



wwPDB EM Validation Summary Report ⓘ

Jun 2, 2024 – 08:40 AM EDT

PDB ID : 7UQJ
EMDB ID : EMD-26696
Title : Cryo-EM structure of the *S. cerevisiae* chromatin remodeler Yta7 hexamer bound to ATPgS and histone H3 tail in state II
Authors : Wang, F.; Feng, X.; Li, H.
Deposited on : 2022-04-19
Resolution : 3.00 Å(reported)

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

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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.dev92
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	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

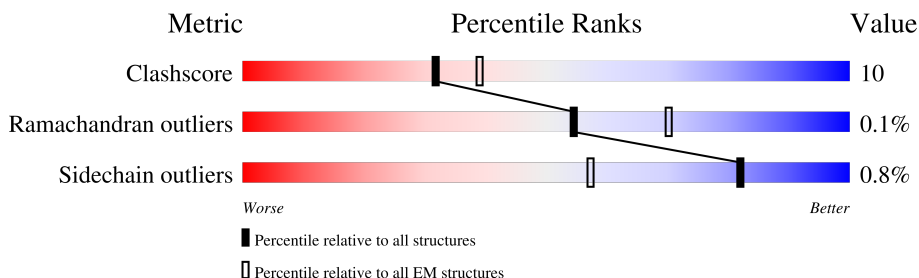
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	1416	
1	B	1416	
1	C	1416	
1	D	1416	
1	E	1416	
1	F	1416	
2	G	25	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 27983 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 ATPase histone chaperone YTA7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	585	Total	C	N	O	S	0	0
			4646	2978	785	866	17		
1	B	574	Total	C	N	O	S	0	0
			4573	2933	775	848	17		
1	C	581	Total	C	N	O	S	0	0
			4622	2965	782	858	17		
1	D	581	Total	C	N	O	S	0	0
			4622	2965	782	858	17		
1	E	578	Total	C	N	O	S	0	0
			4598	2949	779	853	17		
1	F	581	Total	C	N	O	S	0	0
			4628	2965	785	861	17		

There are 222 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-36	HIS	-	expression tag	UNP P40340
A	-35	HIS	-	expression tag	UNP P40340
A	-34	HIS	-	expression tag	UNP P40340
A	-33	HIS	-	expression tag	UNP P40340
A	-32	HIS	-	expression tag	UNP P40340
A	-31	HIS	-	expression tag	UNP P40340
A	-30	HIS	-	expression tag	UNP P40340
A	-29	HIS	-	expression tag	UNP P40340
A	-28	HIS	-	expression tag	UNP P40340
A	-27	HIS	-	expression tag	UNP P40340
A	-26	THR	-	expression tag	UNP P40340
A	-25	SER	-	expression tag	UNP P40340
A	-24	GLY	-	expression tag	UNP P40340
A	-23	SER	-	expression tag	UNP P40340
A	-22	MET	-	expression tag	UNP P40340
A	-21	ASP	-	expression tag	UNP P40340
A	-20	TYR	-	expression tag	UNP P40340
A	-19	LYS	-	expression tag	UNP P40340

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	ASP	-	expression tag	UNP P40340
A	-17	HIS	-	expression tag	UNP P40340
A	-16	ASP	-	expression tag	UNP P40340
A	-15	GLY	-	expression tag	UNP P40340
A	-14	ASP	-	expression tag	UNP P40340
A	-13	TYR	-	expression tag	UNP P40340
A	-12	LYS	-	expression tag	UNP P40340
A	-11	ASP	-	expression tag	UNP P40340
A	-10	HIS	-	expression tag	UNP P40340
A	-9	ASP	-	expression tag	UNP P40340
A	-8	ILE	-	expression tag	UNP P40340
A	-7	ASP	-	expression tag	UNP P40340
A	-6	TYR	-	expression tag	UNP P40340
A	-5	LYS	-	expression tag	UNP P40340
A	-4	ASP	-	expression tag	UNP P40340
A	-3	ASP	-	expression tag	UNP P40340
A	-2	ASP	-	expression tag	UNP P40340
A	-1	ASP	-	expression tag	UNP P40340
A	0	LYS	-	expression tag	UNP P40340
B	-36	HIS	-	expression tag	UNP P40340
B	-35	HIS	-	expression tag	UNP P40340
B	-34	HIS	-	expression tag	UNP P40340
B	-33	HIS	-	expression tag	UNP P40340
B	-32	HIS	-	expression tag	UNP P40340
B	-31	HIS	-	expression tag	UNP P40340
B	-30	HIS	-	expression tag	UNP P40340
B	-29	HIS	-	expression tag	UNP P40340
B	-28	HIS	-	expression tag	UNP P40340
B	-27	HIS	-	expression tag	UNP P40340
B	-26	THR	-	expression tag	UNP P40340
B	-25	SER	-	expression tag	UNP P40340
B	-24	GLY	-	expression tag	UNP P40340
B	-23	SER	-	expression tag	UNP P40340
B	-22	MET	-	expression tag	UNP P40340
B	-21	ASP	-	expression tag	UNP P40340
B	-20	TYR	-	expression tag	UNP P40340
B	-19	LYS	-	expression tag	UNP P40340
B	-18	ASP	-	expression tag	UNP P40340
B	-17	HIS	-	expression tag	UNP P40340
B	-16	ASP	-	expression tag	UNP P40340
B	-15	GLY	-	expression tag	UNP P40340
B	-14	ASP	-	expression tag	UNP P40340

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	TYR	-	expression tag	UNP P40340
B	-12	LYS	-	expression tag	UNP P40340
B	-11	ASP	-	expression tag	UNP P40340
B	-10	HIS	-	expression tag	UNP P40340
B	-9	ASP	-	expression tag	UNP P40340
B	-8	ILE	-	expression tag	UNP P40340
B	-7	ASP	-	expression tag	UNP P40340
B	-6	TYR	-	expression tag	UNP P40340
B	-5	LYS	-	expression tag	UNP P40340
B	-4	ASP	-	expression tag	UNP P40340
B	-3	ASP	-	expression tag	UNP P40340
B	-2	ASP	-	expression tag	UNP P40340
B	-1	ASP	-	expression tag	UNP P40340
B	0	LYS	-	expression tag	UNP P40340
C	-36	HIS	-	expression tag	UNP P40340
C	-35	HIS	-	expression tag	UNP P40340
C	-34	HIS	-	expression tag	UNP P40340
C	-33	HIS	-	expression tag	UNP P40340
C	-32	HIS	-	expression tag	UNP P40340
C	-31	HIS	-	expression tag	UNP P40340
C	-30	HIS	-	expression tag	UNP P40340
C	-29	HIS	-	expression tag	UNP P40340
C	-28	HIS	-	expression tag	UNP P40340
C	-27	HIS	-	expression tag	UNP P40340
C	-26	THR	-	expression tag	UNP P40340
C	-25	SER	-	expression tag	UNP P40340
C	-24	GLY	-	expression tag	UNP P40340
C	-23	SER	-	expression tag	UNP P40340
C	-22	MET	-	expression tag	UNP P40340
C	-21	ASP	-	expression tag	UNP P40340
C	-20	TYR	-	expression tag	UNP P40340
C	-19	LYS	-	expression tag	UNP P40340
C	-18	ASP	-	expression tag	UNP P40340
C	-17	HIS	-	expression tag	UNP P40340
C	-16	ASP	-	expression tag	UNP P40340
C	-15	GLY	-	expression tag	UNP P40340
C	-14	ASP	-	expression tag	UNP P40340
C	-13	TYR	-	expression tag	UNP P40340
C	-12	LYS	-	expression tag	UNP P40340
C	-11	ASP	-	expression tag	UNP P40340
C	-10	HIS	-	expression tag	UNP P40340
C	-9	ASP	-	expression tag	UNP P40340

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	ILE	-	expression tag	UNP P40340
C	-7	ASP	-	expression tag	UNP P40340
C	-6	TYR	-	expression tag	UNP P40340
C	-5	LYS	-	expression tag	UNP P40340
C	-4	ASP	-	expression tag	UNP P40340
C	-3	ASP	-	expression tag	UNP P40340
C	-2	ASP	-	expression tag	UNP P40340
C	-1	ASP	-	expression tag	UNP P40340
C	0	LYS	-	expression tag	UNP P40340
D	-36	HIS	-	expression tag	UNP P40340
D	-35	HIS	-	expression tag	UNP P40340
D	-34	HIS	-	expression tag	UNP P40340
D	-33	HIS	-	expression tag	UNP P40340
D	-32	HIS	-	expression tag	UNP P40340
D	-31	HIS	-	expression tag	UNP P40340
D	-30	HIS	-	expression tag	UNP P40340
D	-29	HIS	-	expression tag	UNP P40340
D	-28	HIS	-	expression tag	UNP P40340
D	-27	HIS	-	expression tag	UNP P40340
D	-26	THR	-	expression tag	UNP P40340
D	-25	SER	-	expression tag	UNP P40340
D	-24	GLY	-	expression tag	UNP P40340
D	-23	SER	-	expression tag	UNP P40340
D	-22	MET	-	expression tag	UNP P40340
D	-21	ASP	-	expression tag	UNP P40340
D	-20	TYR	-	expression tag	UNP P40340
D	-19	LYS	-	expression tag	UNP P40340
D	-18	ASP	-	expression tag	UNP P40340
D	-17	HIS	-	expression tag	UNP P40340
D	-16	ASP	-	expression tag	UNP P40340
D	-15	GLY	-	expression tag	UNP P40340
D	-14	ASP	-	expression tag	UNP P40340
D	-13	TYR	-	expression tag	UNP P40340
D	-12	LYS	-	expression tag	UNP P40340
D	-11	ASP	-	expression tag	UNP P40340
D	-10	HIS	-	expression tag	UNP P40340
D	-9	ASP	-	expression tag	UNP P40340
D	-8	ILE	-	expression tag	UNP P40340
D	-7	ASP	-	expression tag	UNP P40340
D	-6	TYR	-	expression tag	UNP P40340
D	-5	LYS	-	expression tag	UNP P40340
D	-4	ASP	-	expression tag	UNP P40340

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	ASP	-	expression tag	UNP P40340
D	-2	ASP	-	expression tag	UNP P40340
D	-1	ASP	-	expression tag	UNP P40340
D	0	LYS	-	expression tag	UNP P40340
E	-36	HIS	-	expression tag	UNP P40340
E	-35	HIS	-	expression tag	UNP P40340
E	-34	HIS	-	expression tag	UNP P40340
E	-33	HIS	-	expression tag	UNP P40340
E	-32	HIS	-	expression tag	UNP P40340
E	-31	HIS	-	expression tag	UNP P40340
E	-30	HIS	-	expression tag	UNP P40340
E	-29	HIS	-	expression tag	UNP P40340
E	-28	HIS	-	expression tag	UNP P40340
E	-27	HIS	-	expression tag	UNP P40340
E	-26	THR	-	expression tag	UNP P40340
E	-25	SER	-	expression tag	UNP P40340
E	-24	GLY	-	expression tag	UNP P40340
E	-23	SER	-	expression tag	UNP P40340
E	-22	MET	-	expression tag	UNP P40340
E	-21	ASP	-	expression tag	UNP P40340
E	-20	TYR	-	expression tag	UNP P40340
E	-19	LYS	-	expression tag	UNP P40340
E	-18	ASP	-	expression tag	UNP P40340
E	-17	HIS	-	expression tag	UNP P40340
E	-16	ASP	-	expression tag	UNP P40340
E	-15	GLY	-	expression tag	UNP P40340
E	-14	ASP	-	expression tag	UNP P40340
E	-13	TYR	-	expression tag	UNP P40340
E	-12	LYS	-	expression tag	UNP P40340
E	-11	ASP	-	expression tag	UNP P40340
E	-10	HIS	-	expression tag	UNP P40340
E	-9	ASP	-	expression tag	UNP P40340
E	-8	ILE	-	expression tag	UNP P40340
E	-7	ASP	-	expression tag	UNP P40340
E	-6	TYR	-	expression tag	UNP P40340
E	-5	LYS	-	expression tag	UNP P40340
E	-4	ASP	-	expression tag	UNP P40340
E	-3	ASP	-	expression tag	UNP P40340
E	-2	ASP	-	expression tag	UNP P40340
E	-1	ASP	-	expression tag	UNP P40340
E	0	LYS	-	expression tag	UNP P40340
F	-36	HIS	-	expression tag	UNP P40340

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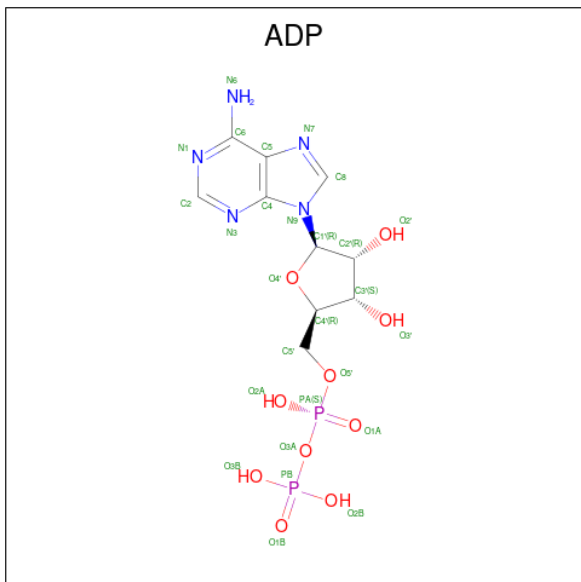
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Chain	Residue	Modelled	Actual	Comment	Reference
F	-35	HIS	-	expression tag	UNP P40340
F	-34	HIS	-	expression tag	UNP P40340
F	-33	HIS	-	expression tag	UNP P40340
F	-32	HIS	-	expression tag	UNP P40340
F	-31	HIS	-	expression tag	UNP P40340
F	-30	HIS	-	expression tag	UNP P40340
F	-29	HIS	-	expression tag	UNP P40340
F	-28	HIS	-	expression tag	UNP P40340
F	-27	HIS	-	expression tag	UNP P40340
F	-26	THR	-	expression tag	UNP P40340
F	-25	SER	-	expression tag	UNP P40340
F	-24	GLY	-	expression tag	UNP P40340
F	-23	SER	-	expression tag	UNP P40340
F	-22	MET	-	expression tag	UNP P40340
F	-21	ASP	-	expression tag	UNP P40340
F	-20	TYR	-	expression tag	UNP P40340
F	-19	LYS	-	expression tag	UNP P40340
F	-18	ASP	-	expression tag	UNP P40340
F	-17	HIS	-	expression tag	UNP P40340
F	-16	ASP	-	expression tag	UNP P40340
F	-15	GLY	-	expression tag	UNP P40340
F	-14	ASP	-	expression tag	UNP P40340
F	-13	TYR	-	expression tag	UNP P40340
F	-12	LYS	-	expression tag	UNP P40340
F	-11	ASP	-	expression tag	UNP P40340
F	-10	HIS	-	expression tag	UNP P40340
F	-9	ASP	-	expression tag	UNP P40340
F	-8	ILE	-	expression tag	UNP P40340
F	-7	ASP	-	expression tag	UNP P40340
F	-6	TYR	-	expression tag	UNP P40340
F	-5	LYS	-	expression tag	UNP P40340
F	-4	ASP	-	expression tag	UNP P40340
F	-3	ASP	-	expression tag	UNP P40340
F	-2	ASP	-	expression tag	UNP P40340
F	-1	ASP	-	expression tag	UNP P40340
F	0	LYS	-	expression tag	UNP P40340

- Molecule 2 is a protein called Histone H3.

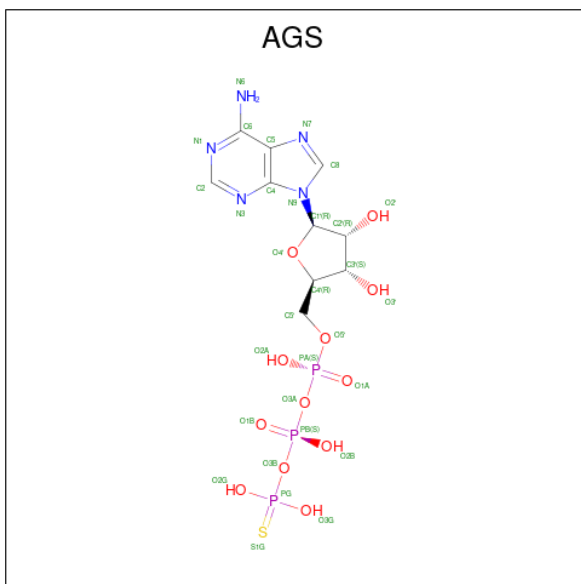
Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	15	Total	C	N	O	0	0
			108	66	23	19		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
4	B	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

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Mol	Chain	Residues	Atoms						AltConf
4	C	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
4	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
4	E	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
4	F	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

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

Mol	Chain	Residues	Atoms		AltConf
5	C	1	Total	Mg	0
			1	1	
5	D	1	Total	Mg	0
			1	1	
5	E	1	Total	Mg	0
			1	1	
5	F	1	Total	Mg	0
			1	1	

- Molecule 1: ATPase histone chaperone YTA7



1673	1520	LYS	ARG	LYS	THR	GLU	ASP	GLU	THR	HIS
A678	3528	ASN	PHE	GLU	ARG	GLN	ASP	GLN	THR	HIS
R679		THR	THR	PRO	SER	LEU	TYR	ASP	ILE	HIS
S680	0531	GLN	GLY	ARG	GLI	ARG	ASP	ASP	ASP	HIS
T681	E532	LYS	GLY	ARG	PRO	GLU	GLU	VAL	GLU	HIS
G682	Q533	LYS	PRO	THR	THR	ASP	ASP	ASP	ASN	HIS
S683		LYS	PHE	GLY	PRO	LEU	SER	VAL	GLY	HIS
S684	L542	LYS	GLY	VAL	PRO	ASP	ASP	VAL	ILE	HIS
	L543	LYS	ASN	ASN	PRO	ASN	PRO	PRO	THR	SER
F689	M546	PRO	ASP	TYR	VAL	ASN	HIS	HIS	THR	GLY
	D547	GLU	VAL	LYS	ARG	ARG	GLU	THR	THR	SER
T692	G548	ILE	LEU	LEU	ARG	ARG	MET	THR	THR	SER
L696	M549	ALA	THR	PRO	ALA	ARG	ALA	ASP	ASP	HIS
	D550	ASP	ILE	PRO	PRO	ARG	ARG	ARG	SER	TYR
L707	L401	LYS	PHE	PRO	ARG	ALA	THR	THR	LEU	LYS
D708		GLY	GLY	LEU	SER	ALA	ASN	ARG	ASP	ASP
	V557	LYS	ASN	THR	ARG	ASP	GLU	GLU	LYS	HIS
L711		D414	THR	ALA	THR	ARG	GLU	ILE	ILE	GLY
T717	M561	ASN	PHE	ASN	HIS	PHE	THR	THR	TYR	GLY
F718	N562	ASN	THR	THR	SER	ARG	LEU	ASN	ASN	GLY
Q719	R563	ASN	THR	THR	ASN	ALA	LEU	LEU	ASN	GLY
R720	E427	THR	TYR	GLU	ALA	GLU	VAL	VAL	ALA	TYR
T721	M428	ASN	ASN	GLU	ALA	ARG	VAL	GLU	GLU	LYS
T722	V429	ASN	ASN	GLU	GLU	THR	PRO	ARG	ILE	ASP
	E437	ILE	VAL	ILE	ILE	ASN	PRO	LEU	ASP	ILE
R576	E437	PRO	SER	PRO	LYS	GLU	ASP	ASP	LYS	ASP
F577	Q440	ASN	PHE	ASN	ASN	ASN	ASP	ASP	TYR	ASP
D578		ALA	ALA	ASN	ASN	ASP	GLU	LYS	ASP	LYS
R579	G449	SER	SER	SER	ASN	GLU	TYR	ALA	ASP	ASP
E580		P455	ASN	ASN	LEU	ASP	ASP	ASP	ASP	ASP
F583	P456	ASN	ASN	ASN	LEU	ASN	ASP	PRO	ASP	ASP
	G457	ASN	ASN	SER	SER	ASN	GLU	GLN	LYS	LYS
R600	T458	ASN	ASN	PHE	ASN	ASP	ASP	GLU	VAL	MET
	G459	ASN	LYS	ASN	HIS	ARG	GLU	ASP	MET	ALA
K613		LEU	LEU	PRO	PRO	ASN	GLY	ASP	ARG	ARG
	C471	ILE	ILE	SER	ASN	GLU	GLY	GLU	ASP	GLY
L617		LEU	LEU	PRO	ALA	ASP	SER	SER	VAL	SER
	D474	ASN	ASP	ALA	THR	LEU	PHE	GLU	THR	ASN
R627	E475	SER	SER	ARG	THR	THR	ILE	THR	THR	ASN
	R476	ASP	ASP	GLY	LEU	SER	GLU	GLU	PRO	ARG
E632	E477	SER	SER	ARG	ALA	HIS	GLU	VAL	ARG	ARG
K633	K477	SER	SER	ARG	ALA	HIS	SER	ASP	GLY	GLY
A634	1478	SER	SER	ASP	GLU	ASP	VAL	VAL	ASP	GLY
L635		ASP	GLY	GLY	GLU	ILE	ASP	VAL	SER	SER
	M482	ASP	GLY	TRP	ILE	SER	ASP	THR	THR	ASP
	R483	ASN	GLU	ASN	ARG	GLY	SER	ASP	VAL	ASP
	K484	ILE	GLU	TRP	GLU	LYS	ASP	ASP	SER	VAL
		LEU	ALA	ALA	LEU	ARG	GLU	ASP	GLU	ALA
	D487	PRO	LEU	SER	GLN	LEU	GLU	GLU	HIS	ALA
	L488	LEU	LEU	GLN	GLU	LYS	LYS	HIS	ALA	ASP
	L489	GLY	VAL	ASN	ASP	ARG	GLU	ASN	ASN	ASN
	S490	THR	GLY	SER	SER	ALA	ALA	GLU	ALA	ASN
		PRO	THR	GLY	PRO	ILE	ASN	ASN	GLN	LYS
	K508	THR	THR	PRO	ILE	SER	ASP	GLY	GLN	VAL
	K509	LYS	THR	PRO	THR	ARG	ASP	GLY	GLN	LYS



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	431065	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 ($e^-/\text{\AA}^2$)	65	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.228	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.015	Depositor
Map size (\AA)	331.2, 331.2, 331.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.828, 0.828, 0.828	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, AGS, 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	0.44	0/4735	0.58	0/6401
1	B	0.47	0/4661	0.59	0/6298
1	C	0.50	0/4711	0.61	0/6368
1	D	0.47	0/4711	0.58	0/6368
1	E	0.45	0/4686	0.59	0/6332
1	F	0.43	0/4717	0.59	0/6373
2	G	0.47	0/108	0.82	1/140 (0.7%)
All	All	0.46	0/28329	0.59	1/38280 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	21	LEU	CA-CB-CG	5.78	128.59	115.30

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	4646	0	4756	113	0
1	B	4573	0	4690	91	0
1	C	4622	0	4741	106	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	4622	0	4741	78	0
1	E	4598	0	4717	91	0
1	F	4628	0	4737	111	0
2	G	108	0	123	13	0
3	A	27	0	12	1	0
4	B	31	0	12	2	0
4	C	31	0	12	7	0
4	D	31	0	12	1	0
4	E	31	0	12	1	0
4	F	31	0	12	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
All	All	27983	0	28577	539	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 10.

The worst 5 of 539 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:F:412:PHE:CD1	1:F:422:ILE:HD13	1.76	1.20
1:B:546:MET:HB2	1:B:576:ARG:HD2	1.23	1.19
1:E:493:VAL:HG23	2:G:18:ARG:HB3	1.25	1.13
1:C:456:PRO:HB3	4:C:1401:AGS:S1G	1.90	1.11
1:F:511:GLN:HB3	1:F:512:PRO:CD	1.83	1.08

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	579/1416 (41%)	540 (93%)	39 (7%)	0	100	100
1	B	568/1416 (40%)	545 (96%)	23 (4%)	0	100	100
1	C	575/1416 (41%)	543 (94%)	31 (5%)	1 (0%)	47	82
1	D	575/1416 (41%)	551 (96%)	23 (4%)	1 (0%)	47	82
1	E	572/1416 (40%)	540 (94%)	32 (6%)	0	100	100
1	F	575/1416 (41%)	543 (94%)	30 (5%)	2 (0%)	41	76
2	G	13/25 (52%)	12 (92%)	1 (8%)	0	100	100
All	All	3457/8521 (41%)	3274 (95%)	179 (5%)	4 (0%)	54	85

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	511	GLN
1	D	827	LYS
1	C	509	LYS
1	F	488	ILE

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	524/1281 (41%)	517 (99%)	7 (1%)	69	89
1	B	516/1281 (40%)	514 (100%)	2 (0%)	91	97
1	C	522/1281 (41%)	517 (99%)	5 (1%)	76	91
1	D	522/1281 (41%)	519 (99%)	3 (1%)	86	95
1	E	519/1281 (40%)	517 (100%)	2 (0%)	91	97
1	F	523/1281 (41%)	517 (99%)	6 (1%)	73	90
2	G	11/18 (61%)	10 (91%)	1 (9%)	9	34
All	All	3137/7704 (41%)	3111 (99%)	26 (1%)	82	93

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	450	VAL
1	E	477	LYS
1	F	863	ASN
1	D	803	LEU
1	E	847	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	639	GLN
1	F	863	ASN
1	E	533	GLN
1	F	843	ASN
1	F	1350	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 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
4	AGS	C	1401	5	26,33,33	0.86	1 (3%)	26,52,52	0.88	2 (7%)
3	ADP	A	1401	-	24,29,29	0.98	1 (4%)	29,45,45	1.35	4 (13%)
4	AGS	B	1401	-	26,33,33	0.86	2 (7%)	26,52,52	1.00	2 (7%)
4	AGS	E	1401	5	26,33,33	0.82	1 (3%)	26,52,52	1.02	2 (7%)
4	AGS	F	1401	5	26,33,33	0.82	0	26,52,52	1.00	2 (7%)
4	AGS	D	1401	5	26,33,33	0.92	2 (7%)	26,52,52	0.80	1 (3%)

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	AGS	C	1401	5	-	5/17/38/38	0/3/3/3
3	ADP	A	1401	-	-	2/12/32/32	0/3/3/3
4	AGS	B	1401	-	-	7/17/38/38	0/3/3/3
4	AGS	E	1401	5	-	5/17/38/38	0/3/3/3
4	AGS	F	1401	5	-	0/17/38/38	0/3/3/3
4	AGS	D	1401	5	-	3/17/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1401	AGS	PA-O1A	-2.36	1.42	1.50
4	C	1401	AGS	PA-O1A	-2.35	1.42	1.50
4	D	1401	AGS	PG-S1G	2.29	1.95	1.90
4	E	1401	AGS	PA-O1A	-2.24	1.43	1.50
3	A	1401	ADP	C5-C4	2.22	1.46	1.40

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1401	AGS	PA-O3A-PB	-3.39	121.18	132.83
3	A	1401	ADP	N3-C2-N1	-3.32	123.49	128.68
4	F	1401	AGS	PA-O3A-PB	-3.03	122.42	132.83
3	A	1401	ADP	C3'-C2'-C1'	2.97	105.44	100.98
4	B	1401	AGS	PA-O3A-PB	-2.84	123.09	132.83

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

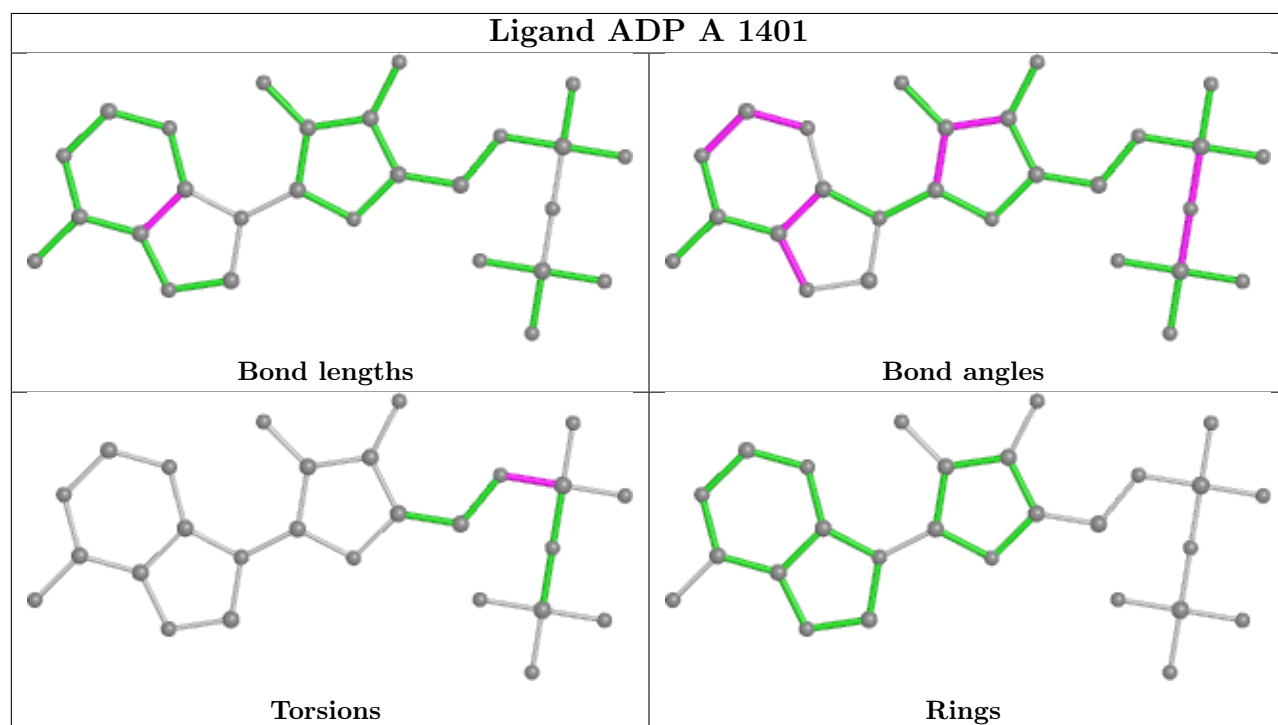
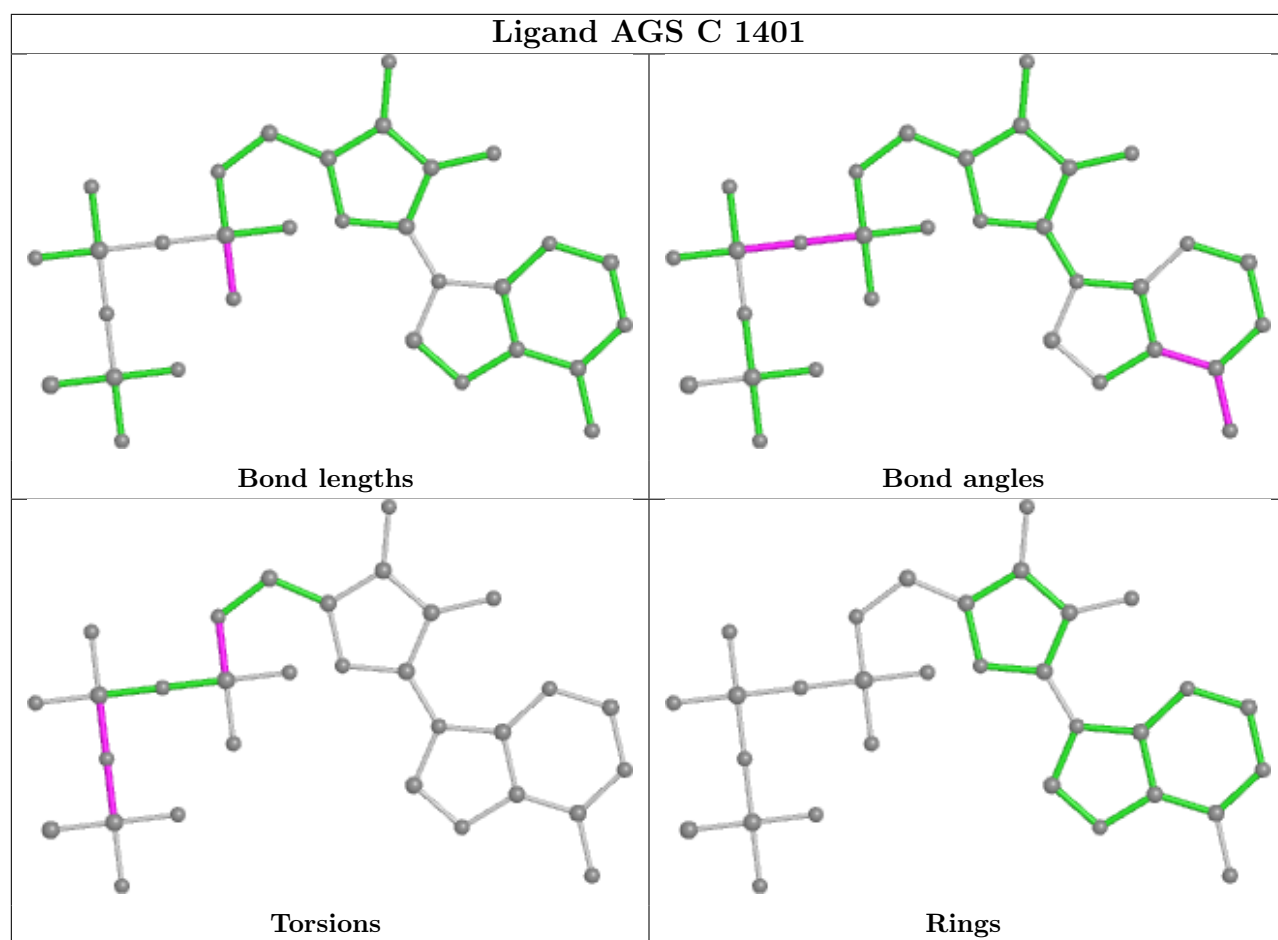
Mol	Chain	Res	Type	Atoms
3	A	1401	ADP	C5'-O5'-PA-O2A
3	A	1401	ADP	C5'-O5'-PA-O3A
4	B	1401	AGS	C5'-O5'-PA-O1A
4	C	1401	AGS	PB-O3B-PG-O2G
4	D	1401	AGS	PB-O3B-PG-O3G

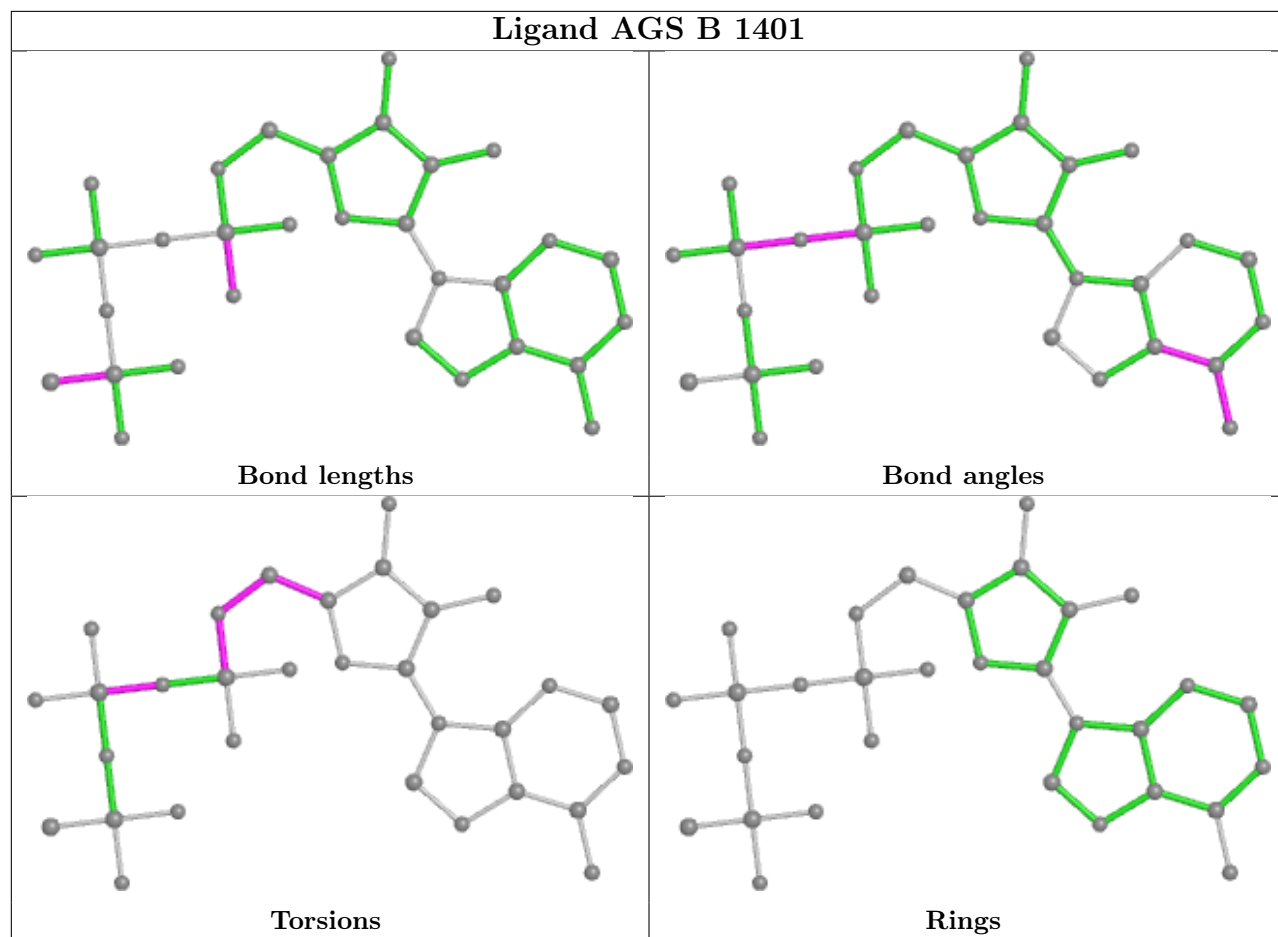
There are no ring outliers.

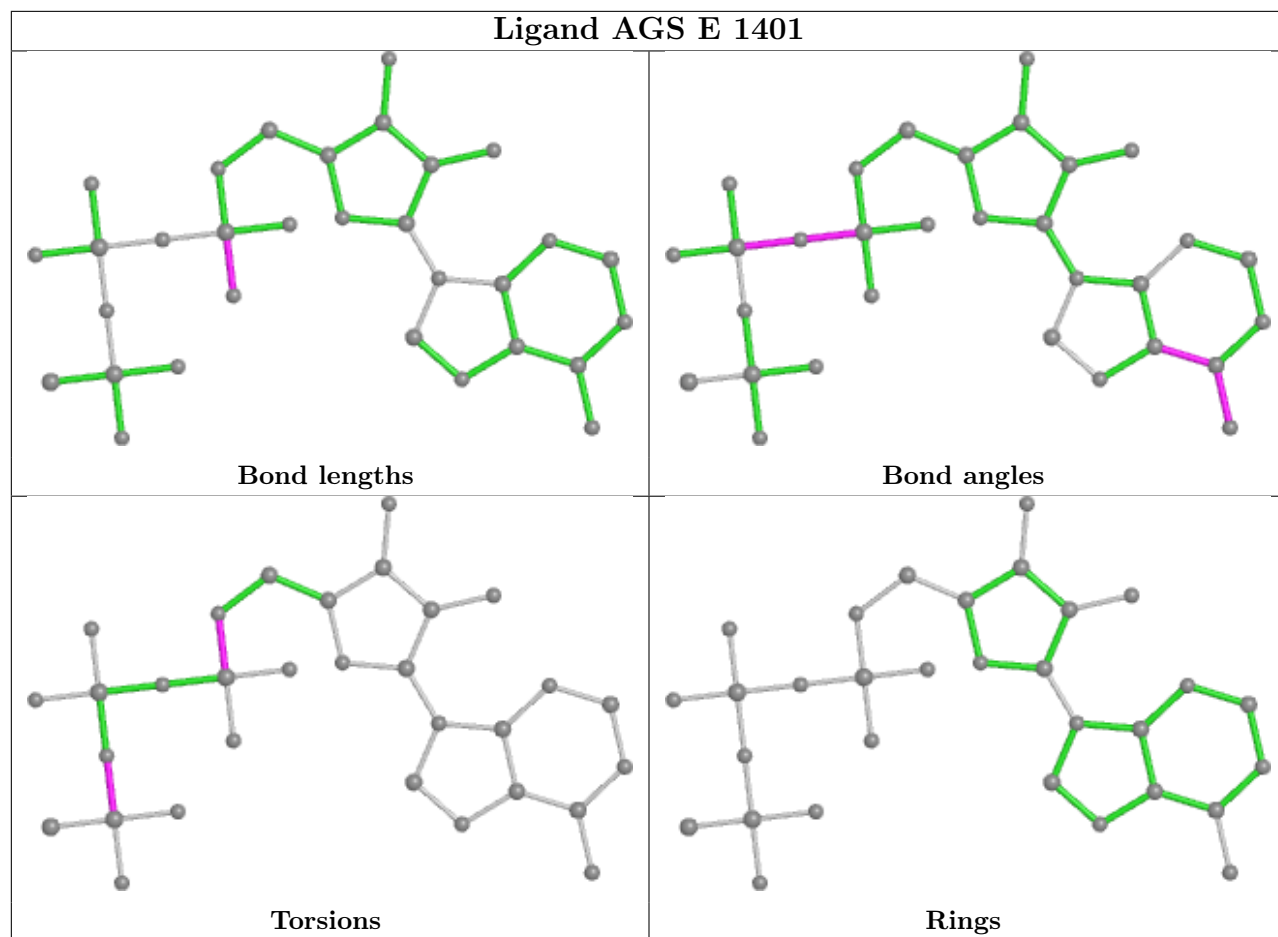
5 monomers are involved in 12 short contacts:

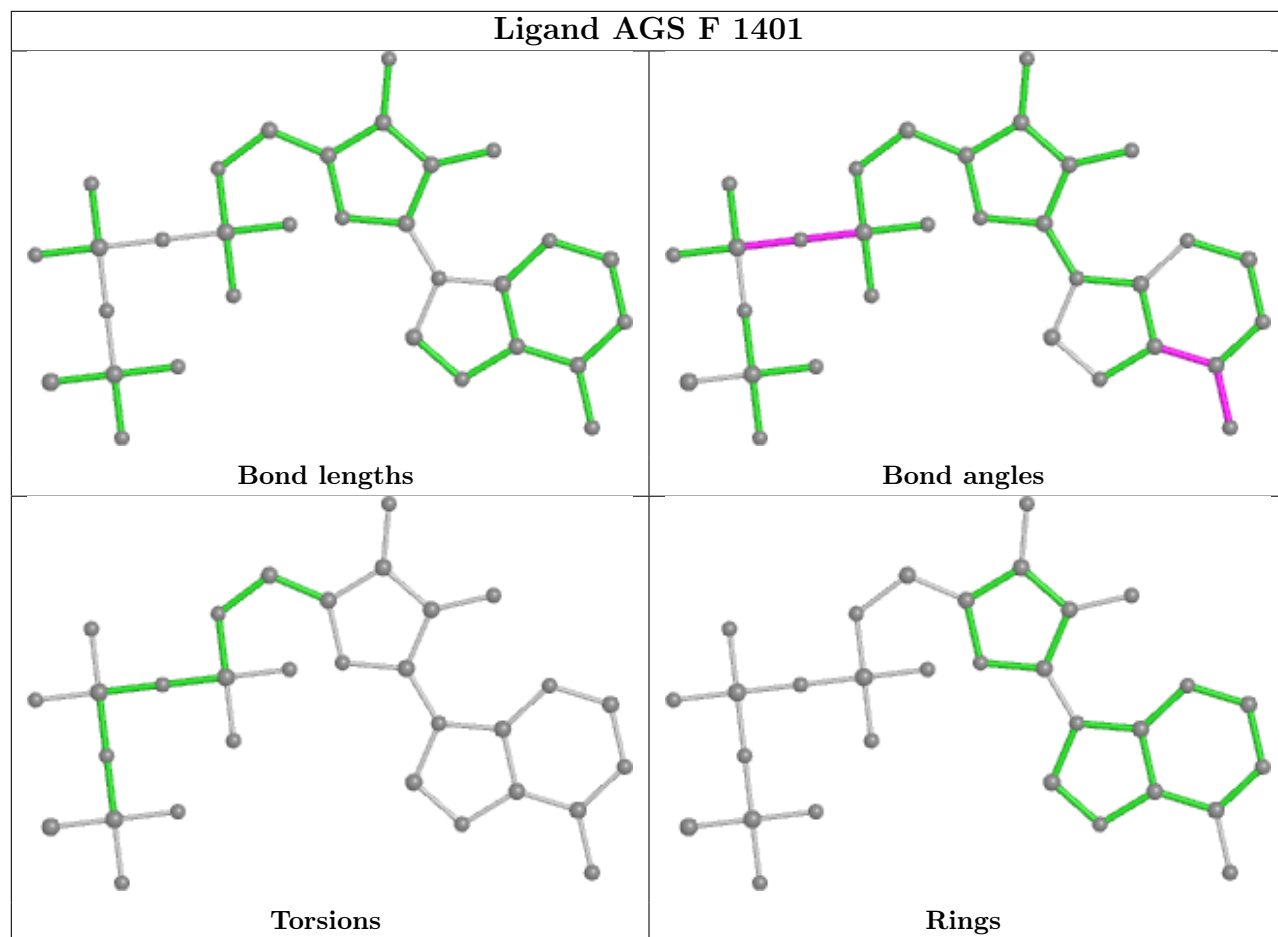
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	1401	AGS	7	0
3	A	1401	ADP	1	0
4	B	1401	AGS	2	0
4	E	1401	AGS	1	0
4	D	1401	AGS	1	0

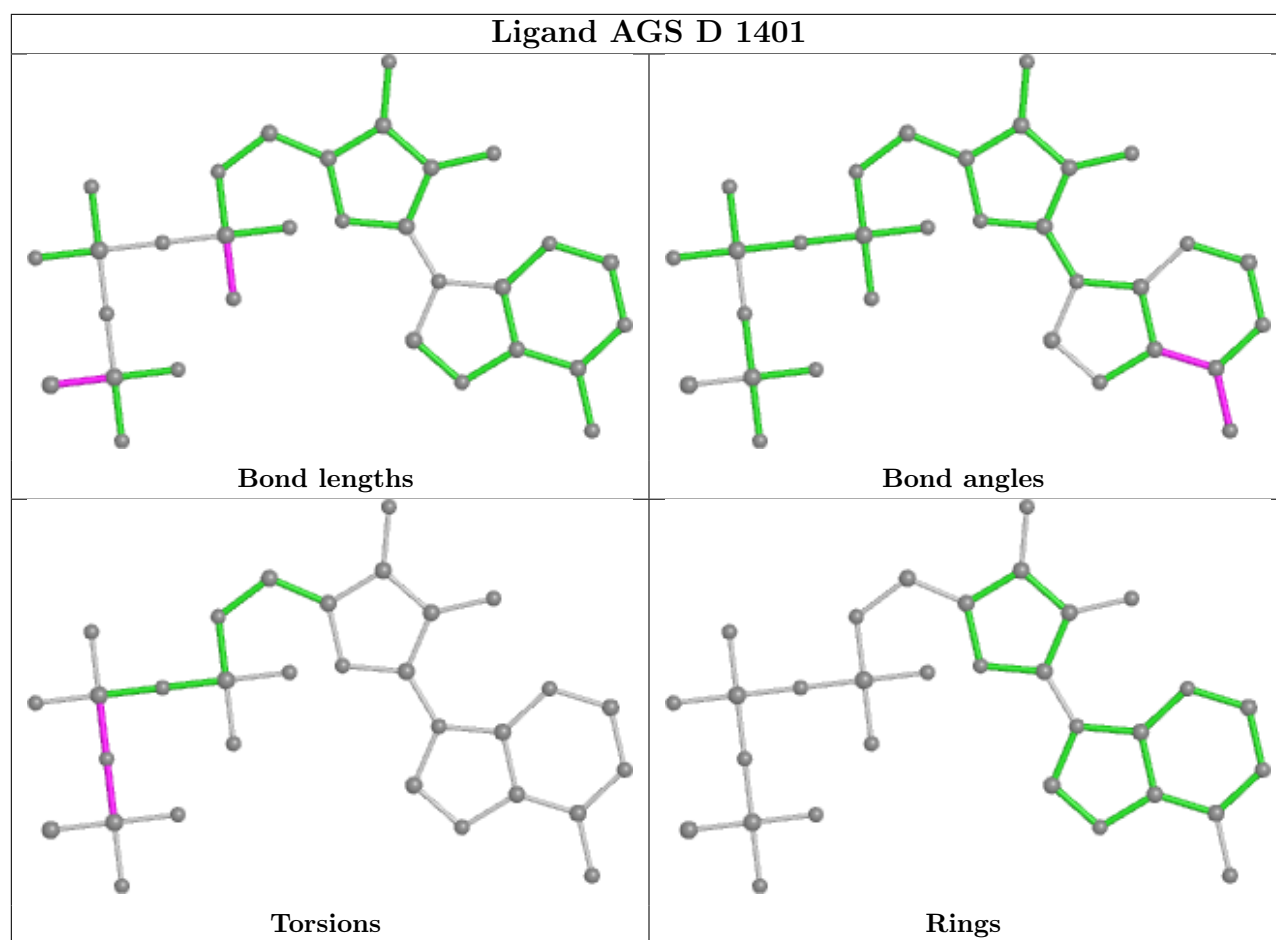
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

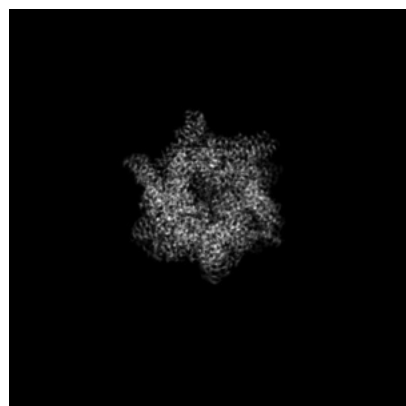
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26696. These allow visual inspection of the internal detail of the map and identification of artifacts.

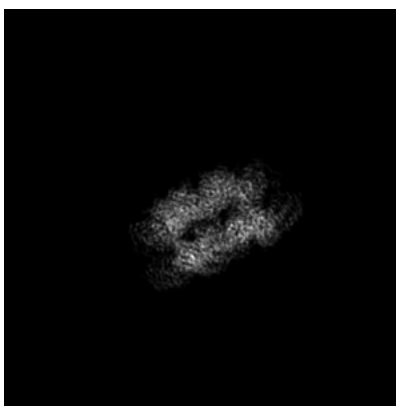
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

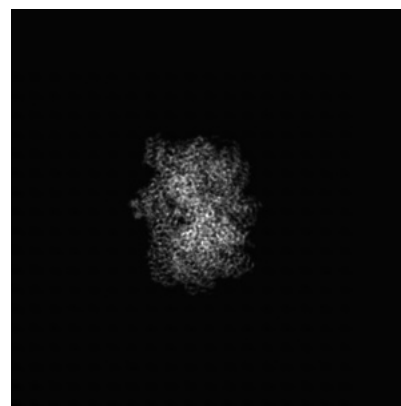
6.1.1 Primary map



X

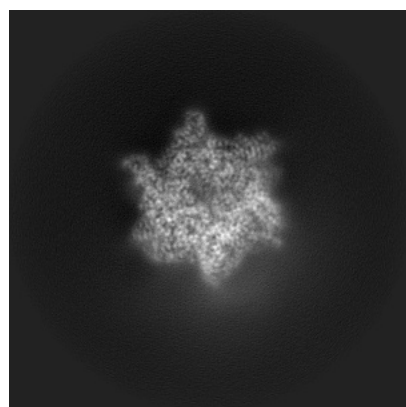


Y

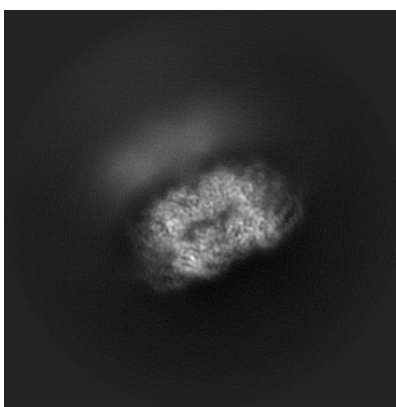


Z

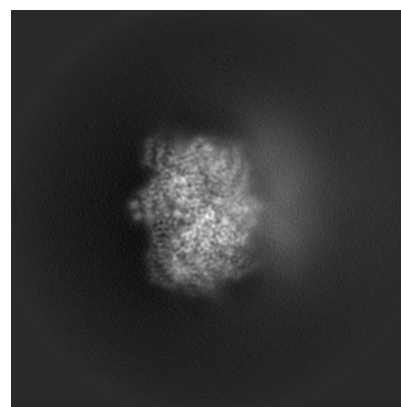
6.1.2 Raw map



X



Y

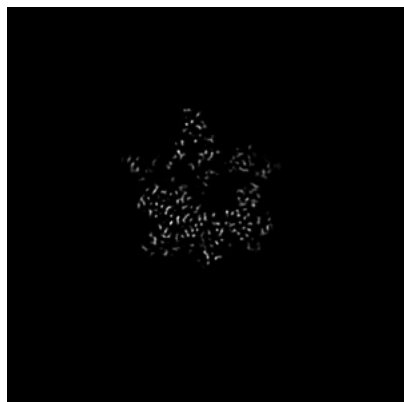


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 200

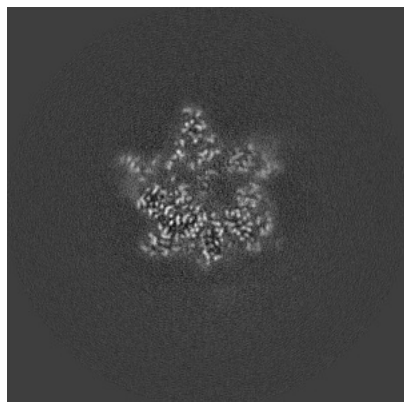


Y Index: 200

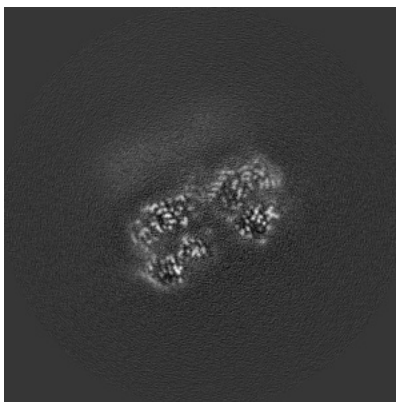


Z Index: 200

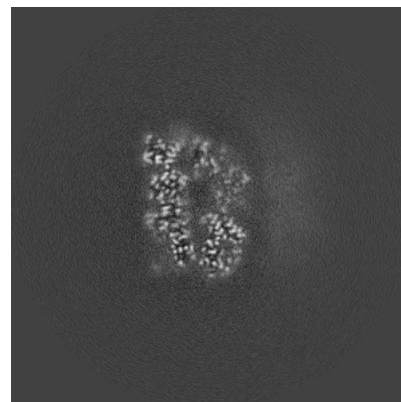
6.2.2 Raw map



X Index: 200



Y Index: 200



Z Index: 200

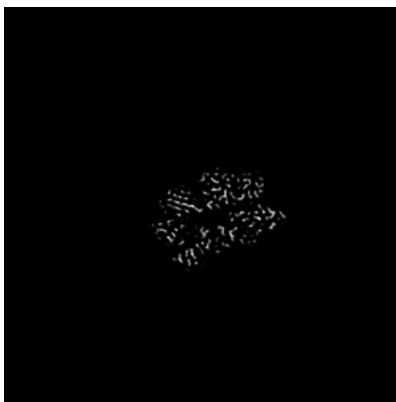
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 183

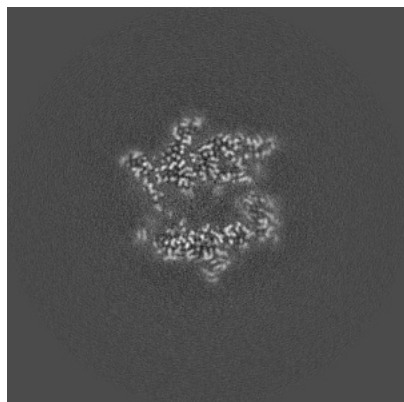


Y Index: 170

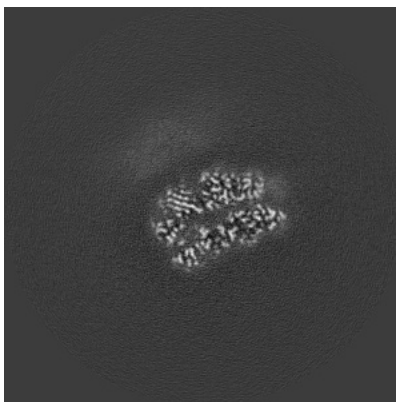


Z Index: 176

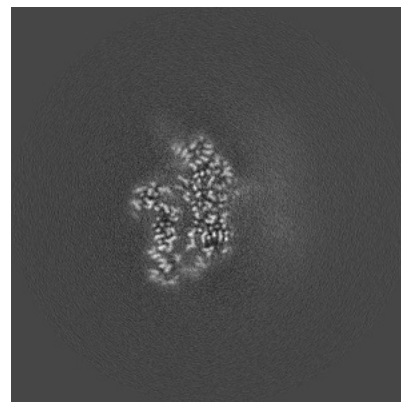
6.3.2 Raw map



X Index: 183



Y Index: 170

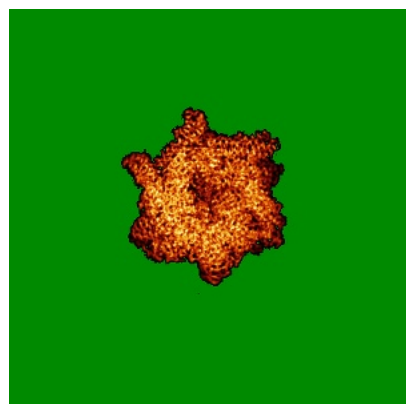


Z Index: 176

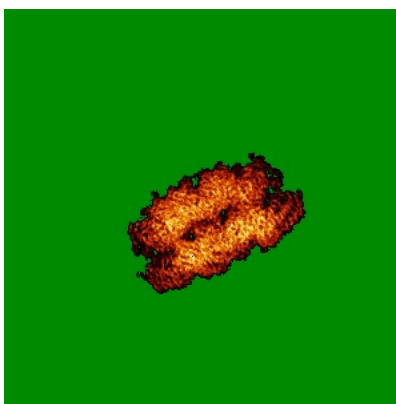
The images above show the largest variance slices of the map in three orthogonal directions.

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

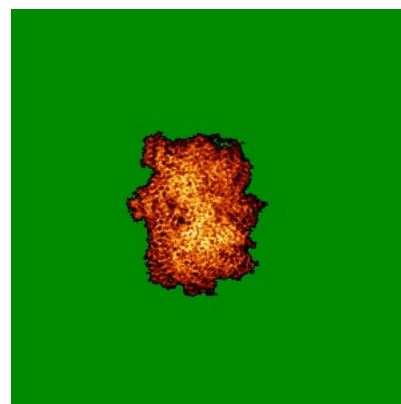
6.4.1 Primary map



X

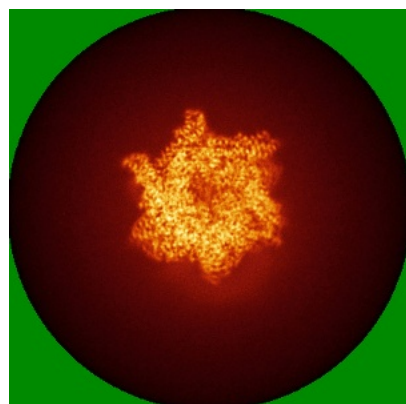


Y

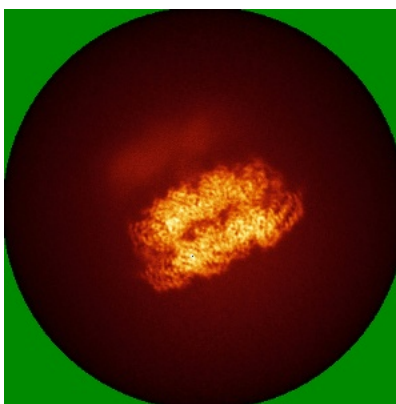


Z

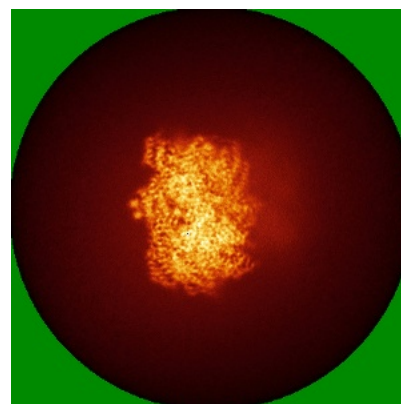
6.4.2 Raw map



X



Y

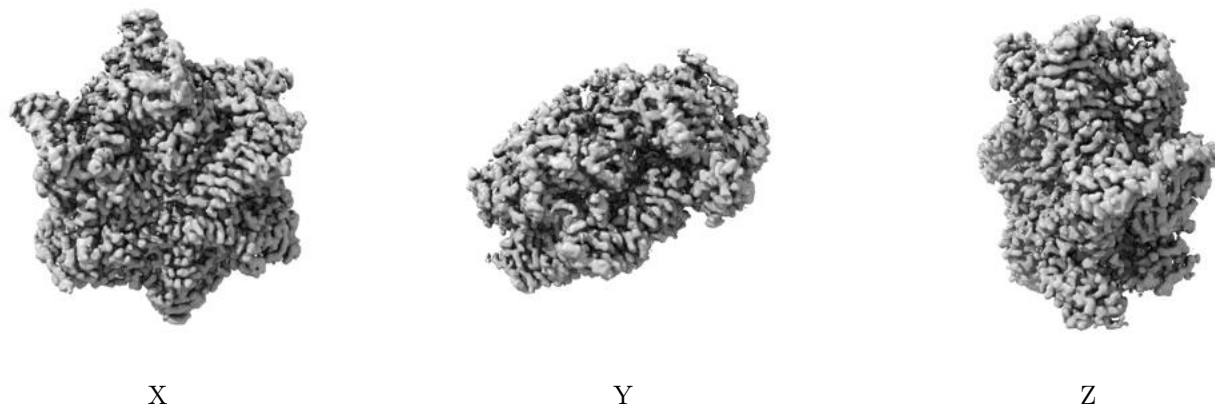


Z

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.

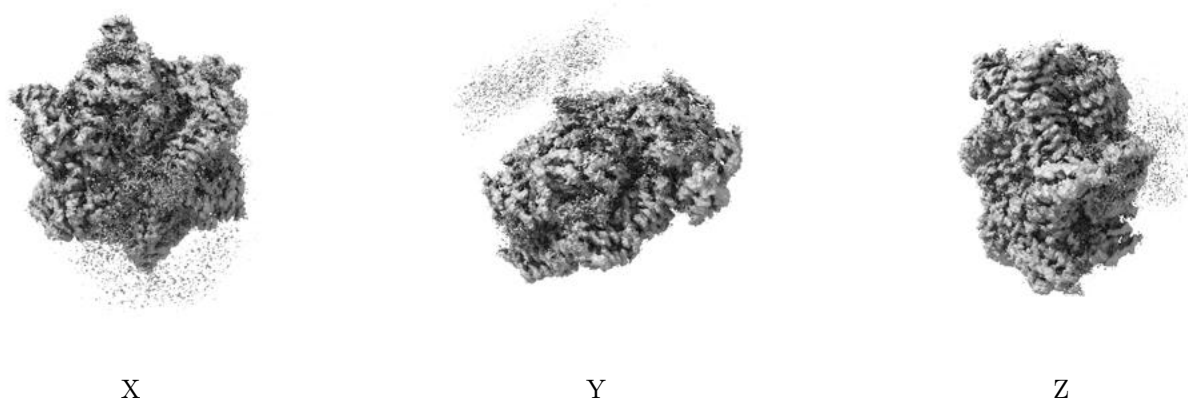
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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.

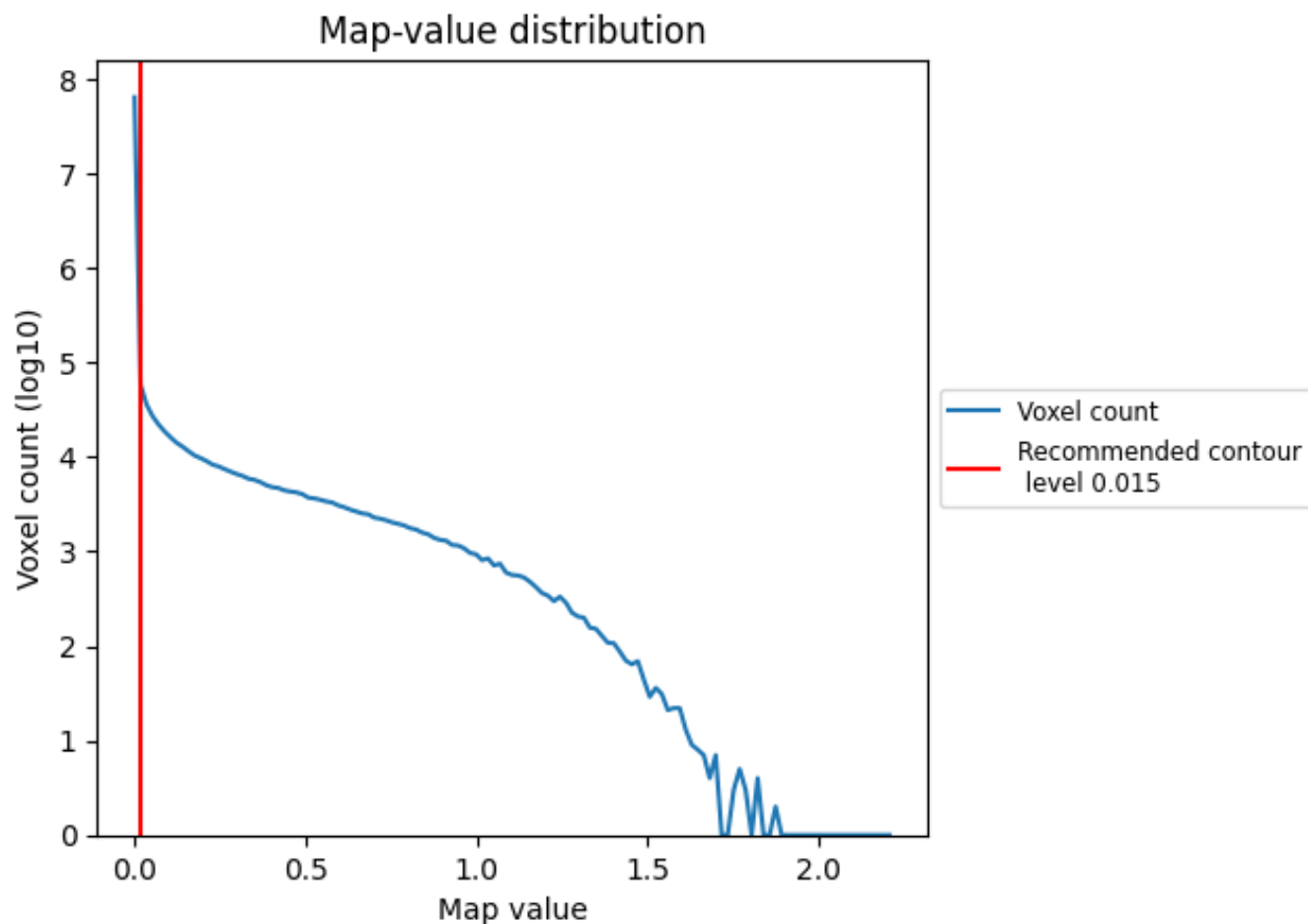
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

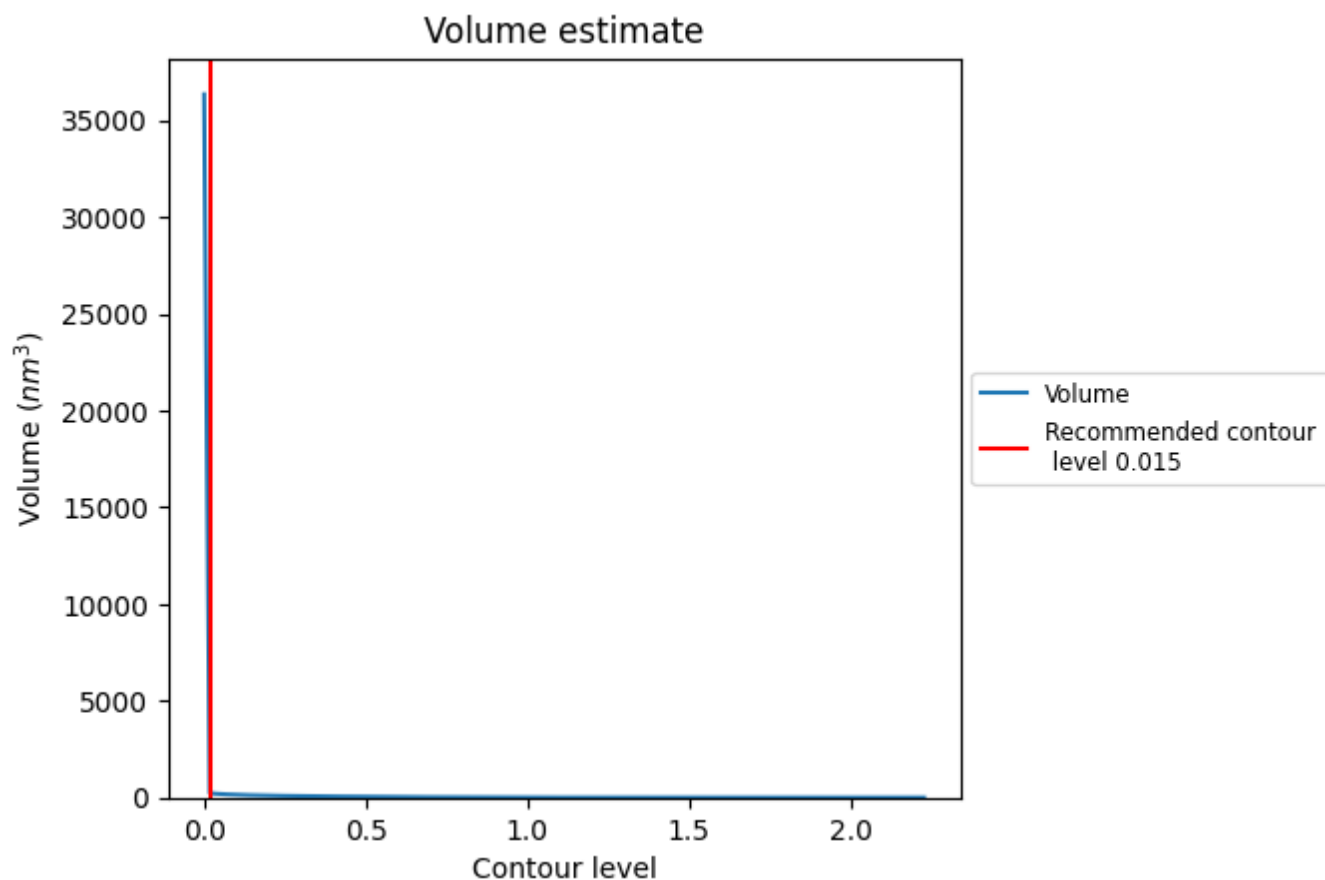
This section contains the results of statistical analysis of the map.

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.

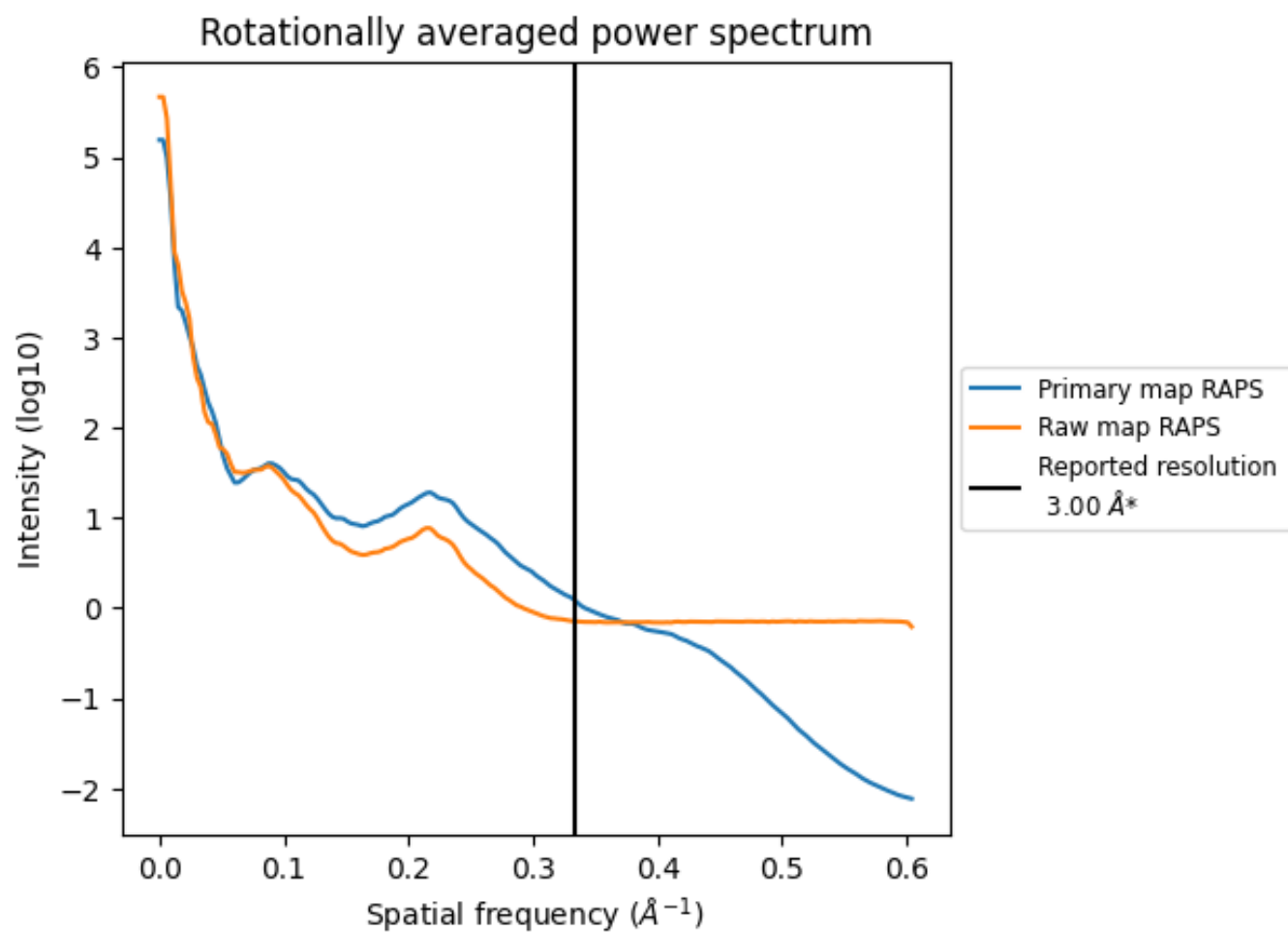
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1555 nm³; this corresponds to an approximate mass of 1405 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 ⓘ

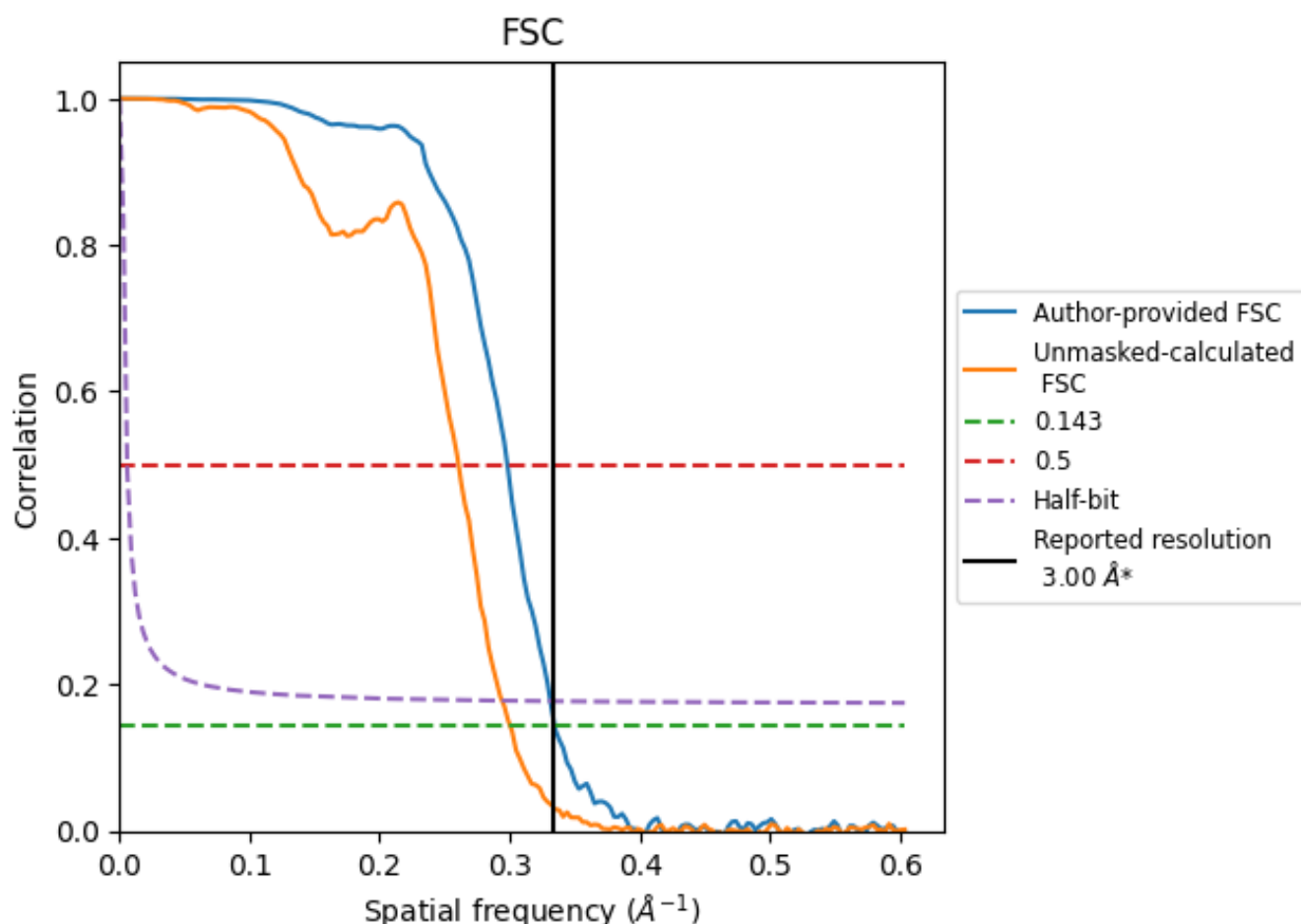


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 \AA^{-1}

8.2 Resolution estimates [i](#)

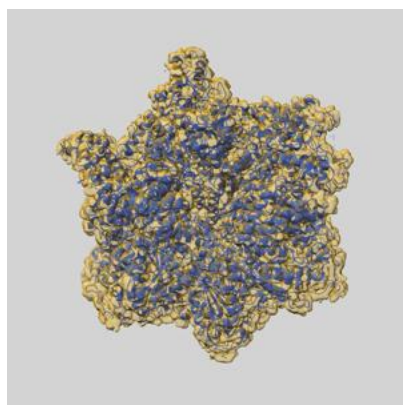
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.99	3.35	3.02
Unmasked-calculated*	3.33	3.84	3.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.33 differs from the reported value 3.0 by more than 10 %

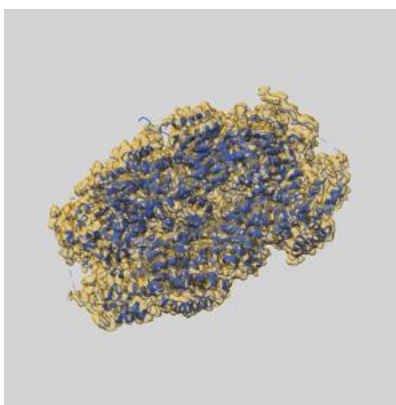
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26696 and PDB model 7UQJ. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

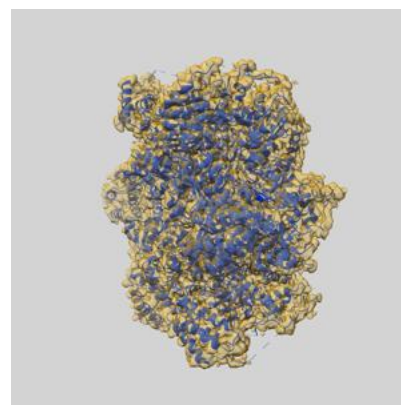
9.1 Map-model overlay [i](#)



X



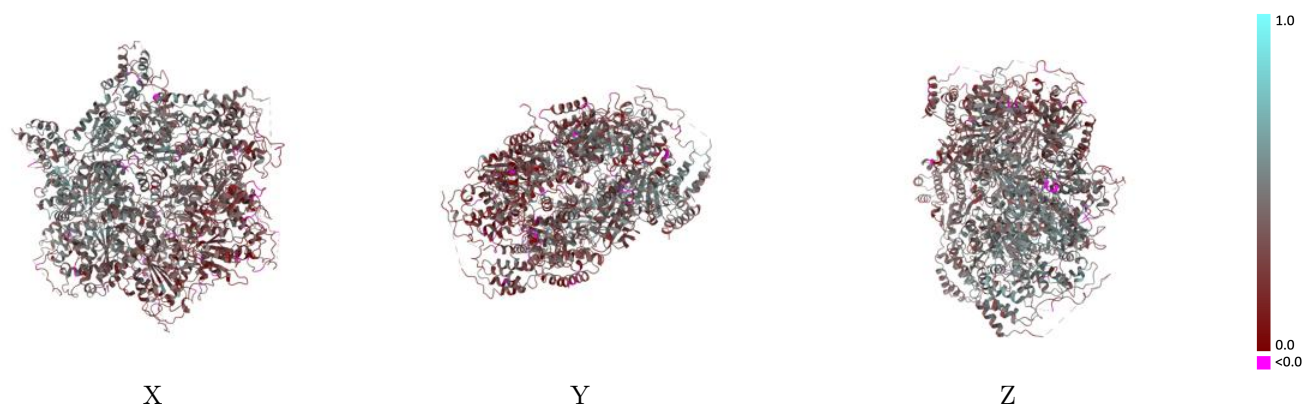
Y



Z

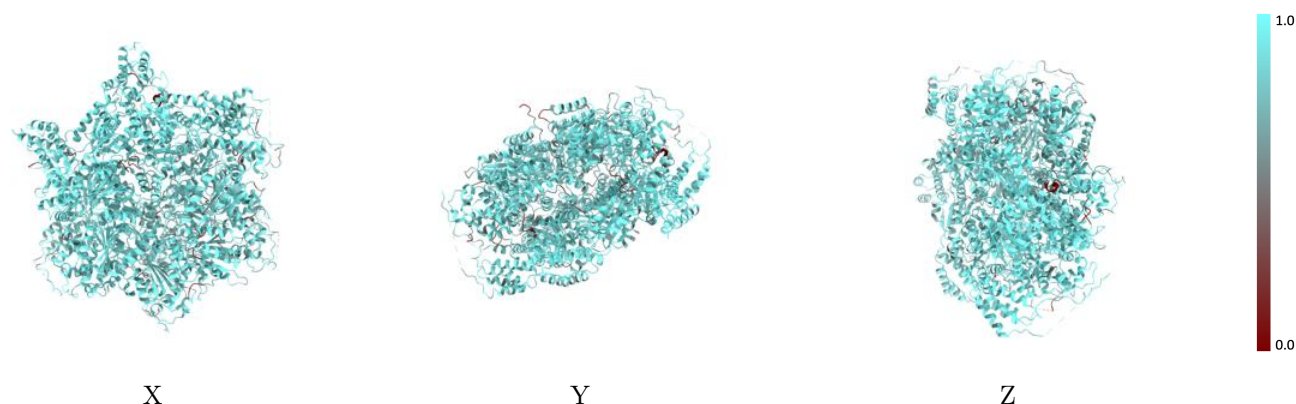
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



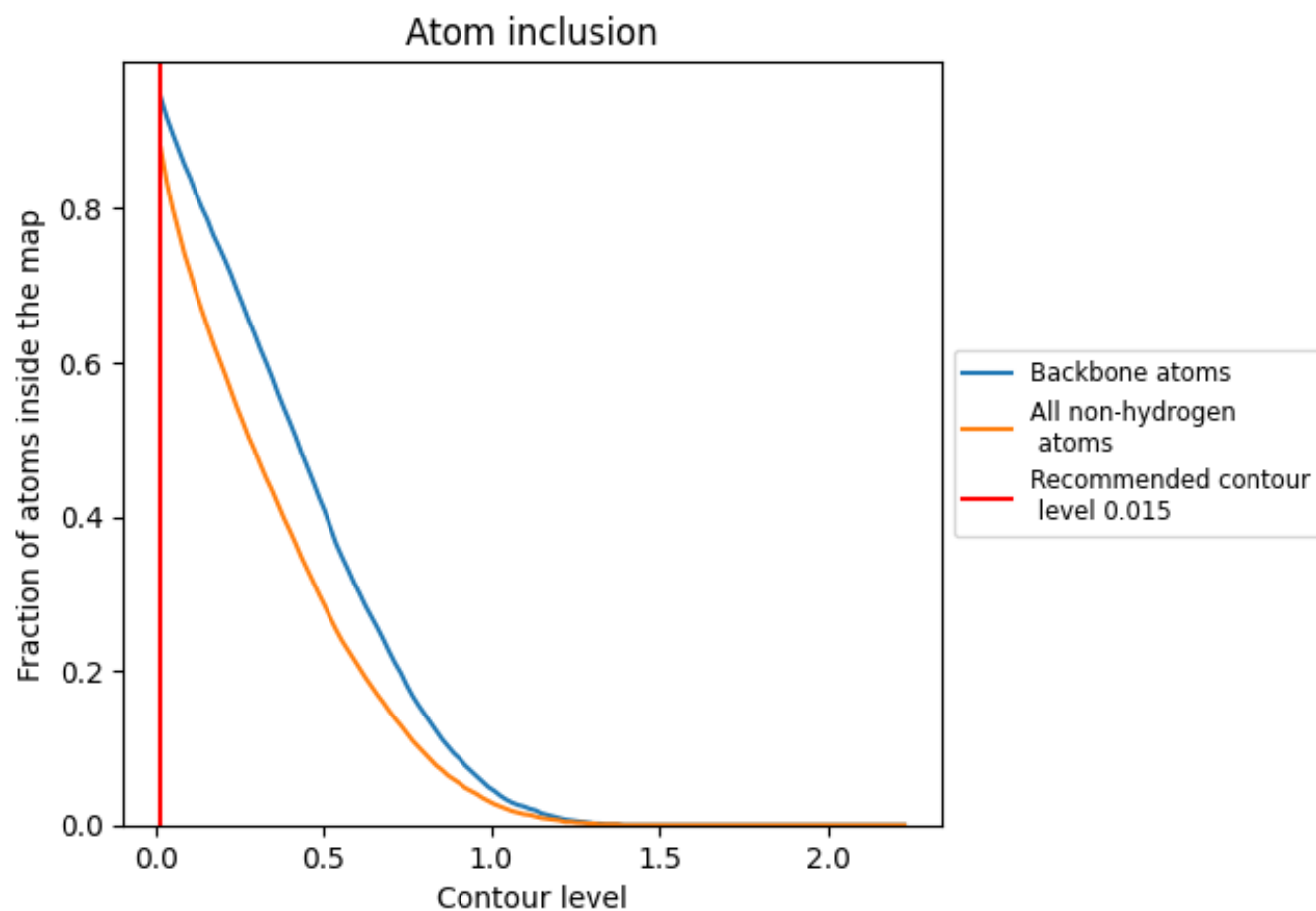
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8780	<div><div></div></div> 0.3620
A	<div><div></div></div> 0.8720	<div><div></div></div> 0.3920
B	<div><div></div></div> 0.9160	<div><div></div></div> 0.4480
C	<div><div></div></div> 0.9120	<div><div></div></div> 0.4320
D	<div><div></div></div> 0.8860	<div><div></div></div> 0.3390
E	<div><div></div></div> 0.8570	<div><div></div></div> 0.2710
F	<div><div></div></div> 0.8390	<div><div></div></div> 0.2940
G	<div><div></div></div> 0.3680	<div><div></div></div> 0.1090

1.0

0.0

<0.0