



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:49 AM UTC

PDB ID : 8S91 / pdb_00008s91
EMDB ID : EMD-40234
Title : Structure of Walker B mutated MCM8/9 heterohexamer complex with ADP
Authors : Li, C.; Gao, Y.
Deposited on : 2023-03-27
Resolution : 4.30 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 : 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

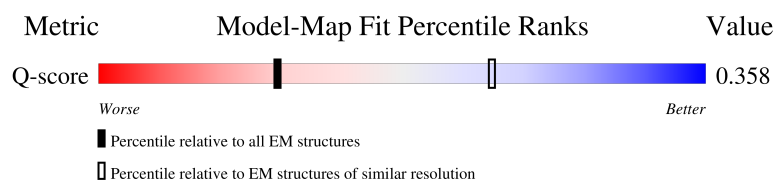
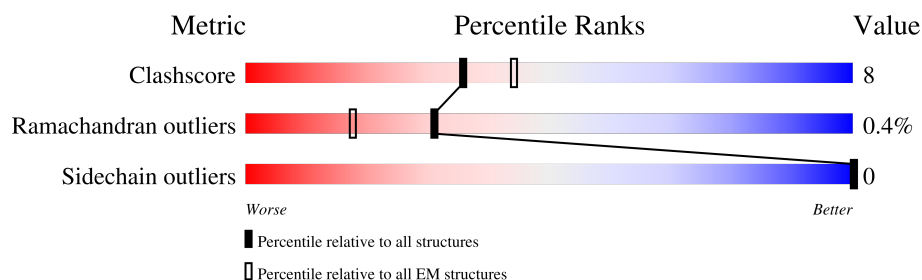
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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.



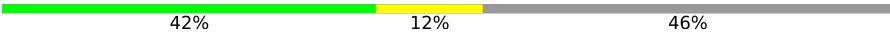
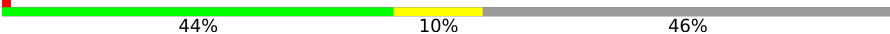
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	 42% 12% 46%
2	F	1143	 44% 10% 46%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 29019 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	602	Total	C	N	O	S	0	0
			4703	2984	809	884	26		
1	B	602	Total	C	N	O	S	0	0
			4703	2984	809	884	26		
1	C	602	Total	C	N	O	S	0	0
			4703	2984	809	884	26		

There are 3 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called DNA helicase MCM9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	621	Total	C	N	O	S	0	0
			4914	3099	841	941	33		
2	E	621	Total	C	N	O	S	0	0
			4914	3099	841	941	33		
2	F	621	Total	C	N	O	S	0	0
			4914	3099	841	941	33		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	415	GLN	GLU	engineered mutation	UNP Q9NXL9
E	415	GLN	GLU	engineered mutation	UNP Q9NXL9
F	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	B	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	D	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
3	F	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	B	1	Total Mg 1 1	0
4	C	1	Total Mg 1 1	0
4	D	1	Total Mg 1 1	0
4	E	1	Total Mg 1 1	0

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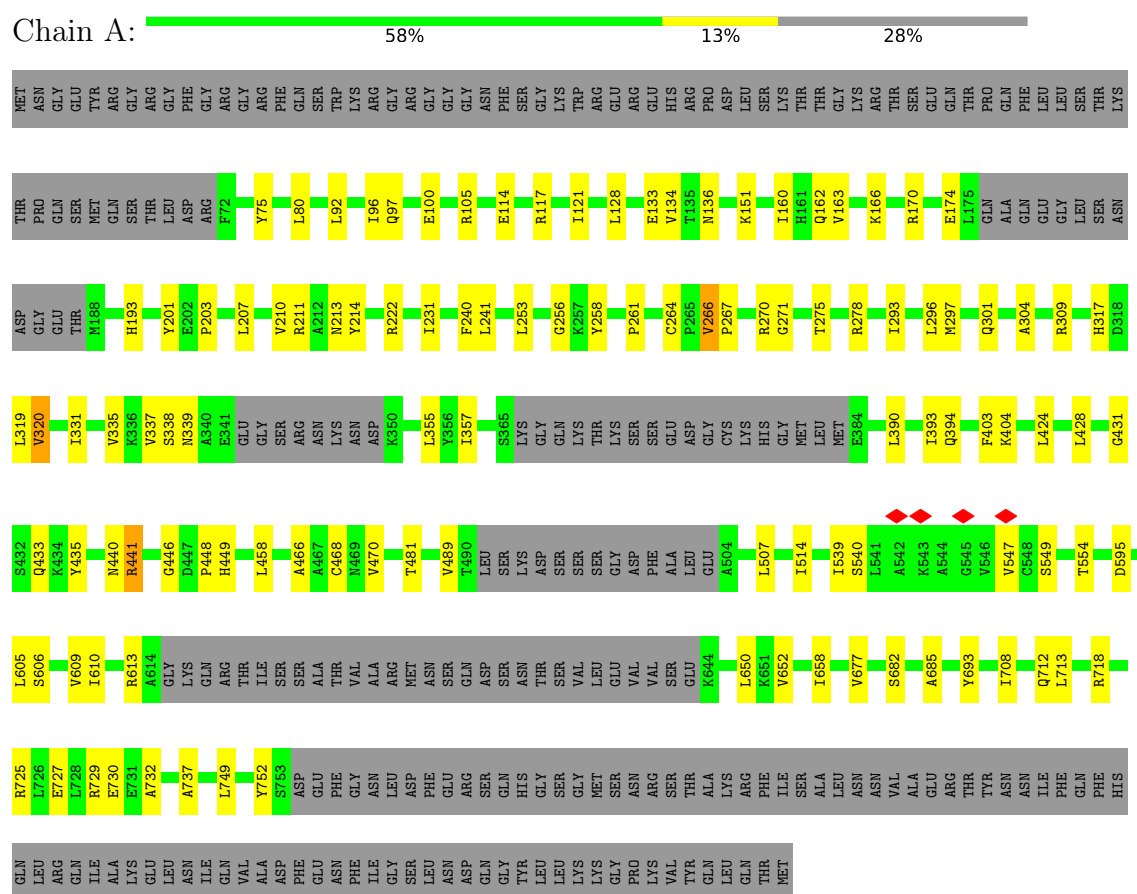
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Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
4	F	1	1	1	0

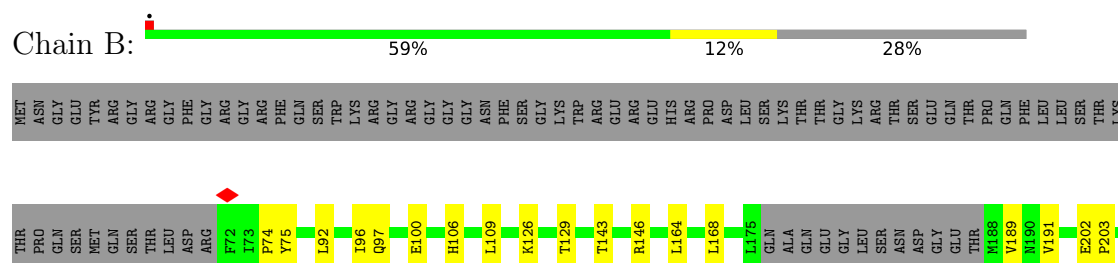
3 Residue-property plots

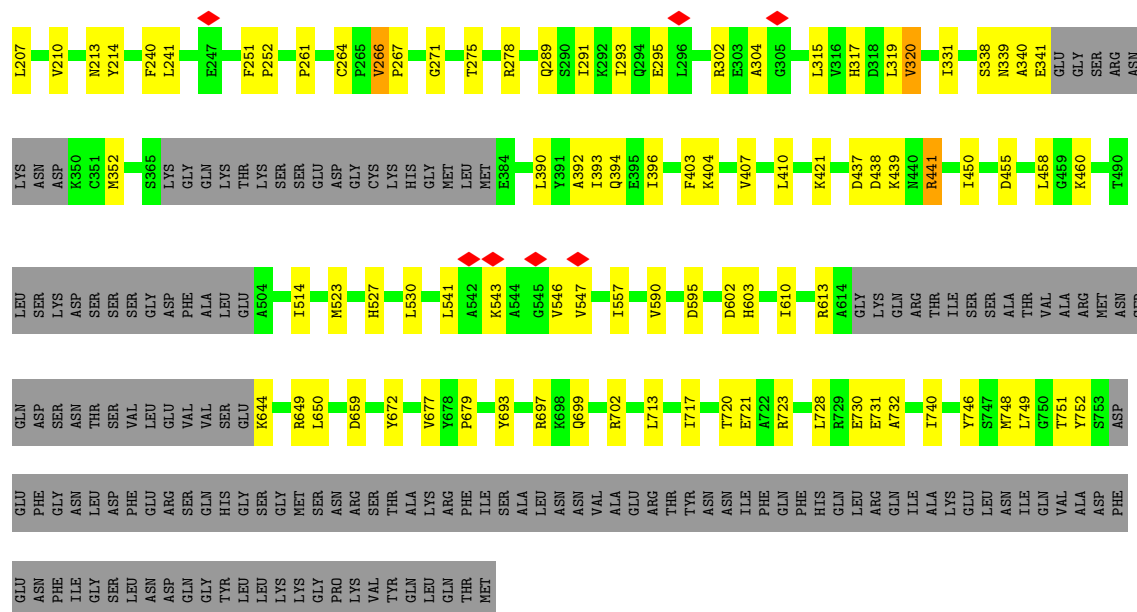
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

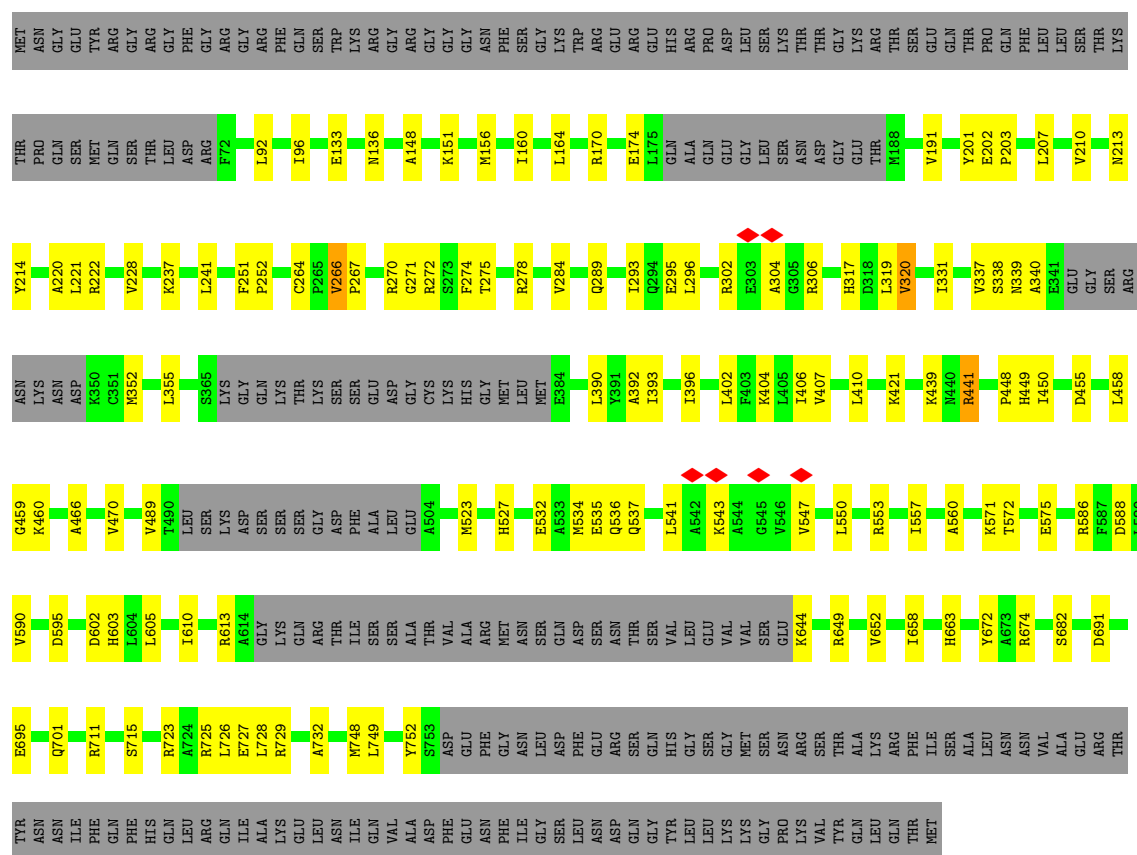


• Molecule 1: DNA helicase MCM8



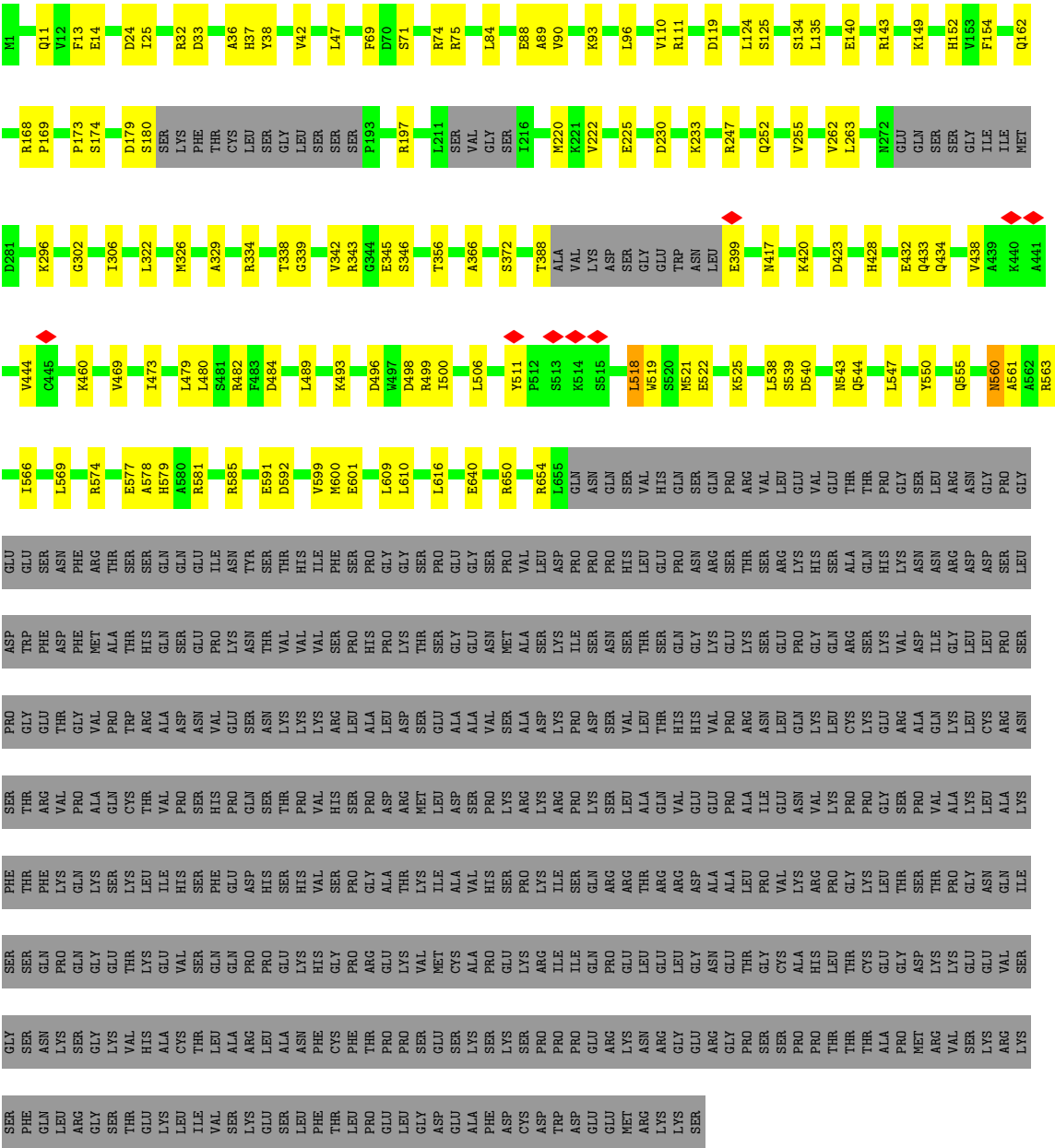


• Molecule 1: DNA helicase MCM8

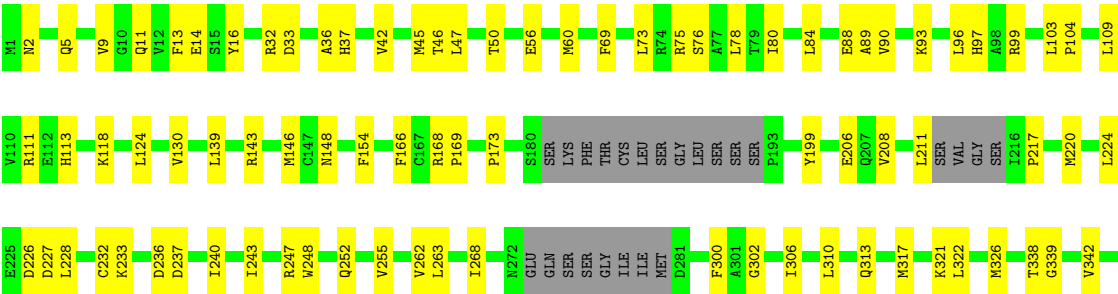


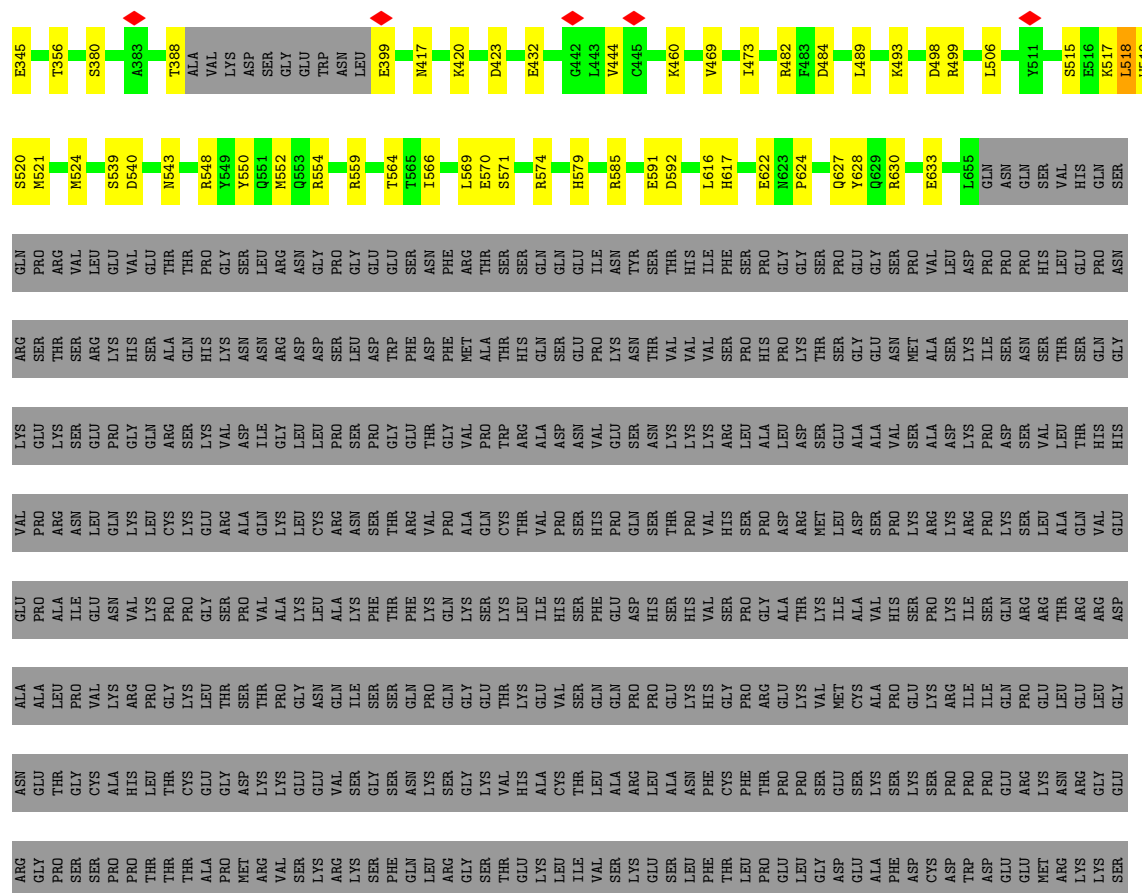
• Molecule 2: DNA helicase MCM9



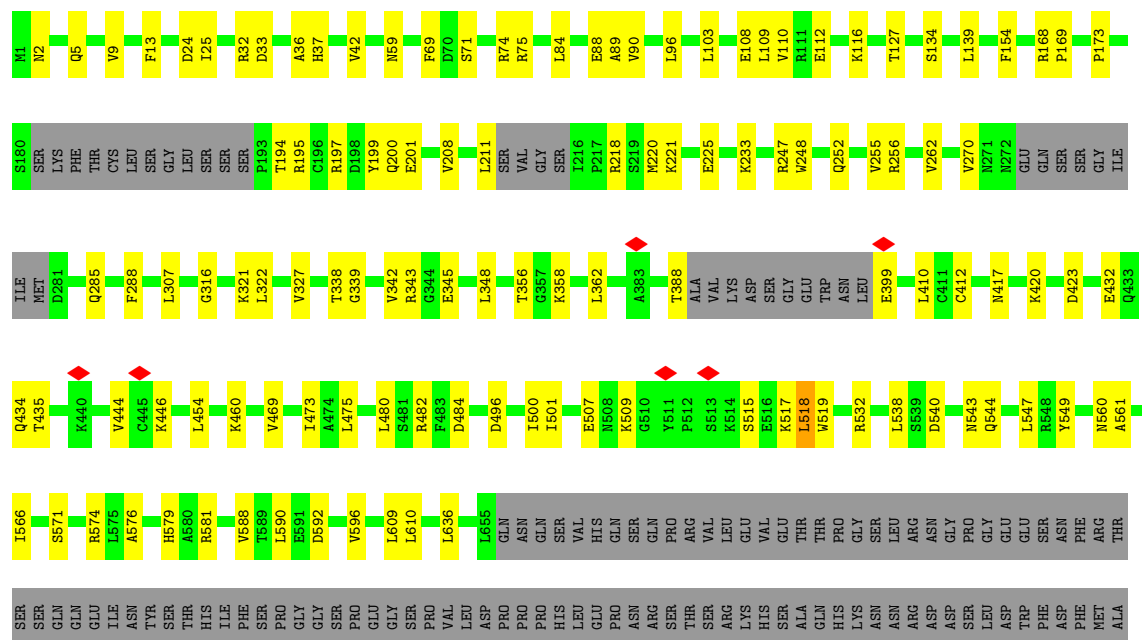


● Molecule 2: DNA helicase MCM9





• Molecule 2: DNA helicase MCM9



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

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	1.189	Depositor
Minimum map value	-0.833	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.06	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

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.13	0/4785	0.39	0/6474
1	B	0.13	0/4785	0.40	0/6474
1	C	0.12	0/4785	0.40	2/6474 (0.0%)
2	D	0.13	0/4992	0.38	2/6746 (0.0%)
2	E	0.14	0/4992	0.40	3/6746 (0.0%)
2	F	0.12	0/4992	0.37	2/6746 (0.0%)
All	All	0.13	0/29331	0.39	9/39660 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	560	ALA	CA-C-N	6.85	138.35	122.31
1	C	560	ALA	C-N-CA	6.85	138.35	122.31
2	F	518	LEU	CA-C-N	6.02	133.04	121.54
2	F	518	LEU	C-N-CA	6.02	133.04	121.54
2	E	518	LEU	CB-CA-C	-6.00	109.64	116.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4703	0	4773	74	0
1	B	4703	0	4773	73	0
1	C	4703	0	4773	79	0
2	D	4914	0	4947	85	0
2	E	4914	0	4947	97	0
2	F	4914	0	4947	80	0
3	A	27	0	12	0	0
3	B	27	0	12	1	0
3	C	27	0	12	1	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	29019	0	29232	455	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 8.

The worst 5 of 455 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:390:LEU:O	1:A:394:GLN:NE2	2.12	0.82
2:F:469:VAL:HG13	2:F:473:ILE:HD13	1.61	0.82
1:B:390:LEU:O	1:B:394:GLN:NE2	2.15	0.79
2:E:310:LEU:O	2:E:321:LYS:NZ	2.19	0.76
1:B:677:VAL:HG12	1:B:679:PRO:HD3	1.69	0.74

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	590/840 (70%)	527 (89%)	59 (10%)	4 (1%)	18	55
1	B	590/840 (70%)	527 (89%)	59 (10%)	4 (1%)	18	55
1	C	590/840 (70%)	525 (89%)	61 (10%)	4 (1%)	18	55
2	D	611/1143 (54%)	561 (92%)	48 (8%)	2 (0%)	36	71
2	E	611/1143 (54%)	555 (91%)	55 (9%)	1 (0%)	43	77
2	F	611/1143 (54%)	553 (90%)	57 (9%)	1 (0%)	43	77
All	All	3603/5949 (61%)	3248 (90%)	339 (9%)	16 (0%)	31	66

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	VAL
1	B	266	VAL
1	C	266	VAL
1	A	320	VAL
1	A	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	519/723 (72%)	519 (100%)	0	100	100
1	B	519/723 (72%)	519 (100%)	0	100	100
1	C	519/723 (72%)	519 (100%)	0	100	100
2	D	555/1020 (54%)	555 (100%)	0	100	100
2	E	555/1020 (54%)	555 (100%)	0	100	100
2	F	555/1020 (54%)	555 (100%)	0	100	100
All	All	3222/5229 (62%)	3222 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	360	GLN
2	F	95	ASN
2	E	448	ASN
2	F	37	HIS
2	F	266	ASN

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	1.43	4 (14%)	43,45,45	1.87	8 (18%)
3	ADP	A	2001	-	28,29,29	1.43	4 (14%)	43,45,45	1.86	8 (18%)
3	ADP	F	2001	4	28,29,29	1.41	4 (14%)	43,45,45	1.86	8 (18%)
3	ADP	D	2001	4	28,29,29	1.41	4 (14%)	43,45,45	1.84	8 (18%)
3	ADP	E	2001	4	28,29,29	1.41	4 (14%)	43,45,45	1.84	8 (18%)
3	ADP	B	2001	-	28,29,29	1.42	4 (14%)	43,45,45	1.84	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	A	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	-	2/16/32/32	0/3/3/3
3	ADP	E	2001	4	-	2/16/32/32	0/3/3/3
3	ADP	B	2001	-	-	2/16/32/32	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	A	2001	ADP	C5-C4	4.77	1.47	1.39
3	C	2001	ADP	C5-C4	4.77	1.47	1.39
3	D	2001	ADP	C5-C4	4.76	1.47	1.39
3	F	2001	ADP	C5-C4	4.73	1.47	1.39
3	E	2001	ADP	C5-C4	4.71	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	-6.05	118.38	126.72
3	A	2001	ADP	C5-C4-N3	-6.01	118.44	126.72
3	F	2001	ADP	C5-C4-N3	-5.94	118.53	126.72
3	B	2001	ADP	C5-C4-N3	-5.90	118.60	126.72
3	E	2001	ADP	C5-C4-N3	-5.87	118.64	126.72

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

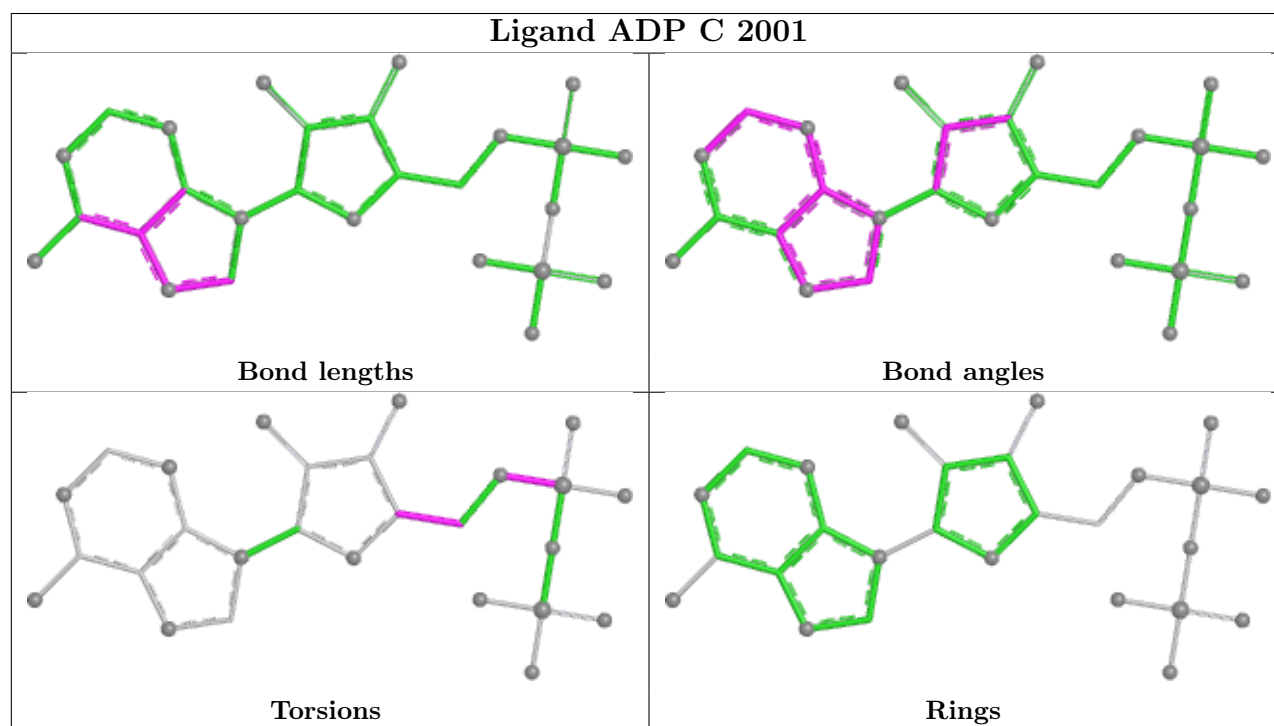
Mol	Chain	Res	Type	Atoms
3	A	2001	ADP	C5'-O5'-PA-O2A
3	A	2001	ADP	C5'-O5'-PA-O3A
3	B	2001	ADP	C5'-O5'-PA-O2A
3	B	2001	ADP	C5'-O5'-PA-O3A
3	C	2001	ADP	C5'-O5'-PA-O2A

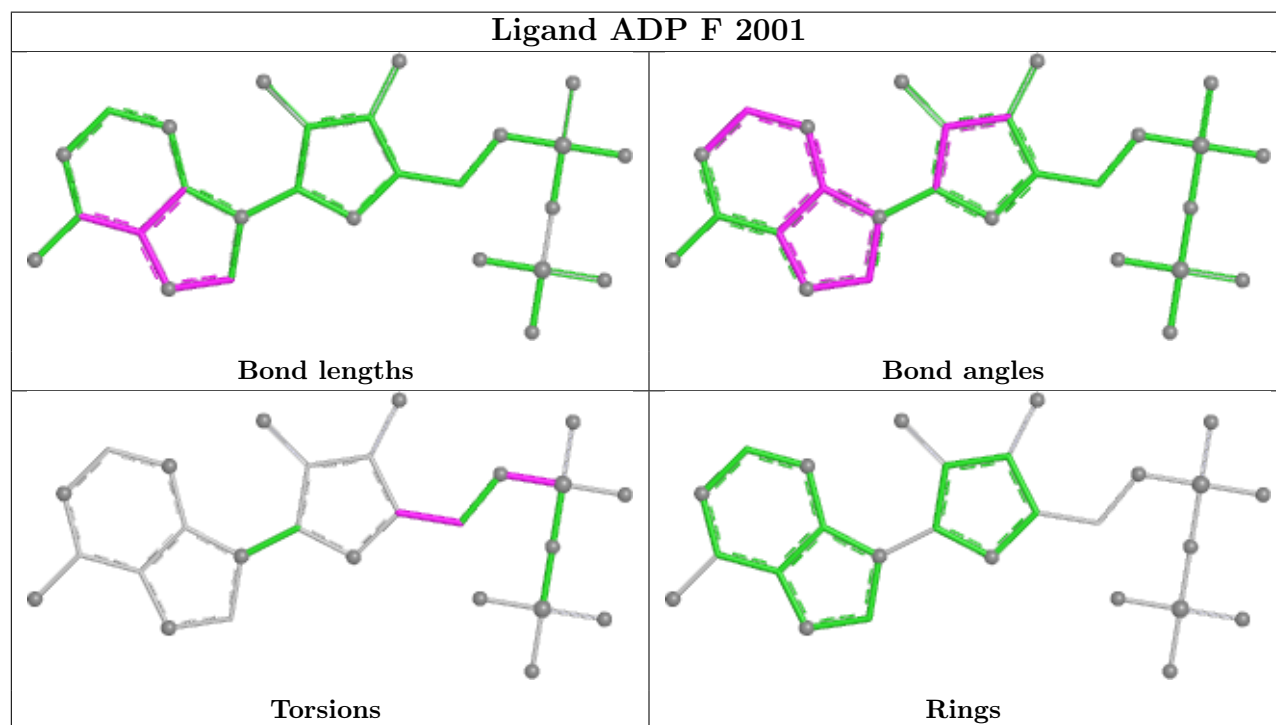
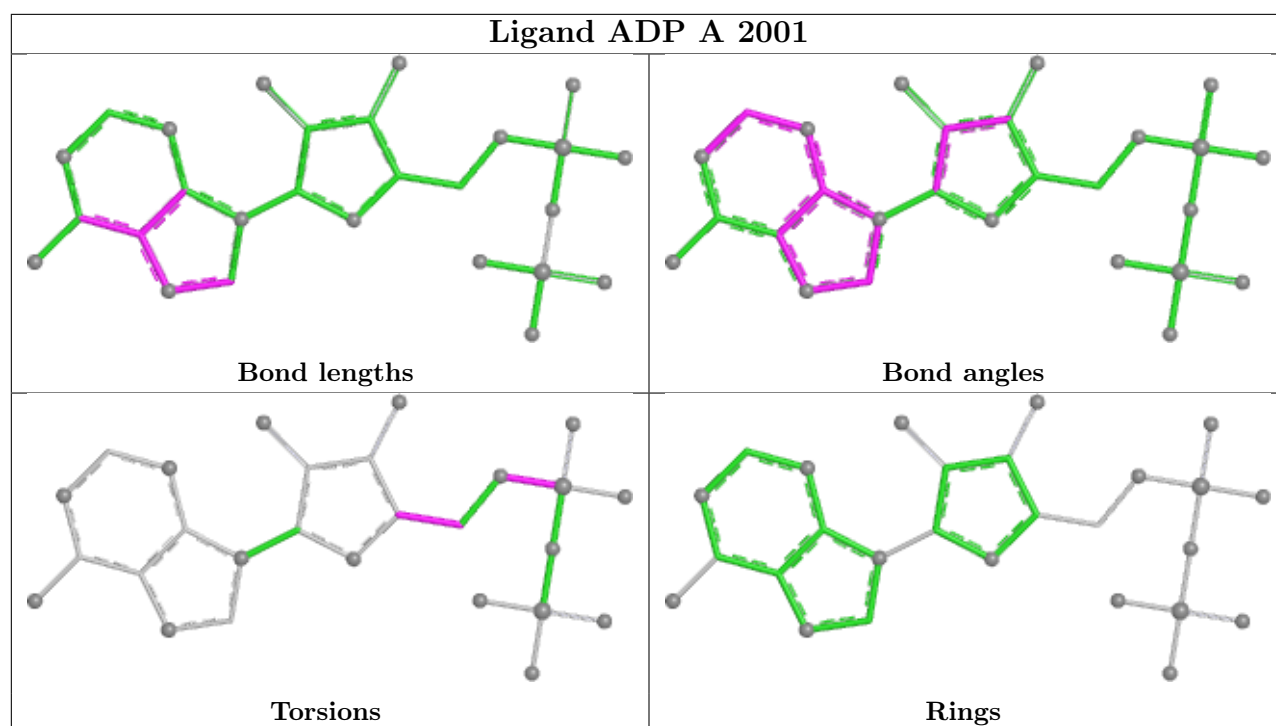
There are no ring outliers.

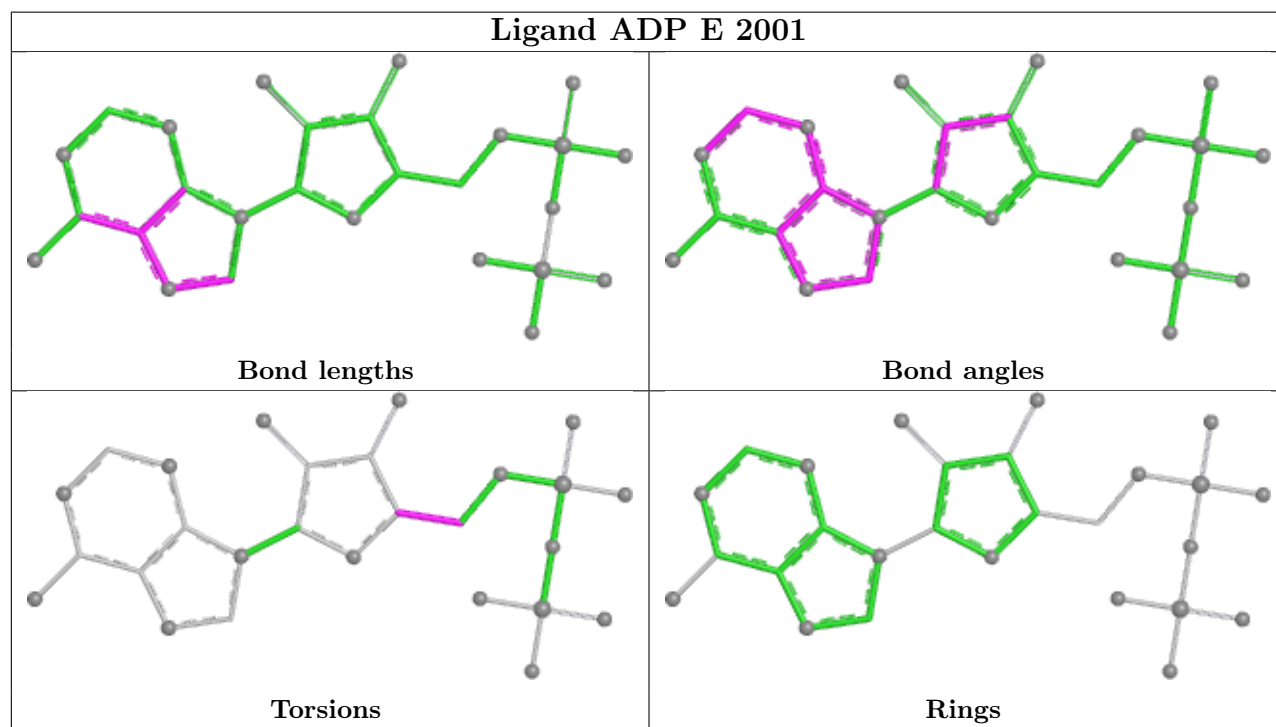
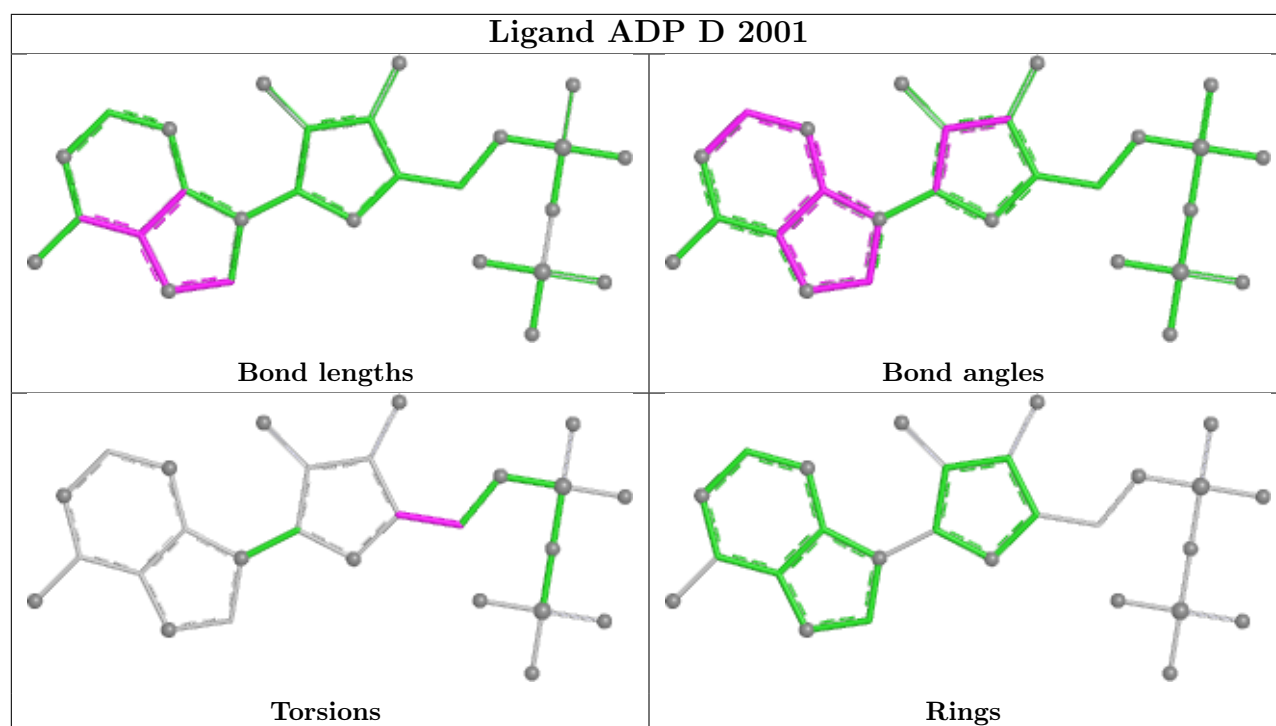
2 monomers are involved in 2 short contacts:

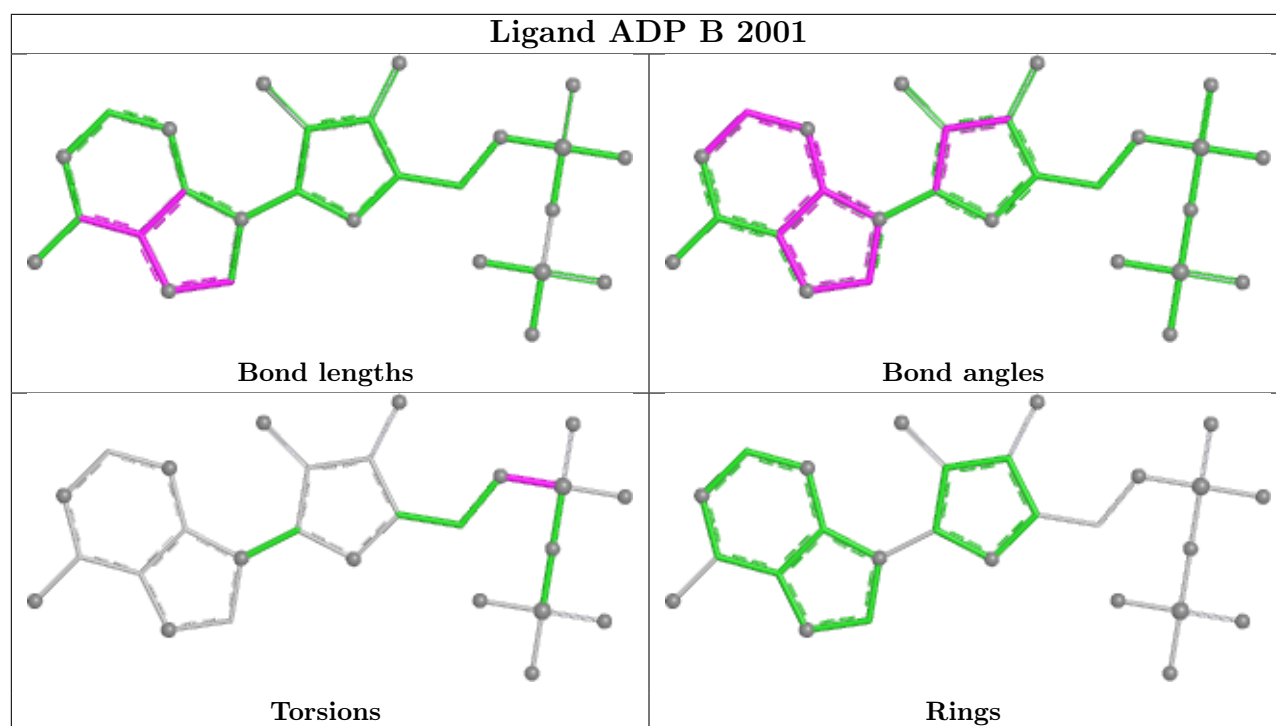
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2001	ADP	1	0
3	B	2001	ADP	1	0

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 [i](#)

There are no chain breaks in this entry.

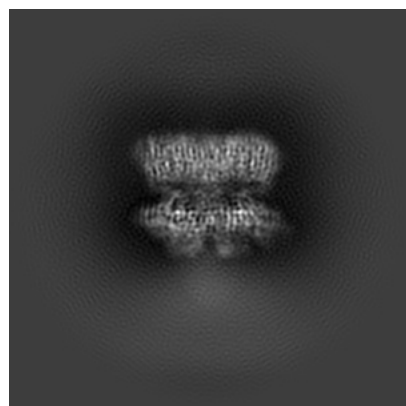
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40234. These allow visual inspection of the internal detail of the map and identification of artifacts.

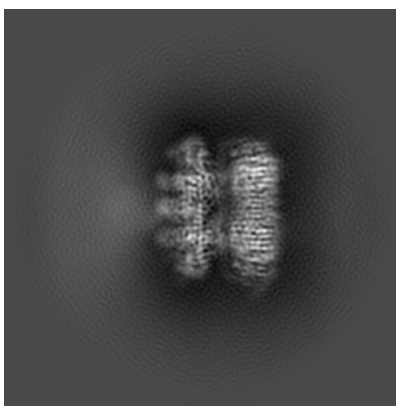
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

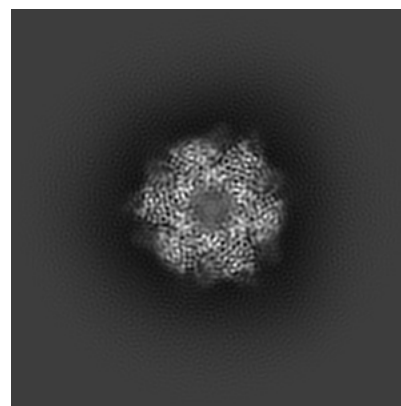
6.1.1 Primary map



X

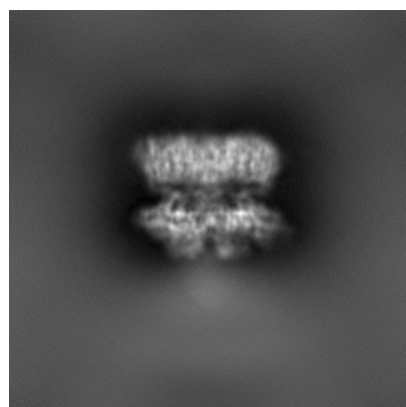


Y

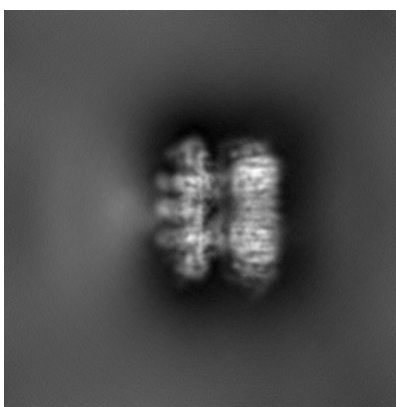


Z

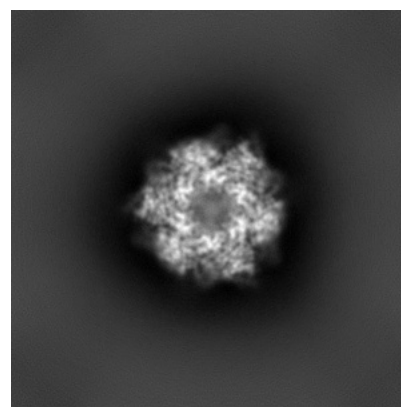
6.1.2 Raw map



X



Y

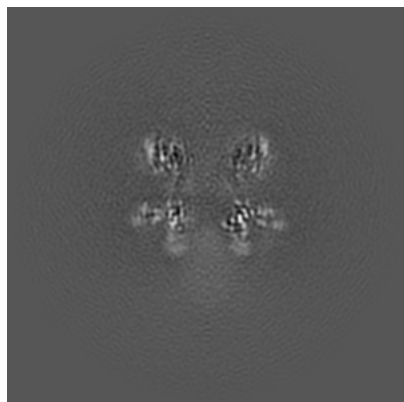


Z

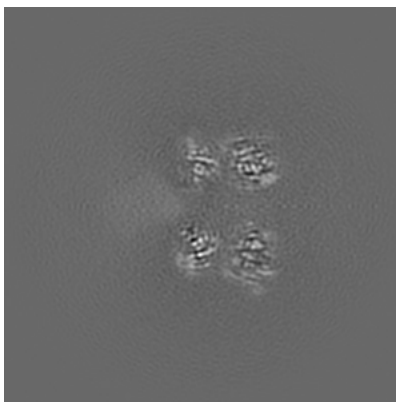
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

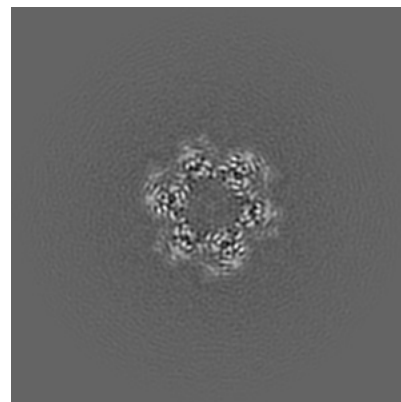
6.2.1 Primary map



X Index: 160

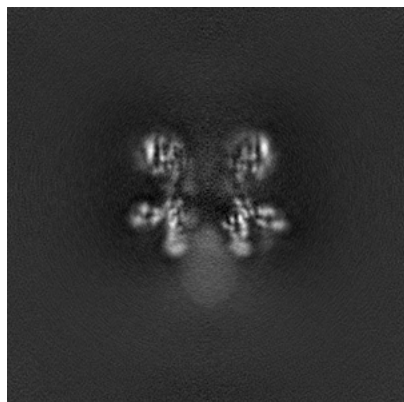


Y Index: 160

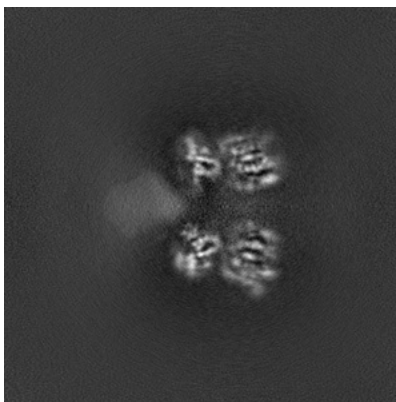


Z Index: 160

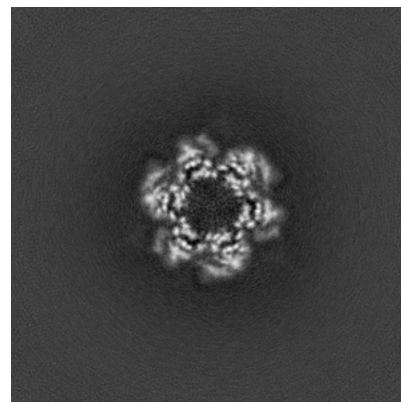
6.2.2 Raw map



X Index: 160



Y Index: 160

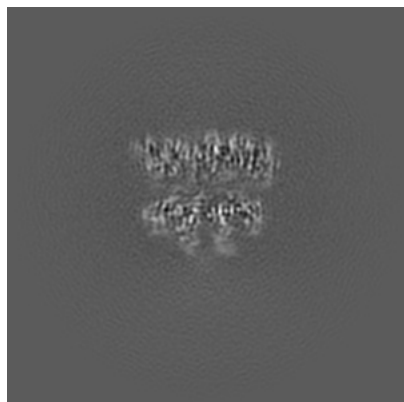


Z Index: 160

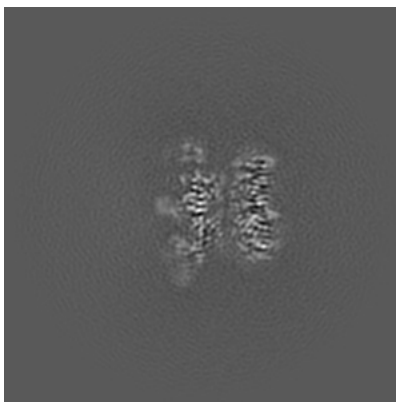
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

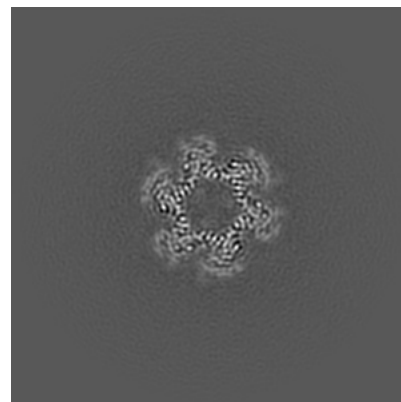
6.3.1 Primary map



X Index: 183

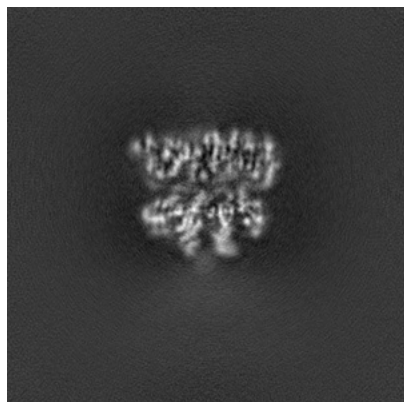


Y Index: 135

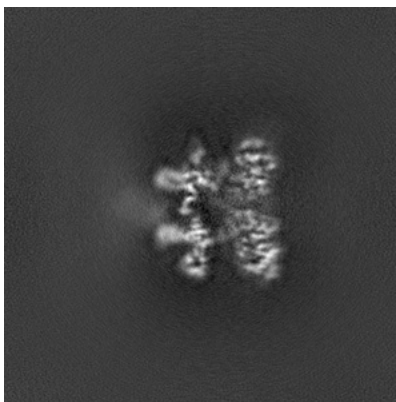


Z Index: 157

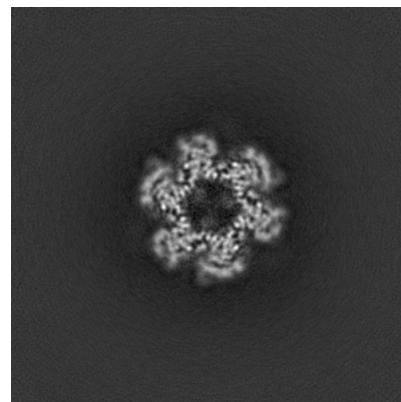
6.3.2 Raw map



X Index: 184



Y Index: 175

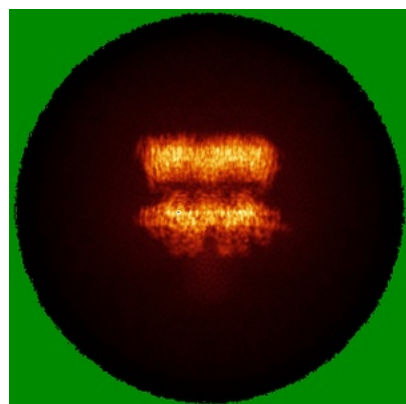


Z Index: 157

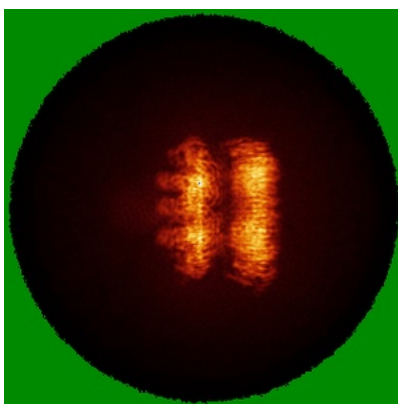
The images above show the largest variance slices of the map in three orthogonal directions.

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

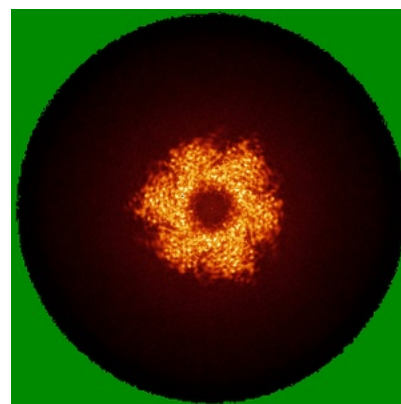
6.4.1 Primary map



X

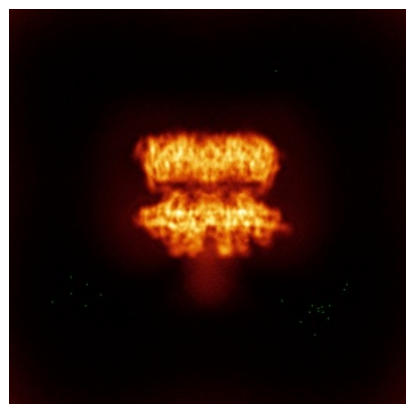


Y

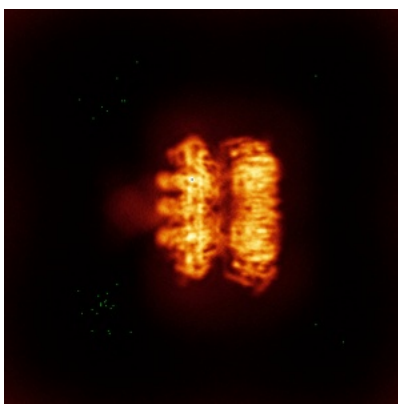


Z

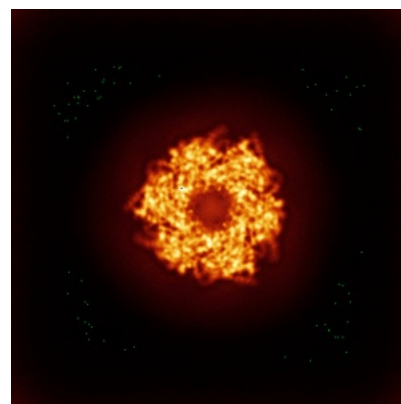
6.4.2 Raw map



X



Y

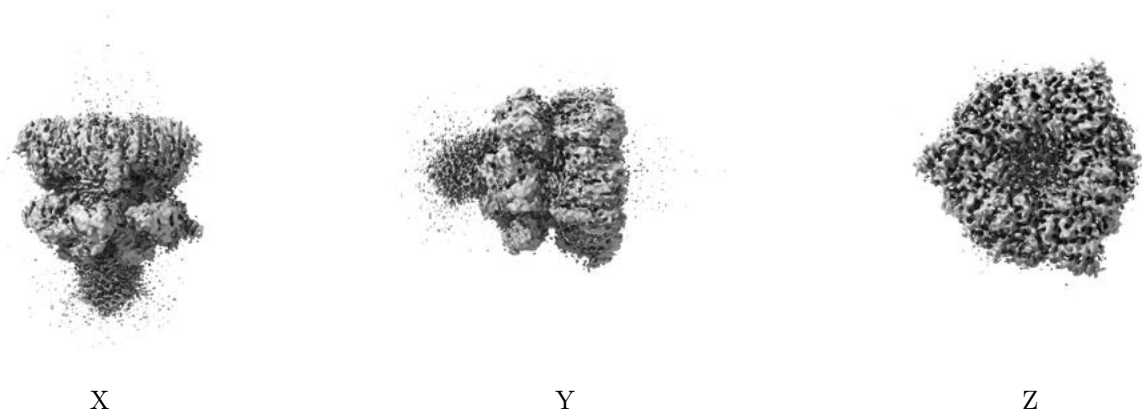


Z

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.

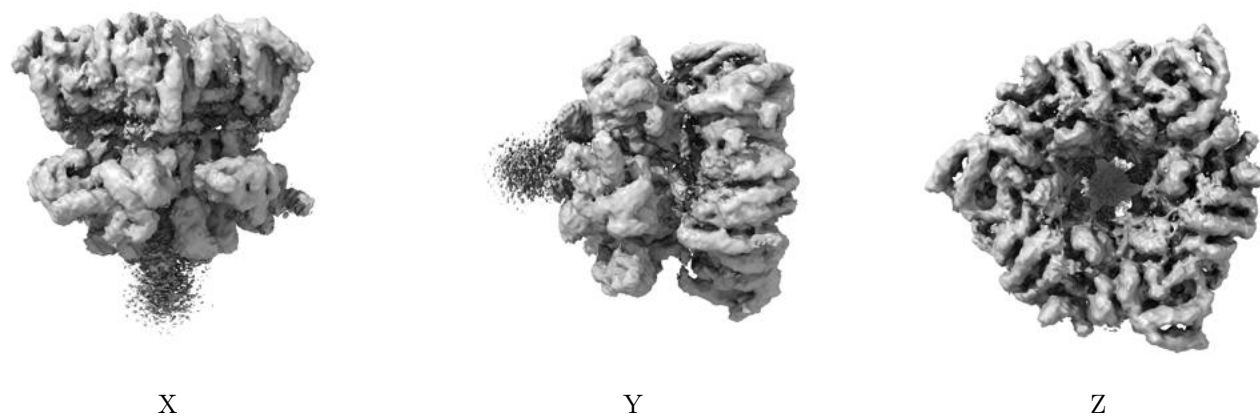
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. 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.

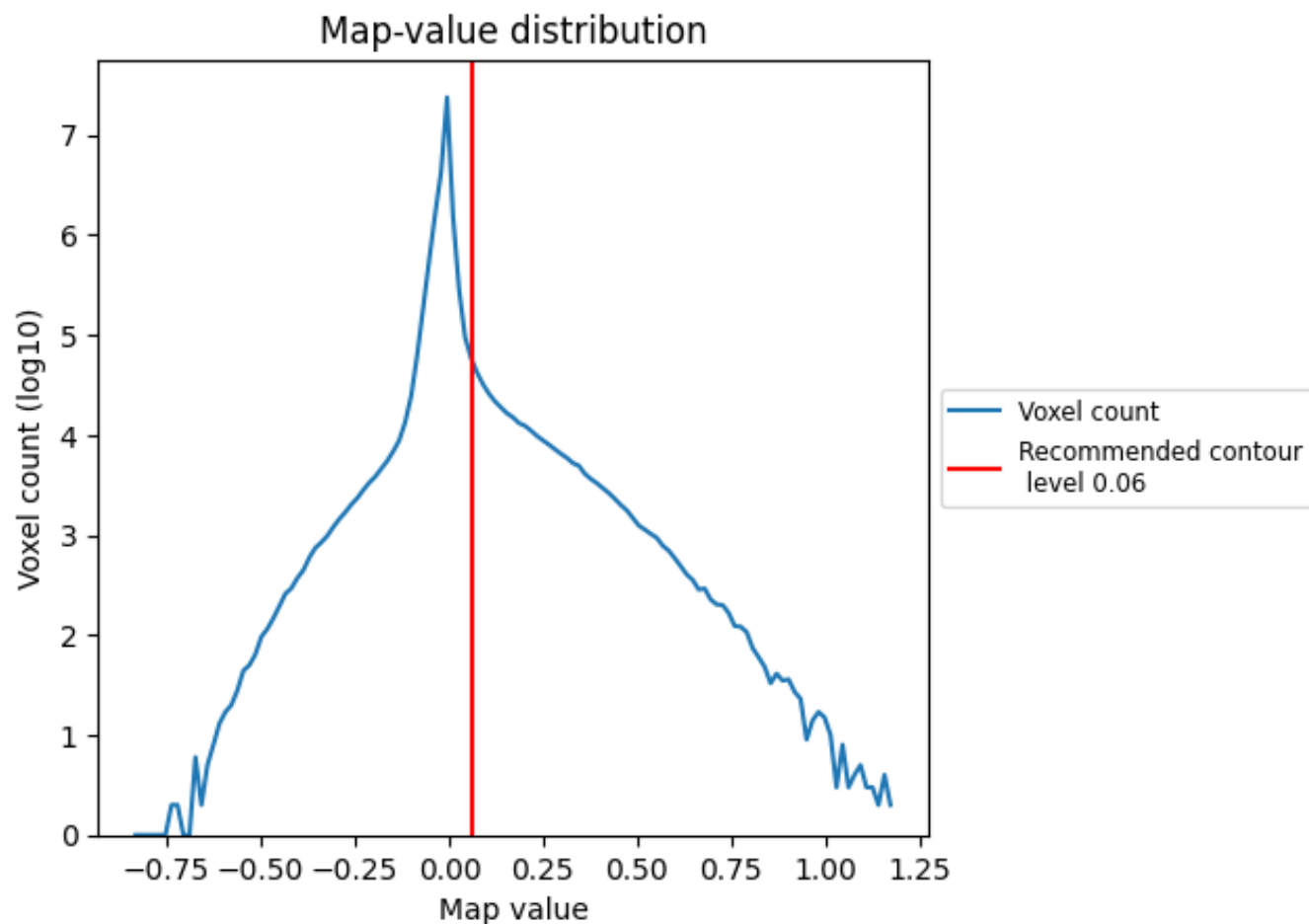
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

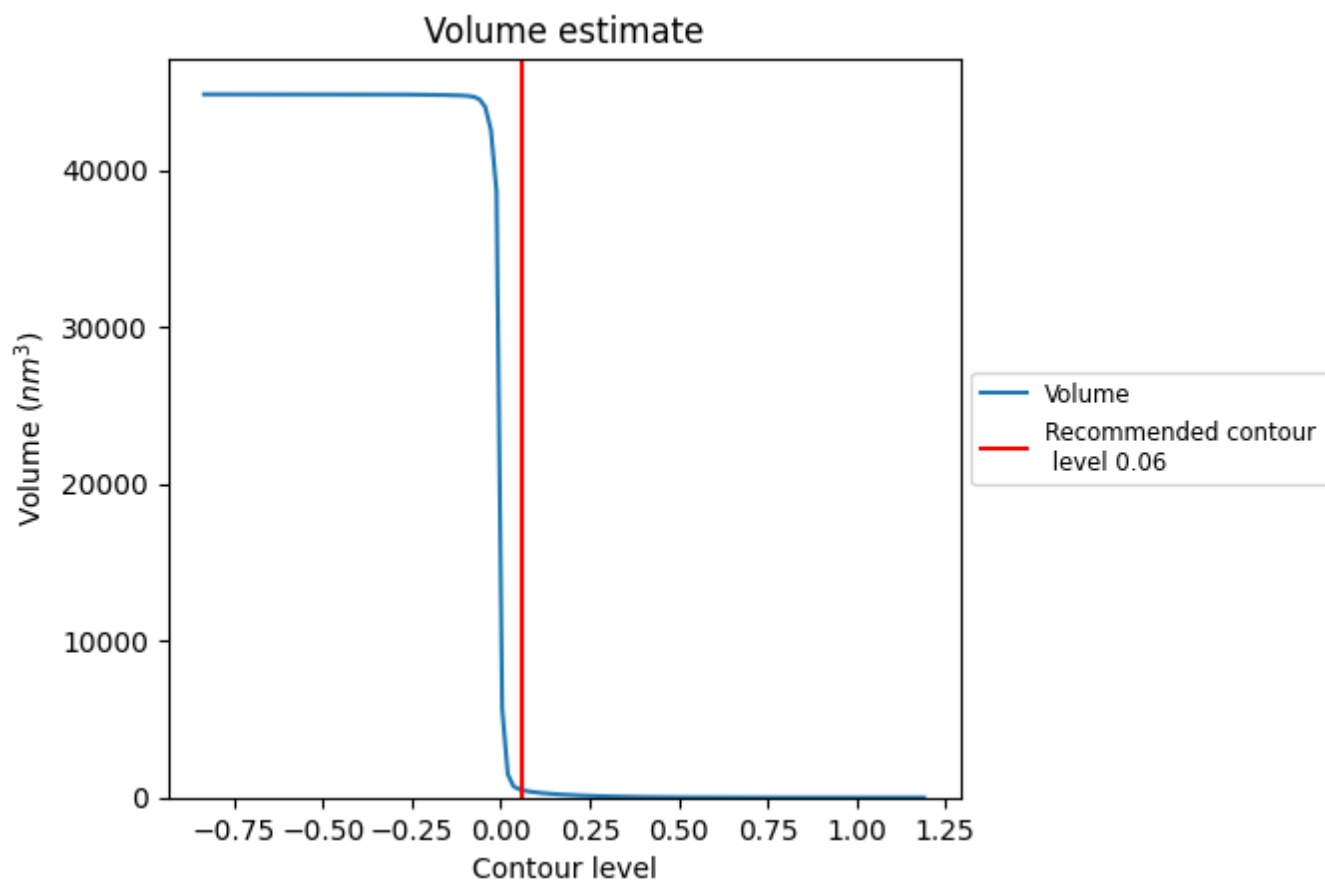
This section contains the results of statistical analysis of the map.

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.

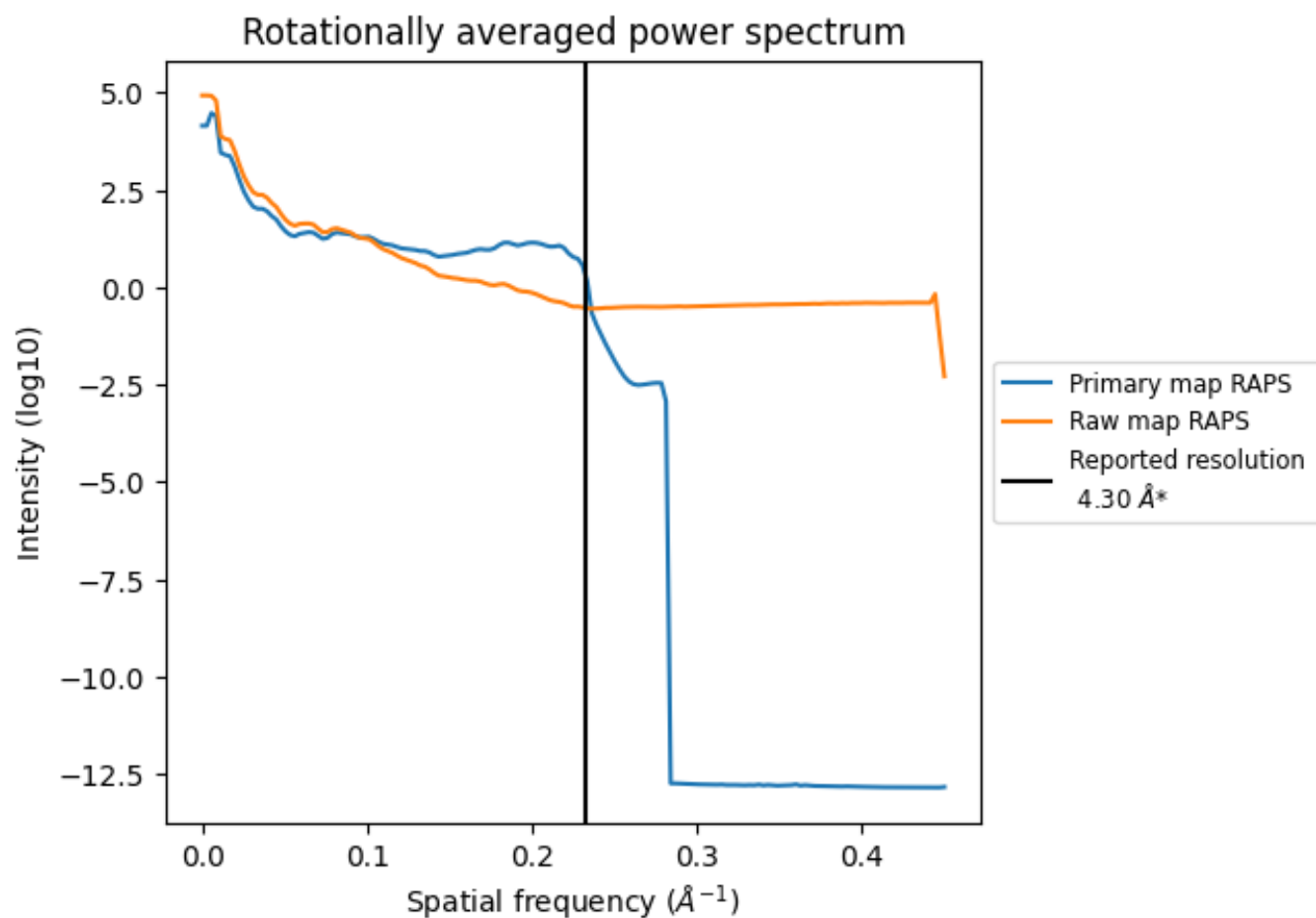
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 485 nm³; this corresponds to an approximate mass of 438 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 ⓘ

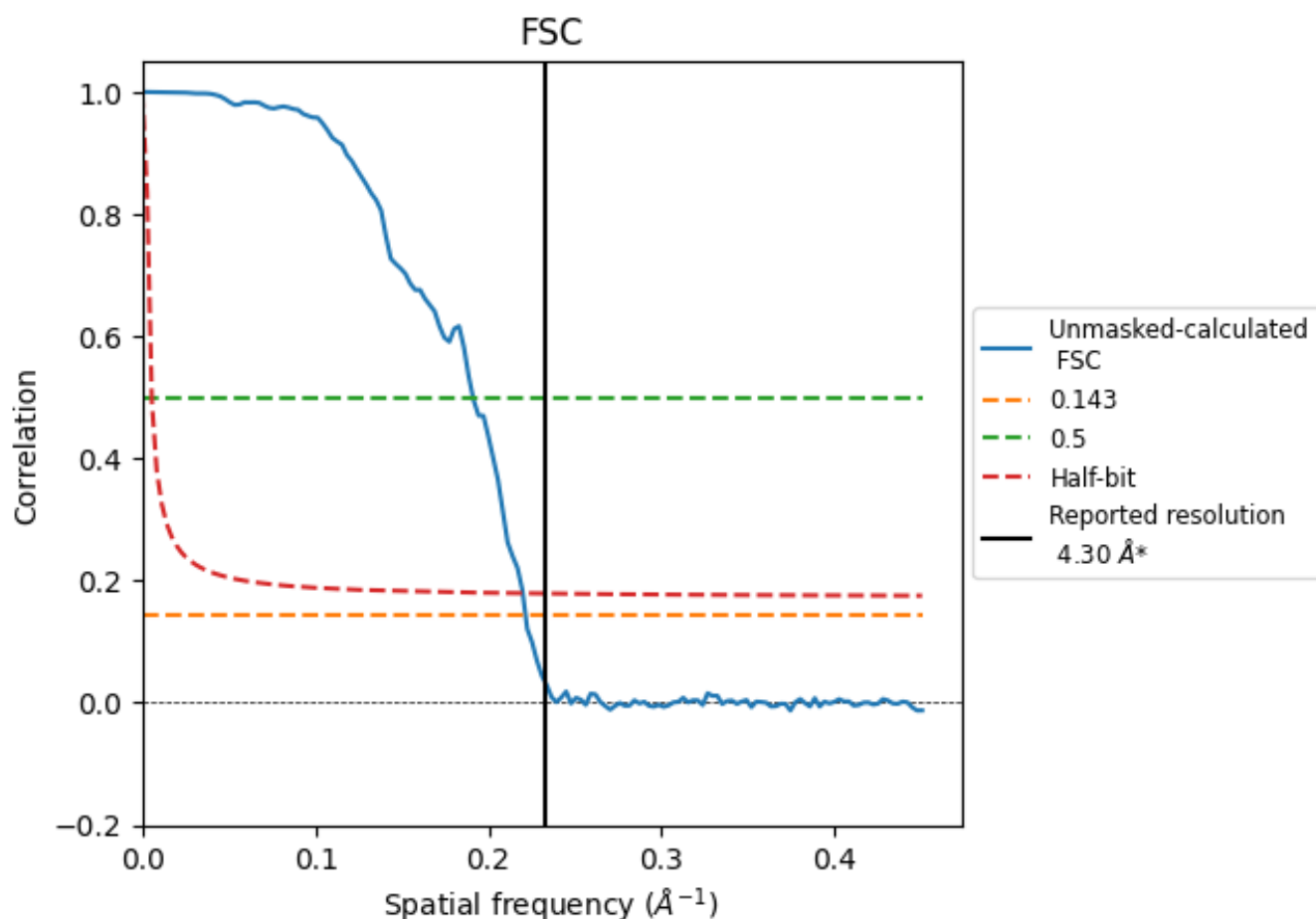


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 Å⁻¹

8.2 Resolution estimates [i](#)

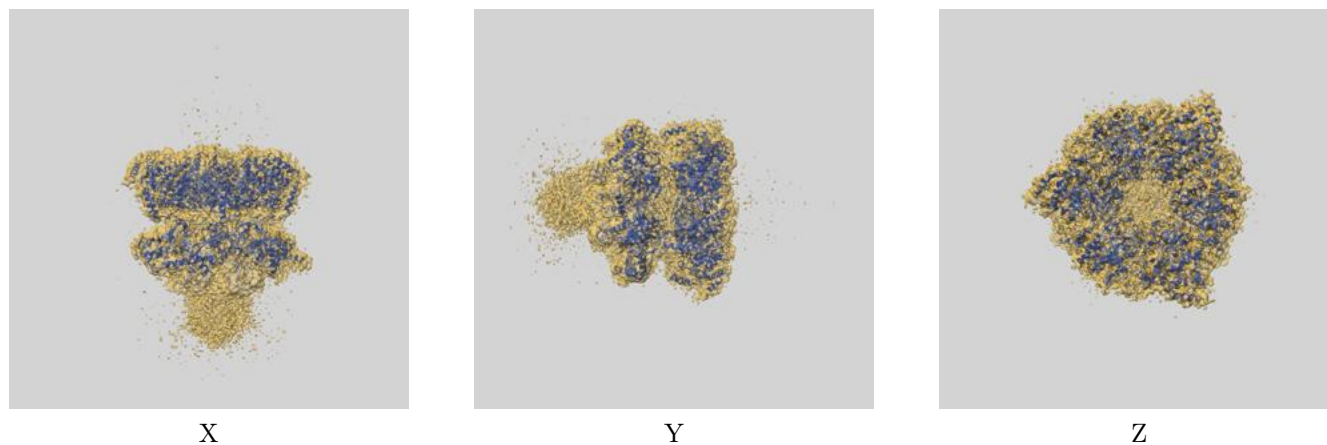
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.52	5.23	4.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

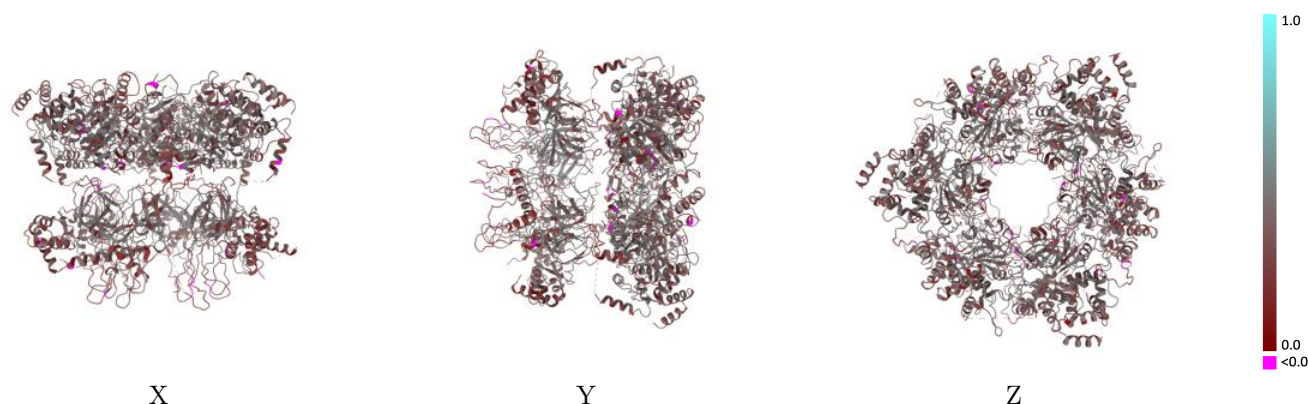
This section contains information regarding the fit between EMDB map EMD-40234 and PDB model 8S91. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



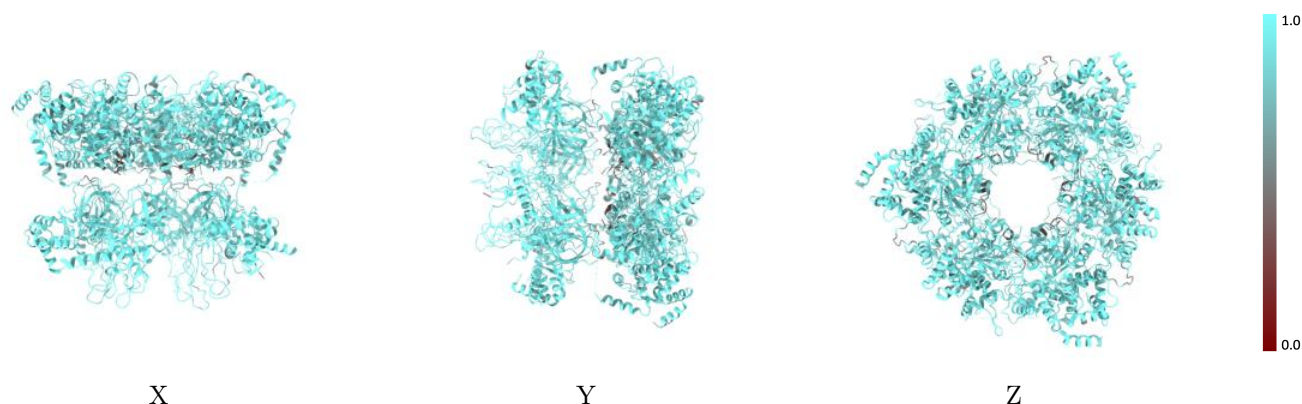
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



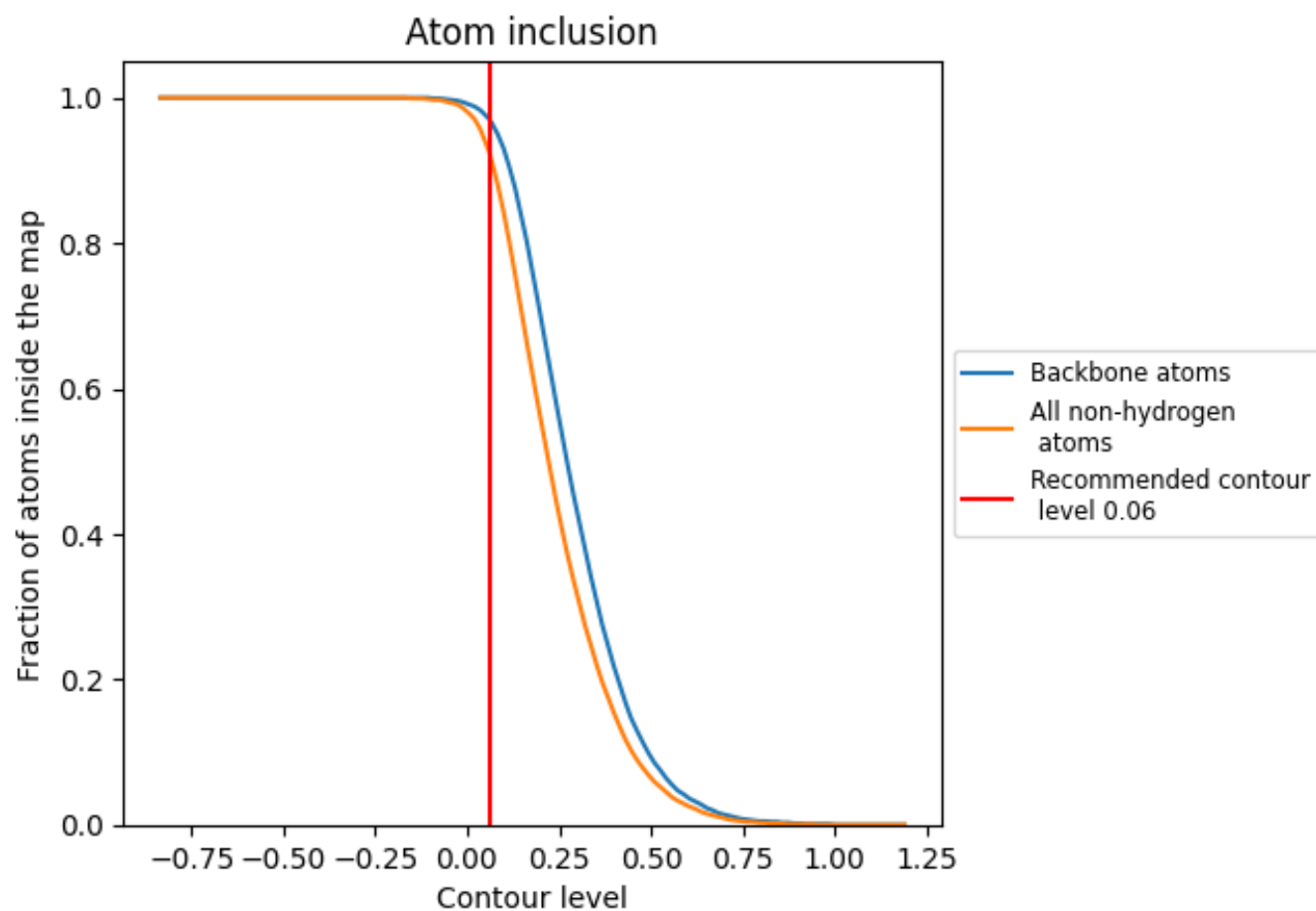
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9260	0.3580
A	0.9240	0.3540
B	0.9270	0.3580
C	0.9250	0.3620
D	0.9210	0.3560
E	0.9290	0.3630
F	0.9280	0.3580

1.0

0.0

<0.0