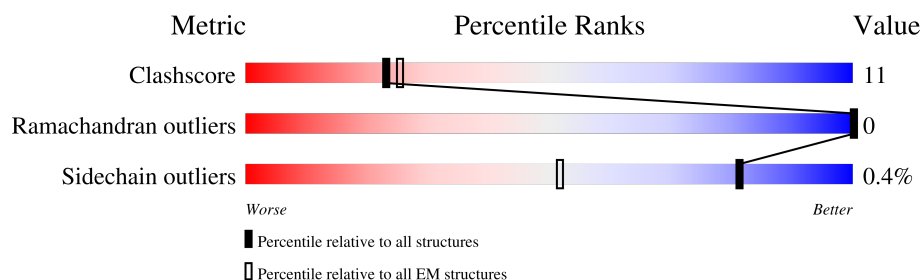
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.60 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	12797 (3.10 - 4.10)

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	782	
1	B	782	
1	C	782	
1	D	782	

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Mol	Chain	Length	Quality of chain
1	E	782	31%10%60%
1	F	782	30%10%60%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15192 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 Internal virion protein gp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	B	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	C	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	D	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	E	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		
1	F	316	Total	C	N	O	S	0	0
			2532	1558	457	507	10		

There are 210 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-34	MET	-	initiating methionine	UNP P03725
A	-33	ARG	-	expression tag	UNP P03725
A	-32	GLY	-	expression tag	UNP P03725
A	-31	SER	-	expression tag	UNP P03725
A	-30	HIS	-	expression tag	UNP P03725
A	-29	HIS	-	expression tag	UNP P03725
A	-28	HIS	-	expression tag	UNP P03725
A	-27	HIS	-	expression tag	UNP P03725
A	-26	HIS	-	expression tag	UNP P03725
A	-25	HIS	-	expression tag	UNP P03725
A	-24	GLY	-	expression tag	UNP P03725
A	-23	MET	-	expression tag	UNP P03725
A	-22	ALA	-	expression tag	UNP P03725
A	-21	SER	-	expression tag	UNP P03725
A	-20	MET	-	expression tag	UNP P03725
A	-19	THR	-	expression tag	UNP P03725
A	-18	GLY	-	expression tag	UNP P03725
A	-17	GLY	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	GLN	-	expression tag	UNP P03725
A	-15	GLN	-	expression tag	UNP P03725
A	-14	MET	-	expression tag	UNP P03725
A	-13	GLY	-	expression tag	UNP P03725
A	-12	ARG	-	expression tag	UNP P03725
A	-11	ASP	-	expression tag	UNP P03725
A	-10	LEU	-	expression tag	UNP P03725
A	-9	TYR	-	expression tag	UNP P03725
A	-8	ASP	-	expression tag	UNP P03725
A	-7	ASP	-	expression tag	UNP P03725
A	-6	ASP	-	expression tag	UNP P03725
A	-5	ASP	-	expression tag	UNP P03725
A	-4	LYS	-	expression tag	UNP P03725
A	-3	ASP	-	expression tag	UNP P03725
A	-2	PRO	-	expression tag	UNP P03725
A	-1	SER	-	expression tag	UNP P03725
A	0	SER	-	expression tag	UNP P03725
B	-34	MET	-	initiating methionine	UNP P03725
B	-33	ARG	-	expression tag	UNP P03725
B	-32	GLY	-	expression tag	UNP P03725
B	-31	SER	-	expression tag	UNP P03725
B	-30	HIS	-	expression tag	UNP P03725
B	-29	HIS	-	expression tag	UNP P03725
B	-28	HIS	-	expression tag	UNP P03725
B	-27	HIS	-	expression tag	UNP P03725
B	-26	HIS	-	expression tag	UNP P03725
B	-25	HIS	-	expression tag	UNP P03725
B	-24	GLY	-	expression tag	UNP P03725
B	-23	MET	-	expression tag	UNP P03725
B	-22	ALA	-	expression tag	UNP P03725
B	-21	SER	-	expression tag	UNP P03725
B	-20	MET	-	expression tag	UNP P03725
B	-19	THR	-	expression tag	UNP P03725
B	-18	GLY	-	expression tag	UNP P03725
B	-17	GLY	-	expression tag	UNP P03725
B	-16	GLN	-	expression tag	UNP P03725
B	-15	GLN	-	expression tag	UNP P03725
B	-14	MET	-	expression tag	UNP P03725
B	-13	GLY	-	expression tag	UNP P03725
B	-12	ARG	-	expression tag	UNP P03725
B	-11	ASP	-	expression tag	UNP P03725
B	-10	LEU	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	TYR	-	expression tag	UNP P03725
B	-8	ASP	-	expression tag	UNP P03725
B	-7	ASP	-	expression tag	UNP P03725
B	-6	ASP	-	expression tag	UNP P03725
B	-5	ASP	-	expression tag	UNP P03725
B	-4	LYS	-	expression tag	UNP P03725
B	-3	ASP	-	expression tag	UNP P03725
B	-2	PRO	-	expression tag	UNP P03725
B	-1	SER	-	expression tag	UNP P03725
B	0	SER	-	expression tag	UNP P03725
C	-34	MET	-	initiating methionine	UNP P03725
C	-33	ARG	-	expression tag	UNP P03725
C	-32	GLY	-	expression tag	UNP P03725
C	-31	SER	-	expression tag	UNP P03725
C	-30	HIS	-	expression tag	UNP P03725
C	-29	HIS	-	expression tag	UNP P03725
C	-28	HIS	-	expression tag	UNP P03725
C	-27	HIS	-	expression tag	UNP P03725
C	-26	HIS	-	expression tag	UNP P03725
C	-25	HIS	-	expression tag	UNP P03725
C	-24	GLY	-	expression tag	UNP P03725
C	-23	MET	-	expression tag	UNP P03725
C	-22	ALA	-	expression tag	UNP P03725
C	-21	SER	-	expression tag	UNP P03725
C	-20	MET	-	expression tag	UNP P03725
C	-19	THR	-	expression tag	UNP P03725
C	-18	GLY	-	expression tag	UNP P03725
C	-17	GLY	-	expression tag	UNP P03725
C	-16	GLN	-	expression tag	UNP P03725
C	-15	GLN	-	expression tag	UNP P03725
C	-14	MET	-	expression tag	UNP P03725
C	-13	GLY	-	expression tag	UNP P03725
C	-12	ARG	-	expression tag	UNP P03725
C	-11	ASP	-	expression tag	UNP P03725
C	-10	LEU	-	expression tag	UNP P03725
C	-9	TYR	-	expression tag	UNP P03725
C	-8	ASP	-	expression tag	UNP P03725
C	-7	ASP	-	expression tag	UNP P03725
C	-6	ASP	-	expression tag	UNP P03725
C	-5	ASP	-	expression tag	UNP P03725
C	-4	LYS	-	expression tag	UNP P03725
C	-3	ASP	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PRO	-	expression tag	UNP P03725
C	-1	SER	-	expression tag	UNP P03725
C	0	SER	-	expression tag	UNP P03725
D	-34	MET	-	initiating methionine	UNP P03725
D	-33	ARG	-	expression tag	UNP P03725
D	-32	GLY	-	expression tag	UNP P03725
D	-31	SER	-	expression tag	UNP P03725
D	-30	HIS	-	expression tag	UNP P03725
D	-29	HIS	-	expression tag	UNP P03725
D	-28	HIS	-	expression tag	UNP P03725
D	-27	HIS	-	expression tag	UNP P03725
D	-26	HIS	-	expression tag	UNP P03725
D	-25	HIS	-	expression tag	UNP P03725
D	-24	GLY	-	expression tag	UNP P03725
D	-23	MET	-	expression tag	UNP P03725
D	-22	ALA	-	expression tag	UNP P03725
D	-21	SER	-	expression tag	UNP P03725
D	-20	MET	-	expression tag	UNP P03725
D	-19	THR	-	expression tag	UNP P03725
D	-18	GLY	-	expression tag	UNP P03725
D	-17	GLY	-	expression tag	UNP P03725
D	-16	GLN	-	expression tag	UNP P03725
D	-15	GLN	-	expression tag	UNP P03725
D	-14	MET	-	expression tag	UNP P03725
D	-13	GLY	-	expression tag	UNP P03725
D	-12	ARG	-	expression tag	UNP P03725
D	-11	ASP	-	expression tag	UNP P03725
D	-10	LEU	-	expression tag	UNP P03725
D	-9	TYR	-	expression tag	UNP P03725
D	-8	ASP	-	expression tag	UNP P03725
D	-7	ASP	-	expression tag	UNP P03725
D	-6	ASP	-	expression tag	UNP P03725
D	-5	ASP	-	expression tag	UNP P03725
D	-4	LYS	-	expression tag	UNP P03725
D	-3	ASP	-	expression tag	UNP P03725
D	-2	PRO	-	expression tag	UNP P03725
D	-1	SER	-	expression tag	UNP P03725
D	0	SER	-	expression tag	UNP P03725
E	-34	MET	-	initiating methionine	UNP P03725
E	-33	ARG	-	expression tag	UNP P03725
E	-32	GLY	-	expression tag	UNP P03725
E	-31	SER	-	expression tag	UNP P03725

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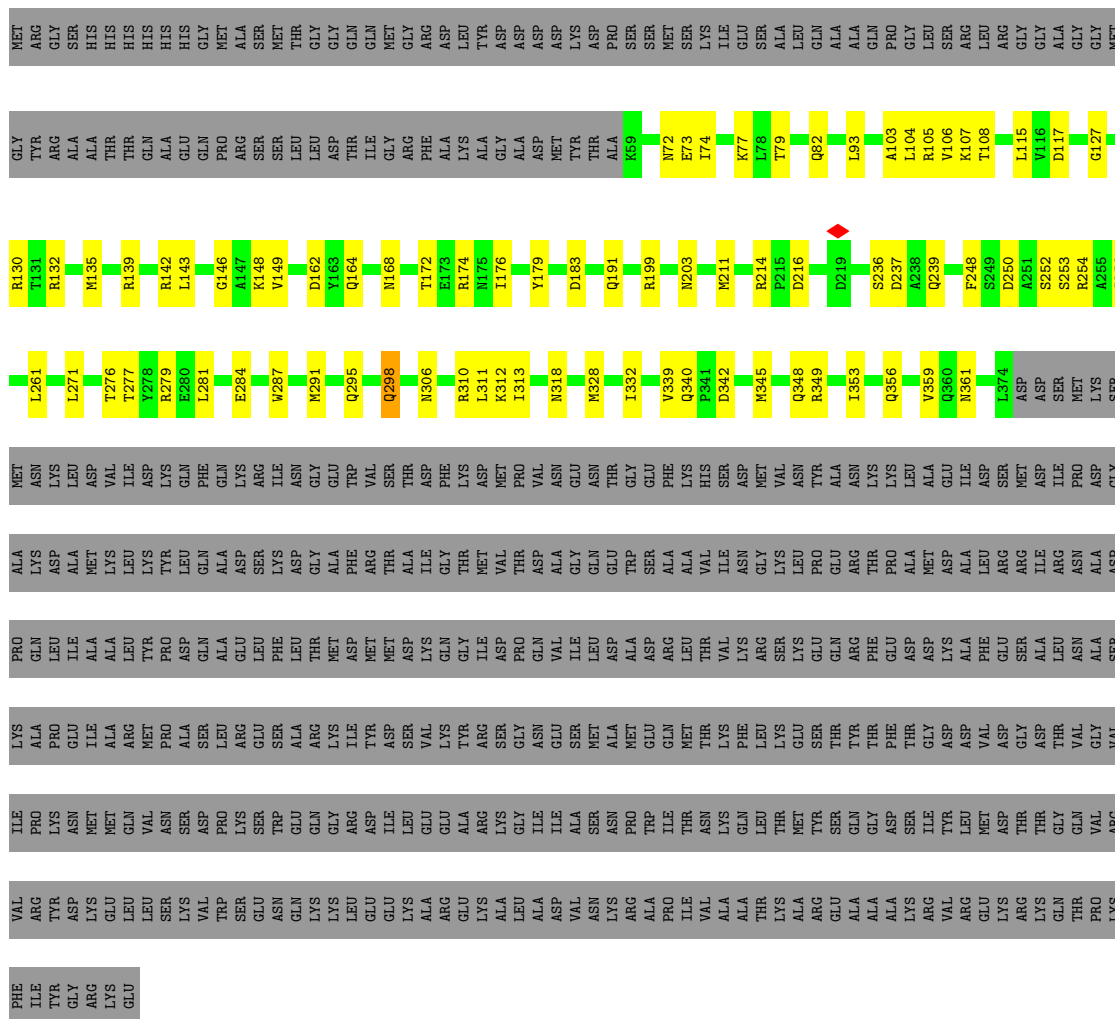
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Chain	Residue	Modelled	Actual	Comment	Reference
E	-30	HIS	-	expression tag	UNP P03725
E	-29	HIS	-	expression tag	UNP P03725
E	-28	HIS	-	expression tag	UNP P03725
E	-27	HIS	-	expression tag	UNP P03725
E	-26	HIS	-	expression tag	UNP P03725
E	-25	HIS	-	expression tag	UNP P03725
E	-24	GLY	-	expression tag	UNP P03725
E	-23	MET	-	expression tag	UNP P03725
E	-22	ALA	-	expression tag	UNP P03725
E	-21	SER	-	expression tag	UNP P03725
E	-20	MET	-	expression tag	UNP P03725
E	-19	THR	-	expression tag	UNP P03725
E	-18	GLY	-	expression tag	UNP P03725
E	-17	GLY	-	expression tag	UNP P03725
E	-16	GLN	-	expression tag	UNP P03725
E	-15	GLN	-	expression tag	UNP P03725
E	-14	MET	-	expression tag	UNP P03725
E	-13	GLY	-	expression tag	UNP P03725
E	-12	ARG	-	expression tag	UNP P03725
E	-11	ASP	-	expression tag	UNP P03725
E	-10	LEU	-	expression tag	UNP P03725
E	-9	TYR	-	expression tag	UNP P03725
E	-8	ASP	-	expression tag	UNP P03725
E	-7	ASP	-	expression tag	UNP P03725
E	-6	ASP	-	expression tag	UNP P03725
E	-5	ASP	-	expression tag	UNP P03725
E	-4	LYS	-	expression tag	UNP P03725
E	-3	ASP	-	expression tag	UNP P03725
E	-2	PRO	-	expression tag	UNP P03725
E	-1	SER	-	expression tag	UNP P03725
E	0	SER	-	expression tag	UNP P03725
F	-34	MET	-	initiating methionine	UNP P03725
F	-33	ARG	-	expression tag	UNP P03725
F	-32	GLY	-	expression tag	UNP P03725
F	-31	SER	-	expression tag	UNP P03725
F	-30	HIS	-	expression tag	UNP P03725
F	-29	HIS	-	expression tag	UNP P03725
F	-28	HIS	-	expression tag	UNP P03725
F	-27	HIS	-	expression tag	UNP P03725
F	-26	HIS	-	expression tag	UNP P03725
F	-25	HIS	-	expression tag	UNP P03725
F	-24	GLY	-	expression tag	UNP P03725

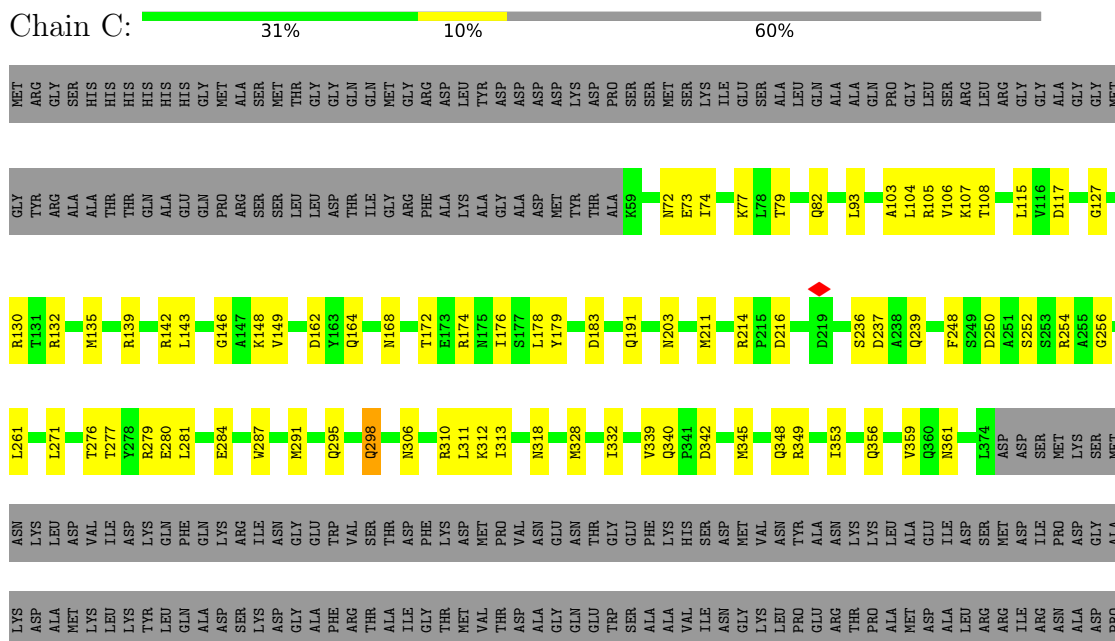
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Chain	Residue	Modelled	Actual	Comment	Reference
F	-23	MET	-	expression tag	UNP P03725
F	-22	ALA	-	expression tag	UNP P03725
F	-21	SER	-	expression tag	UNP P03725
F	-20	MET	-	expression tag	UNP P03725
F	-19	THR	-	expression tag	UNP P03725
F	-18	GLY	-	expression tag	UNP P03725
F	-17	GLY	-	expression tag	UNP P03725
F	-16	GLN	-	expression tag	UNP P03725
F	-15	GLN	-	expression tag	UNP P03725
F	-14	MET	-	expression tag	UNP P03725
F	-13	GLY	-	expression tag	UNP P03725
F	-12	ARG	-	expression tag	UNP P03725
F	-11	ASP	-	expression tag	UNP P03725
F	-10	LEU	-	expression tag	UNP P03725
F	-9	TYR	-	expression tag	UNP P03725
F	-8	ASP	-	expression tag	UNP P03725
F	-7	ASP	-	expression tag	UNP P03725
F	-6	ASP	-	expression tag	UNP P03725
F	-5	ASP	-	expression tag	UNP P03725
F	-4	LYS	-	expression tag	UNP P03725
F	-3	ASP	-	expression tag	UNP P03725
F	-2	PRO	-	expression tag	UNP P03725
F	-1	SER	-	expression tag	UNP P03725
F	0	SER	-	expression tag	UNP P03725



- Molecule 1: Internal virion protein gp15



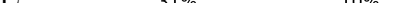
ILE	TRP	ARG	TRP	LYS	PRO	ALA	GLN
TRP	ASP	ASP	ASN	LYS	PRO	LEU	LEU
GLY	LYS	GLU	MET	MET	ILE	ILE	ILE
ARG	GLU	LEU	GLN	ALA	ARG	ALA	ALA
LYS	LEU	LEU	VAL	VAL	MET	TRP	TRP
GLU	SER	SER	ASN	ASN	PRO	PRO	PRO
	LYS	LYS	SER	SER	ALA	ASP	ASP
	VAL	VAL	ASP	ASP	SER	GLN	GLN
	TRP	TRP	PRO	PRO	LEU	ALA	ALA
	SER	SER	LYS	LYS	ARG	GLU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

- Molecule 1: Internal virion protein gp15

Chain D: 31% 9% 60%

[illegible]

- Molecule 1: Internal virion protein gp15

Chain E:  31% 10% 60%



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	50980	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.225	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0114	Depositor
Map size (Å)	204.0, 204.0, 204.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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	0.19	0/2569	0.35	0/3463
1	B	0.19	0/2569	0.35	0/3463
1	C	0.19	0/2569	0.35	0/3463
1	D	0.19	0/2569	0.35	0/3463
1	E	0.19	0/2569	0.35	0/3463
1	F	0.19	0/2569	0.35	0/3463
All	All	0.19	0/15414	0.35	0/20778

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	2532	0	2453	68	0
1	B	2532	0	2453	71	0
1	C	2532	0	2453	69	0
1	D	2532	0	2453	68	0
1	E	2532	0	2453	70	0
1	F	2532	0	2453	73	0
All	All	15192	0	14718	332	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 11.

All (332) 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:C:311:LEU:HD11	1:D:356:GLN:OE1	1.89	0.73
1:A:356:GLN:OE1	1:F:311:LEU:HD11	1.88	0.72
1:E:311:LEU:HD11	1:F:356:GLN:OE1	1.88	0.72
1:B:311:LEU:HD11	1:C:356:GLN:OE1	1.89	0.71
1:D:311:LEU:HD11	1:E:356:GLN:OE1	1.90	0.71
1:D:271:LEU:HD12	1:D:281:LEU:HD11	1.73	0.70
1:A:311:LEU:HD11	1:B:356:GLN:OE1	1.90	0.70
1:E:271:LEU:HD12	1:E:281:LEU:HD11	1.73	0.70
1:B:306:ASN:ND2	1:C:345:MET:HE3	2.07	0.70
1:A:271:LEU:HD12	1:A:281:LEU:HD11	1.73	0.69
1:C:271:LEU:HD12	1:C:281:LEU:HD11	1.73	0.69
1:E:306:ASN:ND2	1:F:345:MET:HE3	2.08	0.69
1:F:271:LEU:HD12	1:F:281:LEU:HD11	1.73	0.69
1:B:271:LEU:HD12	1:B:281:LEU:HD11	1.73	0.68
1:A:345:MET:HE3	1:F:306:ASN:ND2	2.08	0.68
1:C:306:ASN:ND2	1:D:345:MET:HE3	2.09	0.67
1:D:306:ASN:ND2	1:E:345:MET:HE3	2.11	0.66
1:E:306:ASN:HD22	1:F:345:MET:HE3	1.61	0.65
1:F:191:GLN:NE2	1:F:239:GLN:OE1	2.30	0.65
1:B:306:ASN:HD22	1:C:345:MET:HE3	1.62	0.65
1:B:191:GLN:NE2	1:B:239:GLN:OE1	2.30	0.65
1:C:191:GLN:NE2	1:C:239:GLN:OE1	2.30	0.65
1:E:191:GLN:NE2	1:E:239:GLN:OE1	2.30	0.65
1:D:191:GLN:NE2	1:D:239:GLN:OE1	2.30	0.65
1:A:254:ARG:HH11	1:B:284:GLU:CD	2.05	0.64
1:C:306:ASN:HD22	1:D:345:MET:HE3	1.63	0.64
1:C:72:ASN:OD1	1:C:107:LYS:NZ	2.30	0.64
1:A:191:GLN:NE2	1:A:239:GLN:OE1	2.30	0.64
1:A:72:ASN:OD1	1:A:107:LYS:NZ	2.30	0.63
1:D:306:ASN:HD22	1:E:345:MET:HE3	1.63	0.63
1:F:72:ASN:OD1	1:F:107:LYS:NZ	2.30	0.63
1:E:72:ASN:OD1	1:E:107:LYS:NZ	2.30	0.63
1:A:306:ASN:ND2	1:B:345:MET:HE3	2.13	0.63
1:A:345:MET:HE3	1:F:306:ASN:HD22	1.62	0.63
1:C:254:ARG:HH11	1:D:284:GLU:CD	2.07	0.62
1:E:254:ARG:HH11	1:F:284:GLU:CD	2.07	0.62
1:D:254:ARG:HH11	1:E:284:GLU:CD	2.08	0.62
1:A:284:GLU:CD	1:F:254:ARG:HH11	2.08	0.61
1:D:72:ASN:OD1	1:D:107:LYS:NZ	2.30	0.61
1:A:211:MET:SD	1:A:214:ARG:NH2	2.74	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:211:MET:SD	1:E:214:ARG:NH2	2.74	0.60
1:F:211:MET:SD	1:F:214:ARG:NH2	2.74	0.60
1:B:72:ASN:OD1	1:B:107:LYS:NZ	2.30	0.60
1:D:211:MET:SD	1:D:214:ARG:NH2	2.74	0.60
1:A:306:ASN:HD22	1:B:345:MET:HE3	1.66	0.60
1:C:310:ARG:HD3	1:D:353:ILE:HG21	1.83	0.60
1:B:211:MET:SD	1:B:214:ARG:NH2	2.74	0.60
1:E:310:ARG:HD3	1:F:353:ILE:HG21	1.82	0.60
1:A:353:ILE:HG21	1:F:310:ARG:HD3	1.83	0.60
1:C:211:MET:SD	1:C:214:ARG:NH2	2.74	0.60
1:B:254:ARG:HH11	1:C:284:GLU:CD	2.10	0.59
1:B:310:ARG:HD3	1:C:353:ILE:HG21	1.85	0.59
1:D:310:ARG:HD3	1:E:353:ILE:HG21	1.85	0.59
1:A:254:ARG:NH1	1:B:284:GLU:OE1	2.33	0.58
1:A:130:ARG:NH1	1:B:237:ASP:OD1	2.37	0.58
1:A:284:GLU:OE1	1:F:254:ARG:NH1	2.34	0.58
1:A:310:ARG:HD3	1:B:353:ILE:HG21	1.86	0.58
1:E:254:ARG:NH1	1:F:284:GLU:OE1	2.35	0.57
1:D:356:GLN:HA	1:D:359:VAL:HG12	1.88	0.55
1:A:73:GLU:HG3	1:B:164:GLN:OE1	2.06	0.55
1:D:130:ARG:NH1	1:E:237:ASP:OD1	2.39	0.55
1:D:73:GLU:HG3	1:E:164:GLN:OE1	2.06	0.55
1:E:356:GLN:HA	1:E:359:VAL:HG12	1.88	0.55
1:B:254:ARG:NH1	1:C:284:GLU:OE1	2.35	0.55
1:B:356:GLN:HA	1:B:359:VAL:HG12	1.88	0.55
1:E:132:ARG:NH2	1:E:183:ASP:OD2	2.40	0.55
1:C:356:GLN:HA	1:C:359:VAL:HG12	1.88	0.55
1:A:130:ARG:NE	1:B:237:ASP:OD2	2.40	0.55
1:A:356:GLN:HA	1:A:359:VAL:HG12	1.88	0.54
1:D:254:ARG:NH1	1:E:284:GLU:OE1	2.35	0.54
1:E:74:ILE:HG21	1:E:104:LEU:HD22	1.89	0.54
1:F:132:ARG:NH2	1:F:183:ASP:OD2	2.40	0.54
1:D:132:ARG:NH2	1:D:183:ASP:OD2	2.40	0.54
1:B:132:ARG:NH2	1:B:183:ASP:OD2	2.40	0.54
1:C:132:ARG:NH2	1:C:183:ASP:OD2	2.40	0.54
1:A:132:ARG:NH2	1:A:183:ASP:OD2	2.40	0.54
1:B:73:GLU:HG3	1:C:164:GLN:OE1	2.07	0.54
1:F:356:GLN:HA	1:F:359:VAL:HG12	1.88	0.54
1:C:130:ARG:NH1	1:D:237:ASP:OD1	2.41	0.54
1:F:74:ILE:HG21	1:F:104:LEU:HD22	1.89	0.54
1:B:73:GLU:OE2	1:B:77:LYS:NZ	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ILE:HG21	1:B:104:LEU:HD22	1.89	0.53
1:D:74:ILE:HG21	1:D:104:LEU:HD22	1.89	0.53
1:A:74:ILE:HG21	1:A:104:LEU:HD22	1.89	0.53
1:C:254:ARG:NH1	1:D:284:GLU:OE1	2.34	0.53
1:F:214:ARG:NH1	1:F:216:ASP:OD2	2.42	0.53
1:A:115:LEU:HD21	1:B:179:TYR:CD2	2.44	0.53
1:E:130:ARG:NH1	1:F:237:ASP:OD1	2.42	0.53
1:C:214:ARG:NH1	1:C:216:ASP:OD2	2.42	0.53
1:B:214:ARG:NH1	1:B:216:ASP:OD2	2.42	0.53
1:E:276:THR:OG1	1:E:277:THR:N	2.42	0.53
1:A:214:ARG:NH1	1:A:216:ASP:OD2	2.42	0.53
1:C:74:ILE:HG21	1:C:104:LEU:HD22	1.89	0.53
1:A:237:ASP:OD1	1:F:130:ARG:NH1	2.43	0.52
1:E:214:ARG:NH1	1:E:216:ASP:OD2	2.42	0.52
1:D:214:ARG:NH1	1:D:216:ASP:OD2	2.42	0.52
1:A:72:ASN:HB3	1:B:168:ASN:HB3	1.92	0.52
1:A:256:GLY:N	1:A:298:GLN:OE1	2.38	0.52
1:B:248:PHE:O	1:B:252:SER:N	2.43	0.52
1:B:276:THR:OG1	1:B:277:THR:N	2.42	0.52
1:D:73:GLU:OE2	1:D:77:LYS:NZ	2.41	0.52
1:A:73:GLU:OE2	1:A:77:LYS:NZ	2.41	0.52
1:A:127:GLY:O	1:B:236:SER:HA	2.09	0.52
1:C:248:PHE:O	1:C:252:SER:N	2.43	0.52
1:C:276:THR:OG1	1:C:277:THR:N	2.42	0.51
1:B:130:ARG:NH1	1:C:237:ASP:OD1	2.43	0.51
1:D:248:PHE:O	1:D:252:SER:N	2.43	0.51
1:D:130:ARG:NE	1:E:237:ASP:OD2	2.43	0.51
1:A:276:THR:OG1	1:A:277:THR:N	2.42	0.51
1:C:127:GLY:O	1:D:236:SER:HA	2.11	0.51
1:C:73:GLU:OE2	1:C:77:LYS:NZ	2.41	0.51
1:D:115:LEU:HD21	1:E:179:TYR:CD2	2.46	0.51
1:B:349:ARG:O	1:B:353:ILE:HG12	2.11	0.51
1:C:349:ARG:O	1:C:353:ILE:HG12	2.12	0.51
1:E:73:GLU:OE2	1:E:77:LYS:NZ	2.41	0.51
1:F:349:ARG:O	1:F:353:ILE:HG12	2.11	0.51
1:C:130:ARG:NE	1:D:237:ASP:OD2	2.45	0.50
1:D:349:ARG:O	1:D:353:ILE:HG12	2.11	0.50
1:B:115:LEU:HD21	1:C:179:TYR:CD2	2.47	0.50
1:D:127:GLY:O	1:E:236:SER:HA	2.11	0.50
1:D:276:THR:OG1	1:D:277:THR:N	2.42	0.50
1:F:73:GLU:OE2	1:F:77:LYS:NZ	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:GLN:OE1	1:F:73:GLU:HG3	2.12	0.50
1:D:72:ASN:HB3	1:E:168:ASN:HB3	1.94	0.50
1:E:127:GLY:O	1:F:236:SER:HA	2.11	0.49
1:F:117:ASP:OD2	1:F:174:ARG:HD2	2.12	0.49
1:A:117:ASP:OD2	1:A:174:ARG:HD2	2.12	0.49
1:A:349:ARG:O	1:A:353:ILE:HG12	2.11	0.49
1:E:117:ASP:OD2	1:E:174:ARG:HD2	2.12	0.49
1:E:349:ARG:O	1:E:353:ILE:HG12	2.11	0.49
1:F:256:GLY:N	1:F:298:GLN:OE1	2.38	0.49
1:B:117:ASP:OD2	1:B:174:ARG:HD2	2.12	0.49
1:A:361:ASN:OD1	1:F:318:ASN:ND2	2.46	0.49
1:D:256:GLY:N	1:D:298:GLN:OE1	2.38	0.49
1:E:130:ARG:NE	1:F:237:ASP:OD2	2.46	0.49
1:F:248:PHE:O	1:F:252:SER:N	2.43	0.49
1:B:127:GLY:O	1:C:236:SER:HA	2.12	0.49
1:D:117:ASP:OD2	1:D:174:ARG:HD2	2.12	0.49
1:B:72:ASN:HB3	1:C:168:ASN:HB3	1.95	0.49
1:F:276:THR:OG1	1:F:277:THR:N	2.42	0.49
1:C:103:ALA:HA	1:C:106:VAL:HG12	1.95	0.48
1:E:73:GLU:HG3	1:F:164:GLN:OE1	2.13	0.48
1:C:117:ASP:OD2	1:C:174:ARG:HD2	2.12	0.48
1:C:203:ASN:HD21	1:C:254:ARG:HH12	1.61	0.48
1:A:318:ASN:ND2	1:B:361:ASN:OD1	2.46	0.48
1:B:203:ASN:HD21	1:B:254:ARG:HH12	1.61	0.48
1:C:73:GLU:HG3	1:D:164:GLN:OE1	2.12	0.48
1:A:203:ASN:HD21	1:A:254:ARG:HH12	1.61	0.48
1:B:103:ALA:HA	1:B:106:VAL:HG12	1.95	0.48
1:D:203:ASN:HD21	1:D:254:ARG:HH12	1.61	0.48
1:A:236:SER:HA	1:F:127:GLY:O	2.13	0.48
1:E:248:PHE:O	1:E:252:SER:N	2.43	0.48
1:E:256:GLY:N	1:E:298:GLN:OE1	2.38	0.48
1:C:256:GLY:N	1:C:298:GLN:OE1	2.38	0.48
1:B:130:ARG:NE	1:C:237:ASP:OD2	2.46	0.48
1:C:318:ASN:ND2	1:D:361:ASN:OD1	2.47	0.48
1:D:103:ALA:HA	1:D:106:VAL:HG12	1.95	0.48
1:E:318:ASN:ND2	1:F:361:ASN:HA	2.29	0.48
1:A:237:ASP:OD2	1:F:130:ARG:NE	2.46	0.48
1:F:103:ALA:HA	1:F:106:VAL:HG12	1.95	0.47
1:A:248:PHE:O	1:A:252:SER:N	2.43	0.47
1:F:203:ASN:HD21	1:F:254:ARG:HH12	1.61	0.47
1:A:103:ALA:HA	1:A:106:VAL:HG12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:ASN:HA	1:F:318:ASN:ND2	2.29	0.47
1:C:115:LEU:HD21	1:D:179:TYR:CD2	2.49	0.47
1:E:103:ALA:HA	1:E:106:VAL:HG12	1.95	0.47
1:C:72:ASN:HB3	1:D:168:ASN:HB3	1.96	0.47
1:E:203:ASN:HD21	1:E:254:ARG:HH12	1.61	0.47
1:C:250:ASP:OD2	1:C:254:ARG:NH1	2.48	0.47
1:E:318:ASN:ND2	1:F:361:ASN:OD1	2.48	0.47
1:A:179:TYR:CD2	1:F:115:LEU:HD21	2.49	0.47
1:E:72:ASN:HB3	1:F:168:ASN:HB3	1.98	0.46
1:B:250:ASP:OD2	1:B:254:ARG:NH1	2.48	0.46
1:D:250:ASP:OD2	1:D:254:ARG:NH1	2.48	0.46
1:A:250:ASP:OD2	1:A:254:ARG:NH1	2.48	0.46
1:F:250:ASP:OD2	1:F:254:ARG:NH1	2.48	0.46
1:E:115:LEU:HD21	1:F:179:TYR:CD2	2.50	0.46
1:E:295:GLN:HB3	1:E:340:GLN:HG2	1.98	0.46
1:F:295:GLN:HB3	1:F:340:GLN:HG2	1.98	0.46
1:B:148:LYS:HE3	1:B:148:LYS:HB2	1.75	0.46
1:D:295:GLN:HB3	1:D:340:GLN:HG2	1.98	0.46
1:C:318:ASN:ND2	1:D:361:ASN:HA	2.31	0.45
1:A:168:ASN:HB3	1:F:72:ASN:HB3	1.98	0.45
1:E:250:ASP:OD2	1:E:254:ARG:NH1	2.48	0.45
1:A:280:GLU:O	1:F:199:ARG:NH1	2.44	0.45
1:B:318:ASN:ND2	1:C:361:ASN:HA	2.31	0.45
1:F:146:GLY:HA2	1:F:149:VAL:HG12	1.99	0.45
1:A:295:GLN:HB3	1:A:340:GLN:HG2	1.98	0.45
1:C:295:GLN:HB3	1:C:340:GLN:HG2	1.98	0.45
1:B:295:GLN:HB3	1:B:340:GLN:HG2	1.98	0.45
1:E:146:GLY:HA2	1:E:149:VAL:HG12	1.99	0.45
1:A:148:LYS:HE3	1:A:148:LYS:HB2	1.75	0.45
1:B:256:GLY:N	1:B:298:GLN:OE1	2.38	0.45
1:A:146:GLY:HA2	1:A:149:VAL:HG12	1.99	0.45
1:B:142:ARG:HD3	1:B:142:ARG:HA	1.71	0.45
1:F:271:LEU:HD23	1:F:271:LEU:HA	1.80	0.45
1:A:271:LEU:HD23	1:A:271:LEU:HA	1.80	0.45
1:B:146:GLY:HA2	1:B:149:VAL:HG12	1.99	0.45
1:E:291:MET:HG2	1:E:342:ASP:OD2	2.17	0.45
1:B:291:MET:HG2	1:B:342:ASP:OD2	2.17	0.44
1:D:148:LYS:HB2	1:D:148:LYS:HE3	1.75	0.44
1:A:291:MET:HG2	1:A:342:ASP:OD2	2.18	0.44
1:D:318:ASN:ND2	1:E:361:ASN:HA	2.33	0.44
1:B:318:ASN:ND2	1:C:361:ASN:OD1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:ARG:NH1	1:C:280:GLU:O	2.41	0.44
1:C:148:LYS:HB2	1:C:148:LYS:HE3	1.75	0.44
1:D:146:GLY:HA2	1:D:149:VAL:HG12	1.99	0.44
1:F:291:MET:HG2	1:F:342:ASP:OD2	2.18	0.44
1:C:146:GLY:HA2	1:C:149:VAL:HG12	1.99	0.44
1:F:105:ARG:HA	1:F:108:THR:HG22	2.00	0.44
1:A:105:ARG:HA	1:A:108:THR:HG22	2.00	0.44
1:F:172:THR:O	1:F:176:ILE:HG13	2.18	0.43
1:C:172:THR:O	1:C:176:ILE:HG13	2.18	0.43
1:D:172:THR:O	1:D:176:ILE:HG13	2.18	0.43
1:D:318:ASN:ND2	1:E:361:ASN:OD1	2.51	0.43
1:B:328:MET:HE3	1:B:328:MET:HB2	1.91	0.43
1:C:291:MET:HG2	1:C:342:ASP:OD2	2.17	0.43
1:E:142:ARG:HA	1:E:142:ARG:HD3	1.71	0.43
1:A:172:THR:O	1:A:176:ILE:HG13	2.18	0.43
1:D:135:MET:HE1	1:D:179:TYR:CD1	2.54	0.43
1:E:105:ARG:HA	1:E:108:THR:HG22	2.00	0.43
1:B:271:LEU:HD23	1:B:271:LEU:HA	1.80	0.43
1:C:135:MET:HE1	1:C:179:TYR:CD1	2.54	0.43
1:D:291:MET:HG2	1:D:342:ASP:OD2	2.18	0.43
1:E:135:MET:HE1	1:E:179:TYR:CD1	2.54	0.43
1:B:135:MET:HE1	1:B:179:TYR:CD1	2.54	0.43
1:A:162:ASP:OD1	1:A:162:ASP:N	2.51	0.43
1:D:312:LYS:HG2	1:D:332:ILE:HD11	2.01	0.43
1:F:135:MET:HE1	1:F:179:TYR:CD1	2.54	0.43
1:F:328:MET:HE3	1:F:328:MET:HB2	1.91	0.43
1:A:135:MET:HE1	1:A:179:TYR:CD1	2.54	0.43
1:B:105:ARG:HA	1:B:108:THR:HG22	2.00	0.43
1:D:105:ARG:NE	1:D:162:ASP:OD2	2.35	0.43
1:A:348:GLN:N	1:A:348:GLN:OE1	2.52	0.43
1:B:312:LYS:HG2	1:B:332:ILE:HD11	2.01	0.43
1:C:312:LYS:HG2	1:C:332:ILE:HD11	2.01	0.43
1:E:162:ASP:OD1	1:E:162:ASP:N	2.51	0.43
1:E:199:ARG:NH1	1:F:280:GLU:O	2.43	0.43
1:C:348:GLN:N	1:C:348:GLN:OE1	2.52	0.42
1:E:312:LYS:HG2	1:E:332:ILE:HD11	2.01	0.42
1:F:348:GLN:N	1:F:348:GLN:OE1	2.52	0.42
1:B:295:GLN:HB3	1:B:340:GLN:HE21	1.84	0.42
1:B:348:GLN:N	1:B:348:GLN:OE1	2.52	0.42
1:C:295:GLN:HB3	1:C:340:GLN:HE21	1.84	0.42
1:D:348:GLN:N	1:D:348:GLN:OE1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:MET:HE3	1:C:328:MET:HB2	1.91	0.42
1:D:105:ARG:HA	1:D:108:THR:HG22	2.00	0.42
1:A:312:LYS:HG2	1:A:332:ILE:HD11	2.01	0.42
1:A:318:ASN:ND2	1:B:361:ASN:HA	2.35	0.42
1:C:77:LYS:HD2	1:C:93:LEU:HD21	2.02	0.42
1:C:105:ARG:HA	1:C:108:THR:HG22	2.00	0.42
1:D:295:GLN:HB3	1:D:340:GLN:HE21	1.84	0.42
1:E:172:THR:O	1:E:176:ILE:HG13	2.18	0.42
1:F:312:LYS:HG2	1:F:332:ILE:HD11	2.01	0.42
1:A:298:GLN:NE2	1:A:339:VAL:HB	2.35	0.42
1:B:172:THR:O	1:B:176:ILE:HG13	2.18	0.42
1:E:295:GLN:HB3	1:E:340:GLN:HE21	1.84	0.42
1:F:162:ASP:OD1	1:F:162:ASP:N	2.51	0.42
1:F:313:ILE:HD11	1:F:332:ILE:HG21	2.01	0.42
1:B:77:LYS:HD2	1:B:93:LEU:HD21	2.02	0.42
1:B:298:GLN:NE2	1:B:339:VAL:HB	2.35	0.42
1:B:313:ILE:HD11	1:B:332:ILE:HG21	2.01	0.42
1:D:77:LYS:HE3	1:D:77:LYS:HB2	1.88	0.42
1:D:162:ASP:N	1:D:162:ASP:OD1	2.51	0.42
1:F:142:ARG:HD3	1:F:142:ARG:HA	1.71	0.42
1:A:328:MET:HE3	1:A:328:MET:HB2	1.91	0.42
1:B:139:ARG:NH2	1:B:143:LEU:HG	2.35	0.42
1:B:313:ILE:HD13	1:B:313:ILE:HA	1.90	0.42
1:D:77:LYS:HD2	1:D:93:LEU:HD21	2.02	0.42
1:A:77:LYS:HD2	1:A:93:LEU:HD21	2.02	0.42
1:C:139:ARG:NH2	1:C:143:LEU:HG	2.35	0.42
1:E:77:LYS:HD2	1:E:93:LEU:HD21	2.02	0.42
1:F:139:ARG:NH2	1:F:143:LEU:HG	2.35	0.42
1:A:139:ARG:NH2	1:A:143:LEU:HG	2.35	0.42
1:A:295:GLN:HB3	1:A:340:GLN:HE21	1.84	0.42
1:E:313:ILE:HD11	1:E:332:ILE:HG21	2.01	0.42
1:F:298:GLN:NE2	1:F:339:VAL:HB	2.35	0.42
1:B:105:ARG:NE	1:B:162:ASP:OD2	2.35	0.41
1:D:139:ARG:NH2	1:D:143:LEU:HG	2.35	0.41
1:E:348:GLN:OE1	1:E:348:GLN:N	2.52	0.41
1:B:261:LEU:HB2	1:B:291:MET:HE1	2.02	0.41
1:C:261:LEU:HB2	1:C:291:MET:HE1	2.02	0.41
1:C:298:GLN:NE2	1:C:339:VAL:HB	2.35	0.41
1:F:77:LYS:HD2	1:F:93:LEU:HD21	2.02	0.41
1:F:77:LYS:HE3	1:F:77:LYS:HB2	1.88	0.41
1:F:261:LEU:HB2	1:F:291:MET:HE1	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:295:GLN:HB3	1:F:340:GLN:HE21	1.84	0.41
1:A:261:LEU:HB2	1:A:291:MET:HE1	2.02	0.41
1:E:298:GLN:NE2	1:E:339:VAL:HB	2.35	0.41
1:E:313:ILE:HD13	1:E:313:ILE:HA	1.90	0.41
1:E:328:MET:HE3	1:E:328:MET:HB2	1.91	0.41
1:A:313:ILE:HD11	1:A:332:ILE:HG21	2.01	0.41
1:D:252:SER:OG	1:D:253:SER:N	2.54	0.41
1:D:298:GLN:NE2	1:D:339:VAL:HB	2.35	0.41
1:D:313:ILE:HD11	1:D:332:ILE:HG21	2.01	0.41
1:A:142:ARG:HA	1:A:142:ARG:HD3	1.71	0.41
1:C:79:THR:OG1	1:C:82:GLN:HG3	2.21	0.41
1:C:313:ILE:HD11	1:C:332:ILE:HG21	2.01	0.41
1:D:261:LEU:HB2	1:D:291:MET:HE1	2.02	0.41
1:E:139:ARG:NH2	1:E:143:LEU:HG	2.35	0.41
1:A:252:SER:OG	1:A:253:SER:N	2.54	0.41
1:C:279:ARG:HG3	1:C:287:TRP:CD1	2.56	0.41
1:C:328:MET:O	1:C:332:ILE:HG12	2.21	0.41
1:D:142:ARG:HD3	1:D:142:ARG:HA	1.71	0.41
1:E:79:THR:OG1	1:E:82:GLN:HG3	2.21	0.41
1:E:105:ARG:NE	1:E:162:ASP:OD2	2.35	0.41
1:E:271:LEU:HA	1:E:271:LEU:HD23	1.80	0.41
1:B:162:ASP:N	1:B:162:ASP:OD1	2.51	0.41
1:B:252:SER:OG	1:B:253:SER:N	2.54	0.41
1:C:162:ASP:OD1	1:C:162:ASP:N	2.51	0.41
1:D:79:THR:OG1	1:D:82:GLN:HG3	2.21	0.41
1:D:328:MET:O	1:D:332:ILE:HG12	2.21	0.41
1:E:261:LEU:HB2	1:E:291:MET:HE1	2.03	0.41
1:F:328:MET:O	1:F:332:ILE:HG12	2.21	0.41
1:B:328:MET:O	1:B:332:ILE:HG12	2.21	0.41
1:C:142:ARG:HA	1:C:142:ARG:HD3	1.71	0.41
1:E:279:ARG:HG3	1:E:287:TRP:CD1	2.56	0.41
1:F:79:THR:OG1	1:F:82:GLN:HG3	2.21	0.41
1:F:252:SER:OG	1:F:253:SER:N	2.54	0.41
1:F:70:ARG:NH1	1:F:97:ASP:OD2	2.55	0.40
1:F:279:ARG:HG3	1:F:287:TRP:CD1	2.56	0.40
1:B:279:ARG:HG3	1:B:287:TRP:CD1	2.56	0.40
1:F:148:LYS:HE3	1:F:148:LYS:HB2	1.75	0.40
1:F:311:LEU:HD23	1:F:311:LEU:HA	1.94	0.40
1:A:279:ARG:HG3	1:A:287:TRP:CD1	2.56	0.40
1:C:117:ASP:OD1	1:C:178:LEU:HD11	2.21	0.40
1:D:313:ILE:HD13	1:D:313:ILE:HA	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:252:SER:OG	1:E:253:SER:N	2.54	0.40
1:A:79:THR:OG1	1:A:82:GLN:HG3	2.21	0.40
1:B:79:THR:OG1	1:B:82:GLN:HG3	2.21	0.40
1:C:313:ILE:HD13	1:C:313:ILE:HA	1.90	0.40
1:E:328:MET:O	1:E:332:ILE:HG12	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	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	B	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	C	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	D	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	E	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
1	F	314/782 (40%)	305 (97%)	9 (3%)	0	100	100
All	All	1884/4692 (40%)	1830 (97%)	54 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	B	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	C	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	D	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	E	266/653 (41%)	265 (100%)	1 (0%)	84	81
1	F	266/653 (41%)	265 (100%)	1 (0%)	84	81
All	All	1596/3918 (41%)	1590 (100%)	6 (0%)	81	81

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	298	GLN
1	B	298	GLN
1	C	298	GLN
1	D	298	GLN
1	E	298	GLN
1	F	298	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	203	ASN
1	A	246	GLN
1	A	286	GLN
1	A	318	ASN
1	A	319	GLN
1	A	340	GLN
1	A	344	GLN
1	A	361	ASN
1	A	364	ASN
1	B	203	ASN
1	B	246	GLN
1	B	286	GLN
1	B	318	ASN
1	B	319	GLN
1	B	340	GLN
1	B	344	GLN
1	B	361	ASN
1	B	364	ASN
1	C	203	ASN

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Mol	Chain	Res	Type
1	C	246	GLN
1	C	286	GLN
1	C	318	ASN
1	C	319	GLN
1	C	340	GLN
1	C	344	GLN
1	C	361	ASN
1	C	364	ASN
1	D	203	ASN
1	D	246	GLN
1	D	286	GLN
1	D	318	ASN
1	D	319	GLN
1	D	344	GLN
1	D	361	ASN
1	D	364	ASN
1	E	203	ASN
1	E	246	GLN
1	E	286	GLN
1	E	318	ASN
1	E	319	GLN
1	E	340	GLN
1	E	344	GLN
1	E	361	ASN
1	E	364	ASN
1	F	203	ASN
1	F	246	GLN
1	F	286	GLN
1	F	318	ASN
1	F	319	GLN
1	F	340	GLN
1	F	344	GLN
1	F	361	ASN
1	F	364	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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-10911. These allow visual inspection of the internal detail of the map and identification of artifacts.

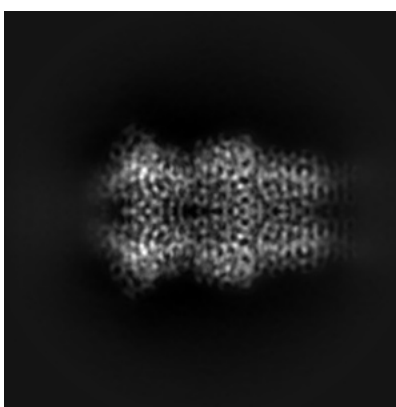
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

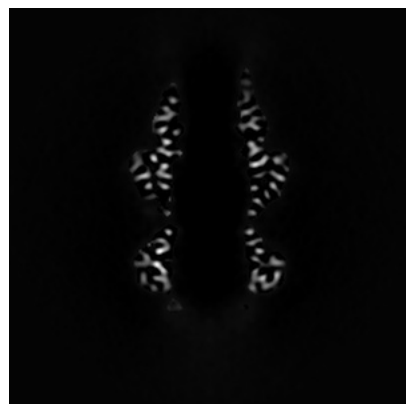


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 120



Y Index: 120



Z Index: 120

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: 140



Y Index: 94

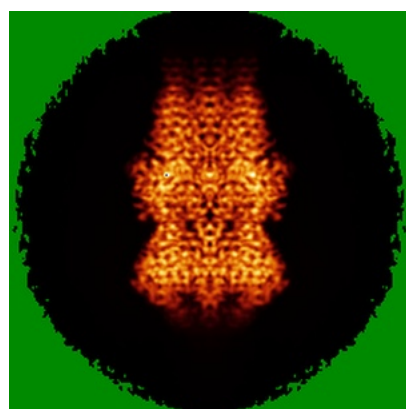


Z Index: 82

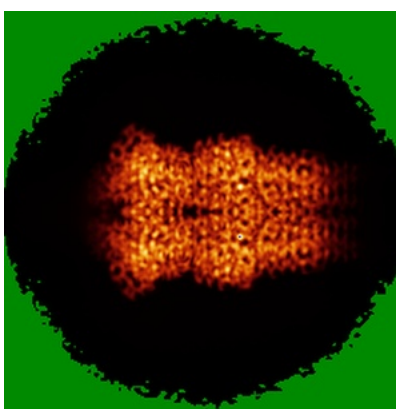
The images above show the largest variance slices of the map in three orthogonal directions.

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

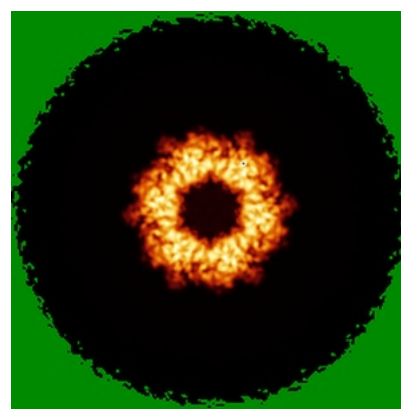
6.4.1 Primary map



X



Y

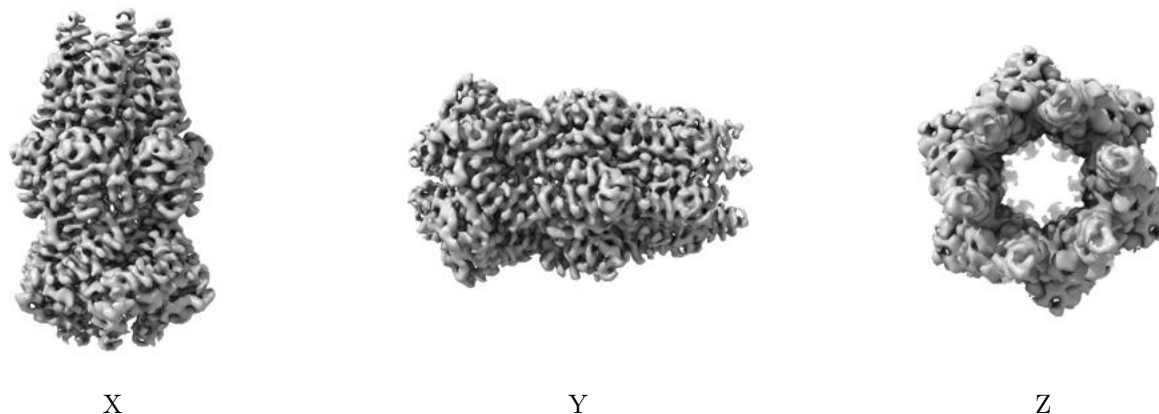


Z

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 0.0114. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

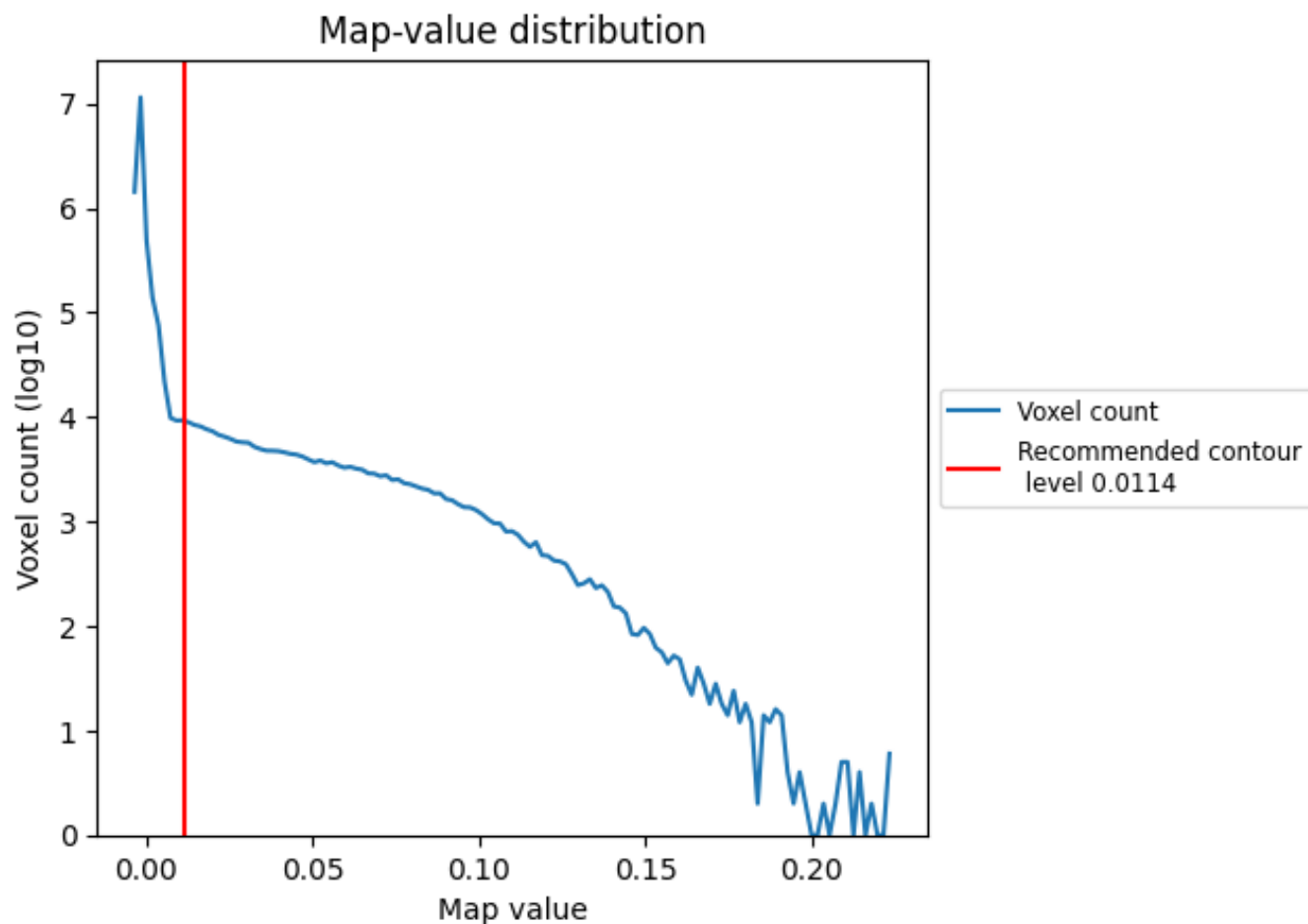
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

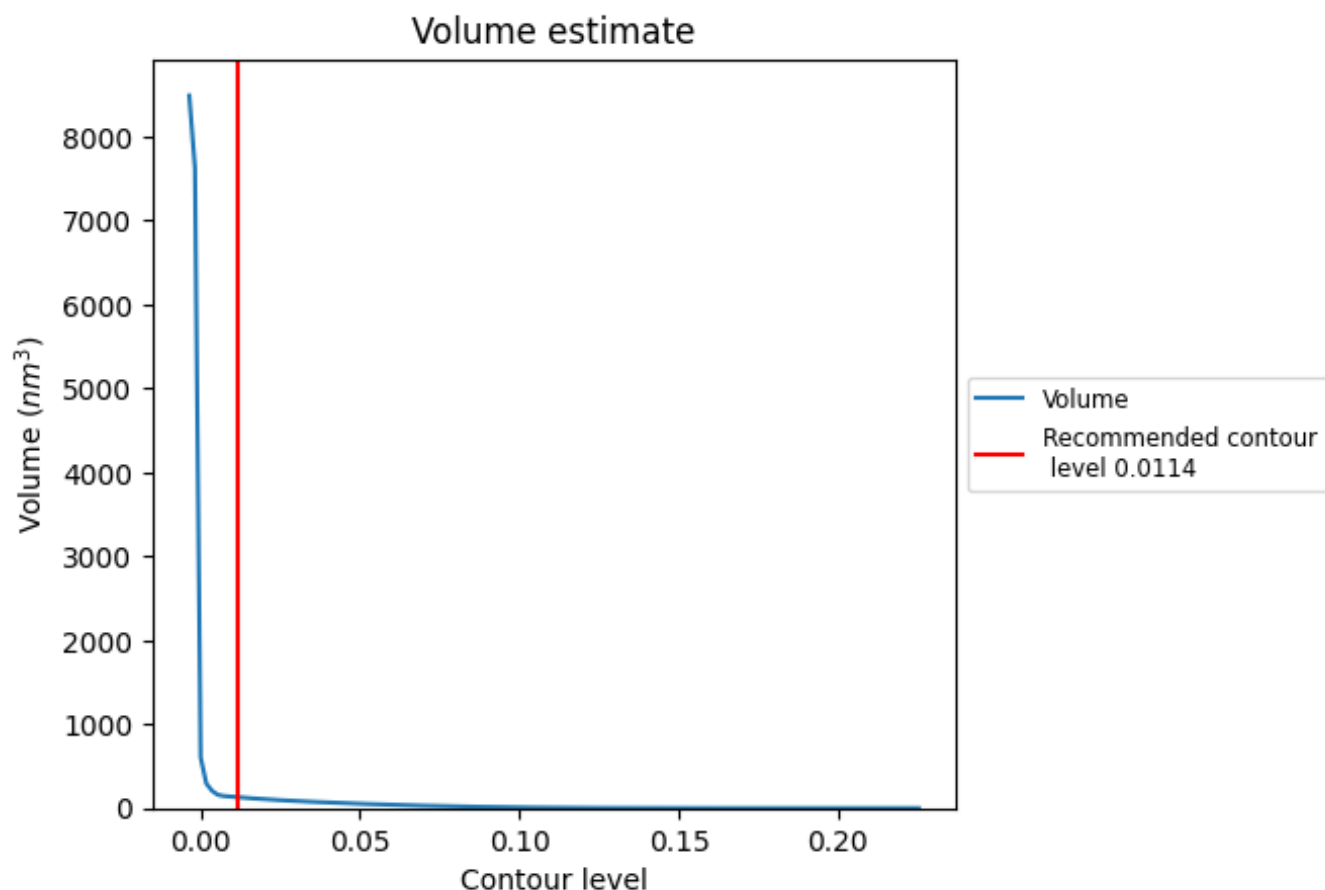
This section contains the results of statistical analysis of the map.

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.

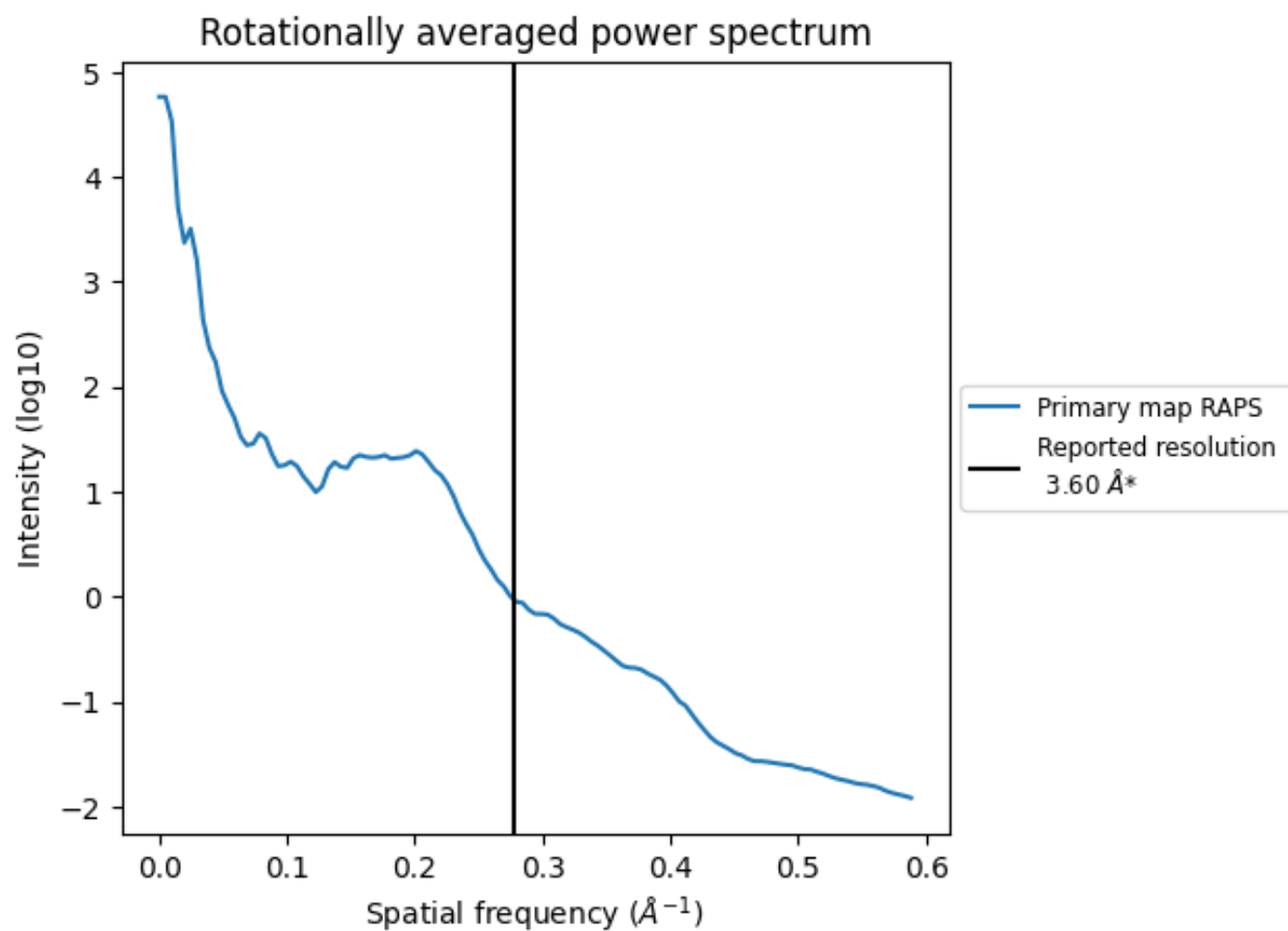
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 131 nm^3 ; this corresponds to an approximate mass of 119 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 ⓘ

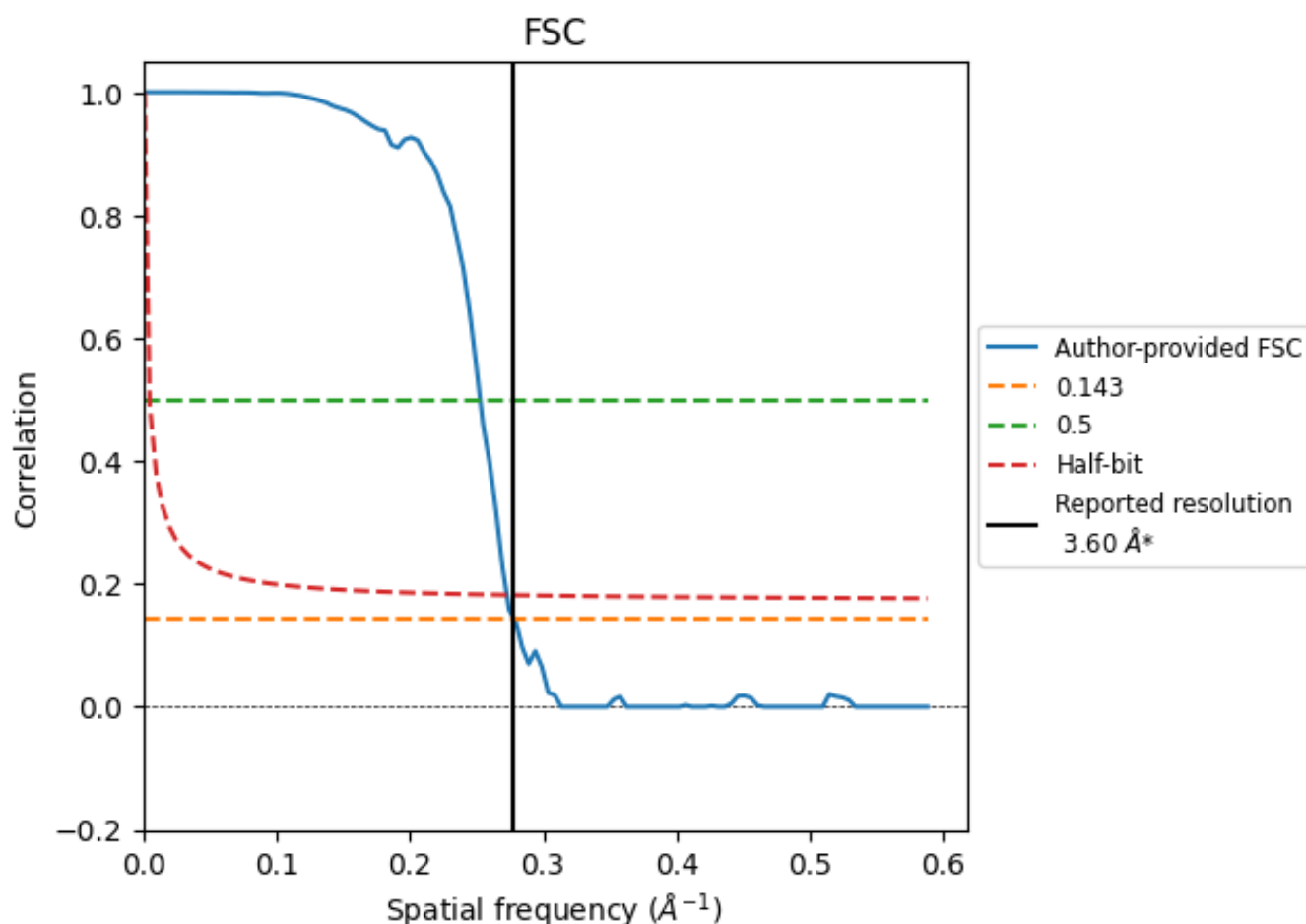


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

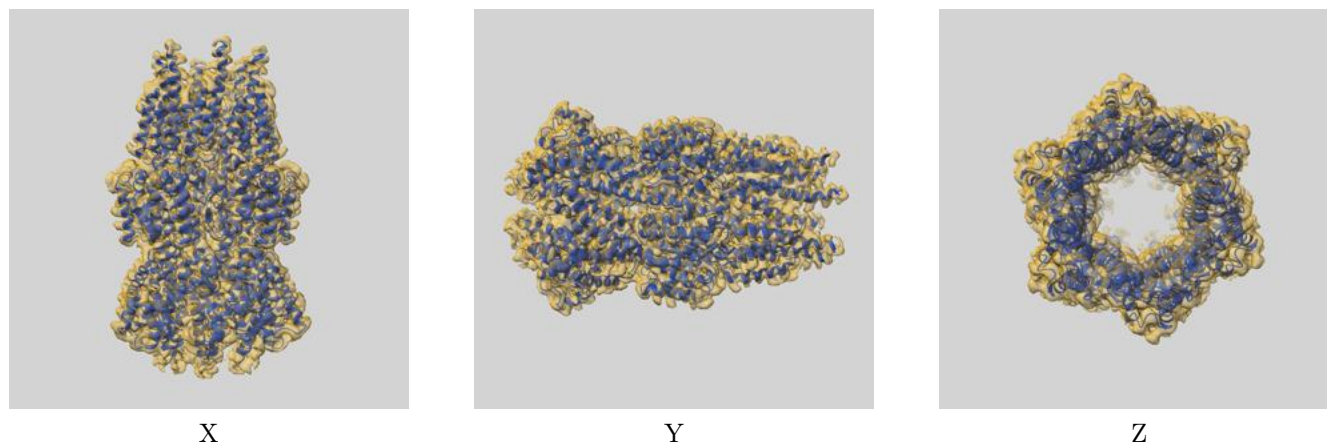
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	3.96	3.67
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

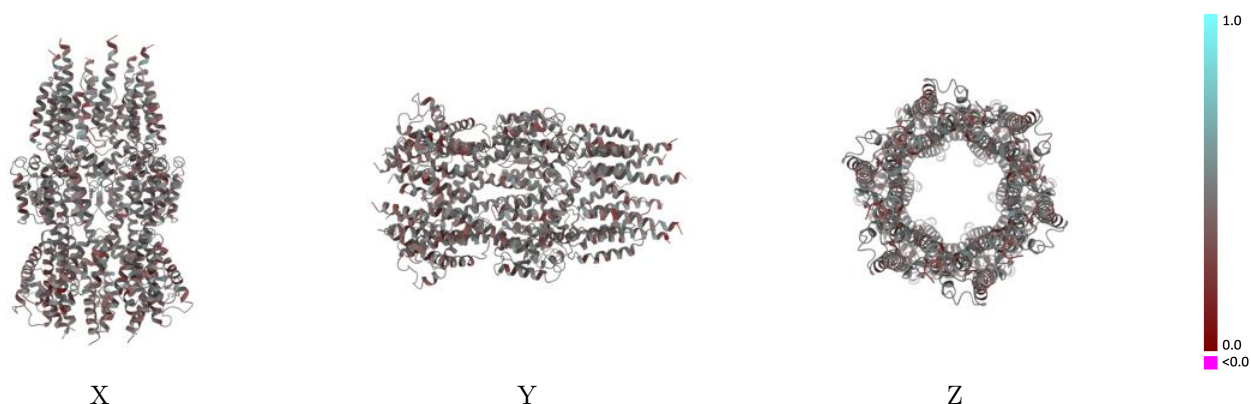
This section contains information regarding the fit between EMDB map EMD-10911 and PDB model 6YSZ. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



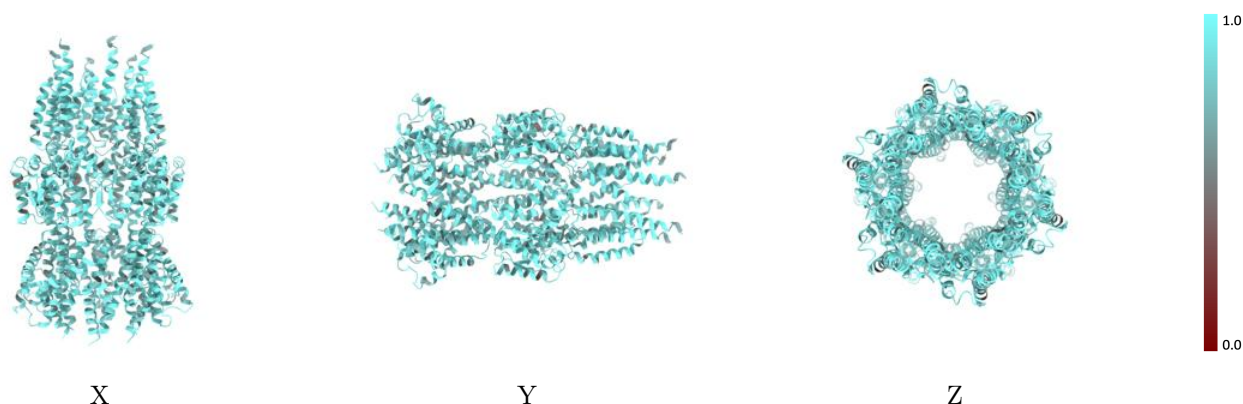
The images above show the 3D surface view of the map at the recommended contour level 0.0114 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



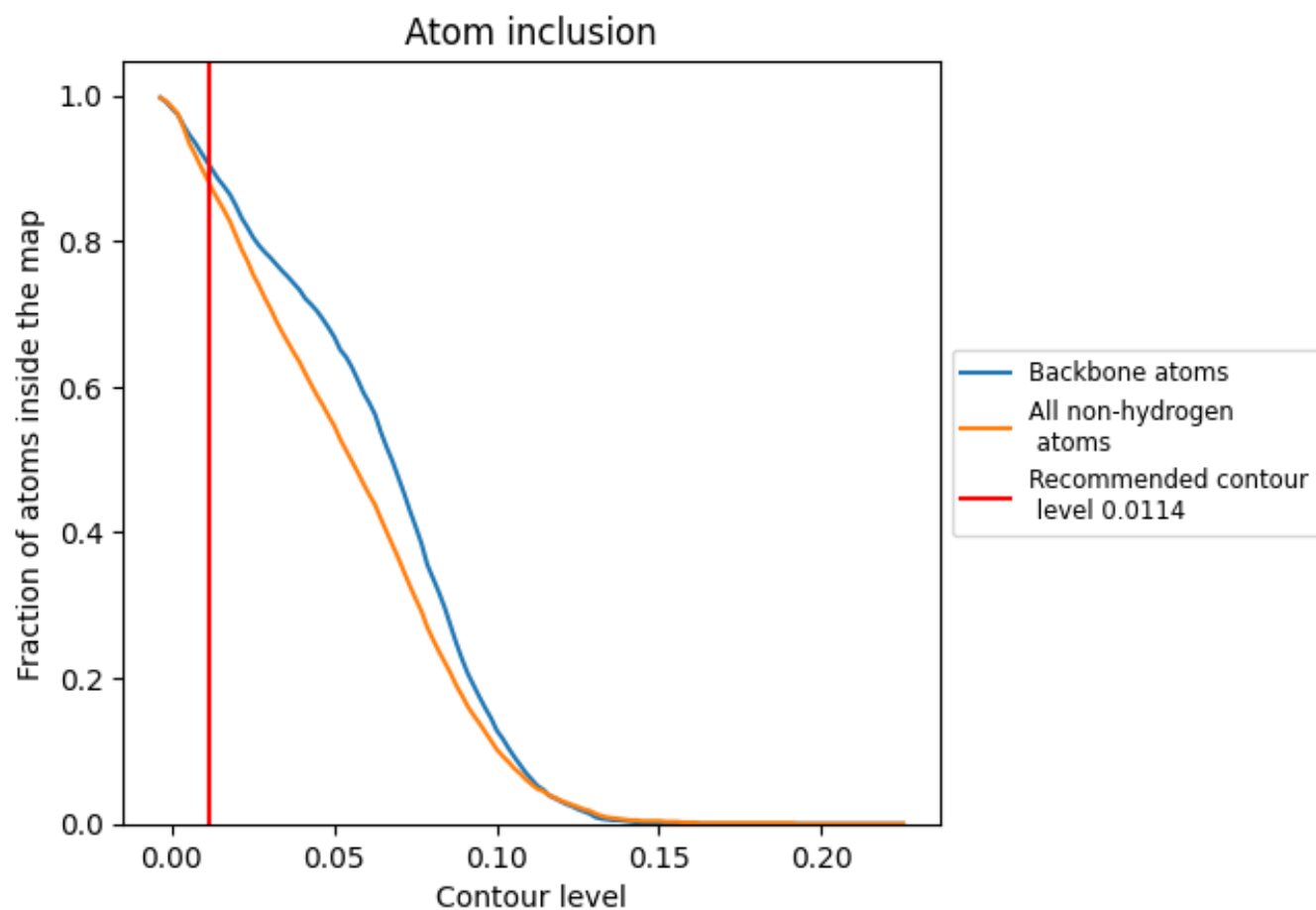
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0114).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.0114) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8810	0.4340
A	0.8830	0.4390
B	0.8810	0.4340
C	0.8810	0.4320
D	0.8830	0.4360
E	0.8790	0.4310
F	0.8800	0.4320

1.0

0.0

<0.0