



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 03:28 AM UTC

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 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:

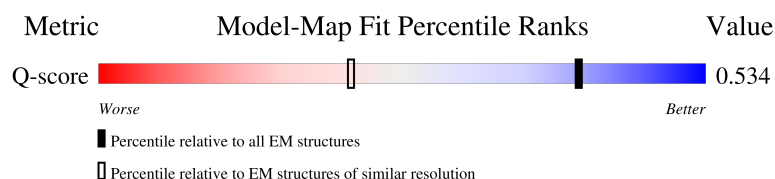
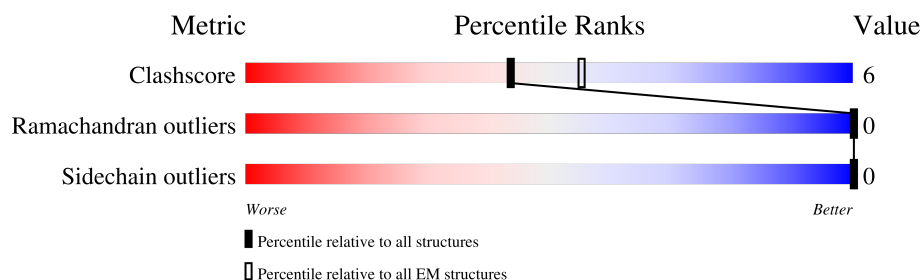
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	438	
1	B	438	
1	C	438	
1	D	438	

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Mol	Chain	Length	Quality of chain
1	E	438	 33% 9% 58%
1	F	438	 37% 5% 58%
1	G	438	 37% 5% 58%
1	H	438	 34% 8% 58%
1	I	438	 34% 8% 58%
1	J	438	 34% 8% 58%
1	K	438	 36% 6% 58%

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
I	-15	HIS	-	expression tag	UNP P43351
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I	-13	HIS	-	expression tag	UNP P43351
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I	-10	HIS	-	expression tag	UNP P43351
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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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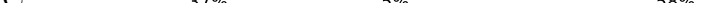
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I	0	HIS	-	expression tag	UNP P43351
J	-19	MET	-	initiating methionine	UNP P43351
J	-18	GLY	-	expression tag	UNP P43351
J	-17	SER	-	expression tag	UNP P43351
J	-16	SER	-	expression tag	UNP P43351
J	-15	HIS	-	expression tag	UNP P43351
J	-14	HIS	-	expression tag	UNP P43351
J	-13	HIS	-	expression tag	UNP P43351
J	-12	HIS	-	expression tag	UNP P43351
J	-11	HIS	-	expression tag	UNP P43351
J	-10	HIS	-	expression tag	UNP P43351
J	-9	SER	-	expression tag	UNP P43351
J	-8	SER	-	expression tag	UNP P43351
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
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J	-1	SER	-	expression tag	UNP P43351
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K	-16	SER	-	expression tag	UNP P43351
K	-15	HIS	-	expression tag	UNP P43351
K	-14	HIS	-	expression tag	UNP P43351
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K	-12	HIS	-	expression tag	UNP P43351
K	-11	HIS	-	expression tag	UNP P43351
K	-10	HIS	-	expression tag	UNP P43351
K	-9	SER	-	expression tag	UNP P43351
K	-8	SER	-	expression tag	UNP P43351
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K	-6	LEU	-	expression tag	UNP P43351
K	-5	VAL	-	expression tag	UNP P43351
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K	-2	GLY	-	expression tag	UNP P43351

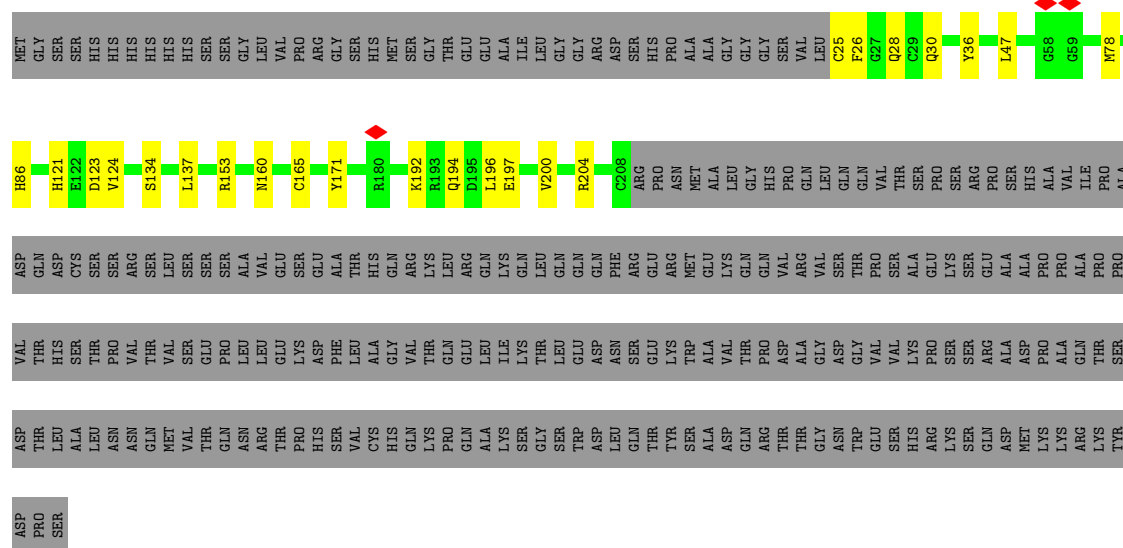
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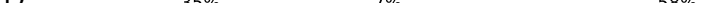
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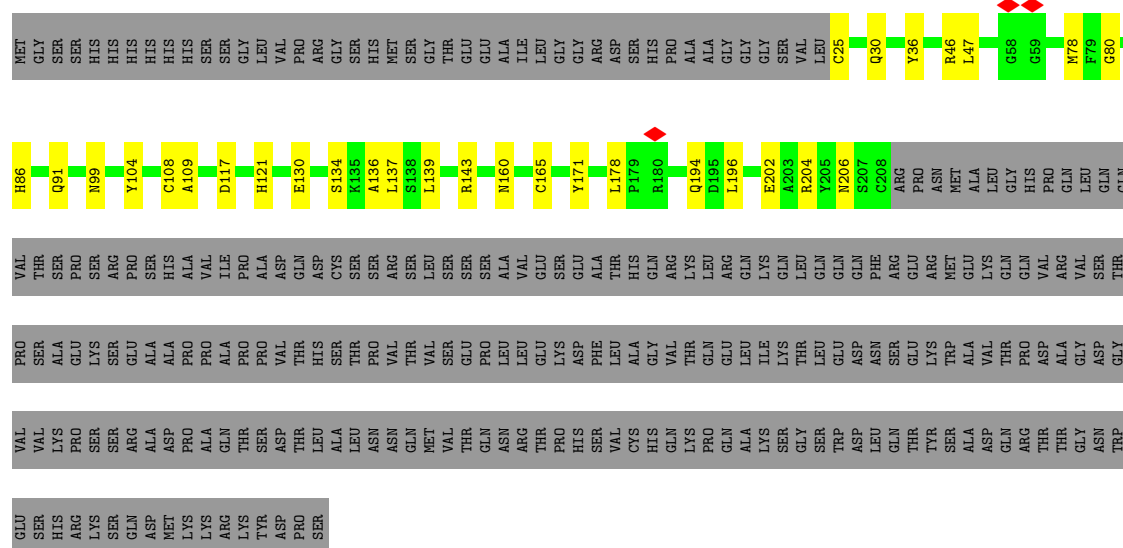
- Molecule 1: DNA repair protein RAD52 homolog

Chain C:  37% 5% 58%



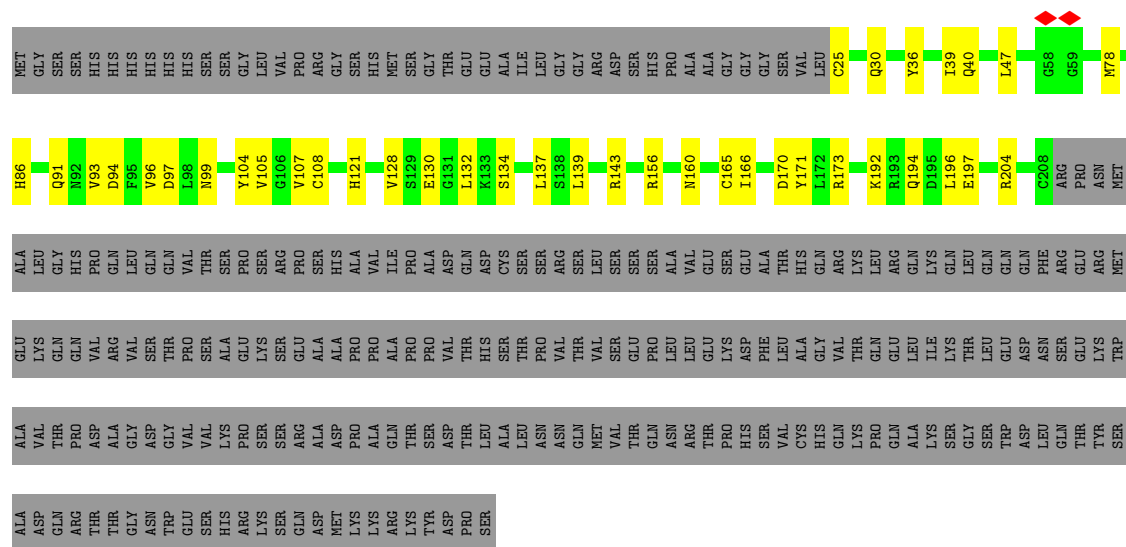
- Molecule 1: DNA repair protein RAD52 homolog

Chain D:  35% 7% 58%

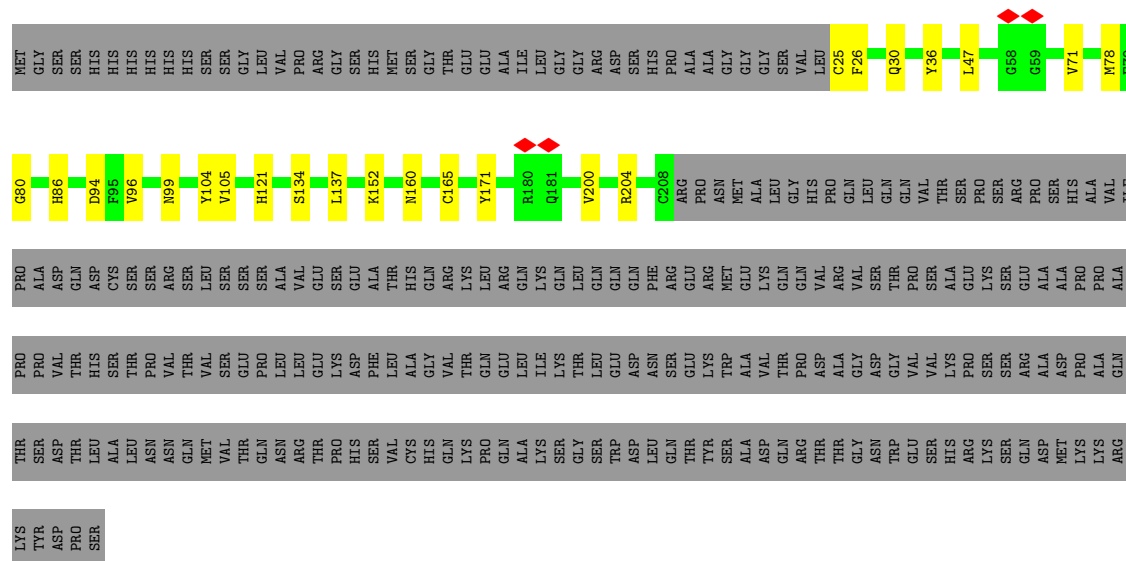
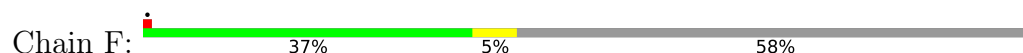


- Molecule 1: DNA repair protein RAD52 homolog

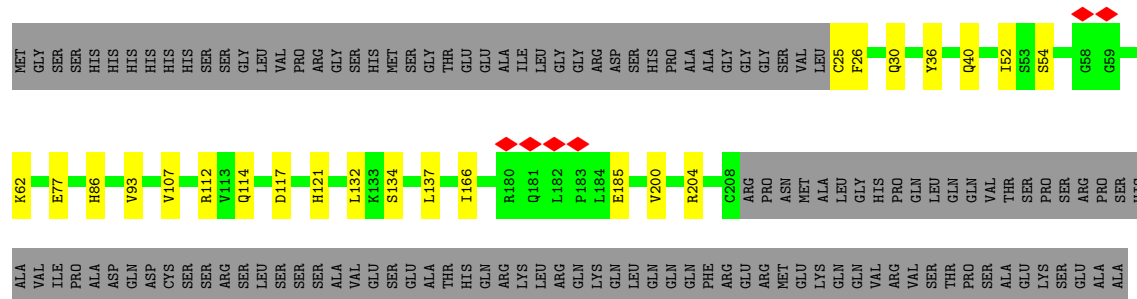
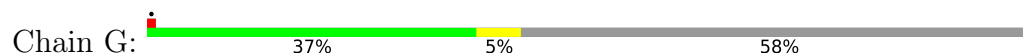
Chain E: 33% 9% 58%



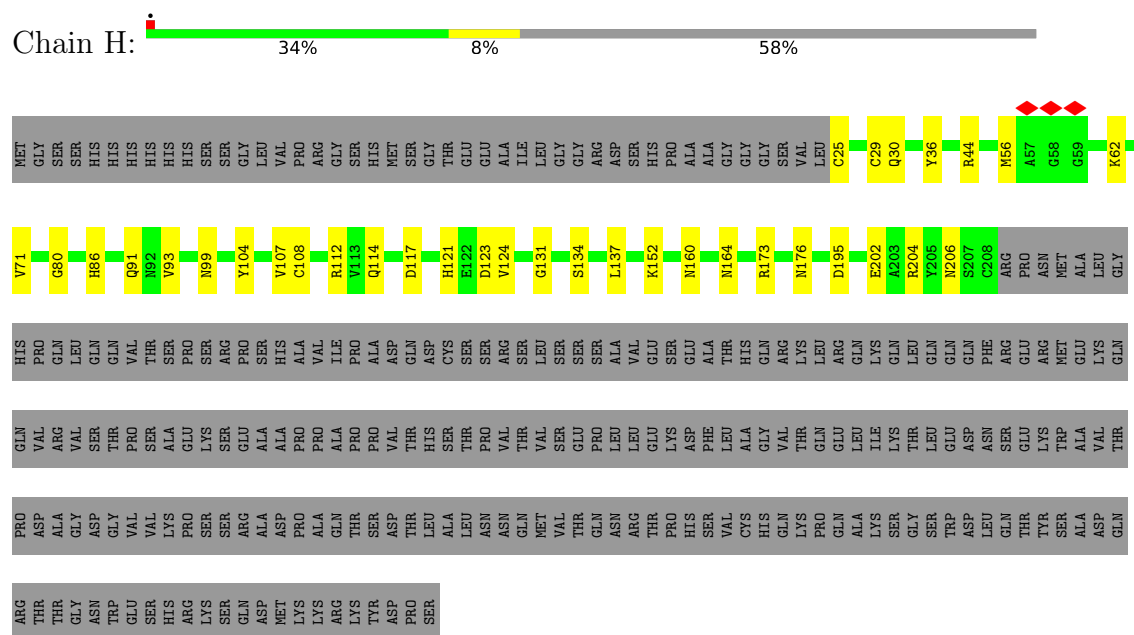
- Molecule 1: DNA repair protein RAD52 homolog



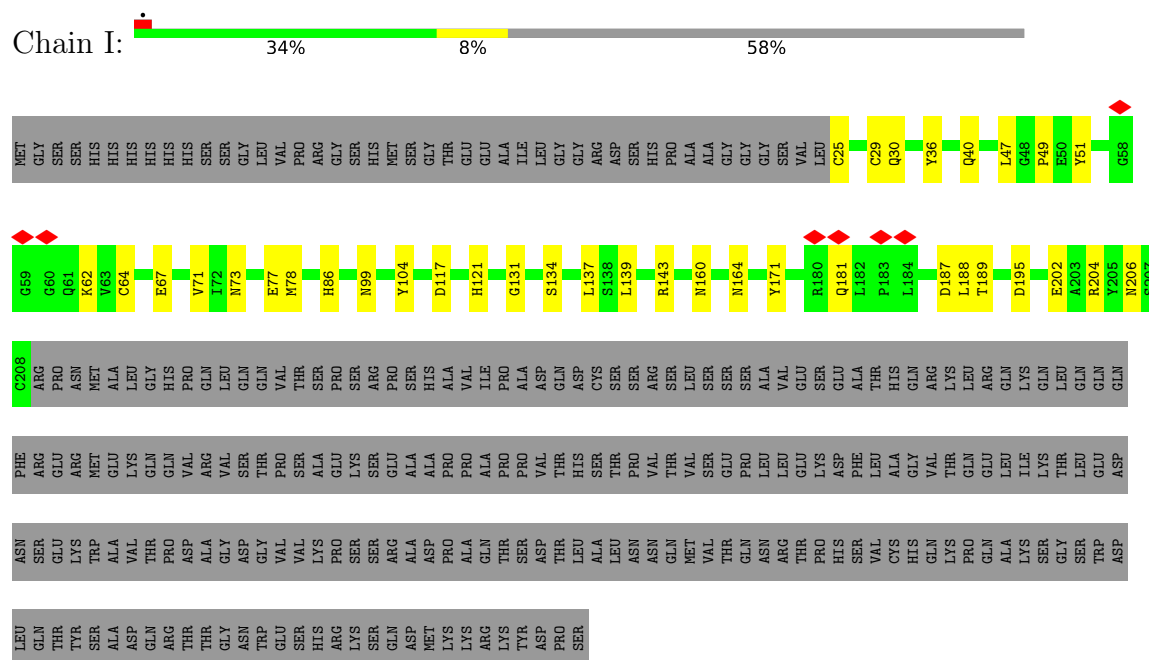
- Molecule 1: DNA repair protein RAD52 homolog



- Molecule 1: DNA repair protein RAD52 homolog



- Molecule 1: DNA repair protein RAD52 homolog



- Molecule 1: DNA repair protein RAD52 homolog

TRP	GLY	THR	GLN	Y65	MET
GLU	VAL	PRO	VAL	GLY	GLY
SER	VAL	SER	THR	SER	SER
HIS	LYS	ALA	SER	Y71	HIS
ARG	PRO	GLU	PRO	Y72	HIS
LYS	SER	LYS	SER	N73	HIS
SER	SER	SER	ARG	L74	HIS
GLN	ARG	GLU	PRO	GLY	HIS
ASP	ALA	ALA	SER	E77	HIS
MET	ASP	ALA	HIS	GLY	SER
LYS	PRO	PRO	ALA	H86	SER
LYS	ALA	PRO	VAL	GLY	SER
ARG	GLN	ALA	ILE	Q90	GLY
LYS	THR	ALA	PRO	Q91	LEU
TYR	SER	PRO	PRO	N92	VAL
ASP	ASP	VAL	ASP	Y93	PRO
PRO	THR	THR	GLN	D94	ARG
SER	LEU	HIS	ASP	Y107	GLY
ALA	ALA	SER	CYS	GLY	SER
LEU	LEU	THR	SER	K116	HIS
ASN	ASN	PRO	SER	D117	MET
ASN	GLN	VAL	ARG	GLY	SER
GLN	GLN	THR	SER	H121	GLY
MET	VAL	VAL	LEU	GLY	THR
VAL	VAL	SER	SER	GLU	GLU
THR	THR	GLU	SER	S134	GLU
GLN	GLN	PRO	SER	GLY	ALA
ASN	ASN	LEU	ALA	L137	ILE
ARG	ARG	LEU	VAL	S138	LEU
THR	THR	GLU	GLU	L139	GLY
PRO	PRO	LYS	SER	GLY	GLY
HIS	HIS	ASP	ALA	R143	ASP
VAL	VAL	PHE	ALA	SER	SER
VAL	VAL	LEU	THR	K152	SER
CYS	CYS	ALA	HIS	GLY	HIS
HIS	HIS	GLY	GLN	Y171	PRO
GLN	GLN	VAL	ARG	GLY	ALA
LYS	LYS	THR	LYS	L175	ALA
PRO	PRO	GLN	LEU	GLY	GLY
GLN	GLN	GLU	ARG	K192	GLY
ALA	ALA	LEU	GLN	GLY	GLY
LYS	LYS	ILE	LYS	D195	SER
SER	SER	LYS	GLN	L196	VAL
GLY	GLY	THR	LEU	E197	VAL
TRP	TRP	GLU	GLN	GLY	LEU
ASP	ASP	ASP	GLN	R204	C25
LEU	LEU	ASN	GLN	GLY	C28
GLN	GLN	SER	PHE	C298	C29
THR	THR	GLU	ARG	ARG	Q30
TYR	TYR	LYS	GLU	PRO	Y36
SER	SER	TRP	MET	MET	ALA7
ALA	ALA	ALA	ALA	ALA	LEU
ASP	ASP	VAL	LYS	LEU	Y61
GLN	GLN	THR	GLN	GLY	152
ARG	ARG	PRO	GLN	HIS	ALA
THR	THR	ASP	VAL	PRO	R55
THR	THR	ALA	ARG	GLN	GLY
GLY	GLY	GLY	VAL	LEU	ALA
ASN	ASN	ASP	SER	GLN	ALA

Chain K:

[illegible]

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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/1474	0.43	0/1981
1	B	0.30	0/1474	0.41	0/1981
1	C	0.31	0/1474	0.42	0/1981
1	D	0.31	0/1474	0.43	0/1981
1	E	0.32	0/1474	0.48	0/1981
1	F	0.31	0/1474	0.46	0/1981
1	G	0.31	0/1474	0.45	0/1981
1	H	0.30	0/1474	0.46	2/1981 (0.1%)
1	I	0.31	0/1474	0.45	2/1981 (0.1%)
1	J	0.30	0/1474	0.42	0/1981
1	K	0.31	0/1474	0.43	0/1981
All	All	0.31	0/16214	0.44	4/21791 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	131	GLY	CA-C-N	5.49	129.49	121.31
1	I	131	GLY	C-N-CA	5.49	129.49	121.31
1	H	131	GLY	CA-C-N	5.39	129.35	121.31
1	H	131	GLY	C-N-CA	5.39	129.35	121.31

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1450	0	1433	22	0
1	B	1450	0	1433	21	0
1	C	1450	0	1433	23	0
1	D	1450	0	1433	26	0
1	E	1450	0	1433	33	0
1	F	1450	0	1433	20	0
1	G	1450	0	1433	20	0
1	H	1450	0	1433	29	0
1	I	1450	0	1433	30	0
1	J	1450	0	1433	32	0
1	K	1450	0	1433	23	0
All	All	15950	0	15763	205	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.

All (205) 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
1:A:204:ARG:NH2	1:B:78:MET:O	2.25	0.70
1:G:25:CYS:N	1:H:30:GLN:OE1	2.25	0.69
1:C:25:CYS:N	1:D:30:GLN:OE1	2.26	0.68
1:B:86:HIS:HD2	1:C:121:HIS:HD2	1.42	0.68
1:D:80:GLY:HA2	1:E:40:GLN:HE22	1.58	0.68
1:G:54:SER:HB2	1:G:62:LYS:HD2	1.74	0.68
1:I:25:CYS:N	1:J:30:GLN:OE1	2.27	0.68
1:J:25:CYS:N	1:K:30:GLN:OE1	2.27	0.67
1:E:104:TYR:HD2	1:E:130:GLU:HG2	1.60	0.66
1:J:204:ARG:NH2	1:K:78:MET:O	2.29	0.66
1:F:71:VAL:HG21	1:F:152:LYS:HG2	1.79	0.65
1:I:62:LYS:NZ	1:I:64:CYS:SG	2.69	0.65
1:J:71:VAL:HG11	1:J:152:LYS:HG2	1.77	0.65
1:D:204:ARG:NH2	1:E:78:MET:O	2.30	0.65
1:C:204:ARG:NH2	1:D:78:MET:O	2.31	0.64
1:D:86:HIS:HD2	1:E:121:HIS:HD2	1.45	0.64
1:A:77:GLU:HG3	1:K:195:ASP:HB3	1.80	0.64
1:B:61:GLN:HG3	1:B:62:LYS:H	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:71:VAL:HG11	1:H:152:LYS:HG2	1.78	0.63
1:A:86:HIS:HD2	1:B:121:HIS:HD2	1.48	0.62
1:I:188:LEU:HD11	1:J:175:LEU:HD12	1.81	0.62
1:J:86:HIS:HD2	1:K:121:HIS:HD2	1.45	0.62
1:H:25:CYS:N	1:I:30:GLN:OE1	2.33	0.62
1:G:132:LEU:HD12	1:G:132:LEU:H	1.65	0.61
1:J:143:ARG:NH2	1:K:108:CYS:SG	2.73	0.61
1:I:195:ASP:HB3	1:J:77:GLU:HG3	1.83	0.61
1:B:25:CYS:N	1:C:30:GLN:HE21	1.99	0.61
1:E:204:ARG:NH2	1:F:78:MET:O	2.33	0.61
1:B:107:VAL:HG11	1:B:143:ARG:HD2	1.83	0.60
1:G:86:HIS:HD2	1:H:121:HIS:HD2	1.47	0.60
1:A:194:GLN:NE2	1:A:196:LEU:O	2.34	0.60
1:C:86:HIS:CD2	1:D:121:HIS:HD2	2.18	0.59
1:A:160:ASN:HB3	1:A:165:CYS:SG	2.43	0.59
1:K:25:CYS:SG	1:K:28:GLN:NE2	2.76	0.59
1:E:99:ASN:HB3	1:E:104:TYR:HE1	1.68	0.58
1:G:93:VAL:HA	1:G:107:VAL:HG23	1.86	0.57
1:A:78:MET:O	1:K:204:ARG:NH2	2.38	0.57
1:D:25:CYS:N	1:E:30:GLN:HE21	2.01	0.57
1:B:86:HIS:CD2	1:C:121:HIS:HD2	2.23	0.56
1:H:99:ASN:HB3	1:H:104:TYR:HE1	1.69	0.56
1:H:80:GLY:HA2	1:I:40:GLN:HE22	1.69	0.56
1:D:91:GLN:HG3	1:D:108:CYS:O	2.05	0.56
1:C:25:CYS:HB3	1:C:28:GLN:HE21	1.69	0.56
1:E:86:HIS:HD2	1:F:121:HIS:HD2	1.53	0.56
1:F:25:CYS:SG	1:F:26:PHE:N	2.78	0.56
1:J:192:LYS:NZ	1:J:197:GLU:OE2	2.35	0.56
1:K:96:VAL:HG13	1:K:105:VAL:HG22	1.87	0.55
1:B:194:GLN:NE2	1:B:196:LEU:O	2.38	0.55
1:C:25:CYS:SG	1:C:26:PHE:N	2.74	0.55
1:H:204:ARG:HD2	1:J:36:TYR:OH	2.06	0.55
1:B:189:THR:HG23	1:B:190:LYS:HG2	1.89	0.54
1:A:123:ASP:OD2	1:A:153:ARG:NE	2.39	0.54
1:I:99:ASN:HB3	1:I:104:TYR:HE1	1.72	0.53
1:A:36:TYR:OH	1:J:204:ARG:HD2	2.09	0.53
1:J:139:LEU:O	1:J:143:ARG:HG2	2.08	0.53
1:K:73:ASN:O	1:K:77:GLU:HG2	2.09	0.53
1:B:139:LEU:O	1:B:143:ARG:HG2	2.09	0.53
1:E:25:CYS:N	1:F:30:GLN:HE21	2.07	0.53
1:F:25:CYS:N	1:G:30:GLN:HE21	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:90:GLN:NE2	1:J:92:ASN:OD1	2.42	0.52
1:D:194:GLN:NE2	1:D:196:LEU:O	2.42	0.52
1:H:204:ARG:NH2	1:I:78:MET:O	2.43	0.52
1:G:200:VAL:HG12	1:G:204:ARG:HH21	1.74	0.52
1:E:194:GLN:NE2	1:E:196:LEU:O	2.43	0.52
1:E:192:LYS:NZ	1:E:197:GLU:OE1	2.37	0.52
1:D:204:ARG:HD2	1:F:36:TYR:OH	2.10	0.52
1:D:47:LEU:O	1:D:171:TYR:OH	2.27	0.52
1:I:204:ARG:HD2	1:K:36:TYR:OH	2.09	0.52
1:J:25:CYS:HB2	1:J:28:GLN:HG2	1.92	0.51
1:E:47:LEU:O	1:E:171:TYR:OH	2.19	0.51
1:E:160:ASN:HB3	1:E:165:CYS:SG	2.51	0.51
1:A:204:ARG:HD2	1:C:36:TYR:OH	2.09	0.51
1:E:132:LEU:HD12	1:E:132:LEU:H	1.76	0.51
1:E:156:ARG:HH21	1:E:166:ILE:HD11	1.77	0.50
1:A:132:LEU:HD12	1:A:132:LEU:H	1.76	0.50
1:G:25:CYS:SG	1:G:26:PHE:N	2.76	0.50
1:D:108:CYS:SG	1:D:109:ALA:N	2.85	0.50
1:E:96:VAL:HG13	1:E:105:VAL:HG22	1.94	0.50
1:A:121:HIS:HD2	1:K:86:HIS:HD2	1.60	0.50
1:F:96:VAL:HG13	1:F:105:VAL:HG22	1.92	0.50
1:I:73:ASN:O	1:I:77:GLU:HG2	2.12	0.50
1:A:73:ASN:O	1:A:77:GLU:HG2	2.12	0.49
1:E:86:HIS:HD2	1:F:121:HIS:CD2	2.29	0.49
1:C:204:ARG:HD2	1:E:36:TYR:OH	2.11	0.49
1:K:93:VAL:HG13	1:K:107:VAL:HG22	1.95	0.49
1:B:25:CYS:SG	1:C:28:GLN:HA	2.51	0.49
1:B:204:ARG:NH2	1:C:78:MET:O	2.46	0.49
1:H:134:SER:OG	1:H:137:LEU:HB2	2.13	0.49
1:E:134:SER:OG	1:E:137:LEU:HB2	2.13	0.48
1:H:91:GLN:HE21	1:H:107:VAL:HG11	1.77	0.48
1:B:200:VAL:HG12	1:B:204:ARG:HH21	1.77	0.48
1:A:134:SER:OG	1:A:137:LEU:HB2	2.14	0.48
1:F:200:VAL:HG12	1:F:204:ARG:HH21	1.78	0.48
1:G:86:HIS:CD2	1:H:121:HIS:HD2	2.29	0.48
1:E:91:GLN:HG3	1:E:108:CYS:O	2.13	0.48
1:A:139:LEU:O	1:A:143:ARG:HG3	2.13	0.48
1:B:134:SER:OG	1:B:137:LEU:HB2	2.13	0.48
1:F:204:ARG:HD2	1:H:36:TYR:OH	2.12	0.48
1:H:99:ASN:HB3	1:H:104:TYR:CE1	2.49	0.48
1:C:123:ASP:OD1	1:C:124:VAL:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:202:GLU:OE2	1:H:206:ASN:ND2	2.47	0.48
1:I:86:HIS:HD2	1:J:121:HIS:CD2	2.32	0.48
1:H:56:MET:HE1	1:H:62:LYS:HB2	1.95	0.48
1:H:62:LYS:NZ	1:H:176:ASN:OD1	2.38	0.47
1:I:86:HIS:HD2	1:J:121:HIS:HD2	1.60	0.47
1:K:156:ARG:HH21	1:K:166:ILE:HD11	1.79	0.47
1:F:47:LEU:O	1:F:171:TYR:OH	2.17	0.47
1:J:107:VAL:HG11	1:J:143:ARG:HD2	1.96	0.47
1:I:99:ASN:HB3	1:I:104:TYR:CE1	2.50	0.47
1:K:160:ASN:HB3	1:K:165:CYS:SG	2.54	0.47
1:A:86:HIS:CD2	1:B:121:HIS:HD2	2.32	0.47
1:K:155:LEU:HD22	1:K:162:LEU:HD13	1.97	0.47
1:B:204:ARG:HD2	1:D:36:TYR:OH	2.15	0.47
1:J:47:LEU:HD12	1:J:51:TYR:CG	2.50	0.47
1:J:29:CYS:O	1:J:117:ASP:HA	2.15	0.46
1:C:123:ASP:OD2	1:C:153:ARG:HB3	2.15	0.46
1:E:204:ARG:HD2	1:G:36:TYR:OH	2.16	0.46
1:G:134:SER:OG	1:G:137:LEU:HB2	2.14	0.46
1:I:134:SER:OG	1:I:137:LEU:HB2	2.15	0.46
1:H:86:HIS:HD2	1:I:121:HIS:HD2	1.64	0.46
1:E:139:LEU:O	1:E:143:ARG:HG3	2.16	0.46
1:C:47:LEU:O	1:C:171:TYR:OH	2.28	0.45
1:F:160:ASN:HB3	1:F:165:CYS:SG	2.56	0.45
1:G:112:ARG:HH21	1:G:114:GLN:NE2	2.14	0.45
1:C:197:GLU:HB2	1:C:200:VAL:HG12	1.99	0.45
1:D:136:ALA:HB1	1:E:128:VAL:HG22	1.98	0.45
1:H:86:HIS:CD2	1:I:121:HIS:HD2	2.34	0.45
1:E:93:VAL:HG13	1:E:107:VAL:HG22	1.99	0.45
1:J:73:ASN:O	1:J:77:GLU:HG2	2.17	0.45
1:A:30:GLN:OE1	1:K:25:CYS:N	2.49	0.45
1:I:47:LEU:O	1:I:171:TYR:OH	2.26	0.45
1:A:112:ARG:HH21	1:A:114:GLN:NE2	2.15	0.45
1:I:86:HIS:CD2	1:J:121:HIS:HD2	2.33	0.45
1:A:47:LEU:O	1:A:171:TYR:OH	2.23	0.44
1:I:29:CYS:O	1:I:117:ASP:HA	2.15	0.44
1:K:47:LEU:O	1:K:171:TYR:OH	2.23	0.44
1:J:86:HIS:CD2	1:K:121:HIS:HD2	2.31	0.44
1:K:139:LEU:O	1:K:143:ARG:HG3	2.17	0.44
1:B:36:TYR:OH	1:K:204:ARG:HD2	2.17	0.44
1:H:123:ASP:OD1	1:H:124:VAL:N	2.44	0.44
1:I:202:GLU:OE2	1:I:206:ASN:ND2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:143:ARG:NH1	1:E:94:ASP:OD2	2.51	0.44
1:D:160:ASN:HB3	1:D:165:CYS:SG	2.58	0.44
1:E:97:ASP:OD1	1:E:104:TYR:HB2	2.18	0.44
1:C:194:GLN:NE2	1:C:196:LEU:O	2.51	0.44
1:D:86:HIS:CD2	1:E:121:HIS:HD2	2.31	0.44
1:H:112:ARG:HH21	1:H:114:GLN:HE21	1.65	0.44
1:G:166:ILE:HD12	1:G:166:ILE:HA	1.89	0.44
1:A:121:HIS:HD2	1:K:86:HIS:CD2	2.36	0.43
1:H:91:GLN:HG3	1:H:108:CYS:O	2.17	0.43
1:J:47:LEU:HD11	1:J:74:LEU:HD11	1.99	0.43
1:D:104:TYR:HD2	1:D:130:GLU:OE1	2.00	0.43
1:G:185:GLU:OE1	1:H:173:ARG:NH2	2.49	0.43
1:I:47:LEU:HD12	1:I:51:TYR:CG	2.52	0.43
1:I:139:LEU:O	1:I:143:ARG:HG3	2.18	0.43
1:C:160:ASN:HB3	1:C:165:CYS:SG	2.58	0.43
1:F:86:HIS:HD2	1:G:121:HIS:HD2	1.67	0.43
1:E:91:GLN:HE21	1:E:107:VAL:HG11	1.83	0.43
1:H:29:CYS:O	1:H:117:ASP:HA	2.17	0.43
1:H:160:ASN:HA	1:H:164:ASN:HB3	2.00	0.43
1:J:25:CYS:SG	1:K:28:GLN:HA	2.59	0.43
1:J:196:LEU:HD23	1:J:197:GLU:N	2.33	0.43
1:A:136:ALA:HB1	1:B:128:VAL:HG22	2.00	0.43
1:B:47:LEU:HD12	1:B:51:TYR:CD1	2.54	0.43
1:G:52:ILE:HD12	1:G:166:ILE:HD13	1.99	0.43
1:A:54:SER:OG	1:A:62:LYS:HG3	2.18	0.43
1:I:143:ARG:NH1	1:J:94:ASP:OD2	2.52	0.43
1:F:26:PHE:HB2	1:G:117:ASP:O	2.19	0.43
1:J:55:ARG:HD3	1:J:65:TYR:CE2	2.54	0.43
1:F:134:SER:OG	1:F:137:LEU:HB2	2.18	0.43
1:G:77:GLU:OE2	1:H:44:ARG:NH1	2.51	0.42
1:C:134:SER:OG	1:C:137:LEU:HB2	2.19	0.42
1:D:178:LEU:HD23	1:D:178:LEU:HA	1.85	0.42
1:I:187:ASP:OD1	1:I:189:THR:HG23	2.20	0.42
1:A:160:ASN:HA	1:A:164:ASN:HB3	2.01	0.42
1:E:143:ARG:NH1	1:F:94:ASP:OD2	2.53	0.42
1:E:86:HIS:CD2	1:F:121:HIS:HD2	2.35	0.42
1:J:134:SER:OG	1:J:137:LEU:HB2	2.19	0.42
1:D:139:LEU:O	1:D:143:ARG:HG3	2.20	0.42
1:H:86:HIS:HD2	1:I:121:HIS:CD2	2.38	0.41
1:E:99:ASN:HB3	1:E:104:TYR:CE1	2.51	0.41
1:F:99:ASN:HB3	1:F:104:TYR:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:46:ARG:HG2	1:D:165:CYS:SG	2.60	0.41
1:D:134:SER:OG	1:D:137:LEU:HB2	2.20	0.41
1:E:39:ILE:HG23	1:E:78:MET:CE	2.51	0.41
1:I:160:ASN:HA	1:I:164:ASN:HB3	2.03	0.41
1:J:52:ILE:HG13	1:J:175:LEU:HD21	2.03	0.41
1:I:67:GLU:O	1:I:71:VAL:HG23	2.21	0.41
1:J:47:LEU:O	1:J:171:TYR:OH	2.21	0.41
1:D:202:GLU:OE2	1:D:206:ASN:ND2	2.51	0.41
1:C:192:LYS:NZ	1:C:197:GLU:OE2	2.42	0.41
1:C:26:PHE:HB2	1:D:117:ASP:O	2.21	0.41
1:F:80:GLY:HA2	1:G:40:GLN:HE22	1.86	0.40
1:H:112:ARG:HH21	1:H:114:GLN:NE2	2.18	0.40
1:D:99:ASN:HB3	1:D:104:TYR:CE1	2.57	0.40
1:G:204:ARG:NH1	1:I:36:TYR:OH	2.54	0.40
1:B:47:LEU:HD12	1:B:51:TYR:CG	2.56	0.40
1:B:86:HIS:HD2	1:C:121:HIS:CD2	2.31	0.40
1:H:93:VAL:HG13	1:H:107:VAL:HG22	2.03	0.40
1:J:29:CYS:SG	1:J:116:LYS:HE3	2.61	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	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
1	F	182/438 (42%)	177 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	153 (100%)	0	100	100
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%)	1683 (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 (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	45	GLN
1	A	69	HIS
1	A	86	HIS
1	A	91	GLN
1	A	100	ASN
1	A	114	GLN
1	A	121	HIS
1	B	37	GLN
1	B	86	HIS
1	B	91	GLN
1	B	121	HIS
1	C	28	GLN
1	C	37	GLN
1	C	69	HIS
1	C	86	HIS
1	C	90	GLN
1	C	91	GLN
1	C	121	HIS
1	D	30	GLN
1	D	37	GLN
1	D	61	GLN
1	D	86	HIS
1	D	90	GLN
1	D	121	HIS
1	E	37	GLN
1	E	40	GLN
1	E	86	HIS
1	E	121	HIS
1	E	176	ASN
1	F	37	GLN
1	F	86	HIS
1	F	90	GLN
1	F	91	GLN
1	G	37	GLN
1	G	40	GLN
1	G	45	GLN
1	G	86	HIS
1	G	91	GLN
1	G	92	ASN
1	G	114	GLN
1	H	30	GLN
1	H	37	GLN

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Mol	Chain	Res	Type
1	H	45	GLN
1	H	86	HIS
1	H	91	GLN
1	H	92	ASN
1	H	114	GLN
1	H	121	HIS
1	I	30	GLN
1	I	37	GLN
1	I	86	HIS
1	I	91	GLN
1	I	121	HIS
1	J	28	GLN
1	J	30	GLN
1	J	37	GLN
1	J	86	HIS
1	J	90	GLN
1	J	91	GLN
1	J	92	ASN
1	J	121	HIS
1	K	28	GLN
1	K	30	GLN
1	K	37	GLN
1	K	86	HIS
1	K	91	GLN
1	K	100	ASN
1	K	181	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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.

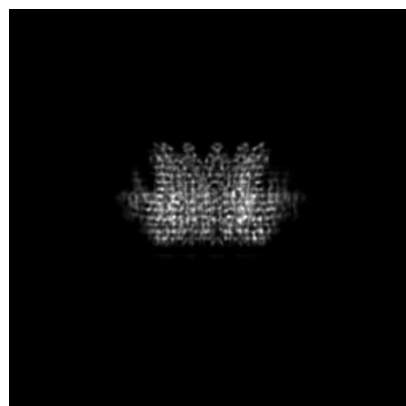
6 Map visualisation [i](#)

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.

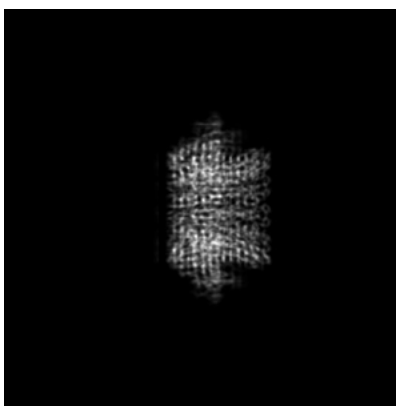
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

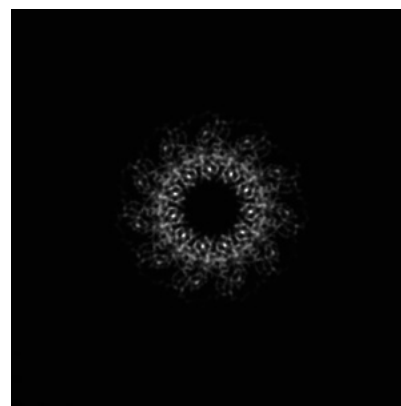
6.1.1 Primary map



X

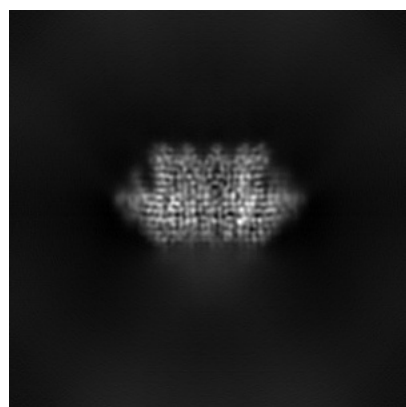


Y

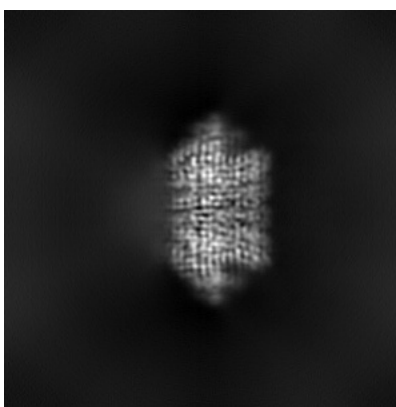


Z

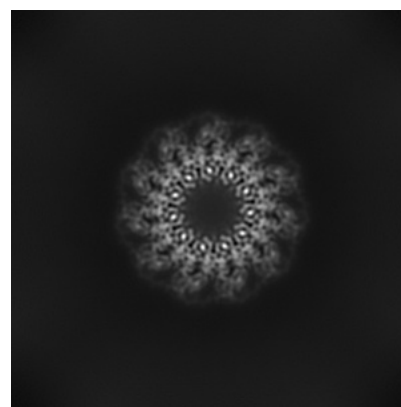
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

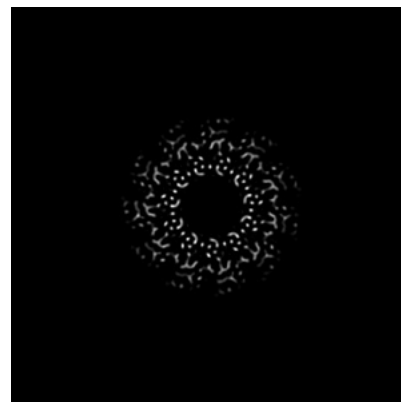
6.2.1 Primary map



X Index: 150

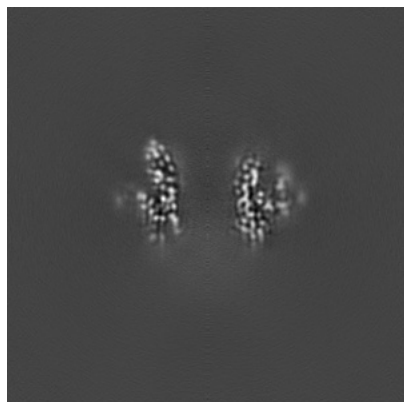


Y Index: 150

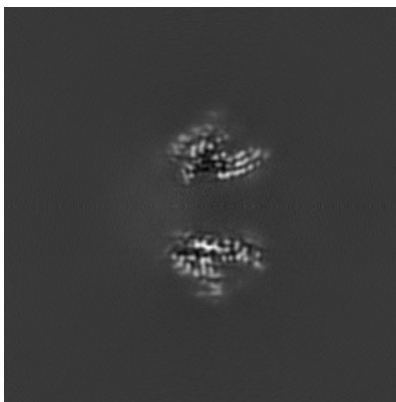


Z Index: 150

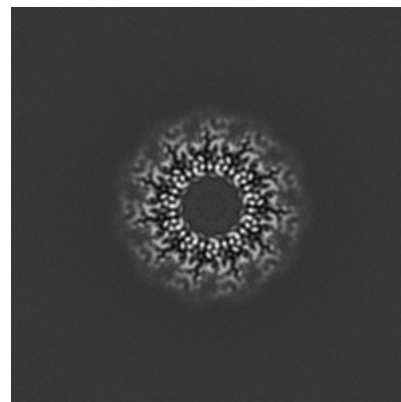
6.2.2 Raw map



X Index: 150



Y Index: 150

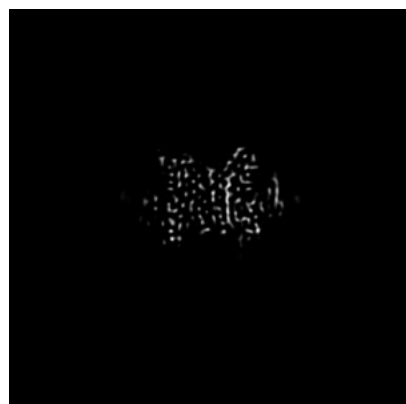


Z Index: 150

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

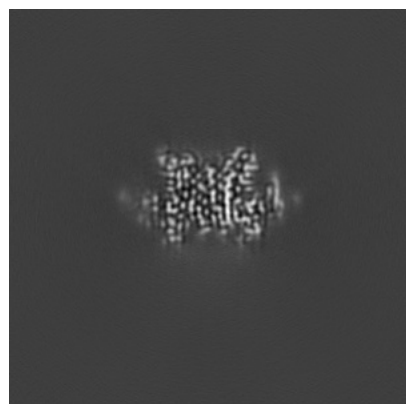


Y Index: 122

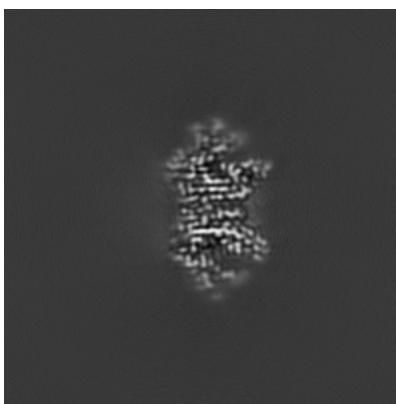


Z Index: 149

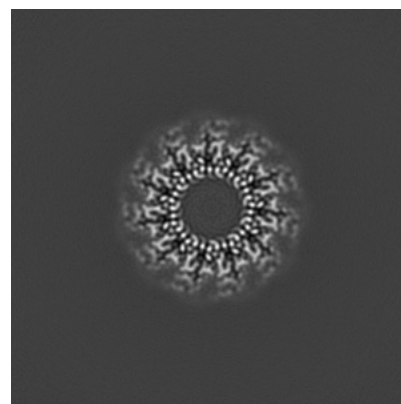
6.3.2 Raw map



X Index: 176



Y Index: 174

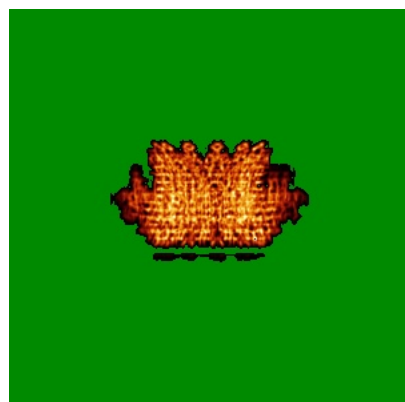


Z Index: 149

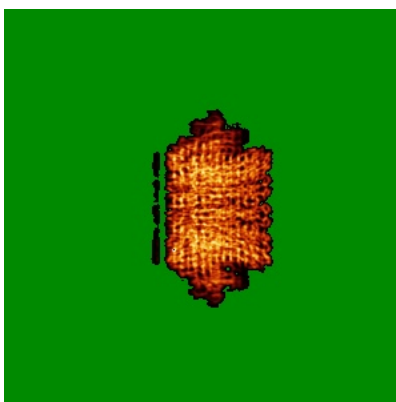
The images above show the largest variance slices of the map in three orthogonal directions.

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

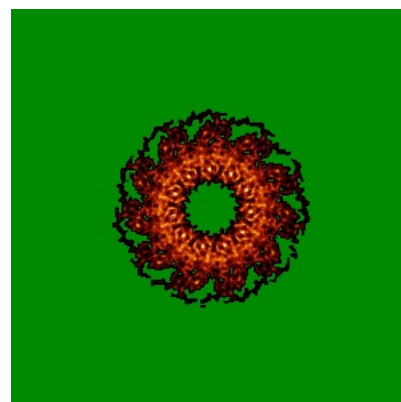
6.4.1 Primary map



X

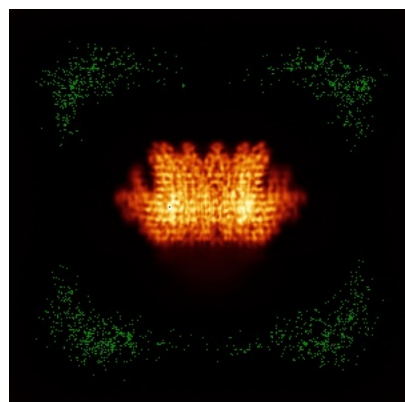


Y

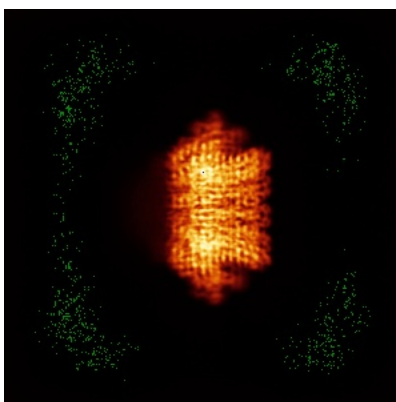


Z

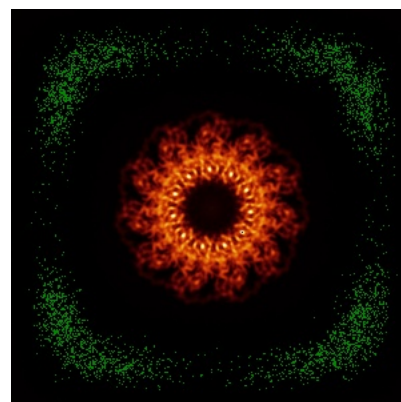
6.4.2 Raw map



X



Y

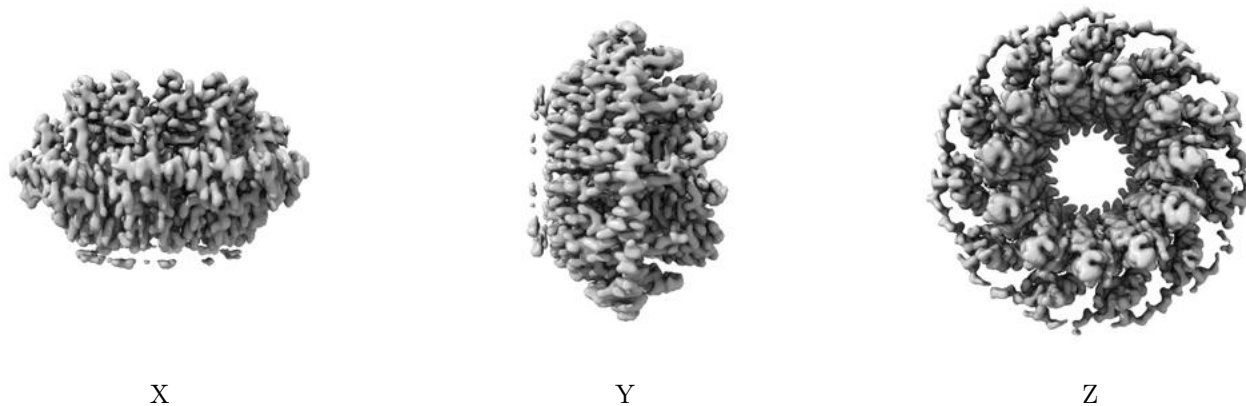


Z

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.

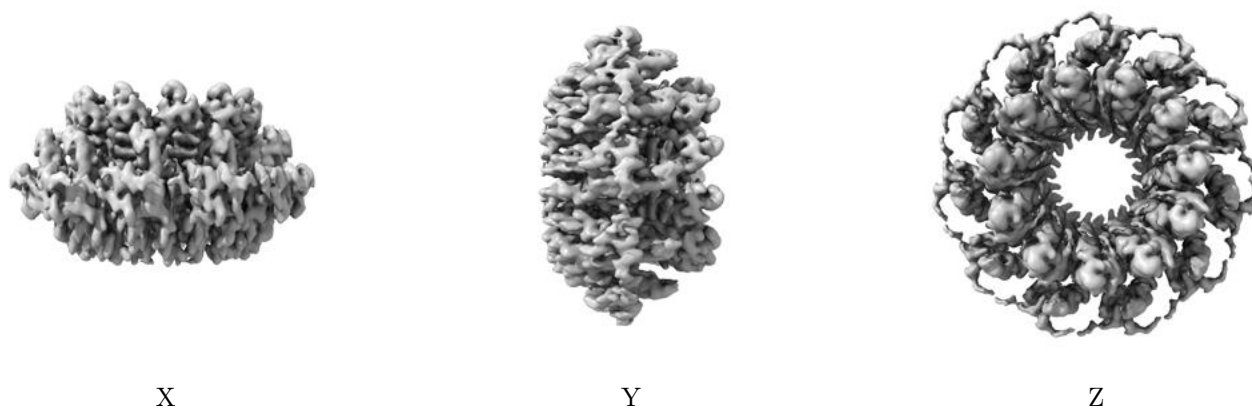
6.5 Orthogonal surface views [i](#)

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.

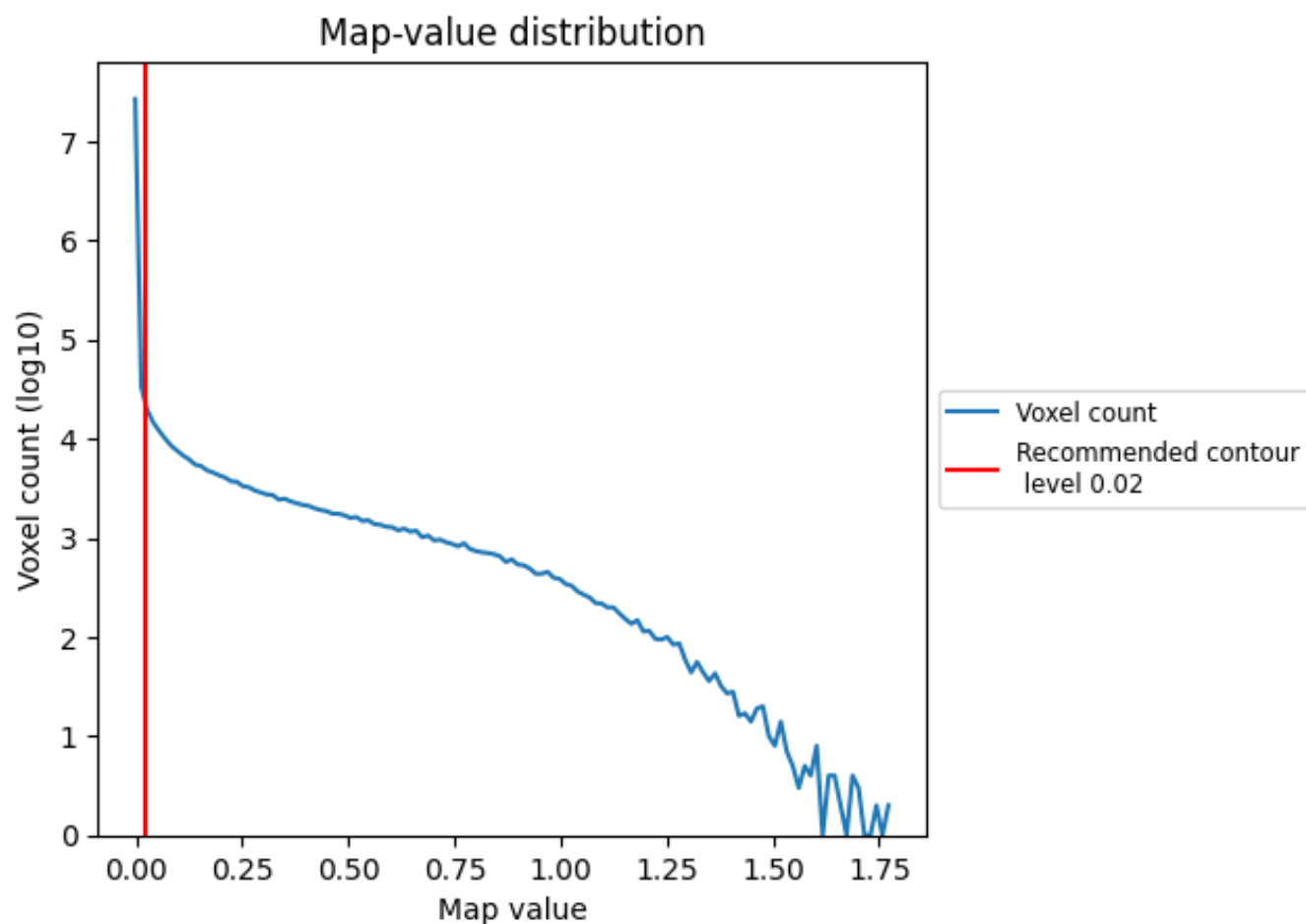
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

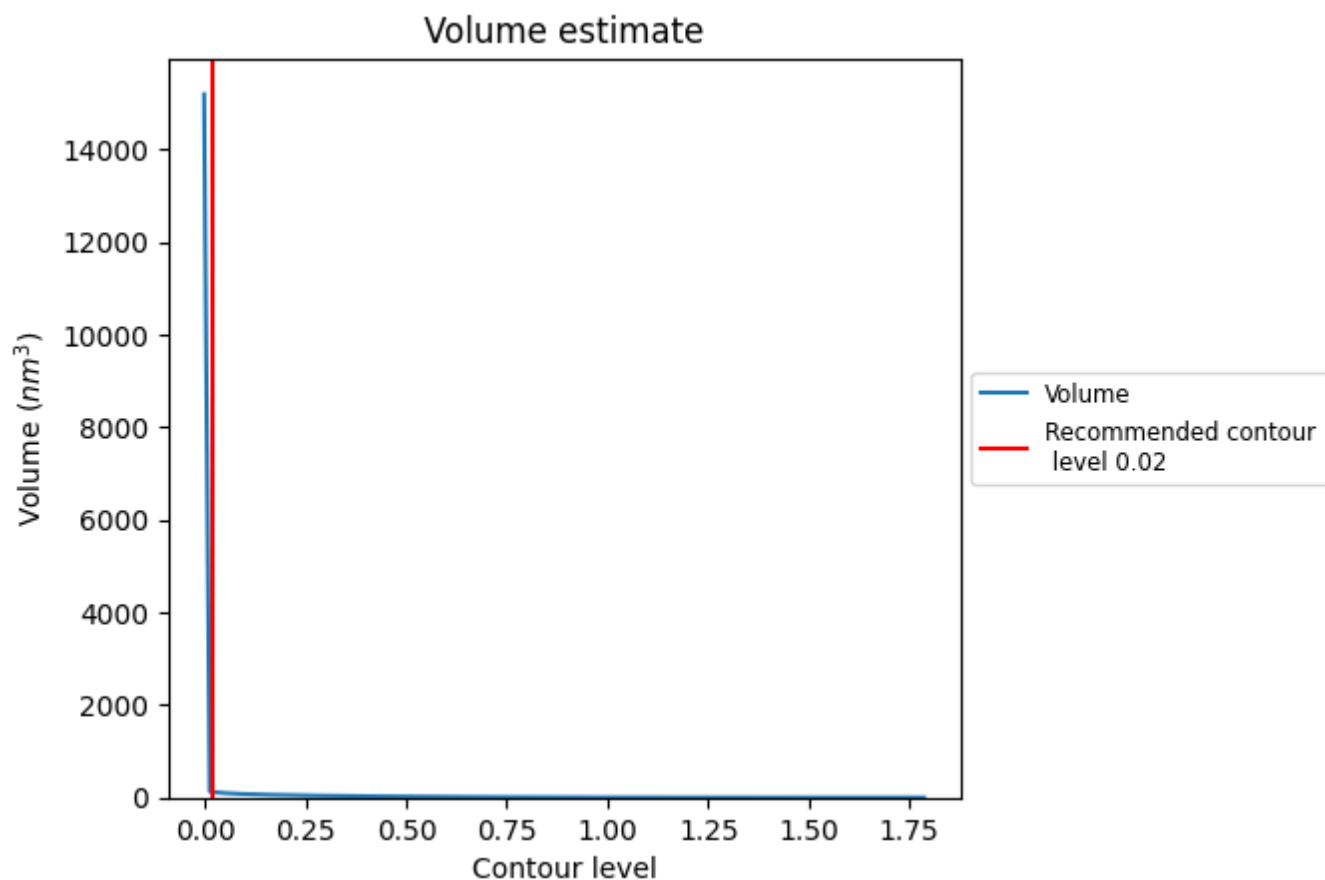
This section contains the results of statistical analysis of the map.

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.

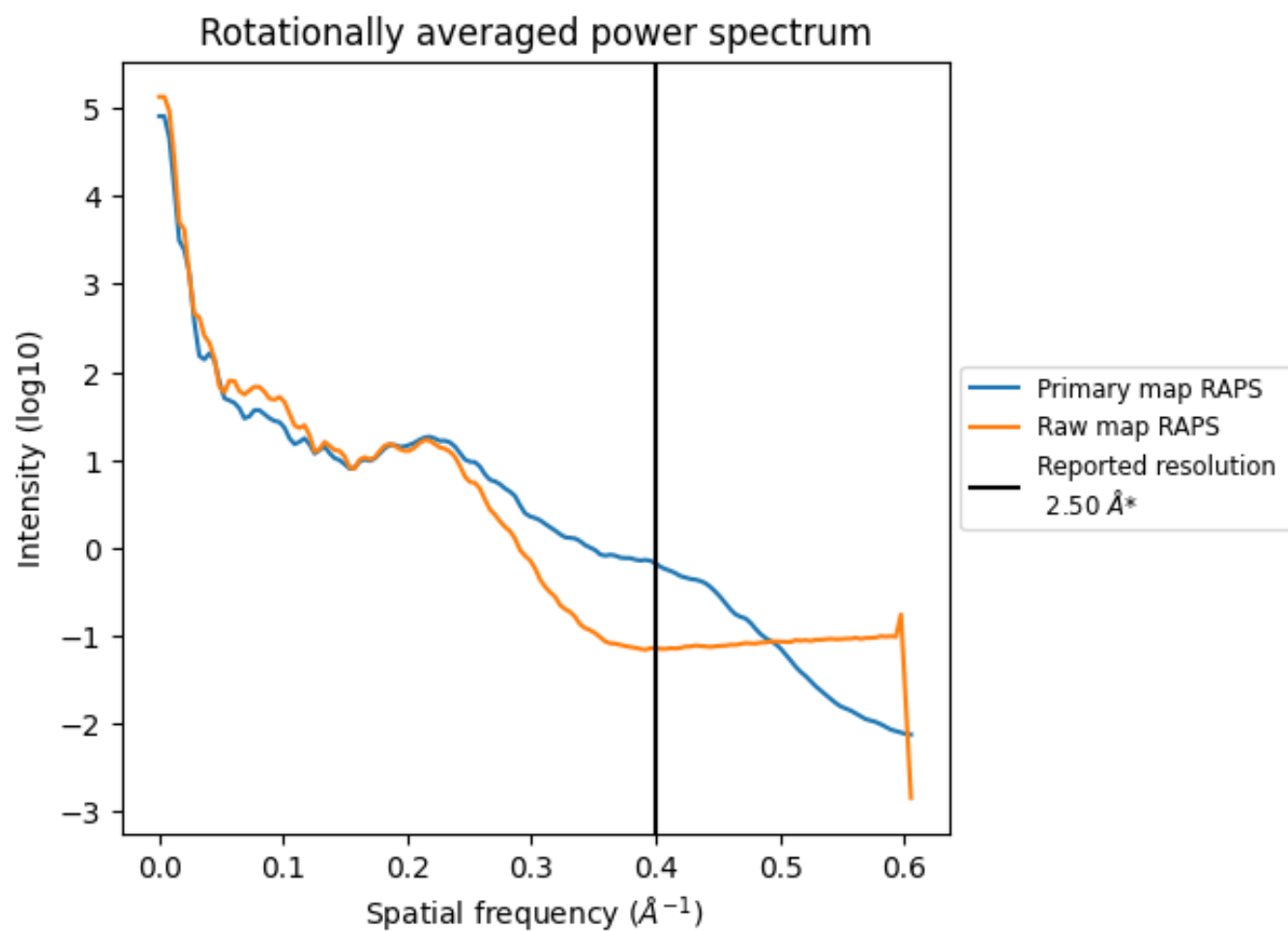
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 122 nm³; 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 ⓘ

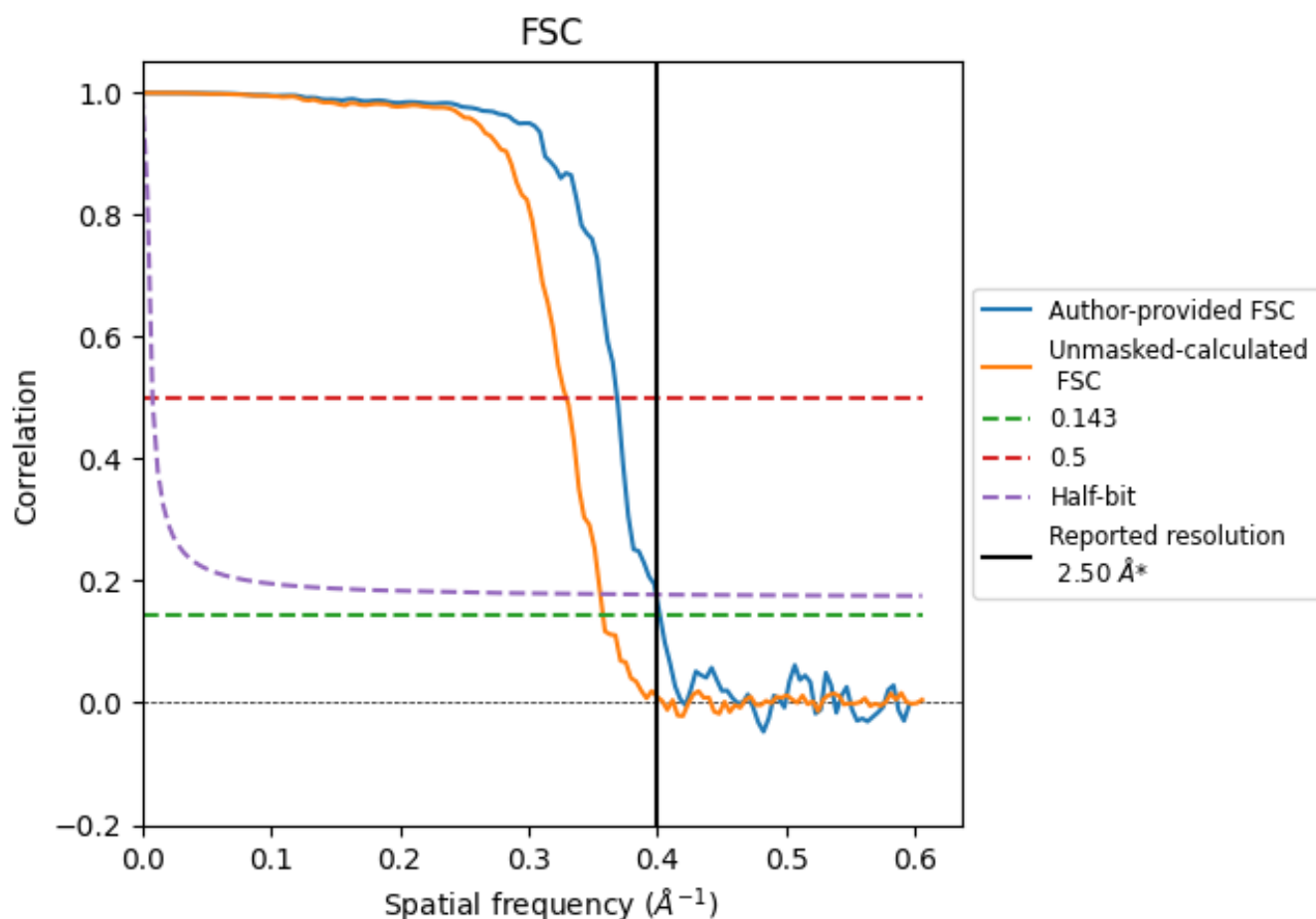


*Reported resolution corresponds to spatial frequency of $0.400 \text{ \AA}^{-1}$

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

8.2 Resolution estimates [i](#)

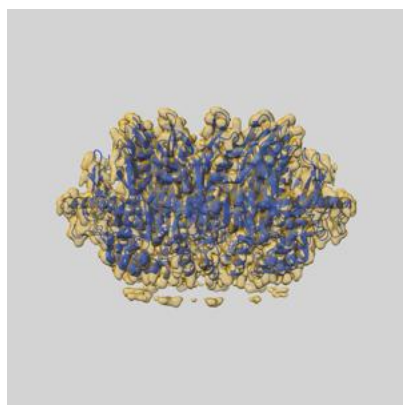
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.49	2.71	2.51
Unmasked-calculated*	2.79	3.04	2.81

*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 %

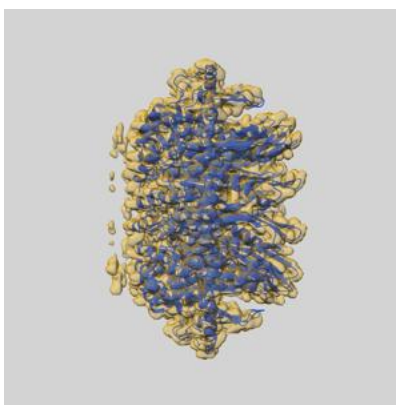
9 Map-model fit [i](#)

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](#).

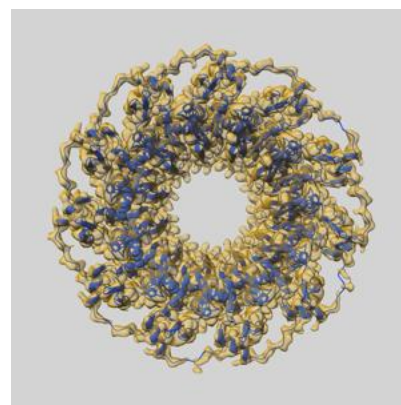
9.1 Map-model overlay [i](#)



X



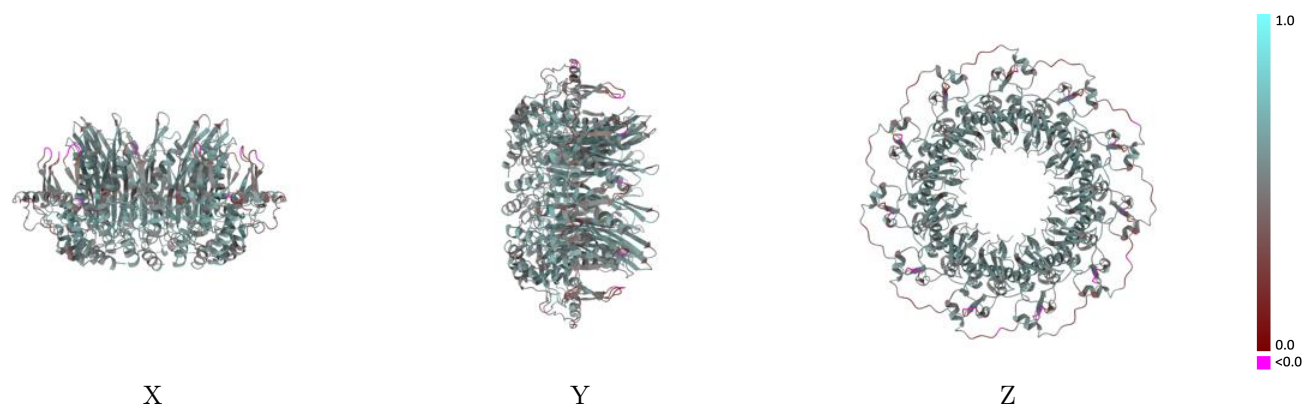
Y



Z

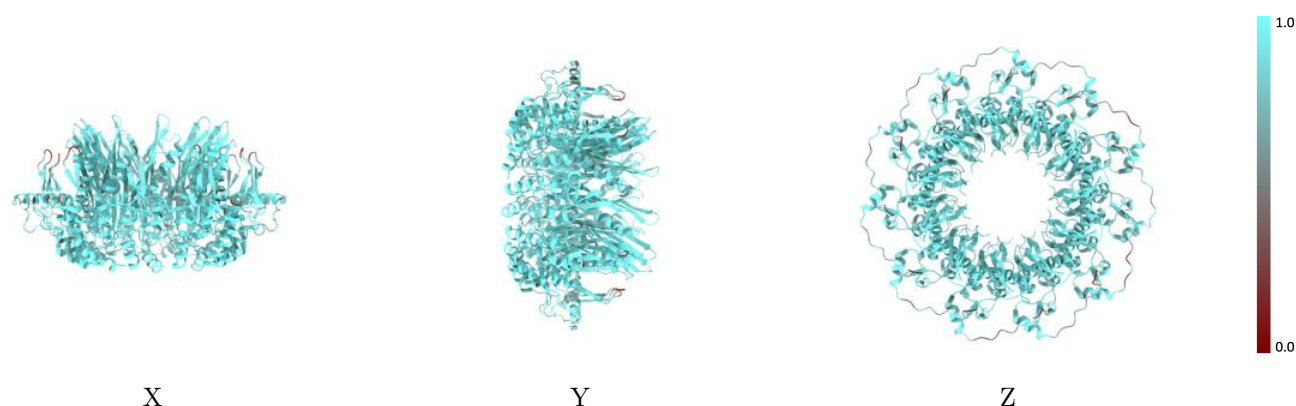
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



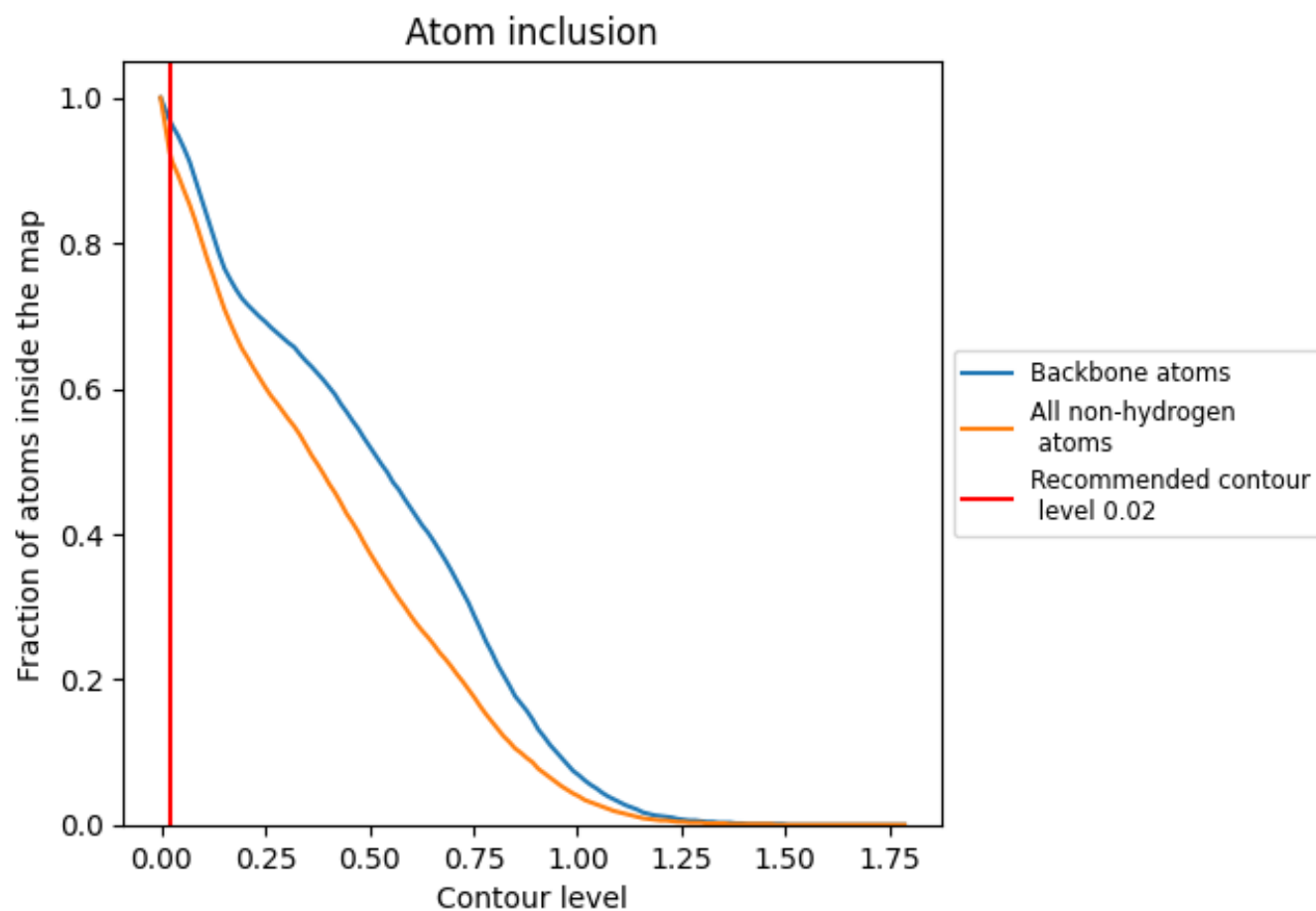
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	0.9250	0.5340
A	0.9270	0.5330
B	0.9250	0.5290
C	0.9310	0.5390
D	0.9280	0.5320
E	0.9400	0.5440
F	0.9290	0.5350
G	0.9170	0.5290
H	0.9220	0.5340
I	0.9140	0.5290
J	0.9310	0.5320
K	0.9050	0.5330

1.0

0.0

<0.0