



wwPDB EM Validation Summary Report ⓘ

Nov 29, 2022 – 08:16 PM EST

PDB ID : 8DR7
EMDB ID : EMD-27673
Title : Open state of RFC:PCNA bound to a nicked dsDNA
Authors : Schrecker, M.; Hite, R.K.
Deposited on : 2022-07-20
Resolution : 2.70 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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

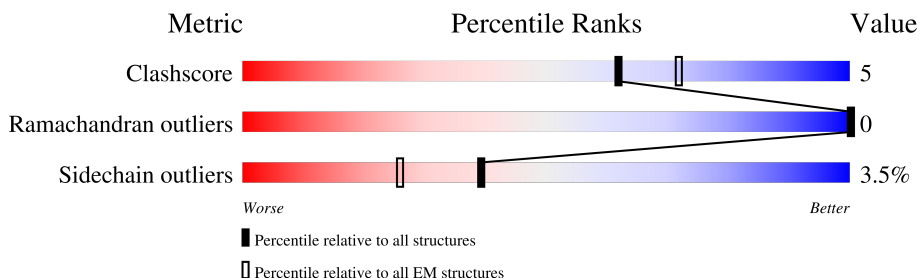
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.



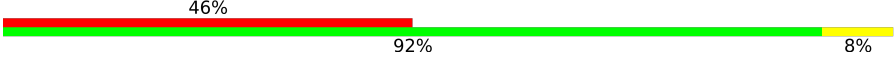


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	918	
2	B	323	
3	C	340	
4	D	353	
5	E	354	
6	F	277	
6	G	277	
6	H	277	

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Mol	Chain	Length	Quality of chain
7	I	26	
8	J	12	
9	K	11	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 43128 atoms, of which 21473 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 Replication factor C subunit 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	497	Total	C	H	N	O	S	0	0
			7919	2499	3982	691	729	18		

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	862	GLY	-	expression tag	UNP P38630
A	863	LEU	-	expression tag	UNP P38630
A	864	ASN	-	expression tag	UNP P38630
A	865	GLU	-	expression tag	UNP P38630
A	866	ASN	-	expression tag	UNP P38630
A	867	LEU	-	expression tag	UNP P38630
A	868	TYR	-	expression tag	UNP P38630
A	869	PHE	-	expression tag	UNP P38630
A	870	GLN	-	expression tag	UNP P38630
A	871	GLY	-	expression tag	UNP P38630
A	872	GLY	-	expression tag	UNP P38630
A	873	GLY	-	expression tag	UNP P38630
A	874	ASP	-	expression tag	UNP P38630
A	875	TYR	-	expression tag	UNP P38630
A	876	LYS	-	expression tag	UNP P38630
A	877	ASP	-	expression tag	UNP P38630
A	878	ASP	-	expression tag	UNP P38630
A	879	ASP	-	expression tag	UNP P38630
A	880	ASP	-	expression tag	UNP P38630
A	881	LYS	-	expression tag	UNP P38630
A	882	ASP	-	expression tag	UNP P38630
A	883	TYR	-	expression tag	UNP P38630
A	884	LYS	-	expression tag	UNP P38630
A	885	ASP	-	expression tag	UNP P38630
A	886	ASP	-	expression tag	UNP P38630
A	887	ASP	-	expression tag	UNP P38630
A	888	ASP	-	expression tag	UNP P38630
A	889	LYS	-	expression tag	UNP P38630

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Chain	Residue	Modelled	Actual	Comment	Reference
A	890	ASP	-	expression tag	UNP P38630
A	891	TYR	-	expression tag	UNP P38630
A	892	LYS	-	expression tag	UNP P38630
A	893	ASP	-	expression tag	UNP P38630
A	894	ASP	-	expression tag	UNP P38630
A	895	ASP	-	expression tag	UNP P38630
A	896	ASP	-	expression tag	UNP P38630
A	897	LYS	-	expression tag	UNP P38630
A	898	GLY	-	expression tag	UNP P38630
A	899	GLY	-	expression tag	UNP P38630
A	900	LYS	-	expression tag	UNP P38630
A	901	ASP	-	expression tag	UNP P38630
A	902	HIS	-	expression tag	UNP P38630
A	903	LEU	-	expression tag	UNP P38630
A	904	ILE	-	expression tag	UNP P38630
A	905	HIS	-	expression tag	UNP P38630
A	906	ASN	-	expression tag	UNP P38630
A	907	VAL	-	expression tag	UNP P38630
A	908	HIS	-	expression tag	UNP P38630
A	909	LYS	-	expression tag	UNP P38630
A	910	GLU	-	expression tag	UNP P38630
A	911	GLU	-	expression tag	UNP P38630
A	912	HIS	-	expression tag	UNP P38630
A	913	ALA	-	expression tag	UNP P38630
A	914	HIS	-	expression tag	UNP P38630
A	915	ALA	-	expression tag	UNP P38630
A	916	HIS	-	expression tag	UNP P38630
A	917	ASN	-	expression tag	UNP P38630
A	918	LYS	-	expression tag	UNP P38630

- Molecule 2 is a protein called Replication factor C subunit 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	318	Total	C	H	N	O	S	0	0
			5083	1574	2587	444	465	13		

- Molecule 3 is a protein called Replication factor C subunit 3.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	330	Total	C	H	N	O	S	0	0
			5254	1643	2643	458	502	8		

- Molecule 4 is a protein called Replication factor C subunit 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	332	Total	C	H	N	O	S	0	0
			5282	1659	2655	454	504	10		

- Molecule 5 is a protein called Replication factor C subunit 5.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	352	Total	C	H	N	O	S	0	0
			5675	1758	2897	483	519	18		

- Molecule 6 is a protein called Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	257	Total	C	H	N	O	S	0	0
			4044	1287	2030	318	399	10		
6	G	256	Total	C	H	N	O	S	0	0
			4037	1284	2028	317	398	10		
6	H	258	Total	C	H	N	O	S	0	0
			4060	1293	2035	319	403	10		

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	MET	-	expression tag	UNP A0A6B7JGY6
F	-17	GLY	-	expression tag	UNP A0A6B7JGY6
F	-16	SER	-	expression tag	UNP A0A6B7JGY6
F	-15	SER	-	expression tag	UNP A0A6B7JGY6
F	-14	HIS	-	expression tag	UNP A0A6B7JGY6
F	-13	HIS	-	expression tag	UNP A0A6B7JGY6
F	-12	HIS	-	expression tag	UNP A0A6B7JGY6
F	-11	HIS	-	expression tag	UNP A0A6B7JGY6
F	-10	HIS	-	expression tag	UNP A0A6B7JGY6
F	-9	HIS	-	expression tag	UNP A0A6B7JGY6
F	-8	SER	-	expression tag	UNP A0A6B7JGY6
F	-7	SER	-	expression tag	UNP A0A6B7JGY6
F	-6	GLY	-	expression tag	UNP A0A6B7JGY6
F	-5	LEU	-	expression tag	UNP A0A6B7JGY6
F	-4	VAL	-	expression tag	UNP A0A6B7JGY6
F	-3	PRO	-	expression tag	UNP A0A6B7JGY6
F	-2	ARG	-	expression tag	UNP A0A6B7JGY6
F	-1	ALA	-	expression tag	UNP A0A6B7JGY6
F	0	SER	-	expression tag	UNP A0A6B7JGY6

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-18	MET	-	expression tag	UNP A0A6B7JGY6
G	-17	GLY	-	expression tag	UNP A0A6B7JGY6
G	-16	SER	-	expression tag	UNP A0A6B7JGY6
G	-15	SER	-	expression tag	UNP A0A6B7JGY6
G	-14	HIS	-	expression tag	UNP A0A6B7JGY6
G	-13	HIS	-	expression tag	UNP A0A6B7JGY6
G	-12	HIS	-	expression tag	UNP A0A6B7JGY6
G	-11	HIS	-	expression tag	UNP A0A6B7JGY6
G	-10	HIS	-	expression tag	UNP A0A6B7JGY6
G	-9	HIS	-	expression tag	UNP A0A6B7JGY6
G	-8	SER	-	expression tag	UNP A0A6B7JGY6
G	-7	SER	-	expression tag	UNP A0A6B7JGY6
G	-6	GLY	-	expression tag	UNP A0A6B7JGY6
G	-5	LEU	-	expression tag	UNP A0A6B7JGY6
G	-4	VAL	-	expression tag	UNP A0A6B7JGY6
G	-3	PRO	-	expression tag	UNP A0A6B7JGY6
G	-2	ARG	-	expression tag	UNP A0A6B7JGY6
G	-1	ALA	-	expression tag	UNP A0A6B7JGY6
G	0	SER	-	expression tag	UNP A0A6B7JGY6
H	-18	MET	-	expression tag	UNP A0A6B7JGY6
H	-17	GLY	-	expression tag	UNP A0A6B7JGY6
H	-16	SER	-	expression tag	UNP A0A6B7JGY6
H	-15	SER	-	expression tag	UNP A0A6B7JGY6
H	-14	HIS	-	expression tag	UNP A0A6B7JGY6
H	-13	HIS	-	expression tag	UNP A0A6B7JGY6
H	-12	HIS	-	expression tag	UNP A0A6B7JGY6
H	-11	HIS	-	expression tag	UNP A0A6B7JGY6
H	-10	HIS	-	expression tag	UNP A0A6B7JGY6
H	-9	HIS	-	expression tag	UNP A0A6B7JGY6
H	-8	SER	-	expression tag	UNP A0A6B7JGY6
H	-7	SER	-	expression tag	UNP A0A6B7JGY6
H	-6	GLY	-	expression tag	UNP A0A6B7JGY6
H	-5	LEU	-	expression tag	UNP A0A6B7JGY6
H	-4	VAL	-	expression tag	UNP A0A6B7JGY6
H	-3	PRO	-	expression tag	UNP A0A6B7JGY6
H	-2	ARG	-	expression tag	UNP A0A6B7JGY6
H	-1	ALA	-	expression tag	UNP A0A6B7JGY6
H	0	SER	-	expression tag	UNP A0A6B7JGY6

- Molecule 7 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
7	I	26	Total	C	H	N	O	P	0	0
			814	247	293	86	162	26		

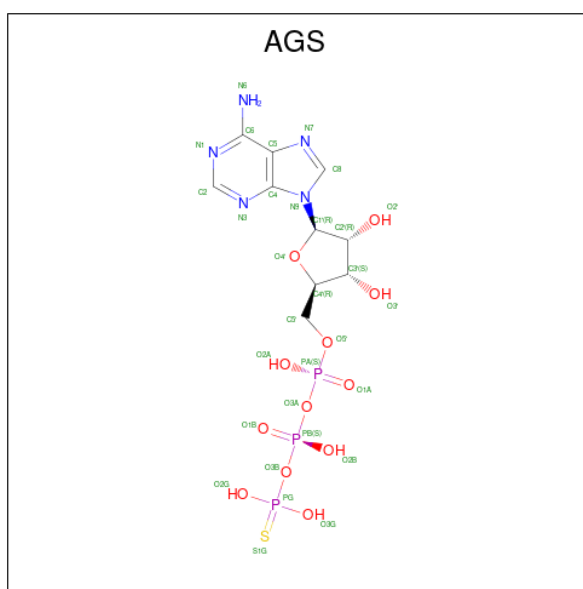
- Molecule 8 is a DNA chain called DNA (5'-D(P*GP*GP*CP*CP*CP*CP*CP*CP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
8	J	12	Total	C	H	N	O	P	0	0
			373	112	133	44	72	12		

- Molecule 9 is a DNA chain called DNA (5'-D(P*AP*GP*GP*GP*GP*GP*GP*GP*GP*GP*G P*G)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
9	K	11	Total	C	H	N	O	P	0	0
			363	110	122	55	65	11		

- Molecule 10 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							AltConf
10	A	1	Total	C	H	N	O	P	S	0
			45	10	14	5	12	3	1	
10	B	1	Total	C	H	N	O	P	S	0
			45	10	14	5	12	3	1	
10	C	1	Total	C	H	N	O	P	S	0
			45	10	14	5	12	3	1	

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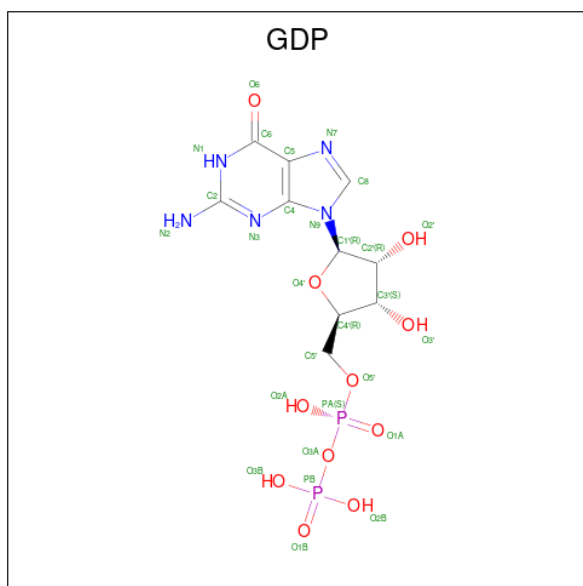
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Mol	Chain	Residues	Atoms							AltConf
10	D	1	Total	C	H	N	O	P	S	0
			45	10	14	5	12	3	1	

- Molecule 11 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
11	B	2	Total	Mg	0
			2	2	
11	C	1	Total	Mg	0
			1	1	
11	D	1	Total	Mg	0
			1	1	

- Molecule 12 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).

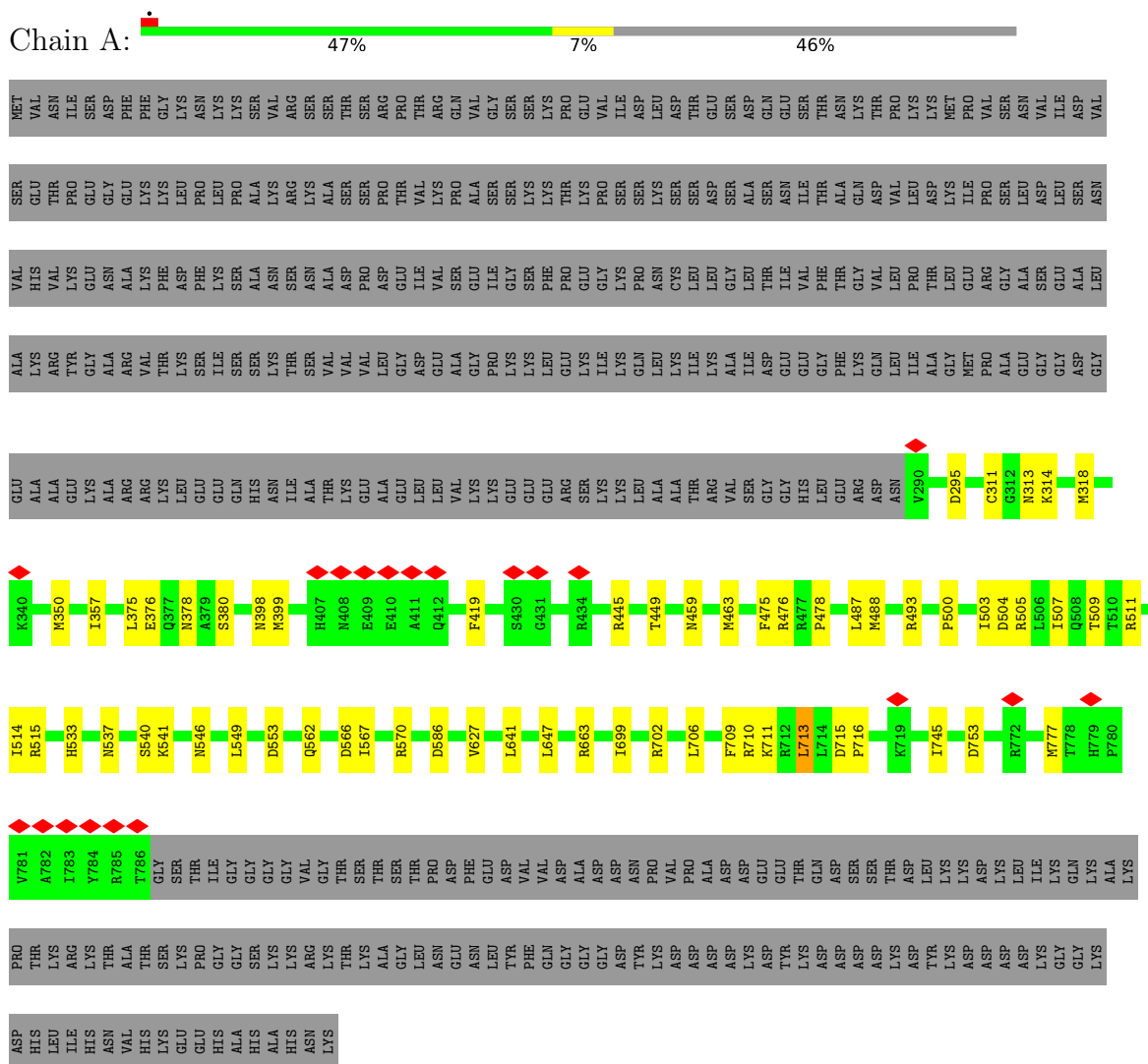


Mol	Chain	Residues	Atoms						AltConf
12	E	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	

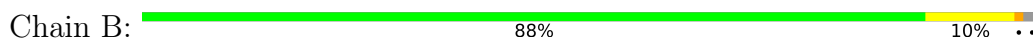
3 Residue-property plots

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: Replication factor C subunit 1



• Molecule 2: Replication factor C subunit 4





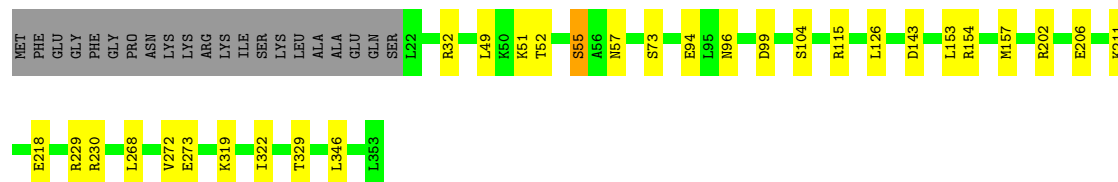
- Molecule 3: Replication factor C subunit 3

Chain C: 86% 11% .



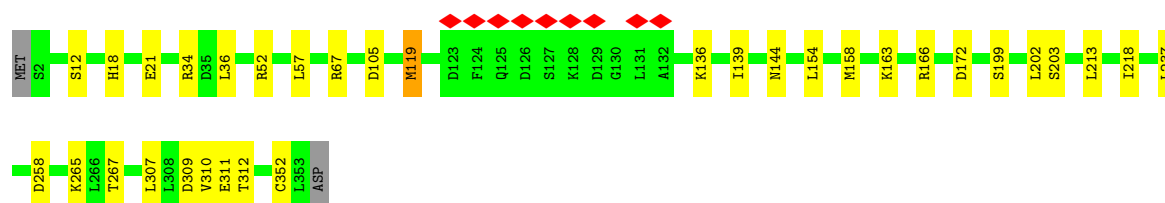
- Molecule 4: Replication factor C subunit 2

Chain D: 86% 8% 6%



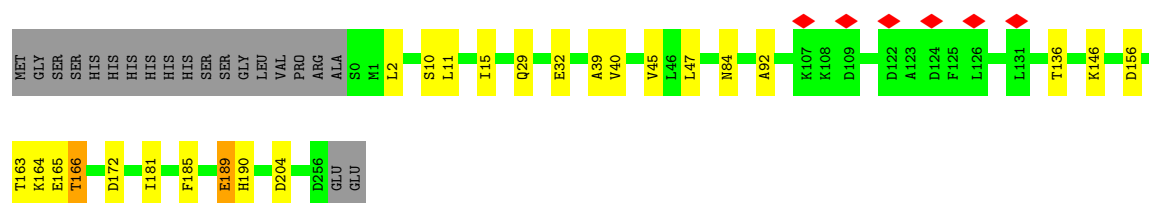
- Molecule 5: Replication factor C subunit 5

Chain E: 90% 9% .

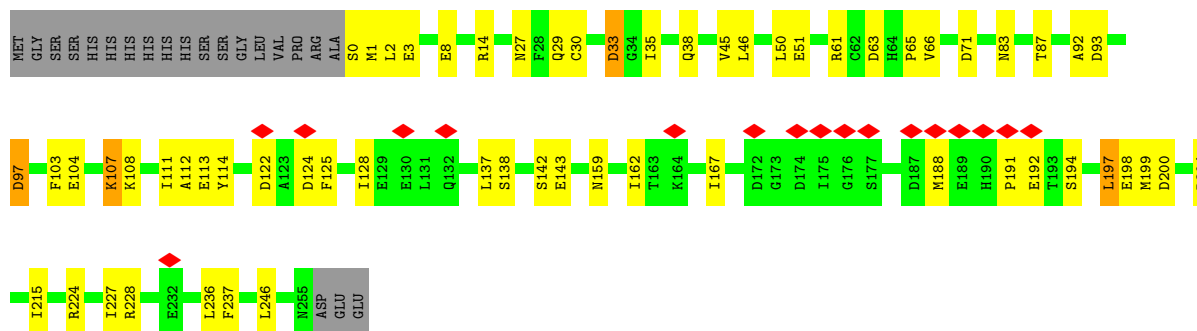


- Molecule 6: Proliferating cell nuclear antigen

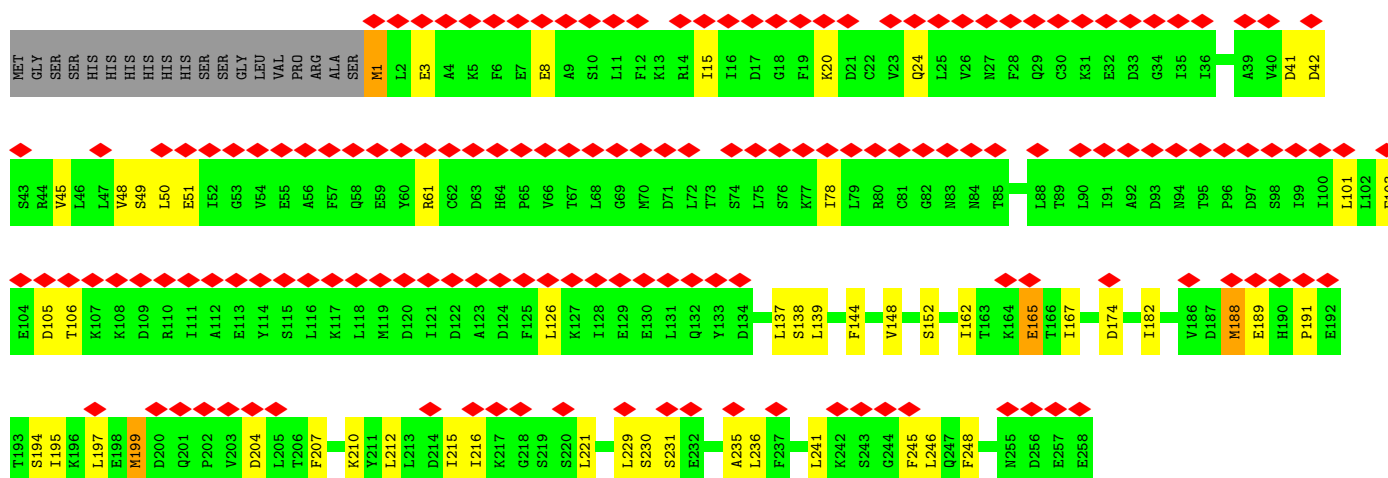
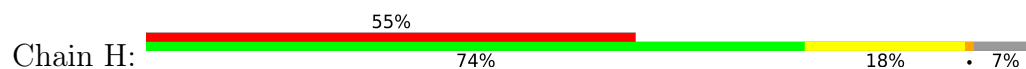
Chain F: 84% 8% 7%



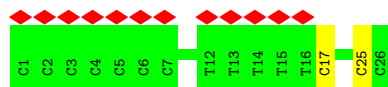
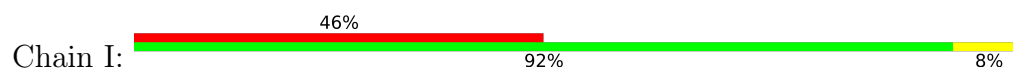
- Molecule 6: Proliferating cell nuclear antigen



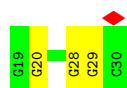
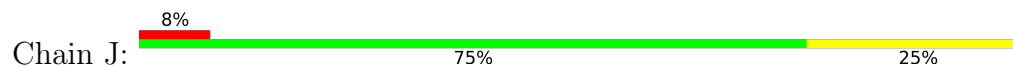
• Molecule 6: Proliferating cell nuclear antigen



• Molecule 7: DNA (26-MER)



• Molecule 8: DNA (5'-D(P*GP*GP*CP*CP*CP*CP*CP*CP*GP*GP*C)-3')



• Molecule 9: DNA (5'-D(P*AP*GP*GP*GP*GP*GP*GP*GP*GP*G)-3')





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	142294	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	66	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.881	Depositor
Minimum map value	-0.614	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	317.184, 317.184, 317.184	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	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: MG, AGS, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/4016	0.48	0/5428
2	B	0.24	0/2531	0.48	0/3414
3	C	0.24	0/2651	0.47	0/3584
4	D	0.24	0/2672	0.45	0/3614
5	E	0.24	0/2818	0.47	0/3808
6	F	0.25	0/2044	0.47	0/2757
6	G	0.26	0/2039	0.53	0/2750
6	H	0.25	0/2055	0.50	0/2772
7	I	0.54	0/579	0.92	0/889
8	J	0.48	0/267	0.75	0/408
9	K	0.46	0/273	0.68	0/423
All	All	0.27	0/21945	0.51	0/29847

There are no bond length outliers.

There are no bond angle outliers.

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	3937	3982	3982	38	0
2	B	2496	2587	2587	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	2611	2643	2642	21	0
4	D	2627	2655	2655	14	0
5	E	2778	2897	2897	16	0
6	F	2014	2030	2032	17	0
6	G	2009	2028	2030	42	0
6	H	2025	2035	2037	33	0
7	I	521	293	293	2	0
8	J	240	133	133	3	0
9	K	241	122	122	0	0
10	A	31	14	12	3	0
10	B	31	14	12	2	0
10	C	31	14	12	2	0
10	D	31	14	12	1	0
11	B	2	0	0	0	0
11	C	1	0	0	0	0
11	D	1	0	0	0	0
12	E	28	12	11	0	0
All	All	21655	21473	21469	195	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 5.

The worst 5 of 195 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)
6:G:128:ILE:HD12	6:G:128:ILE:O	1.75	0.86
6:F:10:SER:OG	6:F:84:ASN:OD1	1.94	0.84
6:G:8:GLU:N	6:G:8:GLU:OE1	2.14	0.80
3:C:294:GLU:N	3:C:294:GLU:OE2	2.15	0.79
4:D:55:SER:OG	4:D:57:ASN:OD1	1.98	0.79

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	495/918 (54%)	493 (100%)	2 (0%)	0	100	100
2	B	316/323 (98%)	308 (98%)	8 (2%)	0	100	100
3	C	328/340 (96%)	326 (99%)	2 (1%)	0	100	100
4	D	330/353 (94%)	325 (98%)	5 (2%)	0	100	100
5	E	350/354 (99%)	346 (99%)	4 (1%)	0	100	100
6	F	255/277 (92%)	252 (99%)	3 (1%)	0	100	100
6	G	254/277 (92%)	251 (99%)	3 (1%)	0	100	100
6	H	256/277 (92%)	248 (97%)	8 (3%)	0	100	100
All	All	2584/3119 (83%)	2549 (99%)	35 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	432/791 (55%)	417 (96%)	15 (4%)	36	65
2	B	279/283 (99%)	270 (97%)	9 (3%)	39	68
3	C	286/296 (97%)	280 (98%)	6 (2%)	53	80
4	D	294/312 (94%)	286 (97%)	8 (3%)	44	74
5	E	322/324 (99%)	312 (97%)	10 (3%)	40	69
6	F	231/249 (93%)	224 (97%)	7 (3%)	41	70
6	G	231/249 (93%)	218 (94%)	13 (6%)	21	45
6	H	232/249 (93%)	219 (94%)	13 (6%)	21	45
All	All	2307/2753 (84%)	2226 (96%)	81 (4%)	39	65

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	G	29	GLN
6	H	138	SER
6	G	38	GLN
6	G	188	MET
6	H	174	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	41	ASN
6	F	58	GLN
6	F	201	GLN
6	G	27	ASN
6	G	29	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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
10	AGS	A	1001	11	26,33,33	3.63	12 (46%)	26,52,52	2.00	6 (23%)
10	AGS	D	402	11	26,33,33	3.63	12 (46%)	26,52,52	2.01	6 (23%)
12	GDP	E	401	-	24,30,30	3.70	13 (54%)	30,47,47	1.40	6 (20%)
10	AGS	B	403	11	26,33,33	3.63	12 (46%)	26,52,52	2.01	6 (23%)
10	AGS	C	402	11	26,33,33	3.63	12 (46%)	26,52,52	2.02	6 (23%)

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
10	AGS	A	1001	11	-	3/17/38/38	0/3/3/3
10	AGS	D	402	11	-	5/17/38/38	0/3/3/3
12	GDP	E	401	-	-	3/12/32/32	0/3/3/3
10	AGS	B	403	11	-	3/17/38/38	0/3/3/3
10	AGS	C	402	11	-	5/17/38/38	0/3/3/3

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	D	402	AGS	C2'-C3'	-10.58	1.24	1.53
10	B	403	AGS	C2'-C3'	-10.56	1.24	1.53
10	C	402	AGS	C2'-C3'	-10.56	1.24	1.53
10	A	1001	AGS	C2'-C3'	-10.52	1.24	1.53
12	E	401	GDP	C3'-C4'	-8.58	1.31	1.53

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1001	AGS	N3-C2-N1	-5.53	120.04	128.68
10	B	403	AGS	N3-C2-N1	-5.50	120.08	128.68
10	D	402	AGS	N3-C2-N1	-5.49	120.09	128.68
10	C	402	AGS	N3-C2-N1	-5.45	120.15	128.68
10	A	1001	AGS	C1'-N9-C4	-4.82	118.18	126.64

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

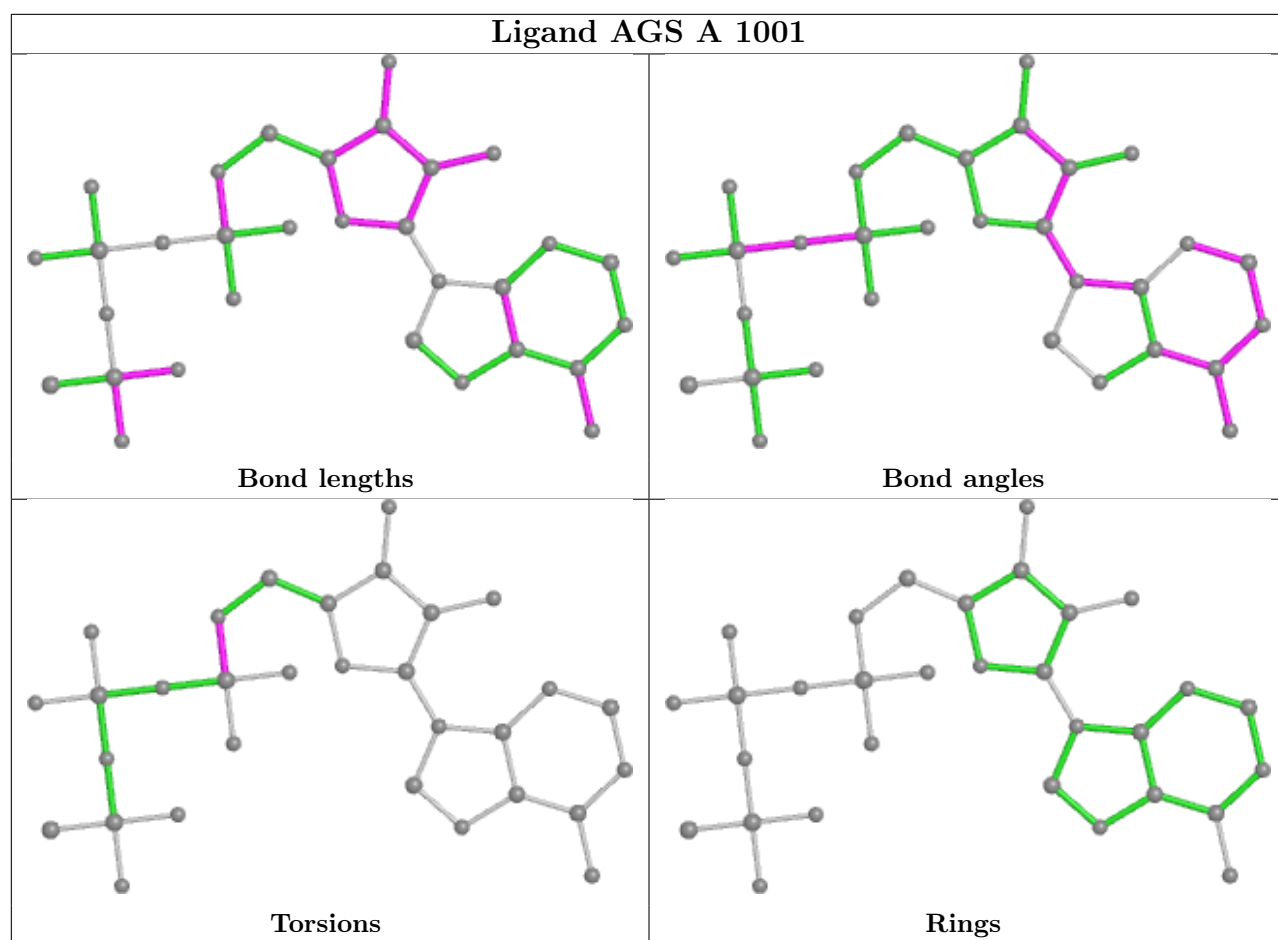
Mol	Chain	Res	Type	Atoms
10	A	1001	AGS	C5'-O5'-PA-O1A
10	A	1001	AGS	C5'-O5'-PA-O2A
10	B	403	AGS	C5'-O5'-PA-O1A
10	B	403	AGS	C5'-O5'-PA-O2A
10	C	402	AGS	C5'-O5'-PA-O1A

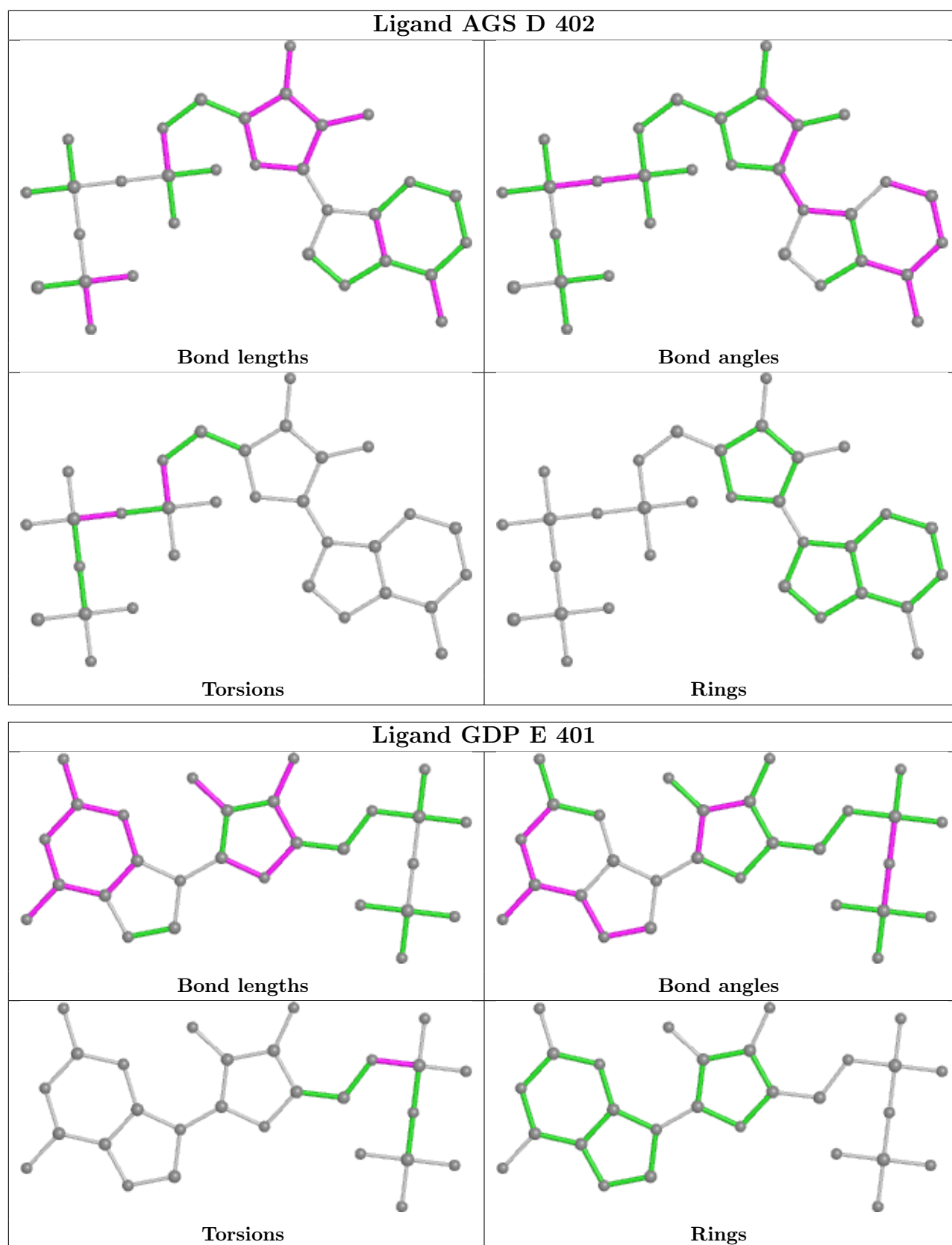
There are no ring outliers.

4 monomers are involved in 8 short contacts:

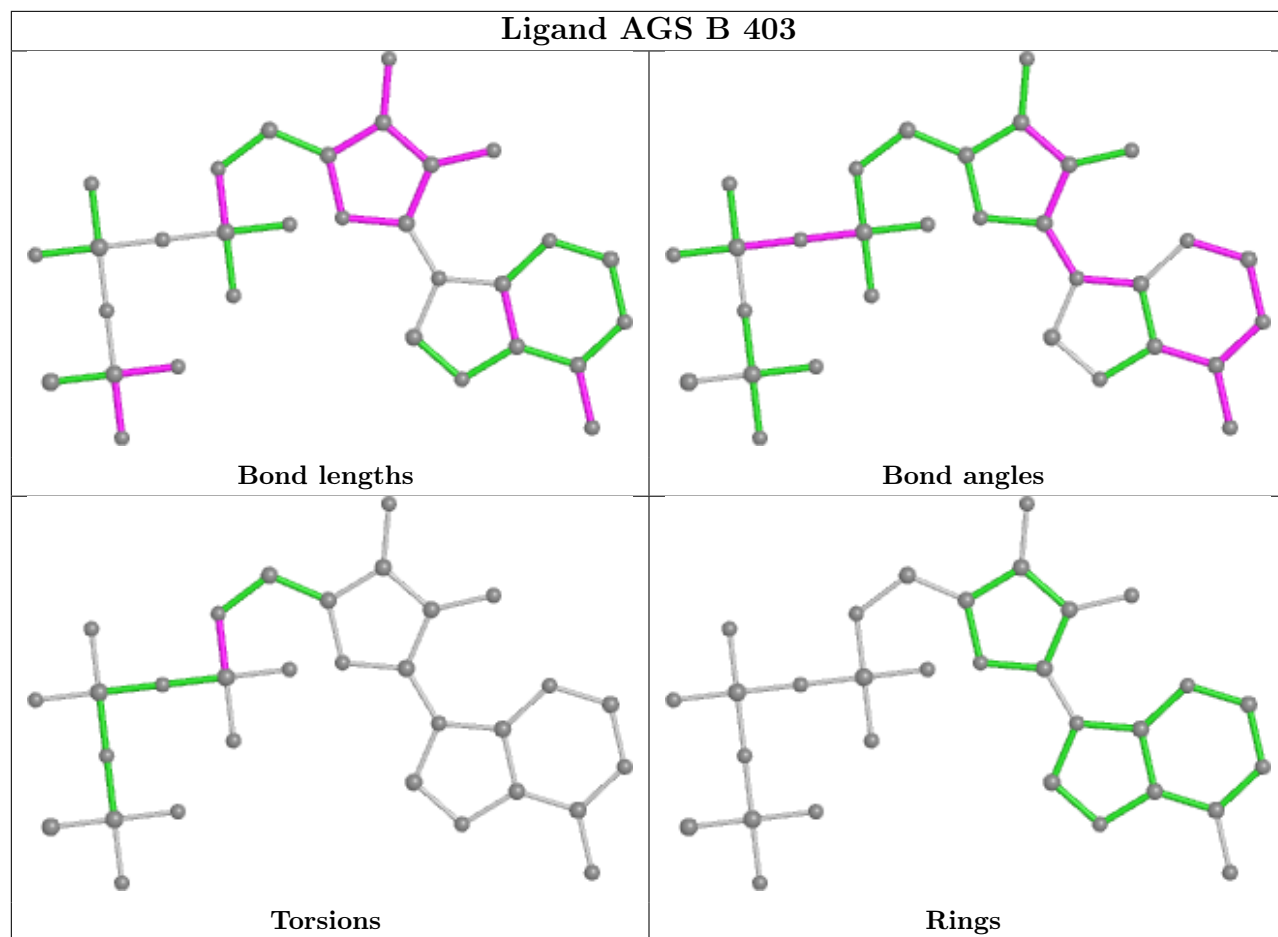
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	1001	AGS	3	0
10	D	402	AGS	1	0
10	B	403	AGS	2	0
10	C	402	AGS	2	0

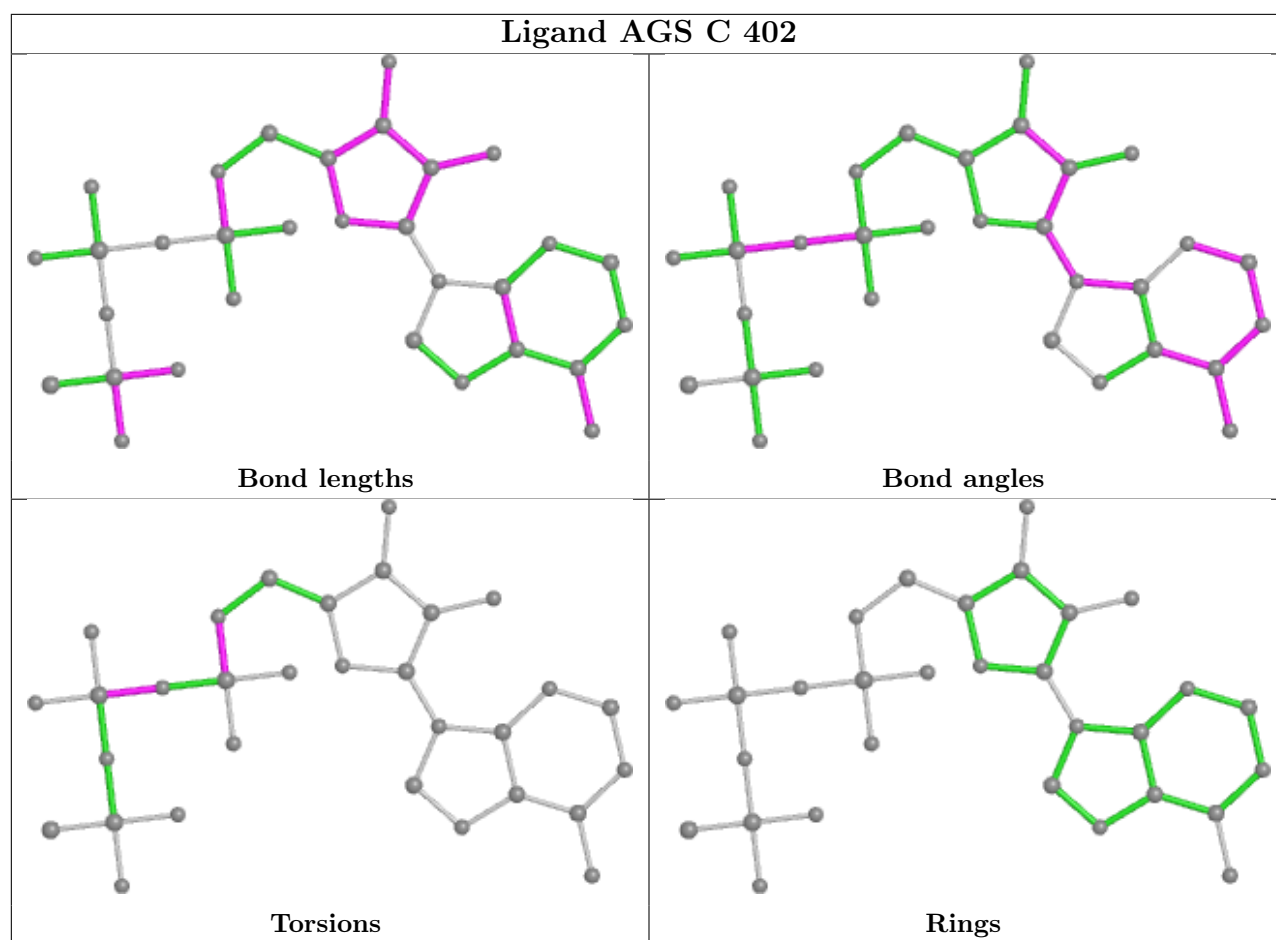
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





Ligand AGS B 403





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.

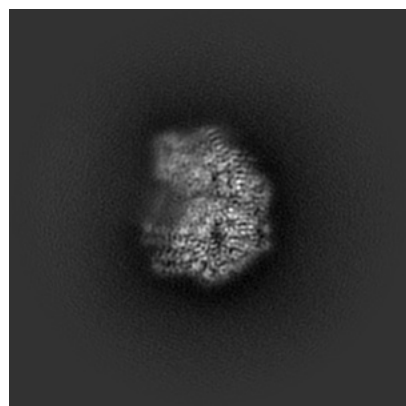
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27673. These allow visual inspection of the internal detail of the map and identification of artifacts.

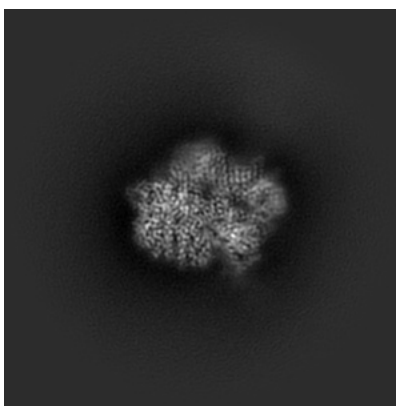
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

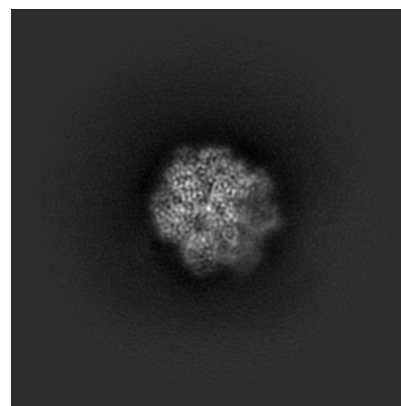
6.1.1 Primary map



X

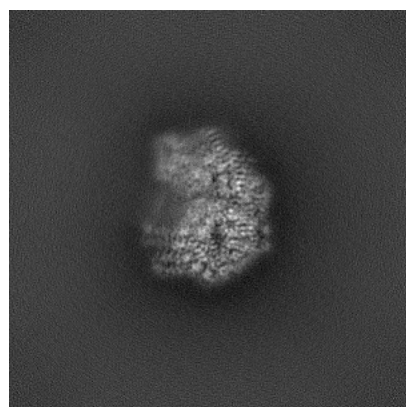


Y

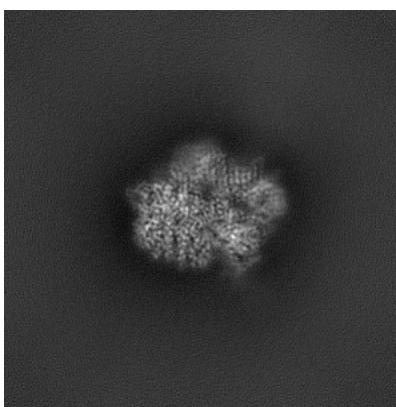


Z

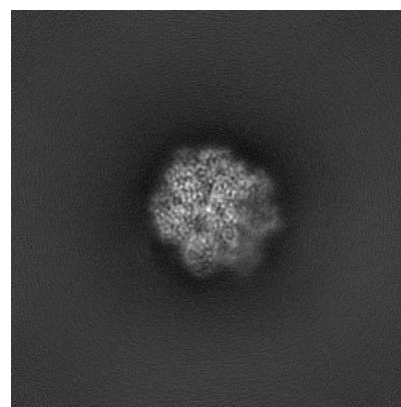
6.1.2 Raw map



X



Y

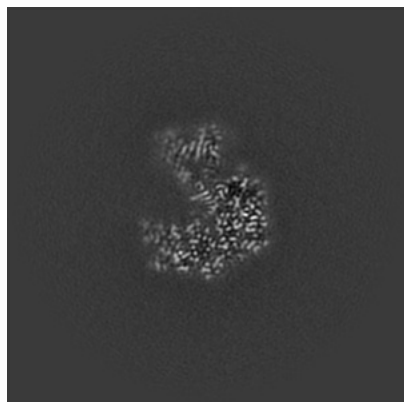


Z

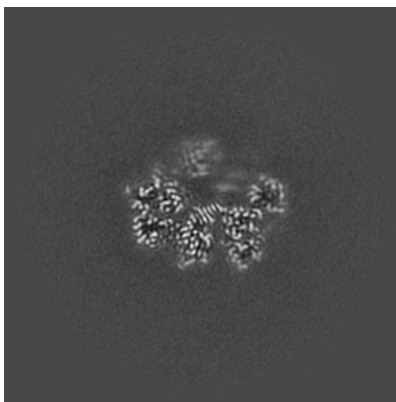
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

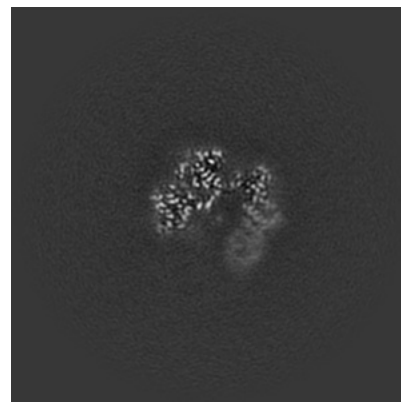
6.2.1 Primary map



X Index: 192

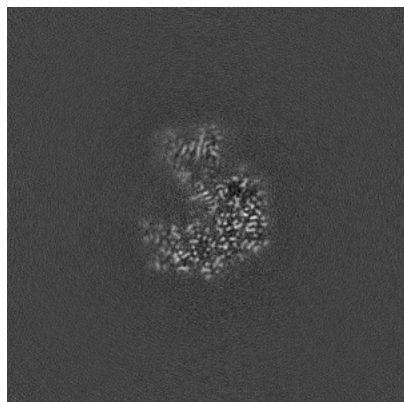


Y Index: 192

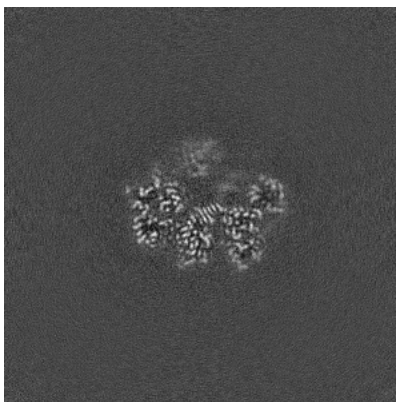


Z Index: 192

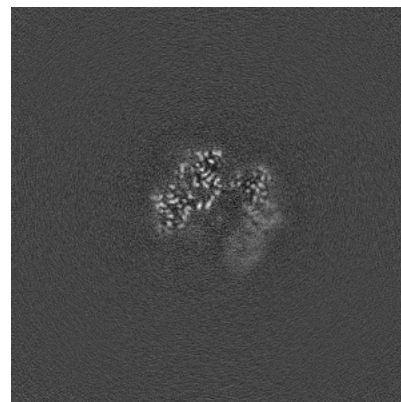
6.2.2 Raw map



X Index: 192



Y Index: 192

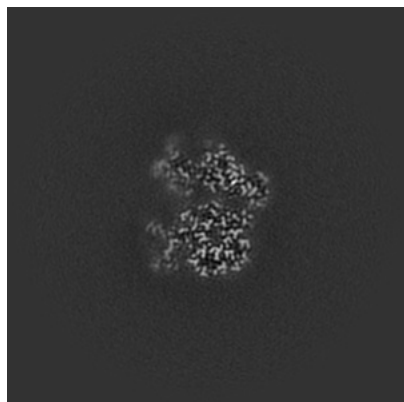


Z Index: 192

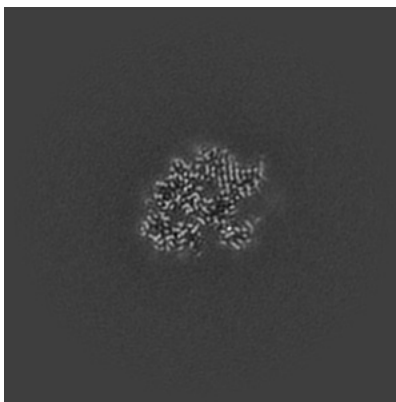
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

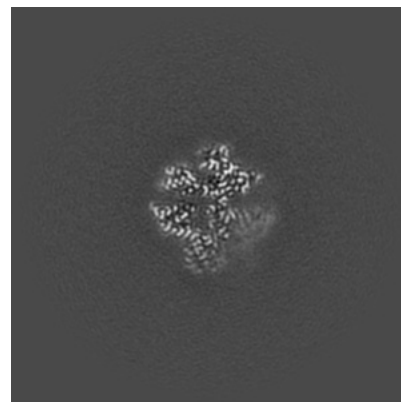
6.3.1 Primary map



X Index: 170

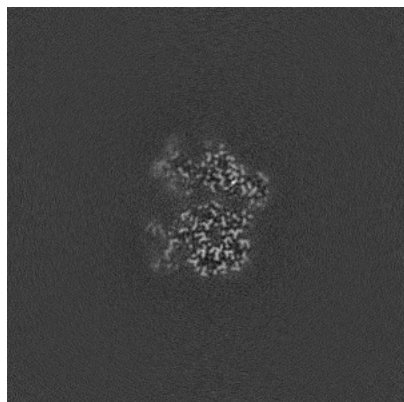


Y Index: 218

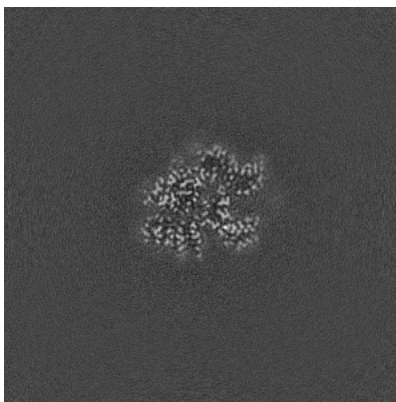


Z Index: 169

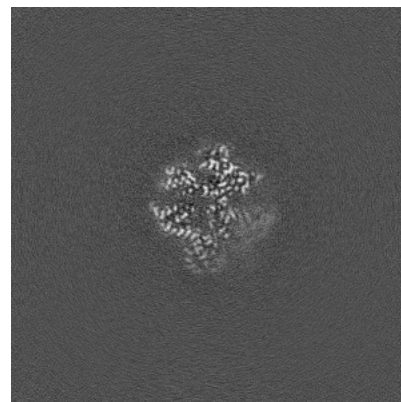
6.3.2 Raw map



X Index: 170



Y Index: 215

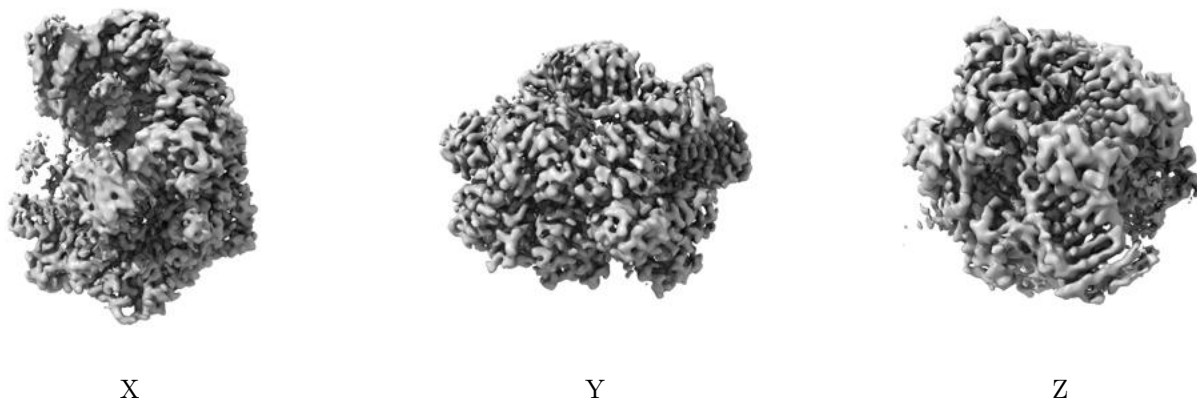


Z Index: 169

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

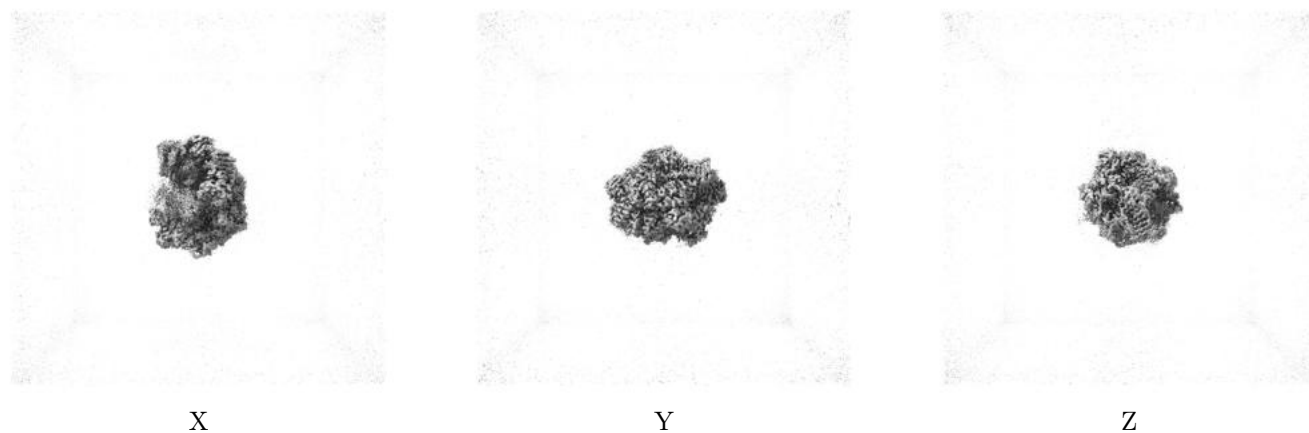
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

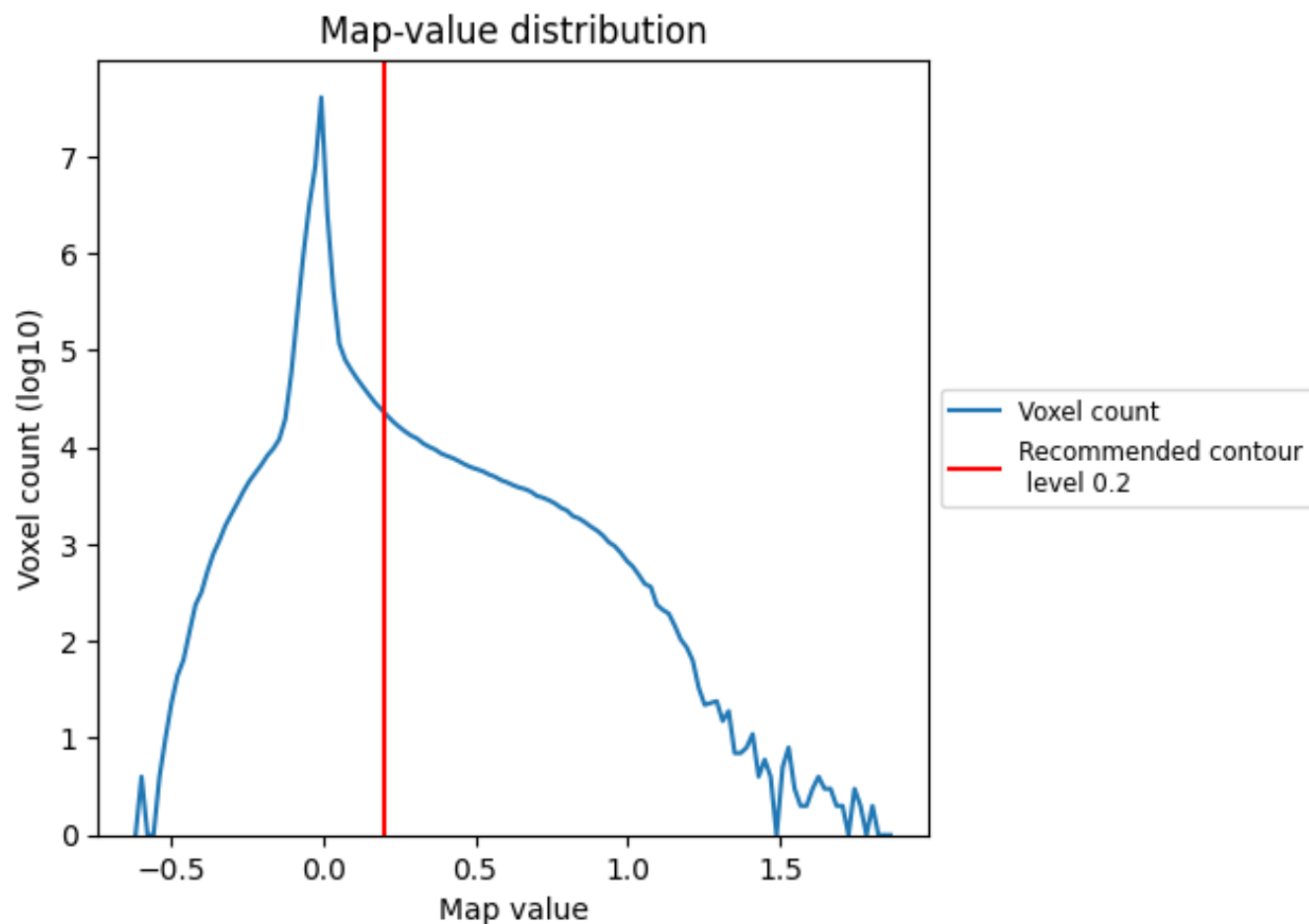
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

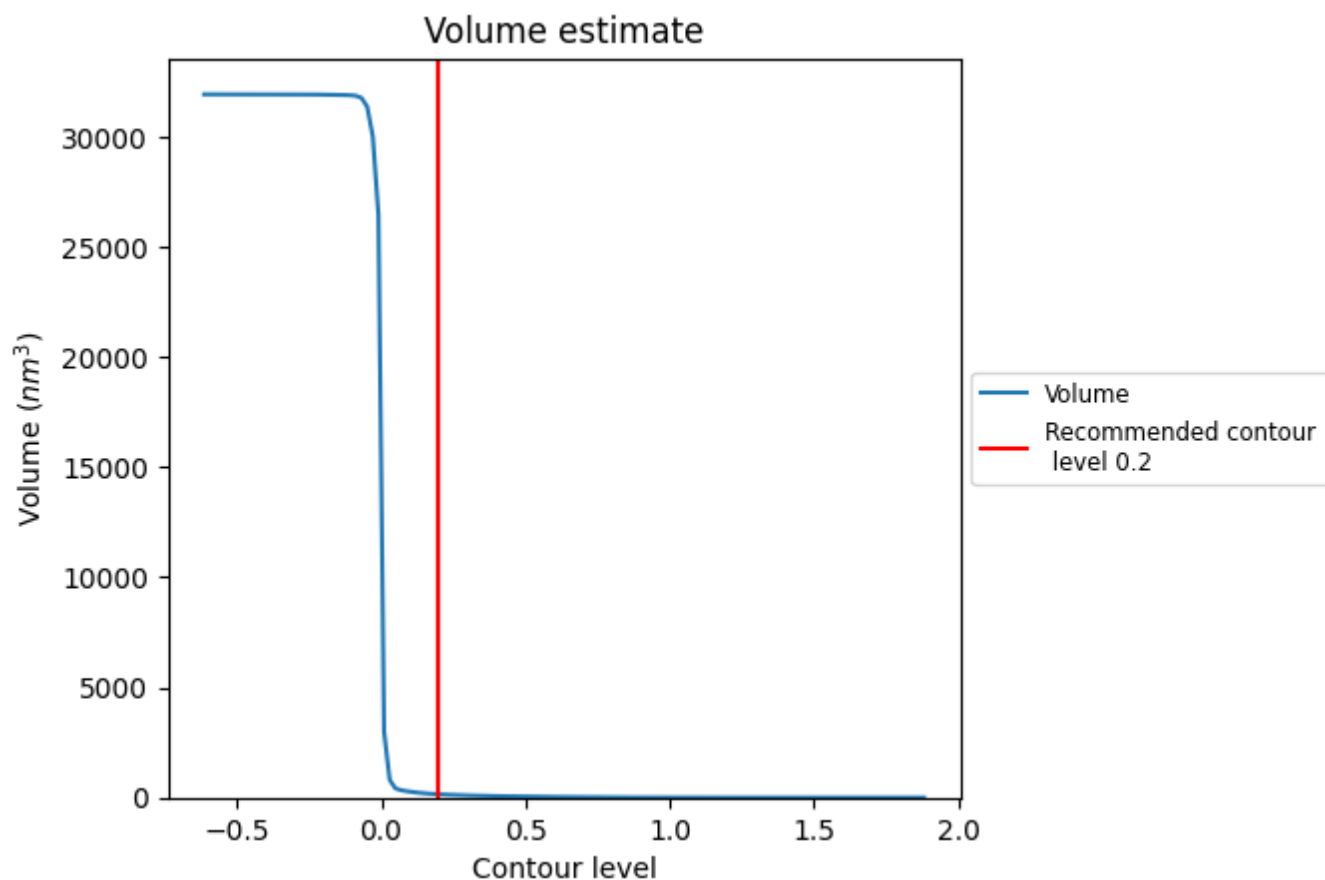
This section contains the results of statistical analysis of the map.

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.

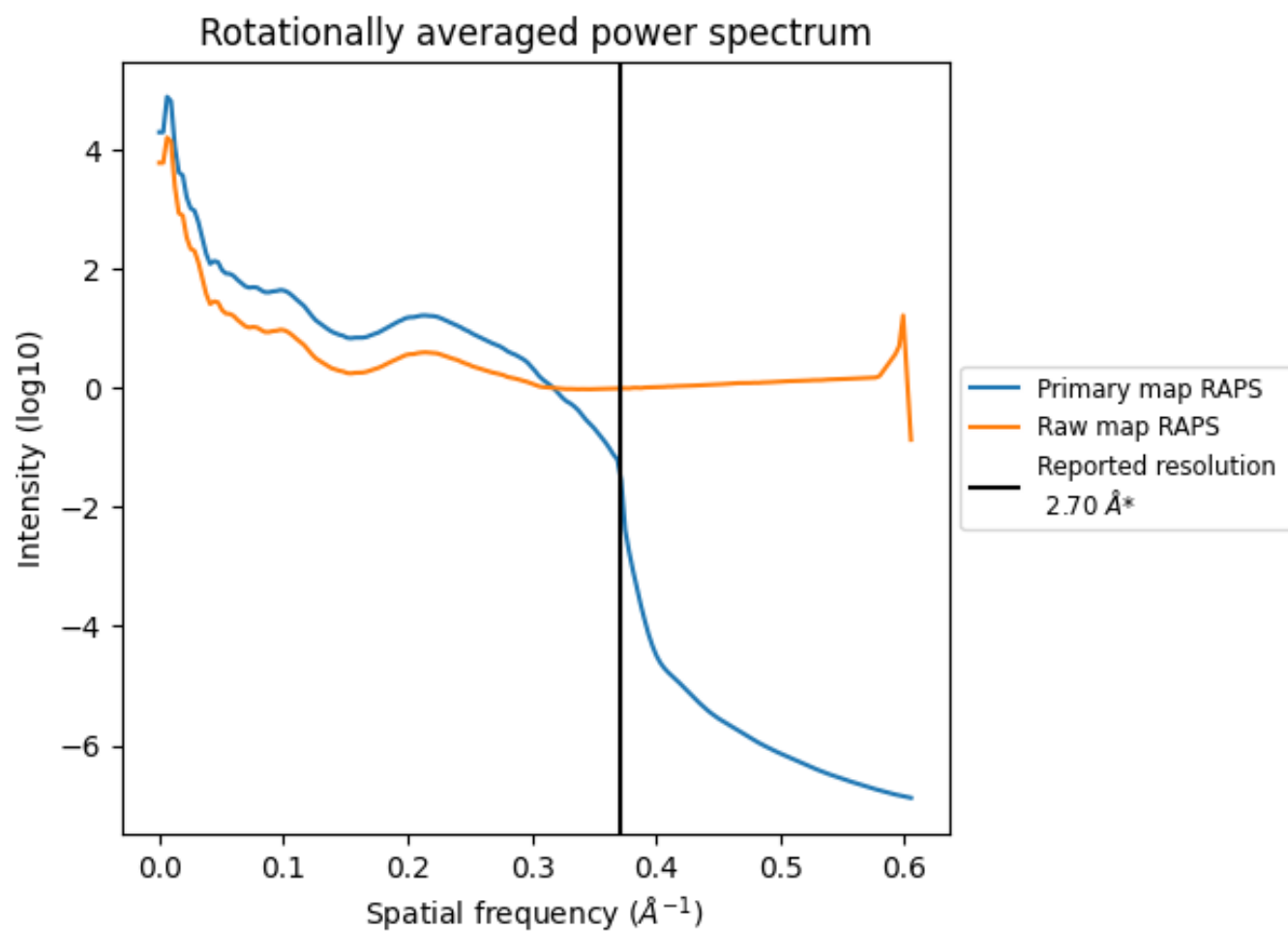
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 148 nm^3 ; this corresponds to an approximate mass of 134 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 ⓘ

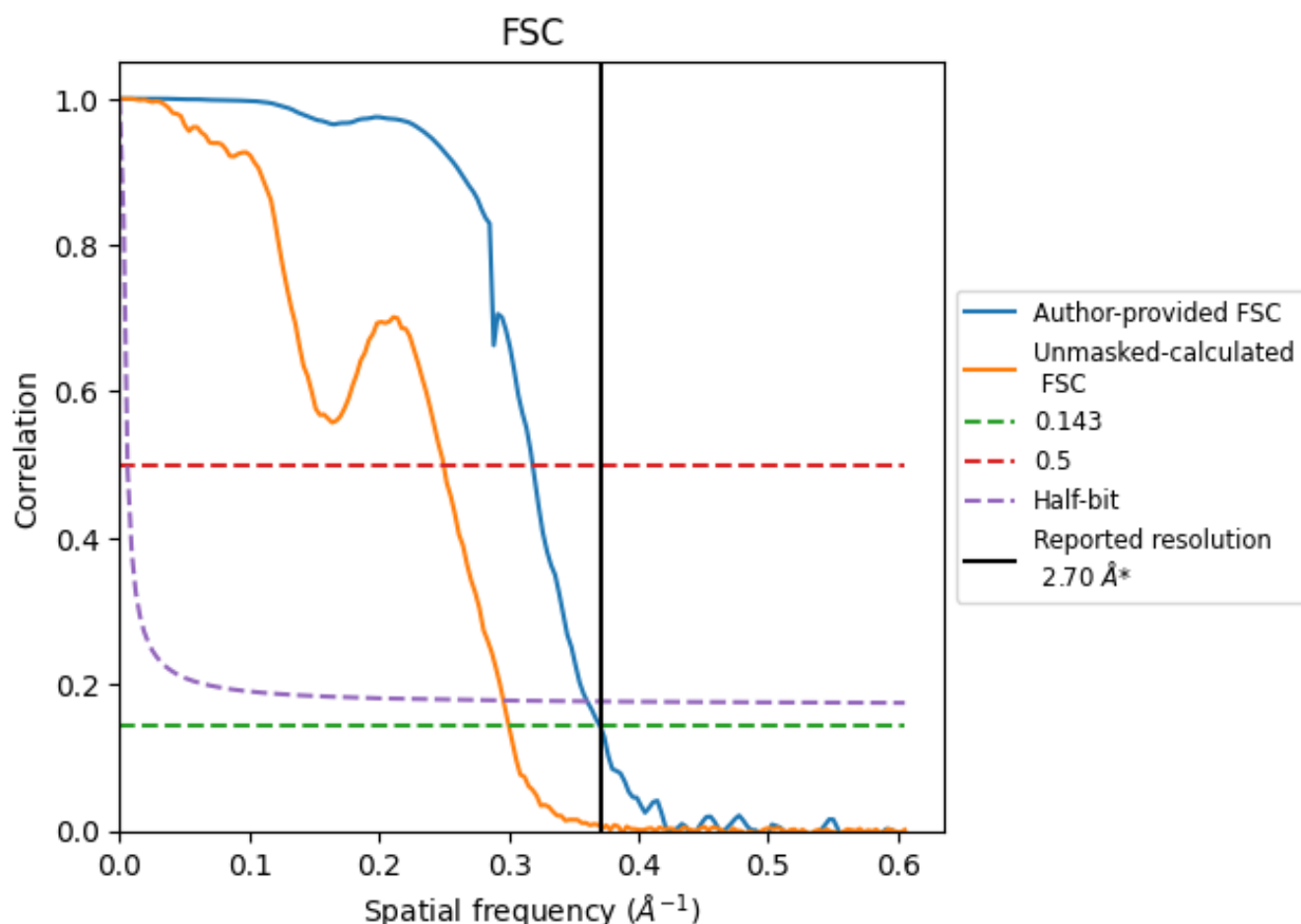


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 \AA^{-1}

8.2 Resolution estimates [i](#)

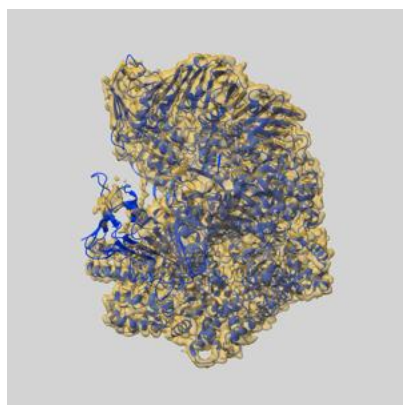
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	3.14	2.77
Unmasked-calculated*	3.33	4.00	3.38

*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 3.33 differs from the reported value 2.7 by more than 10 %

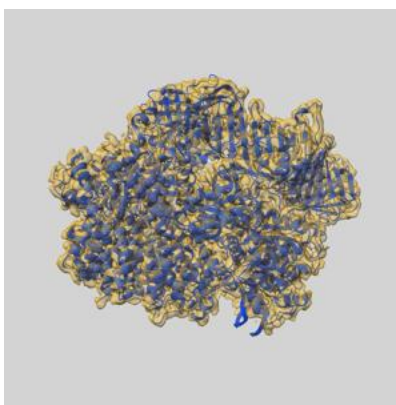
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27673 and PDB model 8DR7. Per-residue inclusion information can be found in section [3](#) on page [10](#).

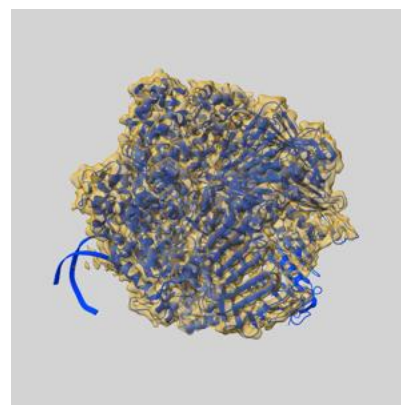
9.1 Map-model overlay [i](#)



X



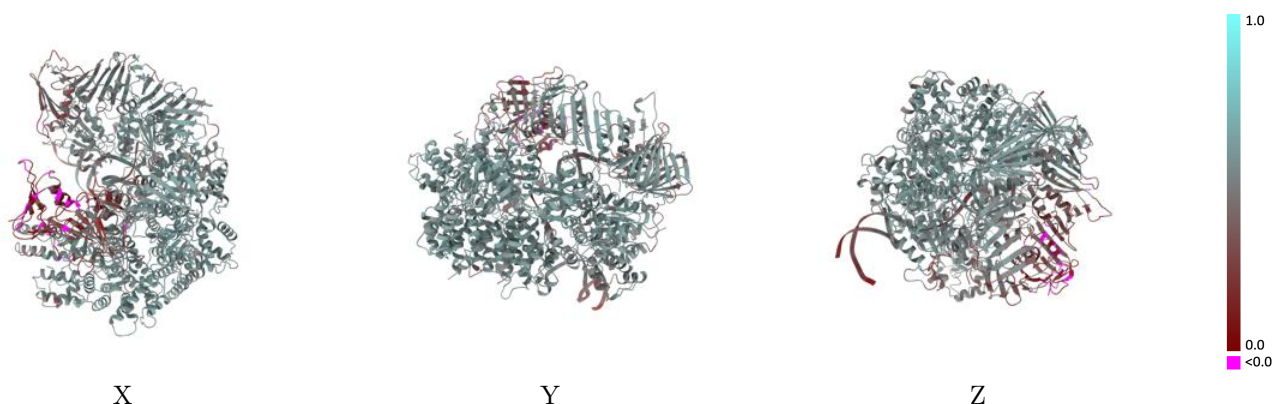
Y



Z

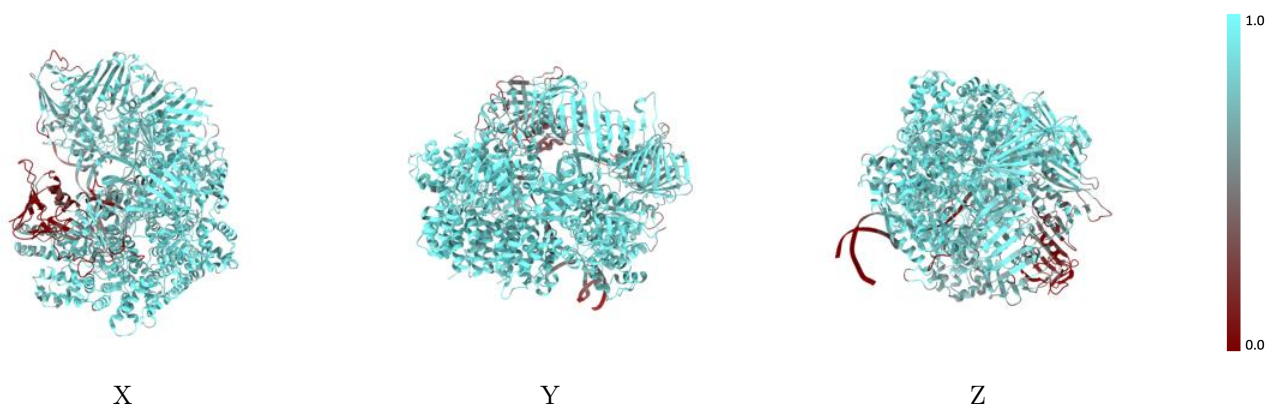
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



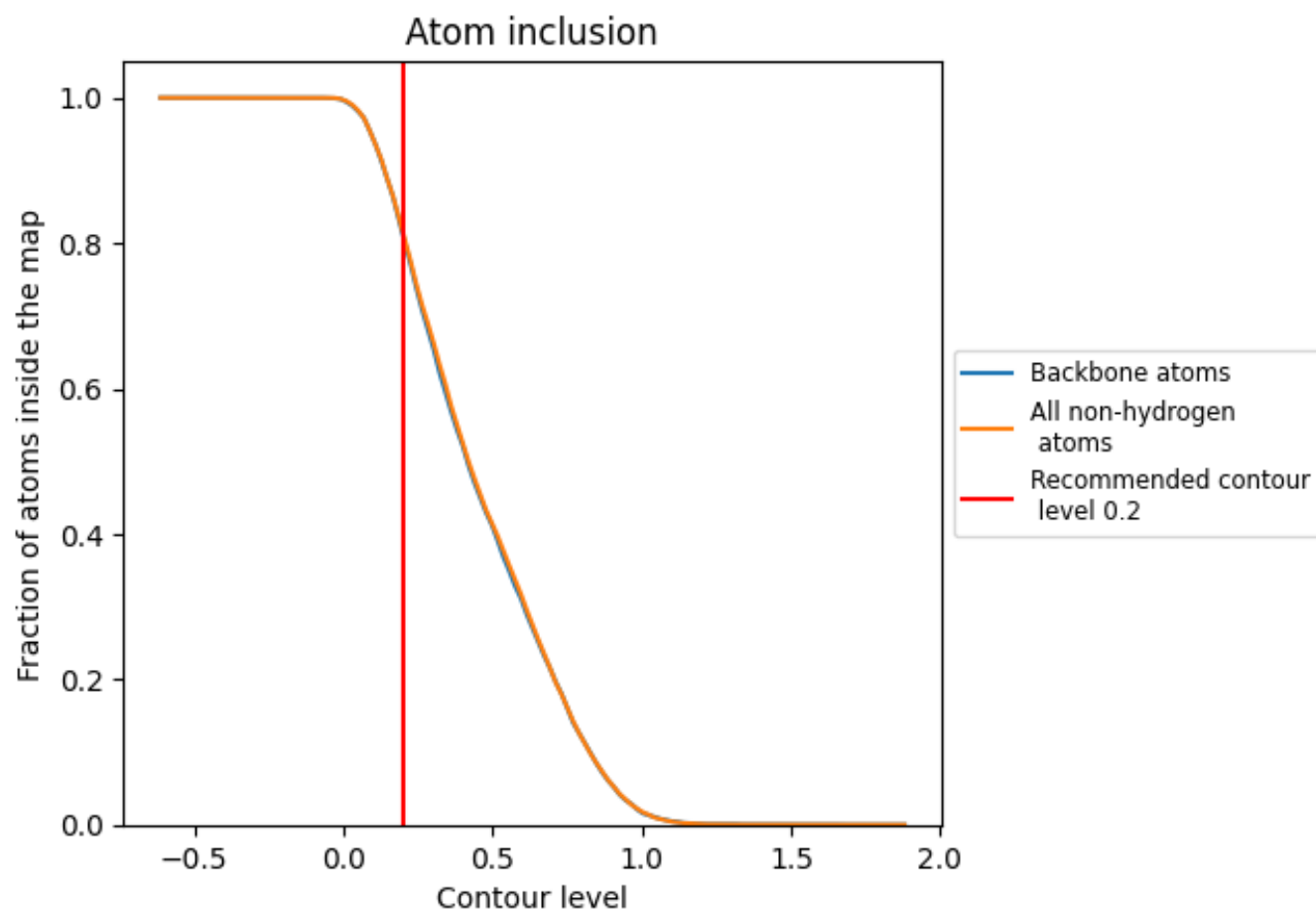
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8134	<div></div> 0.5050
A	<div></div> 0.8330	<div></div> 0.5210
B	<div></div> 0.9252	<div></div> 0.5620
C	<div></div> 0.9258	<div></div> 0.5730
D	<div></div> 0.9437	<div></div> 0.5810
E	<div></div> 0.8940	<div></div> 0.5510
F	<div></div> 0.8601	<div></div> 0.5220
G	<div></div> 0.7511	<div></div> 0.4540
H	<div></div> 0.3327	<div></div> 0.2230
I	<div></div> 0.5528	<div></div> 0.4170
J	<div></div> 0.8292	<div></div> 0.5020
K	<div></div> 0.3320	<div></div> 0.3940

1.0
0.0
<0.0