



## Full wwPDB EM Validation Report ⓘ

Oct 6, 2024 – 01:43 AM JST

PDB ID : 7BY0  
EMDB ID : EMD-30239  
Title : The cryo-EM structure of CENP-A nucleosome in complex with the phosphorylated CENP-C  
Authors : Ariyoshi, M.; Makino, F.; Fukagawa, T.  
Deposited on : 2020-04-21  
Resolution : 4.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.dev113  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

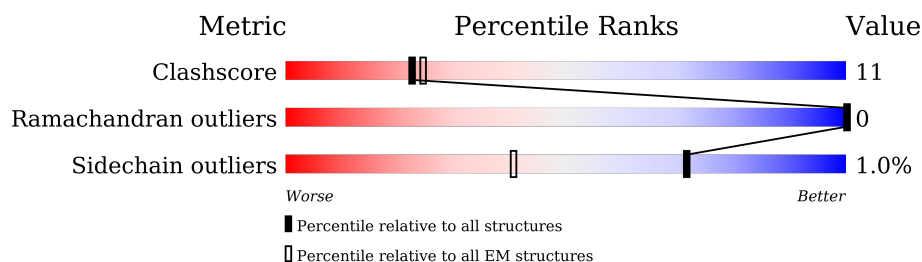
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	141	 55% 18% 27%
1	E	141	 45% 27% 27%
2	B	102	 53% 24% 24%
2	F	102	 52% 25% 24%
3	C	130	 63% 20% 17%
3	G	130	 62% 22% 17%
4	D	126	 60% 14% 25%
4	H	126	 58% 17% 25%

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	I	145	<div><div></div><div>72%25%..</div></div>
6	J	145	<div><div></div><div>68%28%. .</div></div>
7	K	664	<div><div></div><div>5% .92%</div></div>
7	L	664	<div><div></div><div>6% .92%</div></div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12693 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 H3.2,Histone H3-like centromeric protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	103	Total	C	N	O	S	0	0
			854	544	167	140	3		
1	E	103	Total	C	N	O	S	0	0
			854	544	167	140	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	78	Total	C	N	O	S	0	0
			629	397	123	108	1		
2	F	78	Total	C	N	O	S	0	0
			629	397	123	108	1		

- Molecule 3 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	108	Total	C	N	O	0	0
			832	525	164	143		
3	G	108	Total	C	N	O	0	0
			835	526	165	144		

- Molecule 4 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	94	Total	C	N	O	S	0	0
			732	459	133	138	2		
4	H	94	Total	C	N	O	S	0	0
			736	462	134	138	2		

- Molecule 5 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	143	Total	C	N	O	P	0	0
			2914	1384	530	857	143		

- Molecule 6 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	143	Total	C	N	O	P	0	0
			2949	1396	551	859	143		

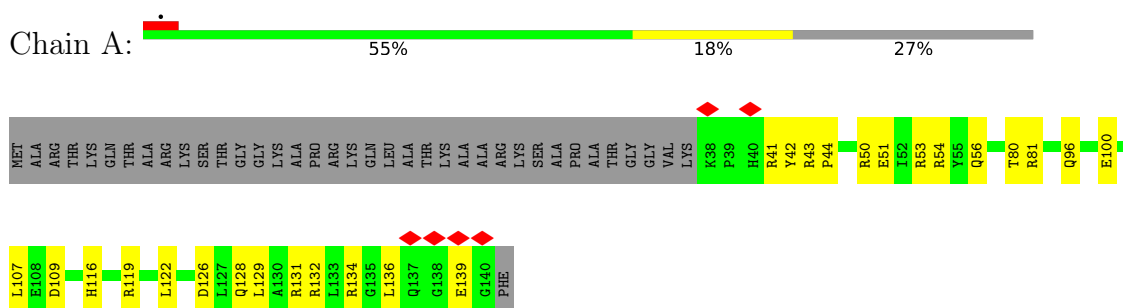
- Molecule 7 is a protein called Maltose Binding Protein tag, linker,CENP-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	51	Total	C	N	O	P	0	0
			363	223	75	64	1		
7	L	51	Total	C	N	O	P	0	0
			366	226	75	64	1		

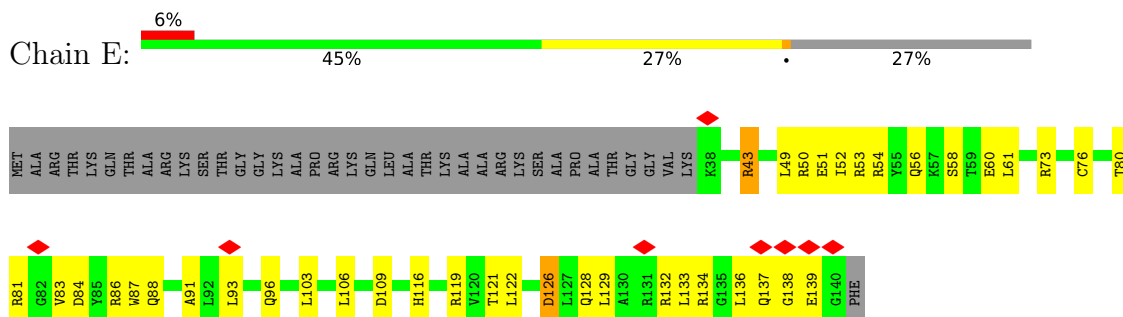
### 3 Residue-property plots [i](#)

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.

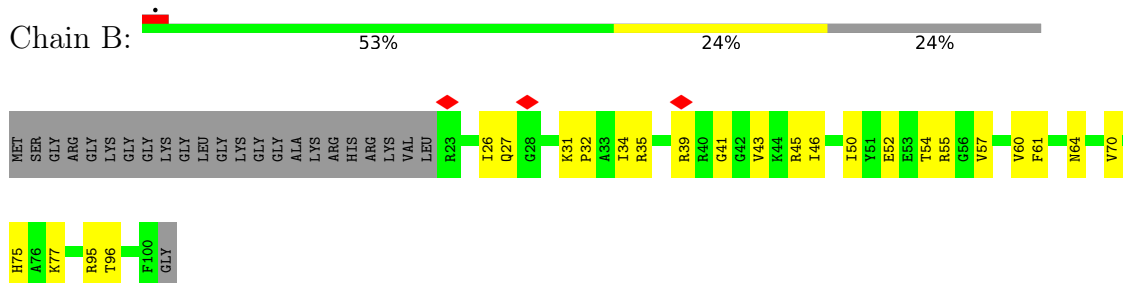
- Molecule 1: Histone H3.2,Histone H3-like centromeric protein A



- Molecule 1: Histone H3.2,Histone H3-like centromeric protein A

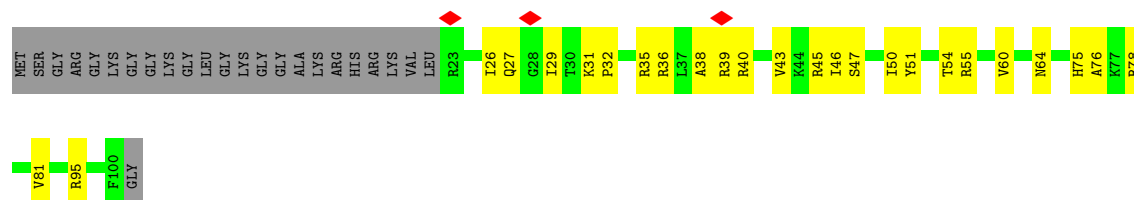


- Molecule 2: Histone H4

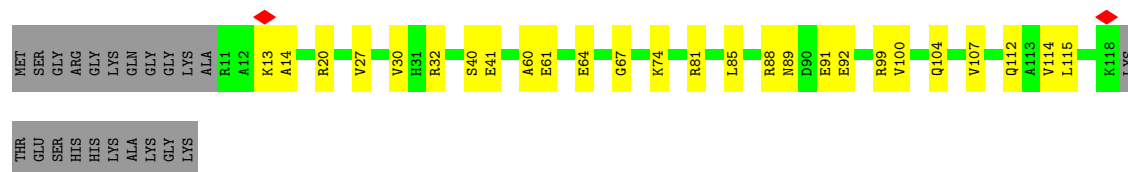


- Molecule 2: Histone H4

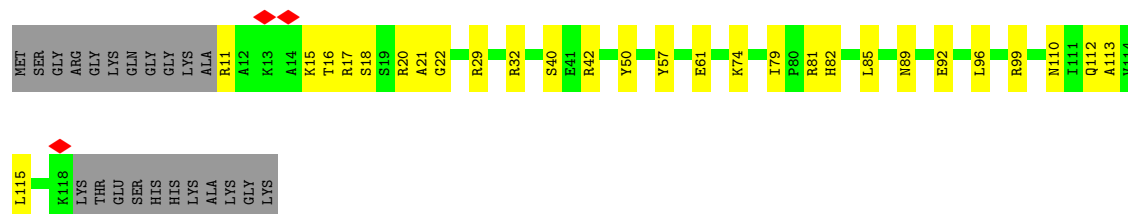




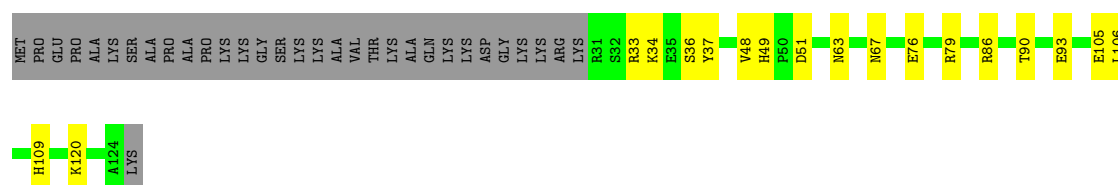
- Molecule 3: Histone H2A type 1-B/E



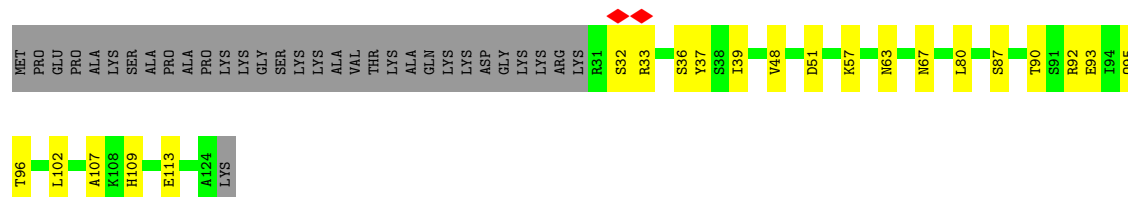
- Molecule 3: Histone H2A type 1-B/E



- Molecule 4: Histone H2B type 1-J



- Molecule 4: Histone H2B type 1-J



- Molecule 5: DNA (145-MER)

A144	DT	DA	T2	G5	C25	T26	A29	T30	T31	G32	G33	A40	C53	G54	C55	T56	A59	A60	C61	G62	C65	G66	T67	A68	C69	T74	G75	C81	G82	G100	A112	T116	A119	G120	G121	G125	T126	G127	A134	T135	A138	C139	G142	C143
------	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Chain J:  68% 28% .

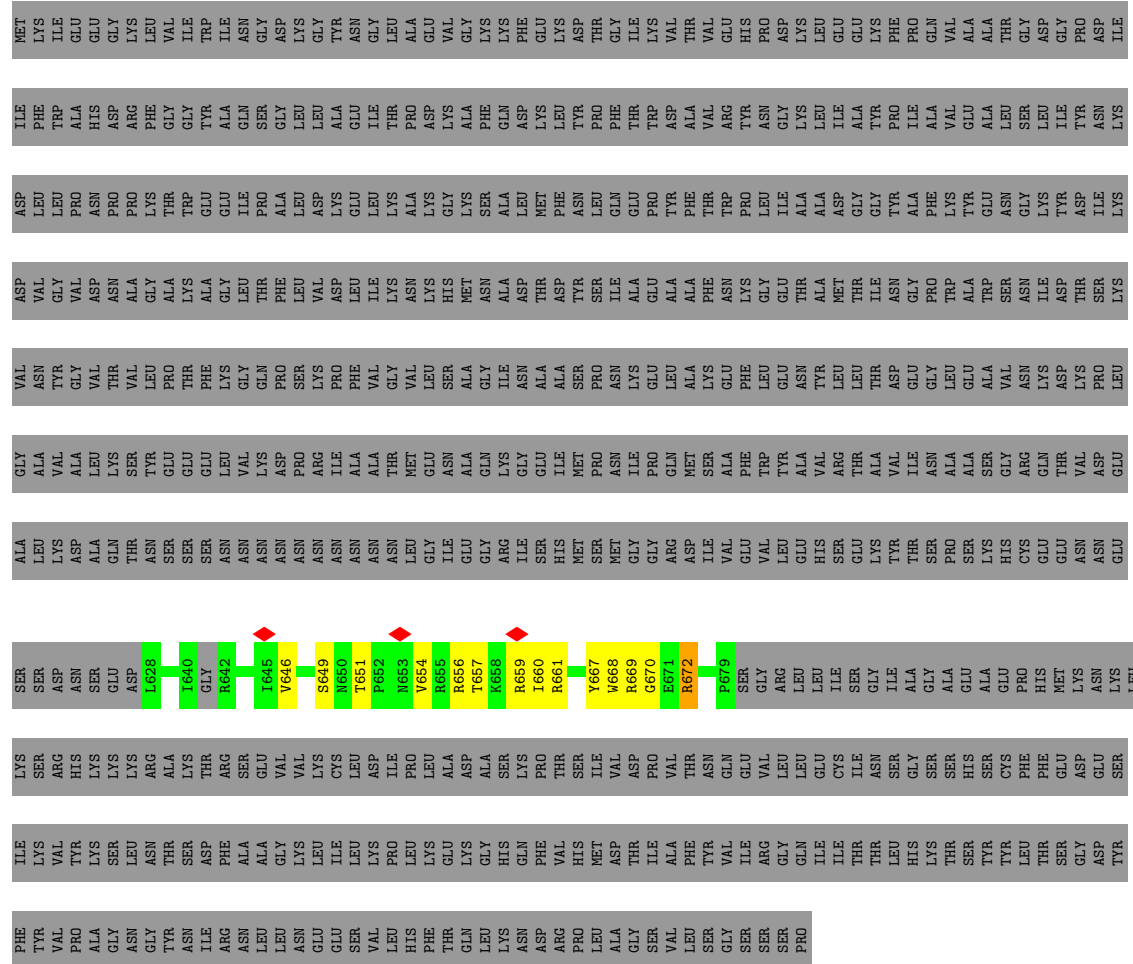
T284	T285	T286	T287	G288	A289	DT	DA	T147	T153	A163	G164	A165	G169	C170	G174	A175	G176	G182	G183	T186	A187	T194	T201	T202	A203	A204	A205	G214	A215	G226	G236	G237	G238	G239	T240	C248	T249	C259	A260	A261	G266	C267	G268	C271	T272	G273	T274	G275	C276	A282
------	------	------	------	------	------	----	----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Chain K: 5% . 92%

ser	glu	lys	ser	ala	gly	val	asp	ile	met
ser	asp	asn	ser	leu	ala	asn	val	phe	lys
asp	glu	lys	asp	lys	val	tyr	leu	trp	ile
tyr	ser	leu	asn	asp	ala	gly	pro	glu	trp
tyr	lys	ser	glu	asn	leu	val	asn	his	glu
val	val	arg	asp	asn	thr	thr	pro	asp	gly
tyr	arg	his	lys	thr	ser	val	ala	arg	lys
pro	lys	lys	lys	asn	tyr	leu	lys	phe	leu
ala	lys	lys	ser	ser	glu	pro	ala	gly	val
asn	lys	lys	glu	ser	glu	thr	lys	trp	ile
gly	arg	ala	glu	asn	leu	phe	glu	tyr	trp
tyr	asn	ala	glu	asn	leu	lys	glu	ala	ile
tyr	thr	ala	glu	asn	val	gly	ile	ala	asn
ser	ser	thr	v646	asn	val	gly	ile	asn	asn
ile	asp	thr	l647	asn	asn	thr	phe	glu	gly
arg	phe	arg	p648	asn	asp	pro	thr	ala	asp
asn	ala	ser	s649	asn	pro	ser	leu	leu	lys
leu	ala	ser	k650	asn	arg	val	val	asp	lys
leu	glu	val	t651	asn	ile	pro	asp	ala	tyr
glu	lys	val	p652	asn	ala	phe	leu	glu	asn
glu	lys	val	n653	asn	ala	val	leu	gly	ile
ile	ile	cys	v654	leu	met	thr	asn	pro	leu
leu	leu	leu	r655	gly	asn	leu	lys	asp	glu
val	asp	asp	r656	ile	asn	ser	gly	lys	val
pro	ile	ile	t657	glu	ala	ala	met	ala	gly
his	leu	pro	k658	gly	glu	gly	asn	phe	lys
lys	lys	leu	r659	arg	lys	ile	ala	glu	lys
glu	glu	ala	i660	ile	gly	asn	asp	leu	phe
lys	asp	asp	r661	ser	glu	ala	thr	met	glu
gly	ala	ala	l662	his	ile	ala	asp	phe	lys
lys	ser	lys	k663	met	met	ser	tyr	asn	thr
asn	lys	ser	p664	ser	pro	pro	leu	trp	asp
asp	phe	pro	l665	met	asn	asn	ile	glu	gly
arg	val	thr	l666	gly	ile	lys	ala	thr	lys
his	his	ser	e667	gly	pro	glu	glu	trp	val
leu	met	ile	w668	arg	glu	leu	ala	asp	lys
ala	asp	val	r669	asn	met	ala	ala	phe	thr
gly	asp	glu	c670	ile	ser	lys	thr	val	glu
ser	ile	pro	e671	val	ala	glu	asn	trp	arg
ala	val	ala	r672	val	phe	thr	lys	tyr	thr
leu	phe	thr	o673	val	val	leu	glu	asn	pro
ser	tyr	asn	p679	leu	tyr	glu	ile	gly	asp
gly	val	glu	ser	glu	ala	thr	ile	gly	lys
ser	ile	glu	gly	his	val	tyr	ala	leu	lys
ser	arg	val	arg	ser	arg	leu	ala	leu	glu
ser	gly	leu	leu	glu	thr	leu	met	ile	glu
ser	glu	leu	leu	lys	ala	thr	gly	ala	glu
pro	ile	glu	ile	thr	val	asp	ile	tyr	phe
pro	thr	cys	ile	thr	val	asn	asn	pro	lys
thr	thr	ile	gly	thr	ile	glu	gly	ile	pro
thr	thr	asn	ile	pro	ala	leu	phe	val	val
his	leu	ser	ala	ser	ala	glu	trp	glu	ala
lys	his	gly	gly	his	lys	val	trp	ala	ala
thr	thr	ser	ala	cys	arg	asn	ser	leu	thr
ser	ser	his	glu	glu	thr	asn	gly	ser	gly
tyr	tyr	cys	ala	glu	val	asp	tyr	ile	pro
tyr	tyr	lys	glu	asn	thr	asp	thr	tyr	lys
leu	leu	phe	pro	thr	val	ser	ile	asn	asn
thr	thr	thr	his	glu	glu	leu	lys	lys	lys



Chain L:  6% . 92%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	38542	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 200	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.2	Depositor
Minimum defocus (nm)	-500	Depositor
Maximum defocus (nm)	-7000	Depositor
Magnification	45454	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	233.20001, 233.20001, 233.20001	wwPDB
Map dimensions	212, 212, 212	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.33	0/870	0.57	0/1172
1	E	0.35	0/870	0.56	0/1172
2	B	0.35	0/636	0.59	0/852
2	F	0.34	0/636	0.54	0/852
3	C	0.31	0/842	0.53	0/1135
3	G	0.33	0/845	0.54	0/1139
4	D	0.32	0/743	0.50	0/1000
4	H	0.34	0/747	0.48	0/1004
5	I	0.91	1/3265 (0.0%)	1.12	5/5032 (0.1%)
6	J	0.92	1/3311 (0.0%)	1.08	5/5113 (0.1%)
7	K	0.29	0/355	0.59	0/478
7	L	0.30	0/358	0.61	0/482
All	All	0.68	2/13478 (0.0%)	0.88	10/19431 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	165	DA	C1'-N9	-7.02	1.37	1.47
5	I	60	DA	N9-C4	-5.26	1.34	1.37

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	32	DG	O4'-C4'-C3'	-7.26	101.60	104.50
5	I	55	DC	O4'-C4'-C3'	-6.00	102.10	104.50
6	J	286	DC	O4'-C4'-C3'	-5.76	102.20	104.50
6	J	163	DA	O4'-C4'-C3'	-5.63	102.25	104.50
6	J	285	DT	C3'-C2'-C1'	-5.42	95.99	102.50
6	J	226	DG	O4'-C4'-C3'	-5.40	102.34	104.50
5	I	31	DT	O4'-C1'-N1	5.38	111.77	108.00

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	5	DG	O4'-C1'-N9	5.11	111.57	108.00
5	I	55	DC	C4'-C3'-C2'	-5.02	98.58	103.10
6	J	215	DA	O4'-C4'-C3'	-5.01	102.50	104.50

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	A	854	0	891	35	0
1	E	854	0	891	40	0
2	B	629	0	670	18	0
2	F	629	0	670	24	0
3	C	832	0	893	24	0
3	G	835	0	897	26	0
4	D	732	0	747	26	0
4	H	736	0	758	19	0
5	I	2914	0	1605	31	0
6	J	2949	0	1606	38	0
7	K	363	0	306	41	0
7	L	366	0	315	18	0
All	All	12693	0	10249	233	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 11.

All (233) 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)
1:A:131:ARG:NH1	7:K:668:TRP:HA	1.61	1.15
3:C:91:GLU:HG3	7:K:665:LEU:HB3	1.09	1.05
3:C:92:GLU:OE1	7:K:659:ARG:NH1	1.95	0.98
3:G:92:GLU:OE2	7:L:659:ARG:NH1	2.05	0.90
3:C:91:GLU:HG3	7:K:665:LEU:CB	2.00	0.87

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:ARG:HG3	7:K:668:TRP:CE3	2.09	0.86
4:D:106:LEU:HD23	7:K:659:ARG:HD2	1.56	0.85
1:A:139:GLU:OE2	7:K:667:TYR:CE2	2.30	0.84
1:E:128:GLN:HE22	7:L:669:ARG:HH21	1.28	0.82
4:D:109:HIS:CE1	7:K:659:ARG:HA	2.14	0.82
1:E:139:GLU:OE2	7:L:667:TYR:HB2	1.80	0.81
1:A:132:ARG:HG3	7:K:668:TRP:CD2	2.17	0.80
1:A:131:ARG:HH12	7:K:668:TRP:HA	1.45	0.79
1:A:131:ARG:HH11	7:K:668:TRP:HA	1.51	0.76
1:E:128:GLN:NE2	7:L:669:ARG:HH21	1.85	0.75
5:I:127:DG:N2	6:J:165:DA:C2	2.55	0.75
1:E:128:GLN:HE22	7:L:669:ARG:HD3	1.51	0.74
4:D:105:GLU:OE2	7:K:660:ILE:N	2.21	0.73
4:D:106:LEU:CD2	7:K:659:ARG:HD2	2.19	0.72
2:F:46:ILE:HG22	2:F:47:SER:O	1.90	0.71
1:A:132:ARG:HD2	7:K:668:TRP:CE2	2.26	0.70
1:E:86:ARG:HH11	5:I:100:DG:H5'	1.57	0.70
1:E:128:GLN:HG2	7:L:668:TRP:HD1	1.57	0.69
1:E:128:GLN:HG2	7:L:668:TRP:CD1	2.28	0.68
1:A:131:ARG:NH1	7:K:668:TRP:CA	2.51	0.68
2:F:38:ALA:HB1	2:F:46:ILE:HD11	1.76	0.67
4:D:106:LEU:HD23	7:K:659:ARG:CD	2.25	0.67
4:D:33:ARG:NH2	6:J:266:DG:N3	2.43	0.66
1:A:132:ARG:HD2	7:K:668:TRP:CZ2	2.31	0.66
1:E:132:ARG:HG3	7:L:668:TRP:CZ3	2.32	0.65
3:C:91:GLU:CG	7:K:665:LEU:HB3	2.05	0.64
1:E:136:LEU:HB2	3:G:99:ARG:HH12	1.63	0.63
4:D:48:VAL:O	7:K:654:VAL:HG13	1.98	0.63
5:I:81:DC:H2''	5:I:82:DG:H2'	1.81	0.63
5:I:74:DT:H2''	5:I:75:DG:H2'	1.80	0.63
5:I:61:DC:H2''	5:I:62:DG:H2'	1.80	0.62
4:H:80:LEU:HD21	4:H:96:THR:OG1	1.99	0.62
5:I:125:DG:H2''	5:I:126:DT:C5	2.35	0.62
2:B:32:PRO:HG3	5:I:59:DA:H3'	1.82	0.62
2:F:81:VAL:HG13	2:F:81:VAL:O	2.00	0.62
1:A:50:ARG:HG2	1:A:53:ARG:HH21	1.65	0.61
1:E:76:CYS:HG	1:E:87:TRP:HE1	1.45	0.61
1:E:87:TRP:CE3	2:F:81:VAL:HG11	2.36	0.61
3:G:29:ARG:HG3	3:G:32:ARG:HH21	1.65	0.61
4:D:105:GLU:OE2	7:K:660:ILE:HG22	2.03	0.59
1:A:128:GLN:NE2	7:K:669:ARG:HD3	2.17	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:52:GLU:OE2	2:B:55:ARG:NH1	2.36	0.59
7:L:659:ARG:NH1	7:L:660:ILE:O	2.36	0.58
3:C:91:GLU:HB2	7:K:663:LYS:O	2.03	0.58
3:C:64:GLU:OE2	7:K:656:ARG:HA	2.04	0.58
3:C:32:ARG:NH1	5:I:29:DA:OP1	2.37	0.57
4:D:63:ASN:O	4:D:67:ASN:ND2	2.37	0.57
4:D:51:ASP:OD1	4:D:51:ASP:N	2.38	0.57
3:C:20:ARG:O	4:D:120:LYS:NZ	2.38	0.56
3:C:40:SER:OG	3:C:41:GLU:N	2.36	0.56
4:H:90:THR:HG23	4:H:92:ARG:H	1.70	0.56
2:B:31:LYS:HA	2:B:34:ILE:HD12	1.88	0.56
1:E:128:GLN:NE2	7:L:669:ARG:HD3	2.20	0.56
3:G:40:SER:OG	4:H:87:SER:O	2.23	0.56
6:J:273:DC:H4'	6:J:274:DG:H5'	1.87	0.56
1:A:134:ARG:HD2	2:B:95:ARG:HH22	1.70	0.56
7:K:646:VAL:HB	7:K:661:ARG:HB2	1.86	0.56
3:C:14:ALA:HA	5:I:31:DT:H5'	1.89	0.55
4:D:48:VAL:HG23	7:K:654:VAL:CG1	2.37	0.55
3:G:16:THR:HA	6:J:175:DA:H5'	1.89	0.55
2:F:39:ARG:NH1	2:F:43:VAL:O	2.40	0.54
4:D:33:ARG:NH1	6:J:267:DC:O4'	2.40	0.54
3:C:13:LYS:NZ	3:C:14:ALA:O	2.41	0.54
3:G:15:LYS:O	3:G:20:ARG:NH1	2.41	0.54
1:A:56:GLN:O	3:G:81:ARG:NH2	2.41	0.54
5:I:138:DA:H1'	5:I:139:DC:H5'	1.91	0.53
4:D:36:SER:OG	4:D:37:TYR:N	2.41	0.53
2:F:51:TYR:O	2:F:55:ARG:NH1	2.42	0.53
5:I:56:DT:O2	6:J:236:DG:N2	2.41	0.53
7:K:670:GLY:O	7:K:672:ARG:NH1	2.40	0.53
4:D:86:ARG:NH2	5:I:40:DA:OP1	2.41	0.53
1:E:43:ARG:NH2	6:J:287:DT:OP2	2.35	0.53
2:F:29:ILE:O	2:F:55:ARG:NH2	2.41	0.53
4:H:102:LEU:HB2	4:H:107:ALA:HB2	1.91	0.53
1:E:88:GLN:OE1	1:E:91:ALA:N	2.41	0.52
2:F:76:ALA:HB1	2:F:78:ARG:HE	1.75	0.52
1:E:86:ARG:NH1	5:I:100:DG:OP1	2.42	0.52
1:E:134:ARG:O	1:E:137:GLN:NE2	2.42	0.52
3:G:42:ARG:HG2	5:I:112:DA:H4'	1.92	0.52
1:A:128:GLN:HE22	7:K:669:ARG:HD3	1.75	0.52
3:C:104:GLN:HE22	1:E:60:GLU:HA	1.75	0.52
1:E:132:ARG:HG3	7:L:668:TRP:CE3	2.44	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:GLU:OE1	1:A:54:ARG:NH1	2.43	0.52
6:J:174:DG:H2''	6:J:175:DA:C8	2.45	0.52
1:A:50:ARG:NH2	6:J:153:DT:OP1	2.43	0.51
3:G:85:LEU:O	3:G:89:ASN:ND2	2.42	0.51
1:A:42:TYR:HA	5:I:142:DC:H4'	1.91	0.51
7:K:647:LEU:HD12	7:K:648:PRO:HD2	1.91	0.51
2:B:50:ILE:HG13	2:B:54:THR:HG23	1.92	0.51
2:F:35:ARG:NH1	5:I:81:DC:OP2	2.43	0.51
3:G:42:ARG:NH2	6:J:182:DG:O3'	2.44	0.50
7:L:670:GLY:O	7:L:672:ARG:NH1	2.44	0.50
5:I:65:DC:H1'	5:I:66:DG:H5'	1.93	0.50
2:F:26:ILE:HG23	2:F:27:GLN:HE21	1.77	0.50
1:E:61:LEU:HD12	1:E:96:GLN:HE21	1.75	0.50
4:H:37:TYR:N	4:H:63:ASN:OD1	2.43	0.50
6:J:203:DA:H2''	6:J:204:DA:H5''	1.93	0.50
4:H:48:VAL:O	7:L:654:VAL:HG13	2.11	0.50
1:A:41:ARG:NH2	1:A:42:TYR:O	2.45	0.50
1:A:122:LEU:HD23	2:B:46:ILE:HD13	1.93	0.50
4:D:105:GLU:CD	7:K:660:ILE:HG22	2.31	0.50
3:G:17:ARG:O	3:G:21:ALA:N	2.43	0.50
4:H:109:HIS:CE1	7:L:659:ARG:HA	2.47	0.50
5:I:33:DG:N2	6:J:259:DC:O2	2.45	0.50
3:C:88:ARG:NH2	3:C:100:VAL:O	2.45	0.50
1:A:119:ARG:NH2	1:A:126:ASP:OD1	2.45	0.49
2:B:45:ARG:HH22	5:I:69:DC:H5''	1.76	0.49
4:D:33:ARG:NH1	6:J:266:DG:O3'	2.44	0.49
2:F:75:HIS:HE1	4:H:93:GLU:HG3	1.77	0.49
7:L:649:SER:HB2	7:L:656:ARG:HH21	1.77	0.49
4:D:76:GLU:OE2	4:D:79:ARG:NH1	2.46	0.49
2:B:61:PHE:HA	2:B:64:ASN:HD22	1.77	0.49
3:C:81:ARG:NH1	3:C:107:VAL:O	2.46	0.49
3:G:11:ARG:NH2	5:I:116:DT:O2	2.46	0.49
3:G:61:GLU:OE1	7:L:657:THR:HG21	2.13	0.49
6:J:248:DC:H2''	6:J:249:DT:H5''	1.94	0.49
4:H:32:SER:OG	4:H:33:ARG:N	2.46	0.49
3:G:112:GLN:HB3	3:G:115:LEU:HG	1.95	0.48
1:A:80:THR:HG22	2:B:70:VAL:HG21	1.95	0.48
3:C:112:GLN:HE22	3:C:114:VAL:HG22	1.78	0.48
2:F:35:ARG:NH2	2:F:51:TYR:OH	2.41	0.48
6:J:201:DT:H4'	6:J:202:DT:H5'	1.94	0.48
5:I:59:DA:H2''	5:I:60:DA:C8	2.49	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:25:DC:H2''	5:I:26:DT:C5	2.48	0.48
1:E:51:GLU:OE1	1:E:54:ARG:NH1	2.47	0.48
1:A:43:ARG:NH2	5:I:68:DA:OP1	2.47	0.48
3:G:112:GLN:HG3	3:G:113:ALA:N	2.29	0.48
1:E:73:ARG:NH2	6:J:194:DT:OP2	2.47	0.48
4:H:36:SER:OG	4:H:37:TYR:N	2.47	0.47
6:J:202:DT:H4'	6:J:203:DA:H5'	1.96	0.47
4:H:39:ILE:HG21	5:I:121:DG:H5'	1.95	0.47
5:I:81:DC:H1'	5:I:82:DG:H5'	1.96	0.47
5:I:119:DA:H1'	5:I:120:DG:C5	2.49	0.47
1:A:43:ARG:HE	1:A:44:PRO:HD2	1.78	0.47
1:E:84:ASP:OD1	1:E:84:ASP:N	2.48	0.47
6:J:283:DA:H3'	6:J:284:DT:H71	1.96	0.47
2:B:39:ARG:NH1	2:B:43:VAL:O	2.46	0.47
2:B:60:VAL:O	2:B:64:ASN:ND2	2.48	0.47
3:G:18:SER:O	3:G:22:GLY:N	2.48	0.47
3:G:92:GLU:O	3:G:96:LEU:N	2.46	0.47
6:J:267:DC:H2''	6:J:268:DG:H8	1.80	0.47
5:I:53:DC:H2'	5:I:54:DG:C8	2.50	0.46
1:E:58:SER:O	2:F:40:ARG:NH2	2.49	0.46
2:F:75:HIS:CE1	4:H:93:GLU:HG3	2.50	0.46
3:G:20:ARG:NH2	6:J:176:DG:OP1	2.49	0.46
1:A:128:GLN:O	1:A:132:ARG:HB2	2.15	0.46
1:E:137:GLN:O	2:F:95:ARG:NH1	2.49	0.46
2:F:45:ARG:NH2	6:J:214:DG:O3'	2.46	0.46
2:F:75:HIS:HB2	4:H:96:THR:HG21	1.97	0.46
3:G:57:TYR:HB2	4:H:113:GLU:HG2	1.97	0.46
1:A:131:ARG:HH12	7:K:668:TRP:CA	2.19	0.46
1:E:49:LEU:HA	1:E:52:ILE:HD12	1.98	0.46
1:A:56:GLN:HE22	3:G:110:ASN:H	1.64	0.46
2:B:75:HIS:O	2:B:77:LYS:NZ	2.49	0.46
7:L:646:VAL:HB	7:L:661:ARG:HB2	1.98	0.46
1:E:132:ARG:O	7:L:667:TYR:OH	2.34	0.46
2:F:60:VAL:O	2:F:64:ASN:ND2	2.48	0.45
4:H:63:ASN:O	4:H:67:ASN:ND2	2.49	0.45
4:D:93:GLU:OE1	4:D:93:GLU:N	2.48	0.45
1:E:119:ARG:NH2	1:E:126:ASP:OD1	2.49	0.45
2:B:35:ARG:NH2	6:J:226:DG:OP2	2.46	0.45
4:D:106:LEU:CD2	7:K:659:ARG:CD	2.91	0.45
4:H:51:ASP:OD1	4:H:51:ASP:N	2.50	0.44
7:K:649:SER:HB2	7:K:656:ARG:HH21	1.82	0.44

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:32:PRO:O	2:F:36:ARG:N	2.50	0.44
5:I:74:DT:H1'	5:I:75:DG:H5'	1.99	0.44
6:J:237:DC:N4	6:J:238:DG:O6	2.51	0.44
6:J:169:DG:H1'	6:J:170:DC:H5'	1.99	0.44
4:D:105:GLU:OE1	7:K:660:ILE:O	2.36	0.44
1:E:138:GLY:HA2	2:F:95:ARG:HH12	1.83	0.44
6:J:175:DA:H2''	6:J:176:DG:C8	2.53	0.44
2:F:36:ARG:HH22	6:J:204:DA:H3'	1.83	0.44
5:I:125:DG:H2''	5:I:126:DT:C7	2.47	0.44
2:F:50:ILE:HG13	2:F:54:THR:HG23	2.00	0.44
1:A:136:LEU:O	3:C:99:ARG:NH2	2.52	0.43
1:E:80:THR:OG1	1:E:83:VAL:O	2.25	0.43
1:E:121:THR:OG1	1:E:122:LEU:N	2.51	0.43
6:J:182:DG:H2''	6:J:183:DG:C8	2.53	0.43
6:J:214:DG:H2''	6:J:215:DA:C8	2.53	0.43
3:C:85:LEU:O	3:C:89:ASN:CB	2.67	0.43
1:E:103:LEU:HD13	1:E:106:LEU:HD11	2.01	0.43
6:J:272:DT:H2''	6:J:273:DC:H2'	2.00	0.43
1:A:96:GLN:HE21	1:A:100:GLU:HG3	1.84	0.43
4:D:90:THR:OG1	4:D:93:GLU:OE1	2.30	0.43
4:D:105:GLU:HG3	7:K:659:ARG:CG	2.48	0.43
6:J:275:DG:H1'	6:J:276:DC:H5'	1.99	0.43
4:H:87:SER:OG	6:J:183:DG:OP1	2.32	0.43
1:A:132:ARG:NE	7:K:668:TRP:CH2	2.86	0.43
4:D:105:GLU:HG3	7:K:659:ARG:HG2	2.01	0.43
5:I:134:DA:H3'	5:I:135:DT:H71	2.01	0.43
2:F:38:ALA:CB	2:F:46:ILE:HD11	2.45	0.42
1:E:109:ASP:OD2	1:E:134:ARG:NH2	2.52	0.42
1:A:132:ARG:CD	7:K:668:TRP:CZ2	3.00	0.42
3:C:60:ALA:HB1	7:K:655:ARG:HG2	2.01	0.42
6:J:271:DC:H2''	6:J:272:DT:C5	2.55	0.42
1:A:109:ASP:HB3	1:E:133:LEU:HD11	2.01	0.42
1:A:107:LEU:HD22	2:B:41:GLY:HA3	2.01	0.42
2:B:35:ARG:HD2	2:B:35:ARG:HA	1.90	0.42
3:C:61:GLU:OE1	7:K:657:THR:HG21	2.19	0.42
1:E:50:ARG:HG2	1:E:53:ARG:HH21	1.85	0.42
2:F:32:PRO:HG2	6:J:205:DA:H5''	2.02	0.42
3:C:74:LYS:HE3	3:C:74:LYS:HB2	1.89	0.42
2:B:26:ILE:HG23	2:B:27:GLN:HE21	1.85	0.42
3:G:50:TYR:OH	4:H:95:GLN:NE2	2.53	0.41
5:I:125:DG:C2'	5:I:126:DT:C7	2.98	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:34:LYS:H	6:J:267:DC:H5'	1.85	0.41
3:G:79:ILE:HG22	3:G:82:HIS:CE1	2.55	0.41
2:B:96:THR:N	3:G:99:ARG:O	2.54	0.41
6:J:284:DT:H2'	6:J:285:DT:C5	2.56	0.41
3:C:81:ARG:NH2	1:E:56:GLN:O	2.45	0.41
1:E:83:VAL:HG12	1:E:84:ASP:N	2.35	0.41
1:A:129:LEU:HD22	1:E:116:HIS:CG	2.56	0.41
2:B:57:VAL:HA	2:B:60:VAL:HG22	2.02	0.41
3:C:112:GLN:HB3	3:C:115:LEU:HG	2.02	0.41
3:G:112:GLN:HG3	3:G:113:ALA:H	1.86	0.41
3:C:27:VAL:HA	3:C:30:VAL:HG22	2.02	0.41
3:C:67:GLY:HA3	4:D:49:HIS:CD2	2.55	0.41
1:E:76:CYS:O	1:E:80:THR:OG1	2.38	0.41
1:E:93:LEU:HA	1:E:96:GLN:HB3	2.03	0.41
4:H:57:LYS:HA	4:H:57:LYS:HD3	1.89	0.41
6:J:186:DT:O4	6:J:187:DA:N6	2.54	0.41
6:J:239:DG:H2''	6:J:240:DT:H5'	2.03	0.41
7:K:646:VAL:N	7:K:661:ARG:O	2.54	0.41
3:G:17:ARG:HA	3:G:20:ARG:HB2	2.03	0.41
1:A:139:GLU:OE2	7:K:667:TYR:CD2	2.70	0.40
1:A:116:HIS:CG	1:E:129:LEU:HD22	2.56	0.40
3:G:74:LYS:HE3	3:G:74:LYS:HB2	1.84	0.40
6:J:260:DA:H2''	6:J:261:DA:C8	2.56	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	A	101/141 (72%)	99 (98%)	2 (2%)	0	100	100
1	E	101/141 (72%)	98 (97%)	3 (3%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	76/102 (74%)	74 (97%)	2 (3%)	0	100	100
2	F	76/102 (74%)	74 (97%)	2 (3%)	0	100	100
3	C	106/130 (82%)	103 (97%)	3 (3%)	0	100	100
3	G	106/130 (82%)	102 (96%)	4 (4%)	0	100	100
4	D	92/126 (73%)	92 (100%)	0	0	100	100
4	H	92/126 (73%)	88 (96%)	4 (4%)	0	100	100
7	K	46/664 (7%)	43 (94%)	3 (6%)	0	100	100
7	L	46/664 (7%)	43 (94%)	3 (6%)	0	100	100
All	All	842/2326 (36%)	816 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	87/113 (77%)	86 (99%)	1 (1%)	70	80
1	E	87/113 (77%)	84 (97%)	3 (3%)	32	53
2	B	65/79 (82%)	65 (100%)	0	100	100
2	F	65/79 (82%)	64 (98%)	1 (2%)	60	75
3	C	84/100 (84%)	84 (100%)	0	100	100
3	G	85/100 (85%)	85 (100%)	0	100	100
4	D	79/105 (75%)	79 (100%)	0	100	100
4	H	80/105 (76%)	80 (100%)	0	100	100
7	K	26/562 (5%)	25 (96%)	1 (4%)	28	50
7	L	27/562 (5%)	26 (96%)	1 (4%)	29	51
All	All	685/1918 (36%)	678 (99%)	7 (1%)	71	81

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	ARG
1	E	43	ARG
1	E	81	ARG
1	E	126	ASP
2	F	31	LYS
7	K	672	ARG
7	L	672	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	A	88	GLN
1	A	96	GLN
1	A	128	GLN
2	B	27	GLN
2	B	64	ASN
3	C	38	ASN
3	C	104	GLN
4	D	63	ASN
4	D	95	GLN
1	E	96	GLN
1	E	128	GLN
2	F	64	ASN
2	F	75	HIS
3	G	68	ASN
4	H	49	HIS
4	H	95	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
7	TPO	L	651	7	8,10,11	1.04	0	10,14,16	1.80	1 (10%)
7	TPO	K	651	7	8,10,11	1.03	0	10,14,16	1.78	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	TPO	L	651	7	-	2/9/11/13	-
7	TPO	K	651	7	-	1/9/11/13	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	651	TPO	P-OG1-CB	-5.20	107.50	123.21
7	K	651	TPO	P-OG1-CB	-5.15	107.64	123.21

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	K	651	TPO	CB-OG1-P-O1P
7	L	651	TPO	CB-OG1-P-O1P
7	L	651	TPO	CB-OG1-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates

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.

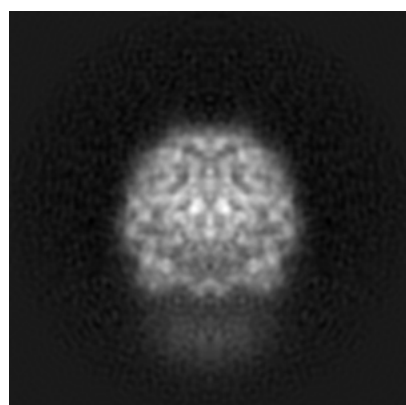
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30239. These allow visual inspection of the internal detail of the map and identification of artifacts.

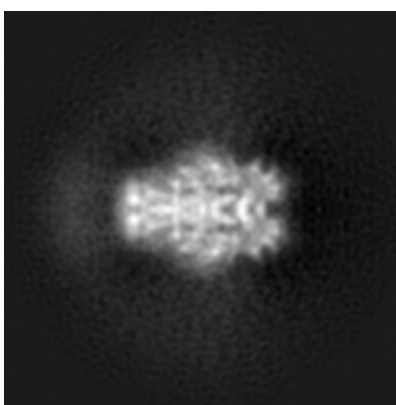
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

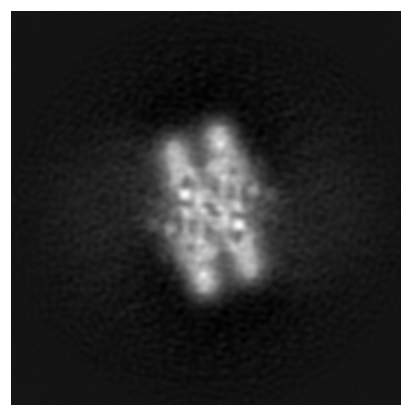
#### 6.1.1 Primary map



X



Y

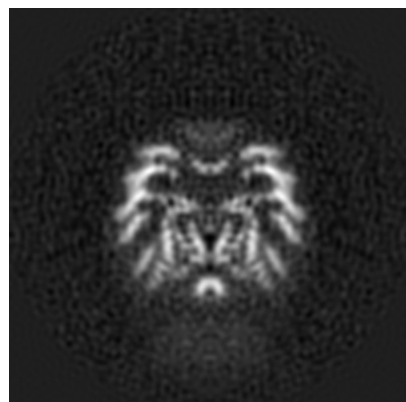


Z

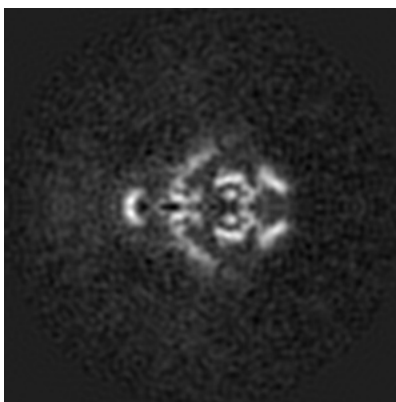
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

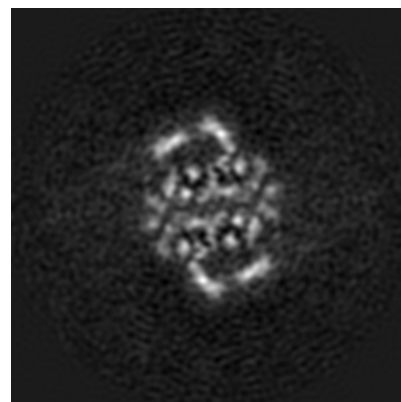
#### 6.2.1 Primary map



X Index: 106



Y Index: 106

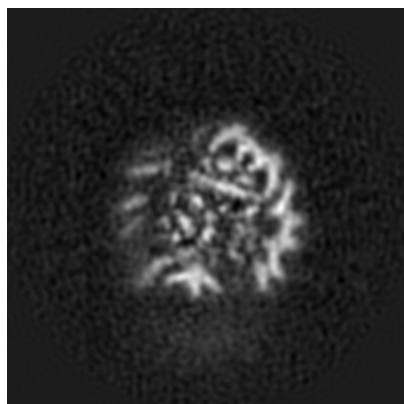


Z Index: 106

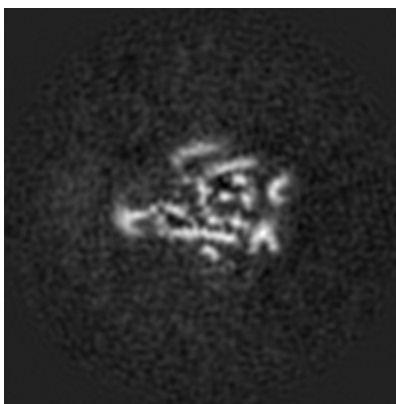
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

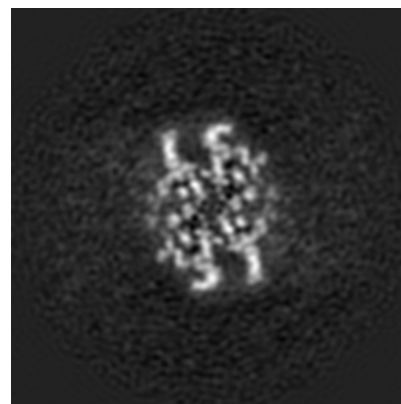
### 6.3.1 Primary map



X Index: 111



Y Index: 114

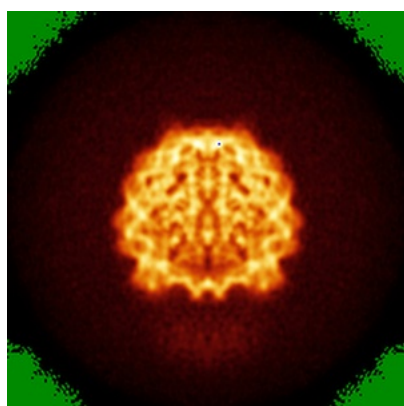


Z Index: 112

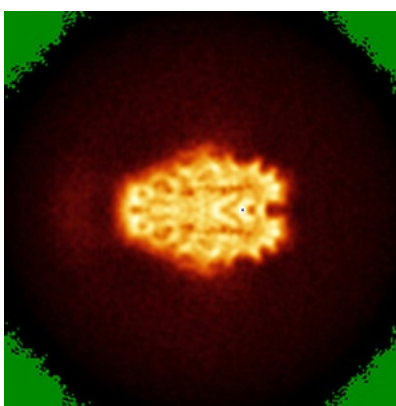
The images above show the largest variance slices of the map in three orthogonal directions.

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

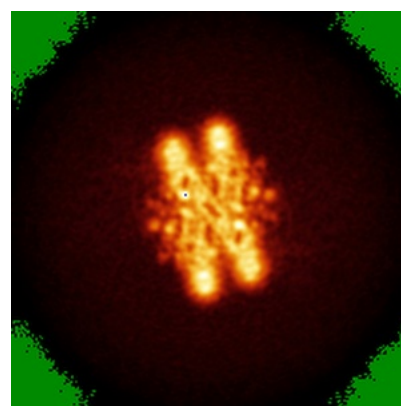
### 6.4.1 Primary map



X



Y



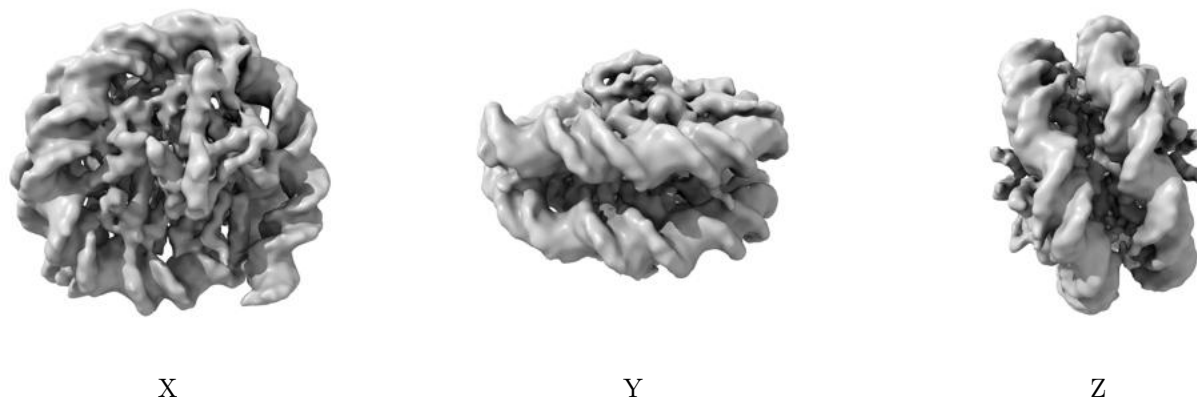
Z

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

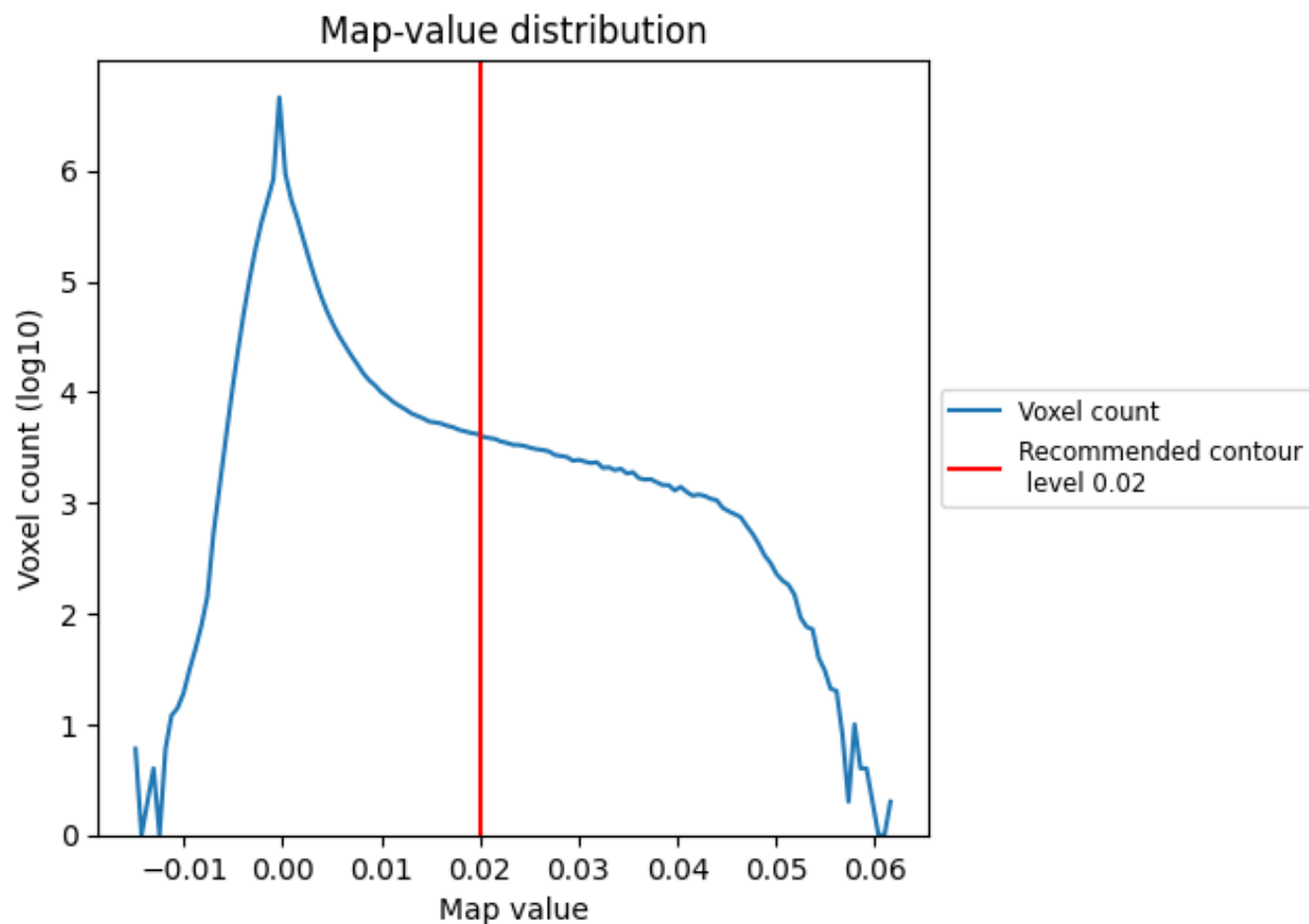
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

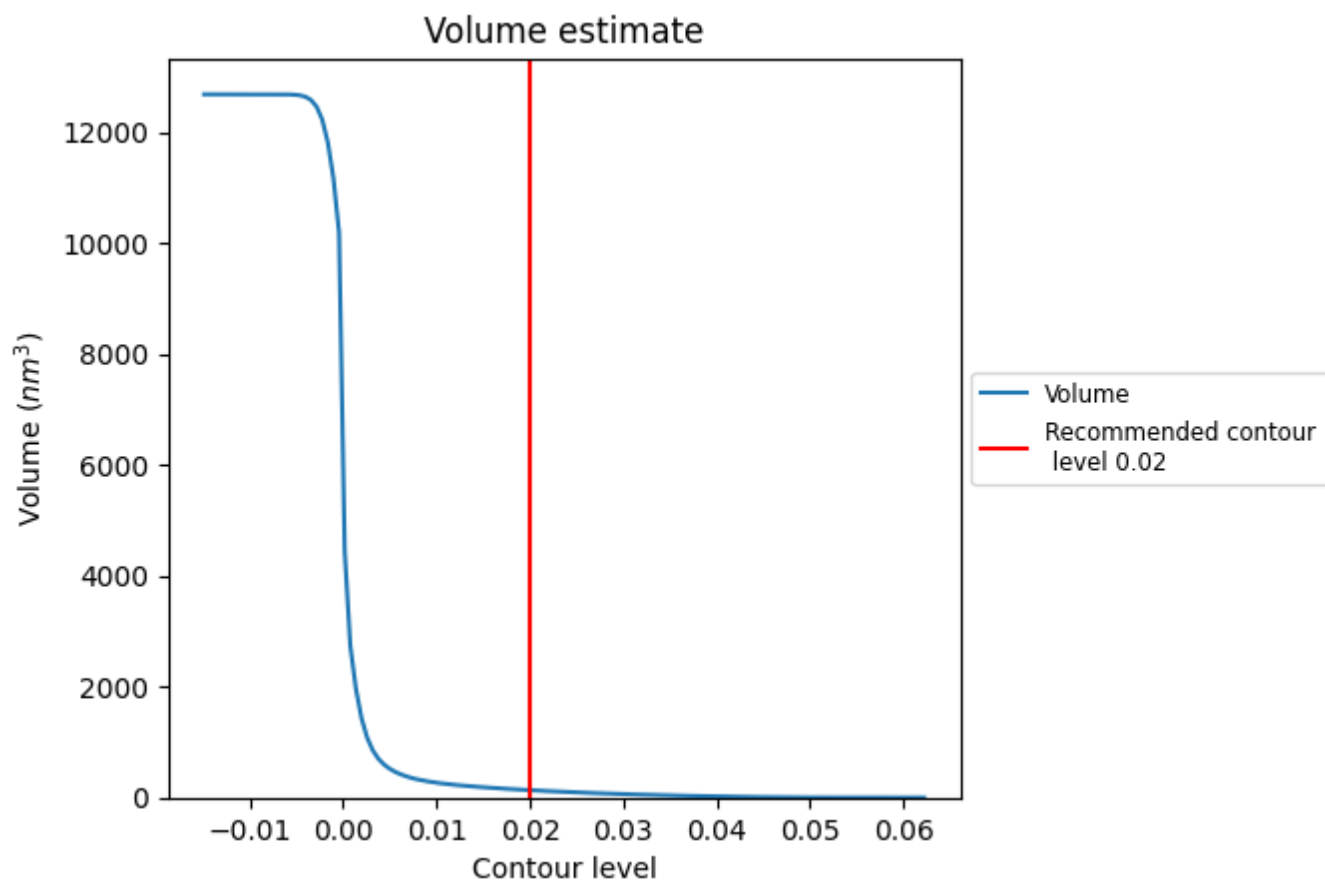
This section contains the results of statistical analysis of the map.

### 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.

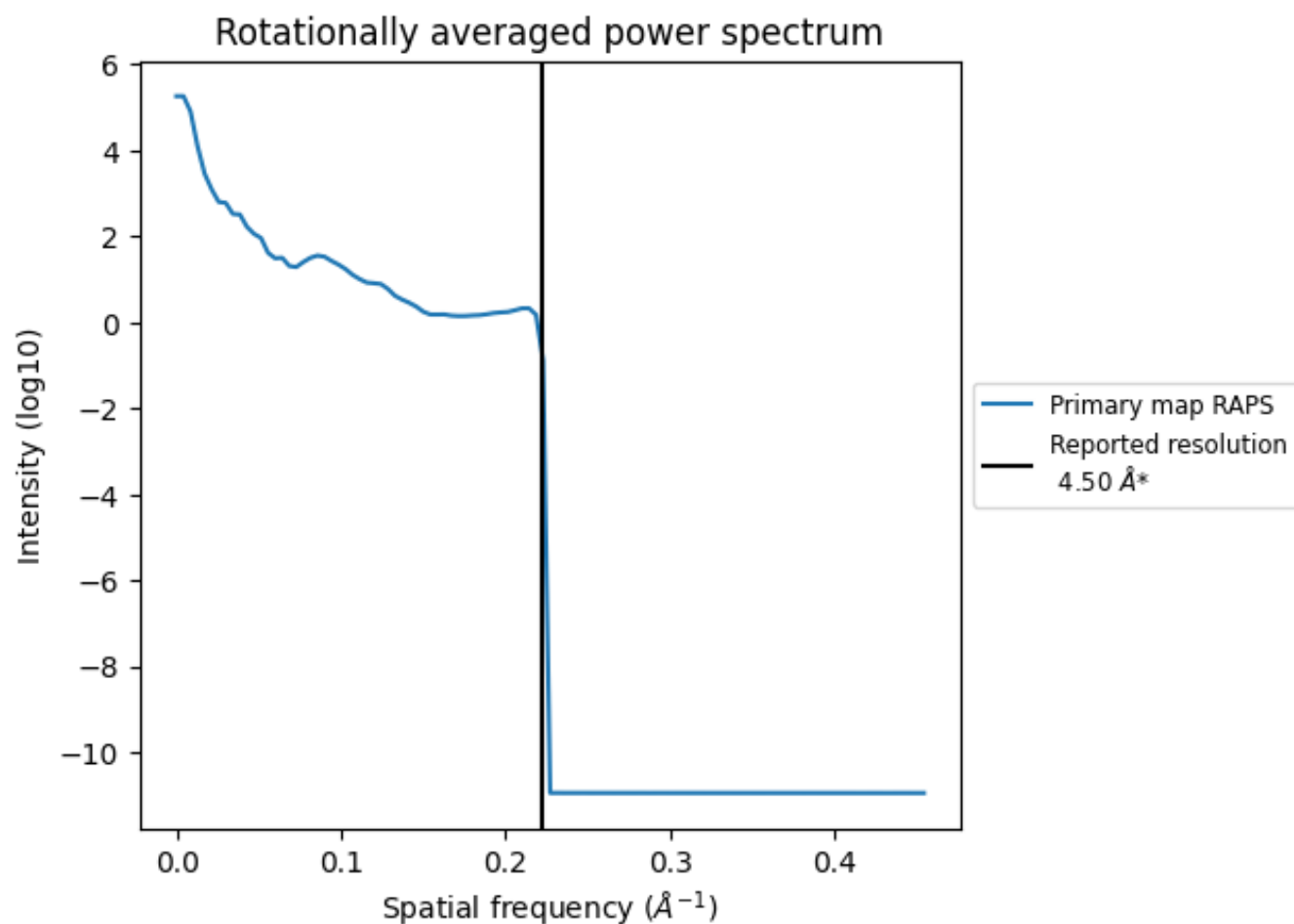
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 133 nm<sup>3</sup>; this corresponds to an approximate mass of 120 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 ⓘ

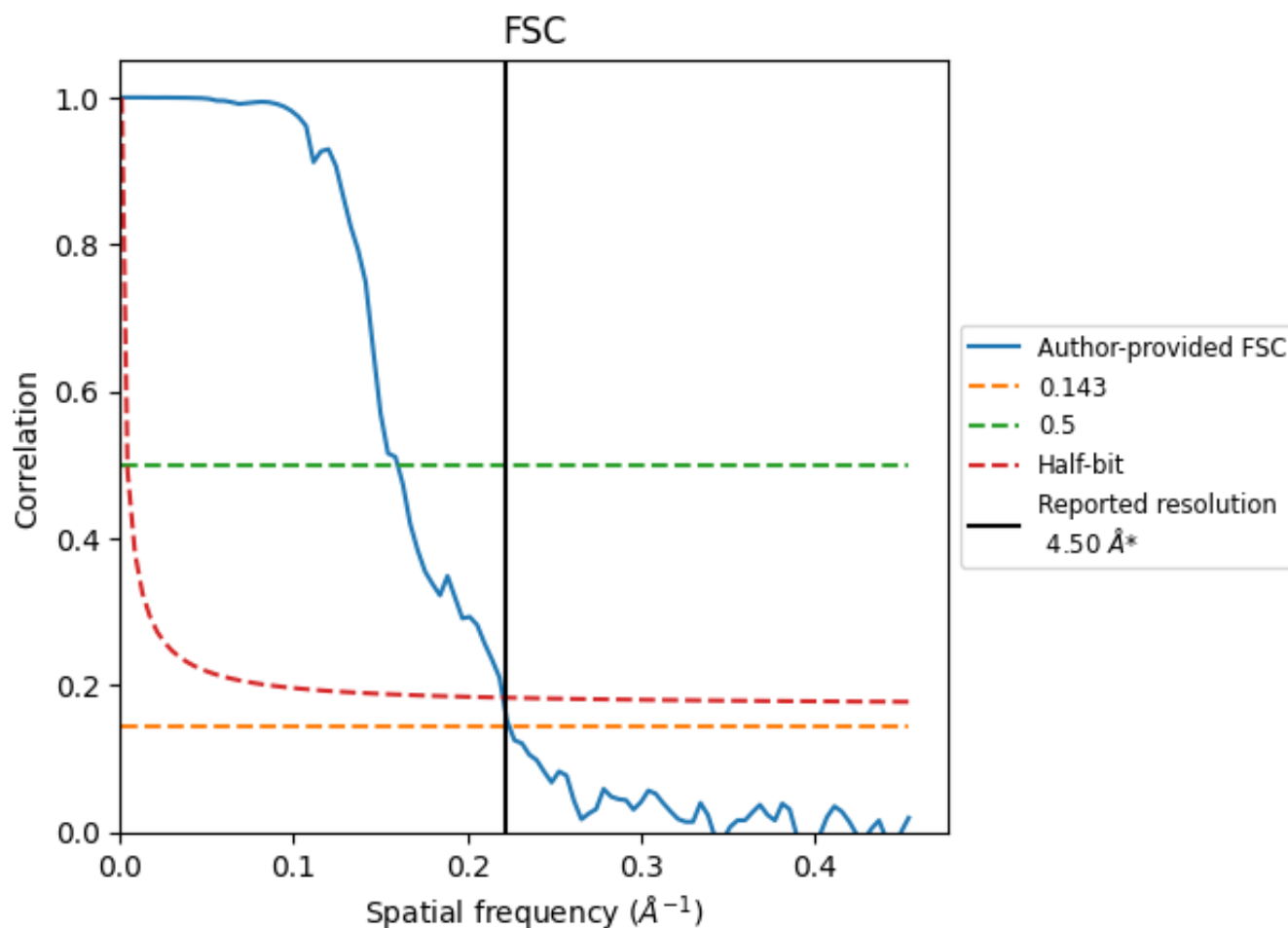


\*Reported resolution corresponds to spatial frequency of 0.222 Å<sup>-1</sup>

## 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 0.222 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

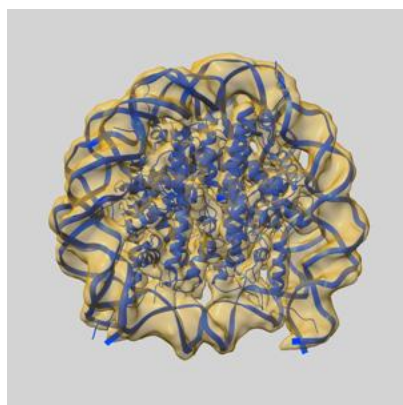
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.46	6.25	4.53
Unmasked-calculated*	-	-	-

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

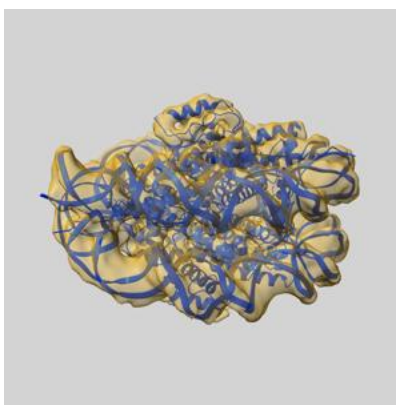
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30239 and PDB model 7BY0. Per-residue inclusion information can be found in section [3](#) on page [6](#).

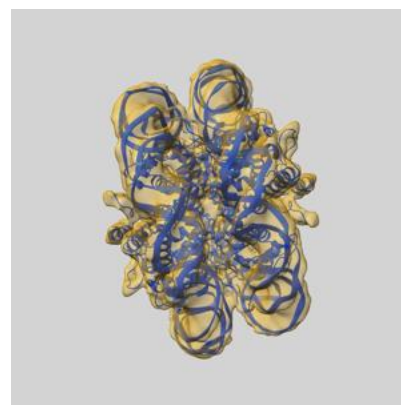
### 9.1 Map-model overlay [i](#)



X



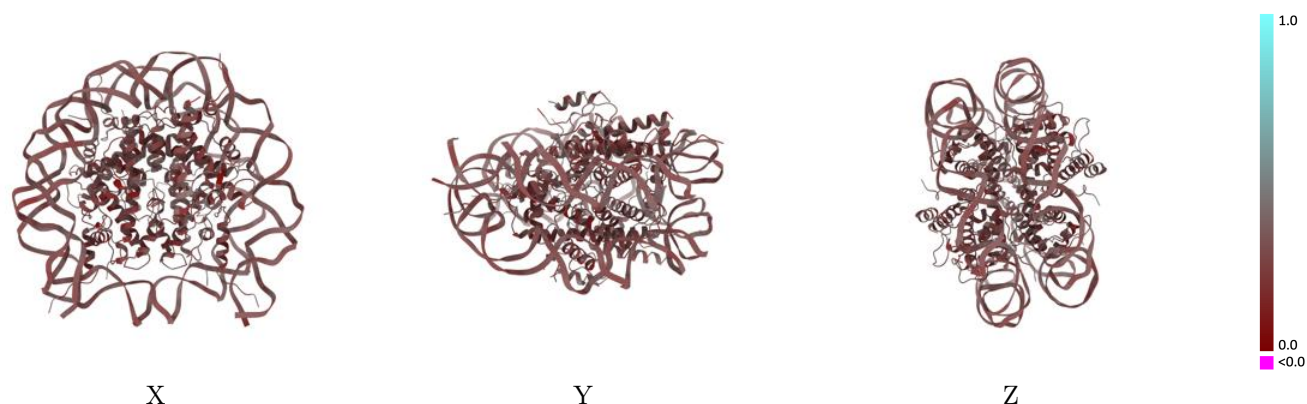
Y



Z

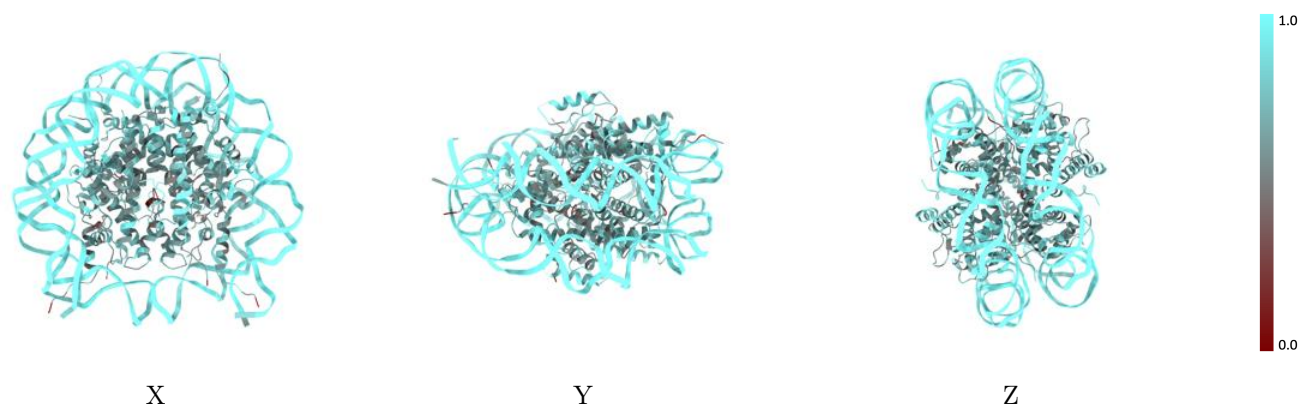
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

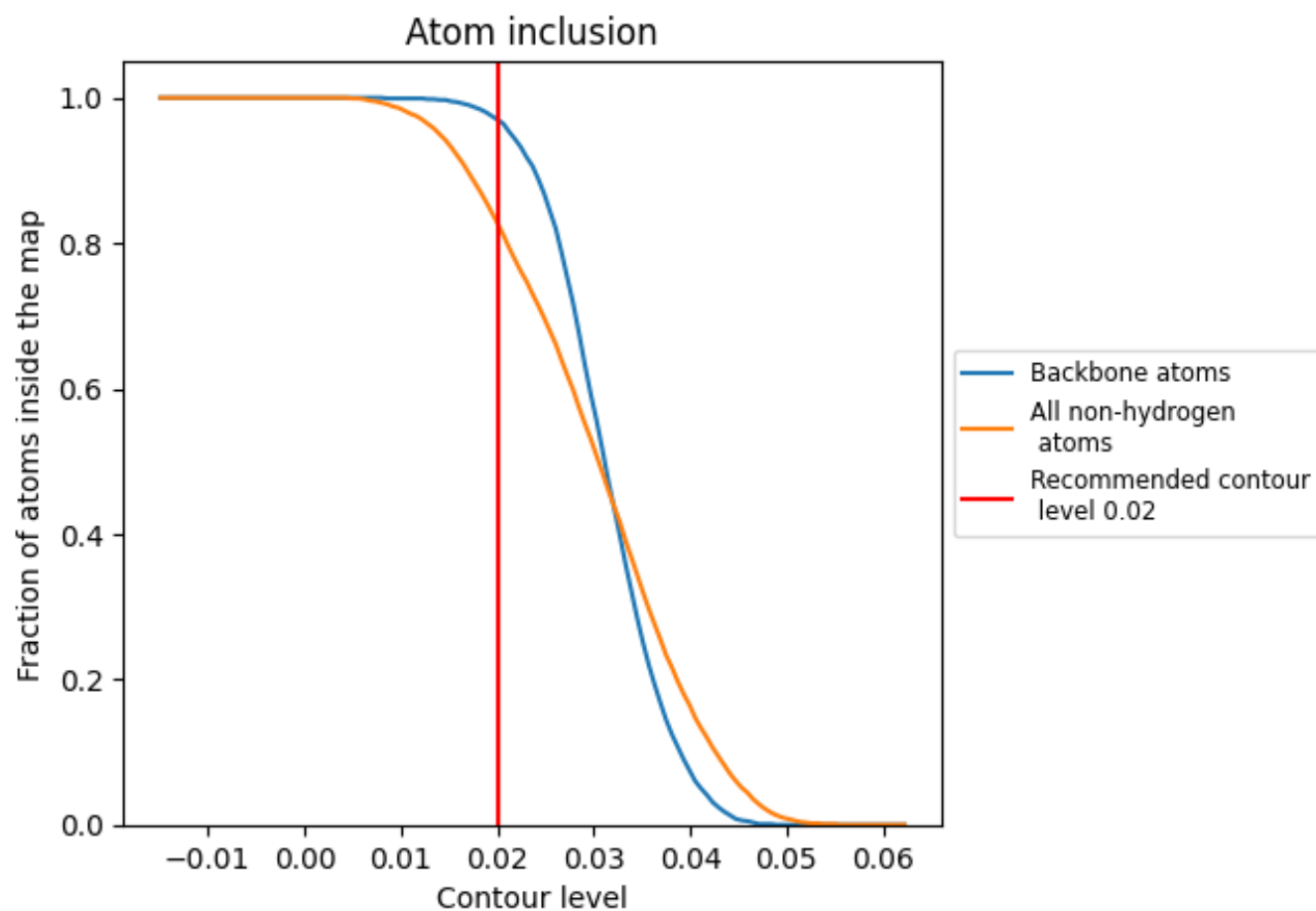
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.02).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8280</div>	<div><div></div>0.2970</div>
A	<div><div></div>0.6720</div>	<div><div></div>0.2680</div>
B	<div><div></div>0.6970</div>	<div><div></div>0.2710</div>
C	<div><div></div>0.7220</div>	<div><div></div>0.2900</div>
D	<div><div></div>0.7530</div>	<div><div></div>0.2950</div>
E	<div><div></div>0.6720</div>	<div><div></div>0.2690</div>
F	<div><div></div>0.7080</div>	<div><div></div>0.2850</div>
G	<div><div></div>0.7030</div>	<div><div></div>0.2870</div>
H	<div><div></div>0.7290</div>	<div><div></div>0.2920</div>
I	<div><div></div>0.9590</div>	<div><div></div>0.3090</div>
J	<div><div></div>0.9590</div>	<div><div></div>0.3070</div>
K	<div><div></div>0.7590</div>	<div><div></div>0.3340</div>
L	<div><div></div>0.7470</div>	<div><div></div>0.3350</div>

1.0

0.0

<0.0