



Full wwPDB EM Validation Report ⓘ

Sep 28, 2026 – 12:30 PM EDT

PDB ID : 9PC7 / pdb_00009pc7
EMDB ID : EMD-71498
Title : Core Mediator of PIC-Med-SWI/SNF-Nucleosome
Authors : Yang, C.; Nagai, S.; Chen, D.-H.
Deposited on : 2025-06-27
Resolution : 3.40 Å(reported)
Based on initial model : 8cen

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

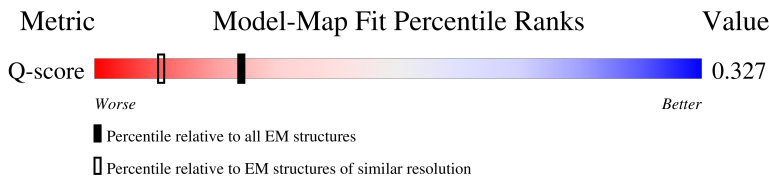
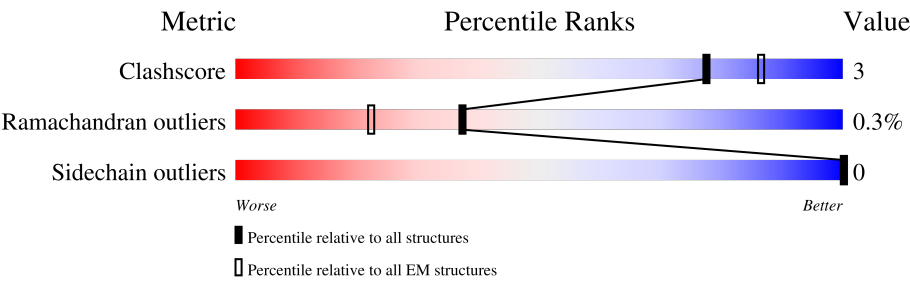
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



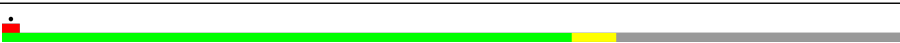
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	b	223	59%6%35%
2	f	210	95%5%
3	h	284	16%57%5%38%
4	n	140	96%

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Mol	Chain	Length	Quality of chain
5	o	127	
6	d	687	
7	a	295	
8	c	115	
9	e	307	
10	g	121	
11	i	222	
12	k	157	
13	l	1082	
14	m	220	
15	A	1733	
16	j	149	
17	p	566	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 29226 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 Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	144	Total	C	N	O	S	0	0
			1185	747	208	227	3		

- Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	f	210	Total	C	N	O	S	0	0
			1609	1016	270	317	6		

- Molecule 3 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	h	177	Total	C	N	O	S	0	0
			1441	910	242	284	5		

- Molecule 4 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	n	140	Total	C	N	O	S	0	0
			1124	701	189	228	6		

- Molecule 5 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	o	109	Total	C	N	O	S	0	0
			914	603	141	164	6		

- Molecule 6 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	535	Total	C	N	O	S	0	0
			4325	2766	730	816	13		

- Molecule 7 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	a	171	Total	C	N	O	S	0	0
			1420	913	236	265	6		

- Molecule 8 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	c	108	Total	C	N	O	S	0	0
			876	546	149	177	4		

- Molecule 9 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	253	Total	C	N	O	S	0	0
			1995	1271	331	383	10		

- Molecule 10 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	g	106	Total	C	N	O	S	0	0
			847	528	139	175	5		

- Molecule 11 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	i	185	Total	C	N	O	S	0	0
			1538	989	259	284	6		

- Molecule 12 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	k	144	Total	C	N	O	S	0	0
			1157	715	204	235	3		

- Molecule 13 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	l	654	Total	C	N	O	S	0	0
			5367	3465	924	954	24		

- Molecule 14 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	m	83	Total	C	N	O	S	0	0
			671	424	111	135	1		

- Molecule 15 is a protein called DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	A	79	Total	C	N	O	0	0
			575	361	79	135		

- Molecule 16 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	j	102	Total	C	N	O	S	0	0
			852	533	156	162	1		

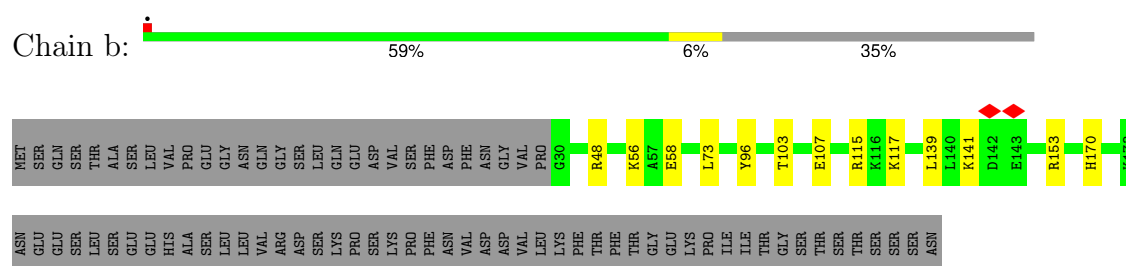
- Molecule 17 is a protein called Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	p	409	Total	C	N	O	S	0	0
			3330	2115	535	669	11		

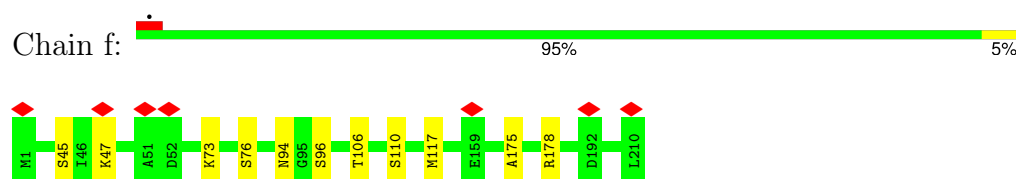
3 Residue-property plots

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.

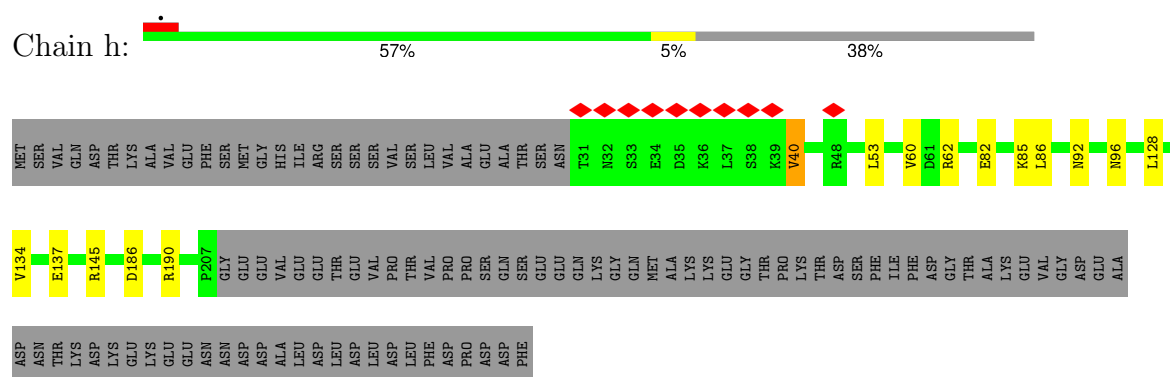
- Molecule 1: Mediator of RNA polymerase II transcription subunit 8



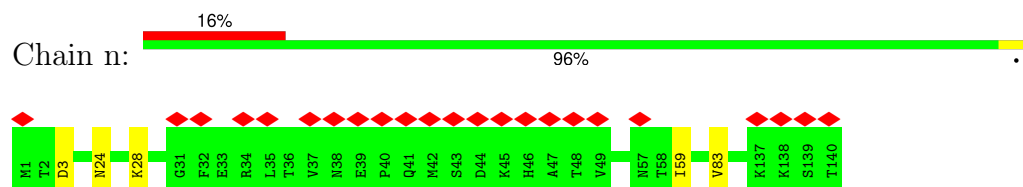
- Molecule 2: Mediator of RNA polymerase II transcription subunit 20



- Molecule 3: Mediator of RNA polymerase II transcription subunit 4

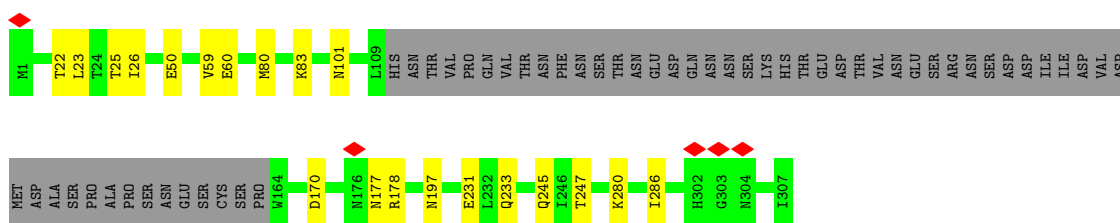


- Molecule 4: Mediator of RNA polymerase II transcription subunit 21



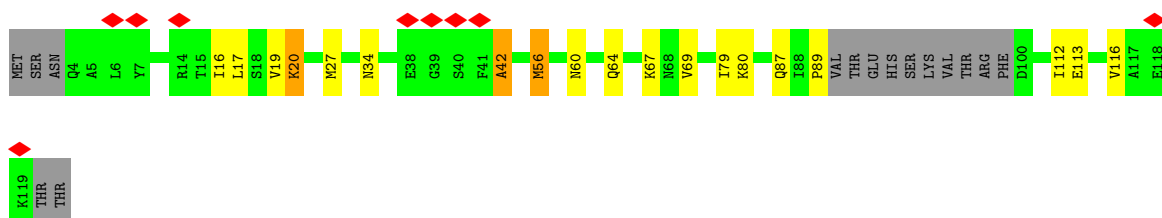
- Molecule 9: Mediator of RNA polymerase II transcription subunit 18

Chain e: 



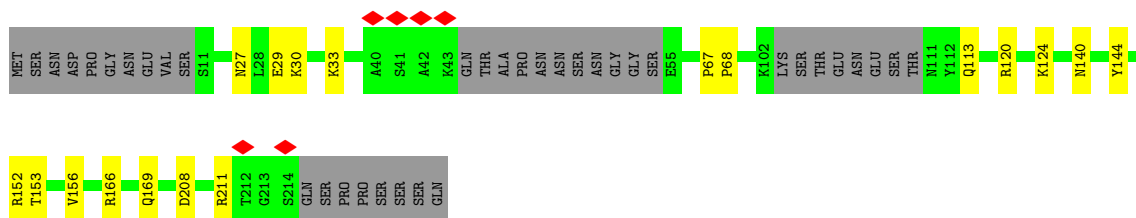
- Molecule 10: Mediator of RNA polymerase II transcription subunit 22

Chain g: 

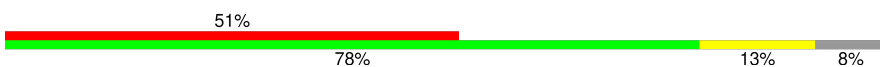


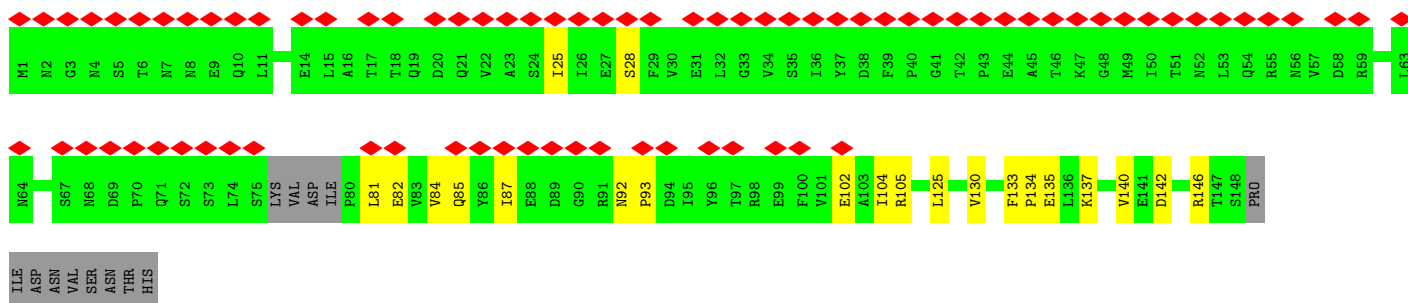
- Molecule 11: Mediator of RNA polymerase II transcription subunit 7

Chain i: 



- Molecule 12: Mediator of RNA polymerase II transcription subunit 10

Chain k: 



- Molecule 13: Mediator of RNA polymerase II transcription subunit 14

Chain l: 





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	418209	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.225	Depositor
Minimum map value	-3.190	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.079	Depositor
Recommended contour level	0.523	Depositor
Map size ($\text{\AA}$)	537.6, 537.6, 537.6	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.4, 1.4, 1.4	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.32	0/1207	0.70	2/1636 (0.1%)
2	f	0.26	0/1635	0.61	2/2215 (0.1%)
3	h	0.34	0/1462	0.88	4/1970 (0.2%)
4	n	0.36	0/1135	0.73	0/1526
5	o	0.37	1/941 (0.1%)	0.76	1/1282 (0.1%)
6	d	0.30	0/4389	0.61	0/5901
7	a	0.31	0/1455	0.71	0/1969
8	c	0.40	0/885	0.75	0/1183
9	e	0.26	0/2030	0.63	0/2747
10	g	0.51	0/851	1.12	4/1148 (0.3%)
11	i	0.42	1/1569 (0.1%)	0.79	2/2117 (0.1%)
12	k	0.46	0/1172	0.93	0/1581
13	l	0.30	0/5460	0.71	7/7373 (0.1%)
14	m	0.34	0/684	0.79	3/928 (0.3%)
15	A	0.34	0/606	0.84	0/848
16	j	0.43	0/865	0.93	2/1166 (0.2%)
17	p	0.26	0/3394	0.59	0/4589
All	All	0.33	2/29740 (0.0%)	0.73	27/40179 (0.1%)

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	b	0	1
3	h	0	1
5	o	0	1
7	a	0	1
8	c	0	1
12	k	0	1
14	m	0	1
All	All	0	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	i	166	ARG	C-N	6.88	1.43	1.34
5	o	106	LEU	C-N	6.12	1.42	1.34

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	g	89	PRO	CA-N-CD	-8.03	100.76	112.00
14	m	26	GLN	CA-C-N	6.84	138.48	121.80
14	m	26	GLN	C-N-CA	6.84	138.48	121.80
13	l	194	LYS	N-CA-C	6.79	119.06	110.24
13	l	193	ALA	N-CA-C	6.54	118.07	111.07
13	l	187	LEU	N-CA-C	6.50	119.20	111.33
3	h	86	LEU	CA-C-N	6.23	128.91	120.38
3	h	86	LEU	C-N-CA	6.23	128.91	120.38
11	i	144	TYR	CA-C-N	5.76	128.27	120.38
11	i	144	TYR	C-N-CA	5.76	128.27	120.38
3	h	62	ARG	CA-C-N	5.75	130.57	122.46
3	h	62	ARG	C-N-CA	5.75	130.57	122.46
10	g	20	LYS	CA-CB-CG	5.74	125.59	114.10
14	m	27	GLN	CA-CB-CG	5.68	125.45	114.10
10	g	27	MET	CB-CG-SD	5.37	128.82	112.70
2	f	73	LYS	CA-C-N	5.29	130.33	122.82
2	f	73	LYS	C-N-CA	5.29	130.33	122.82
13	l	458	ASN	CA-C-N	5.25	130.40	122.68
13	l	458	ASN	C-N-CA	5.25	130.40	122.68
1	b	170	HIS	CA-C-N	5.25	130.27	122.82
1	b	170	HIS	C-N-CA	5.25	130.27	122.82
5	o	89	MET	CA-CB-CG	5.20	124.50	114.10
10	g	56	MET	CB-CG-SD	5.17	128.21	112.70
13	l	193	ALA	CA-C-N	5.10	128.32	120.82
13	l	193	ALA	C-N-CA	5.10	128.32	120.82
16	j	82	ASN	CA-C-N	5.00	131.09	121.54
16	j	82	ASN	C-N-CA	5.00	131.09	121.54

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	a	144	GLY	Peptide
1	b	96	TYR	Peptide
8	c	39	ARG	Peptide

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Mol	Chain	Res	Type	Group
3	h	40	VAL	Peptide
12	k	133	PHE	Peptide
14	m	26	GLN	Peptide
5	o	67	PRO	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	1185	0	1193	8	0
2	f	1609	0	1626	7	0
3	h	1441	0	1461	7	0
4	n	1124	0	1147	4	0
5	o	914	0	902	3	0
6	d	4325	0	4482	25	0
7	a	1420	0	1398	9	0
8	c	876	0	885	7	0
9	e	1995	0	2018	12	0
10	g	847	0	858	13	0
11	i	1538	0	1576	10	0
12	k	1157	0	1142	13	0
13	l	5367	0	5607	36	0
14	m	671	0	650	8	0
15	A	575	0	507	3	0
16	j	852	0	857	5	0
17	p	3330	0	3243	28	0
All	All	29226	0	29552	169	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 3.

All (169) 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)
9:e:59:VAL:HG23	9:e:60:GLU:HG2	1.82	0.62
2:f:45:SER:HB2	2:f:117:MET:HE1	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:115:ARG:HE	1:b:117:LYS:HB3	1.68	0.59
17:p:167:TYR:O	17:p:171:LEU:HB2	2.02	0.59
12:k:87:ILE:HG23	12:k:93:PRO:HD3	1.86	0.58
8:c:2:GLN:HB2	8:c:7:GLN:HE21	1.69	0.57
1:b:56:LYS:HD3	1:b:58:GLU:H	1.70	0.57
12:k:130:VAL:HG11	12:k:140:VAL:HG21	1.87	0.56
6:d:634:MET:HB3	6:d:646:HIS:HB3	1.86	0.56
1:b:103:THR:O	1:b:107:GLU:HB3	2.05	0.55
9:e:177:ASN:OD1	9:e:178:ARG:NH1	2.40	0.55
6:d:281:LEU:HD21	8:c:39:ARG:HE	1.72	0.55
12:k:92:ASN:ND2	14:m:62:LYS:O	2.40	0.55
13:l:165:LEU:HD21	14:m:34:LEU:HD21	1.89	0.54
13:l:749:LEU:HD13	13:l:767:MET:HE3	1.88	0.54
8:c:79:THR:O	10:g:87:GLN:NE2	2.41	0.54
17:p:298:PRO:HA	17:p:301:ASP:HB2	1.90	0.53
1:b:56:LYS:O	6:d:204:ARG:NH2	2.42	0.53
13:l:290:THR:HB	13:l:297:LEU:HD13	1.91	0.53
6:d:316:ILE:O	8:c:2:GLN:NE2	2.42	0.52
13:l:515:LEU:HD11	13:l:524:PHE:HB3	1.91	0.52
6:d:320:ASP:OD1	6:d:320:ASP:N	2.43	0.52
10:g:16:ILE:HA	10:g:19:VAL:HG12	1.92	0.52
13:l:123:ASN:ND2	14:m:145:PHE:O	2.43	0.52
3:h:186:ASP:O	3:h:190:ARG:NH1	2.42	0.52
13:l:414:ARG:NH1	13:l:415:TYR:O	2.42	0.51
6:d:455:TYR:O	6:d:550:ARG:NH2	2.44	0.51
17:p:531:ILE:HB	17:p:538:ILE:HB	1.93	0.51
6:d:327:ASP:HB3	6:d:331:GLY:H	1.76	0.51
11:i:140:ASN:ND2	14:m:24:THR:O	2.43	0.51
12:k:130:VAL:O	12:k:137:LYS:NZ	2.42	0.51
17:p:95:ASP:OD1	17:p:189:ARG:NH1	2.43	0.51
5:o:78:CYS:SG	5:o:79:LEU:N	2.84	0.51
3:h:60:VAL:HG11	16:j:87:LEU:HD22	1.93	0.51
17:p:261:ASN:ND2	17:p:325:ILE:O	2.44	0.51
6:d:361:ILE:O	6:d:364:GLN:NE2	2.44	0.50
11:i:120:ARG:HG3	11:i:124:LYS:HE2	1.93	0.50
4:n:3:ASP:OD2	11:i:169:GLN:NE2	2.41	0.50
6:d:338:LYS:O	8:c:89:LYS:NZ	2.39	0.50
6:d:469:LEU:HD11	6:d:549:VAL:HG11	1.94	0.50
13:l:771:ILE:HG12	13:l:778:ILE:HG23	1.94	0.50
17:p:297:PRO:HG2	17:p:300:ILE:HD12	1.93	0.50
17:p:53:ARG:NH1	17:p:66:ASP:OD1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:i:27:ASN:HA	11:i:30:LYS:HG2	1.94	0.49
5:o:19:LEU:HD12	5:o:20:PRO:HD2	1.94	0.49
7:a:168:LYS:HA	7:a:171:GLN:HG2	1.95	0.49
13:l:248:ASP:OD1	13:l:293:ARG:NH2	2.45	0.49
14:m:24:THR:OG1	14:m:25:TYR:N	2.45	0.49
2:f:175:ALA:O	2:f:178:ARG:NH2	2.46	0.49
6:d:86:LEU:HD12	6:d:87:VAL:HG23	1.95	0.49
10:g:113:GLU:HA	10:g:116:VAL:HG12	1.95	0.49
13:l:245:ARG:NH2	13:l:248:ASP:OD2	2.46	0.49
13:l:722:MET:HA	13:l:725:GLU:HB2	1.95	0.48
9:e:231:GLU:OE1	9:e:233:GLN:NE2	2.46	0.48
17:p:351:VAL:HA	17:p:558:ILE:HD11	1.96	0.48
2:f:47:LYS:NZ	9:e:50:GLU:OE2	2.46	0.48
6:d:203:ARG:NH1	7:a:190:ASP:OD2	2.47	0.48
14:m:51:ASN:ND2	14:m:55:THR:O	2.46	0.48
3:h:92:ASN:O	3:h:96:ASN:ND2	2.47	0.48
4:n:24:ASN:O	4:n:28:LYS:NZ	2.46	0.48
7:a:39:LYS:O	7:a:44:GLN:NE2	2.47	0.48
13:l:559:ASP:HA	13:l:562:ILE:HB	1.96	0.48
1:b:139:LEU:O	1:b:141:LYS:NZ	2.43	0.47
17:p:76:ASP:N	17:p:76:ASP:OD1	2.46	0.47
1:b:153:ARG:NH1	10:g:34:ASN:O	2.46	0.47
17:p:315:MET:HE3	17:p:316:ASN:H	1.80	0.47
2:f:106:THR:O	2:f:110:SER:HB3	2.14	0.47
17:p:45:GLU:HB3	17:p:53:ARG:HB2	1.96	0.47
17:p:200:ILE:HB	17:p:213:ALA:HB3	1.96	0.47
3:h:134:VAL:HA	3:h:137:GLU:HG2	1.94	0.47
6:d:563:LYS:HG3	6:d:567:LEU:HD23	1.97	0.47
12:k:130:VAL:HG21	12:k:140:VAL:HG11	1.95	0.47
7:a:7:ASP:OD1	7:a:7:ASP:N	2.45	0.47
11:i:208:ASP:OD1	11:i:211:ARG:NH1	2.48	0.47
13:l:174:MET:O	13:l:178:ASN:ND2	2.48	0.47
13:l:163:ILE:HD12	15:A:1671:THR:HG22	1.96	0.46
3:h:82:GLU:HA	3:h:85:LYS:HG2	1.97	0.46
7:a:124:ASP:N	7:a:124:ASP:OD1	2.48	0.46
13:l:516:LYS:HB2	13:l:525:TYR:HD2	1.81	0.46
17:p:62:VAL:HB	17:p:80:VAL:HB	1.97	0.46
17:p:537:ILE:HB	17:p:545:CYS:HB3	1.98	0.46
13:l:628:ARG:NH1	13:l:629:LEU:O	2.49	0.46
11:i:29:GLU:O	11:i:33:LYS:NZ	2.49	0.46
12:k:102:GLU:HA	12:k:105:ARG:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:l:772:ASP:OD2	13:l:775:ASN:ND2	2.49	0.46
1:b:48:ARG:HD3	15:A:1573:THR:HG21	1.97	0.45
6:d:606:PHE:HB3	6:d:610:LEU:HD23	1.96	0.45
17:p:35:CYS:SG	17:p:36:GLN:N	2.90	0.45
12:k:135:GLU:HA	12:k:137:LYS:HE2	1.99	0.45
6:d:563:LYS:O	6:d:567:LEU:HB3	2.16	0.45
14:m:42:ASP:OD1	14:m:42:ASP:N	2.50	0.45
8:c:63:THR:HG21	10:g:17:LEU:HD12	1.99	0.45
13:l:745:ILE:HG22	13:l:769:LEU:HB3	1.97	0.45
17:p:190:THR:HG22	17:p:198:ILE:HA	1.99	0.45
17:p:549:ASP:OD1	17:p:554:TRP:NE1	2.47	0.45
6:d:467:ILE:HB	6:d:474:PHE:HB2	1.98	0.45
13:l:739:ASN:HB2	13:l:742:ILE:HD12	1.99	0.44
14:m:64:TYR:HB2	14:m:67:GLN:HB2	1.97	0.44
4:n:83:VAL:O	11:i:113:GLN:NE2	2.51	0.44
13:l:700:ILE:HG12	13:l:819:LEU:HD11	1.99	0.44
13:l:159:PHE:HA	13:l:162:LEU:HD13	1.99	0.44
7:a:135:ASN:HA	7:a:145:PRO:HG3	2.00	0.44
8:c:73:LEU:HD22	10:g:79:ILE:HG23	2.00	0.44
10:g:20:LYS:HZ1	10:g:69:VAL:HG23	1.83	0.43
17:p:61:ILE:HD12	17:p:128:ASP:HB2	2.00	0.43
12:k:82:GLU:OE1	12:k:85:GLN:NE2	2.51	0.43
15:A:1634:SER:OG	15:A:1637:SER:O	2.37	0.43
3:h:53:LEU:HD23	16:j:95:ARG:HG3	2.00	0.43
7:a:107:LEU:O	7:a:133:ARG:NH1	2.51	0.43
9:e:80:MET:HG3	9:e:83:LYS:HD2	2.00	0.43
16:j:75:GLN:OE1	16:j:78:LYS:NZ	2.52	0.43
13:l:251:LEU:HB3	13:l:293:ARG:HH22	1.83	0.43
3:h:145:ARG:HE	6:d:20:ALA:HB2	1.83	0.42
9:e:23:LEU:HA	9:e:26:ILE:HG22	2.01	0.42
17:p:113:ASP:N	17:p:113:ASP:OD1	2.50	0.42
13:l:539:LYS:O	13:l:542:ARG:NH1	2.51	0.42
13:l:500:LEU:HD22	13:l:512:PRO:HB2	2.02	0.42
9:e:22:THR:HA	9:e:25:THR:HG22	2.02	0.42
17:p:258:ILE:HB	17:p:261:ASN:HB2	2.00	0.42
1:b:73:LEU:HD22	10:g:56:MET:HE1	2.01	0.42
7:a:133:ARG:HE	7:a:147:ILE:HD11	1.85	0.42
6:d:355:ALA:HA	6:d:370:PRO:HA	2.02	0.42
6:d:437:PHE:HE2	6:d:509:ARG:HG2	1.85	0.42
6:d:442:MET:HG2	6:d:478:LEU:HD22	2.02	0.42
13:l:747:LEU:HB2	13:l:767:MET:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:p:93:GLN:O	17:p:189:ARG:NH2	2.52	0.42
16:j:77:ARG:HH12	17:p:147:LYS:HG3	1.84	0.42
2:f:94:ASN:ND2	2:f:96:SER:OG	2.52	0.42
9:e:286:ILE:HD12	9:e:286:ILE:HA	1.94	0.42
13:l:405:ASP:OD1	13:l:405:ASP:N	2.53	0.41
13:l:750:GLU:HB3	13:l:760:ASN:HD21	1.85	0.41
5:o:30:ILE:HD11	5:o:82:LEU:HD22	2.02	0.41
10:g:112:ILE:HD12	10:g:112:ILE:HA	1.95	0.41
12:k:81:LEU:HA	12:k:84:VAL:HG22	2.02	0.41
2:f:117:MET:SD	2:f:117:MET:N	2.93	0.41
6:d:24:ASN:HD21	6:d:87:VAL:HB	1.86	0.41
6:d:309:TRP:CE2	10:g:80:LYS:HE2	2.55	0.41
9:e:170:ASP:N	9:e:170:ASP:OD1	2.53	0.41
4:n:59:ILE:HD11	12:k:125:LEU:HD23	2.02	0.41
12:k:25:ILE:O	12:k:28:SER:OG	2.38	0.41
13:l:711:LEU:HD11	13:l:823:VAL:HG13	2.01	0.41
2:f:76:SER:OG	9:e:197:ASN:OD1	2.37	0.41
10:g:34:ASN:HD21	10:g:42:ALA:HB3	1.86	0.41
10:g:64:GLN:HA	10:g:67:LYS:HG2	2.03	0.41
6:d:469:LEU:HD23	6:d:471:ASN:H	1.85	0.41
13:l:408:LYS:HA	13:l:408:LYS:HD2	1.92	0.41
13:l:701:ASN:OD1	13:l:773:TYR:OH	2.33	0.41
6:d:317:SER:OG	6:d:318:ASN:N	2.53	0.41
13:l:89:GLN:HG3	13:l:159:PHE:HB3	2.01	0.41
13:l:536:TYR:OH	13:l:559:ASP:OD2	2.34	0.41
7:a:6:LEU:HA	7:a:9:LEU:HD23	2.02	0.41
9:e:245:GLN:NE2	9:e:247:THR:O	2.54	0.41
13:l:747:LEU:N	13:l:767:MET:O	2.51	0.41
13:l:814:GLU:OE2	13:l:832:LYS:NZ	2.53	0.41
17:p:19:LYS:HD2	17:p:118:HIS:CE1	2.56	0.41
16:j:78:LYS:O	17:p:147:LYS:NZ	2.44	0.41
17:p:184:CYS:SG	17:p:343:LYS:NZ	2.94	0.41
12:k:104:ILE:HG23	13:l:169:PHE:HE2	1.86	0.40
17:p:77:VAL:HG11	17:p:104:LEU:HB2	2.03	0.40
17:p:256:MET:HB2	17:p:330:ILE:HG12	2.03	0.40
11:i:67:PRO:HA	11:i:68:PRO:HD3	1.95	0.40
11:i:153:THR:HA	11:i:156:VAL:HG22	2.03	0.40
11:i:152:ARG:HH21	13:l:186:SER:HA	1.86	0.40
6:d:674:LEU:HA	6:d:677:ILE:HG22	2.02	0.40
9:e:280:LYS:HA	9:e:280:LYS:HD3	1.88	0.40
10:g:56:MET:O	10:g:60:ASN:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:l:413:VAL:HB	13:l:427:ILE:HB	2.02	0.40
12:k:142:ASP:O	12:k:146:ARG:HB2	2.22	0.40
17:p:227:ARG:NH1	17:p:250:ASN:OD1	2.54	0.40

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	
1	b	142/223 (64%)	141 (99%)	1 (1%)	0	100	100
2	f	208/210 (99%)	203 (98%)	5 (2%)	0	100	100
3	h	175/284 (62%)	167 (95%)	6 (3%)	2 (1%)	11	38
4	n	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
5	o	107/127 (84%)	101 (94%)	6 (6%)	0	100	100
6	d	525/687 (76%)	521 (99%)	4 (1%)	0	100	100
7	a	167/295 (57%)	162 (97%)	5 (3%)	0	100	100
8	c	104/115 (90%)	100 (96%)	4 (4%)	0	100	100
9	e	249/307 (81%)	238 (96%)	10 (4%)	1 (0%)	30	59
10	g	102/121 (84%)	99 (97%)	2 (2%)	1 (1%)	12	40
11	i	179/222 (81%)	175 (98%)	4 (2%)	0	100	100
12	k	140/157 (89%)	137 (98%)	2 (1%)	1 (1%)	18	47
13	l	640/1082 (59%)	620 (97%)	19 (3%)	1 (0%)	43	71
14	m	79/220 (36%)	77 (98%)	2 (2%)	0	100	100
15	A	73/1733 (4%)	64 (88%)	7 (10%)	2 (3%)	4	20
16	j	98/149 (66%)	93 (95%)	4 (4%)	1 (1%)	12	40
17	p	405/566 (72%)	390 (96%)	15 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	3531/6638 (53%)	3421 (97%)	101 (3%)	9 (0%)	37	65

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	h	128	LEU
12	k	134	PRO
3	h	40	VAL
10	g	42	ALA
16	j	64	GLU
15	A	1573	THR
15	A	1613	SER
9	e	101	ASN
13	l	461	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	135/207 (65%)	135 (100%)	0	100	100
2	f	178/178 (100%)	178 (100%)	0	100	100
3	h	164/258 (64%)	164 (100%)	0	100	100
4	n	132/132 (100%)	132 (100%)	0	100	100
5	o	102/117 (87%)	102 (100%)	0	100	100
6	d	499/642 (78%)	499 (100%)	0	100	100
7	a	160/259 (62%)	160 (100%)	0	100	100
8	c	101/108 (94%)	101 (100%)	0	100	100
9	e	228/280 (81%)	228 (100%)	0	100	100
10	g	98/113 (87%)	98 (100%)	0	100	100
11	i	175/208 (84%)	175 (100%)	0	100	100
12	k	132/145 (91%)	132 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	l	618/1001 (62%)	618 (100%)	0	100	100
14	m	77/195 (40%)	77 (100%)	0	100	100
15	A	79/1520 (5%)	79 (100%)	0	100	100
16	j	100/144 (69%)	100 (100%)	0	100	100
17	p	390/528 (74%)	390 (100%)	0	100	100
All	All	3368/6035 (56%)	3368 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	84	GLN
1	b	87	GLN
1	b	157	ASN
1	b	165	ASN
2	f	68	GLN
2	f	94	ASN
2	f	141	ASN
3	h	96	ASN
3	h	143	GLN
4	n	18	GLN
4	n	74	ASN
5	o	35	ASN
6	d	255	ASN
6	d	285	ASN
6	d	310	ASN
6	d	428	GLN
6	d	444	GLN
6	d	646	HIS
8	c	7	GLN
8	c	50	ASN
8	c	65	GLN
9	e	3	GLN
9	e	62	ASN
10	g	34	ASN
10	g	45	ASN
10	g	60	ASN
10	g	64	GLN
11	i	129	ASN

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Mol	Chain	Res	Type
11	i	150	ASN
11	i	207	GLN
12	k	68	ASN
12	k	116	HIS
13	l	123	ASN
13	l	160	HIS
13	l	167	ASN
13	l	192	ASN
13	l	340	ASN
13	l	344	ASN
13	l	452	ASN
13	l	502	GLN
13	l	726	GLN
13	l	741	ASN
13	l	775	ASN
16	j	86	GLN
16	j	123	GLN
16	j	127	HIS
17	p	36	GLN
17	p	118	HIS
17	p	220	ASN
17	p	247	ASN
17	p	313	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1652:PRO	C	1667:SER	N	31.63
1	A	1614:PRO	C	1629:THR	N	22.64

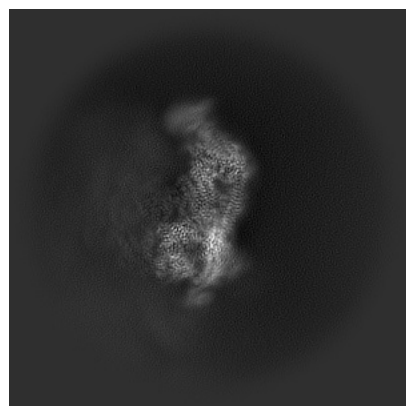
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71498. These allow visual inspection of the internal detail of the map and identification of artifacts.

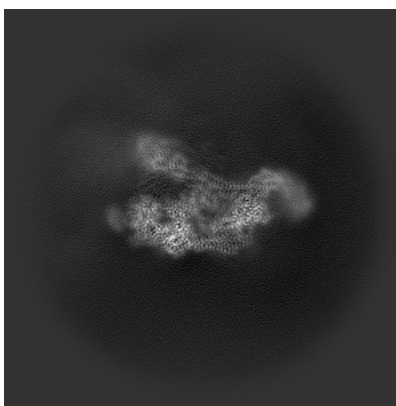
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

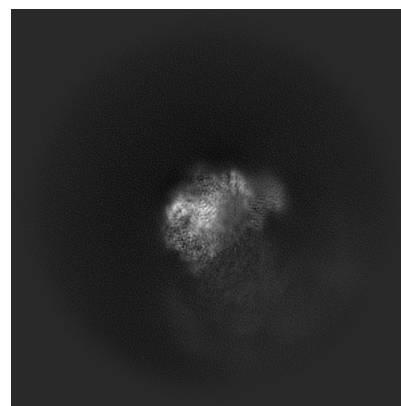
6.1.1 Primary map



X

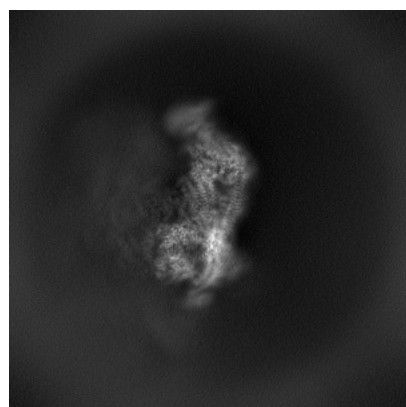


Y

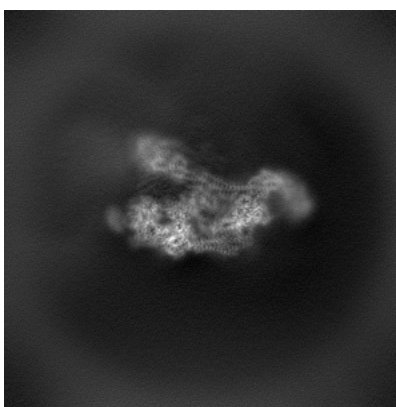


Z

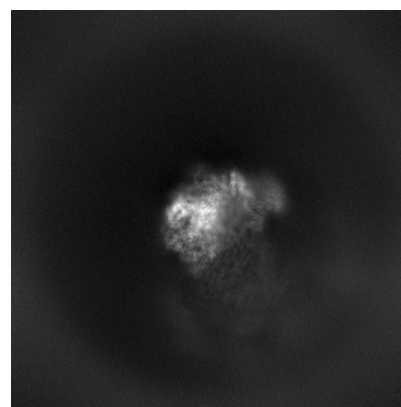
6.1.2 Raw map



X



Y

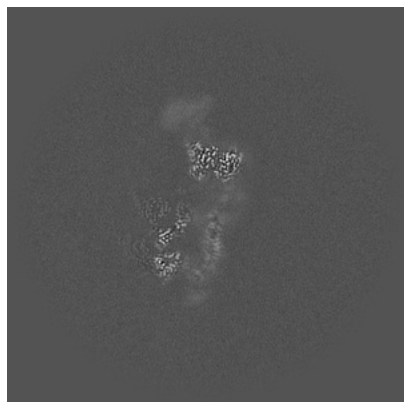


Z

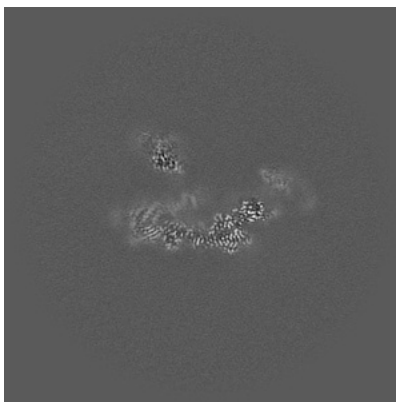
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 192

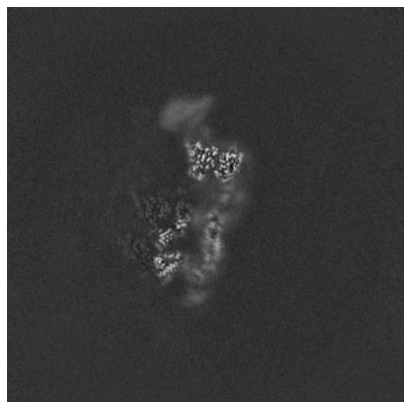


Y Index: 192

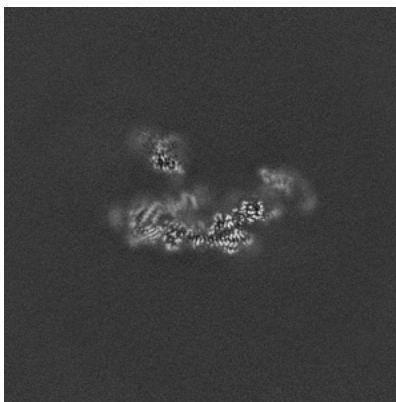


Z Index: 192

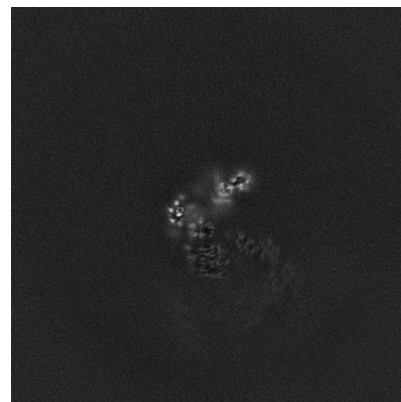
6.2.2 Raw map



X Index: 192



Y Index: 192

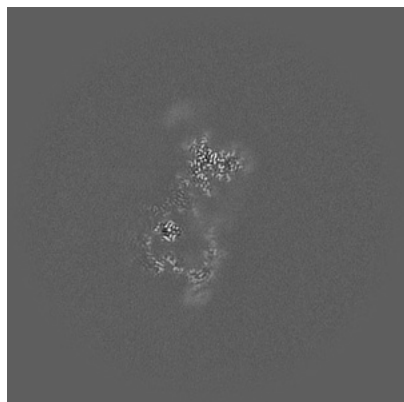


Z Index: 192

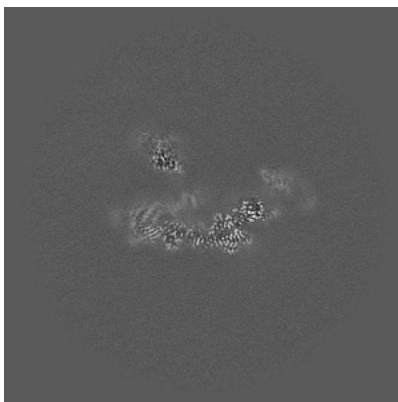
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

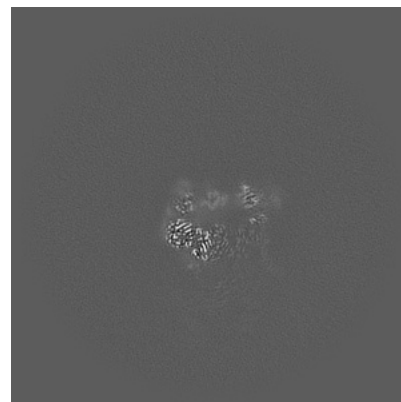
6.3.1 Primary map



X Index: 184

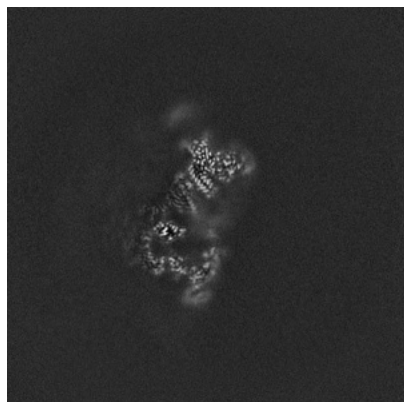


Y Index: 192

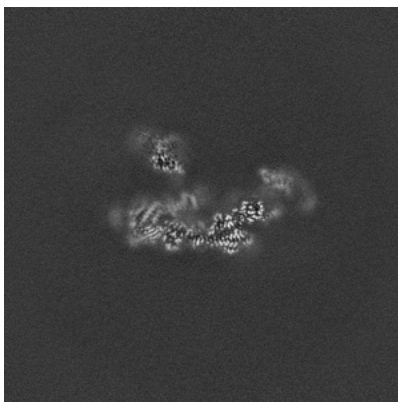


Z Index: 169

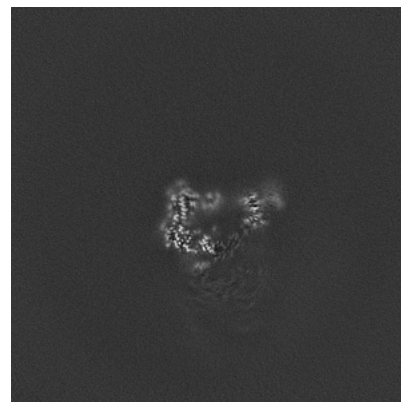
6.3.2 Raw map



X Index: 182



Y Index: 192

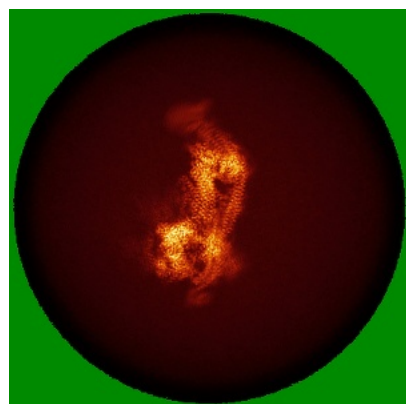


Z Index: 162

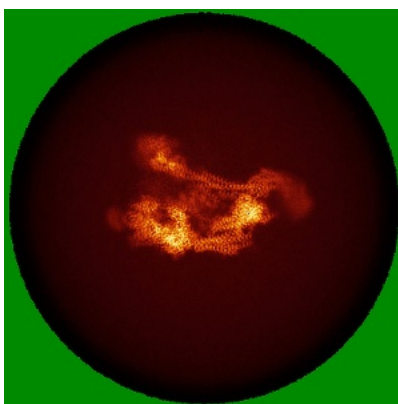
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

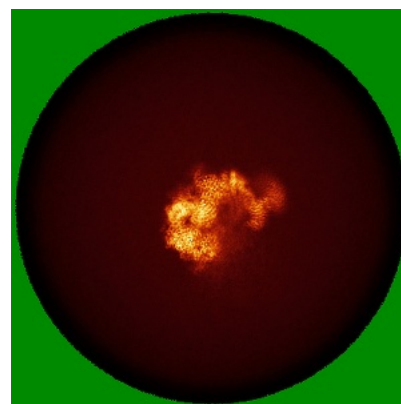
6.4.1 Primary map



X

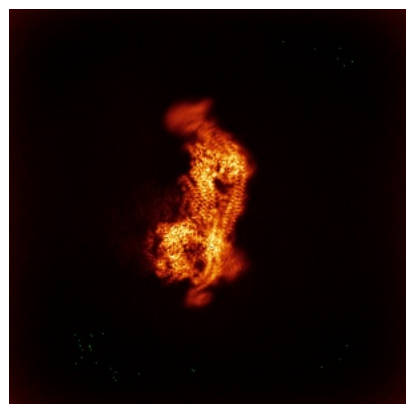


Y

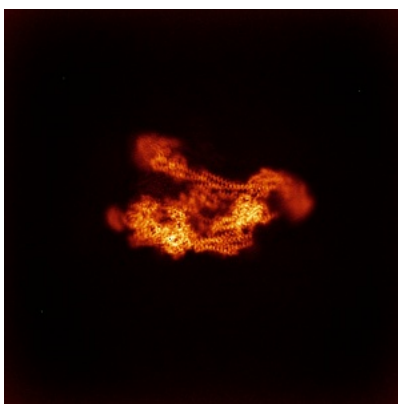


Z

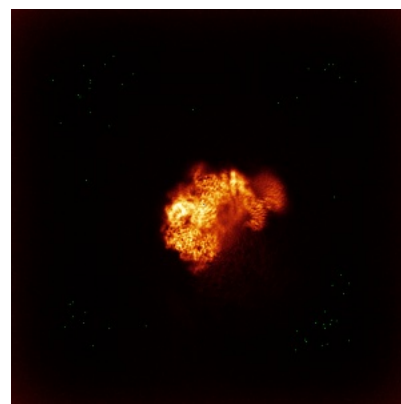
6.4.2 Raw map



X



Y

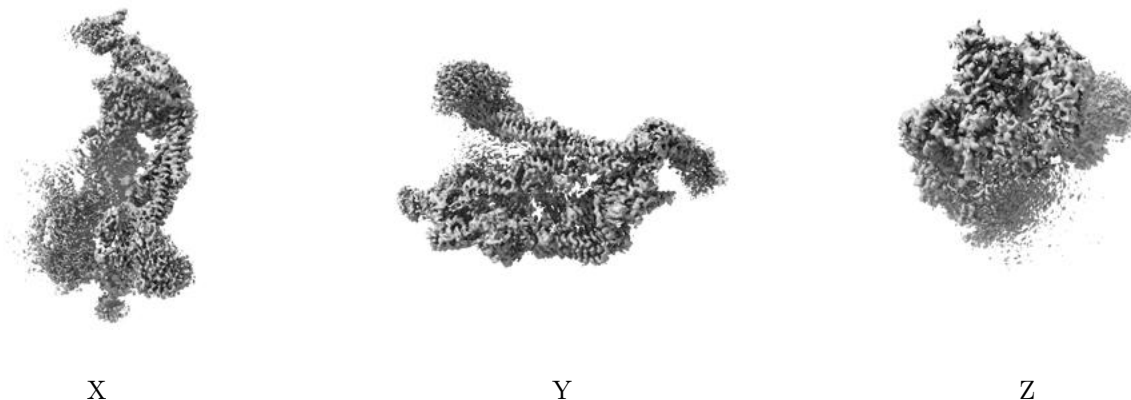


Z

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

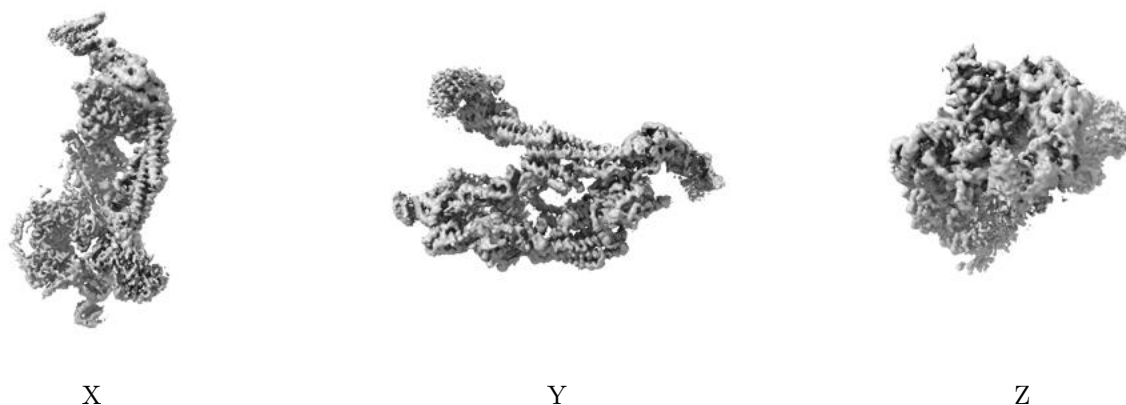
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.523. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

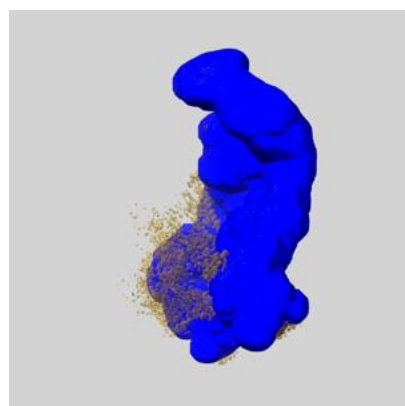
6.6 Mask visualisation [i](#)

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

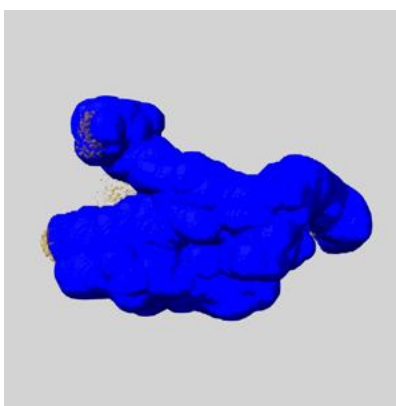
A mask typically either:

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

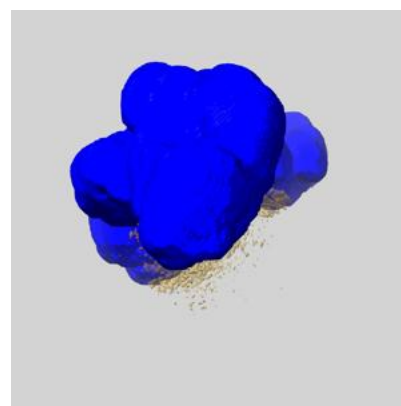
6.6.1 emd_71498_msk_1.map [i](#)



X



Y

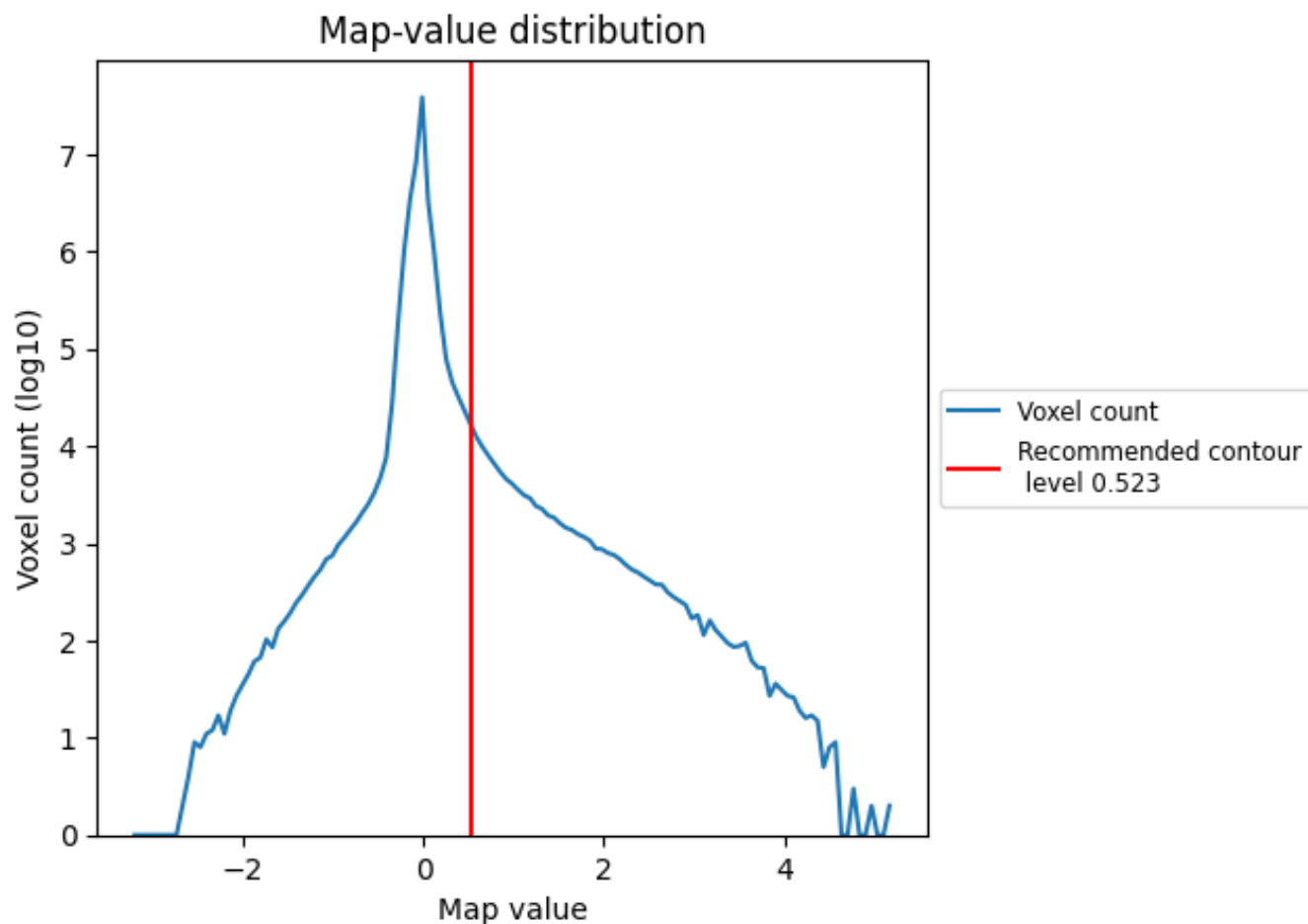


Z

7 Map analysis [i](#)

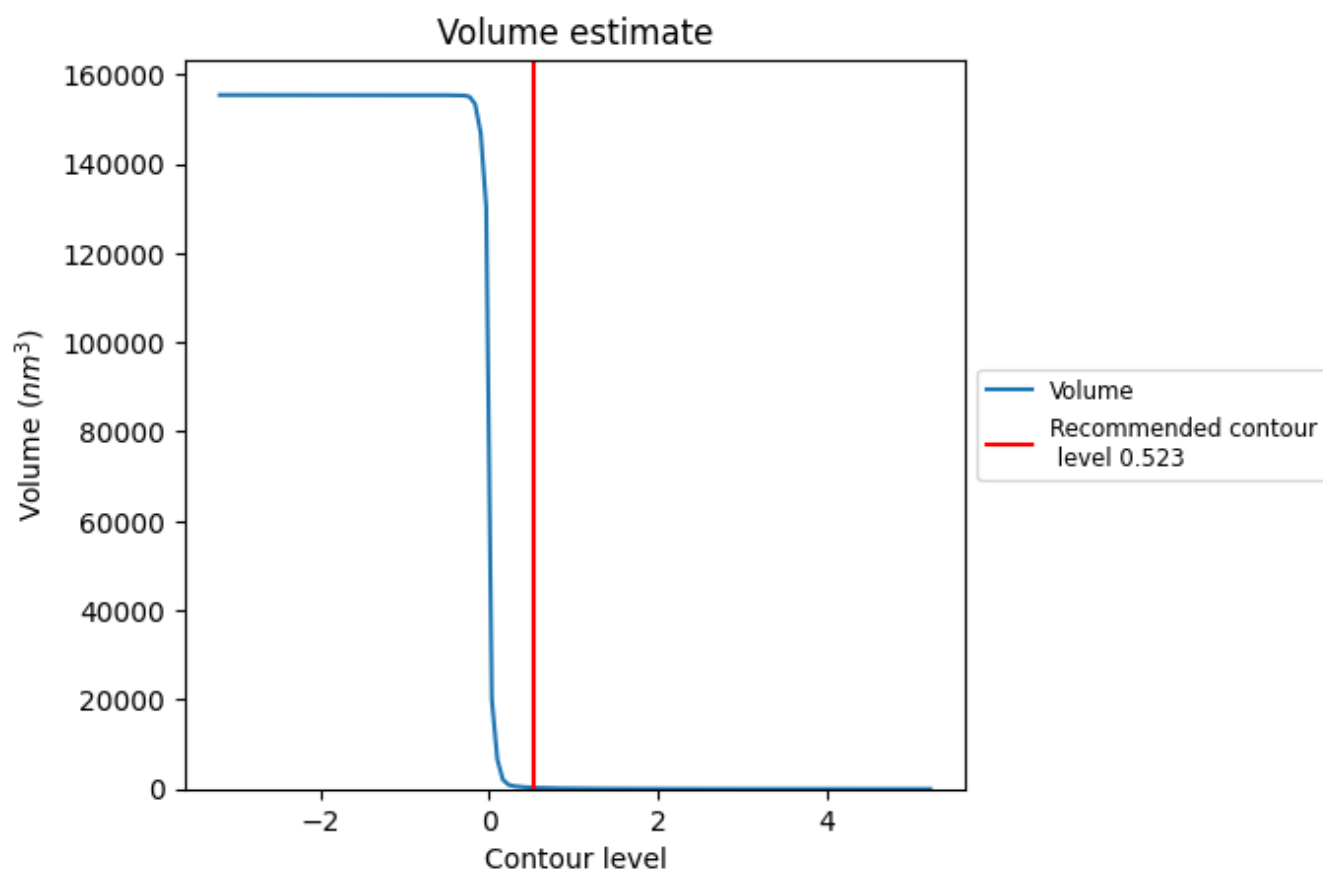
This section contains the results of statistical analysis of the map.

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.

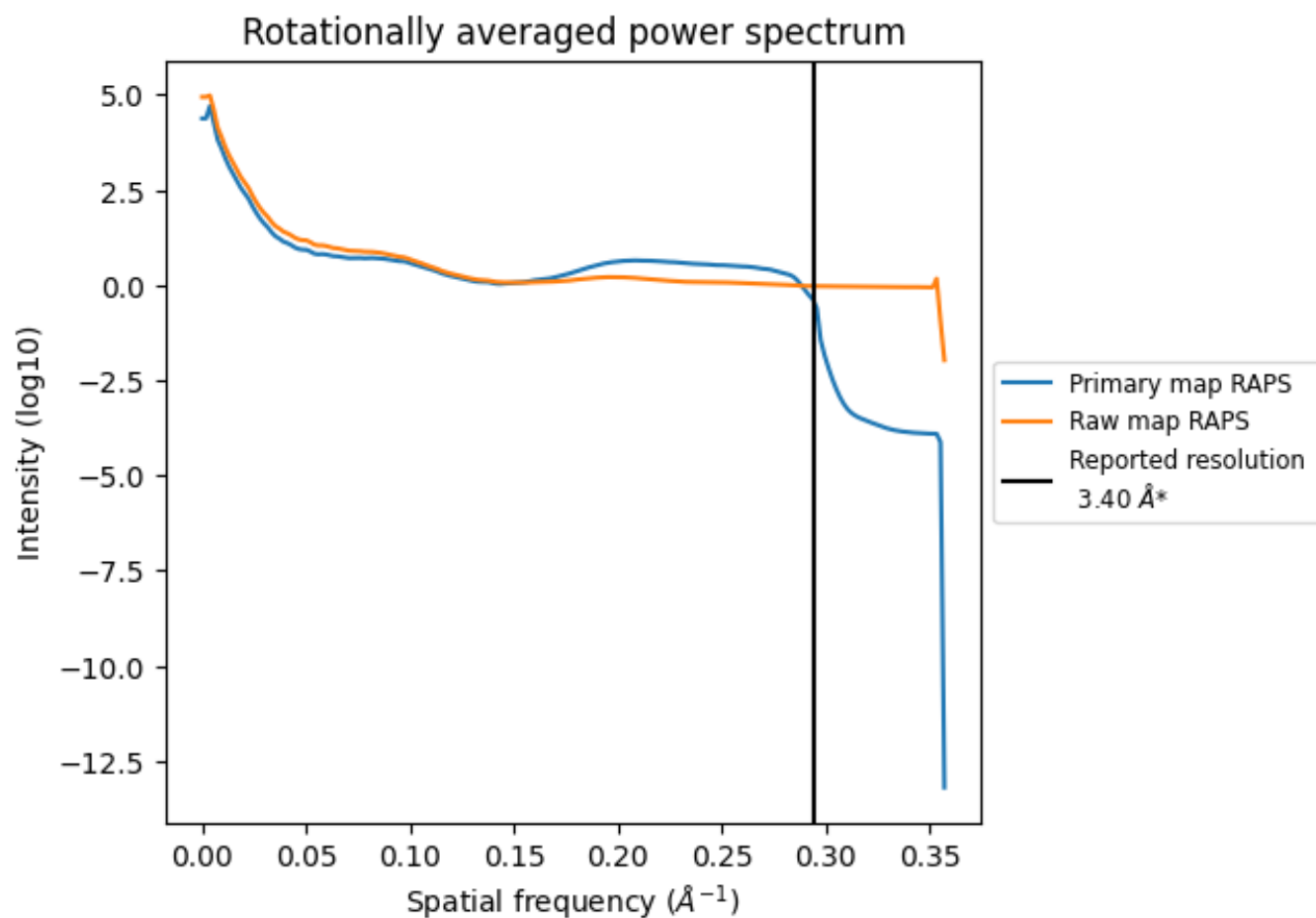
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 287 nm³; this corresponds to an approximate mass of 259 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 ⓘ

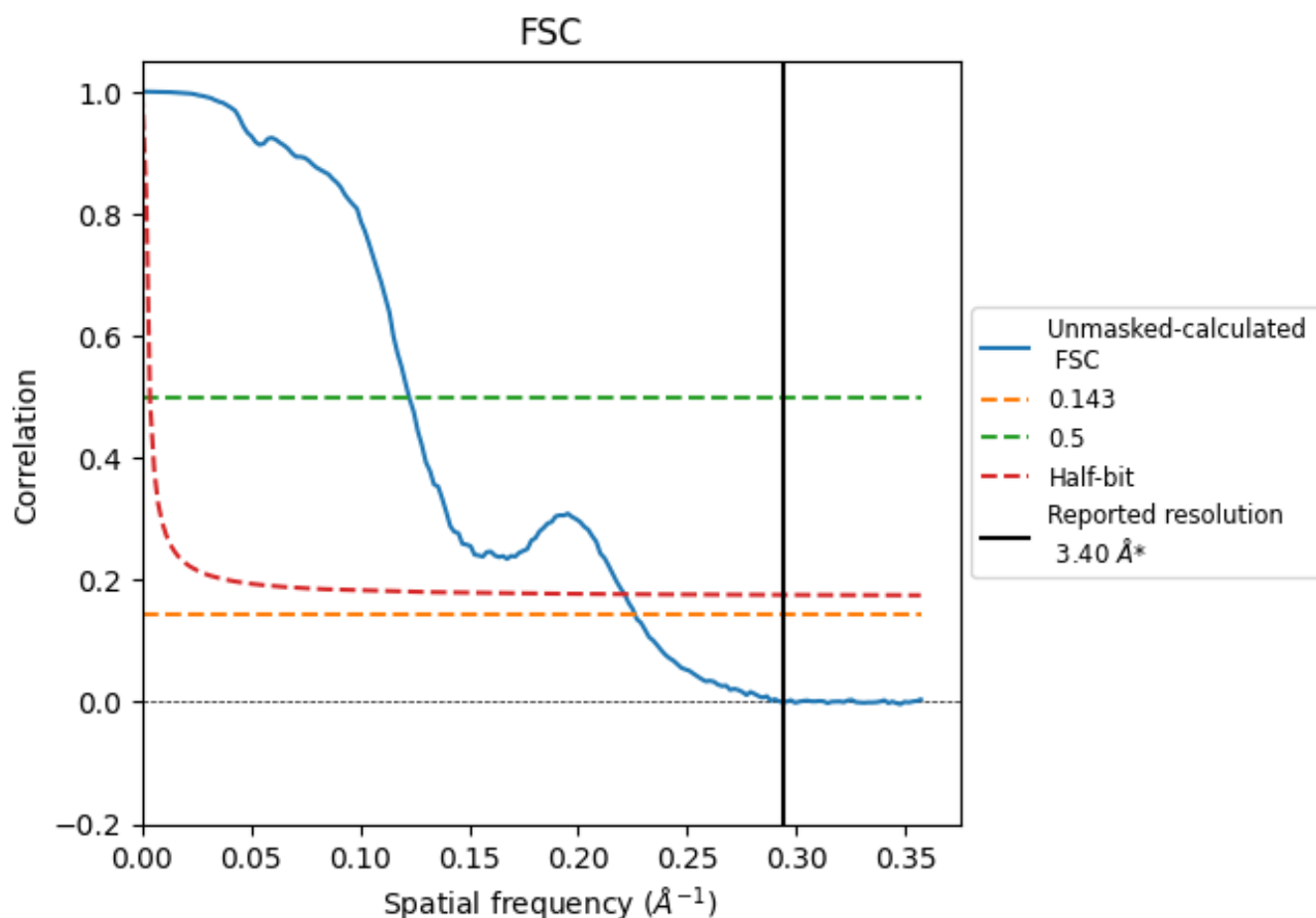


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

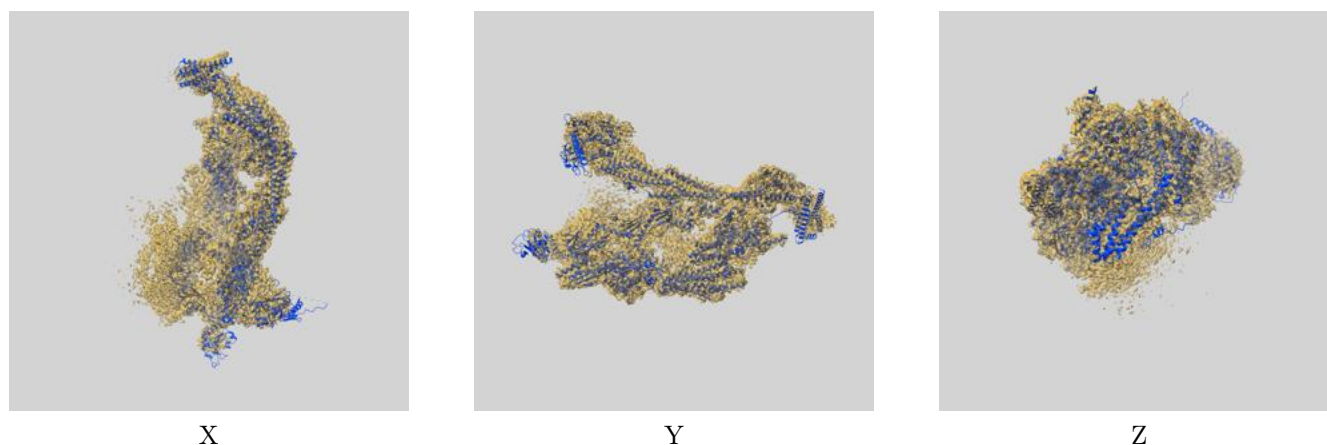
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.42	8.17	4.52

*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 4.42 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

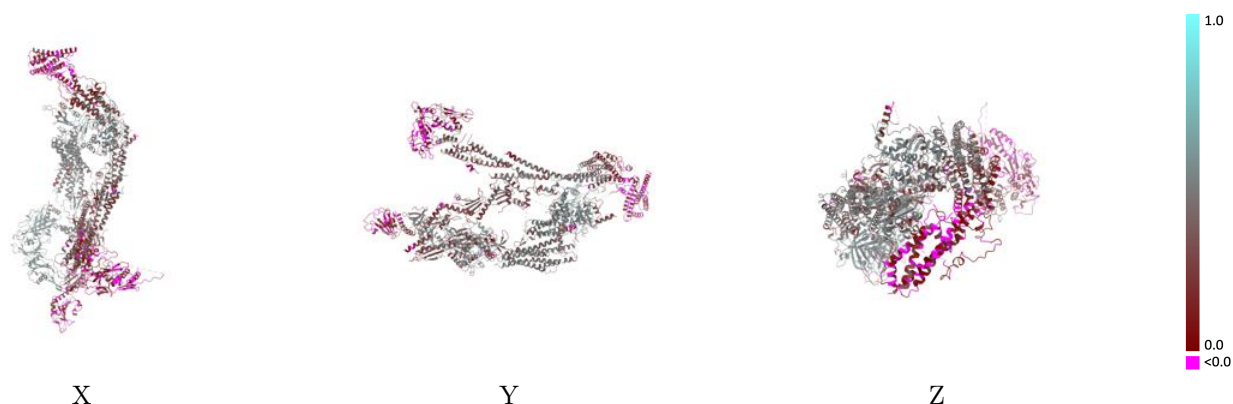
This section contains information regarding the fit between EMDB map EMD-71498 and PDB model 9PC7. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



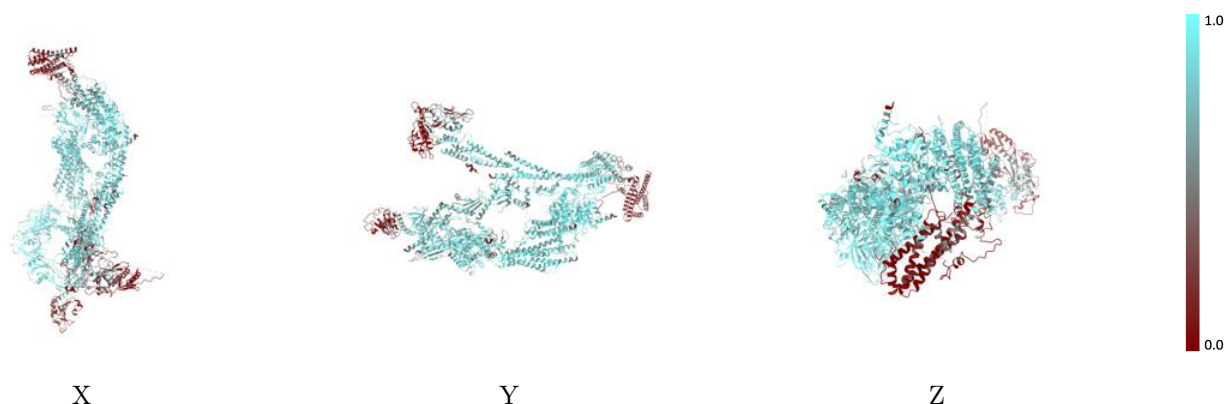
The images above show the 3D surface view of the map at the recommended contour level 0.523 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



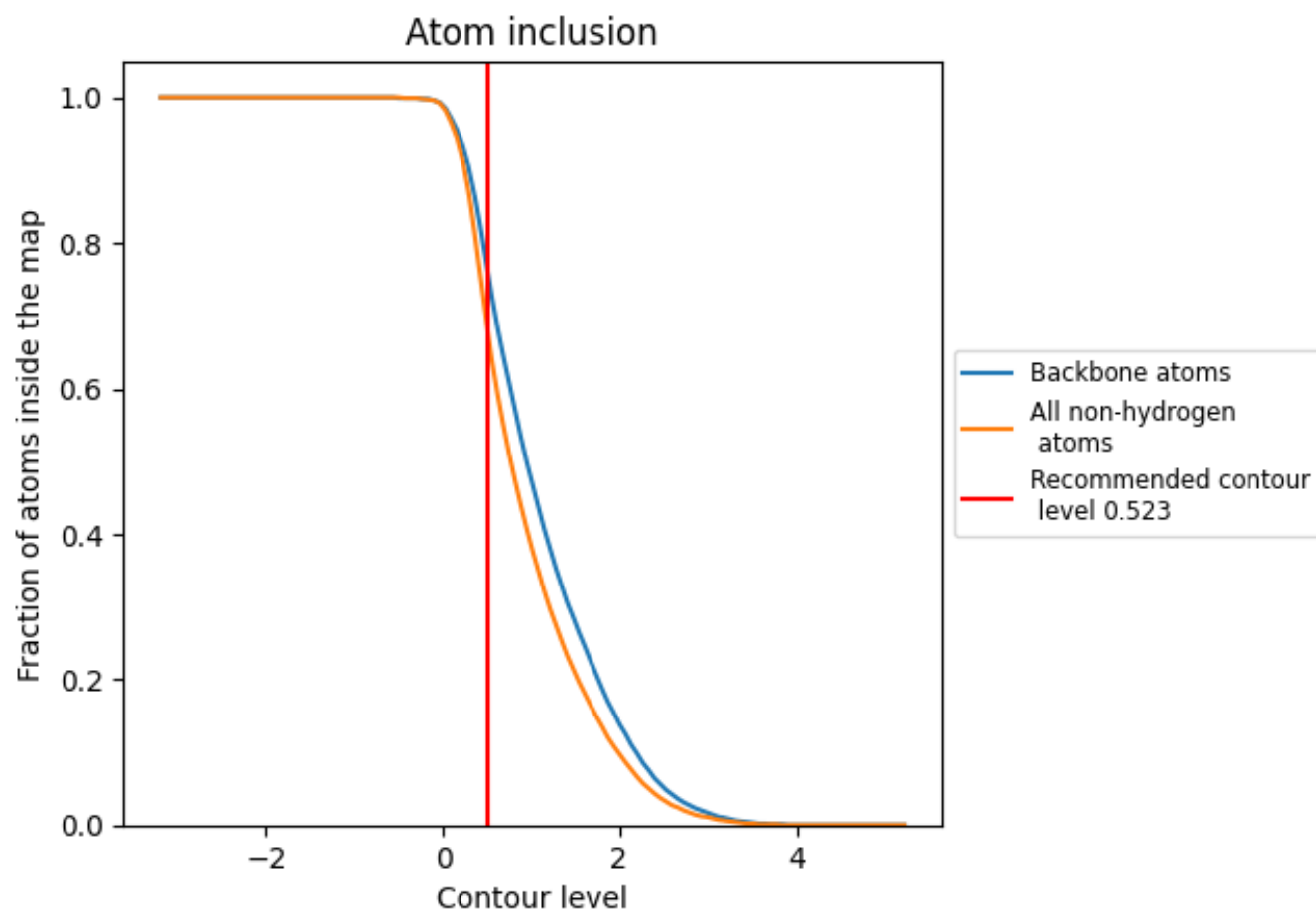
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.523).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 67% 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 (0.523) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6690	 0.3270
A	 0.7480	 0.4310
a	 0.8450	 0.4560
b	 0.8580	 0.4510
c	 0.8350	 0.4290
d	 0.7480	 0.3740
e	 0.9030	 0.4980
f	 0.8810	 0.4840
g	 0.7510	 0.3660
h	 0.7860	 0.3910
i	 0.8220	 0.3960
j	 0.7930	 0.3500
k	 0.3670	 0.1020
l	 0.5380	 0.2380
m	 0.2470	 0.1280
n	 0.6800	 0.3240
o	 0.8940	 0.4950
p	 0.2870	 0.0860

