



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 07:27 AM UTC

PDB ID : 7YYH / pdb_00007yyh
EMDB ID : EMD-14375
Title : Structure of the human CCANdeltaT CENP-A alpha-satellite complex
Authors : Yatskevich, S.; Muir, K.W.; Bellini, D.; Zhang, Z.; Yang, J.; Tischer, T.; Predin, M.; Dendooven, T.; McLaughlin, S.H.; Barford, D.
Deposited on : 2022-02-17
Resolution : 8.90 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:

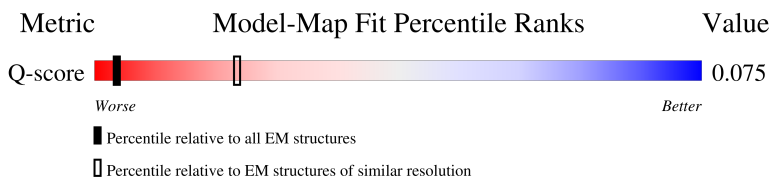
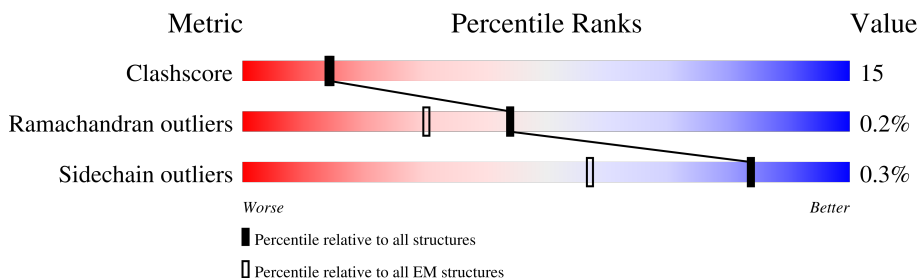
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 8.90 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	258 (8.40 - 9.40)

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	140	10% 59% 11% 29%
1	E	140	5% 57% 10% 33%
2	B	103	6% 68% 8% 24%
2	F	103	7% 62% 16% 22%

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Mol	Chain	Length	Quality of chain
3	C	130	
3	G	130	
4	D	126	
4	h	126	
5	H	247	
6	I	756	
7	J	171	
8	K	269	
9	L	344	
10	M	180	
11	N	339	
12	O	300	
13	P	288	
14	Q	268	
15	R	177	
16	U	418	
17	k	544	
17	l	544	
18	i	171	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 33344 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 Histone H3-like centromeric protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	99	Total	C	N	O	S	0	0
			799	518	147	133	1		
1	E	94	Total	C	N	O	S	0	0
			770	501	141	127	1		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	78	Total	C	N	O	S	0	0
			622	393	120	108	1		
2	F	80	Total	C	N	O	S	0	0
			641	405	125	110	1		

- Molecule 3 is a protein called Histone H2A type 1-C.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	98	Total	C	N	O	0	0
			755	474	149	132		
3	G	103	Total	C	N	O	0	0
			784	491	155	138		

- Molecule 4 is a protein called Histone H2B type 1-C/E/F/G/I.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	92	Total	C	N	O	S	0	0
			719	452	129	136	2		
4	h	92	Total	C	N	O	S	0	0
			719	452	129	136	2		

- Molecule 5 is a protein called Centromere protein H.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	171	Total	C	N	O	S	0	0
			1384	874	236	266	8		

- Molecule 6 is a protein called Centromere protein I.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	543	Total	C	N	O	S	0	0
			4402	2897	709	770	26		

- Molecule 7 is a DNA chain called DNA (171-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	153	Total	C	N	O	P	0	0
			3133	1501	557	922	153		

- Molecule 8 is a protein called Centromere protein K.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	217	Total	C	N	O	S	0	0
			1793	1139	297	347	10		

- Molecule 9 is a protein called Centromere protein L.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	297	Total	C	N	O	S	0	0
			2397	1563	392	428	14		

- Molecule 10 is a protein called Centromere protein M.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	172	Total	C	N	O	S	0	0
			1325	839	236	243	7		

- Molecule 11 is a protein called Centromere protein N.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	297	Total	C	N	O	S	0	0
			2452	1581	425	436	10		

- Molecule 12 is a protein called Centromere protein O.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	210	Total	C	N	O	S	0	0
			1642	1060	277	298	7		

- Molecule 13 is a protein called Centromere protein P.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	219	Total	C	N	O	S	0	0
			1732	1107	293	324	8		

- Molecule 14 is a protein called Centromere protein Q.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	189	Total	C	N	O	S	0	0
			1506	943	253	299	11		

- Molecule 15 is a protein called Centromere protein R.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	80	Total	C	N	O	S	0	0
			649	412	105	125	7		

- Molecule 16 is a protein called Centromere protein U.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	165	Total	C	N	O	S	0	0
			1346	851	234	256	5		

- Molecule 17 is a protein called Centromere protein C.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	k	21	Total	C	N	O	0	0
			178	111	37	30		
17	l	57	Total	C	N	O	0	0
			476	298	85	93		

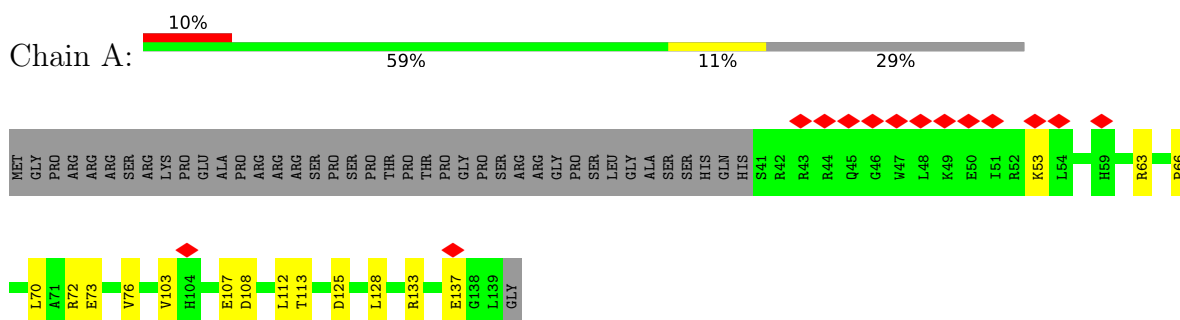
- Molecule 18 is a DNA chain called DNA (171-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	i	152	Total	C	N	O	P	0	0
			3120	1492	569	907	152		

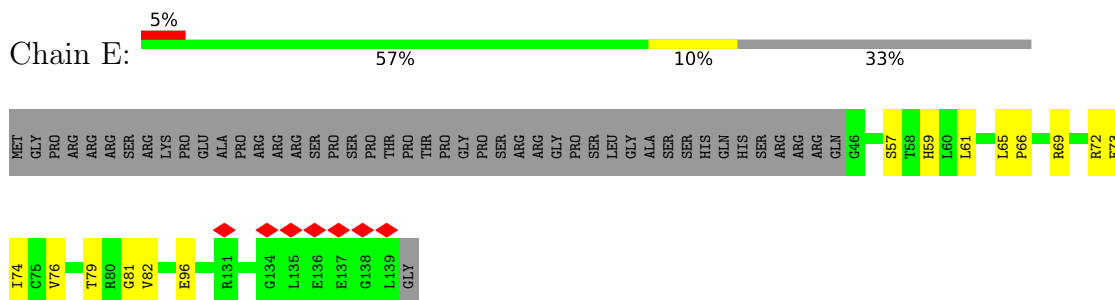
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

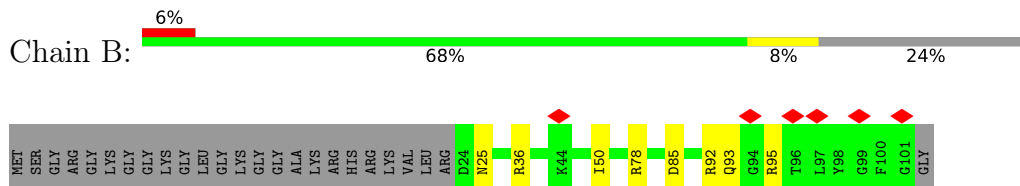
- Molecule 1: Histone H3-like centromeric protein A



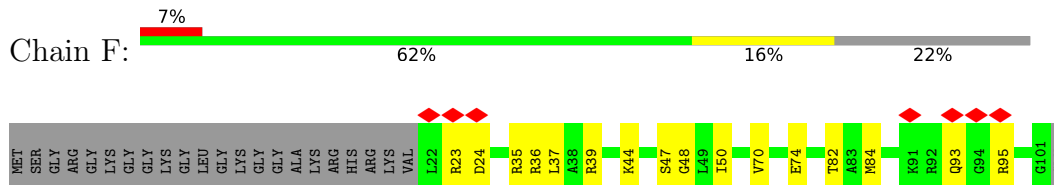
- Molecule 1: Histone H3-like centromeric protein A



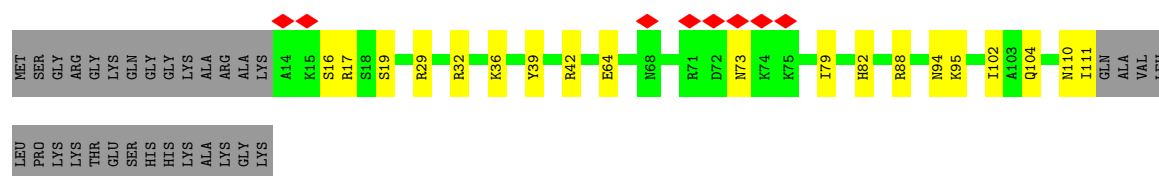
- Molecule 2: Histone H4



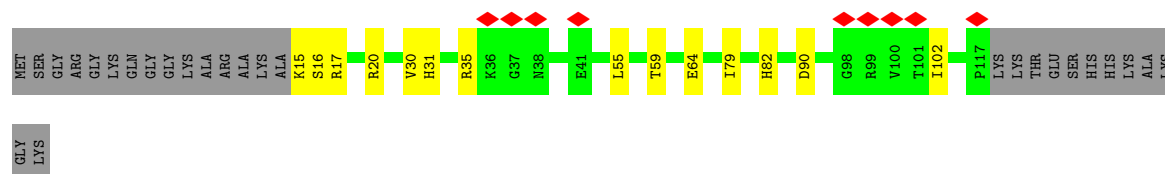
- Molecule 2: Histone H4



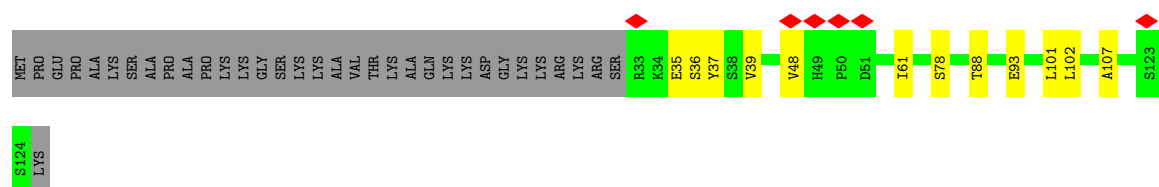
- Molecule 3: Histone H2A type 1-C



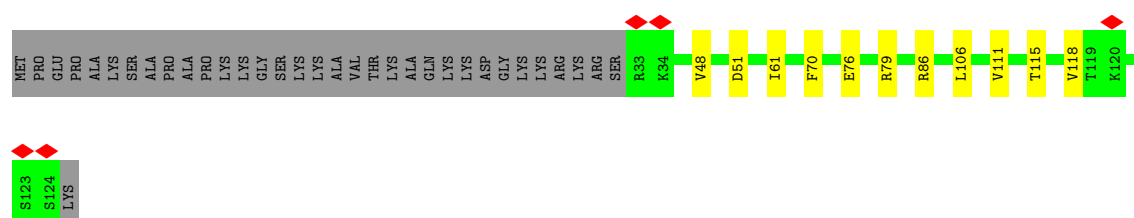
- Molecule 3: Histone H2A type 1-C



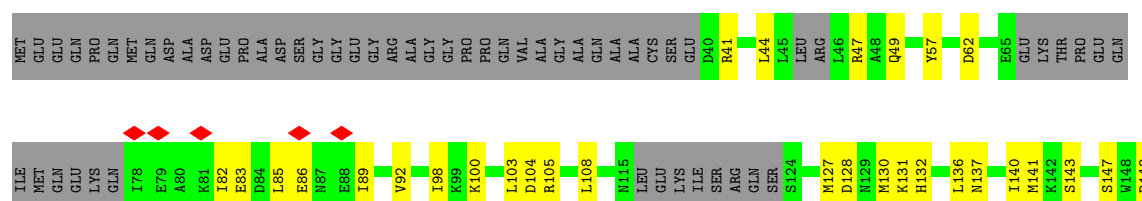
- Molecule 4: Histone H2B type 1-C/E/F/G/I

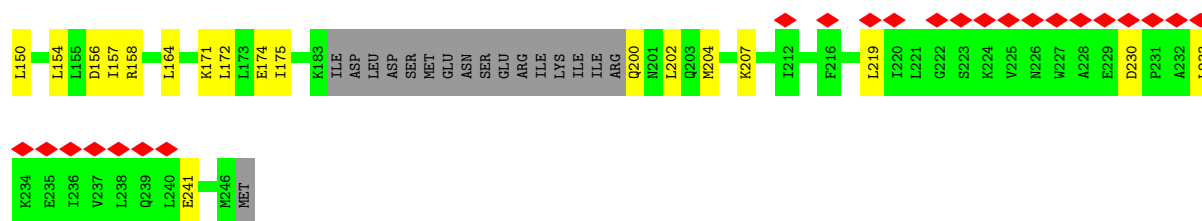


- Molecule 4: Histone H2B type 1-C/E/F/G/I

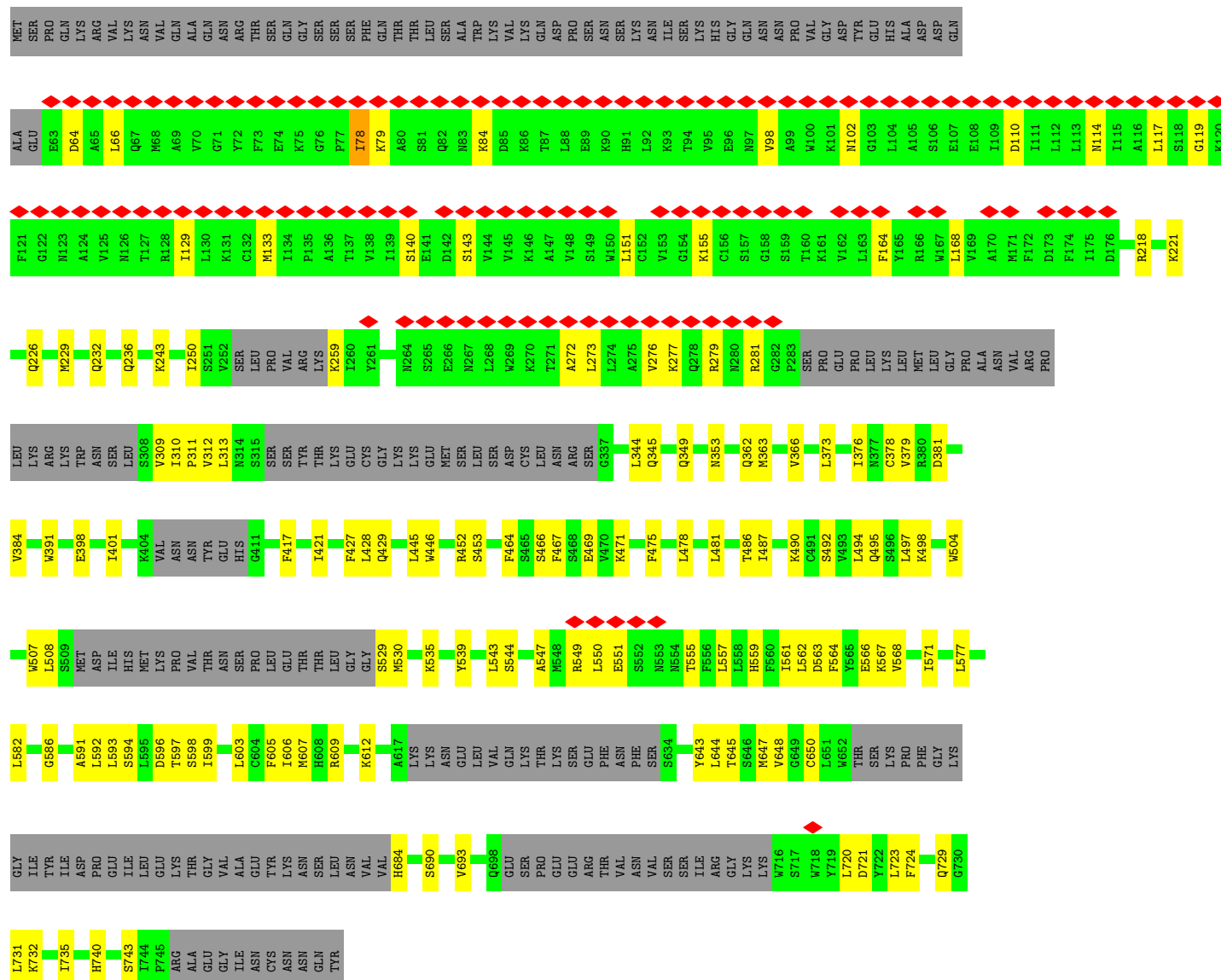


- Molecule 5: Centromere protein H



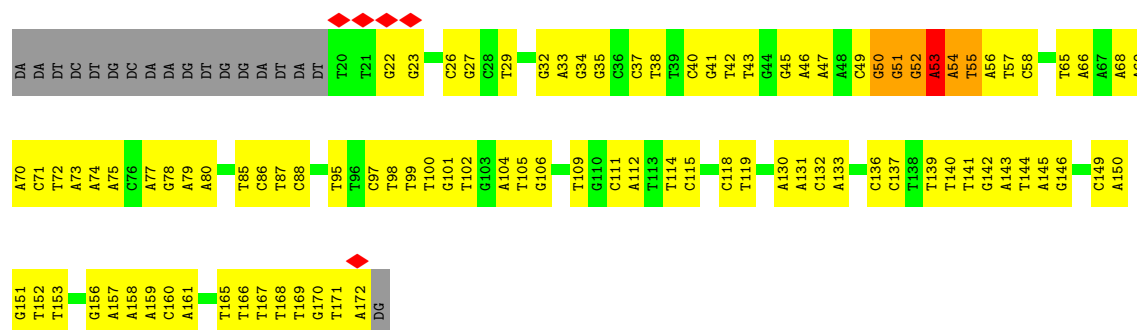


• Molecule 6: Centromere protein I

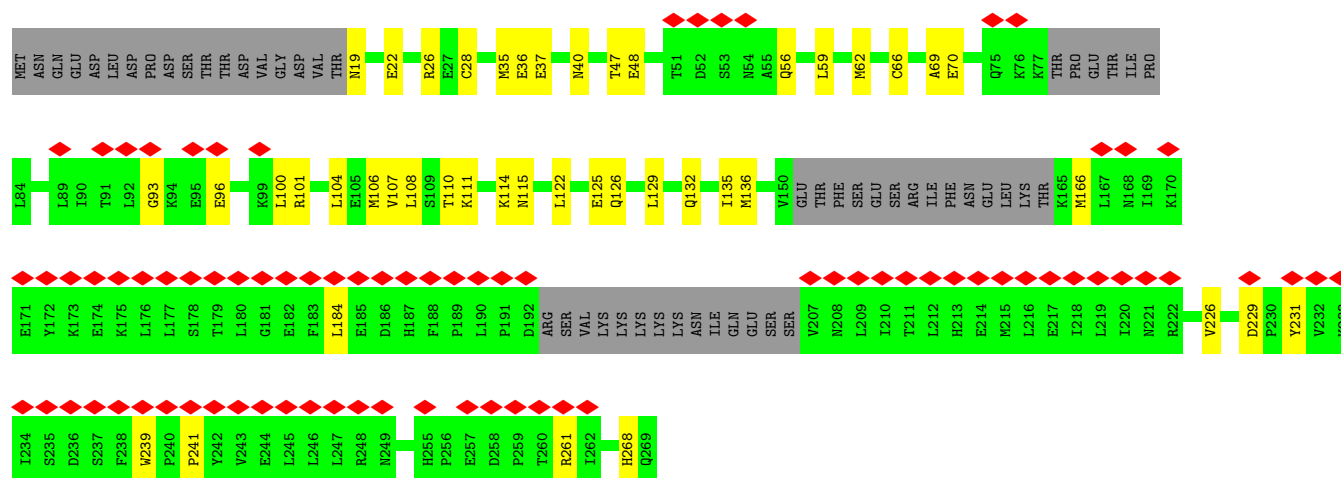


• Molecule 7: DNA (171-MER)

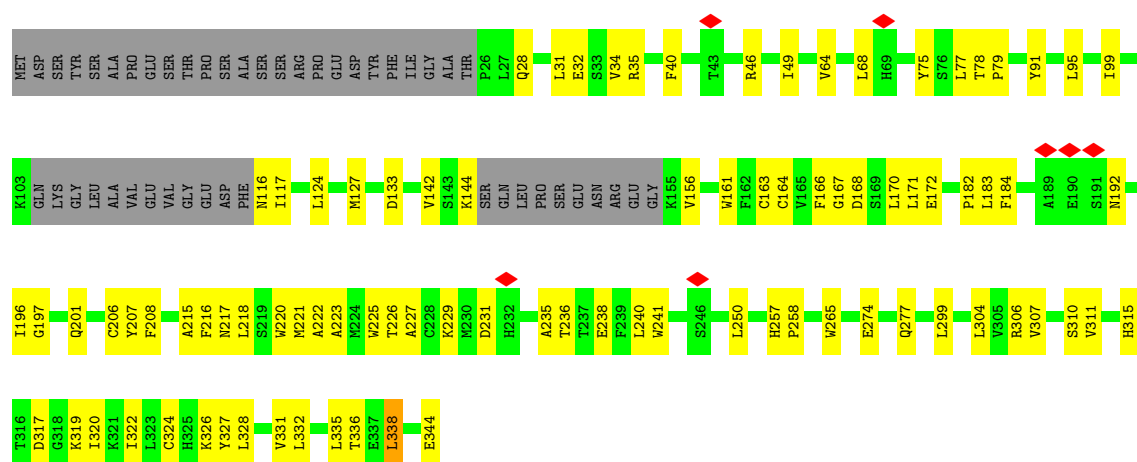




- Molecule 8: Centromere protein K

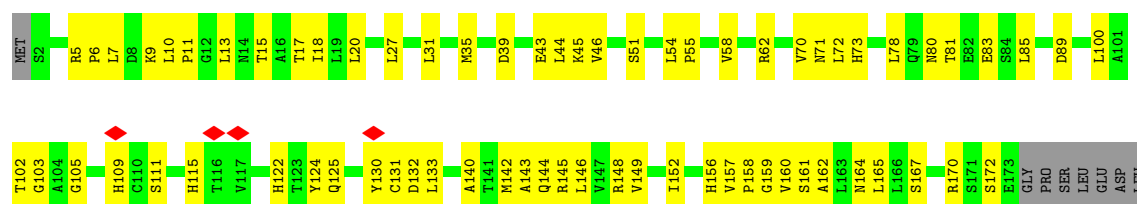


- Molecule 9: Centromere protein L



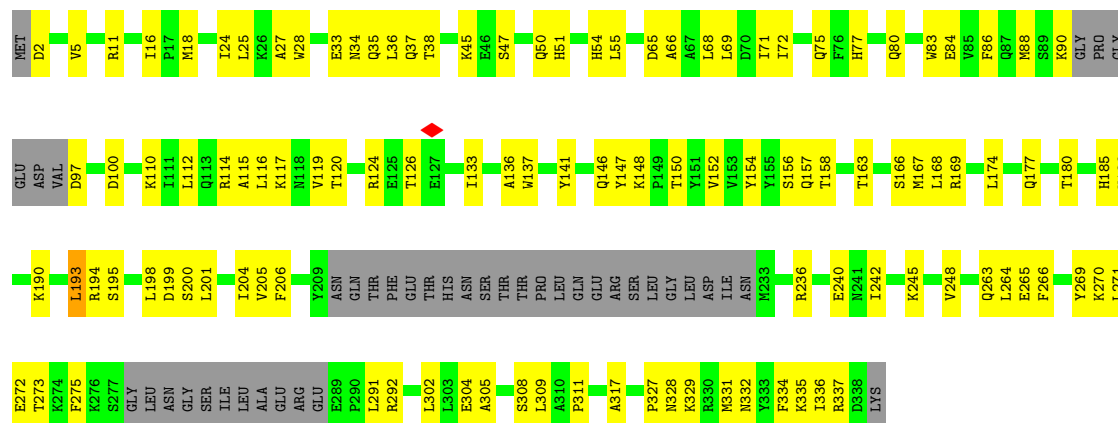
- Molecule 10: Centromere protein M





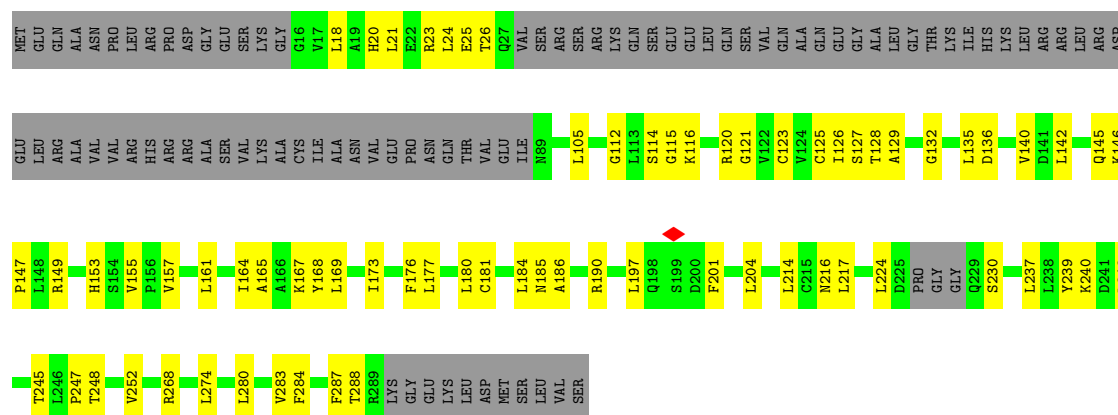
• Molecule 11: Centromere protein N

Chain N: 54% 33% 12%



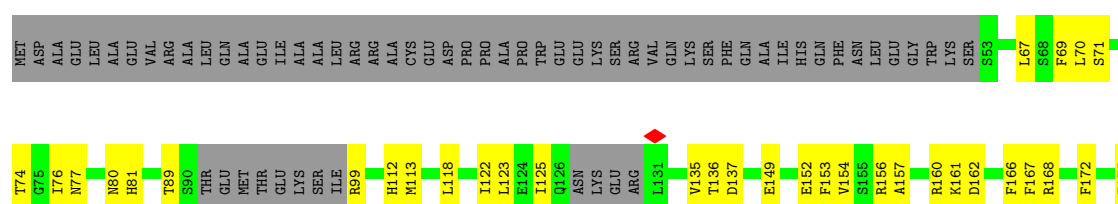
• Molecule 12: Centromere protein O

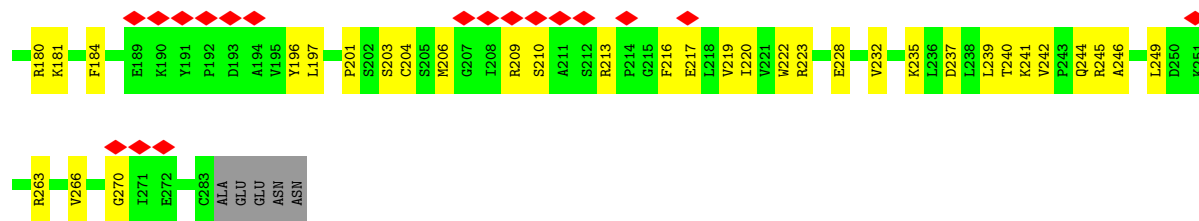
Chain O: 47% 23% 30%



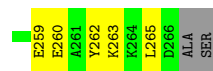
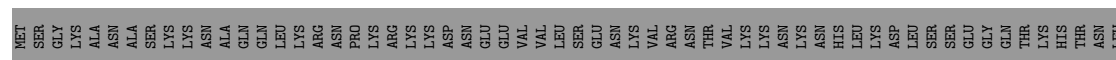
• Molecule 13: Centromere protein P

Chain P: 7% 53% 23% 24%

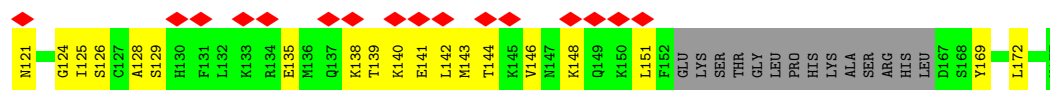
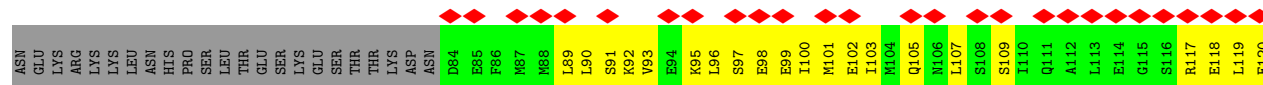
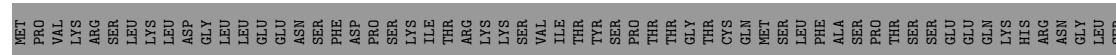




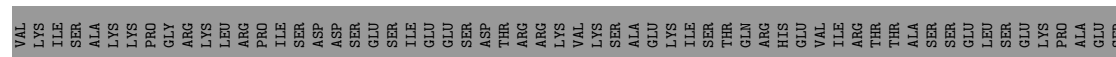
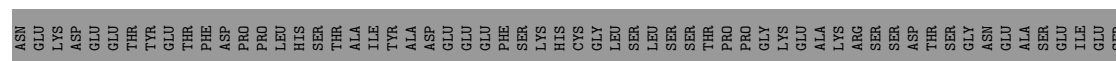
• Molecule 14: Centromere protein Q

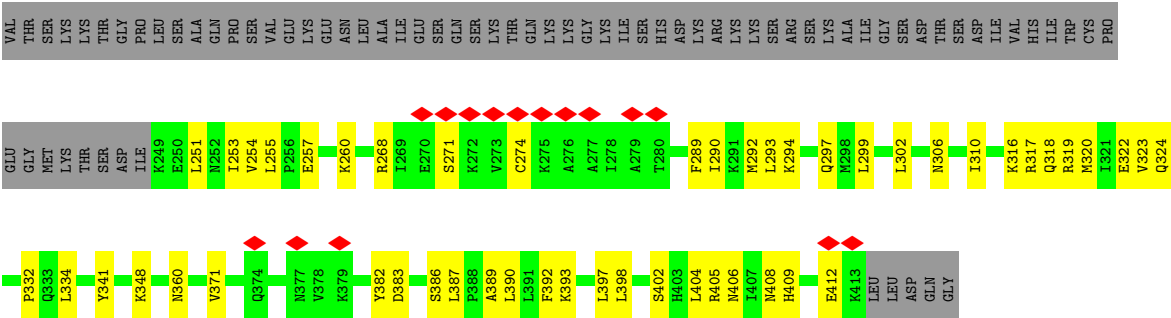


• Molecule 15: Centromere protein R

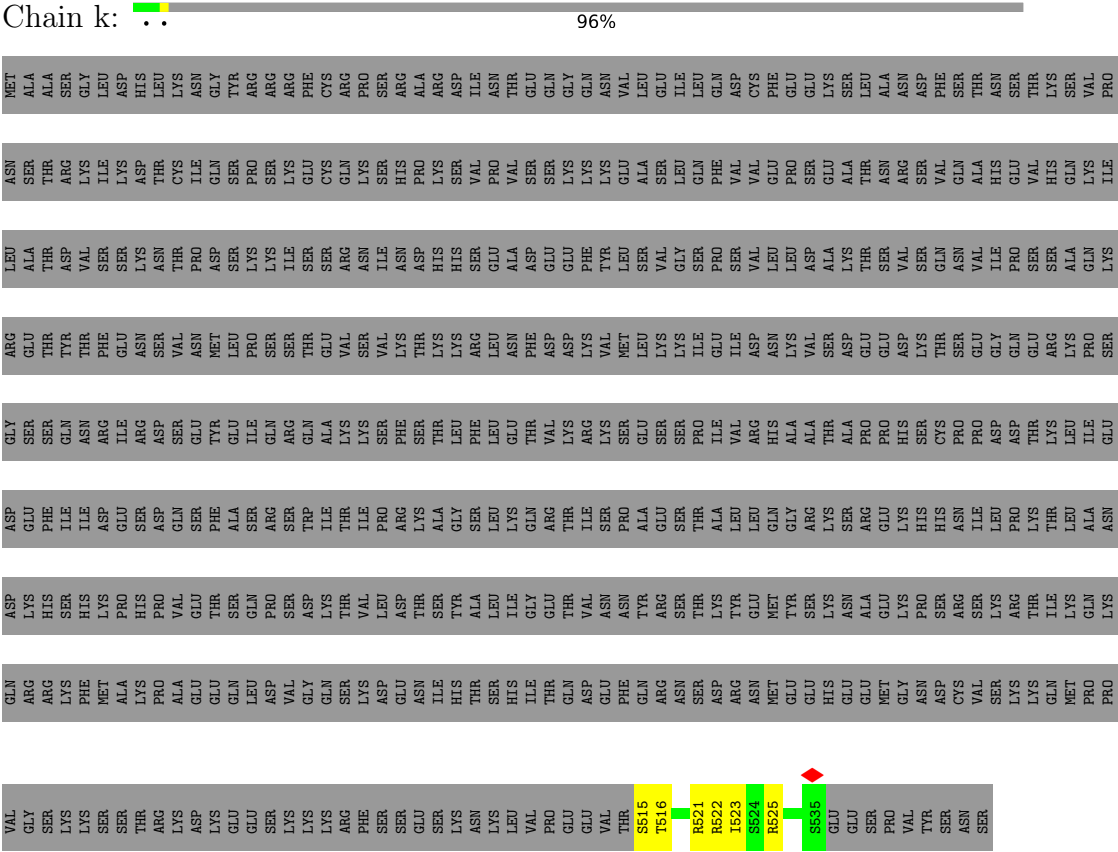


• Molecule 16: Centromere protein U

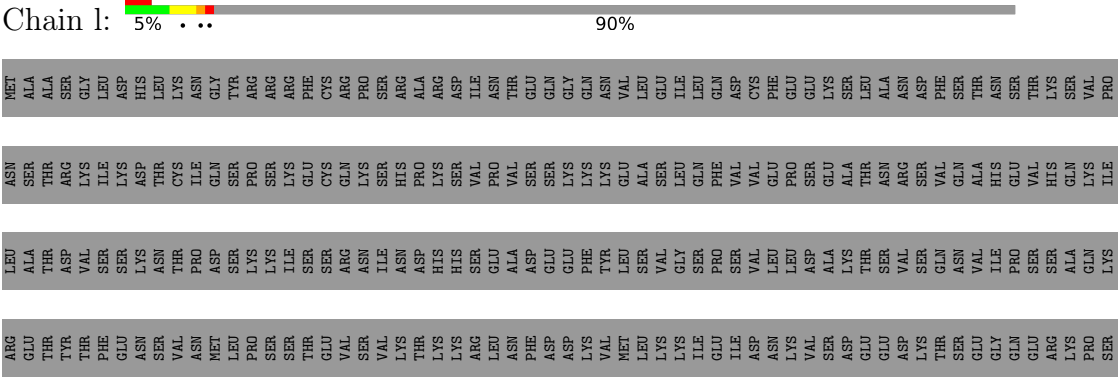




● Molecule 17: Centromere protein C



● Molecule 17: Centromere protein C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52144	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)	1200	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.745	Depositor
Minimum map value	-0.777	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.239	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	312.456, 312.456, 312.456	wwPDB
Map dimensions	188, 188, 188	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.662, 1.662, 1.662	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	0.49	0/814	0.42	0/1097
1	E	0.58	0/785	0.59	0/1057
2	B	0.56	0/629	0.65	0/843
2	F	0.51	0/648	0.56	0/868
3	C	0.47	0/764	0.51	0/1030
3	G	0.47	0/793	0.45	0/1070
4	D	0.52	0/730	0.52	0/982
4	h	0.49	0/730	0.46	0/982
5	H	0.21	0/1390	0.46	0/1856
6	I	0.16	0/4515	0.36	1/6118 (0.0%)
7	J	0.43	1/3512 (0.0%)	0.76	20/5418 (0.4%)
8	K	0.24	0/1820	0.36	0/2450
9	L	0.18	0/2462	0.39	0/3340
10	M	0.15	0/1347	0.41	0/1827
11	N	0.30	1/2505 (0.0%)	0.51	1/3380 (0.0%)
12	O	0.15	0/1678	0.41	0/2280
13	P	0.25	0/1763	0.47	0/2377
14	Q	0.22	0/1518	0.47	0/2036
15	R	0.13	0/653	0.41	0/865
16	U	0.15	0/1364	0.40	0/1831
17	k	0.68	0/182	0.86	0/245
17	l	1.30	10/481 (2.1%)	1.97	18/641 (2.8%)
18	i	0.37	1/3502 (0.0%)	0.69	7/5403 (0.1%)
All	All	0.36	13/34585 (0.0%)	0.57	47/47996 (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
7	J	0	1
17	l	0	13

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	14

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	l	301	ASP	C-N	11.45	1.51	1.33
17	l	300	GLU	C-N	10.15	1.48	1.33
17	l	296	THR	C-N	9.88	1.47	1.33
17	l	299	ILE	C-N	9.09	1.46	1.33
7	J	54	DA	O3'-P	-8.65	1.48	1.61

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	l	274	SER	O-C-N	-19.42	95.61	121.83
17	l	258	ALA	O-C-N	-18.01	98.64	122.59
17	l	256	ARG	O-C-N	-16.50	96.60	123.00
17	l	257	GLN	O-C-N	-15.72	101.68	122.59
18	i	201	DA	O3'-P-O5'	-14.64	82.04	104.00

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	J	53	DA	Sidechain
17	l	256	ARG	Mainchain
17	l	257	GLN	Mainchain
17	l	258	ALA	Mainchain
17	l	259	LYS	Mainchain

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	A	799	0	823	10	0
1	E	770	0	807	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	622	0	660	7	0
2	F	641	0	684	11	0
3	C	755	0	800	16	0
3	G	784	0	815	11	0
4	D	719	0	738	10	0
4	h	719	0	738	9	0
5	H	1384	0	1447	51	0
6	I	4402	0	4398	136	0
7	J	3133	0	1734	167	0
8	K	1793	0	1795	41	0
9	L	2397	0	2395	68	0
10	M	1325	0	1370	57	0
11	N	2452	0	2481	122	0
12	O	1642	0	1616	63	0
13	P	1732	0	1715	52	0
14	Q	1506	0	1561	78	0
15	R	649	0	673	103	0
16	U	1346	0	1367	82	0
17	k	178	0	185	5	0
17	l	476	0	483	16	0
18	i	3120	0	1718	131	0
All	All	33344	0	31003	970	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 15.

The worst 5 of 970 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)
6:I:259:LYS:CD	6:I:312:VAL:HG12	1.29	1.55
14:Q:254:MET:HE1	15:R:93:VAL:CG1	1.13	1.55
15:R:151:LEU:HG	16:U:412:GLU:CB	1.11	1.54
14:Q:250:GLN:CB	15:R:96:LEU:HD21	1.38	1.53
6:I:259:LYS:HD3	6:I:312:VAL:CG1	1.34	1.53

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	97/140 (69%)	95 (98%)	2 (2%)	0	100	100
1	E	92/140 (66%)	88 (96%)	4 (4%)	0	100	100
2	B	76/103 (74%)	75 (99%)	1 (1%)	0	100	100
2	F	78/103 (76%)	76 (97%)	2 (3%)	0	100	100
3	C	96/130 (74%)	92 (96%)	4 (4%)	0	100	100
3	G	101/130 (78%)	97 (96%)	4 (4%)	0	100	100
4	D	90/126 (71%)	86 (96%)	4 (4%)	0	100	100
4	h	90/126 (71%)	88 (98%)	2 (2%)	0	100	100
5	H	163/247 (66%)	161 (99%)	2 (1%)	0	100	100
6	I	525/756 (69%)	505 (96%)	19 (4%)	1 (0%)	43	78
8	K	209/269 (78%)	205 (98%)	4 (2%)	0	100	100
9	L	291/344 (85%)	282 (97%)	9 (3%)	0	100	100
10	M	170/180 (94%)	166 (98%)	4 (2%)	0	100	100
11	N	289/339 (85%)	277 (96%)	12 (4%)	0	100	100
12	O	204/300 (68%)	196 (96%)	8 (4%)	0	100	100
13	P	213/288 (74%)	209 (98%)	4 (2%)	0	100	100
14	Q	185/268 (69%)	179 (97%)	6 (3%)	0	100	100
15	R	76/177 (43%)	72 (95%)	4 (5%)	0	100	100
16	U	163/418 (39%)	162 (99%)	1 (1%)	0	100	100
17	k	19/544 (4%)	14 (74%)	5 (26%)	0	100	100
17	l	51/544 (9%)	44 (86%)	3 (6%)	4 (8%)	1	10
All	All	3278/5672 (58%)	3169 (97%)	104 (3%)	5 (0%)	44	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	l	257	GLN
17	l	258	ALA
17	l	259	LYS
17	l	273	LYS
6	I	78	ILE

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	80/118 (68%)	80 (100%)	0	100	100
1	E	79/118 (67%)	78 (99%)	1 (1%)	61	74
2	B	64/79 (81%)	64 (100%)	0	100	100
2	F	66/79 (84%)	66 (100%)	0	100	100
3	C	76/99 (77%)	76 (100%)	0	100	100
3	G	77/99 (78%)	77 (100%)	0	100	100
4	D	79/106 (74%)	78 (99%)	1 (1%)	61	74
4	h	79/106 (74%)	79 (100%)	0	100	100
5	H	156/224 (70%)	156 (100%)	0	100	100
6	I	490/691 (71%)	489 (100%)	1 (0%)	87	87
8	K	205/260 (79%)	205 (100%)	0	100	100
9	L	267/306 (87%)	266 (100%)	1 (0%)	84	84
10	M	151/158 (96%)	151 (100%)	0	100	100
11	N	270/311 (87%)	268 (99%)	2 (1%)	76	81
12	O	177/263 (67%)	177 (100%)	0	100	100
13	P	191/259 (74%)	190 (100%)	1 (0%)	81	83
14	Q	176/248 (71%)	176 (100%)	0	100	100
15	R	75/166 (45%)	75 (100%)	0	100	100
16	U	149/379 (39%)	149 (100%)	0	100	100
17	k	21/508 (4%)	21 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
17	l	56/508 (11%)	54 (96%)	2 (4%)	31 52
All	All	2984/5085 (59%)	2975 (100%)	9 (0%)	84 86

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	l	269	THR
17	l	296	THR
9	L	338	LEU
11	N	126	THR
11	N	193	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
12	O	133	ASN
15	R	147	ASN
12	O	172	ASN
13	P	59	GLN
4	h	63	ASN

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](#)

There are no chain breaks in this entry.

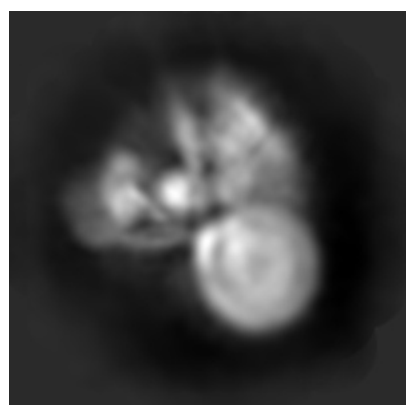
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14375. These allow visual inspection of the internal detail of the map and identification of artifacts.

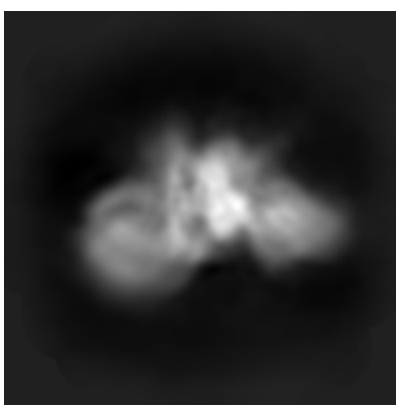
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

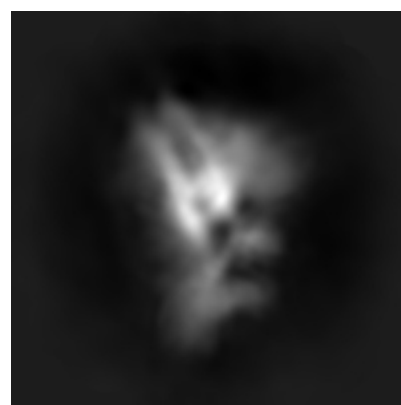
6.1.1 Primary map



X



Y

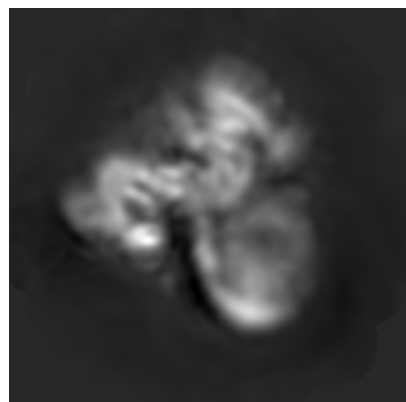


Z

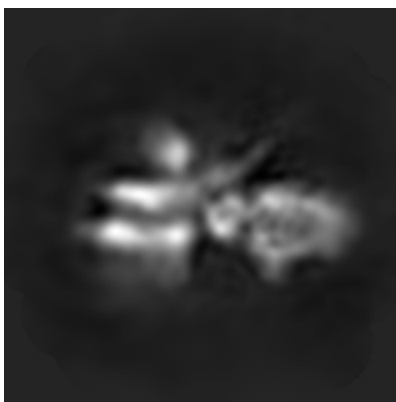
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

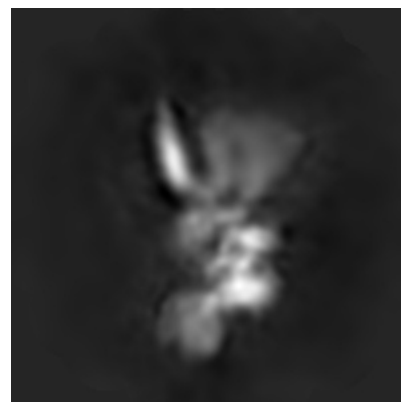
6.2.1 Primary map



X Index: 94



Y Index: 94

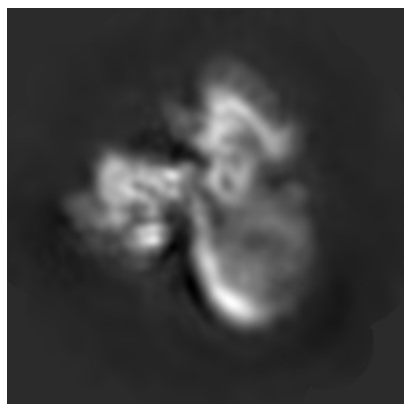


Z Index: 94

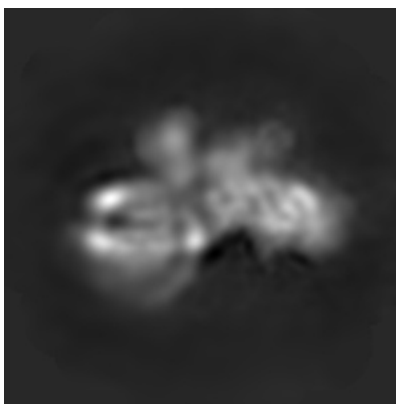
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 97



Y Index: 105

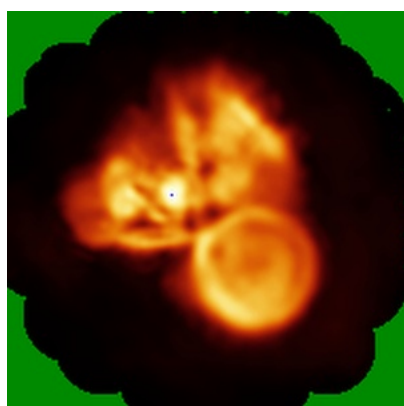


Z Index: 101

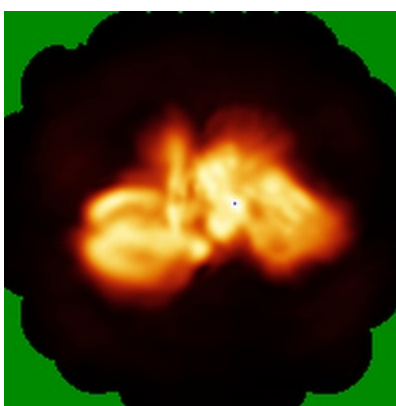
The images above show the largest variance slices of the map in three orthogonal directions.

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

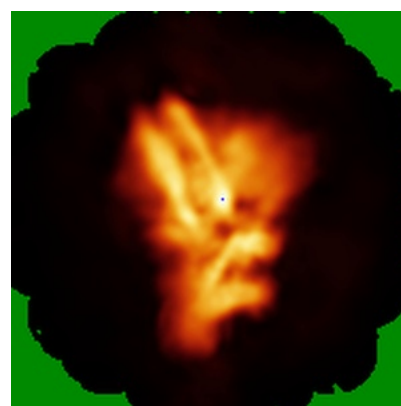
6.4.1 Primary map



X



Y

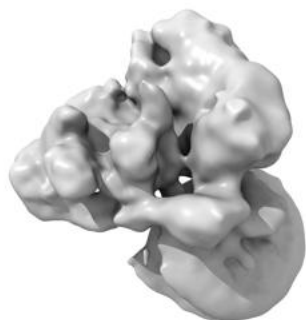


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

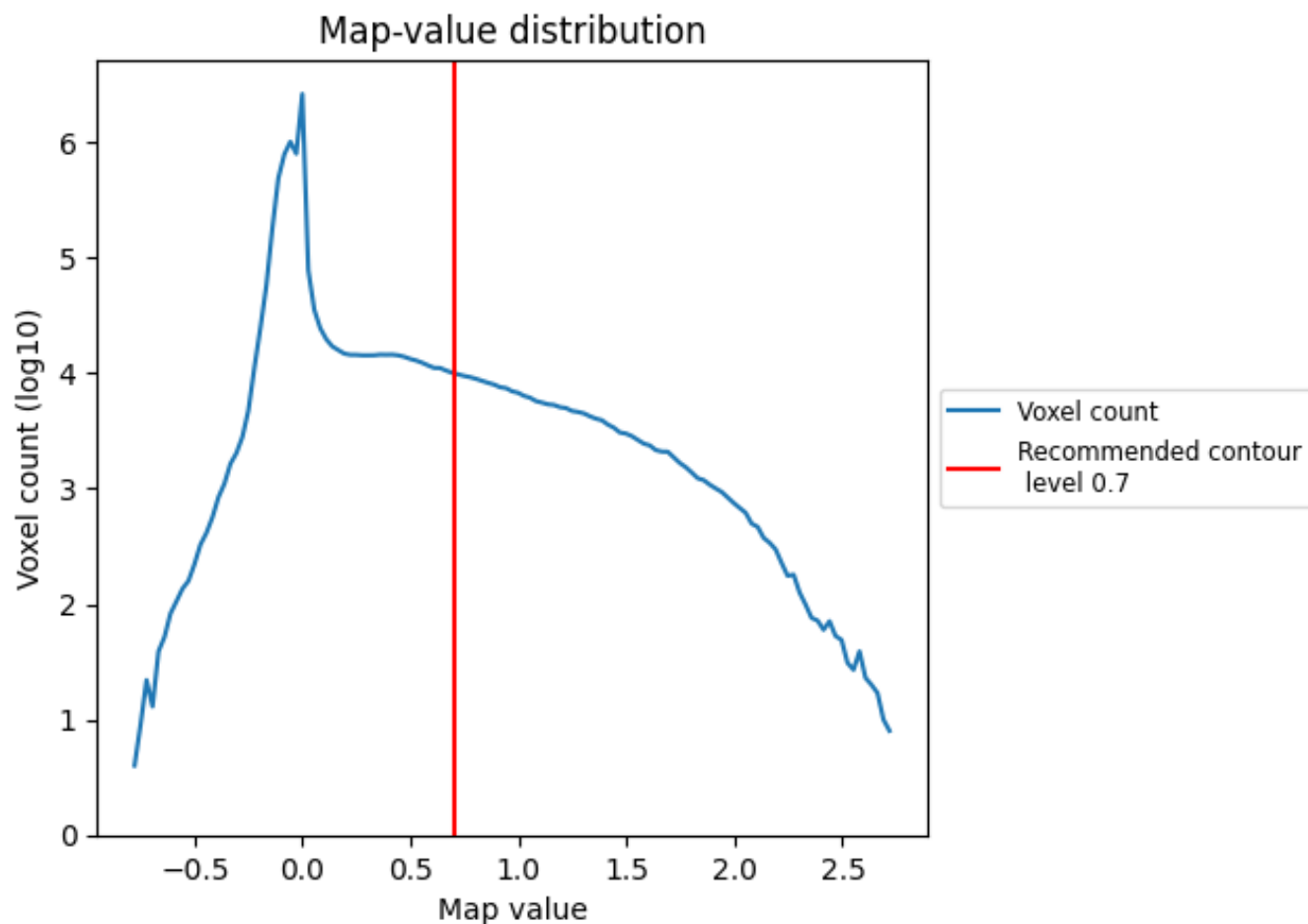
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

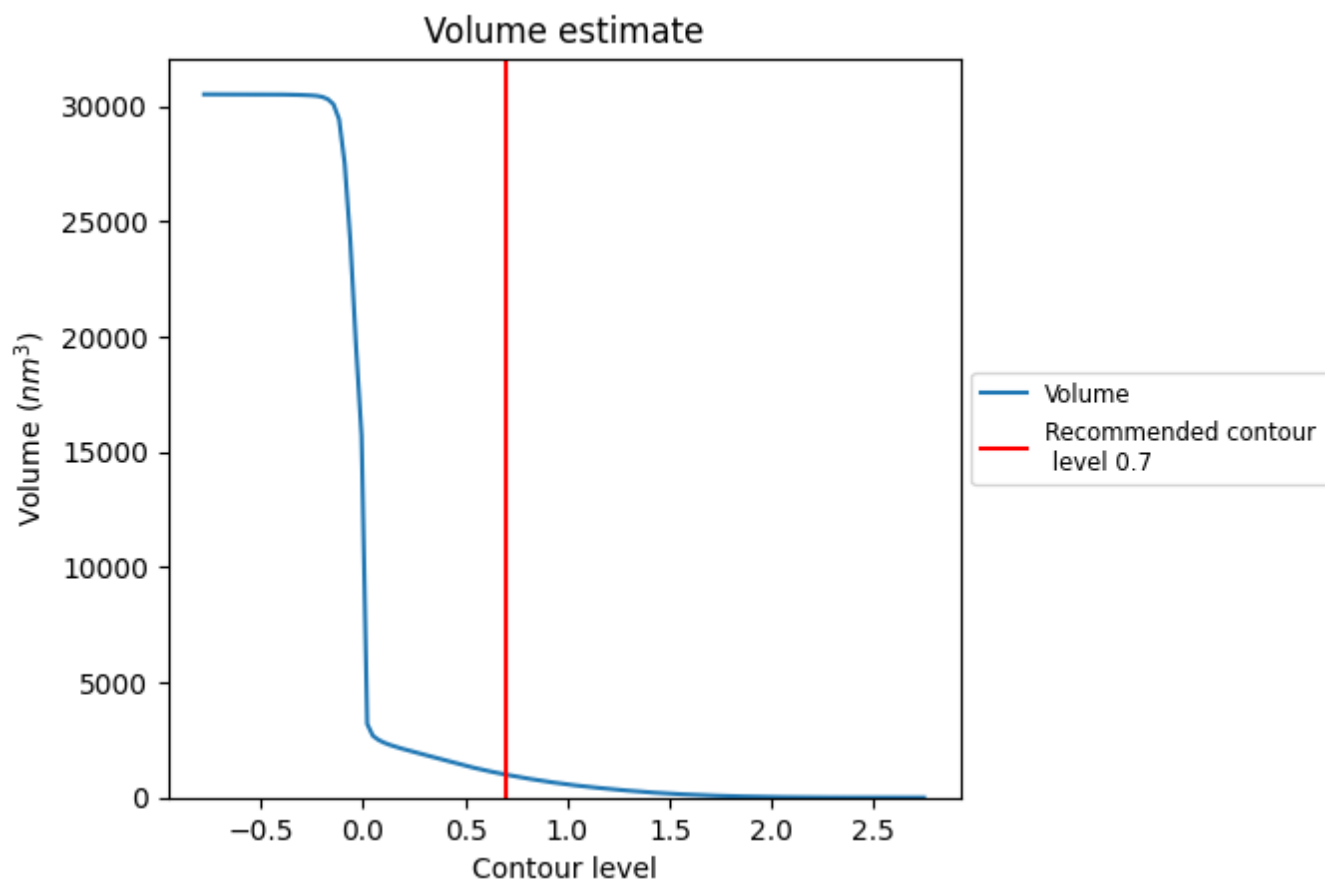
This section contains the results of statistical analysis of the map.

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.

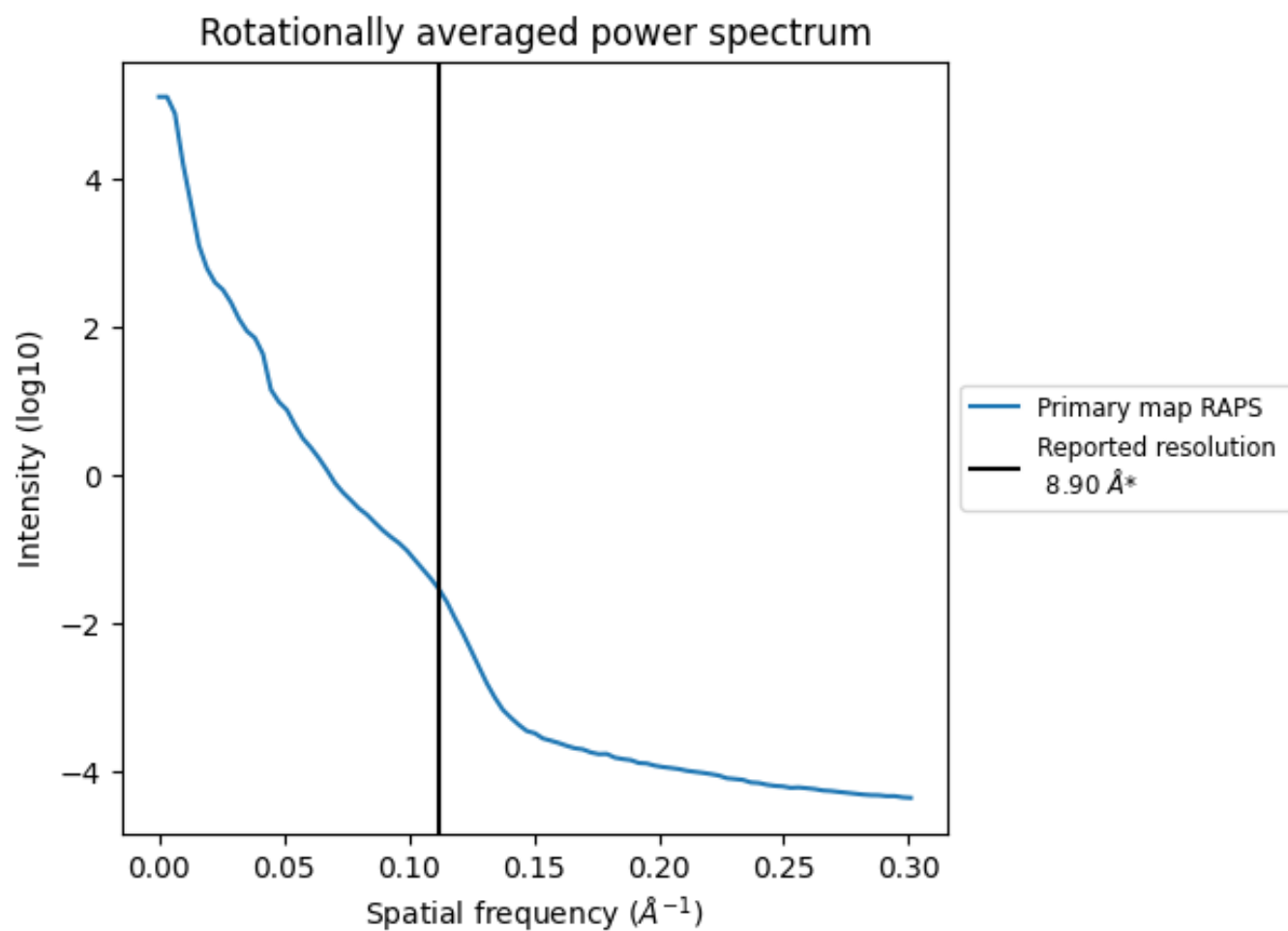
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 995 nm³; this corresponds to an approximate mass of 899 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 ⓘ

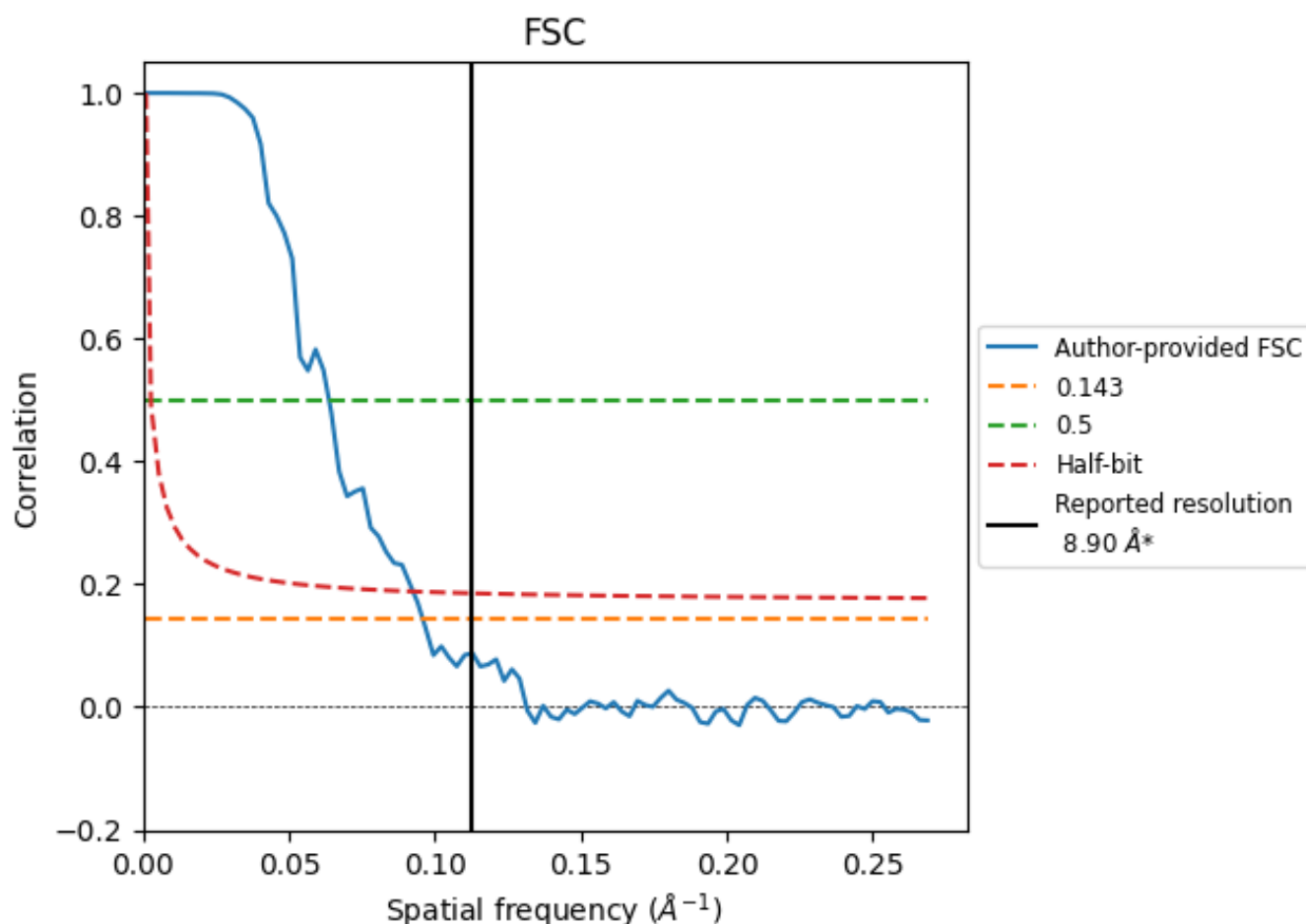


*Reported resolution corresponds to spatial frequency of 0.112 Å⁻¹

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 0.112 Å⁻¹

8.2 Resolution estimates [i](#)

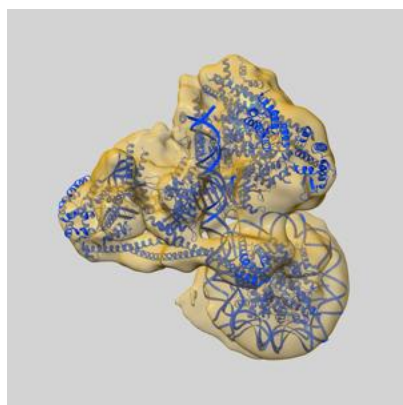
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.90	-	-
Author-provided FSC curve	10.44	15.70	10.81
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 10.44 differs from the reported value 8.9 by more than 10 %

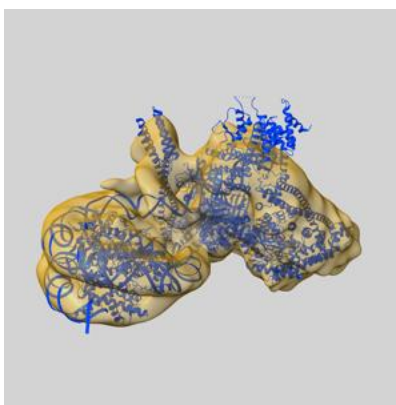
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14375 and PDB model 7YYH. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

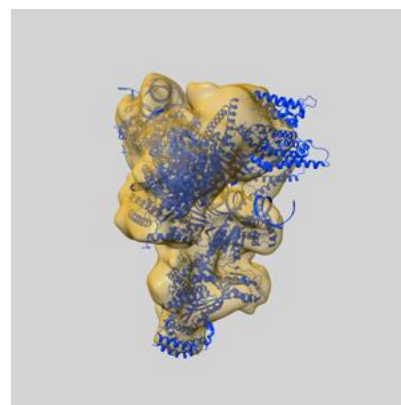
9.1 Map-model overlay [i](#)



X



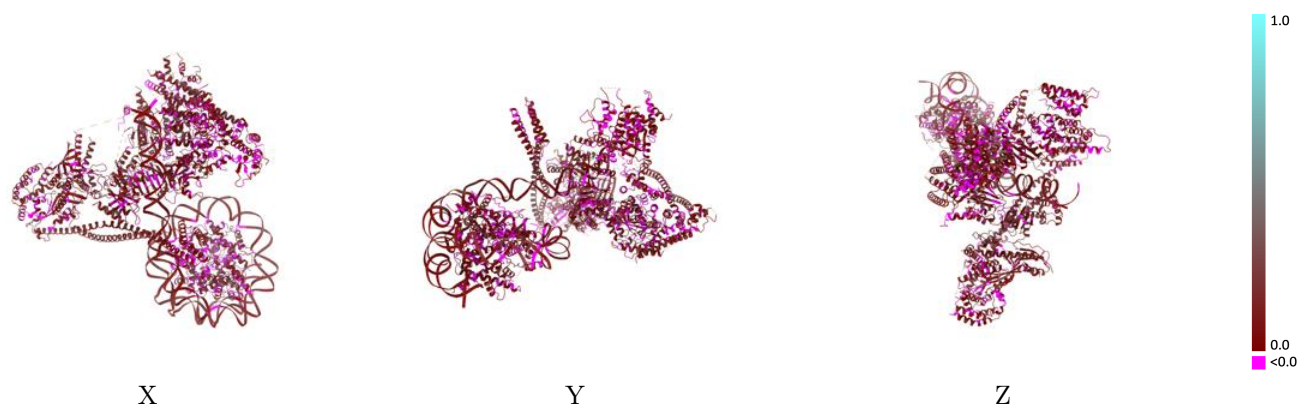
Y



Z

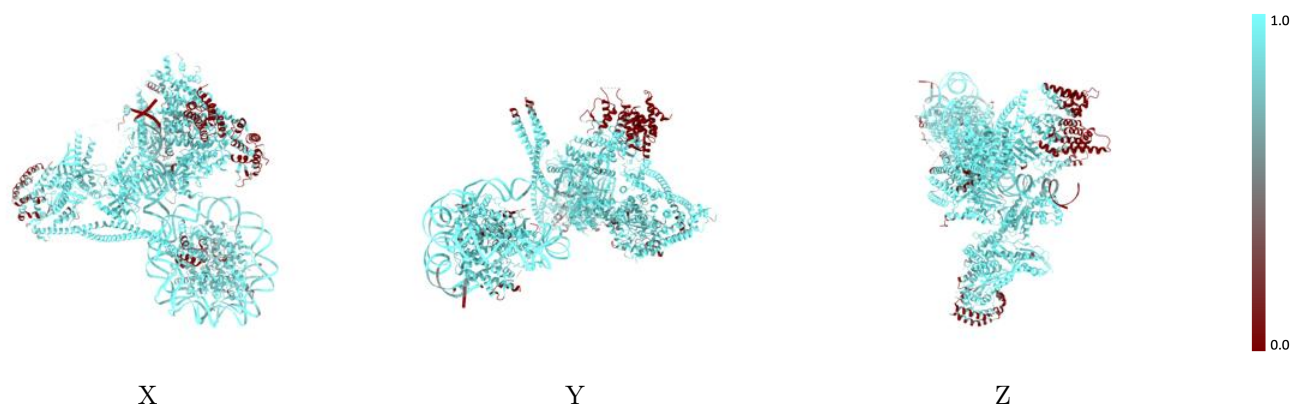
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



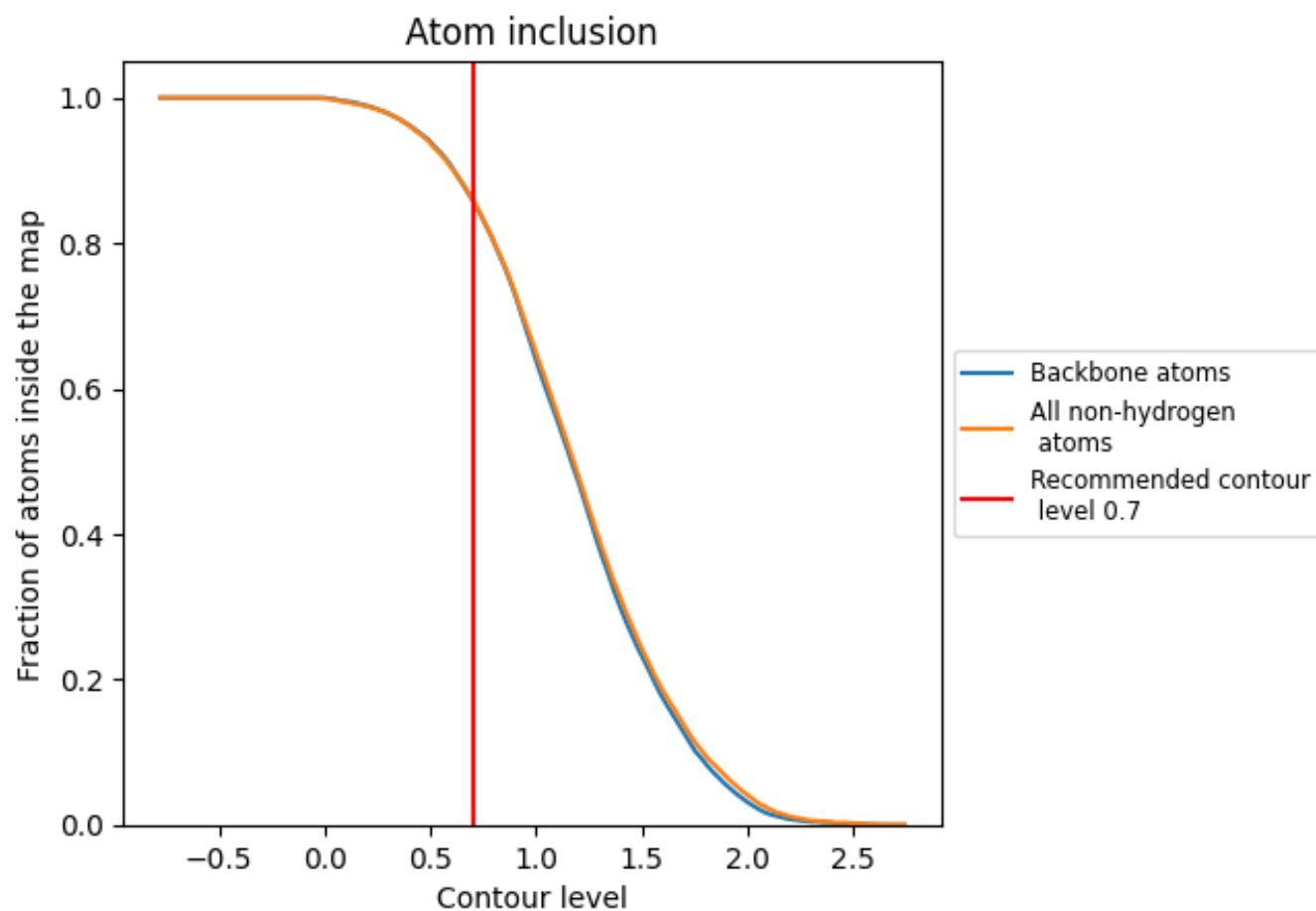
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8600	 0.0750
A	 0.8480	 0.0280
B	 0.8910	 0.0440
C	 0.8900	 0.0550
D	 0.9300	 0.0670
E	 0.9210	 0.0290
F	 0.8860	 0.0200
G	 0.8870	 0.0550
H	 0.8100	 0.0740
I	 0.7550	 0.0460
J	 0.9040	 0.1020
K	 0.6040	 0.0710
L	 0.9630	 0.0800
M	 0.9380	 0.0640
N	 0.9800	 0.0990
O	 0.9850	 0.1140
P	 0.8930	 0.0750
Q	 0.8240	 0.1050
R	 0.4320	 0.0640
U	 0.8920	 0.1080
h	 0.9130	 0.0380
i	 0.8890	 0.1000
k	 0.8810	 0.0180
l	 0.7340	 0.0260

