



# wwPDB EM Validation Summary Report ⓘ

Apr 7, 2025 – 07:10 PM EDT

PDB ID : 8TKQ / pdb\_00008tkq  
EMDB ID : EMD-41357  
Title : Cryo-EM structure of human full-length RAD52  
Authors : Schnicker, N.J.; Razzaghi, M.; Spies, M.  
Deposited on : 2023-07-25  
Resolution : 2.50 Å(reported)  
Based on initial model : 1KN0

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

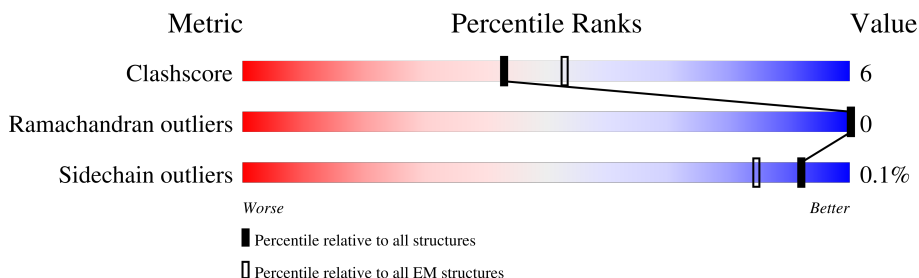
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.50 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	438	
1	B	438	
1	C	438	
1	D	438	
1	E	438	
1	F	438	
1	G	438	
1	H	438	

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Mol	Chain	Length	Quality of chain
1	I	438	
1	J	438	
1	K	438	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15950 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 DNA repair protein RAD52 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	B	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	C	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	D	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	E	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	F	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	G	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	H	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	I	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	J	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		
1	K	184	Total	C	N	O	S	0	0
			1450	907	261	274	8		

There are 220 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P43351
A	-18	GLY	-	expression tag	UNP P43351
A	-17	SER	-	expression tag	UNP P43351
A	-16	SER	-	expression tag	UNP P43351
A	-15	HIS	-	expression tag	UNP P43351
A	-14	HIS	-	expression tag	UNP P43351
A	-13	HIS	-	expression tag	UNP P43351
A	-12	HIS	-	expression tag	UNP P43351

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	HIS	-	expression tag	UNP P43351
A	-10	HIS	-	expression tag	UNP P43351
A	-9	SER	-	expression tag	UNP P43351
A	-8	SER	-	expression tag	UNP P43351
A	-7	GLY	-	expression tag	UNP P43351
A	-6	LEU	-	expression tag	UNP P43351
A	-5	VAL	-	expression tag	UNP P43351
A	-4	PRO	-	expression tag	UNP P43351
A	-3	ARG	-	expression tag	UNP P43351
A	-2	GLY	-	expression tag	UNP P43351
A	-1	SER	-	expression tag	UNP P43351
A	0	HIS	-	expression tag	UNP P43351
B	-19	MET	-	initiating methionine	UNP P43351
B	-18	GLY	-	expression tag	UNP P43351
B	-17	SER	-	expression tag	UNP P43351
B	-16	SER	-	expression tag	UNP P43351
B	-15	HIS	-	expression tag	UNP P43351
B	-14	HIS	-	expression tag	UNP P43351
B	-13	HIS	-	expression tag	UNP P43351
B	-12	HIS	-	expression tag	UNP P43351
B	-11	HIS	-	expression tag	UNP P43351
B	-10	HIS	-	expression tag	UNP P43351
B	-9	SER	-	expression tag	UNP P43351
B	-8	SER	-	expression tag	UNP P43351
B	-7	GLY	-	expression tag	UNP P43351
B	-6	LEU	-	expression tag	UNP P43351
B	-5	VAL	-	expression tag	UNP P43351
B	-4	PRO	-	expression tag	UNP P43351
B	-3	ARG	-	expression tag	UNP P43351
B	-2	GLY	-	expression tag	UNP P43351
B	-1	SER	-	expression tag	UNP P43351
B	0	HIS	-	expression tag	UNP P43351
C	-19	MET	-	initiating methionine	UNP P43351
C	-18	GLY	-	expression tag	UNP P43351
C	-17	SER	-	expression tag	UNP P43351
C	-16	SER	-	expression tag	UNP P43351
C	-15	HIS	-	expression tag	UNP P43351
C	-14	HIS	-	expression tag	UNP P43351
C	-13	HIS	-	expression tag	UNP P43351
C	-12	HIS	-	expression tag	UNP P43351
C	-11	HIS	-	expression tag	UNP P43351
C	-10	HIS	-	expression tag	UNP P43351

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-9	SER	-	expression tag	UNP P43351
C	-8	SER	-	expression tag	UNP P43351
C	-7	GLY	-	expression tag	UNP P43351
C	-6	LEU	-	expression tag	UNP P43351
C	-5	VAL	-	expression tag	UNP P43351
C	-4	PRO	-	expression tag	UNP P43351
C	-3	ARG	-	expression tag	UNP P43351
C	-2	GLY	-	expression tag	UNP P43351
C	-1	SER	-	expression tag	UNP P43351
C	0	HIS	-	expression tag	UNP P43351
D	-19	MET	-	initiating methionine	UNP P43351
D	-18	GLY	-	expression tag	UNP P43351
D	-17	SER	-	expression tag	UNP P43351
D	-16	SER	-	expression tag	UNP P43351
D	-15	HIS	-	expression tag	UNP P43351
D	-14	HIS	-	expression tag	UNP P43351
D	-13	HIS	-	expression tag	UNP P43351
D	-12	HIS	-	expression tag	UNP P43351
D	-11	HIS	-	expression tag	UNP P43351
D	-10	HIS	-	expression tag	UNP P43351
D	-9	SER	-	expression tag	UNP P43351
D	-8	SER	-	expression tag	UNP P43351
D	-7	GLY	-	expression tag	UNP P43351
D	-6	LEU	-	expression tag	UNP P43351
D	-5	VAL	-	expression tag	UNP P43351
D	-4	PRO	-	expression tag	UNP P43351
D	-3	ARG	-	expression tag	UNP P43351
D	-2	GLY	-	expression tag	UNP P43351
D	-1	SER	-	expression tag	UNP P43351
D	0	HIS	-	expression tag	UNP P43351
E	-19	MET	-	initiating methionine	UNP P43351
E	-18	GLY	-	expression tag	UNP P43351
E	-17	SER	-	expression tag	UNP P43351
E	-16	SER	-	expression tag	UNP P43351
E	-15	HIS	-	expression tag	UNP P43351
E	-14	HIS	-	expression tag	UNP P43351
E	-13	HIS	-	expression tag	UNP P43351
E	-12	HIS	-	expression tag	UNP P43351
E	-11	HIS	-	expression tag	UNP P43351
E	-10	HIS	-	expression tag	UNP P43351
E	-9	SER	-	expression tag	UNP P43351
E	-8	SER	-	expression tag	UNP P43351

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-7	GLY	-	expression tag	UNP P43351
E	-6	LEU	-	expression tag	UNP P43351
E	-5	VAL	-	expression tag	UNP P43351
E	-4	PRO	-	expression tag	UNP P43351
E	-3	ARG	-	expression tag	UNP P43351
E	-2	GLY	-	expression tag	UNP P43351
E	-1	SER	-	expression tag	UNP P43351
E	0	HIS	-	expression tag	UNP P43351
F	-19	MET	-	initiating methionine	UNP P43351
F	-18	GLY	-	expression tag	UNP P43351
F	-17	SER	-	expression tag	UNP P43351
F	-16	SER	-	expression tag	UNP P43351
F	-15	HIS	-	expression tag	UNP P43351
F	-14	HIS	-	expression tag	UNP P43351
F	-13	HIS	-	expression tag	UNP P43351
F	-12	HIS	-	expression tag	UNP P43351
F	-11	HIS	-	expression tag	UNP P43351
F	-10	HIS	-	expression tag	UNP P43351
F	-9	SER	-	expression tag	UNP P43351
F	-8	SER	-	expression tag	UNP P43351
F	-7	GLY	-	expression tag	UNP P43351
F	-6	LEU	-	expression tag	UNP P43351
F	-5	VAL	-	expression tag	UNP P43351
F	-4	PRO	-	expression tag	UNP P43351
F	-3	ARG	-	expression tag	UNP P43351
F	-2	GLY	-	expression tag	UNP P43351
F	-1	SER	-	expression tag	UNP P43351
F	0	HIS	-	expression tag	UNP P43351
G	-19	MET	-	initiating methionine	UNP P43351
G	-18	GLY	-	expression tag	UNP P43351
G	-17	SER	-	expression tag	UNP P43351
G	-16	SER	-	expression tag	UNP P43351
G	-15	HIS	-	expression tag	UNP P43351
G	-14	HIS	-	expression tag	UNP P43351
G	-13	HIS	-	expression tag	UNP P43351
G	-12	HIS	-	expression tag	UNP P43351
G	-11	HIS	-	expression tag	UNP P43351
G	-10	HIS	-	expression tag	UNP P43351
G	-9	SER	-	expression tag	UNP P43351
G	-8	SER	-	expression tag	UNP P43351
G	-7	GLY	-	expression tag	UNP P43351
G	-6	LEU	-	expression tag	UNP P43351

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-5	VAL	-	expression tag	UNP P43351
G	-4	PRO	-	expression tag	UNP P43351
G	-3	ARG	-	expression tag	UNP P43351
G	-2	GLY	-	expression tag	UNP P43351
G	-1	SER	-	expression tag	UNP P43351
G	0	HIS	-	expression tag	UNP P43351
H	-19	MET	-	initiating methionine	UNP P43351
H	-18	GLY	-	expression tag	UNP P43351
H	-17	SER	-	expression tag	UNP P43351
H	-16	SER	-	expression tag	UNP P43351
H	-15	HIS	-	expression tag	UNP P43351
H	-14	HIS	-	expression tag	UNP P43351
H	-13	HIS	-	expression tag	UNP P43351
H	-12	HIS	-	expression tag	UNP P43351
H	-11	HIS	-	expression tag	UNP P43351
H	-10	HIS	-	expression tag	UNP P43351
H	-9	SER	-	expression tag	UNP P43351
H	-8	SER	-	expression tag	UNP P43351
H	-7	GLY	-	expression tag	UNP P43351
H	-6	LEU	-	expression tag	UNP P43351
H	-5	VAL	-	expression tag	UNP P43351
H	-4	PRO	-	expression tag	UNP P43351
H	-3	ARG	-	expression tag	UNP P43351
H	-2	GLY	-	expression tag	UNP P43351
H	-1	SER	-	expression tag	UNP P43351
H	0	HIS	-	expression tag	UNP P43351
I	-19	MET	-	initiating methionine	UNP P43351
I	-18	GLY	-	expression tag	UNP P43351
I	-17	SER	-	expression tag	UNP P43351
I	-16	SER	-	expression tag	UNP P43351
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I	-13	HIS	-	expression tag	UNP P43351
I	-12	HIS	-	expression tag	UNP P43351
I	-11	HIS	-	expression tag	UNP P43351
I	-10	HIS	-	expression tag	UNP P43351
I	-9	SER	-	expression tag	UNP P43351
I	-8	SER	-	expression tag	UNP P43351
I	-7	GLY	-	expression tag	UNP P43351
I	-6	LEU	-	expression tag	UNP P43351
I	-5	VAL	-	expression tag	UNP P43351
I	-4	PRO	-	expression tag	UNP P43351

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	ARG	-	expression tag	UNP P43351
I	-2	GLY	-	expression tag	UNP P43351
I	-1	SER	-	expression tag	UNP P43351
I	0	HIS	-	expression tag	UNP P43351
J	-19	MET	-	initiating methionine	UNP P43351
J	-18	GLY	-	expression tag	UNP P43351
J	-17	SER	-	expression tag	UNP P43351
J	-16	SER	-	expression tag	UNP P43351
J	-15	HIS	-	expression tag	UNP P43351
J	-14	HIS	-	expression tag	UNP P43351
J	-13	HIS	-	expression tag	UNP P43351
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J	-7	GLY	-	expression tag	UNP P43351
J	-6	LEU	-	expression tag	UNP P43351
J	-5	VAL	-	expression tag	UNP P43351
J	-4	PRO	-	expression tag	UNP P43351
J	-3	ARG	-	expression tag	UNP P43351
J	-2	GLY	-	expression tag	UNP P43351
J	-1	SER	-	expression tag	UNP P43351
J	0	HIS	-	expression tag	UNP P43351
K	-19	MET	-	initiating methionine	UNP P43351
K	-18	GLY	-	expression tag	UNP P43351
K	-17	SER	-	expression tag	UNP P43351
K	-16	SER	-	expression tag	UNP P43351
K	-15	HIS	-	expression tag	UNP P43351
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K	-9	SER	-	expression tag	UNP P43351
K	-8	SER	-	expression tag	UNP P43351
K	-7	GLY	-	expression tag	UNP P43351
K	-6	LEU	-	expression tag	UNP P43351
K	-5	VAL	-	expression tag	UNP P43351
K	-4	PRO	-	expression tag	UNP P43351
K	-3	ARG	-	expression tag	UNP P43351
K	-2	GLY	-	expression tag	UNP P43351

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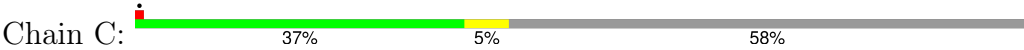
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Chain	Residue	Modelled	Actual	Comment	Reference
K	-1	SER	-	expression tag	UNP P43351
K	0	HIS	-	expression tag	UNP P43351



LEU	ASN	ASN	GLN	MET	HIS	THR	GLN	ASN	THR	THR	PRO	HIS	SER	VAL	CYS	GLN	LYS	PRO	GLN	ALA	LYS	SER	GLY	SER	THR	ASP	LEU	GLN	THR	TYR	ARG	ASP	ALA	ASP	GLN	ARG	THR	THR	GLY	ASN	TRP	GLY	SER	HIS	SER	LEU
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● Molecule 1: DNA repair protein RAD52 homolog



SER	LEU	HIS	ASP	CYS	H86	MET
GLY	LEU	SER	SER	SER	H121	GLY
THR	ASN	PRO	SER	SER	E122	SER
VAL	ASN	VAL	ARG	ARG	D123	HIS
GLN	GLN	THR	SER	SER	V124	HIS
MET	MET	VAL	LEU	LEU	S134	HIS
VAL	THR	SER	SER	SER	L137	HIS
GLN	GLN	PRO	SER	SER	L137	SER
ASN	ASN	LEU	ALA	ALA	R153	SER
ARG	ARG	LEU	VAL	VAL	R153	GLY
THR	THR	GLU	GLU	GLU	N160	LEU
PRO	PRO	LYS	SER	SER	N160	VAL
HIS	HIS	ASP	GLU	GLU	C165	PRO
SER	SER	PHE	ALA	ALA	C165	ARG
VAL	VAL	LEU	THR	THR	Y171	GLY
CYS	CYS	ALA	HIS	HIS	Y171	SER
HIS	HIS	GLY	GLN	GLN	R190	HIS
GLN	GLN	VAL	ARG	ARG	R190	GLY
LYS	LYS	THR	LYS	LYS	R190	MET
PRO	PRO	GLN	LEU	LEU	Q194	SER
GLN	GLN	GLU	ARG	ARG	Q194	GLY
ALA	ALA	LEU	GLN	GLN	D195	THR
LYS	LYS	ILE	LYS	LYS	L196	GLU
SER	SER	LYS	GLN	GLN	E197	GLU
GLY	GLY	THR	LEU	LEU	V200	ALA
SER	SER	LEU	GLN	GLN	V200	ILE
TRP	TRP	GLU	GLN	GLN	R204	LEU
ASP	ASP	ASP	PHE	PHE	R204	GLY
LEU	LEU	ASN	ARG	ARG	C208	GLY
GLN	GLN	SER	ARG	ARG	C208	GLY
THR	THR	GLU	GLU	GLU	ARG	ARG
TYR	TYR	LYS	ARG	ARG	PRO	ASP
SER	SER	TRP	MET	MET	ASN	SER
ALA	ALA	ALA	GLU	GLU	ALA	HIS
ASP	ASP	VAL	LYS	LYS	ALA	PRO
GLN	GLN	THR	GLN	GLN	GLY	ALA
ARG	ARG	PRO	GLN	GLN	LEU	ALA
THR	THR	ASP	VAL	VAL	HIS	GLY
THR	THR	ALA	ARG	ARG	PRO	GLY
GLY	GLY	GLY	VAL	VAL	GLN	SER
ASN	ASN	ASP	SER	SER	LEU	VAL
TRP	TRP	GLY	THR	THR	GLN	LEU
GLU	GLU	VAL	PRO	PRO	VAL	LEU
SER	SER	VAL	SER	SER	THR	C25
HIS	HIS	LYS	ALA	ALA	THR	F26
ARG	ARG	PRO	GLU	GLU	ALA	G27
LYS	LYS	SER	SER	SER	PRO	Q28
SER	SER	SER	LYS	LYS	PRO	C29
GLN	GLN	ARG	GLU	GLU	SER	Q30
ASP	ASP	ALA	ALA	ALA	PRO	Y36
MET	MET	ASP	ALA	ALA	PRO	Y36
LYS	LYS	PRO	PRO	PRO	HIS	L47
ARG	ARG	ALA	PRO	PRO	ALA	L47
LYS	LYS	GLN	ALA	ALA	VAL	G58
TYR	TYR	THR	ALA	ALA	ILE	G59
ASP	ASP	SER	PRO	PRO	PRO	M78
PRO	PRO	ASP	VAL	VAL	ALA	M78
		THR	THR	THR	GLN	GLN

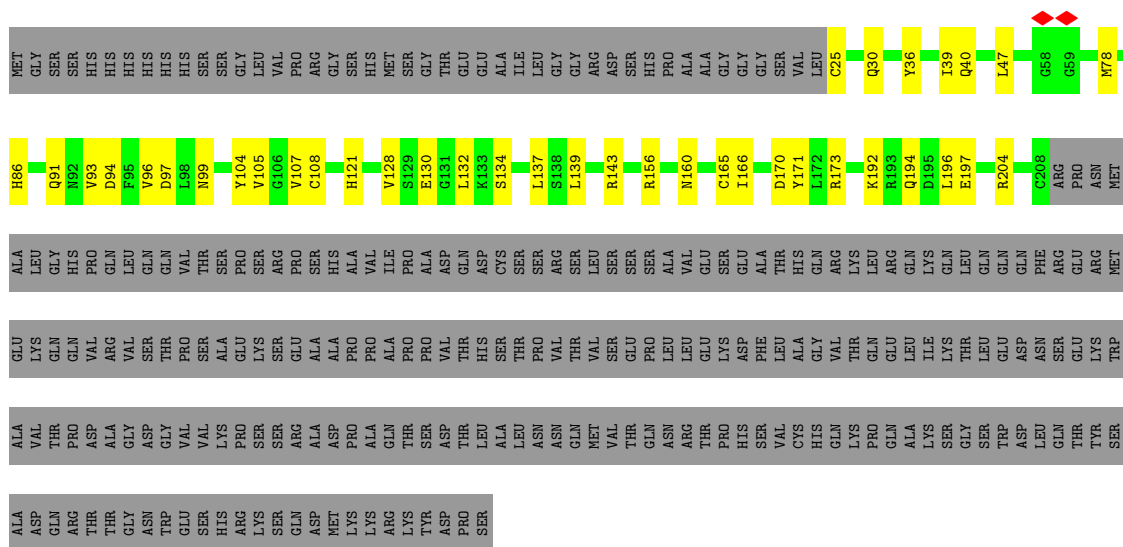
● Molecule 1: DNA repair protein RAD52 homolog



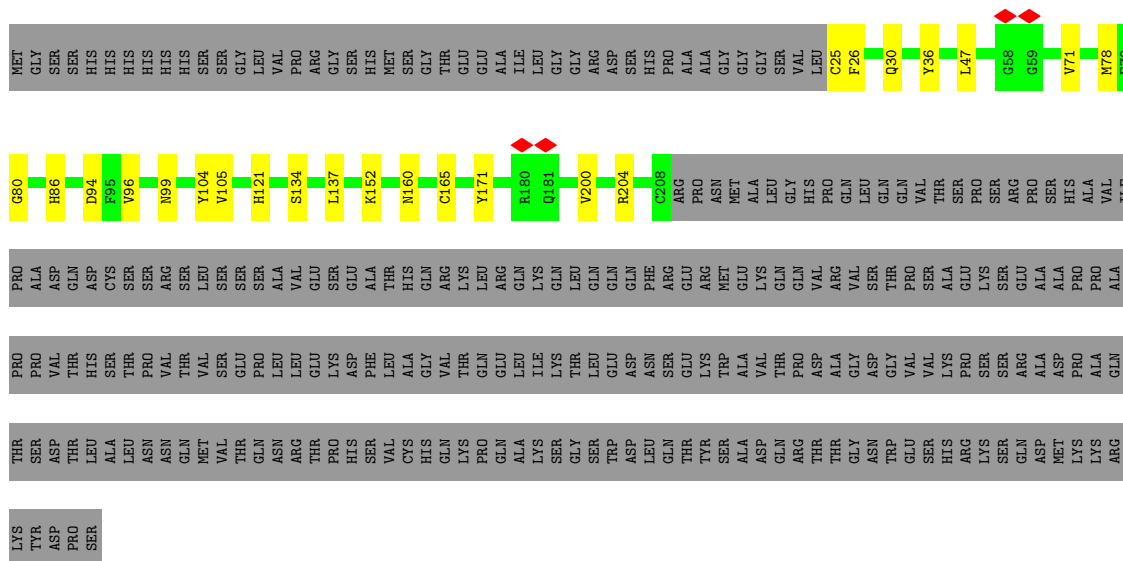
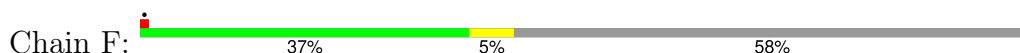
GLY	SER	HIS	ARG	SER	SER	GLN	ASP	MET	LYS	ARG	THR	ASP	THR	LEU	ALA	ASN	ASN	GLN	THR	VAL	VAL	GLN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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● Molecule 1: DNA repair protein RAD52 homolog

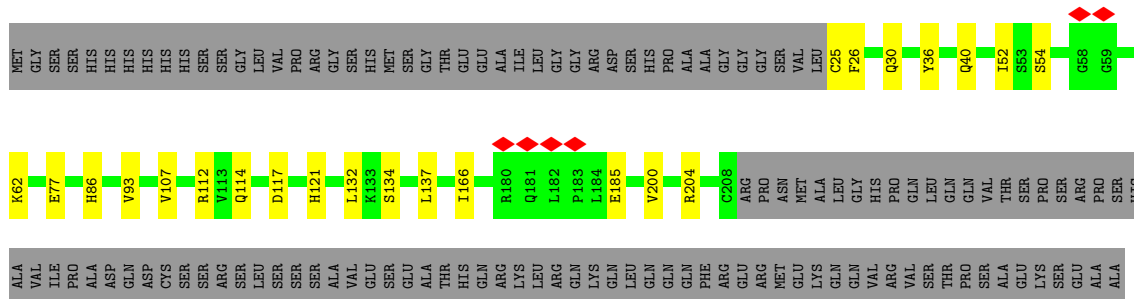
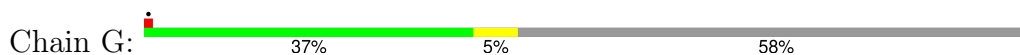




- Molecule 1: DNA repair protein RAD52 homolog

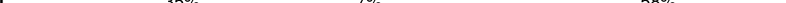


- Molecule 1: DNA repair protein RAD52 homolog



LYS LYS ARG LYS TYR ASP PRO SER	PRO	ALA	GLN	THR	SER	ASP	THR	LEU	THR	ASN	GLN	MET	VAL	THR	GLN	ASN	ARG	THR	PRO	HIS	ASP	PHE	LEU	ALA	GLY	THR	GLN	LEU	ILE	LYS	THR	LEU	GLU	ASP	ASN	SER	GLU	LYS	TRP	ALA	VAL	THR	PRO	ASP	ALA	GLY	GLY	VAL	VAL	LYS	PRO	SER	SER	ARG	ASP	MET
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- Molecule 1: DNA repair protein RAD52 homolog

Chain H: 

[illegible]

- Molecule 1: DNA repair protein RAD52 homolog

Chain I: 

[illegible]

- Molecule 1: DNA repair protein RAD52 homolog

Response	Percentage
Yes	34%
No	8%
Don't know	58%



Frequency	Percentage
Daily	36%
Weekly	6%
Monthly	58%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C11	Depositor
Number of particles used	623559	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.786	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	247.65001, 247.65001, 247.65001	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8255, 0.8255, 0.8255	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	0.42	0/1474	0.44	0/1981
1	B	0.42	0/1474	0.44	0/1981
1	C	0.42	0/1474	0.44	0/1981
1	D	0.42	0/1474	0.44	0/1981
1	E	0.42	0/1474	0.46	0/1981
1	F	0.41	0/1474	0.45	0/1981
1	G	0.42	0/1474	0.45	0/1981
1	H	0.42	0/1474	0.45	0/1981
1	I	0.41	0/1474	0.46	0/1981
1	J	0.40	0/1474	0.45	0/1981
1	K	0.41	0/1474	0.44	0/1981
All	All	0.42	0/16214	0.45	0/21791

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	1450	0	1433	21	0
1	B	1450	0	1433	22	0
1	C	1450	0	1433	22	0
1	D	1450	0	1433	26	0
1	E	1450	0	1433	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1450	0	1433	20	0
1	G	1450	0	1433	20	0
1	H	1450	0	1433	28	0
1	I	1450	0	1433	29	0
1	J	1450	0	1433	32	0
1	K	1450	0	1433	23	0
All	All	15950	0	15763	202	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 202 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:H:195:ASP:HB3	1:I:77:GLU:HG3	1.67	0.76
1:C:86:HIS:HD2	1:D:121:HIS:HD2	1.33	0.73
1:I:49:PRO:HB2	1:I:181:GLN:HE22	1.53	0.72
1:J:195:ASP:HB3	1:K:77:GLU:HG3	1.69	0.72
1:E:170:ASP:OD2	1:E:173:ARG:NH2	2.23	0.71

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	182/438 (42%)	177 (97%)	5 (3%)	0	100	100
1	B	182/438 (42%)	180 (99%)	2 (1%)	0	100	100
1	C	182/438 (42%)	179 (98%)	3 (2%)	0	100	100
1	D	182/438 (42%)	176 (97%)	6 (3%)	0	100	100
1	E	182/438 (42%)	177 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	182/438 (42%)	177 (97%)	5 (3%)	0	100	100
1	G	182/438 (42%)	179 (98%)	3 (2%)	0	100	100
1	H	182/438 (42%)	179 (98%)	3 (2%)	0	100	100
1	I	182/438 (42%)	178 (98%)	4 (2%)	0	100	100
1	J	182/438 (42%)	181 (100%)	1 (0%)	0	100	100
1	K	182/438 (42%)	181 (100%)	1 (0%)	0	100	100
All	All	2002/4818 (42%)	1964 (98%)	38 (2%)	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	153/372 (41%)	153 (100%)	0	100	100
1	B	153/372 (41%)	153 (100%)	0	100	100
1	C	153/372 (41%)	153 (100%)	0	100	100
1	D	153/372 (41%)	153 (100%)	0	100	100
1	E	153/372 (41%)	153 (100%)	0	100	100
1	F	153/372 (41%)	153 (100%)	0	100	100
1	G	153/372 (41%)	153 (100%)	0	100	100
1	H	153/372 (41%)	153 (100%)	0	100	100
1	I	153/372 (41%)	152 (99%)	1 (1%)	81	93
1	J	153/372 (41%)	153 (100%)	0	100	100
1	K	153/372 (41%)	153 (100%)	0	100	100
All	All	1683/4092 (41%)	1682 (100%)	1 (0%)	92	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	177	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	164	ASN
1	J	121	HIS
1	G	92	ASN
1	J	92	ASN
1	K	86	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.

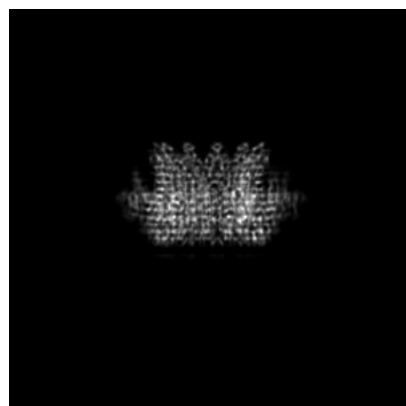
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41357. These allow visual inspection of the internal detail of the map and identification of artifacts.

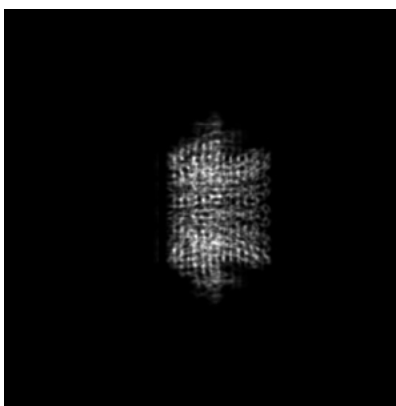
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

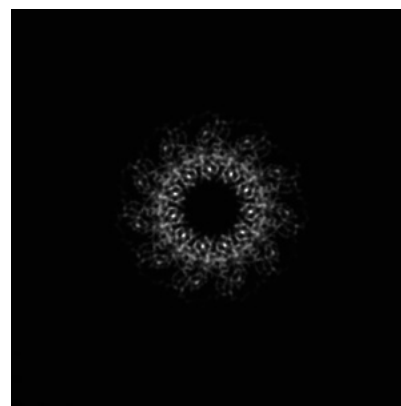
#### 6.1.1 Primary map



X

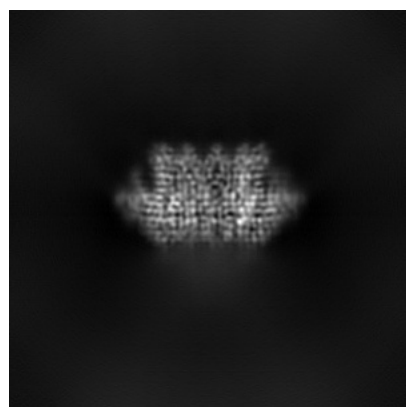


Y

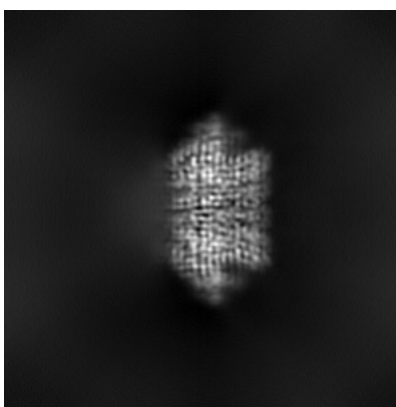


Z

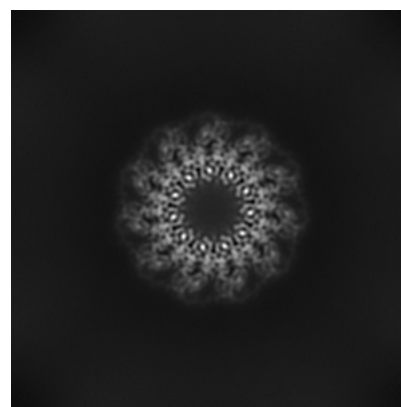
#### 6.1.2 Raw map



X



Y



Z

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

## 6.2 Central slices [i](#)

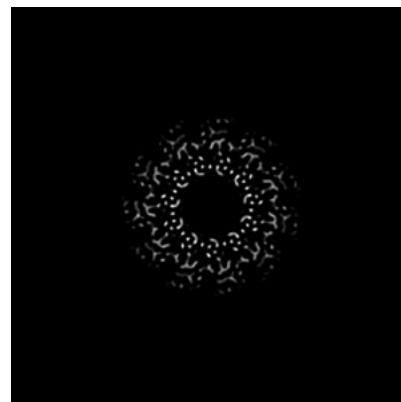
### 6.2.1 Primary map



X Index: 150

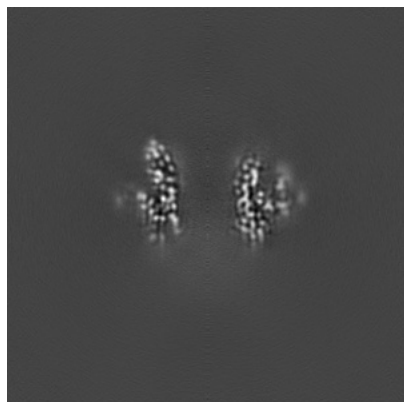


Y Index: 150

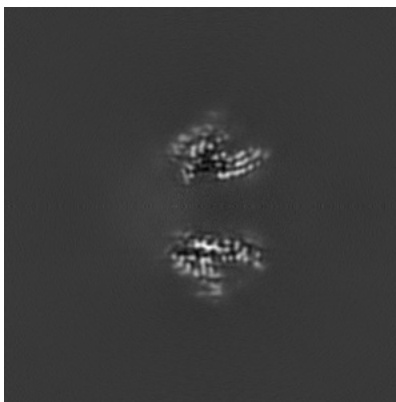


Z Index: 150

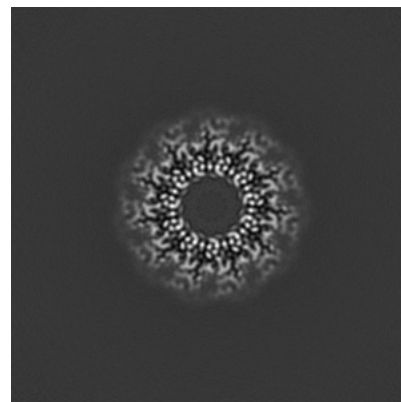
### 6.2.2 Raw map



X Index: 150



Y Index: 150

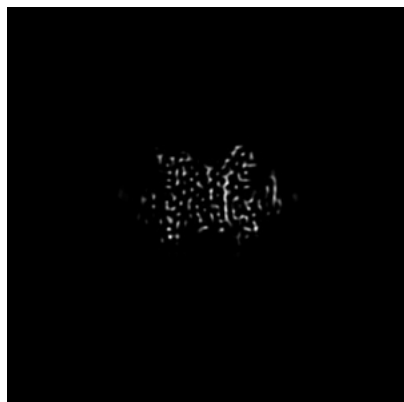


Z Index: 150

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: 176

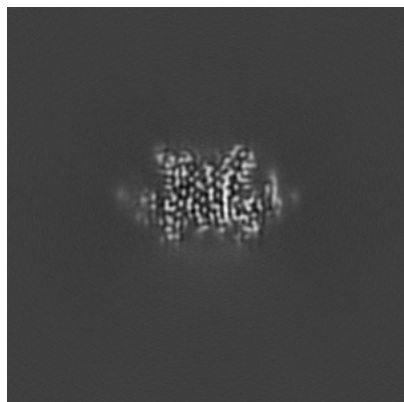


Y Index: 122

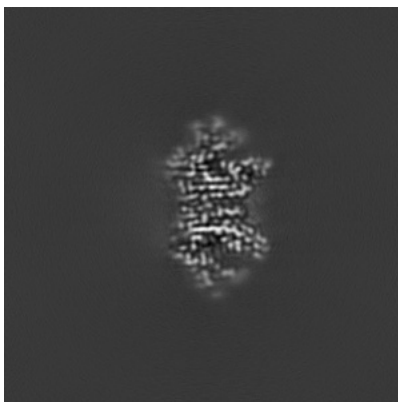


Z Index: 149

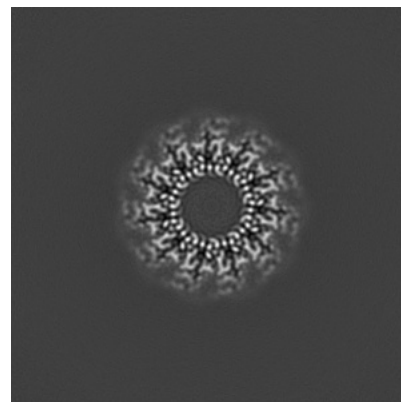
### 6.3.2 Raw map



X Index: 176



Y Index: 174

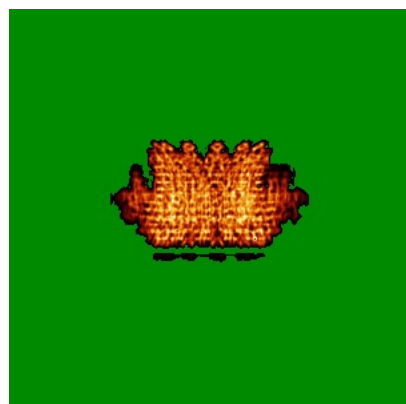


Z Index: 149

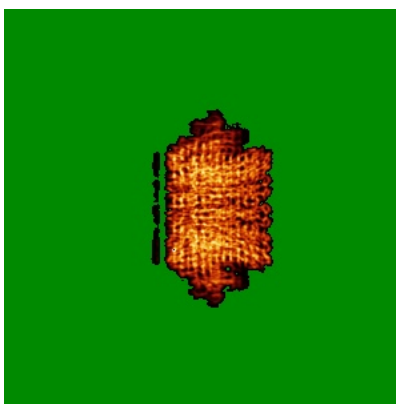
The images above show the largest variance slices of the map in three orthogonal directions.

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

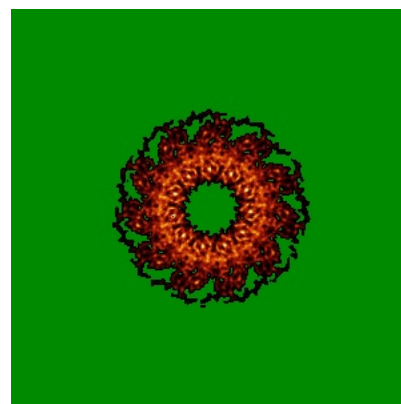
### 6.4.1 Primary map



X

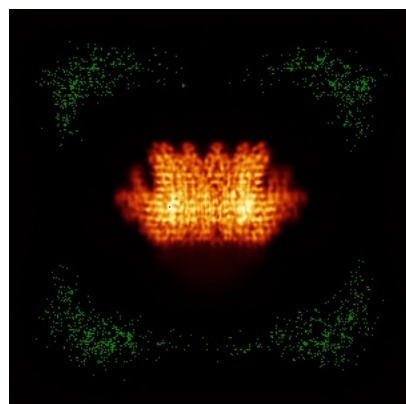


Y

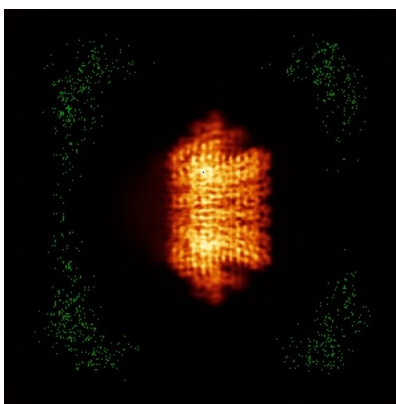


Z

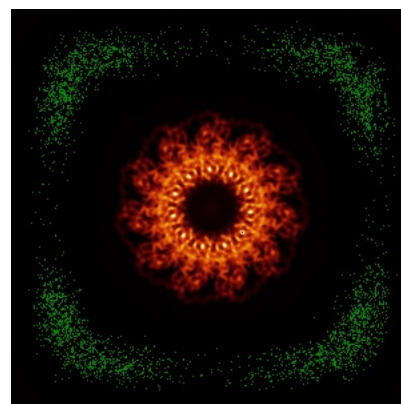
### 6.4.2 Raw map



X



Y



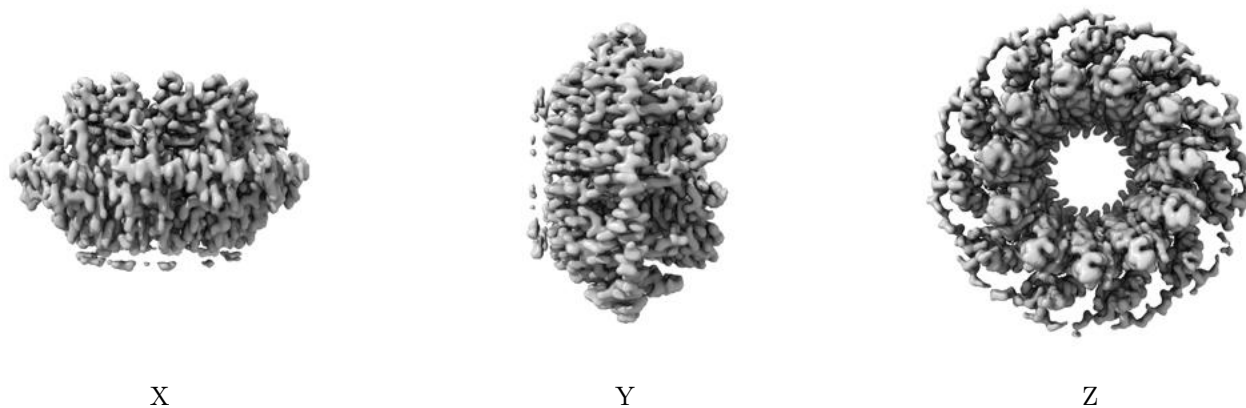
Z

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



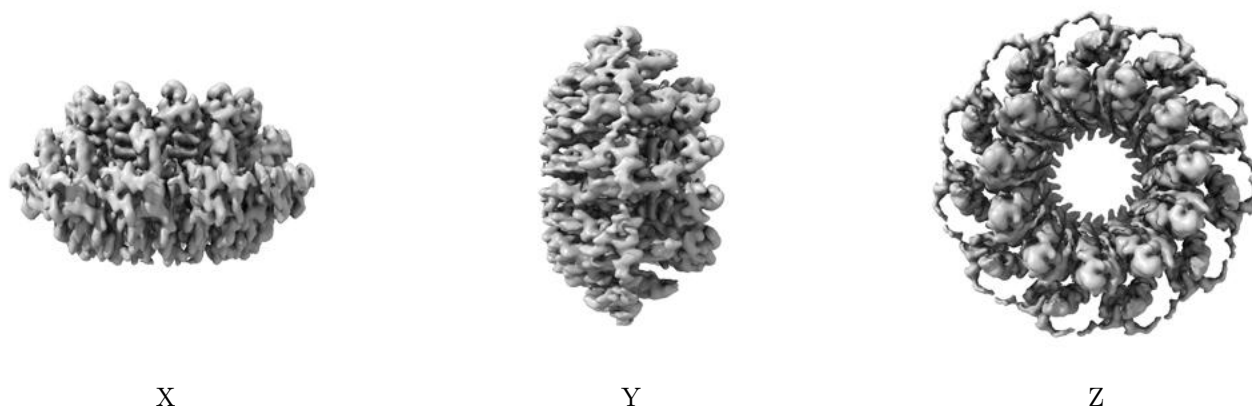
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

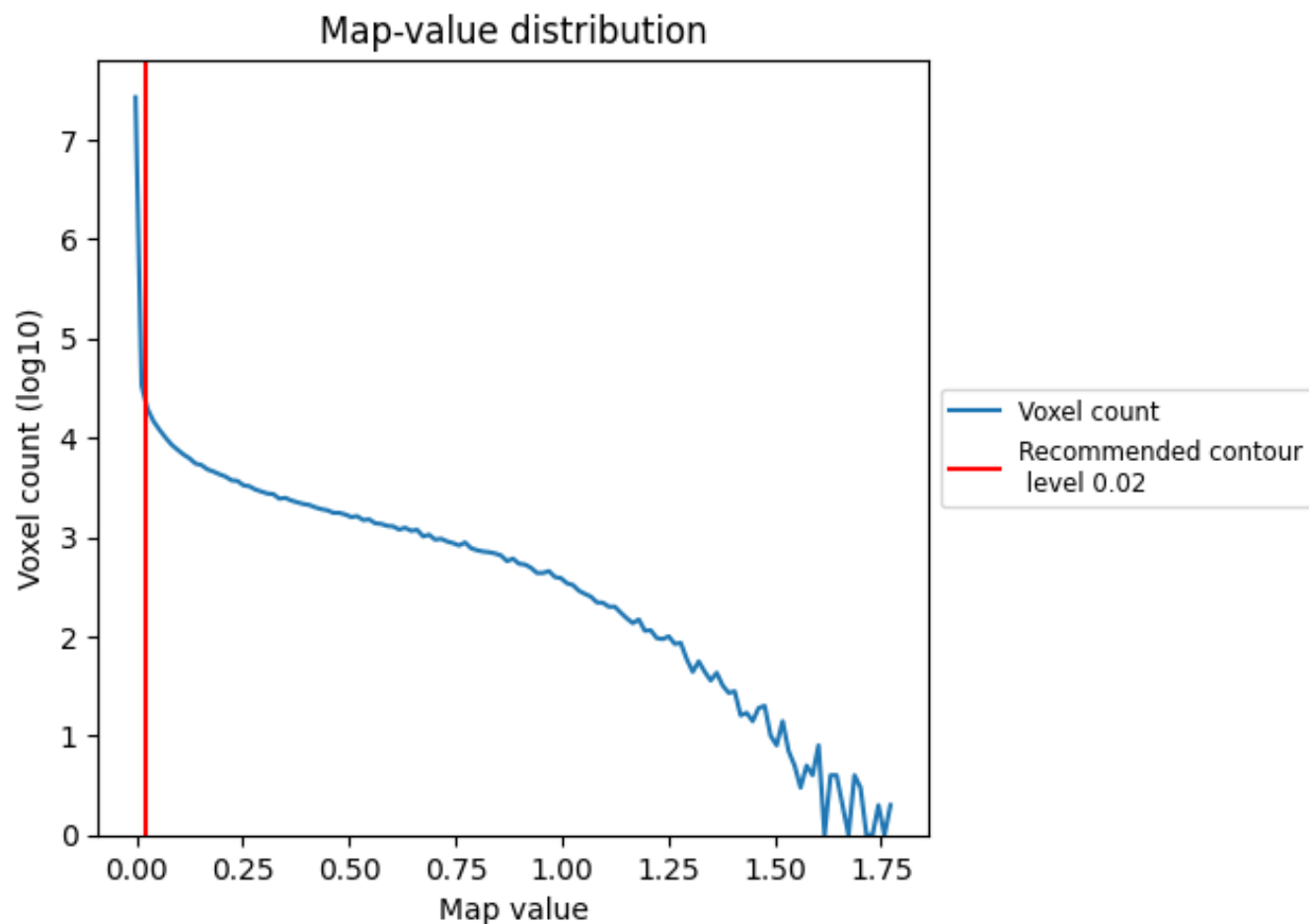
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

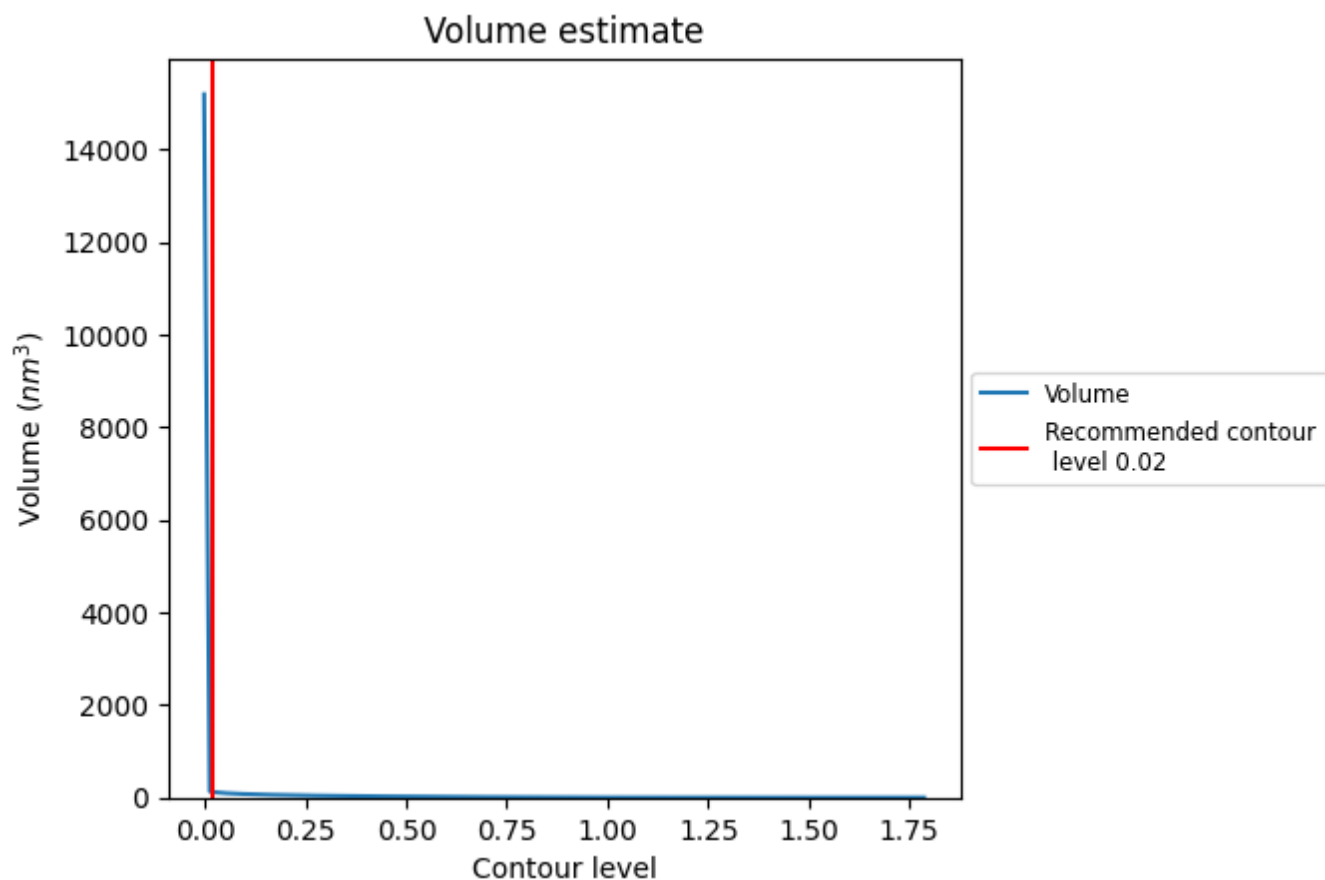
This section contains the results of statistical analysis of the map.

### 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.

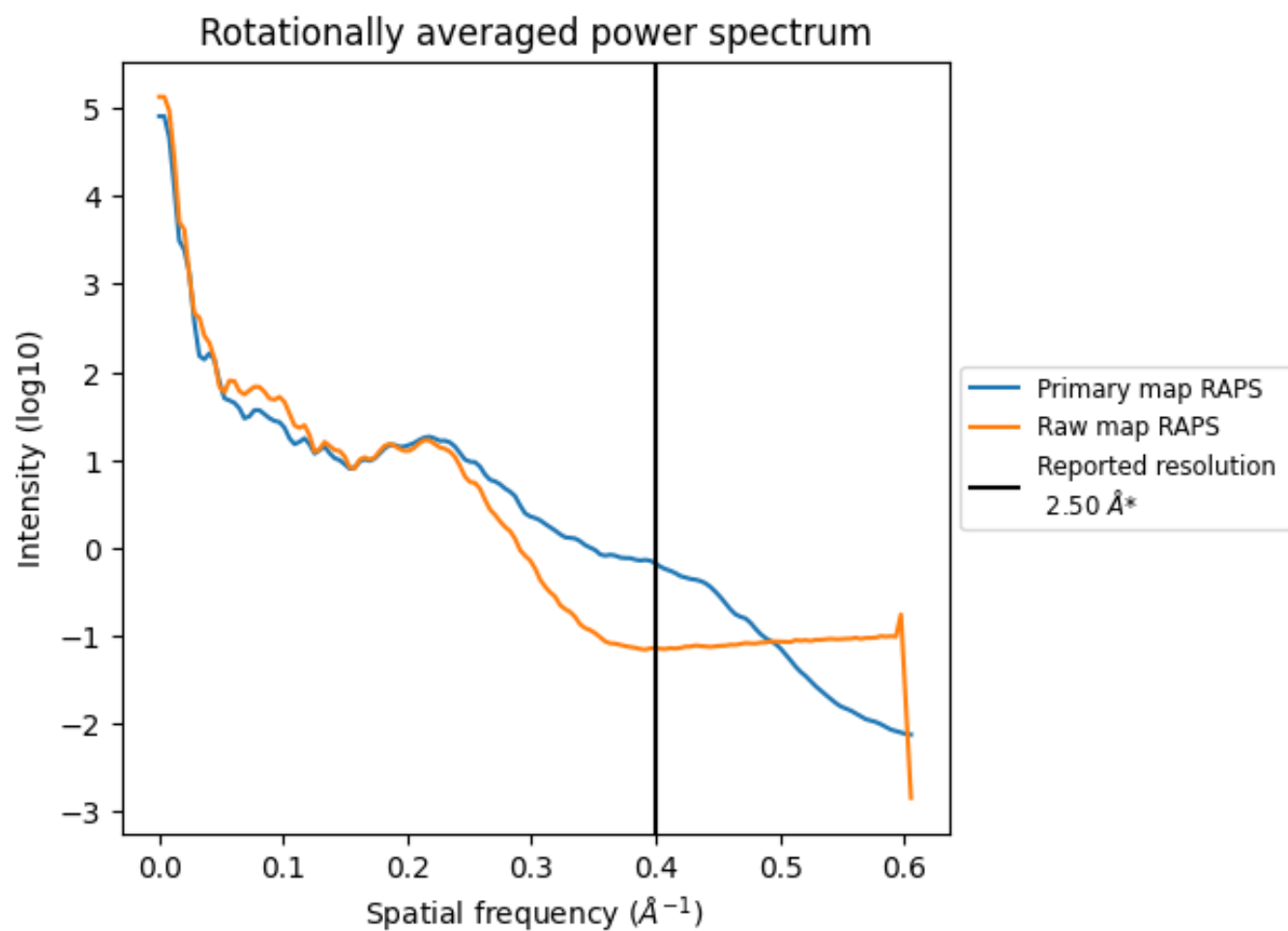
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 122 nm<sup>3</sup>; this corresponds to an approximate mass of 110 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 ⓘ

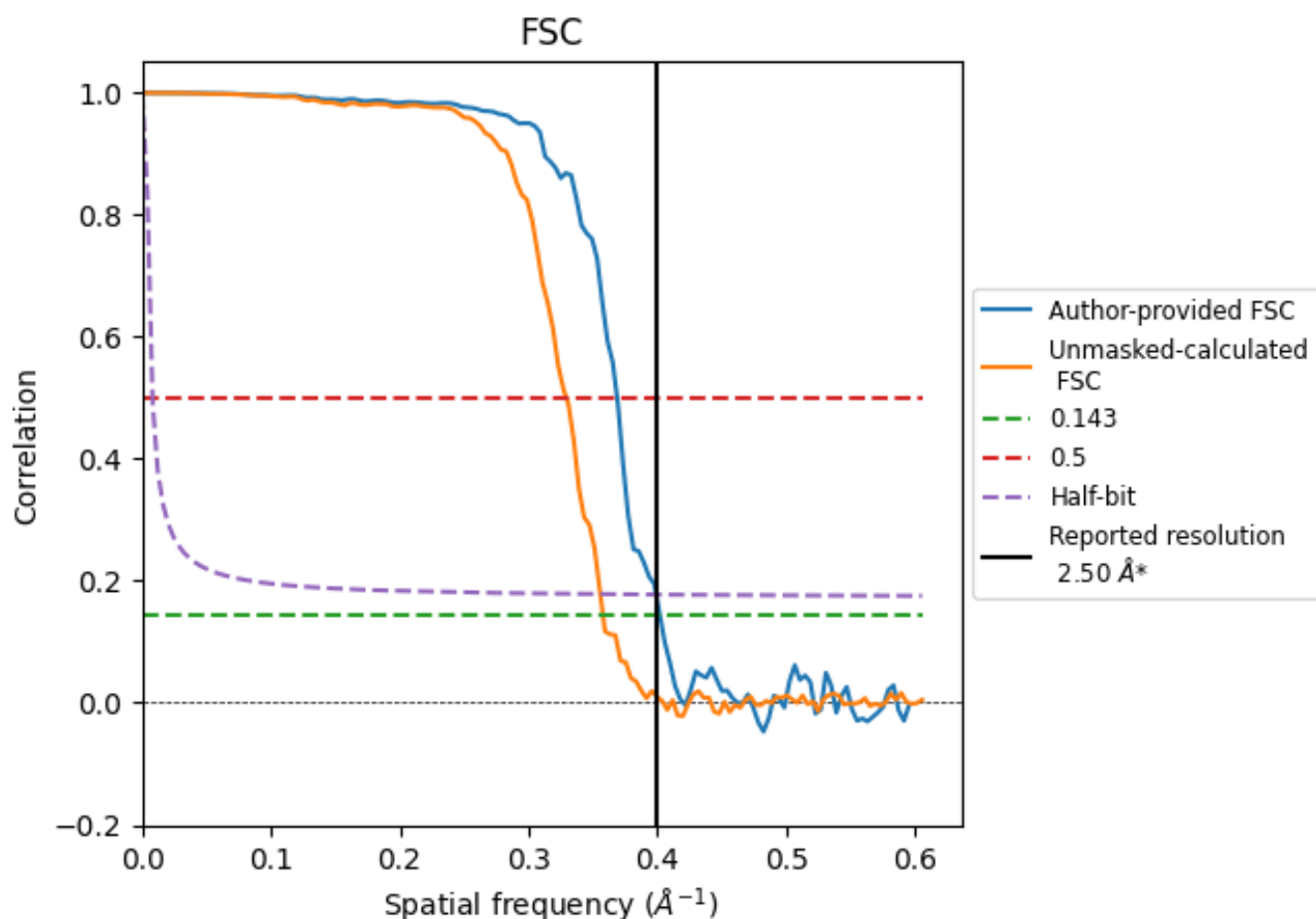


\*Reported resolution corresponds to spatial frequency of 0.400 Å<sup>-1</sup>

## 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 0.400  $\text{\AA}^{-1}$

## 8.2 Resolution estimates

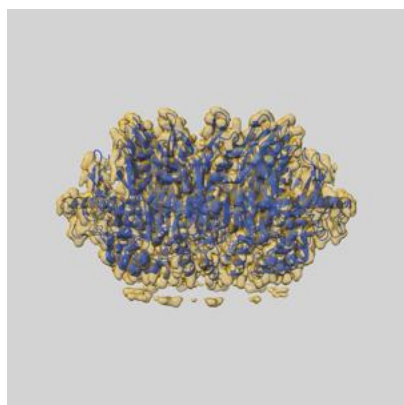
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.49	2.71	2.51
Unmasked-calculated*	2.79	3.04	2.81

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.79 differs from the reported value 2.5 by more than 10 %

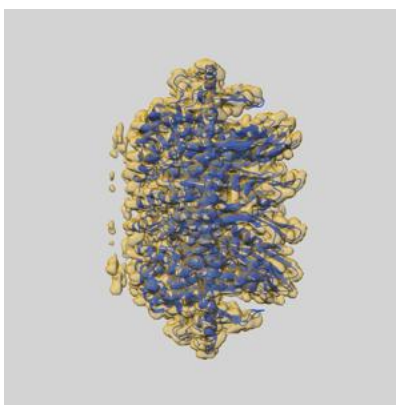
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41357 and PDB model 8TKQ. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

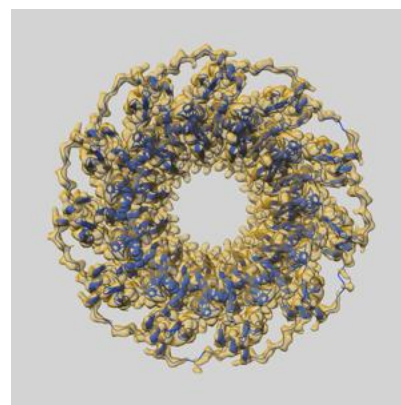
### 9.1 Map-model overlay [i](#)



X



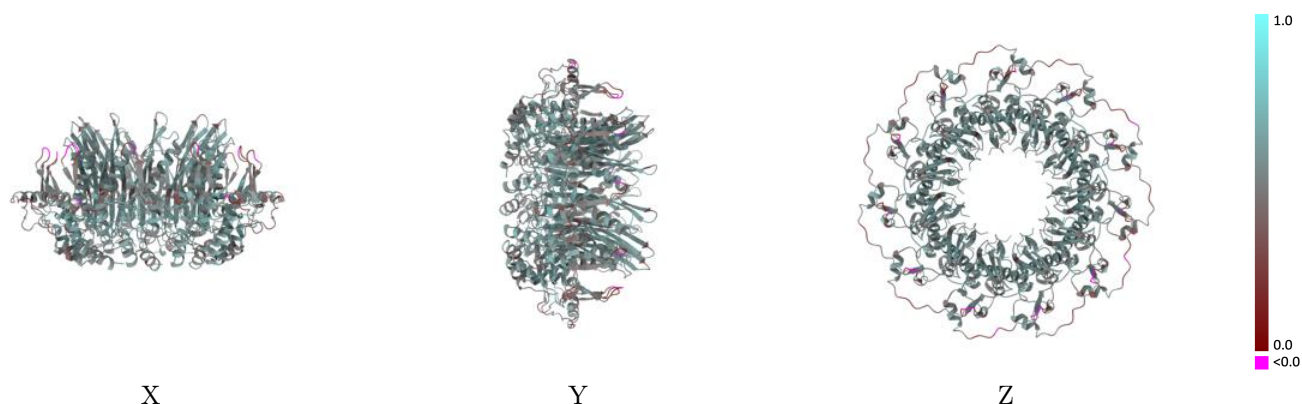
Y



Z

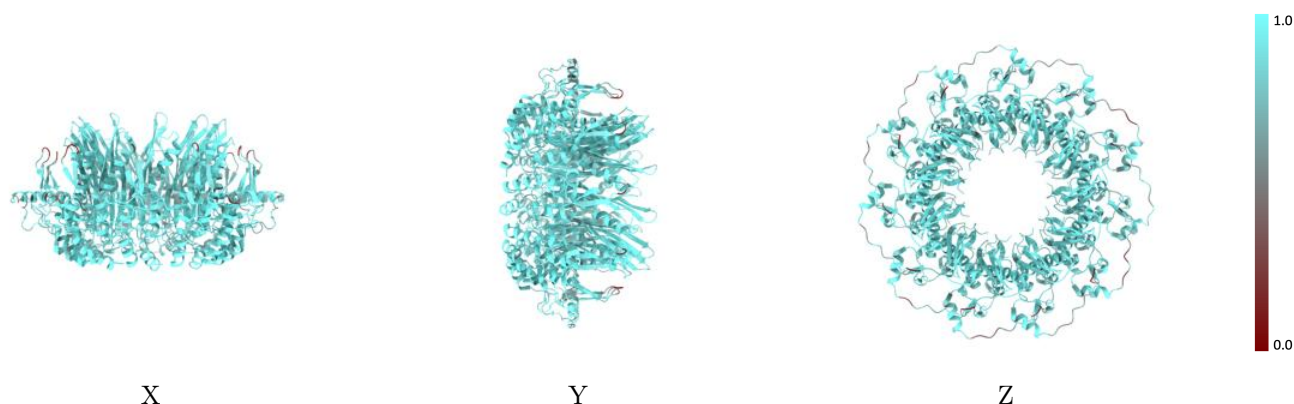
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

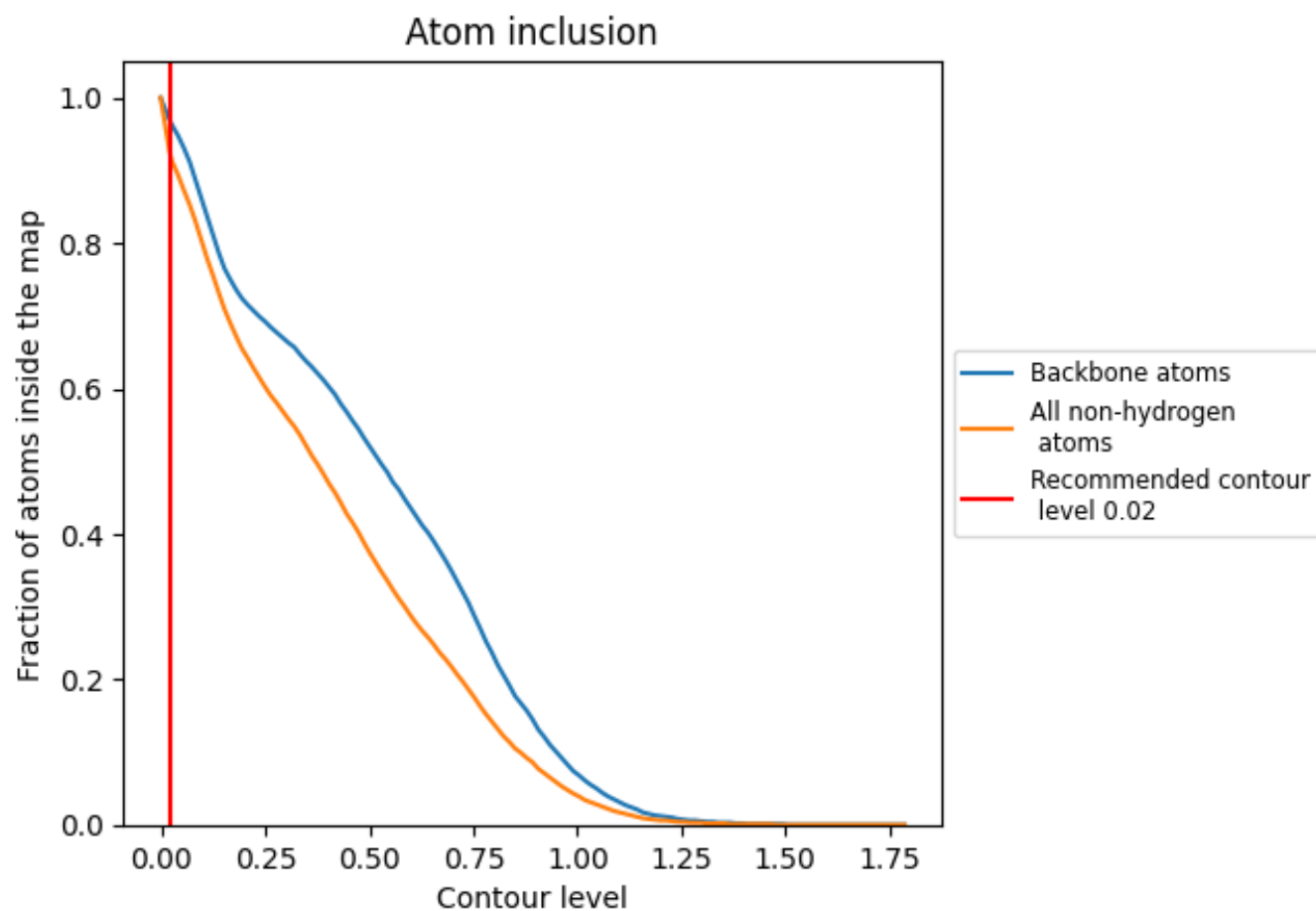
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.02).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 92% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9250	<div><div></div></div> 0.5340
A	<div><div></div></div> 0.9270	<div><div></div></div> 0.5330
B	<div><div></div></div> 0.9250	<div><div></div></div> 0.5290
C	<div><div></div></div> 0.9310	<div><div></div></div> 0.5390
D	<div><div></div></div> 0.9280	<div><div></div></div> 0.5320
E	<div><div></div></div> 0.9400	<div><div></div></div> 0.5440
F	<div><div></div></div> 0.9290	<div><div></div></div> 0.5350
G	<div><div></div></div> 0.9170	<div><div></div></div> 0.5290
H	<div><div></div></div> 0.9220	<div><div></div></div> 0.5340
I	<div><div></div></div> 0.9140	<div><div></div></div> 0.5290
J	<div><div></div></div> 0.9310	<div><div></div></div> 0.5320
K	<div><div></div></div> 0.9050	<div><div></div></div> 0.5330

1.0

0.0

<0.0