



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:34 AM UTC

PDB ID : 8S94 / pdb_00008s94
EMDB ID : EMD-40236
Title : Structure of C-terminal domains of Walker B mutated MCM8/9 heterohexamer complex with ADP
Authors : Li, C.; Gao, Y.
Deposited on : 2023-03-27
Resolution : 3.94 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

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<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 : 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) : 2.49

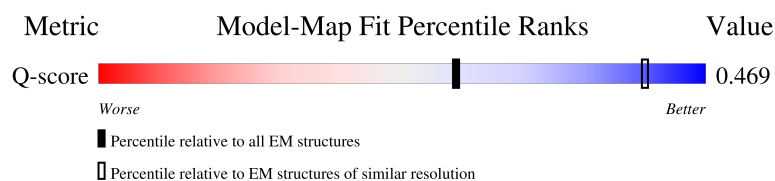
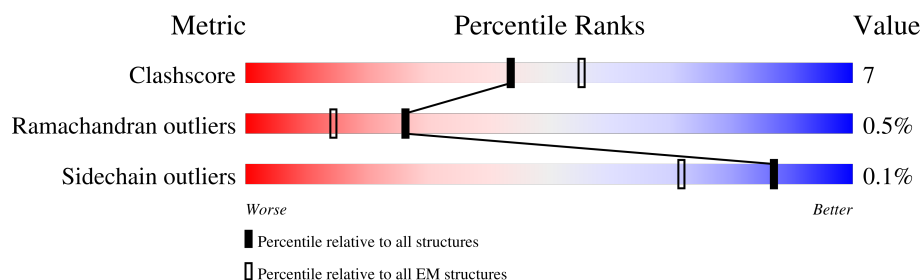
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.94 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	7757 (3.44 - 4.43)

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	840	
1	B	840	
1	C	840	
2	D	1143	

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Mol	Chain	Length	Quality of chain
2	E	1143	 A horizontal bar chart showing the quality of chain E. The bar is divided into three segments: a red segment at the start (0-27%), a green segment (27-5%), and a grey segment (5-100%). The percentages 27%, 5%, and 68% are labeled below the bar.
2	F	1143	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment at the start (0-26%), a green segment (26-6%), and a grey segment (6-100%). The percentages 26%, 6%, and 68% are labeled below the bar.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16305 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 DNA helicase MCM8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	328	Total	C	N	O	S	0	0
			2535	1601	445	478	11		
1	C	328	Total	C	N	O	S	0	0
			2535	1601	445	478	11		
1	B	328	Total	C	N	O	S	0	0
			2535	1601	445	478	11		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	519	GLN	GLU	engineered mutation	UNP Q9UJA3
C	519	GLN	GLU	engineered mutation	UNP Q9UJA3
B	519	GLN	GLU	engineered mutation	UNP Q9UJA3

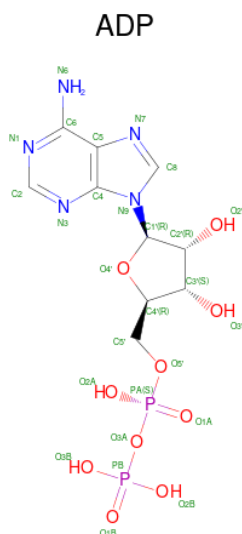
- Molecule 2 is a protein called DNA helicase MCM9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	365	Total	C	N	O	S	0	0
			2844	1789	492	547	16		
2	F	365	Total	C	N	O	S	0	0
			2844	1789	492	547	16		
2	E	365	Total	C	N	O	S	0	0
			2844	1789	492	547	16		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	415	GLN	GLU	engineered mutation	UNP Q9NXL9
F	415	GLN	GLU	engineered mutation	UNP Q9NXL9
E	415	GLN	GLU	engineered mutation	UNP Q9NXL9

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total 27	C 10	N 5	O 10	P 2	0
3	D	1	Total 27	C 10	N 5	O 10	P 2	0
3	C	1	Total 27	C 10	N 5	O 10	P 2	0
3	F	1	Total 27	C 10	N 5	O 10	P 2	0
3	B	1	Total 27	C 10	N 5	O 10	P 2	0
3	E	1	Total 27	C 10	N 5	O 10	P 2	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
4	A	1	Total Mg 1 1	0
4	D	1	Total Mg 1 1	0
4	C	1	Total Mg 1 1	0
4	F	1	Total Mg 1 1	0
4	B	1	Total Mg 1 1	0

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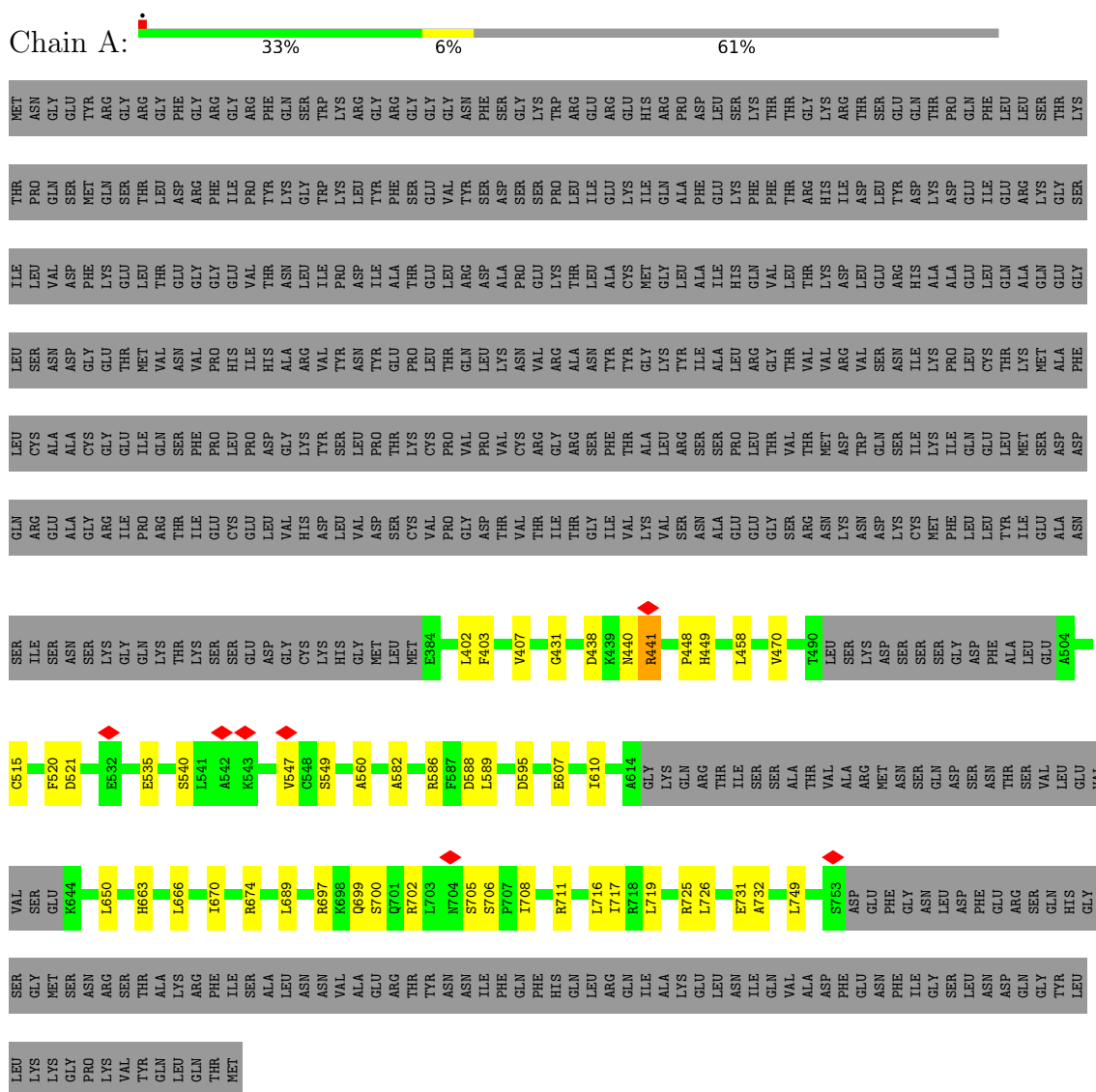
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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
4	E	1	1	1	0

3 Residue-property plots

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: DNA helicase MCM8



• Molecule 1: DNA helicase MCM8





[illegible]

- Molecule 2: DNA helicase MCM9

[illegible]

ARG	VAL	HIS	GLN	PRO	GLN	Y511
ASP	GLU	HIS	GLY	ASN	SER	P512
ALA	ALA	VAL	LYS	ARG	GLN	S512
LEU	PRO	PRO	GLU	SER	PRO	S513
PRO	ILE	ARG	LYS	THR	ARG	S514
VAL	ILE	ASN	SER	SER	VAL	K514
PRO	GLU	LEU	GLU	ARG	LEU	S515
LYS	ASN	GLN	PRO	LYS	GLU	E516
ARG	VAL	LYS	GLN	HIS	VAL	K517
PRO	LYS	LEU	GLY	SER	GLU	F528
LYS	PRO	CYS	ARG	ALA	THR	F529
LEU	GLY	GLU	LYS	GLN	THR	R532
THR	SER	ARG	VAL	HIS	PRO	R532
SER	PRO	ALA	ASP	ASN	GLY	S539
THR	VAL	GLN	ILE	ASN	SER	D540
PRO	ALA	LYS	GLY	ARG	LEU	V541
GLY	LYS	LEU	GLY	ARG	ARG	V541
ASN	LEU	LEU	LEU	ASP	ASN	L546
GLN	ALA	CYS	LEU	ASP	GLY	L546
ILE	LYS	ARG	PRO	SER	PRO	R554
SER	PHE	ASN	SER	LEU	GLY	R554
SER	THR	SER	PRO	ASP	GLU	R559
GLN	PHE	ARG	GLY	TRP	THR	R559
GLN	PHE	GLU	GLU	PHE	SER	T564
PRO	LYS	VAL	THR	ASP	ASN	T564
GLN	GLN	PRO	GLY	PHE	PHE	I566
GLY	LYS	ALA	VAL	MET	ARG	I566
GLU	SER	GLN	PRO	ALA	THR	R567
THR	LYS	CYS	TRP	THR	SER	S571
LYS	LYS	THR	ARG	HIS	SER	L572
LYS	ILE	VAL	ALA	GLN	GLN	I573
VAL	HIS	PRO	ASP	SER	GLN	R574
SER	SER	SER	ASN	GLU	GLU	L575
GLN	PHE	HIS	VAL	PRO	ILE	H579
PRO	GLU	PRO	GLU	LYS	ASN	H579
PRO	ASP	GLN	SER	ASN	TYR	A580
PRO	HIS	SER	ASN	THR	THR	R581
GLU	GLU	THR	LYS	VAL	THR	R581
LYS	HIS	PRO	LYS	VAL	HIS	D592
HIS	VAL	VAL	LYS	VAL	ILE	D592
GLY	SER	HIS	ARG	SER	PHE	E601
PRO	PRO	SER	LEU	PRO	SER	E601
ARG	GLY	PRO	ALA	HIS	PRO	L610
GLU	ALA	ASP	LEU	PRO	GLY	L610
LYS	THR	ARG	ASP	LYS	GLY	N614
VAL	LYS	MET	SER	THR	SER	N614
MET	ILE	LEU	GLU	SER	PRO	N623
CYS	ALA	ASP	ALA	GLY	GLU	N623
ALA	VAL	SER	ALA	GLY	GLY	K638
PRO	HIS	PRO	VAL	ASN	SER	L639
GLU	SER	LYS	VAL	MET	PRO	E640
LYS	PRO	ARG	ALA	ALA	VAL	L641
ARG	LYS	LYS	ASP	SER	LEU	L641
ILE	ILE	ARG	LYS	LYS	ASP	L655
ILE	SER	PRO	PRO	ILE	PRO	L655
GLN	GLN	LYS	ASP	ASN	GLN	ASN
PRO	ARG	SER	SER	ASN	PRO	ASN
LEU	ARG	LEU	VAL	HIS	GLN	SER
GLU	THR	ALA	LEU	THR	LEU	SER
GLU	ARG	GLN	THR	SER	GLU	THR

LYS	GLY	LEU
SER	GLU	ASN
	ARG	GLU
	GLY	THR
	PRO	GLY
	SER	CYS
	SER	ALA
	PRO	HIS
	PRO	LEU
	THR	THR
	THR	CYS
	ALA	GLU
	PRO	GLY
	MET	ASP
	ARG	LYS
	VAL	LYS
	SER	GLU
	LYS	GLU
	ARG	VAL
	LYS	SER
	SER	GLY
	PHE	SER
	GLN	ASN
	LEU	LYS
	ARG	GLY
	GLY	GLY
	SER	LYS
	THR	VAL
	THR	HIS
	GLU	ALA
	LYS	CYS
	LEU	THR
	ILE	THR
	VAL	LEU
	SER	ALA
	LYS	ARG
	GLU	LEU
	SER	ALA
	LEU	ASN
	PHE	CYS
	THR	PHE
	LEU	THR
	PRO	THR
	GLU	PRO
	LEU	PRO
	GLY	SER
	ASP	GLU
	GLU	SER
	ALA	LYS
	PHE	LYS
	ASP	LYS
	CYS	SER
	ASP	PRO
	TRP	PRO
	ASP	PRO
	GLU	ARG
	GLU	LYS
	MET	LYS
	ARG	ASN
	LYS	ARG

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	227818	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 ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.025	Depositor
Minimum map value	-1.294	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	355.2, 355.2, 355.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.11, 1.11, 1.11	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, 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	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.13	0/2574	0.38	0/3480
1	B	0.12	0/2574	0.37	0/3480
1	C	0.12	0/2574	0.36	0/3480
2	D	0.14	0/2885	0.41	0/3899
2	E	0.13	0/2885	0.41	1/3899 (0.0%)
2	F	0.13	0/2885	0.39	1/3899 (0.0%)
All	All	0.13	0/16377	0.39	2/22137 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	541	VAL	N-CA-C	-5.22	106.45	112.98
2	E	541	VAL	N-CA-C	-5.10	106.60	112.98

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	2535	0	2586	32	0
1	B	2535	0	2586	31	0
1	C	2535	0	2586	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	2844	0	2883	43	0
2	E	2844	0	2883	43	0
2	F	2844	0	2883	46	0
3	A	27	0	12	0	0
3	B	27	0	12	0	0
3	C	27	0	12	0	0
3	D	27	0	12	0	0
3	E	27	0	12	0	0
3	F	27	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
All	All	16305	0	16479	214	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 7.

The worst 5 of 214 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)
2:F:285:GLN:N	2:F:285:GLN:OE1	2.24	0.70
2:F:460:LYS:HA	2:F:460:LYS:HE3	1.73	0.69
1:C:531:LEU:HD23	1:C:586:ARG:HH21	1.56	0.68
2:E:285:GLN:OE1	2:E:285:GLN:N	2.27	0.68
2:E:420:LYS:O	2:E:423:ASP:N	2.27	0.67

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	322/840 (38%)	292 (91%)	28 (9%)	2 (1%)	21	56
1	B	322/840 (38%)	294 (91%)	26 (8%)	2 (1%)	21	56
1	C	322/840 (38%)	296 (92%)	24 (8%)	2 (1%)	21	56
2	D	361/1143 (32%)	323 (90%)	36 (10%)	2 (1%)	21	56
2	E	361/1143 (32%)	320 (89%)	40 (11%)	1 (0%)	36	70
2	F	361/1143 (32%)	322 (89%)	37 (10%)	2 (1%)	21	56
All	All	2049/5949 (34%)	1847 (90%)	191 (9%)	11 (0%)	26	60

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	441	ARG
1	A	547	VAL
2	D	518	LEU
1	C	441	ARG
1	C	547	VAL

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	275/723 (38%)	275 (100%)	0	100	100
1	B	275/723 (38%)	274 (100%)	1 (0%)	84	84
1	C	275/723 (38%)	275 (100%)	0	100	100
2	D	314/1020 (31%)	314 (100%)	0	100	100
2	E	314/1020 (31%)	314 (100%)	0	100	100
2	F	314/1020 (31%)	313 (100%)	1 (0%)	86	86
All	All	1767/5229 (34%)	1765 (100%)	2 (0%)	87	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	373	VAL
1	B	661	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	608	HIS
2	E	360	GLN
2	E	333	GLN
2	E	434	GLN
2	F	333	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 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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
3	ADP	C	2001	-	28,29,29	1.42	4 (14%)	43,45,45	1.86	8 (18%)
3	ADP	F	2001	4	28,29,29	1.40	4 (14%)	43,45,45	1.86	8 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ADP	D	2001	4	28,29,29	1.41	4 (14%)	43,45,45	1.85	8 (18%)
3	ADP	B	2001	-	28,29,29	1.41	4 (14%)	43,45,45	1.85	8 (18%)
3	ADP	E	2001	4	28,29,29	1.40	4 (14%)	43,45,45	1.84	8 (18%)
3	ADP	A	2001	-	28,29,29	1.42	4 (14%)	43,45,45	1.85	8 (18%)

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
3	ADP	C	2001	-	-	3/16/32/32	0/3/3/3
3	ADP	F	2001	4	-	4/16/32/32	0/3/3/3
3	ADP	D	2001	4	-	3/16/32/32	0/3/3/3
3	ADP	B	2001	-	-	2/16/32/32	0/3/3/3
3	ADP	E	2001	4	-	3/16/32/32	0/3/3/3
3	ADP	A	2001	-	-	3/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2001	ADP	C5-C4	4.74	1.47	1.39
3	A	2001	ADP	C5-C4	4.72	1.47	1.39
3	B	2001	ADP	C5-C4	4.72	1.47	1.39
3	F	2001	ADP	C5-C4	4.70	1.47	1.39
3	D	2001	ADP	C5-C4	4.70	1.47	1.39

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2001	ADP	C5-C4-N3	-6.13	118.27	126.72
3	B	2001	ADP	C5-C4-N3	-6.11	118.31	126.72
3	A	2001	ADP	C5-C4-N3	-6.10	118.32	126.72
3	F	2001	ADP	C5-C4-N3	-6.04	118.40	126.72
3	D	2001	ADP	C5-C4-N3	-6.03	118.41	126.72

There are no chirality outliers.

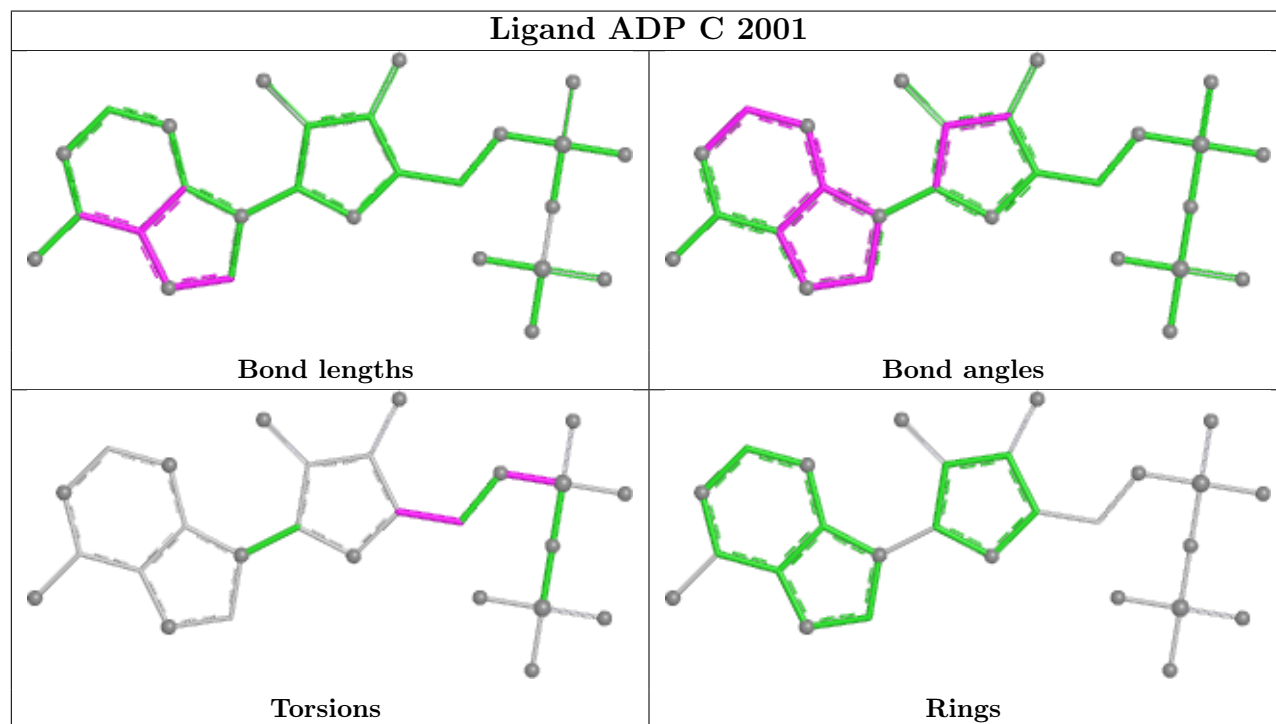
5 of 18 torsion outliers are listed below:

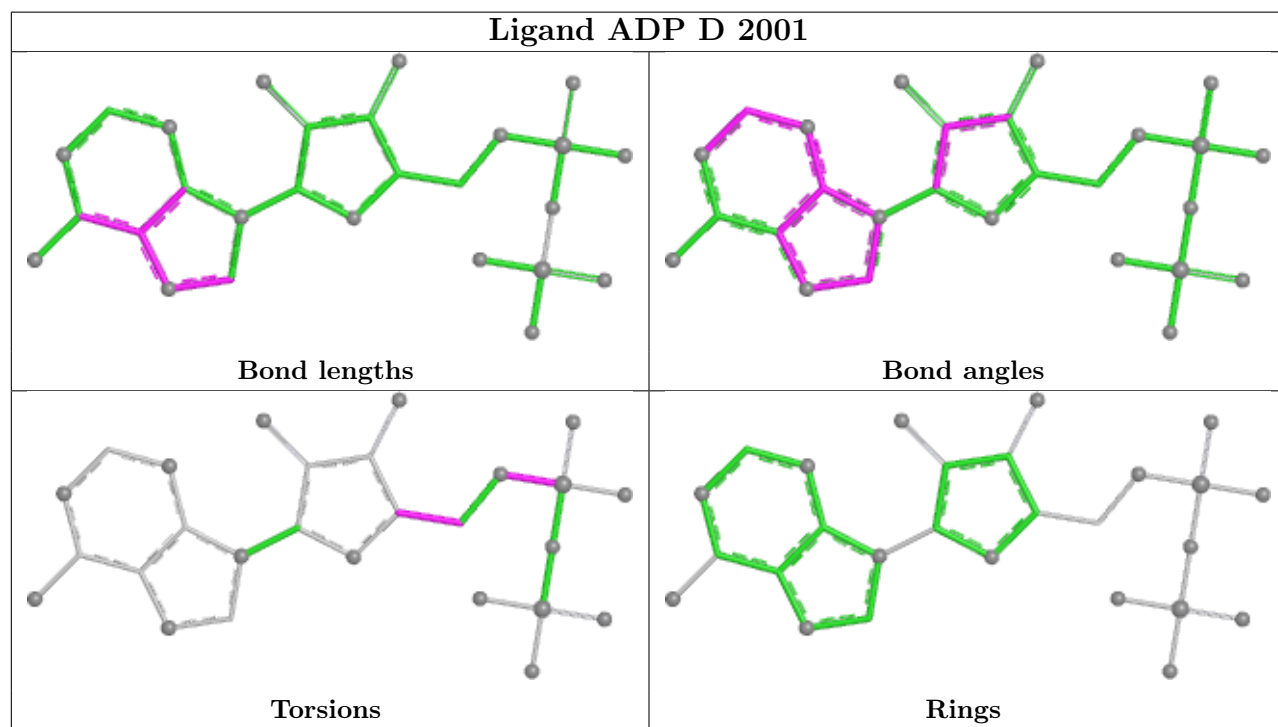
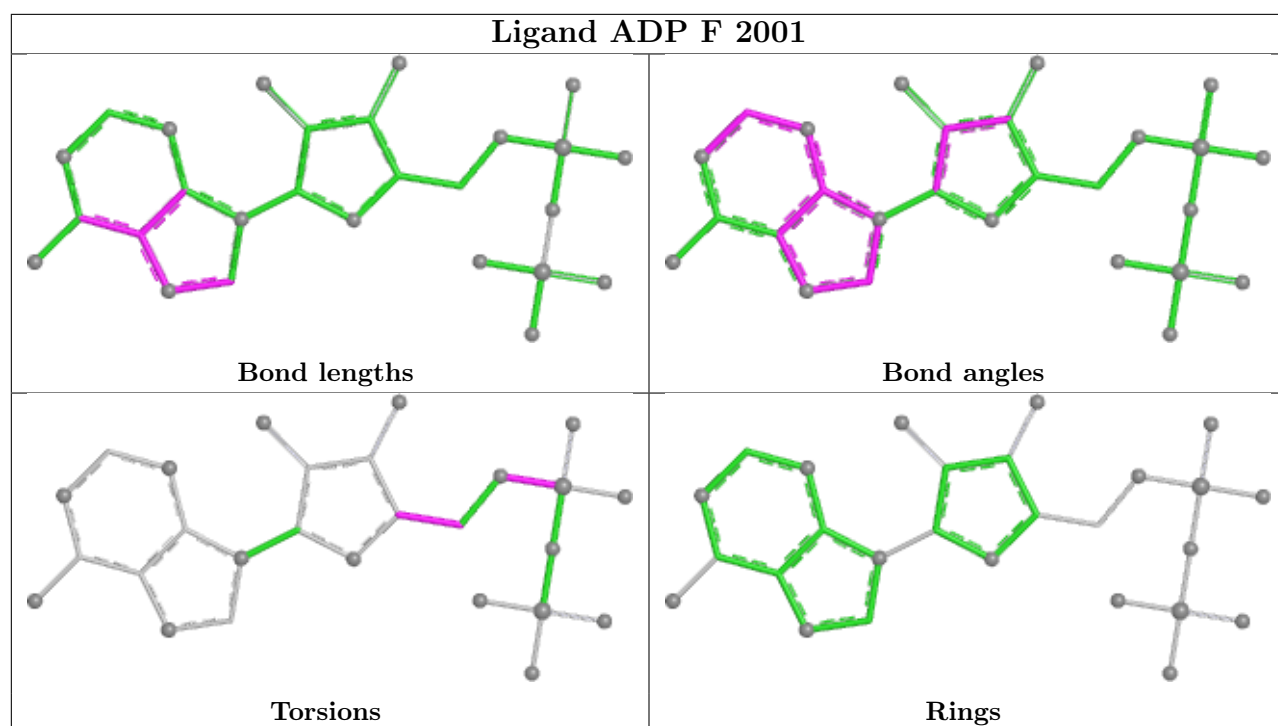
Mol	Chain	Res	Type	Atoms
3	A	2001	ADP	C5'-O5'-PA-O3A
3	D	2001	ADP	C5'-O5'-PA-O1A
3	D	2001	ADP	C3'-C4'-C5'-O5'
3	C	2001	ADP	C5'-O5'-PA-O3A
3	F	2001	ADP	C5'-O5'-PA-O1A

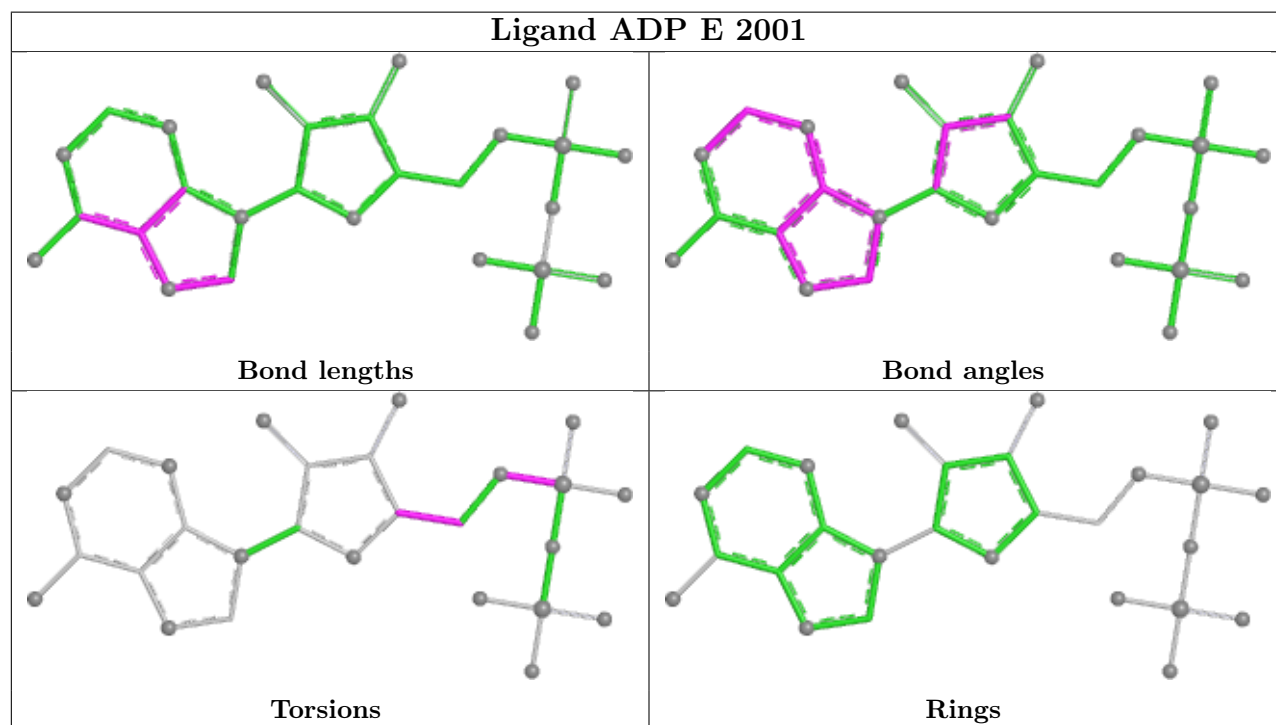
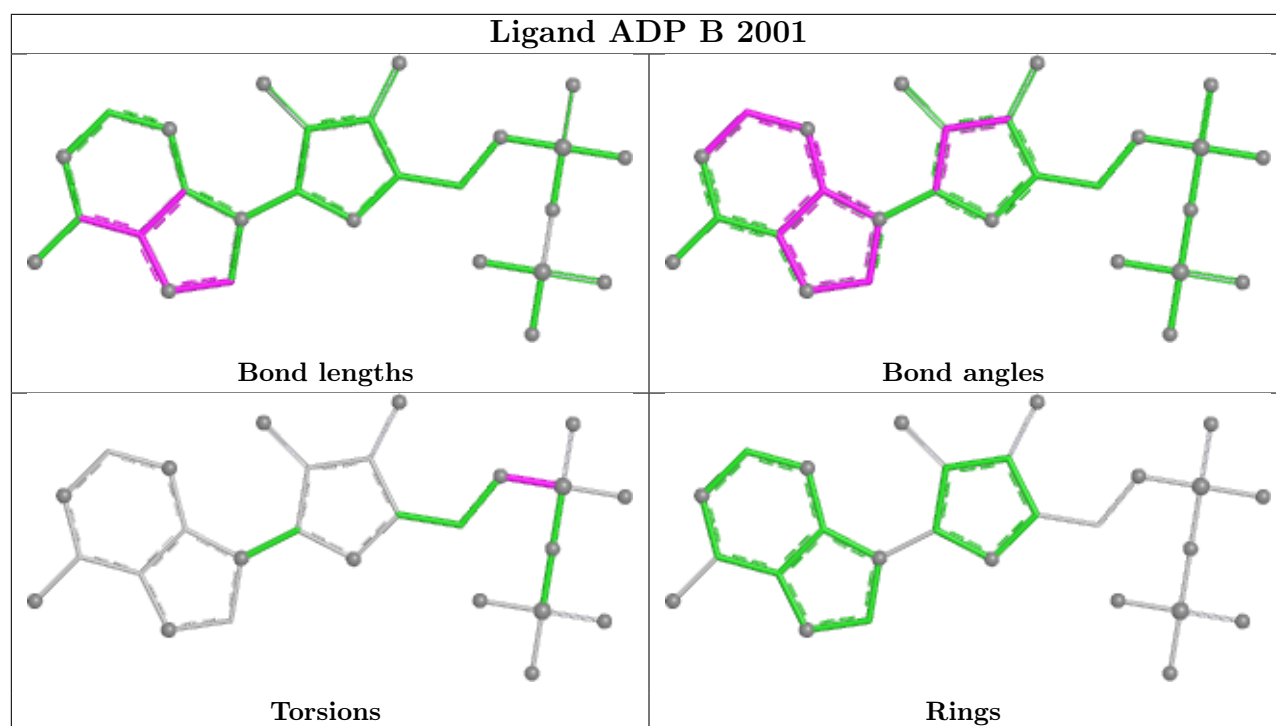
There are no ring outliers.

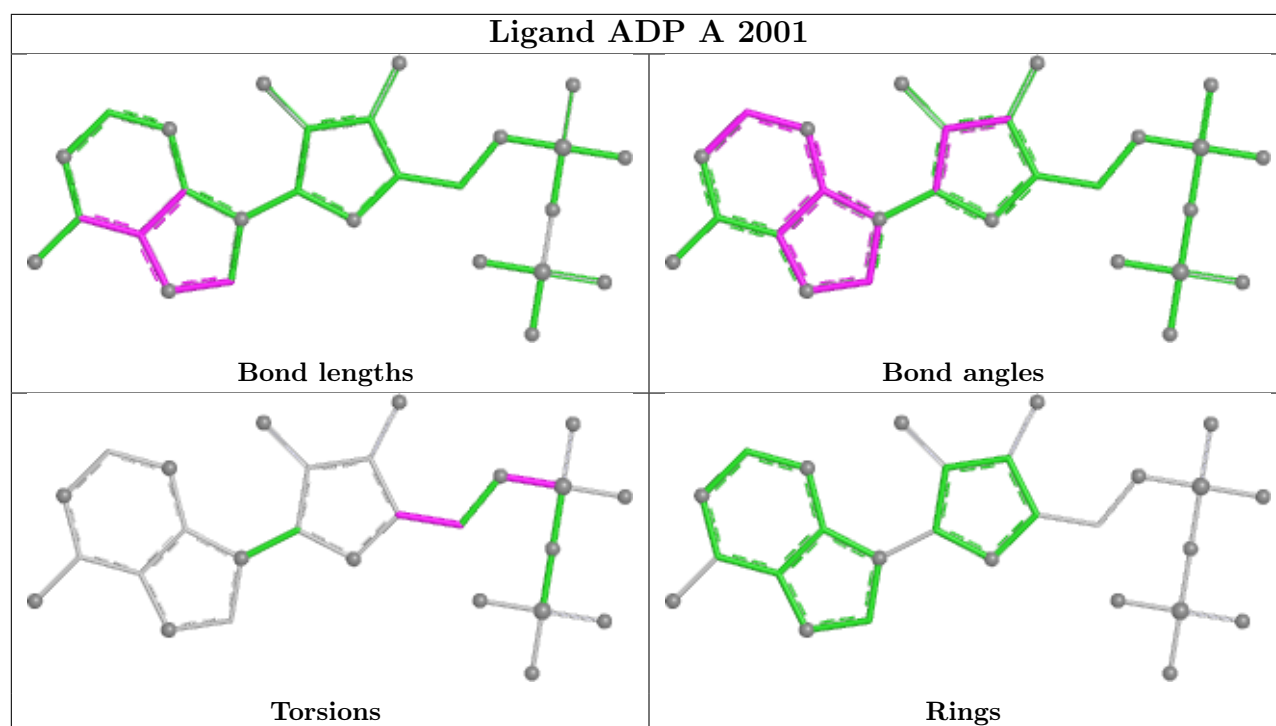
No monomer is involved in short contacts.

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.









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.

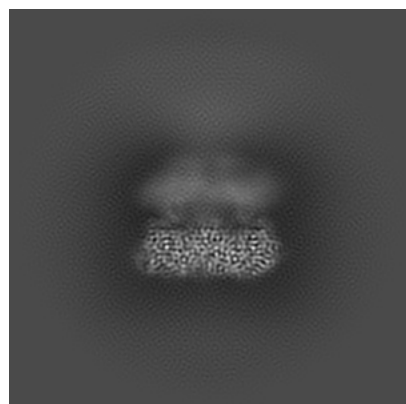
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40236. These allow visual inspection of the internal detail of the map and identification of artifacts.

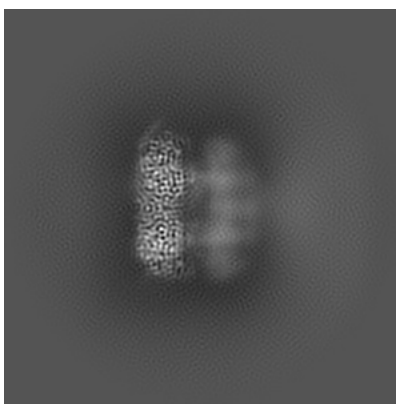
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

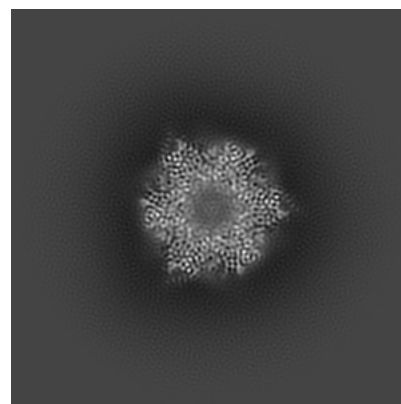
6.1.1 Primary map



X

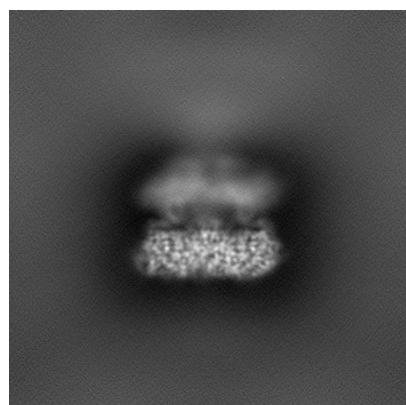


Y

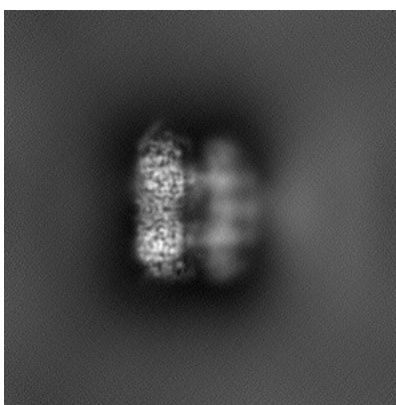


Z

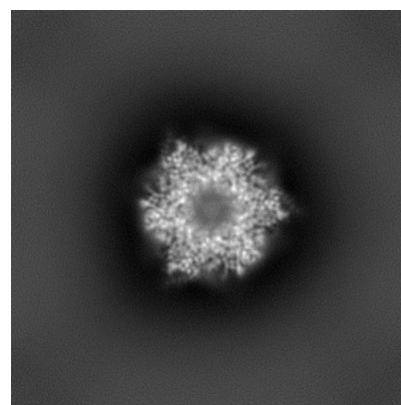
6.1.2 Raw map



X



Y

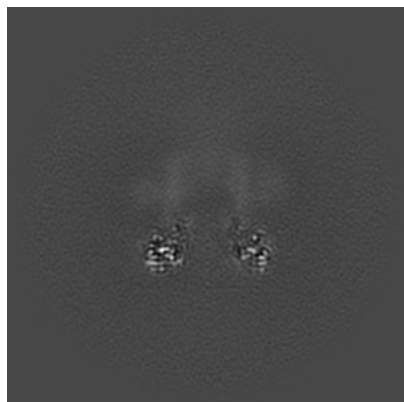


Z

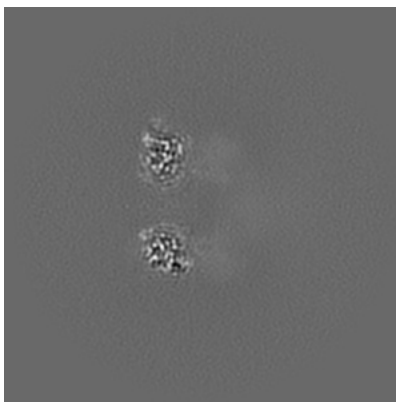
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

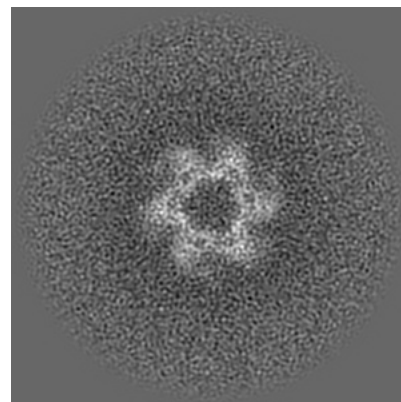
6.2.1 Primary map



X Index: 160

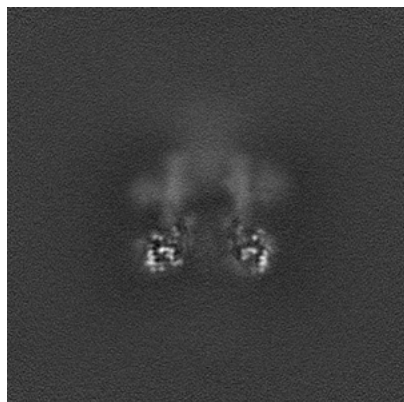


Y Index: 160

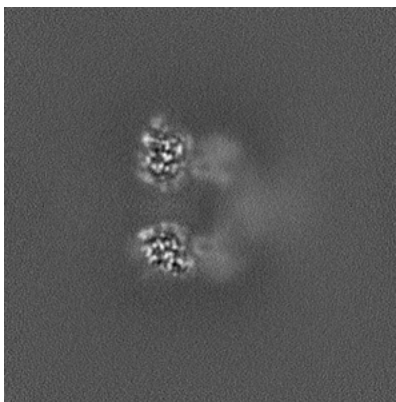


Z Index: 160

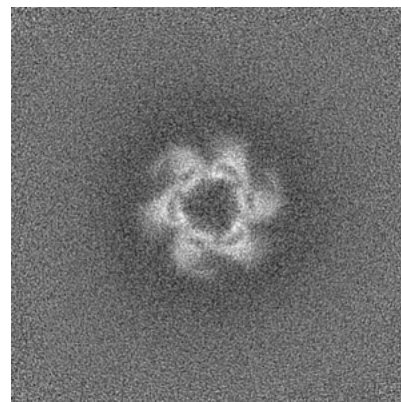
6.2.2 Raw map



X Index: 160



Y Index: 160

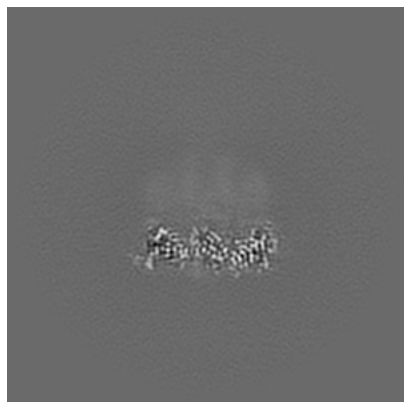


Z Index: 160

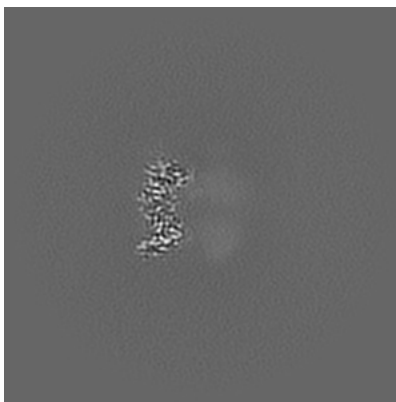
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

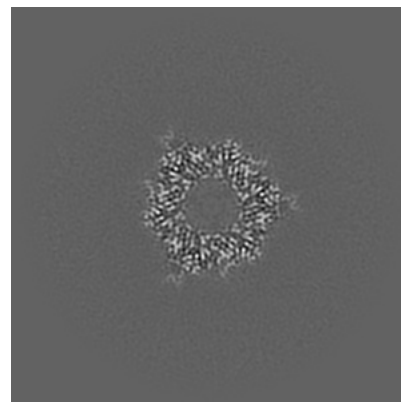
6.3.1 Primary map



X Index: 133

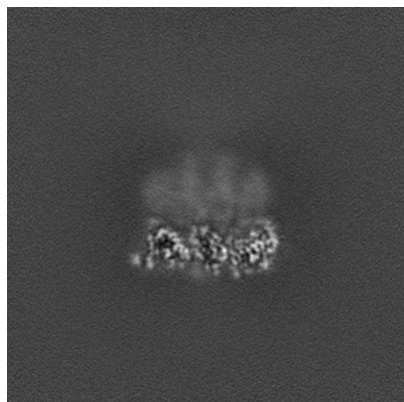


Y Index: 199

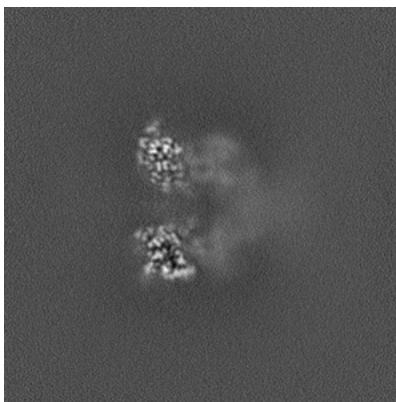


Z Index: 121

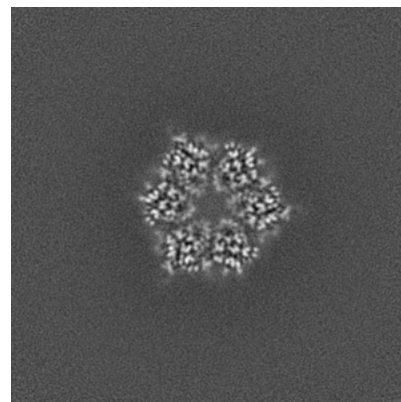
6.3.2 Raw map



X Index: 134



Y Index: 165

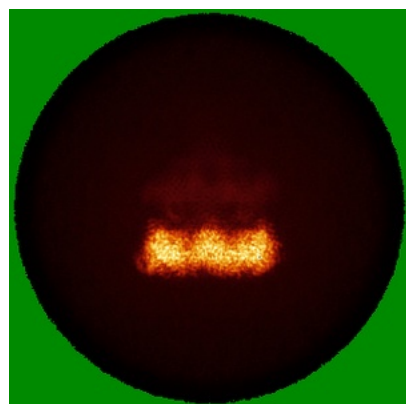


Z Index: 129

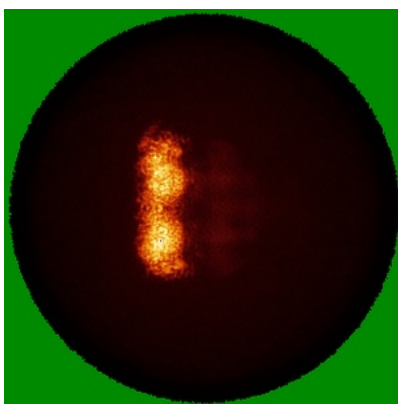
The images above show the largest variance slices of the map in three orthogonal directions.

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

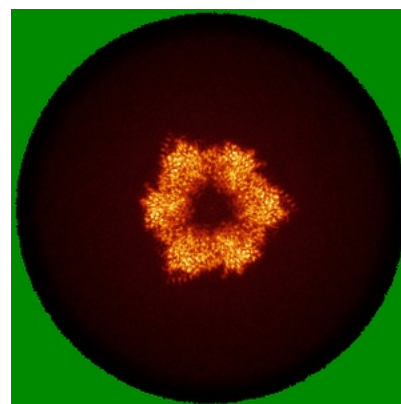
6.4.1 Primary map



X

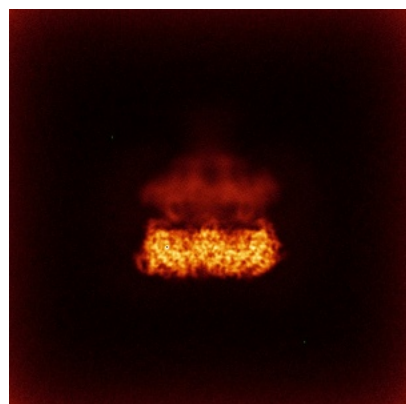


Y

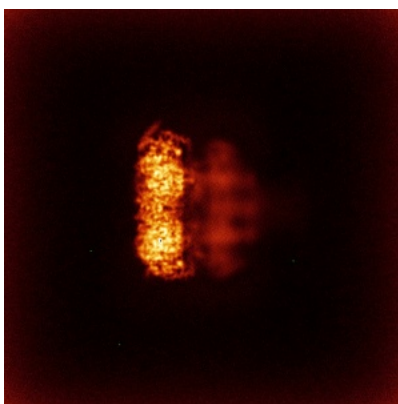


Z

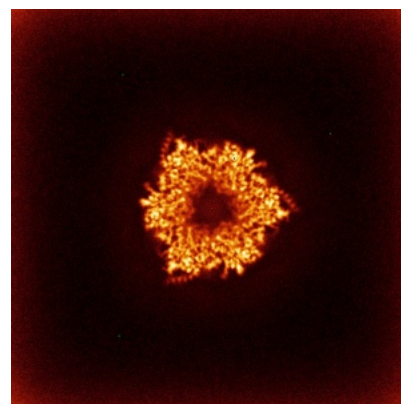
6.4.2 Raw map



X



Y

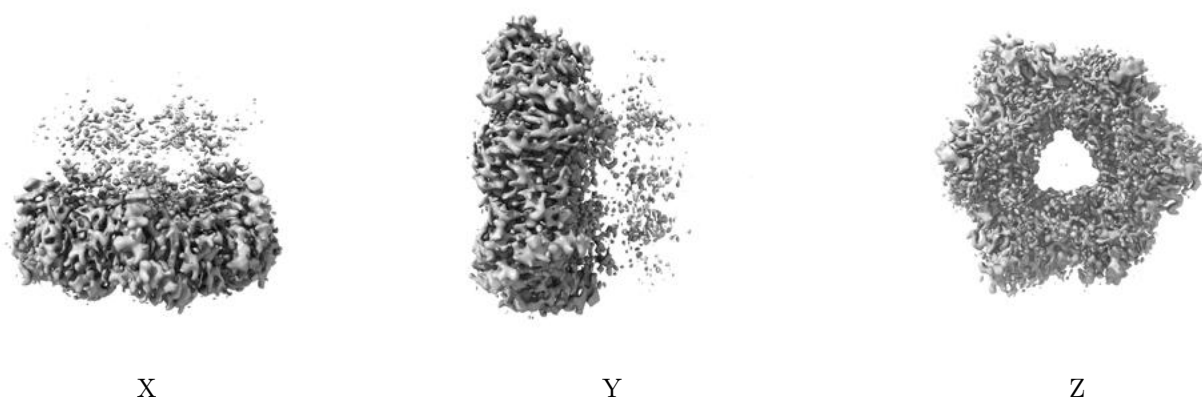


Z

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

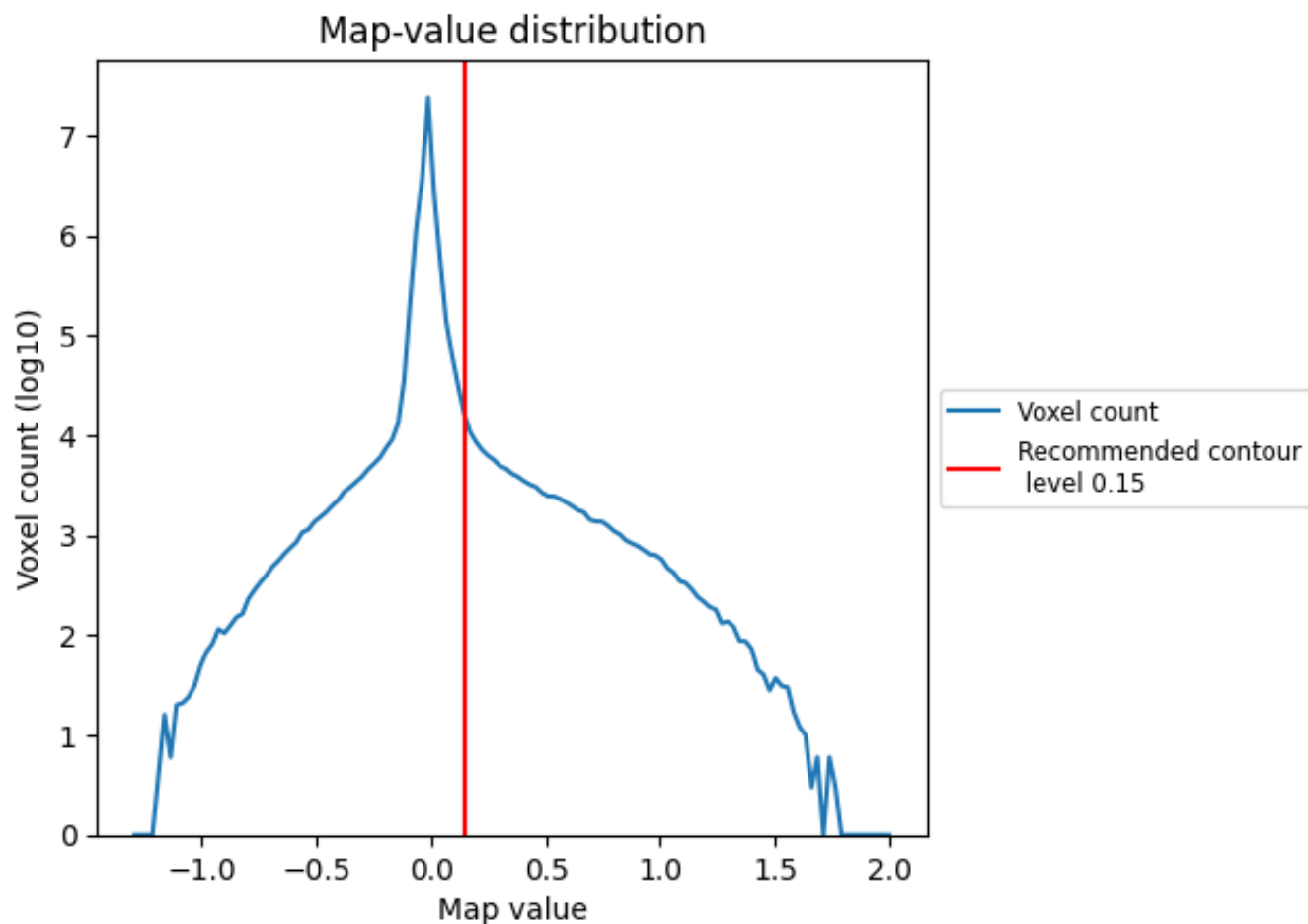
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

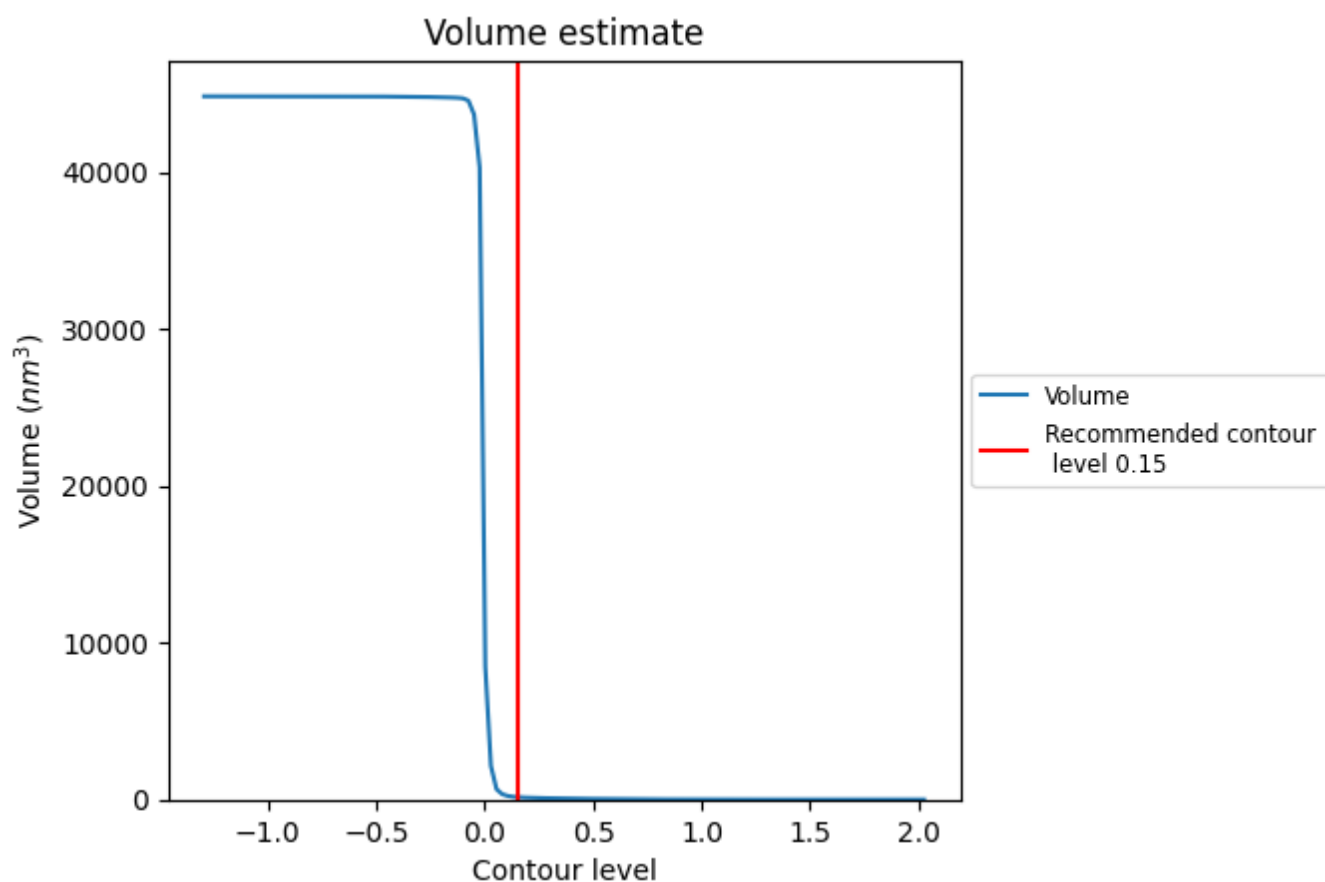
This section contains the results of statistical analysis of the map.

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.

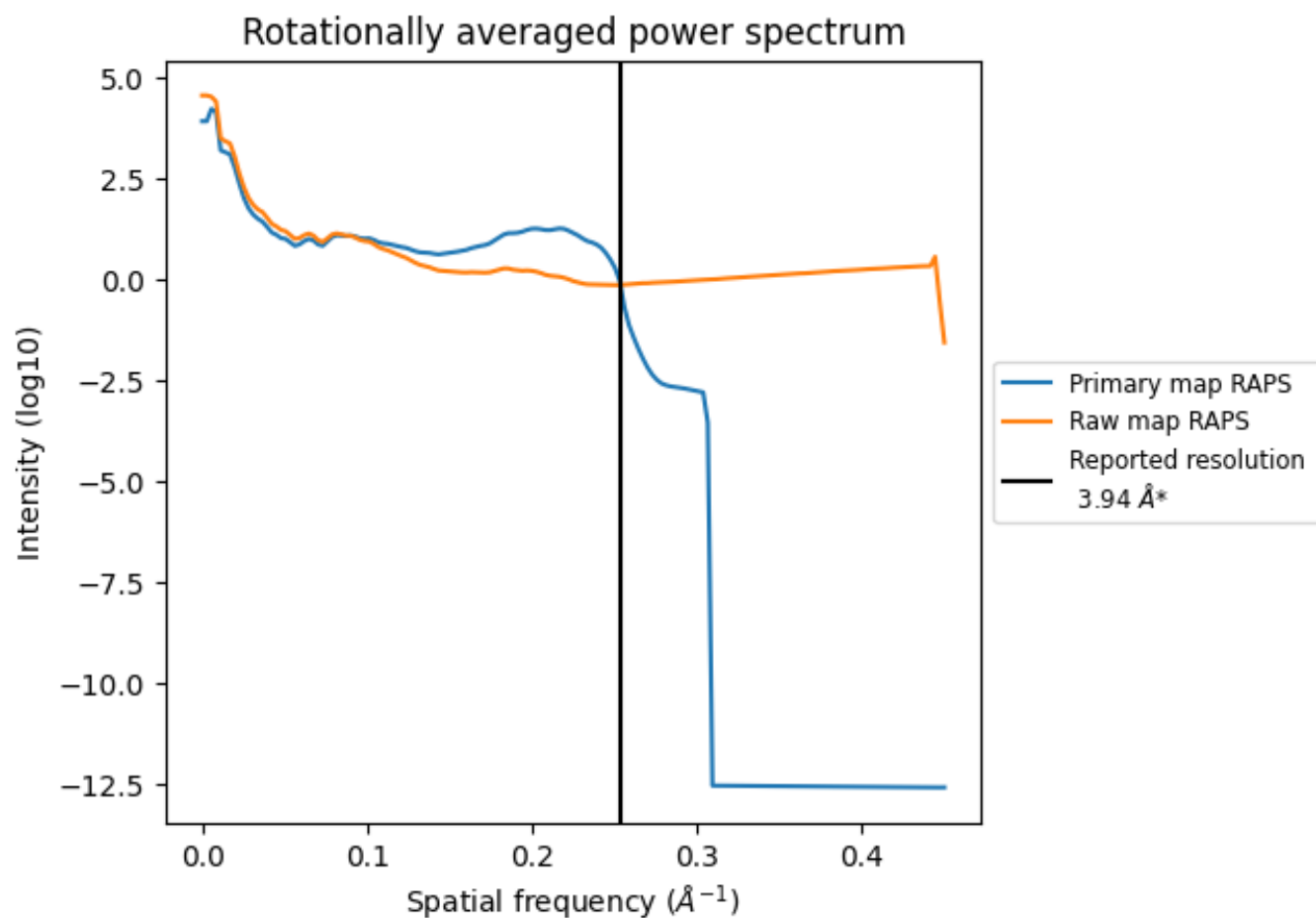
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm³; this corresponds to an approximate mass of 138 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 ⓘ

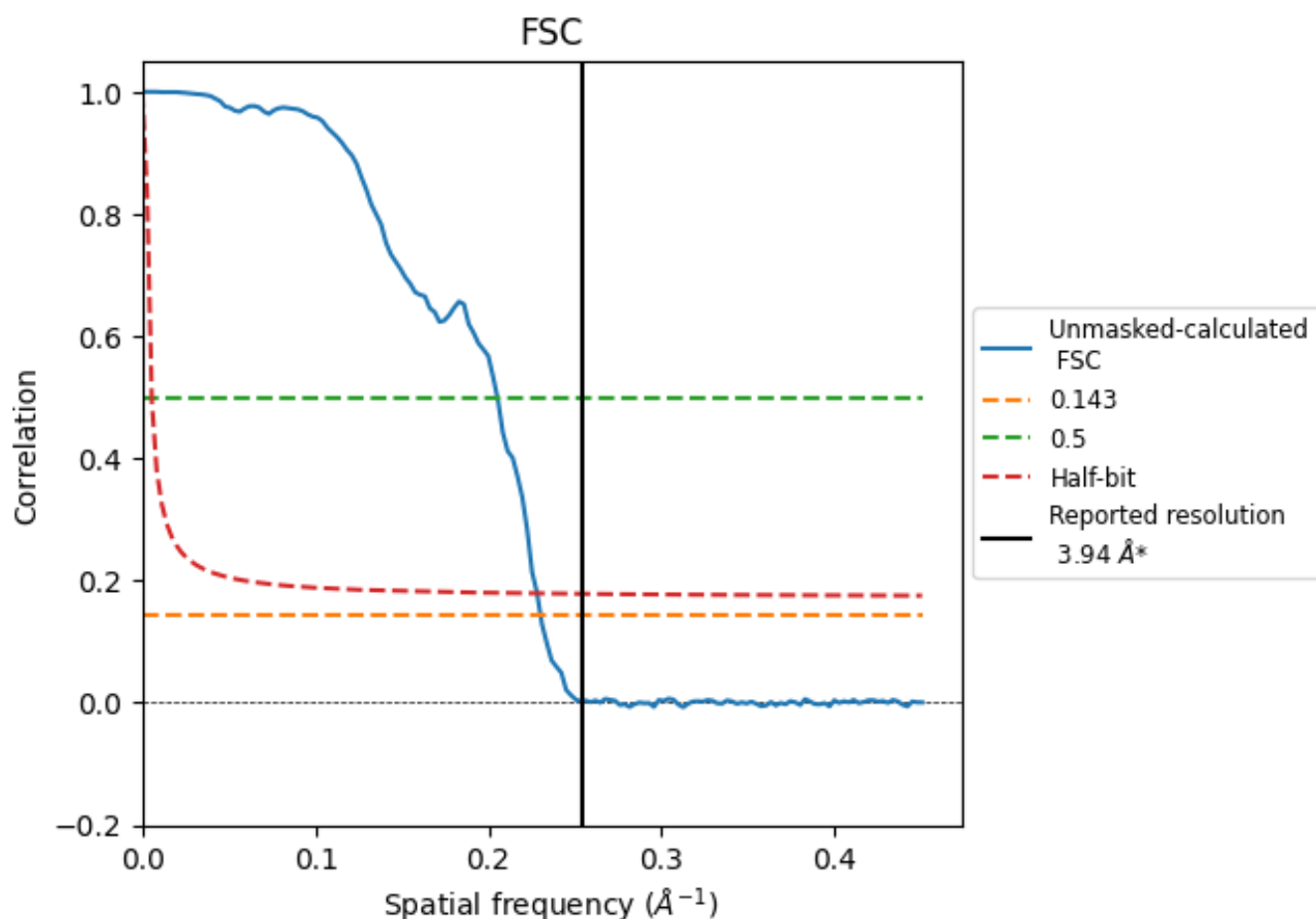


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 $0.254 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

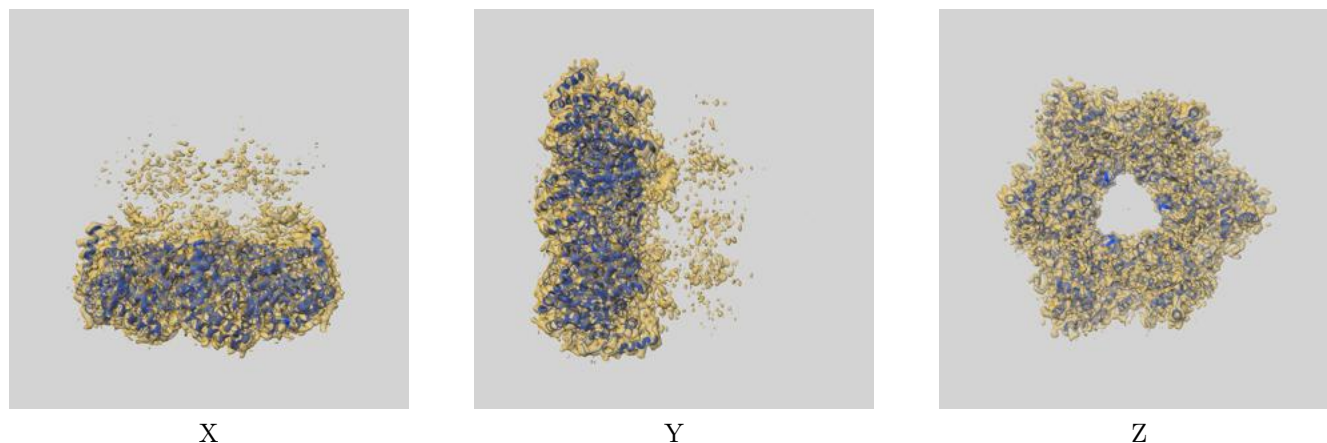
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.35	4.87	4.38

*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 4.35 differs from the reported value 3.94 by more than 10 %

9 Map-model fit [i](#)

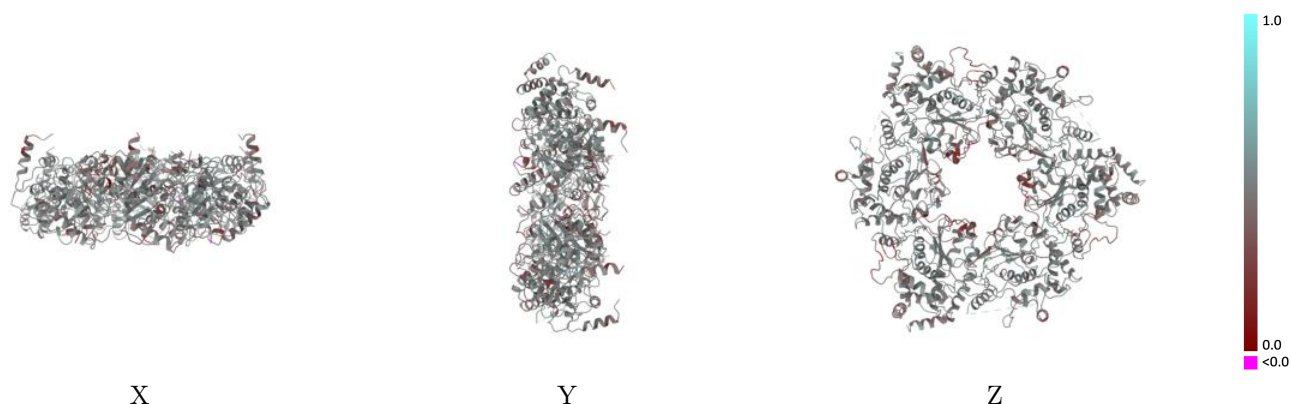
This section contains information regarding the fit between EMDB map EMD-40236 and PDB model 8S94. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



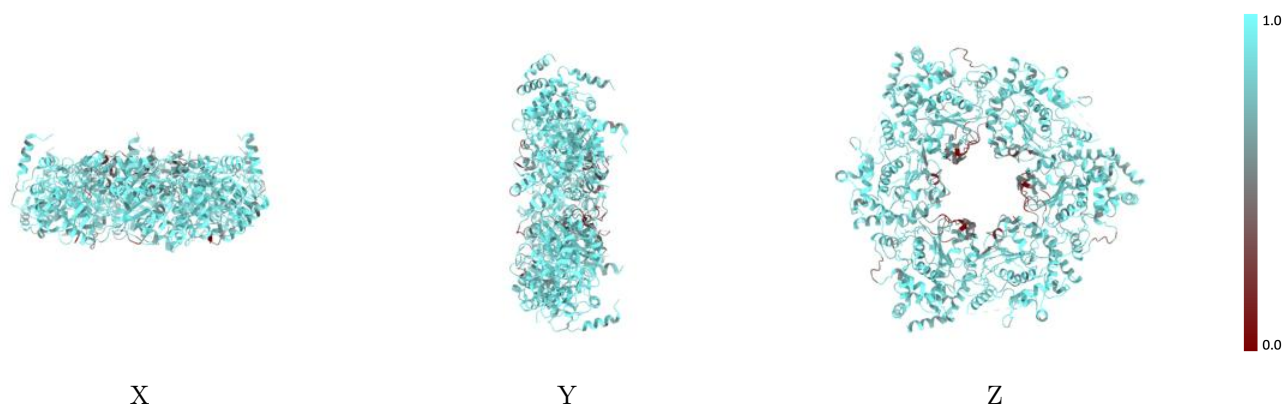
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



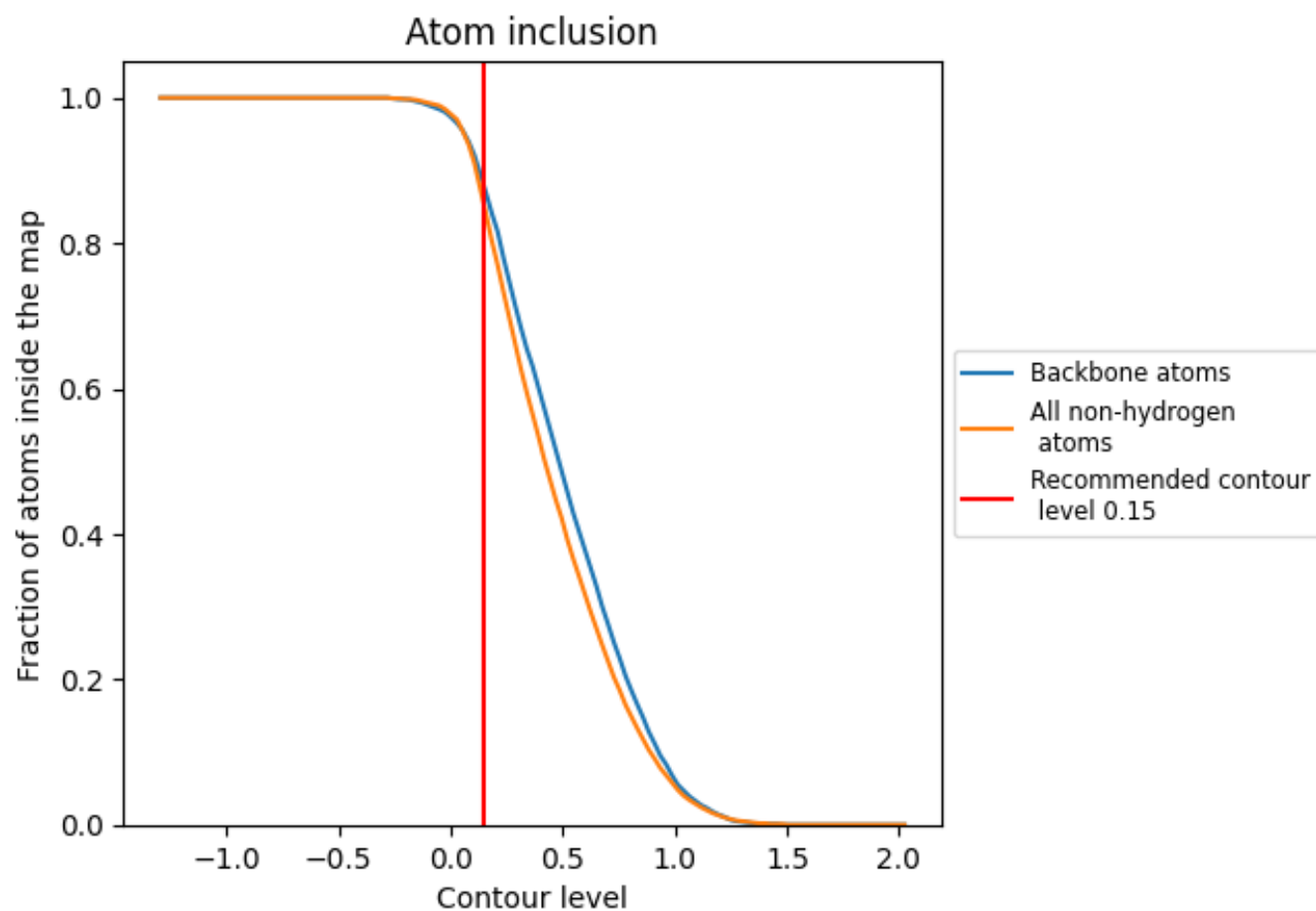
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8520	0.4690
A	0.8670	0.4730
B	0.8700	0.4740
C	0.8700	0.4720
D	0.8380	0.4640
E	0.8330	0.4660
F	0.8360	0.4650

1.0

0.0

<0.0