Full wwPDB EM Validation Report (i)

Nov 27, 2022 – 05:31 AM EST

PDB ID	:	6O1O
EMDB ID	:	EMD-0454
Title	:	Cryo-EM structure of the T. thermophilus Csm complex bound to target ss-RNA
Authors	:	Liu, J.J.; Liu, T.Y.
Deposited on	:	2019-02-21
Resolution	:	3.80 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 (i) 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 (i)) were used in the production of this report:

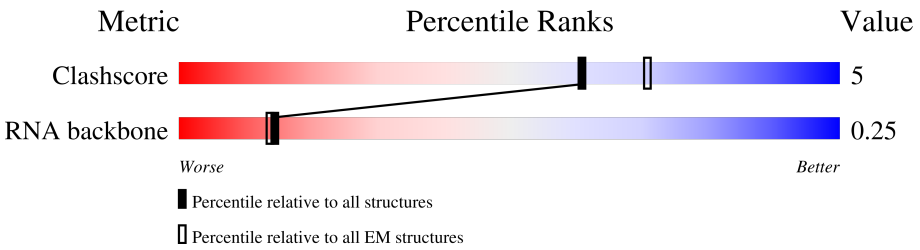
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 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	158937	4297
RNA backbone	4643	859

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 <=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	716	12% 93% 7%
2	B	279	15% 93% 7%
2	G	279	15% 73% • 25%
2	H	279	41% 68% 7% 25%
3	C	218	5% 91% 9%
3	D	218	• 91% 9%
3	E	218	• 96% •
3	F	218	• 96% • •
4	I	118	• 92% 8%

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Mol	Chain	Length	Quality of chain
4	J	118	92% 8%
4	K	118	9% 92% 8%
4	L	118	51% 92% 8%
5	M	48	10% 38% 23% 25%
6	N	50	18% 20% 14% 8% 40%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 15193 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 Csm1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	716	3580	2148	716	716	0	0

- Molecule 2 is a protein called Csm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	279	1395	837	279	279	0	0
2	G	210	1050	630	210	210	0	0
2	H	210	1050	630	210	210	0	0

- Molecule 3 is a protein called Csm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	218	1090	654	218	218	0	0
3	D	218	1090	654	218	218	0	0
3	E	218	1090	654	218	218	0	0
3	F	216	1080	648	216	216	0	0

- Molecule 4 is a protein called Csm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	I	118	590	354	118	118	0	0
4	J	118	590	354	118	118	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	K	118	590	354	118	118	0	0
4	L	118	590	354	118	118	0	0

- Molecule 5 is a RNA chain called RNA (36-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	M	36	775	345	147	247	36	0	0

- Molecule 6 is a RNA chain called RNA (30-MER).

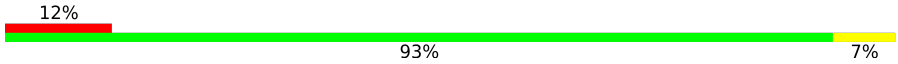
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	N	30	633	282	106	215	30	0	0

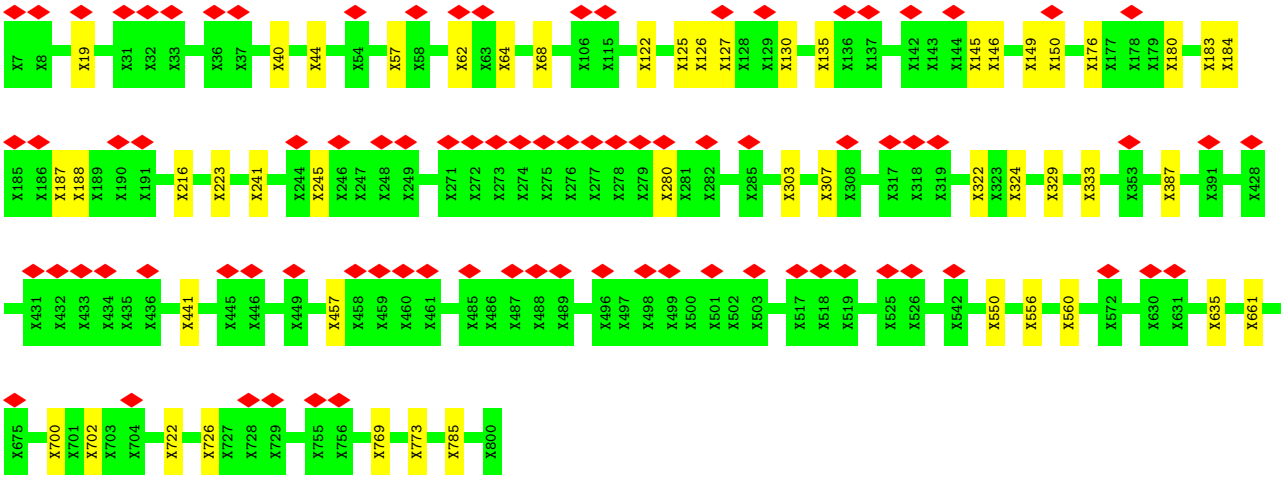
3 Residue-property plots (i)

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: Csm1

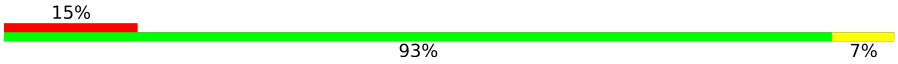
Chain A:

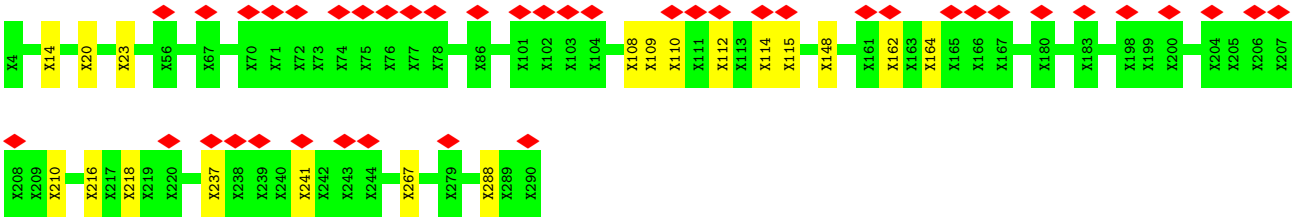




- Molecule 2: Csm4

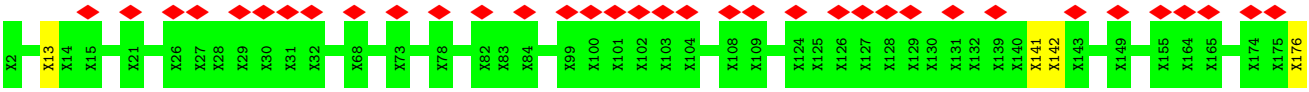
Chain B:

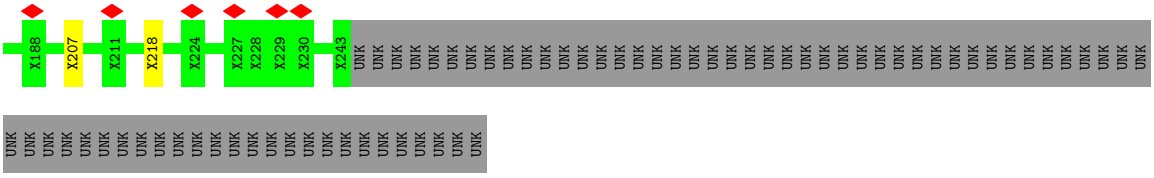




- Molecule 2: Csm4

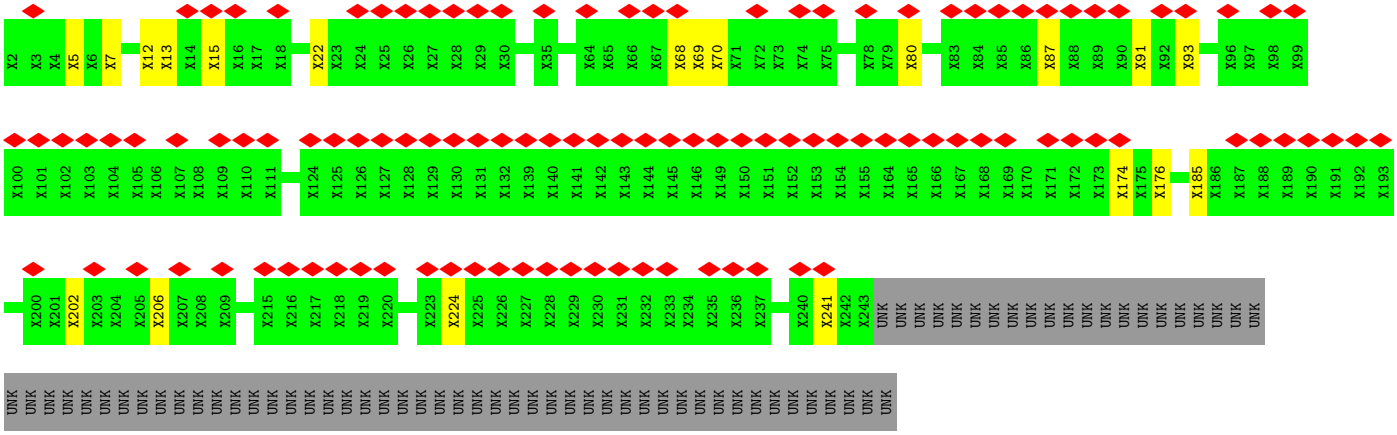
Chain G:





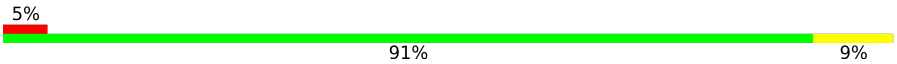
- Molecule 2: Csm4

Chain H:



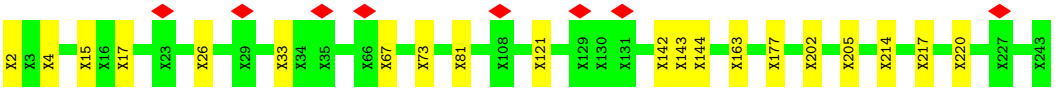
- Molecule 3: Csm3

Chain C:



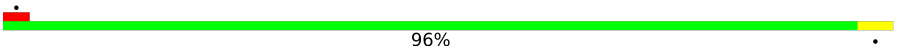
- Molecule 3: Csm3

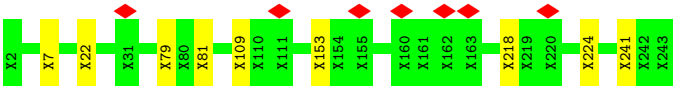
Chain D:



- Molecule 3: Csm3

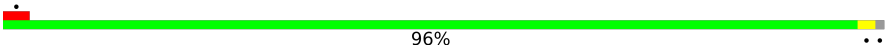
Chain E:

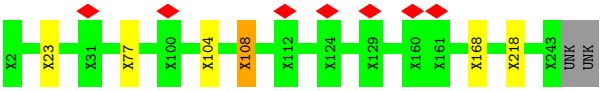




- Molecule 3: Csm3

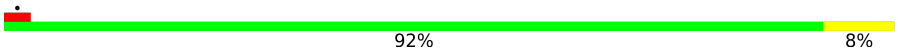
Chain F:

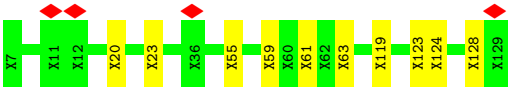




• Molecule 4: Csm2

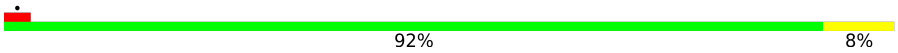
Chain I:

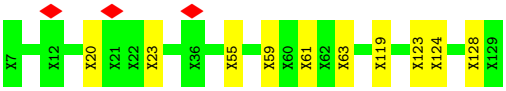




• Molecule 4: Csm2

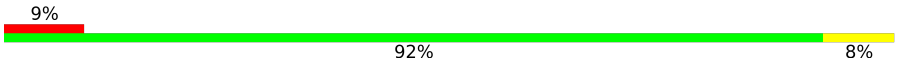
Chain J:

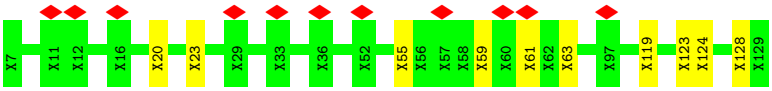




• Molecule 4: Csm2

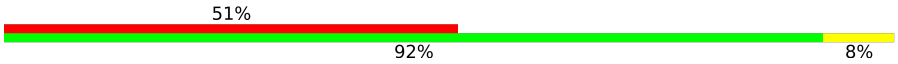
Chain K:

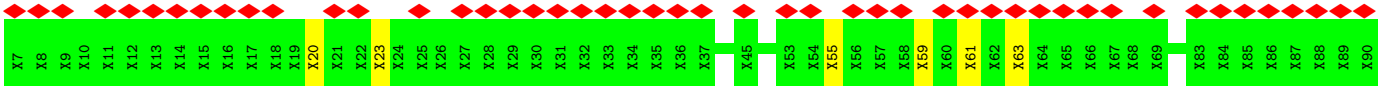


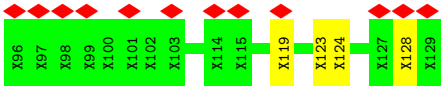


• Molecule 4: Csm2

Chain L:

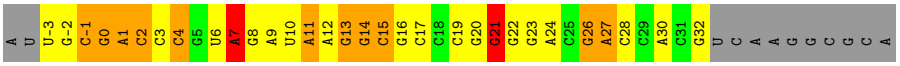






• Molecule 5: RNA (36-MER)

Chain M:



• Molecule 6: RNA (30-MER)

Chain N:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	87321	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.282	Depositor
Minimum map value	-1.862	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.074	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	410.40002, 410.40002, 410.40002	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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
5	M	2.04	21/867 (2.4%)	2.24	65/1351 (4.8%)
6	N	1.48	2/704 (0.3%)	1.56	13/1094 (1.2%)
All	All	1.81	23/1571 (1.5%)	1.96	78/2445 (3.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
2	B	0	1
2	G	0	3
2	H	0	1
3	C	0	9
3	D	0	9
3	E	0	5
3	F	0	3
All	All	0	38

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	7	A	N9-C4	-10.78	1.31	1.37
5	M	12	A	N9-C4	-9.48	1.32	1.37
5	M	11	A	N9-C4	-7.12	1.33	1.37
5	M	12	A	C5-C4	-7.09	1.33	1.38
5	M	30	A	N9-C4	-6.93	1.33	1.37
5	M	27	A	N9-C4	-6.72	1.33	1.37
5	M	7	A	C5-C6	-6.35	1.35	1.41
5	M	11	A	N3-C4	-6.24	1.31	1.34
5	M	15	C	N1-C6	-6.13	1.33	1.37
5	M	11	A	C5-C4	-5.83	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	24	A	N9-C4	-5.79	1.34	1.37
5	M	15	C	N3-C4	-5.75	1.29	1.33
5	M	11	A	N9-C8	-5.75	1.33	1.37
5	M	11	A	N7-C5	-5.70	1.35	1.39
5	M	9	A	N9-C4	-5.44	1.34	1.37
6	N	33	A	N9-C4	-5.42	1.34	1.37
5	M	21	G	C8-N7	-5.31	1.27	1.30
5	M	22	G	C5-C4	-5.27	1.34	1.38
5	M	12	A	N9-C8	-5.10	1.33	1.37
5	M	16	G	N7-C5	-5.08	1.36	1.39
5	M	12	A	C5-C6	-5.08	1.36	1.41
5	M	21	G	N9-C8	-5.06	1.34	1.37
6	N	37	A	N9-C4	-5.01	1.34	1.37

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	M	20	G	C4-C5-N7	10.86	115.14	110.80
5	M	1	A	C8-N9-C4	-10.32	101.67	105.80
5	M	12	A	C8-N9-C4	9.55	109.62	105.80
5	M	0	G	O5'-P-OP1	9.41	121.99	110.70
5	M	2	C	C5-C6-N1	9.25	125.63	121.00
5	M	21	G	N3-C4-N9	9.10	131.46	126.00
5	M	21	G	N1-C2-N2	-8.77	108.31	116.20
5	M	20	G	N9-C4-C5	-8.52	101.99	105.40
5	M	14	G	C4-C5-N7	8.14	114.06	110.80
5	M	-2	G	C4-C5-N7	8.09	114.04	110.80
5	M	15	C	O4'-C1'-N1	8.06	114.65	108.20
5	M	21	G	O4'-C1'-N9	7.93	114.55	108.20
5	M	-2	G	C6-C5-N7	-7.71	125.78	130.40
5	M	7	A	O4'-C1'-N9	7.66	114.32	108.20
5	M	20	G	C6-C5-N7	-7.57	125.86	130.40
5	M	22	G	C8-N9-C4	7.48	109.39	106.40
5	M	-2	G	C4-N9-C1'	7.33	136.03	126.50
5	M	7	A	C5-N7-C8	-7.31	100.24	103.90
6	N	37	A	C5-N7-C8	-7.08	100.36	103.90
5	M	7	A	C4-C5-N7	7.04	114.22	110.70
5	M	20	G	C5-N7-C8	-6.96	100.82	104.30
5	M	1	A	N7-C8-N9	6.84	117.22	113.80
5	M	-2	G	C8-N9-C1'	-6.77	118.20	127.00
6	N	37	A	C4-C5-N7	6.77	114.08	110.70
5	M	27	A	C8-N9-C4	6.71	108.48	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	M	6	U	C5-C6-N1	6.66	126.03	122.70
6	N	17	C	C6-N1-C2	6.54	122.92	120.30
5	M	21	G	N3-C2-N2	6.43	124.40	119.90
6	N	28	G	N1-C6-O6	-6.43	116.04	119.90
6	N	22	C	C2-N3-C4	-6.31	116.75	119.90
5	M	-2	G	C5-C6-O6	-6.28	124.83	128.60
5	M	21	G	N9-C4-C5	-6.18	102.93	105.40
5	M	-2	G	N1-C6-O6	6.14	123.58	119.90
5	M	23	G	C5-C6-O6	-6.13	124.92	128.60
6	N	35	C	P-O3'-C3'	6.07	126.98	119.70
5	M	21	G	N3-C4-C5	-6.05	125.58	128.60
5	M	16	G	C4-C5-N7	6.01	113.21	110.80
6	N	22	C	N3-C2-O2	-6.00	117.70	121.90
5	M	26	G	N9-C4-C5	-5.89	103.04	105.40
6	N	11	C	C6-N1-C2	-5.88	117.95	120.30
5	M	2	C	N3-C4-N4	5.82	122.07	118.00
6	N	20	C	N3-C4-C5	5.77	124.21	121.90
5	M	14	G	N9-C4-C5	-5.73	103.11	105.40
5	M	20	G	C8-N9-C1'	-5.73	119.55	127.00
5	M	21	G	C6-C5-N7	-5.70	126.98	130.40
5	M	0	G	C2-N3-C4	-5.69	109.06	111.90
5	M	-1	C	C2-N1-C1'	5.69	125.05	118.80
5	M	21	G	N1-C2-N3	5.64	127.28	123.90
5	M	-2	G	N9-C4-C5	-5.63	103.15	105.40
5	M	12	A	N9-C4-C5	-5.63	103.55	105.80
5	M	21	G	C6-N1-C2	-5.56	121.76	125.10
5	M	2	C	O5'-P-OP2	-5.48	100.77	105.70
5	M	14	G	P-O3'-C3'	5.43	126.22	119.70
5	M	2	C	C6-N1-C2	-5.41	118.14	120.30
6	N	33	A	C5-N7-C8	-5.36	101.22	103.90
5	M	-3	U	C2-N1-C1'	-5.31	111.33	117.70
5	M	14	G	O4'-C1'-N9	5.30	112.44	108.20
5	M	4	C	C5-C6-N1	5.30	123.65	121.00
5	M	-2	G	N3-C4-N9	5.27	129.16	126.00
6	N	36	U	N1-C2-O2	5.22	126.46	122.80
5	M	-3	U	C6-N1-C1'	5.22	128.51	121.20
5	M	-2	G	C5-N7-C8	-5.18	101.71	104.30
5	M	13	G	O4'-C1'-N9	5.17	112.34	108.20
5	M	4	C	C6-N1-C2	-5.16	118.23	120.30
5	M	16	G	N9-C4-C5	-5.16	103.34	105.40
5	M	14	G	C5-N7-C8	-5.14	101.73	104.30
5	M	12	A	C5-C6-N1	5.12	120.26	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	M	20	G	C5-C6-O6	-5.12	125.53	128.60
5	M	7	A	N3-C4-C5	5.07	130.35	126.80
5	M	20	G	C4-N9-C1'	5.07	133.09	126.50
5	M	23	G	N1-C6-O6	5.07	122.94	119.90
5	M	22	G	O5'-P-OP2	-5.06	101.14	105.70
5	M	14	G	C5-C6-O6	-5.06	125.56	128.60
6	N	28	G	O4'-C1'-N9	5.05	112.24	108.20
5	M	28	C	C2-N1-C1'	5.04	124.35	118.80
5	M	17	C	C5-C6-N1	5.02	123.51	121.00
6	N	27	C	N3-C4-C5	5.02	123.91	121.90
5	M	28	C	C5-C6-N1	5.01	123.51	121.00

There are no chirality outliers.

All (38) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	125	UNK	Peptide
1	A	126	UNK	Peptide
1	A	19	UNK	Peptide
1	A	223	UNK	Peptide
1	A	280	UNK	Peptide
1	A	387	UNK	Peptide
1	A	785	UNK	Peptide
2	B	267	UNK	Peptide
3	C	113	UNK	Peptide
3	C	143	UNK	Peptide
3	C	17	UNK	Peptide
3	C	174	UNK	Peptide
3	C	214	UNK	Peptide
3	C	26	UNK	Peptide
3	C	66	UNK	Peptide
3	C	67	UNK	Peptide
3	C	78	UNK	Peptide
3	D	143	UNK	Peptide
3	D	17	UNK	Peptide
3	D	214	UNK	Peptide
3	D	217	UNK	Peptide
3	D	26	UNK	Peptide
3	D	33	UNK	Peptide
3	D	67	UNK	Peptide
3	D	73	UNK	Peptide
3	D	81	UNK	Peptide

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Mol	Chain	Res	Type	Group
3	E	109	UNK	Peptide
3	E	153	UNK	Peptide
3	E	218	UNK	Peptide
3	E	22	UNK	Peptide
3	E	224	UNK	Peptide
3	F	108	UNK	Peptide
3	F	218	UNK	Peptide
3	F	77	UNK	Peptide
2	G	142	UNK	Peptide
2	G	207	UNK	Peptide
2	G	218	UNK	Peptide
2	H	93	UNK	Peptide

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	3580	0	794	21	0
2	B	1395	0	327	9	0
2	G	1050	0	244	2	0
2	H	1050	0	248	10	0
3	C	1090	0	251	5	0
3	D	1090	0	249	6	0
3	E	1090	0	250	2	0
3	F	1080	0	246	2	0
4	I	590	0	122	5	0
4	J	590	0	122	5	0
4	K	590	0	122	5	0
4	L	590	0	122	5	0
5	M	775	0	394	5	0
6	N	633	0	323	8	0
All	All	15193	0	3814	85	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 5.

All (85) 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)
5:M:7:A:H61	6:N:37:A:HO3'	1.25	0.81
3:F:23:UNK:HA	3:F:168:UNK:HA	1.71	0.72
5:M:7:A:N6	6:N:37:A:HO3'	1.89	0.70
1:A:127:UNK:N	1:A:135:UNK:O	2.31	0.63
2:G:13:UNK:O	2:G:176:UNK:HA	1.99	0.62
1:A:145:UNK:O	1:A:149:UNK:N	2.34	0.61
3:D:121:UNK:O	3:D:177:UNK:HA	2.00	0.61
6:N:24:G:H2'	6:N:25:G:H8	1.65	0.60
2:B:210:UNK:HA	2:B:288:UNK:HA	1.83	0.59
1:A:722:UNK:O	1:A:726:UNK:N	2.35	0.59
1:A:183:UNK:O	1:A:187:UNK:N	2.37	0.56
2:H:12:UNK:N	2:H:224:UNK:O	2.40	0.55
1:A:241:UNK:O	1:A:245:UNK:N	2.40	0.55
2:H:15:UNK:O	2:H:174:UNK:N	2.41	0.54
2:H:87:UNK:O	2:H:91:UNK:N	2.41	0.54
1:A:64:UNK:O	1:A:68:UNK:N	2.41	0.54
3:C:3:UNK:HA	3:C:186:UNK:HA	1.90	0.53
2:H:13:UNK:O	2:H:176:UNK:HA	2.10	0.52
2:B:108:UNK:O	2:B:112:UNK:N	2.43	0.51
4:K:119:UNK:O	4:K:123:UNK:N	2.44	0.51
4:L:119:UNK:O	4:L:123:UNK:N	2.44	0.51
4:I:119:UNK:O	4:I:123:UNK:N	2.44	0.51
1:A:329:UNK:O	1:A:333:UNK:N	2.44	0.51
2:B:237:UNK:O	2:B:241:UNK:N	2.42	0.51
2:H:5:UNK:CB	2:H:185:UNK:O	2.59	0.51
1:A:130:UNK:N	1:A:661:UNK:O	2.44	0.51
3:C:14:UNK:HA	3:C:176:UNK:HA	1.93	0.51
4:J:119:UNK:O	4:J:123:UNK:N	2.44	0.51
1:A:40:UNK:O	1:A:44:UNK:N	2.45	0.50
1:A:700:UNK:O	1:A:702:UNK:N	2.45	0.50
1:A:769:UNK:O	1:A:773:UNK:N	2.45	0.49
4:I:124:UNK:O	4:I:128:UNK:N	2.45	0.49
4:K:124:UNK:O	4:K:128:UNK:N	2.45	0.49
2:B:20:UNK:O	2:B:23:UNK:N	2.46	0.49
4:L:124:UNK:O	4:L:128:UNK:N	2.45	0.48
2:H:69:UNK:O	2:H:80:UNK:N	2.45	0.48
4:J:124:UNK:O	4:J:128:UNK:N	2.45	0.48
1:A:556:UNK:O	1:A:560:UNK:N	2.45	0.48
2:B:216:UNK:O	2:B:218:UNK:N	2.46	0.48
1:A:303:UNK:O	1:A:307:UNK:N	2.47	0.47
5:M:21:G:N2	6:N:22:C:O2	2.43	0.47
3:E:7:UNK:HA	3:E:241:UNK:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:7:UNK:HA	2:H:241:UNK:HA	1.97	0.47
2:B:110:UNK:O	2:B:115:UNK:N	2.48	0.47
1:A:122:UNK:N	1:A:216:UNK:O	2.48	0.46
2:B:109:UNK:O	2:B:114:UNK:N	2.48	0.46
6:N:24:G:H2'	6:N:25:G:C8	2.48	0.46
1:A:441:UNK:N	1:A:457:UNK:O	2.48	0.46
3:D:202:UNK:O	3:D:205:UNK:N	2.49	0.46
2:H:202:UNK:O	2:H:206:UNK:CB	2.63	0.46
3:C:114:UNK:O	3:C:116:UNK:N	2.48	0.46
3:F:104:UNK:O	3:F:108:UNK:N	2.49	0.45
5:M:10:U:H2'	5:M:11:A:H8	1.81	0.45
4:I:55:UNK:O	4:I:59:UNK:N	2.50	0.45
4:K:55:UNK:O	4:K:59:UNK:N	2.50	0.45
4:L:20:UNK:O	4:L:23:UNK:N	2.50	0.45
4:L:55:UNK:O	4:L:59:UNK:N	2.50	0.45
4:J:20:UNK:O	4:J:23:UNK:N	2.50	0.45
6:N:35:C:O2'	6:N:36:U:OP2	2.32	0.44
1:A:176:UNK:O	1:A:180:UNK:CB	2.65	0.44
4:J:55:UNK:O	4:J:59:UNK:N	2.50	0.44
4:I:20:UNK:O	4:I:23:UNK:N	2.50	0.44
4:K:20:UNK:O	4:K:23:UNK:N	2.50	0.44
2:G:141:UNK:O	2:H:22:UNK:N	2.51	0.44
1:A:322:UNK:O	1:A:324:UNK:N	2.51	0.43
4:I:61:UNK:O	4:I:63:UNK:N	2.52	0.43
3:C:122:UNK:HA	3:C:177:UNK:HA	2.00	0.43
1:A:184:UNK:O	1:A:188:UNK:N	2.52	0.43
1:A:550:UNK:O	1:A:635:UNK:HA	2.19	0.43
3:E:79:UNK:O	3:E:81:UNK:N	2.52	0.43
4:K:61:UNK:O	4:K:63:UNK:N	2.52	0.43
4:J:61:UNK:O	4:J:63:UNK:N	2.52	0.42
3:C:10:UNK:O	3:C:238:UNK:N	2.53	0.42
3:D:163:UNK:O	6:N:28:G:O2'	2.36	0.42
4:L:61:UNK:O	4:L:63:UNK:N	2.52	0.42
3:D:2:UNK:O	3:D:4:UNK:N	2.52	0.42
3:D:142:UNK:O	3:D:144:UNK:N	2.53	0.42
3:D:15:UNK:HA	3:D:220:UNK:HA	2.02	0.42
6:N:33:A:N6	6:N:34:U:O4	2.53	0.41
1:A:146:UNK:HA	1:A:150:UNK:HA	2.02	0.41
1:A:57:UNK:O	1:A:62:UNK:N	2.54	0.41
5:M:10:U:H2'	5:M:11:A:C8	2.54	0.41
2:B:162:UNK:O	2:B:164:UNK:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:14:UNK:O	2:B:148:UNK:N	2.54	0.41
2:H:68:UNK:C	2:H:70:UNK:H	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

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)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	M	35/48 (72%)	15 (42%)	3 (8%)
6	N	29/50 (58%)	16 (55%)	1 (3%)
All	All	64/98 (65%)	31 (48%)	4 (6%)

All (31) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	M	-1	C
5	M	0	G
5	M	1	A
5	M	2	C
5	M	3	C
5	M	4	C
5	M	7	A
5	M	8	G
5	M	14	G
5	M	15	C
5	M	19	C
5	M	21	G
5	M	26	G
5	M	27	A

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Mol	Chain	Res	Type
5	M	32	G
6	N	9	G
6	N	10	A
6	N	11	C
6	N	12	G
6	N	17	C
6	N	18	G
6	N	20	C
6	N	21	C
6	N	24	G
6	N	26	G
6	N	30	C
6	N	32	U
6	N	33	A
6	N	34	U
6	N	36	U
6	N	37	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	M	0	G
5	M	13	G
5	M	14	G
6	N	35	C

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 monosaccharides 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	6
2	H	4
2	G	4
3	F	3
3	D	3
3	C	3
3	E	3
2	B	1
4	I	1
4	J	1
4	K	1
4	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	146:UNK	C	149:UNK	N	27.10
1	A	106:UNK	C	115:UNK	N	19.08
1	A	391:UNK	C	422:UNK	N	15.92
1	G	146:UNK	C	149:UNK	N	15.91
1	F	146:UNK	C	149:UNK	N	14.97
1	D	35:UNK	C	52:UNK	N	13.31
1	C	146:UNK	C	149:UNK	N	12.73
1	E	146:UNK	C	149:UNK	N	12.11
1	C	35:UNK	C	52:UNK	N	11.14
1	D	132:UNK	C	139:UNK	N	11.05
1	D	146:UNK	C	149:UNK	N	10.87
1	G	35:UNK	C	52:UNK	N	10.69
1	H	155:UNK	C	164:UNK	N	10.23
1	F	35:UNK	C	52:UNK	N	10.14
1	B	131:UNK	C	140:UNK	N	9.68
1	E	35:UNK	C	52:UNK	N	9.18
1	H	35:UNK	C	52:UNK	N	8.95
1	C	132:UNK	C	139:UNK	N	8.77
1	I	90:UNK	C	96:UNK	N	8.76

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	90:UNK	C	96:UNK	N	8.76
1	K	90:UNK	C	96:UNK	N	8.76
1	L	90:UNK	C	96:UNK	N	8.76
1	H	132:UNK	C	139:UNK	N	7.78
1	G	132:UNK	C	139:UNK	N	7.76
1	E	132:UNK	C	139:UNK	N	7.59
1	G	155:UNK	C	164:UNK	N	7.41
1	A	75:UNK	C	86:UNK	N	7.22
1	F	131:UNK	C	140:UNK	N	6.98
1	A	464:UNK	C	480:UNK	N	6.73
1	A	605:UNK	C	616:UNK	N	5.00
1	A	566:UNK	C	572:UNK	N	4.57

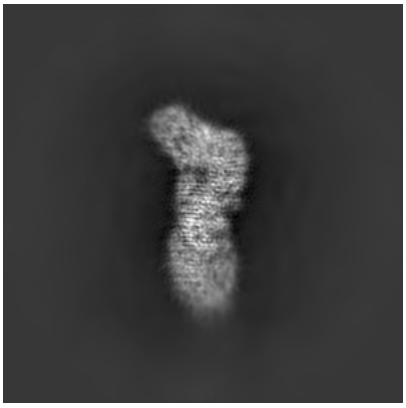
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0454. These allow visual inspection of the internal detail of the map and identification of artifacts.

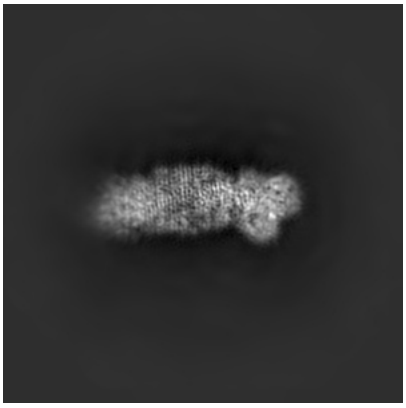
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

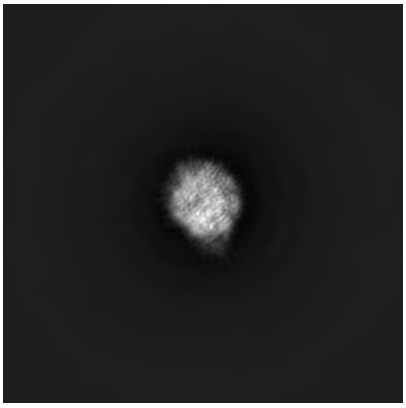
6.1.1 Primary map



X



Y

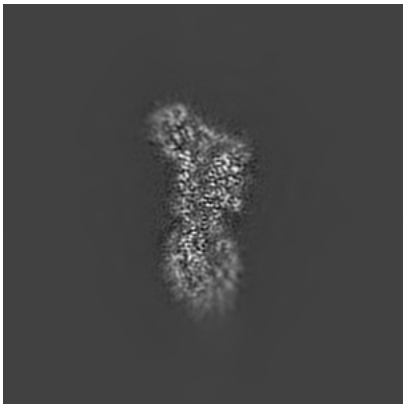


Z

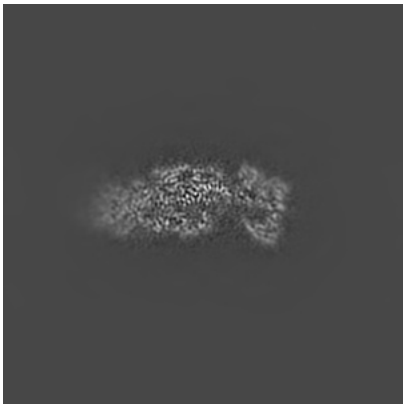
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

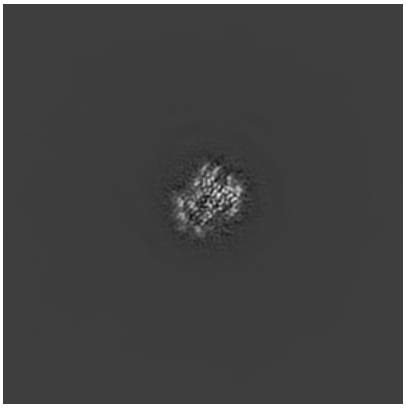
6.2.1 Primary map



X Index: 190



Y Index: 190



Z Index: 190

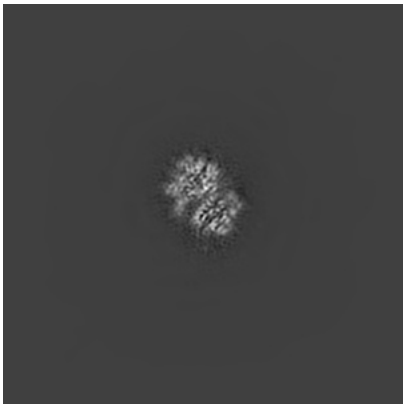
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 194

Y Index: 181



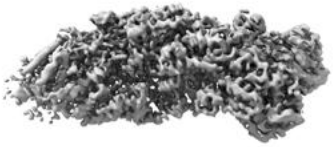
Z Index: 232

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

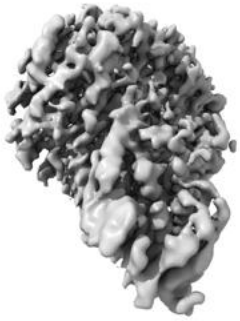
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

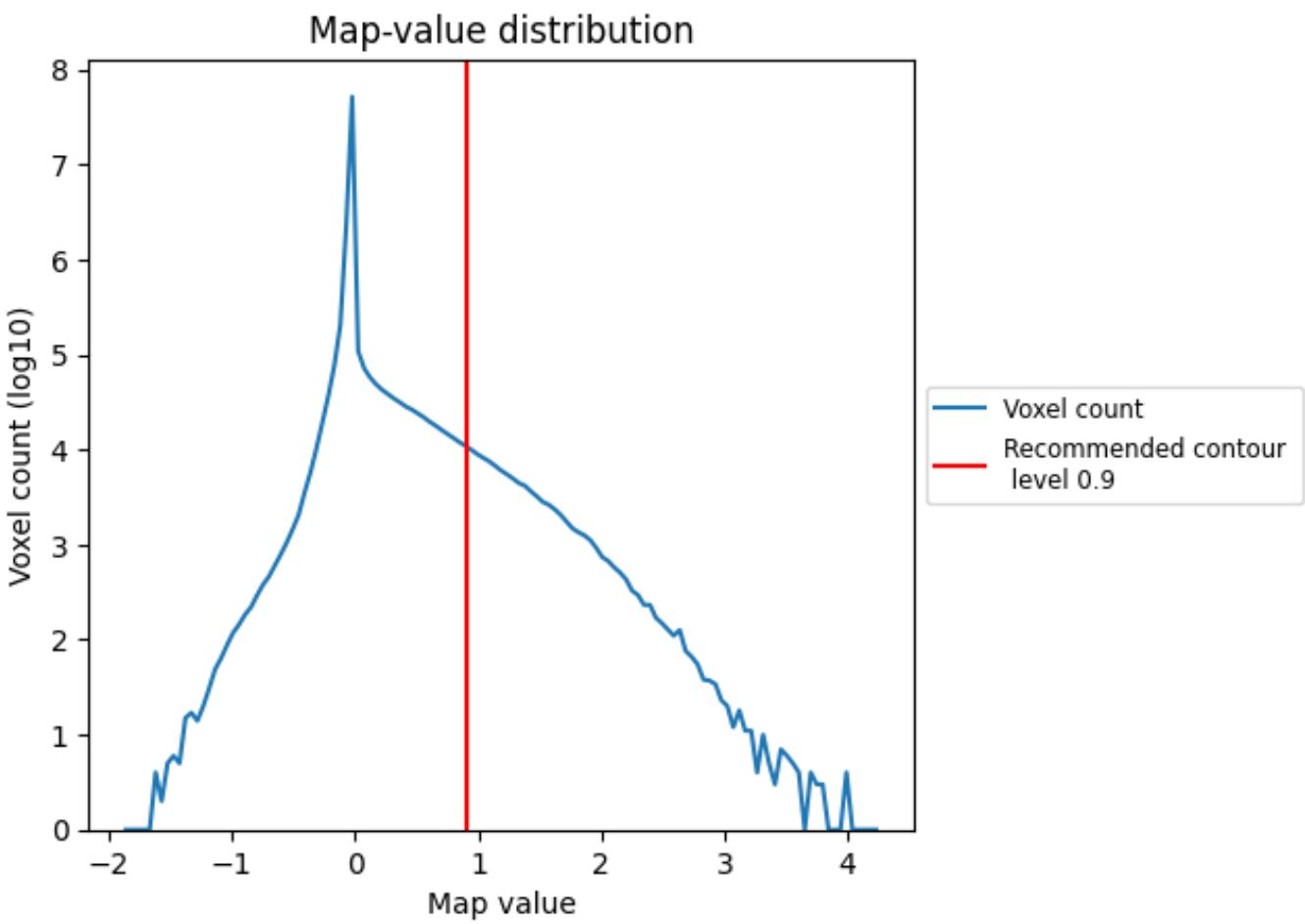
6.5 Mask visualisation (i)

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

7 Map analysis (i)

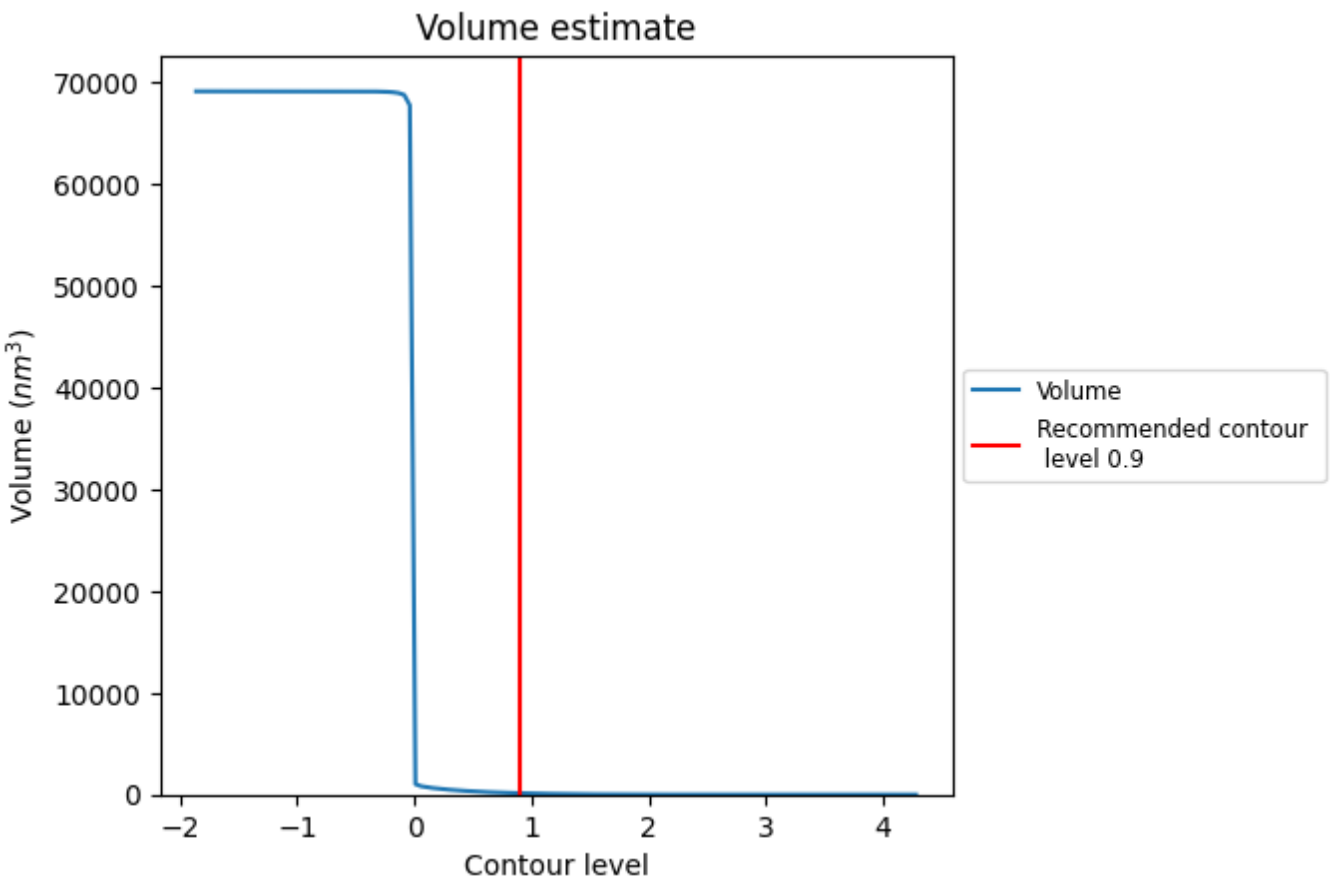
This section contains the results of statistical analysis of the map.

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.

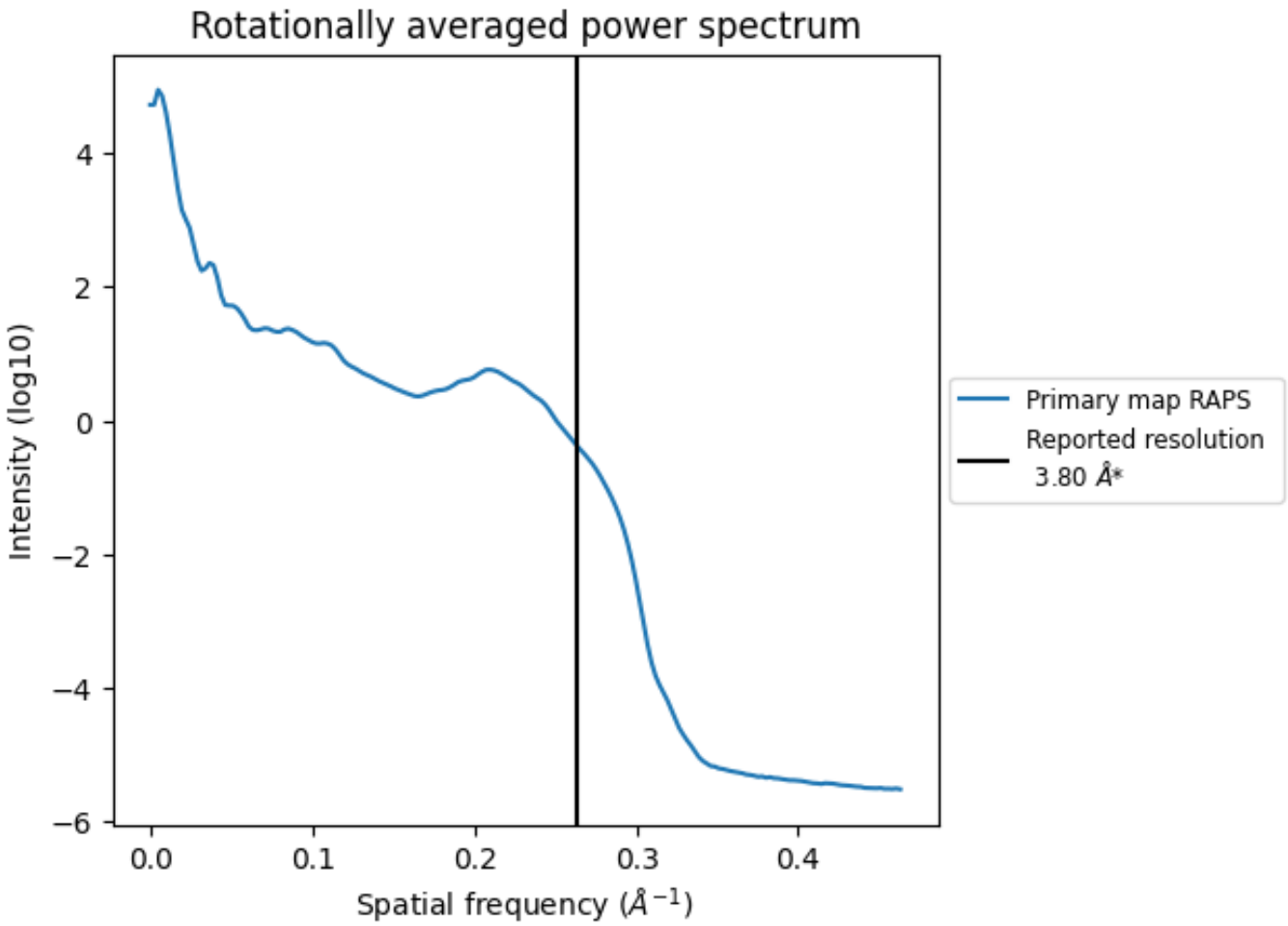
7.2 Volume estimate (i)



The volume at the recommended contour level is 134 nm^3; this corresponds to an approximate mass of 121 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 (i)



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

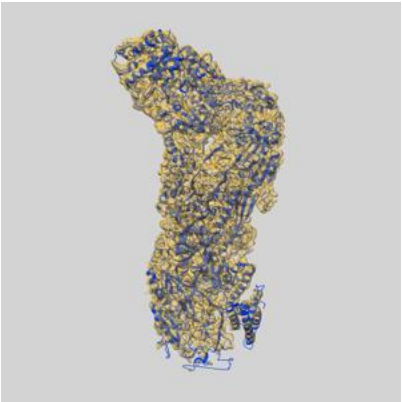
8 Fourier-Shell correlation (i)

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

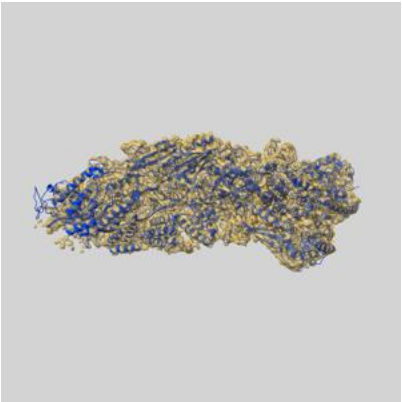
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-0454 and PDB model 6O1O. Per-residue inclusion information can be found in section 3 on page 6.

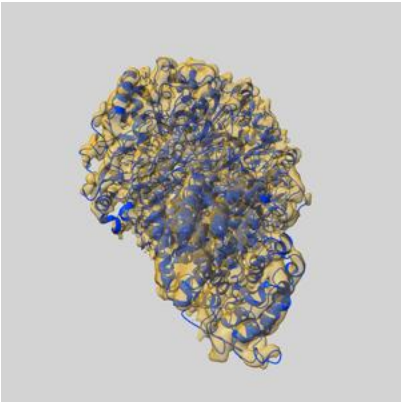
9.1 Map-model overlay (i)



X



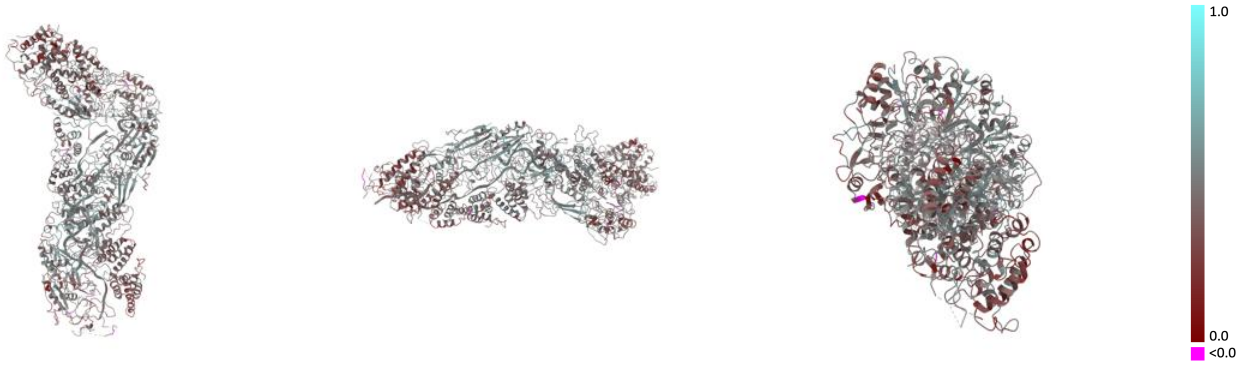
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.9 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.

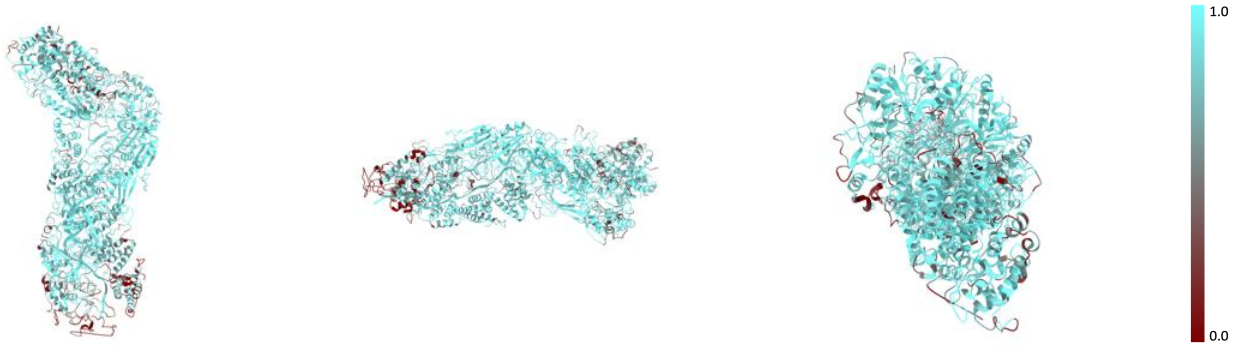
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

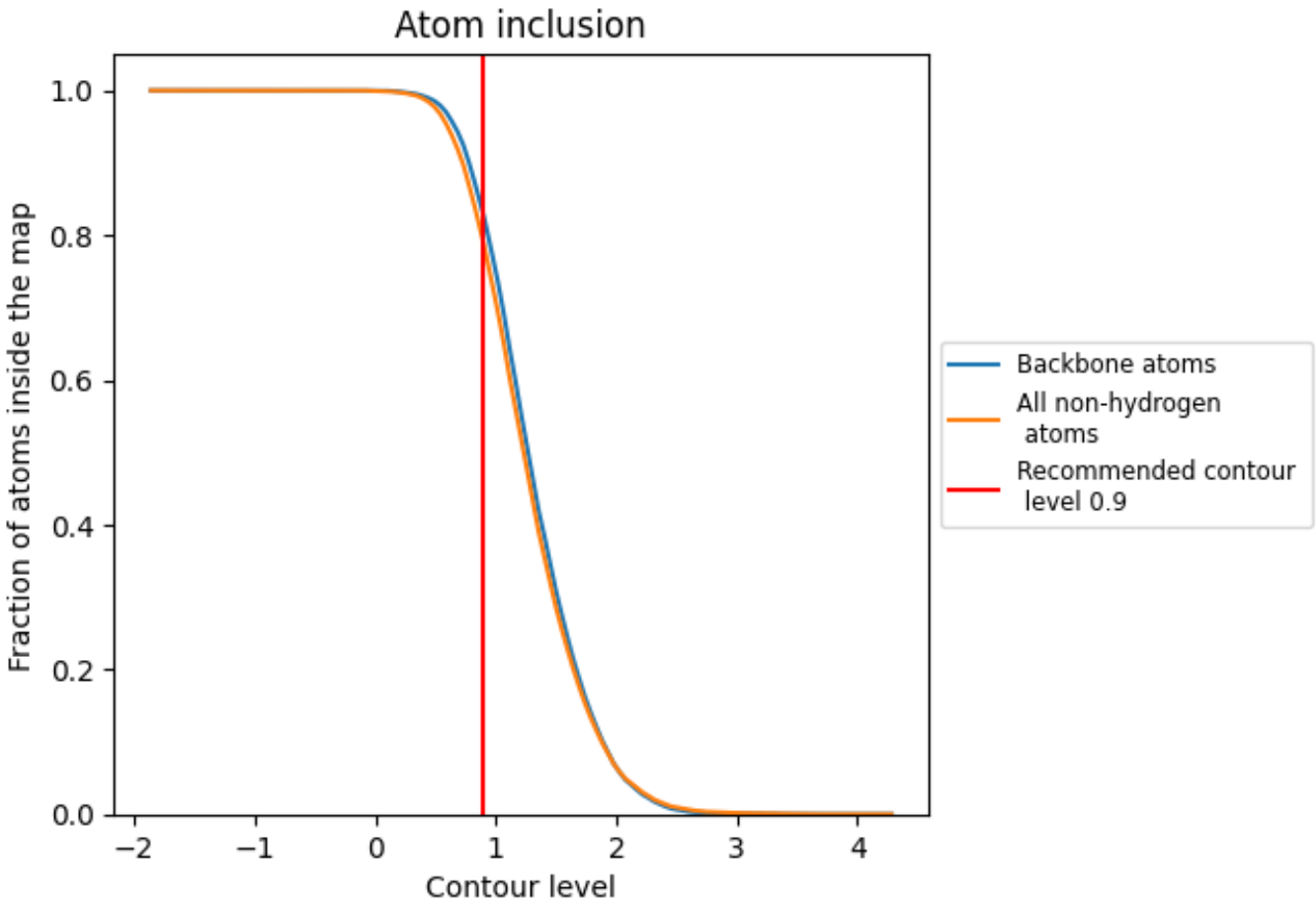
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.9).

9.4 Atom inclusion (i)



At the recommended contour level, 83% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7874	0.4330
A	0.8034	0.4190
B	0.7692	0.4080
C	0.8697	0.4660
D	0.8826	0.4780
E	0.8789	0.4780
F	0.8657	0.4830
G	0.7410	0.4430
H	0.4352	0.3450
I	0.8508	0.4310
J	0.8458	0.4250
K	0.7847	0.3700
L	0.4034	0.3310
M	0.9213	0.4890
N	0.8847	0.4890