wwPDB EM Validation Summary Report ⓘ

Dec 11, 2022 – 02:43 pm GMT

PDB ID	:	6SIC
EMDB ID	:	EMD-10209
Title	:	Cryo-EM structure of the Type III-B Cmr-beta bound to cognate target RNA
Authors	:	Sofos, N.; Montoya, G.; Stella, S.
Deposited on	:	2019-08-09
Resolution	:	3.52 Å(reported)
Based on initial model	:	6S8B

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

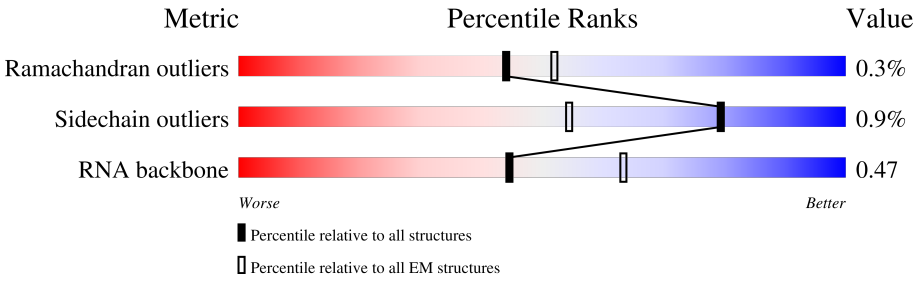
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 3.52 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
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	155	99%
1	B	155	99%
1	C	155	99%
2	D	286	99%
2	E	286	100%
2	F	286	98%
2	G	286	99%
3	H	313	99%

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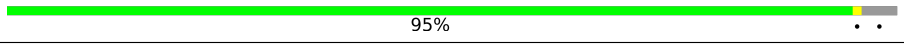
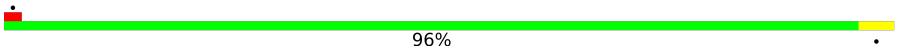
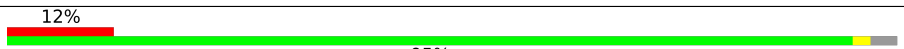
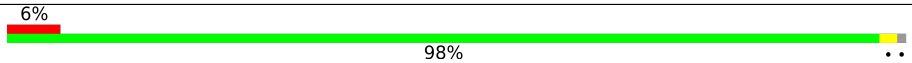
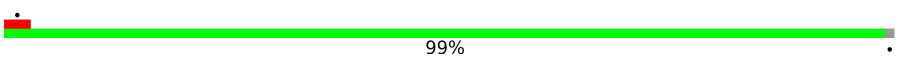
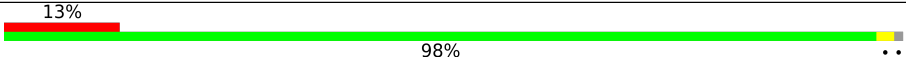
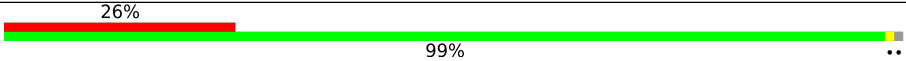
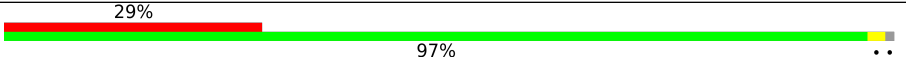
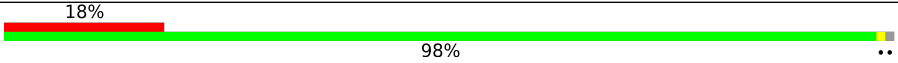
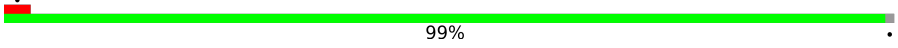
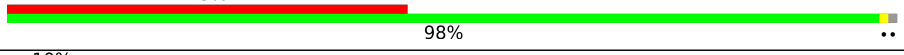
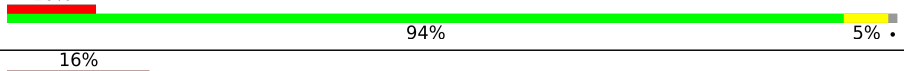
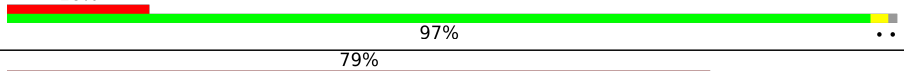
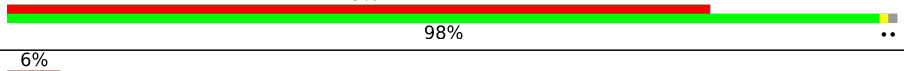
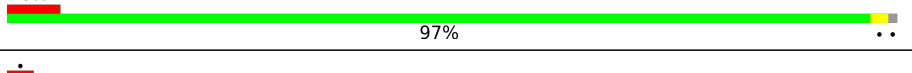
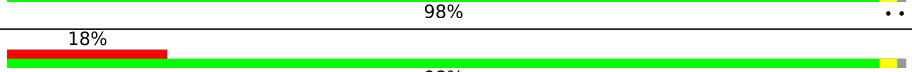
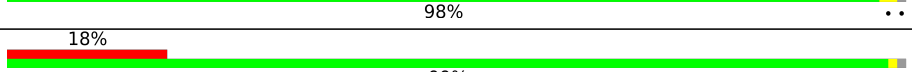
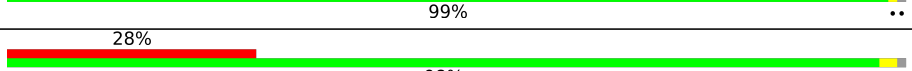
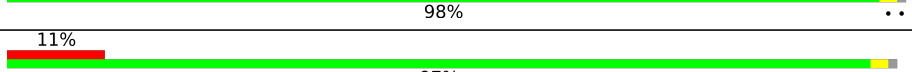
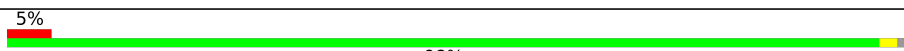
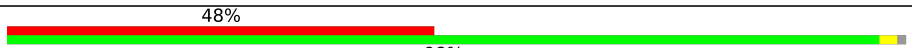
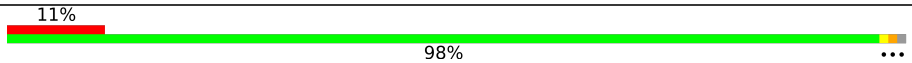
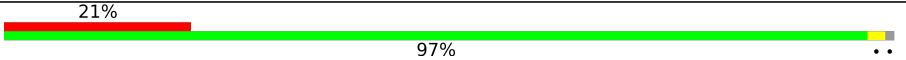
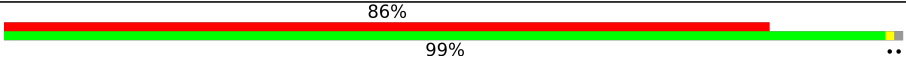
Mol	Chain	Length	Quality of chain
4	I	296	
5	J	476	
6	K	1037	
7	L	174	
7	M	174	
7	N	174	
7	O	174	
7	P	174	
7	Q	174	
7	R	174	
7	S	174	
7	T	174	
7	W	174	
7	X	174	
7	l	174	
7	m	174	
7	n	174	
7	o	174	
7	p	174	
7	q	174	
7	r	174	
7	s	174	
7	t	174	
7	w	174	
7	x	174	

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Mol	Chain	Length	Quality of chain
8	U	46	59% 33% 9%
9	V	51	65% 25% 6%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 62079 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 CRISPR-associated protein, Cmr5 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	153	Total	C	N	O	S	0	0
			1253	817	205	230	1		
1	B	154	Total	C	N	O	S	0	0
			1261	823	206	231	1		
1	C	154	Total	C	N	O	S	0	0
			1261	823	206	231	1		

- Molecule 2 is a protein called CRISPR-associated RAMP protein, Cmr4 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	285	Total	C	N	O	S	0	0
			2274	1478	369	425	2		
2	E	285	Total	C	N	O	S	0	0
			2274	1478	369	425	2		
2	F	285	Total	C	N	O	S	0	0
			2274	1478	369	425	2		
2	G	285	Total	C	N	O	S	0	0
			2273	1478	369	424	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	31	ALA	ASP	engineered mutation	UNP F0NDX6
E	31	ALA	ASP	engineered mutation	UNP F0NDX6
F	31	ALA	ASP	engineered mutation	UNP F0NDX6
G	31	ALA	ASP	engineered mutation	UNP F0NDX6

- Molecule 3 is a protein called CRISPR-associated protein, Cmr3 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	312	Total	C	N	O	S	0	0
			2528	1630	418	473	7		

- Molecule 4 is a protein called CRISPR-associated RAMP protein, Cmr6 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	284	Total	C	N	O	S	0	0
			2282	1470	381	427	4		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	284	ALA	-	expression tag	UNP F0NDX3
I	285	ALA	-	expression tag	UNP F0NDX3
I	286	ALA	-	expression tag	UNP F0NDX3
I	287	HIS	-	expression tag	UNP F0NDX3
I	288	HIS	-	expression tag	UNP F0NDX3
I	289	HIS	-	expression tag	UNP F0NDX3
I	290	HIS	-	expression tag	UNP F0NDX3
I	291	HIS	-	expression tag	UNP F0NDX3
I	292	HIS	-	expression tag	UNP F0NDX3
I	293	HIS	-	expression tag	UNP F0NDX3
I	294	HIS	-	expression tag	UNP F0NDX3
I	295	HIS	-	expression tag	UNP F0NDX3
I	296	HIS	-	expression tag	UNP F0NDX3

- Molecule 5 is a protein called CRISPR-associated RAMP protein, Cmr1 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	475	Total	C	N	O	S	0	0
			3889	2517	632	727	13		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	MET	-	initiating methionine	UNP F0NDX4
J	2	GLU	-	expression tag	UNP F0NDX4
J	3	GLU	-	expression tag	UNP F0NDX4
J	4	LEU	-	expression tag	UNP F0NDX4
J	5	LEU	-	expression tag	UNP F0NDX4

- Molecule 6 is a protein called CRISPR-associated protein, Cmr2 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	1009	Total	C	N	O	S	0	0
			8282	5360	1366	1532	24		

- Molecule 7 is a protein called CRISPR-associated protein Cmrx.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	M	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	N	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	O	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	P	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	Q	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	R	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	S	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	T	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	W	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	l	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	m	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	n	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	o	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	p	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	q	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	r	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	s	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	t	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	w	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		
7	X	173	Total	C	N	O	S	0	0
			1378	880	227	269	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	x	173	Total 1378	C 880	N 227	O 269	S 2	0	0

- Molecule 8 is a RNA chain called Cognate target RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	U	42	Total 886	C 398	N 152	O 295	P 41	0	0

- Molecule 9 is a RNA chain called crRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	V	48	Total 1025	C 461	N 192	O 325	P 47	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	1	A	C	conflict	GB 323473489
V	3	U	G	conflict	GB 323473489

- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

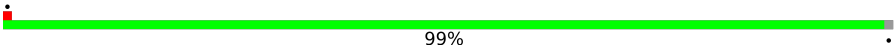
Mol	Chain	Residues	Atoms		AltConf
10	K	1	Total 1	Zn 1	0

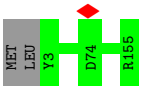
3 Residue-property plots (i)

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: CRISPR-associated protein, Cmr5 family

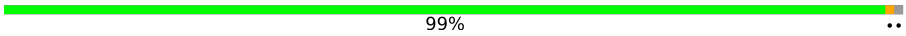
Chain A:

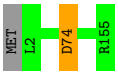




• Molecule 1: CRISPR-associated protein, Cmr5 family

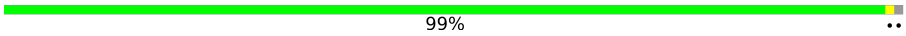
Chain B:





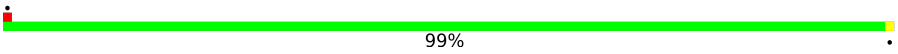
• Molecule 1: CRISPR-associated protein, Cmr5 family

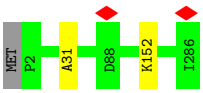
Chain C:



• Molecule 2: CRISPR-associated RAMP protein, Cmr4 family

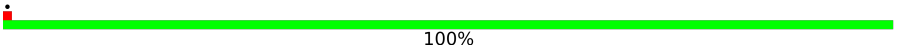
Chain D:

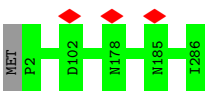




• Molecule 2: CRISPR-associated RAMP protein, Cmr4 family

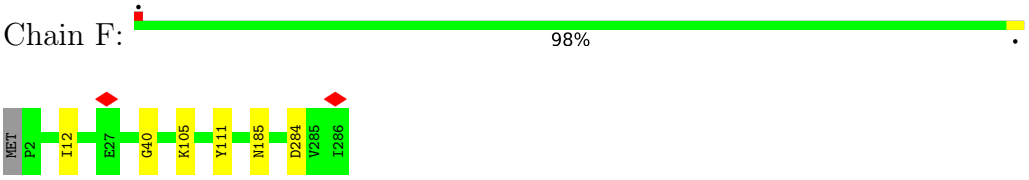
Chain E:





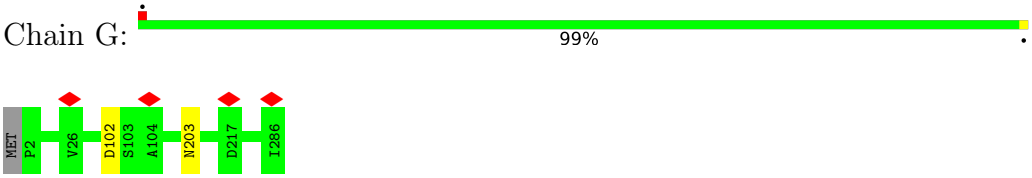
• Molecule 2: CRISPR-associated RAMP protein, Cmr4 family

Chain F:



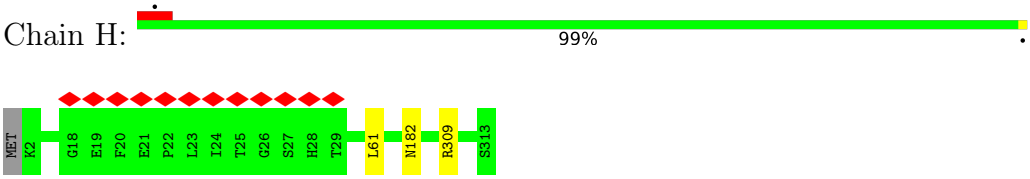
• Molecule 2: CRISPR-associated RAMP protein, Cmr4 family

Chain G:



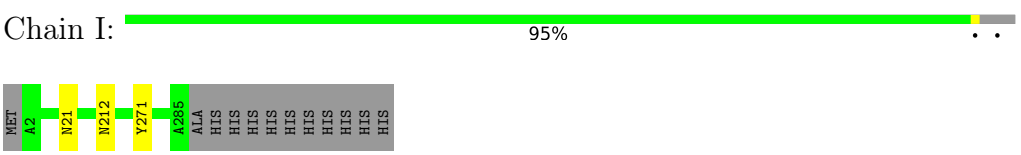
• Molecule 3: CRISPR-associated protein, Cmr3 family

Chain H:



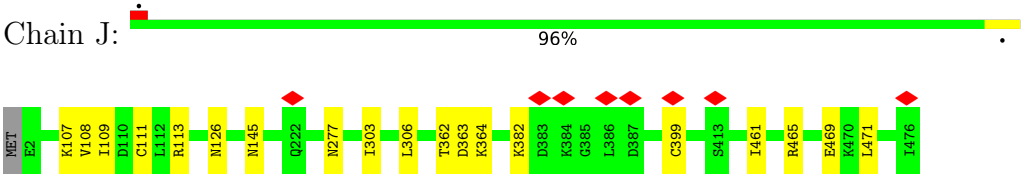
• Molecule 4: CRISPR-associated RAMP protein, Cmr6 family

Chain I:



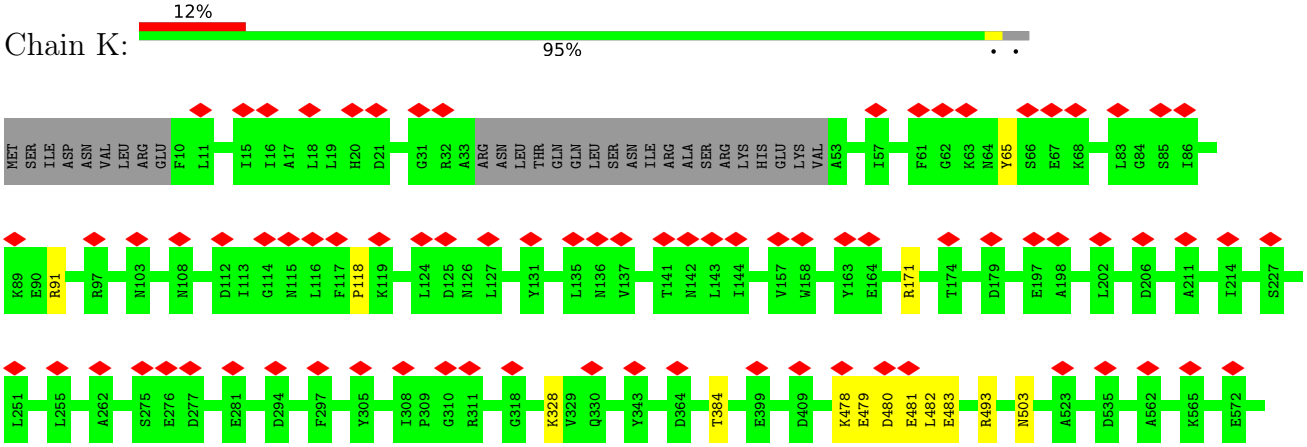
• Molecule 5: CRISPR-associated RAMP protein, Cmr1 family

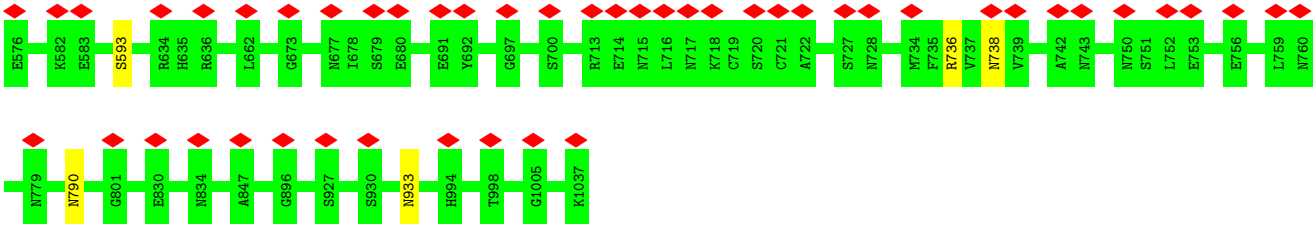
Chain J:



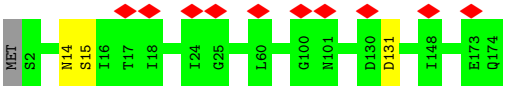
• Molecule 6: CRISPR-associated protein, Cmr2 family

Chain K:

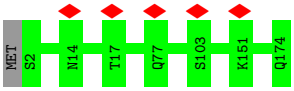




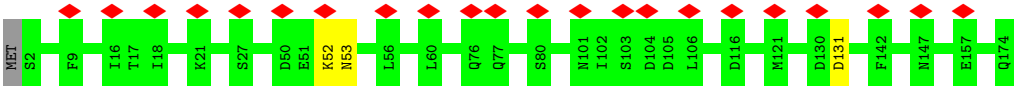
• Molecule 7: CRISPR-associated protein Cmrx



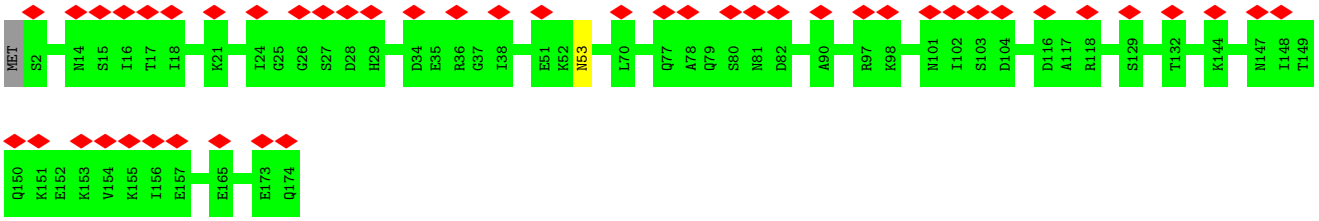
• Molecule 7: CRISPR-associated protein Cmrx



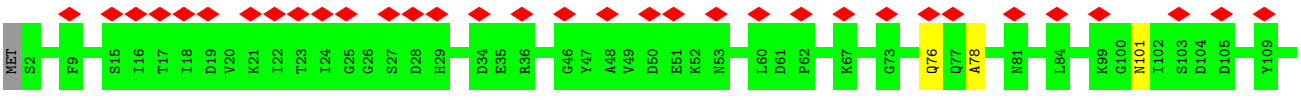
• Molecule 7: CRISPR-associated protein Cmrx

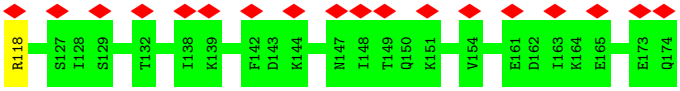


• Molecule 7: CRISPR-associated protein Cmrx

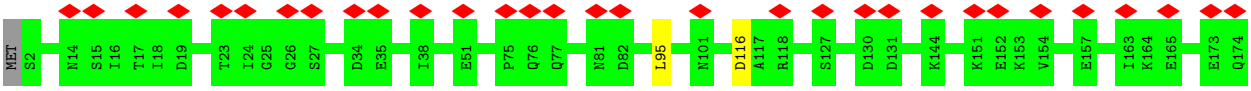


• Molecule 7: CRISPR-associated protein Cmrx

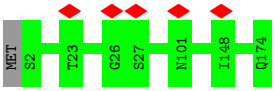




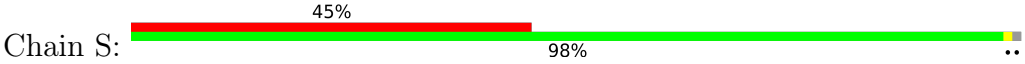
• Molecule 7: CRISPR-associated protein Cmrx

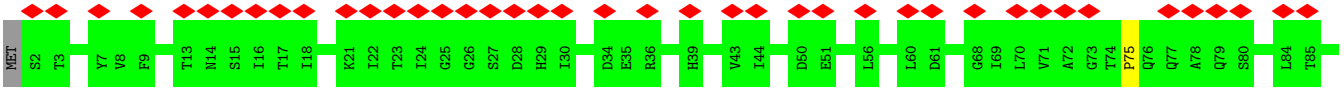


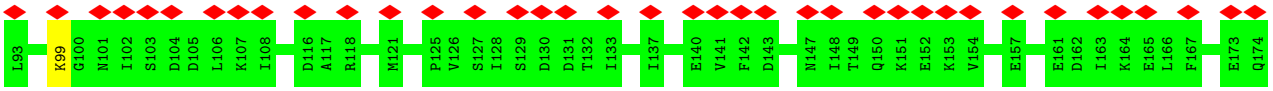
• Molecule 7: CRISPR-associated protein Cmrx



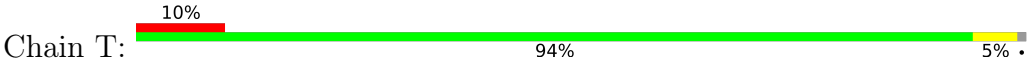
• Molecule 7: CRISPR-associated protein Cmrx

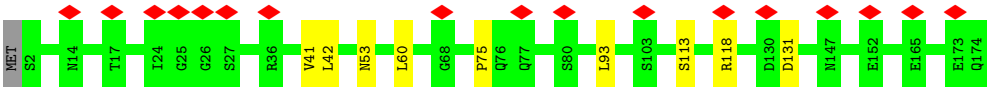




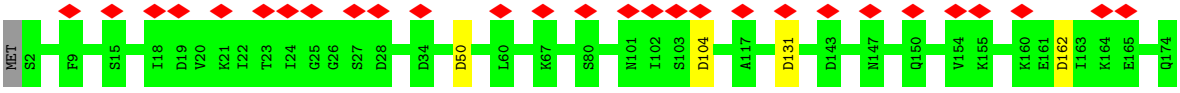


• Molecule 7: CRISPR-associated protein Cmrx

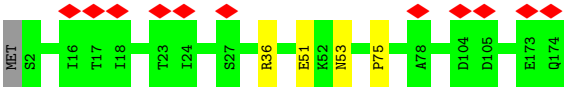




• Molecule 7: CRISPR-associated protein Cmrx

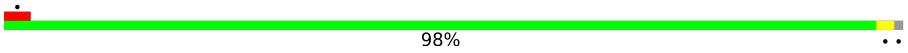


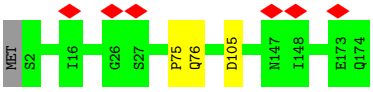
• Molecule 7: CRISPR-associated protein Cmrx



• Molecule 7: CRISPR-associated protein Cmrx

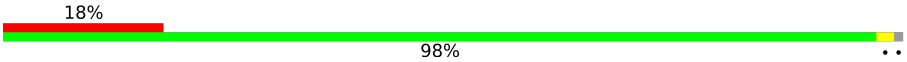
Chain m:

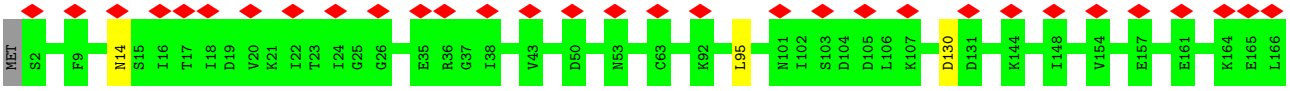




• Molecule 7: CRISPR-associated protein Cmrx

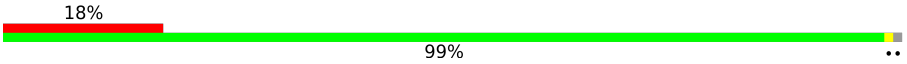
Chain n:

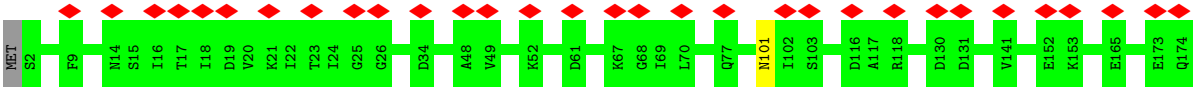




• Molecule 7: CRISPR-associated protein Cmrx

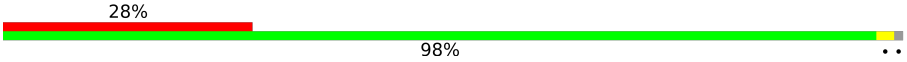
Chain o:

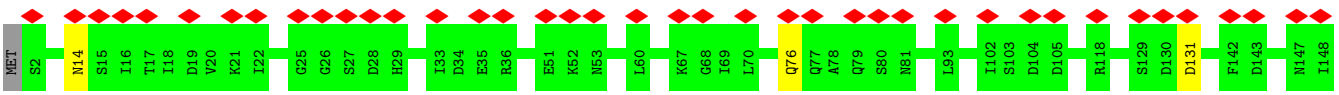


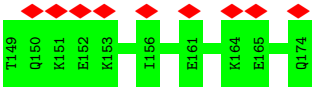


• Molecule 7: CRISPR-associated protein Cmrx

Chain p:

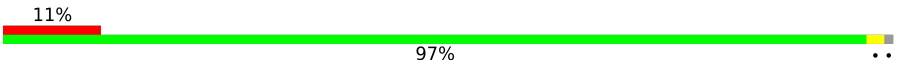


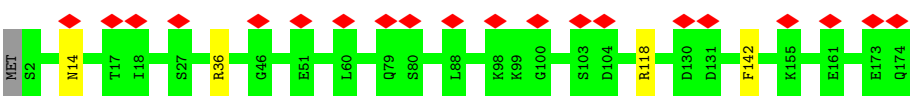




• Molecule 7: CRISPR-associated protein Cmrx

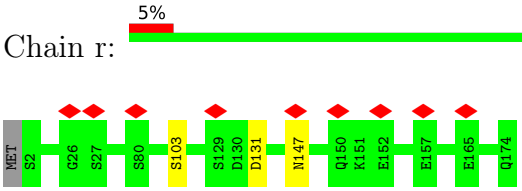
Chain q:





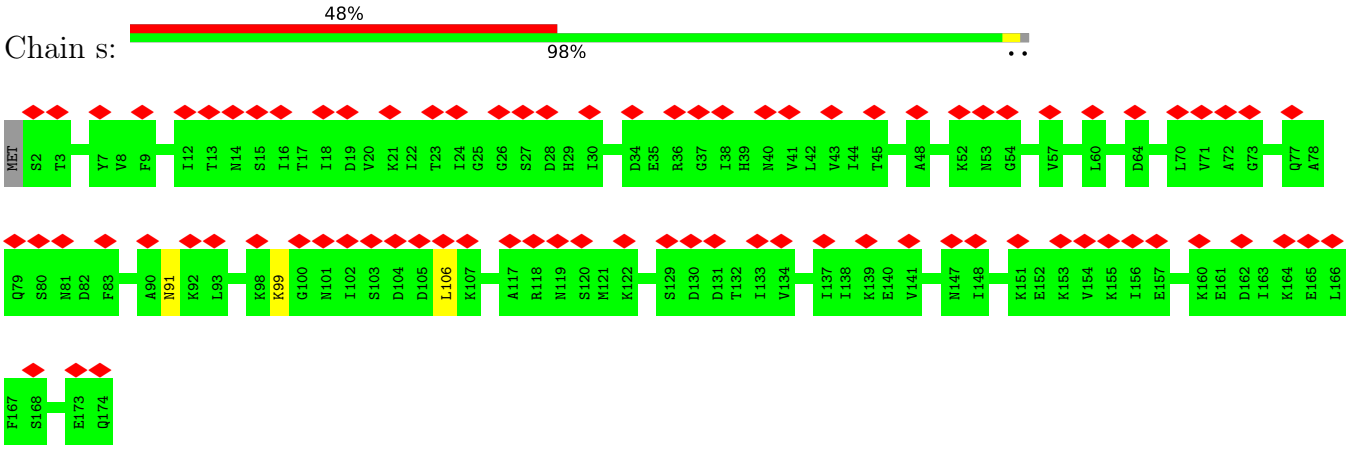
• Molecule 7: CRISPR-associated protein Cmrx

Chain r:



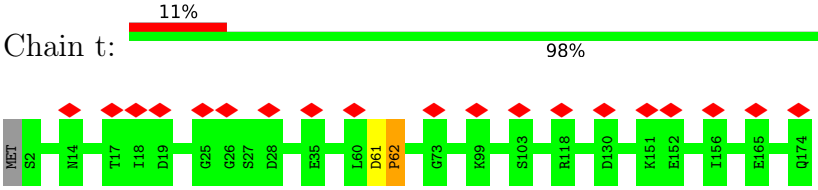
• Molecule 7: CRISPR-associated protein Cmrx

Chain s:



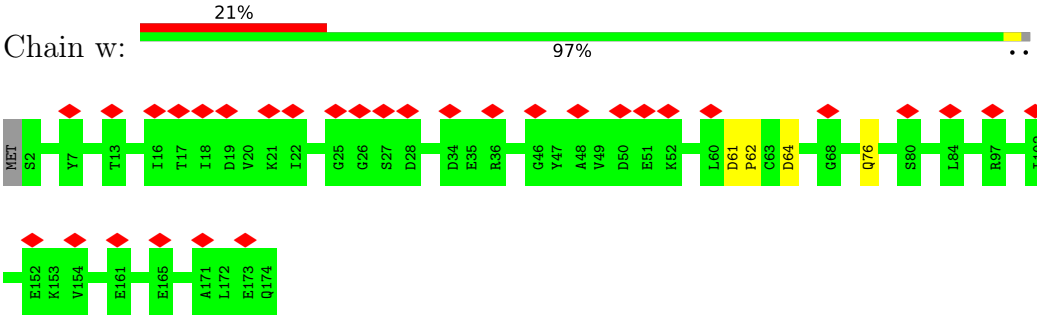
• Molecule 7: CRISPR-associated protein Cmrx

Chain t:



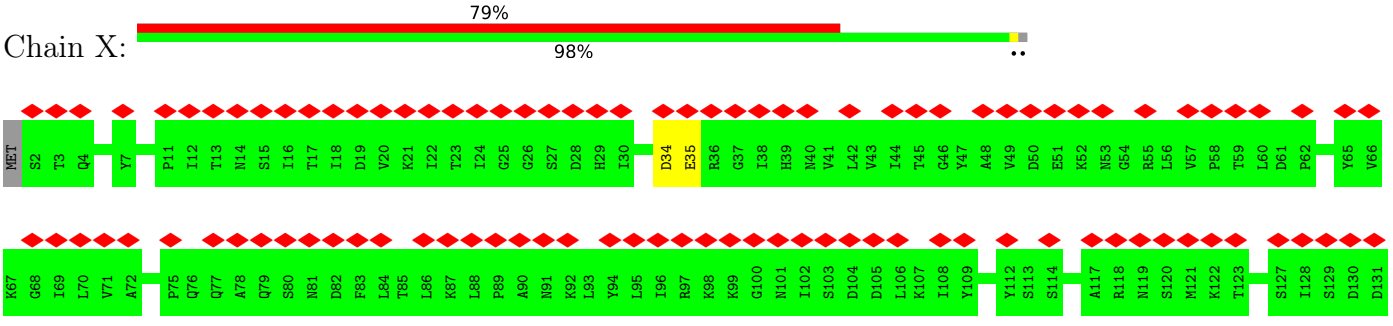
• Molecule 7: CRISPR-associated protein Cmrx

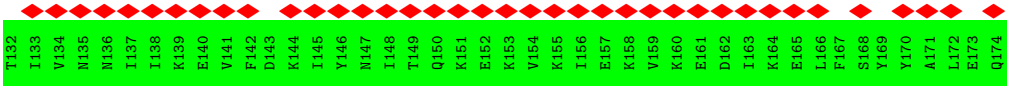
Chain w:



• Molecule 7: CRISPR-associated protein Cmrx

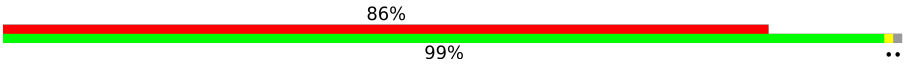
Chain X:

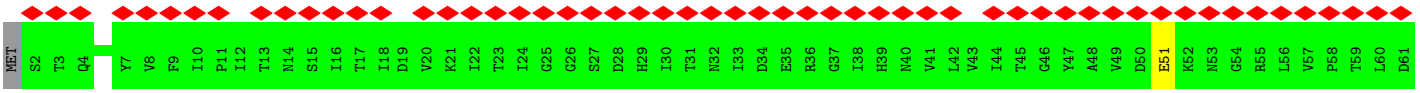


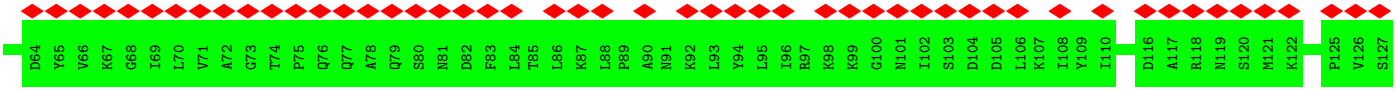


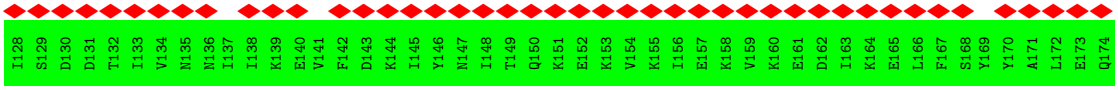
• Molecule 7: CRISPR-associated protein Cmrx

Chain x:



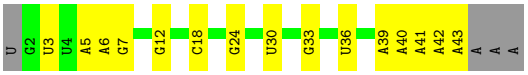






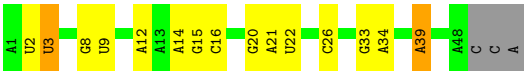
• Molecule 8: Cognate target RNA

Chain U:



• Molecule 9: crRNA

Chain V:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30455	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 ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	1700	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	19.604	Depositor
Minimum map value	-9.825	Depositor
Average map value	-0.007	Depositor
Map value standard deviation	0.637	Depositor
Recommended contour level	2.25	Depositor
Map size (Å)	480.0, 480.0, 480.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.58	0/1275	0.59	0/1716
1	B	0.55	0/1283	0.64	1/1727 (0.1%)
1	C	0.59	0/1283	0.60	0/1727
2	D	0.63	0/2318	0.65	0/3134
2	E	0.62	0/2318	0.63	0/3134
2	F	0.63	1/2318 (0.0%)	0.66	2/3134 (0.1%)
2	G	0.56	0/2317	0.62	1/3133 (0.0%)
3	H	0.44	0/2574	0.60	0/3469
4	I	0.57	0/2325	0.61	0/3138
5	J	0.53	0/3956	0.66	3/5319 (0.1%)
6	K	0.39	0/8452	0.61	0/11416
7	L	0.38	0/1400	0.64	0/1895
7	M	0.40	0/1400	0.64	0/1895
7	N	0.34	0/1400	0.64	0/1895
7	O	0.34	0/1400	0.60	0/1895
7	P	0.35	0/1400	0.61	0/1895
7	Q	0.33	0/1400	0.68	2/1895 (0.1%)
7	R	0.38	0/1400	0.62	0/1895
7	S	0.34	0/1400	0.64	0/1895
7	T	0.36	1/1400 (0.1%)	0.66	0/1895
7	W	0.34	0/1400	0.65	2/1895 (0.1%)
7	X	0.28	0/1400	0.53	0/1895
7	l	0.40	0/1400	0.62	0/1895
7	m	0.41	0/1400	0.66	0/1895
7	n	0.35	0/1400	0.66	1/1895 (0.1%)
7	o	0.34	0/1400	0.65	0/1895
7	p	0.35	0/1400	0.66	0/1895
7	q	0.35	0/1400	0.62	0/1895
7	r	0.39	0/1400	0.63	0/1895
7	s	0.34	0/1400	0.65	1/1895 (0.1%)
7	t	0.50	2/1400 (0.1%)	0.65	1/1895 (0.1%)
7	w	0.53	2/1400 (0.1%)	0.69	1/1895 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
7	x	0.28	0/1400	0.52	0/1895
8	U	1.00	0/989	1.04	0/1538
9	V	1.30	1/1149 (0.1%)	1.15	8/1789 (0.4%)
All	All	0.50	7/63357 (0.0%)	0.65	23/86064 (0.0%)

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
2	D	0	1
2	F	0	1
5	J	0	2
6	K	0	5
7	L	0	1
7	N	0	2
7	P	0	2
7	W	0	1
7	X	0	1
7	m	0	1
7	n	0	1
7	p	0	1
7	q	0	1
7	r	0	1
All	All	0	21

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	w	62	PRO	N-CA	13.42	1.70	1.47
7	t	62	PRO	N-CA	13.09	1.69	1.47
7	w	61	ASP	C-N	5.85	1.45	1.34
2	F	40	GLY	C-N	-5.79	1.20	1.34
7	t	61	ASP	C-N	5.44	1.44	1.34

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	V	3	U	C2-N1-C1'	8.39	127.77	117.70
9	V	3	U	N1-C2-O2	7.46	128.02	122.80
7	w	62	PRO	CA-N-CD	-7.42	101.11	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	V	3	U	N3-C2-O2	-6.92	117.36	122.20
9	V	15	G	O4'-C1'-N9	6.53	113.42	108.20

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	31	ALA	Peptide
2	F	105	LYS	Peptide
5	J	303	ILE	Peptide
5	J	363	ASP	Peptide
6	K	65	TYR	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	151/155 (97%)	145 (96%)	6 (4%)	0	100	100
1	B	152/155 (98%)	143 (94%)	8 (5%)	1 (1%)	22	62
1	C	152/155 (98%)	146 (96%)	6 (4%)	0	100	100
2	D	283/286 (99%)	257 (91%)	26 (9%)	0	100	100
2	E	283/286 (99%)	261 (92%)	22 (8%)	0	100	100
2	F	283/286 (99%)	258 (91%)	25 (9%)	0	100	100
2	G	283/286 (99%)	255 (90%)	28 (10%)	0	100	100
3	H	310/313 (99%)	280 (90%)	30 (10%)	0	100	100
4	I	282/296 (95%)	263 (93%)	19 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	J	473/476 (99%)	429 (91%)	43 (9%)	1 (0%)	47	80
6	K	1005/1037 (97%)	891 (89%)	113 (11%)	1 (0%)	51	84
7	L	171/174 (98%)	142 (83%)	28 (16%)	1 (1%)	25	64
7	M	171/174 (98%)	147 (86%)	24 (14%)	0	100	100
7	N	171/174 (98%)	149 (87%)	21 (12%)	1 (1%)	25	64
7	O	171/174 (98%)	137 (80%)	34 (20%)	0	100	100
7	P	171/174 (98%)	143 (84%)	28 (16%)	0	100	100
7	Q	171/174 (98%)	139 (81%)	32 (19%)	0	100	100
7	R	171/174 (98%)	143 (84%)	28 (16%)	0	100	100
7	S	171/174 (98%)	146 (85%)	24 (14%)	1 (1%)	25	64
7	T	171/174 (98%)	138 (81%)	31 (18%)	2 (1%)	13	51
7	W	171/174 (98%)	141 (82%)	29 (17%)	1 (1%)	25	64
7	X	171/174 (98%)	139 (81%)	31 (18%)	1 (1%)	25	64
7	l	171/174 (98%)	139 (81%)	30 (18%)	2 (1%)	13	51
7	m	171/174 (98%)	140 (82%)	29 (17%)	2 (1%)	13	51
7	n	171/174 (98%)	141 (82%)	30 (18%)	0	100	100
7	o	171/174 (98%)	143 (84%)	28 (16%)	0	100	100
7	p	171/174 (98%)	146 (85%)	24 (14%)	1 (1%)	25	64
7	q	171/174 (98%)	148 (86%)	23 (14%)	0	100	100
7	r	171/174 (98%)	139 (81%)	31 (18%)	1 (1%)	25	64
7	s	171/174 (98%)	149 (87%)	22 (13%)	0	100	100
7	t	171/174 (98%)	145 (85%)	25 (15%)	1 (1%)	25	64
7	w	171/174 (98%)	142 (83%)	28 (16%)	1 (1%)	25	64
7	x	171/174 (98%)	129 (75%)	41 (24%)	1 (1%)	25	64
All	All	7419/7559 (98%)	6453 (87%)	947 (13%)	19 (0%)	44	75

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	K	482	LEU
5	J	364	LYS
7	N	131	ASP
7	T	131	ASP
7	W	131	ASP

5.3.2 Protein sidechains (i)

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	134/136 (98%)	134 (100%)	0	100	100
1	B	135/136 (99%)	135 (100%)	0	100	100
1	C	135/136 (99%)	134 (99%)	1 (1%)	84	93
2	D	252/253 (100%)	251 (100%)	1 (0%)	91	96
2	E	252/253 (100%)	252 (100%)	0	100	100
2	F	252/253 (100%)	250 (99%)	2 (1%)	81	91
2	G	251/253 (99%)	250 (100%)	1 (0%)	91	96
3	H	279/280 (100%)	276 (99%)	3 (1%)	73	87
4	I	255/266 (96%)	252 (99%)	3 (1%)	71	87
5	J	442/445 (99%)	429 (97%)	13 (3%)	42	71
6	K	921/949 (97%)	908 (99%)	13 (1%)	67	85
7	L	159/160 (99%)	158 (99%)	1 (1%)	86	94
7	M	159/160 (99%)	159 (100%)	0	100	100
7	N	159/160 (99%)	159 (100%)	0	100	100
7	O	159/160 (99%)	158 (99%)	1 (1%)	86	94
7	P	159/160 (99%)	157 (99%)	2 (1%)	69	86
7	Q	159/160 (99%)	159 (100%)	0	100	100
7	R	159/160 (99%)	159 (100%)	0	100	100
7	S	159/160 (99%)	158 (99%)	1 (1%)	86	94
7	T	159/160 (99%)	153 (96%)	6 (4%)	33	65
7	W	159/160 (99%)	159 (100%)	0	100	100
7	X	159/160 (99%)	159 (100%)	0	100	100
7	l	159/160 (99%)	157 (99%)	2 (1%)	69	86
7	m	159/160 (99%)	159 (100%)	0	100	100
7	n	159/160 (99%)	158 (99%)	1 (1%)	86	94
7	o	159/160 (99%)	158 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
7	p	159/160 (99%)	158 (99%)	1 (1%)	86 94
7	q	159/160 (99%)	156 (98%)	3 (2%)	57 80
7	r	159/160 (99%)	158 (99%)	1 (1%)	86 94
7	s	159/160 (99%)	157 (99%)	2 (1%)	69 86
7	t	159/160 (99%)	159 (100%)	0	100 100
7	w	159/160 (99%)	158 (99%)	1 (1%)	86 94
7	x	159/160 (99%)	159 (100%)	0	100 100
All	All	6806/6880 (99%)	6746 (99%)	60 (1%)	79 90

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	K	478	LYS
7	q	118	ARG
6	K	738	ASN
7	q	36	ARG
7	w	64	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
7	o	40	ASN
7	X	39	HIS
7	p	14	ASN
7	t	4	GLN
7	x	32	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	U	41/46 (89%)	15 (36%)	2 (4%)
9	V	47/51 (92%)	12 (25%)	0
All	All	88/97 (90%)	27 (30%)	2 (2%)

5 of 27 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	U	3	U
8	U	5	A
8	U	6	A
8	U	7	G
8	U	12	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	U	5	A
8	U	42	A

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)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

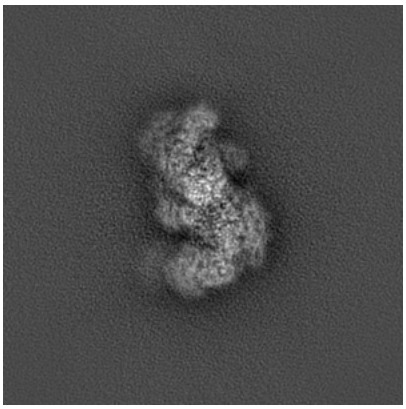
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10209. These allow visual inspection of the internal detail of the map and identification of artifacts.

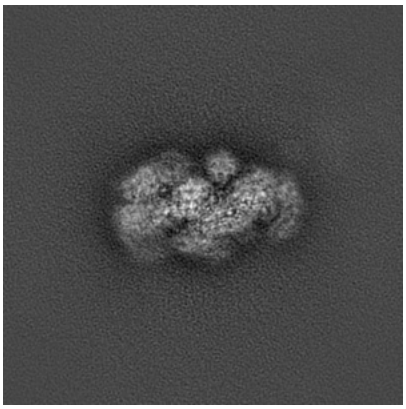
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

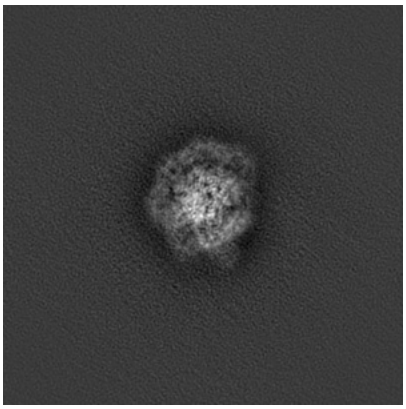
6.1.1 Primary map



X

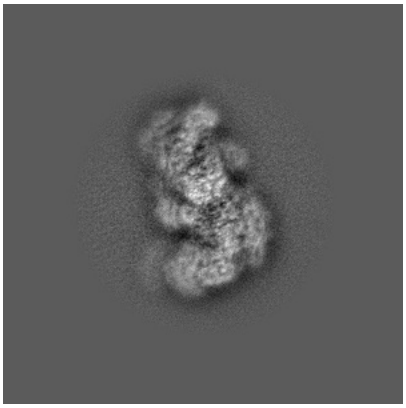


Y

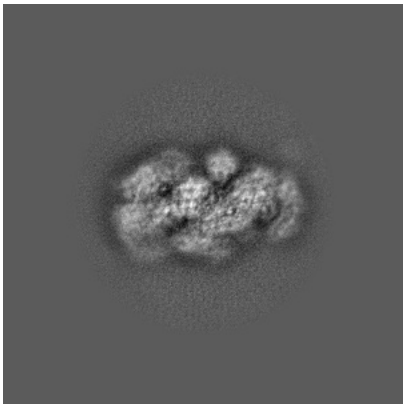


Z

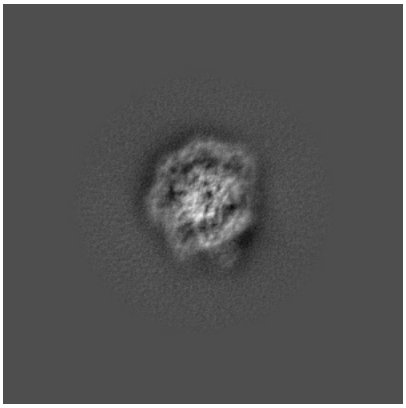
6.1.2 Raw map



X



Y

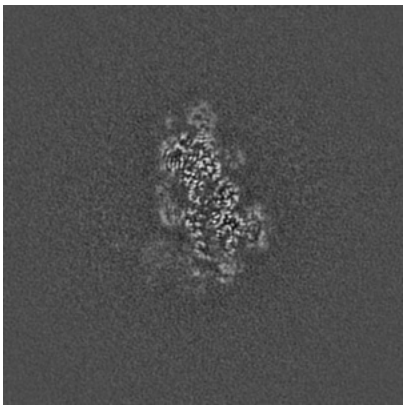


Z

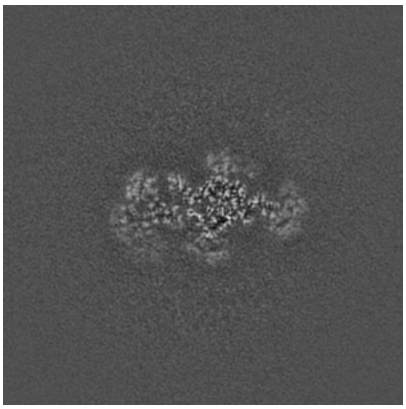
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

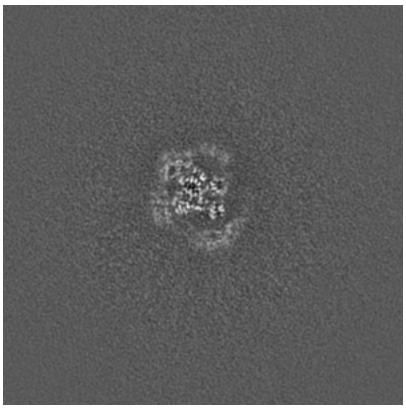
6.2.1 Primary map



X Index: 240

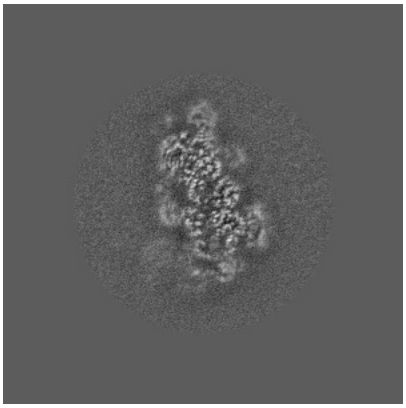


Y Index: 240

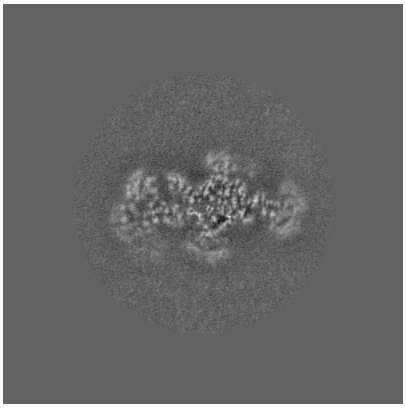


Z Index: 240

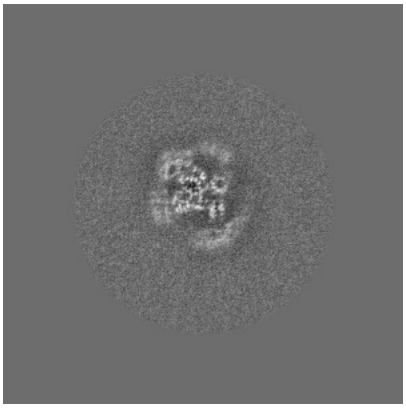
6.2.2 Raw map



X Index: 240



Y Index: 240

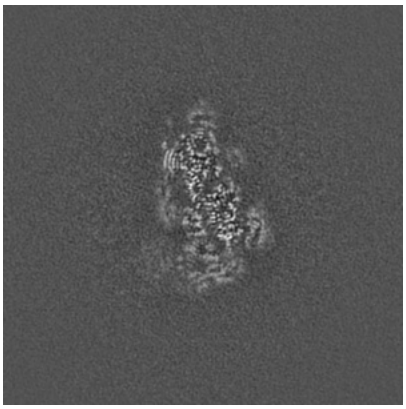


Z Index: 240

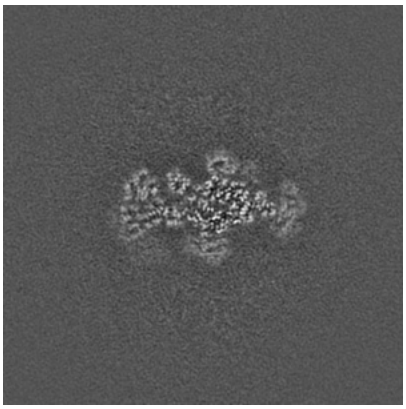
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

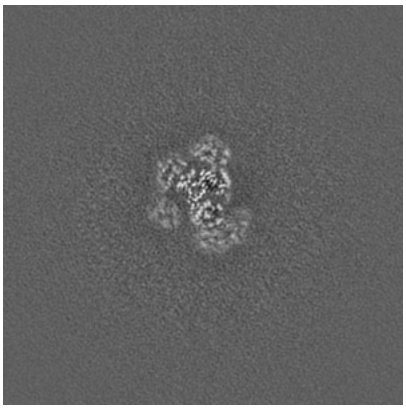
6.3.1 Primary map



X Index: 237

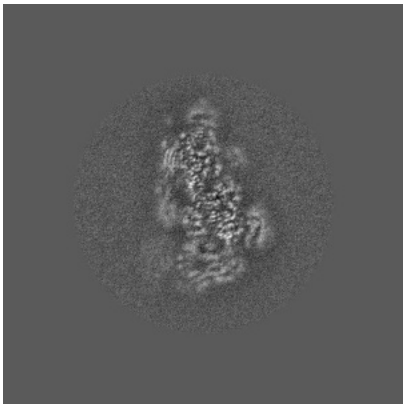


Y Index: 243

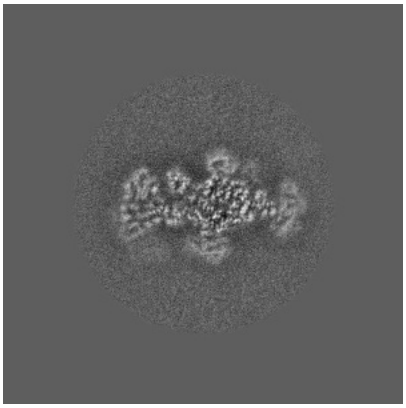


Z Index: 225

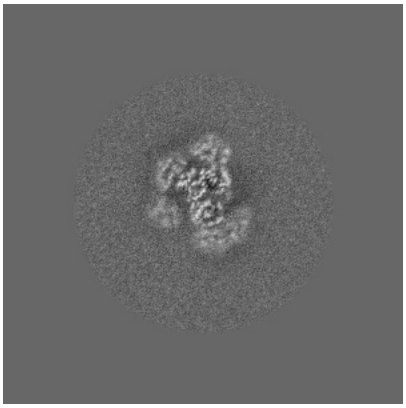
6.3.2 Raw map



X Index: 237



Y Index: 243



Z Index: 225

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

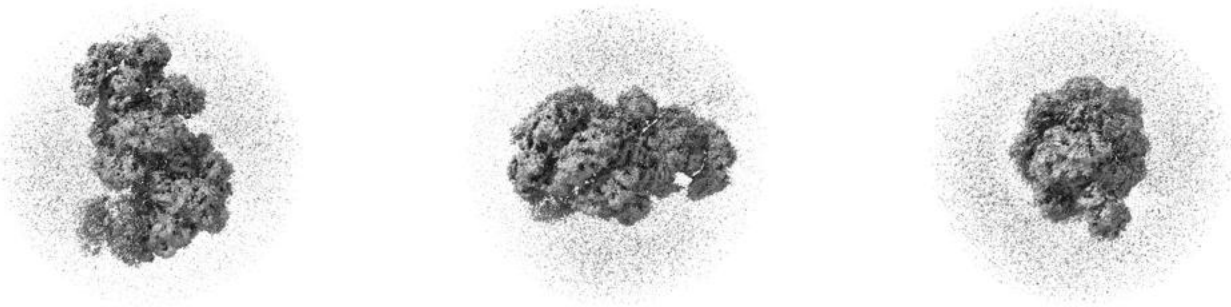
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 2.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

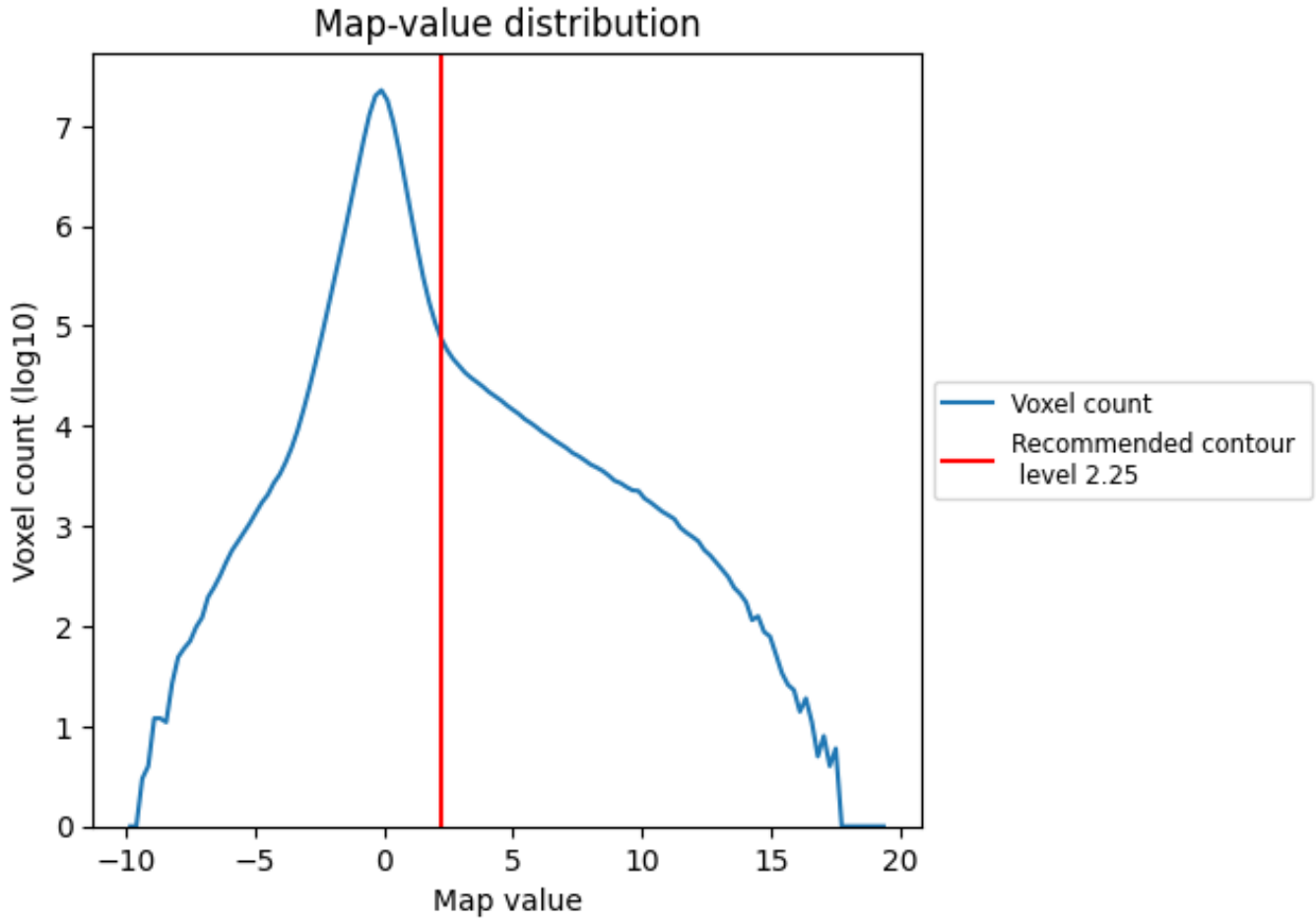
6.5 Mask visualisation (i)

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

7 Map analysis

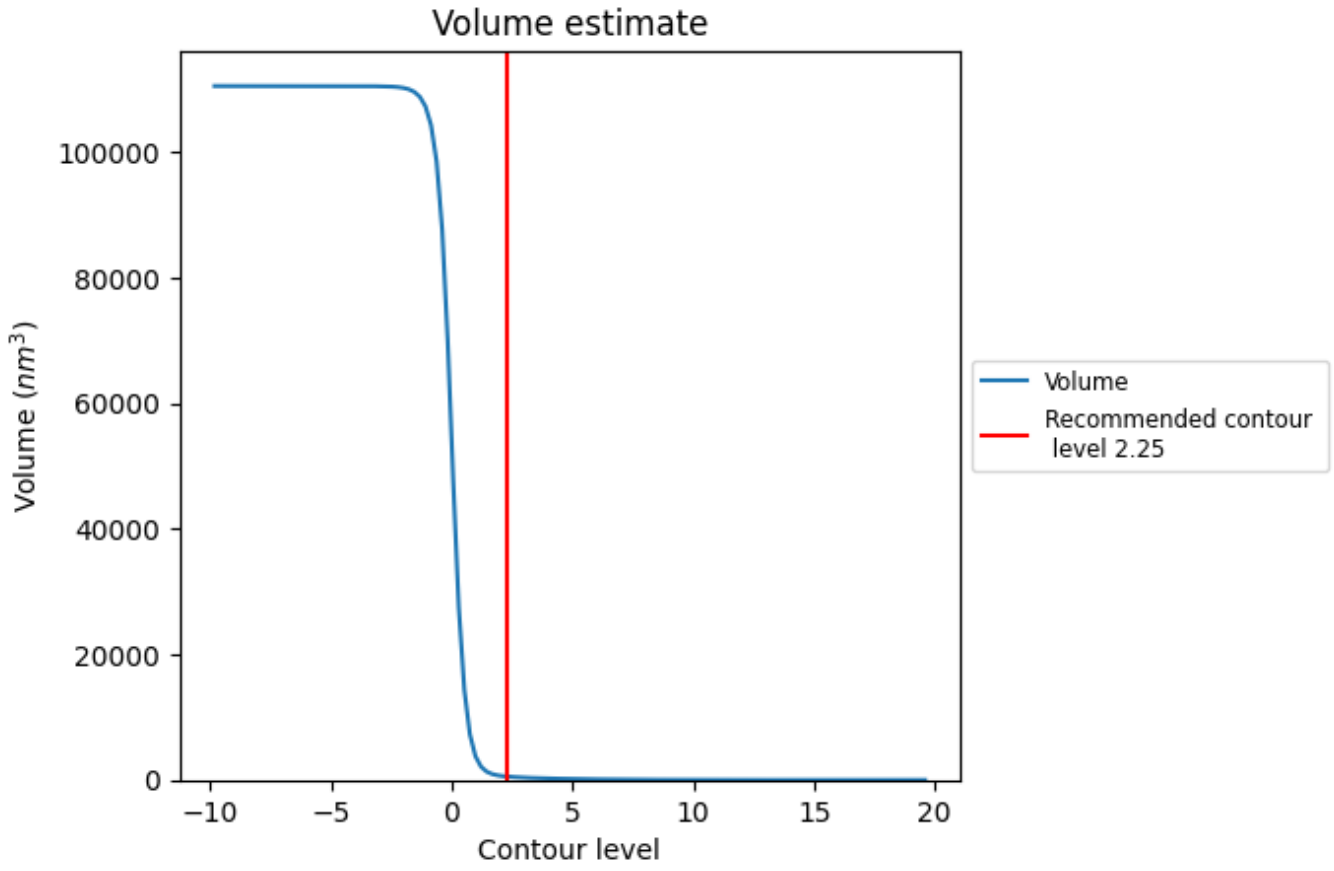
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

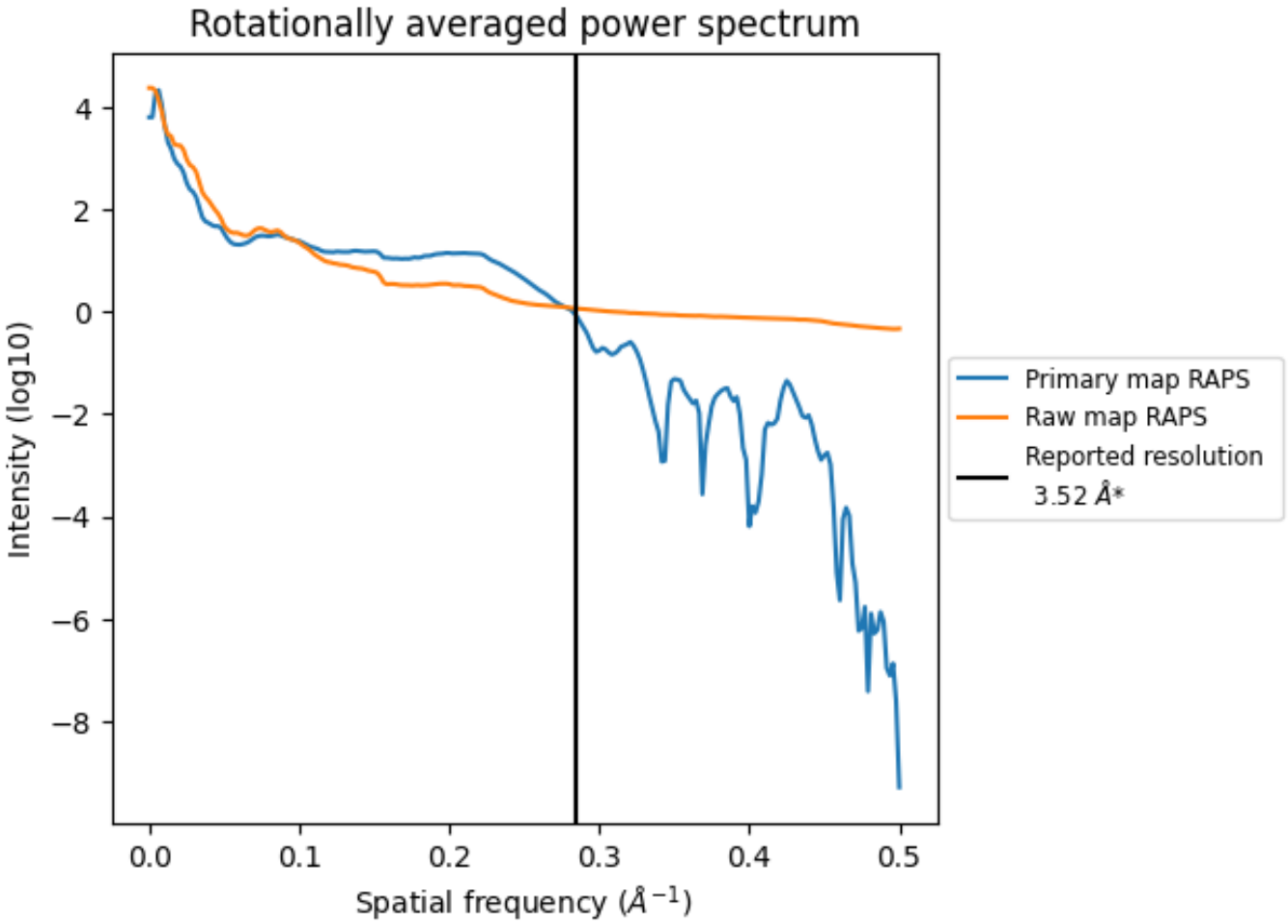
7.2 Volume estimate (i)



The volume at the recommended contour level is 561 nm^3; this corresponds to an approximate mass of 506 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)

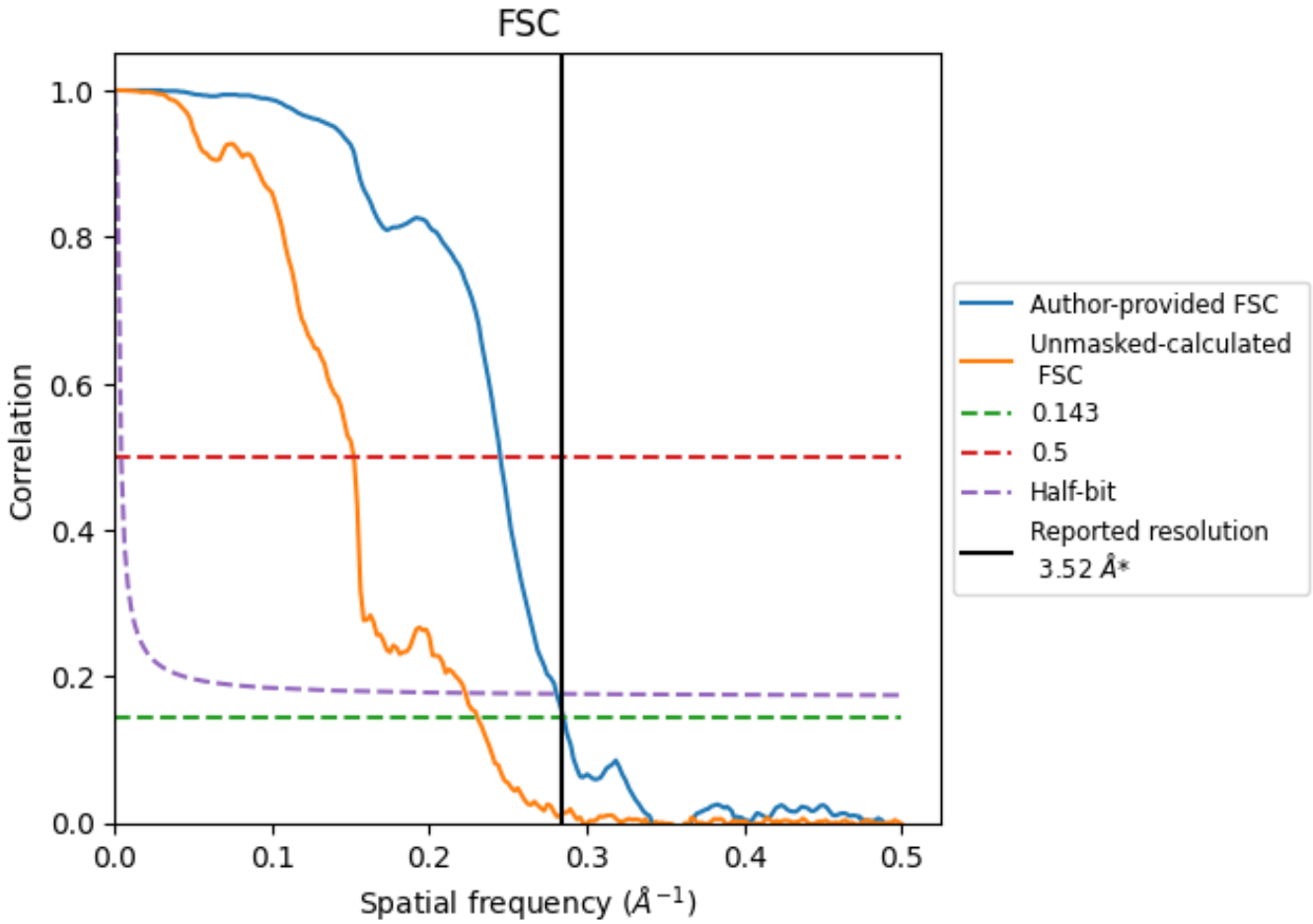


*Reported resolution corresponds to spatial frequency of 0.284 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.284 Å^{-1}

8.2 Resolution estimates (i)

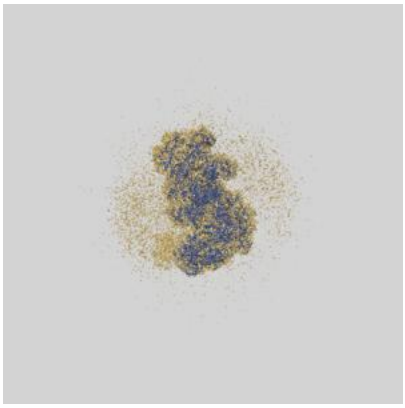
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.52	-	-
Author-provided FSC curve	3.51	4.08	3.56
Unmasked-calculated*	4.33	6.58	4.49

*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 4.33 differs from the reported value 3.52 by more than 10 %

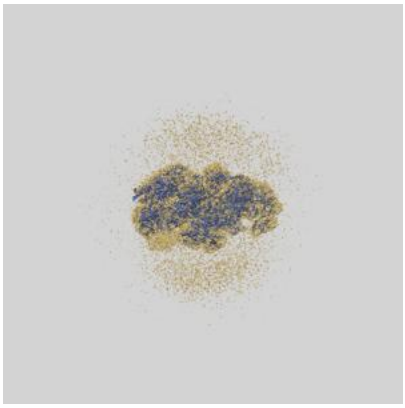
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10209 and PDB model 6SIC. Per-residue inclusion information can be found in section 3 on page 9.

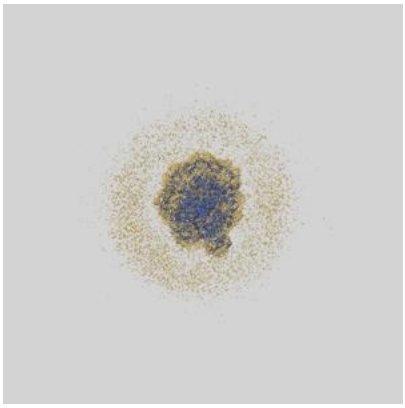
9.1 Map-model overlay



X



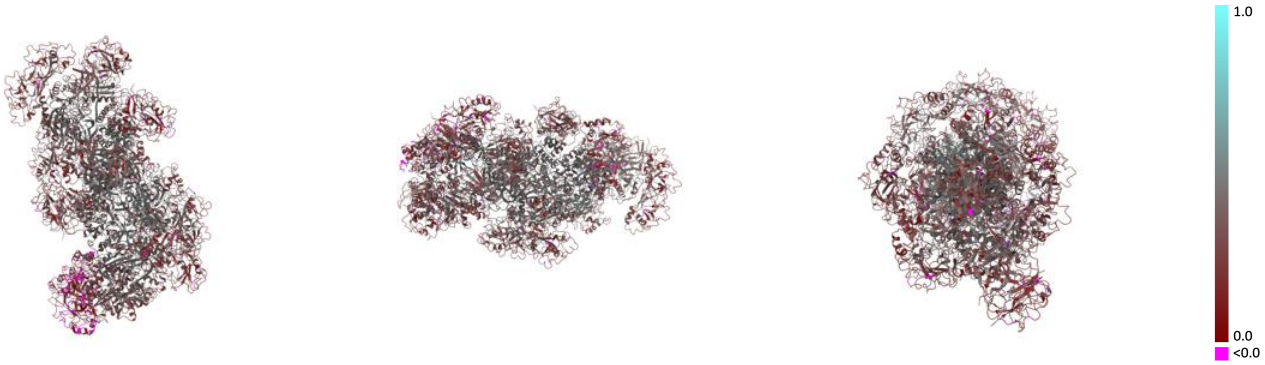
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.25 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.

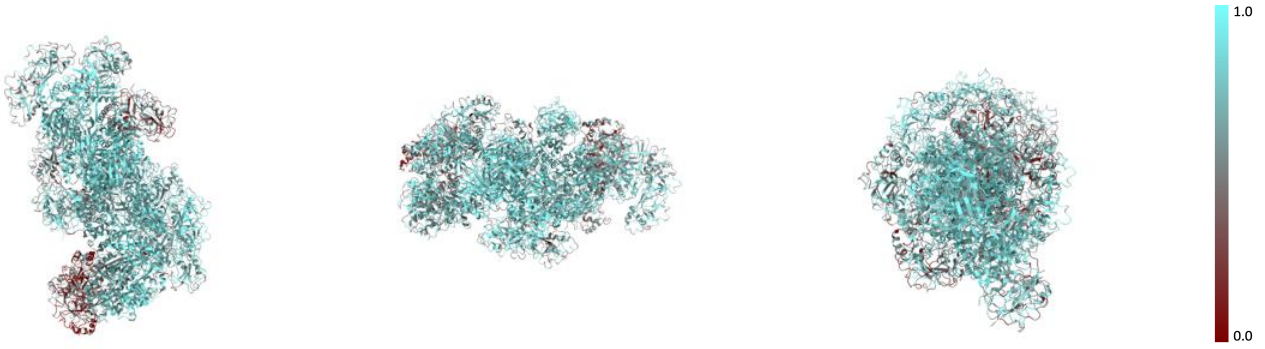
9.2 Q-score mapped to coordinate model (i)



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.

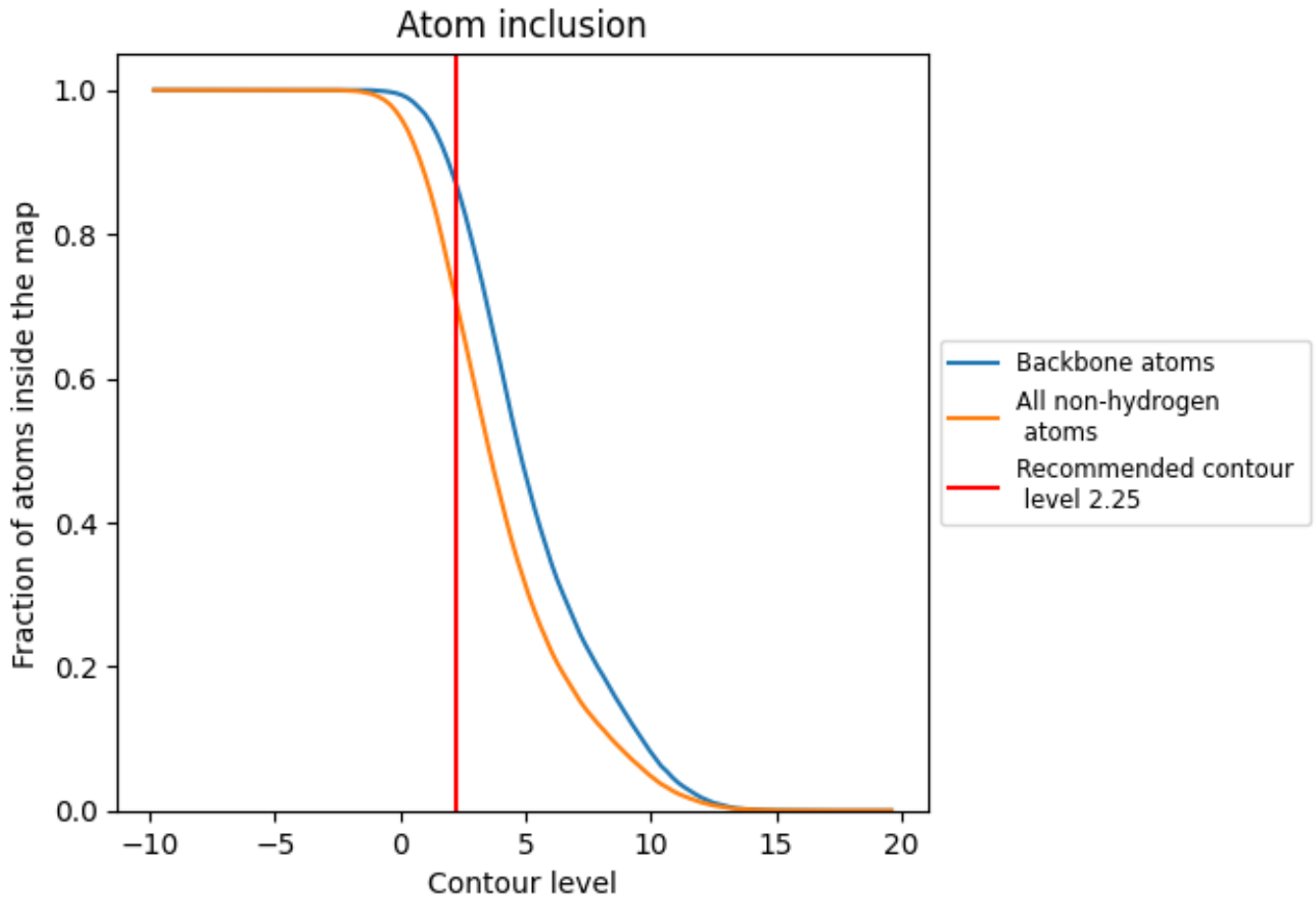
9.3 Atom inclusion mapped to coordinate model (i)



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 (2.25).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 70% 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 (2.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7047	0.3430
A	0.8216	0.4420
B	0.8252	0.4160
C	0.8374	0.4370
D	0.8352	0.4440
E	0.8316	0.4490
F	0.8271	0.4450
G	0.8275	0.4250
H	0.7867	0.3750
I	0.8450	0.4350
J	0.8229	0.4020
K	0.6677	0.3130
L	0.7638	0.3470
M	0.7947	0.3300
N	0.6446	0.2730
O	0.5982	0.3070
P	0.5386	0.3050
Q	0.6336	0.2990
R	0.7925	0.3140
S	0.4444	0.2810
T	0.7005	0.2940
U	0.9560	0.4680
V	0.9717	0.4820
W	0.6380	0.3010
X	0.2163	0.1150
l	0.7697	0.3440
m	0.8013	0.3520
n	0.6255	0.2640
o	0.6372	0.3050
p	0.5526	0.2970
q	0.7027	0.2940
r	0.7800	0.3170
s	0.4047	0.2770
t	0.6733	0.2870
w	0.5997	0.2790
x	0.1759	0.1090