



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 11:42 AM EST

PDB ID : 7MK9
EMDB ID : EMD-23887
Title : Complex structure of trailing EC of EC+EC (trailing EC-focused)
Authors : Yang, C.; Murakami, K.
Deposited on : 2021-04-22
Resolution : 3.54 Å(reported)
Based on initial models : 3PO2, 5C4J

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) : 2.31.2

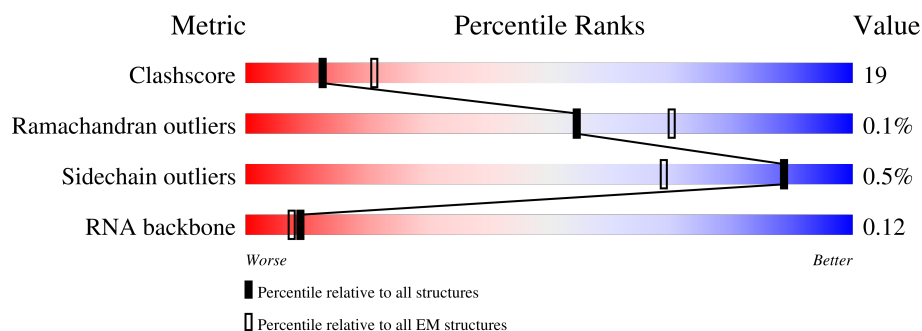
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.54 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.



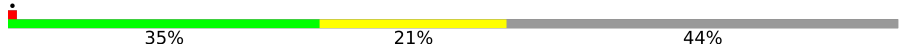


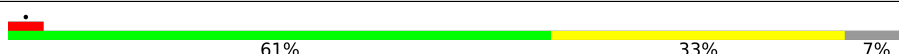
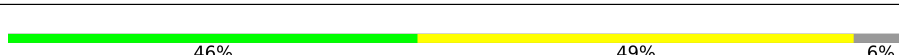
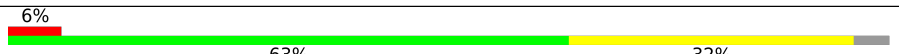
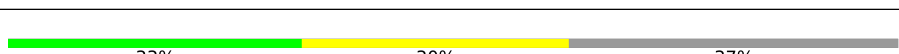
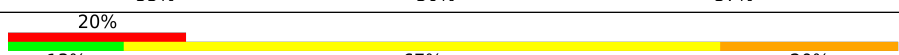
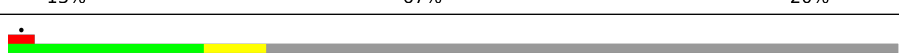
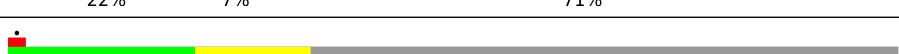
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. 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	N	40	
2	O	40	
3	A	1733	
4	B	1224	
5	C	318	
6	D	221	
7	E	215	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	F	155	
9	G	171	
10	H	146	
11	I	122	
12	J	70	
13	K	120	
14	L	70	
15	R	15	
16	Q	735	
17	M	400	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 36122 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 DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	40	Total	C	N	O	P	0	0
			822	393	162	227	40		

- Molecule 2 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	40	Total	C	N	O	P	0	0
			827	396	141	250	40		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	1425	Total	C	N	O	S	0	0
			11167	7036	1948	2121	62		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	1166	Total	C	N	O	S	0	0
			9227	5823	1619	1729	56		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	265	Total	C	N	O	S	0	0
			2086	1312	347	414	13		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	168	Total	C	N	O	S	0	0
			1331	822	237	270	2		

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	214	Total	C	N	O	S	0	0
			1752	1111	309	321	11		

- Molecule 8 is a protein called DNA-directed RNA polymerases I,II,and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	87	Total	C	N	O	S	0	0
			705	451	119	132	3		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	171	Total	C	N	O	S	0	0
			1335	858	221	248	8		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	135	Total	C	N	O	S	0	0
			1080	679	182	214	5		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	114	Total	C	N	O	S	0	0
			927	571	168	178	10		

- Molecule 12 is a protein called DNA-directed RNA polymerases II subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	66	Total	C	N	O	S	0	0
			540	345	94	95	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	115	Total	C	N	O	S	0	0
			924	593	157	172	2		

- Molecule 14 is a protein called DNA-directed RNA polymerases II subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	44	Total	C	N	O	S	0	0
			352	217	70	61	4		

- Molecule 15 is a RNA chain called RNA (5'-R(P*UP*CP*GP*AP*GP*AP*GP*GP*AP*UP*CP*CP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	15	Total	C	N	O	P	0	0
			312	141	56	100	15		

- Molecule 16 is a protein called Transcription initiation factor IIF subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	214	Total	C	N	O	S	0	0
			1619	1017	297	299	6		

- Molecule 17 is a protein called Transcription initiation factor IIF subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	135	Total	C	N	O	S	0	0
			1106	694	197	210	5		

- Molecule 18 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
18	A	2	Total	Zn	0
			2	2	
18	B	1	Total	Zn	0
			1	1	
18	C	1	Total	Zn	0
			1	1	
18	I	2	Total	Zn	0
			2	2	
18	J	1	Total	Zn	0
			1	1	
18	L	1	Total	Zn	0
			1	1	

- Molecule 19 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
19	A	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

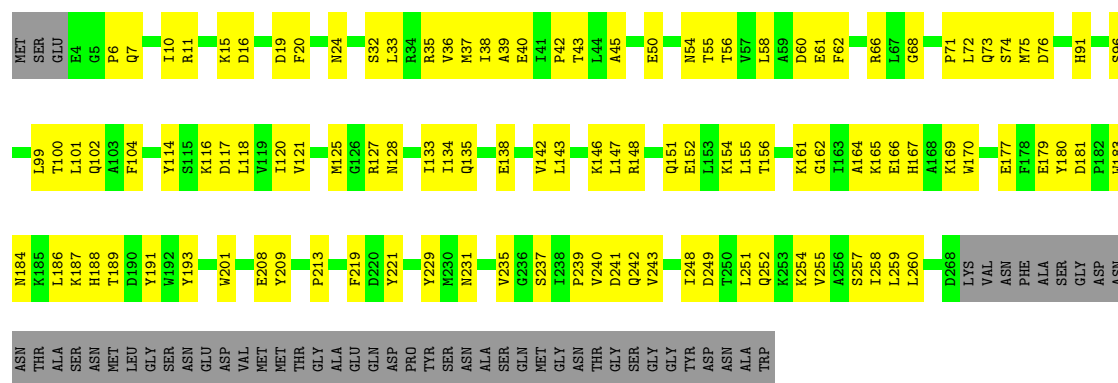
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
19	R	1	1	1	0

- Molecule 4: DNA-directed RNA polymerase subunit beta



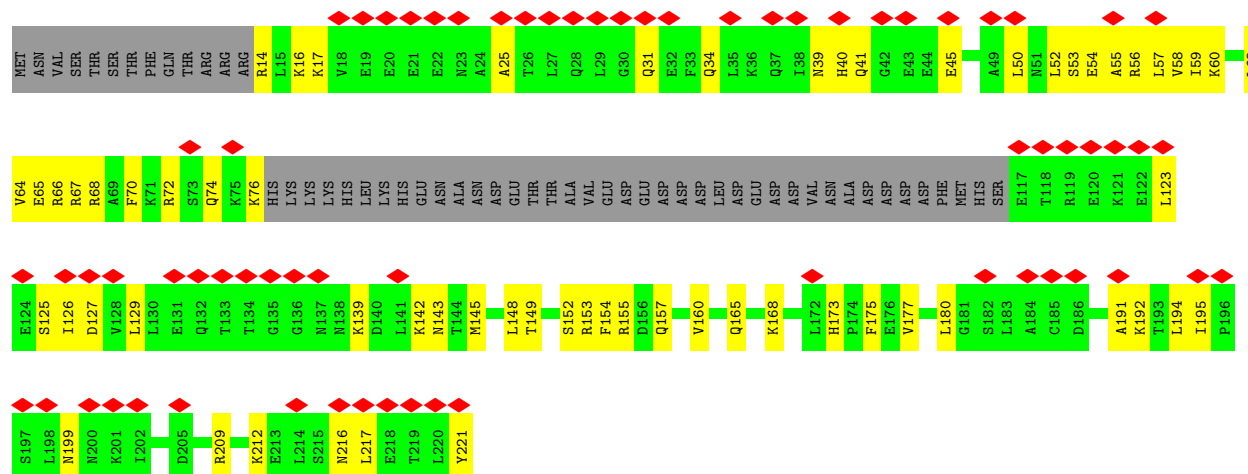


Chain C: 



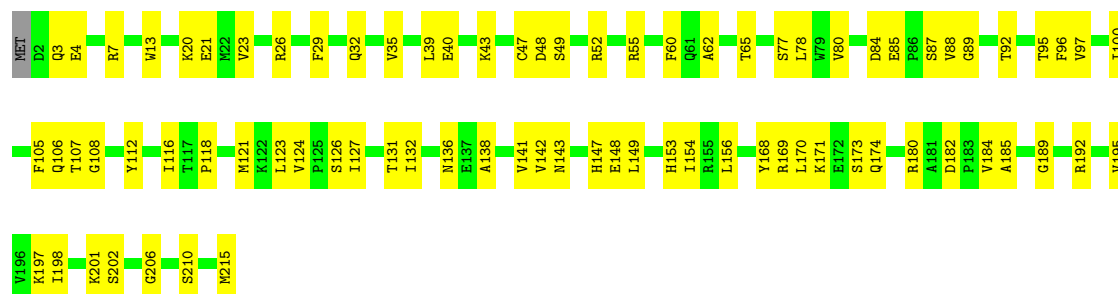
• Molecule 6: DNA-directed RNA polymerase II subunit RPB4

Chain D: 

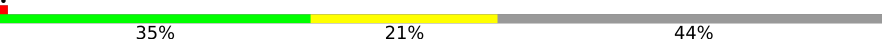


• Molecule 7: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 



• Molecule 8: DNA-directed RNA polymerases I,II,and III subunit RPABC2

Chain F: 

MET SER GLN TYR GLU ALA PHE ASN ASP GLY ASN GLU PHE GLU ASP PHE ASP VAL GLU HIS PHE SER ASP ASP GLU LYS PHE GLN ASP LYS ASP GLY GLU THR THR ASP ALA ASN GLY LYS THR ILE VAL THR GLY GLY ASN GLY PRO GLU ASP PHE GLN GLN

HIS GLU GLN ILE ARG ARG LYS THR L69 E70 E71 K72 D77 P78 Q78 R79 T82 P83 Y84 Y85 T86 E89 R92 R93 L94 R97 Q100 Q101 F108 D116 R119 L125 T130 P131 L132 V133 P139 D140 G141 S142 V148 E149 E150 L151 L152 L155

• Molecule 9: DNA-directed RNA polymerase II subunit RPB7

Chain G: 36% 54% 46%

M1 F2 I4 K5 D6 L7 N10 L13 H14 P15 F17 R21 Q24 Y25 L26 K27 T28 E33 C38 T39 G40 K41 Y44 I45 L46 C47 V48 L49 D52 N53 T56 Q57 R58 I61 L62 P63 N71 V72 K73 Y74 R75 A76 V77 V78 F79 F82

K83 G84 E85 V86 V87 D88 G89 T90 V91 V92 S93 S94 C94 S95 S96 H97 G98 F99 E100 V101 V102 G104 P105 M106 K107 V108 F109 V110 T111 K112 H113 L114 M115 P116 Q117 D118 L119 T120 F121 M122 A123 G124 S125 M126 P127 P128 S129 Y130 Q131 S132 S133 E134 D135 V136 I137 T138 I139 K140 S141 R142

I143 R144 V145 K146 I147 E148 G149 C150 I151 S152 Q153 V154 S155 S156 S157 H158 A159 I160 G161 S162 I163 K164 E165 D166 Y167 L168 G169 A170 I171

• Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 47% 44% 8%

M1 L5 F6 D7 D8 I9 V12 S13 P17 G18 R19 K22 V23 C24 R25 L26 E27 Q33 D34 G35 C36 K37 L40 D41 I42 D53 S54 L55 T58 I59 A60 S61 S62 L63 K64 L65 L66 L67 L68 L69 L70 L71 L72 L73 L74 L75 L76 L77 L78 L79 L80 L81 L82 L83 L84 L85 L86 L87 L88 L89 L90 L91 L92 L93 L94 L95 L96 L97 L98 L99 L100 L101 L102 L103 L104 L105 L106 L107 L108 L109 L110 L111 L112 L113 L114 L115 L116 L117 L118 L119 L120 L121 L122 L123 L124 L125 L126 L127 L128 L129 L130 L131 L132 L133 L134 L135 L136 L137 L138 L139 L140 L141 L142 L143 L144 L145 L146

• Molecule 11: DNA-directed RNA polymerase II subunit RPB9

Chain I: 61% 33% 7%

MET T2 C7 C10 N11 R17 E21 N22 K23 R24 L25 L26 F27 E28 V35 E36 E37 V43 Y44 R45 H46 I52 G53 G54 E55 A56 G57 Q60 D61 I62 P66 P67 T67 L68 P69 R73 P76 K77 C78 N83 V84 F85 F86 Q87 S88 Q89 Q90 R91

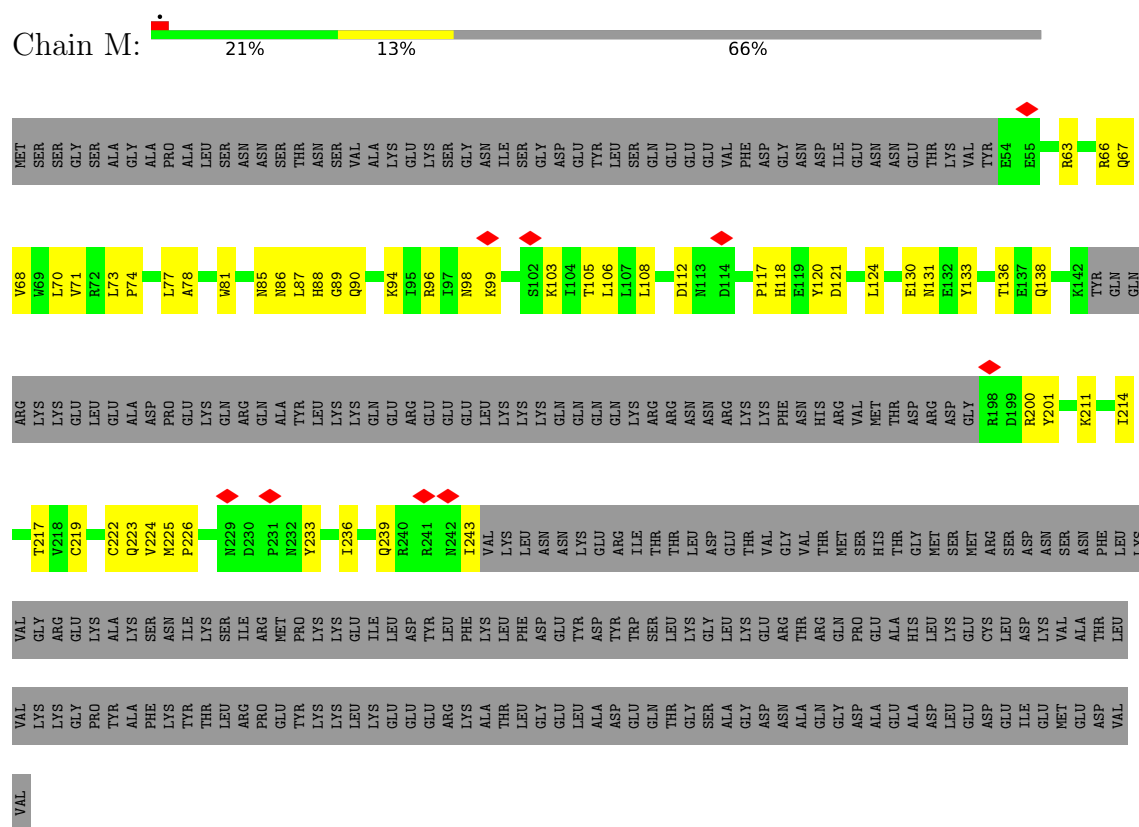
F100 C103 L104 S105 C106 I109 D113 Q114 K115 ASN LYS ARG THR PHE SER

• Molecule 12: DNA-directed RNA polymerases II subunit RPABC5

Chain J: 46% 49% 6%

M1 T2 V3 P4 V5 F8 S9 C10 G11 D16 K17 W18 E19 S20 L22 L23 L24 E27 D28 E32 L39 Y44 C45 R47 R48 M49 T52 H53 V54 D55 L56 I57 L61 R62 Y63 R64 L66 L67 L68 L69 L70 L71 L72 L73 L74 L75 L76 L77 L78 L79 L80 L81 L82 L83 L84 L85 L86 L87 L88 L89 L90 L91

- Molecule 17: Transcription initiation factor IIF subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	66261	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 ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.056	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0084	Depositor
Map size (\AA)	237.6, 237.6, 237.6	wwPDB
Map dimensions	220, 220, 220	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	N	0.54	0/926	0.87	0/1425
2	O	0.60	0/925	0.99	0/1429
3	A	0.33	0/11368	0.49	0/15383
4	B	0.34	0/9402	0.52	0/12680
5	C	0.32	0/2124	0.50	0/2879
6	D	0.24	0/1339	0.44	0/1793
7	E	0.32	0/1788	0.45	0/2406
8	F	0.35	0/717	0.51	0/967
9	G	0.29	0/1363	0.49	0/1840
10	H	0.33	0/1097	0.52	0/1484
11	I	0.30	0/945	0.45	0/1273
12	J	0.40	0/549	0.51	0/738
13	K	0.32	0/942	0.48	0/1272
14	L	0.28	0/354	0.57	0/468
15	R	0.58	0/347	0.85	1/536 (0.2%)
16	Q	0.27	0/1648	0.45	1/2226 (0.0%)
17	M	0.25	0/1124	0.47	0/1517
All	All	0.34	0/36958	0.53	2/50316 (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
3	A	0	3
4	B	0	3
9	G	0	1
All	All	0	7

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	R	12	A	O5'-P-OP1	-5.83	100.45	105.70
16	Q	421	PRO	N-CA-CB	5.72	110.16	103.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	252	PHE	Peptide
3	A	55	ASP	Peptide
3	A	750	GLY	Peptide
4	B	363	HIS	Peptide
4	B	510	LYS	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	N	822	0	449	19	0
2	O	827	0	458	19	0
3	A	11167	0	11188	458	0
4	B	9227	0	9200	393	0
5	C	2086	0	2045	96	0
6	D	1331	0	1344	56	0
7	E	1752	0	1776	63	0
8	F	705	0	731	30	0
9	G	1335	0	1346	56	0
10	H	1080	0	1049	58	0
11	I	927	0	881	33	0
12	J	540	0	553	37	0
13	K	924	0	934	39	0
14	L	352	0	375	20	0
15	R	312	0	165	12	0
16	Q	1619	0	1452	41	0
17	M	1106	0	1099	43	0
18	A	2	0	0	0	0
18	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	C	1	0	0	0	0
18	I	2	0	0	0	0
18	J	1	0	0	0	0
18	L	1	0	0	0	0
19	A	1	0	0	0	0
19	R	1	0	0	0	0
All	All	36122	0	35045	1329	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 19.

The worst 5 of 1329 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:510:LYS:HG3	4:B:511:PRO:HD3	1.45	0.98
14:L:48:CYS:SG	14:L:51:CYS:HB2	2.09	0.93
3:A:110:CYS:HB3	3:A:167:CYS:SG	2.09	0.92
3:A:802:ASN:HD21	3:A:806:ARG:HB2	1.35	0.91
4:B:334:ILE:HA	4:B:347:LYS:HG3	1.52	0.90

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	1417/1733 (82%)	1266 (89%)	148 (10%)	3 (0%)	47	80
4	B	1150/1224 (94%)	1001 (87%)	147 (13%)	2 (0%)	47	80
5	C	263/318 (83%)	231 (88%)	32 (12%)	0	100	100
6	D	164/221 (74%)	159 (97%)	5 (3%)	0	100	100
7	E	212/215 (99%)	196 (92%)	16 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	F	85/155 (55%)	77 (91%)	8 (9%)	0	100	100
9	G	169/171 (99%)	155 (92%)	14 (8%)	0	100	100
10	H	129/146 (88%)	110 (85%)	19 (15%)	0	100	100
11	I	112/122 (92%)	102 (91%)	10 (9%)	0	100	100
12	J	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
13	K	113/120 (94%)	108 (96%)	5 (4%)	0	100	100
14	L	42/70 (60%)	30 (71%)	12 (29%)	0	100	100
16	Q	208/735 (28%)	202 (97%)	6 (3%)	0	100	100
17	M	131/400 (33%)	123 (94%)	8 (6%)	0	100	100
All	All	4259/5700 (75%)	3814 (90%)	440 (10%)	5 (0%)	54	84

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	188	ASP
4	B	364	ILE
3	A	195	ASP
3	A	253	ASN
4	B	363	HIS

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	
3	A	1235/1520 (81%)	1228 (99%)	7 (1%)	86	94
4	B	1000/1061 (94%)	995 (100%)	5 (0%)	88	95
5	C	233/274 (85%)	232 (100%)	1 (0%)	91	97
6	D	146/200 (73%)	146 (100%)	0	100	100
7	E	196/197 (100%)	196 (100%)	0	100	100
8	F	77/137 (56%)	77 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	G	151/152 (99%)	151 (100%)	0	100	100
10	H	118/128 (92%)	115 (98%)	3 (2%)	47	76
11	I	108/116 (93%)	108 (100%)	0	100	100
12	J	61/65 (94%)	61 (100%)	0	100	100
13	K	99/102 (97%)	99 (100%)	0	100	100
14	L	39/57 (68%)	39 (100%)	0	100	100
16	Q	147/641 (23%)	145 (99%)	2 (1%)	67	85
17	M	125/363 (34%)	125 (100%)	0	100	100
All	All	3735/5013 (74%)	3717 (100%)	18 (0%)	89	95

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	H	130	ARG
16	Q	333	LYS
16	Q	330	ARG
4	B	265	SER
10	H	77	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
6	D	41	GLN
8	F	100	GLN
13	K	40	HIS
11	I	87	GLN
6	D	150	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	R	14/15 (93%)	8 (57%)	0

5 of 8 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	R	5	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	R	8	A
15	R	9	C
15	R	10	A
15	R	11	A

There are no RNA pucker outliers to report.

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 10 ligands modelled in this entry, 10 are 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.

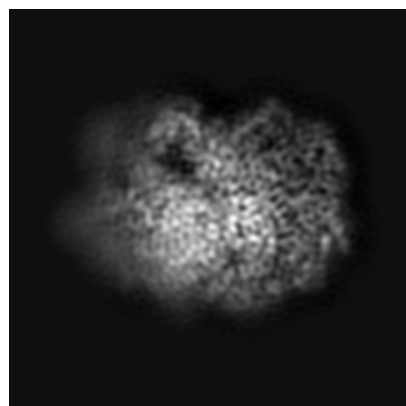
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23887. These allow visual inspection of the internal detail of the map and identification of artifacts.

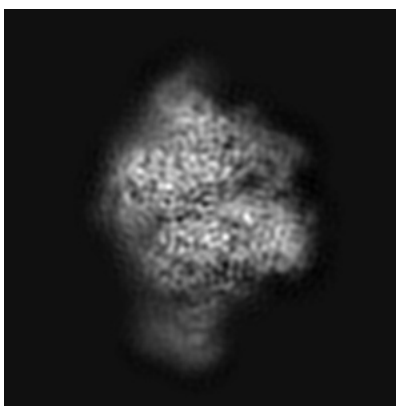
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

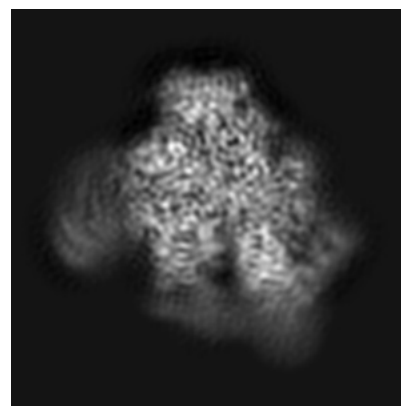
6.1.1 Primary map



X

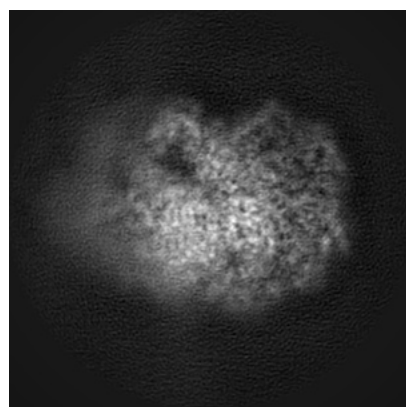


Y

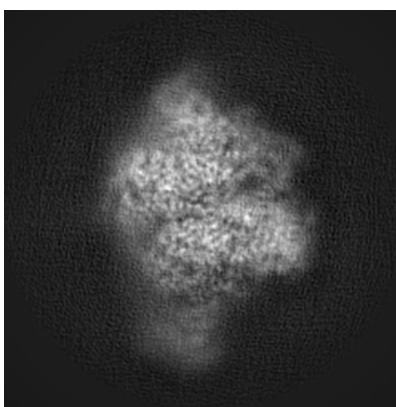


Z

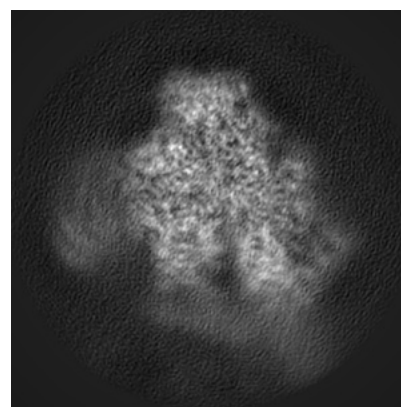
6.1.2 Raw map



X



Y

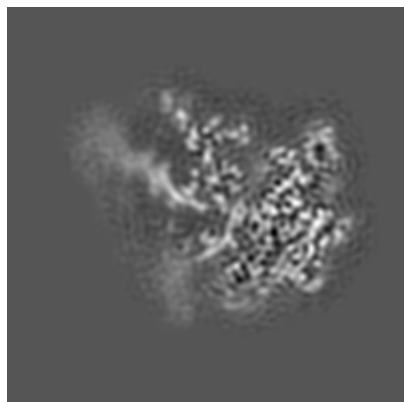


Z

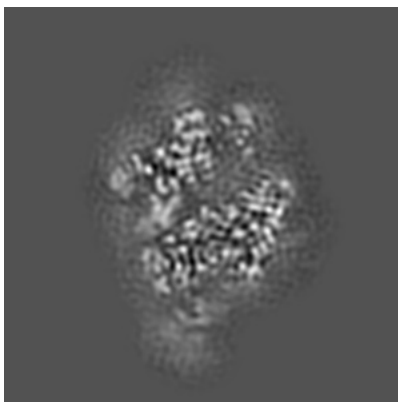
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

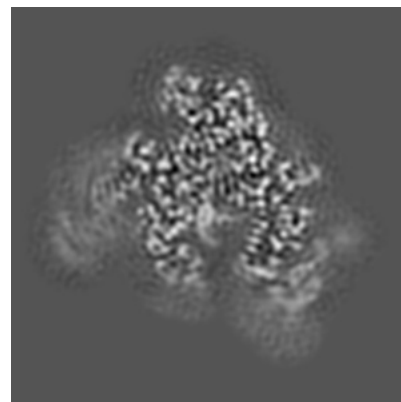
6.2.1 Primary map



X Index: 110

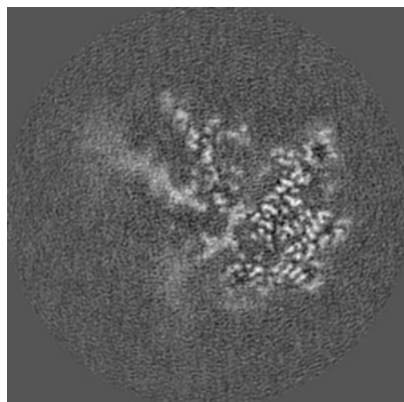


Y Index: 110

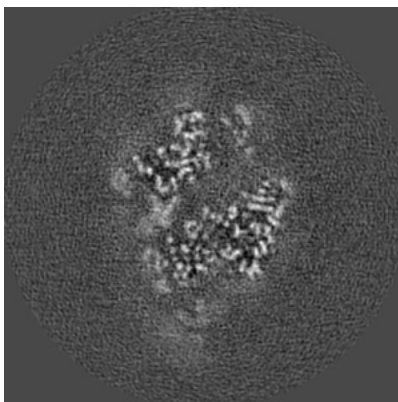


Z Index: 110

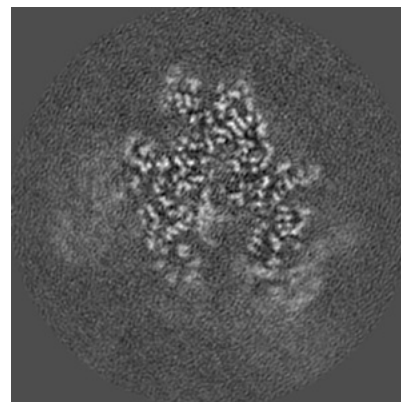
6.2.2 Raw map



X Index: 110



Y Index: 110

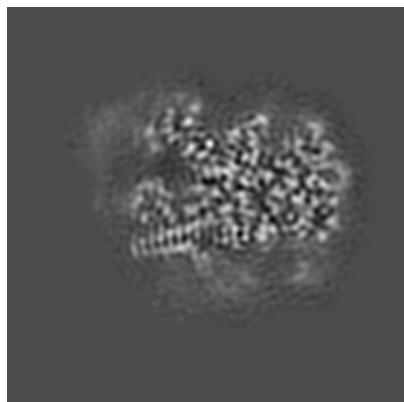


Z Index: 110

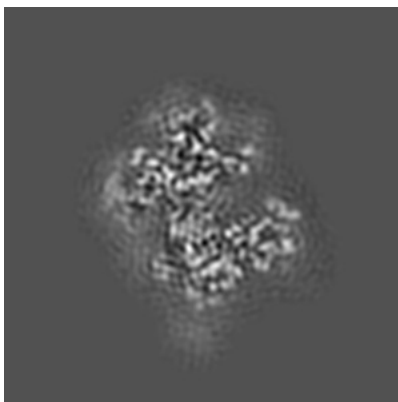
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

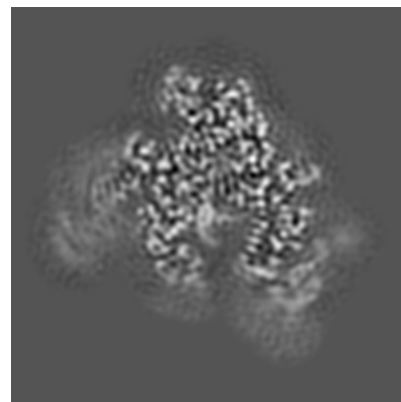
6.3.1 Primary map



X Index: 96

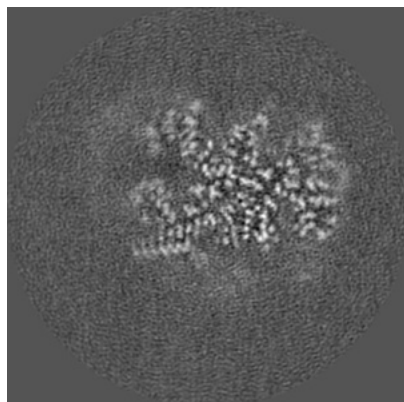


Y Index: 131

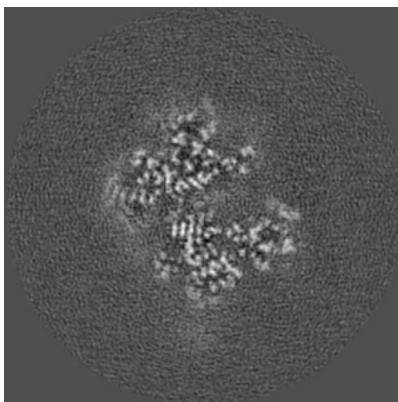


Z Index: 110

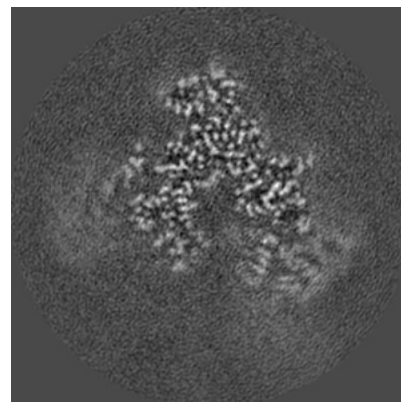
6.3.2 Raw map



X Index: 95



Y Index: 131

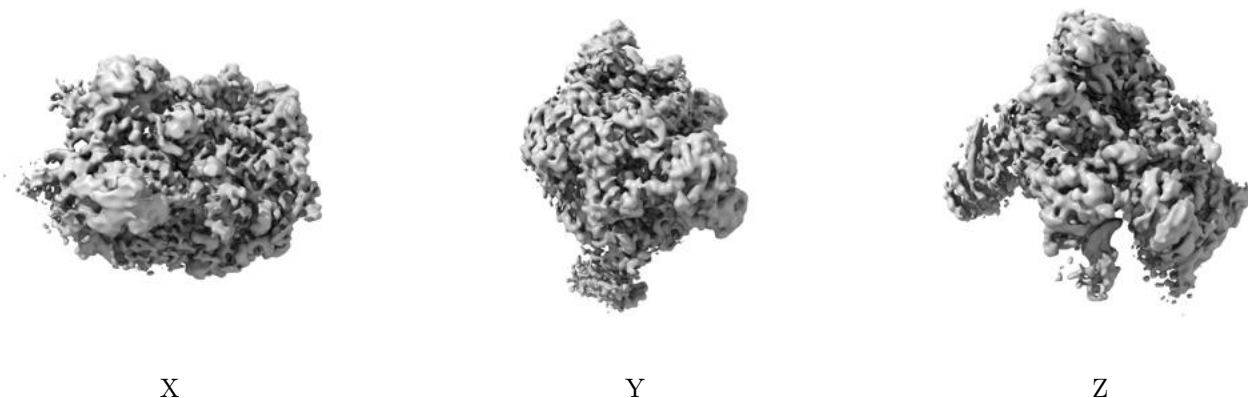


Z Index: 101

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

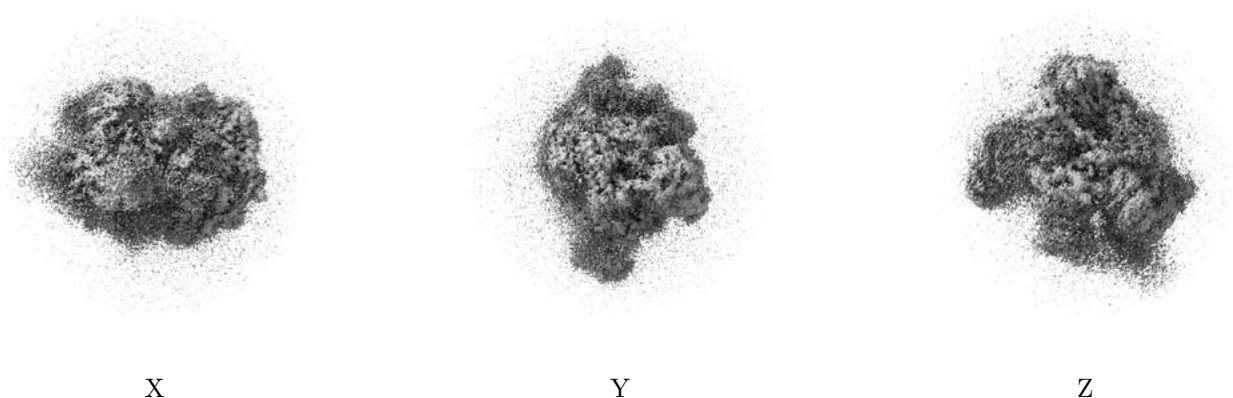
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0084. 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



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.

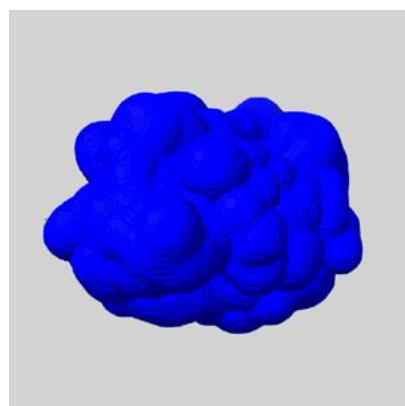
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

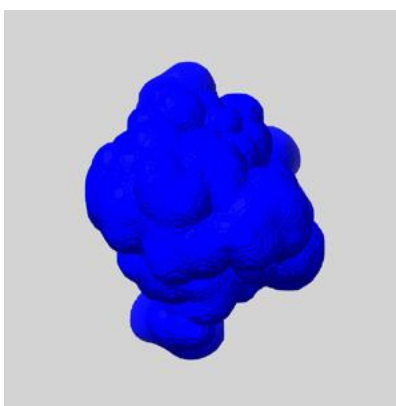
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

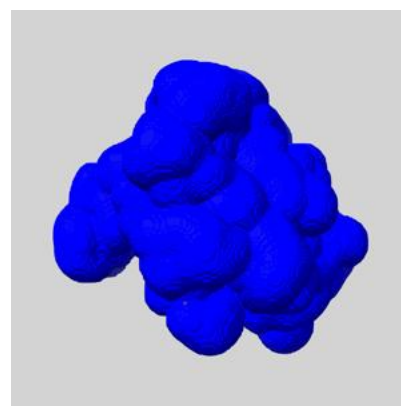
6.5.1 emd_23887_msk_1.map [i](#)



X



Y

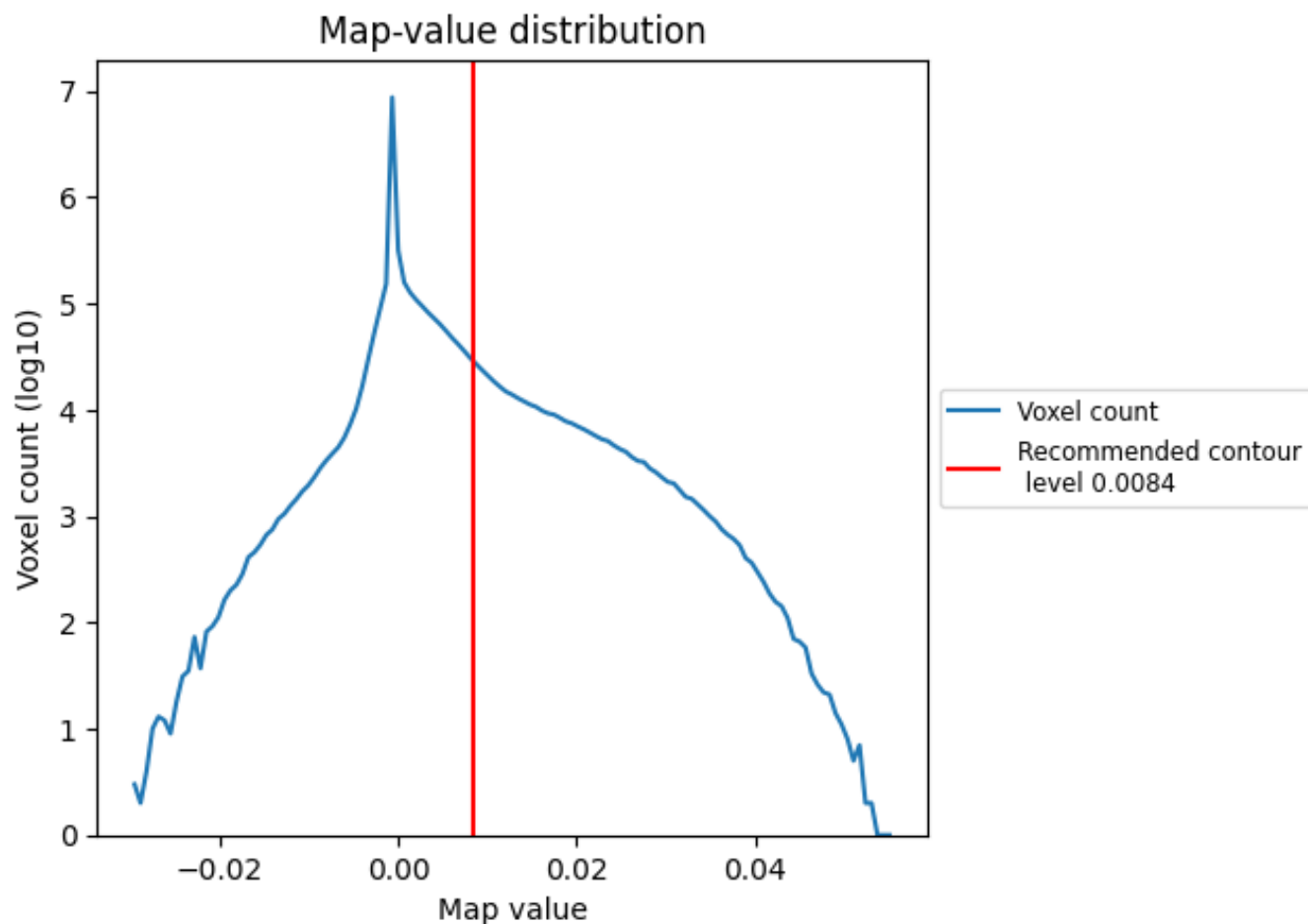


Z

7 Map analysis [i](#)

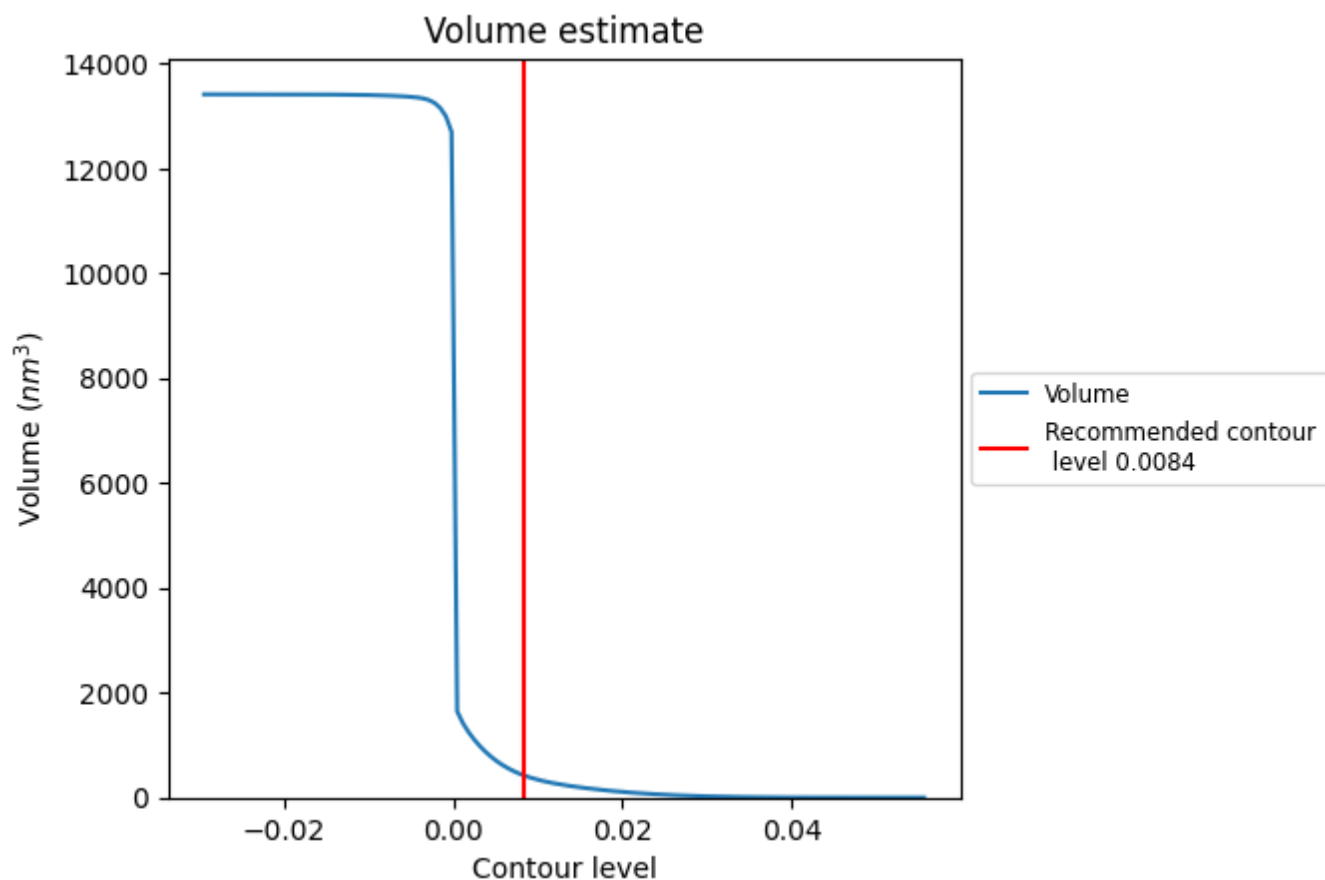
This section contains the results of statistical analysis of the map.

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.

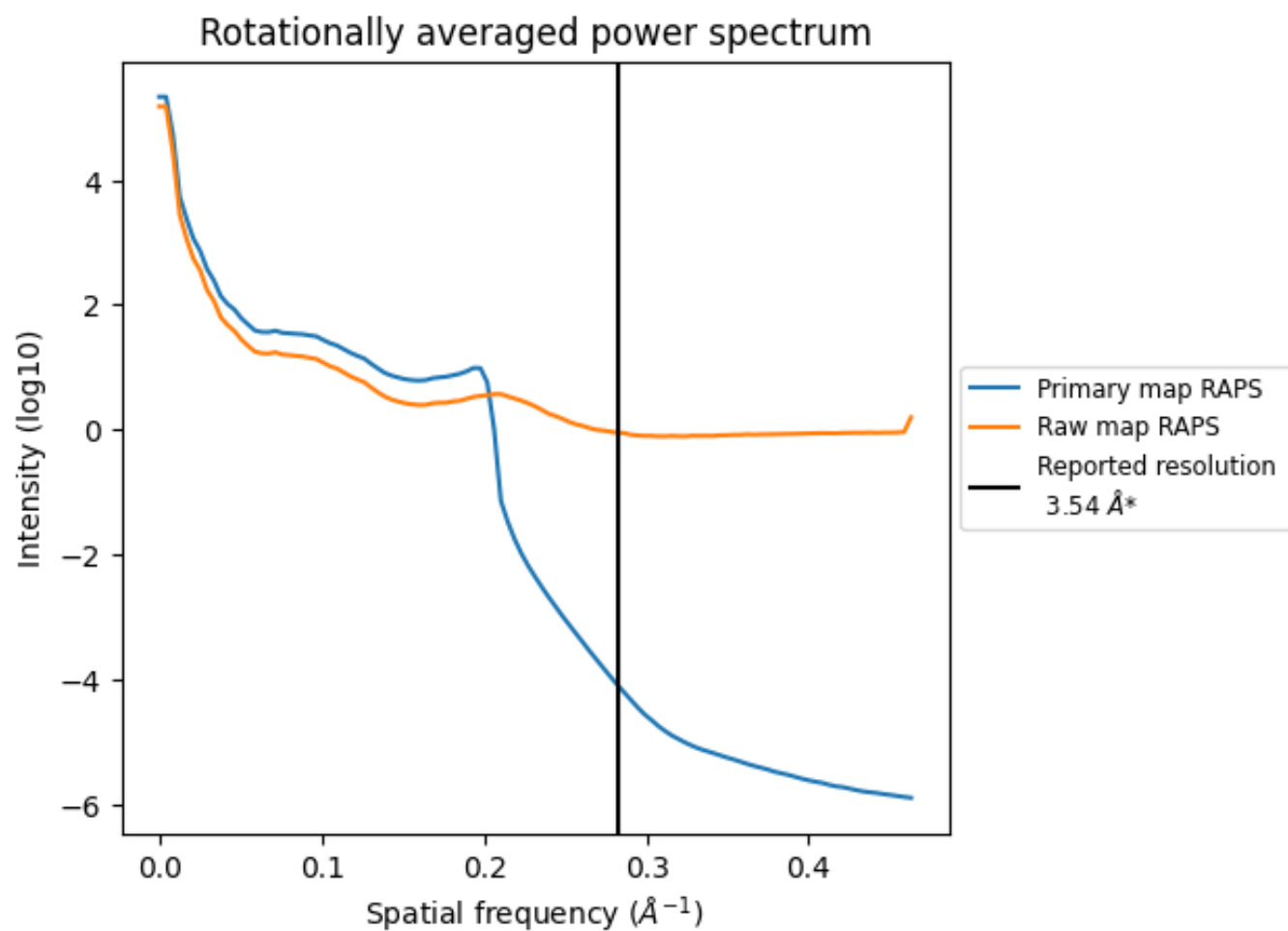
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 420 nm³; this corresponds to an approximate mass of 379 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 ⓘ

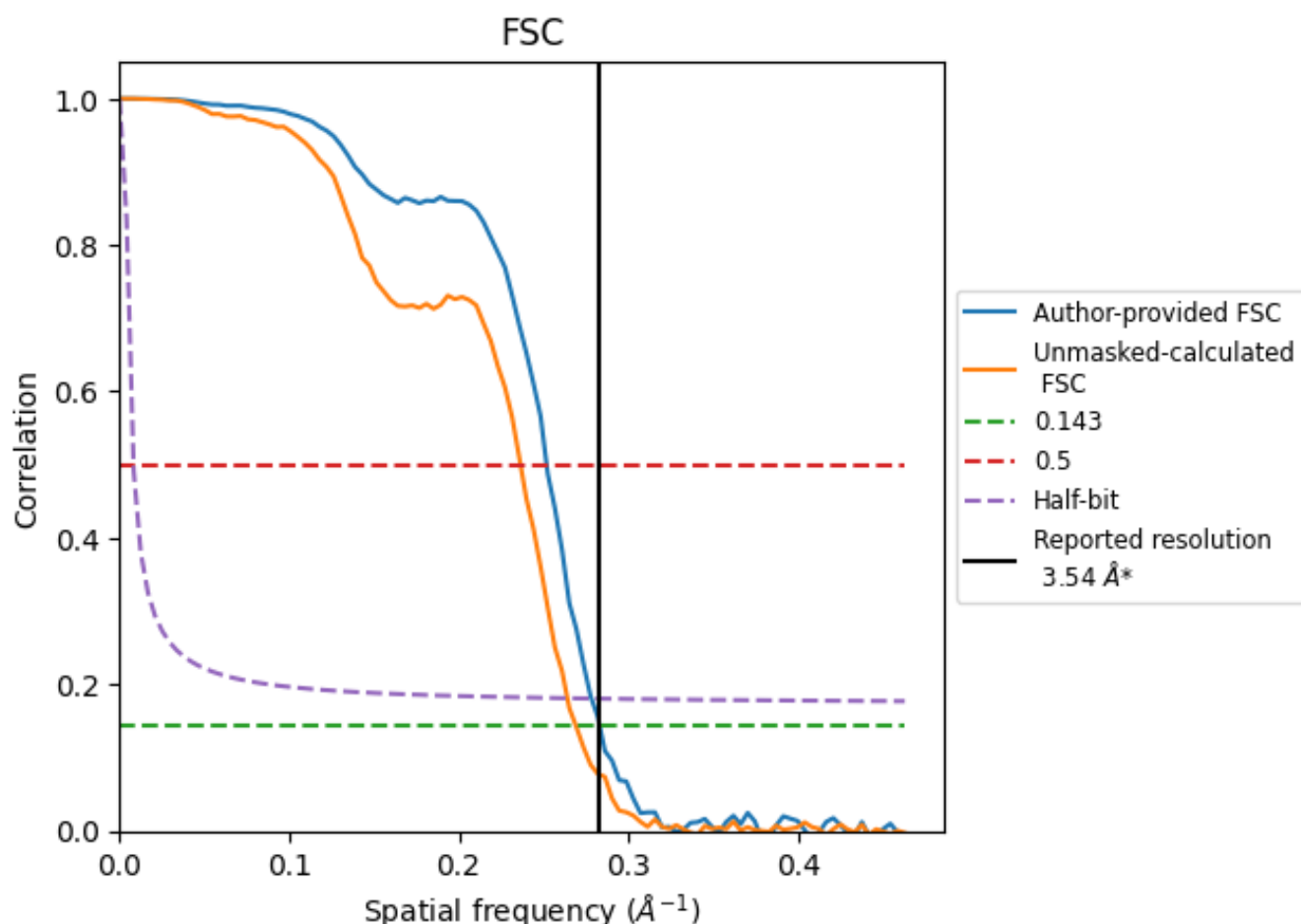


*Reported resolution corresponds to spatial frequency of 0.282 Å⁻¹

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 0.282 \AA^{-1}

8.2 Resolution estimates [i](#)

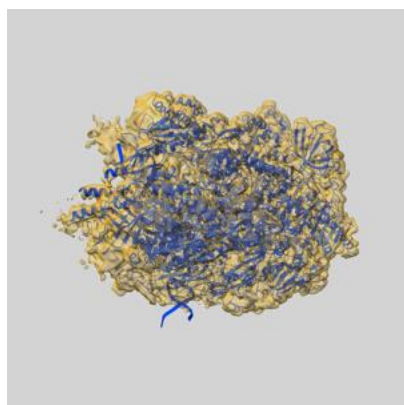
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.53	3.97	3.59
Unmasked-calculated*	3.72	4.23	3.79

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

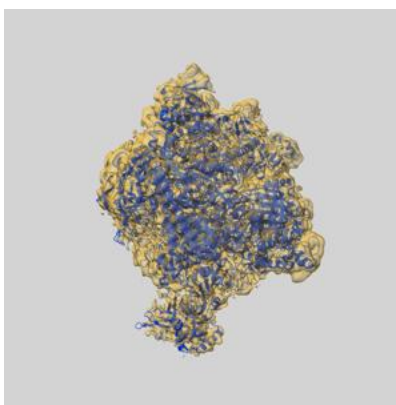
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23887 and PDB model 7MK9. Per-residue inclusion information can be found in section [3](#) on page [8](#).

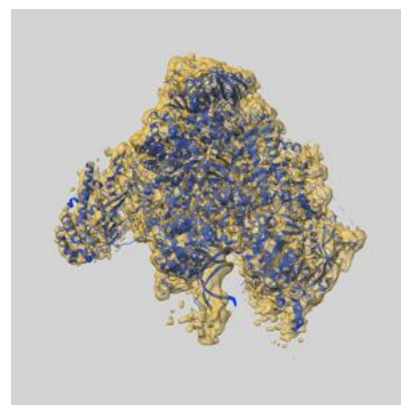
9.1 Map-model overlay [i](#)



X



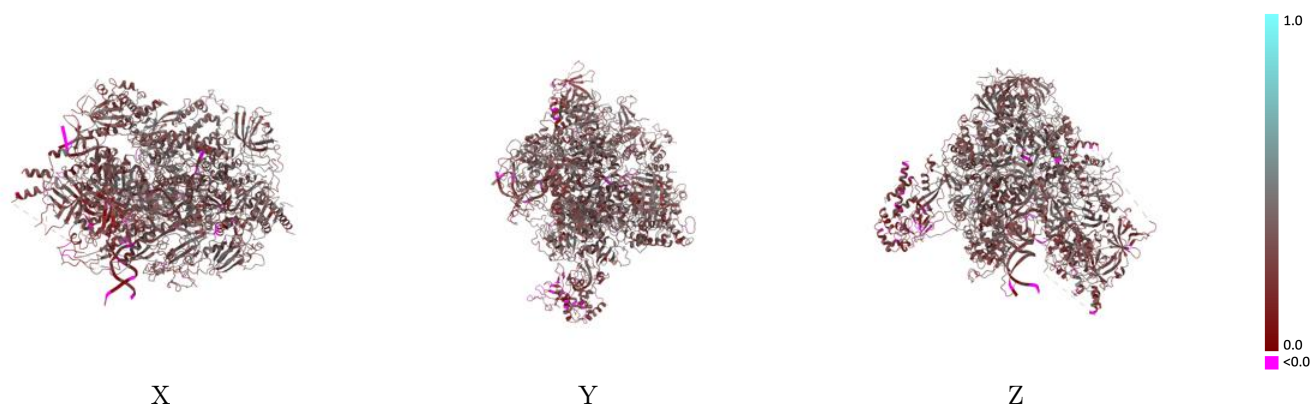
Y



Z

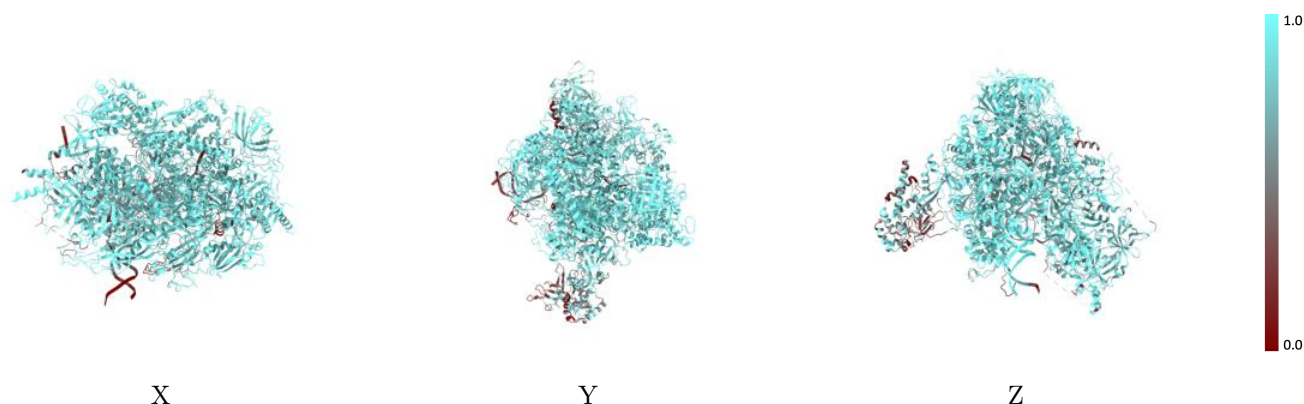
The images above show the 3D surface view of the map at the recommended contour level 0.0084 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



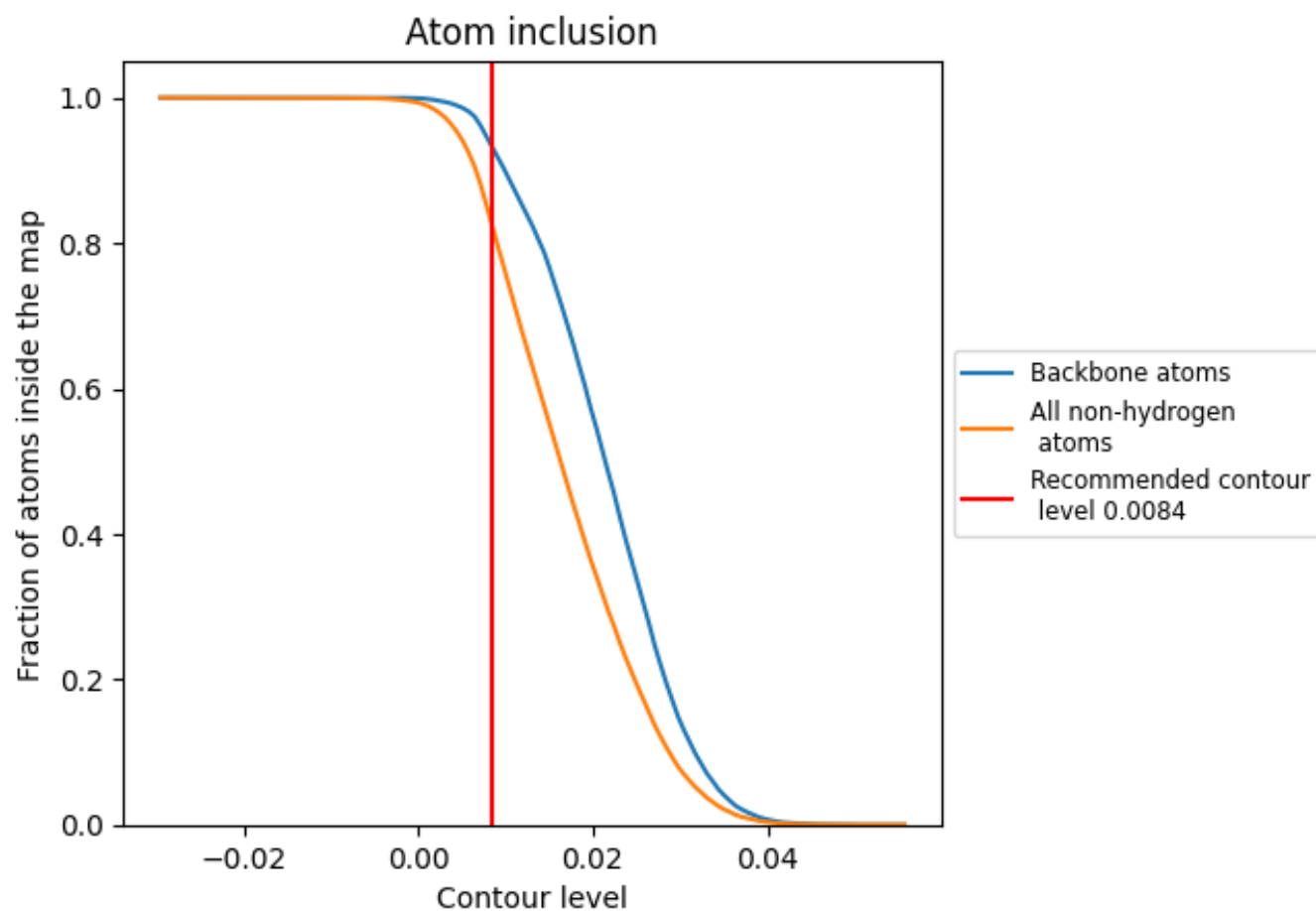
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0084).





































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 83% 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 (0.0084) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8274	 0.3170
A	 0.8810	 0.3470
B	 0.8382	 0.3360
C	 0.9004	 0.3600
D	 0.5134	 0.1930
E	 0.9046	 0.3440
F	 0.8748	 0.3580
G	 0.5475	 0.1910
H	 0.9297	 0.3400
I	 0.8805	 0.3390
J	 0.9295	 0.3570
K	 0.8332	 0.3200
L	 0.9000	 0.3260
M	 0.7832	 0.2340
N	 0.5912	 0.1750
O	 0.7400	 0.2100
Q	 0.7516	 0.2700
R	 0.7444	 0.2300

