

# Full wwPDB EM Validation Report (i)

Jul 22, 2023 – 01:23 pm BST

PDB ID : 8009

EMDB ID : EMD-17007

Title : CryoEM Structure INO80core Hexasome complex ATPase-DNA refinement

state1

Authors: Zhang, M.; Jungblut, A.; Hoffmann, T.; Eustermann, S.

Deposited on : 2023-04-04

Resolution : 3.20 Å(reported)

Based on initial models : 8AV6, 3I62

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

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 (1)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev50

Mogul : 1.8.4, CSD as541be (2020)

MolProbity : 4.02b-467 buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

MapQ : 1.9.9

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

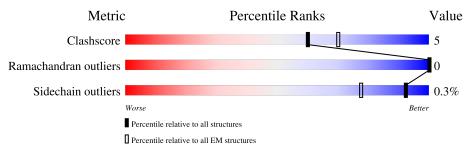
Validation Pipeline (wwPDB-VP) : 2.34

# 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 3.20 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 $(\# \mathrm{Entries})$	${ m EM\ structures} \ (\#{ m Entries})$
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	G	1134	37% • 61%					
2	K	226	· 7% 91%					
3	L	226	• 5% 91%					



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4516 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 Chromatin-remodeling ATPase INO80.

Mol	Chain	Residues		At	oms			AltConf	Trace
1	G	439	Total 3622	C 2319	N 638	O 641	S 24	0	0

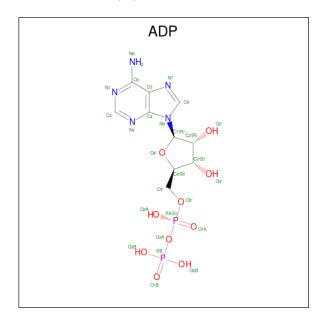
• Molecule 2 is a DNA chain called DNA strand 1.

Mol	Chain	Residues		At	oms			AltConf	Trace
2	K	21	Total 431	C 204	N 81	O 125	P 21	0	0

• Molecule 3 is a DNA chain called DNA strand 2.

Mol	Chain	Residues		At	oms	}		AltConf	Trace
3	L	21	Total 430			O 127	P 21	0	0

• Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).



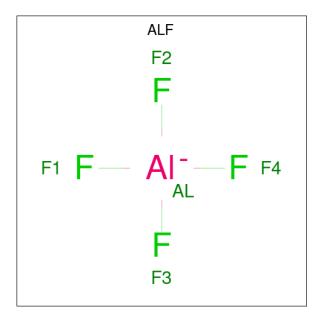


Mol	Chain	Residues	Atoms			AltConf		
4	С	1	Total	С	N	О	Р	0
4	G	1	27	10	5	10	2	0

• Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	G	1	Total 1	Mg 1	0

• Molecule 6 is TETRAFLUOROALUMINATE ION (three-letter code: ALF) (formula: AlF<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



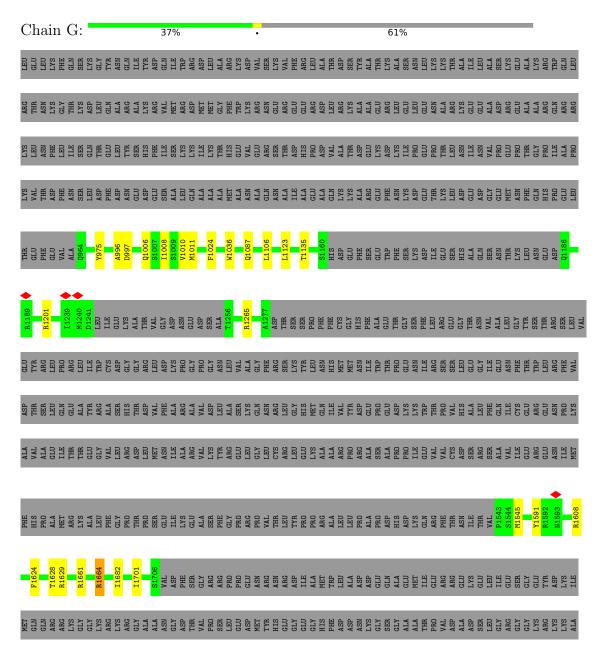
Mol	Chain	Residues	Atoms	AltConf
6	G	1	Total Al F 5 1 4	0



# 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.

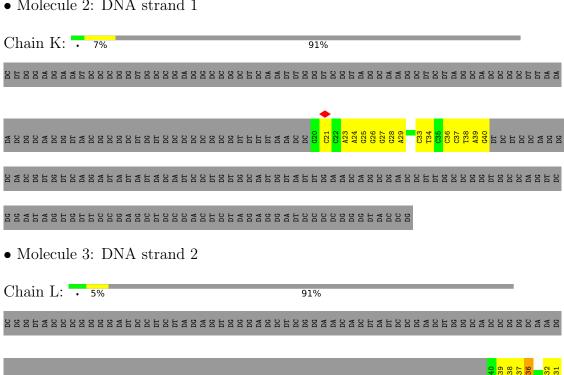
• Molecule 1: Chromatin-remodeling ATPase INO80





#### 

• Molecule 2: DNA strand 1





# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72400	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	50.36	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.239	Depositor
Minimum map value	-0.144	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.158	Depositor
Map size (Å)	295.92, 295.92, 295.92	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	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: ADP, ALF, MG

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	Boı	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z >5	
1	G	0.44	0/3696	0.63	0/4978	
2	K	0.87	0/483	0.63	0/743	
3	L	1.00	2/481~(0.4%)	0.67	0/740	
All	All	0.58	$2/4660 \ (0.0\%)$	0.63	0/6461	

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

M	ol	Chain	#Chirality outliers	#Planarity outliers
	_	G	0	1

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\mathring{A})$	Ideal(A)
3	L	-36	DG	C4'-C3'	5.84	1.59	1.53
3	L	-36	DG	C2'-C1'	-5.09	1.47	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	1664	ARG	Sidechain



### 5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	3622	0	3679	14	0
2	K	431	0	236	16	0
3	L	430	0	237	9	0
4	G	27	0	12	0	0
5	G	1	0	0	0	0
6	G	5	0	0	0	0
All	All	4516	0	4164	37	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.

All (37) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\text{\AA}) \end{array}$	Clash overlap (Å)
2:K:24:DA:H2"	2:K:25:DG:C8	2.03	0.93
2:K:25:DG:H2"	2:K:26:DG:C8	2.06	0.90
2:K:25:DG:H2'	2:K:25:DG:OP2	1.91	0.69
3:L:-39:DT:H2"	3:L:-38:DA:C8	2.28	0.68
3:L:-37:DG:H2"	3:L:-36:DG:C8	2.29	0.68
3:L:-32:DT:H2"	3:L:-31:DA:C8	2.32	0.65
1:G:1008:ILE:HD11	1:G:1036:TRP:HE1	1.62	0.64
1:G:975:TYR:O	1:G:1201:ARG:NH1	2.33	0.62
2:K:28:DG:H2"	2:K:29:DA:C8	2.39	0.56
3:L:-25:DC:H1'	3:L:-24:DT:C6	2.41	0.56
1:G:1608:ARG:NH2	3:L:-28:DC:OP2	2.37	0.56
3:L:-38:DA:H2"	3:L:-37:DG:C8	2.41	0.56
2:K:25:DG:H4'	2:K:26:DG:H5'	1.88	0.55
2:K:26:DG:H2'	2:K:26:DG:OP2	2.09	0.53
2:K:26:DG:H2"	2:K:27:DG:C8	2.43	0.53
2:K:21:DC:C6	2:K:21:DC:OP2	2.63	0.52
1:G:1106:LEU:HD21	1:G:1123:LEU:HD13	1.92	0.51
1:G:997:ASP:OD2	1:G:1201:ARG:NH2	2.44	0.50
1:G:1087:GLN:HG3	3:L:-28:DC:H4'	1.92	0.50
2:K:33:DC:H2"	2:K:34:DT:H71	1.93	0.49
1:G:1701:ILE:O	1:G:1701:ILE:HG22	2.14	0.48

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Atom-1	Atom-2	Interatomic	Clash
		${ m distance}({ m \AA})$	overlap (Å)
1:G:1011:MET:HE2	1:G:1024:PHE:HB3	1.94	0.48
2:K:25:DG:C2'	2:K:26:DG:C8	2.91	0.47
2:K:36:DC:H2"	2:K:37:DC:C5	2.50	0.46
2:K:21:DC:OP2	2:K:21:DC:H6	1.99	0.45
2:K:37:DC:H2"	2:K:38:DT:C6	2.52	0.45
2:K:23:DA:H2"	2:K:24:DA:C8	2.52	0.44
3:L:-31:DA:H2"	3:L:-30:DA:C8	2.52	0.44
3:L:-27:DC:H2"	3:L:-26:DC:C6	2.53	0.44
1:G:1265:ARG:HG3	1:G:1682:ILE:HD11	1.99	0.44
1:G:1545:MET:HB3	1:G:1591:TYR:CD2	2.53	0.43
1:G:1661:ARG:HH21	1:G:1664:ARG:NH1	2.16	0.43
1:G:1006:GLN:O	1:G:1010:VAL:HG23	2.20	0.42
2:K:27:DG:OP2	2:K:27:DG:H8	2.03	0.41
1:G:1628:THR:HG23	1:G:1629:ARG:N	2.36	0.41
1:G:996:ALA:HA	1:G:1135:THR:O	2.21	0.40
2:K:39:DA:H2"	2:K:40:DG:N7	2.36	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			
1	G	431/1134 (38%)	421 (98%)	10 (2%)	0	100 10	00

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains (i)

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	Analysed Rotameric O		Percentiles
1	G	397/989 (40%)	396 (100%)	1 (0%)	92 96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	1624	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	1663	HIS

#### 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 monosaccharides 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	Trus	Chain	Res	Link	Во	ond leng	ths	В	ond ang	les
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	ALF	G	2003	-	0,4,4	-	-	-		
4	ADP	G	2001	5	24,29,29	0.98	2 (8%)	29,45,45	1.48	4 (13%)

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
4	ADP	G	2001	5	-	3/12/32/32	0/3/3/3

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
4	G	2001	ADP	C5-C4	2.14	1.46	1.40
4	G	2001	ADP	C2'-C1'	-2.03	1.50	1.53

#### All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\mathrm{Ideal}(^{o})$
4	G	2001	ADP	PA-O3A-PB	-3.69	120.16	132.83
4	G	2001	ADP	N3-C2-N1	-3.11	123.82	128.68
4	G	2001	ADP	C4-C5-N7	-2.99	106.28	109.40
4	G	2001	ADP	O3B-PB-O2B	2.59	117.53	107.64

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	2001	ADP	PA-O3A-PB-O2B
4	G	2001	ADP	PA-O3A-PB-O1B
4	G	2001	ADP	O4'-C4'-C5'-O5'

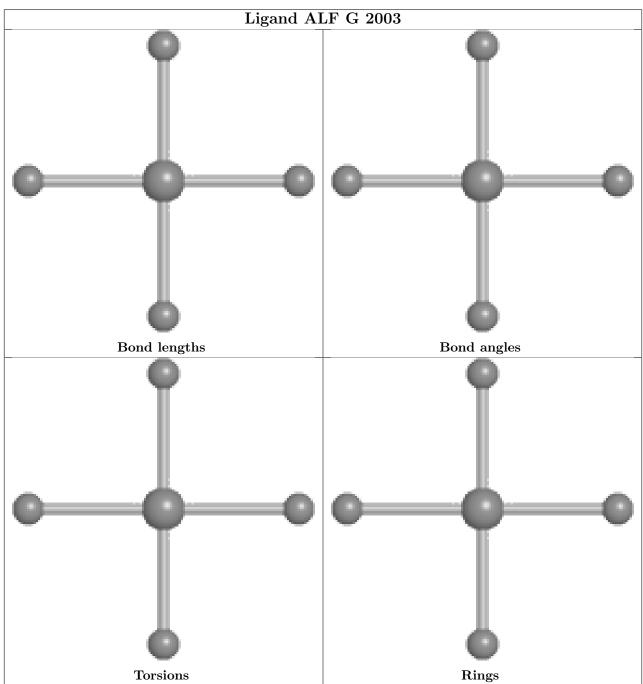
There are no ring outliers.

No monomer is involved in short contacts.

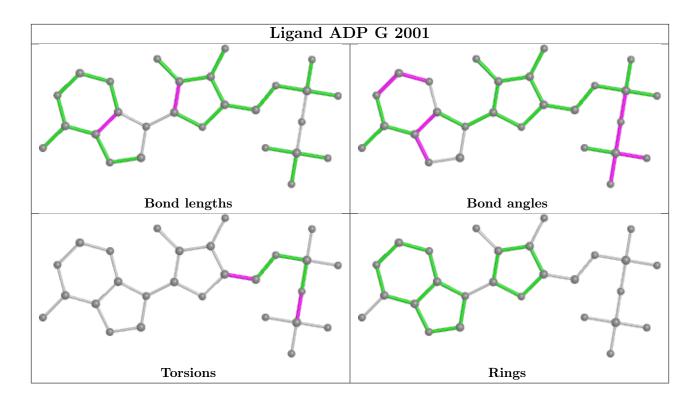
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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 (i)

There are no chain breaks in this entry.



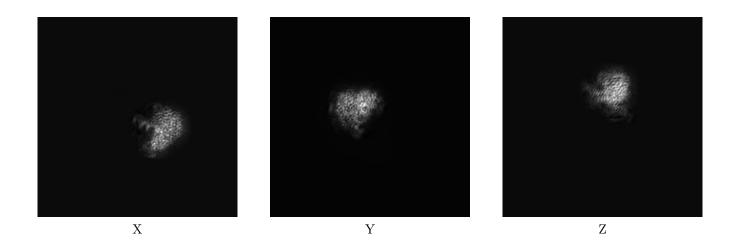
# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-17007. These allow visual inspection of the internal detail of the map and identification of artifacts.

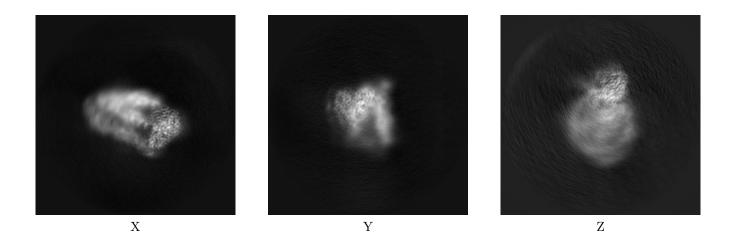
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

#### 6.1 Orthogonal projections (i)

#### 6.1.1 Primary map



#### 6.1.2 Raw map

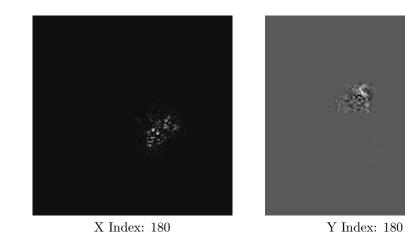


The images above show the map projected in three orthogonal directions.



# 6.2 Central slices (i)

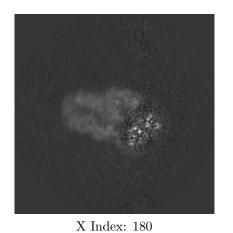
#### 6.2.1 Primary map

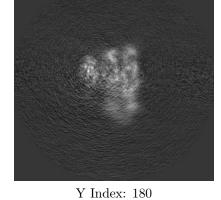


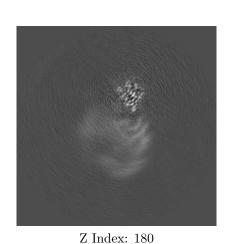


Raw map

6.2.2







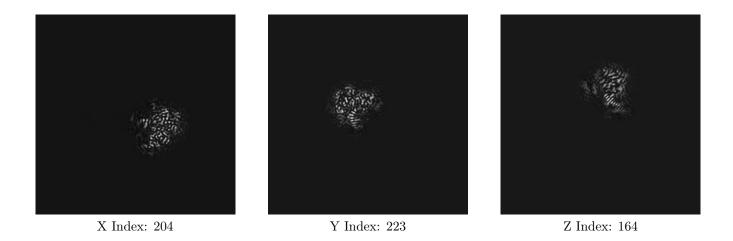
The images above show central slices of the map in three orthogonal directions.

The images above show central shees of the map in timee of thogonal affections

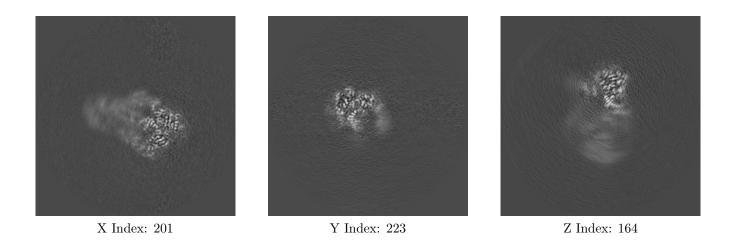


# 6.3 Largest variance slices (i)

#### 6.3.1 Primary map



#### 6.3.2 Raw map

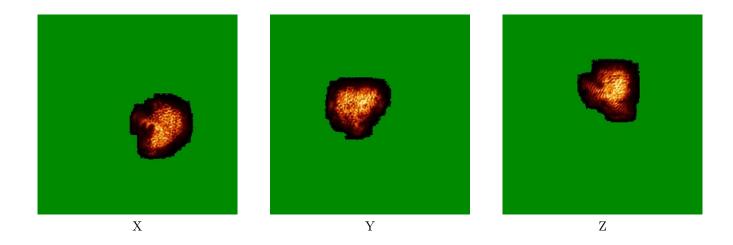


The images above show the largest variance slices of the map in three orthogonal directions.

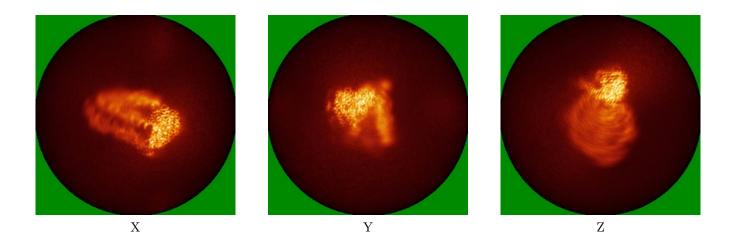


### 6.4 Orthogonal standard-deviation projections (False-color) (i)

#### 6.4.1 Primary map



#### 6.4.2 Raw map

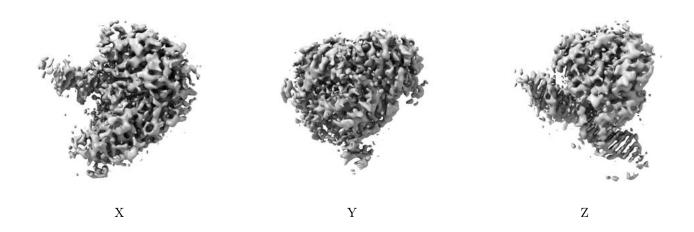


The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



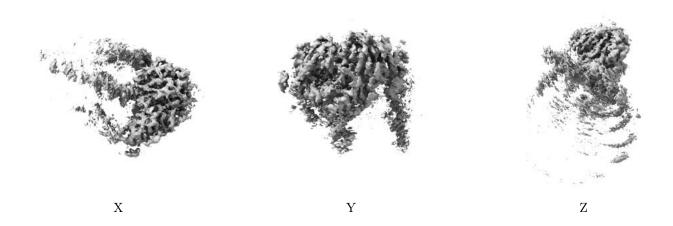
# 6.5 Orthogonal surface views (i)

#### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.158. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

#### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

### 6.6 Mask visualisation (i)

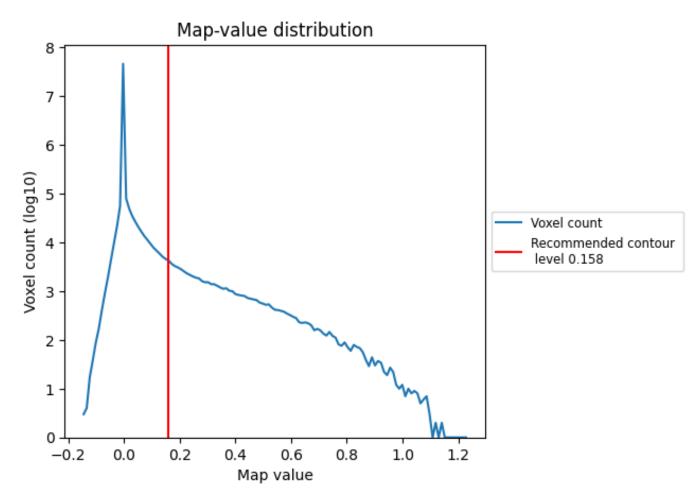
This section was not generated. No masks/segmentation were deposited.



# 7 Map analysis (i)

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

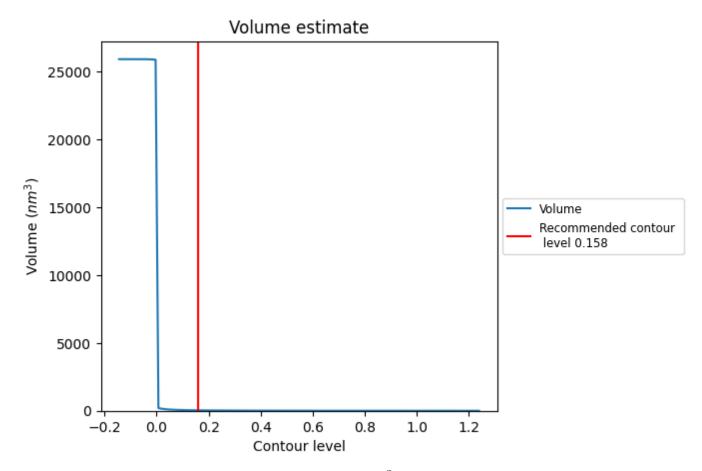
### 7.1 Map-value distribution (i)



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)

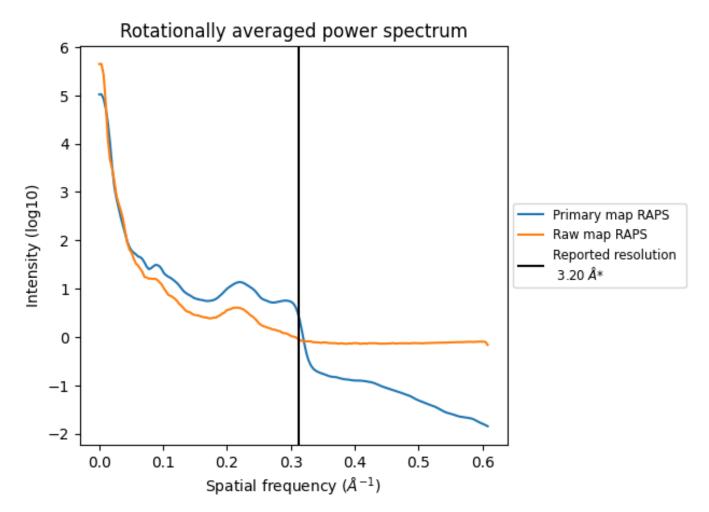


The volume at the recommended contour level is  $33~\mathrm{nm^3}$ ; this corresponds to an approximate mass of  $30~\mathrm{kDa}$ .

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 (i)



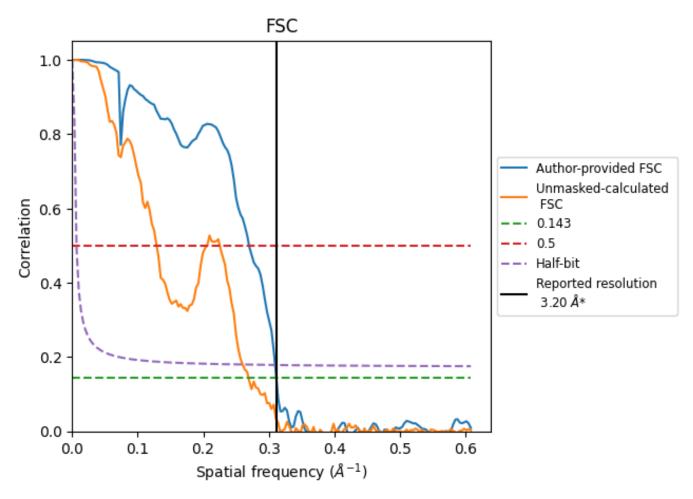
<sup>\*</sup>Reported resolution corresponds to spatial frequency of 0.312  $\rm \mathring{A}^{-1}$ 



# 8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC (i)



\*Reported resolution corresponds to spatial frequency of 0.312  $\rm \mathring{A}^{-1}$ 



# 8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
rtesolution estimate (A)	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.21	3.71	3.23
Unmasked-calculated*	3.71	7.76	3.84

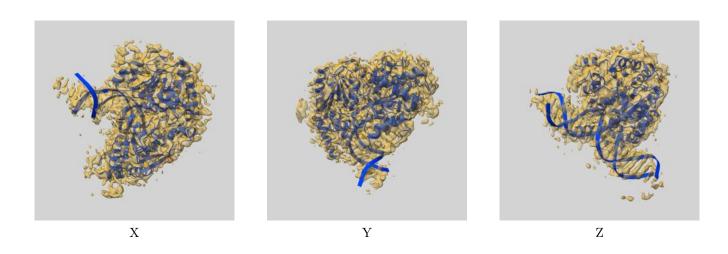
<sup>\*</sup>Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.71 differs from the reported value 3.2 by more than 10 %



# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-17007 and PDB model 8009. Per-residue inclusion information can be found in section 3 on page 5.

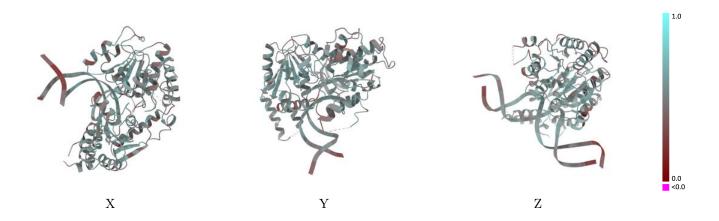
# 9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.158 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

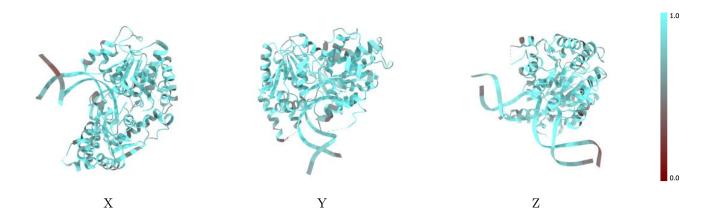


### 9.2 Q-score mapped to coordinate model (i)



The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

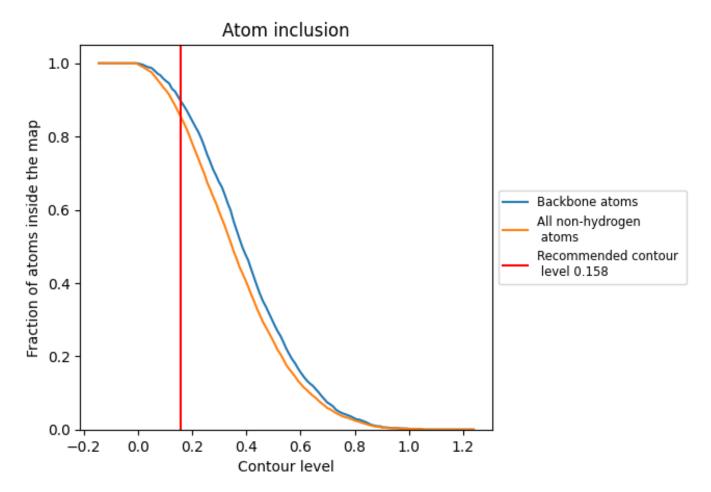
### 9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.158).



# 9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.



# 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.158) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8540	0.5150
G	0.8640	0.5230
K	0.8050	0.4660
L	0.8210	0.4940



