



Full wwPDB EM Validation Report ⓘ

Mar 21, 2026 – 03:29 PM UTC

PDB ID : 7FGF / pdb_00007fgf
EMDB ID : EMD-31579
Title : Cryo-EM structure of CCHFV envelope protein Gc in postfusion conformation
Authors : Li, N.; Rao, G.; Fu, Y.; Cao, S.
Deposited on : 2021-07-26
Resolution : 2.80 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

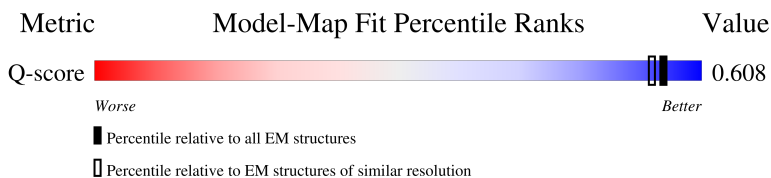
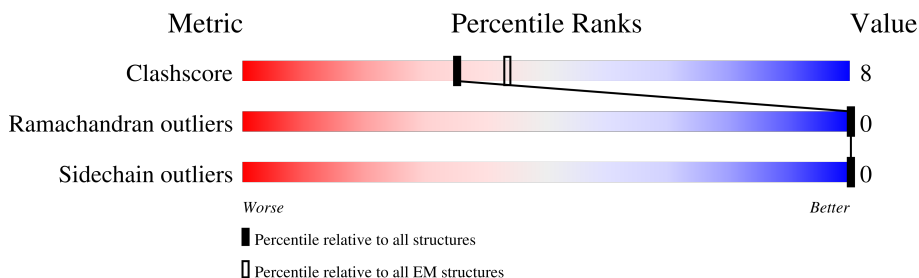
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	591	 58% 15% 27%
1	B	591	 58% 15% 27%
1	C	591	 59% 14% 27%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10143 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 Glycoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	432	Total	C	N	O	S	0	0
			3381	2125	571	651	34		
1	B	432	Total	C	N	O	S	0	0
			3381	2125	571	651	34		
1	C	432	Total	C	N	O	S	0	0
			3381	2125	571	651	34		

There are 210 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1570	SER	-	expression tag	UNP Q8JSZ3
A	1571	ARG	-	expression tag	UNP Q8JSZ3
A	1572	GLY	-	expression tag	UNP Q8JSZ3
A	1573	SER	-	expression tag	UNP Q8JSZ3
A	1574	GLY	-	expression tag	UNP Q8JSZ3
A	1575	GLY	-	expression tag	UNP Q8JSZ3
A	1576	MET	-	expression tag	UNP Q8JSZ3
A	1577	LYS	-	expression tag	UNP Q8JSZ3
A	1578	GLN	-	expression tag	UNP Q8JSZ3
A	1579	ILE	-	expression tag	UNP Q8JSZ3
A	1580	GLU	-	expression tag	UNP Q8JSZ3
A	1581	ASP	-	expression tag	UNP Q8JSZ3
A	1582	LYS	-	expression tag	UNP Q8JSZ3
A	1583	ILE	-	expression tag	UNP Q8JSZ3
A	1584	GLU	-	expression tag	UNP Q8JSZ3
A	1585	GLU	-	expression tag	UNP Q8JSZ3
A	1586	ILE	-	expression tag	UNP Q8JSZ3
A	1587	LEU	-	expression tag	UNP Q8JSZ3
A	1588	SER	-	expression tag	UNP Q8JSZ3
A	1589	LYS	-	expression tag	UNP Q8JSZ3
A	1590	ILE	-	expression tag	UNP Q8JSZ3
A	1591	TYR	-	expression tag	UNP Q8JSZ3
A	1592	HIS	-	expression tag	UNP Q8JSZ3
A	1593	ILE	-	expression tag	UNP Q8JSZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1594	GLU	-	expression tag	UNP Q8JSZ3
A	1595	ASN	-	expression tag	UNP Q8JSZ3
A	1596	GLU	-	expression tag	UNP Q8JSZ3
A	1597	ILE	-	expression tag	UNP Q8JSZ3
A	1598	ALA	-	expression tag	UNP Q8JSZ3
A	1599	ARG	-	expression tag	UNP Q8JSZ3
A	1600	ILE	-	expression tag	UNP Q8JSZ3
A	1601	LYS	-	expression tag	UNP Q8JSZ3
A	1602	LYS	-	expression tag	UNP Q8JSZ3
A	1603	LEU	-	expression tag	UNP Q8JSZ3
A	1604	ILE	-	expression tag	UNP Q8JSZ3
A	1605	GLY	-	expression tag	UNP Q8JSZ3
A	1606	GLU	-	expression tag	UNP Q8JSZ3
A	1607	GLY	-	expression tag	UNP Q8JSZ3
A	1608	SER	-	expression tag	UNP Q8JSZ3
A	1609	GLY	-	expression tag	UNP Q8JSZ3
A	1610	GLY	-	expression tag	UNP Q8JSZ3
A	1611	SER	-	expression tag	UNP Q8JSZ3
A	1612	ARG	-	expression tag	UNP Q8JSZ3
A	1613	GLY	-	expression tag	UNP Q8JSZ3
A	1614	PRO	-	expression tag	UNP Q8JSZ3
A	1615	PHE	-	expression tag	UNP Q8JSZ3
A	1616	GLU	-	expression tag	UNP Q8JSZ3
A	1617	GLY	-	expression tag	UNP Q8JSZ3
A	1618	LYS	-	expression tag	UNP Q8JSZ3
A	1619	PRO	-	expression tag	UNP Q8JSZ3
A	1620	ILE	-	expression tag	UNP Q8JSZ3
A	1621	PRO	-	expression tag	UNP Q8JSZ3
A	1622	ASN	-	expression tag	UNP Q8JSZ3
A	1623	PRO	-	expression tag	UNP Q8JSZ3
A	1624	LEU	-	expression tag	UNP Q8JSZ3
A	1625	LEU	-	expression tag	UNP Q8JSZ3
A	1626	GLY	-	expression tag	UNP Q8JSZ3
A	1627	LEU	-	expression tag	UNP Q8JSZ3
A	1628	ASP	-	expression tag	UNP Q8JSZ3
A	1629	SER	-	expression tag	UNP Q8JSZ3
A	1630	THR	-	expression tag	UNP Q8JSZ3
A	1631	ARG	-	expression tag	UNP Q8JSZ3
A	1632	THR	-	expression tag	UNP Q8JSZ3
A	1633	GLY	-	expression tag	UNP Q8JSZ3
A	1634	HIS	-	expression tag	UNP Q8JSZ3
A	1635	HIS	-	expression tag	UNP Q8JSZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1636	HIS	-	expression tag	UNP Q8JSZ3
A	1637	HIS	-	expression tag	UNP Q8JSZ3
A	1638	HIS	-	expression tag	UNP Q8JSZ3
A	1639	HIS	-	expression tag	UNP Q8JSZ3
B	1570	SER	-	expression tag	UNP Q8JSZ3
B	1571	ARG	-	expression tag	UNP Q8JSZ3
B	1572	GLY	-	expression tag	UNP Q8JSZ3
B	1573	SER	-	expression tag	UNP Q8JSZ3
B	1574	GLY	-	expression tag	UNP Q8JSZ3
B	1575	GLY	-	expression tag	UNP Q8JSZ3
B	1576	MET	-	expression tag	UNP Q8JSZ3
B	1577	LYS	-	expression tag	UNP Q8JSZ3
B	1578	GLN	-	expression tag	UNP Q8JSZ3
B	1579	ILE	-	expression tag	UNP Q8JSZ3
B	1580	GLU	-	expression tag	UNP Q8JSZ3
B	1581	ASP	-	expression tag	UNP Q8JSZ3
B	1582	LYS	-	expression tag	UNP Q8JSZ3
B	1583	ILE	-	expression tag	UNP Q8JSZ3
B	1584	GLU	-	expression tag	UNP Q8JSZ3
B	1585	GLU	-	expression tag	UNP Q8JSZ3
B	1586	ILE	-	expression tag	UNP Q8JSZ3
B	1587	LEU	-	expression tag	UNP Q8JSZ3
B	1588	SER	-	expression tag	UNP Q8JSZ3
B	1589	LYS	-	expression tag	UNP Q8JSZ3
B	1590	ILE	-	expression tag	UNP Q8JSZ3
B	1591	TYR	-	expression tag	UNP Q8JSZ3
B	1592	HIS	-	expression tag	UNP Q8JSZ3
B	1593	ILE	-	expression tag	UNP Q8JSZ3
B	1594	GLU	-	expression tag	UNP Q8JSZ3
B	1595	ASN	-	expression tag	UNP Q8JSZ3
B	1596	GLU	-	expression tag	UNP Q8JSZ3
B	1597	ILE	-	expression tag	UNP Q8JSZ3
B	1598	ALA	-	expression tag	UNP Q8JSZ3
B	1599	ARG	-	expression tag	UNP Q8JSZ3
B	1600	ILE	-	expression tag	UNP Q8JSZ3
B	1601	LYS	-	expression tag	UNP Q8JSZ3
B	1602	LYS	-	expression tag	UNP Q8JSZ3
B	1603	LEU	-	expression tag	UNP Q8JSZ3
B	1604	ILE	-	expression tag	UNP Q8JSZ3
B	1605	GLY	-	expression tag	UNP Q8JSZ3
B	1606	GLU	-	expression tag	UNP Q8JSZ3
B	1607	GLY	-	expression tag	UNP Q8JSZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1608	SER	-	expression tag	UNP Q8JSZ3
B	1609	GLY	-	expression tag	UNP Q8JSZ3
B	1610	GLY	-	expression tag	UNP Q8JSZ3
B	1611	SER	-	expression tag	UNP Q8JSZ3
B	1612	ARG	-	expression tag	UNP Q8JSZ3
B	1613	GLY	-	expression tag	UNP Q8JSZ3
B	1614	PRO	-	expression tag	UNP Q8JSZ3
B	1615	PHE	-	expression tag	UNP Q8JSZ3
B	1616	GLU	-	expression tag	UNP Q8JSZ3
B	1617	GLY	-	expression tag	UNP Q8JSZ3
B	1618	LYS	-	expression tag	UNP Q8JSZ3
B	1619	PRO	-	expression tag	UNP Q8JSZ3
B	1620	ILE	-	expression tag	UNP Q8JSZ3
B	1621	PRO	-	expression tag	UNP Q8JSZ3
B	1622	ASN	-	expression tag	UNP Q8JSZ3
B	1623	PRO	-	expression tag	UNP Q8JSZ3
B	1624	LEU	-	expression tag	UNP Q8JSZ3
B	1625	LEU	-	expression tag	UNP Q8JSZ3
B	1626	GLY	-	expression tag	UNP Q8JSZ3
B	1627	LEU	-	expression tag	UNP Q8JSZ3
B	1628	ASP	-	expression tag	UNP Q8JSZ3
B	1629	SER	-	expression tag	UNP Q8JSZ3
B	1630	THR	-	expression tag	UNP Q8JSZ3
B	1631	ARG	-	expression tag	UNP Q8JSZ3
B	1632	THR	-	expression tag	UNP Q8JSZ3
B	1633	GLY	-	expression tag	UNP Q8JSZ3
B	1634	HIS	-	expression tag	UNP Q8JSZ3
B	1635	HIS	-	expression tag	UNP Q8JSZ3
B	1636	HIS	-	expression tag	UNP Q8JSZ3
B	1637	HIS	-	expression tag	UNP Q8JSZ3
B	1638	HIS	-	expression tag	UNP Q8JSZ3
B	1639	HIS	-	expression tag	UNP Q8JSZ3
C	1570	SER	-	expression tag	UNP Q8JSZ3
C	1571	ARG	-	expression tag	UNP Q8JSZ3
C	1572	GLY	-	expression tag	UNP Q8JSZ3
C	1573	SER	-	expression tag	UNP Q8JSZ3
C	1574	GLY	-	expression tag	UNP Q8JSZ3
C	1575	GLY	-	expression tag	UNP Q8JSZ3
C	1576	MET	-	expression tag	UNP Q8JSZ3
C	1577	LYS	-	expression tag	UNP Q8JSZ3
C	1578	GLN	-	expression tag	UNP Q8JSZ3
C	1579	ILE	-	expression tag	UNP Q8JSZ3

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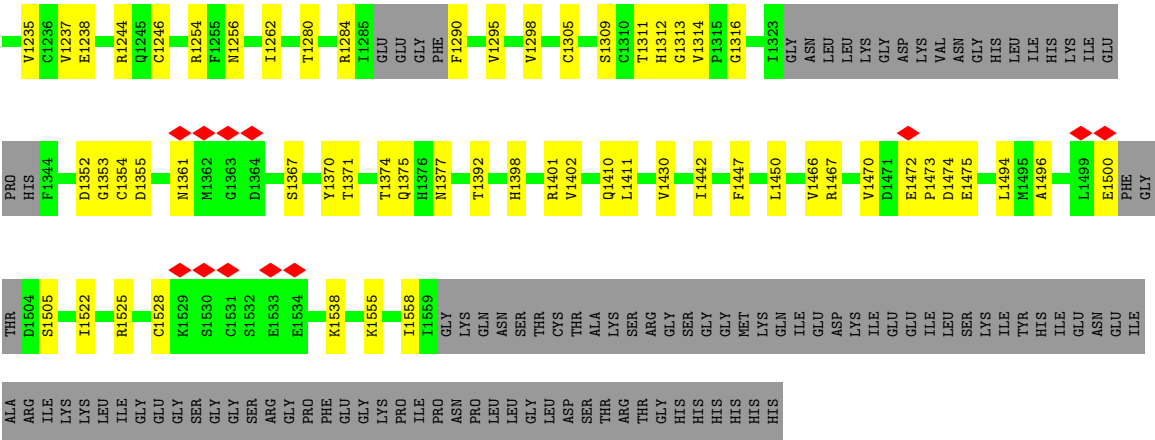
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Chain	Residue	Modelled	Actual	Comment	Reference
C	1580	GLU	-	expression tag	UNP Q8JSZ3
C	1581	ASP	-	expression tag	UNP Q8JSZ3
C	1582	LYS	-	expression tag	UNP Q8JSZ3
C	1583	ILE	-	expression tag	UNP Q8JSZ3
C	1584	GLU	-	expression tag	UNP Q8JSZ3
C	1585	GLU	-	expression tag	UNP Q8JSZ3
C	1586	ILE	-	expression tag	UNP Q8JSZ3
C	1587	LEU	-	expression tag	UNP Q8JSZ3
C	1588	SER	-	expression tag	UNP Q8JSZ3
C	1589	LYS	-	expression tag	UNP Q8JSZ3
C	1590	ILE	-	expression tag	UNP Q8JSZ3
C	1591	TYR	-	expression tag	UNP Q8JSZ3
C	1592	HIS	-	expression tag	UNP Q8JSZ3
C	1593	ILE	-	expression tag	UNP Q8JSZ3
C	1594	GLU	-	expression tag	UNP Q8JSZ3
C	1595	ASN	-	expression tag	UNP Q8JSZ3
C	1596	GLU	-	expression tag	UNP Q8JSZ3
C	1597	ILE	-	expression tag	UNP Q8JSZ3
C	1598	ALA	-	expression tag	UNP Q8JSZ3
C	1599	ARG	-	expression tag	UNP Q8JSZ3
C	1600	ILE	-	expression tag	UNP Q8JSZ3
C	1601	LYS	-	expression tag	UNP Q8JSZ3
C	1602	LYS	-	expression tag	UNP Q8JSZ3
C	1603	LEU	-	expression tag	UNP Q8JSZ3
C	1604	ILE	-	expression tag	UNP Q8JSZ3
C	1605	GLY	-	expression tag	UNP Q8JSZ3
C	1606	GLU	-	expression tag	UNP Q8JSZ3
C	1607	GLY	-	expression tag	UNP Q8JSZ3
C	1608	SER	-	expression tag	UNP Q8JSZ3
C	1609	GLY	-	expression tag	UNP Q8JSZ3
C	1610	GLY	-	expression tag	UNP Q8JSZ3
C	1611	SER	-	expression tag	UNP Q8JSZ3
C	1612	ARG	-	expression tag	UNP Q8JSZ3
C	1613	GLY	-	expression tag	UNP Q8JSZ3
C	1614	PRO	-	expression tag	UNP Q8JSZ3
C	1615	PHE	-	expression tag	UNP Q8JSZ3
C	1616	GLU	-	expression tag	UNP Q8JSZ3
C	1617	GLY	-	expression tag	UNP Q8JSZ3
C	1618	LYS	-	expression tag	UNP Q8JSZ3
C	1619	PRO	-	expression tag	UNP Q8JSZ3
C	1620	ILE	-	expression tag	UNP Q8JSZ3
C	1621	PRO	-	expression tag	UNP Q8JSZ3

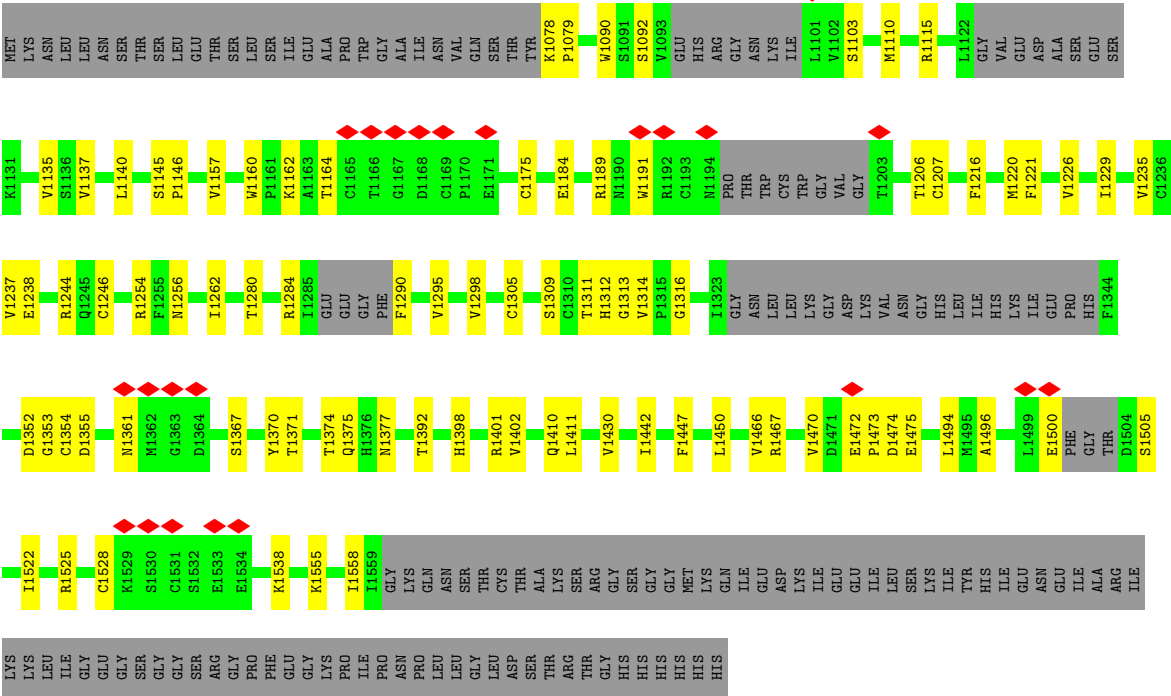
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Chain	Residue	Modelled	Actual	Comment	Reference
C	1622	ASN	-	expression tag	UNP Q8JSZ3
C	1623	PRO	-	expression tag	UNP Q8JSZ3
C	1624	LEU	-	expression tag	UNP Q8JSZ3
C	1625	LEU	-	expression tag	UNP Q8JSZ3
C	1626	GLY	-	expression tag	UNP Q8JSZ3
C	1627	LEU	-	expression tag	UNP Q8JSZ3
C	1628	ASP	-	expression tag	UNP Q8JSZ3
C	1629	SER	-	expression tag	UNP Q8JSZ3
C	1630	THR	-	expression tag	UNP Q8JSZ3
C	1631	ARG	-	expression tag	UNP Q8JSZ3
C	1632	THR	-	expression tag	UNP Q8JSZ3
C	1633	GLY	-	expression tag	UNP Q8JSZ3
C	1634	HIS	-	expression tag	UNP Q8JSZ3
C	1635	HIS	-	expression tag	UNP Q8JSZ3
C	1636	HIS	-	expression tag	UNP Q8JSZ3
C	1637	HIS	-	expression tag	UNP Q8JSZ3
C	1638	HIS	-	expression tag	UNP Q8JSZ3
C	1639	HIS	-	expression tag	UNP Q8JSZ3



• Molecule 1: Glycoprotein C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	187292	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.465	Depositor
Minimum map value	-2.404	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.096	Depositor
Recommended contour level	0.44	Depositor
Map size ($\text{\AA}$)	219.6, 219.6, 219.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.61, 0.61, 0.61	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	A	0.24	0/3451	0.44	0/4674
1	B	0.24	0/3451	0.44	0/4674
1	C	0.24	0/3451	0.44	0/4674
All	All	0.24	0/10353	0.44	0/14022

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 [i](#)

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	3381	0	3295	55	0
1	B	3381	0	3295	57	0
1	C	3381	0	3295	55	0
All	All	10143	0	9885	159	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 8.

All (159) 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:1078:LYS:HZ2	1:A:1115:ARG:HH11	1.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1078:LYS:HZ2	1:B:1115:ARG:HH11	1.40	0.69
1:A:1238:GLU:HG2	1:A:1244:ARG:HG3	1.79	0.65
1:C:1238:GLU:HG2	1:C:1244:ARG:HG3	1.79	0.65
1:B:1238:GLU:HG2	1:B:1244:ARG:HG3	1.79	0.64
1:B:1189:ARG:NH2	1:B:1206:THR:OG1	2.33	0.62
1:C:1078:LYS:HZ2	1:C:1115:ARG:HH11	1.48	0.61
1:C:1189:ARG:NH2	1:C:1206:THR:OG1	2.33	0.61
1:B:1309:SER:HB2	1:C:1314:VAL:HG21	1.83	0.60
1:A:1189:ARG:NH2	1:A:1206:THR:OG1	2.33	0.60
1:A:1314:VAL:HG21	1:C:1309:SER:HB2	1.83	0.60
1:B:1466:VAL:HG21	1:B:1494:LEU:HD13	1.84	0.60
1:A:1309:SER:HB2	1:B:1314:VAL:HG21	1.84	0.59
1:A:1466:VAL:HG21	1:A:1494:LEU:HD13	1.84	0.59
1:C:1466:VAL:HG21	1:C:1494:LEU:HD13	1.84	0.59
1:B:1470:VAL:HG22	1:B:1473:PRO:HD2	1.85	0.58
1:A:1470:VAL:HG22	1:A:1473:PRO:HD2	1.85	0.57
1:C:1470:VAL:HG22	1:C:1473:PRO:HD2	1.85	0.57
1:B:1157:VAL:HG22	1:B:1375:GLN:HA	1.88	0.56
1:B:1160:TRP:HZ2	1:B:1175:CYS:HB2	1.70	0.56
1:A:1160:TRP:HZ2	1:A:1175:CYS:HB2	1.70	0.56
1:C:1157:VAL:HG22	1:C:1375:GLN:HA	1.88	0.56
1:C:1447:PHE:CD2	1:C:1538:LYS:HB2	2.41	0.56
1:A:1157:VAL:HG22	1:A:1375:GLN:HA	1.88	0.55
1:A:1447:PHE:CD2	1:A:1538:LYS:HB2	2.41	0.55
1:C:1447:PHE:HE2	1:C:1450:LEU:HB2	1.72	0.55
1:B:1447:PHE:CD2	1:B:1538:LYS:HB2	2.41	0.55
1:C:1078:LYS:NZ	1:C:1115:ARG:HH11	2.05	0.55
1:A:1447:PHE:HE2	1:A:1450:LEU:HB2	1.72	0.55
1:B:1447:PHE:HE2	1:B:1450:LEU:HB2	1.72	0.54
1:C:1160:TRP:HZ2	1:C:1175:CYS:HB2	1.70	0.54
1:A:1078:LYS:NZ	1:A:1115:ARG:HH11	2.05	0.54
1:C:1146:PRO:HB3	1:C:1226:VAL:HG12	1.89	0.54
1:B:1078:LYS:NZ	1:B:1115:ARG:HH11	2.05	0.54
1:B:1078:LYS:HB3	1:B:1079:PRO:HD3	1.91	0.53
1:A:1146:PRO:HB3	1:A:1226:VAL:HG12	1.89	0.53
1:B:1146:PRO:HB3	1:B:1226:VAL:HG12	1.89	0.53
1:A:1078:LYS:HB3	1:A:1079:PRO:HD3	1.91	0.53
1:A:1254:ARG:NH1	1:A:1256:ASN:OD1	2.42	0.53
1:B:1254:ARG:NH1	1:B:1256:ASN:OD1	2.42	0.53
1:C:1254:ARG:NH1	1:C:1256:ASN:OD1	2.42	0.53
1:C:1522:ILE:O	1:C:1525:ARG:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1522:ILE:O	1:A:1525:ARG:HG3	2.09	0.53
1:C:1078:LYS:HB3	1:C:1079:PRO:HD3	1.91	0.53
1:B:1522:ILE:O	1:B:1525:ARG:HG3	2.09	0.52
1:A:1280:THR:HB	1:A:1295:VAL:HG13	1.92	0.52
1:C:1140:LEU:O	1:C:1398:HIS:NE2	2.41	0.51
1:B:1280:THR:HB	1:B:1295:VAL:HG13	1.92	0.51
1:A:1140:LEU:O	1:A:1398:HIS:NE2	2.41	0.50
1:C:1280:THR:HB	1:C:1295:VAL:HG13	1.92	0.50
1:B:1137:VAL:HG12	1:B:1235:VAL:HG22	1.93	0.50
1:C:1103:SER:OG	1:C:1430:VAL:O	2.30	0.50
1:C:1216:PHE:CE2	1:C:1220:MET:HE2	2.47	0.50
1:A:1137:VAL:HG12	1:A:1235:VAL:HG22	1.93	0.49
1:C:1137:VAL:HG12	1:C:1235:VAL:HG22	1.93	0.49
1:B:1216:PHE:CE2	1:B:1220:MET:HE2	2.47	0.49
1:B:1244:ARG:HD2	1:B:1246:CYS:SG	2.52	0.49
1:A:1216:PHE:CE2	1:A:1220:MET:HE2	2.47	0.49
1:C:1244:ARG:HD2	1:C:1246:CYS:SG	2.52	0.49
1:A:1311:THR:HG22	1:A:1312:HIS:H	1.79	0.48
1:B:1311:THR:HG22	1:B:1312:HIS:H	1.79	0.48
1:A:1228:TYR:HH	1:A:1231:THR:HG1	1.57	0.48
1:A:1244:ARG:HD2	1:A:1246:CYS:SG	2.52	0.48
1:B:1361:ASN:OD1	1:B:1367:SER:OG	2.31	0.48
1:B:1442:ILE:HB	1:B:1528:CYS:HA	1.95	0.48
1:A:1442:ILE:HB	1:A:1528:CYS:HA	1.95	0.48
1:A:1474:ASP:O	1:A:1475:GLU:HB3	2.14	0.48
1:C:1467:ARG:NH2	1:C:1500:GLU:O	2.47	0.48
1:C:1311:THR:HG22	1:C:1312:HIS:H	1.79	0.47
1:C:1442:ILE:HB	1:C:1528:CYS:HA	1.95	0.47
1:A:1374:THR:OG1	1:A:1555:LYS:HE2	2.15	0.47
1:B:1374:THR:OG1	1:B:1555:LYS:HE2	2.15	0.47
1:C:1474:ASP:O	1:C:1475:GLU:HB3	2.14	0.47
1:B:1474:ASP:O	1:B:1475:GLU:HB3	2.14	0.47
1:A:1361:ASN:OD1	1:A:1367:SER:OG	2.31	0.47
1:C:1361:ASN:OD1	1:C:1367:SER:OG	2.31	0.47
1:B:1401:ARG:O	1:B:1411:LEU:HA	2.15	0.47
1:A:1305:CYS:HB3	1:A:1316:GLY:HA3	1.98	0.46
1:A:1401:ARG:O	1:A:1411:LEU:HA	2.15	0.46
1:C:1401:ARG:O	1:C:1411:LEU:HA	2.16	0.46
1:B:1140:LEU:O	1:B:1398:HIS:NE2	2.41	0.46
1:C:1374:THR:OG1	1:C:1555:LYS:HE2	2.15	0.46
1:B:1305:CYS:HB3	1:B:1316:GLY:HA3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1472:GLU:HB3	1:C:1473:PRO:HD3	1.97	0.46
1:B:1472:GLU:HB3	1:B:1473:PRO:HD3	1.97	0.46
1:A:1475:GLU:HA	1:A:1496:ALA:O	2.16	0.46
1:C:1305:CYS:HB3	1:C:1316:GLY:HA3	1.98	0.46
1:C:1475:GLU:HA	1:C:1496:ALA:O	2.17	0.45
1:A:1472:GLU:HB3	1:A:1473:PRO:HD3	1.97	0.45
1:B:1103:SER:OG	1:B:1430:VAL:O	2.30	0.45
1:C:1191:TRP:H	1:C:1191:TRP:CD1	2.34	0.45
1:B:1191:TRP:H	1:B:1191:TRP:CD1	2.34	0.45
1:B:1312:HIS:O	1:B:1312:HIS:CG	2.70	0.45
1:A:1183:LYS:NZ	1:B:1355:ASP:OD2	2.43	0.45
1:B:1475:GLU:HA	1:B:1496:ALA:O	2.17	0.45
1:C:1352:ASP:OD1	1:C:1353:GLY:N	2.50	0.45
1:A:1103:SER:OG	1:A:1430:VAL:O	2.30	0.45
1:B:1164:THR:O	1:B:1189:ARG:NH1	2.50	0.45
1:A:1352:ASP:OD1	1:A:1353:GLY:N	2.50	0.45
1:C:1354:CYS:HA	1:C:1371:THR:O	2.17	0.45
1:A:1354:CYS:HA	1:A:1371:THR:O	2.17	0.44
1:B:1352:ASP:OD1	1:B:1353:GLY:N	2.50	0.44
1:C:1164:THR:O	1:C:1189:ARG:NH1	2.49	0.44
1:C:1494:LEU:HD22	1:C:1505:SER:HB3	2.00	0.44
1:B:1494:LEU:HD22	1:B:1505:SER:HB3	2.00	0.44
1:C:1312:HIS:CG	1:C:1312:HIS:O	2.70	0.44
1:B:1145:SER:HB3	1:B:1229:ILE:HD11	2.00	0.44
1:A:1467:ARG:NH2	1:A:1500:GLU:O	2.47	0.44
1:A:1164:THR:O	1:A:1189:ARG:NH1	2.50	0.44
1:C:1237:VAL:HG11	1:C:1262:ILE:HD12	1.99	0.44
1:A:1191:TRP:CD1	1:A:1191:TRP:H	2.34	0.43
1:A:1312:HIS:O	1:A:1312:HIS:CG	2.70	0.43
1:A:1370:TYR:HD1	1:A:1558:ILE:HB	1.83	0.43
1:A:1494:LEU:HD22	1:A:1505:SER:HB3	2.00	0.43
1:A:1500:GLU:N	1:A:1500:GLU:OE1	2.51	0.43
1:B:1500:GLU:N	1:B:1500:GLU:OE1	2.51	0.43
1:A:1298:VAL:H	1:A:1392:THR:HG23	1.83	0.43
1:C:1145:SER:HB3	1:C:1229:ILE:HD11	2.00	0.43
1:A:1090:TRP:HB2	1:C:1092:SER:HB3	2.00	0.43
1:B:1354:CYS:HA	1:B:1371:THR:O	2.17	0.43
1:B:1237:VAL:HG11	1:B:1262:ILE:HD12	1.99	0.43
1:B:1467:ARG:NH2	1:B:1500:GLU:O	2.47	0.43
1:C:1298:VAL:H	1:C:1392:THR:HG23	1.83	0.43
1:A:1237:VAL:HG11	1:A:1262:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1370:TYR:HD1	1:B:1558:ILE:HB	1.83	0.43
1:C:1500:GLU:OE1	1:C:1500:GLU:N	2.51	0.43
1:C:1313:GLY:O	1:C:1377:ASN:ND2	2.52	0.43
1:C:1370:TYR:HD1	1:C:1558:ILE:HB	1.83	0.43
1:A:1145:SER:HB3	1:A:1229:ILE:HD11	2.00	0.42
1:B:1313:GLY:O	1:B:1377:ASN:ND2	2.52	0.42
1:A:1284:ARG:HG2	1:A:1290:PHE:CE1	2.55	0.42
1:A:1313:GLY:O	1:A:1377:ASN:ND2	2.52	0.42
1:A:1402:VAL:HA	1:A:1410:GLN:O	2.19	0.42
1:B:1298:VAL:H	1:B:1392:THR:HG23	1.83	0.42
1:B:1221:PHE:HA	1:B:1280:THR:O	2.20	0.42
1:B:1402:VAL:HA	1:B:1410:GLN:O	2.19	0.42
1:C:1402:VAL:HA	1:C:1410:GLN:O	2.19	0.42
1:C:1284:ARG:HG2	1:C:1290:PHE:CE1	2.55	0.42
1:A:1162:LYS:HB2	1:A:1207:CYS:SG	2.60	0.42
1:C:1254:ARG:HA	1:C:1262:ILE:O	2.20	0.42
1:B:1092:SER:HB3	1:C:1090:TRP:HB2	2.02	0.42
1:C:1221:PHE:HA	1:C:1280:THR:O	2.20	0.42
1:A:1092:SER:HB3	1:B:1090:TRP:HB2	2.01	0.41
1:B:1162:LYS:HB2	1:B:1207:CYS:SG	2.60	0.41
1:B:1284:ARG:HG2	1:B:1290:PHE:CE1	2.55	0.41
1:C:1110:MET:HE1	1:C:1135:VAL:HG12	2.03	0.41
1:A:1221:PHE:HA	1:A:1280:THR:O	2.20	0.41
1:A:1254:ARG:HA	1:A:1262:ILE:O	2.20	0.41
1:B:1183:LYS:NZ	1:C:1355:ASP:OD2	2.42	0.41
1:B:1254:ARG:HA	1:B:1262:ILE:O	2.20	0.41
1:C:1162:LYS:HB2	1:C:1207:CYS:SG	2.60	0.41
1:B:1447:PHE:HD2	1:B:1538:LYS:HB2	1.86	0.41
1:B:1110:MET:HE1	1:B:1135:VAL:HG12	2.03	0.41
1:C:1184:GLU:HG3	1:C:1207:CYS:HB3	2.03	0.40
1:A:1184:GLU:HG3	1:A:1207:CYS:HB3	2.03	0.40
1:B:1112:LEU:HB3	1:B:1140:LEU:HD22	2.03	0.40
1:C:1447:PHE:HD2	1:C:1538:LYS:HB2	1.86	0.40
1:A:1110:MET:HE1	1:A:1135:VAL:HG12	2.03	0.40
1:B:1184:GLU:HG3	1:B:1207:CYS:HB3	2.03	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	418/591 (71%)	389 (93%)	29 (7%)	0	100	100
1	B	418/591 (71%)	389 (93%)	29 (7%)	0	100	100
1	C	418/591 (71%)	389 (93%)	29 (7%)	0	100	100
All	All	1254/1773 (71%)	1167 (93%)	87 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	391/523 (75%)	391 (100%)	0	100	100
1	B	391/523 (75%)	391 (100%)	0	100	100
1	C	391/523 (75%)	391 (100%)	0	100	100
All	All	1173/1569 (75%)	1173 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1396	HIS
1	B	1396	HIS
1	C	1396	HIS

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.

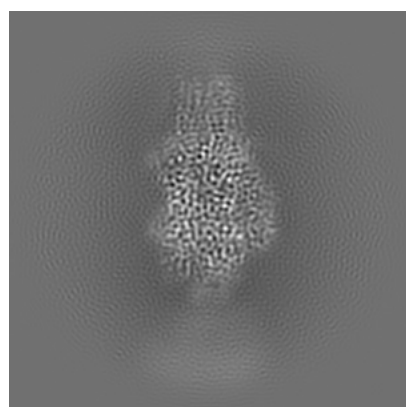
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31579. These allow visual inspection of the internal detail of the map and identification of artifacts.

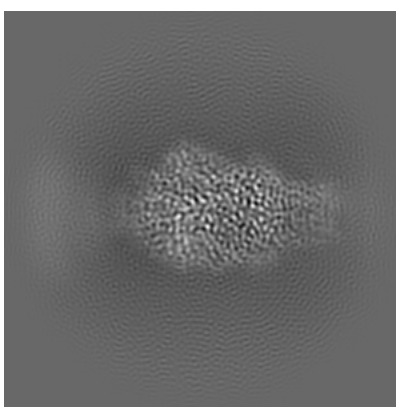
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

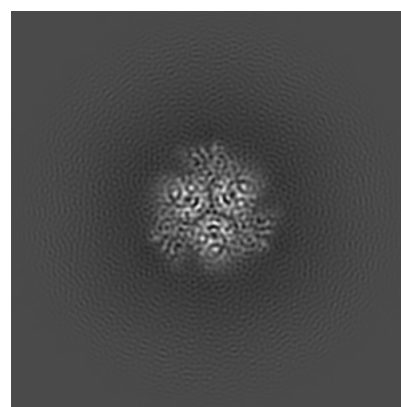
6.1.1 Primary map



X



Y

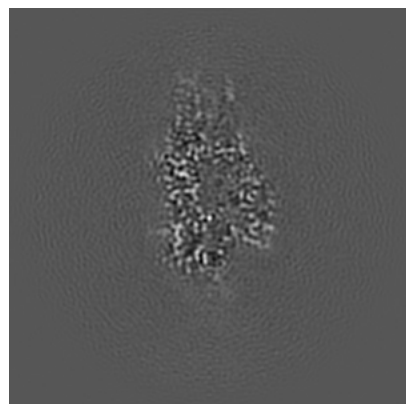


Z

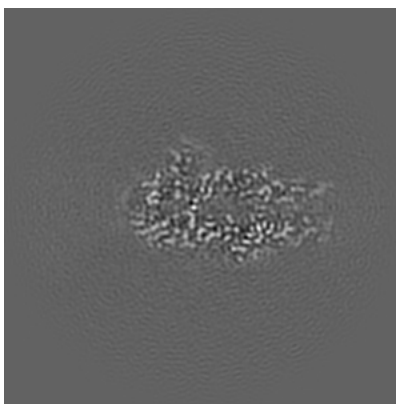
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

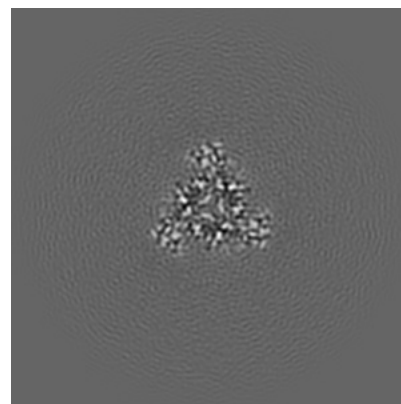
6.2.1 Primary map



X Index: 180



Y Index: 180

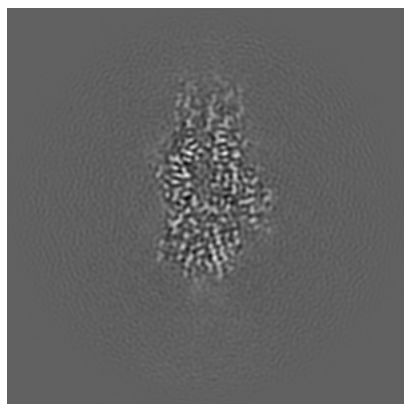


Z Index: 180

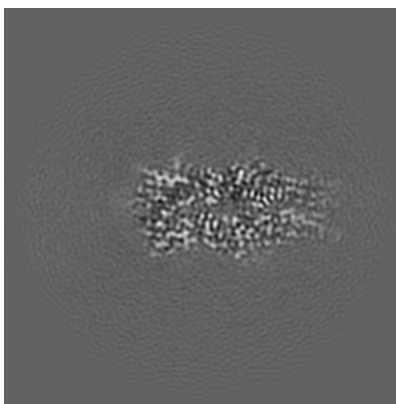
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

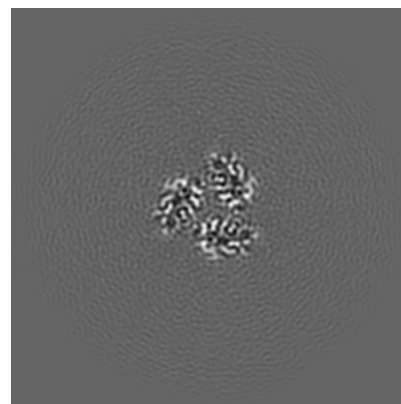
6.3.1 Primary map



X Index: 189



Y Index: 194

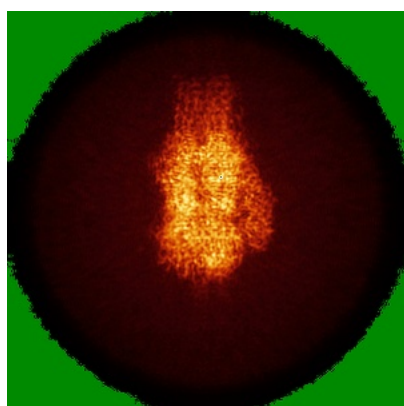


Z Index: 207

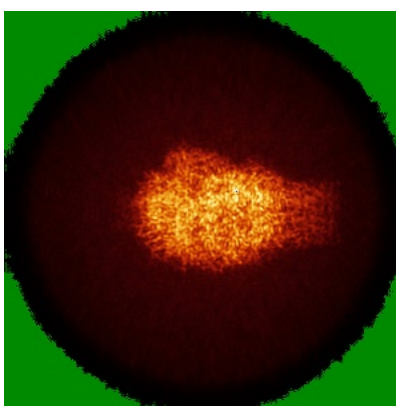
The images above show the largest variance slices of the map in three orthogonal directions.

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

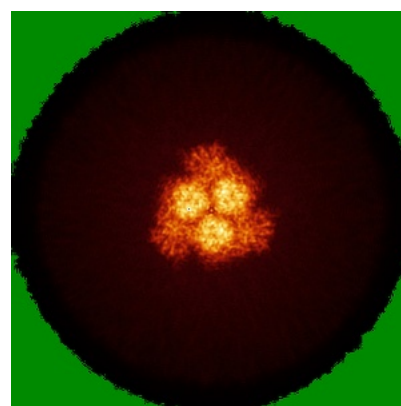
6.4.1 Primary map



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

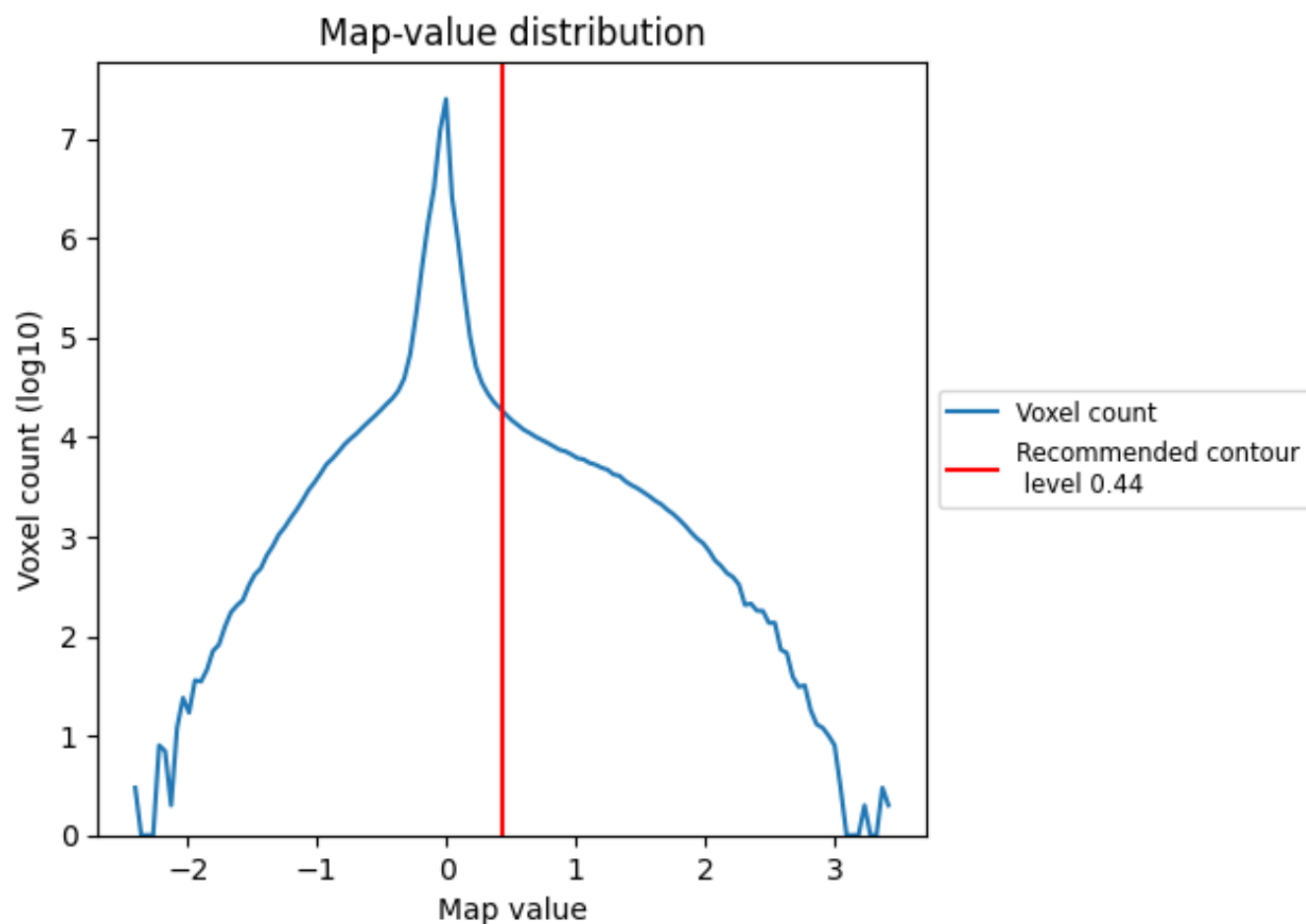
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

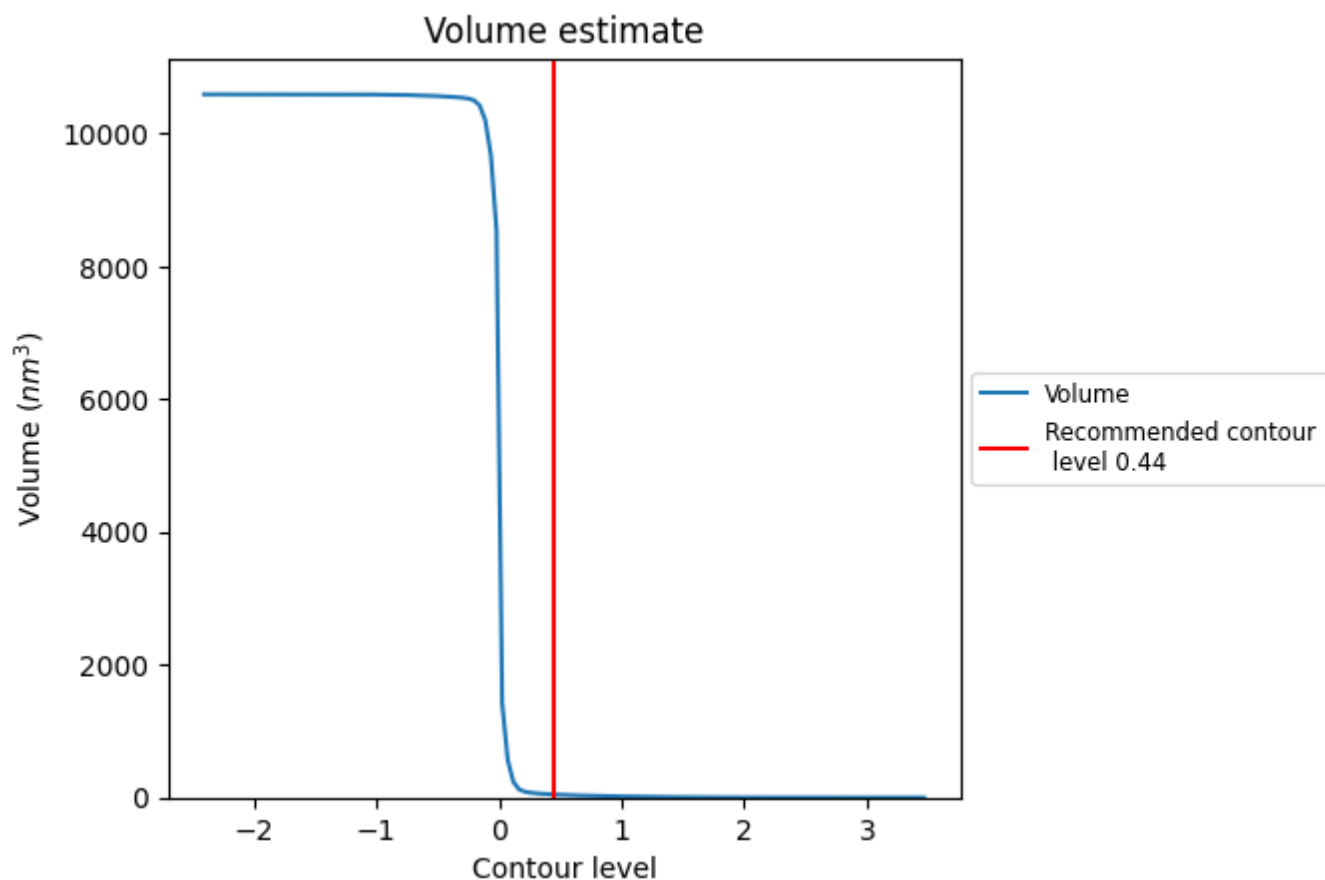
This section contains the results of statistical analysis of the map.

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.

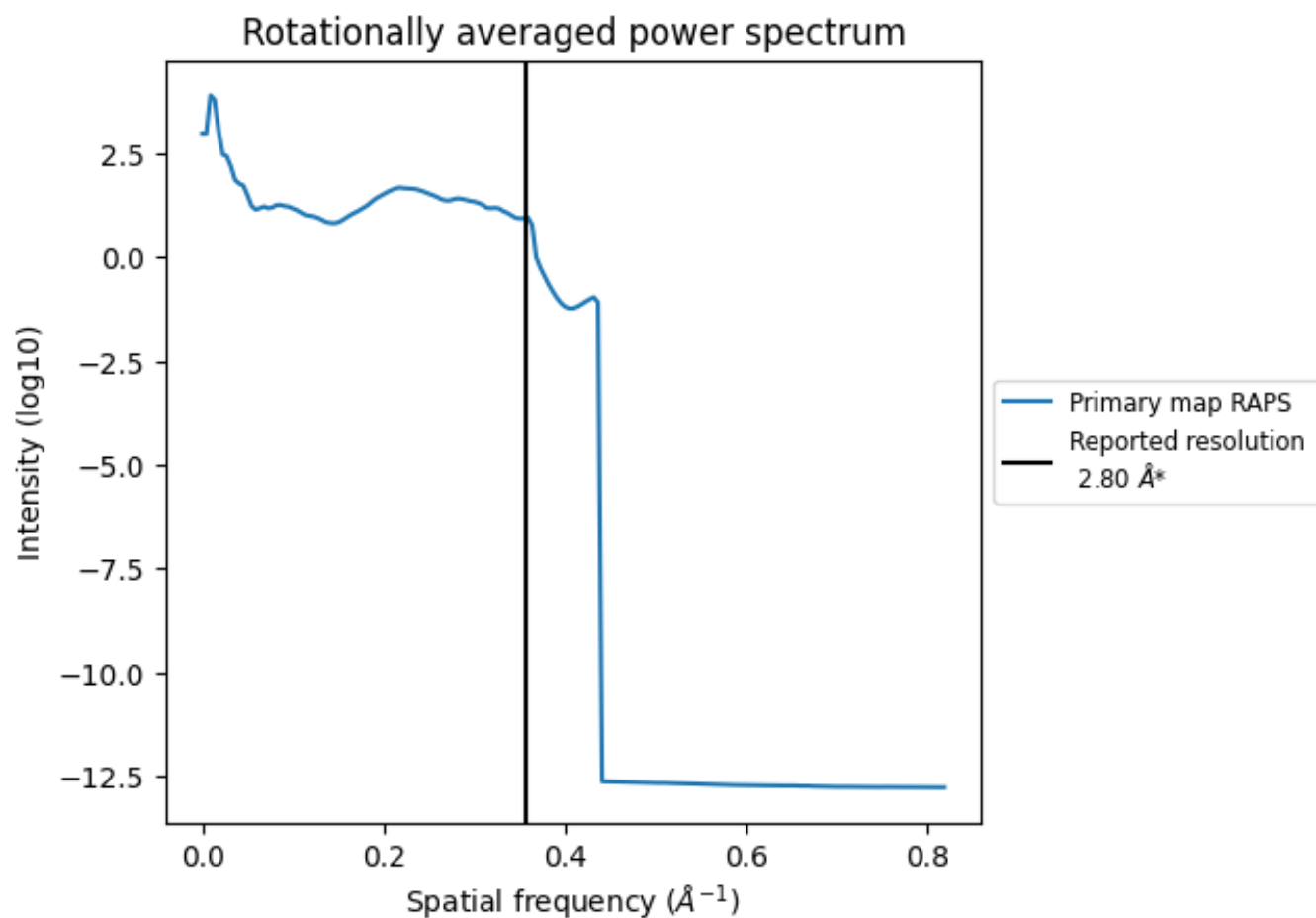
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 47 nm³; this corresponds to an approximate mass of 43 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 0.357 Å⁻¹

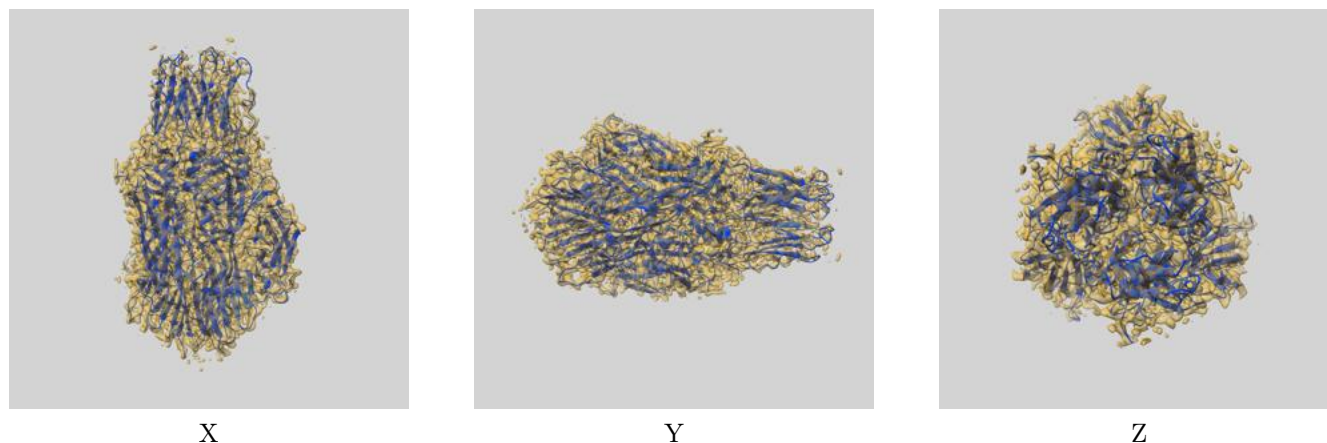
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

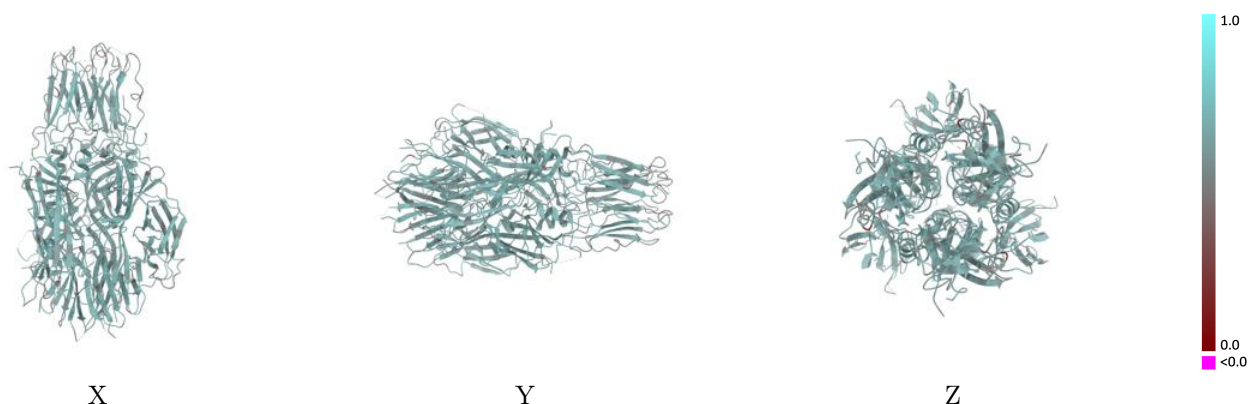
This section contains information regarding the fit between EMDB map EMD-31579 and PDB model 7FGF. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



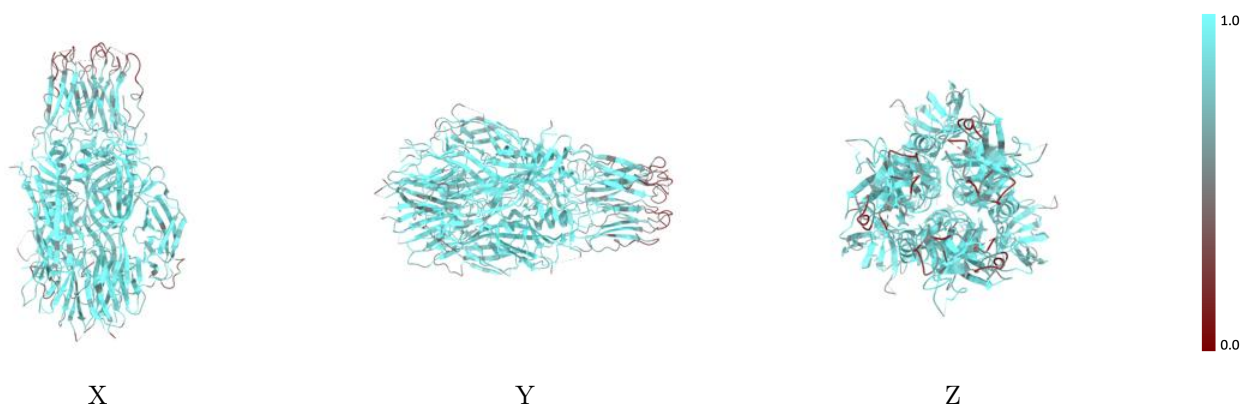
The images above show the 3D surface view of the map at the recommended contour level 0.44 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



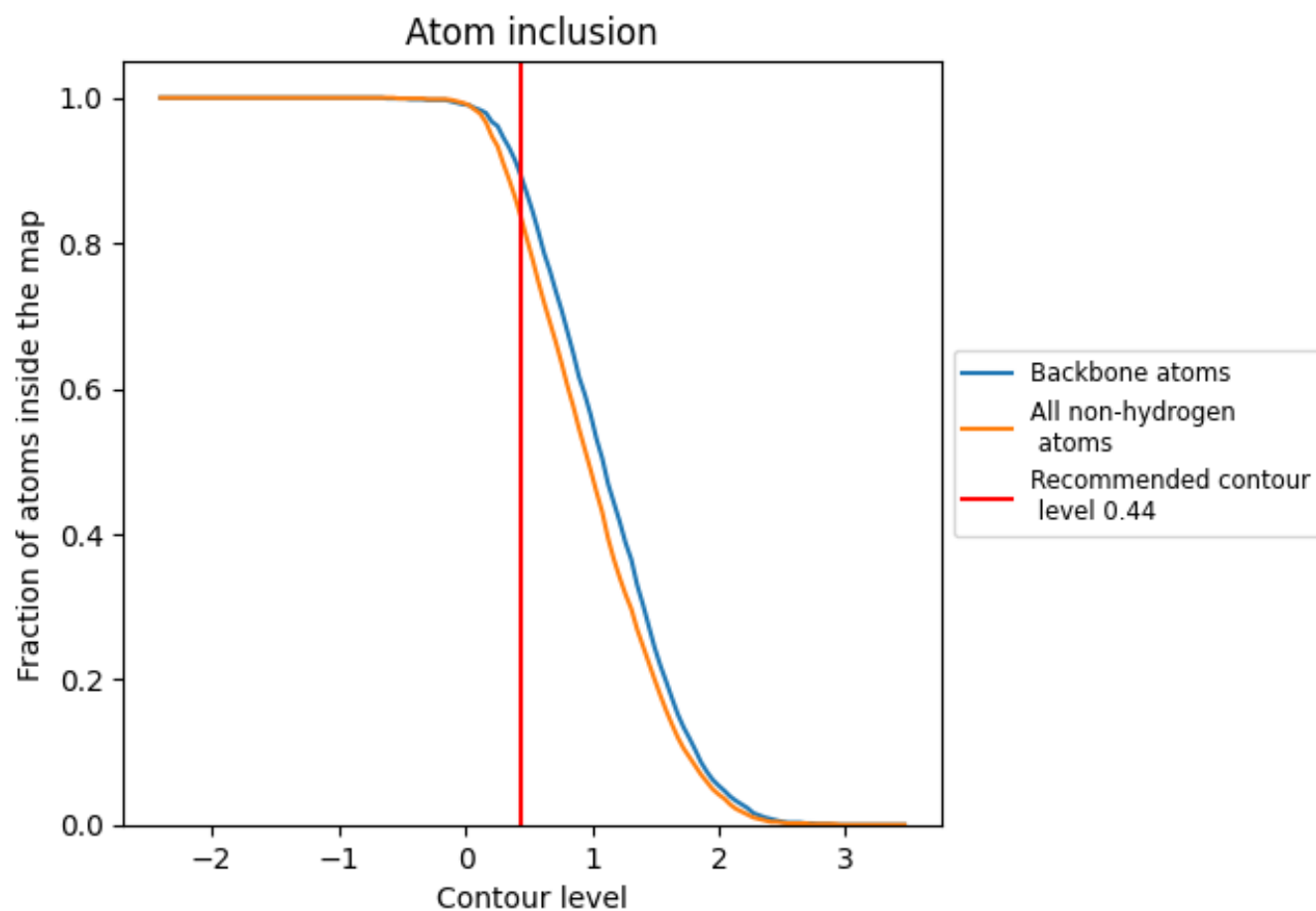
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.44).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.44) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8350	0.6080
A	0.8340	0.6080
B	0.8380	0.6080
C	0.8350	0.6090

