



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:27 AM UTC

PDB ID : 8T9H / pdb_00008t9h
EMDB ID : EMD-41111
Title : Catalytic and non-catalytic mechanisms of histone H4 lysine 20 methyltransferase SUV420H1
Authors : Abini-Agbomson, S.; Armache, K.-J.
Deposited on : 2023-06-24
Resolution : 3.37 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:

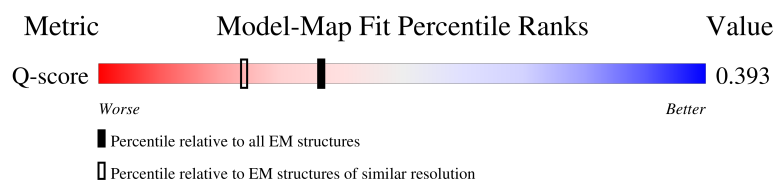
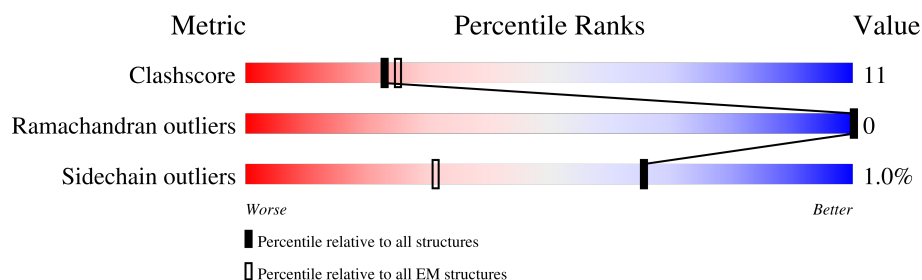
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.37 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	14287 (2.87 - 3.87)

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	 53% 18% 29%
1	E	135	 55% 13% 32%
2	B	103	 64% 19% 17%
2	F	103	 57% 20% 22%

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Mol	Chain	Length	Quality of chain
3	C	130	5% 68% 15% 12%
3	G	130	7% 73% 8% 12%
4	D	123	2% 57% 20% 21%
4	H	123	1% 65% 9% 25%
5	I	146	26% 42% 32%
6	J	146	25% 45% 30%
7	K	394	11% 45% 18% 26%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12039 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	96	Total	C	N	O	S	0	0
			791	498	152	138	3		
1	E	92	Total	C	N	O	S	0	0
			750	472	142	133	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	ALA	GLY	variant	UNP P84233
E	102	ALA	GLY	variant	UNP P84233

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	86	Total	C	N	O	S	0	0
			693	435	139	117	2		
2	F	80	Total	C	N	O	S	0	0
			638	401	125	111	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	20	MET	LYS	conflict	UNP A0A8J1LTD2
F	20	MET	LYS	conflict	UNP A0A8J1LTD2

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	107	Total	C	N	O	0	0
			811	510	158	143		
3	G	107	Total	C	N	O	0	0
			811	510	158	143		

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	95	Total	C	N	O	S	0	0
			745	469	134	140	2		
4	H	91	Total	C	N	O	S	0	0
			709	447	125	135	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	3	MET	-	initiating methionine	UNP P02281
D	32	THR	SER	engineered mutation	UNP P02281
H	4	MET	-	initiating methionine	UNP P02281
H	33	THR	SER	engineered mutation	UNP P02281

- Molecule 5 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	99	Total	C	N	O	P	0	0
			2012	957	360	596	99		

- Molecule 6 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	102	Total	C	N	O	P	0	0
			2110	997	401	610	102		

- Molecule 7 is a protein called Histone-lysine N-methyltransferase KMT5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	249	Total	C	N	O	S	0	0
			1969	1234	343	376	16		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	0	GLY	-	expression tag	UNP Q4FZB7
K	1	SER	-	expression tag	UNP Q4FZB7

- Molecule 3: Histone H2A

Chain G:

Sequence logo for Chain G. The y-axis represents frequency in bits (0.00 to 0.15). The x-axis lists amino acids. A bar chart above the sequence shows the overall frequency of each amino acid: 7% (red), 73% (green), 8% (yellow), and 18% (grey).

Amino Acid	Frequency (bits)
MET	0.00
SER	0.00
GLY	0.00
ARG	0.00
GLY	0.00
LYS	0.00
GLN	0.00
GLY	0.00
GLY	0.00
THR	0.00
ARG	0.00
A12	0.00
K13	0.00
A14	0.00
K15	0.00
T16	0.00
S19	0.00
Q24	0.00
V27	0.00
V30	0.00
Y39	0.00
V49	0.00
E56	0.00
Y57	0.00
E64	0.00
R77	0.00
I102	0.00
I111	0.00
Q112	0.00
S113	0.00
V114	0.00
L115	0.00
L116	0.00
P117	0.00
K118	0.00
LYS	0.00
THR	0.00
GLU	0.00
SER	0.00
SER	0.00
SER	0.00
ALA	0.00
LYS	0.00
SER	0.00

- Molecule 4: Histone H2B 1.1

Chain D:

- Molecule 4: Histone H2B 1.1

Chain H:

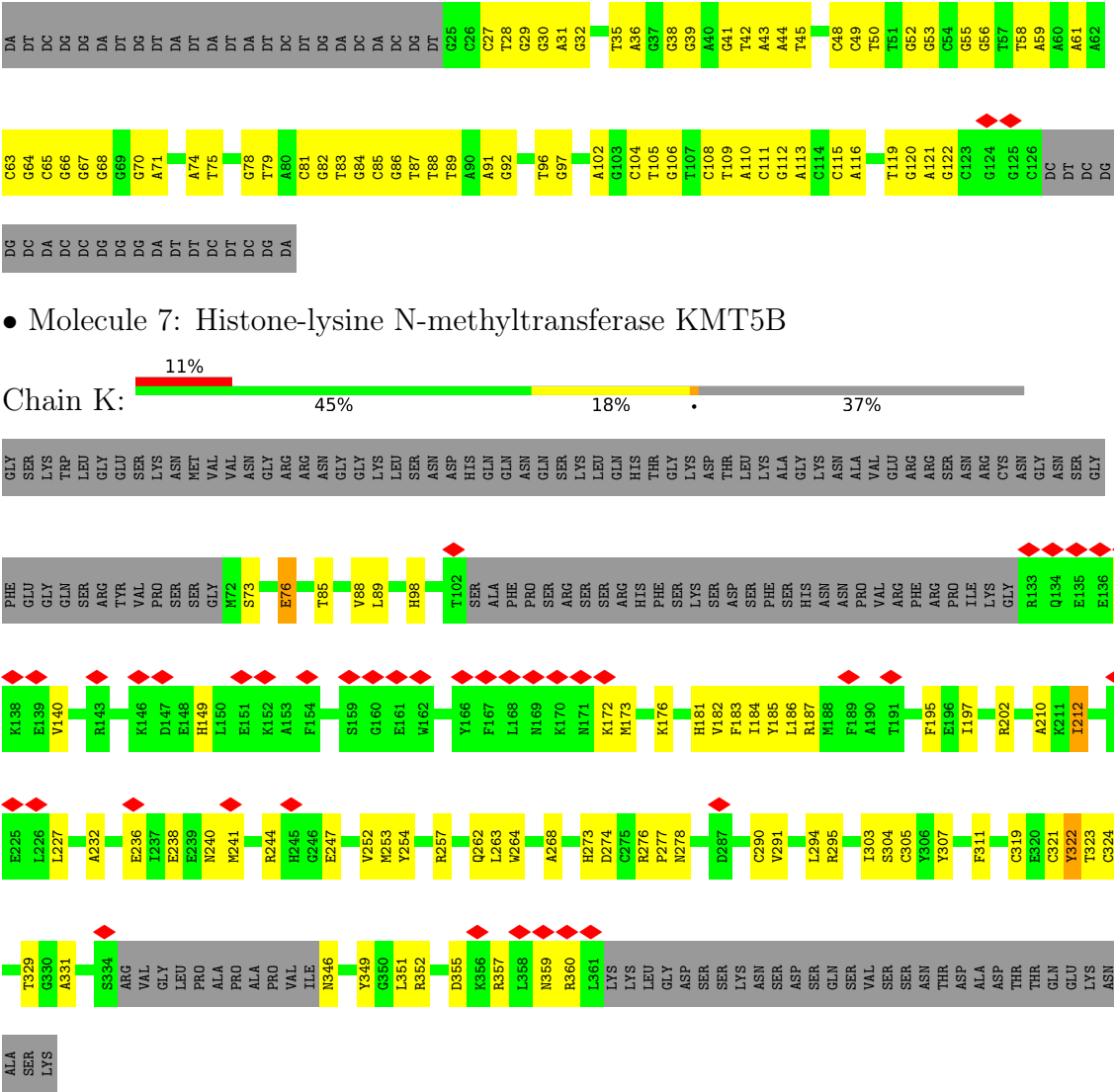
Residue	Category
MET	Green
ALA	Green
LYS	Green
SER	Green
ALA	Green
PRO	Green
PRO	Green
LYS	Green
LYS	Green
GLY	Green
SER	Green
LYS	Green
LYS	Green
ALA	Green
VAL	Green
THR	Green
LYS	Green
THR	Green
GLN	Green
LYS	Green
LYS	Green
ASP	Green
GLY	Green
LYS	Green
LYS	Green
ARG	Green
ARG	Green
LYS	Green
THR	Green
ARG	Green
LYS	Green
LYS	Green
ES6	Green
V42	Yellow
V49	Yellow
S56	Yellow
M60	Yellow
S61	Yellow
I62	Yellow
F71	Yellow
S79	Yellow
H83	Yellow
R87	Yellow
T97	Yellow
E114	Yellow
V126	Grey

- Molecule 5: DNA (146-MER)

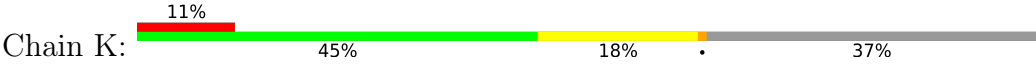
[illegible]

- Molecule 6: DNA (146-MER)





• Molecule 7: Histone-lysine N-methyltransferase KMT5B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	366390	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.295	Depositor
Minimum map value	-0.414	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.22	Depositor
Map size ($\text{\AA}$)	350.71997, 350.71997, 350.71997	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.096, 1.096, 1.096	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	0.12	0/801	0.26	0/1073
1	E	0.12	0/758	0.29	0/1015
2	B	0.14	0/701	0.33	0/936
2	F	0.13	0/645	0.25	0/862
3	C	0.12	0/821	0.24	0/1112
3	G	0.11	0/821	0.26	0/1112
4	D	0.14	0/756	0.30	0/1015
4	H	0.11	0/720	0.24	0/969
5	I	0.20	0/2252	0.45	0/3469
6	J	0.19	0/2371	0.35	0/3662
7	K	0.08	0/2004	0.24	0/2691
All	All	0.15	0/12650	0.32	0/17916

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	791	0	831	19	0
1	E	750	0	789	15	0
2	B	693	0	738	20	0
2	F	638	0	676	21	0
3	C	811	0	849	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	811	0	849	9	0
4	D	745	0	773	20	0
4	H	709	0	727	10	0
5	I	2012	0	1113	51	0
6	J	2110	0	1144	62	0
7	K	1969	0	1870	63	0
All	All	12039	0	10359	247	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 11.

All (247) 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:232:ALA:H	7:K:262:GLN:HE22	1.24	0.85
5:I:48:DT:H2''	5:I:49:DA:N7	1.98	0.78
7:K:276:ARG:HB3	7:K:323:THR:HG21	1.71	0.73
4:H:42:VAL:HB	4:H:60:MET:HE1	1.70	0.73
5:I:85:DG:H2''	5:I:86:DT:H5''	1.70	0.73
6:J:49:DC:H2''	6:J:50:DT:H71	1.71	0.72
1:A:69:ARG:HB3	2:F:25:ASN:HD22	1.54	0.71
3:C:63:LEU:HD12	4:D:45:LEU:HD13	1.74	0.69
7:K:262:GLN:NE2	7:K:263:LEU:O	2.26	0.69
7:K:236:GLU:O	7:K:240:ASN:ND2	2.26	0.67
1:A:120:MET:HG3	1:A:121:PRO:HD2	1.77	0.66
3:C:77:ARG:HH21	4:D:55:SER:HA	1.60	0.66
5:I:55:DG:H2''	5:I:56:DC:H2'	1.78	0.65
7:K:88:VAL:HG13	7:K:89:LEU:HD22	1.79	0.65
7:K:273:HIS:ND1	7:K:321:CYS:SG	2.70	0.65
7:K:232:ALA:N	7:K:262:GLN:HE22	1.92	0.64
5:I:54:DC:H2'	5:I:55:DG:C8	2.32	0.64
7:K:355:ASP:O	7:K:359:ASN:ND2	2.31	0.64
3:C:39:TYR:HB3	4:D:78:SER:HB2	1.80	0.64
7:K:202:ARG:NH2	7:K:321:CYS:O	2.31	0.64
6:J:35:DT:H2''	6:J:36:DA:C8	2.34	0.63
6:J:55:DG:H2'	6:J:56:DG:C8	2.33	0.63
6:J:63:DC:N4	6:J:64:DG:O6	2.33	0.62
2:B:39:ARG:NH1	2:B:44:LYS:O	2.31	0.61
6:J:85:DC:H2''	6:J:86:DG:C8	2.35	0.61
3:G:39:TYR:HB3	4:H:79:SER:HB2	1.83	0.61
7:K:278:ASN:HD21	7:K:303:ILE:HG23	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:30:THR:HG21	5:I:61:DA:H5''	1.83	0.61
5:I:104:DT:H2'	5:I:105:DT:H71	1.84	0.60
6:J:65:DC:H2''	6:J:66:DG:C8	2.37	0.60
3:C:90:ASP:OD2	7:K:352:ARG:NH2	2.35	0.59
2:B:37:LEU:HD23	1:E:61:LEU:HD12	1.85	0.59
7:K:319:CYS:H	7:K:331:ALA:H	1.51	0.58
2:B:20:MET:O	7:K:254:TYR:N	2.36	0.58
1:A:120:MET:HB3	1:A:122:LYS:HG2	1.86	0.58
3:G:77:ARG:HH21	4:H:56:SER:HA	1.69	0.58
5:I:49:DA:H2''	5:I:50:DG:C8	2.39	0.57
1:A:108:ASN:HB2	2:F:43:VAL:HG12	1.85	0.57
7:K:277:PRO:HB3	7:K:305:CYS:HA	1.86	0.57
3:C:112:GLN:HB3	3:C:115:LEU:HD13	1.86	0.57
5:I:38:DT:H1'	5:I:39:DA:C5	2.40	0.57
5:I:86:DT:H2''	5:I:87:DT:H5''	1.87	0.57
6:J:104:DC:H2'	6:J:105:DT:H71	1.86	0.57
7:K:182:VAL:HA	7:K:185:TYR:HD2	1.70	0.57
2:B:80:THR:HG22	1:E:83:ARG:HB2	1.88	0.56
5:I:37:DG:N1	6:J:112:DG:O6	2.38	0.56
2:B:42:GLY:O	1:E:108:ASN:ND2	2.38	0.56
3:C:102:ILE:HG23	4:D:61:ILE:HD13	1.88	0.56
5:I:36:DC:H2''	5:I:37:DG:H5'	1.87	0.56
7:K:273:HIS:ND1	7:K:319:CYS:SG	2.77	0.55
2:F:24:ASP:O	2:F:27:GLN:NE2	2.38	0.55
7:K:351:LEU:HD12	7:K:357:ARG:HH12	1.72	0.55
2:F:36:ARG:NH2	5:I:61:DA:OP1	2.35	0.55
6:J:105:DT:H2'	6:J:106:DG:C8	2.41	0.55
7:K:290:CYS:SG	7:K:291:VAL:N	2.80	0.55
6:J:38:DG:H2''	6:J:39:DG:N7	2.22	0.54
7:K:220:ARG:HG2	7:K:295:ARG:HA	1.88	0.54
1:A:61:LEU:O	2:F:36:ARG:NH1	2.38	0.54
3:C:115:LEU:HG	2:F:44:LYS:HG2	1.89	0.54
6:J:108:DC:H2''	6:J:109:DT:C5	2.43	0.54
6:J:29:DG:H2'	6:J:30:DG:C8	2.43	0.54
4:D:41:VAL:HB	4:D:59:MET:HE1	1.89	0.54
6:J:96:DT:C4	6:J:97:DG:O6	2.61	0.54
7:K:172:LYS:HG2	7:K:176:LYS:HE3	1.90	0.53
1:A:113:HIS:NE2	1:E:123:ASP:OD1	2.33	0.53
2:F:78:ARG:HD2	6:J:102:DA:H5'	1.89	0.53
5:I:46:DT:H2''	5:I:47:DC:C5	2.43	0.53
1:E:64:LYS:N	5:I:92:DC:OP1	2.36	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:40:DG:H1'	5:I:41:DA:C8	2.44	0.53
5:I:68:DT:H2''	5:I:69:DA:N7	2.24	0.52
6:J:115:DC:O2	6:J:116:DA:N6	2.40	0.52
6:J:84:DG:H2''	6:J:85:DC:H5''	1.91	0.52
6:J:81:DC:H2''	6:J:82:DG:C8	2.45	0.52
3:C:55:LEU:HD21	4:D:70:PHE:HB2	1.90	0.52
7:K:273:HIS:CD2	7:K:307:TYR:HB2	2.45	0.52
3:C:38:ASN:HD21	4:H:83:HIS:CE1	2.28	0.51
7:K:173:MET:HA	7:K:176:LYS:HZ2	1.74	0.51
7:K:202:ARG:HH22	7:K:325:GLU:HB2	1.75	0.51
5:I:85:DG:H2'	5:I:86:DT:H72	1.90	0.51
7:K:73:SER:N	7:K:76:GLU:OE1	2.43	0.51
7:K:253:MET:HE3	7:K:264:TRP:HB3	1.91	0.51
6:J:41:DG:H2''	6:J:42:DT:H5''	1.93	0.51
1:E:79:LYS:HD3	1:E:82:LEU:HD21	1.92	0.51
5:I:54:DC:N4	5:I:55:DG:O6	2.43	0.51
6:J:44:DA:H4'	6:J:45:DT:OP1	2.09	0.51
5:I:87:DT:H2''	5:I:88:DT:H5''	1.93	0.51
2:B:35:ARG:O	2:B:39:ARG:HG2	2.10	0.51
2:B:75:HIS:O	4:D:92:ARG:NH1	2.43	0.50
1:A:64:LYS:N	6:J:92:DG:OP1	2.41	0.50
6:J:52:DG:H2''	6:J:53:DG:H5''	1.93	0.50
5:I:119:DC:H2''	5:I:120:DA:C8	2.46	0.50
1:A:128:ARG:NH1	1:A:133:GLU:OE1	2.45	0.50
7:K:85:THR:HA	7:K:89:LEU:HD23	1.93	0.50
5:I:108:DT:O2	6:J:41:DG:N2	2.44	0.50
2:B:74:GLU:OE2	4:D:99:ARG:NH2	2.45	0.49
7:K:273:HIS:CE1	7:K:319:CYS:HG	2.29	0.49
6:J:44:DA:H2'	6:J:45:DT:H71	1.95	0.49
6:J:48:DC:H2''	6:J:49:DC:C6	2.47	0.49
5:I:94:DG:H4'	5:I:95:DC:OP1	2.12	0.49
2:F:73:THR:HG21	2:F:81:VAL:HG22	1.94	0.49
7:K:319:CYS:O	7:K:331:ALA:N	2.40	0.49
5:I:52:DA:C2	6:J:97:DG:N1	2.81	0.49
5:I:96:DC:H2''	5:I:97:DA:H5''	1.94	0.49
6:J:74:DA:H2''	6:J:75:DT:H5'	1.94	0.49
2:B:20:MET:SD	7:K:307:TYR:HA	2.53	0.49
2:B:85:ASP:OD1	4:D:83:TYR:OH	2.26	0.48
7:K:321:CYS:H	7:K:324:CYS:HB2	1.78	0.48
5:I:79:DC:H2''	5:I:80:DC:C6	2.49	0.48
7:K:181:HIS:O	7:K:184:ILE:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:121:DA:H2''	6:J:122:DG:C8	2.48	0.48
5:I:64:DC:H2''	5:I:65:DA:C8	2.48	0.48
2:F:80:THR:OG1	6:J:102:DA:O5'	2.29	0.48
5:I:27:DT:O2	6:J:122:DG:O6	2.31	0.48
6:J:78:DG:H2''	6:J:79:DT:C6	2.48	0.48
2:B:43:VAL:HG22	1:E:108:ASN:HB2	1.94	0.48
3:C:54:VAL:HG21	4:D:98:VAL:HG21	1.96	0.48
6:J:119:DT:H2''	6:J:120:DG:N7	2.28	0.48
6:J:86:DG:H2''	6:J:87:DT:H5'	1.95	0.47
7:K:319:CYS:H	7:K:331:ALA:N	2.11	0.47
3:C:68:ASN:HB3	7:K:360:ARG:HH12	1.78	0.47
6:J:67:DG:H2''	6:J:68:DG:C8	2.49	0.47
2:B:75:HIS:HB2	4:D:96:THR:HG21	1.96	0.47
3:G:27:VAL:HG21	3:G:49:VAL:HG22	1.97	0.47
6:J:61:DA:H5'	6:J:61:DA:C8	2.50	0.47
2:B:25:ASN:HA	7:K:257:ARG:HB2	1.96	0.47
7:K:241:MET:O	7:K:244:ARG:NH1	2.47	0.47
1:A:126:LEU:HD22	1:E:113:HIS:CG	2.50	0.47
1:E:104:PHE:HA	1:E:107:THR:HG22	1.96	0.47
6:J:121:DA:C2	6:J:122:DG:O6	2.69	0.46
1:E:128:ARG:NH2	1:E:135:ALA:O	2.49	0.46
6:J:71:DA:H5''	6:J:71:DA:H8	1.80	0.46
6:J:74:DA:H2'	6:J:75:DT:H71	1.96	0.46
1:A:108:ASN:ND2	2:F:42:GLY:O	2.48	0.46
7:K:253:MET:HB2	7:K:262:GLN:HB3	1.98	0.46
1:A:68:GLN:HE21	1:A:72:ARG:HE	1.64	0.46
7:K:212:ILE:HG23	7:K:303:ILE:HB	1.96	0.46
4:D:31:LYS:N	6:J:105:DT:OP1	2.49	0.46
5:I:40:DG:N2	6:J:109:DT:O2	2.48	0.46
7:K:276:ARG:HG2	7:K:295:ARG:NH2	2.31	0.46
3:C:61:GLU:OE2	7:K:352:ARG:NE	2.48	0.46
3:G:64:GLU:HB2	4:H:49:VAL:HG21	1.98	0.46
7:K:137:LEU:HA	7:K:140:VAL:HG12	1.97	0.45
7:K:149:HIS:O	7:K:149:HIS:ND1	2.45	0.45
7:K:184:ILE:HG22	7:K:187:ARG:HH21	1.81	0.45
7:K:346:ASN:HD22	7:K:349:TYR:H	1.64	0.45
3:C:16:THR:HG23	3:C:19:SER:H	1.80	0.45
5:I:29:DA:H2''	5:I:30:DA:N7	2.31	0.45
6:J:96:DT:H2'	6:J:97:DG:C8	2.50	0.45
3:G:16:THR:HG23	3:G:19:SER:H	1.81	0.45
2:B:18:HIS:HA	7:K:311:PHE:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:30:VAL:HG13	4:H:71:PHE:HE1	1.82	0.45
5:I:84:DC:H2''	5:I:85:DG:H8	1.80	0.45
6:J:30:DG:C5	6:J:31:DA:H2	2.34	0.45
7:K:324:CYS:HG	7:K:329:THR:HG1	1.65	0.45
6:J:52:DG:H2''	6:J:53:DG:C8	2.52	0.45
7:K:232:ALA:H	7:K:262:GLN:NE2	2.05	0.45
2:B:92:ARG:NH1	4:D:100:LEU:HB3	2.32	0.45
1:A:69:ARG:HB3	2:F:25:ASN:ND2	2.29	0.44
5:I:33:DG:H1'	5:I:34:DG:N7	2.32	0.44
6:J:42:DT:H2'	6:J:43:DA:C8	2.52	0.44
3:C:100:VAL:HG21	2:F:98:TYR:CZ	2.53	0.44
3:C:115:LEU:O	2:F:44:LYS:NZ	2.44	0.44
5:I:58:DT:H1'	5:I:59:DA:C5	2.53	0.44
5:I:72:DG:H2''	5:I:73:DA:C8	2.53	0.44
5:I:81:DC:H1'	5:I:82:DC:H5'	2.00	0.44
6:J:31:DA:H1'	6:J:32:DG:N7	2.33	0.44
6:J:91:DA:H2''	6:J:92:DG:C8	2.53	0.44
4:D:109:HIS:O	4:D:112:SER:OG	2.29	0.44
1:E:69:ARG:NH1	5:I:91:DA:OP2	2.50	0.44
2:F:35:ARG:O	2:F:39:ARG:HG2	2.18	0.44
6:J:88:DT:H2''	6:J:89:DT:H5'	1.99	0.43
1:A:62:ILE:O	1:A:93:GLN:NE2	2.51	0.43
2:B:36:ARG:HH12	6:J:61:DA:P	2.41	0.43
1:E:62:ILE:O	1:E:93:GLN:NE2	2.51	0.43
2:F:30:THR:OG1	2:F:32:PRO:HD2	2.18	0.43
5:I:121:DG:H2''	5:I:122:DG:C8	2.53	0.43
1:E:79:LYS:HB3	1:E:82:LEU:HD11	2.00	0.43
4:H:87:ARG:HD3	4:H:87:ARG:HA	1.88	0.43
6:J:58:DT:H2''	6:J:59:DA:N7	2.33	0.43
7:K:273:HIS:HD2	7:K:307:TYR:HB2	1.81	0.43
4:D:90:THR:OG1	4:D:93:GLU:OE1	2.26	0.43
3:G:102:ILE:HG23	4:H:62:ILE:HD13	2.00	0.43
5:I:86:DT:H2'	5:I:87:DT:H72	2.00	0.43
1:A:82:LEU:HD23	1:A:82:LEU:HA	1.91	0.42
6:J:110:DA:H2''	6:J:111:DC:C5	2.53	0.42
7:K:197:ILE:HD11	7:K:210:ALA:HB1	2.01	0.42
7:K:274:ASP:OD2	7:K:304:SER:OG	2.30	0.42
3:C:59:THR:HG23	4:D:62:MET:HE2	2.01	0.42
1:A:99:TYR:OH	1:A:128:ARG:NH1	2.51	0.42
3:C:24:GLN:N	3:C:56:GLU:OE1	2.52	0.42
7:K:244:ARG:NE	7:K:247:GLU:OE1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:THR:HB	2:F:45:ARG:HH11	1.84	0.42
7:K:227:LEU:HG	7:K:268:ALA:HB2	2.01	0.42
1:A:65:LEU:HB2	6:J:92:DG:OP2	2.20	0.42
5:I:27:DT:O2	6:J:122:DG:C6	2.73	0.42
2:B:20:MET:HE3	2:B:20:MET:HB3	1.89	0.42
7:K:220:ARG:NE	7:K:294:LEU:O	2.53	0.42
6:J:120:DG:H2'	6:J:121:DA:O4'	2.20	0.42
7:K:238:GLU:HA	7:K:241:MET:HE2	2.01	0.42
2:F:31:LYS:HG3	2:F:51:TYR:CE1	2.55	0.42
5:I:58:DT:H4'	5:I:59:DA:H5'	2.02	0.42
6:J:63:DC:H2'	6:J:64:DG:C8	2.55	0.42
4:D:102:LEU:HB2	4:D:107:ALA:HB2	2.02	0.41
6:J:108:DC:H2''	6:J:109:DT:C7	2.50	0.41
2:B:31:LYS:HG3	2:B:51:TYR:CE1	2.55	0.41
3:C:56:GLU:HG2	7:K:349:TYR:HE2	1.86	0.41
5:I:26:DC:H2'	5:I:27:DT:O4'	2.20	0.41
5:I:112:DT:H2''	5:I:113:DA:N7	2.35	0.41
6:J:102:DA:H8	6:J:102:DA:H5''	1.85	0.41
7:K:183:PHE:HD1	7:K:186:LEU:HD12	1.85	0.41
5:I:60:DA:H2''	5:I:61:DA:C8	2.55	0.41
6:J:82:DG:H2'	6:J:83:DT:H71	2.01	0.41
5:I:58:DT:H1'	5:I:59:DA:N7	2.35	0.41
5:I:70:DC:H1'	5:I:71:DG:N7	2.35	0.41
5:I:84:DC:H2''	5:I:85:DG:C8	2.55	0.41
7:K:220:ARG:O	7:K:221:ASN:ND2	2.53	0.41
7:K:224:ILE:HG13	7:K:227:LEU:H	1.85	0.41
2:B:20:MET:HB2	7:K:253:MET:HA	2.02	0.41
2:F:39:ARG:HA	2:F:39:ARG:HD3	1.86	0.41
1:E:60:LEU:HD21	1:E:94:GLU:CD	2.46	0.41
7:K:195:PHE:HB2	7:K:212:ILE:HD11	2.03	0.41
3:C:26:PRO:HD3	4:D:40:TYR:CG	2.55	0.41
4:D:84:ASN:OD1	4:D:84:ASN:N	2.54	0.41
4:D:116:LYS:O	4:D:119:THR:OG1	2.30	0.41
3:G:57:TYR:HB2	4:H:114:GLU:HG2	2.03	0.41
5:I:49:DA:H2''	5:I:50:DG:N7	2.36	0.41
5:I:111:DC:H6	5:I:111:DC:H2'	1.69	0.41
6:J:48:DC:H2''	6:J:49:DC:C5	2.56	0.41
6:J:70:DG:H2''	6:J:71:DA:C8	2.56	0.41
7:K:273:HIS:HD2	7:K:307:TYR:H	1.68	0.41
1:A:116:ARG:HH22	1:A:123:ASP:CG	2.27	0.41
2:B:58:LEU:HD13	1:E:100:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:24:GLN:N	3:G:56:GLU:OE1	2.53	0.41
2:F:75:HIS:HB2	4:H:97:THR:HG21	2.02	0.40
5:I:78:DC:H2''	5:I:79:DC:C5	2.55	0.40
6:J:112:DG:H2''	6:J:113:DA:C8	2.56	0.40
5:I:90:DA:H1'	5:I:91:DA:N7	2.36	0.40
6:J:27:DC:H1'	6:J:28:DT:C2	2.57	0.40
7:K:98:HIS:O	7:K:98:HIS:ND1	2.50	0.40
3:C:16:THR:N	3:C:19:SER:OG	2.54	0.40
5:I:25:DG:H2''	5:I:26:DC:H5''	2.04	0.40
2:F:48:GLY:H	6:J:81:DC:P	2.41	0.40
5:I:91:DA:H2''	5:I:92:DC:H5''	2.03	0.40
6:J:83:DT:H2''	6:J:84:DG:C8	2.56	0.40
1:A:60:LEU:HD21	1:A:94:GLU:CD	2.46	0.40
7:K:202:ARG:NH2	7:K:325:GLU:HB2	2.35	0.40
7:K:322:TYR:HD1	7:K:322:TYR:HA	1.77	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	94/135 (70%)	90 (96%)	4 (4%)	0	100	100
1	E	90/135 (67%)	87 (97%)	3 (3%)	0	100	100
2	B	84/103 (82%)	82 (98%)	2 (2%)	0	100	100
2	F	78/103 (76%)	74 (95%)	4 (5%)	0	100	100
3	C	105/130 (81%)	105 (100%)	0	0	100	100
3	G	105/130 (81%)	103 (98%)	2 (2%)	0	100	100
4	D	93/123 (76%)	93 (100%)	0	0	100	100
4	H	89/123 (72%)	88 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	K	243/394 (62%)	235 (97%)	8 (3%)	0	100	100
All	All	981/1376 (71%)	957 (98%)	24 (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	83/110 (76%)	82 (99%)	1 (1%)	63	72
1	E	79/110 (72%)	79 (100%)	0	100	100
2	B	71/79 (90%)	69 (97%)	2 (3%)	38	60
2	F	65/79 (82%)	65 (100%)	0	100	100
3	C	81/102 (79%)	81 (100%)	0	100	100
3	G	81/102 (79%)	80 (99%)	1 (1%)	63	72
4	D	81/103 (79%)	81 (100%)	0	100	100
4	H	77/103 (75%)	77 (100%)	0	100	100
7	K	207/344 (60%)	203 (98%)	4 (2%)	50	66
All	All	825/1132 (73%)	817 (99%)	8 (1%)	65	75

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LEU
2	B	34	ILE
2	B	57	VAL
3	G	27	VAL
7	K	76	GLU
7	K	212	ILE
7	K	252	VAL
7	K	322	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	68	GLN
1	A	85	GLN
1	A	108	ASN
2	B	25	ASN
3	C	38	ASN
3	C	110	ASN
3	C	112	GLN
4	D	109	HIS
2	F	25	ASN
3	G	38	ASN
3	G	73	ASN
3	G	112	GLN
4	H	48	GLN
4	H	50	HIS
4	H	85	ASN
7	K	134	GLN
7	K	221	ASN
7	K	240	ASN
7	K	262	GLN
7	K	346	ASN
7	K	359	ASN

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.

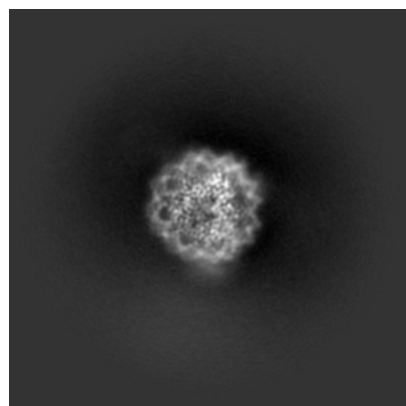
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41111. These allow visual inspection of the internal detail of the map and identification of artifacts.

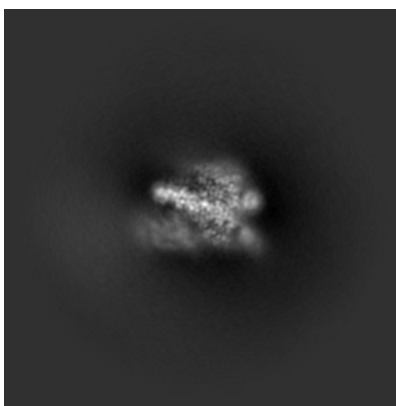
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

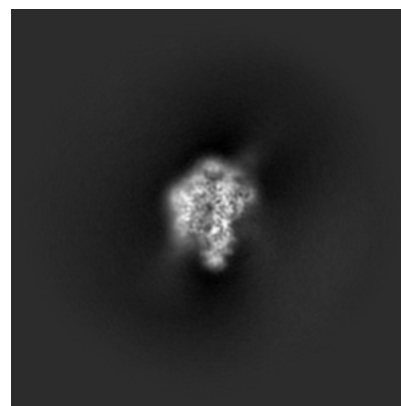
6.1.1 Primary map



X

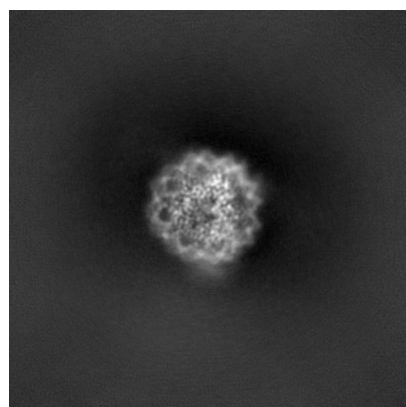


Y

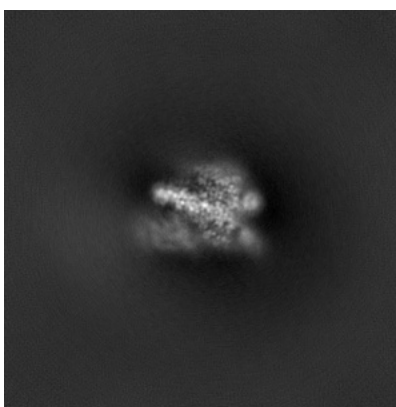


Z

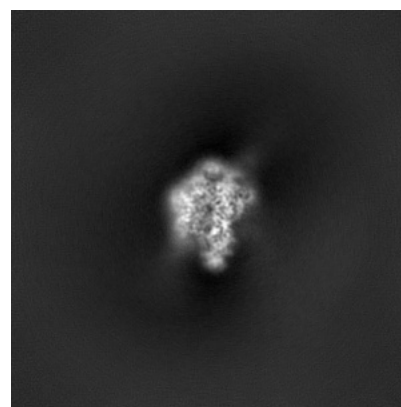
6.1.2 Raw map



X



Y

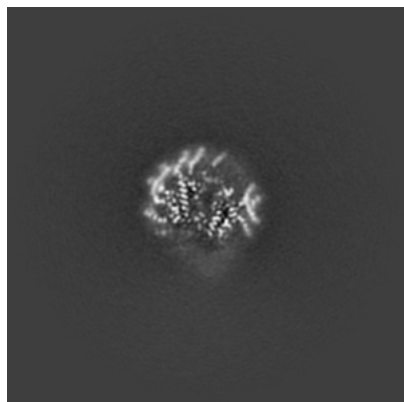


Z

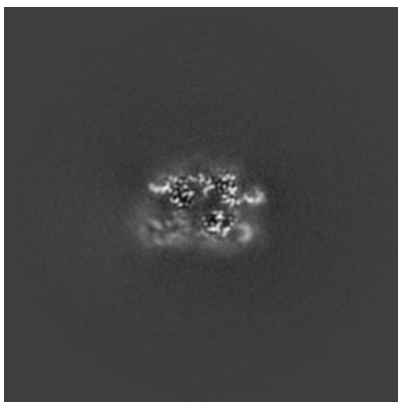
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

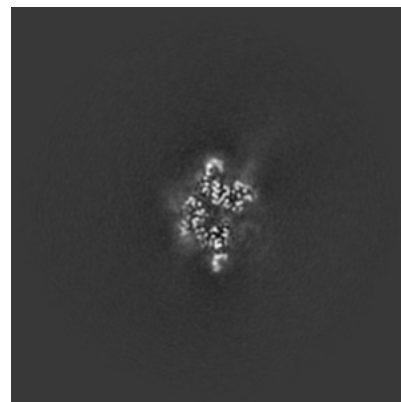
6.2.1 Primary map



X Index: 160

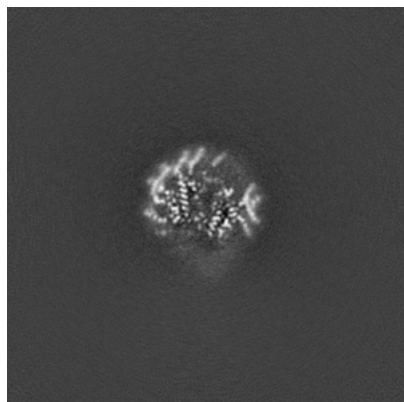


Y Index: 160

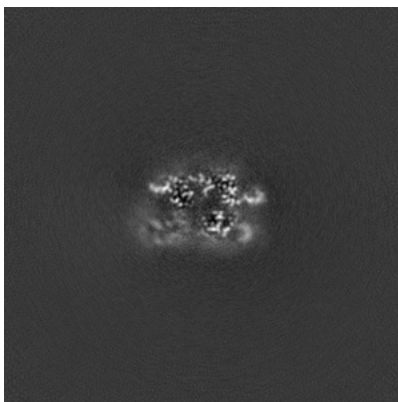


Z Index: 160

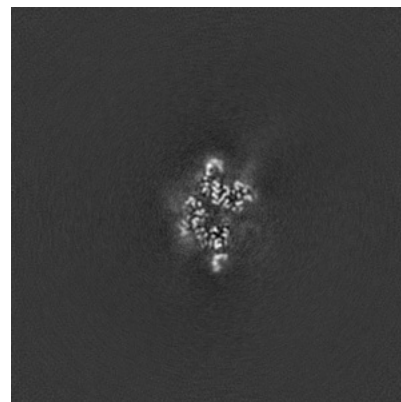
6.2.2 Raw map



X Index: 160



Y Index: 160

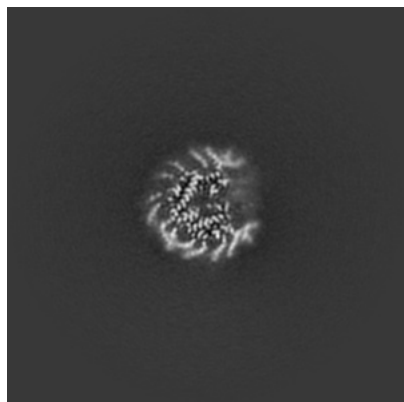


Z Index: 160

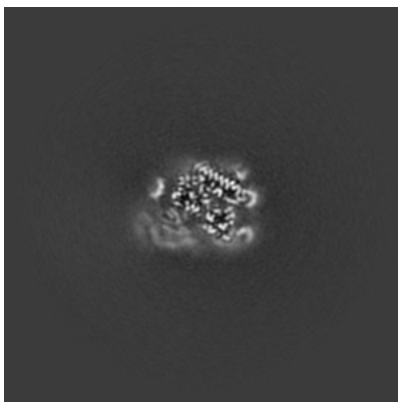
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

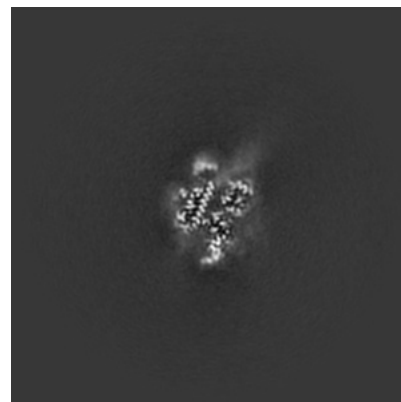
6.3.1 Primary map



X Index: 170

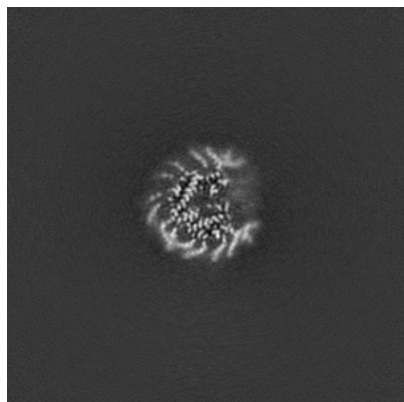


Y Index: 167

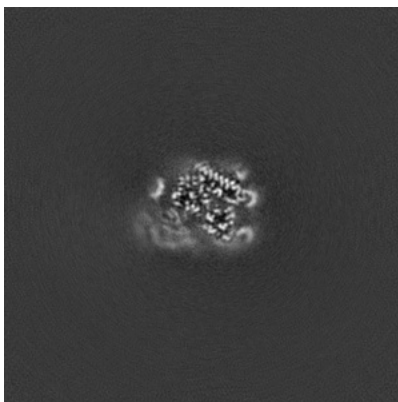


Z Index: 171

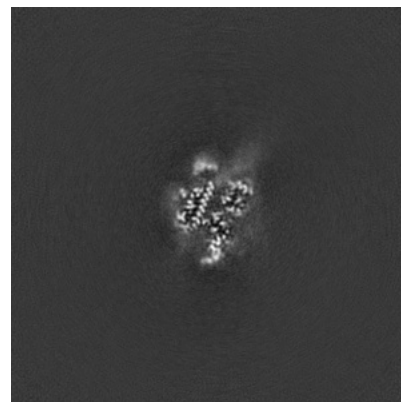
6.3.2 Raw map



X Index: 170



Y Index: 167

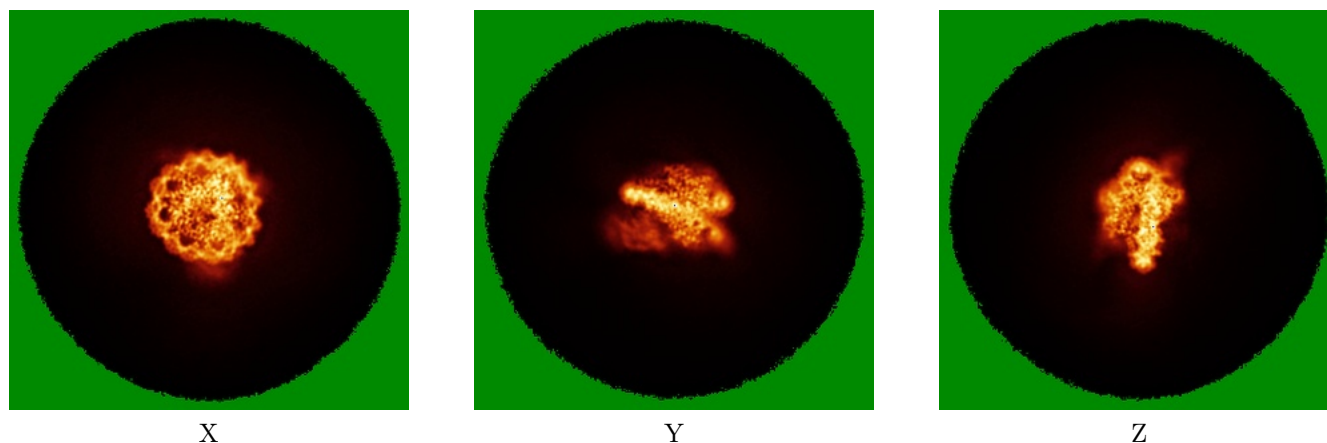


Z Index: 171

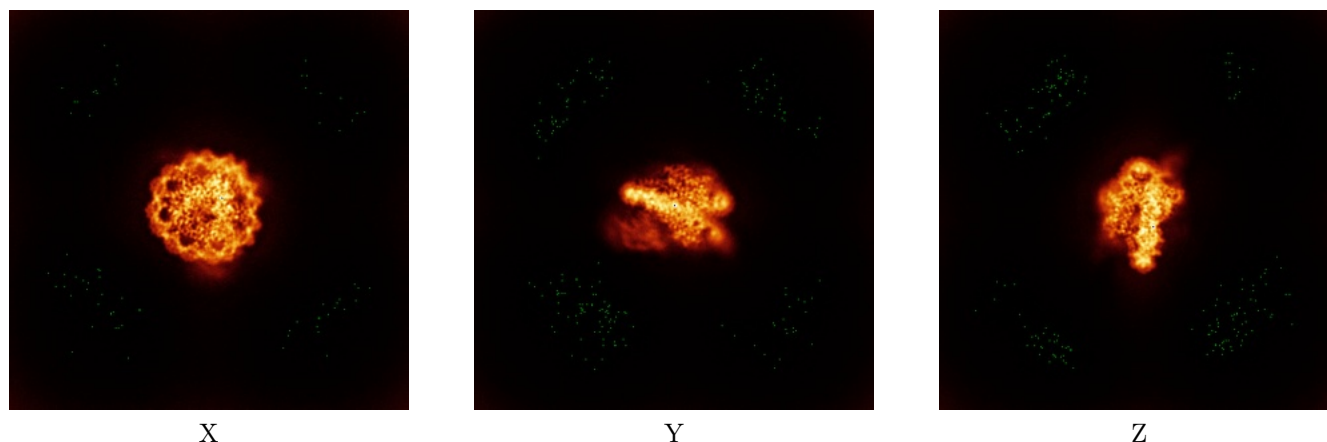
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

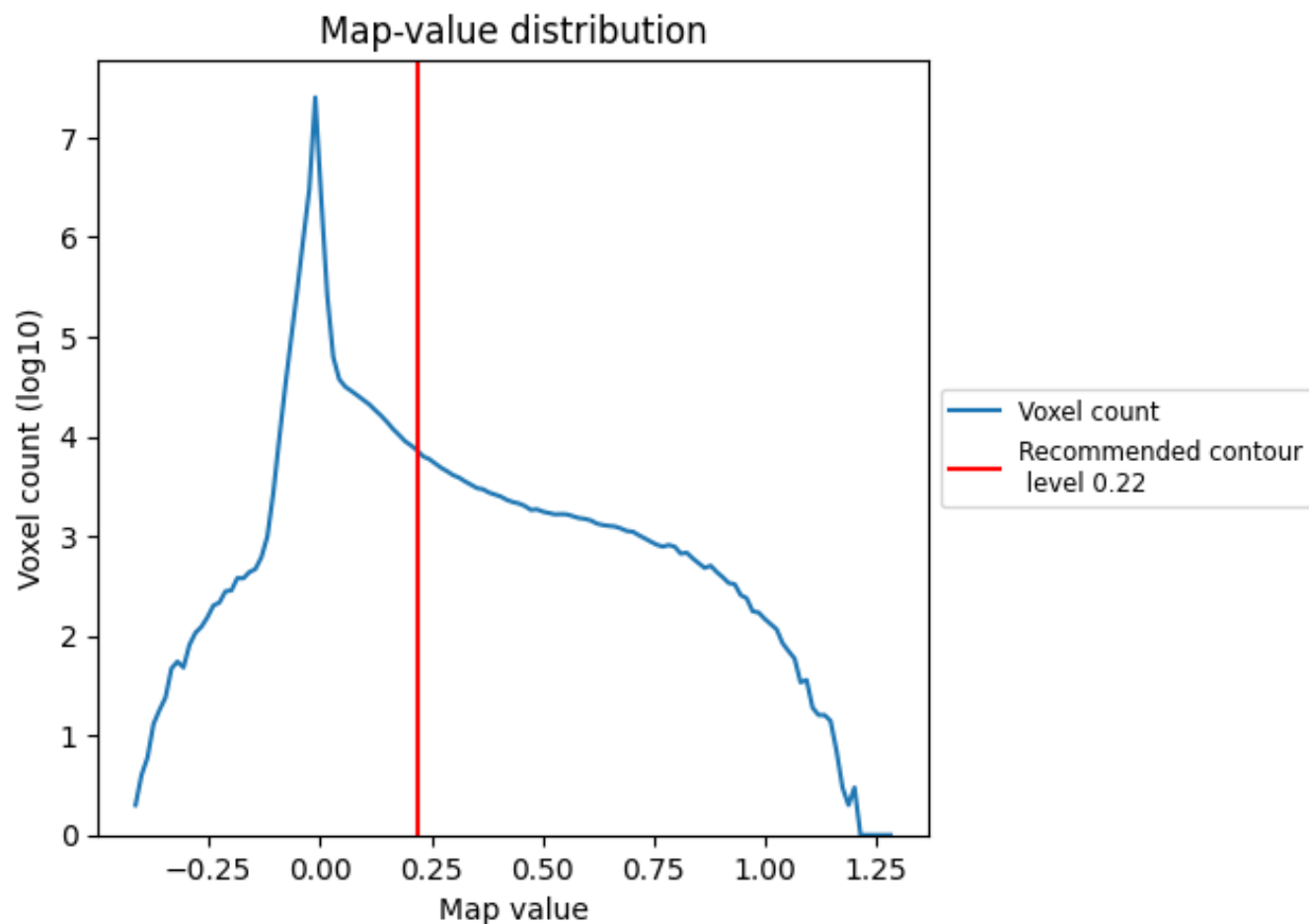
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

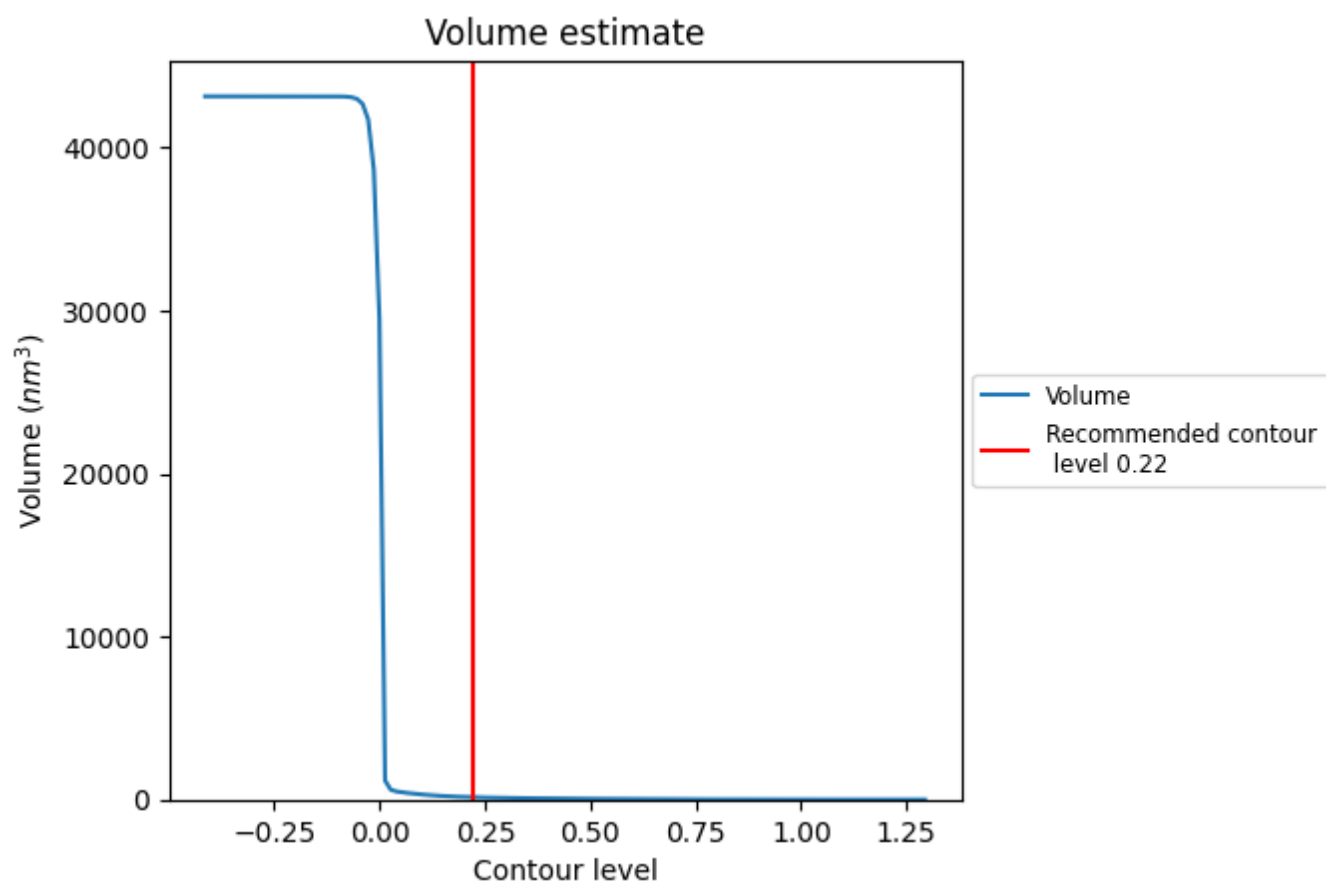
This section contains the results of statistical analysis of the map.

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.

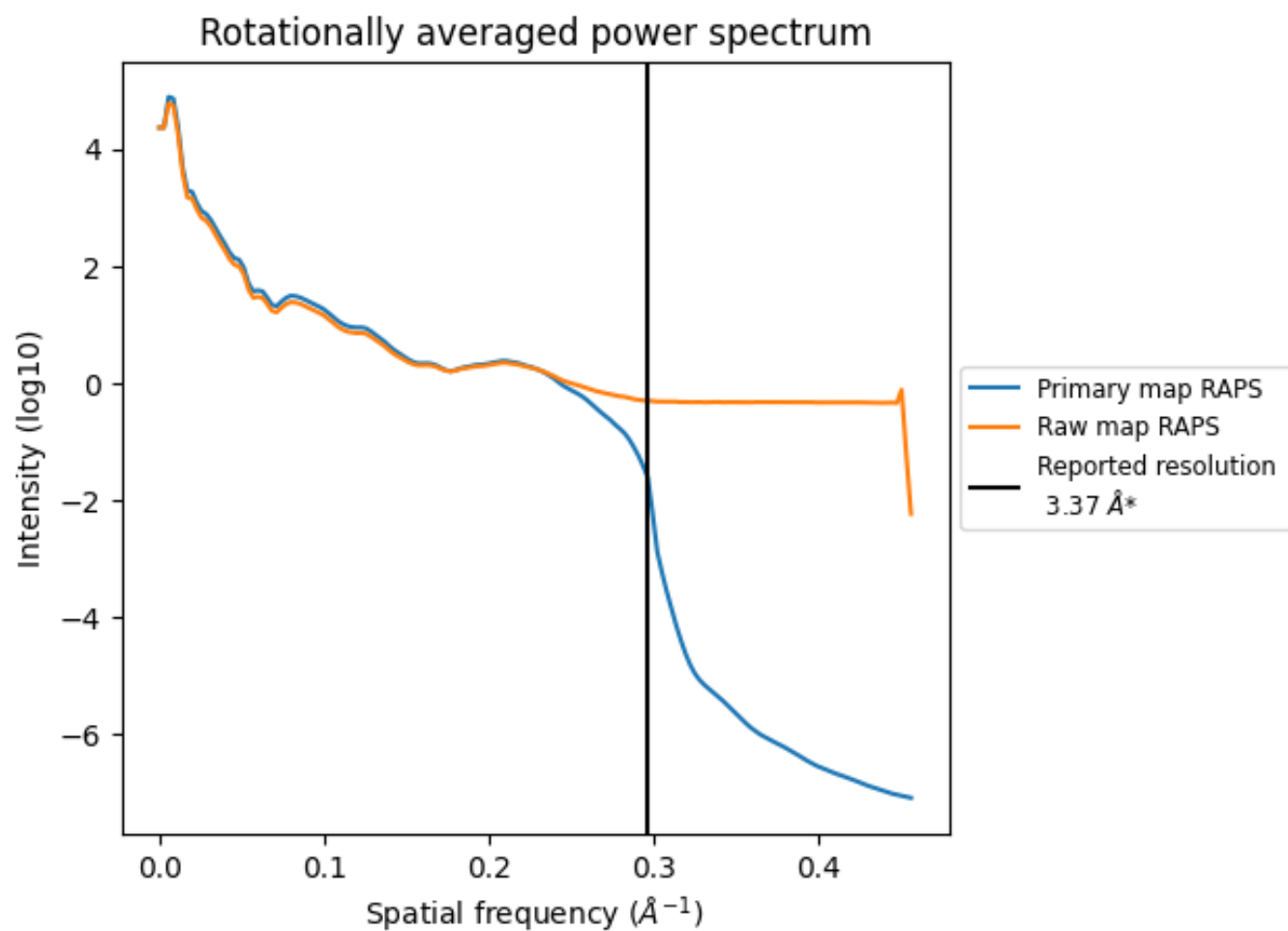
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 144 nm³; this corresponds to an approximate mass of 130 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 ⓘ

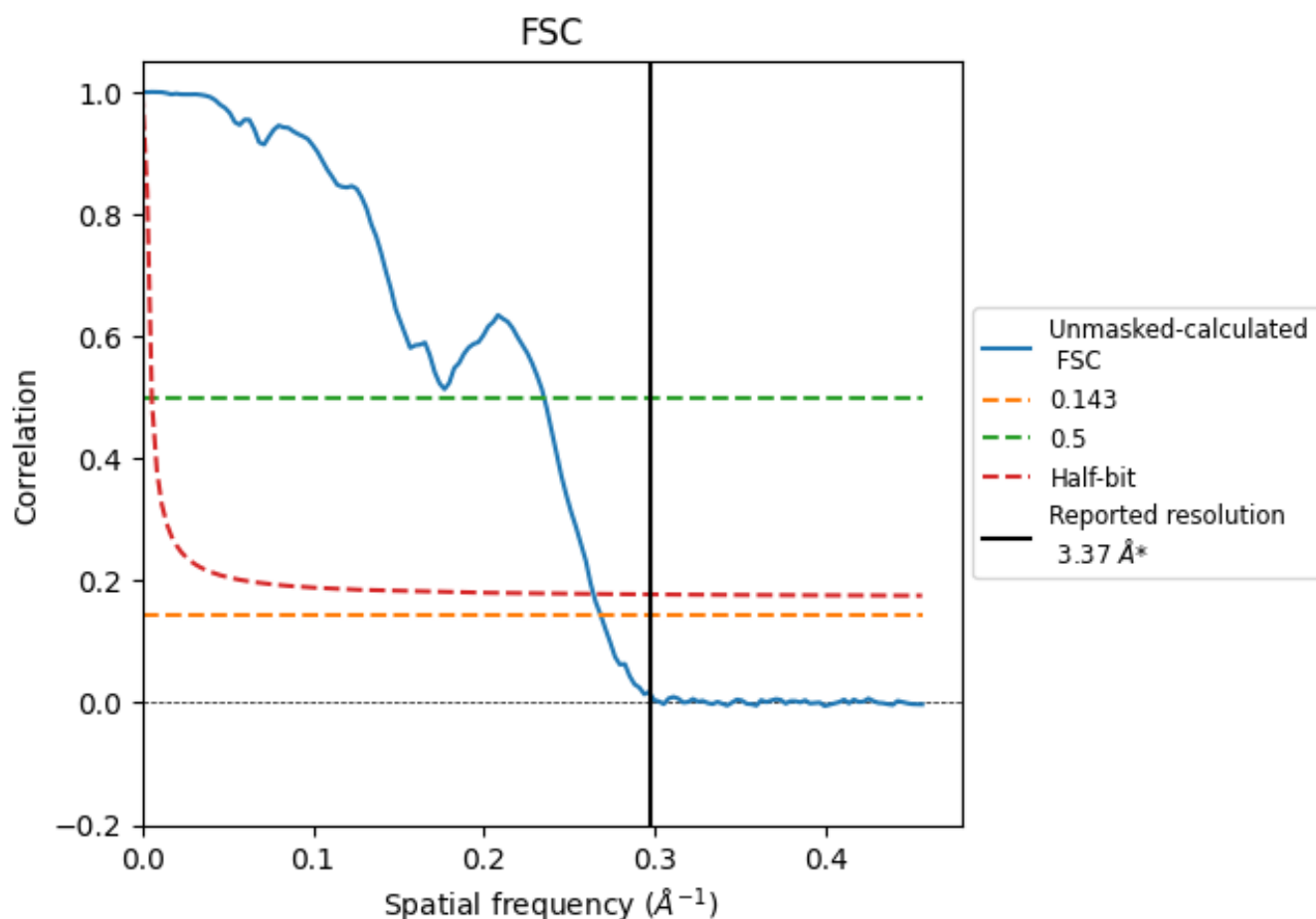


*Reported resolution corresponds to spatial frequency of 0.297 Å⁻¹

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 $0.297 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

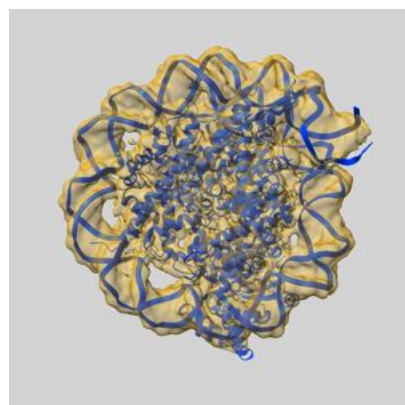
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.37	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.73	4.26	3.79

*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 3.73 differs from the reported value 3.37 by more than 10 %

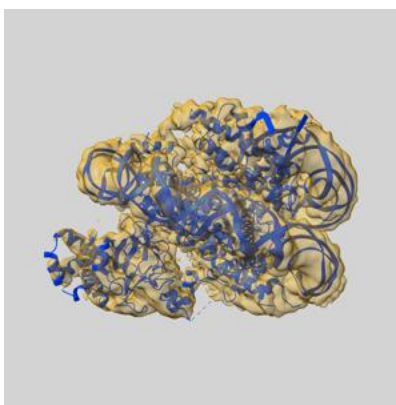
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41111 and PDB model 8T9H. Per-residue inclusion information can be found in section [3](#) on page [6](#).

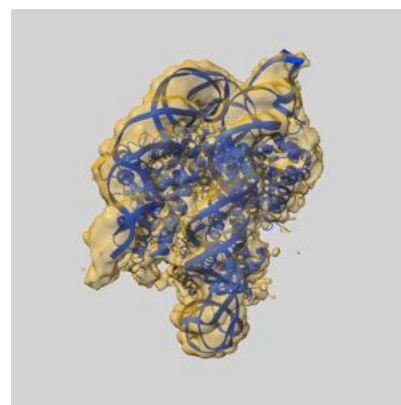
9.1 Map-model overlay [i](#)



X



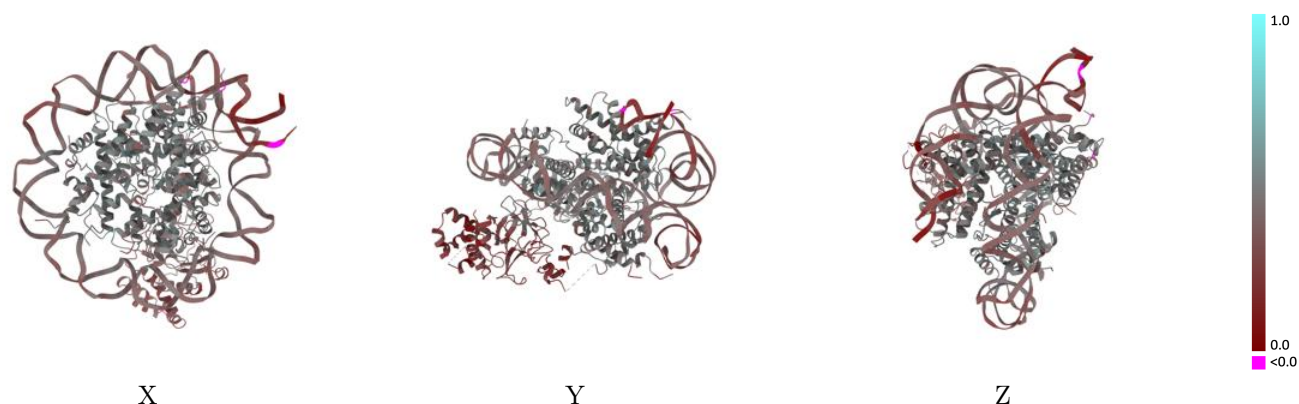
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.22 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](#)

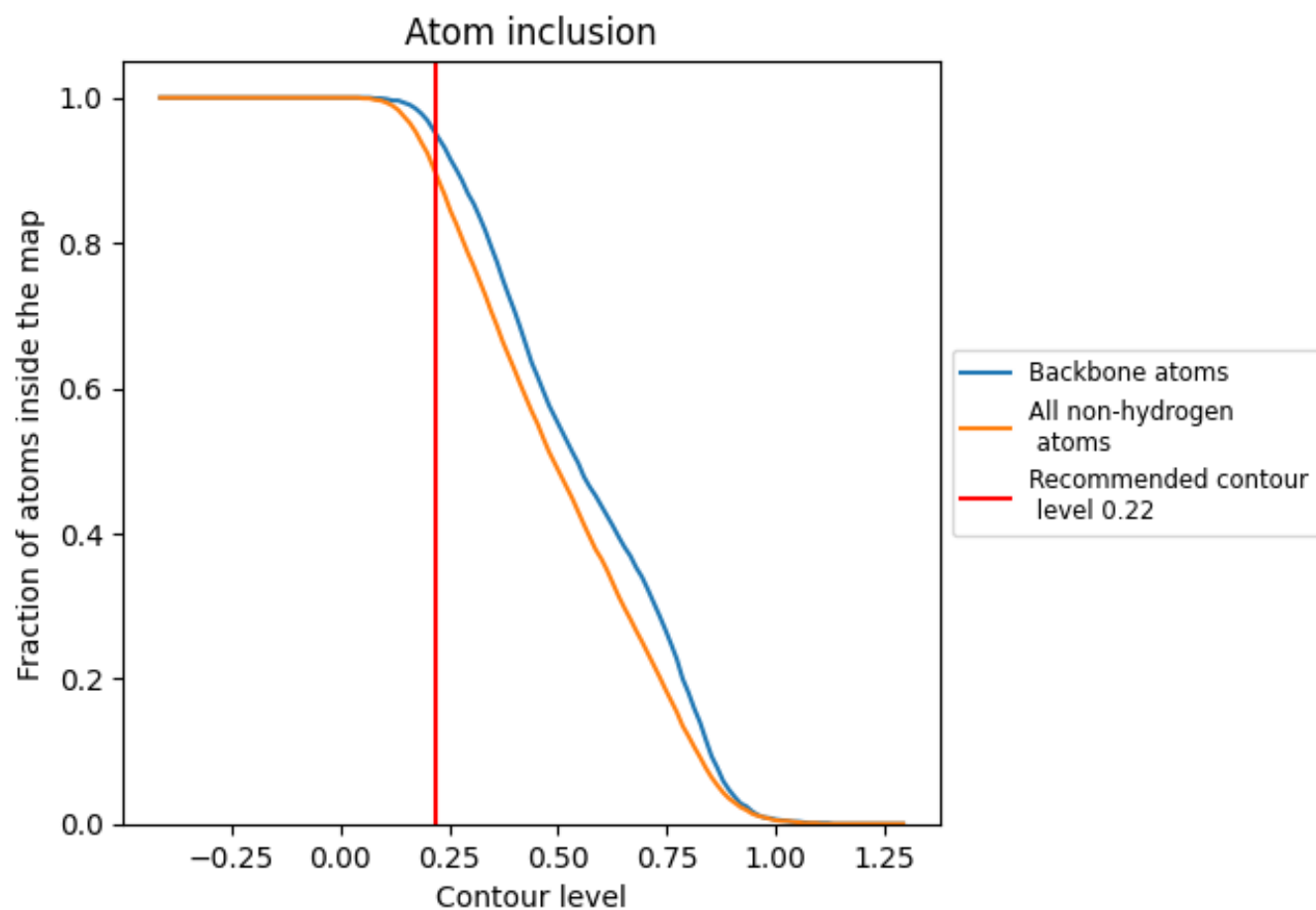


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 89% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8940	0.3930
A	0.8840	0.4770
B	0.9250	0.4750
C	0.8870	0.4610
D	0.9410	0.4550
E	0.9130	0.4790
F	0.9430	0.4910
G	0.8680	0.4640
H	0.9480	0.4650
I	0.9790	0.3570
J	0.9610	0.3430
K	0.6810	0.2500

1.0

0.0

<0.0