



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 01:25 PM UTC

PDB ID : 6ZNA / pdb_00006zna
EMDB ID : EMD-0667
Title : Porcine ATP synthase Fo domain
Authors : Spikes, T.E.; Montgomery, M.G.; Walker, J.E.
Deposited on : 2020-07-06
Resolution : 6.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : **FAILED**
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) : 2.49

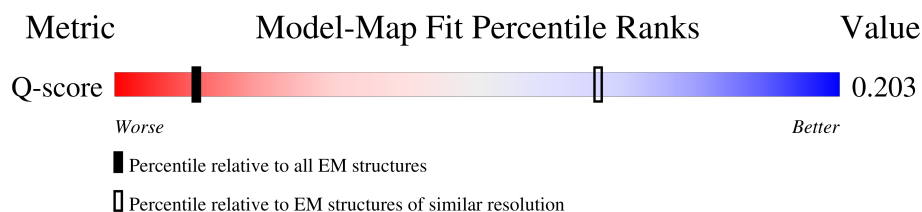
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.20 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	537 (5.70 - 6.70)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 39195 atoms, of which 13428 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 ATP synthase protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A8	34	Total	C	H	N	O	0	0
			238	102	68	34	34		
1	B8	34	Total	C	H	N	O	0	0
			238	102	68	34	34		
1	C8	34	Total	C	H	N	O	0	0
			238	102	68	34	34		
1	8	34	Total	C	H	N	O	0	0
			238	102	68	34	34		

- Molecule 2 is a protein called ATP synthase F(0) complex subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
2	AK	75	Total 565	C 214	H 201	N 75	O 75	0	0	
2	AL	75	Total 565	C 214	H 201	N 75	O 75	0	0	
2	AM	74	Total 558	C 211	H 199	N 74	O 74	0	0	
2	AN	75	Total 565	C 214	H 201	N 75	O 75	0	0	
2	AO	75	Total 1096	C 356	H 559	N 83	O 94	S 4	0	0
2	AP	74	Total 558	C 211	H 199	N 74	O 74	0	0	
2	AQ	74	Total 558	C 211	H 199	N 74	O 74	0	0	
2	AR	75	Total 565	C 214	H 201	N 75	O 75	0	0	
2	BK	74	Total 558	C 211	H 199	N 74	O 74	0	0	
2	BL	75	Total 565	C 214	H 201	N 75	O 75	0	0	
2	BM	75	Total 565	C 214	H 201	N 75	O 75	0	0	

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	BN	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	BO	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	BP	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	BQ	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	BR	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	CK	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	CL	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	CM	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	CN	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	CO	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	CP	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	CQ	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	CR	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	K	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	L	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	M	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	N	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	O	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	P	74	Total	C	H	N	O	0	0
			558	211	199	74	74		
2	Q	75	Total	C	H	N	O	0	0
			565	214	201	75	75		
2	R	75	Total	C	H	N	O	0	0
			565	214	201	75	75		

- Molecule 3 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Aa	223	Total	C	H	N	O	0	0
			1599	659	494	223	223		
3	Ba	223	Total	C	H	N	O	0	0
			1599	659	494	223	223		
3	Ca	223	Total	C	H	N	O	0	0
			1599	659	494	223	223		
3	a	223	Total	C	H	N	O	0	0
			1599	659	494	223	223		

- Molecule 4 is a protein called ATP synthase peripheral stalk-membrane subunit b.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ab	94	Total	C	H	N	O	0	0
			669	272	209	94	94		
4	Bb	94	Total	C	H	N	O	0	0
			669	272	209	94	94		
4	Cb	94	Total	C	H	N	O	0	0
			669	272	209	94	94		
4	b	94	Total	C	H	N	O	0	0
			669	272	209	94	94		

- Molecule 5 is a protein called ATP synthase subunit d, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ad	33	Total	C	H	N	O	0	0
			226	99	61	33	33		
5	Bd	33	Total	C	H	N	O	0	0
			226	99	61	33	33		
5	Cd	33	Total	C	H	N	O	0	0
			226	99	61	33	33		
5	d	33	Total	C	H	N	O	0	0
			226	99	61	33	33		

- Molecule 6 is a protein called ATP synthase subunit e, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Ae	57	Total	C	H	N	O	0	0
			413	168	131	57	57		
6	Be	57	Total	C	H	N	O	0	0
			413	168	131	57	57		
6	Ce	57	Total	C	H	N	O	0	0
			413	168	131	57	57		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	e	57	Total	C	H	N	O	0	0
			413	168	131	57	57		

- Molecule 7 is a protein called ATP synthase subunit f, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Af	83	Total	C	H	N	O	0	0
			593	243	184	83	83		
7	Bf	83	Total	C	H	N	O	0	0
			593	243	184	83	83		
7	Cf	83	Total	C	H	N	O	0	0
			593	243	184	83	83		
7	f	83	Total	C	H	N	O	0	0
			593	243	184	83	83		

- Molecule 8 is a protein called ATP synthase g subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Ag	93	Total	C	H	N	O	0	0
			708	275	247	93	93		
8	Bg	74	Total	C	H	N	O	0	0
			532	218	166	74	74		
8	Cg	93	Total	C	H	N	O	0	0
			708	275	247	93	93		
8	g	74	Total	C	H	N	O	0	0
			532	218	166	74	74		

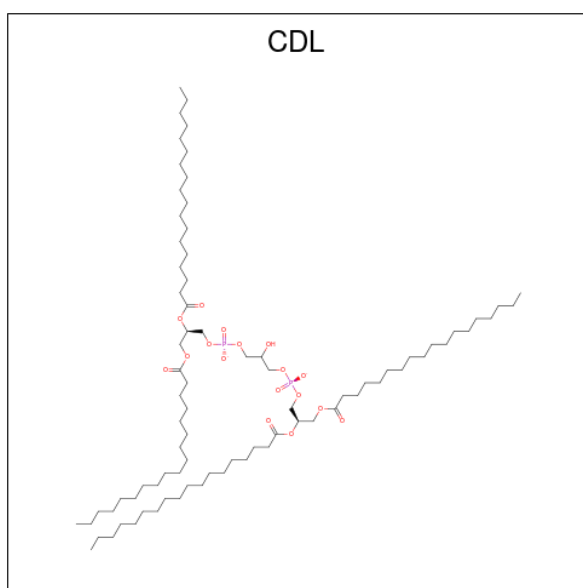
- Molecule 9 is a protein called ATP synthase j subunit (6.8PL).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aj	48	Total	C	H	N	O	0	0
			339	141	102	48	48		
9	Bj	48	Total	C	H	N	O	0	0
			339	141	102	48	48		
9	Cj	48	Total	C	H	N	O	0	0
			339	141	102	48	48		
9	j	48	Total	C	H	N	O	0	0
			339	141	102	48	48		

- Molecule 10 is a protein called ATP synthase membrane subunit DAPIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Ak	35	Total	C	H	N	O	0	0
			250	101	79	35	35		
10	Bk	35	Total	C	H	N	O	0	0
			250	101	79	35	35		
10	Ck	35	Total	C	H	N	O	0	0
			250	101	79	35	35		
10	k	35	Total	C	H	N	O	0	0
			250	101	79	35	35		

- Molecule 11 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms					AltConf
11	Af	1	Total	C	H	O	P	0
			220	70	131	17	2	
11	Bf	1	Total	C	H	O	P	0
			220	70	131	17	2	
11	Cf	1	Total	C	H	O	P	0
			220	70	131	17	2	
11	f	1	Total	C	H	O	P	0
			220	70	131	17	2	

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3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	170000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.571	Depositor
Minimum map value	-0.528	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.315	Depositor
Map size (Å)	662.4, 662.4, 662.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

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4.3.3 RNA [i](#)

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

32 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	$\# Z > 2$
2	M3L	AL	43	2	3,4,12	0.94	0	2,4,16	0.56	0
2	M3L	BQ	43	2	3,4,12	0.89	0	2,4,16	0.64	0
2	M3L	M	43	2	3,4,12	1.00	0	2,4,16	0.14	0
2	M3L	CL	43	2	3,4,12	0.92	0	2,4,16	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	M3L	AO	43	2	10,11,12	0.48	0	9,14,16	0.64	0
2	M3L	BP	43	2	3,4,12	0.99	0	2,4,16	0.63	0
2	M3L	BM	43	2	3,4,12	0.82	0	2,4,16	0.40	0
2	M3L	BK	43	2	3,4,12	1.15	0	2,4,16	0.25	0
2	M3L	BO	43	2	3,4,12	0.86	0	2,4,16	0.15	0
2	M3L	R	43	2	3,4,12	0.90	0	2,4,16	0.65	0
2	M3L	CO	43	2	3,4,12	0.87	0	2,4,16	0.64	0
2	M3L	CP	43	2	3,4,12	0.89	0	2,4,16	0.57	0
2	M3L	AQ	43	2	3,4,12	1.16	0	2,4,16	0.25	0
2	M3L	K	43	2	3,4,12	0.91	0	2,4,16	0.59	0
2	M3L	BN	43	2	3,4,12	0.94	0	2,4,16	0.54	0
2	M3L	CQ	43	2	3,4,12	1.16	0	2,4,16	0.26	0
2	M3L	N	43	2	3,4,12	0.83	0	2,4,16	0.42	0
2	M3L	BR	43	2	3,4,12	0.87	0	2,4,16	0.58	0
2	M3L	AM	43	2	3,4,12	0.88	0	2,4,16	0.15	0
2	M3L	AR	43	2	3,4,12	0.98	0	2,4,16	0.15	0
2	M3L	BL	43	2	3,4,12	1.01	0	2,4,16	0.14	0
2	M3L	AK	43	2	3,4,12	0.83	0	2,4,16	0.42	0
2	M3L	P	43	2	3,4,12	0.89	0	2,4,16	0.14	0
2	M3L	AP	43	2	3,4,12	0.88	0	2,4,16	0.55	0
2	M3L	O	43	2	3,4,12	0.93	0	2,4,16	0.56	0
2	M3L	L	43	2	3,4,12	1.15	0	2,4,16	0.22	0
2	M3L	Q	43	2	3,4,12	0.97	0	2,4,16	0.62	0
2	M3L	AN	43	2	3,4,12	0.97	0	2,4,16	0.61	0
2	M3L	CR	43	2	3,4,12	1.01	0	2,4,16	0.17	0
2	M3L	CK	43	2	3,4,12	0.81	0	2,4,16	0.41	0
2	M3L	CN	43	2	3,4,12	0.97	0	2,4,16	0.61	0
2	M3L	CM	43	2	3,4,12	0.88	0	2,4,16	0.16	0

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
2	M3L	AL	43	2	-	0/1/2/12	-
2	M3L	BQ	43	2	-	1/1/2/12	-
2	M3L	M	43	2	-	0/1/2/12	-
2	M3L	CL	43	2	-	0/1/2/12	-
2	M3L	AO	43	2	-	4/9/10/12	-
2	M3L	BP	43	2	-	0/1/2/12	-
2	M3L	BM	43	2	-	0/1/2/12	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	M3L	BK	43	2	-	0/1/2/12	-
2	M3L	BO	43	2	-	0/1/2/12	-
2	M3L	R	43	2	-	1/1/2/12	-
2	M3L	CO	43	2	-	1/1/2/12	-
2	M3L	CP	43	2	-	0/1/2/12	-
2	M3L	AQ	43	2	-	0/1/2/12	-
2	M3L	K	43	2	-	0/1/2/12	-
2	M3L	BN	43	2	-	0/1/2/12	-
2	M3L	CQ	43	2	-	0/1/2/12	-
2	M3L	N	43	2	-	0/1/2/12	-
2	M3L	BR	43	2	-	0/1/2/12	-
2	M3L	AM	43	2	-	0/1/2/12	-
2	M3L	AR	43	2	-	0/1/2/12	-
2	M3L	BL	43	2	-	0/1/2/12	-
2	M3L	AK	43	2	-	0/1/2/12	-
2	M3L	P	43	2	-	0/1/2/12	-
2	M3L	AP	43	2	-	0/1/2/12	-
2	M3L	O	43	2	-	0/1/2/12	-
2	M3L	L	43	2	-	0/1/2/12	-
2	M3L	Q	43	2	-	0/1/2/12	-
2	M3L	AN	43	2	-	0/1/2/12	-
2	M3L	CR	43	2	-	0/1/2/12	-
2	M3L	CK	43	2	-	0/1/2/12	-
2	M3L	CN	43	2	-	0/1/2/12	-
2	M3L	CM	43	2	-	0/1/2/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	BQ	43	M3L	O-C-CA-CB
2	CO	43	M3L	O-C-CA-CB
2	R	43	M3L	O-C-CA-CB
2	AO	43	M3L	CD-CE-NZ-CM2
2	AO	43	M3L	CD-CE-NZ-CM3

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

4 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
11	CDL	f	101	-	88,88,99	0.96	6 (6%)	94,100,111	1.07	5 (5%)
11	CDL	Bf	101	-	88,88,99	0.96	6 (6%)	94,100,111	1.07	7 (7%)
11	CDL	Cf	101	-	88,88,99	0.95	6 (6%)	94,100,111	1.07	5 (5%)
11	CDL	Af	101	-	88,88,99	0.95	6 (6%)	94,100,111	1.07	6 (6%)

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
11	CDL	f	101	-	-	41/99/99/110	-
11	CDL	Bf	101	-	-	41/99/99/110	-
11	CDL	Cf	101	-	-	41/99/99/110	-
11	CDL	Af	101	-	-	41/99/99/110	-

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	Bf	101	CDL	OA6-CA4	-3.06	1.39	1.46
11	f	101	CDL	OA6-CA4	-3.06	1.39	1.46
11	Af	101	CDL	OA6-CA4	-2.99	1.39	1.46
11	Cf	101	CDL	OA6-CA4	-2.97	1.39	1.46
11	f	101	CDL	OB6-CB4	-2.78	1.40	1.46

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Bf	101	CDL	OA6-CA5-C11	3.98	120.09	111.48
11	Af	101	CDL	OA6-CA5-C11	3.97	120.07	111.48
11	Cf	101	CDL	OA6-CA5-C11	3.95	120.03	111.48
11	f	101	CDL	OA6-CA5-C11	3.95	120.02	111.48
11	f	101	CDL	OB6-CB5-C51	3.63	119.34	111.48

There are no chirality outliers.

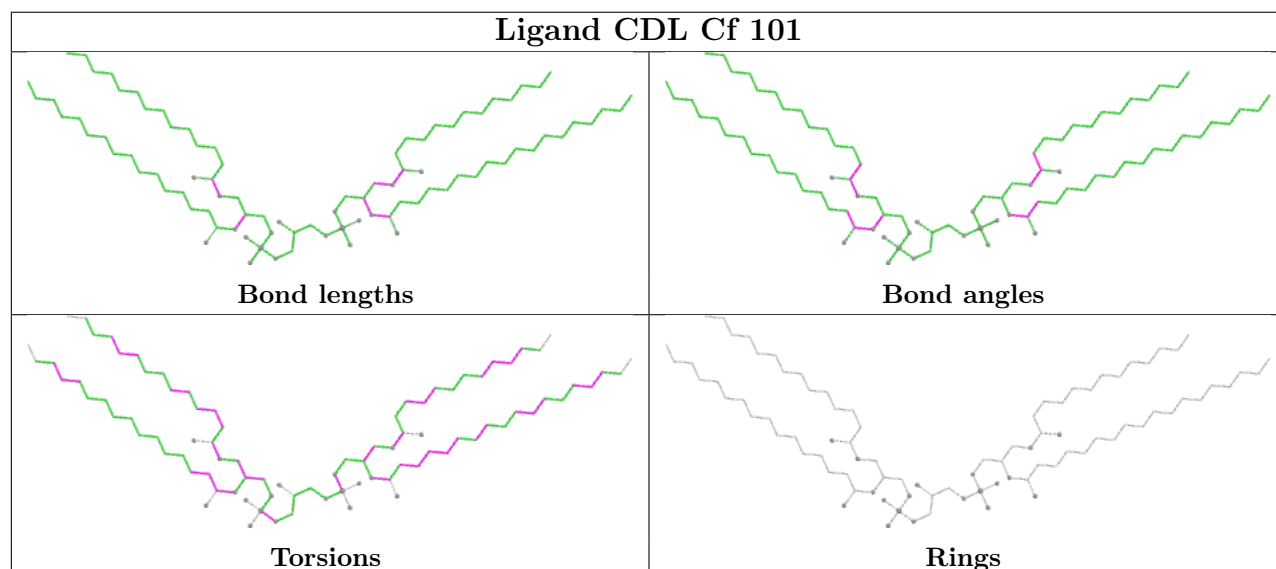
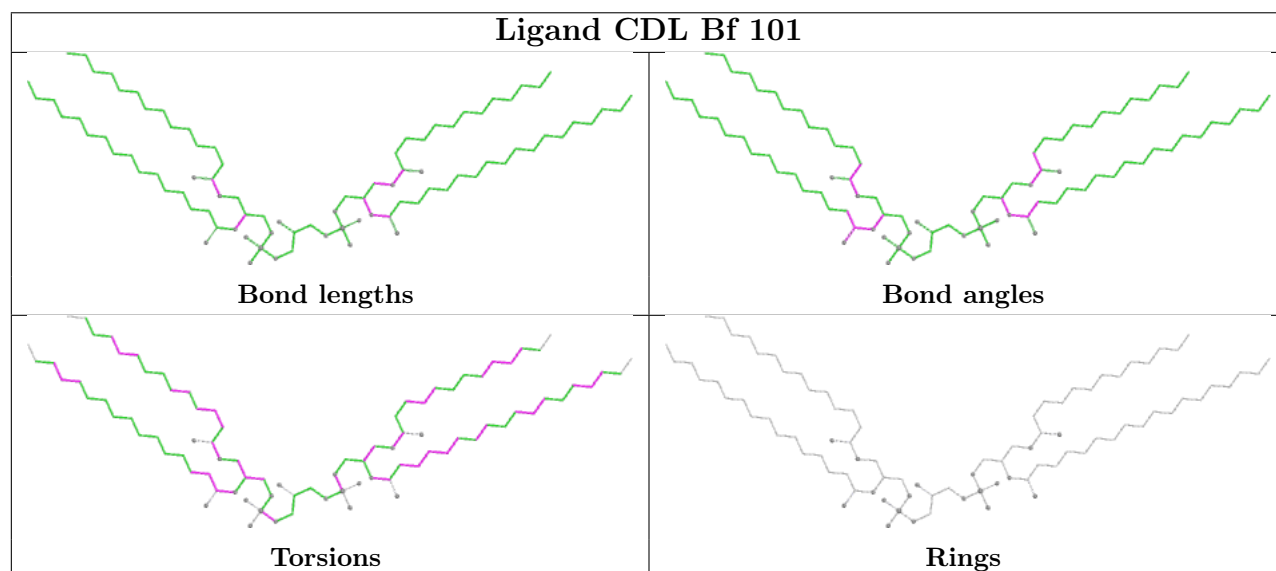
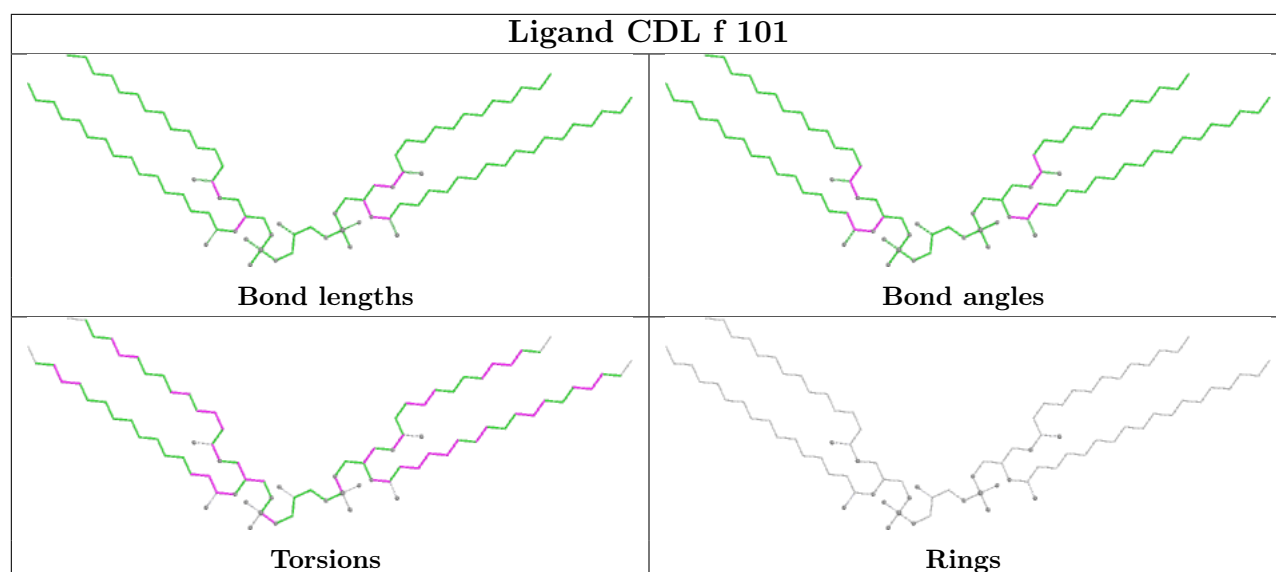
5 of 164 torsion outliers are listed below:

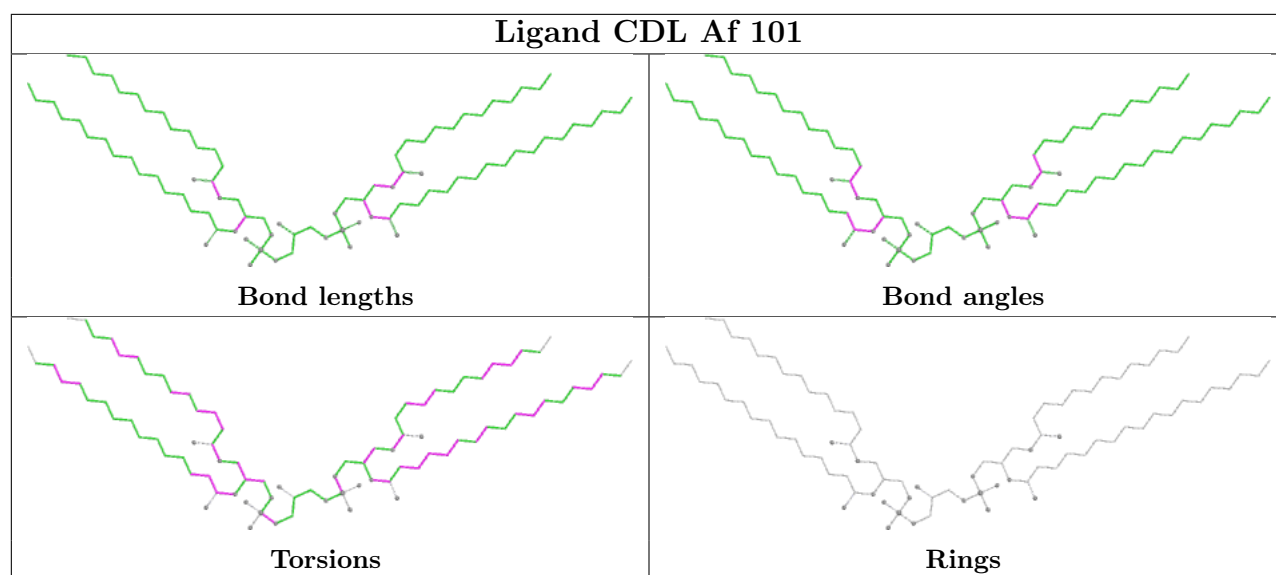
Mol	Chain	Res	Type	Atoms
11	Af	101	CDL	OA5-CA3-CA4-OA6
11	Af	101	CDL	CB3-OB5-PB2-OB2
11	Af	101	CDL	CB3-OB5-PB2-OB3
11	Af	101	CDL	CB3-OB5-PB2-OB4
11	Bf	101	CDL	OA5-CA3-CA4-OA6

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 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.





4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

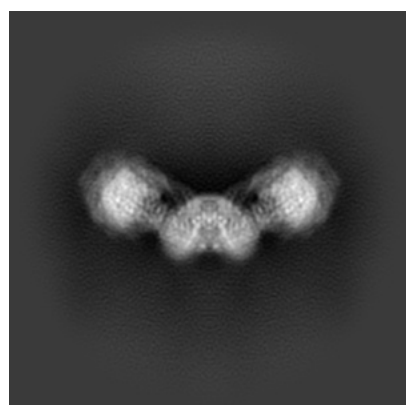
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0667. These allow visual inspection of the internal detail of the map and identification of artifacts.

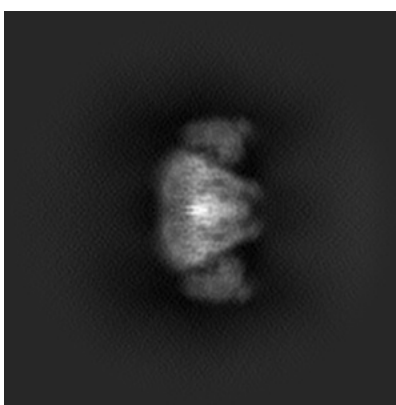
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

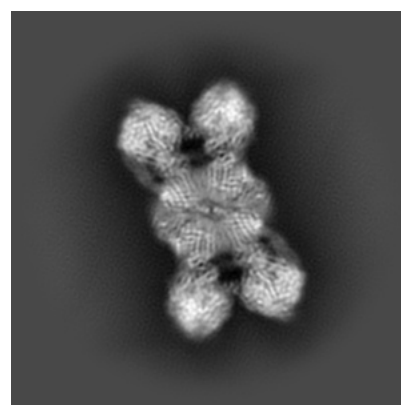
5.1.1 Primary map



X



Y

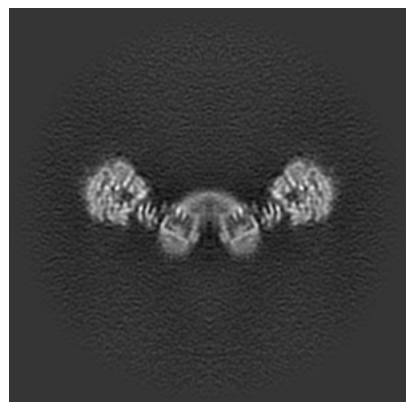


Z

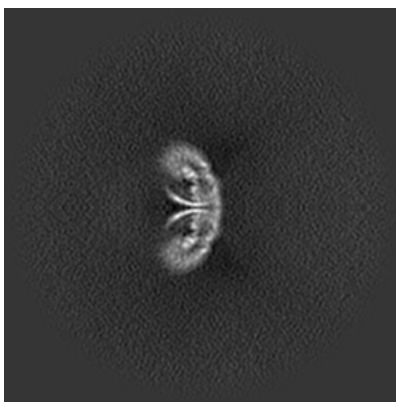
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

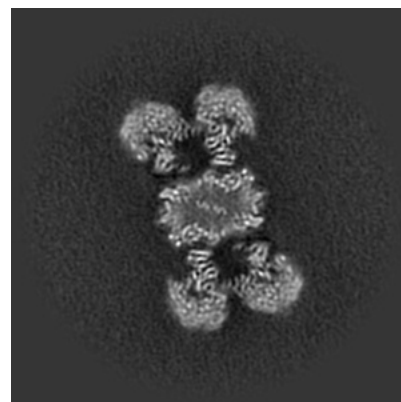
5.2.1 Primary map



X Index: 240



Y Index: 240

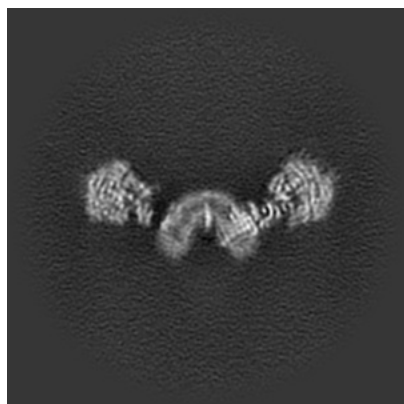


Z Index: 240

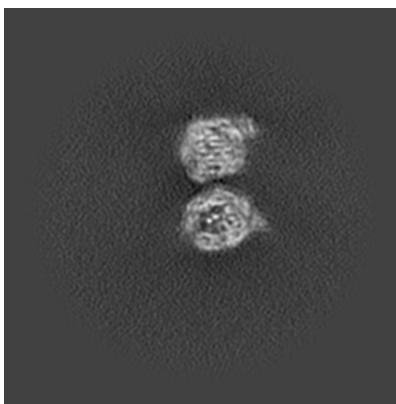
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

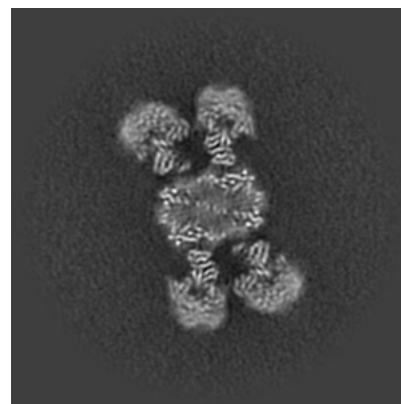
5.3.1 Primary map



X Index: 244



Y Index: 137

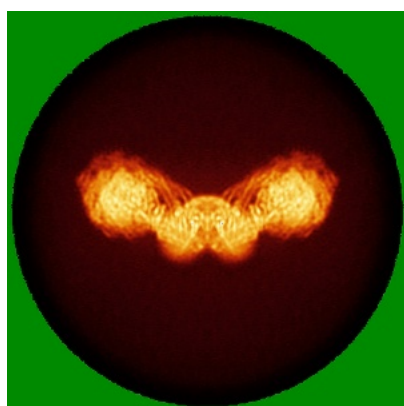


Z Index: 237

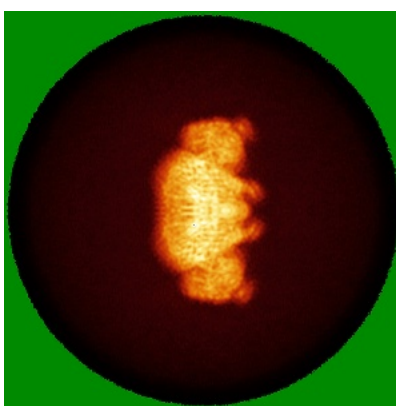
The images above show the largest variance slices of the map in three orthogonal directions.

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

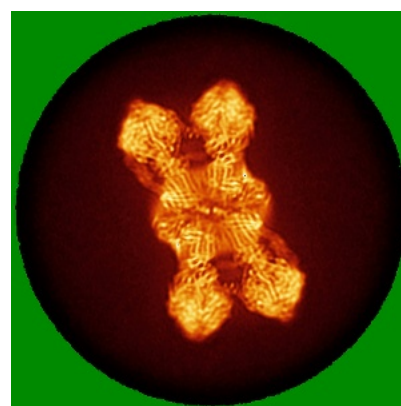
5.4.1 Primary map



X



Y

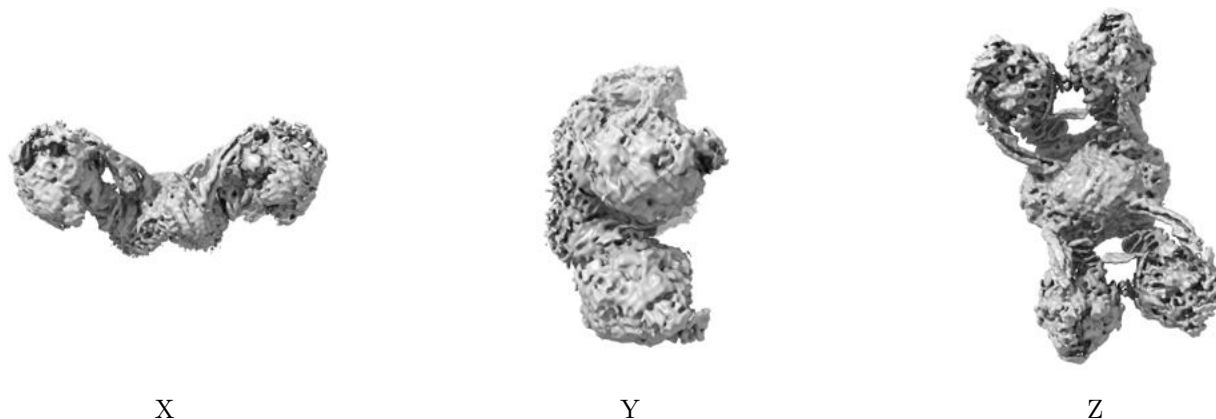


Z

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.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.315. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

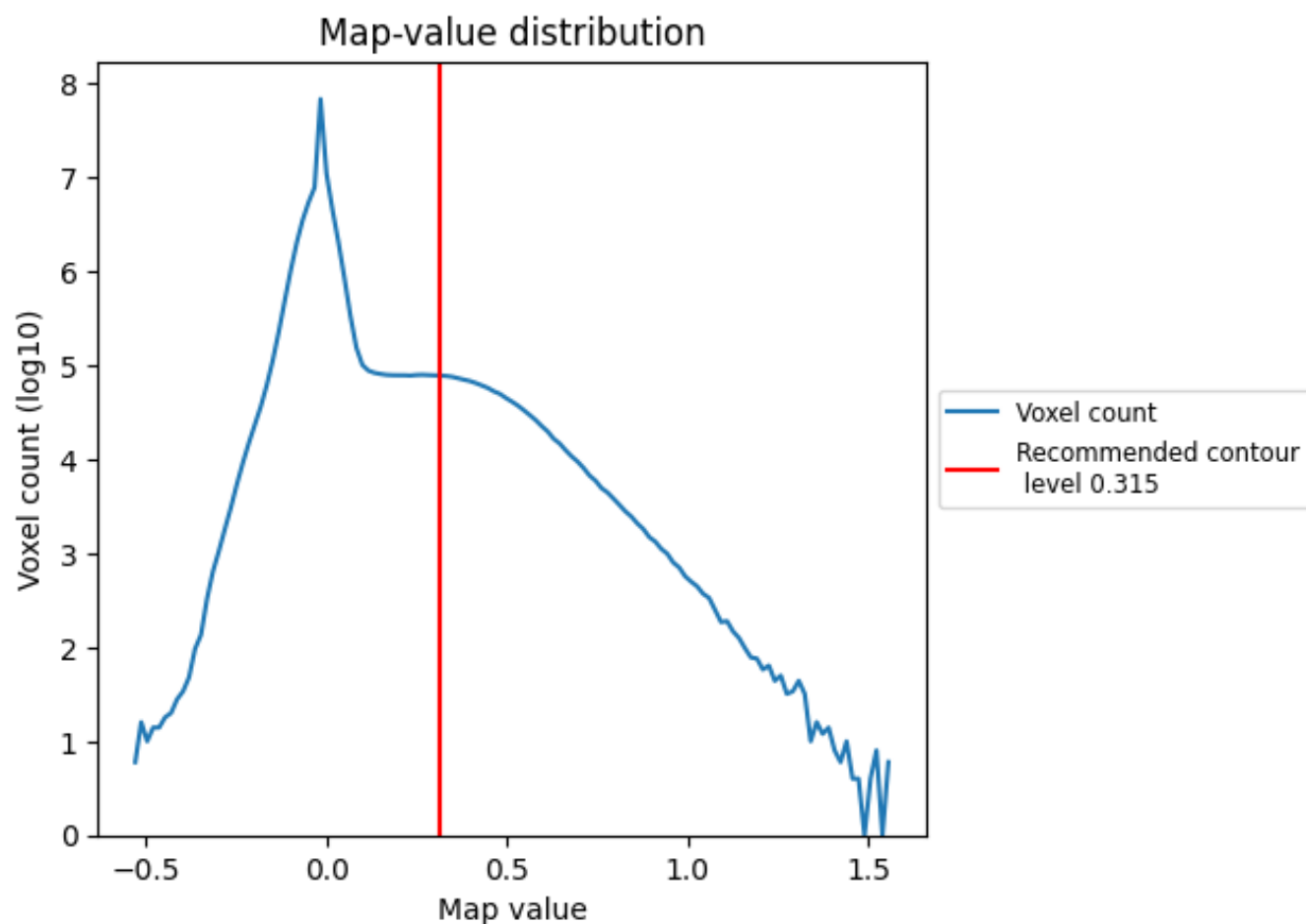
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

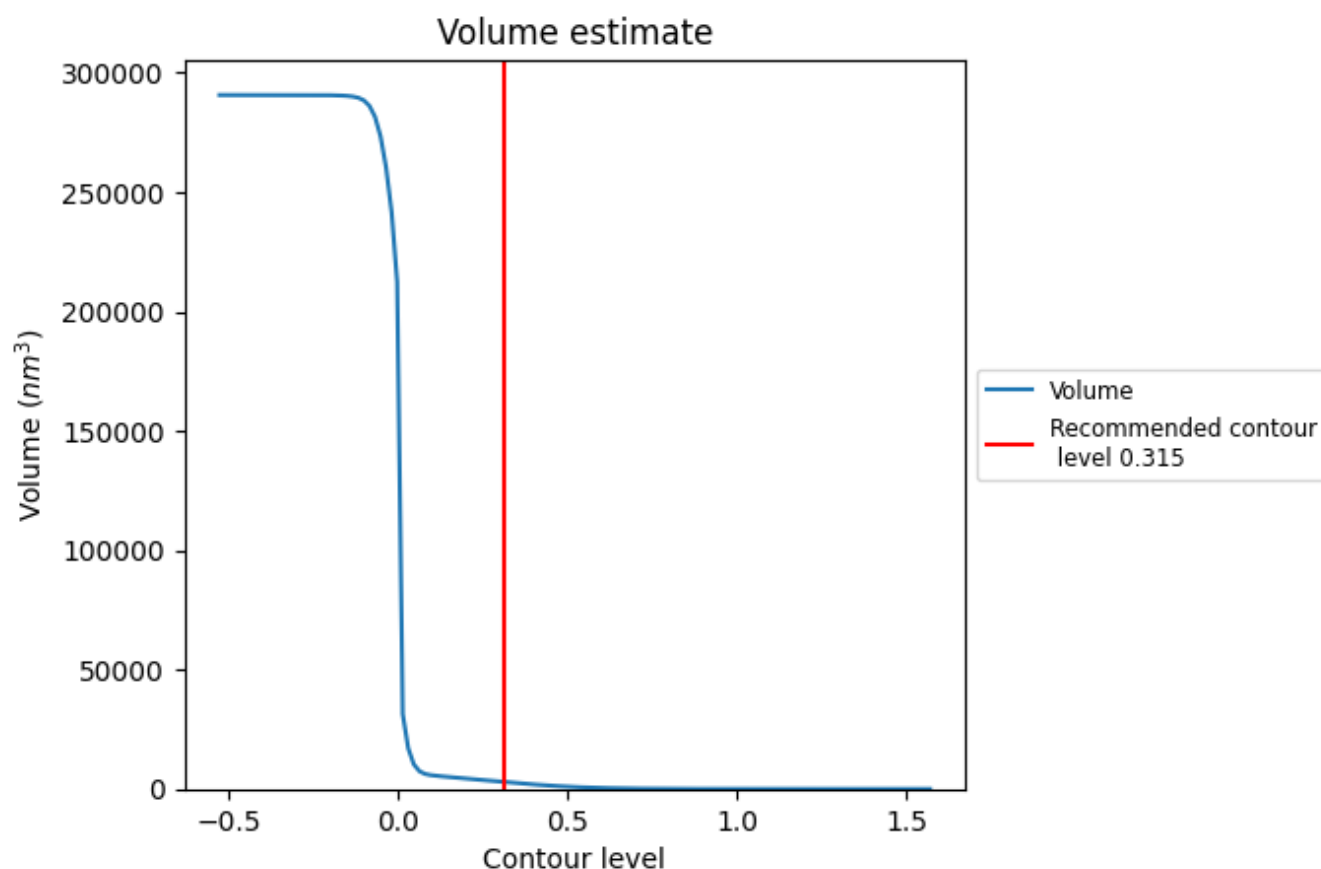
This section contains the results of statistical analysis of the map.

6.1 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.

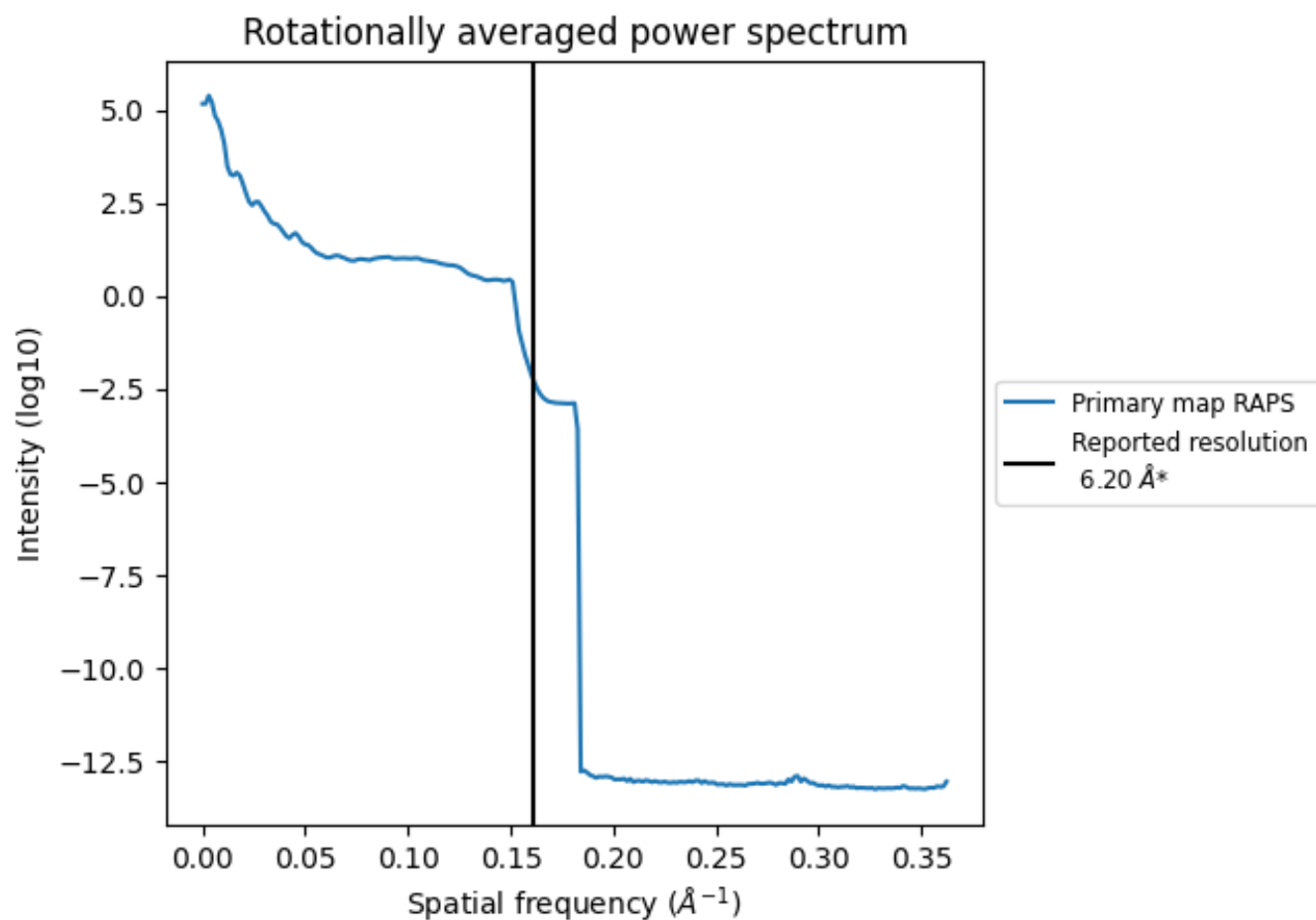
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 2912 nm^3 ; this corresponds to an approximate mass of 2630 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.161 Å⁻¹

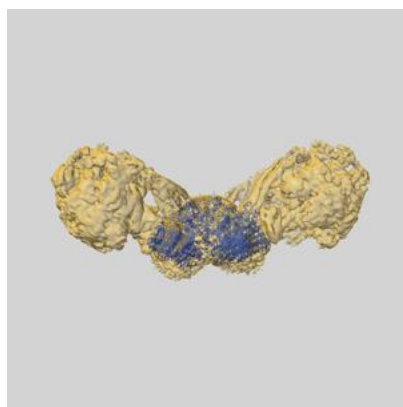
7 Fourier-Shell correlation

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

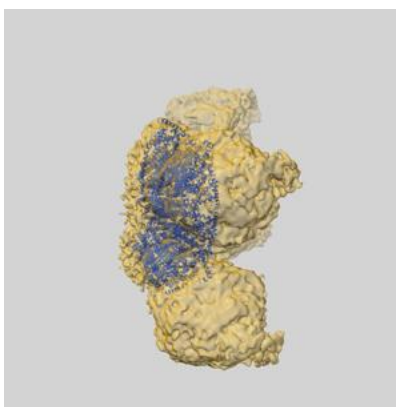
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0667 and PDB model 6ZNA. Per-residue inclusion information can be found in section ?? on page ??.

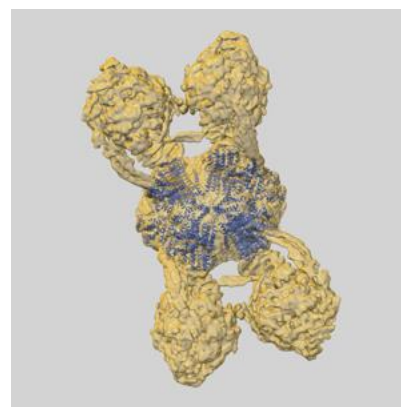
8.1 Map-model overlay [i](#)



X



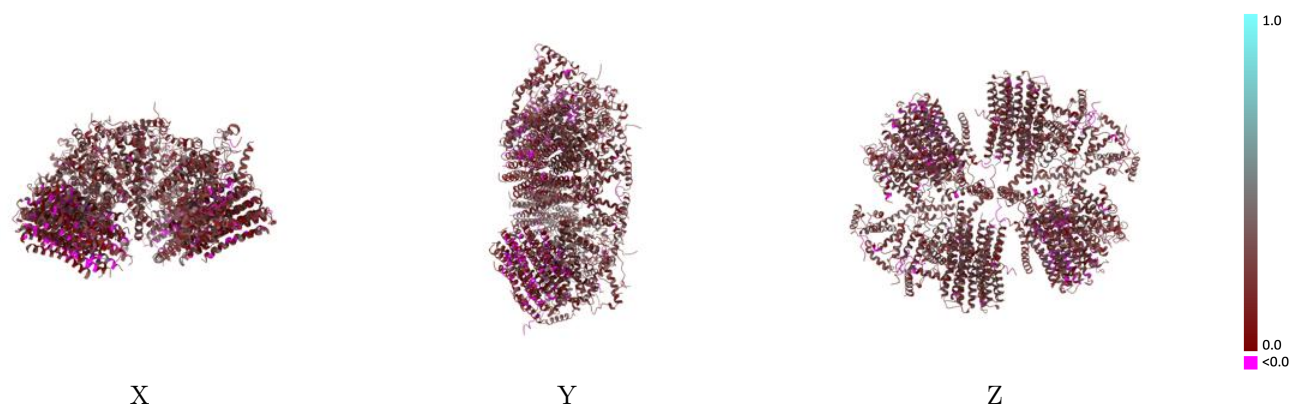
Y



Z

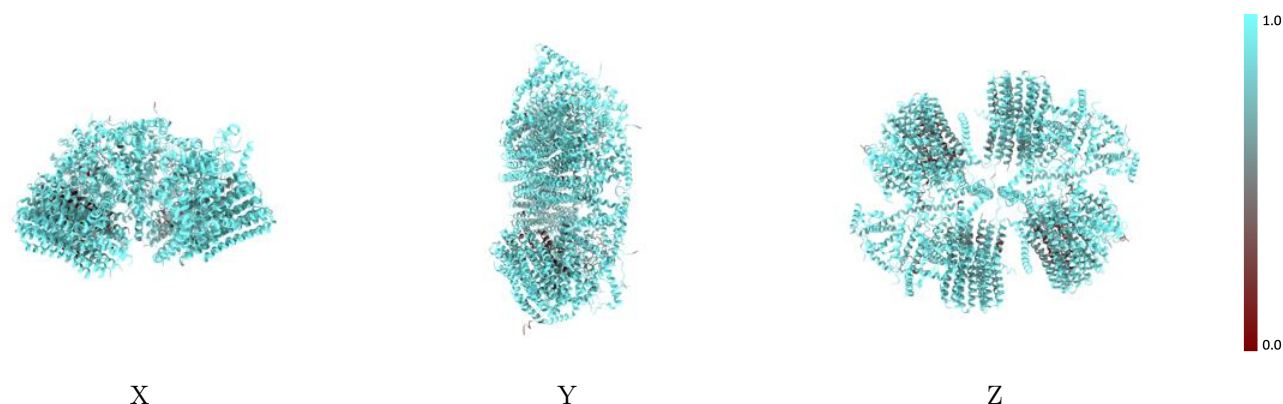
The images above show the 3D surface view of the map at the recommended contour level 0.315 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



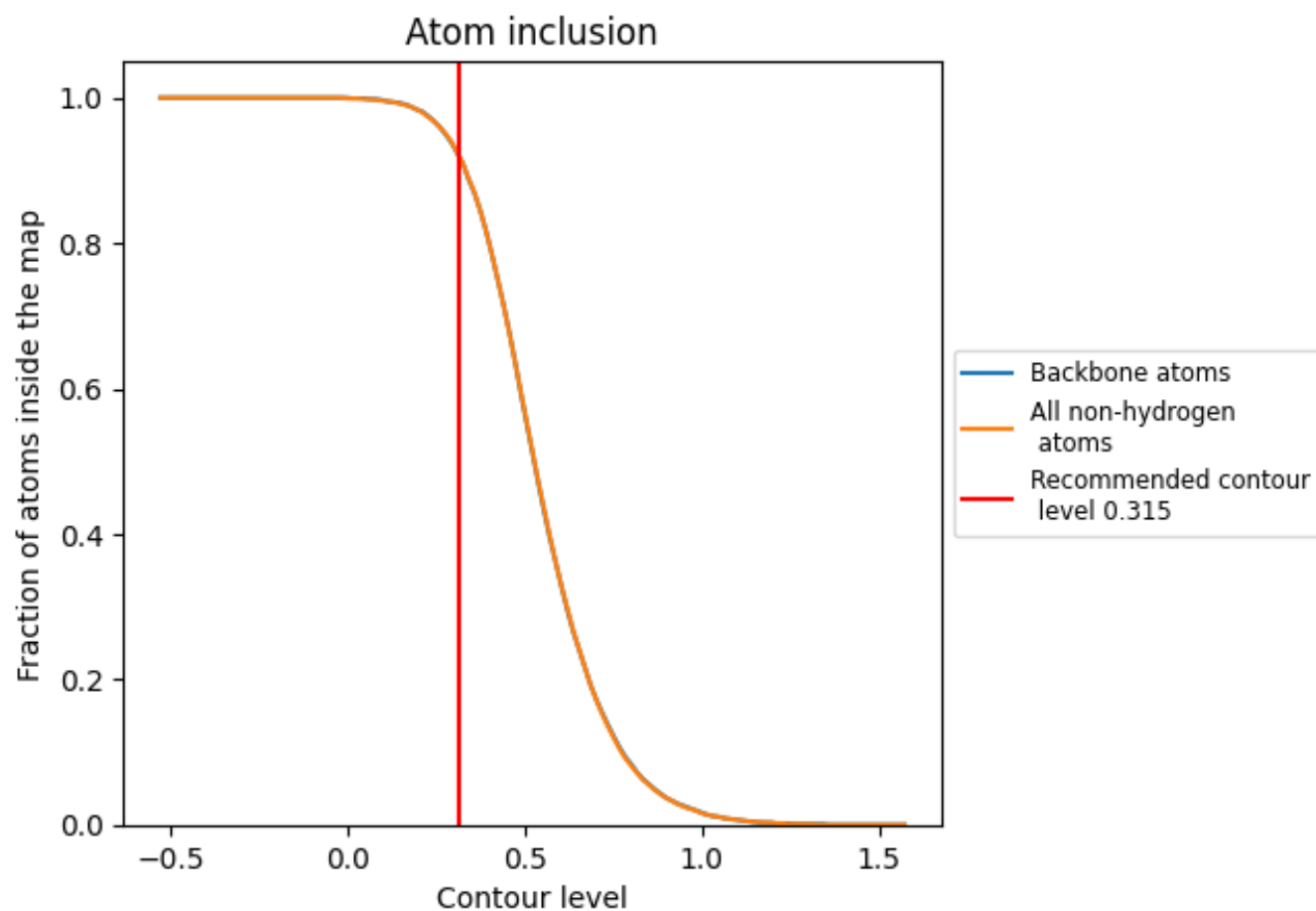
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

8.3 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 (0.315).

8.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.315) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9190	 0.2030
8	 0.9470	 0.2740
A8	 0.9410	 0.2510
AK	 0.9730	 0.1200
AL	 0.9180	 0.1390
AM	 0.8750	 0.1610
AN	 0.6700	 0.1170
AO	 0.6620	 0.0750
AP	 0.8890	 0.1930
AQ	 0.9280	 0.1420
AR	 0.9640	 0.1600
Aa	 0.9490	 0.2510
Ab	 0.9520	 0.2540
Ad	 0.9520	 0.2260
Ae	 0.9570	 0.2560
Af	 0.8680	 0.2040
Ag	 0.9760	 0.2370
Aj	 0.9200	 0.2200
Ak	 0.8010	 0.1840
B8	 0.9530	 0.2720
BK	 0.9860	 0.2150
BL	 0.9510	 0.2360
BM	 0.8740	 0.2060
BN	 0.8740	 0.2100
BO	 0.9280	 0.2330
BP	 0.9260	 0.2190
BQ	 0.9480	 0.1680
BR	 0.9780	 0.1690
Ba	 0.9660	 0.2560
Bb	 0.9720	 0.2420
Bd	 0.9640	 0.2490
Be	 0.9500	 0.2410
Bf	 0.9040	 0.2030
Bg	 0.9700	 0.2440
Bj	 0.9580	 0.2430



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Chain	Atom inclusion	Q-score
Bk	 0.8890	 0.1740
C8	 0.9590	 0.2500
CK	 0.9560	 0.0900
CL	 0.8650	 0.0840
CM	 0.8860	 0.1860
CN	 0.7360	 0.1420
CO	 0.7310	 0.1020
CP	 0.9110	 0.1800
CQ	 0.9110	 0.1080
CR	 0.9530	 0.1370
Ca	 0.9320	 0.2420
Cb	 0.9540	 0.2320
Cd	 0.9820	 0.2060
Ce	 0.9430	 0.2460
Cf	 0.8490	 0.2020
Cg	 0.9630	 0.2300
Cj	 0.9200	 0.2230
Ck	 0.7540	 0.1610
K	 0.9780	 0.1590
L	 0.9690	 0.2060
M	 0.9420	 0.2260
N	 0.8650	 0.1900
O	 0.8740	 0.1990
P	 0.9330	 0.2340
Q	 0.9370	 0.2150
R	 0.9310	 0.1450
a	 0.9580	 0.2490
b	 0.9590	 0.2400
d	 0.9700	 0.2580
e	 0.9500	 0.2410
f	 0.8940	 0.2010
g	 0.9780	 0.2340
j	 0.9660	 0.2350
k	 0.8890	 0.1660