



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 10:48 AM JST

PDB ID : 7VDT / pdb_00007vdt
EMDB ID : EMD-31925
Title : The motor-nucleosome module of human chromatin remodeling PBAF-nucleosome complex
Authors : Chen, Z.C.; Chen, K.J.; Yuan, J.J.
Deposited on : 2021-09-07
Resolution : 2.80 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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.50

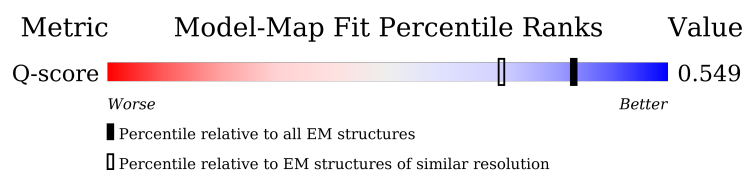
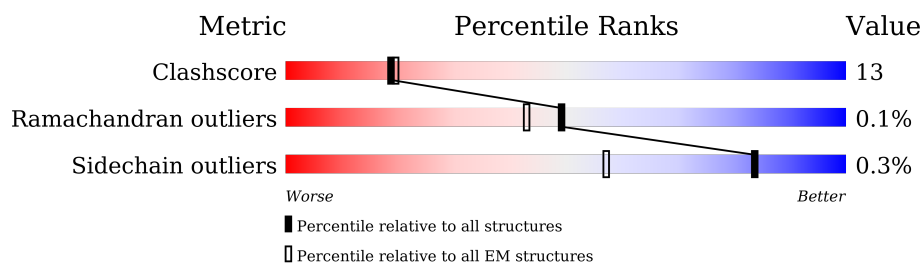
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



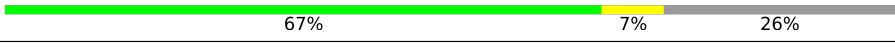
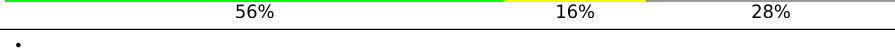
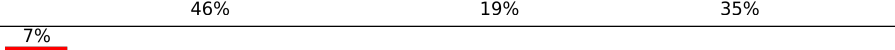
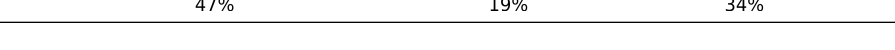
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	1485	 9% 27% 14% 50%
2	B	103	 7% 68% 17% 8%
2	F	103	 7% 70% 14% 9%
3	C	130	 1% 76% 6% 17%

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Mol	Chain	Length	Quality of chain
3	G	130	
4	D	126	
4	H	126	
5	E	136	
5	K	136	
6	I	207	
7	J	207	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 16704 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 Isoform 2 of Transcription activator BRG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	617	Total	C	N	O	S	0	0
			5057	3225	890	915	27		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	159	MET	-	initiating methionine	UNP P51532
A	1615	ALA	-	expression tag	UNP P51532
A	1616	SER	-	expression tag	UNP P51532
A	1617	GLY	-	expression tag	UNP P51532
A	1618	GLY	-	expression tag	UNP P51532
A	1619	SER	-	expression tag	UNP P51532
A	1620	TRP	-	expression tag	UNP P51532
A	1621	SER	-	expression tag	UNP P51532
A	1622	HIS	-	expression tag	UNP P51532
A	1623	PRO	-	expression tag	UNP P51532
A	1624	GLN	-	expression tag	UNP P51532
A	1625	PHE	-	expression tag	UNP P51532
A	1626	GLU	-	expression tag	UNP P51532
A	1627	LYS	-	expression tag	UNP P51532
A	1628	TRP	-	expression tag	UNP P51532
A	1629	SER	-	expression tag	UNP P51532
A	1630	HIS	-	expression tag	UNP P51532
A	1631	PRO	-	expression tag	UNP P51532
A	1632	GLN	-	expression tag	UNP P51532
A	1633	PHE	-	expression tag	UNP P51532
A	1634	GLU	-	expression tag	UNP P51532
A	1635	LYS	-	expression tag	UNP P51532
A	1636	TRP	-	expression tag	UNP P51532
A	1637	SER	-	expression tag	UNP P51532
A	1638	HIS	-	expression tag	UNP P51532
A	1639	PRO	-	expression tag	UNP P51532
A	1640	GLN	-	expression tag	UNP P51532
A	1641	PHE	-	expression tag	UNP P51532

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1642	GLU	-	expression tag	UNP P51532
A	1643	LYS	-	expression tag	UNP P51532

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	F	86	Total	C	N	O	S	0	0
			672	424	130	117	1		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	107	Total	C	N	O	S	0	0
			811	510	158	143			
3	G	108	Total	C	N	O	S	0	0
			828	522	162	144			

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	93	Total	C	N	O	S	0	0
			717	450	128	137	2		
4	H	93	Total	C	N	O	S	0	0
			725	456	130	137	2		

- Molecule 5 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	95	Total	C	N	O	S	0	0
			779	492	148	136	3		
5	K	98	Total	C	N	O	S	0	0
			801	506	153	139	3		

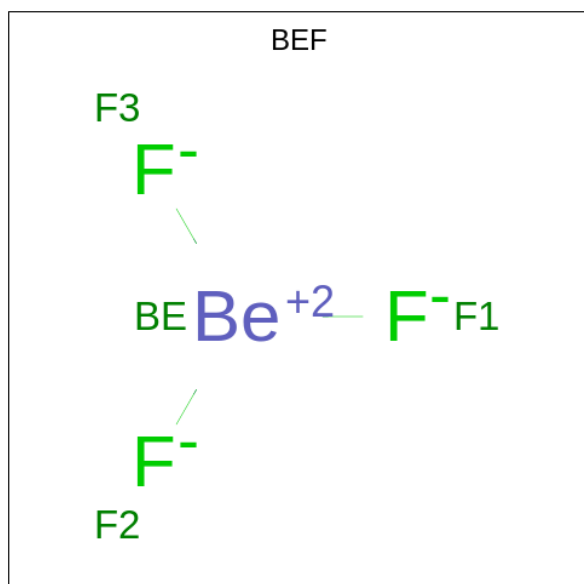
- Molecule 6 is a DNA chain called DNA (207-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	135	Total	C	N	O	P	0	0
			2752	1307	499	811	135		

- Molecule 7 is a DNA chain called DNA (207-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	137	Total	C	N	O	P	0	0
			2827	1337	532	821	137		

- Molecule 8 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3) (labeled as "Ligand of Interest" by depositor).

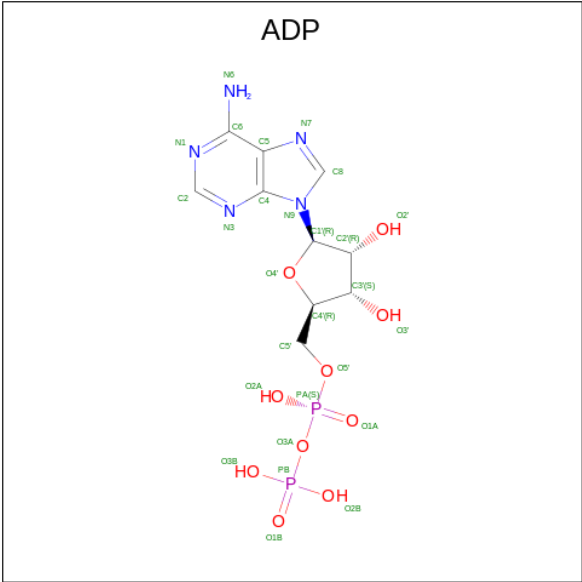


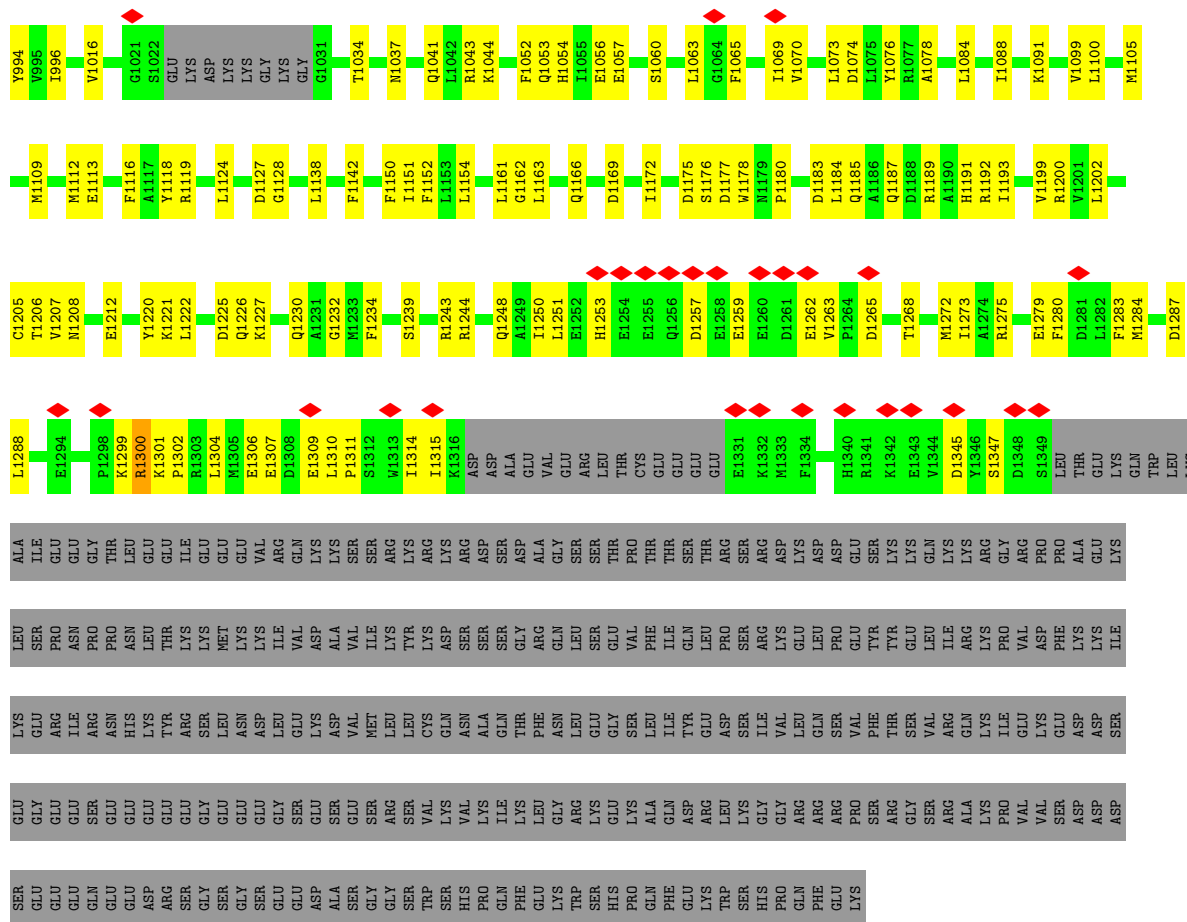
Mol	Chain	Residues	Atoms			AltConf
8	A	1	Total	Be	F	0
			4	1	3	

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
9	A	1	Total	Mg	0
			1	1	

- Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$) (labeled as "Ligand of Interest" by depositor).





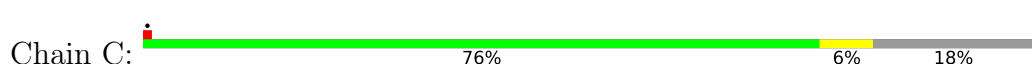
- Molecule 2: Histone H4



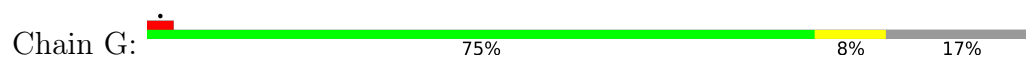
- Molecule 2: Histone H4



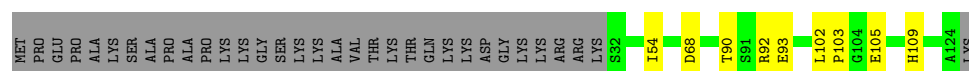
- Molecule 3: Histone H2A



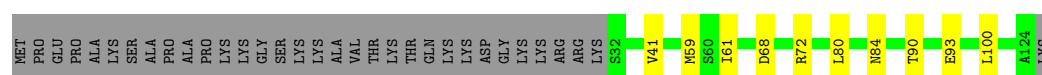
- Molecule 3: Histone H2A



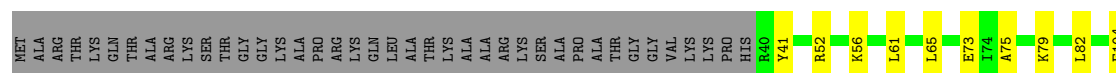
- Molecule 4: Histone H2B 1.1



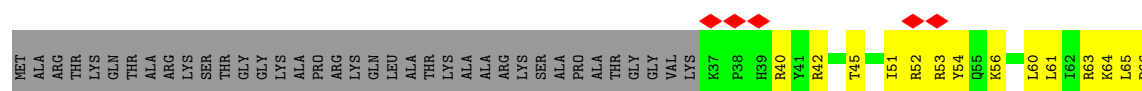
- Molecule 4: Histone H2B 1.1



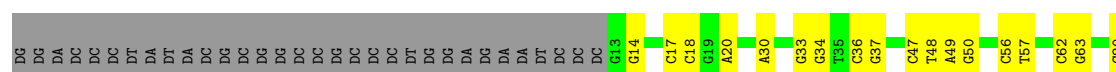
- Molecule 5: Histone H3



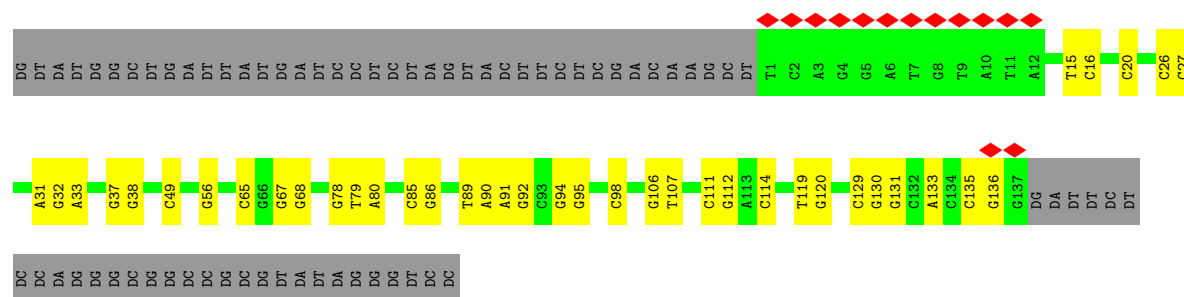
- Molecule 5: Histone H3



- Molecule 6: DNA (207-MER)



- Molecule 7: DNA (207-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	208905	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.013	Depositor
Map size ($\text{\AA}$)	389.69998, 389.69998, 389.69998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0825, 1.0825, 1.0825	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, BEF, ADP

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	0.23	0/5156	0.43	0/6943
2	B	0.31	0/711	0.42	0/950
2	F	0.30	0/680	0.40	0/912
3	C	0.27	0/821	0.34	0/1112
3	G	0.25	0/838	0.37	0/1131
4	D	0.28	0/728	0.35	0/983
4	H	0.26	0/736	0.31	0/991
5	E	0.30	0/789	0.43	1/1059 (0.1%)
5	K	0.29	0/813	0.38	0/1093
6	I	0.32	0/3083	0.40	0/4752
7	J	0.31	0/3175	0.38	0/4903
All	All	0.28	0/17530	0.40	1/24829 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	117	VAL	N-CA-C	-5.41	108.01	113.47

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	5057	0	5115	197	0
2	B	703	0	757	19	0
2	F	672	0	698	11	0
3	C	811	0	849	7	0
3	G	828	0	884	8	0
4	D	717	0	723	13	0
4	H	725	0	745	6	0
5	E	779	0	815	11	0
5	K	801	0	831	15	0
6	I	2752	0	1516	50	0
7	J	2827	0	1537	49	0
8	A	4	0	0	0	0
9	A	1	0	0	0	0
10	A	27	0	12	3	0
All	All	16704	0	14482	327	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 13.

The worst 5 of 327 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:553:LEU:O	1:A:557:THR:HG23	1.40	1.21
1:A:1076:TYR:OH	1:A:1301:LYS:NZ	1.72	1.20
1:A:556:GLN:HG3	1:A:932:ILE:HD13	1.15	1.09
1:A:552:TYR:HA	1:A:555:GLN:NE2	1.67	1.08
1:A:552:TYR:CA	1:A:555:GLN:NE2	2.21	1.04

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	609/1485 (41%)	556 (91%)	52 (8%)	1 (0%)	43	72
2	B	85/103 (82%)	81 (95%)	4 (5%)	0	100	100
2	F	84/103 (82%)	83 (99%)	1 (1%)	0	100	100
3	C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	G	106/130 (82%)	105 (99%)	1 (1%)	0	100	100
4	D	91/126 (72%)	90 (99%)	1 (1%)	0	100	100
4	H	91/126 (72%)	90 (99%)	1 (1%)	0	100	100
5	E	93/136 (68%)	93 (100%)	0	0	100	100
5	K	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
All	All	1360/2475 (55%)	1295 (95%)	64 (5%)	1 (0%)	49	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	541	LEU

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	551/1303 (42%)	547 (99%)	4 (1%)	76	91
2	B	72/79 (91%)	72 (100%)	0	100	100
2	F	67/79 (85%)	67 (100%)	0	100	100
3	C	81/102 (79%)	81 (100%)	0	100	100
3	G	84/102 (82%)	84 (100%)	0	100	100
4	D	77/106 (73%)	77 (100%)	0	100	100
4	H	79/106 (74%)	79 (100%)	0	100	100
5	E	82/111 (74%)	82 (100%)	0	100	100
5	K	84/111 (76%)	84 (100%)	0	100	100
All	All	1177/2099 (56%)	1173 (100%)	4 (0%)	84	95

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	554	LEU
1	A	555	GLN
1	A	1257	ASP
1	A	1300	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	76	GLN
5	E	85	GLN
5	K	85	GLN
3	G	104	GLN
3	C	24	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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
10	ADP	A	1703	9,1	27,29,29	1.35	4 (14%)	42,45,45	1.98	8 (19%)
8	BEF	A	1701	-	0,3,3	-	-	-		

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
10	ADP	A	1703	9,1	-	2/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1703	ADP	C5-C4	4.37	1.47	1.39
10	A	1703	ADP	C5-C6	2.50	1.48	1.41
10	A	1703	ADP	C5-N7	-2.45	1.34	1.39
10	A	1703	ADP	C8-N7	2.17	1.35	1.31

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1703	ADP	C5-C4-N3	-6.30	118.53	126.75
10	A	1703	ADP	N3-C4-N9	5.03	135.37	127.08
10	A	1703	ADP	C2-N3-C4	3.83	120.79	111.75
10	A	1703	ADP	PA-O3A-PB	-3.81	119.76	132.83
10	A	1703	ADP	C4-C5-N7	-3.04	106.91	110.62

There are no chirality outliers.

All (2) torsion outliers are listed below:

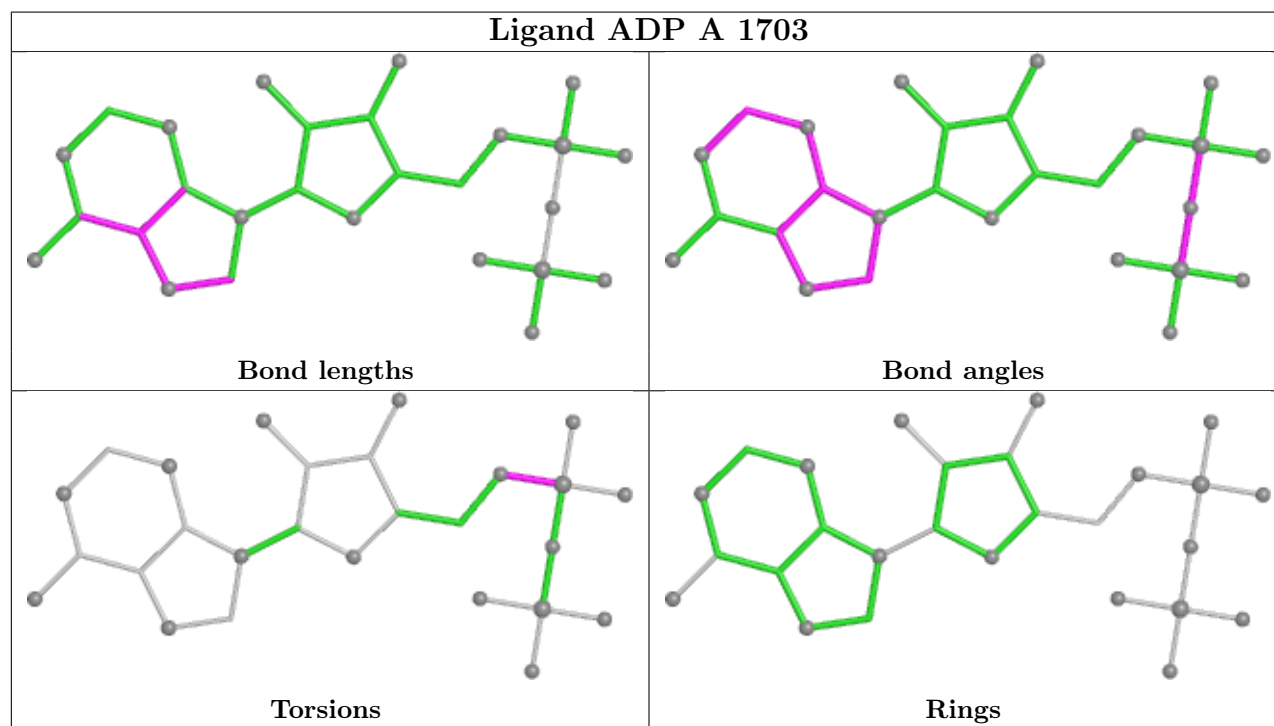
Mol	Chain	Res	Type	Atoms
10	A	1703	ADP	C5'-O5'-PA-O1A
10	A	1703	ADP	C5'-O5'-PA-O3A

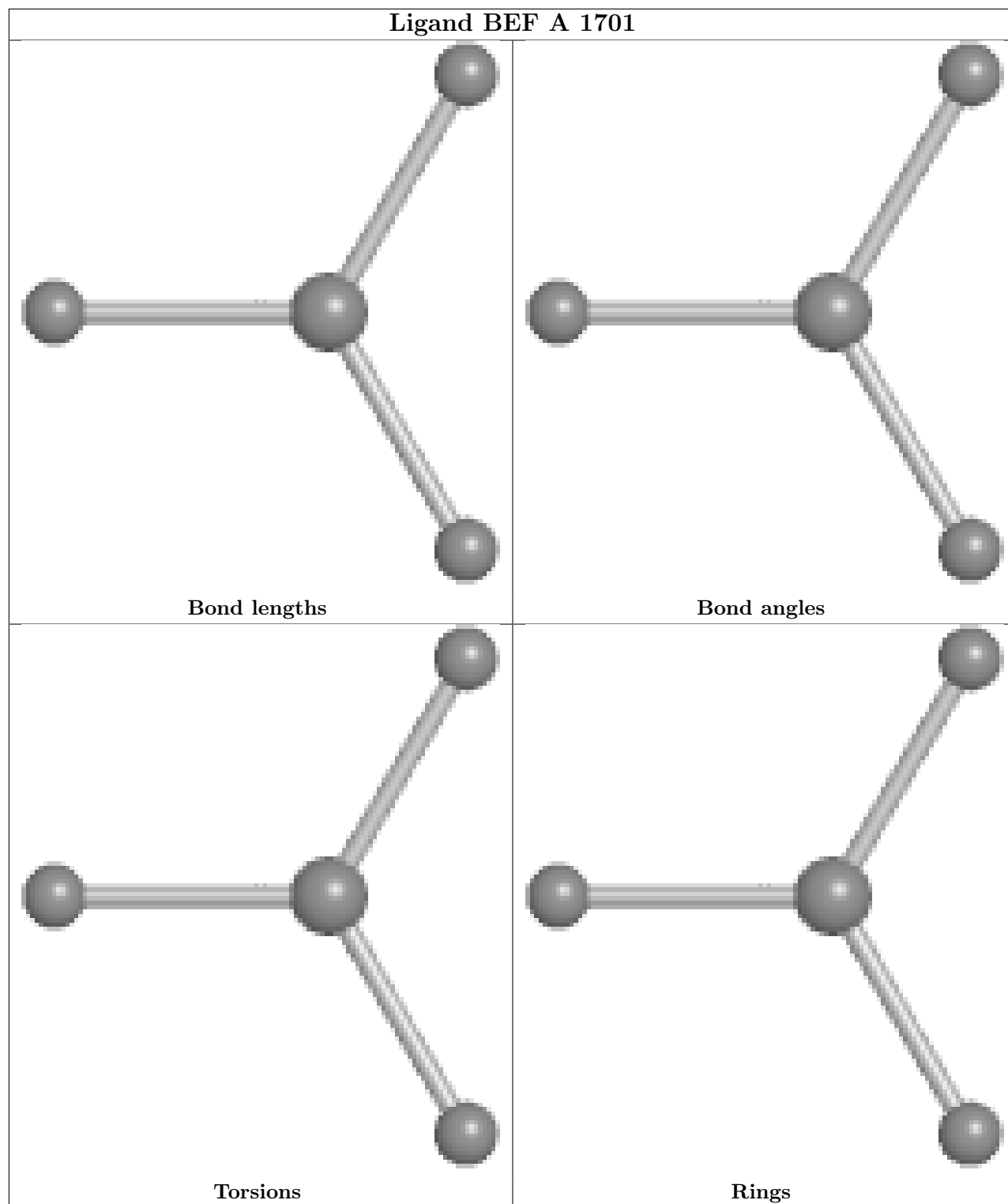
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	1703	ADP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

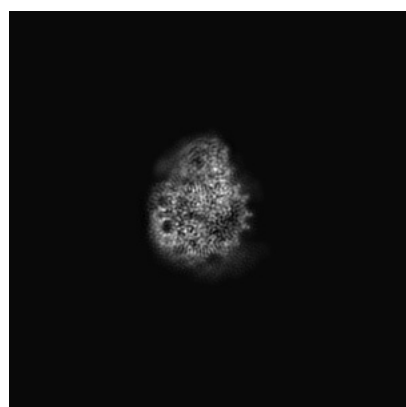
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31925. These allow visual inspection of the internal detail of the map and identification of artifacts.

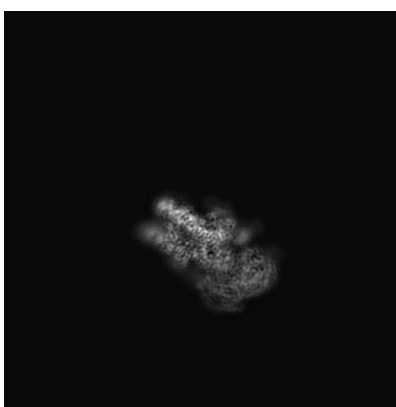
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

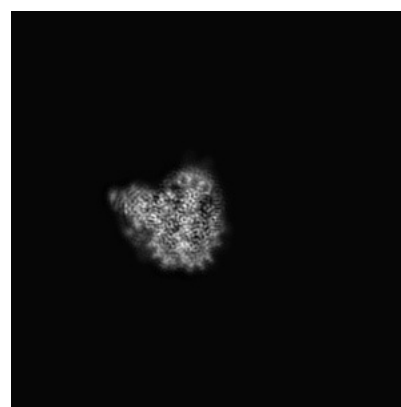
6.1.1 Primary map



X



Y



Z

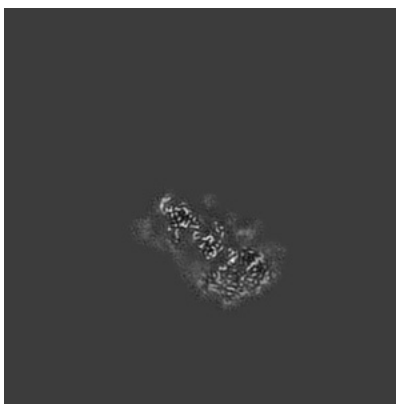
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

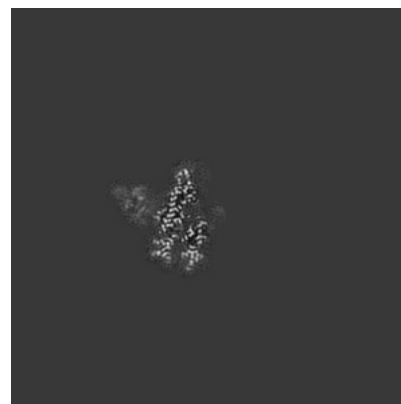
6.2.1 Primary map



X Index: 180



Y Index: 180

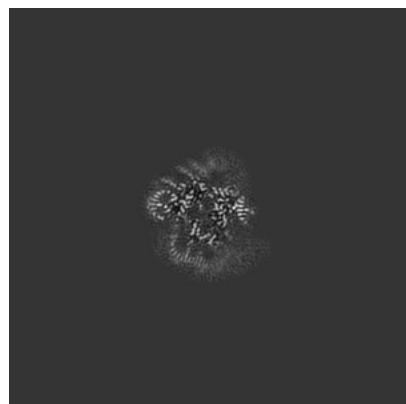


Z Index: 180

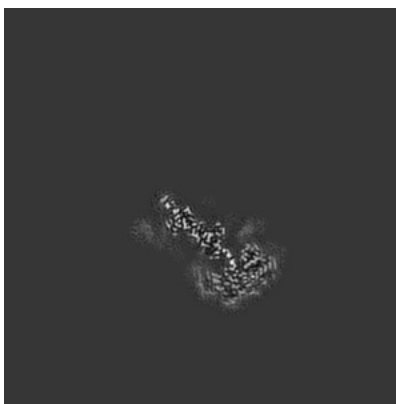
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

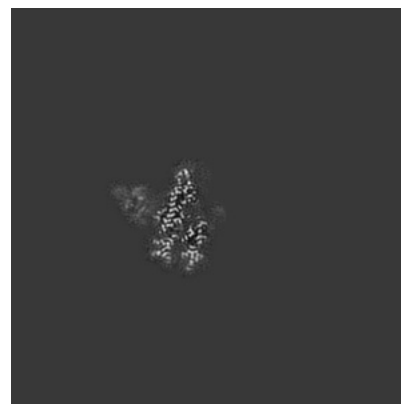
6.3.1 Primary map



X Index: 160



Y Index: 184

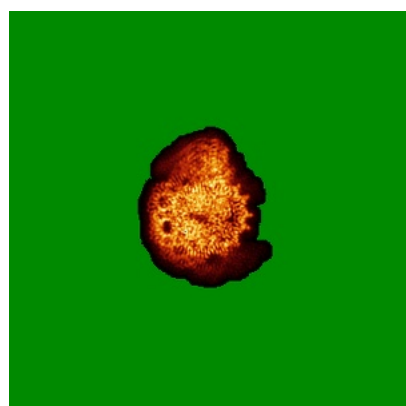


Z Index: 180

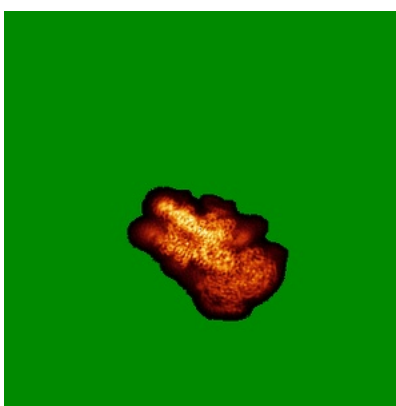
The images above show the largest variance slices of the map in three orthogonal directions.

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

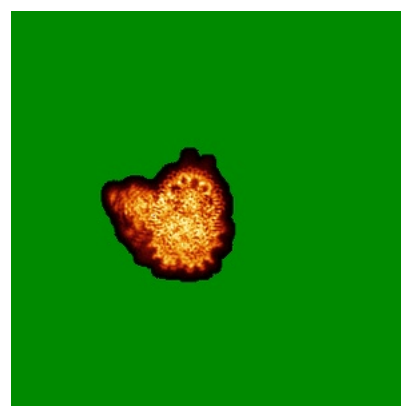
6.4.1 Primary map



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

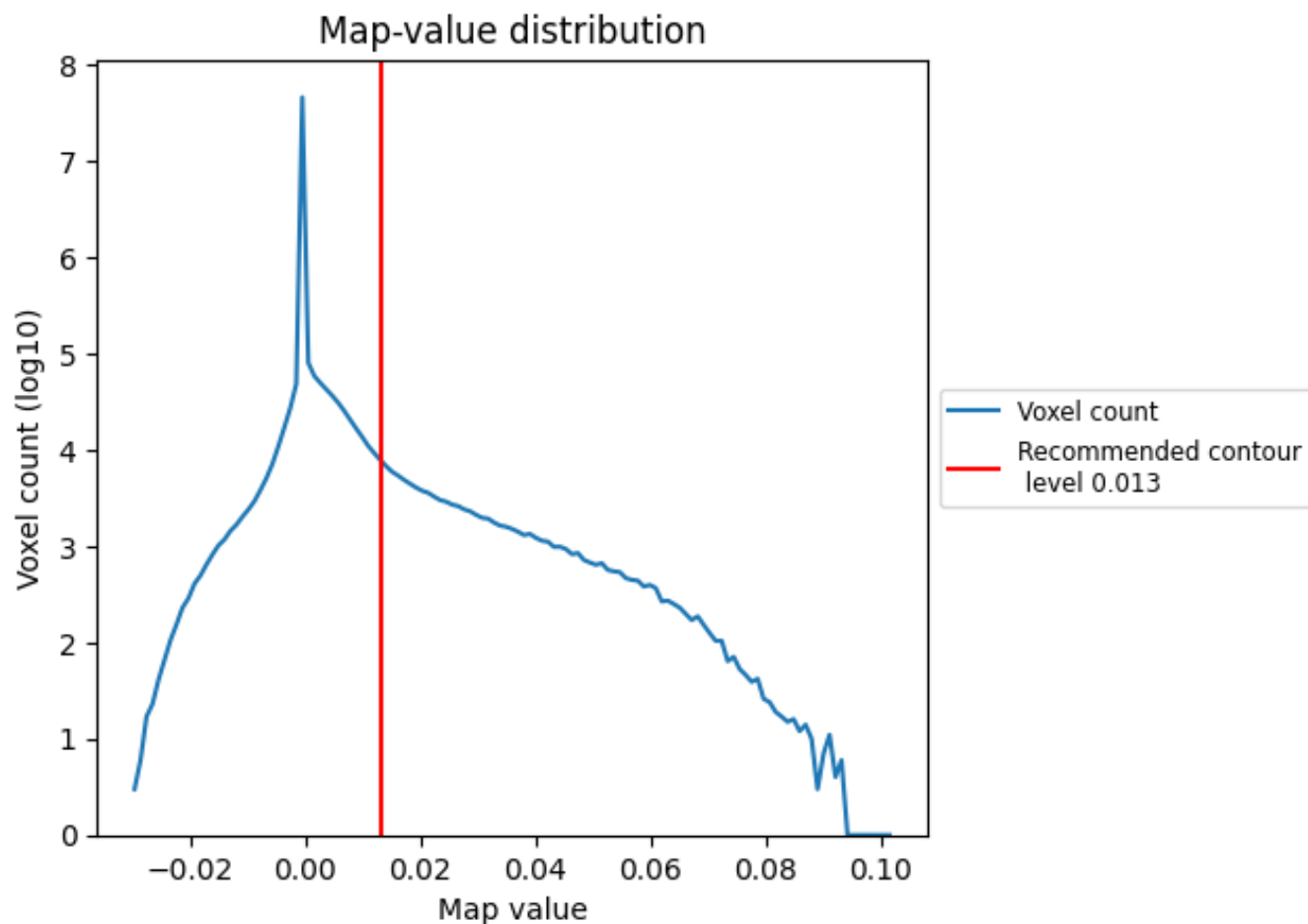
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

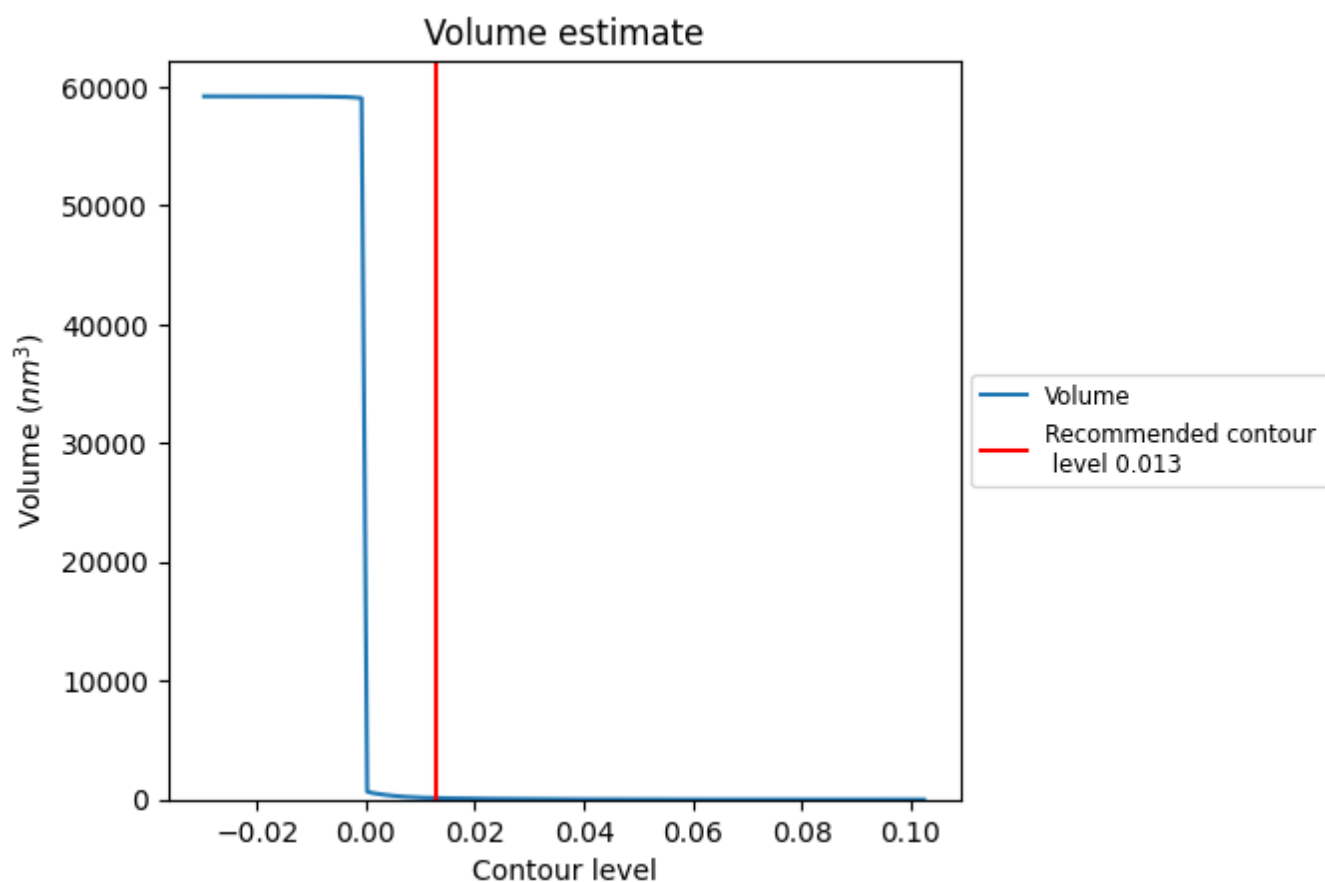
This section contains the results of statistical analysis of the map.

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.

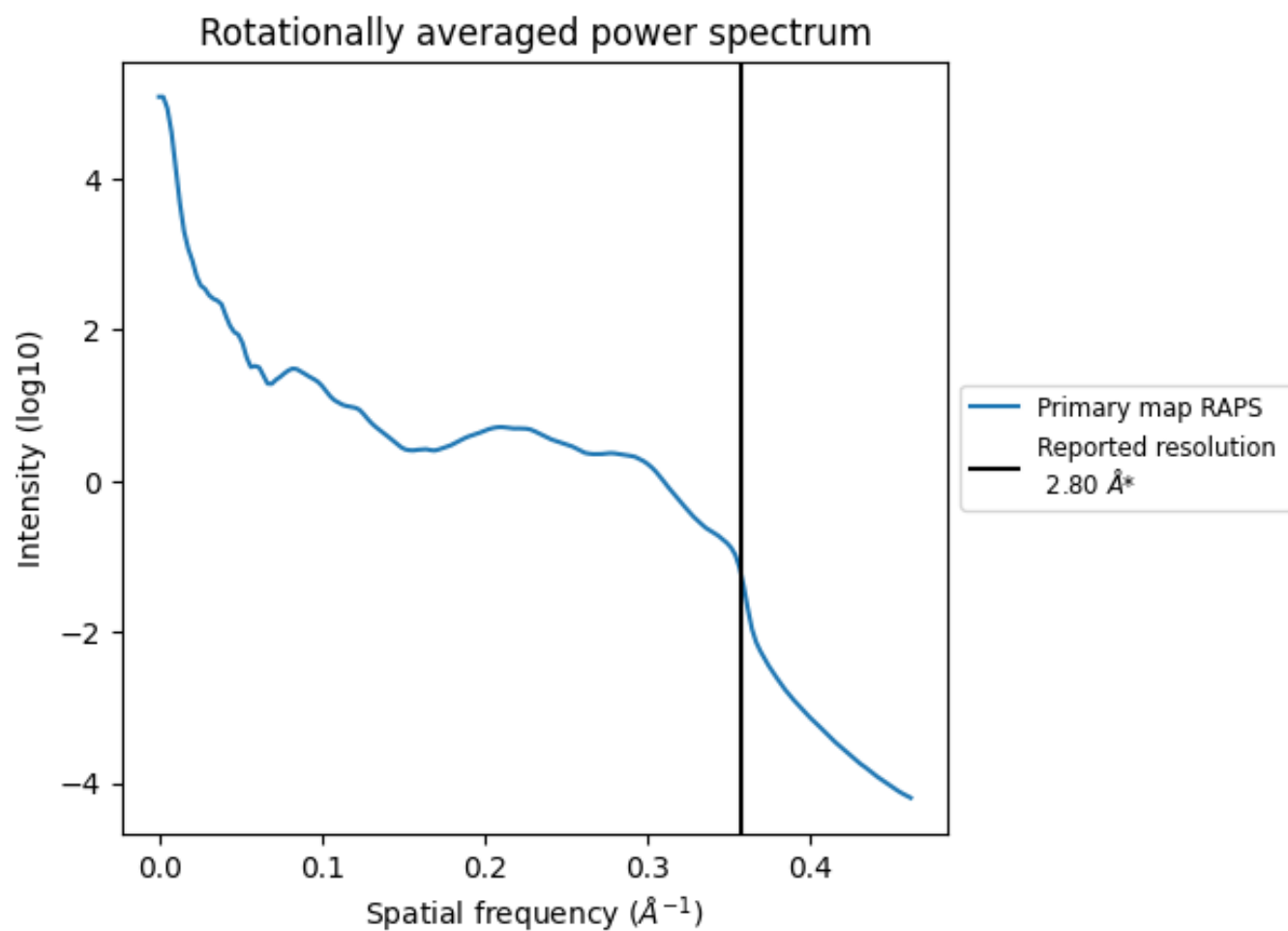
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 127 nm^3 ; this corresponds to an approximate mass of 114 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 0.357 Å⁻¹

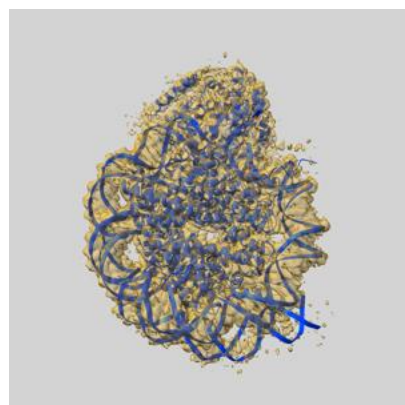
8 Fourier-Shell correlation

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

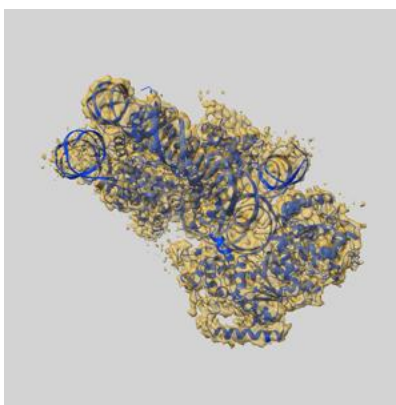
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31925 and PDB model 7VDT. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

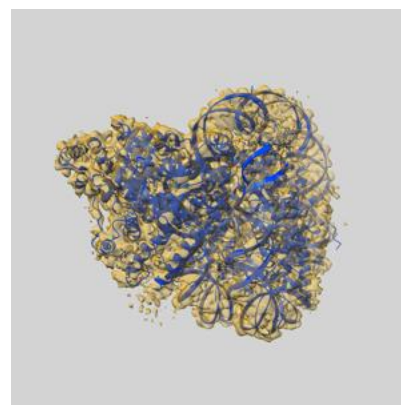
9.1 Map-model overlay [i](#)



X



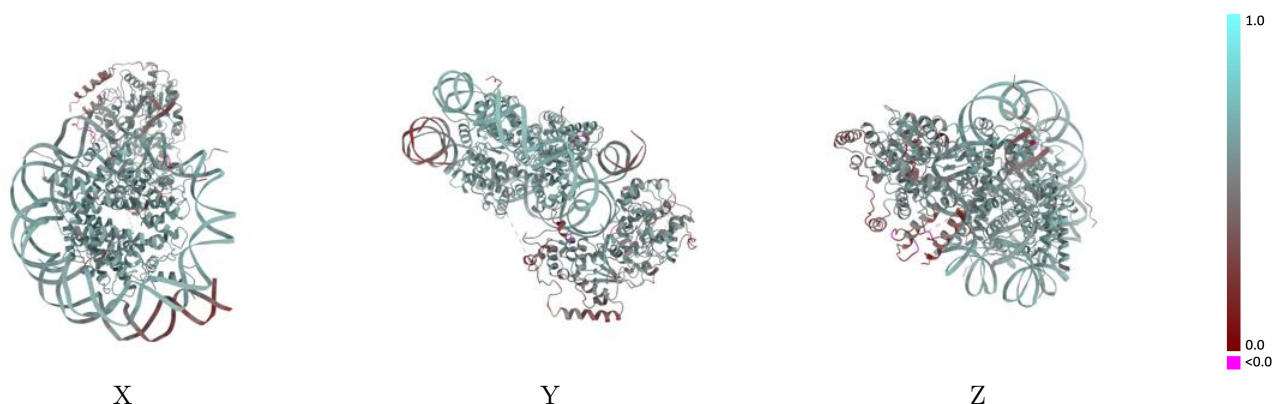
Y



Z

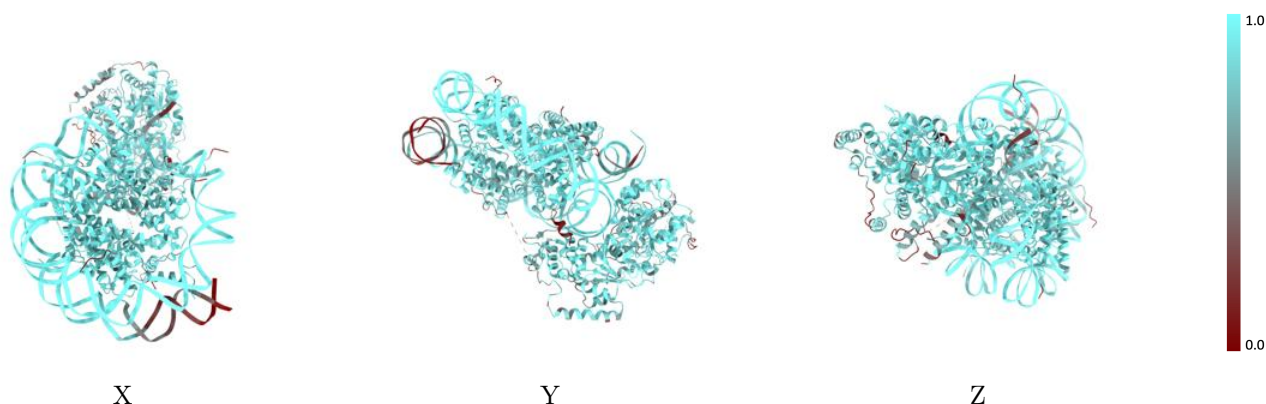
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



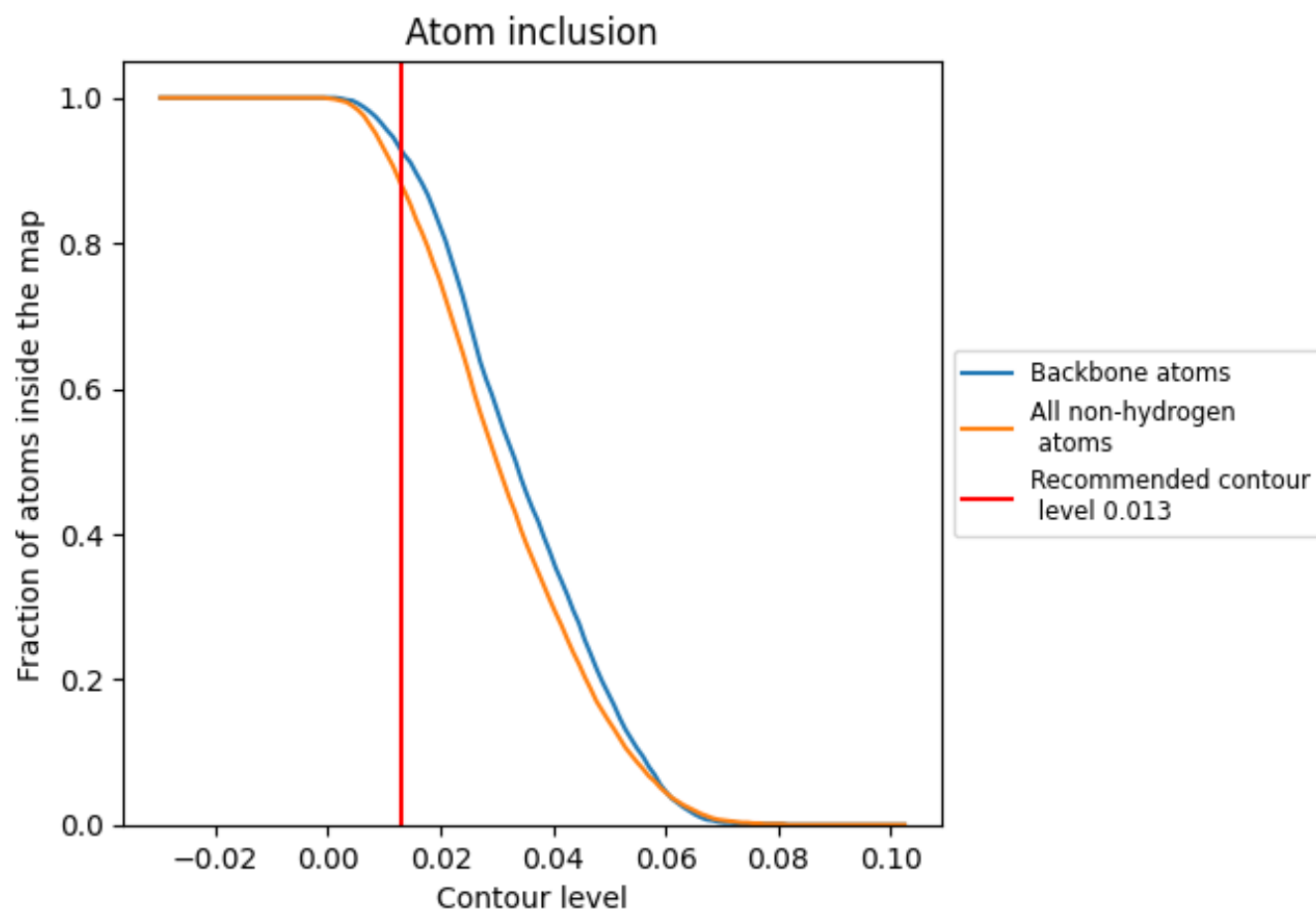
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8810	0.5490
A	0.8070	0.4740
B	0.8840	0.5750
C	0.9500	0.6150
D	0.9660	0.6050
E	0.9520	0.6150
F	0.9090	0.6050
G	0.8930	0.5900
H	0.9440	0.6020
I	0.9170	0.5690
J	0.8900	0.5610
K	0.8910	0.5740

1.0

0.0

<0.0