



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:03 PM UTC

PDB ID : 7W68 / pdb_00007w68
EMDB ID : EMD-32326
Title : human single hexameric Mcm2-7 complex
Authors : Xu, N.N.; Lin, Q.P.; Liu, C.D.; Tian, H.L.; Xiang, Y.; Zhu, G.
Deposited on : 2021-12-01
Resolution : 4.40 Å(reported)

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:

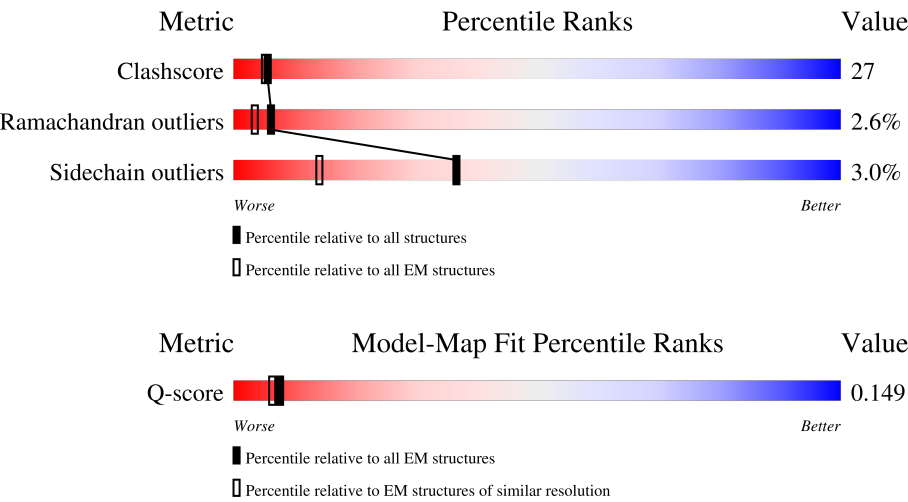
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	A	904	18% 32%26%38%
2	B	808	14% 30%26%38%
3	C	863	14% 30%27%39%
4	D	734	15% 29%27%42%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	821	24%39%35%. .19%
6	F	719	22%41%36%. .20%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 25833 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 DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	560	Total	C	N	O	S	0	0
			4443	2800	797	823	23		

- Molecule 2 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	498	Total	C	N	O	S	0	0
			3912	2456	700	733	23		

- Molecule 3 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	529	Total	C	N	O	S	0	0
			4227	2670	745	788	24		

- Molecule 4 is a protein called DNA replication licensing factor MCM5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	426	Total	C	N	O	S	0	0
			3349	2106	591	627	25		

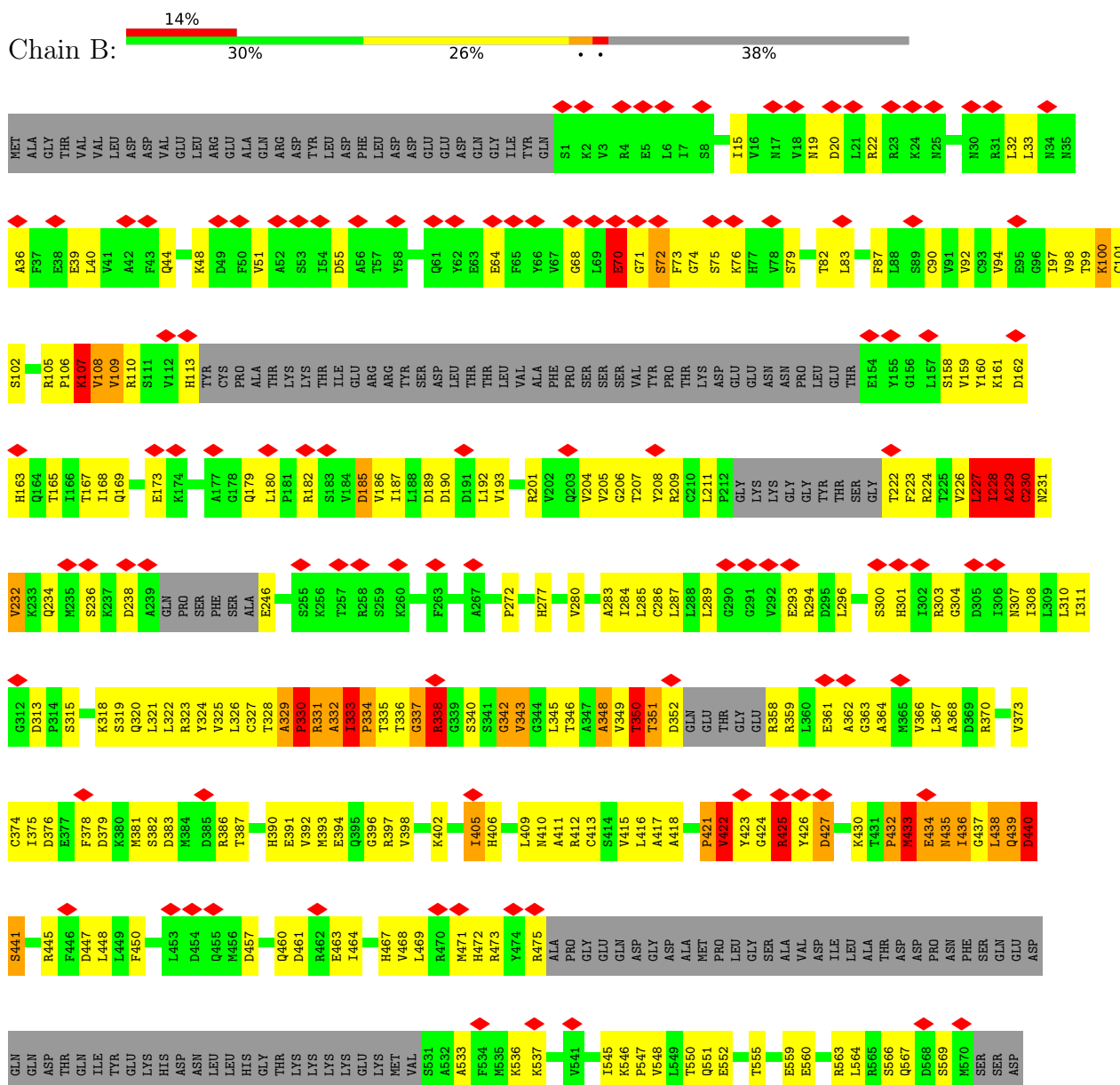
- Molecule 5 is a protein called DNA replication licensing factor MCM6.

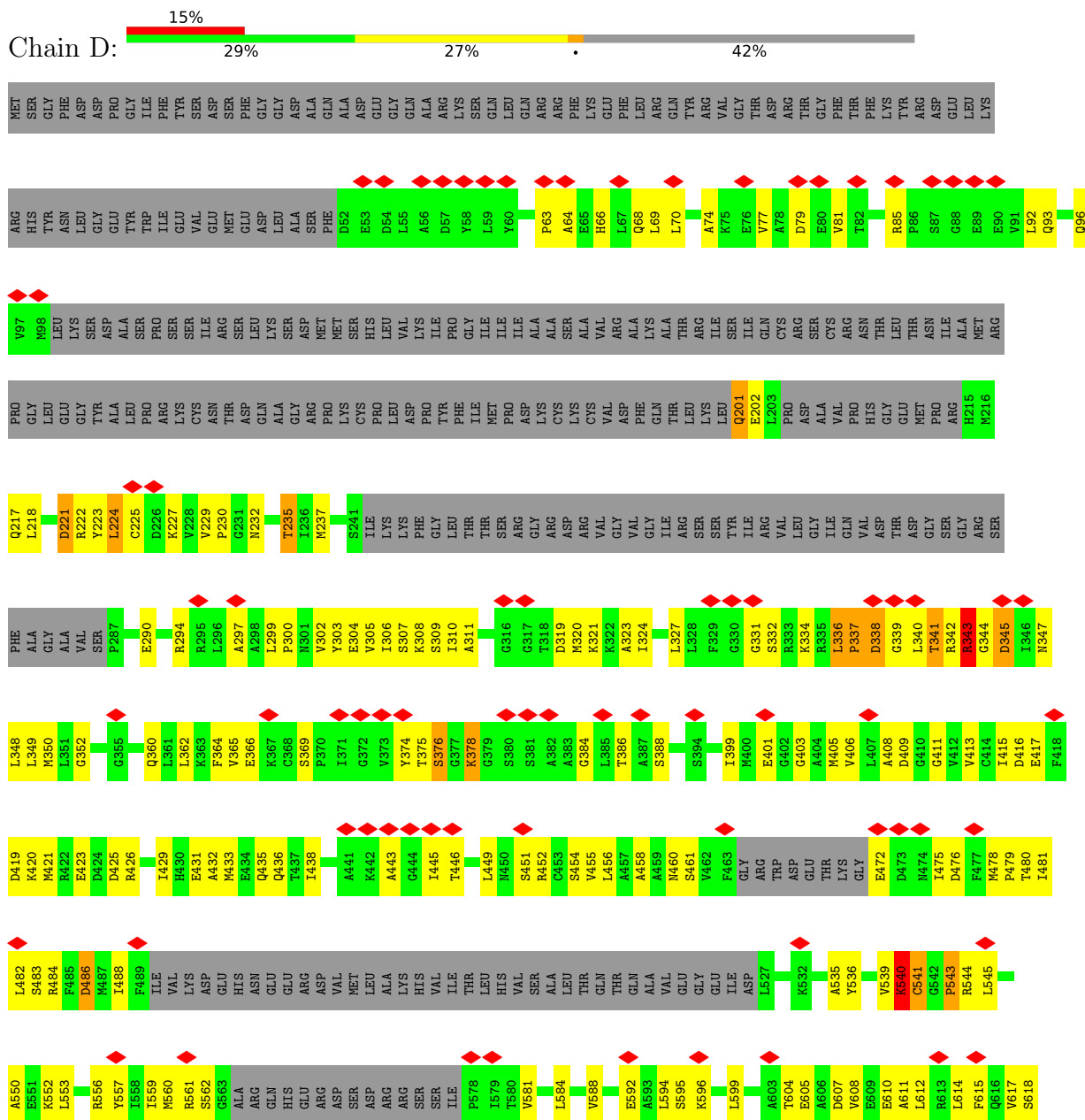
Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	661	Total	C	N	O	S	0	0
			5335	3355	946	1007	27		

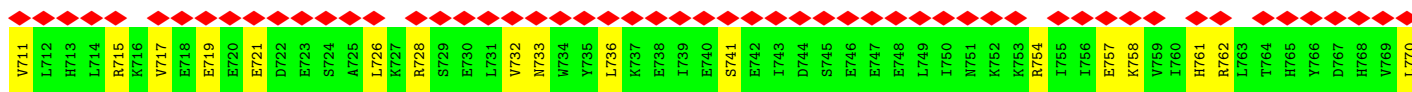
- Molecule 6 is a protein called DNA replication licensing factor MCM7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	575	Total	C	N	O	S	0	0
			4567	2866	815	861	25		

- Molecule 2: DNA replication licensing factor MCM3







ILE
GLU
THR
GLN
ALA
GLY
LEU
LYS
SER
THR
GLU
GLY
SER
GLU
TVR
GLU
ASP
PRD
TRP
LEU
VAL
VAL
ASN
PRD
ASN
TVR
LEU
GLU
ASP

• Molecule 6: DNA replication licensing factor MCM7



MET
ALA
LEU
LYS
D1
Y2
R68
R69
A70
K6
E7
K8
V9
F12
L13
Q14
E15
Q18
D19
D20
E21
L22
C23
K24
K25
Q26
Y29
G30
N31
Q32
L33
V34
R35
A37
Q41
V42
A43
L44
Y45
V46
D47
L48
D49
VAL
D50
V51
A52
E53
D54
D55
P56
E57
L58
V59
D60
S61

E64
N65
A66
R67
R68
Y69
A70
K71
L72
F73
A74
D75
A76
V77
O78
E79
L80
L81
P82
Q83
Y84
K85
E86
R87
GLU
VAL
ARG
ASN
LYS
ASP
VAL
LEU
ASP
VAL
VAL
TVR
ILE
GLU
HIS
ARG
LEU
MET
GLU
GLN
ARG
SER
PRD
GLN
ASN
Q121
A124

E125
L126
M127
R128
R129
F130
E131
L132
Y133
F134
Q135
G136
P137
S138
S139
N140
K141
P142
R143
Y144
C145
I146
E147
V148
R149
A150
D151
S152
V153
G154
K155
L156
V157
T158
V159
Q160
I161
I162
V163
T164
R165
V166
S167
E168
V169
K170
P171
K172
M173
V174
V175
A176
T177
Y178
T179
C180
Q181
Q182
C183
G184

A185
E186
T187
Y188
Q189
P190
L191
GLN
SER
PRO
THR
PHE
MET
PRO
LEU
ILE
MET
CYS
PRO
SER
GLU
GLN
CYS
THR
ASN
ARG
SER
GLY
G214
L218
Q219
T220
R221
G222
S223
R224
F225
I226
K227
F228
Q229
E230
W231
K232
K233
Q234
E235
H236
S237
P241
V242
G243
N244
T245
P246
R247
S248

L249
L252
V253
E256
W257
T258
R259
L260
Q262
H266
V267
S268
V269
T270
G271
T272
F273
L274
P275
T276
L277
R278
T279
Q280
F281
R282
Q283
W284
V285
Q286
Q287
L288
L289
S290
E291
L294
E295
A296
H297
V300
K301
K302
S305
GLU
ASP
ASP
GLU
SER
GLY
ALA
GLU
LEU

T316
R317
E318
E319
L320
A324
D327
F328
Y329
E330
K331
L332
A333
A334
S335
I336
A337
Y341
D345
V346
K347
K348
L351
L352
G356
G357
V358
D359
Q360
S361
P362
R363
G364
K365
K366
I367
R368
G369
N370
I371
N372
I373
G377
D378
P379
G380
V381
A382
K383
L386
L387
S388

Y389
L390
D391
R392
L393
A394
S397
T400
G401
G402
R403
G404
S405
S406
G407
V408
G409
L410
T411
A412
A413
V414
L415
R416
D417
S418
V419
S420
G421
E422
L423
T424
G428
A429
L432
A433
L440
D441
E442
F443
A447
E448
A449
D450
R451
T452
A453
I454
H455
E456
V457
M458
E459
Q460

Q461
T462
I463
S464
A465
A466
K467
A468
G469
I470
L471
T472
T473
L474
N475
A476
R477
C478
S479
I480
M483
A484
M485
P486
R487
Y488
G489
R490
Y491
N492
P493
R494
R495
S496
L497
F498
Q499
N500
A506
L507
L508
S509
R510
F511
D512
L513
L516
I517
Q518
D519
D524
H525
D526
L527
R528
L529

A530
Q531
H532
I533
T534
Y535
V536
H537
R541
Q542
P543
P544
S545
Q546
F547
E548
P549
L550
D551
M552
K553
L554
M555
R556
R557
Y558
I559
A560
M561
C562
K565
M568
V569
P570
L573
A574
D575
Y576
A579
A580
ASP
Y581
V582
R585
W589
K592
D593
A594
T595
Y596
T597
S598
R599
A599

R600
T601
L602
L603
L606
R607
T610
L615
R616
M617
V618
V619
Q620
V621
E624
E628
A629
I630
R631
L632
M633
R634
M635
S636
S639
L640
LEU
GLY
TRP
ASP
LYS
GLY
GLN
THR
ALA
ARG
THR
ARG
GLN
ARG
PRO
ALA
ASP
VAL
ILE
PHE
THR
VAL
ARG
GLU
LEU
VAL
SER
GLY

ARG
SER
VAL
L602
L603
L606
R607
T610
L615
R616
M617
V618
V619
Q620
V621
E624
E628
A629
I630
R631
L632
M633
R634
M635
S636
S639
L640
LEU
GLY
TRP
ASP
LYS
GLY
GLN
THR
ALA
ARG
THR
ARG
GLN
ARG
PRO
ALA
ASP
VAL
ILE
PHE
THR
VAL
ARG
GLU
LEU
VAL
SER
GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	186918	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.293	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.050	Depositor
Recommended contour level	0.14	Depositor
Map size ($\text{\AA}$)	254.4, 254.4, 254.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	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	A	0.64	3/4518 (0.1%)	1.01	30/6093 (0.5%)
2	B	0.98	22/3965 (0.6%)	1.21	58/5341 (1.1%)
3	C	0.73	6/4299 (0.1%)	1.07	39/5809 (0.7%)
4	D	0.61	3/3390 (0.1%)	0.87	6/4541 (0.1%)
5	E	0.88	16/5420 (0.3%)	1.24	76/7302 (1.0%)
6	F	0.69	4/4637 (0.1%)	0.90	18/6257 (0.3%)
All	All	0.77	54/26229 (0.2%)	1.07	227/35343 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	14
2	B	0	8
3	C	0	17
4	D	0	9
5	E	0	13
6	F	0	7
All	All	0	68

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	153	GLN	N-CA	14.41	1.64	1.46
5	E	203	ILE	C-N	13.83	1.50	1.33
5	E	153	GLN	CA-C	-13.68	1.34	1.52
2	B	436	ILE	CA-CB	12.73	1.69	1.54
2	B	433	MET	N-CA	-12.42	1.30	1.46

The worst 5 of 227 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	380	ASP	CA-C-N	26.88	153.44	119.84
5	E	380	ASP	C-N-CA	26.88	153.44	119.84
1	A	98	LEU	CA-C-N	20.71	145.73	119.84
1	A	98	LEU	C-N-CA	20.71	145.73	119.84
2	B	436	ILE	CB-CA-C	18.20	133.76	111.20

There are no chirality outliers.

5 of 68 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	102	GLU	Peptide
1	A	190	GLU	Peptide
1	A	243	PRO	Peptide
1	A	289	ALA	Peptide
1	A	32	MET	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4443	0	4483	211	0
2	B	3912	0	3993	259	0
3	C	4227	0	4258	249	0
4	D	3349	0	3429	201	0
5	E	5335	0	5360	381	0
6	F	4567	0	4622	212	0
All	All	25833	0	26145	1427	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 27.

The worst 5 of 1427 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)
3:C:552:ARG:CG	5:E:542:ILE:HG13	1.22	1.62
5:E:153:GLN:CB	5:E:153:GLN:CG	1.74	1.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:594:LYS:HE3	5:E:597:TRP:CD1	1.37	1.59
2:B:436:ILE:CD1	2:B:436:ILE:CG1	1.82	1.54
2:B:386:ARG:NE	2:B:438:LEU:CD2	1.68	1.53

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	A	546/904 (60%)	454 (83%)	79 (14%)	13 (2%)	4	27
2	B	484/808 (60%)	402 (83%)	67 (14%)	15 (3%)	3	22
3	C	515/863 (60%)	400 (78%)	100 (19%)	15 (3%)	3	23
4	D	410/734 (56%)	355 (87%)	50 (12%)	5 (1%)	10	42
5	E	653/821 (80%)	517 (79%)	109 (17%)	27 (4%)	2	18
6	F	567/719 (79%)	484 (85%)	74 (13%)	9 (2%)	7	36
All	All	3175/4849 (66%)	2612 (82%)	479 (15%)	84 (3%)	6	25

5 of 84 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	PRO
1	A	374	PRO
1	A	424	ALA
2	B	229	ALA
2	B	230	CYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	488/781 (62%)	475 (97%)	13 (3%)	39	59
2	B	429/707 (61%)	414 (96%)	15 (4%)	32	53
3	C	470/753 (62%)	460 (98%)	10 (2%)	47	65
4	D	364/625 (58%)	355 (98%)	9 (2%)	42	62
5	E	595/724 (82%)	568 (96%)	27 (4%)	24	46
6	F	494/619 (80%)	484 (98%)	10 (2%)	48	66
All	All	2840/4209 (68%)	2756 (97%)	84 (3%)	37	57

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	173	ARG
5	E	599	ILE
5	E	176	LEU
5	E	383	THR
6	F	253	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	192	GLN
6	F	189	GLN
5	E	195	GLN
5	E	636	ASN
6	F	461	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

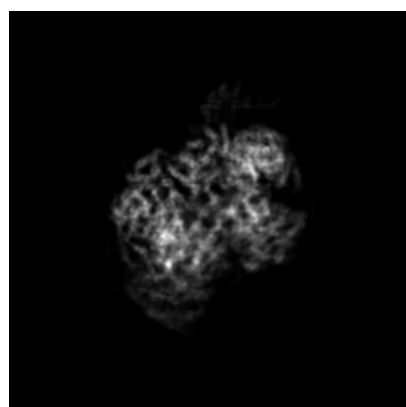
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32326. These allow visual inspection of the internal detail of the map and identification of artifacts.

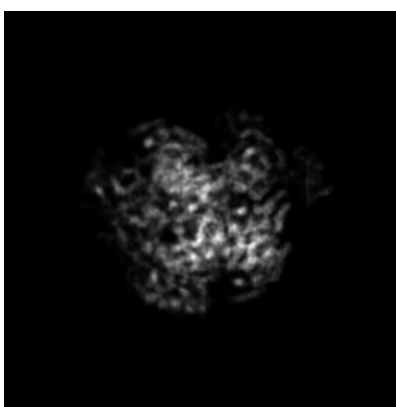
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

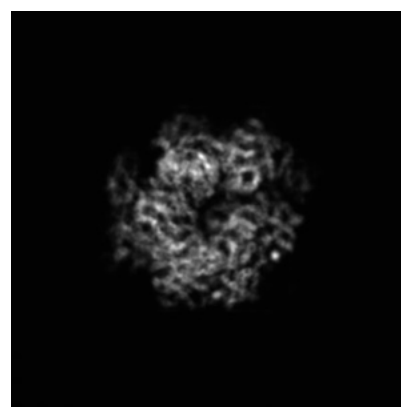
6.1.1 Primary map



X



Y

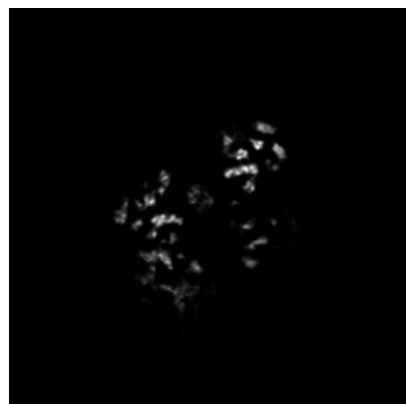


Z

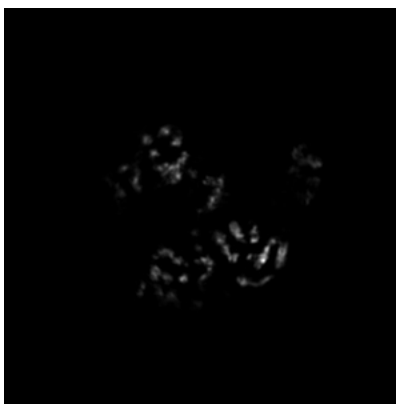
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

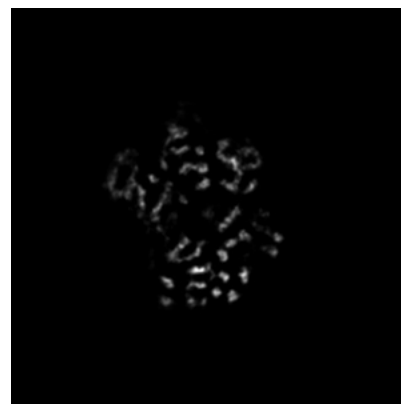
6.2.1 Primary map



X Index: 120



Y Index: 120

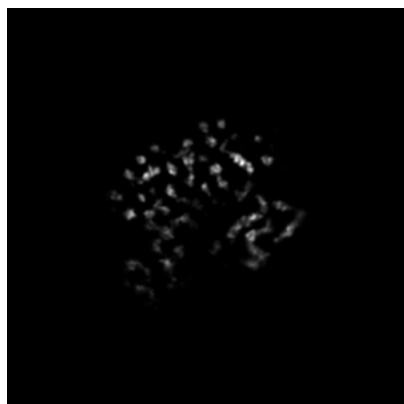


Z Index: 120

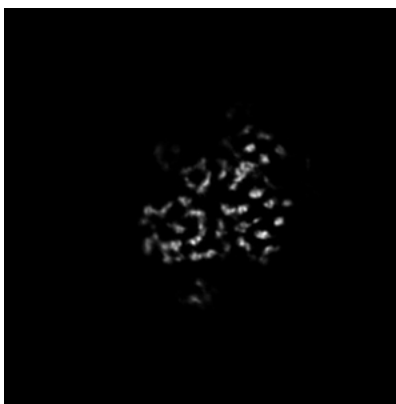
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 98



Y Index: 146

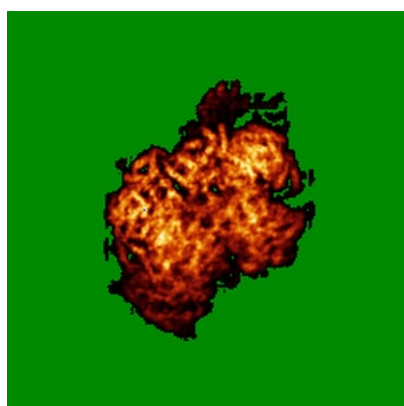


Z Index: 119

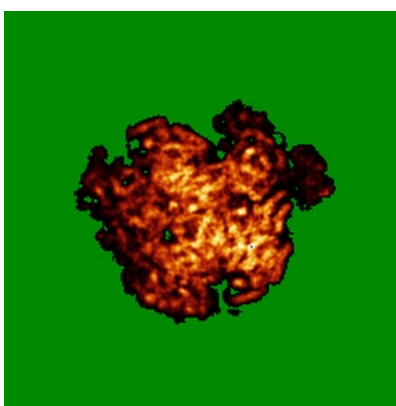
The images above show the largest variance slices of the map in three orthogonal directions.

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

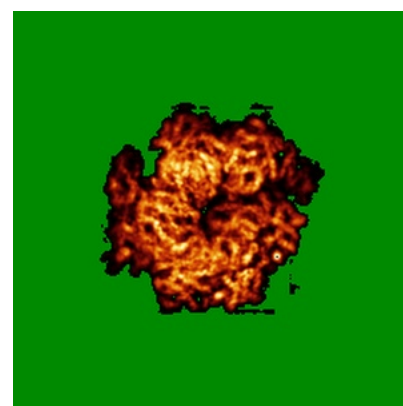
6.4.1 Primary map



X



Y

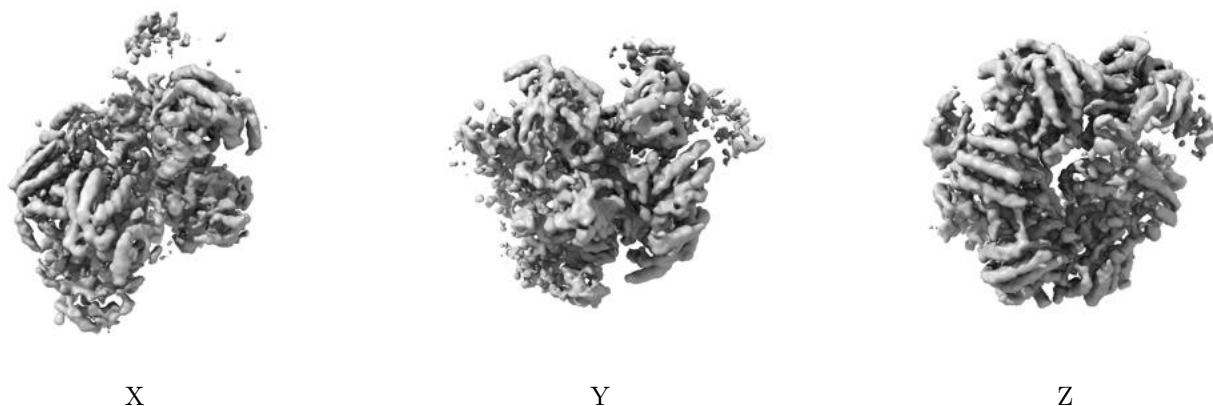


Z

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 0.14. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

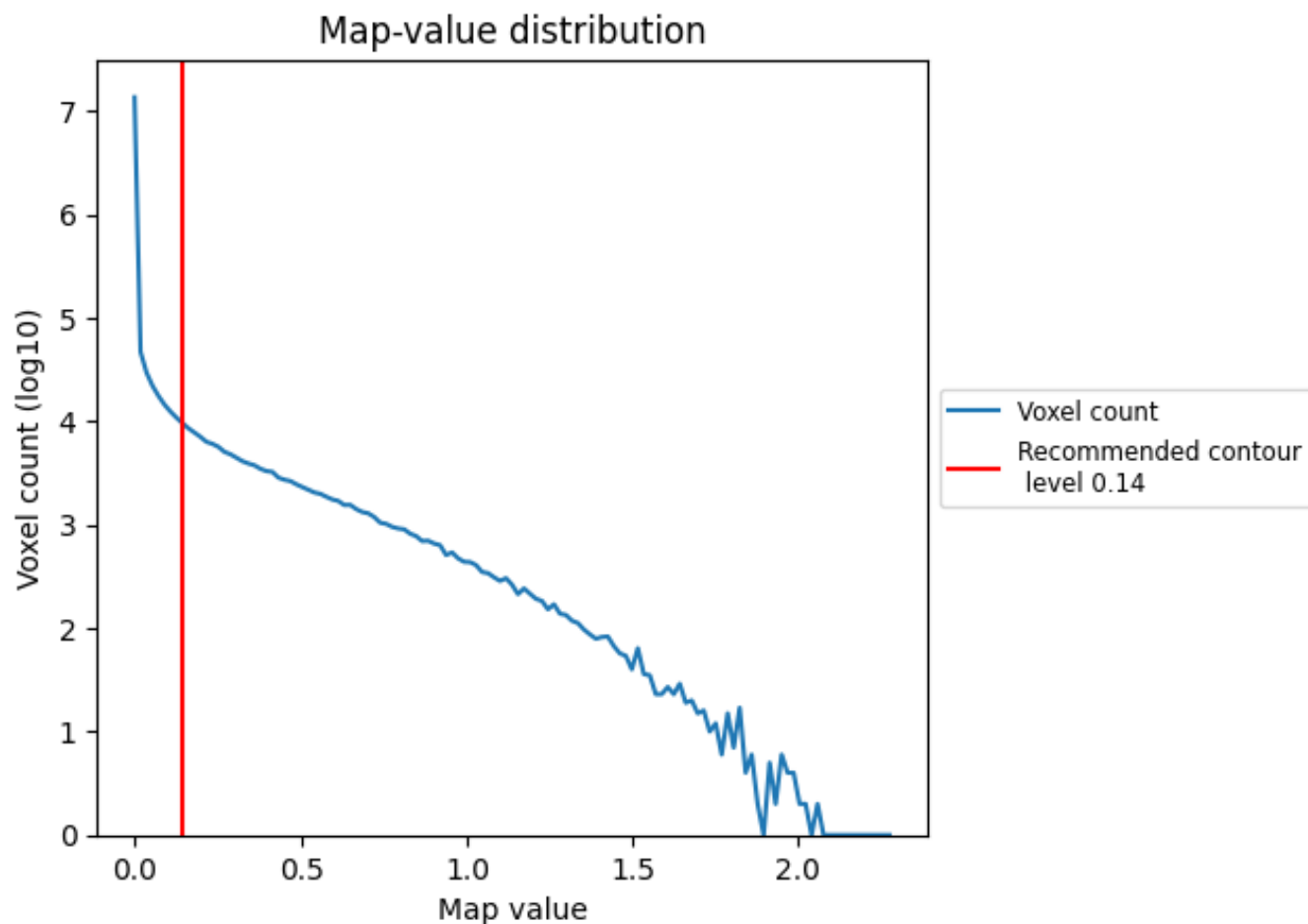
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

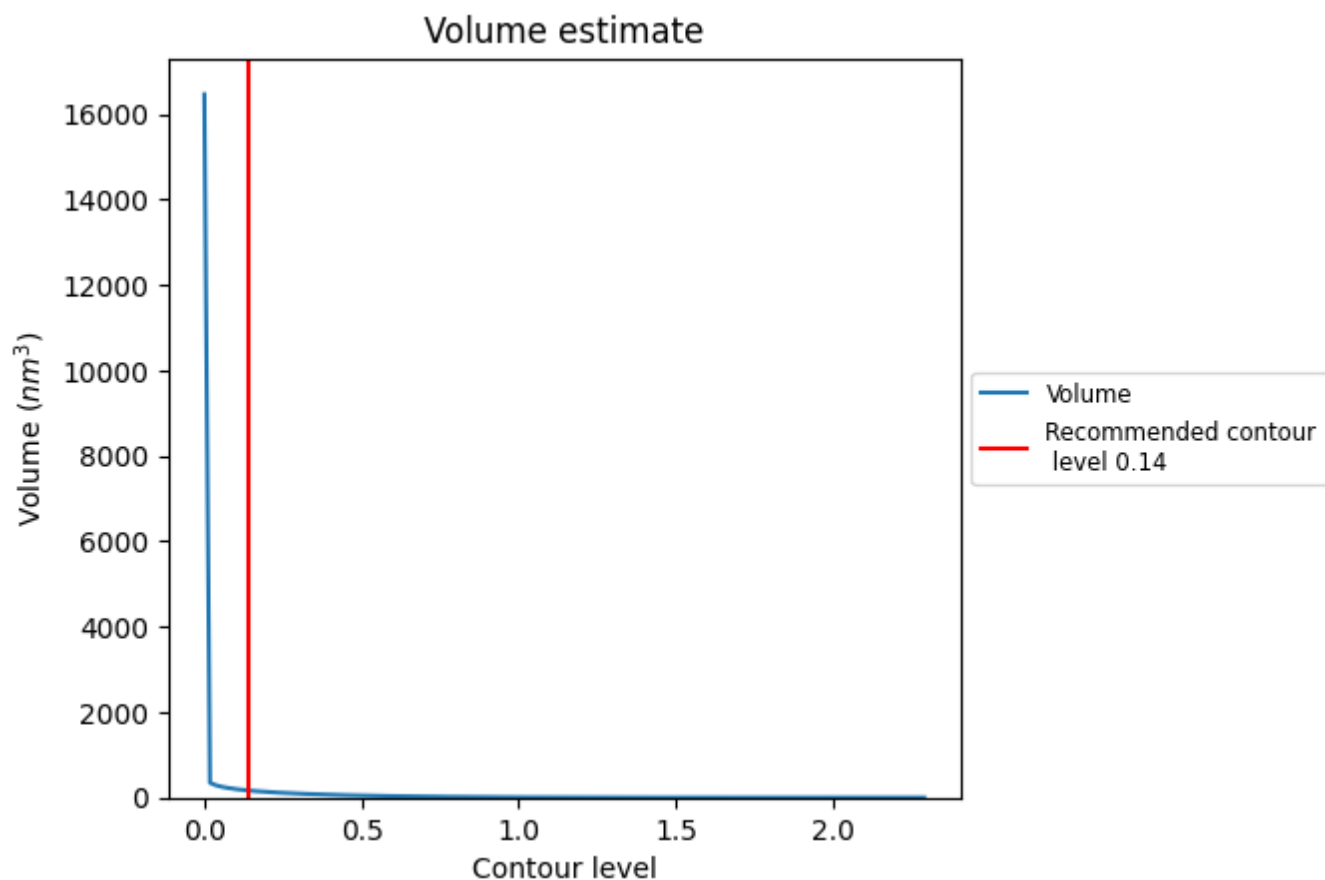
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

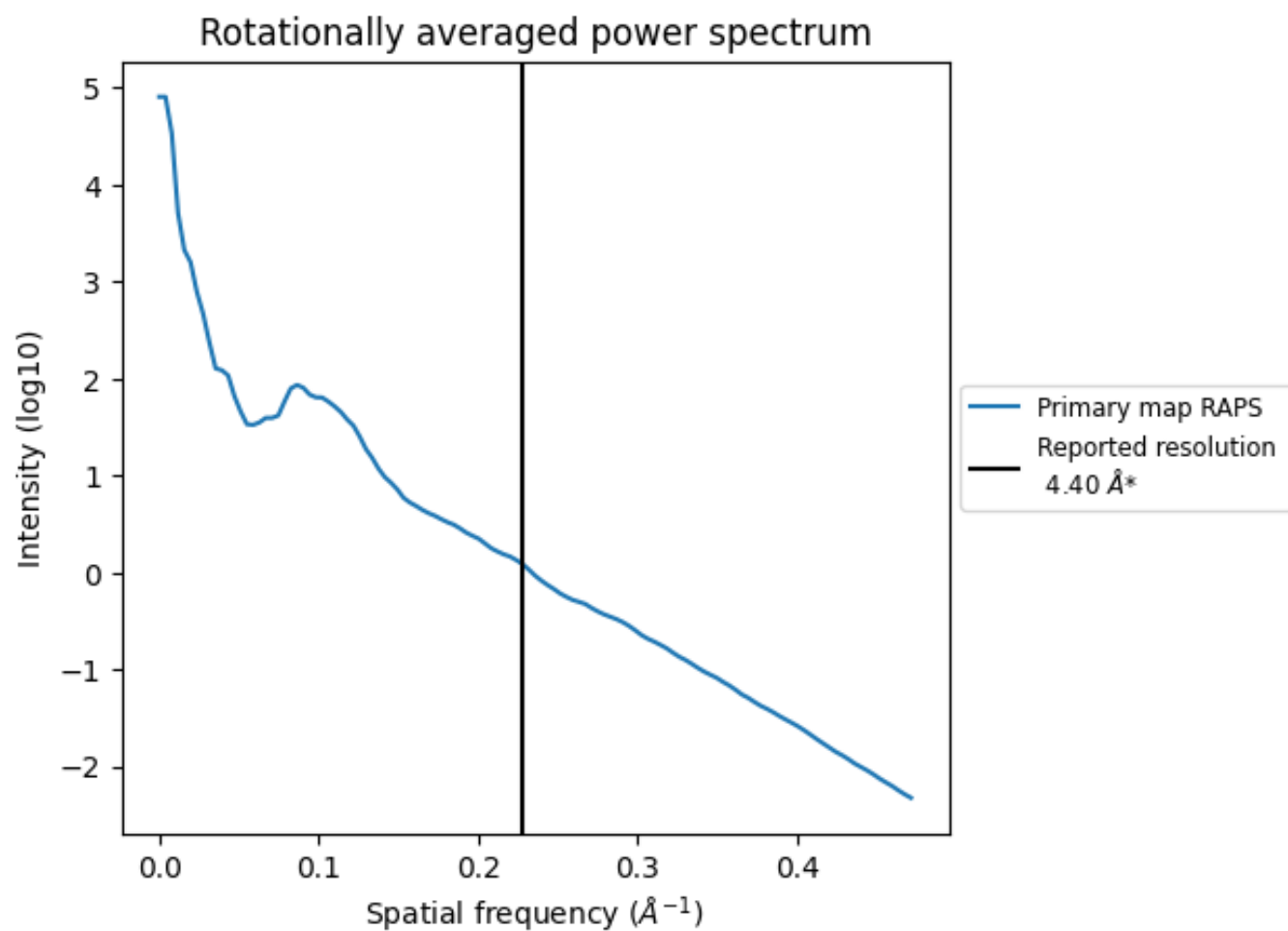
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 165 nm^3 ; this corresponds to an approximate mass of 149 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 ⓘ

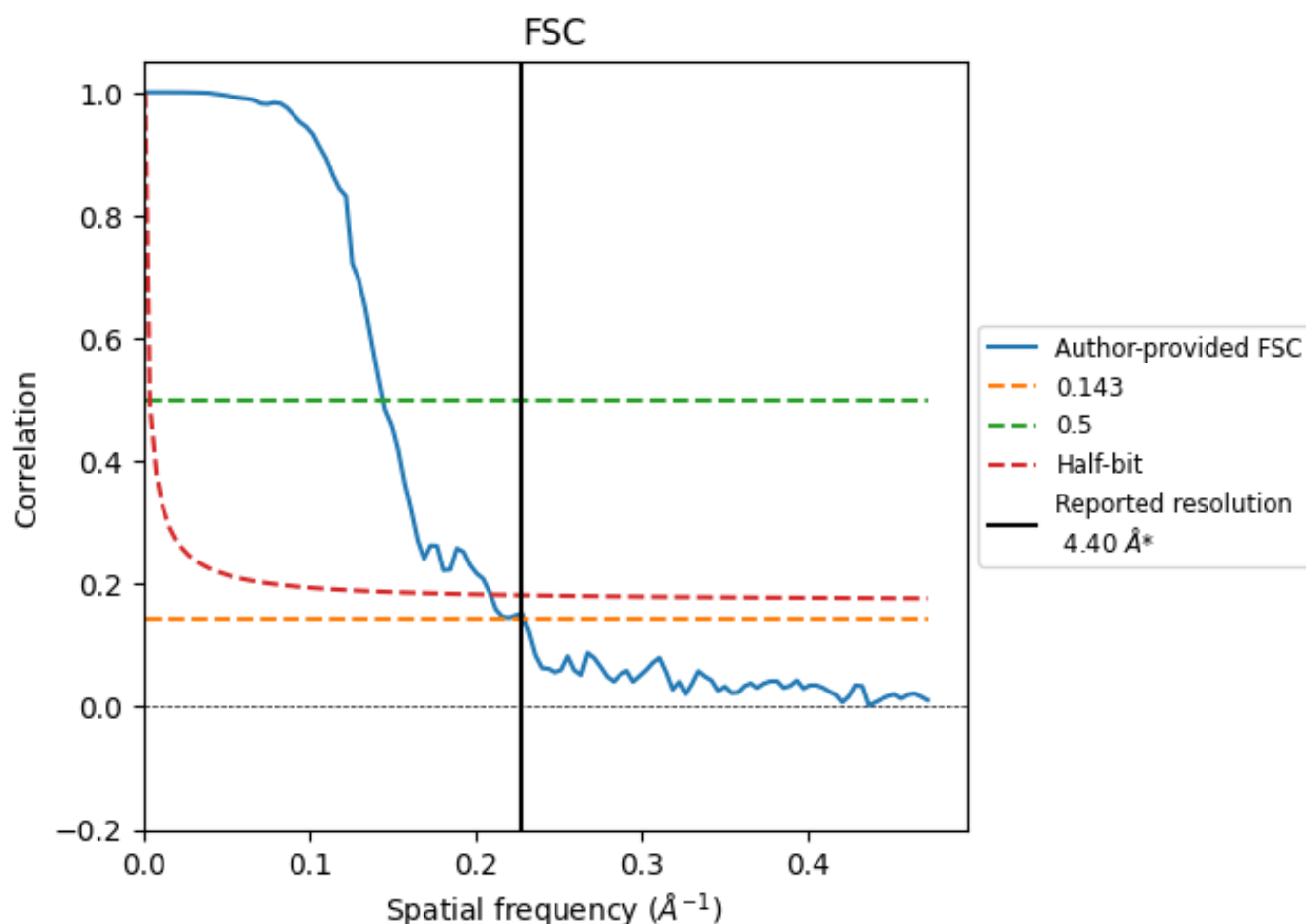


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

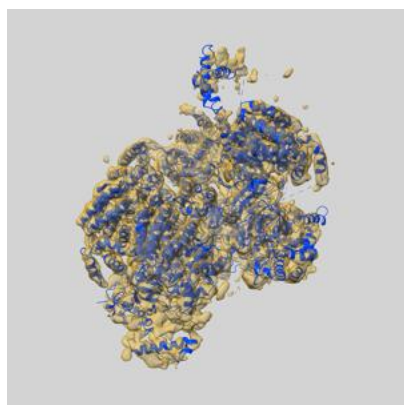
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.36	6.93	4.79
Unmasked-calculated*	-	-	-

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

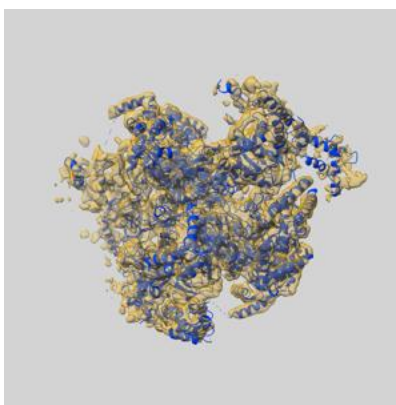
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32326 and PDB model 7W68. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

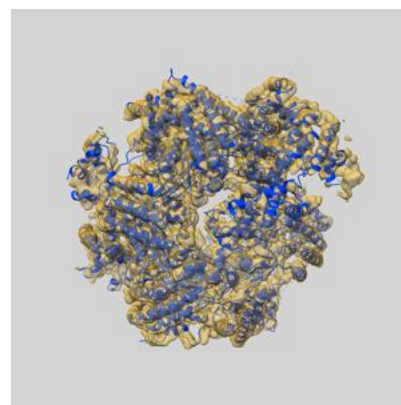
9.1 Map-model overlay [i](#)



X



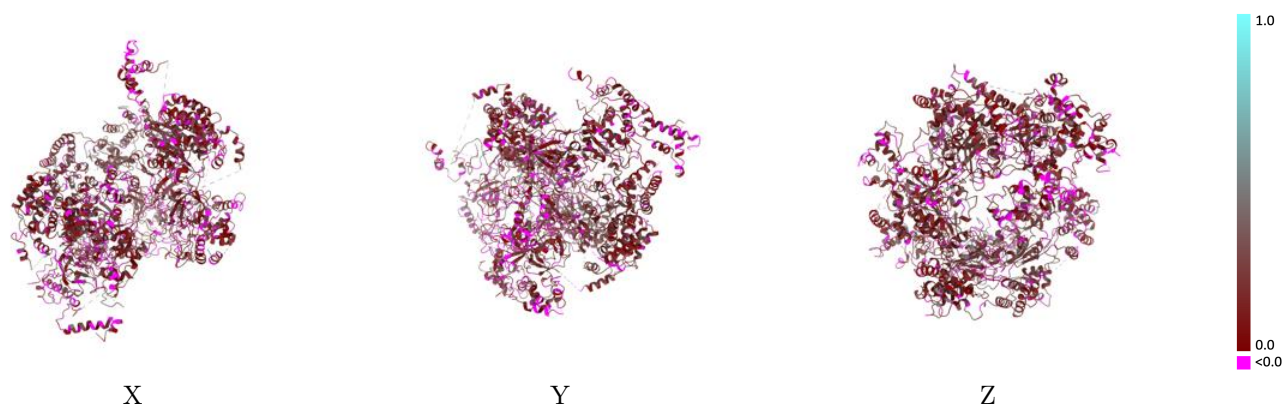
Y



Z

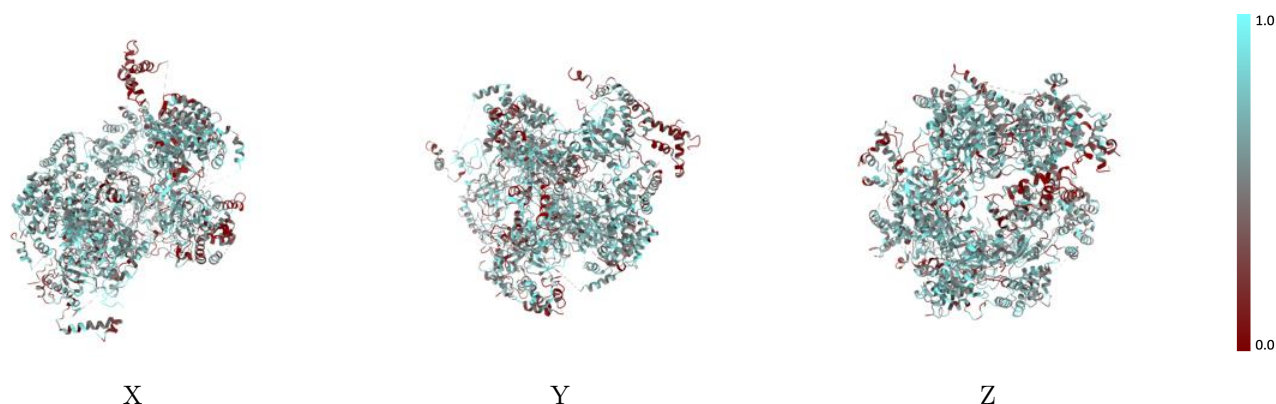
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



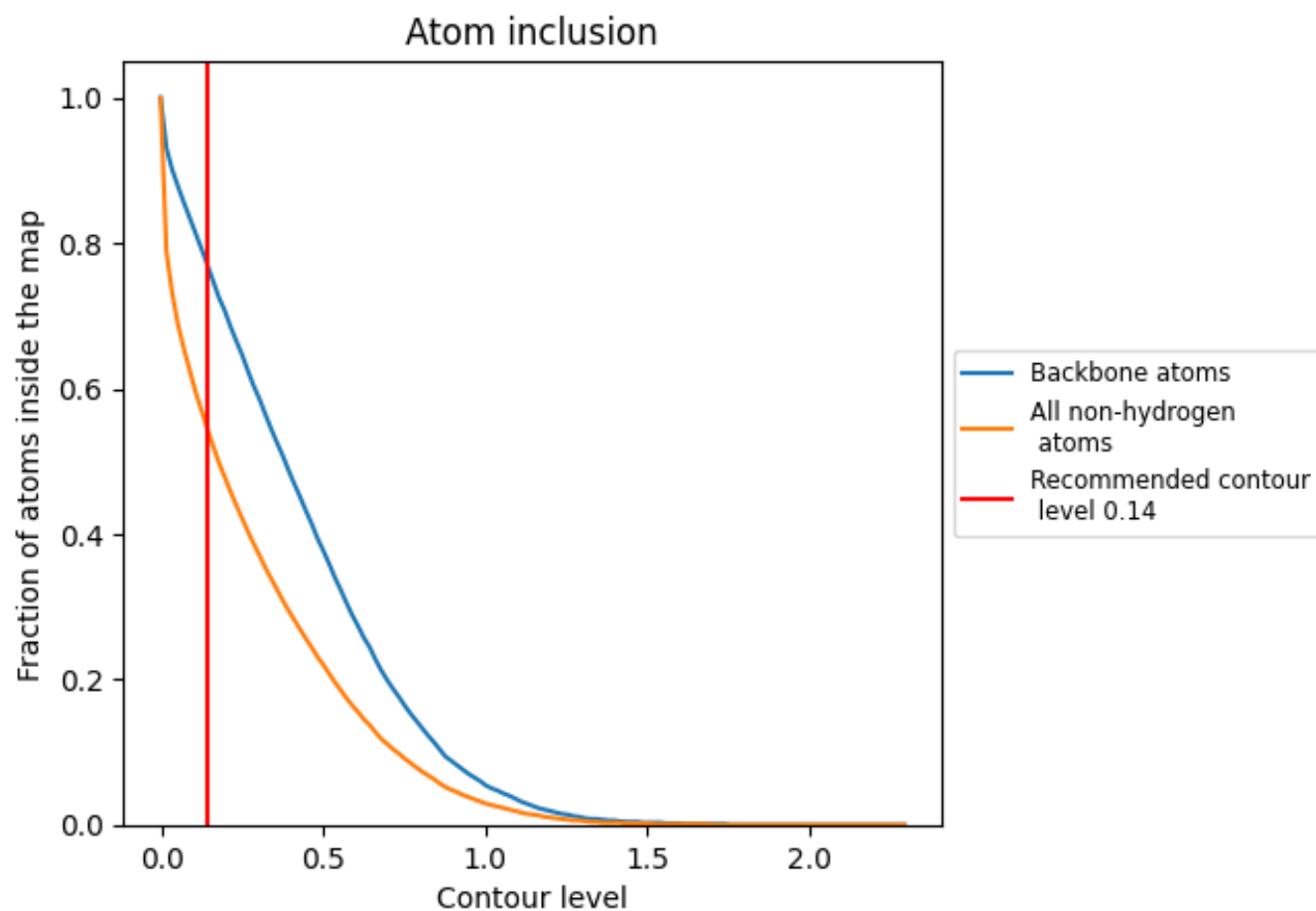
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 55% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5480	0.1490
A	0.5300	0.1370
B	0.5780	0.1690
C	0.5760	0.1560
D	0.5560	0.1460
E	0.5200	0.1450
F	0.5370	0.1440

1.0

0.0

<0.0