



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:45 PM UTC

PDB ID : 6QLD / pdb_00006qld
EMDB ID : EMD-4579
Title : Structure of inner kinetochore CCAN-Cenp-A complex
Authors : Yan, K.; Yang, J.; Zhang, Z.; McLaughlin, S.H.; Chang, L.; Fasci, D.; Heck, A.J.R.; Barford, D.
Deposited on : 2019-01-31
Resolution : 4.15 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:

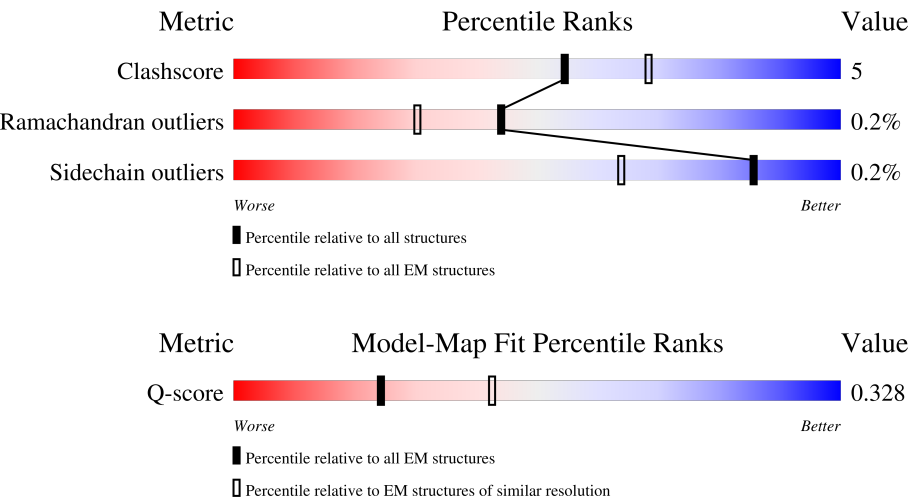
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.15 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	5475 (3.66 - 4.65)

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	C	22	86% 86%14%
2	G	124	8% 89%10%
3	H	133	8% 81%13%6%
4	I	408	6% 77%11%11%

Continued on next page...

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Mol	Chain	Length	Quality of chain
5	J	124	
6	K	122	
7	L	241	
8	N	447	
9	O	212	
10	P	270	
11	Q	231	
12	U	190	
13	Y	237	
14	Z	151	
15	a	90	
16	b	79	
16	f	79	
17	d	93	
18	e	115	
19	g	105	
20	h	94	
21	i	102	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 29086 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 Inner kinetochore subunit MIF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	C	22	Total	C	N	O	0	0
			194	127	37	30		

- Molecule 2 is a DNA chain called DNA (125-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	124	Total	C	N	O	P	0	0
			2524	1197	459	744	124		

- Molecule 3 is a protein called Inner kinetochore subunit MCM16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	125	Total	C	N	O	S	0	0
			948	607	173	167	1		

- Molecule 4 is a protein called Inner kinetochore subunit CTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	362	Total	C	N	O	S	0	0
			2701	1761	450	471	19		

- Molecule 5 is a DNA chain called DNA (125-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	124	Total	C	N	O	P	0	0
			2560	1209	483	744	124		

- Molecule 6 is a protein called Inner kinetochore subunit MCM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	106	Total	C	N	O	S	0	0
			774	491	138	142	3		

- Molecule 7 is a protein called Inner kinetochore subunit IML3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	241	Total	C	N	O	S	0	0
			1937	1242	320	364	11		

- Molecule 8 is a protein called Inner kinetochore subunit CHL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	371	Total	C	N	O	S	0	0
			2929	1906	507	504	12		

- Molecule 9 is a protein called Inner kinetochore subunit MCM21.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	205	Total	C	N	O	S	0	0
			1658	1078	271	305	4		

- Molecule 10 is a protein called Inner kinetochore subunit CTF19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	P	242	Total	C	N	O	S	0	0
			1865	1208	323	322	12		

- Molecule 11 is a protein called Inner kinetochore subunit OKP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Q	204	Total	C	N	O	S	0	0
			1421	885	261	270	5		

- Molecule 12 is a protein called Inner kinetochore subunit AME1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	U	171	Total	C	N	O	S	0	0
			1229	768	227	231	3		

- Molecule 13 is a protein called Inner kinetochore subunit NKP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Y	223	Total	C	N	O	S	0	0
			1541	965	275	296	5		

- Molecule 14 is a protein called Inner kinetochore subunit NKP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Z	140	Total	C	N	O	S	0	0
			995	632	181	181	1		

- Molecule 15 is a protein called Histone H3-like centromeric protein CSE4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	a	87	Total	C	N	O	S	0	0
			706	450	127	125	4		

- Molecule 16 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	b	79	Total	C	N	O		0	0
			625	393	120	112			
16	f	79	Total	C	N	O		0	0
			627	395	120	112			

- Molecule 17 is a protein called Histone H2B.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	d	93	Total	C	N	O	S	0	0
			719	450	127	141	1		

- Molecule 18 is a protein called Histone H3-like centromeric protein CSE4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	e	106	Total	C	N	O	S	0	0
			801	507	146	144	4		

- Molecule 19 is a protein called Histone H2A.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	g	105	Total	C	N	O		0	0
			813	511	160	142			

- Molecule 20 is a protein called Histone H2B.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	h	94	Total	C	N	O	S	0	0
			731	459	128	143	1		

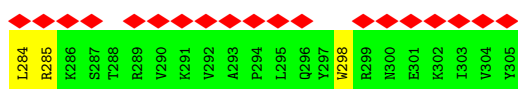
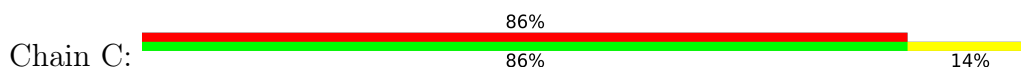
- Molecule 21 is a protein called Histone H2A.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	i	102	Total	C	N	O	0	0
			788	494	155	139		

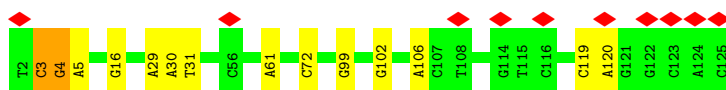
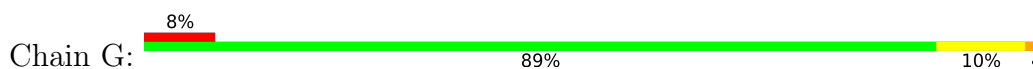
3 Residue-property plots

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.

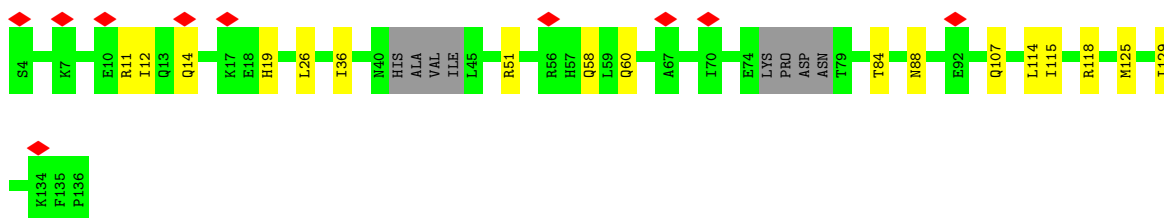
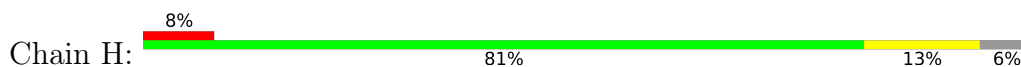
- Molecule 1: Inner kinetochore subunit MIF2



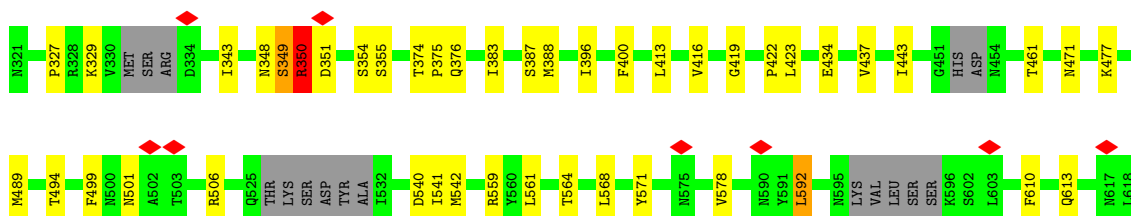
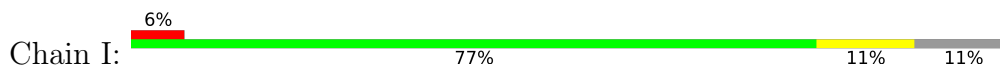
- Molecule 2: DNA (125-MER)

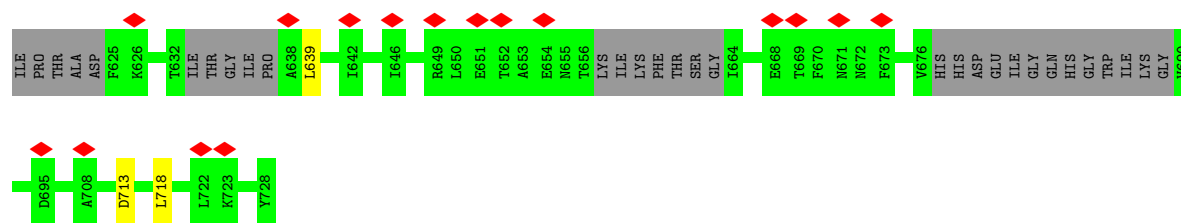


- Molecule 3: Inner kinetochore subunit MCM16

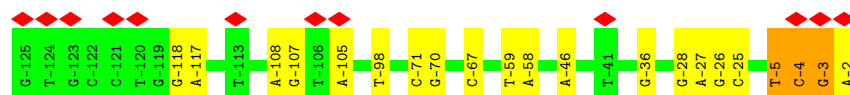
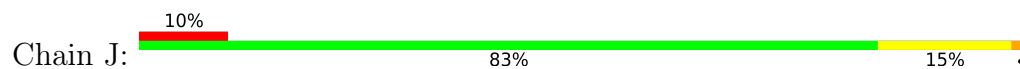


- Molecule 4: Inner kinetochore subunit CTF3

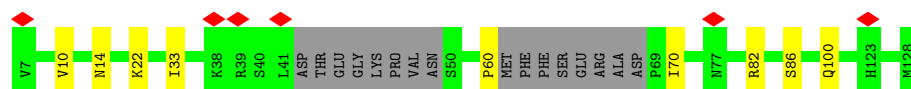
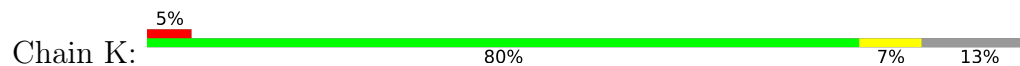




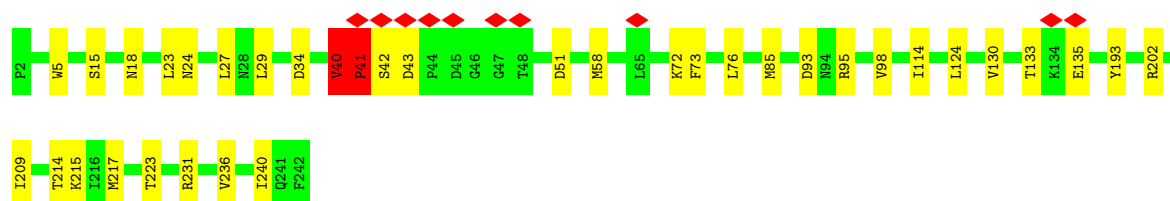
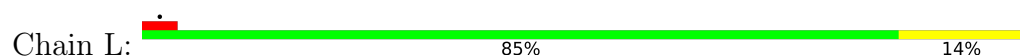
• Molecule 5: DNA (125-MER)



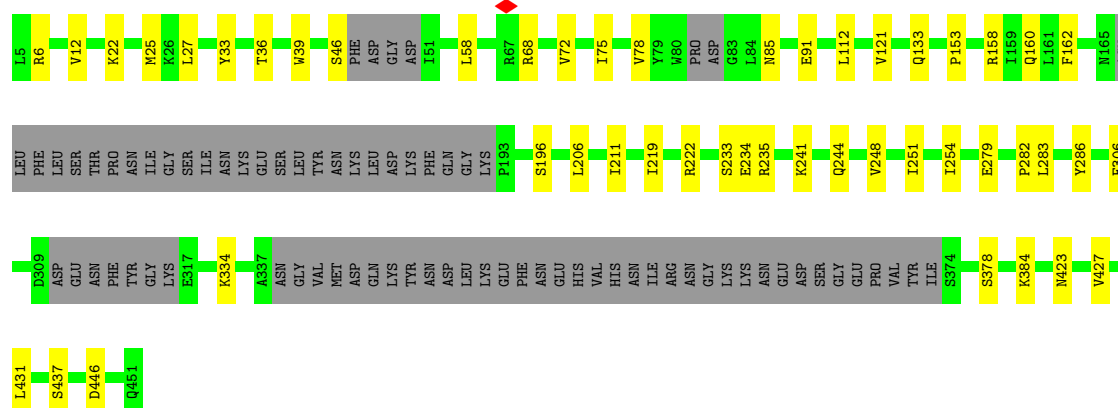
• Molecule 6: Inner kinetochore subunit MCM22



• Molecule 7: Inner kinetochore subunit IML3



• Molecule 8: Inner kinetochore subunit CHL4



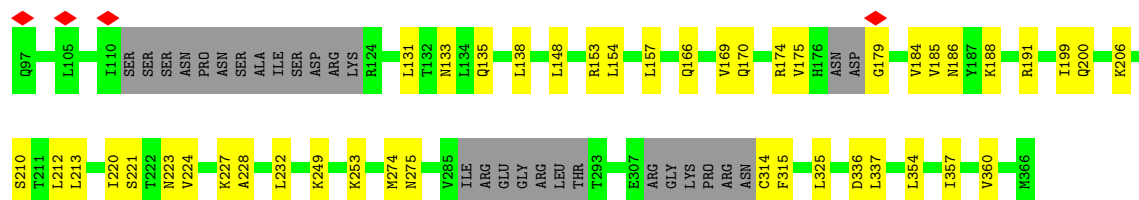
- Molecule 9: Inner kinetochore subunit MCM21

Chain O: 



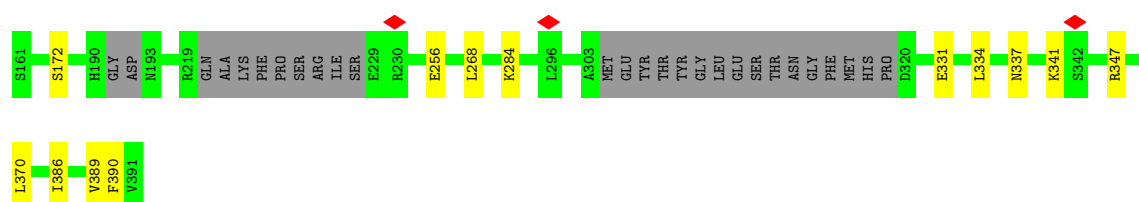
- Molecule 10: Inner kinetochore subunit CTF19

Chain P: 



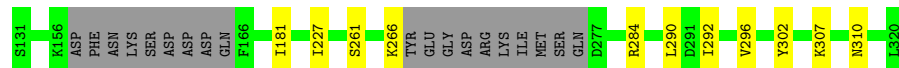
- Molecule 11: Inner kinetochore subunit OKP1

Chain Q: 



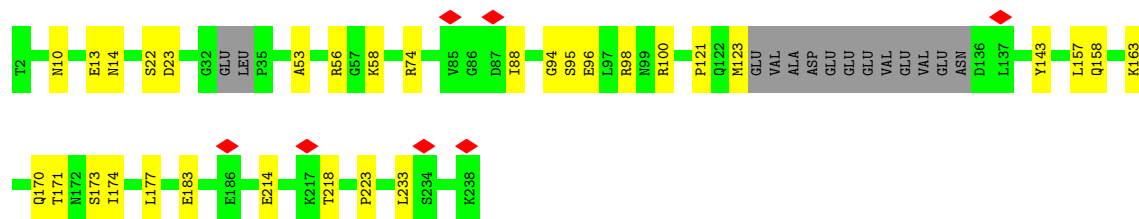
- Molecule 12: Inner kinetochore subunit AME1

Chain U: 



- Molecule 13: Inner kinetochore subunit NKP1

Chain Y: 

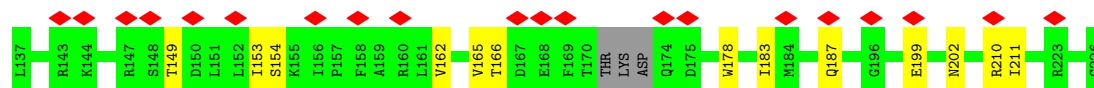
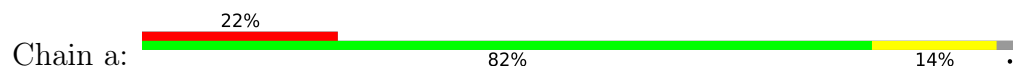


- Molecule 14: Inner kinetochore subunit NKP2

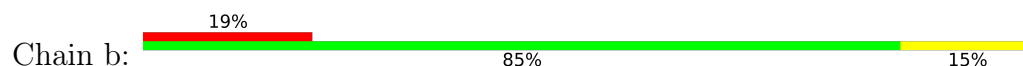
Chain Z: 



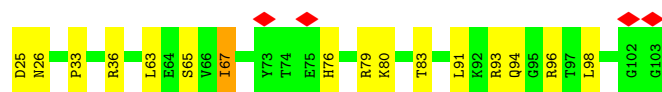
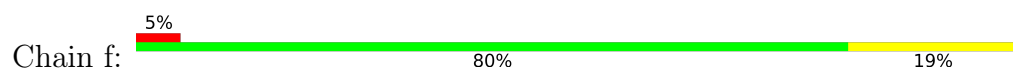
- Molecule 15: Histone H3-like centromeric protein CSE4



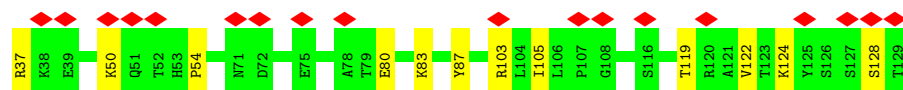
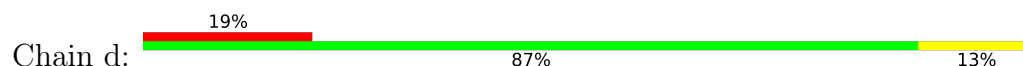
- Molecule 16: Histone H4



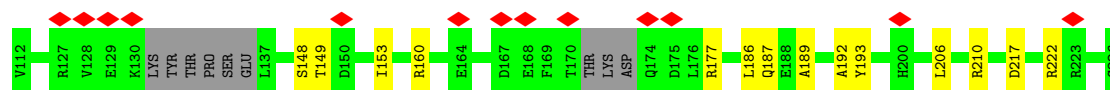
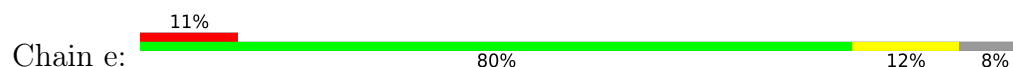
- Molecule 16: Histone H4



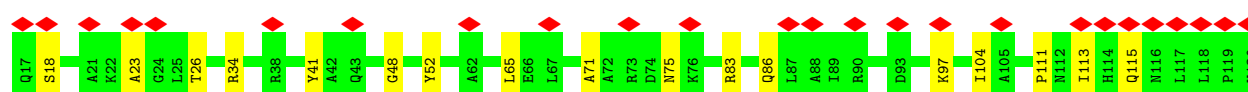
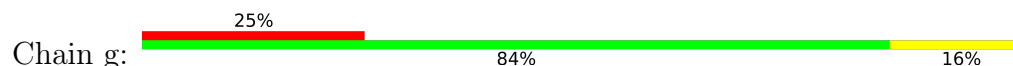
- Molecule 17: Histone H2B.2



- Molecule 18: Histone H3-like centromeric protein CSE4

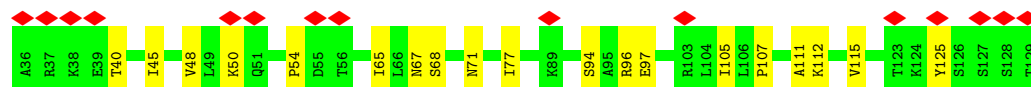
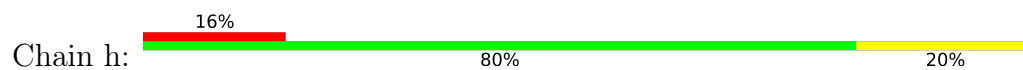


- Molecule 19: Histone H2A.1

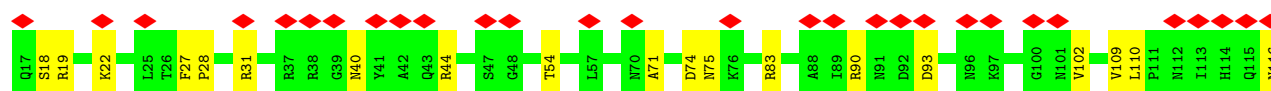
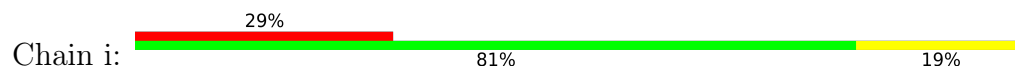




- Molecule 20: Histone H2B.1



- Molecule 21: Histone H2A.1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	145783	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 ($e^-/\text{\AA}^2$)	32	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.122	Depositor
Minimum map value	-0.069	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	348.80002, 348.80002, 348.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	C	0.19	0/198	0.54	0/266
2	G	0.29	1/2827 (0.0%)	0.57	4/4356 (0.1%)
3	H	0.18	0/956	0.49	0/1291
4	I	0.25	0/2750	0.66	6/3736 (0.2%)
5	J	0.23	0/2875	0.49	4/4440 (0.1%)
6	K	0.19	0/780	0.42	0/1055
7	L	0.25	0/1977	0.54	3/2679 (0.1%)
8	N	0.24	0/2994	0.51	0/4046
9	O	0.23	0/1689	0.47	0/2275
10	P	0.21	0/1891	0.52	0/2552
11	Q	0.19	0/1430	0.48	0/1938
12	U	0.20	0/1236	0.48	0/1676
13	Y	0.20	0/1550	0.54	0/2102
14	Z	0.16	0/1005	0.44	0/1367
15	a	0.17	0/714	0.43	0/958
16	b	0.19	0/632	0.50	0/845
16	f	0.19	0/634	0.48	0/848
17	d	0.21	0/728	0.48	0/980
18	e	0.18	0/808	0.44	0/1088
19	g	0.18	0/824	0.45	0/1113
20	h	0.17	0/741	0.40	0/998
21	i	0.20	0/798	0.49	0/1079
All	All	0.22	1/30037 (0.0%)	0.52	17/41688 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	4	DG	O3'-P	-9.91	1.46	1.61

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	4	DG	O3'-P-O5'	11.35	121.03	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	4	DG	OP1-P-O3'	-10.96	75.11	108.00
5	J	-5	DT	P-O3'-C3'	-9.03	106.66	120.20
5	J	-5	DT	O3'-P-O5'	-8.74	90.89	104.00
5	J	-3	DG	C2'-C3'-O3'	-7.76	99.86	111.50

There are no chirality outliers.

There are no planarity outliers.

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	C	194	0	209	2	0
2	G	2524	0	1390	16	0
3	H	948	0	933	16	0
4	I	2701	0	2573	32	0
5	J	2560	0	1390	24	0
6	K	774	0	748	9	0
7	L	1937	0	1942	28	0
8	N	2929	0	2964	35	0
9	O	1658	0	1665	24	0
10	P	1865	0	1855	29	0
11	Q	1421	0	1237	13	0
12	U	1229	0	1117	12	0
13	Y	1541	0	1425	20	0
14	Z	995	0	911	5	0
15	a	706	0	734	9	0
16	b	625	0	657	12	0
16	f	627	0	664	14	0
17	d	719	0	741	9	0
18	e	801	0	771	13	0
19	g	813	0	860	17	0
20	h	731	0	753	14	0
21	i	788	0	827	16	0
All	All	29086	0	26366	284	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 5.

The worst 5 of 284 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)
5:J:-117:DA:H5''	19:g:18:SER:HB2	1.17	1.09
7:L:40:VAL:HG23	7:L:51:ASP:OD1	1.75	0.86
5:J:-117:DA:C5'	19:g:18:SER:HB2	2.09	0.76
7:L:40:VAL:HB	7:L:41:PRO:HD2	1.72	0.70
3:H:125:MET:HE2	4:I:350:ARG:HH11	1.56	0.70

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	C	20/22 (91%)	17 (85%)	3 (15%)	0	100	100
3	H	119/133 (90%)	117 (98%)	2 (2%)	0	100	100
4	I	344/408 (84%)	318 (92%)	24 (7%)	2 (1%)	21	58
6	K	100/122 (82%)	100 (100%)	0	0	100	100
7	L	239/241 (99%)	218 (91%)	19 (8%)	2 (1%)	16	52
8	N	359/447 (80%)	336 (94%)	23 (6%)	0	100	100
9	O	201/212 (95%)	192 (96%)	9 (4%)	0	100	100
10	P	232/270 (86%)	218 (94%)	14 (6%)	0	100	100
11	Q	196/231 (85%)	191 (97%)	5 (3%)	0	100	100
12	U	165/190 (87%)	163 (99%)	2 (1%)	0	100	100
13	Y	217/237 (92%)	199 (92%)	17 (8%)	1 (0%)	24	61
14	Z	136/151 (90%)	134 (98%)	2 (2%)	0	100	100
15	a	83/90 (92%)	77 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	b	77/79 (98%)	74 (96%)	3 (4%)	0	100	100
16	f	77/79 (98%)	76 (99%)	1 (1%)	0	100	100
17	d	91/93 (98%)	84 (92%)	7 (8%)	0	100	100
18	e	100/115 (87%)	95 (95%)	5 (5%)	0	100	100
19	g	103/105 (98%)	101 (98%)	2 (2%)	0	100	100
20	h	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
21	i	100/102 (98%)	93 (93%)	7 (7%)	0	100	100
All	All	3051/3421 (89%)	2891 (95%)	155 (5%)	5 (0%)	44	76

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	L	41	PRO
4	I	350	ARG
7	L	42	SER
13	Y	223	PRO
4	I	327	PRO

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	C	21/21 (100%)	21 (100%)	0	100	100
3	H	94/128 (73%)	94 (100%)	0	100	100
4	I	270/380 (71%)	267 (99%)	3 (1%)	65	73
6	K	78/113 (69%)	78 (100%)	0	100	100
7	L	216/217 (100%)	214 (99%)	2 (1%)	70	75
8	N	316/408 (78%)	316 (100%)	0	100	100
9	O	185/199 (93%)	185 (100%)	0	100	100
10	P	193/255 (76%)	193 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	Q	120/221 (54%)	120 (100%)	0	100	100
12	U	111/181 (61%)	111 (100%)	0	100	100
13	Y	140/218 (64%)	140 (100%)	0	100	100
14	Z	87/141 (62%)	87 (100%)	0	100	100
15	a	74/79 (94%)	74 (100%)	0	100	100
16	b	65/66 (98%)	65 (100%)	0	100	100
16	f	66/66 (100%)	65 (98%)	1 (2%)	57	70
17	d	80/81 (99%)	80 (100%)	0	100	100
18	e	74/104 (71%)	74 (100%)	0	100	100
19	g	84/84 (100%)	84 (100%)	0	100	100
20	h	81/81 (100%)	81 (100%)	0	100	100
21	i	81/81 (100%)	81 (100%)	0	100	100
All	All	2436/3124 (78%)	2430 (100%)	6 (0%)	85	85

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	L	40	VAL
7	L	41	PRO
16	f	67	ILE
4	I	350	ARG
4	I	349	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
10	P	276	ASN
14	Z	80	GLN
12	U	196	ASN
13	Y	155	GLN
14	Z	106	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	596:LYS	C	602:SER	N	6.10

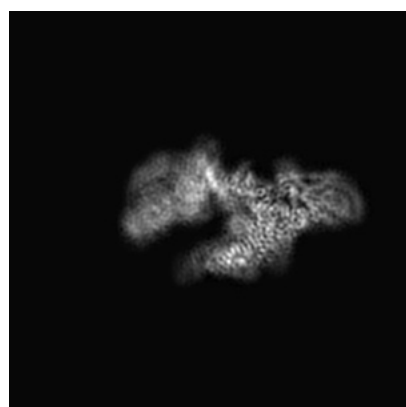
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4579. These allow visual inspection of the internal detail of the map and identification of artifacts.

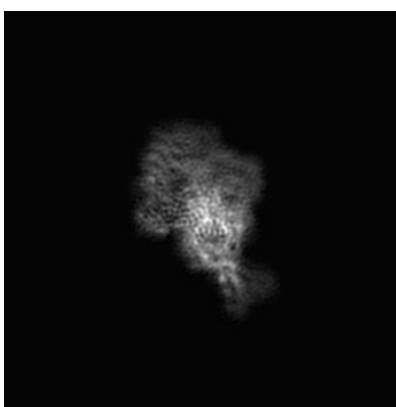
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

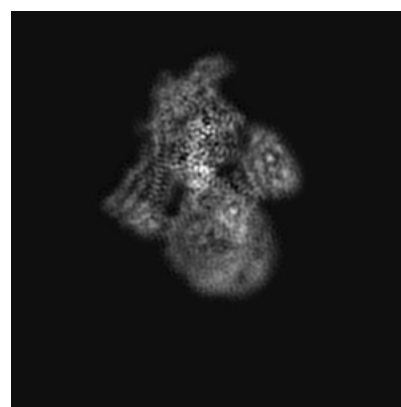
6.1.1 Primary map



X



Y

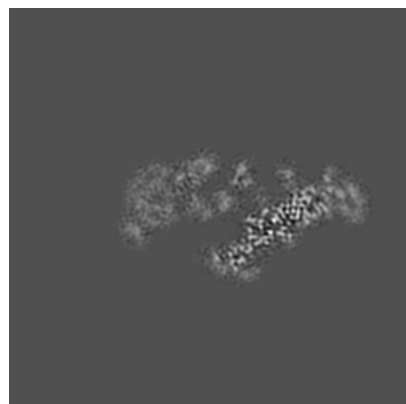


Z

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

6.2 Central slices [i](#)

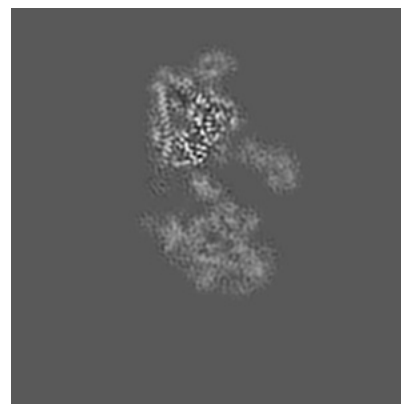
6.2.1 Primary map



X Index: 160



Y Index: 160

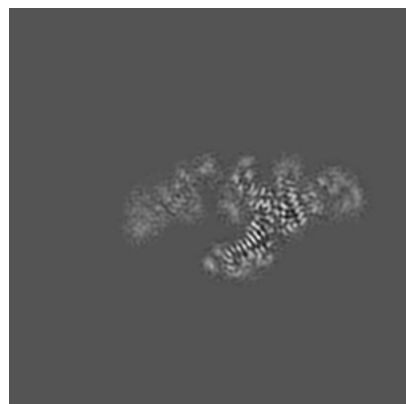


Z Index: 160

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

6.3 Largest variance slices [i](#)

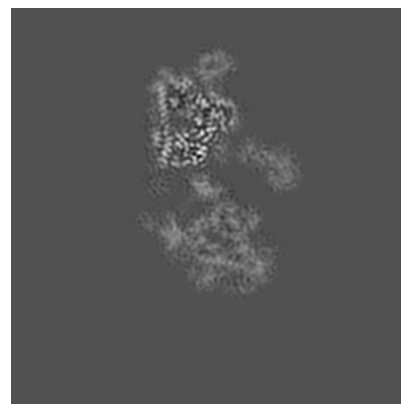
6.3.1 Primary map



X Index: 152



Y Index: 192

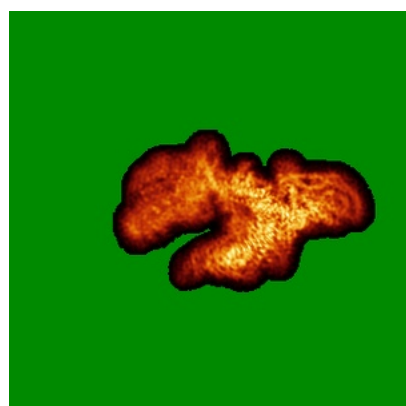


Z Index: 161

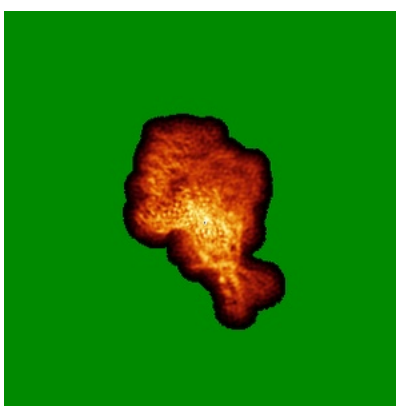
The images above show the largest variance slices of the map in three orthogonal directions.

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

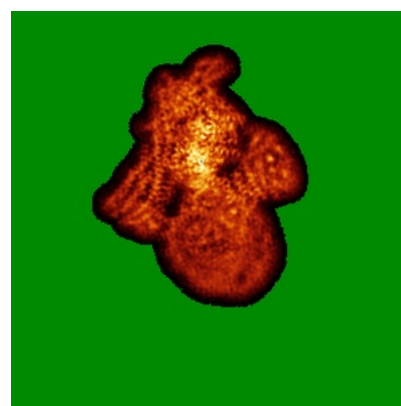
6.4.1 Primary map



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

This section was not generated.

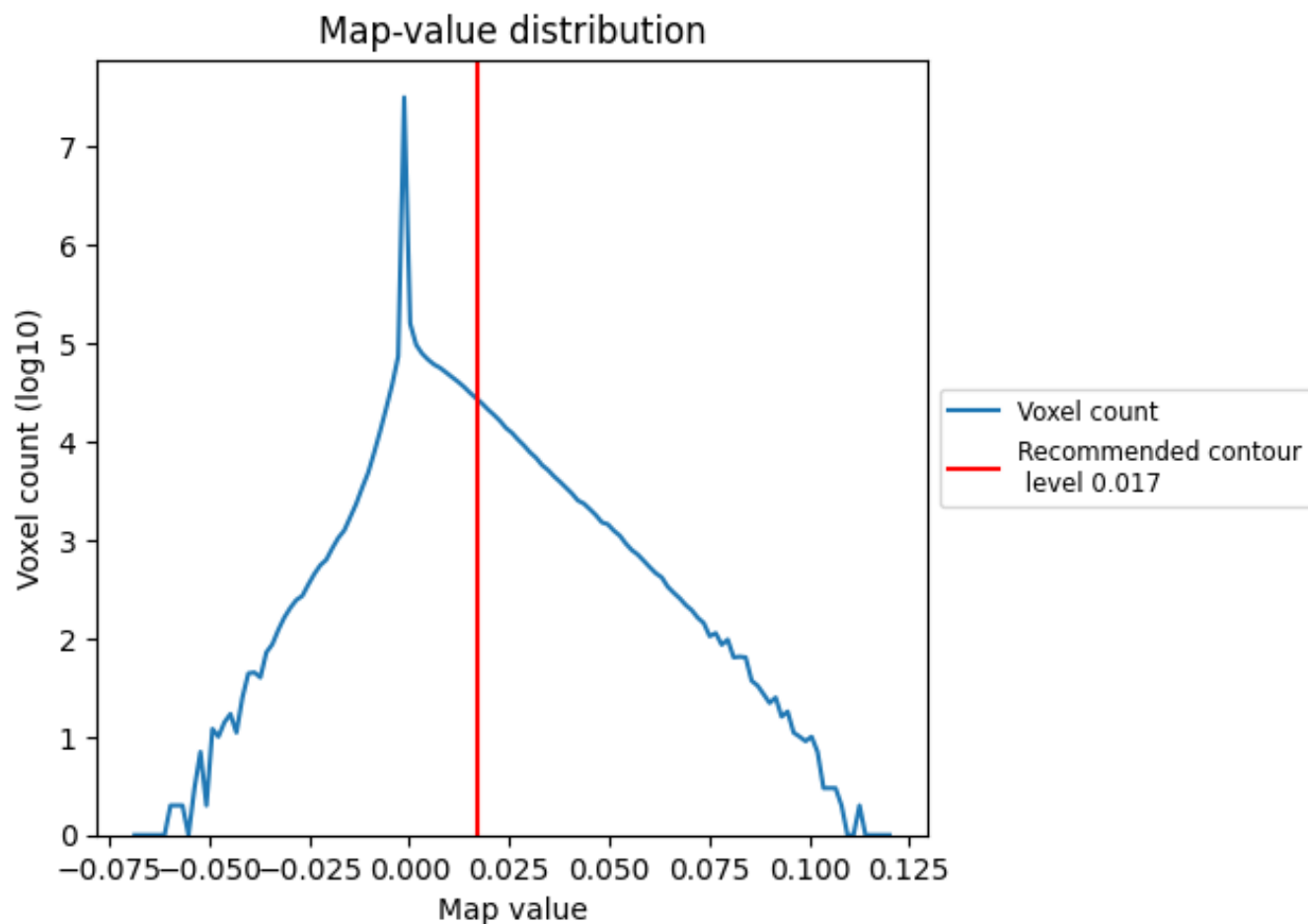
6.6 Mask visualisation

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

7 Map analysis [i](#)

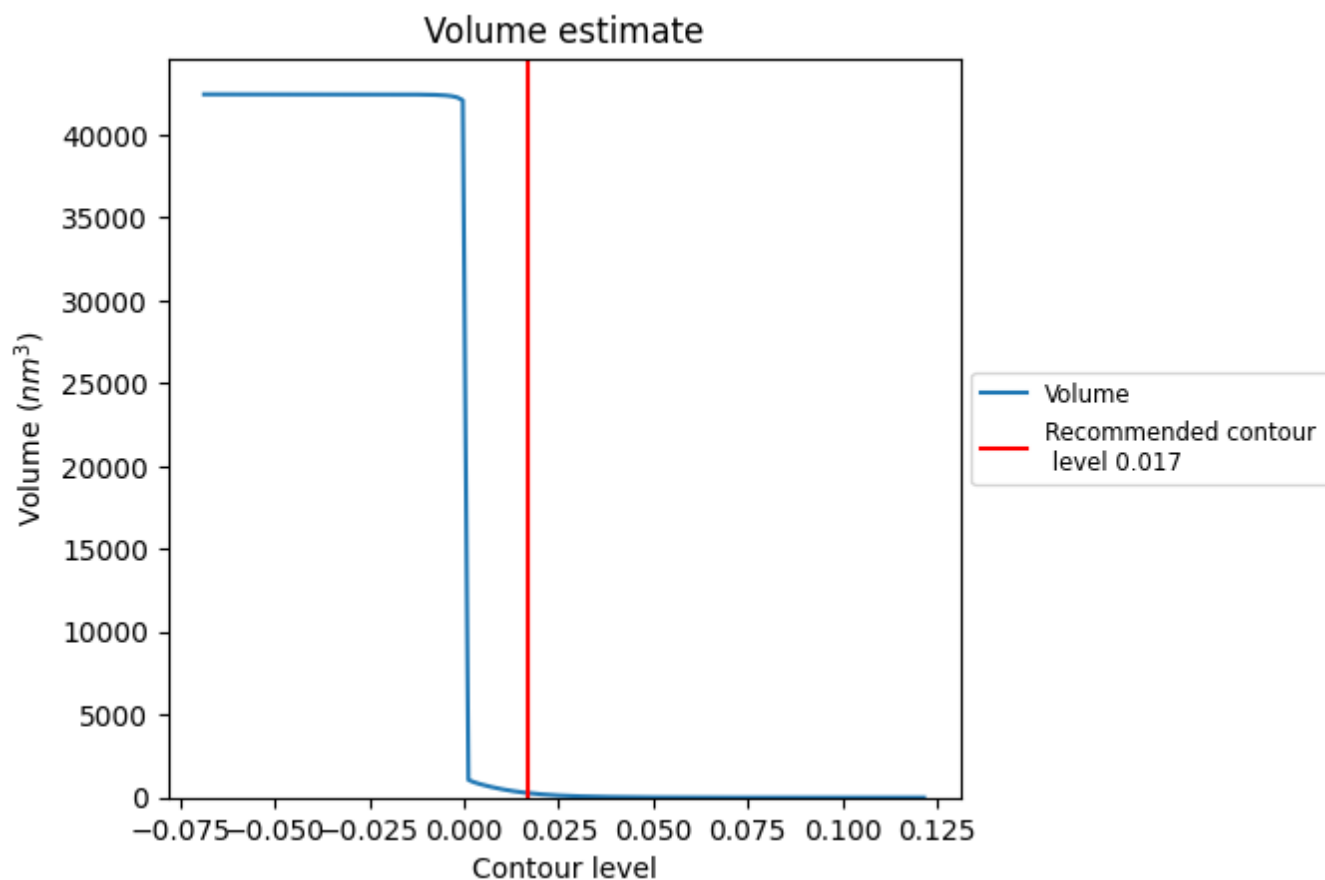
This section contains the results of statistical analysis of the map.

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.

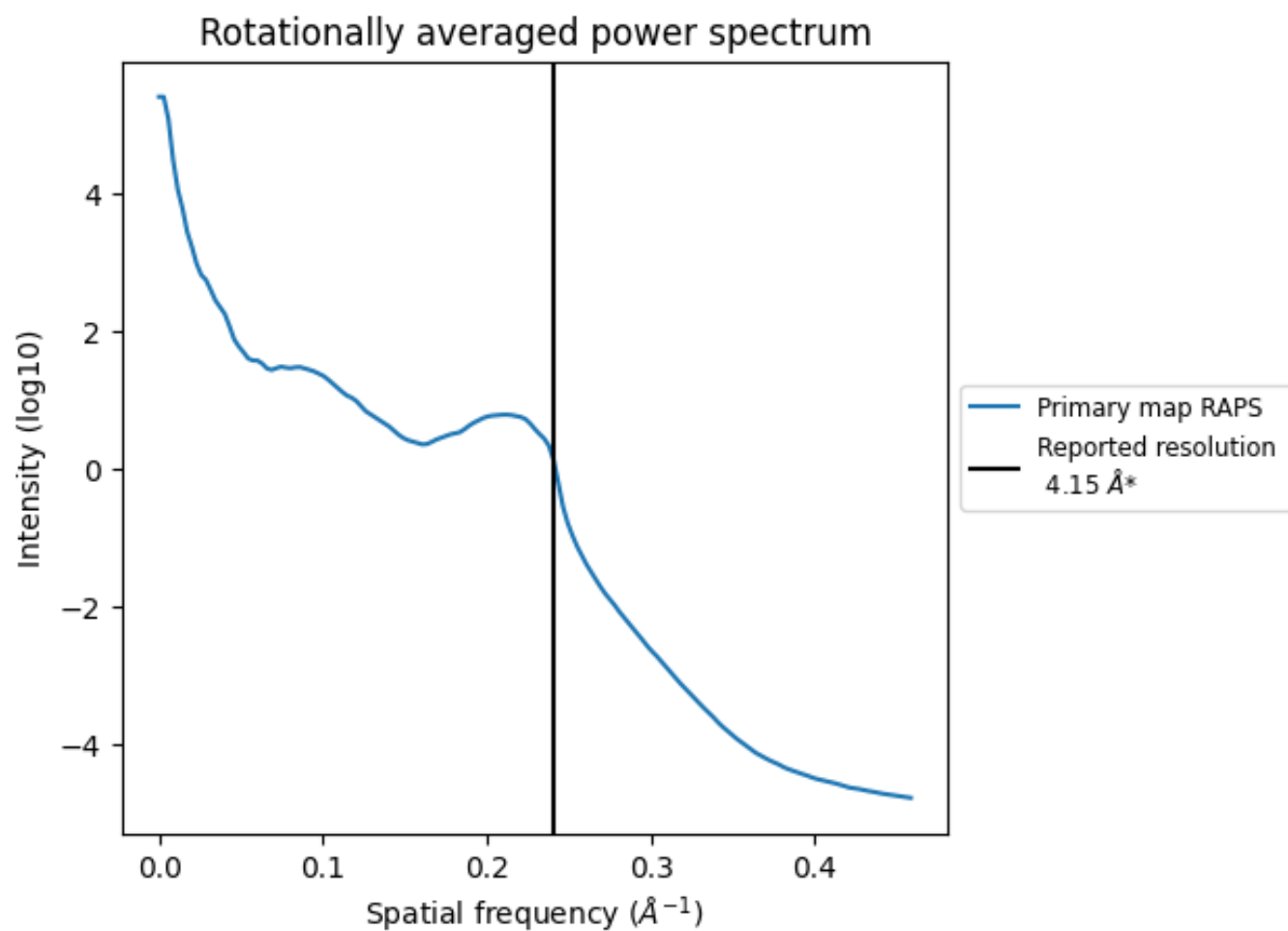
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 272 nm^3 ; this corresponds to an approximate mass of 246 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 0.241 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

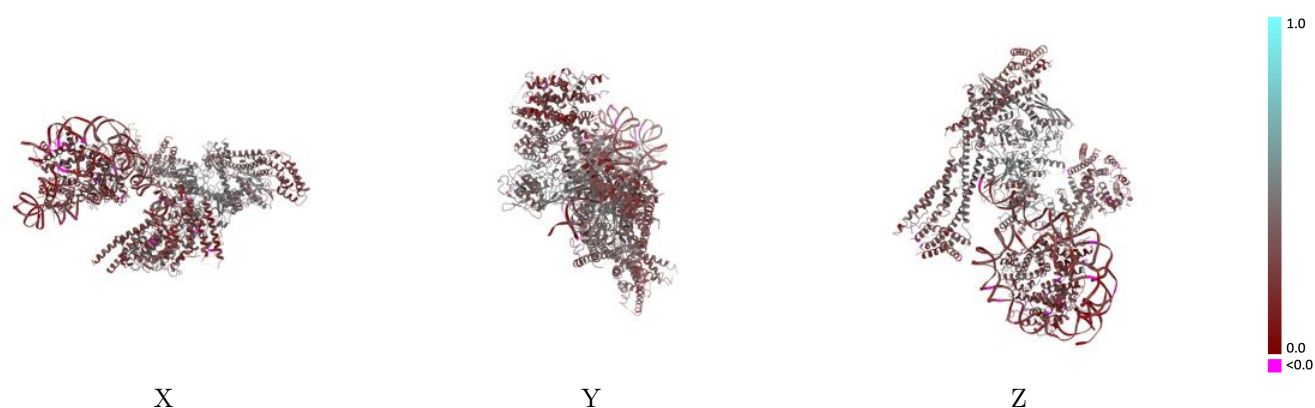
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4579 and PDB model 6QLD. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

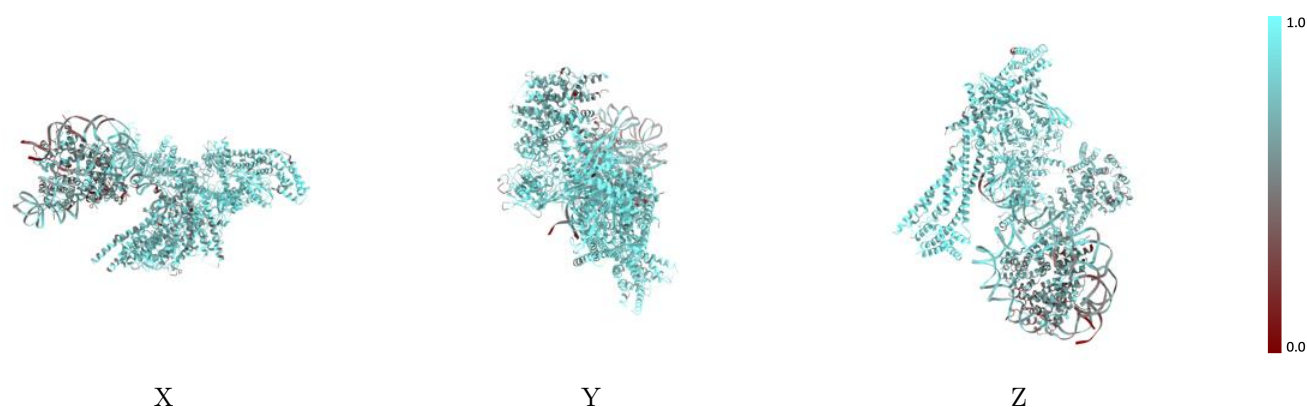
This section was not generated.

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



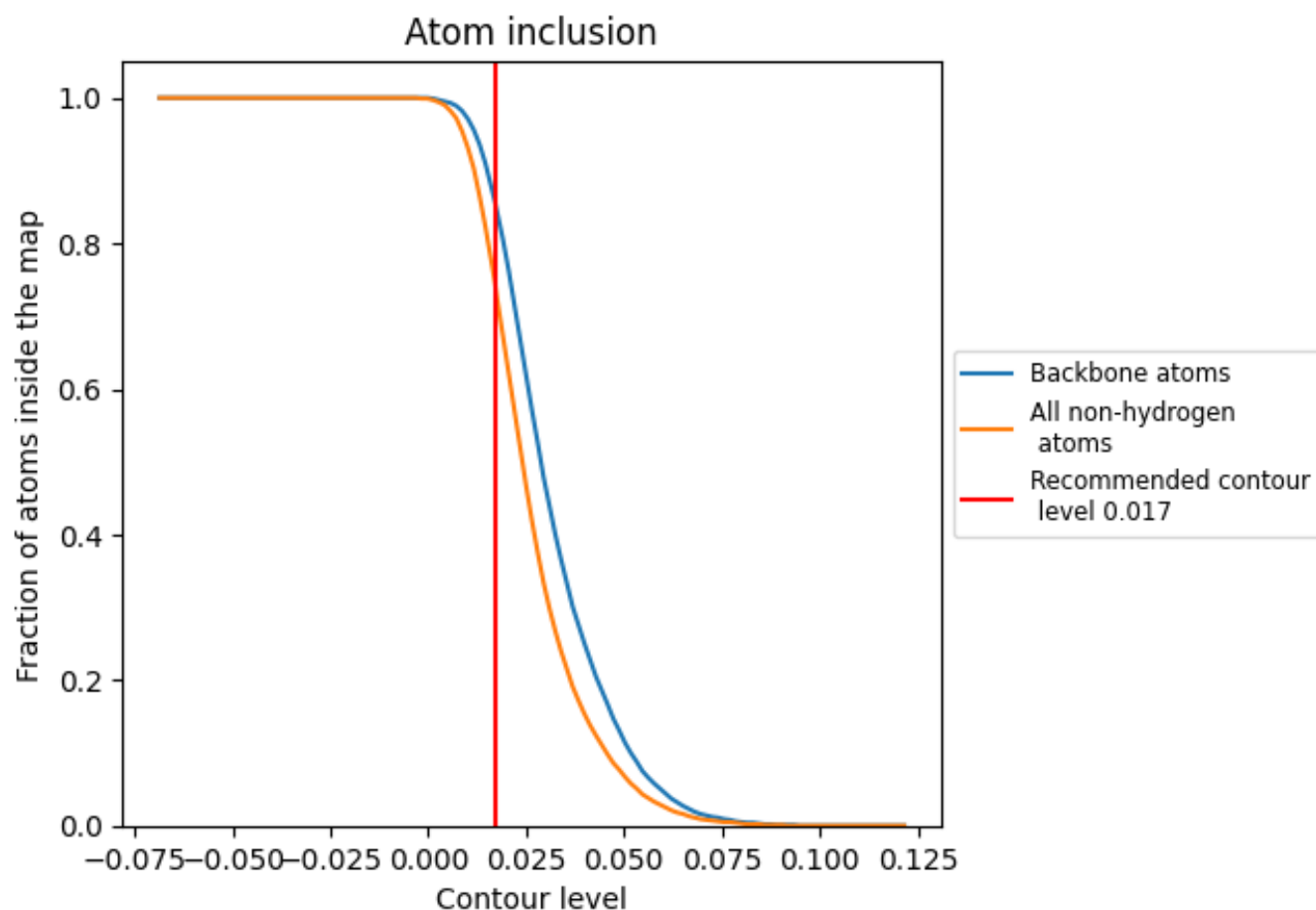
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 75% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7470	 0.3280
C	 0.1620	 0.2560
G	 0.6640	 0.1990
H	 0.7170	 0.2860
I	 0.7600	 0.3230
J	 0.6580	 0.1970
K	 0.7440	 0.2900
L	 0.8230	 0.4110
N	 0.8740	 0.4470
O	 0.8440	 0.4370
P	 0.8600	 0.4230
Q	 0.8390	 0.3540
U	 0.8430	 0.3470
Y	 0.8190	 0.3450
Z	 0.8300	 0.3210
a	 0.5830	 0.2720
b	 0.6040	 0.2810
d	 0.6060	 0.2890
e	 0.6700	 0.3430
f	 0.7050	 0.3390
g	 0.5800	 0.2780
h	 0.6170	 0.2790
i	 0.5290	 0.2880

