



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2025 – 10:16 am BST

PDB ID : 9R2M / pdb_00009r2m
EMDB ID : EMD-53532
Title : p53 bound to nucleosome at position SHL+5.9 (non-crosslinked sample, composite map)
Authors : Chakraborty, D.; Kater, L.; Kempf, G.; Cavadini, S.; Thoma, N.H.
Deposited on : 2025-04-30
Resolution : 3.50 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.44

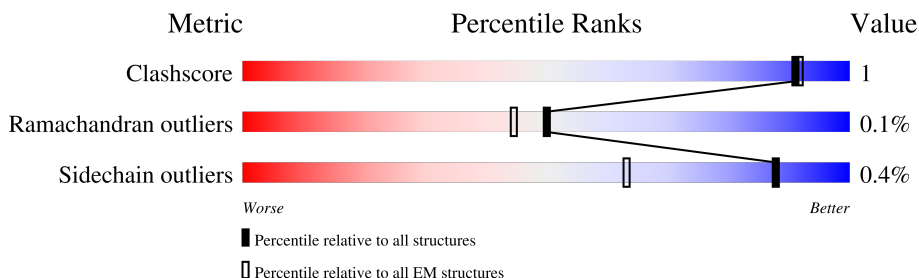
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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 ≥ 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	139	
1	E	139	
2	B	106	
2	F	106	
3	C	133	
3	G	133	
4	D	128	
4	H	128	

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Mol	Chain	Length	Quality of chain
5	I	153	 91% • 7%
6	J	153	 88% 6% 7%
7	K	417	 13% 47% • 52%
7	L	417	 6% 47% • 52%
7	M	417	 • 47% • 52%
7	N	417	 5% 47% • 52%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15971 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 Histone H3.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	97	Total	C	N	O	S	0	0
			801	505	155	137	4		
1	E	96	Total	C	N	O	S	0	0
			790	499	151	136	4		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P68431
A	-1	SER	-	expression tag	UNP P68431
A	0	HIS	-	expression tag	UNP P68431
E	-2	GLY	-	expression tag	UNP P68431
E	-1	SER	-	expression tag	UNP P68431
E	0	HIS	-	expression tag	UNP P68431

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	82	Total	C	N	O	S	0	0
			653	412	127	113	1		
2	F	82	Total	C	N	O	S	0	0
			653	412	127	113	1		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP P62805
B	-1	SER	-	expression tag	UNP P62805
B	0	HIS	-	expression tag	UNP P62805
F	-2	GLY	-	expression tag	UNP P62805
F	-1	SER	-	expression tag	UNP P62805
F	0	HIS	-	expression tag	UNP P62805

- Molecule 3 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	108	Total	C	N	O	0	0
			835	526	165	144		
3	G	108	Total	C	N	O	0	0
			835	526	165	144		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP P04908
C	-1	SER	-	expression tag	UNP P04908
C	0	HIS	-	expression tag	UNP P04908
G	-2	GLY	-	expression tag	UNP P04908
G	-1	SER	-	expression tag	UNP P04908
G	0	HIS	-	expression tag	UNP P04908

- Molecule 4 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	97	Total	C	N	O	S	0	0
			765	480	142	141	2		
4	H	91	Total	C	N	O	S	0	0
			708	447	125	134	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	GLY	-	expression tag	UNP P06899
D	-1	SER	-	expression tag	UNP P06899
D	0	HIS	-	expression tag	UNP P06899
H	-2	GLY	-	expression tag	UNP P06899
H	-1	SER	-	expression tag	UNP P06899
H	0	HIS	-	expression tag	UNP P06899

- Molecule 5 is a DNA chain called DNA-for.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	143	Total	C	N	O	P	0	0
			2912	1381	530	858	143		

- Molecule 6 is a DNA chain called DNA-rev.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	143	Total	C	N	O	P	0	0
			2951	1394	556	858	143		

- Molecule 7 is a protein called Cellular tumor antigen p53.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	200	Total	C	N	O		0	0
			1017	617	200	200			
7	L	200	Total	C	N	O		0	0
			1017	617	200	200			
7	M	200	Total	C	N	O		0	0
			1017	617	200	200			
7	N	200	Total	C	N	O		0	0
			1017	617	200	200			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-23	MET	-	initiating methionine	UNP P04637
K	-22	ASP	-	expression tag	UNP P04637
K	-21	TRP	-	expression tag	UNP P04637
K	-20	SER	-	expression tag	UNP P04637
K	-19	HIS	-	expression tag	UNP P04637
K	-18	PRO	-	expression tag	UNP P04637
K	-17	GLN	-	expression tag	UNP P04637
K	-16	PHE	-	expression tag	UNP P04637
K	-15	GLU	-	expression tag	UNP P04637
K	-14	LYS	-	expression tag	UNP P04637
K	-13	SER	-	expression tag	UNP P04637
K	-12	ALA	-	expression tag	UNP P04637
K	-11	VAL	-	expression tag	UNP P04637
K	-10	ASP	-	expression tag	UNP P04637
K	-9	GLU	-	expression tag	UNP P04637
K	-8	ASN	-	expression tag	UNP P04637
K	-7	LEU	-	expression tag	UNP P04637
K	-6	TYR	-	expression tag	UNP P04637
K	-5	PHE	-	expression tag	UNP P04637
K	-4	GLN	-	expression tag	UNP P04637
K	-3	GLY	-	expression tag	UNP P04637
K	-2	GLY	-	expression tag	UNP P04637
K	-1	GLY	-	expression tag	UNP P04637
K	0	ARG	-	expression tag	UNP P04637
L	-23	MET	-	initiating methionine	UNP P04637

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-22	ASP	-	expression tag	UNP P04637
L	-21	TRP	-	expression tag	UNP P04637
L	-20	SER	-	expression tag	UNP P04637
L	-19	HIS	-	expression tag	UNP P04637
L	-18	PRO	-	expression tag	UNP P04637
L	-17	GLN	-	expression tag	UNP P04637
L	-16	PHE	-	expression tag	UNP P04637
L	-15	GLU	-	expression tag	UNP P04637
L	-14	LYS	-	expression tag	UNP P04637
L	-13	SER	-	expression tag	UNP P04637
L	-12	ALA	-	expression tag	UNP P04637
L	-11	VAL	-	expression tag	UNP P04637
L	-10	ASP	-	expression tag	UNP P04637
L	-9	GLU	-	expression tag	UNP P04637
L	-8	ASN	-	expression tag	UNP P04637
L	-7	LEU	-	expression tag	UNP P04637
L	-6	TYR	-	expression tag	UNP P04637
L	-5	PHE	-	expression tag	UNP P04637
L	-4	GLN	-	expression tag	UNP P04637
L	-3	GLY	-	expression tag	UNP P04637
L	-2	GLY	-	expression tag	UNP P04637
L	-1	GLY	-	expression tag	UNP P04637
L	0	ARG	-	expression tag	UNP P04637
M	-23	MET	-	initiating methionine	UNP P04637
M	-22	ASP	-	expression tag	UNP P04637
M	-21	TRP	-	expression tag	UNP P04637
M	-20	SER	-	expression tag	UNP P04637
M	-19	HIS	-	expression tag	UNP P04637
M	-18	PRO	-	expression tag	UNP P04637
M	-17	GLN	-	expression tag	UNP P04637
M	-16	PHE	-	expression tag	UNP P04637
M	-15	GLU	-	expression tag	UNP P04637
M	-14	LYS	-	expression tag	UNP P04637
M	-13	SER	-	expression tag	UNP P04637
M	-12	ALA	-	expression tag	UNP P04637
M	-11	VAL	-	expression tag	UNP P04637
M	-10	ASP	-	expression tag	UNP P04637
M	-9	GLU	-	expression tag	UNP P04637
M	-8	ASN	-	expression tag	UNP P04637
M	-7	LEU	-	expression tag	UNP P04637
M	-6	TYR	-	expression tag	UNP P04637
M	-5	PHE	-	expression tag	UNP P04637

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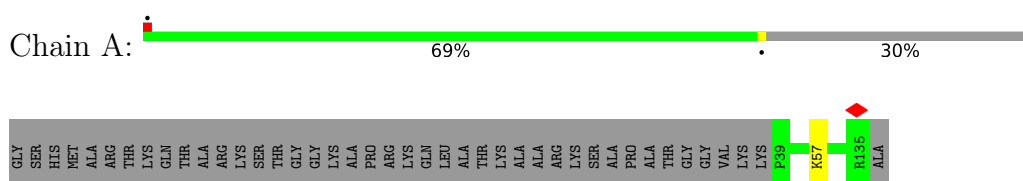
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Chain	Residue	Modelled	Actual	Comment	Reference
M	-4	GLN	-	expression tag	UNP P04637
M	-3	GLY	-	expression tag	UNP P04637
M	-2	GLY	-	expression tag	UNP P04637
M	-1	GLY	-	expression tag	UNP P04637
M	0	ARG	-	expression tag	UNP P04637
N	-23	MET	-	initiating methionine	UNP P04637
N	-22	ASP	-	expression tag	UNP P04637
N	-21	TRP	-	expression tag	UNP P04637
N	-20	SER	-	expression tag	UNP P04637
N	-19	HIS	-	expression tag	UNP P04637
N	-18	PRO	-	expression tag	UNP P04637
N	-17	GLN	-	expression tag	UNP P04637
N	-16	PHE	-	expression tag	UNP P04637
N	-15	GLU	-	expression tag	UNP P04637
N	-14	LYS	-	expression tag	UNP P04637
N	-13	SER	-	expression tag	UNP P04637
N	-12	ALA	-	expression tag	UNP P04637
N	-11	VAL	-	expression tag	UNP P04637
N	-10	ASP	-	expression tag	UNP P04637
N	-9	GLU	-	expression tag	UNP P04637
N	-8	ASN	-	expression tag	UNP P04637
N	-7	LEU	-	expression tag	UNP P04637
N	-6	TYR	-	expression tag	UNP P04637
N	-5	PHE	-	expression tag	UNP P04637
N	-4	GLN	-	expression tag	UNP P04637
N	-3	GLY	-	expression tag	UNP P04637
N	-2	GLY	-	expression tag	UNP P04637
N	-1	GLY	-	expression tag	UNP P04637
N	0	ARG	-	expression tag	UNP P04637

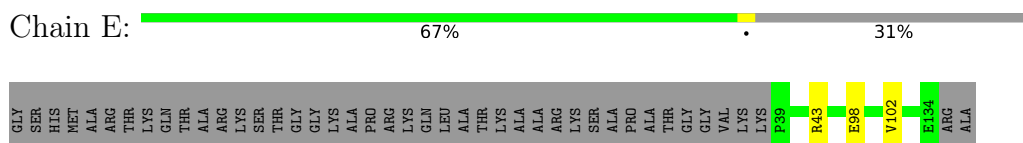
3 Residue-property plots [i](#)

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.

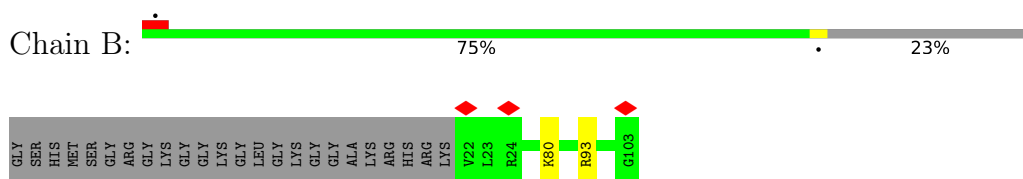
- Molecule 1: Histone H3.1



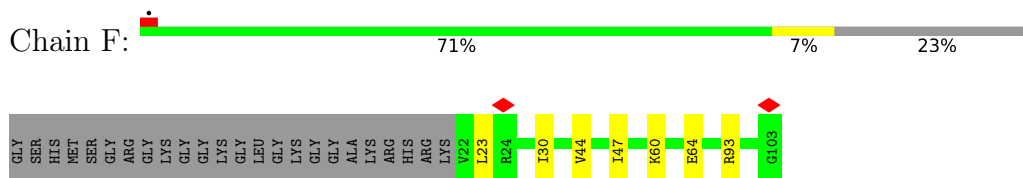
- Molecule 1: Histone H3.1



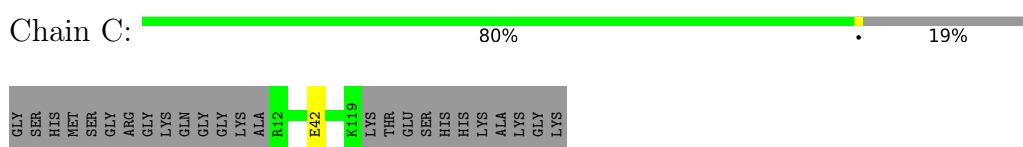
- Molecule 2: Histone H4



- Molecule 2: Histone H4



- Molecule 3: Histone H2A type 1-B/E



- Molecule 3: Histone H2A type 1-B/E

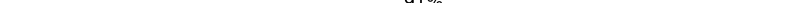
GLY	SER	HIS	MET	SER	GLY	ARG	GLY	LYS	GLN	GLY	GLY	LYS	ALA	R12	R82	E92	E93	K119	LYS	THR	GLU	SER	HIS	HIS	LYS	ALA	LYS	GLY
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- Chain D:  70% 24%

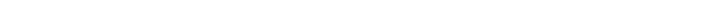
GLY	SER	HIS	MET	PRO	GLU	PRO	ALA	SER	SER	ALA	ALA	ALA	PRO	LYS	GLY	SER	LYS	LYS	ALA	ALA	VAL	THR	LYS	ALA	GLN	LYS	LYS	ASP	GLY	LYS	K29	R30	R31	I40	E94	I95	V99	R100	L101	A125
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- Chain H:  66% 5% 29%

GLY	SER	HIS	THR	PRO	GLU	PRO	ALA	LYS	SER	ALA	PRO	ALA	PRO	LYS	LYS	GLY	SER	LYS	ALA	VAL	THR	LYS	ALA	GLN	LYS	LYS	ASP	GLY	LYS	LYS	ARG	LYS	ARG	SER	ARG	ARG	R35	E94	I95	V99	R100	L101	A108	V112	A125
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- Chain I:  91% • 7%

DA	DT	C-1	C18	G36	A48	C109	C141	DC	DC	DT	DG	DT	DG	DA	DT
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- Chain J:  88% 6% 7%

DA	DT	DC	DA	DC	DA	DA	DG	DG	G7	T24	T25	G38	G69	C99	G102	A111	G123	T129	G149	DA	DT
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- Chain K:  13% 47% 52%

MET	ASP	TRP	SER	HIS	PRO	GLN	PHE	GLY	LYS	SER	ALA	VAL	ASP	ASN	LEU	TYP	PHE	GLN	GLY	GLY	GLY	ARG	MET	GLU	GLU	PRO	GLN	SER	ASP	VAL	GLI	PRO	PRO	LEU	SER	SER	ASP	LEU	TRP	LYS	LEU	LEU	PRO	GLN	ASN	VAL	LEU	SER	PRO	LEU	PRO	LEU
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SER	GLN	ALA	MET	ASP	ASP	LEU	MET	LEU	SER	PRO	ASP	ASP	ILE	GLU	GLN	TRP	PHE	THR	GLU	ASP	PRO	PRO	GLY	PRO	ASP	GLU	ALA	ALA	PRO	ARG	MET	MET	PRO	GLU	ALA	ALA	PRO	PRO	VAL	ALA	PRO	ALA	ALA	PRO	ALA	ALA	ALA	PRO	THR	PRO	ALA	ALA	PRO	ALA	SER	TRP	P92	S95	S96	T97
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P98	S99	Q100	Q101	T102	Q103	Q104	G105	S106	Y107	K120	L145	P153	G154	V157	R158	A159	M160	A161	I162	Y163	Q167	T170	E171	V172	S183	D184	S185	D186	H193	L194	G199	N200	L201	R202	V203	L206	D207	D208	R209	N210	T211	F212	R213	Y220	E221	P222	P223	E224
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V235	G226	S227	D228	C229	T230	S240	G244	R248	T251	L252	T253	S260	S261	G262	N263	L264	K291	LYS	GLY	GLY	PRO	HIS	HIS	HIS	GLU	LEU	PRO	PRO	GLY	SER	THR	LYS	ARG	ALA	LEU	PRO	PRO	ASN	ASN	THR	THR	SER	SER	SER	PRO	PRO	GLN	GLN	LYS	LYS	LYS	LEU	LEU	ASP	GLY	GLU
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[illegible]

- Molecule 7: Cellular tumor antigen p53

[illegible]

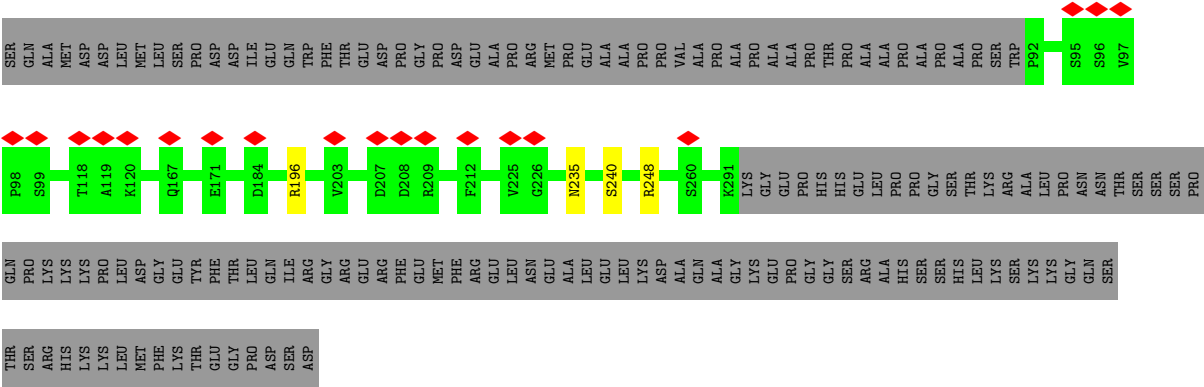
- Molecule 7: Cellular tumor antigen p53

[illegible]

- Molecule 7: Cellular tumor antigen p53



NET	ASP	TRP	SER	HIS	PRO	GLN	PHE	GLU	GLY	LYS	SER	ALA	VAL	ASP	GLU	ASN	LEU	TYR	PHE	GLN	GLY	GLY	GLY	ARG	NET	GLU	GLU	PRO	GLN	SER	ASP	PRO	SER	VAL	GLU	PRO	PRO	LEU	SER	SER	GLN	GLU	THR	PHE	SER	ASP	LEU	TRP	LYS	LEU	LEU	PRO	PRO	ASN	ASN	VAL	LEU	LEU	SER	PRO	PRO	LEU	PRO
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	163724	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.974	Depositor
Minimum map value	-0.295	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.263	Depositor
Map size (Å)	432.65283, 432.65283, 432.65283	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1267, 1.1267, 1.1267	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	0.08	0/813	0.25	0/1090
1	E	0.08	0/802	0.25	0/1076
2	B	0.08	0/660	0.23	0/883
2	F	0.09	0/660	0.26	0/883
3	C	0.09	0/845	0.26	0/1139
3	G	0.08	0/845	0.25	0/1139
4	D	0.08	0/776	0.27	0/1040
4	H	0.07	0/719	0.24	0/968
5	I	0.17	0/3262	0.41	0/5027
6	J	0.17	0/3314	0.40	0/5118
7	K	0.14	0/1031	0.33	0/1445
7	L	0.14	0/1031	0.35	0/1445
7	M	0.13	0/1031	0.35	0/1445
7	N	0.13	0/1031	0.33	0/1445
All	All	0.14	0/16820	0.35	0/24143

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	801	0	839	1	0
1	E	790	0	826	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	653	0	696	2	0
2	F	653	0	696	5	0
3	C	835	0	897	1	0
3	G	835	0	897	3	0
4	D	765	0	797	9	0
4	H	708	0	727	4	0
5	I	2912	0	1603	4	0
6	J	2951	0	1603	8	0
7	K	1017	0	509	2	0
7	L	1017	0	509	2	0
7	M	1017	0	509	2	0
7	N	1017	0	509	2	0
All	All	15971	0	11617	37	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 1.

The worst 5 of 37 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:D:30:ARG:HD3	4:D:30:ARG:H	1.38	0.89
5:I:18:DC:N4	6:J:129:DT:O4	2.20	0.75
4:D:31:LYS:HD3	4:D:31:LYS:H	1.56	0.70
4:D:30:ARG:HD3	4:D:30:ARG:N	2.08	0.67
4:H:95:ILE:O	4:H:99:VAL:HG23	1.98	0.64

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	95/139 (68%)	94 (99%)	1 (1%)	0	100	100
1	E	94/139 (68%)	90 (96%)	4 (4%)	0	100	100
2	B	80/106 (76%)	77 (96%)	3 (4%)	0	100	100
2	F	80/106 (76%)	76 (95%)	3 (4%)	1 (1%)	10	41
3	C	106/133 (80%)	106 (100%)	0	0	100	100
3	G	106/133 (80%)	105 (99%)	1 (1%)	0	100	100
4	D	95/128 (74%)	94 (99%)	1 (1%)	0	100	100
4	H	89/128 (70%)	88 (99%)	1 (1%)	0	100	100
7	K	198/417 (48%)	188 (95%)	10 (5%)	0	100	100
7	L	198/417 (48%)	189 (96%)	9 (4%)	0	100	100
7	M	198/417 (48%)	189 (96%)	9 (4%)	0	100	100
7	N	198/417 (48%)	192 (97%)	6 (3%)	0	100	100
All	All	1537/2680 (57%)	1488 (97%)	48 (3%)	1 (0%)	50	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	30	ILE

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	85/113 (75%)	85 (100%)	0	100	100
1	E	84/113 (74%)	84 (100%)	0	100	100
2	B	67/81 (83%)	67 (100%)	0	100	100
2	F	67/81 (83%)	67 (100%)	0	100	100
3	C	85/102 (83%)	85 (100%)	0	100	100
3	G	85/102 (83%)	85 (100%)	0	100	100
4	D	83/106 (78%)	80 (96%)	3 (4%)	30	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H	77/106 (73%)	77 (100%)	0	100	100
7	K	15/366 (4%)	15 (100%)	0	100	100
7	L	15/366 (4%)	15 (100%)	0	100	100
7	M	15/366 (4%)	15 (100%)	0	100	100
7	N	15/366 (4%)	15 (100%)	0	100	100
All	All	693/2268 (31%)	690 (100%)	3 (0%)	88	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	30	ARG
4	D	31	LYS
4	D	40	ILE

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

Mol	Chain	Res	Type
2	B	76	HIS
3	G	25	GLN
3	G	32	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.

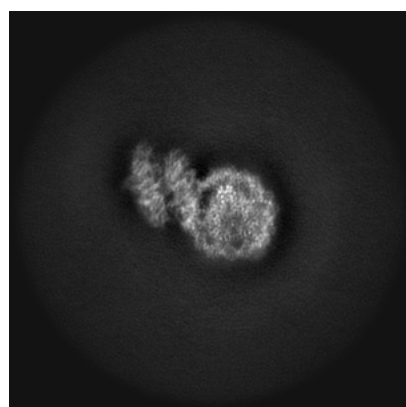
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53532. These allow visual inspection of the internal detail of the map and identification of artifacts.

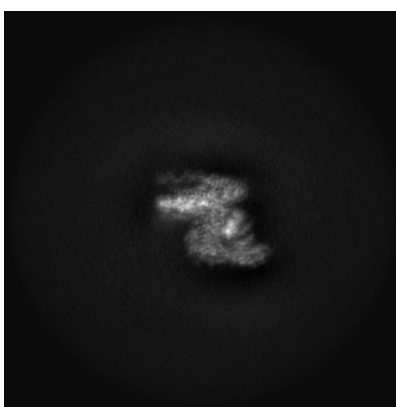
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

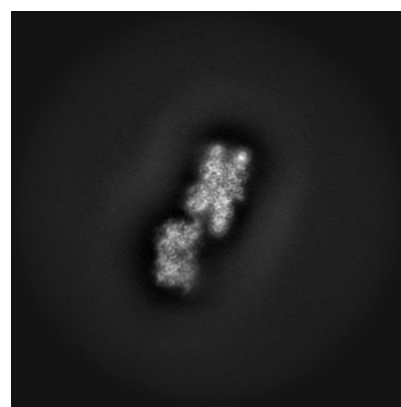
6.1.1 Primary map



X



Y

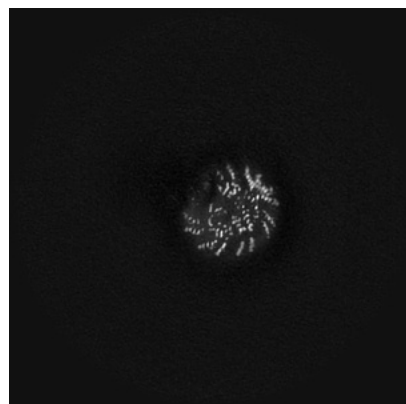


Z

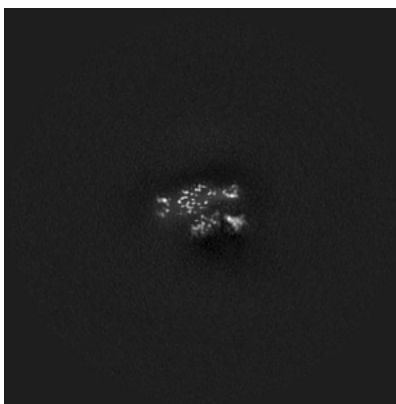
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

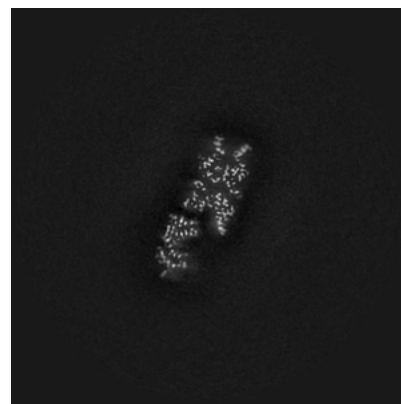
6.2.1 Primary map



X Index: 192



Y Index: 192

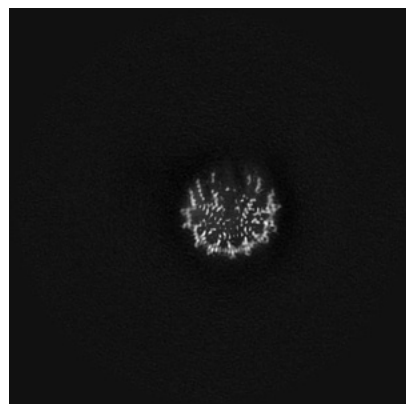


Z Index: 192

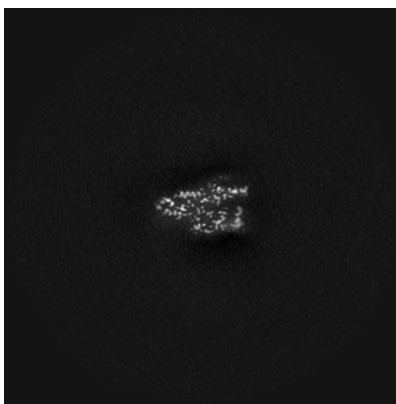
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

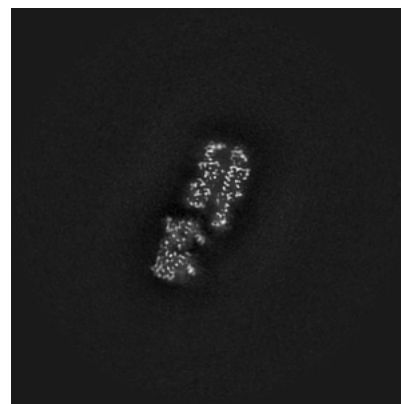
6.3.1 Primary map



X Index: 198



Y Index: 200

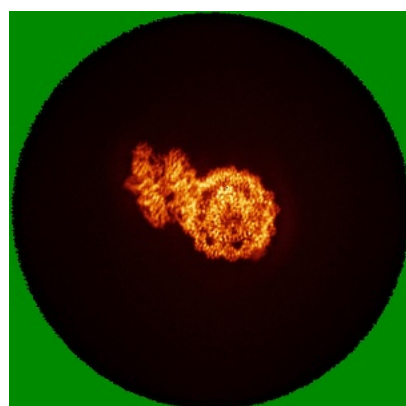


Z Index: 200

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

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

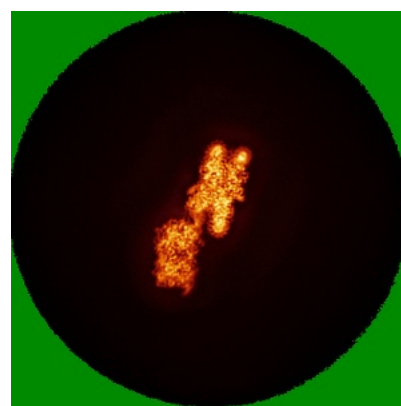
6.4.1 Primary map



X



Y

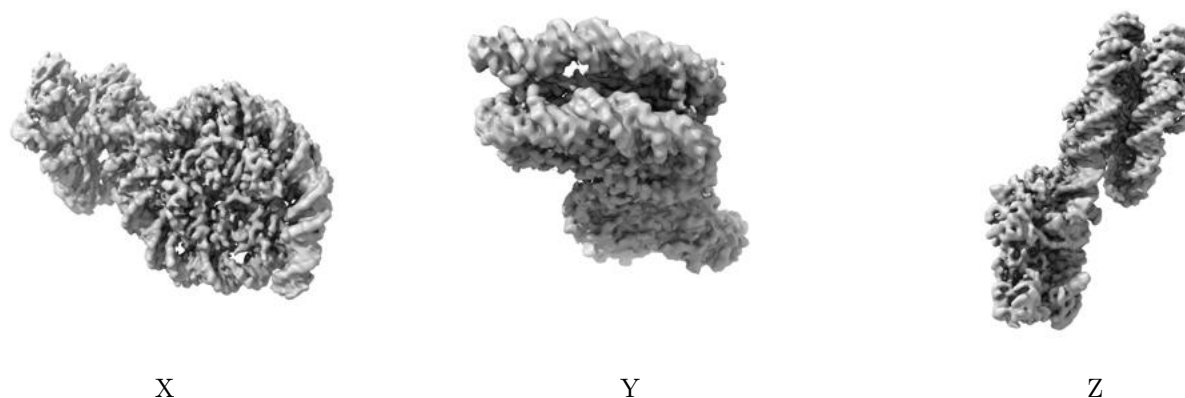


Z

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

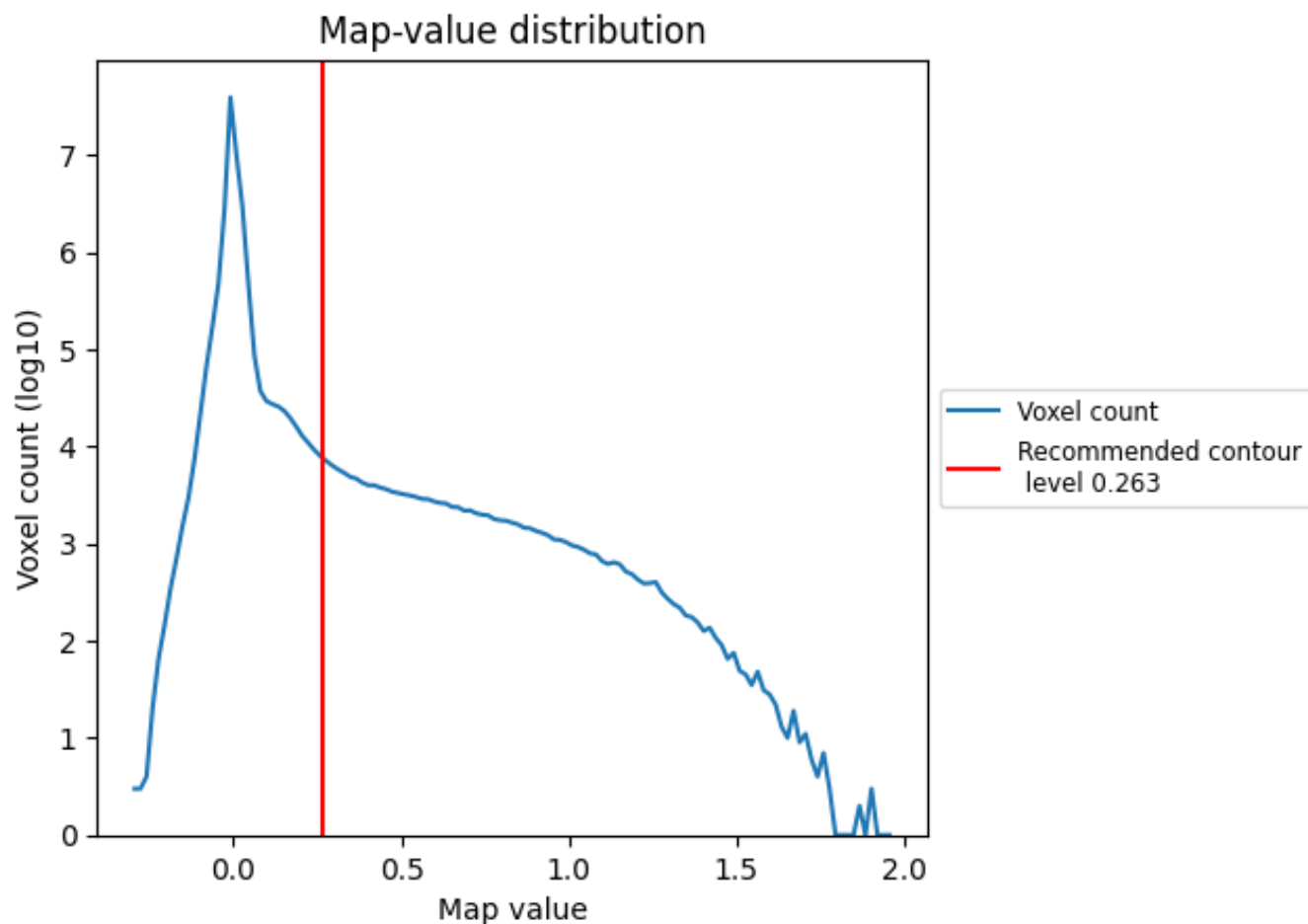
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

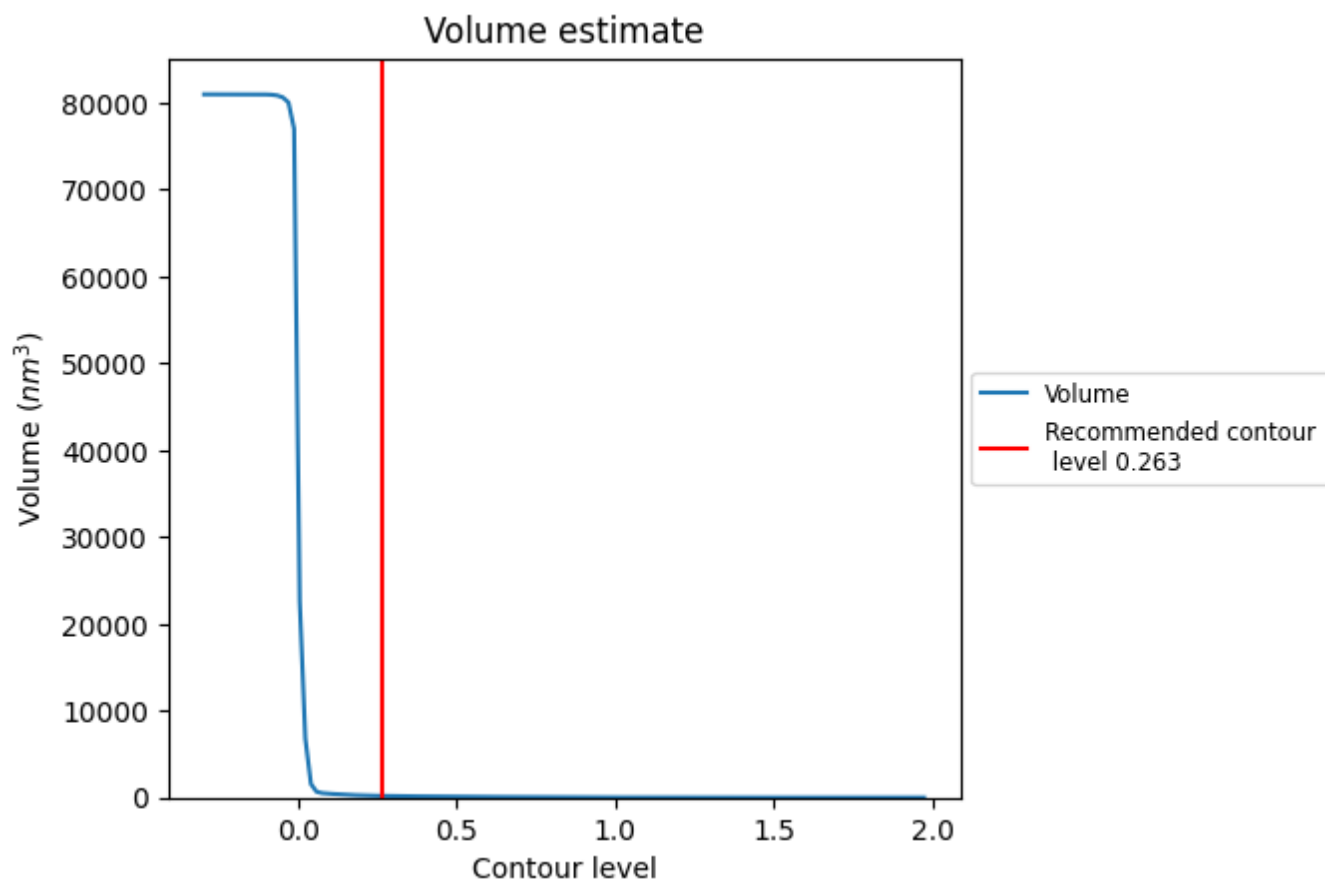
This section contains the results of statistical analysis of the map.

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.

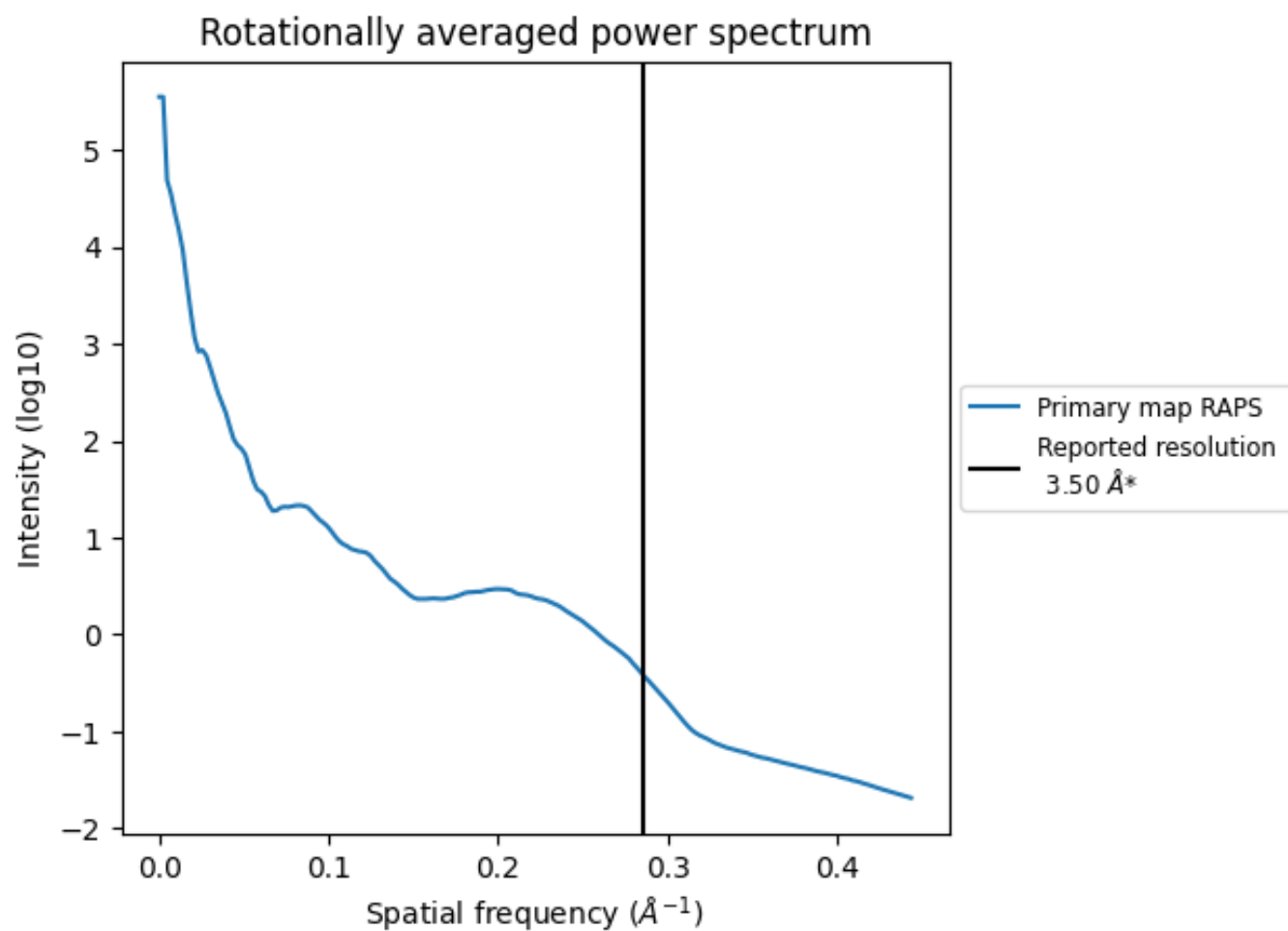
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 193 nm^3 ; this corresponds to an approximate mass of 175 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 0.286 Å⁻¹

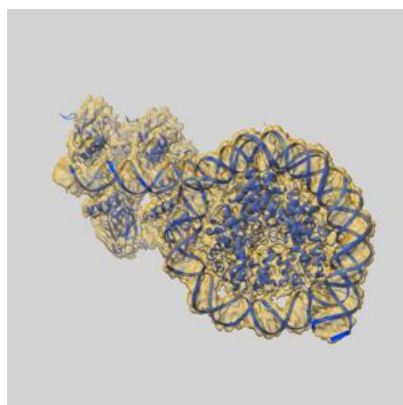
8 Fourier-Shell correlation

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

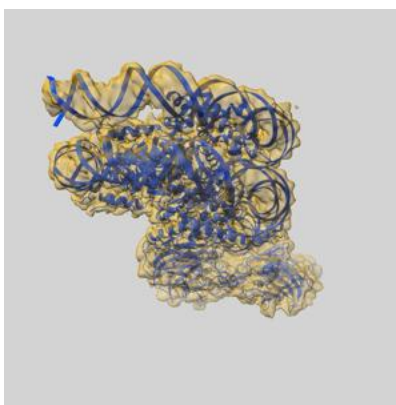
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53532 and PDB model 9R2M. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



X



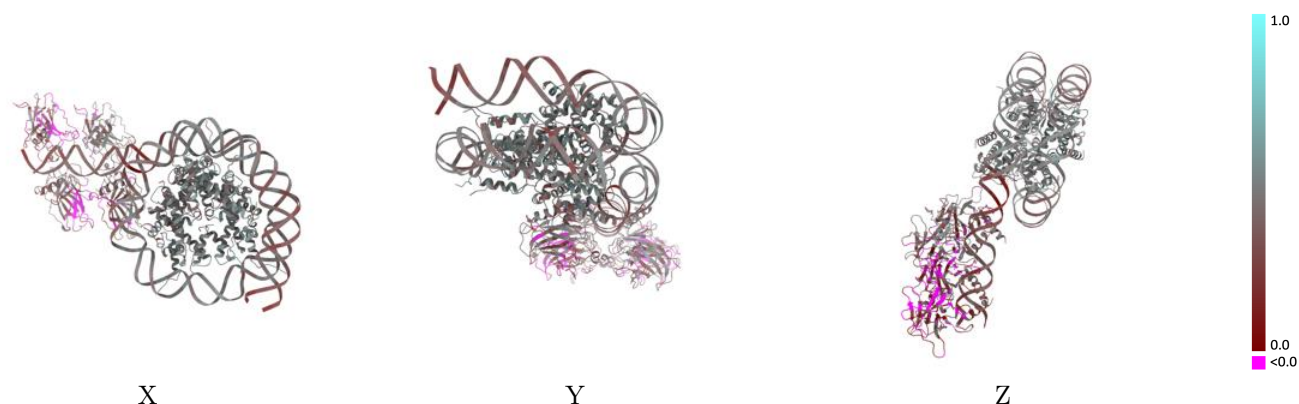
Y



Z

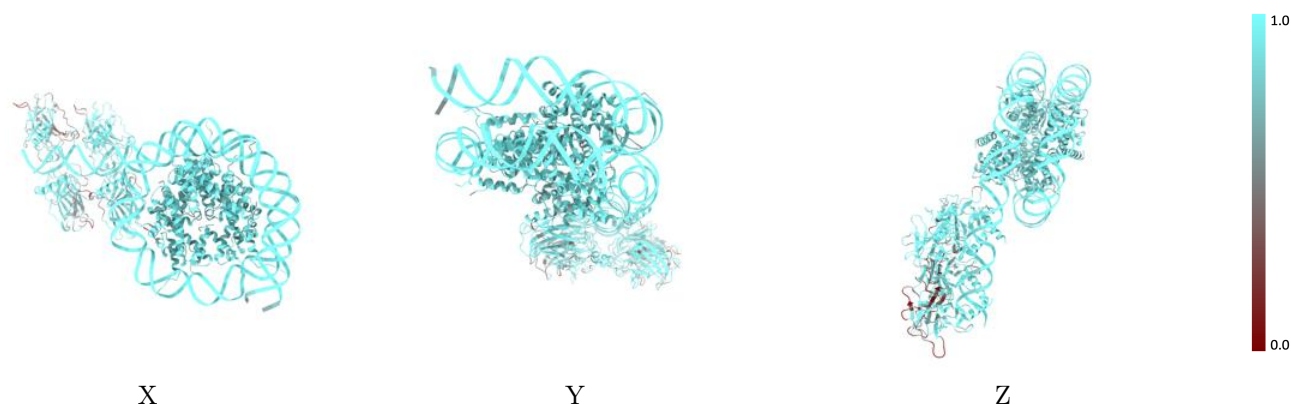
The images above show the 3D surface view of the map at the recommended contour level 0.263 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



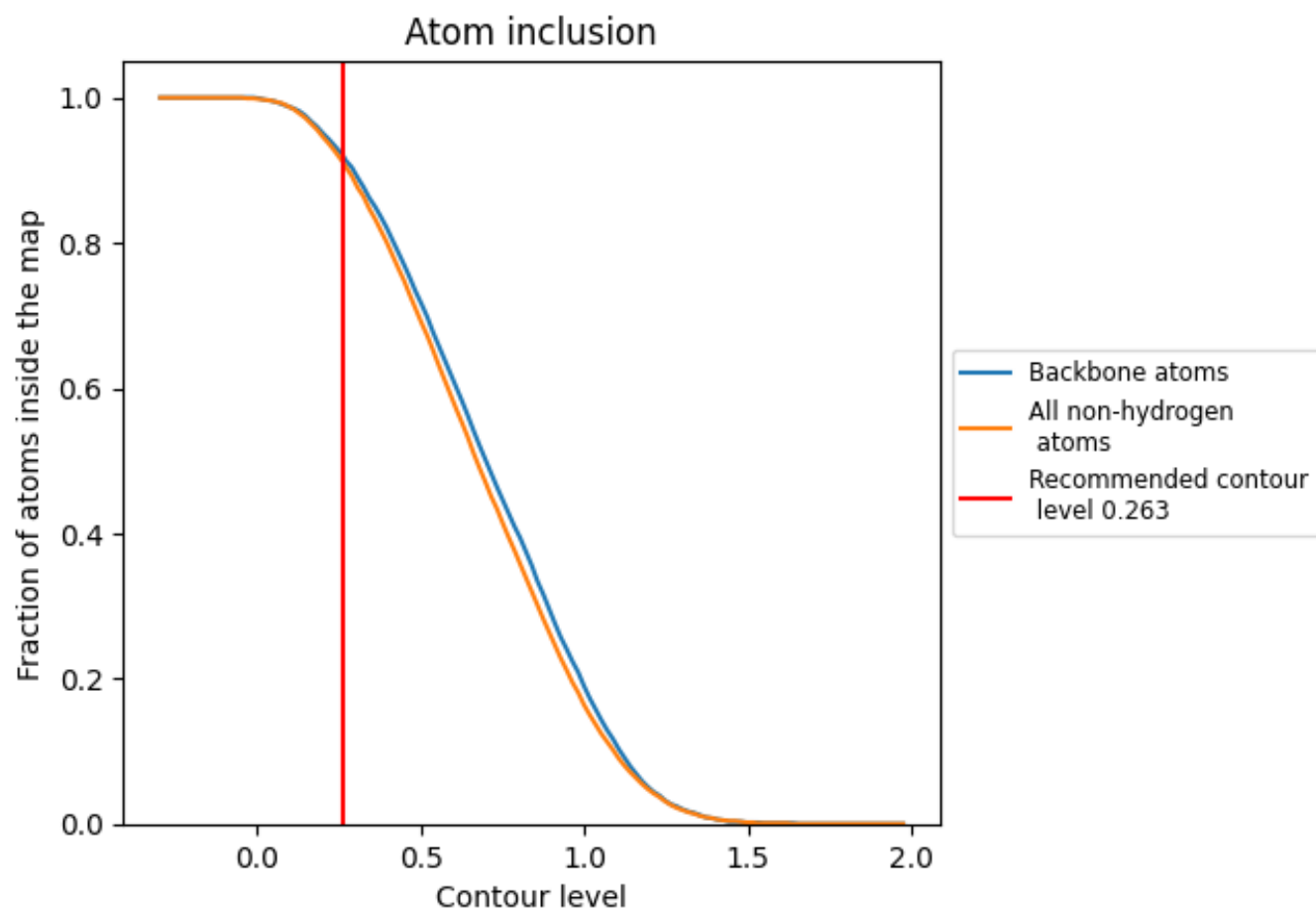
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.263).































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (0.263) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9110	 0.3900
A	 0.9350	 0.4830
B	 0.9230	 0.4820
C	 0.9230	 0.4940
D	 0.9070	 0.4590
E	 0.9320	 0.4920
F	 0.9070	 0.4910
G	 0.9010	 0.4710
H	 0.9060	 0.4650
I	 0.9690	 0.3970
J	 0.9740	 0.4040
K	 0.6580	 0.1350
L	 0.8220	 0.1980
M	 0.9220	 0.3560
N	 0.8560	 0.2760

