



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 02:06 AM EST

PDB ID : 7S6C
EMDB ID : EMD-24868
Title : CryoEM structure of modular PKS holo-Lsd14 stalled at the condensation step and bound to antibody fragment 1B2, composite structure
Authors : Bagde, S.R.; Kim, C.-Y.; Fromme, J.C.
Deposited on : 2021-09-13
Resolution : 3.10 Å (reported)
Based on initial models : 7S6B, 6C9U

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.dev43
Mogul : 1.8.5 (274361), 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) : 2.31.3

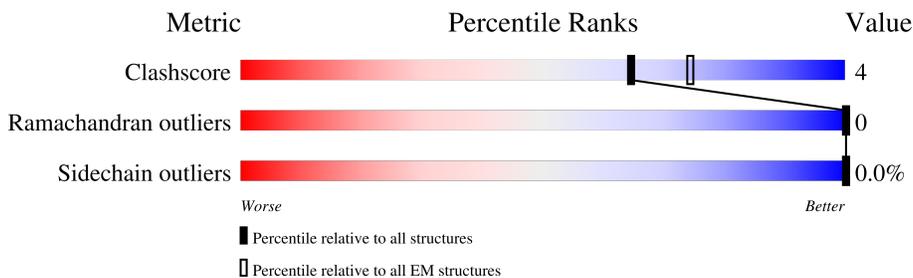
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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	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 $\leq 5\%$. 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	1649	
1	B	1649	
1	C	1649	
1	D	1649	
2	E	249	
2	H	249	
3	F	236	
3	G	236	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 47400 atoms, of which 23451 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 6-deoxyerythronolide-B synthase EryA2, modules 3 and 4, Lsd14 Polyketide synthase fusion.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	895	13235	4176	6542	1220	1277	20	0	0
1	B	891	13199	4162	6521	1218	1278	20	0	0
1	C	480	6988	2208	3471	638	668	3	0	0
1	D	82	1257	388	632	120	115	2	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	initiating methionine	UNP Q03132
A	8	VAL	-	expression tag	UNP Q03132
A	1648	LEU	-	expression tag	UNP B6ZK67
A	1649	GLU	-	expression tag	UNP B6ZK67
A	1650	HIS	-	expression tag	UNP B6ZK67
A	1651	HIS	-	expression tag	UNP B6ZK67
A	1652	HIS	-	expression tag	UNP B6ZK67
A	1653	HIS	-	expression tag	UNP B6ZK67
A	1654	HIS	-	expression tag	UNP B6ZK67
A	1655	HIS	-	expression tag	UNP B6ZK67
B	7	MET	-	initiating methionine	UNP Q03132
B	8	VAL	-	expression tag	UNP Q03132
B	1648	LEU	-	expression tag	UNP B6ZK67
B	1649	GLU	-	expression tag	UNP B6ZK67
B	1650	HIS	-	expression tag	UNP B6ZK67
B	1651	HIS	-	expression tag	UNP B6ZK67
B	1652	HIS	-	expression tag	UNP B6ZK67
B	1653	HIS	-	expression tag	UNP B6ZK67
B	1654	HIS	-	expression tag	UNP B6ZK67
B	1655	HIS	-	expression tag	UNP B6ZK67
C	7	MET	-	initiating methionine	UNP Q03132

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Chain	Residue	Modelled	Actual	Comment	Reference
C	8	VAL	-	expression tag	UNP Q03132
C	1648	LEU	-	expression tag	UNP B6ZK67
C	1649	GLU	-	expression tag	UNP B6ZK67
C	1650	HIS	-	expression tag	UNP B6ZK67
C	1651	HIS	-	expression tag	UNP B6ZK67
C	1652	HIS	-	expression tag	UNP B6ZK67
C	1653	HIS	-	expression tag	UNP B6ZK67
C	1654	HIS	-	expression tag	UNP B6ZK67
C	1655	HIS	-	expression tag	UNP B6ZK67
D	7	MET	-	initiating methionine	UNP Q03132
D	8	VAL	-	expression tag	UNP Q03132
D	1648	LEU	-	expression tag	UNP B6ZK67
D	1649	GLU	-	expression tag	UNP B6ZK67
D	1650	HIS	-	expression tag	UNP B6ZK67
D	1651	HIS	-	expression tag	UNP B6ZK67
D	1652	HIS	-	expression tag	UNP B6ZK67
D	1653	HIS	-	expression tag	UNP B6ZK67
D	1654	HIS	-	expression tag	UNP B6ZK67
D	1655	HIS	-	expression tag	UNP B6ZK67

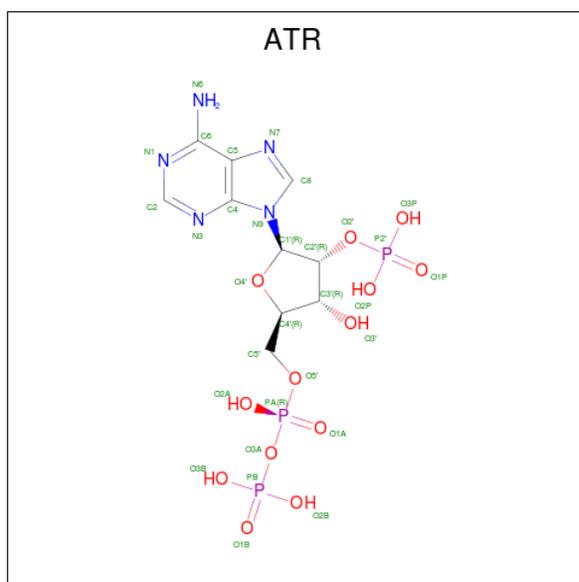
- Molecule 2 is a protein called Fab 1B2 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
2	E	207	Total	C	H	N	O	S	0	0
			3081	987	1526	260	302	6		
2	H	205	Total	C	H	N	O	S	0	0
			3053	979	1513	257	298	6		

- Molecule 3 is a protein called Fab 1B2 light chain.

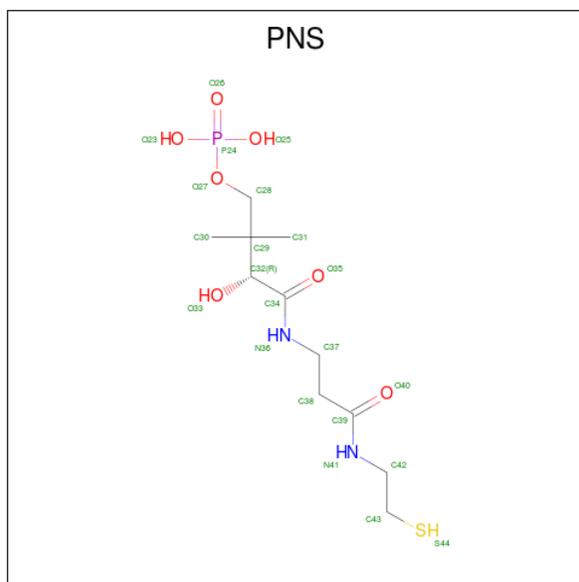
Mol	Chain	Residues	Atoms					AltConf	Trace	
3	F	216	Total	C	H	N	O	S	0	0
			3255	1033	1604	280	332	6		
3	G	214	Total	C	H	N	O	S	0	0
			3249	1029	1611	278	325	6		

- Molecule 4 is 2'-MONOPHOSPHOADENOSINE-5'-DIPHOSPHATE (three-letter code: ATR) (formula: C₁₀H₁₆N₅O₁₃P₃).

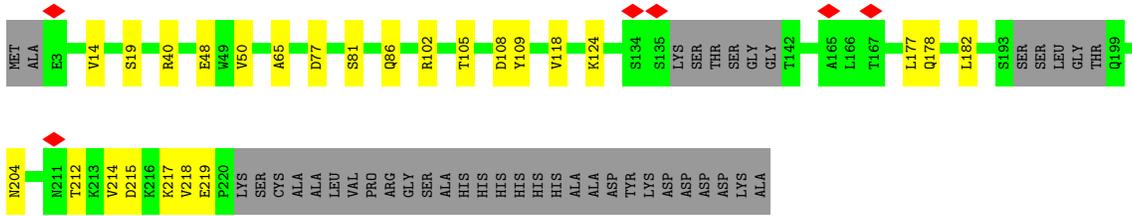


Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
4	C	1	42	10	11	5	13	3	0

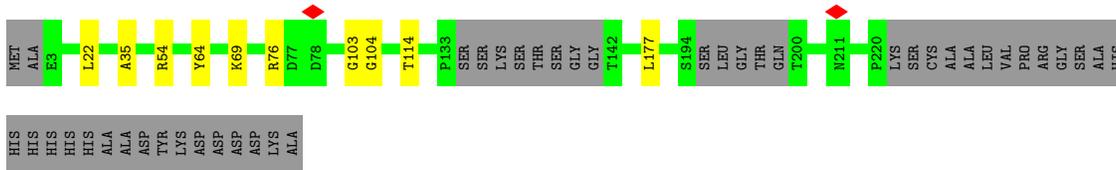
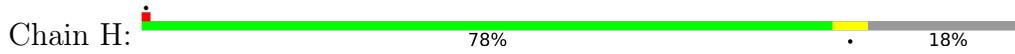
- Molecule 5 is 4'-PHOSPHOPANTETHEINE (three-letter code: PNS) (formula: C₁₁H₂₃N₂O₇PS) (labeled as "Ligand of Interest" by depositor).



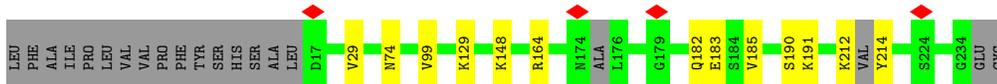
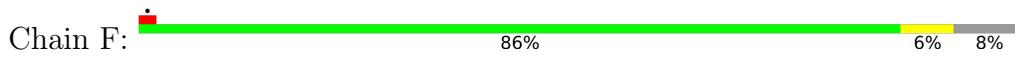
Mol	Chain	Residues	Atoms						AltConf	
			Total	C	H	N	O	P		S
5	D	1	41	11	20	2	6	1	1	0



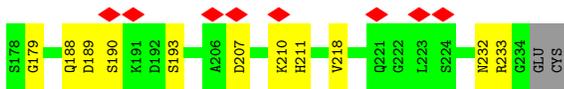
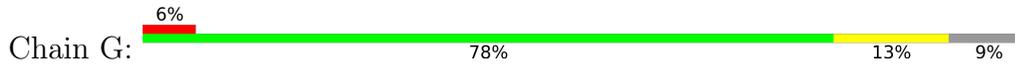
• Molecule 2: Fab 1B2 heavy chain



• Molecule 3: Fab 1B2 light chain



• Molecule 3: Fab 1B2 light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	397539	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	79000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	47.709	Depositor
Minimum map value	-21.716	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	1.126	Depositor
Recommended contour level	7.0	Depositor
Map size (Å)	379.652, 379.652, 379.652	wwPDB
Map dimensions	364, 364, 364	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.043, 1.043, 1.043	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: PNS, ATR

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	0.25	0/6844	0.57	0/9349
1	B	0.25	0/6830	0.58	1/9332 (0.0%)
1	C	0.26	0/3591	0.60	0/4914
1	D	0.25	0/633	0.64	0/857
2	E	0.27	0/1591	0.57	0/2163
2	H	0.27	0/1576	0.55	0/2143
3	F	0.26	0/1686	0.53	0/2289
3	G	0.28	0/1674	0.55	0/2273
All	All	0.26	0/24425	0.57	1/33320 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	884	ASP	CB-CG-OD2	5.37	123.14	118.30

There are no chirality outliers.

There are no planarity outliers.

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	A	6693	6542	6545	54	0
1	B	6678	6521	6524	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3517	3471	3471	35	0
1	D	625	632	632	8	0
2	E	1555	1526	1526	16	0
2	H	1540	1513	1513	6	0
3	F	1651	1604	1604	9	0
3	G	1638	1611	1611	17	0
4	C	31	11	11	2	0
5	D	21	20	21	0	0
All	All	23949	23451	23458	199	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 4.

The worst 5 of 199 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:206:ILE:HD11	1:A:219:LEU:HD12	1.66	0.78
1:B:209:ALA:O	1:B:212:SER:OG	2.07	0.71
1:A:367:GLU:N	1:A:367:GLU:OE1	2.25	0.70
1:C:980:ARG:NH2	1:C:1417:GLU:OE1	2.25	0.70
1:B:38:GLU:O	1:B:225:ARG:NH1	2.25	0.69

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	885/1649 (54%)	849 (96%)	36 (4%)	0	100	100
1	B	885/1649 (54%)	848 (96%)	37 (4%)	0	100	100
1	C	476/1649 (29%)	457 (96%)	19 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	78/1649 (5%)	75 (96%)	3 (4%)	0	100	100
2	E	201/249 (81%)	195 (97%)	6 (3%)	0	100	100
2	H	199/249 (80%)	193 (97%)	6 (3%)	0	100	100
3	F	210/236 (89%)	203 (97%)	7 (3%)	0	100	100
3	G	210/236 (89%)	197 (94%)	13 (6%)	0	100	100
All	All	3144/7566 (42%)	3017 (96%)	127 (4%)	0	100	100

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	Rotameric	Outliers	Percentiles	
1	A	684/1242 (55%)	684 (100%)	0	100	100
1	B	685/1242 (55%)	685 (100%)	0	100	100
1	C	348/1242 (28%)	348 (100%)	0	100	100
1	D	64/1242 (5%)	64 (100%)	0	100	100
2	E	172/203 (85%)	172 (100%)	0	100	100
2	H	170/203 (84%)	170 (100%)	0	100	100
3	F	190/208 (91%)	189 (100%)	1 (0%)	88	94
3	G	189/208 (91%)	189 (100%)	0	100	100
All	All	2502/5790 (43%)	2501 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
3	F	148	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

2 ligands 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
4	ATR	C	1701	-	27,33,33	2.89	4 (14%)	35,52,52	2.03	10 (28%)
5	PNS	D	1701	1	13,20,21	2.44	4 (30%)	18,26,29	1.69	4 (22%)

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	ATR	C	1701	-	-	3/17/37/37	0/3/3/3
5	PNS	D	1701	1	-	10/24/26/27	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1701	ATR	P2'-O2'	12.59	1.83	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	1701	PNS	C39-N41	5.60	1.46	1.33
4	C	1701	ATR	PB-O3B	5.51	1.76	1.54
5	D	1701	PNS	C34-N36	5.43	1.45	1.33
4	C	1701	ATR	O2'-C2'	-2.98	1.33	1.44

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1701	ATR	PA-O3A-PB	-7.33	107.68	132.83
5	D	1701	PNS	C38-C39-N41	4.26	123.59	116.42
4	C	1701	ATR	O2'-P2'-O1P	-3.33	96.53	109.39
4	C	1701	ATR	O2B-PB-O1B	3.30	123.59	110.68
4	C	1701	ATR	PA-O5'-C5'	-2.96	104.30	121.68

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

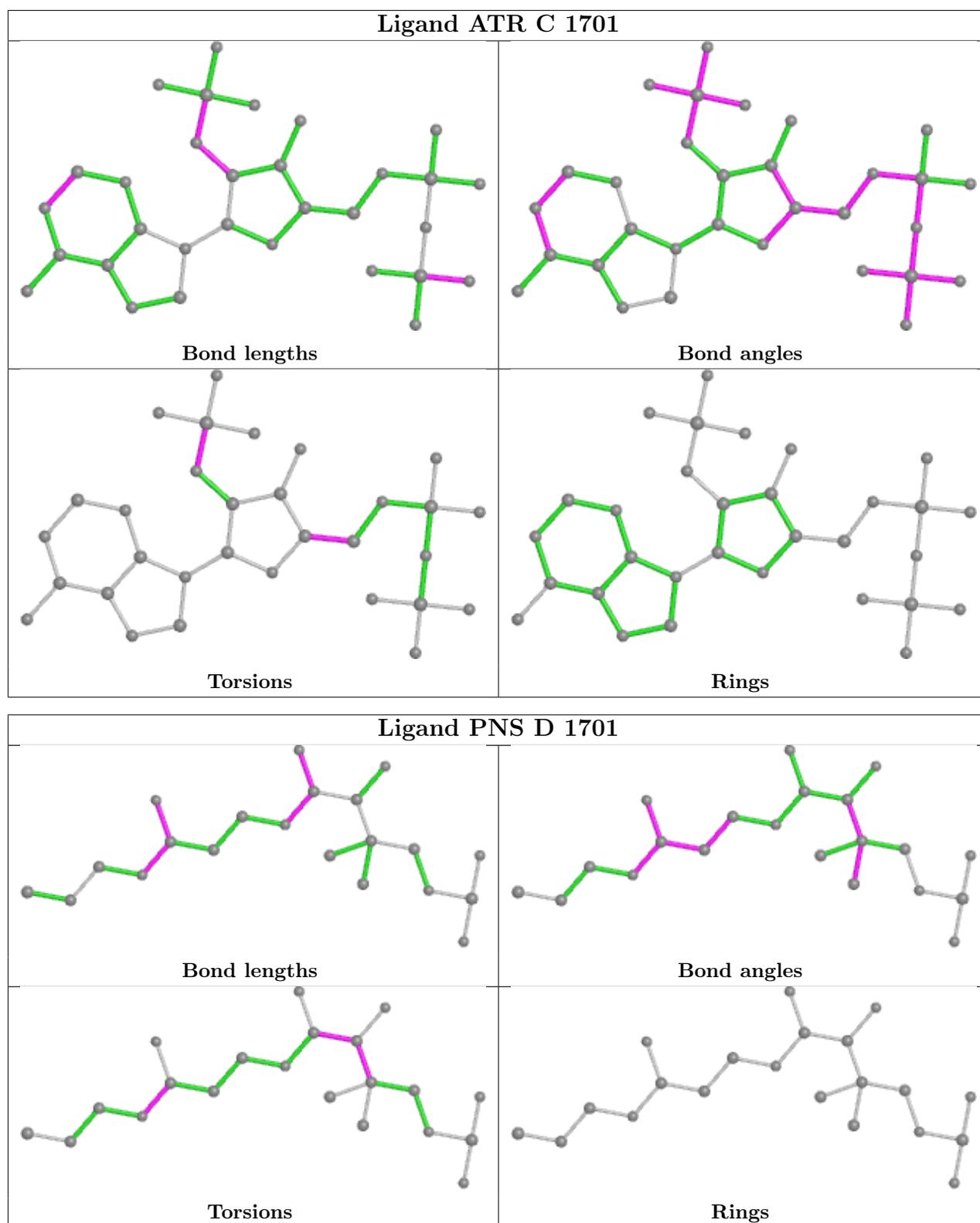
Mol	Chain	Res	Type	Atoms
4	C	1701	ATR	C2'-O2'-P2'-O3P
5	D	1701	PNS	C28-C29-C32-C34
5	D	1701	PNS	C38-C39-N41-C42
5	D	1701	PNS	O40-C39-N41-C42
5	D	1701	PNS	C30-C29-C32-O33

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1701	ATR	2	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.

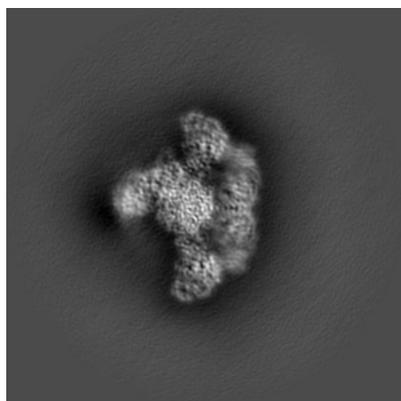
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24868. These allow visual inspection of the internal detail of the map and identification of artifacts.

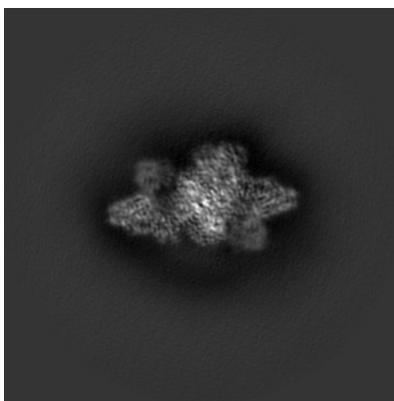
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

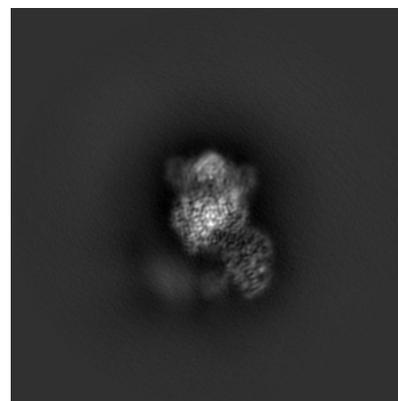
6.1.1 Primary map



X



Y

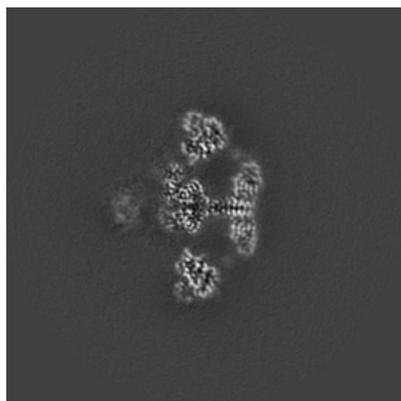


Z

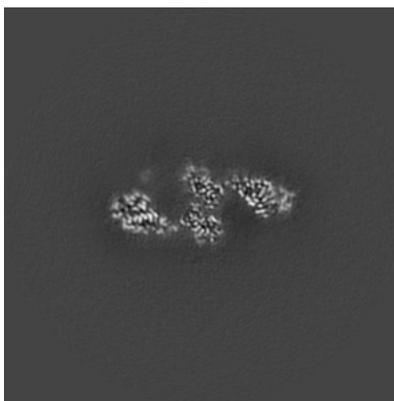
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

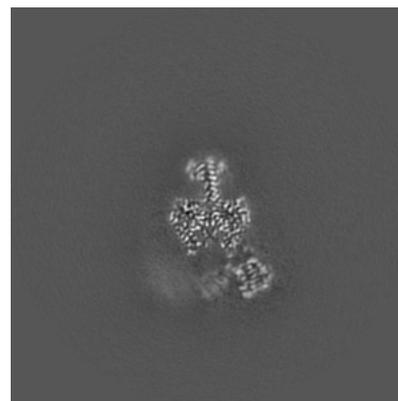
6.2.1 Primary map



X Index: 182



Y Index: 182

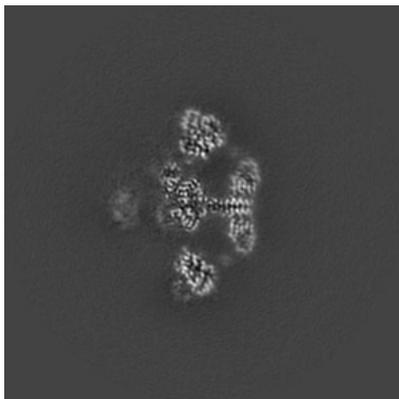


Z Index: 182

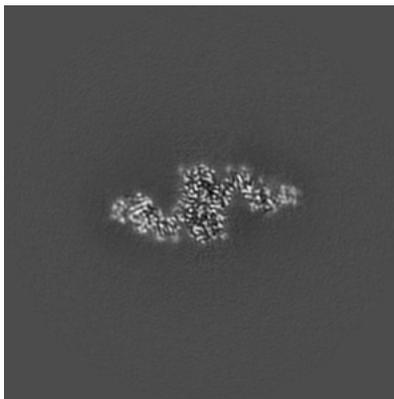
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

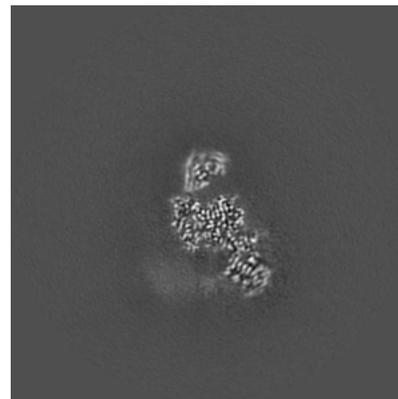
6.3.1 Primary map



X Index: 183



Y Index: 174

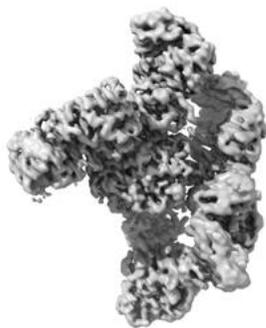


Z Index: 191

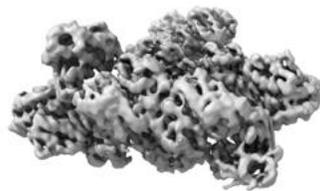
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

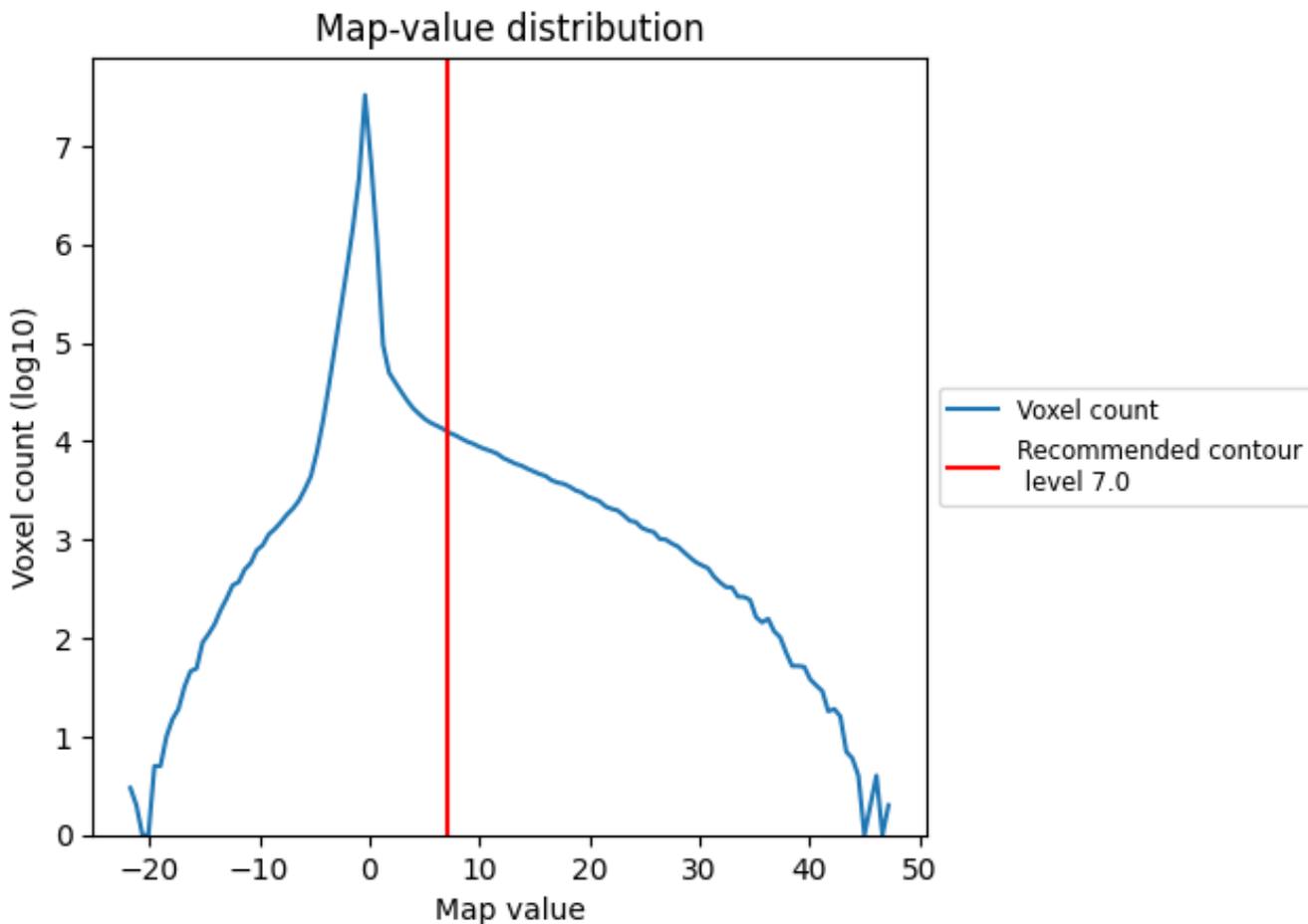
6.5 Mask visualisation

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

7 Map analysis [i](#)

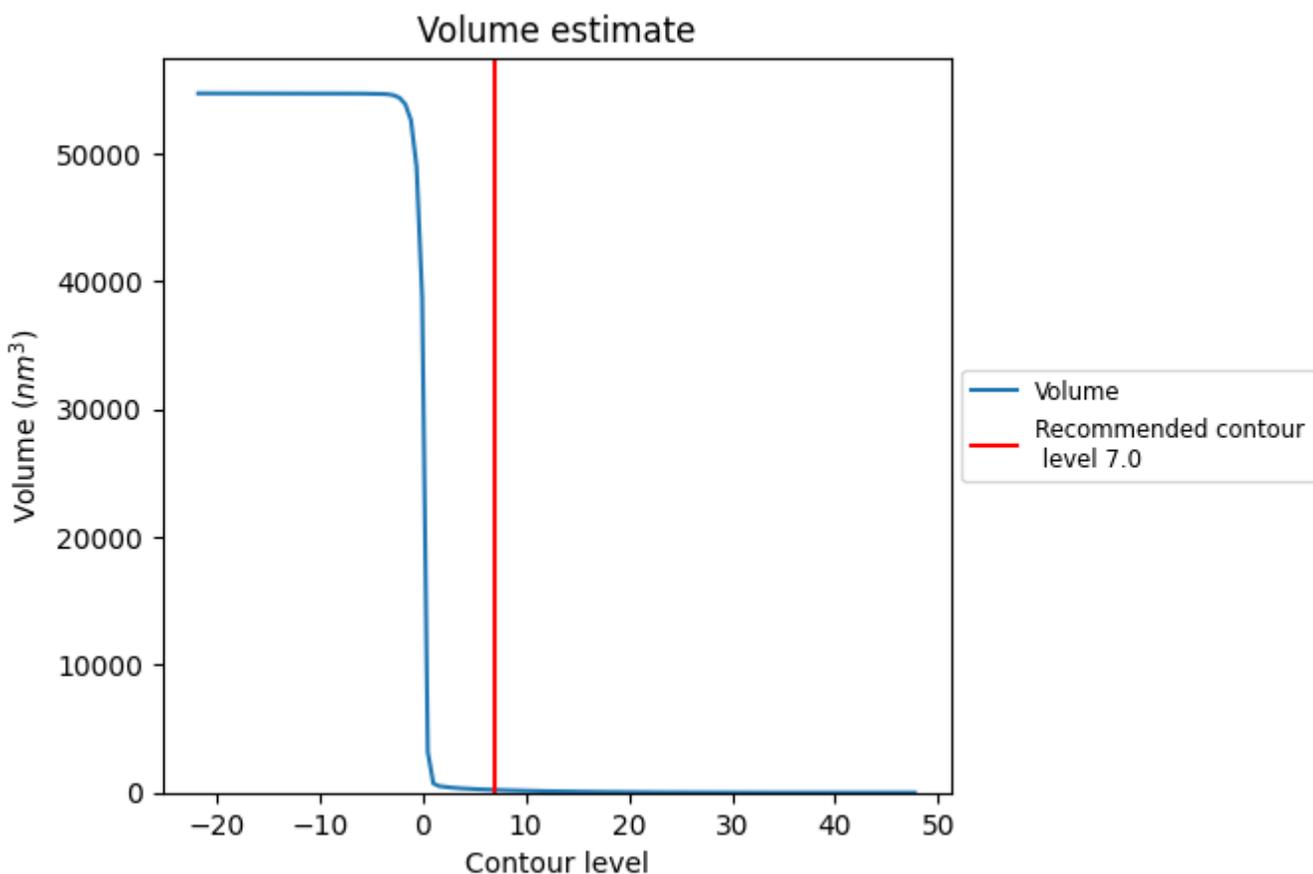
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

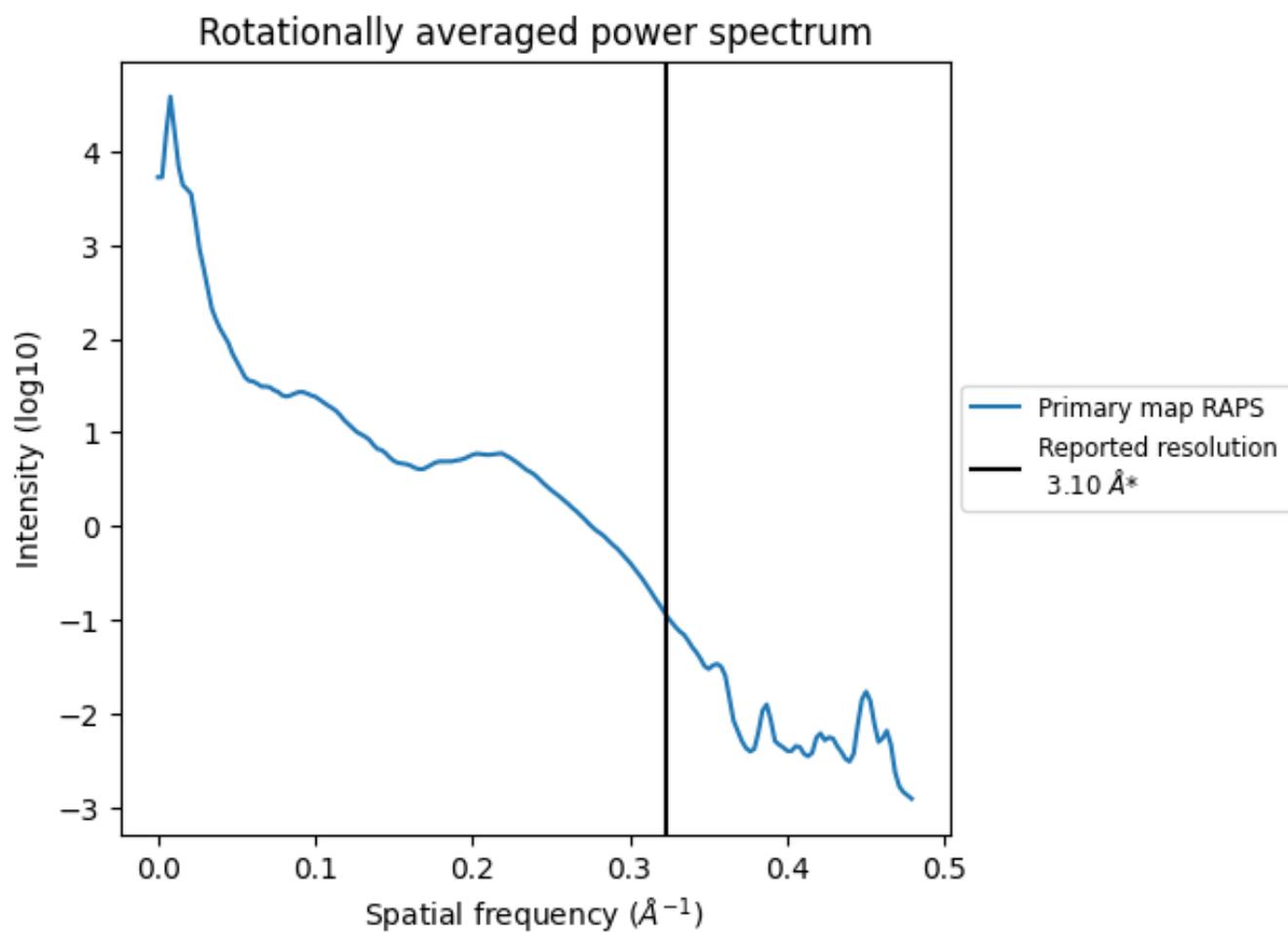
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 215 nm³; this corresponds to an approximate mass of 194 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](#)



*Reported resolution corresponds to spatial frequency of 0.323\AA^{-1}

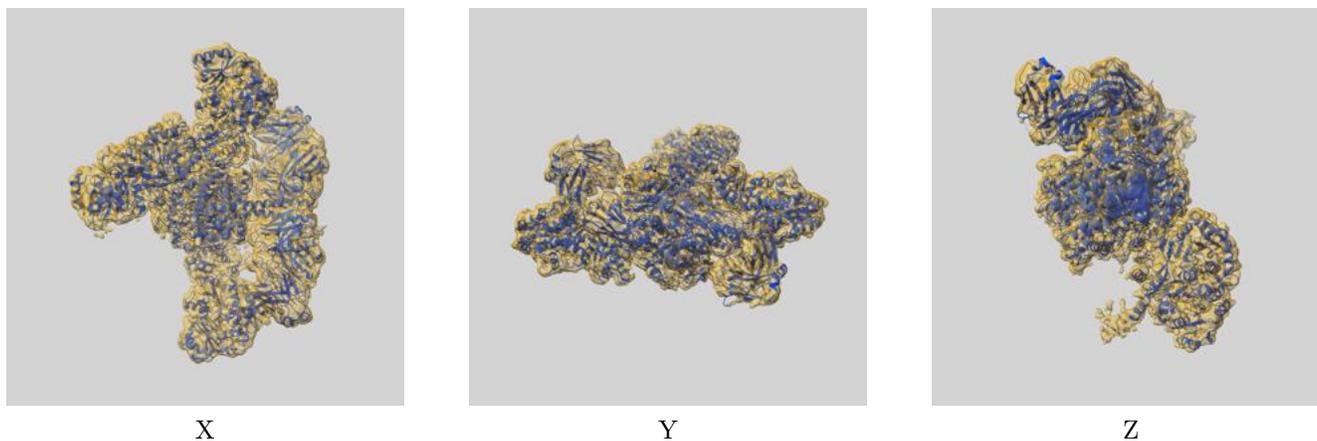
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

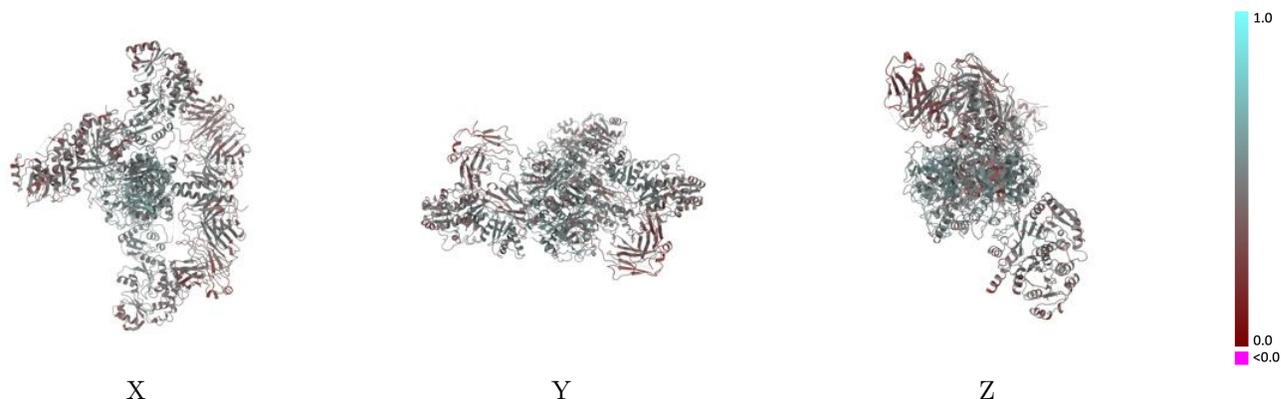
This section contains information regarding the fit between EMDB map EMD-24868 and PDB model 7S6C. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



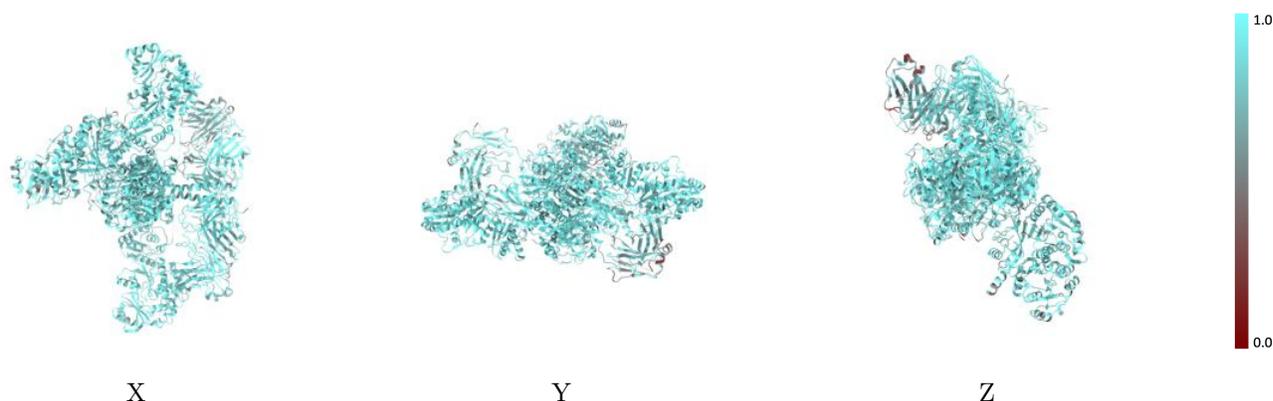
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



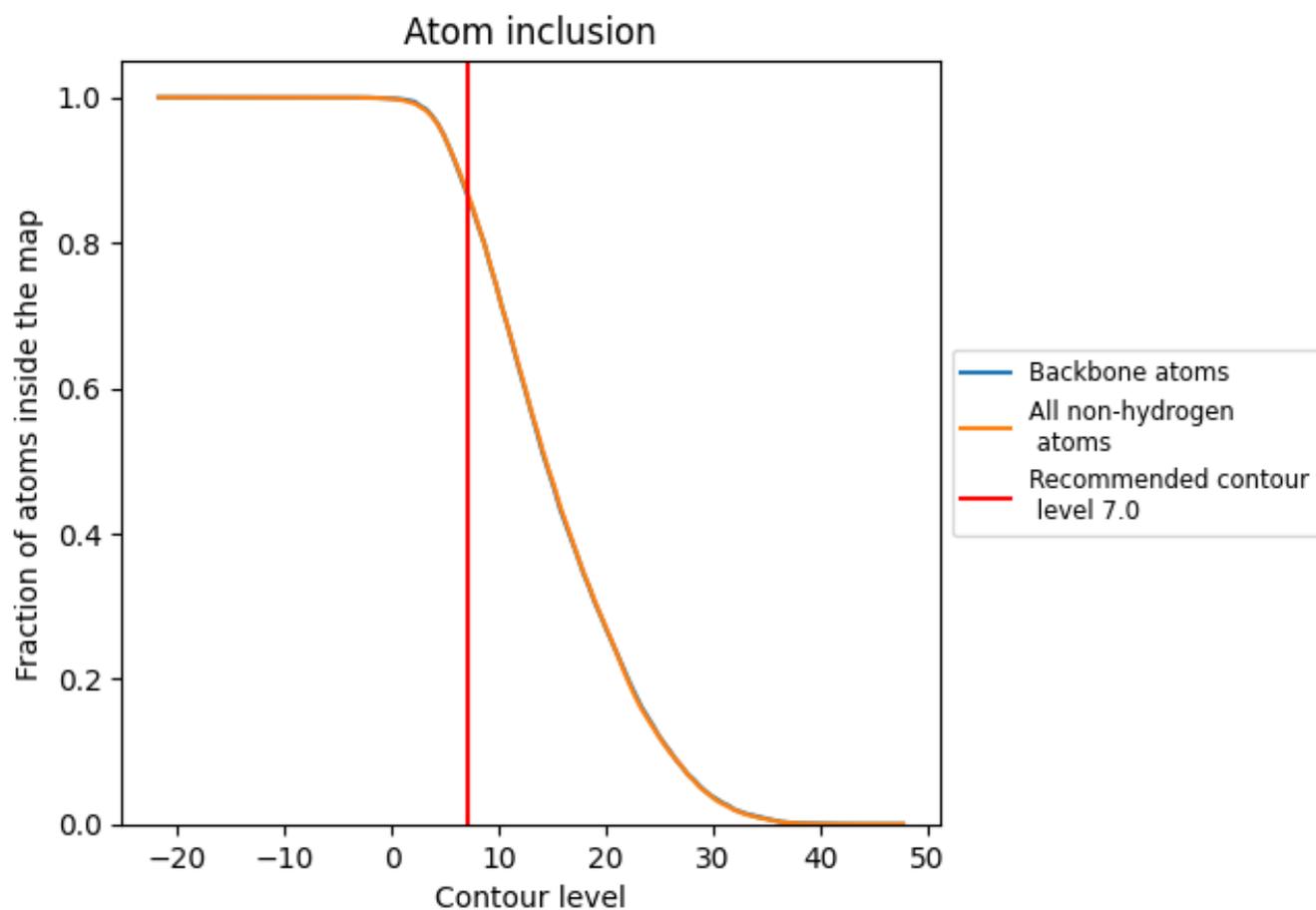
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7.0).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 87% 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 (7.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8708	 0.4700
A	 0.9050	 0.5070
B	 0.9171	 0.5100
C	 0.8361	 0.4370
D	 0.8435	 0.4860
E	 0.8396	 0.4100
F	 0.8644	 0.4070
G	 0.7752	 0.3890
H	 0.8558	 0.4270

