



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 10:05 PM UTC

PDB ID : 6QX3 / pdb_00006qx3
EMDB ID : EMD-4661
Title : Influenza A virus (A/NT/60/1968) polymerase Hetermotrimer in complex with 3'5' cRNA promoter and Nb8205
Authors : Carrique, L.; Keown, J.R.; Fan, H.; Fodor, E.; Grimes, J.M.
Deposited on : 2019-03-07
Resolution : 3.79 Å(reported)
Based on initial model : 6QPG

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:

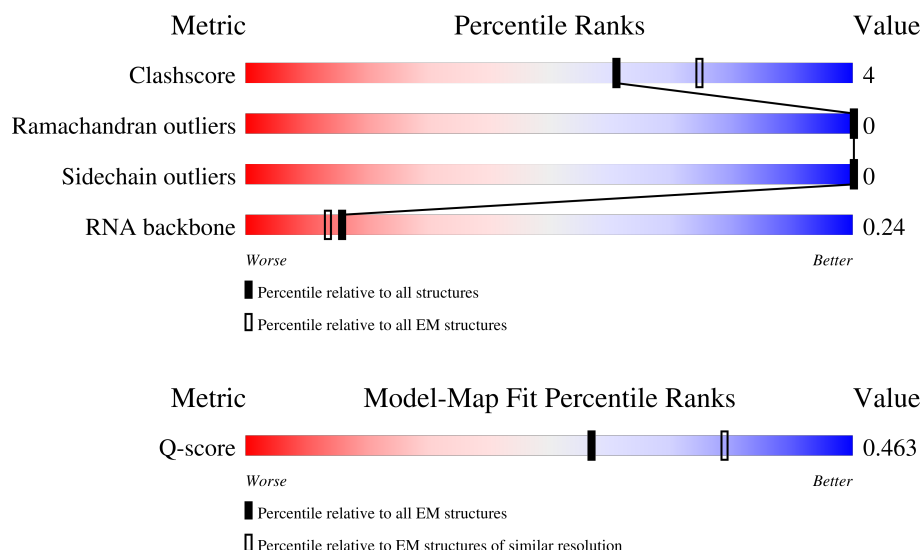
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.79 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	10018 (3.29 - 4.29)

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	D	15	
2	G	15	
3	O	134	

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Mol	Chain	Length	Quality of chain
4	B	757	 72% 9% 19%
5	A	716	 64% 8% 28%
6	C	762	 9% 89%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 21587 atoms, of which 10646 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 RNA chain called RNA (5'-R(P*AP*GP*CP*AP*AP*AP*AP*GP*CP*A)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
1	D	10	Total	C	H	N	O	P	0	0
			329	98	111	46	64	10		

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*CP*U)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
2	G	4	Total	C	H	N	O	P	0	0
			122	36	42	9	31	4		

- Molecule 3 is a protein called Nb8205.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	O	121	Total	C	H	N	O	S	0	0
			1799	572	877	163	181	6		

- Molecule 4 is a protein called RNA-directed RNA polymerase catalytic subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	615	Total	C	H	N	O	S	0	0
			9750	3084	4858	850	923	35		

- Molecule 5 is a protein called Polymerase acidic protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	A	515	Total	C	H	N	O	S	0	0
			8157	2614	4039	691	783	30		

- Molecule 6 is a protein called Polymerase basic protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	C	86	Total	C	H	N	O	S	0	0
			1430	453	719	125	125	8		

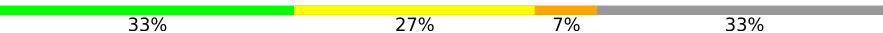
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	757	GLU	-	expression tag	UNP P03429
C	758	ASN	-	expression tag	UNP P03429
C	759	LEU	-	expression tag	UNP P03429
C	760	TYR	-	expression tag	UNP P03429
C	761	PHE	-	expression tag	UNP P03429
C	762	GLN	-	expression tag	UNP P03429

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.

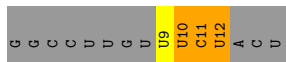
- Molecule 1: RNA (5'-R(P*AP*GP*CP*AP*AP*AP*AP*GP*CP*A)-3')

Chain D: 



- Molecule 2: RNA (5'-R(P*UP*UP*CP*U)-3')

Chain G: 



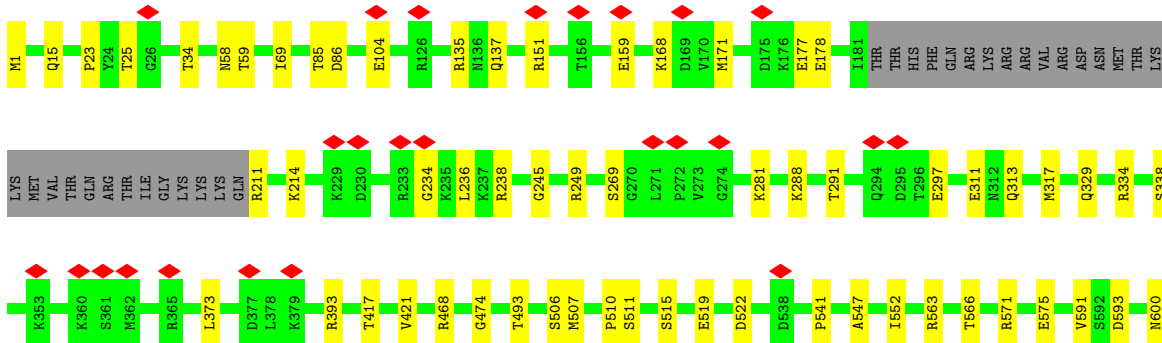
- Molecule 3: Nb8205

Chain O: 



- Molecule 4: RNA-directed RNA polymerase catalytic subunit

Chain B: 



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52932	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 ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.256	Depositor
Minimum map value	-0.160	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	216.00002, 216.00002, 216.00002	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	D	0.14	0/245	0.25	0/380
2	G	0.21	0/87	0.59	0/132
3	O	0.26	0/942	0.39	0/1278
4	B	0.26	0/4991	0.43	0/6744
5	A	0.29	0/4209	0.44	0/5688
6	C	0.19	0/730	0.35	0/985
All	All	0.27	0/11204	0.42	0/15207

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	D	218	111	111	3	0
2	G	80	42	42	6	0
3	O	922	877	877	9	0
4	B	4892	4858	4856	46	0
5	A	4118	4039	4037	43	0
6	C	711	719	719	8	0
All	All	10941	10646	10642	94	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 4.

The worst 5 of 94 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)
4:B:563:ARG:O	4:B:566:THR:OG1	2.05	0.74
5:A:566:ARG:NE	5:A:567:THR:O	2.22	0.72
3:O:90:ASP:OD1	3:O:94:TYR:OH	2.08	0.71
4:B:619:ASP:OD1	4:B:623:ARG:NH1	2.25	0.70
2:G:11:C:OP2	5:A:488:LYS:NZ	2.24	0.69

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	
3	O	119/134 (89%)	108 (91%)	11 (9%)	0	100	100
4	B	609/757 (80%)	549 (90%)	60 (10%)	0	100	100
5	A	513/716 (72%)	463 (90%)	50 (10%)	0	100	100
6	C	84/762 (11%)	77 (92%)	7 (8%)	0	100	100
All	All	1325/2369 (56%)	1197 (90%)	128 (10%)	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	
3	O	97/111 (87%)	97 (100%)	0	100	100
4	B	538/669 (80%)	538 (100%)	0	100	100
5	A	453/644 (70%)	453 (100%)	0	100	100
6	C	79/674 (12%)	79 (100%)	0	100	100
All	All	1167/2098 (56%)	1167 (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 (4) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	77	ASN
4	B	310	ASN
4	B	629	ASN
5	A	587	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	D	9/15 (60%)	3 (33%)	0
2	G	3/15 (20%)	3 (100%)	0
All	All	12/30 (40%)	6 (50%)	0

5 of 6 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	D	5	A
1	D	6	A
1	D	10	A
2	G	10	U
2	G	11	C

There are no RNA pucker outliers to report.

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.

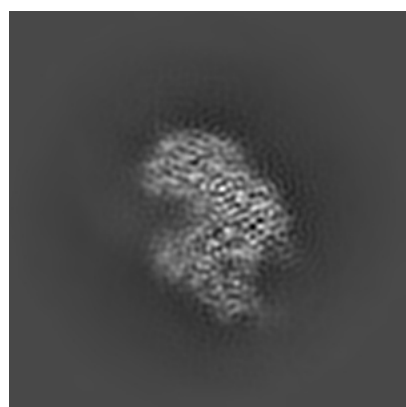
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4661. These allow visual inspection of the internal detail of the map and identification of artifacts.

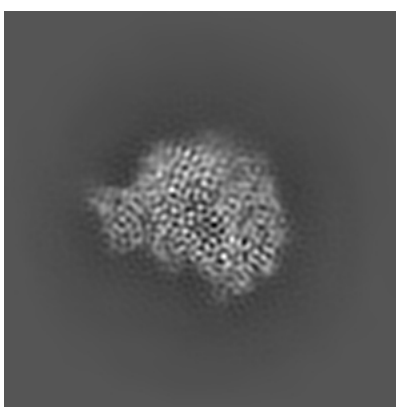
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

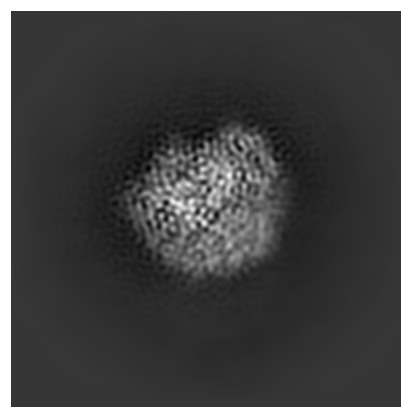
6.1.1 Primary map



X



Y

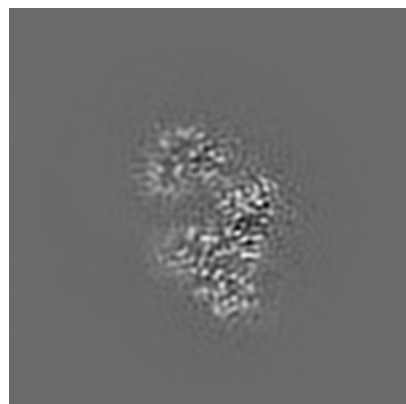


Z

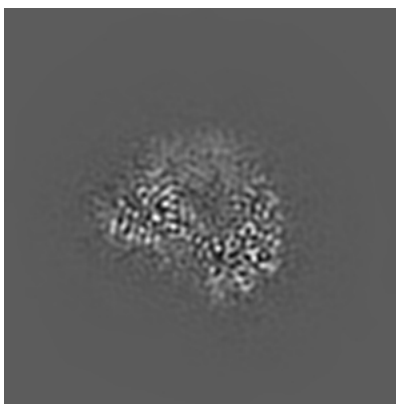
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 100



Y Index: 100



Z Index: 100

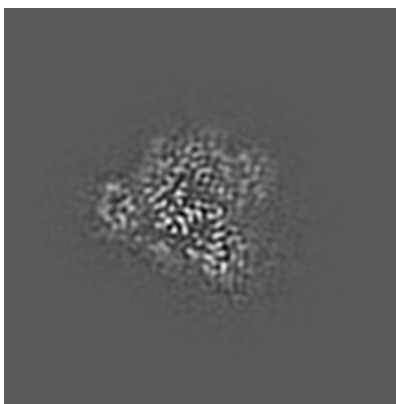
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

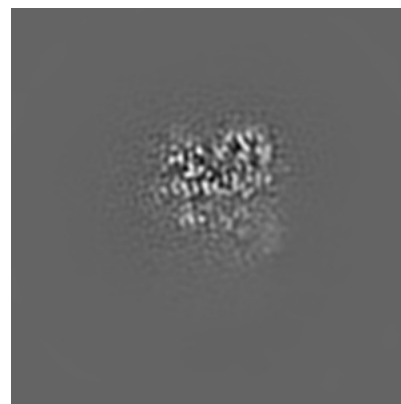
6.3.1 Primary map



X Index: 95



Y Index: 116

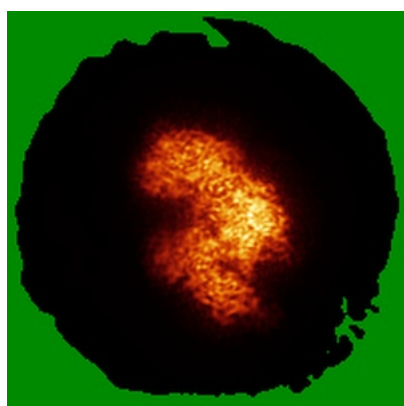


Z Index: 90

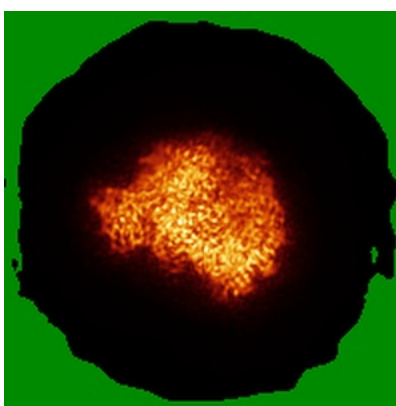
The images above show the largest variance slices of the map in three orthogonal directions.

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

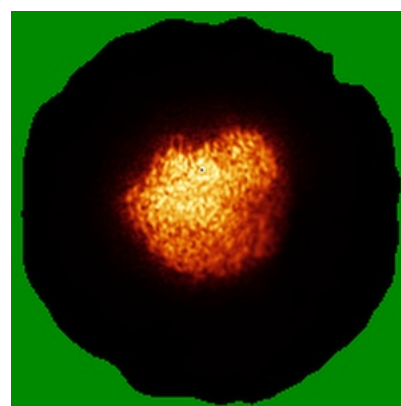
6.4.1 Primary map



X



Y

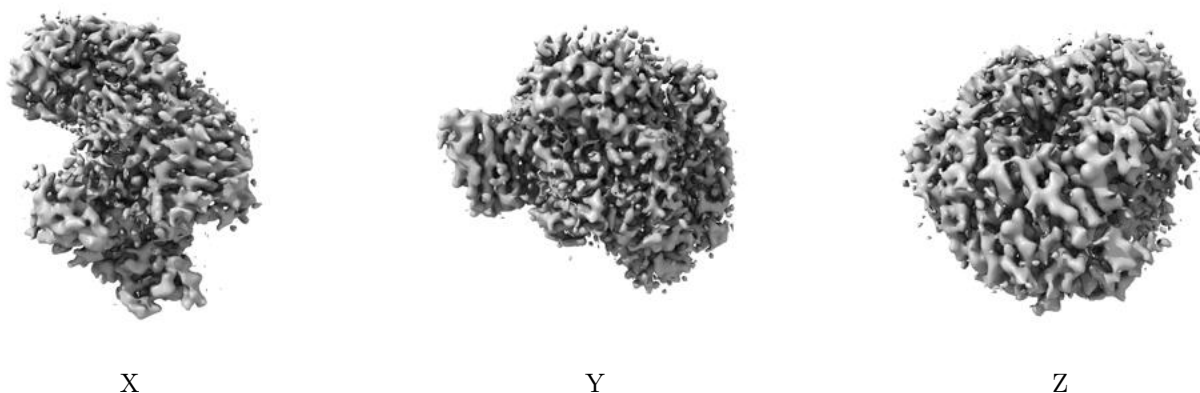


Z

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

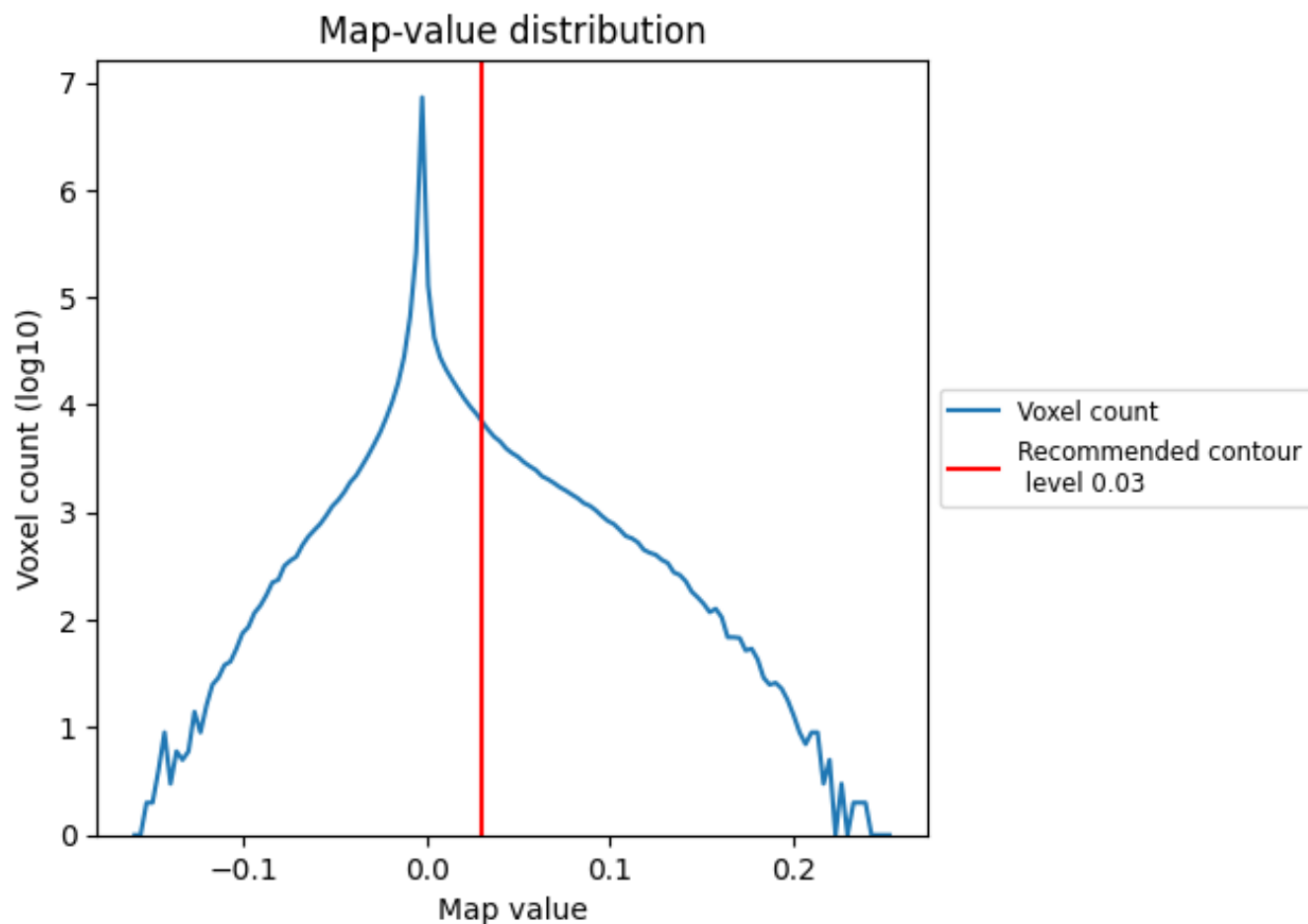
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

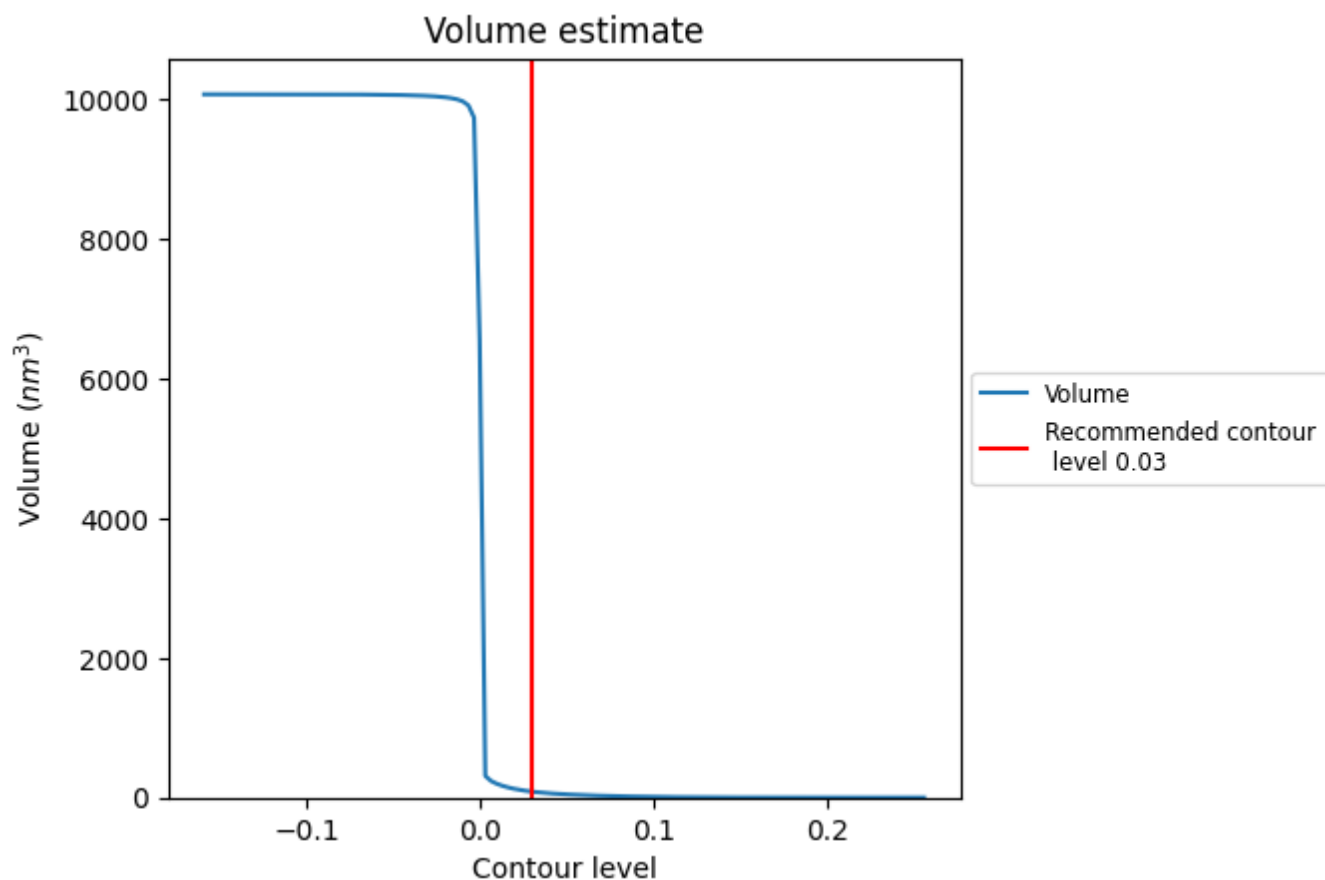
This section contains the results of statistical analysis of the map.

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.

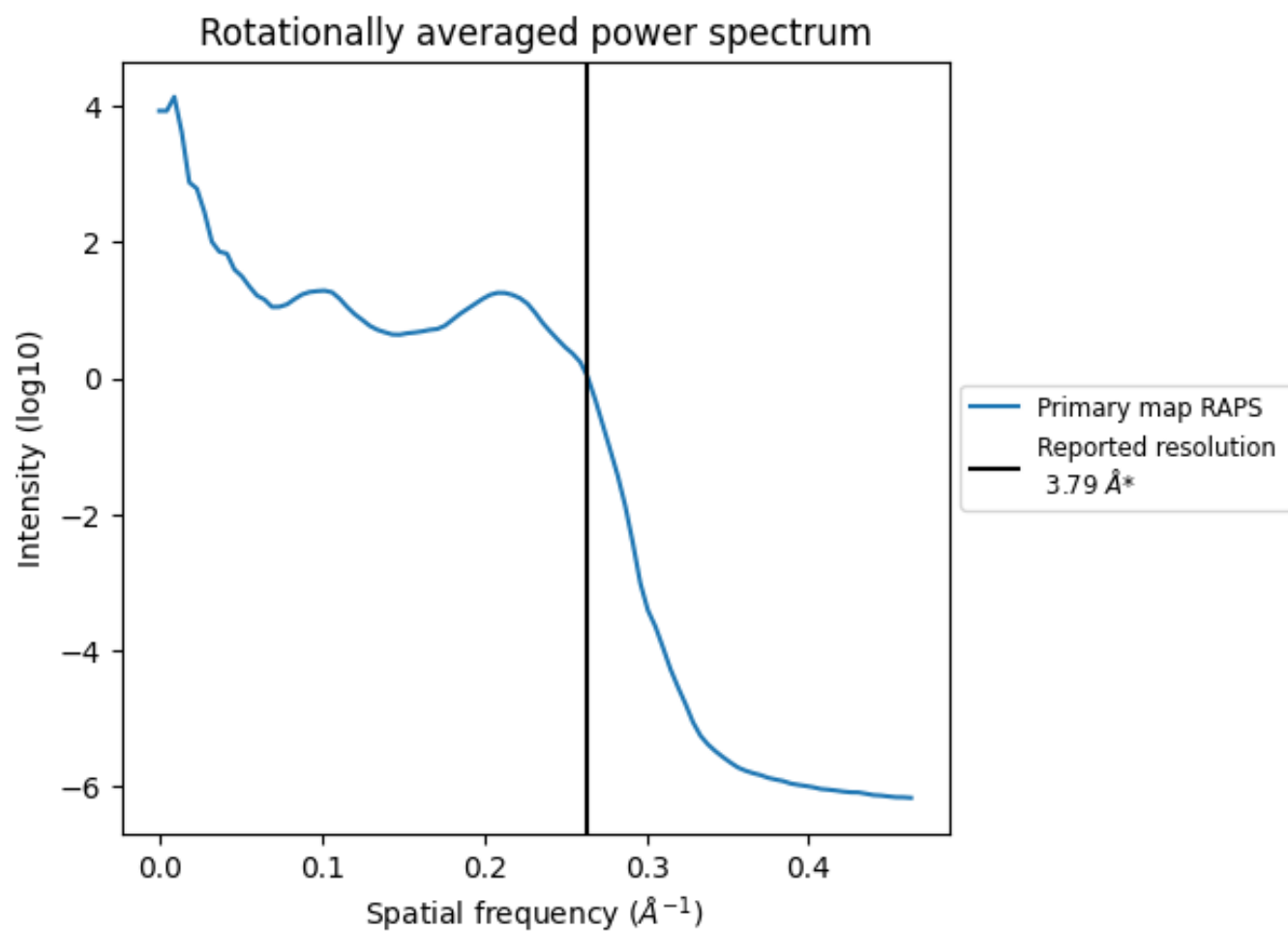
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84 nm³; this corresponds to an approximate mass of 76 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 ⓘ

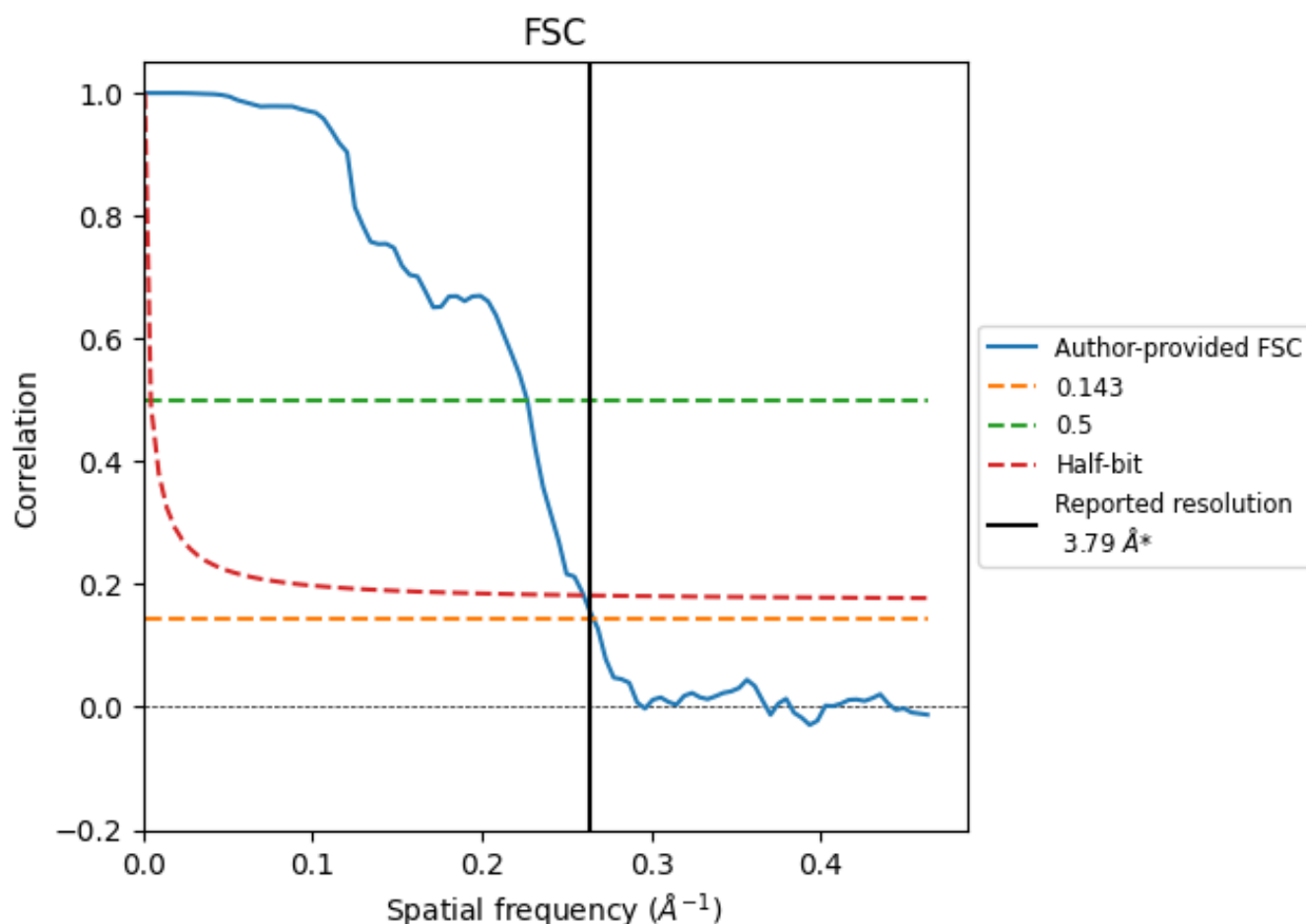


*Reported resolution corresponds to spatial frequency of 0.264 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.264 Å⁻¹

8.2 Resolution estimates [i](#)

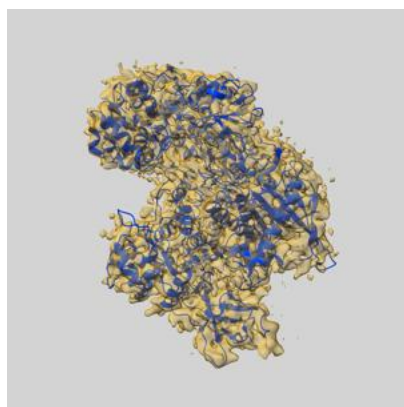
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.79	-	-
Author-provided FSC curve	3.76	4.41	3.85
Unmasked-calculated*	-	-	-

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

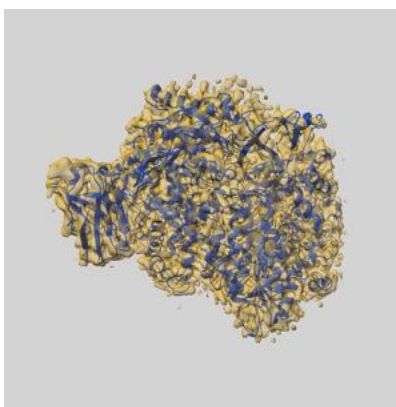
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4661 and PDB model 6QX3. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

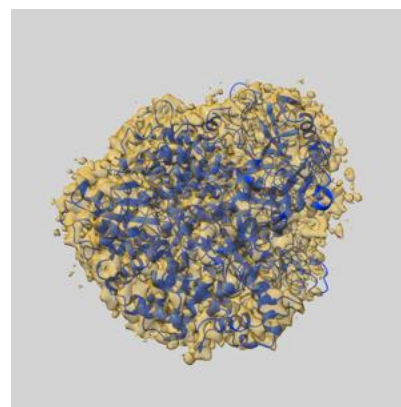
9.1 Map-model overlay [i](#)



X



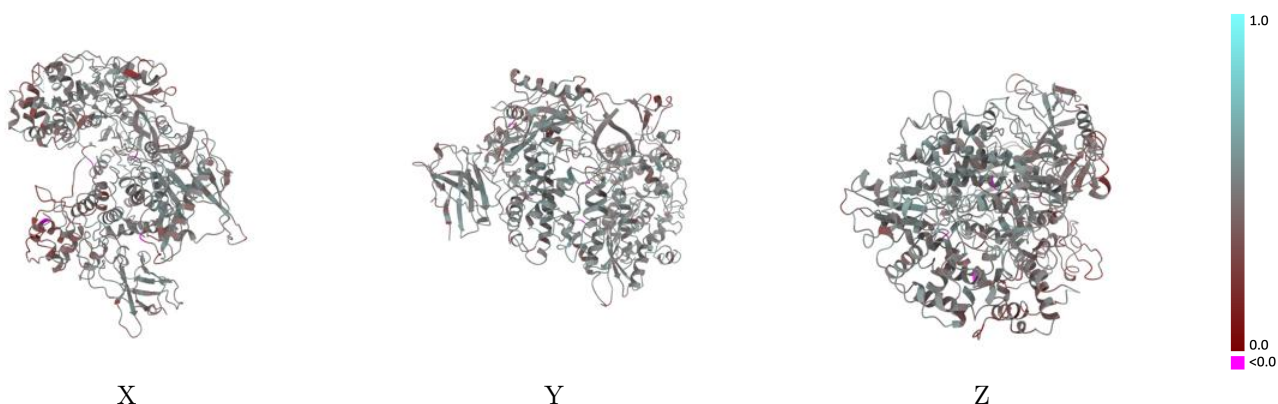
Y



Z

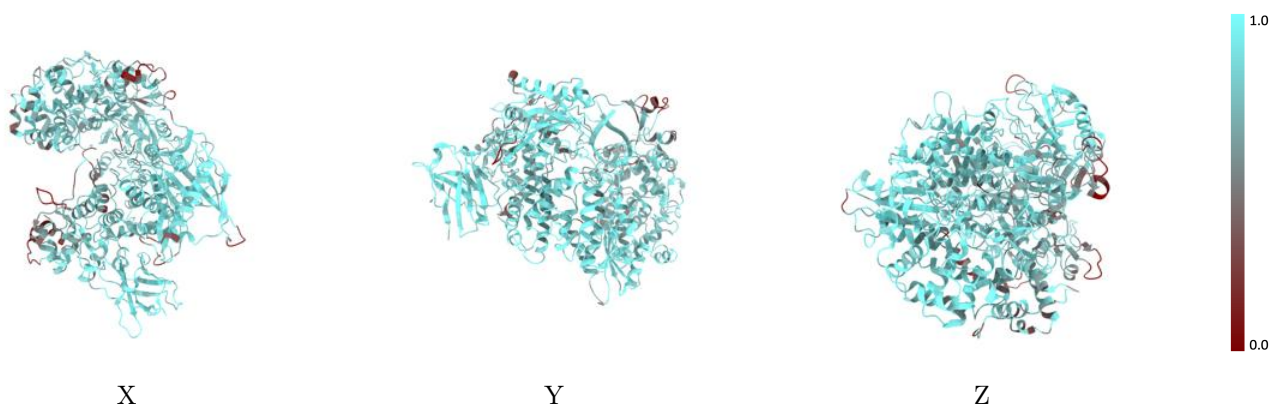
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



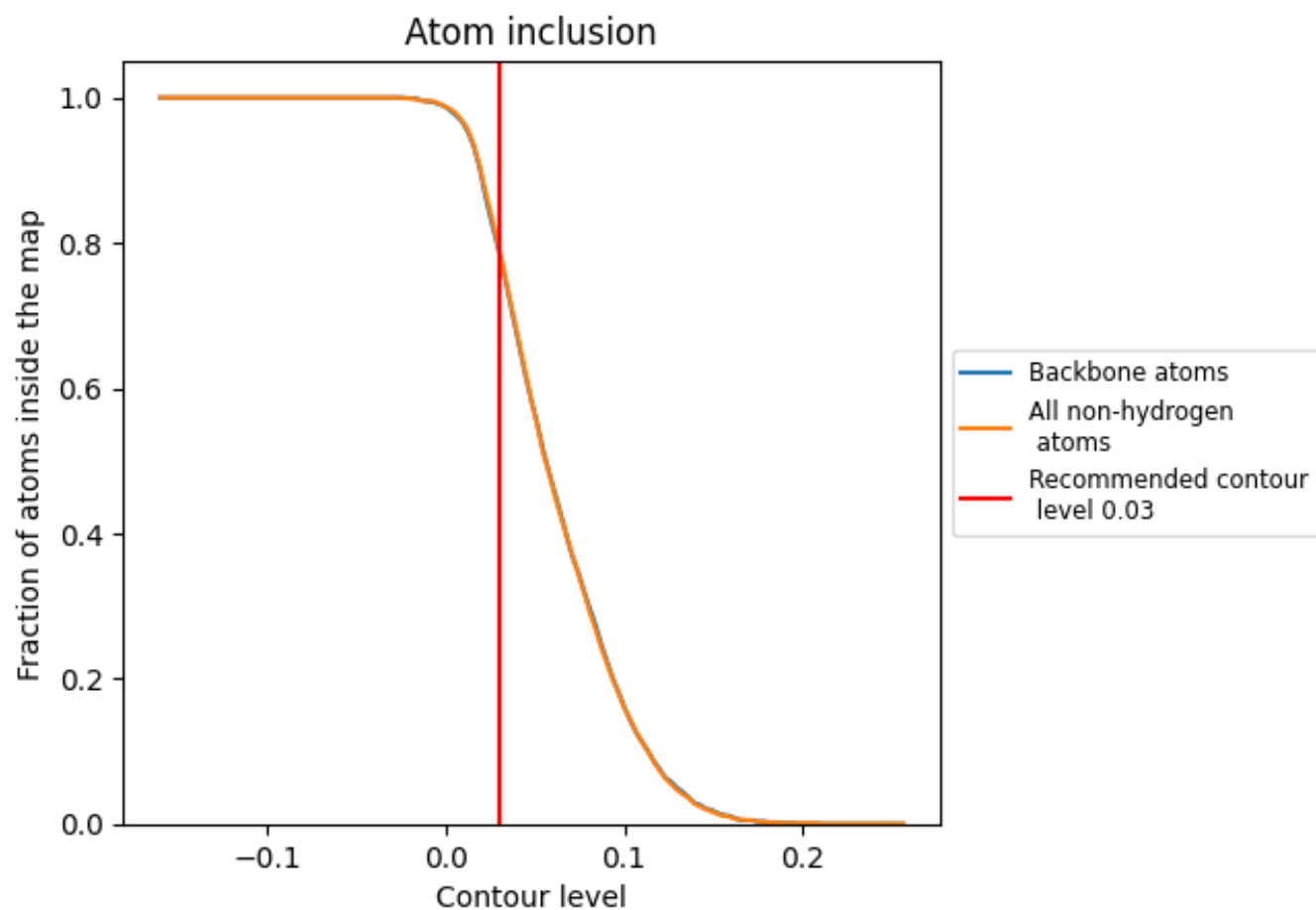
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 79% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7920	0.4630
A	0.8190	0.4750
B	0.7940	0.4690
C	0.5090	0.3410
D	0.8070	0.4620
G	0.7130	0.4720
O	0.8940	0.4780

