



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:00 AM UTC

PDB ID : 8CXG / pdb_00008cxg
EMDB ID : EMD-27055
Title : Structures of Zika Virus in Complex with Antibodies Targeting E Dimer Epitopes and Basis for Neutralization Efficacy
Authors : Liu, W.; Zhang, X.K.; Gong, D.Y.; Dai, X.H.; Sharma, A.; Zhang, T.H.; Rey, F.; Zhou, Z.H.
Deposited on : 2022-05-21
Resolution : 3.20 Å(reported)

This is a wwPDB EM Validation Summary 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:

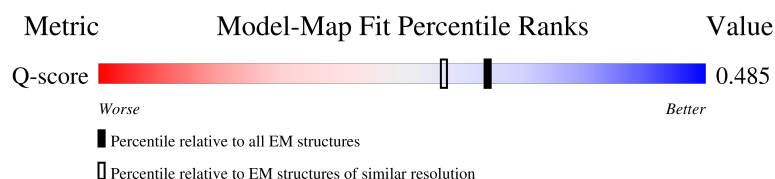
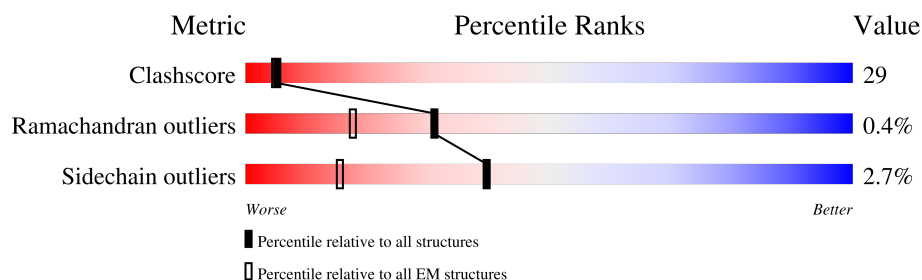
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.20 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	15020 (2.70 - 3.70)

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	1	122	99% 70% 28% ..
1	H	122	55% 80% 18% ..
1	h	122	56% 84% 14% ..
2	2	109	99% 69% 28% ...

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Mol	Chain	Length	Quality of chain
2	L	109	
2	l	109	
3	A	639	
3	B	639	
3	C	639	
4	D	3423	
4	E	3423	
4	F	3423	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 18381 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 C8 scFv heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	121	Total	C	N	O	S	0	0
			933	591	151	186	5		
1	h	121	Total	C	N	O	S	0	0
			933	591	151	186	5		
1	1	121	Total	C	N	O	S	0	0
			933	591	151	186	5		

- Molecule 2 is a protein called C8 scFv light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	109	Total	C	N	O	S	0	0
			852	541	145	164	2		
2	1	109	Total	C	N	O	S	0	0
			852	541	145	164	2		
2	2	108	Total	C	N	O	S	0	0
			846	538	144	162	2		

- Molecule 3 is a protein called Ankyrin repeat family A protein 2,Envelope E protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	492	Total	C	N	O	S	0	0
			3721	2343	645	703	30		
3	B	492	Total	C	N	O	S	0	0
			3721	2343	645	703	30		
3	C	501	Total	C	N	O	S	0	0
			3790	2384	657	718	31		

- Molecule 4 is a protein called Membrane M protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	75	Total	C	N	O	S	0	0
			600	391	105	103	1		

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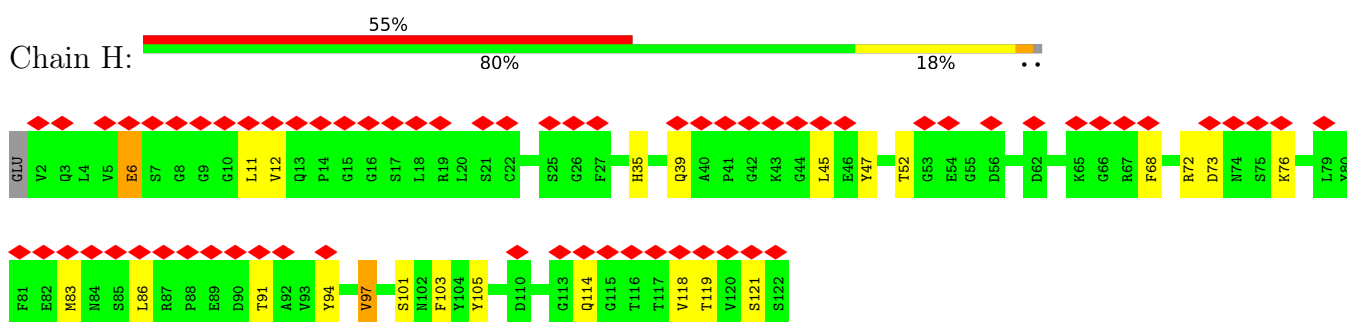
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Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	75	Total	C	N	O	S	0	0
			600	391	105	103	1		
4	F	75	Total	C	N	O	S	0	0
			600	391	105	103	1		

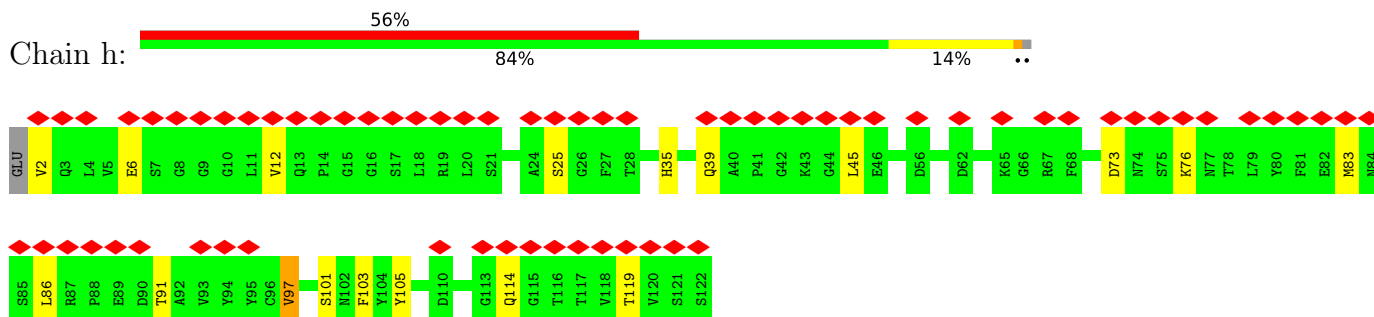
3 Residue-property plots [i](#)

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.

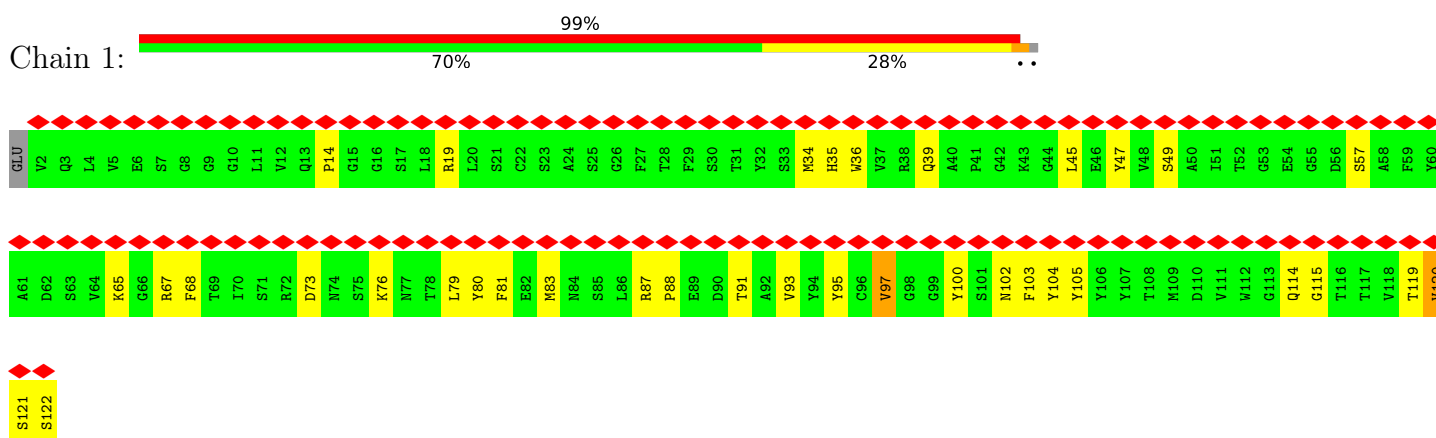
- Molecule 1: C8 scFv heavy chain



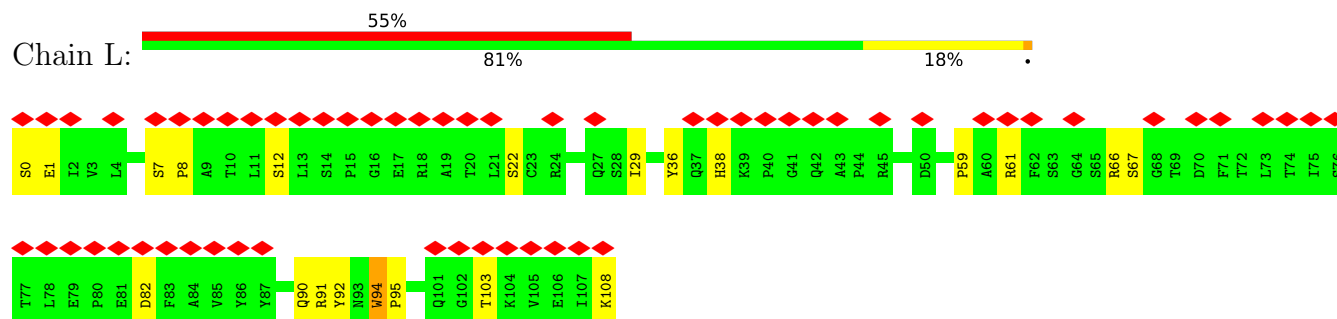
- Molecule 1: C8 scFv heavy chain



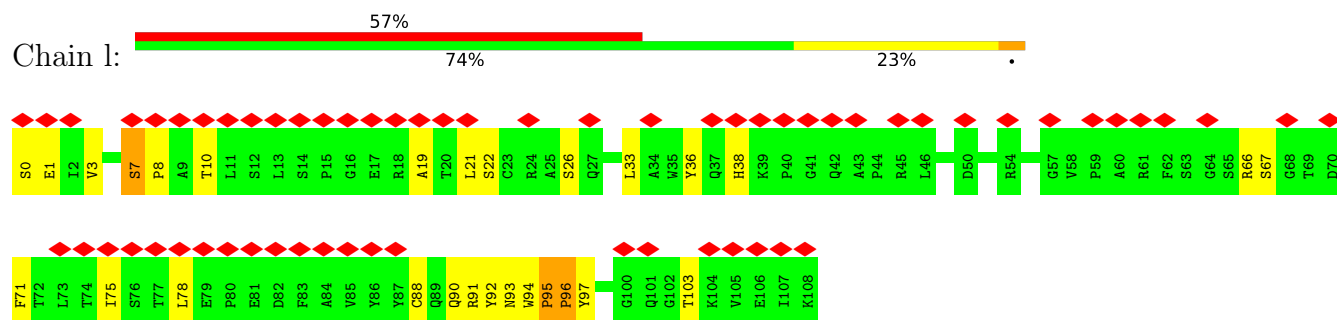
- Molecule 1: C8 scFv heavy chain



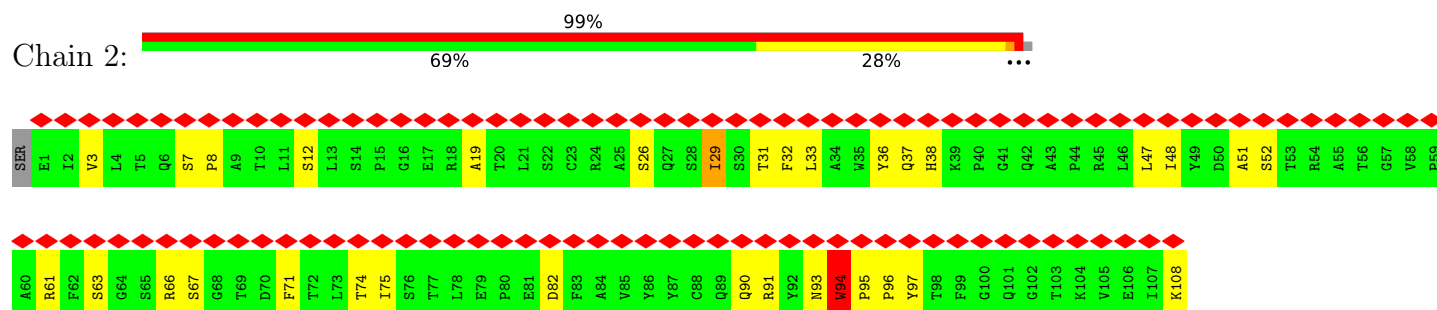
Chain L:



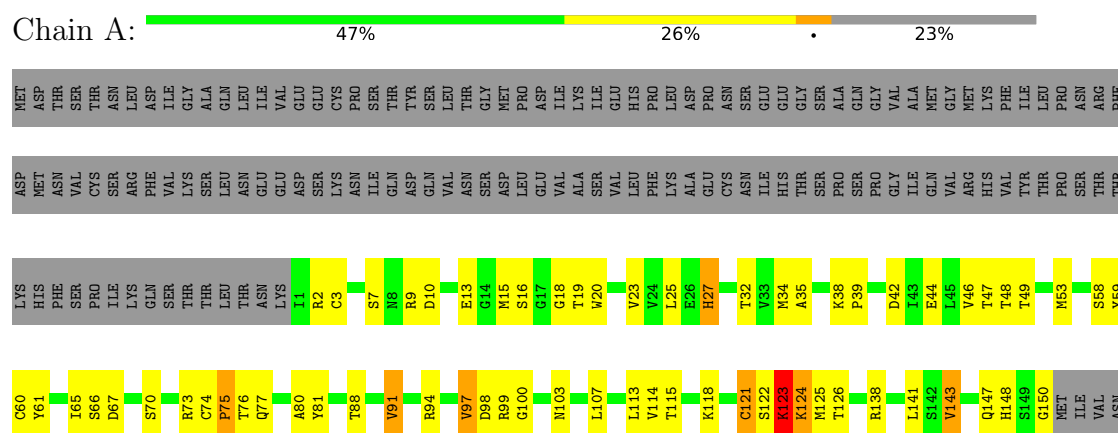
Chain 1:

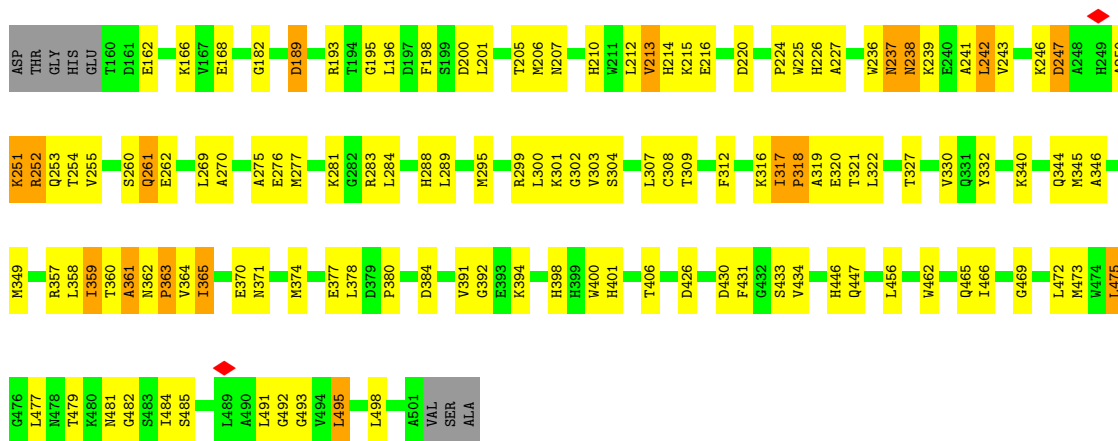


Chain 2:



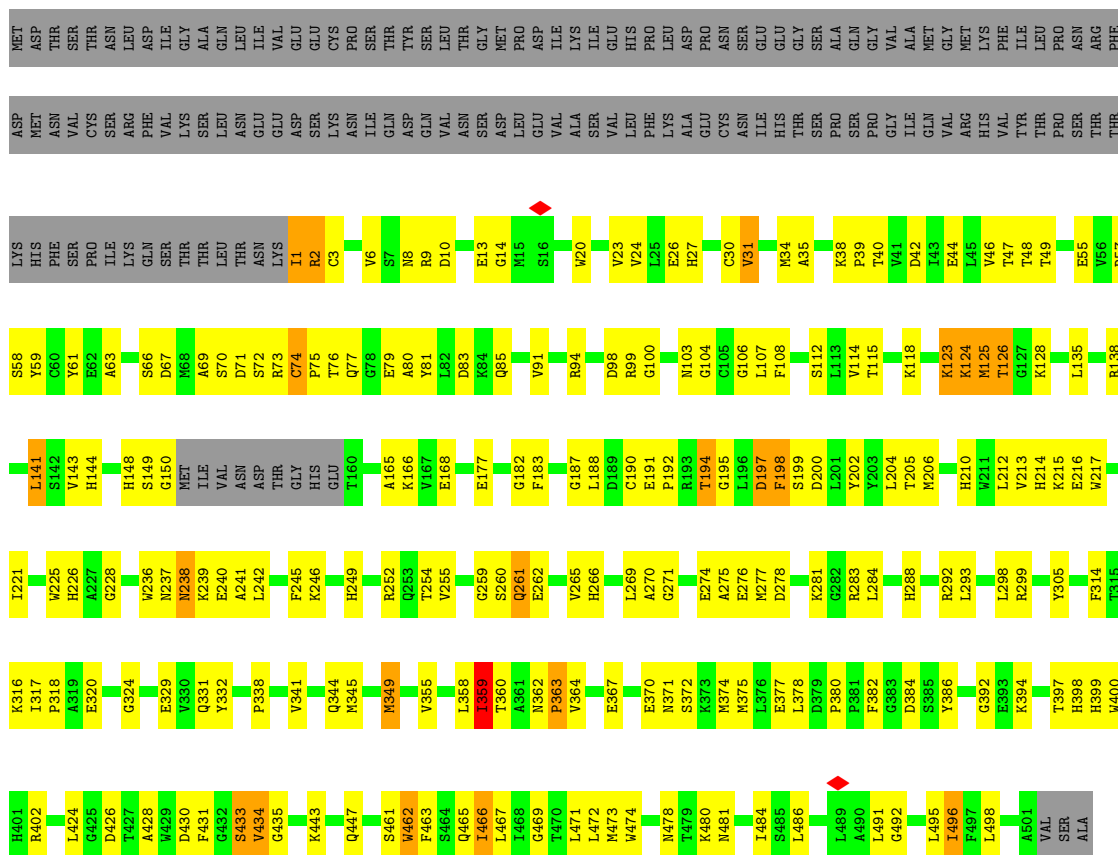
Chain A:





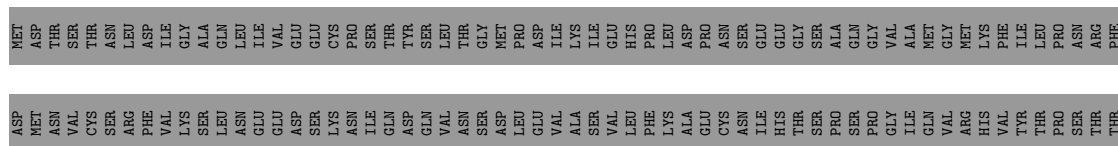
• Molecule 3: Ankyrin repeat family A protein 2,Envelope E protein

Chain B: 43% 30% 23%



• Molecule 3: Ankyrin repeat family A protein 2,Envelope E protein

Chain C: 49% 28% 22%





VAL	VAL	VAL	VAL	VAL	PHE	LYS	ALA	CYS	GLY	MET	PRO	MET
SER	SER	GLY	SER	ILE	GLY	LYS	SER	ILE	VAL	SER	SER	LYS
TYR	TYR	PHE	PHE	MET	GLY	MET	ILE	GLY	GLU	ALA	ALA	ASN
LEU	LEU	LEU	LEU	GLY	LEU	GLY	THR	VAL	PRO	VAL	GLY	PRO
ASP	ASP	GLY	GLY	THR	THR	THR	ASP	SER	ASP	THR	ILE	LYS
ALA	ALA	LEU	LEU	MET	ASP	SER	ASP	ASN	ASP	VAL	ASN	LYS
HIS	HIS	CYS	CYS	ILE	ASP	ILE	ILE	ARG	VAL	ARG	ARG	SER
ALA	ALA	ASP	ASP	GLN	GLU	GLN	ASP	PHE	CYS	GLY	TRP	GLY
LYS	LYS	GLU	GLU	PRO	PRO	PRO	VAL	VAL	TRP	SER	GLY	GLY
PHE	PHE	ARG	ARG	SER	ARG	GLU	VAL	GLY	GLU	ALA	SER	PHE
THR	THR	GLN	GLN	ASN	THR	ASN	CYS	GLY	CYS	ASN	TYR	ARG
THR	THR	THR	THR	LEU	GLY	LEU	PRO	MET	THR	THR	GLY	ILE
LYS	LYS	LEU	LEU	SER	THR	THR	THR	SER	SER	MET	LYS	VAL
ILE	ILE	ASP	ASP	GLN	PHE	GLY	THR	GLY	THR	TYR	TYR	ASN
PRO	PRO	PHE	PHE	ARG	GLY	ILE	GLY	THR	THR	ASP	GLU	MET
ALA	ALA	GLY	GLY	ILE	SER	MET	ALA	TRP	VAL	ARG	ALA	LEU
GLU	GLU	SER	SER	MET	ASP	LEU	TYR	VAL	VAL	ASN	MET	LYS
THR	THR	LEU	LEU	SER	LEU	SER	LEU	ASP	THR	ASN	GLU	ARG
GLY	GLY	TYR	TYR	VAL	TYR	VAL	ASP	VAL	GLY	ASP	ILE	GLY
HIS	HIS	ALA	ALA	GLY	GLY	GLY	ASP	VAL	GLY	ALA	ILE	VAL
THR	THR	THR	THR	THR	THR	THR	THR	GLY	CYS	THR	ILE	ARG
VAL	VAL	HIS	HIS	ASN	ASN	GLN	ASP	HIS	HIS	ILE	LYS	SER
THR	THR	ASN	ASN	SER	THR	SER	THR	GLY	LYS	THR	LYS	PRO
VAL	VAL	ALA	ALA	SER	ASN	HIS	THR	GLY	LYS	PHE	ASP	PHE
GLU	GLU	LEU	LEU	SER	GLN	SER	GLN	GLY	GLY	PRO	LEU	GLY
VAL	VAL	ALA	ALA	HIS	HIS	GLY	VAL	CYS	GLY	THR	ALA	GLY
GLN	GLN	GLY	GLY	VAL	TRP	MET	THR	VAL	GLU	THR	ALA	LEU
TYR	TYR	LEU	LEU	ILE	LEU	ILE	CYS	THR	ALA	THR	ALA	LEU
ALA	ALA	VAL	VAL	VAL	VAL	VAL	LYS	VAL	ARG	LEU	MET	LYS
GLY	GLY	HIS	HIS	ASN	HIS	ASN	ASN	MET	ARG	GLY	GLY	ARG
THR	THR	ALA	ALA	ASP	THR	ASP	THR	ALA	SER	MET	ARG	LEU
ASP	ASP	GLU	GLU	GLY	GLY	THR	LEU	GLN	ARG	ILE	ILE	ARG
GLY	GLY	MET	MET	GLY	TRP	GLY	GLY	ASP	ARG	ILE	ILE	PRO
PRO	PRO	ASP	ASP	THR	THR	HIS	VAL	LYS	A1	CYS	ASN	ALA
GLN	GLN	PHE	PHE	GLY	ASP	GLU	ARG	PRO	V2	THR	ALA	LEU
VAL	VAL	ALA	ALA	ILE	ASP	THR	TRP	THR	T3	ILE	ARG	LEU
PRO	PRO	GLY	GLY	VAL	VAL	ASP	TRP	VAL	L4	GLN	LYS	LEU
ALA	ALA	ARG	ARG	GLY	GLY	ASN	ASN	ASP	H7	ILE	GLY	GLY
LEU	LEU	LEU	LEU	ASN	ASN	GLY	GLY	ILE		MET	LYS	HIS
GLN	GLN	THR	THR	ALA	THR	ALA	ARG	GLU		ASP	LYS	GLY
SER	SER	SER	SER	ALA	TRP	ALA	CYS	VAL	R10	LEU	ARG	PRO
ALA	ALA	HIS	HIS	LYS	GLY	LYS	LYS	VAL	K11	GLY	ARG	ILE
VAL	VAL	GLY	GLY	VAL	THR	VAL	VAL	THR	L12	HIS	GLY	ARG
ASP	ASP	HIS	HIS	PHE	THR	PHE	THR	THR	Q13	MET	ALA	MET
MET	MET	LEU	LEU	GLY	THR	GLY	THR	THR		CYS	ASP	VAL
GLN	GLN	LYS	LYS	VAL	VAL	LYS	VAL	VAL	V19	ASP	THR	LEU
THR	THR	CYS	CYS	SER	SER	GLY	GLY	SER		ALA	SER	ALA
LEU	LEU	ARG	ARG	ASN	THR	ASN	SER					





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

- Molecule 4: Membrane M protein

Chain E: 98%

ALA	VAL	GLY	HIS	LYS	GLY	VAL	VAL	I49	GLY	MET	PRO
VAL	ASP	HIS	GLY	VAL	PHE	THR	THR	A50	VAL	ALA	SER
MET	GLN	LYS	ALA	ILE	GLY	THR	THR	W51	GLU	ALA	LEU
THR	THR	CYS	THR	PRO	GLY	GLY	VAL	L52	ASP	VAL	GLY
LEU	ARG	ARG	GLY	ASN	SER	ASN	SER	L53	ASP	THR	ILE
THR	LEU	LEU	THR	ASN	SER	ASN	ASN	K60	VAL	ARG	ASN
PRO	LYS	PRO	PRO	SER	LEU	MET	MET		ASP	ARG	SER
HIS	ASP	HIS	THR	ARG	THR	GLU	GLU	M66	CYS	ARG	GLY
TRP	LYS	TRP	TRP	ALA	CYS	VAL	VAL	I67	TRP	SER	TRP
ASN	LYS	ASN	ASN	GLU	ALA	ARG	ARG	L68	CYS	ALA	SER
ASN	ALA	ASN	ASN	ALA	LYS	SER	SER	L69	ASN	TYR	VAL
LYS	THR	THR	LYS	THR	PHE	TYR	TYR	I70	THR	TYR	GLY
GLY	LEU	LEU	GLY	LEU	CYS	CYS	CYS	S75	SER	MET	LYS
ALA	ALA	ALA	ALA	ALA	CYS	TYR	TYR	ILE	THR	GLU	VAL
ASN	VAL	GLY	VAL	GLY	SER	GLU	GLU	THR	THR	ASP	ALA
PRO	VAL	GLY	GLY	PHE	LYS	LYS	ILE	VAL	VAL	ARG	MET
ILE	THR	THR	PHE	GLY	MET	SER	SER	VAL	ASP	ASN	GLU
THR	THR	THR	LYS	LEU	LYS	THR	ILE	TYR	THR	ASN	ILE
GLU	GLU	LEU	ASP	GLY	GLY	THR	SER	VAL	GLY	ALA	VAL
THR	THR	CYS	ALA	LEU	LYS	MET	MET	THR	THR	GLY	LYS
SER	GLU	THR	HIS	ASP	ILE	SER	ALA	ARG	HIS	ALA	PHE
GLU	GLU	ALA	ALA	CYS	GLY	SER	ASP	ASP	HIS	ALA	VAL
ASN	ASN	ALA	LYS	GLU	GLN	ASP	GLN	PHE	LYS	VAL	SER
SER	PHE	ALA	ARG	PRO	PRO	SER	SER	VAL	VAL	GLY	PRO
LYS	THR	THR	GLN	ARG	GLU	THR	VAL	GLU	GLY	PRO	GLY
MET	MET	PHE	THR	THR	ASN	CYS	CYS	GLY	GLU	THR	ALA
MET	MET	THR	VAL	GLY	LEU	PRO	PRO	MET	ALA	THR	VAL
LEU	LEU	LYS	VAL	LEU	GLU	THR	GLN	VAL	VAL	THR	ILE
GLU	GLU	ILE	VAL	LEU	TYR	THR	GLY	T3	ILE	ARG	LEU
ASP	ASP	GLY	ALA	LEU	HIS	VAL	ASP	T3	ILE	ARG	LEU
SER	SER	THR	VAL	THR	GLY	THR	GLY	L4	GLN	LYS	LEU
TYR	VAL	HIS	VAL	MET	SER	SER	SER	S6	ILE	GLY	GLY
ILE	THR	THR	HIS	ASN	GLN	ASP	THR	S6	MET	LYS	HIS
VAL	VAL	ALA	THR	ASN	ILE	ASP	ASP	H7	ASP	LYS	GLY
VAL	GLU	VAL	ALA	ASN	SER	THR	THR		LEU	PRO	ARG
ILE	GLU	GLY	LEU	LYS	HIS	GLY	GLY	R10	GLY	ILE	ILE
VAL	VAL	VAL	ALA	HIS	GLY	THR	THR	CYS	HIS	ARG	GLY
VAL	VAL	GLN	GLY	THR	GLY	VAL	VAL	R15	MET	ALA	MET
GLY	GLY	TYR	ALA	LEU	ILE	CYS	THR		CYS	VAL	VAL
LYS	GLY	ALA	LEU	VAL	ASN	VAL	VAL	T18	ASP	THR	THR
GLY	THR	GLY	GLU	HIS	ASN	ARG	MET	W19	ALA	SER	ALA
ILE	THR	ASP	ALA	THR	THR	THR	THR		THR	VAL	VAL
THR	GLY	THR	GLY	THR	THR	THR	GLN	R23	MET	GLY	ILE
THR	GLY	THR	GLY	ASP	THR	VAL	GLN	E24	SER	ILE	ALA
GLY	GLY	GLY	GLY	VAL	VAL	VAL	ASP	Y25	VAL	VAL	PHE
HIS	HIS	CYS	GLY	ASP	HIS	ARG	PRO	T26	GLY	TYR	VAL
TRP	TRP	LYS	ALA	THR	GLY	THR	THR	R27	CYS	GLU	LEU
ARG	ARG	GLY	GLY	ASP	ASP	THR	VAL	I30	PRO	GLY	ARG
SER	SER	ALA	ARG	LEU	ASN	ASN	ILE		LEU	THR	THR
THR	THR	MET	LEU	PRO	GLY	GLY	THR	N39	ASP	THR	THR
SER	SER	GLY	THR	THR	ALA	CYS	LEU		GLU	ALA	ALA









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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1007280	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	14.196	Depositor
Minimum map value	-6.057	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	265.0, 265.0, 265.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.19	0/957	0.47	1/1298 (0.1%)
1	H	0.15	0/957	0.38	0/1298
1	h	0.14	0/957	0.34	0/1298
2	2	0.22	0/869	0.61	2/1185 (0.2%)
2	L	0.26	0/875	0.46	1/1193 (0.1%)
2	l	0.17	0/875	0.62	3/1193 (0.3%)
3	A	0.56	8/3798 (0.2%)	0.69	10/5138 (0.2%)
3	B	0.60	7/3798 (0.2%)	0.74	14/5138 (0.3%)
3	C	0.50	3/3869 (0.1%)	0.67	7/5236 (0.1%)
4	D	0.32	0/615	0.40	0/838
4	E	0.46	1/615 (0.2%)	0.52	0/838
4	F	0.28	0/615	0.48	0/838
All	All	0.46	19/18800 (0.1%)	0.62	38/25491 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	0	1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	121	CYS	CA-C	-9.51	1.41	1.52
3	A	243	VAL	C-O	-8.72	1.15	1.24
3	A	243	VAL	CA-CB	-6.44	1.46	1.54
3	B	198	PHE	CA-C	-6.22	1.44	1.52
3	C	126	THR	CA-C	-6.18	1.44	1.52

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	242	LEU	N-CA-C	-9.79	100.84	113.17
3	B	237	ASN	N-CA-C	9.03	121.20	111.36
2	1	95	PRO	N-CA-C	8.93	121.59	110.70
3	B	433	SER	N-CA-C	8.79	124.32	110.70
3	A	361	ALA	N-CA-C	8.47	120.20	110.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	238	ASN	Mainchain

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	1	933	0	868	66	0
1	H	933	0	868	17	0
1	h	933	0	868	11	0
2	2	846	0	824	55	0
2	L	852	0	831	25	0
2	l	852	0	831	32	0
3	A	3721	0	3682	268	0
3	B	3721	0	3682	286	0
3	C	3790	0	3748	318	0
4	D	600	0	624	10	0
4	E	600	0	624	32	0
4	F	600	0	624	26	0
All	All	18381	0	18074	1039	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 29.

The worst 5 of 1039 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)
3:A:113:LEU:CD2	3:A:253:GLN:CD	1.79	1.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:249:HIS:HE1	4:F:16:SER:CB	0.93	1.55
3:C:225:TRP:CH2	3:C:237:ASN:ND2	1.69	1.55
3:A:74:CYS:HB3	3:A:77:GLN:CG	1.34	1.54
3:B:249:HIS:CE1	4:F:16:SER:HB2	1.02	1.53

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	1	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
1	H	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
1	h	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
2	2	106/109 (97%)	99 (93%)	6 (6%)	1 (1%)	14	47
2	L	107/109 (98%)	100 (94%)	7 (6%)	0	100	100
2	l	107/109 (98%)	96 (90%)	10 (9%)	1 (1%)	14	47
3	A	488/639 (76%)	435 (89%)	50 (10%)	3 (1%)	21	56
3	B	488/639 (76%)	433 (89%)	51 (10%)	4 (1%)	16	50
3	C	499/639 (78%)	441 (88%)	57 (11%)	1 (0%)	43	73
4	D	73/3423 (2%)	66 (90%)	7 (10%)	0	100	100
4	E	73/3423 (2%)	66 (90%)	7 (10%)	0	100	100
4	F	73/3423 (2%)	65 (89%)	8 (11%)	0	100	100
All	All	2371/12879 (18%)	2153 (91%)	208 (9%)	10 (0%)	31	62

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	317	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	A	261	GLN
3	A	318	PRO
3	C	261	GLN
2	l	96	PRO

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	1	100/101 (99%)	99 (99%)	1 (1%)	68	80
1	H	100/101 (99%)	98 (98%)	2 (2%)	48	72
1	h	100/101 (99%)	99 (99%)	1 (1%)	68	80
2	2	92/93 (99%)	91 (99%)	1 (1%)	65	79
2	L	93/93 (100%)	93 (100%)	0	100	100
2	l	93/93 (100%)	91 (98%)	2 (2%)	45	71
3	A	400/534 (75%)	380 (95%)	20 (5%)	22	55
3	B	400/534 (75%)	385 (96%)	15 (4%)	29	62
3	C	408/534 (76%)	399 (98%)	9 (2%)	45	71
4	D	64/2832 (2%)	63 (98%)	1 (2%)	55	75
4	E	64/2832 (2%)	62 (97%)	2 (3%)	35	66
4	F	64/2832 (2%)	64 (100%)	0	100	100
All	All	1978/10680 (18%)	1924 (97%)	54 (3%)	40	68

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	31	VAL
3	B	274	GLU
3	C	284	LEU
3	B	125	MET
3	B	213	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	266	HIS
3	C	401	HIS
3	C	288	HIS
3	C	344	GLN
3	C	478	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.

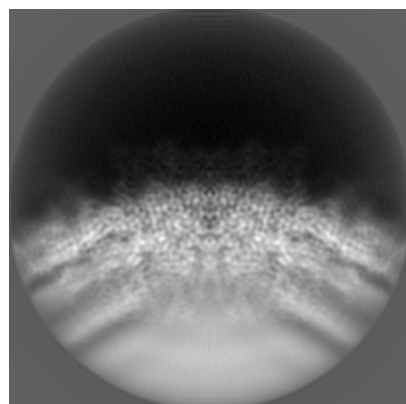
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27055. These allow visual inspection of the internal detail of the map and identification of artifacts.

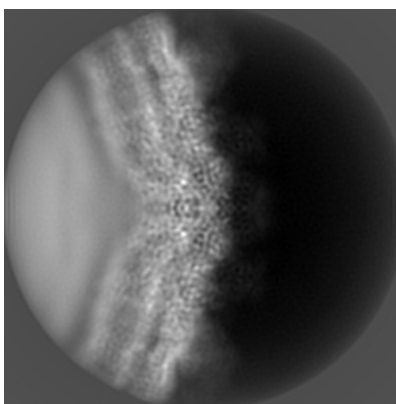
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

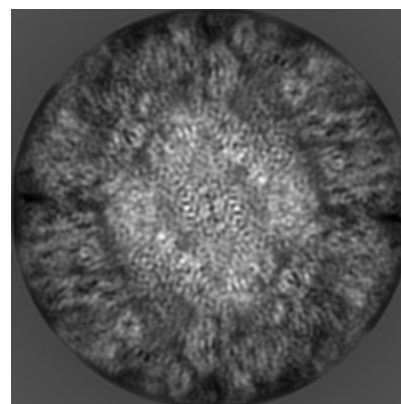
6.1.1 Primary map



X

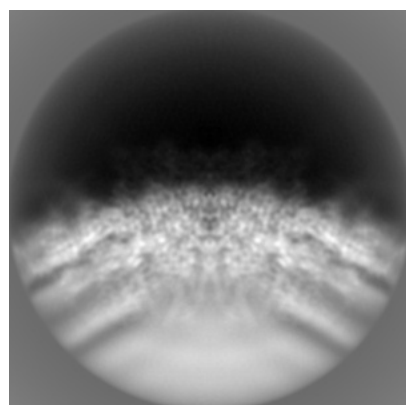


Y

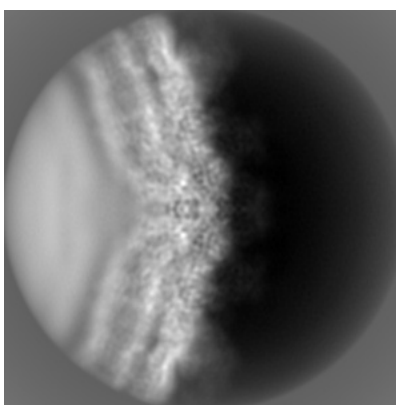


Z

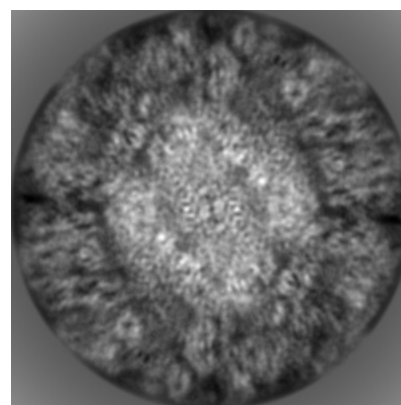
6.1.2 Raw map



X



Y

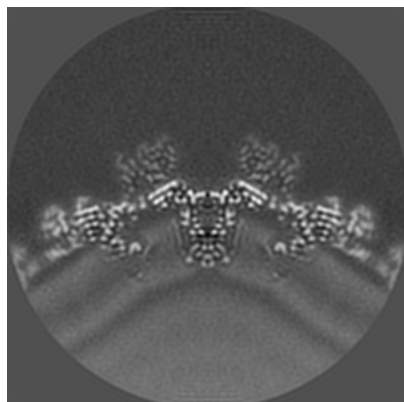


Z

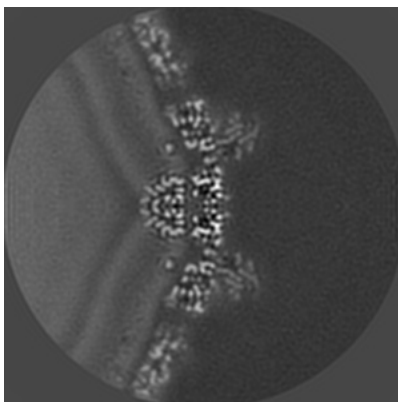
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

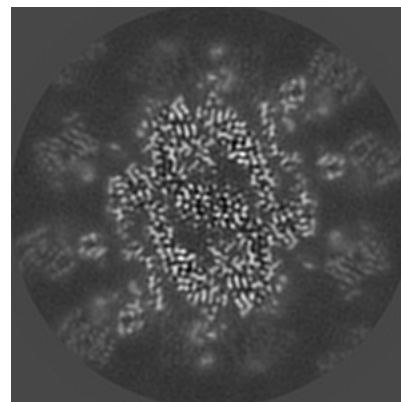
6.2.1 Primary map



X Index: 125

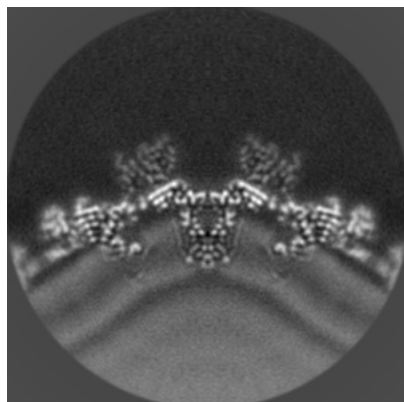


Y Index: 125

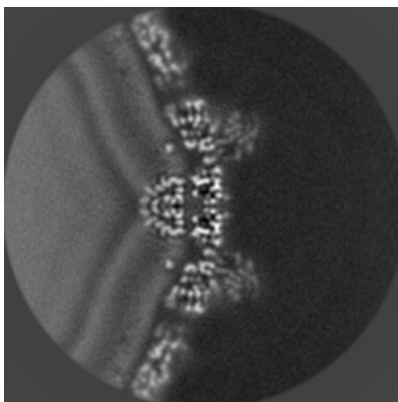


Z Index: 125

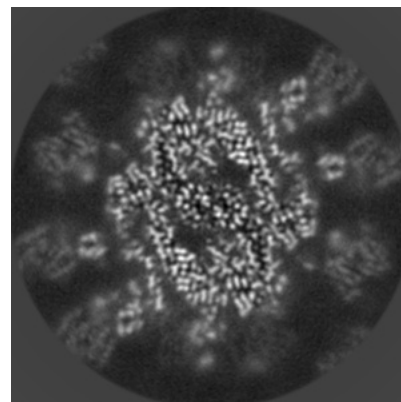
6.2.2 Raw map



X Index: 125



Y Index: 125

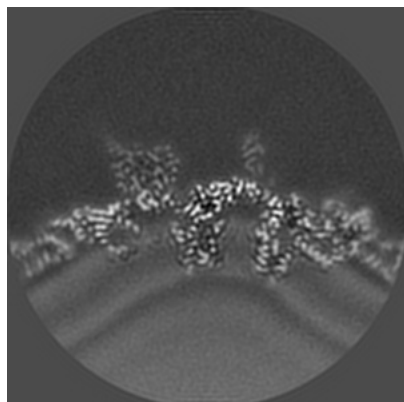


Z Index: 125

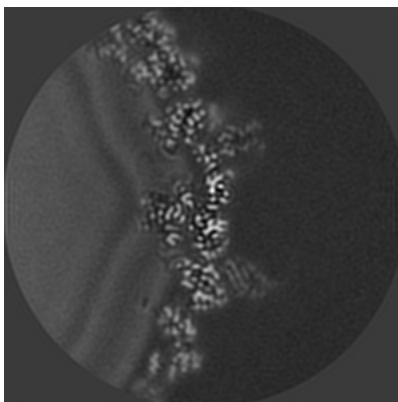
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

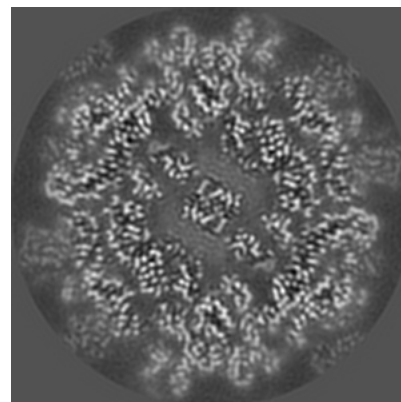
6.3.1 Primary map



X Index: 133

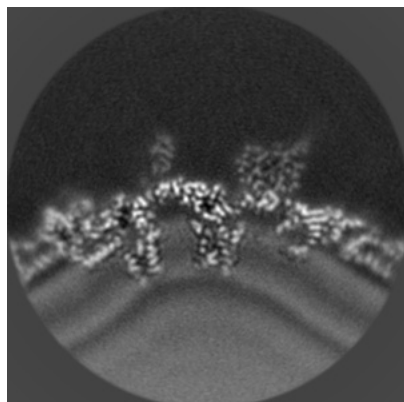


Y Index: 134

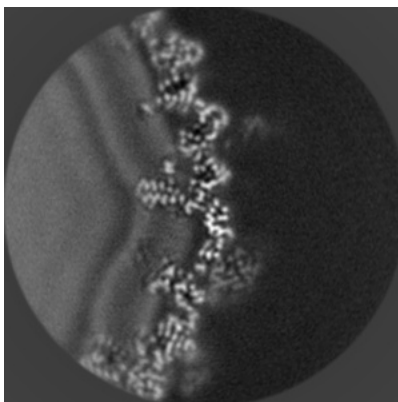


Z Index: 112

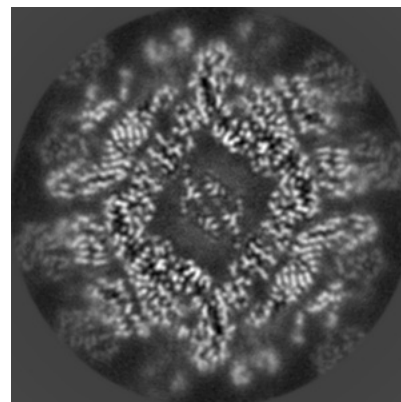
6.3.2 Raw map



X Index: 117



Y Index: 112

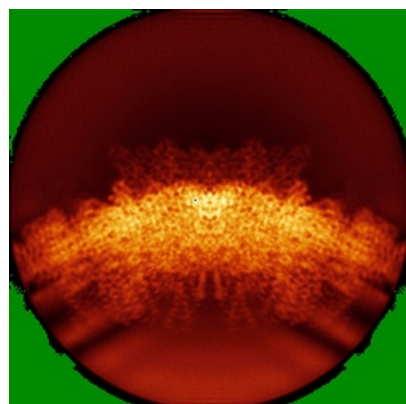


Z Index: 116

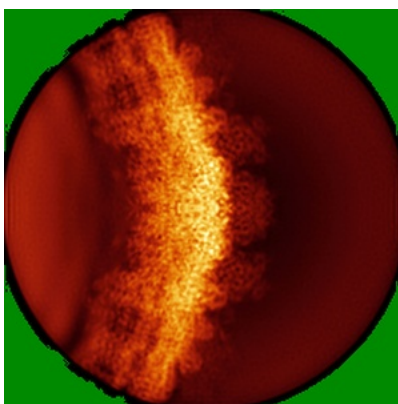
The images above show the largest variance slices of the map in three orthogonal directions.

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

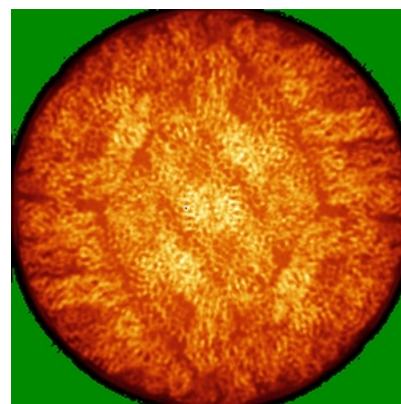
6.4.1 Primary map



X

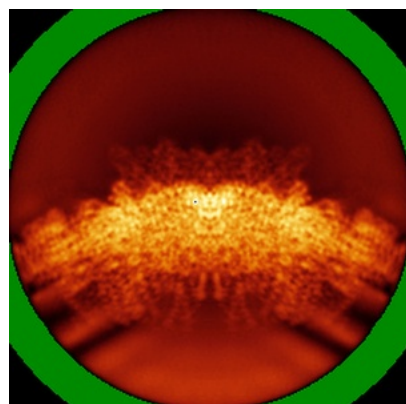


Y

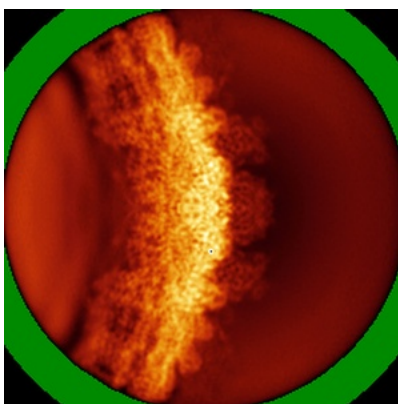


Z

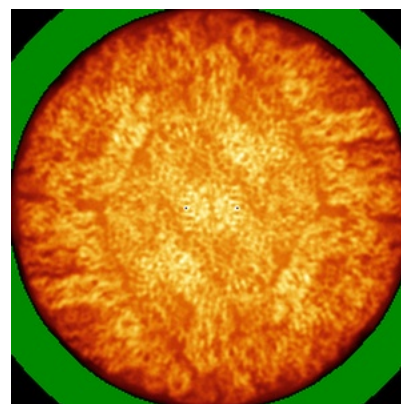
6.4.2 Raw map



X



Y

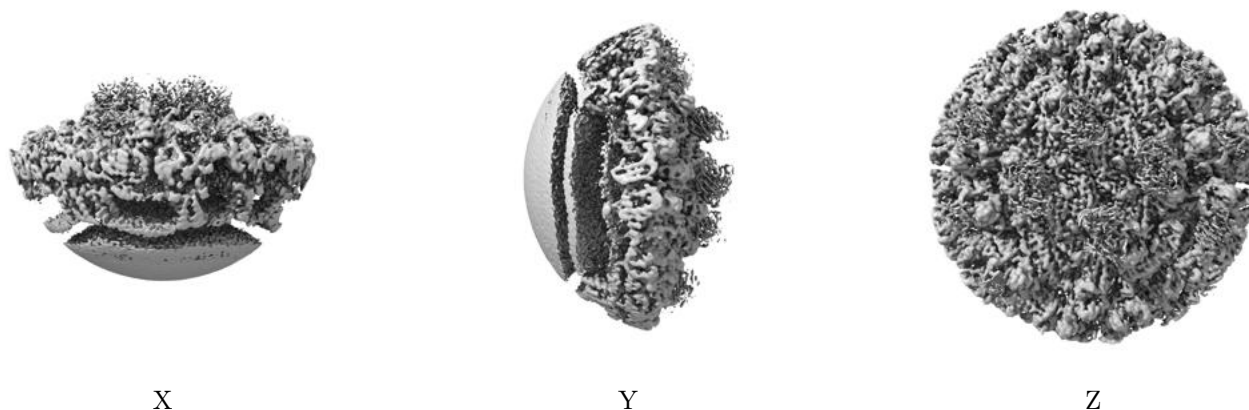


Z

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 1.5. 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.

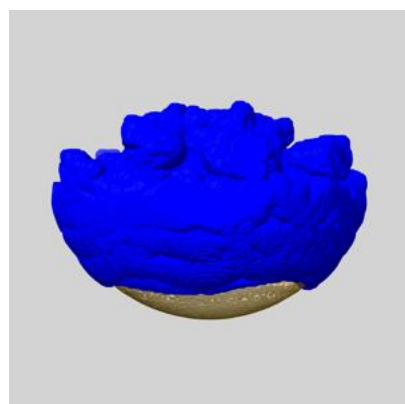
6.6 Mask visualisation [i](#)

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

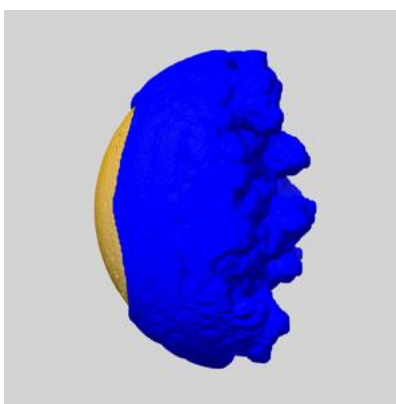
A mask typically either:

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

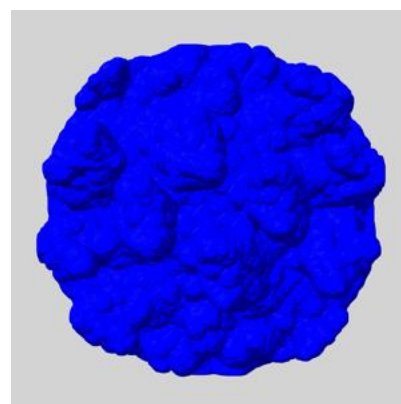
6.6.1 emd_27055_msk_1.map [i](#)



X



Y

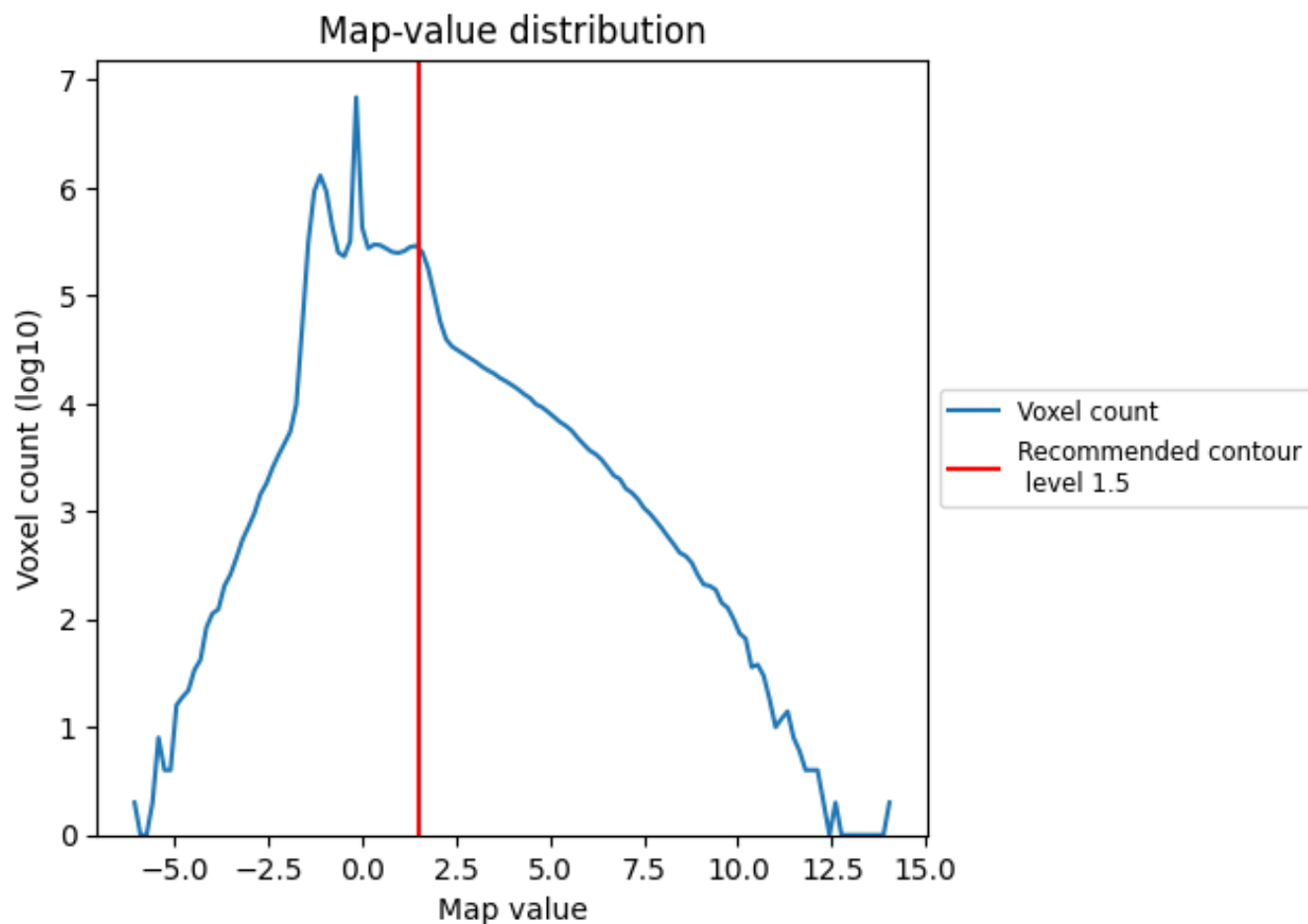


Z

7 Map analysis [i](#)

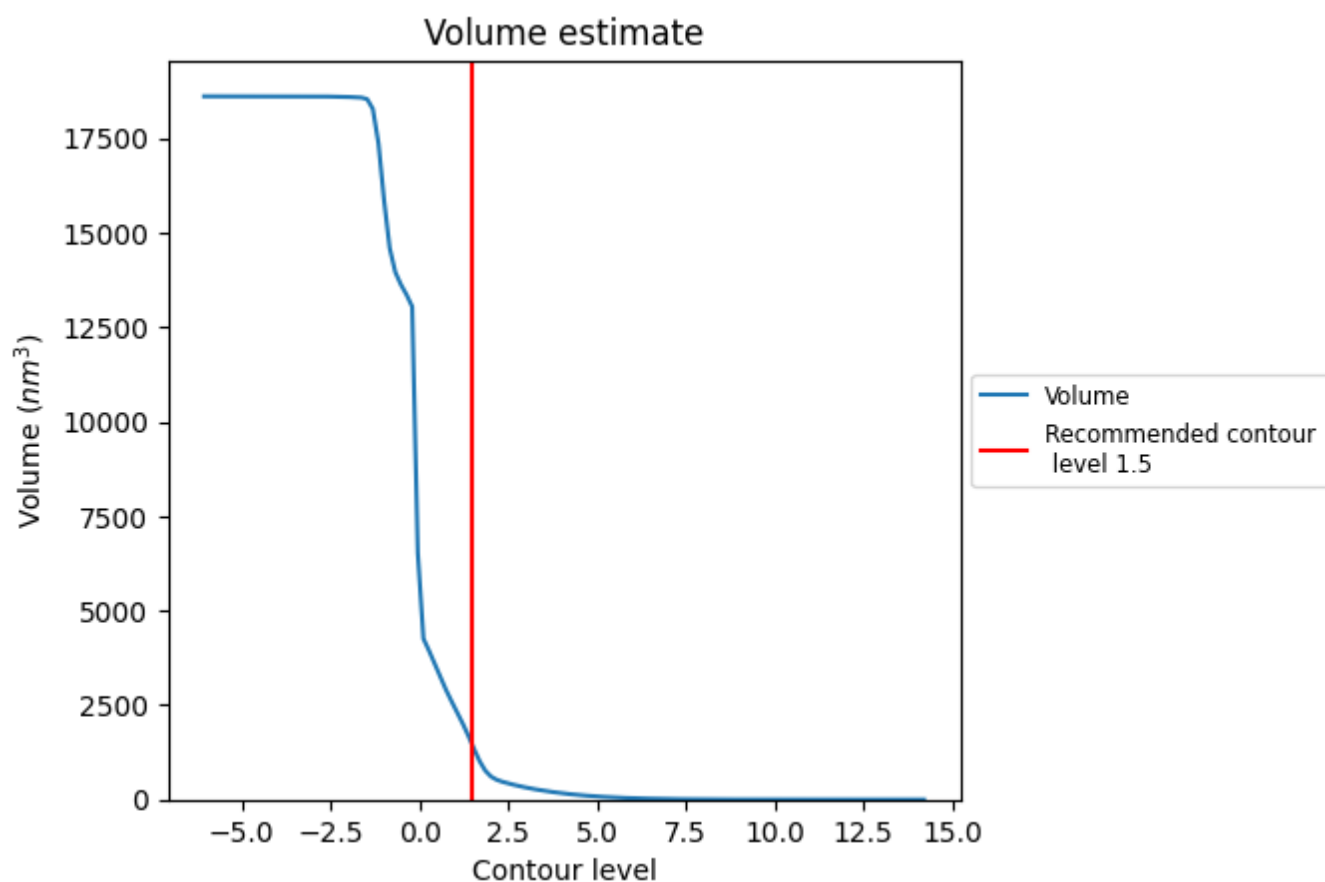
This section contains the results of statistical analysis of the map.

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.

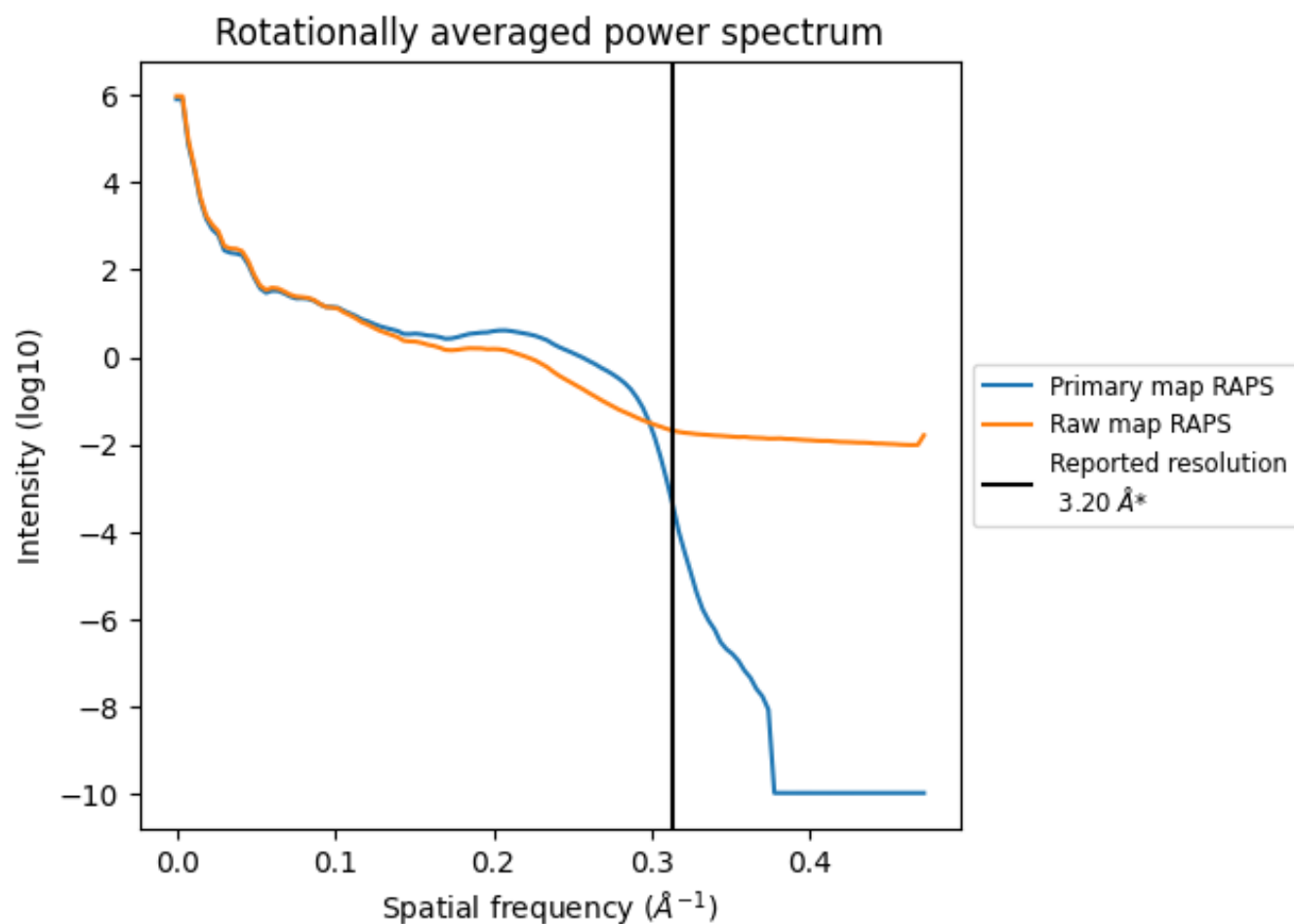
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1420 nm³; this corresponds to an approximate mass of 1283 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 ⓘ

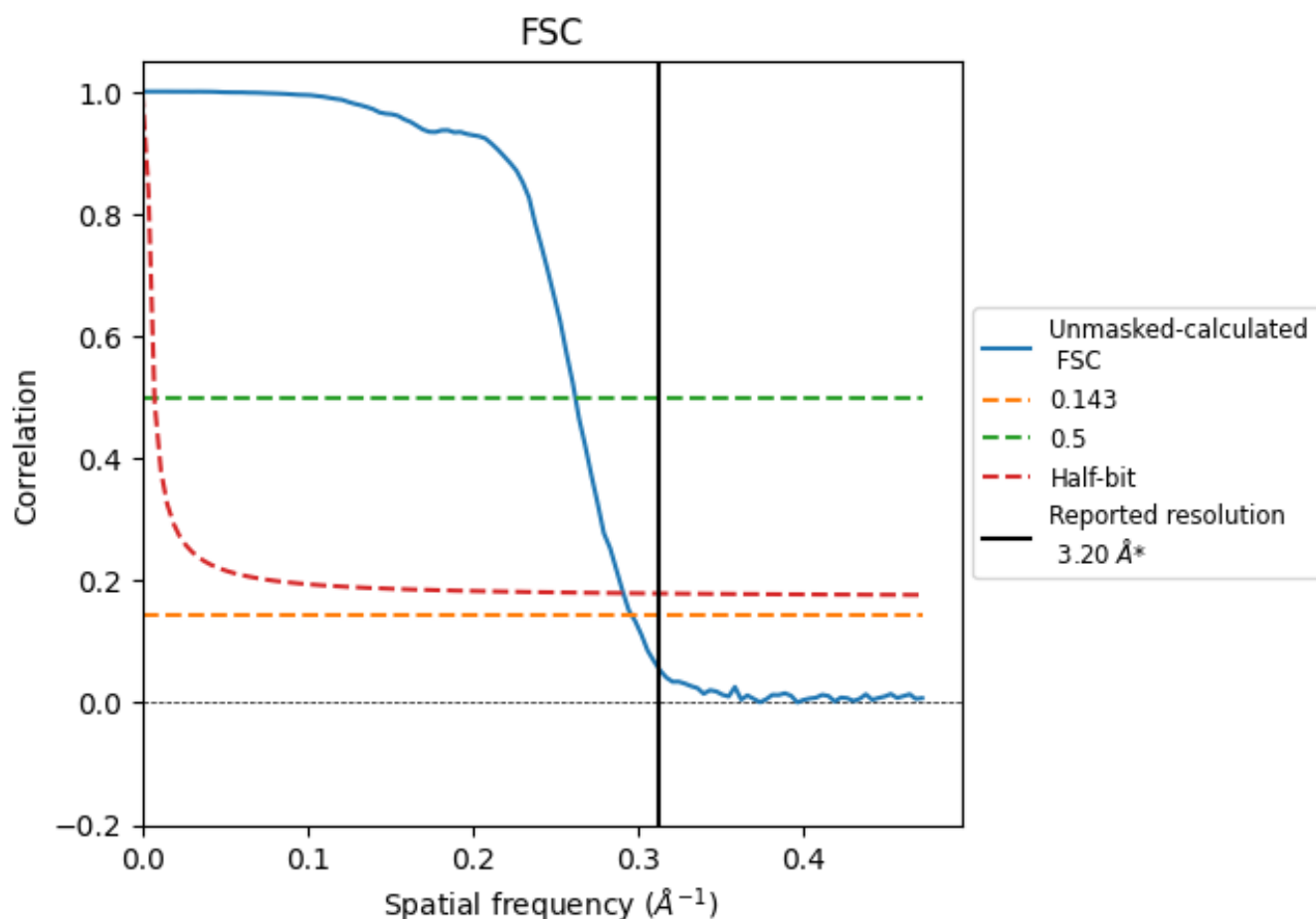


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 $0.312 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

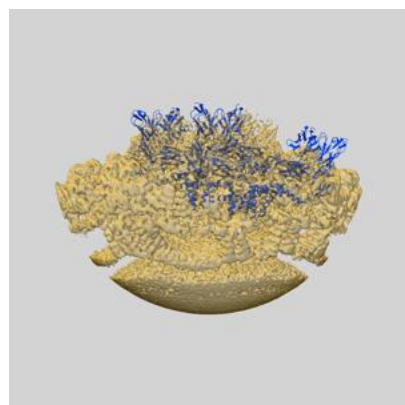
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.38	3.82	3.44

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

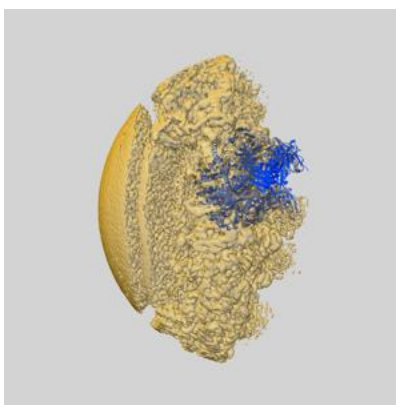
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27055 and PDB model 8CXG. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

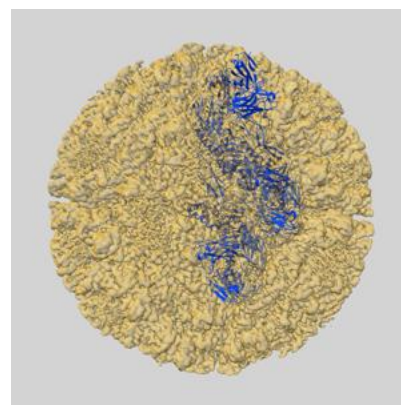
9.1 Map-model overlay [i](#)



X



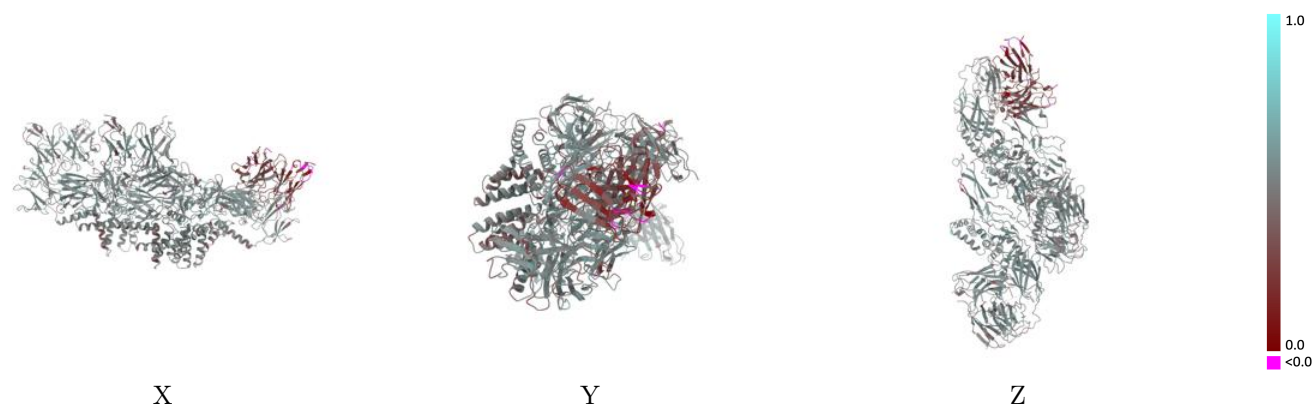
Y



Z

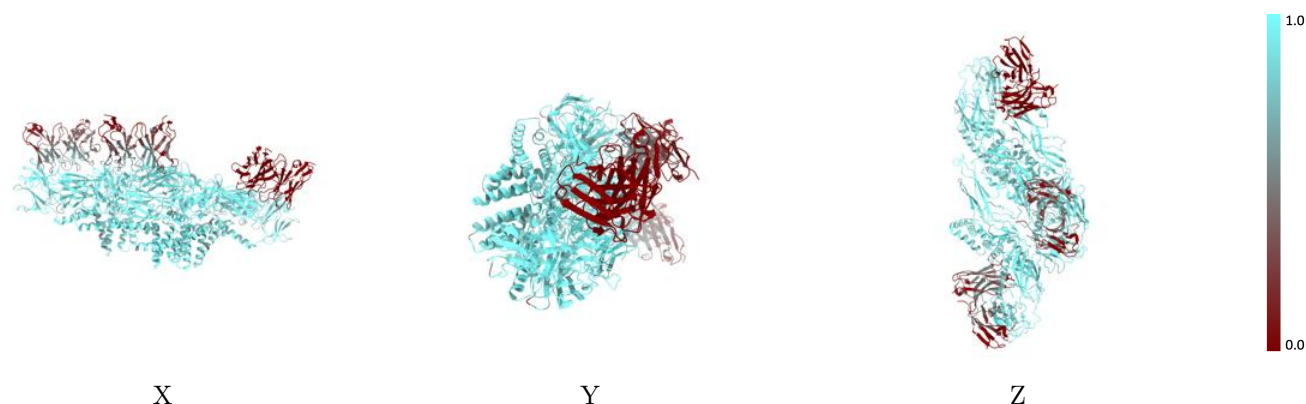
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



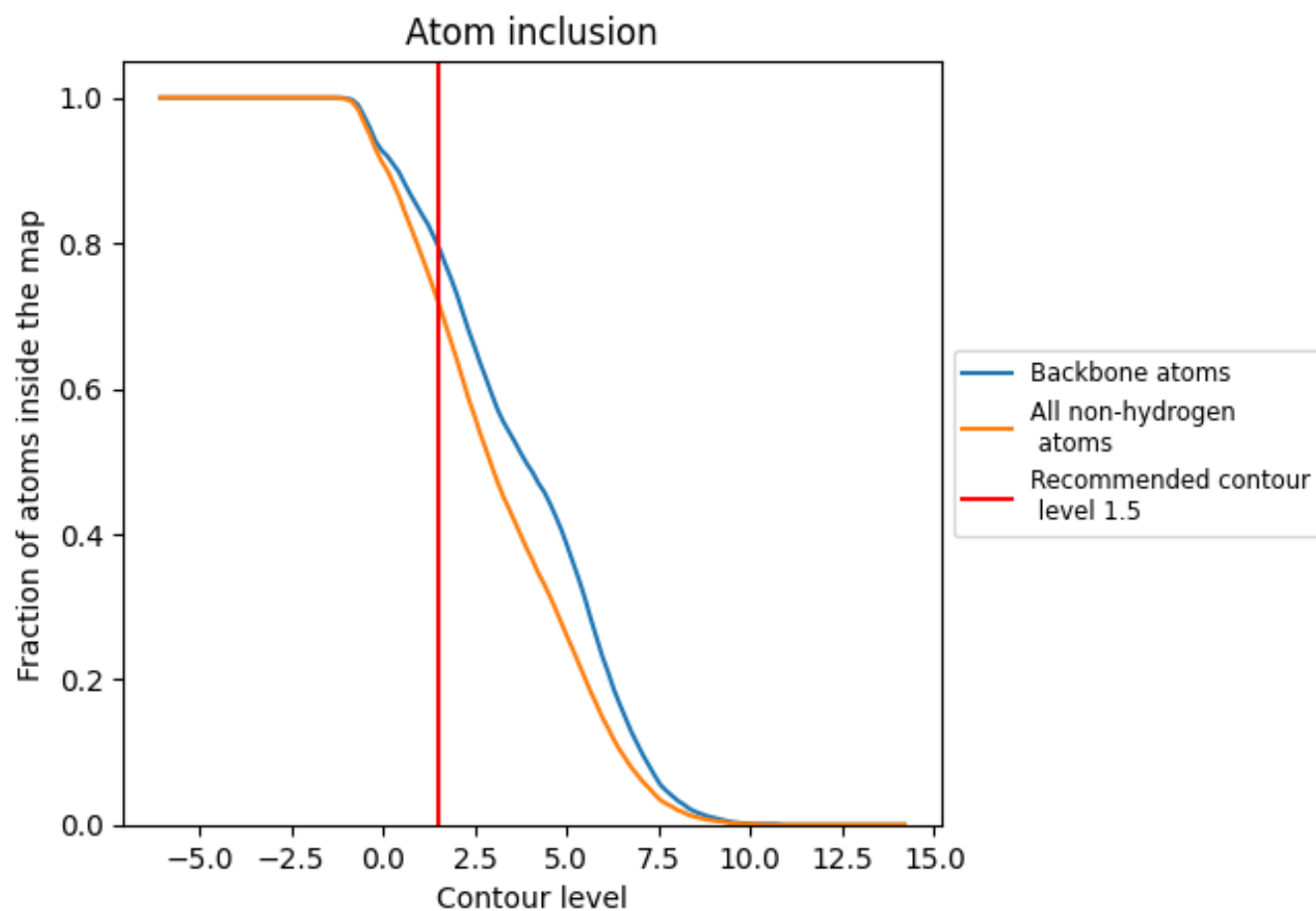
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 72% 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 (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7190	0.4850
1	0.0030	0.3020
2	0.0000	0.2290
A	0.9140	0.5140
B	0.9080	0.5030
C	0.9090	0.5040
D	0.9210	0.5430
E	0.9180	0.5310
F	0.9110	0.5120
H	0.4120	0.5090
L	0.3250	0.4950
h	0.3920	0.5030
l	0.3390	0.4970

1.0

0.0

<0.0