



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 02:22 AM UTC

PDB ID : 9DWK / pdb_00009dwk
EMDB ID : EMD-47253
Title : DNA Polymerase Beta bound to a nucleosome containing a 1-nt gap at SHL-3.5
Authors : Weaver, T.M.; Ryan, B.J.; Freudenthal, B.D.
Deposited on : 2024-10-09
Resolution : 4.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

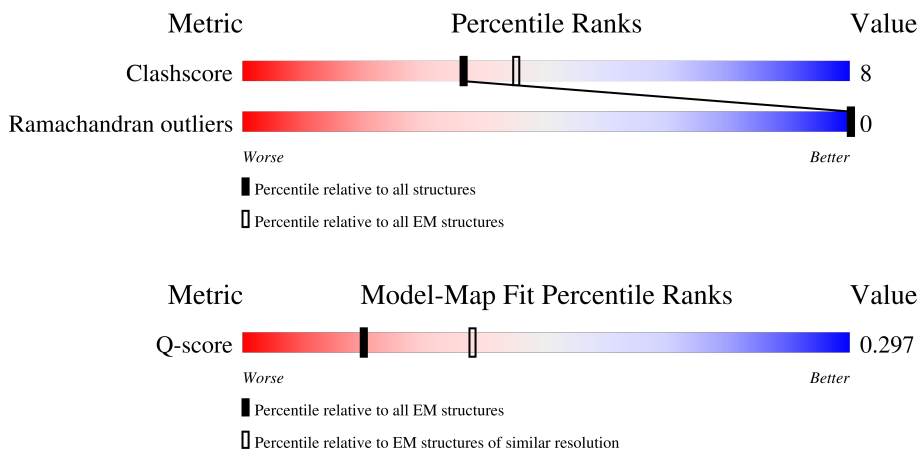
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	135	 67% 30%
1	E	135	 66% 5% 29%
2	B	102	 77% 22%
2	F	102	 78% 19%
3	C	129	 75% 6% 19%

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Mol	Chain	Length	Quality of chain
3	G	129	76% 21%
4	D	125	71% 26%
4	H	125	72% 26%
5	I	106	36% 63%
6	J	147	44% 41% 15%
7	K	40	8% 12% 35% 52%
8	L	335	48% 93%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10375 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 H3.2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	94	Total	C	N	O	0	0
			467	279	94	94		
1	E	96	Total	C	N	O	0	0
			477	285	96	96		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	110	ALA	CYS	engineered mutation	UNP Q71DI3
E	110	ALA	CYS	engineered mutation	UNP Q71DI3

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	80	Total	C	N	O	0	0
			392	232	80	80		
2	F	83	Total	C	N	O	0	0
			407	241	83	83		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	105	Total	C	N	O	0	0
			516	306	105	105		
3	G	102	Total	C	N	O	0	0
			501	297	102	102		

- Molecule 4 is a protein called Histone H2B type 1-C/E/F/G/I.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	93	Total	C	N	O	0	0
			460	274	93	93		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	H	92	Total	C	N	O	0	0
			455	271	92	92		

- Molecule 5 is a DNA chain called 601 I strand (damaged strand 1).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	105	Total	C	N	O	P	0	0
			2144	1016	394	629	105		

- Molecule 6 is a DNA chain called 601 J strand (non-damaged strand).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	125	Total	C	N	O	P	0	0
			2579	1218	486	750	125		

- Molecule 7 is a DNA chain called 601 K strand (damaged strand 2).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	19	Total	C	N	O	P	0	0
			384	182	67	116	19		

- Molecule 8 is a protein called DNA polymerase beta.

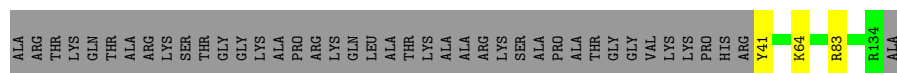
Mol	Chain	Residues	Atoms				AltConf	Trace
8	L	323	Total	C	N	O	0	0
			1593	947	323	323		

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 H3.2

Chain A:  67% 30%



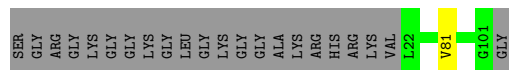
- Molecule 1: Histone H3.2

Chain E:  66% 5% 29%



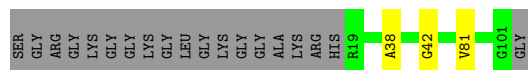
- Molecule 2: Histone H4

Chain B:  77% 22%



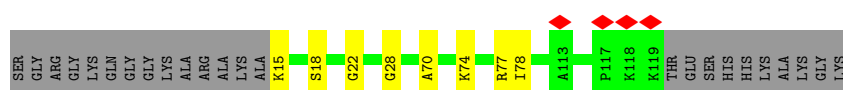
- Molecule 2: Histone H4

Chain F:  78% 19%



- Molecule 3: Histone H2A type 1

Chain C:  75% 6% 19%



- Molecule 3: Histone H2A type 1

SER
GLY
ARG
GLY
LYS
GLN
GLY
LYS
LYS
ALA
ALA
ARG
ALA
LYS
ALA
LYS
T16
R20
G44
I78
N110
A113
V114
L115
L116
P117
LYS
LYS
THR
GLU
GLU
SER
HIS
HIS
LYS
LYS
ALA
LYS
LYS
GLY
GLY

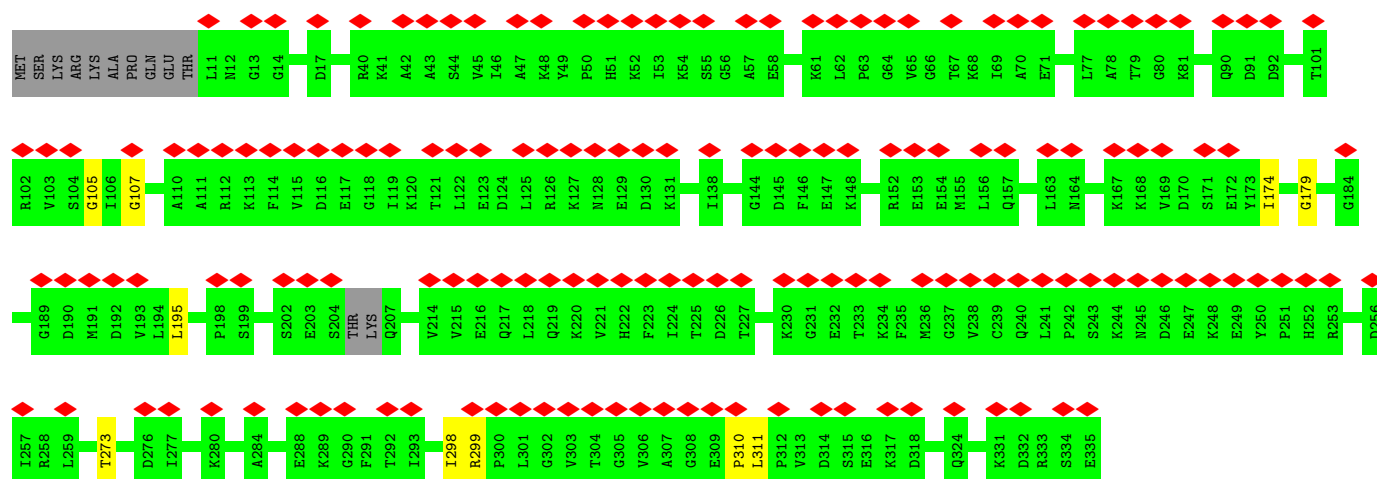
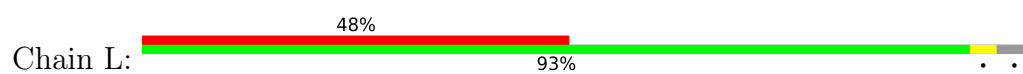
PRO	GLU	PRO	ALA	LYS	SER	ALA	PRO	ALA	PRO	LYS	GLY	SER	LYS	LYS	ALA	ALA	VAL	THR	LYS	ALA	GLN	LYS	LYS	ASP	GLY	LYS	ARG	ARG	LYS	ARG	S32	R33	R33	I54	A81	K85	R86	S87	I124	S124
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PRO	GLU	PRO	ALA	LYS	SER	ALA	PRO	ALA	ALA	PRO	LYS	LYS	GLY	SER	LYS	LYS	ALA	ALA	VAL	THR	LYS	ALA	GLN	LYS	LYS	ASP	GLY	LYS	LYS	ARG	LYS	ARG	ARG	SER	R33	G53	I89	S124	LYS
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[illegible]

C81	C82	T83	G84	C85	G86	T87	T88	A91	G92	G95	T96	T99	A100	G112	A113	T118	T119	G120	C123	G124	T128	C129	G130	G131	C132	A139	T140	G144	G145	A146	DT																			
DA	DT	DC	DG	DG	DA	DT	DT	DA	DA	DT	DT	DC	DT	DG	DA	DC	DC	C22	G23	T24	G25	C26	C27	T28	A36	G37	G38	T42	A43	A44	C49	T50	T51	G52	G53	C54	G55	A60	A61	A62	C63	G64	A71	C72	A73	G74	C75	G76	C77	G78

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15757	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 ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.044	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	236.4, 236.4, 236.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.394, 0.394, 0.394	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	0.17	0/466	0.35	0/649
1	E	0.20	0/476	0.38	0/663
2	B	0.20	0/391	0.33	0/541
2	F	0.19	0/406	0.30	0/562
3	C	0.18	0/515	0.30	0/714
3	G	0.18	0/500	0.33	0/693
4	D	0.18	0/459	0.33	0/638
4	H	0.18	0/454	0.31	0/631
5	I	0.31	0/2403	0.49	0/3704
6	J	0.29	0/2896	0.43	0/4472
7	K	0.48	1/428 (0.2%)	0.57	0/655
8	L	0.11	0/1591	0.26	0/2211
All	All	0.26	1/10985 (0.0%)	0.40	0/16133

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	108	DT	OP3-P	6.57	1.61	1.48

There are no bond angle outliers.

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	467	0	217	3	0
1	E	477	0	221	6	0
2	B	392	0	184	1	0
2	F	407	0	190	2	0
3	C	516	0	252	6	0
3	G	501	0	246	3	0
4	D	460	0	212	3	0
4	H	455	0	210	2	0
5	I	2144	0	1177	50	0
6	J	2579	0	1401	44	0
7	K	384	0	214	7	0
8	L	1593	0	704	6	0
All	All	10375	0	5228	116	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (116) 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)
7:K:117:DT:H4'	7:K:118:DC:OP1	1.90	0.72
1:E:83:ARG:O	2:F:81:VAL:N	2.23	0.69
5:I:50:DG:H2''	5:I:51:DC:H5''	1.76	0.67
6:J:27:DC:H2''	6:J:28:DT:C5	2.37	0.58
3:C:28:GLY:HA3	5:I:30:DA:H3'	1.85	0.58
6:J:91:DA:H2''	6:J:92:DG:H5''	1.86	0.58
1:A:41:TYR:N	6:J:84:DG:OP1	2.38	0.57
1:A:64:LYS:N	6:J:92:DG:OP2	2.38	0.56
1:E:47:ALA:N	5:I:83:DG:OP1	2.37	0.56
5:I:75:DT:H2'	5:I:76:DG:C8	2.41	0.56
5:I:103:DA:H2'	5:I:104:DT:C6	2.40	0.56
1:E:50:GLU:O	1:E:54:TYR:N	2.36	0.55
5:I:74:DC:H2'	5:I:75:DT:C6	2.41	0.55
6:J:119:DT:H2''	6:J:120:DG:C8	2.41	0.55
3:C:15:LYS:N	5:I:32:DT:OP1	2.40	0.54
5:I:17:DC:H2''	5:I:18:DC:C5	2.42	0.54
5:I:64:DC:H2''	5:I:65:DA:C8	2.43	0.54
3:G:44:GLY:N	4:H:89:ILE:O	2.40	0.53
4:D:87:SER:H	5:I:40:DG:P	2.31	0.53
7:K:125:DC:H2''	7:K:126:DG:C8	2.44	0.53
5:I:26:DC:H2''	5:I:27:DT:H5''	1.90	0.52
5:I:78:DC:H2''	5:I:79:DC:C5	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:ARG:O	2:B:81:VAL:N	2.34	0.52
7:K:119:DC:H2''	7:K:120:DA:C8	2.45	0.52
6:J:81:DC:H2''	6:J:82:DG:C8	2.45	0.51
5:I:15:DT:H2''	5:I:16:DG:C8	2.45	0.51
6:J:123:DC:H2''	6:J:124:DG:C8	2.47	0.50
5:I:85:DG:H2'	5:I:86:DT:H71	1.94	0.50
5:I:98:DA:H2''	5:I:99:DG:C8	2.47	0.50
5:I:55:DG:H1'	5:I:56:DC:H5'	1.95	0.49
8:L:179:GLY:H	8:L:273:THR:HA	1.77	0.49
3:G:16:THR:O	3:G:20:ARG:N	2.42	0.49
5:I:97:DA:H2''	5:I:98:DA:C8	2.48	0.49
3:C:77:ARG:N	6:J:132:DC:OP1	2.37	0.48
1:E:118:THR:N	6:J:71:DA:OP1	2.36	0.48
6:J:51:DT:H2''	6:J:52:DG:C8	2.49	0.48
5:I:14:DG:H1'	5:I:15:DT:H5'	1.96	0.48
5:I:104:DT:H3'	8:L:107:GLY:HA3	1.96	0.48
6:J:43:DA:H2''	6:J:44:DA:H8	1.79	0.47
5:I:6:DG:H2''	5:I:7:DA:C8	2.49	0.47
6:J:130:DG:H2''	6:J:131:DG:N7	2.30	0.47
5:I:18:DC:H2''	5:I:19:DG:N7	2.30	0.47
5:I:96:DC:H2'	5:I:97:DA:C8	2.49	0.47
6:J:49:DC:H1'	6:J:50:DT:H5'	1.96	0.47
6:J:77:DC:H2''	6:J:78:DG:N7	2.30	0.47
5:I:89:DT:H2''	5:I:90:DA:N7	2.30	0.47
6:J:99:DT:H2''	6:J:100:DA:N7	2.29	0.47
3:C:70:ALA:O	3:C:74:LYS:N	2.48	0.46
6:J:37:DG:H2''	6:J:38:DG:C8	2.50	0.46
5:I:40:DG:H1'	5:I:41:DA:C8	2.50	0.46
6:J:77:DC:H2''	6:J:78:DG:C8	2.50	0.46
7:K:123:DC:H2''	7:K:124:DA:C8	2.51	0.46
6:J:36:DA:H2''	6:J:37:DG:C8	2.51	0.45
7:K:112:DT:H2''	7:K:113:DA:C8	2.51	0.45
6:J:61:DA:H2''	6:J:62:DA:H8	1.79	0.45
5:I:41:DA:C8	5:I:41:DA:H5'	2.52	0.45
8:L:298:ILE:O	8:L:311:LEU:N	2.47	0.45
6:J:73:DA:H2''	6:J:74:DG:H8	1.81	0.45
5:I:2:DT:H6	5:I:2:DT:H2'	1.67	0.44
5:I:20:DA:H1'	5:I:21:DG:O4'	2.17	0.44
6:J:128:DT:H2''	6:J:129:DC:C5	2.51	0.44
6:J:52:DG:H2''	6:J:53:DG:H8	1.82	0.44
6:J:139:DA:H1'	6:J:140:DT:H5'	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:78:ILE:N	4:H:53:GLY:O	2.47	0.44
4:D:81:ALA:O	4:D:85:LYS:N	2.51	0.44
6:J:23:DG:H2''	6:J:24:DT:H5'	2.00	0.44
6:J:145:DG:H2''	6:J:146:DA:C8	2.53	0.44
5:I:37:DG:H2'	5:I:38:DT:H71	1.98	0.44
5:I:24:DC:H2''	5:I:25:DG:C8	2.52	0.44
3:C:18:SER:O	3:C:22:GLY:N	2.50	0.43
1:E:42:ARG:H	6:J:144:DC:H5''	1.83	0.43
8:L:174:ILE:O	8:L:195:LEU:HA	2.18	0.43
5:I:70:DC:H1'	5:I:71:DG:C8	2.54	0.43
6:J:54:DC:H1'	6:J:55:DG:H5'	2.01	0.43
6:J:83:DT:H2''	6:J:84:DG:C8	2.53	0.43
6:J:75:DC:H1'	6:J:76:DG:H5'	2.00	0.43
5:I:104:DT:H2'	5:I:105:DT:H71	2.01	0.43
6:J:42:DT:H2''	6:J:43:DA:C8	2.54	0.43
6:J:72:DC:H2''	6:J:73:DA:C8	2.53	0.43
5:I:80:DC:H6	5:I:80:DC:H2'	1.71	0.42
8:L:299:ARG:HA	8:L:310:PRO:HA	2.01	0.42
6:J:24:DT:H1'	6:J:25:DG:C8	2.54	0.42
5:I:39:DA:H1'	5:I:40:DG:O4'	2.20	0.42
6:J:37:DG:H2''	6:J:38:DG:H8	1.84	0.42
7:K:115:DT:H2'	7:K:116:DC:C6	2.53	0.42
2:F:38:ALA:O	2:F:42:GLY:N	2.49	0.42
5:I:54:DC:H2''	5:I:55:DG:C8	2.55	0.42
6:J:118:DT:H2''	6:J:119:DT:C5	2.55	0.42
5:I:4:DG:H2''	5:I:5:DA:N7	2.35	0.42
5:I:70:DC:H1'	5:I:71:DG:N7	2.35	0.42
6:J:60:DA:H2''	6:J:61:DA:C8	2.55	0.42
3:C:78:ILE:H	4:D:54:ILE:HA	1.85	0.41
6:J:95:DG:C8	6:J:96:DT:H72	2.54	0.41
5:I:48:DT:H2''	5:I:49:DA:N7	2.35	0.41
5:I:88:DT:C6	5:I:89:DT:H72	2.55	0.41
5:I:28:DC:H1'	5:I:29:DA:C8	2.55	0.41
5:I:58:DT:H2''	5:I:59:DA:N7	2.35	0.41
6:J:82:DG:H2''	6:J:83:DT:O5'	2.19	0.41
6:J:85:DC:H2''	6:J:86:DG:C8	2.56	0.41
7:K:122:DG:H2''	7:K:123:DC:C5	2.55	0.41
5:I:34:DG:C8	5:I:35:DT:H72	2.55	0.41
6:J:63:DC:H2''	6:J:64:DG:H8	1.85	0.41
6:J:88:DT:H2'	6:J:88:DT:OP2	2.21	0.41
6:J:112:DG:H2''	6:J:113:DA:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:76:DG:H2'	5:I:77:DT:H71	2.03	0.41
5:I:51:DC:C2	5:I:52:DA:C8	3.08	0.41
1:E:117:VAL:H	6:J:71:DA:P	2.44	0.41
5:I:46:DT:H2''	5:I:47:DC:C6	2.56	0.40
5:I:7:DA:H2''	5:I:8:DA:C8	2.56	0.40
5:I:34:DG:H2'	5:I:35:DT:C6	2.56	0.40
5:I:98:DA:H2''	5:I:99:DG:H8	1.87	0.40
5:I:105:DT:OP1	8:L:105:GLY:N	2.54	0.40
6:J:52:DG:H2''	6:J:53:DG:C8	2.56	0.40
5:I:2:DT:H2''	5:I:3:DC:H5''	2.03	0.40
5:I:69:DA:H1'	5:I:70:DC:C6	2.57	0.40
6:J:61:DA:H2''	6:J:62:DA:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	92/135 (68%)	92 (100%)	0	0	100	100
1	E	94/135 (70%)	92 (98%)	2 (2%)	0	100	100
2	B	78/102 (76%)	78 (100%)	0	0	100	100
2	F	81/102 (79%)	81 (100%)	0	0	100	100
3	C	103/129 (80%)	103 (100%)	0	0	100	100
3	G	100/129 (78%)	99 (99%)	1 (1%)	0	100	100
4	D	91/125 (73%)	89 (98%)	2 (2%)	0	100	100
4	H	90/125 (72%)	89 (99%)	1 (1%)	0	100	100
8	L	319/335 (95%)	314 (98%)	5 (2%)	0	100	100
All	All	1048/1317 (80%)	1037 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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.

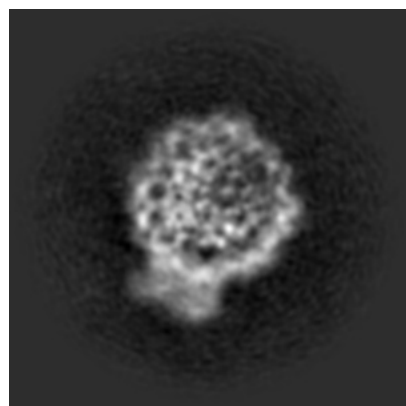
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47253. These allow visual inspection of the internal detail of the map and identification of artifacts.

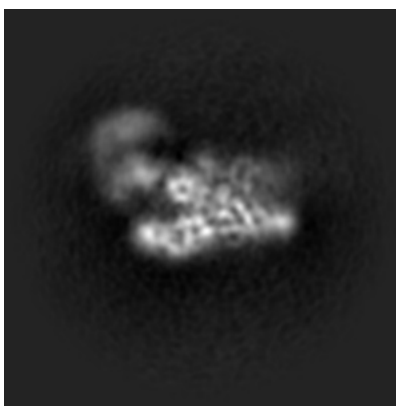
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

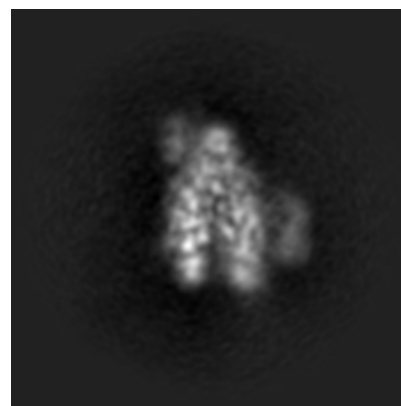
6.1.1 Primary map



X

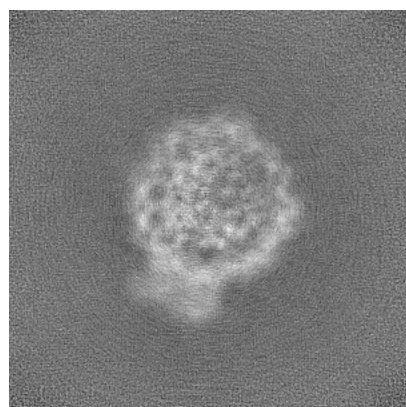


Y

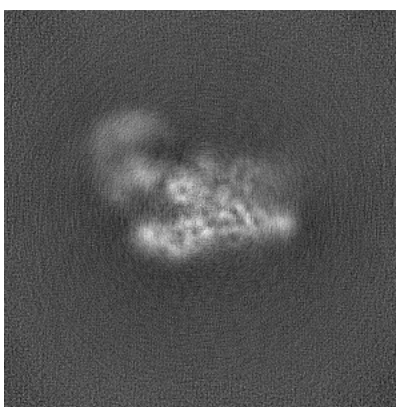


Z

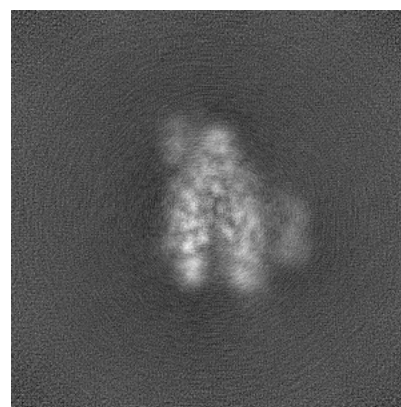
6.1.2 Raw map



X



Y

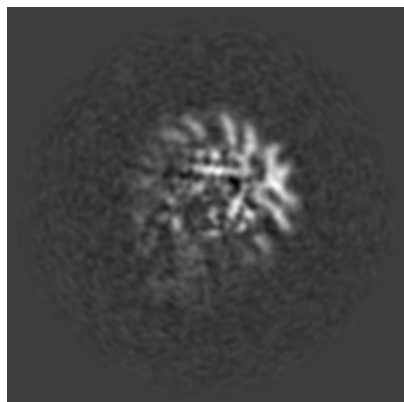


Z

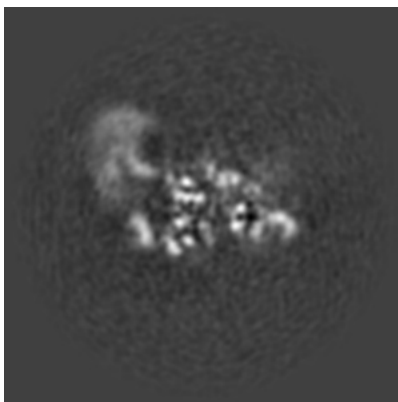
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

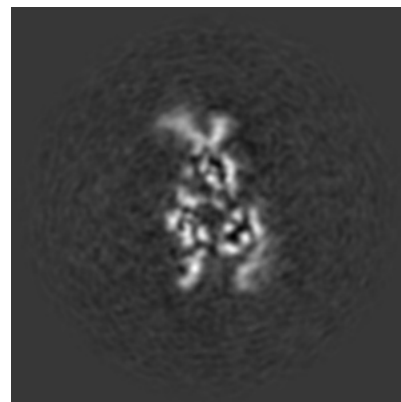
6.2.1 Primary map



X Index: 300

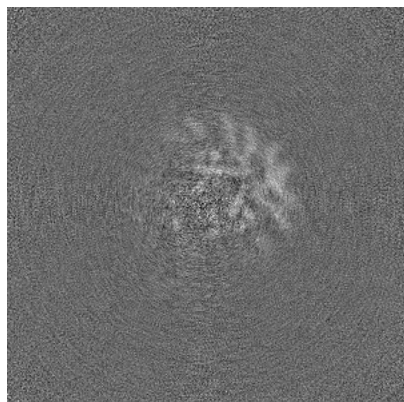


Y Index: 300

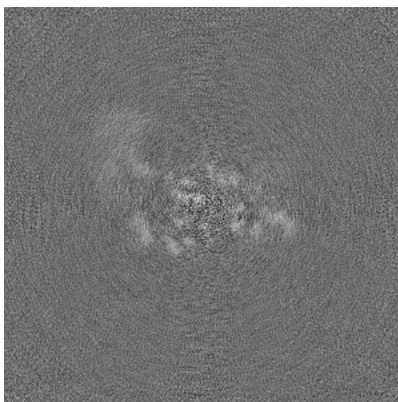


Z Index: 300

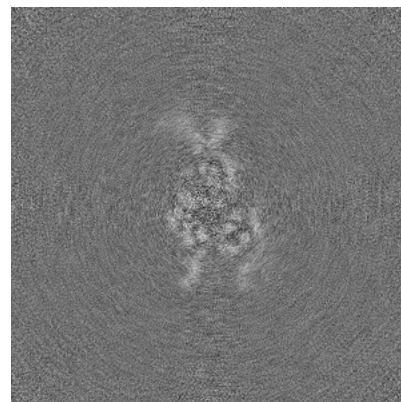
6.2.2 Raw map



X Index: 300



Y Index: 300

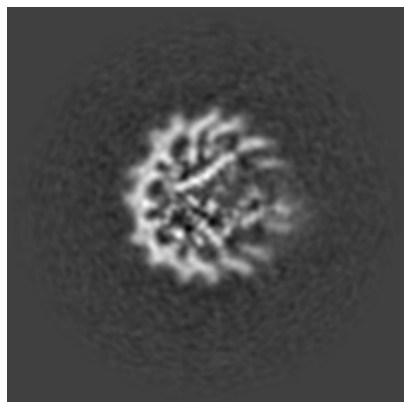


Z Index: 300

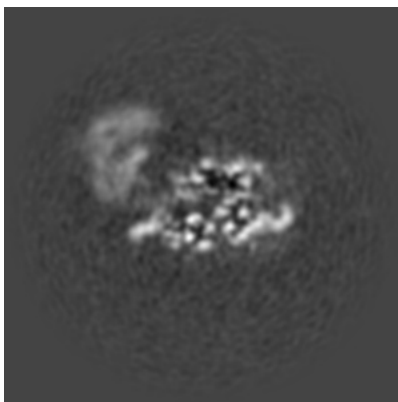
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

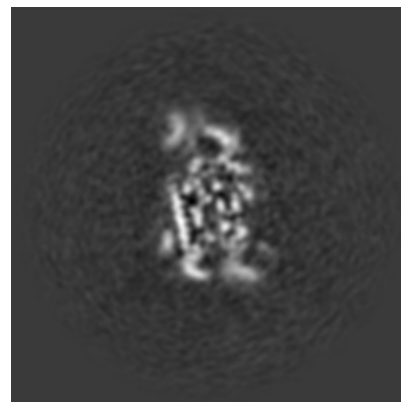
6.3.1 Primary map



X Index: 272

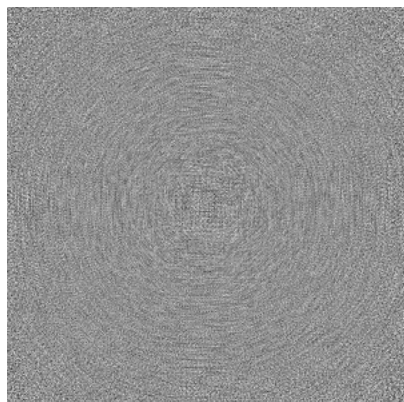


Y Index: 278

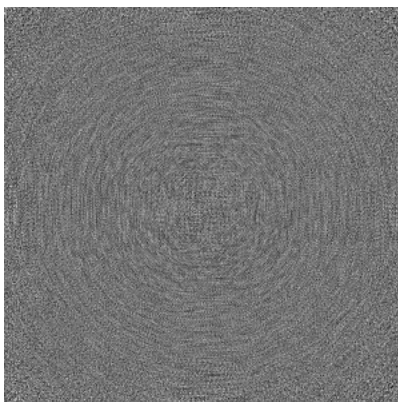


Z Index: 277

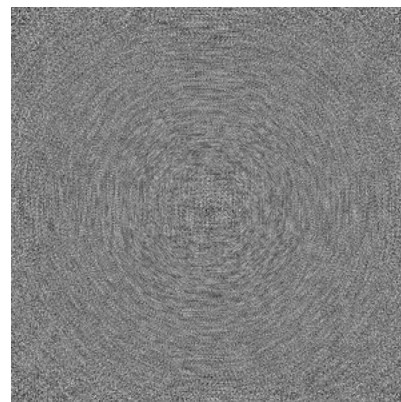
6.3.2 Raw map



X Index: 0



Y Index: 0

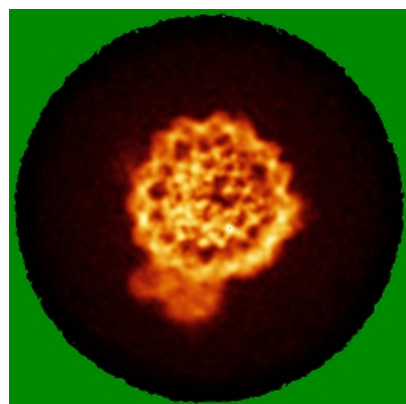


Z Index: 0

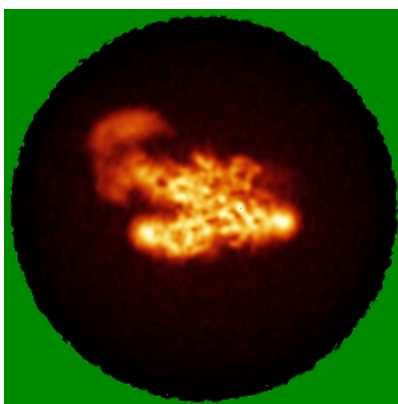
The images above show the largest variance slices of the map in three orthogonal directions.

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

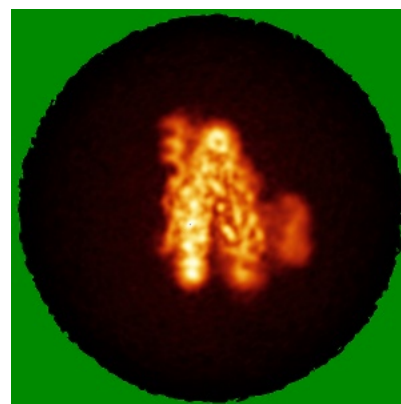
6.4.1 Primary map



X

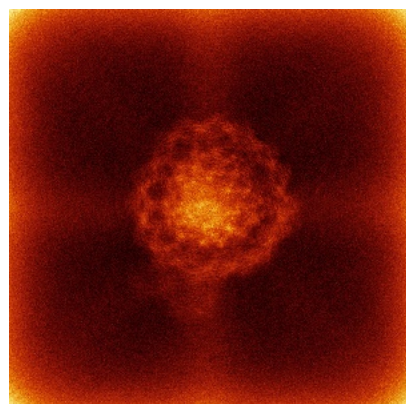


Y

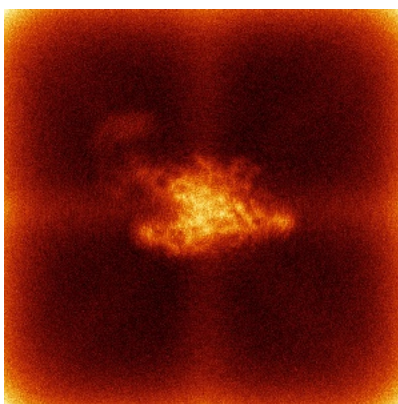


Z

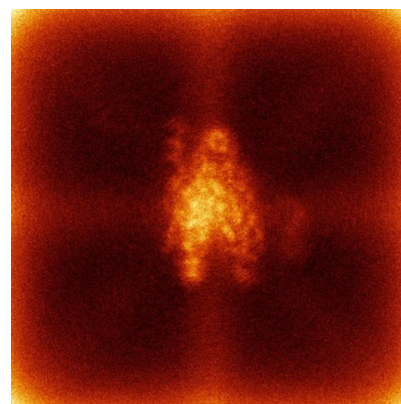
6.4.2 Raw map



X



Y

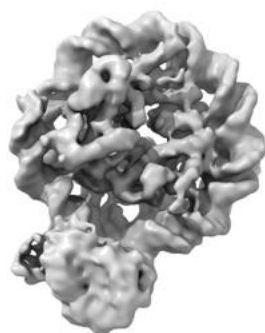


Z

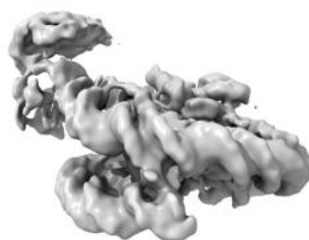
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



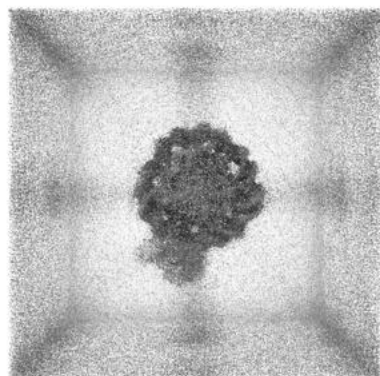
Y



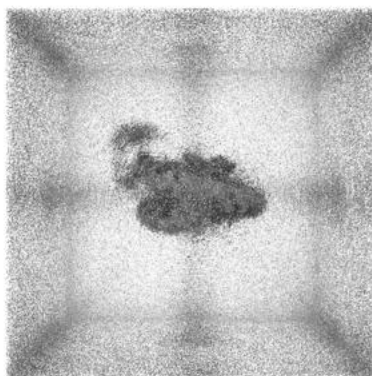
Z

The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

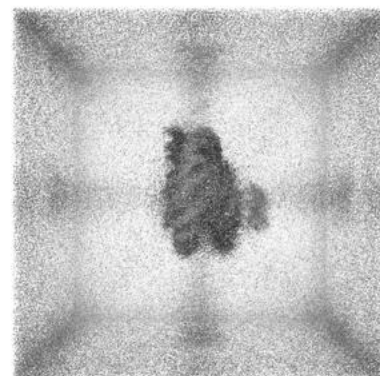
6.5.2 Raw map



X



Y



Z

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.

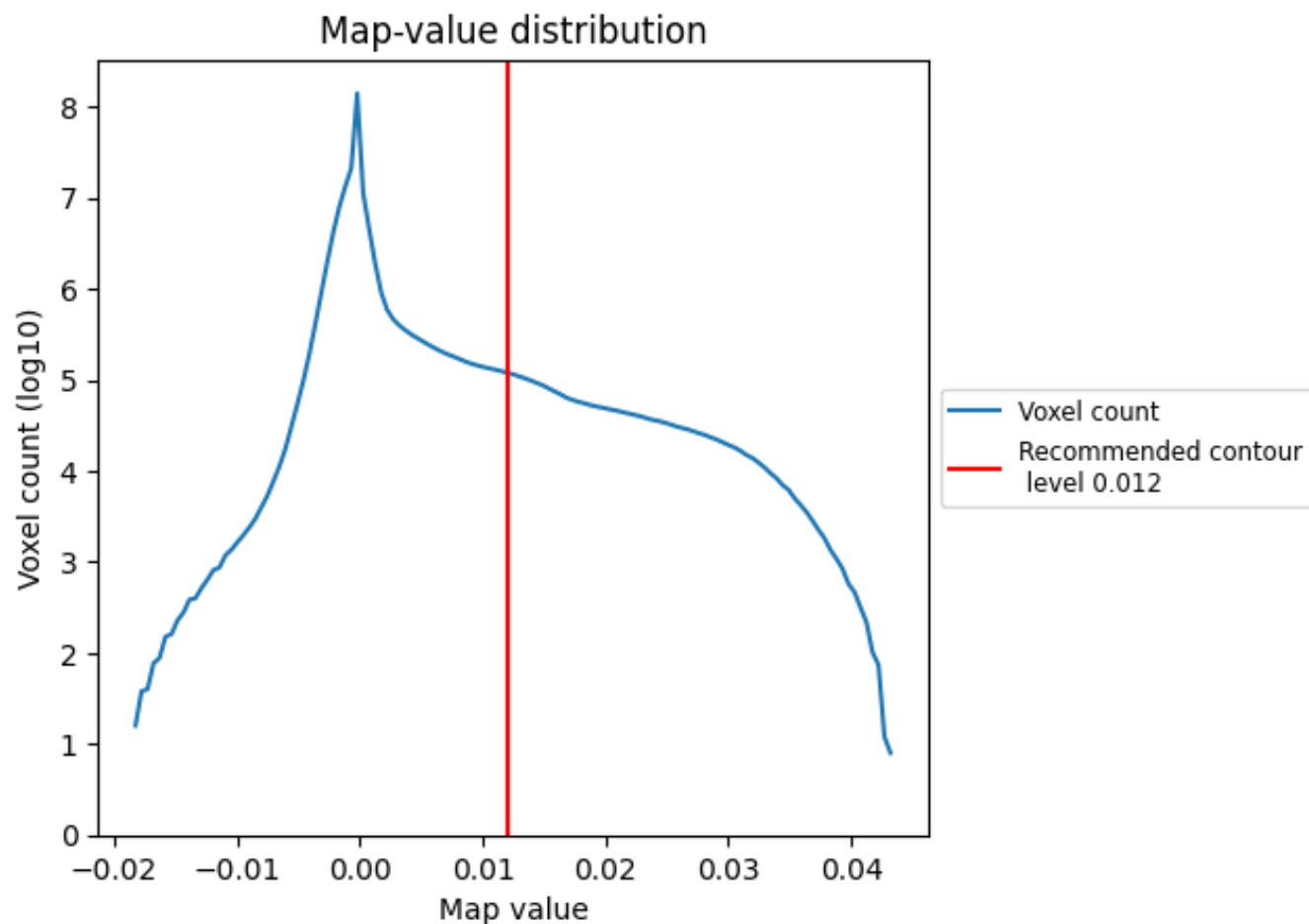
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

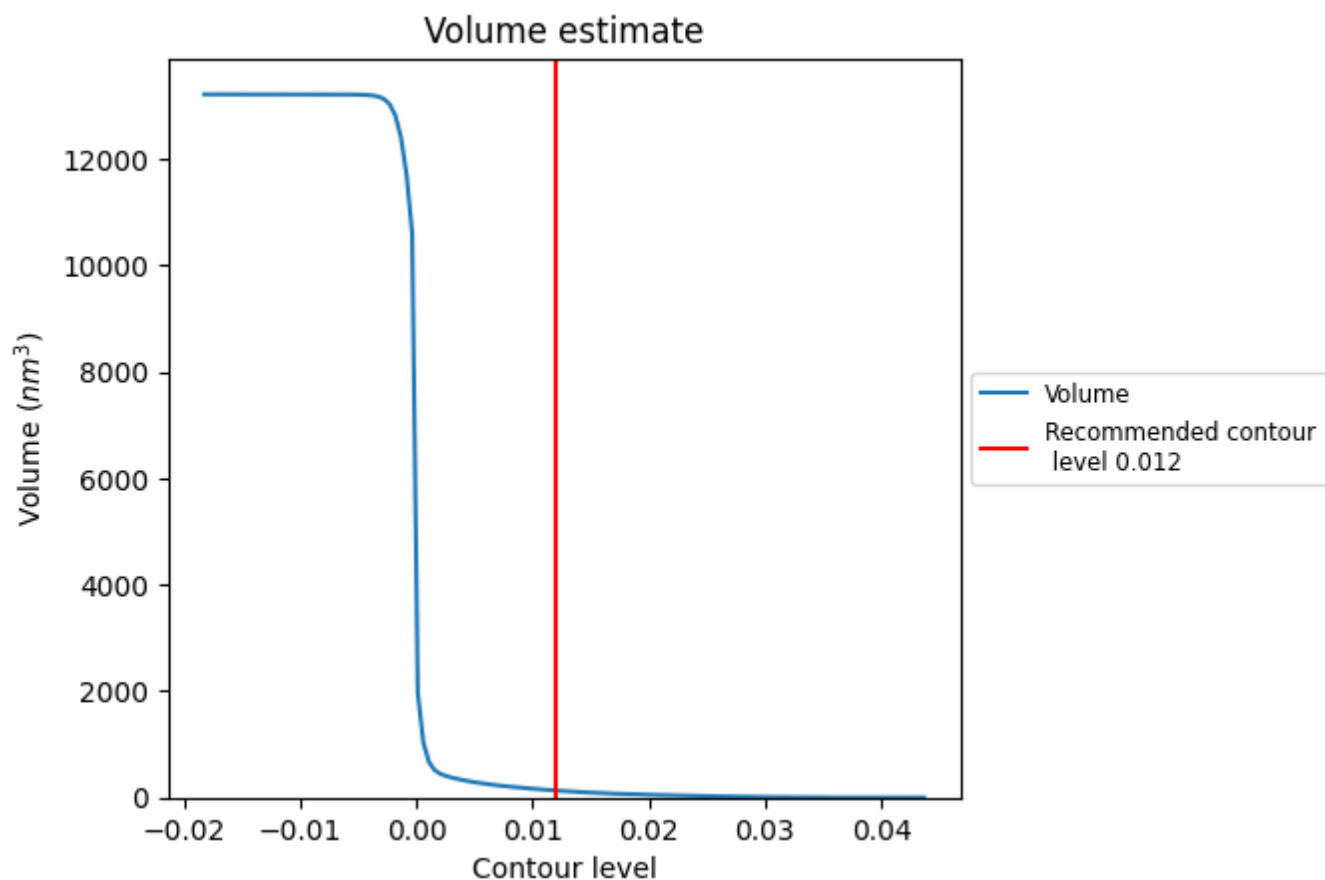
This section contains the results of statistical analysis of the map.

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.

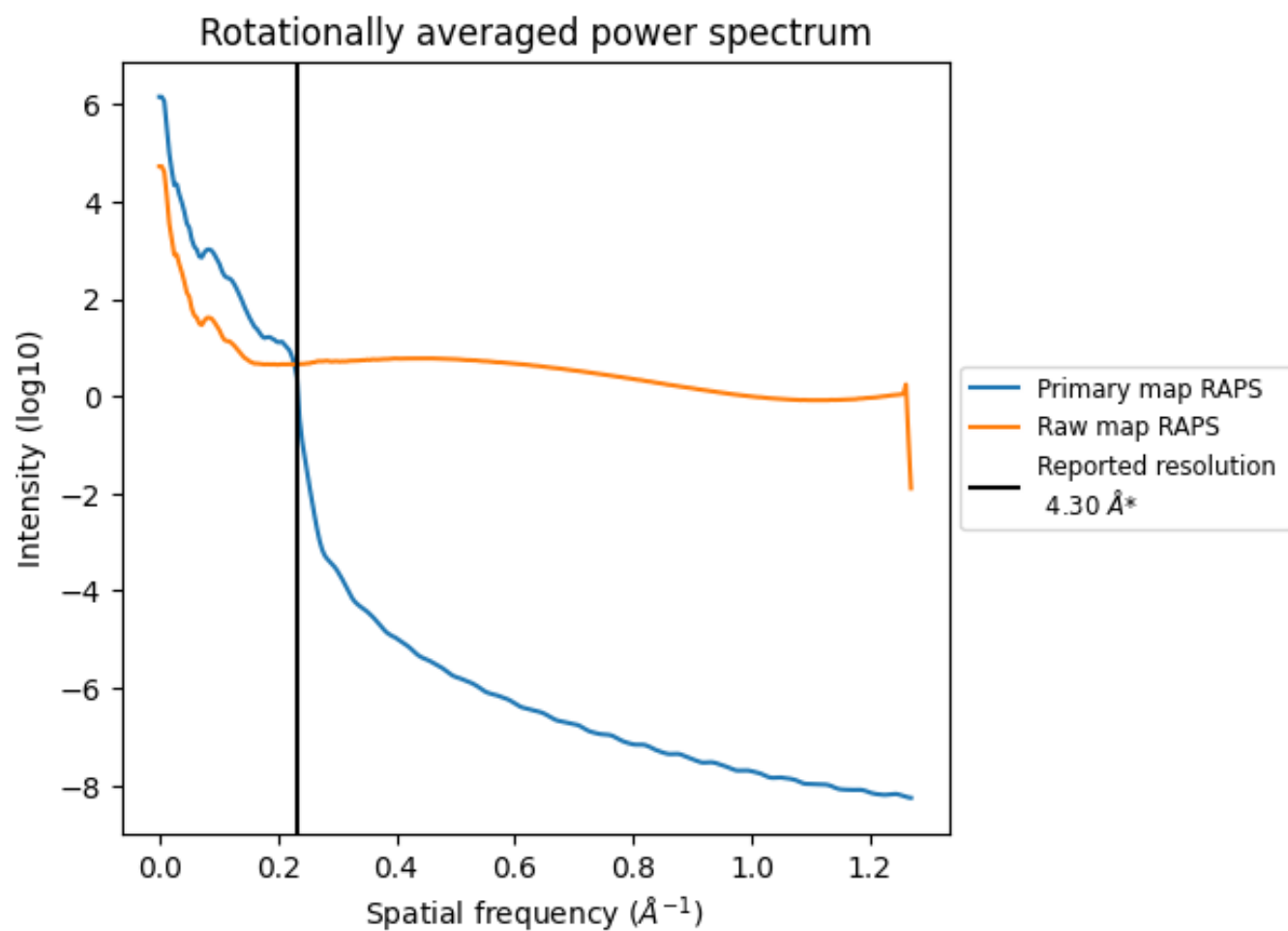
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 133 nm³; this corresponds to an approximate mass of 120 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 ⓘ

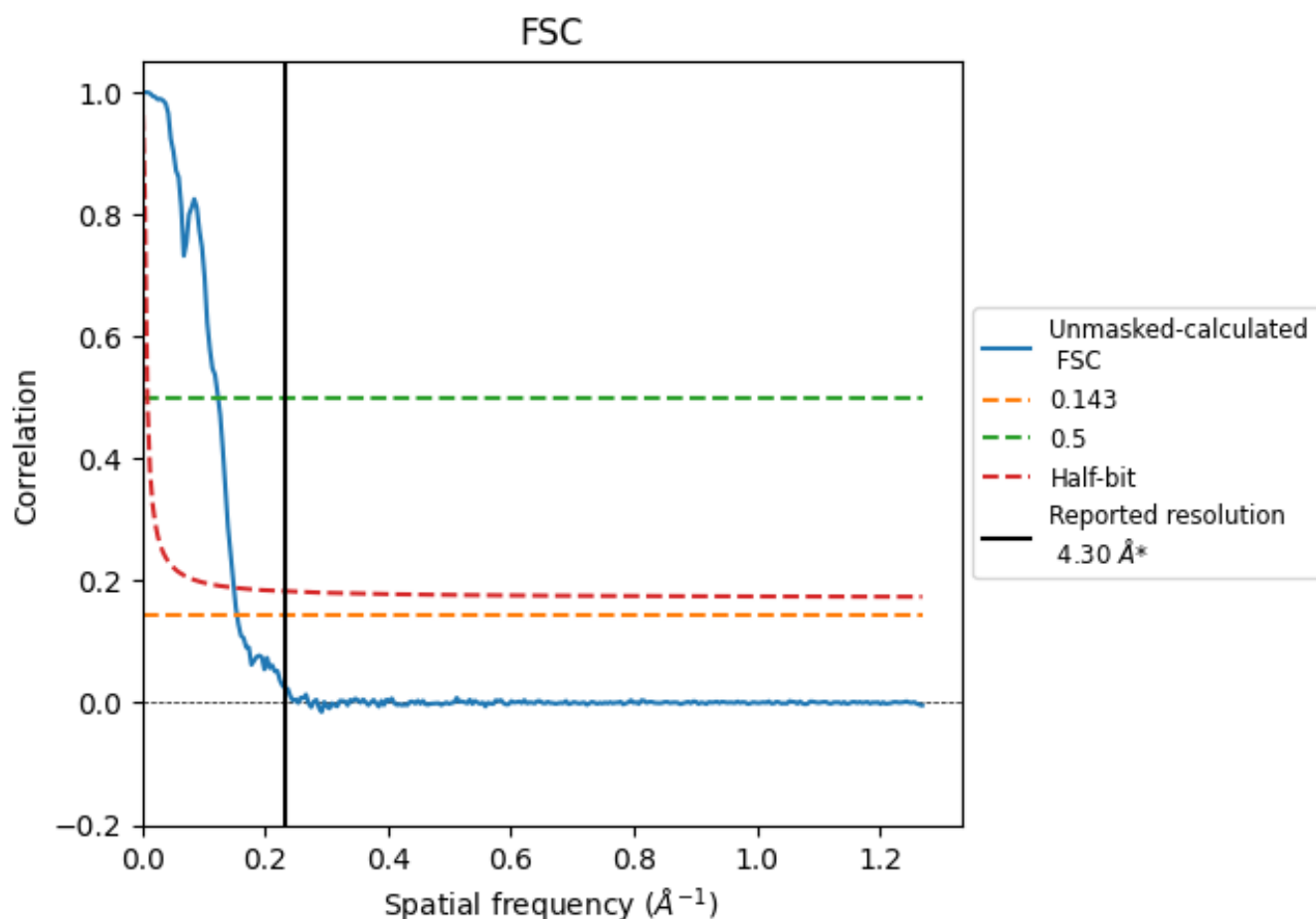


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 $0.233 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

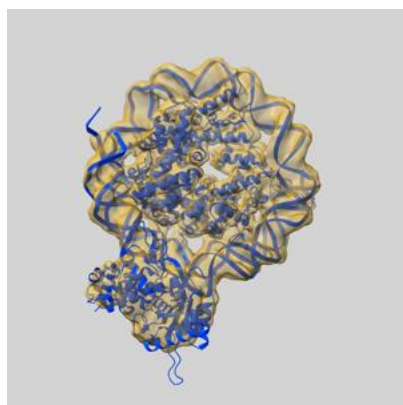
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.48	8.10	6.72

*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 6.48 differs from the reported value 4.3 by more than 10 %

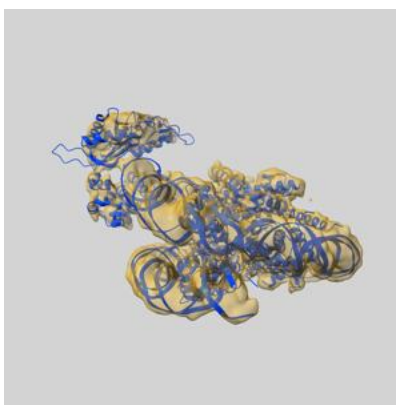
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47253 and PDB model 9DWK. Per-residue inclusion information can be found in section [3](#) on page [6](#).

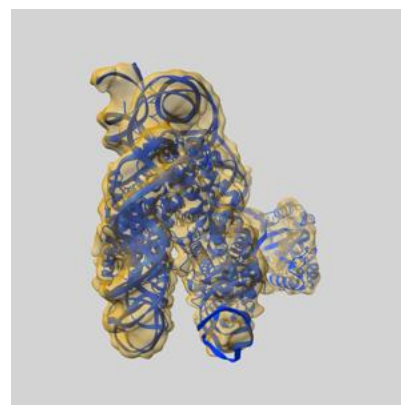
9.1 Map-model overlay [i](#)



X



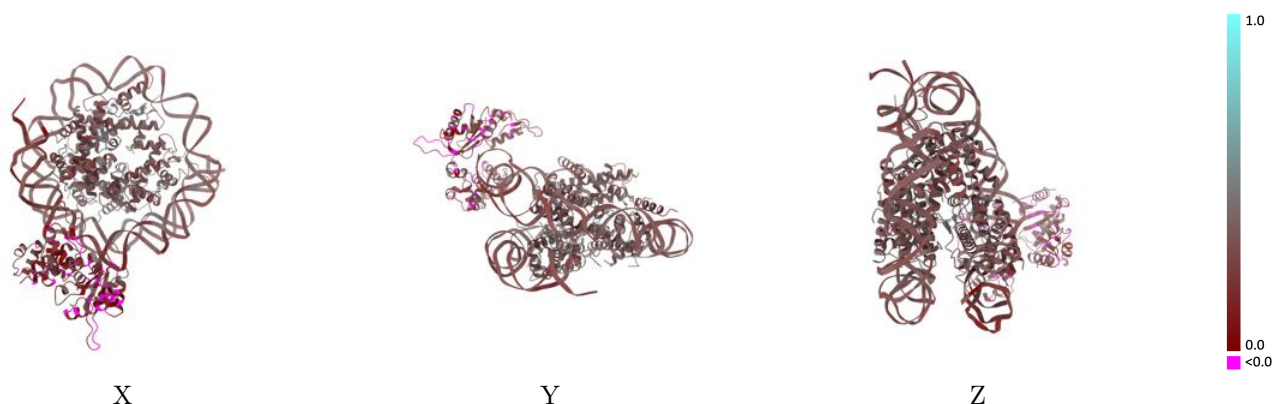
Y



Z

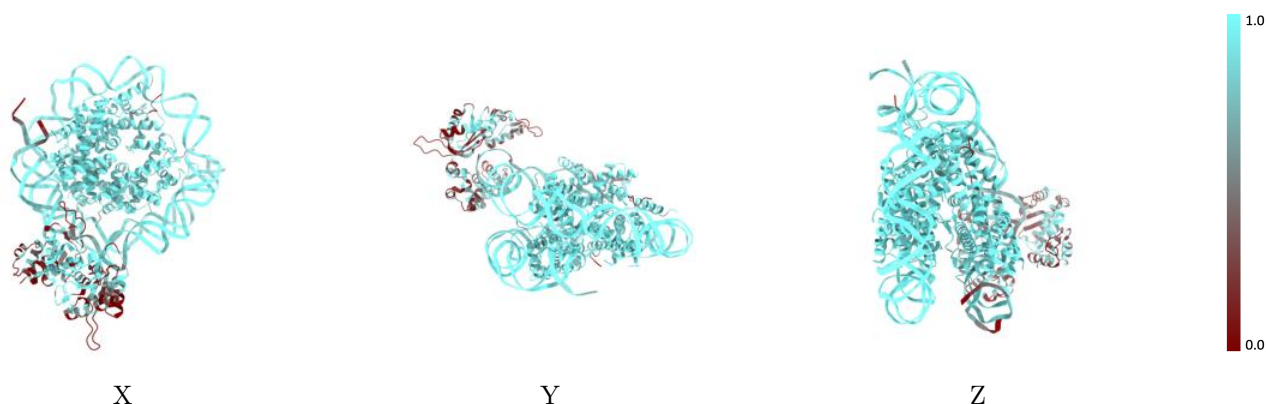
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



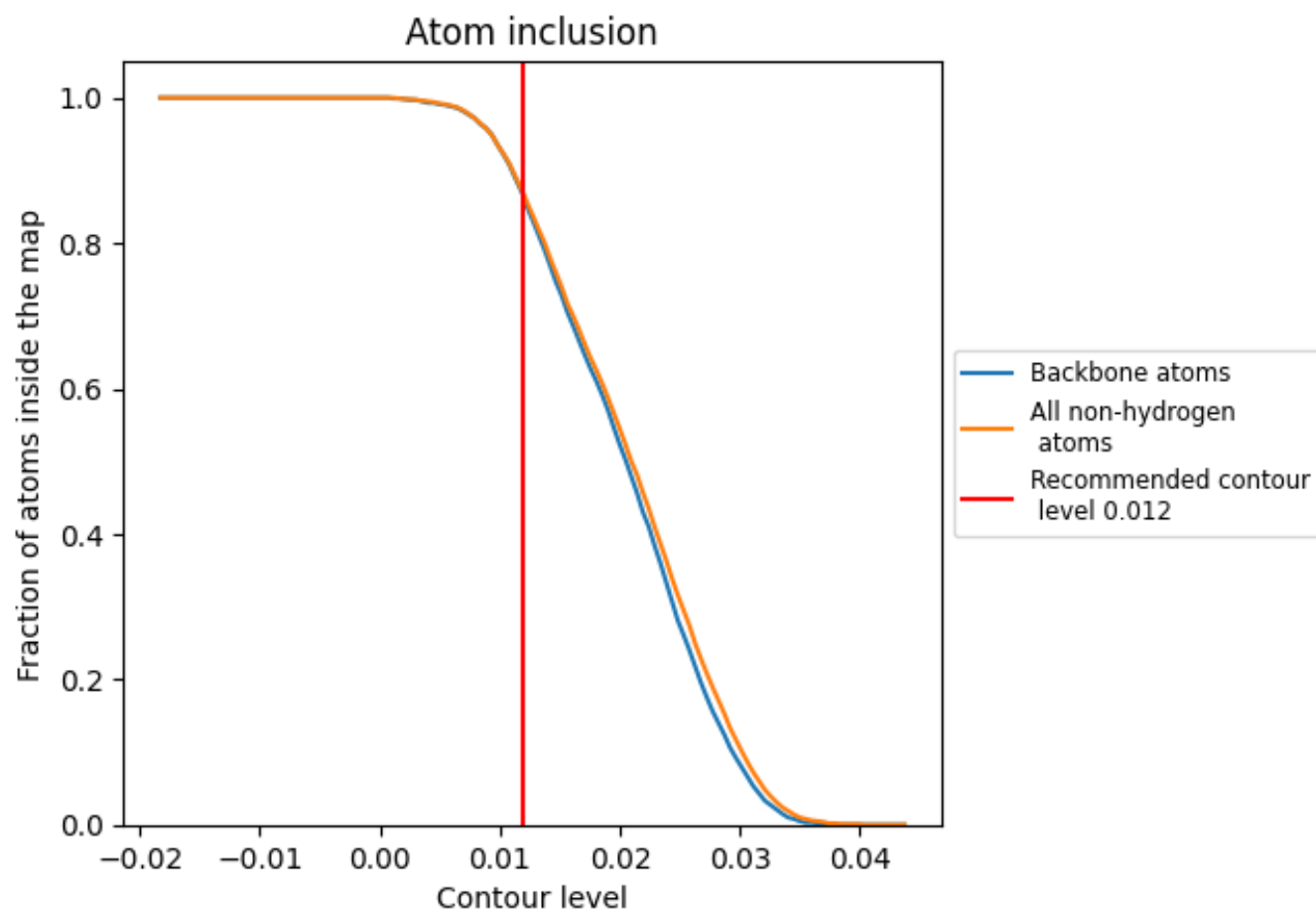
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 87% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8670	 0.2970
A	 0.9530	 0.3410
B	 0.9670	 0.3690
C	 0.9260	 0.3790
D	 0.9570	 0.3560
E	 0.9640	 0.3510
F	 0.9710	 0.3730
G	 0.9160	 0.3650
H	 0.9630	 0.3310
I	 0.9570	 0.3030
J	 0.9140	 0.2950
K	 0.7290	 0.2500
L	 0.5070	 0.1620

