



## wwPDB EM Validation Summary Report ⓘ

Jul 24, 2025 – 05:25 PM EDT

PDB ID : 9C9S / pdb\_00009c9s  
EMDB ID : EMD-45369  
Title : S.c INO80 in complex with S.c 0/40 nucleosome, Class 1  
Authors : Wu, H.; Kaur, U.; Narlikar, G.J.; Cheng, Y.F.  
Deposited on : 2024-06-15  
Resolution : 3.09 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

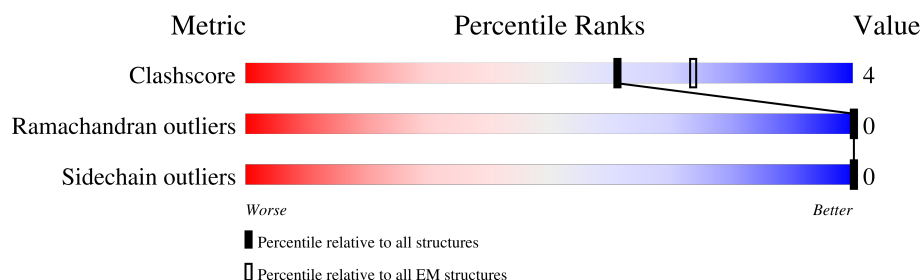
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.09 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.











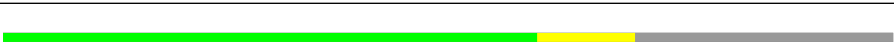

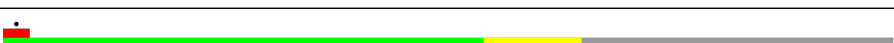

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	Q	1489	
2	R	755	
3	S	166	
4	T	463	
4	V	463	
4	X	463	
5	U	471	
5	W	471	

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Mol	Chain	Length	Quality of chain
5	Y	471	
6	Z	320	
7	A	136	
7	E	136	
8	B	103	
8	F	103	
9	C	132	
9	G	132	
10	D	131	
10	H	131	
11	I	227	
12	J	227	

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 43163 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 Chromatin-remodeling ATPase INO80.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Q	660	Total	C	N	O	S	0	0
			5277	3372	905	977	23		

- Molecule 2 is a protein called Actin-related protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	550	Total	C	N	O	S	0	0
			4067	2566	705	785	11		

- Molecule 3 is a protein called Chromatin-remodeling complex subunit IES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	125	Total	C	N	O	S	0	0
			1014	647	189	176	2		

- Molecule 4 is a protein called RuvB-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	435	Total	C	N	O	S	0	0
			3339	2107	575	647	10		
4	V	442	Total	C	N	O	S	0	0
			3397	2144	584	659	10		
4	X	443	Total	C	N	O	S	0	0
			3404	2149	585	660	10		

- Molecule 5 is a protein called RuvB-like protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	U	445	Total	C	N	O	S	0	0
			3421	2138	594	677	12		
5	W	442	Total	C	N	O	S	0	0
			3394	2120	589	673	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Y	436	Total	C	N	O	S	0	0
			3350	2098	583	658	11		

- Molecule 6 is a protein called Ino eighty subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Z	52	Total	C	N	O	S	0	0
			367	229	69	67	2		

- Molecule 7 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	97	Total	C	N	O		0	0
			801	508	155	138			
7	E	97	Total	C	N	O		0	0
			801	508	155	138			

- Molecule 8 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	79	Total	C	N	O	S	0	0
			624	392	121	110	1		
8	F	79	Total	C	N	O	S	0	0
			620	389	120	110	1		

- Molecule 9 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	106	Total	C	N	O		0	0
			819	514	161	144			
9	G	108	Total	C	N	O		0	0
			827	517	164	146			

- Molecule 10 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	93	Total	C	N	O	S	0	0
			726	456	127	142	1		
10	H	93	Total	C	N	O	S	0	0
			726	456	127	142	1		

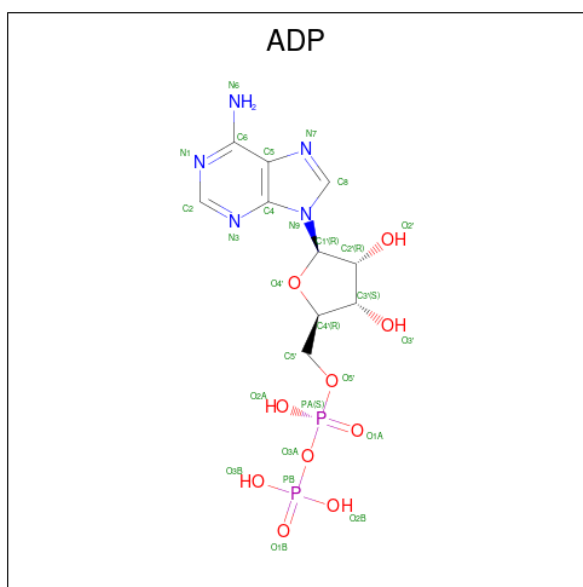
- Molecule 11 is a DNA chain called DNA (227-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	147	Total	C	N	O	P	0	0
			3030	1434	567	882	147		

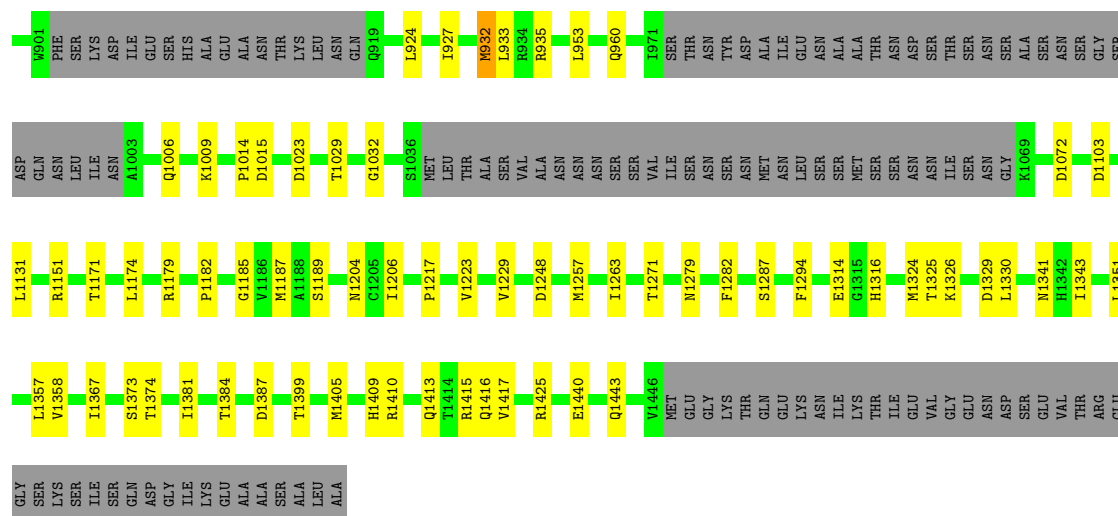
- Molecule 12 is a DNA chain called DNA (227-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	147	Total	C	N	O	P	0	0
			2997	1423	545	882	147		

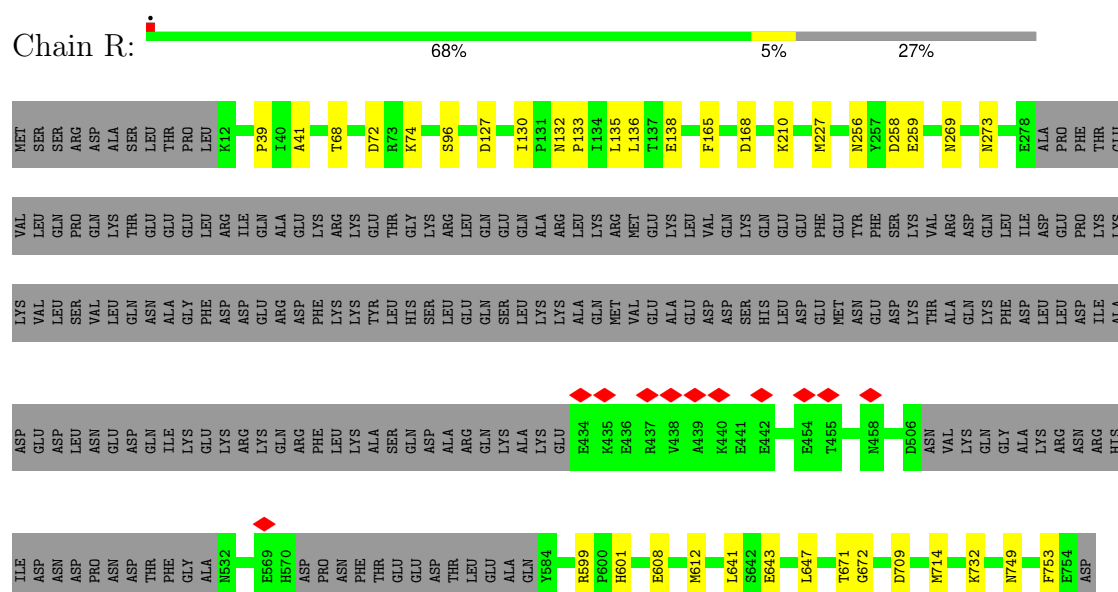
- Molecule 13 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).



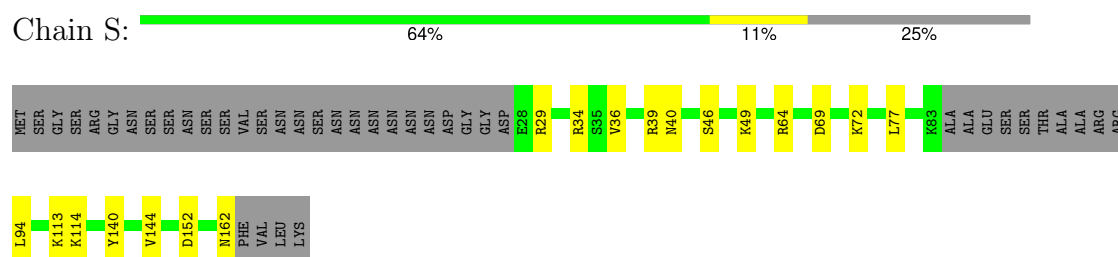




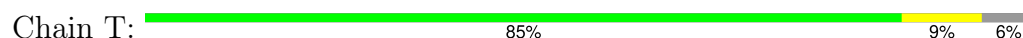
### • Molecule 2: Actin-related protein 5



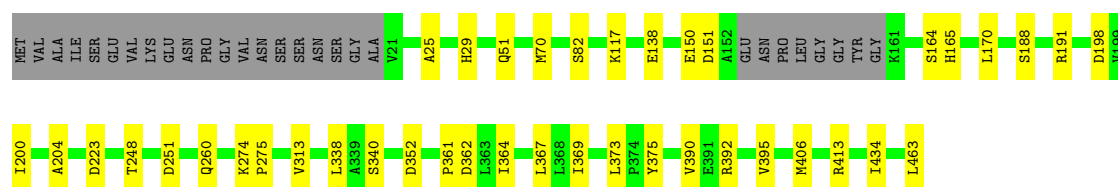
### • Molecule 3: Chromatin-remodeling complex subunit IES6



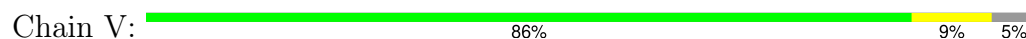
### • Molecule 4: RuvB-like protein 1



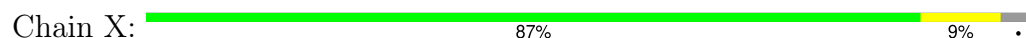




• Molecule 4: RuvB-like protein 1



• Molecule 4: RuvB-like protein 1




• Molecule 5: RuvB-like protein 2

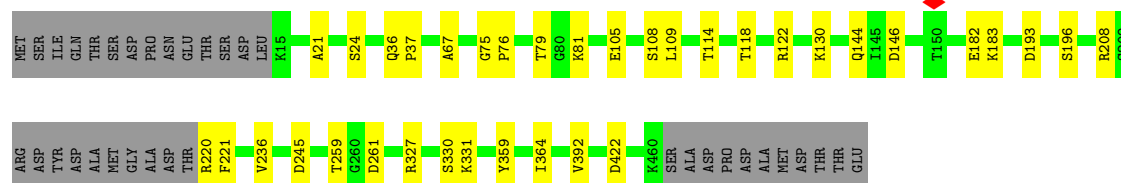


• Molecule 5: RuvB-like protein 2



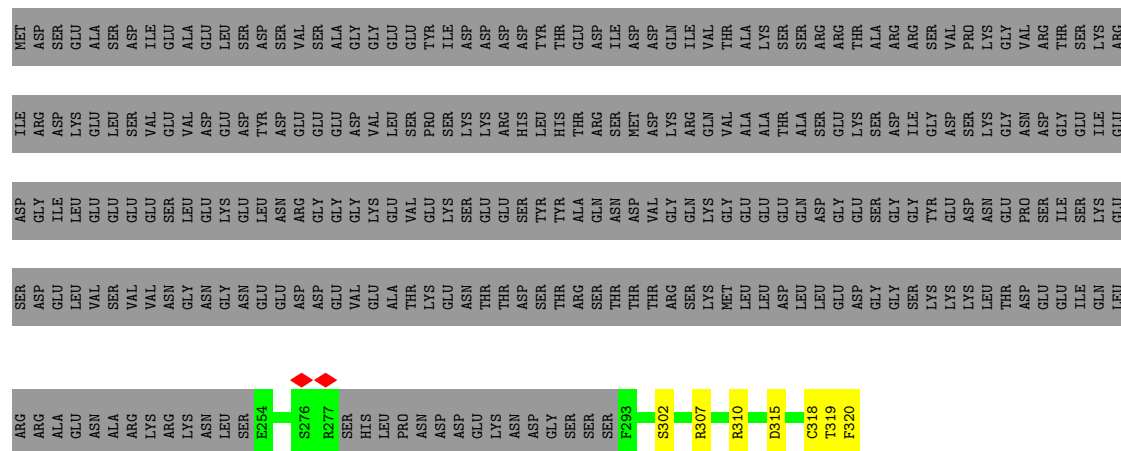
• Molecule 5: RuvB-like protein 2

Chain Y: 



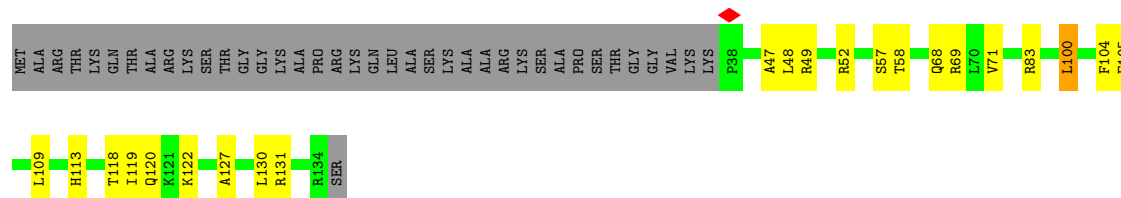
- Molecule 6: Ino eighty subunit 2

Chain Z: 



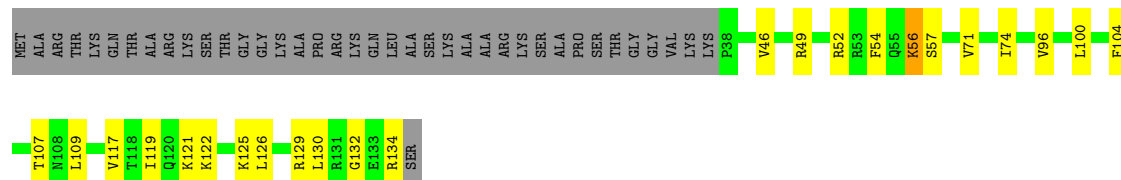
- Molecule 7: Histone H3

Chain A: 



- Molecule 7: Histone H3

Chain E: 

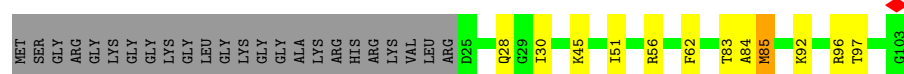


- Molecule 8: Histone H4

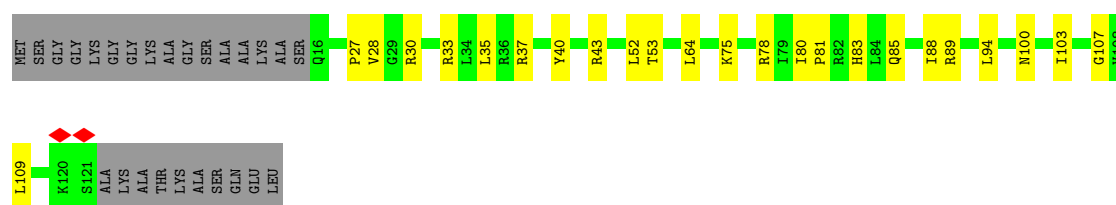
Chain B: 



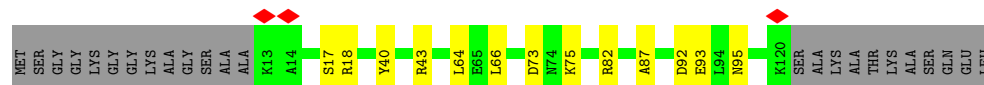
- Molecule 8: Histone H4



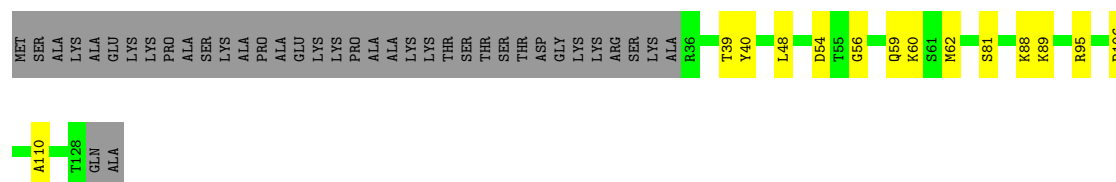
- Molecule 9: Histone H2A



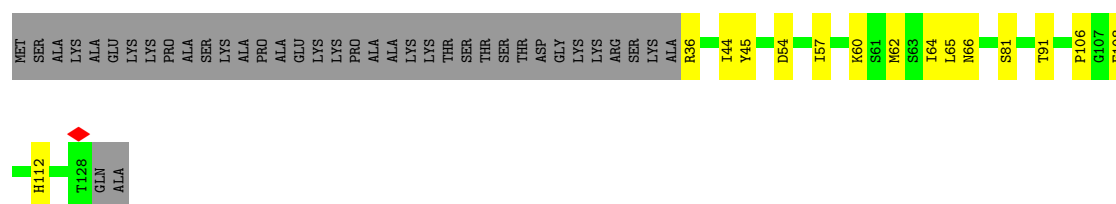
- Molecule 9: Histone H2A



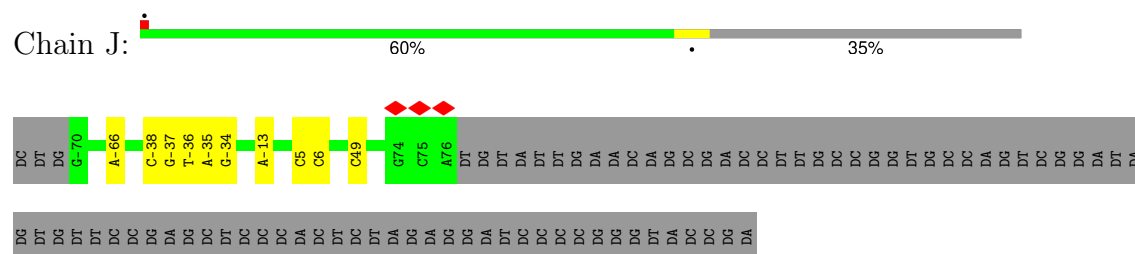
- Molecule 10: Histone H2B



- Molecule 10: Histone H2B



- Molecule 11: DNA (227-MER)



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74790	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 ( $e^-/\text{\AA}^2$ )	45.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.170	Depositor
Minimum map value	-0.357	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.132	Depositor
Map size (Å)	374.08, 374.08, 374.08	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.835, 0.835, 0.835	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	Q	0.21	0/5395	0.48	1/7323 (0.0%)
2	R	0.16	0/4153	0.39	0/5667
3	S	0.20	0/1036	0.49	0/1392
4	T	0.18	0/3378	0.40	0/4569
4	V	0.18	0/3439	0.44	0/4652
4	X	0.19	0/3446	0.44	1/4662 (0.0%)
5	U	0.17	0/3459	0.39	0/4662
5	W	0.18	0/3432	0.40	0/4628
5	Y	0.17	0/3386	0.40	0/4561
6	Z	0.14	0/372	0.29	0/501
7	A	0.29	0/812	0.73	3/1086 (0.3%)
7	E	0.23	0/812	0.61	2/1086 (0.2%)
8	B	0.30	0/631	0.80	0/844
8	F	0.28	0/627	0.78	1/840 (0.1%)
9	C	0.24	0/830	0.61	1/1121 (0.1%)
9	G	0.28	0/838	0.68	0/1131
10	D	0.28	0/736	0.75	1/991 (0.1%)
10	H	0.29	0/736	0.76	0/991
11	I	0.21	0/3402	0.46	0/5253
12	J	0.19	0/3358	0.41	0/5176
All	All	0.20	0/44278	0.47	10/61136 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
8	F	0	1

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	105	GLU	CA-CB-CG	7.13	128.36	114.10
7	E	56	LYS	CA-CB-CG	6.26	126.62	114.10
7	A	105	GLU	N-CA-CB	6.02	120.22	110.40
8	F	85	MET	CB-CG-SD	5.91	130.43	112.70
10	D	88	LYS	CA-CB-CG	5.63	125.35	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	F	96	ARG	Sidechain

## 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	Q	5277	0	5172	64	0
2	R	4067	0	3636	24	0
3	S	1014	0	1050	14	0
4	T	3339	0	3468	30	0
4	V	3397	0	3533	40	0
4	X	3404	0	3542	24	0
5	U	3421	0	3499	31	0
5	W	3394	0	3459	17	0
5	Y	3350	0	3444	26	0
6	Z	367	0	293	4	0
7	A	801	0	851	16	0
7	E	801	0	851	18	0
8	B	624	0	654	12	0
8	F	620	0	643	9	0
9	C	819	0	865	16	0
9	G	827	0	865	9	0
10	D	726	0	748	10	0
10	H	726	0	748	11	0
11	I	3030	0	1650	18	0
12	J	2997	0	1650	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	T	27	0	12	2	0
13	U	27	0	12	0	0
13	V	27	0	12	2	0
13	W	27	0	12	2	0
13	X	27	0	12	0	0
13	Y	27	0	12	2	0
All	All	43163	0	40693	343	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 4.

The worst 5 of 343 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)
5:U:352:ILE:CG2	4:V:446:PHE:HB3	1.79	1.13
5:U:352:ILE:HG21	4:V:446:PHE:HB3	1.58	0.84
1:Q:760:VAL:HG22	1:Q:839:ILE:HB	1.79	0.65
1:Q:1174:LEU:HD23	1:Q:1187:MET:HE1	1.79	0.64
5:W:212:TYR:HB2	5:W:215:MET:HE1	1.80	0.64

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	Q	652/1489 (44%)	618 (95%)	34 (5%)	0	100	100
2	R	542/755 (72%)	531 (98%)	11 (2%)	0	100	100
3	S	121/166 (73%)	116 (96%)	5 (4%)	0	100	100
4	T	431/463 (93%)	418 (97%)	13 (3%)	0	100	100
4	V	440/463 (95%)	426 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	X	441/463 (95%)	427 (97%)	14 (3%)	0	100	100
5	U	443/471 (94%)	424 (96%)	19 (4%)	0	100	100
5	W	440/471 (93%)	422 (96%)	18 (4%)	0	100	100
5	Y	432/471 (92%)	412 (95%)	20 (5%)	0	100	100
6	Z	48/320 (15%)	48 (100%)	0	0	100	100
7	A	95/136 (70%)	93 (98%)	2 (2%)	0	100	100
7	E	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
8	B	77/103 (75%)	73 (95%)	4 (5%)	0	100	100
8	F	77/103 (75%)	73 (95%)	4 (5%)	0	100	100
9	C	104/132 (79%)	99 (95%)	5 (5%)	0	100	100
9	G	106/132 (80%)	103 (97%)	3 (3%)	0	100	100
10	D	91/131 (70%)	91 (100%)	0	0	100	100
10	H	91/131 (70%)	89 (98%)	2 (2%)	0	100	100
All	All	4726/6536 (72%)	4555 (96%)	171 (4%)	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	Q	579/1350 (43%)	579 (100%)	0	100	100
2	R	389/682 (57%)	389 (100%)	0	100	100
3	S	109/142 (77%)	109 (100%)	0	100	100
4	T	367/391 (94%)	367 (100%)	0	100	100
4	V	374/391 (96%)	374 (100%)	0	100	100
4	X	375/391 (96%)	375 (100%)	0	100	100
5	U	378/403 (94%)	378 (100%)	0	100	100
5	W	374/403 (93%)	374 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	Y	371/403 (92%)	371 (100%)	0	100	100
6	Z	27/285 (10%)	27 (100%)	0	100	100
7	A	85/113 (75%)	85 (100%)	0	100	100
7	E	85/113 (75%)	85 (100%)	0	100	100
8	B	63/79 (80%)	63 (100%)	0	100	100
8	F	62/79 (78%)	62 (100%)	0	100	100
9	C	85/99 (86%)	85 (100%)	0	100	100
9	G	84/99 (85%)	84 (100%)	0	100	100
10	D	81/109 (74%)	81 (100%)	0	100	100
10	H	81/109 (74%)	81 (100%)	0	100	100
All	All	3969/5641 (70%)	3969 (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 36 such sidechains are listed below:

Mol	Chain	Res	Type
5	Y	408	GLN
10	H	70	ASN
5	Y	453	ASN
9	C	74	ASN
2	R	132	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
13	ADP	W	1001	-	24,29,29	0.94	1 (4%)	29,45,45	1.29	3 (10%)
13	ADP	X	1001	-	24,29,29	0.87	0	29,45,45	1.20	2 (6%)
13	ADP	U	1001	-	24,29,29	0.85	0	29,45,45	1.23	2 (6%)
13	ADP	T	1001	-	24,29,29	0.87	0	29,45,45	1.24	2 (6%)
13	ADP	Y	1001	-	24,29,29	0.86	0	29,45,45	1.21	2 (6%)
13	ADP	V	1001	-	24,29,29	0.84	0	29,45,45	1.21	2 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	ADP	W	1001	-	-	3/12/32/32	0/3/3/3
13	ADP	X	1001	-	-	0/12/32/32	0/3/3/3
13	ADP	U	1001	-	-	3/12/32/32	0/3/3/3
13	ADP	T	1001	-	-	1/12/32/32	0/3/3/3
13	ADP	Y	1001	-	-	3/12/32/32	0/3/3/3
13	ADP	V	1001	-	-	4/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	W	1001	ADP	PA-O3A	2.14	1.61	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	U	1001	ADP	N3-C2-N1	-3.73	123.61	128.67

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	T	1001	ADP	N3-C2-N1	-3.69	123.67	128.67
13	V	1001	ADP	N3-C2-N1	-3.66	123.71	128.67
13	X	1001	ADP	N3-C2-N1	-3.59	123.80	128.67
13	Y	1001	ADP	N3-C2-N1	-3.55	123.85	128.67

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

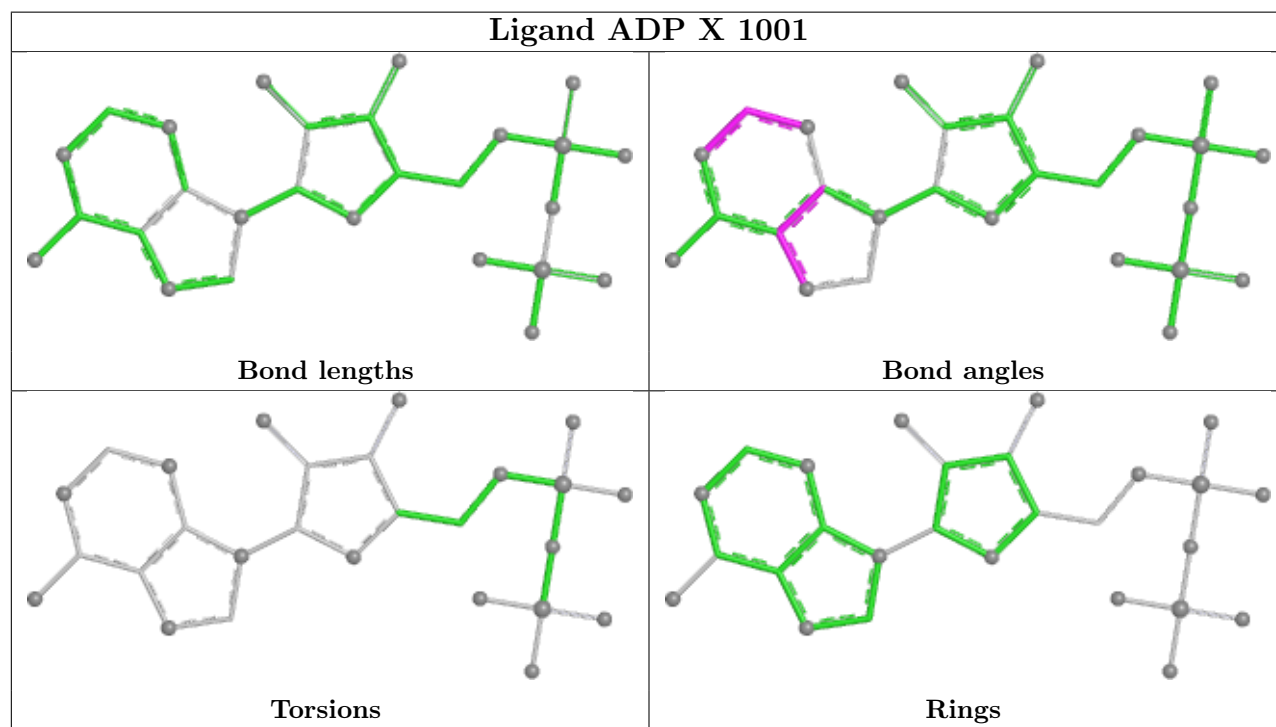
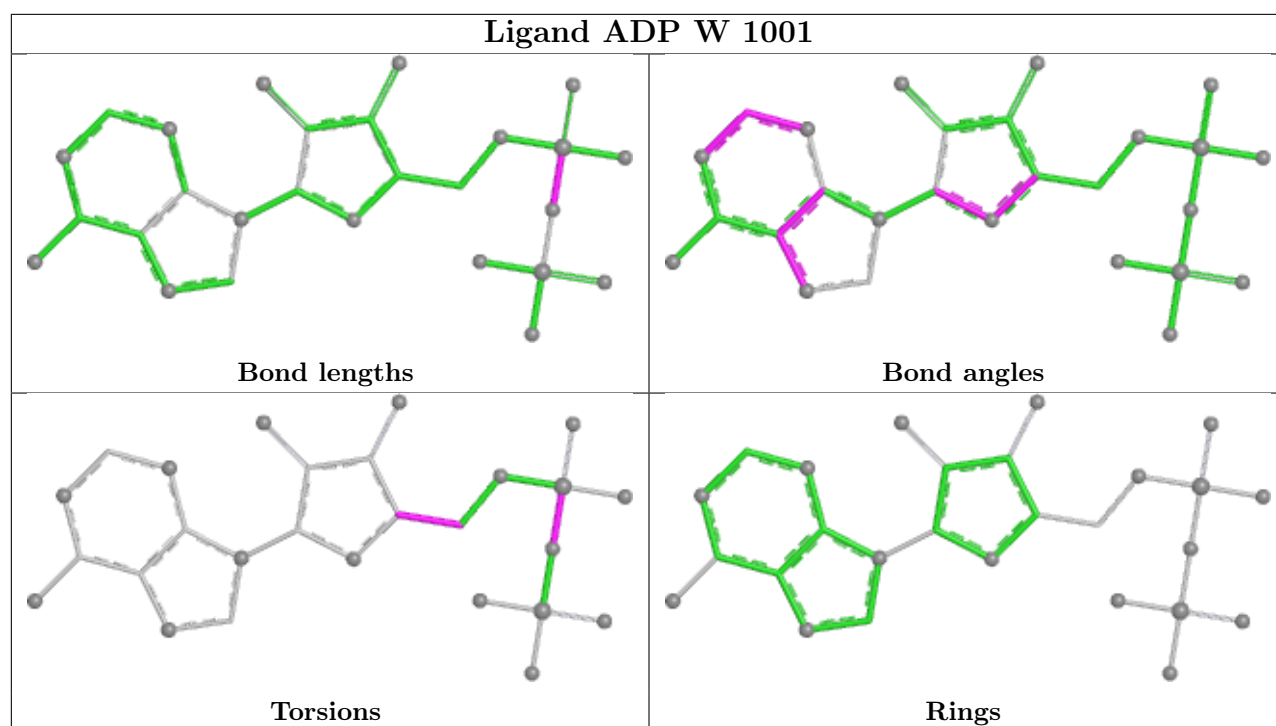
Mol	Chain	Res	Type	Atoms
13	U	1001	ADP	C5'-O5'-PA-O1A
13	U	1001	ADP	C5'-O5'-PA-O2A
13	U	1001	ADP	C5'-O5'-PA-O3A
13	V	1001	ADP	C5'-O5'-PA-O1A
13	V	1001	ADP	C5'-O5'-PA-O2A

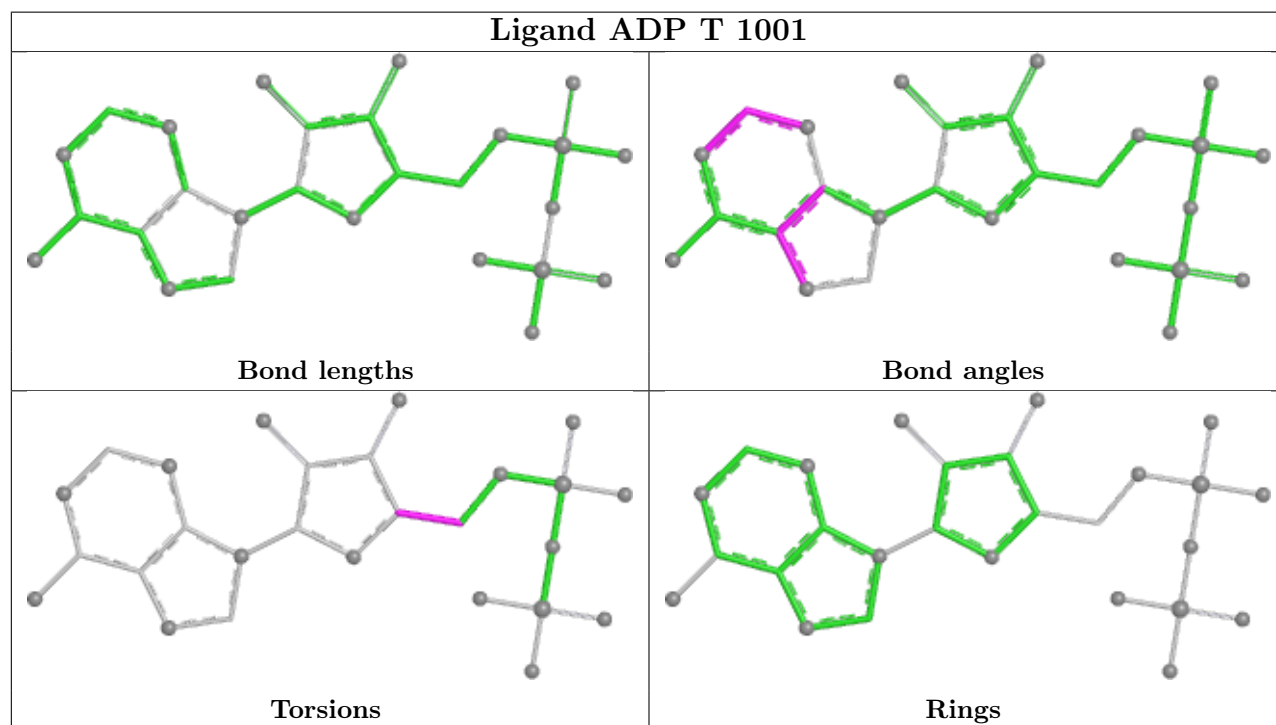
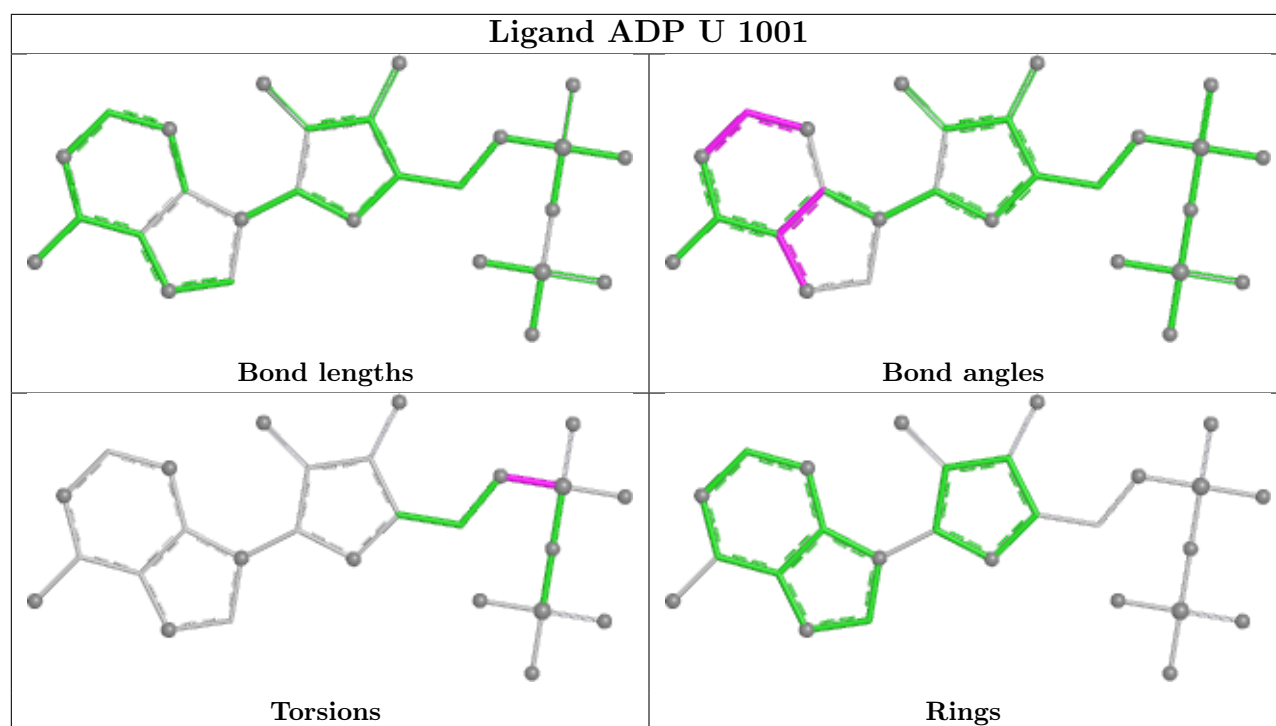
There are no ring outliers.

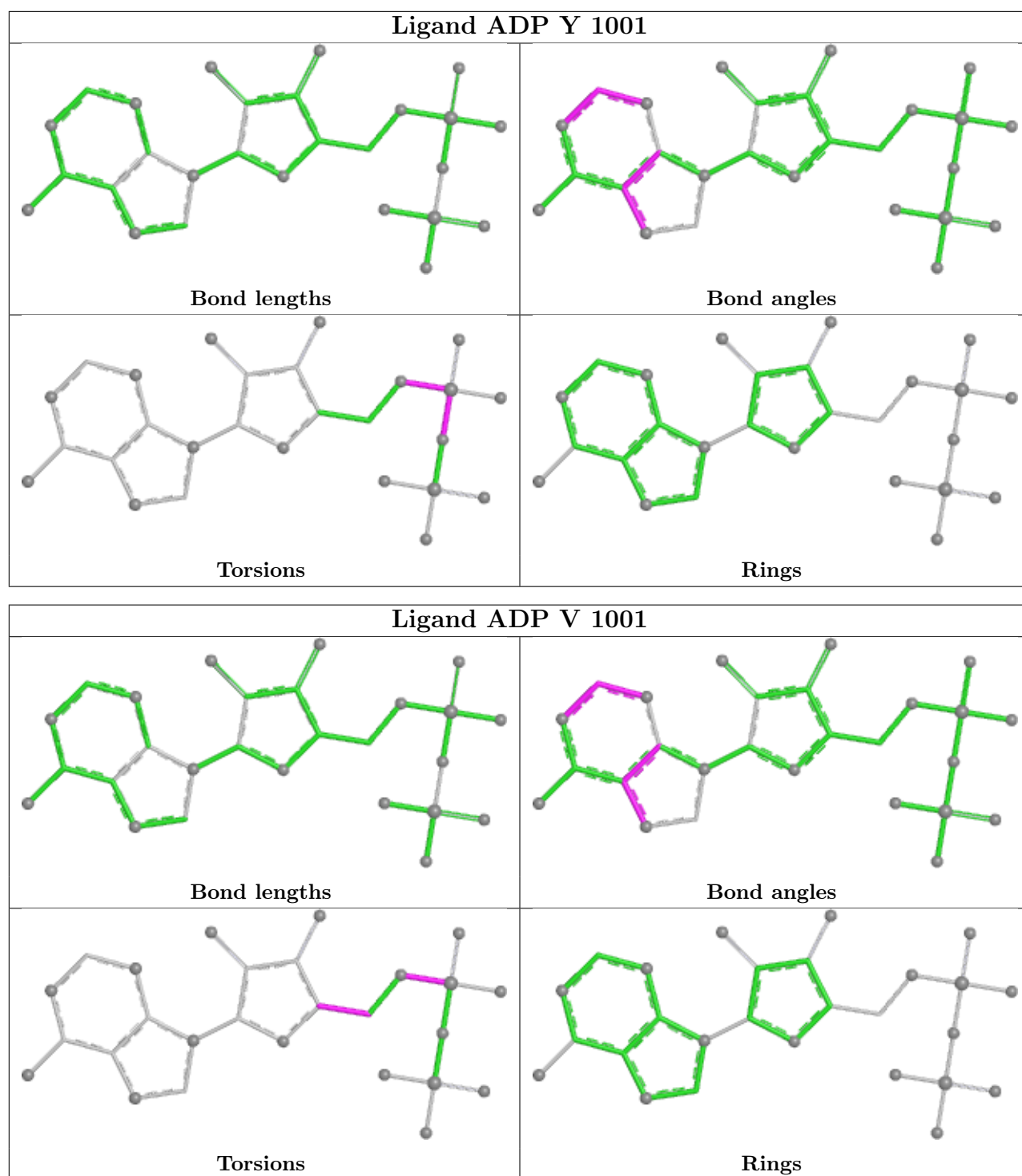
4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	W	1001	ADP	2	0
13	T	1001	ADP	2	0
13	Y	1001	ADP	2	0
13	V	1001	ADP	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.







## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.



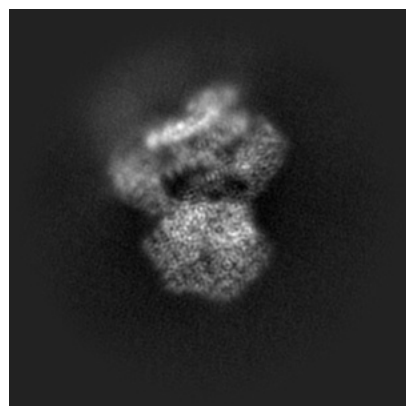
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45369. These allow visual inspection of the internal detail of the map and identification of artifacts.

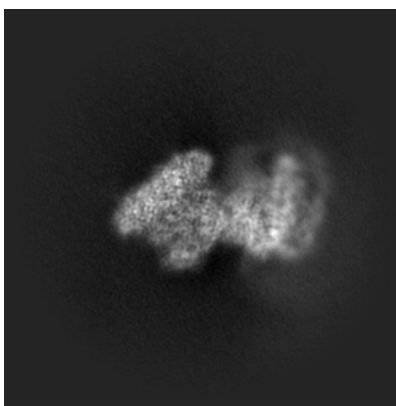
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

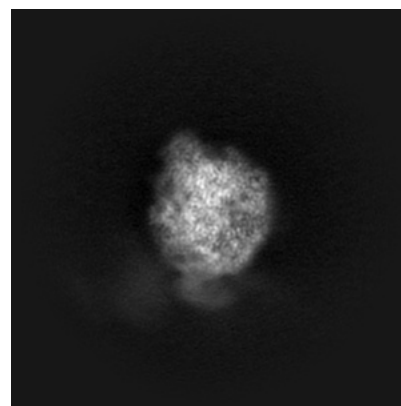
#### 6.1.1 Primary map



X

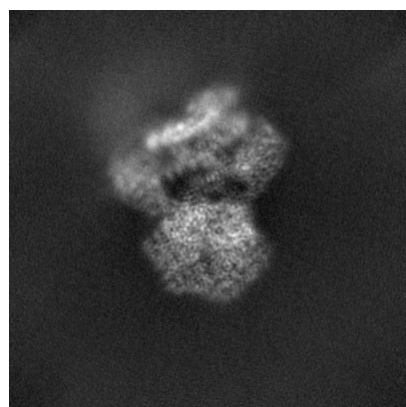


Y

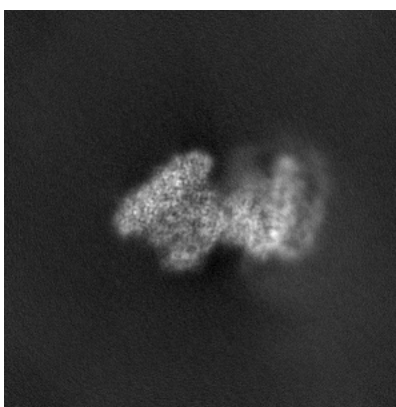


Z

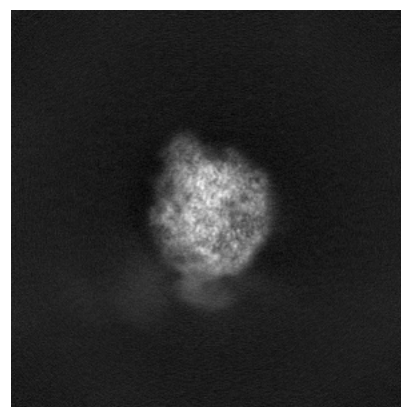
#### 6.1.2 Raw map



X



Y

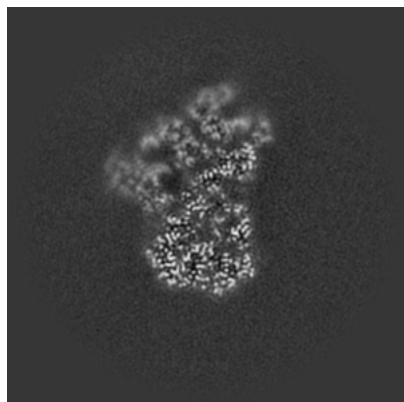


Z

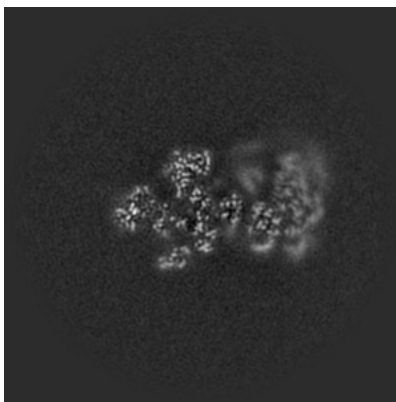
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

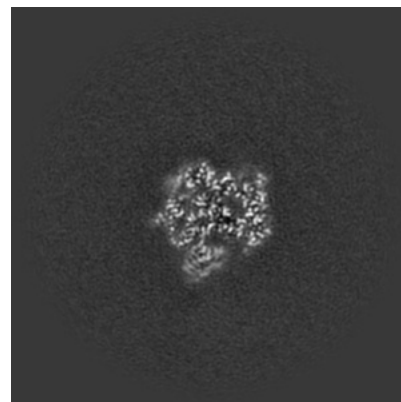
### 6.2.1 Primary map



X Index: 224

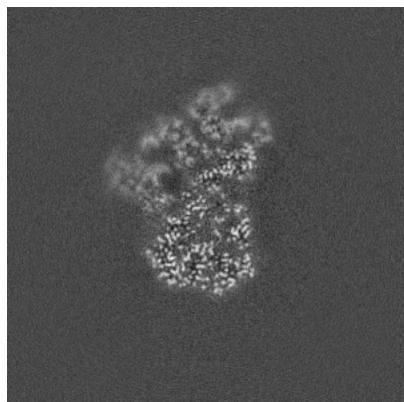


Y Index: 224

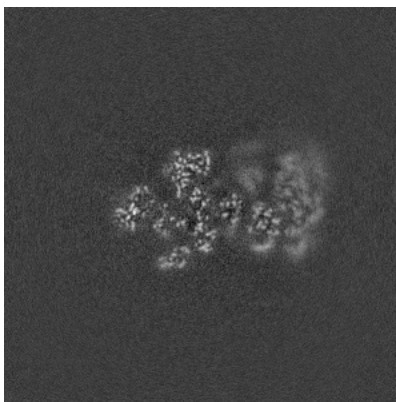


Z Index: 224

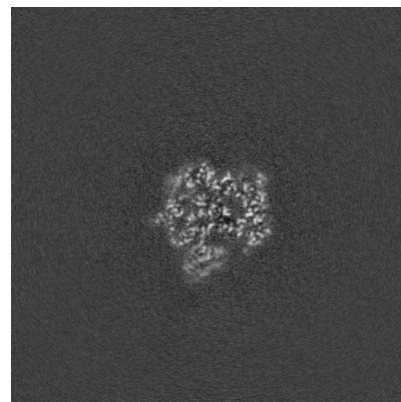
### 6.2.2 Raw map



X Index: 224



Y Index: 224

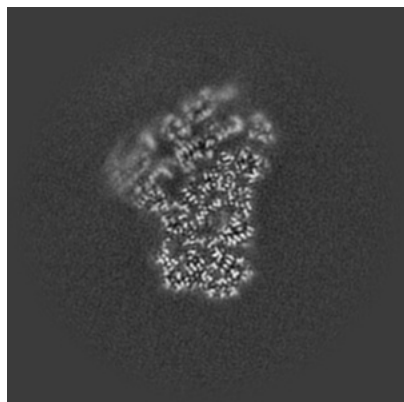


Z Index: 224

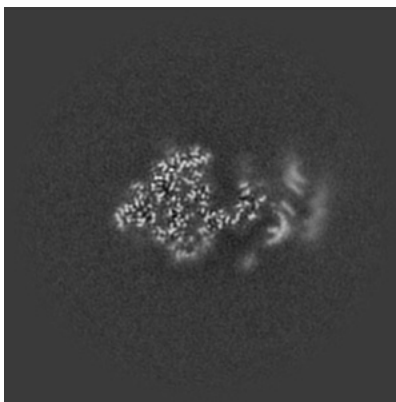
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

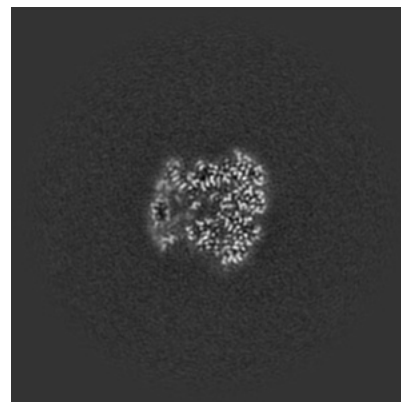
### 6.3.1 Primary map



X Index: 215

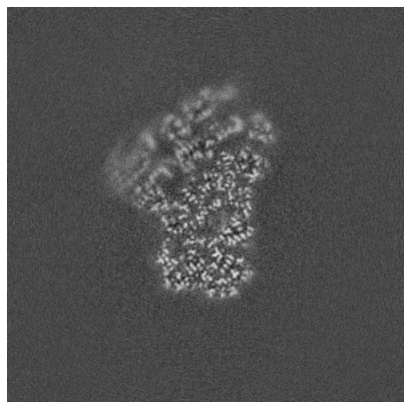


Y Index: 251

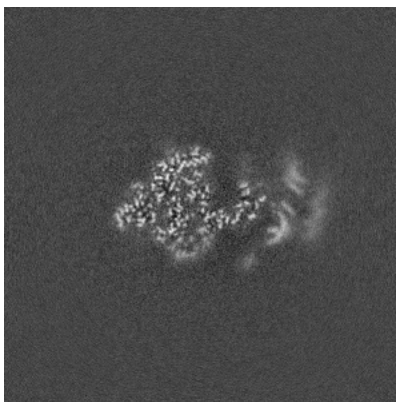


Z Index: 195

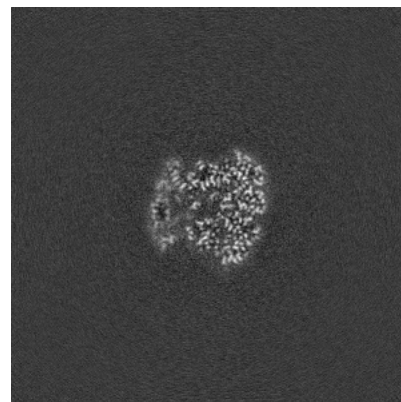
### 6.3.2 Raw map



X Index: 215



Y Index: 251

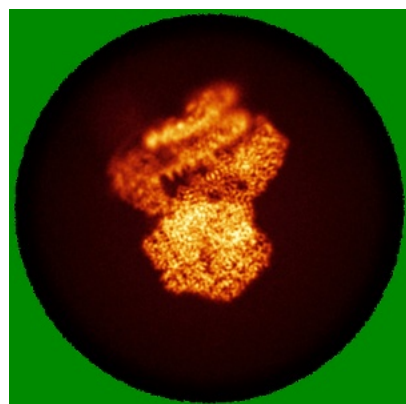


Z Index: 195

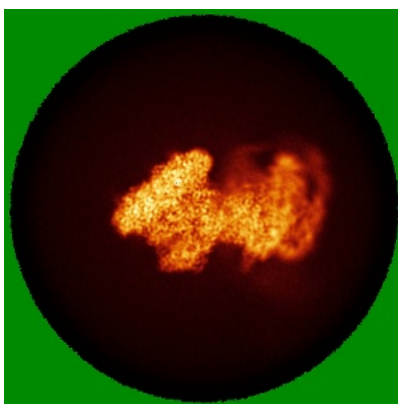
The images above show the largest variance slices of the map in three orthogonal directions.

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

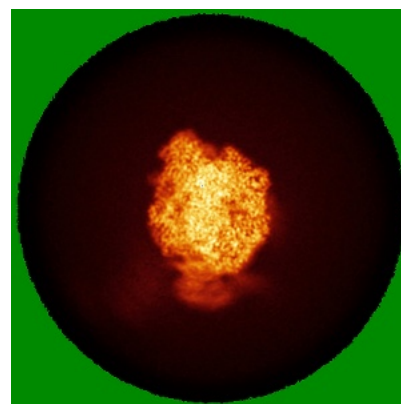
### 6.4.1 Primary map



X

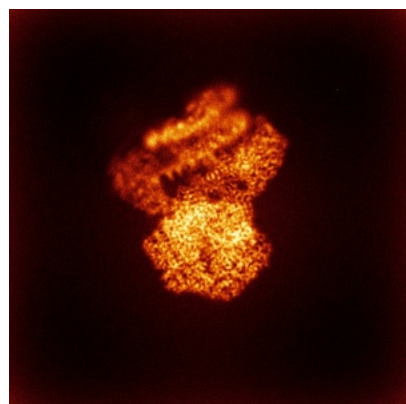


Y

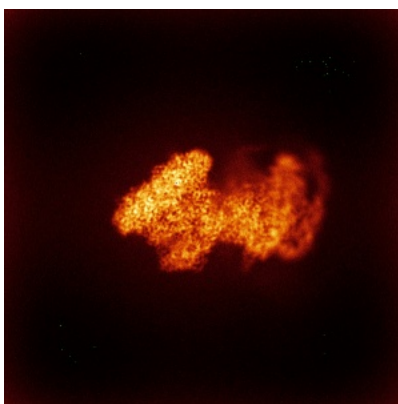


Z

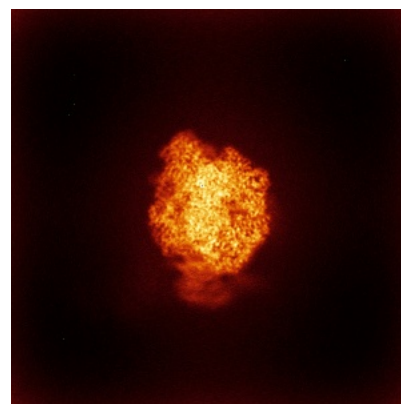
### 6.4.2 Raw map



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



X



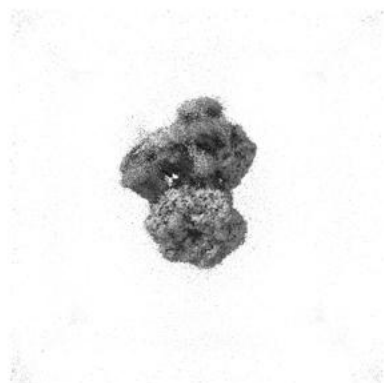
Y



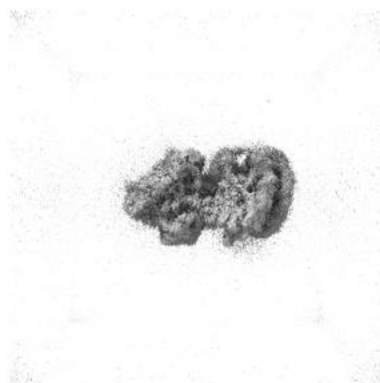
Z

The images above show the 3D surface view of the map at the recommended contour level 0.132. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

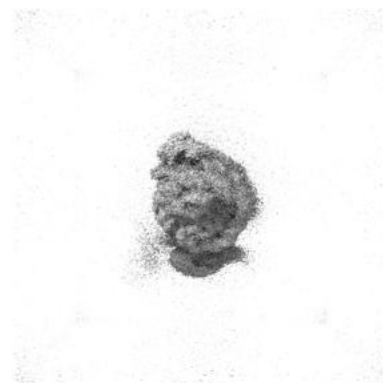
### 6.5.2 Raw map



X



Y



Z

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.

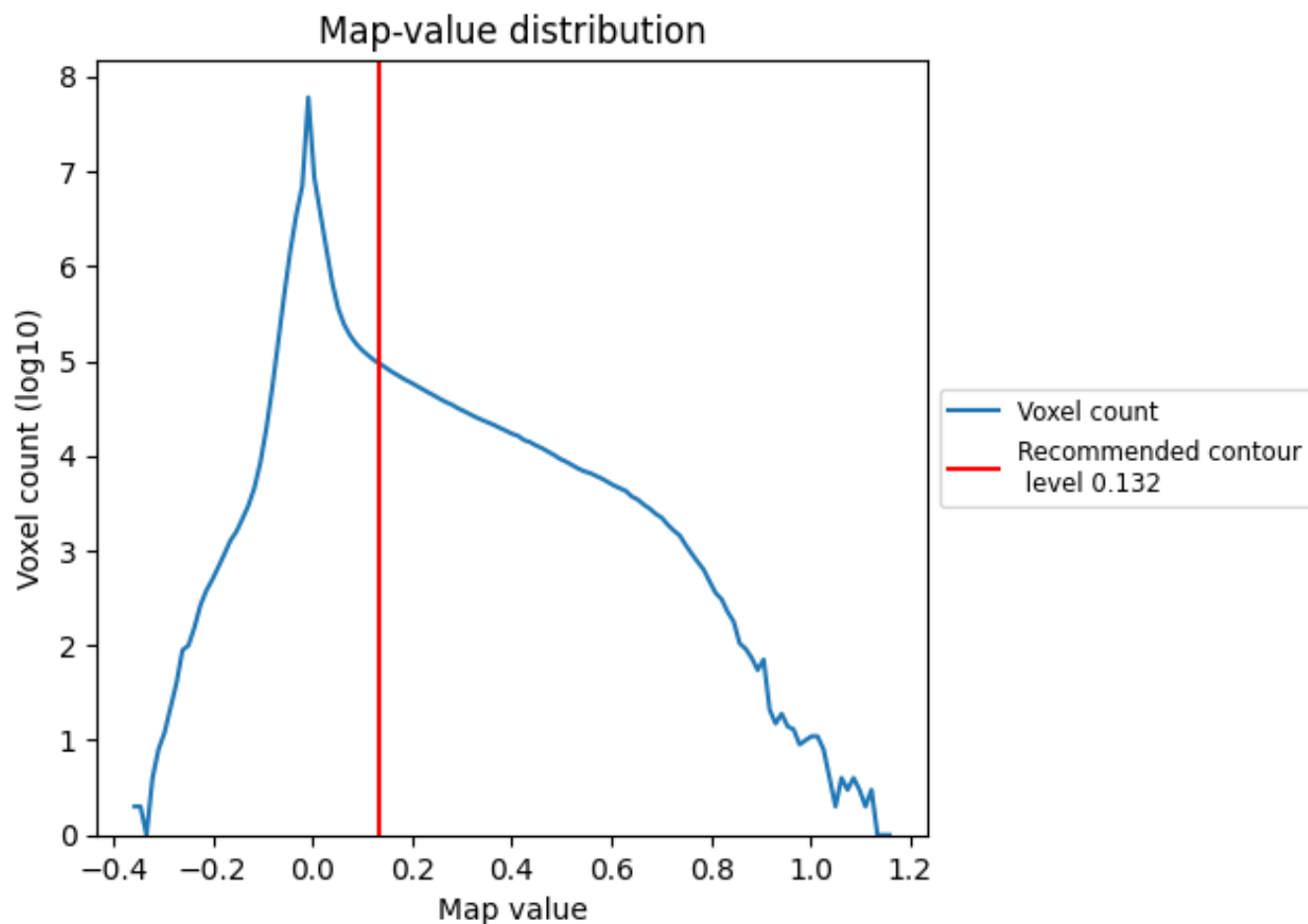
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

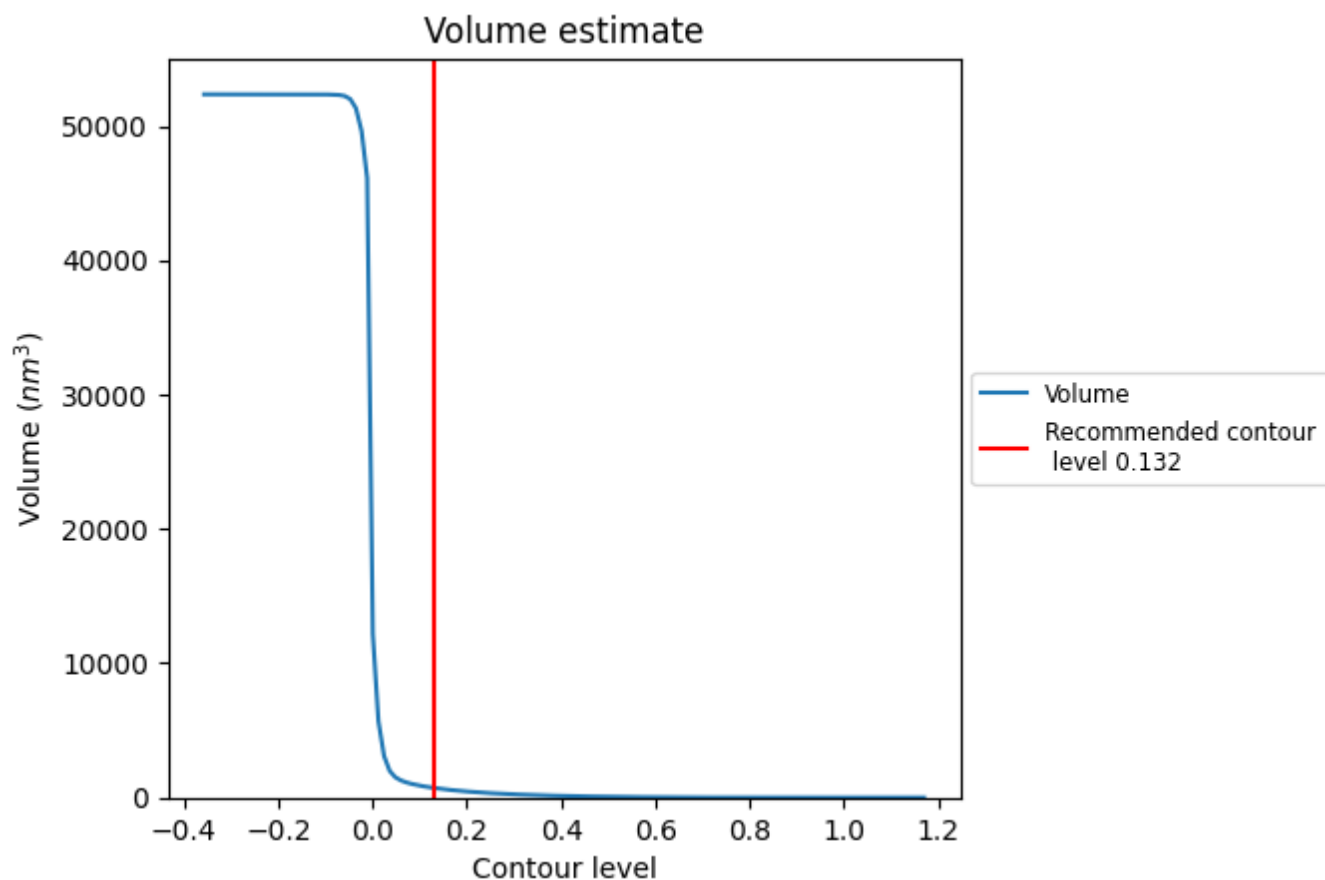
This section contains the results of statistical analysis of the map.

### 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.

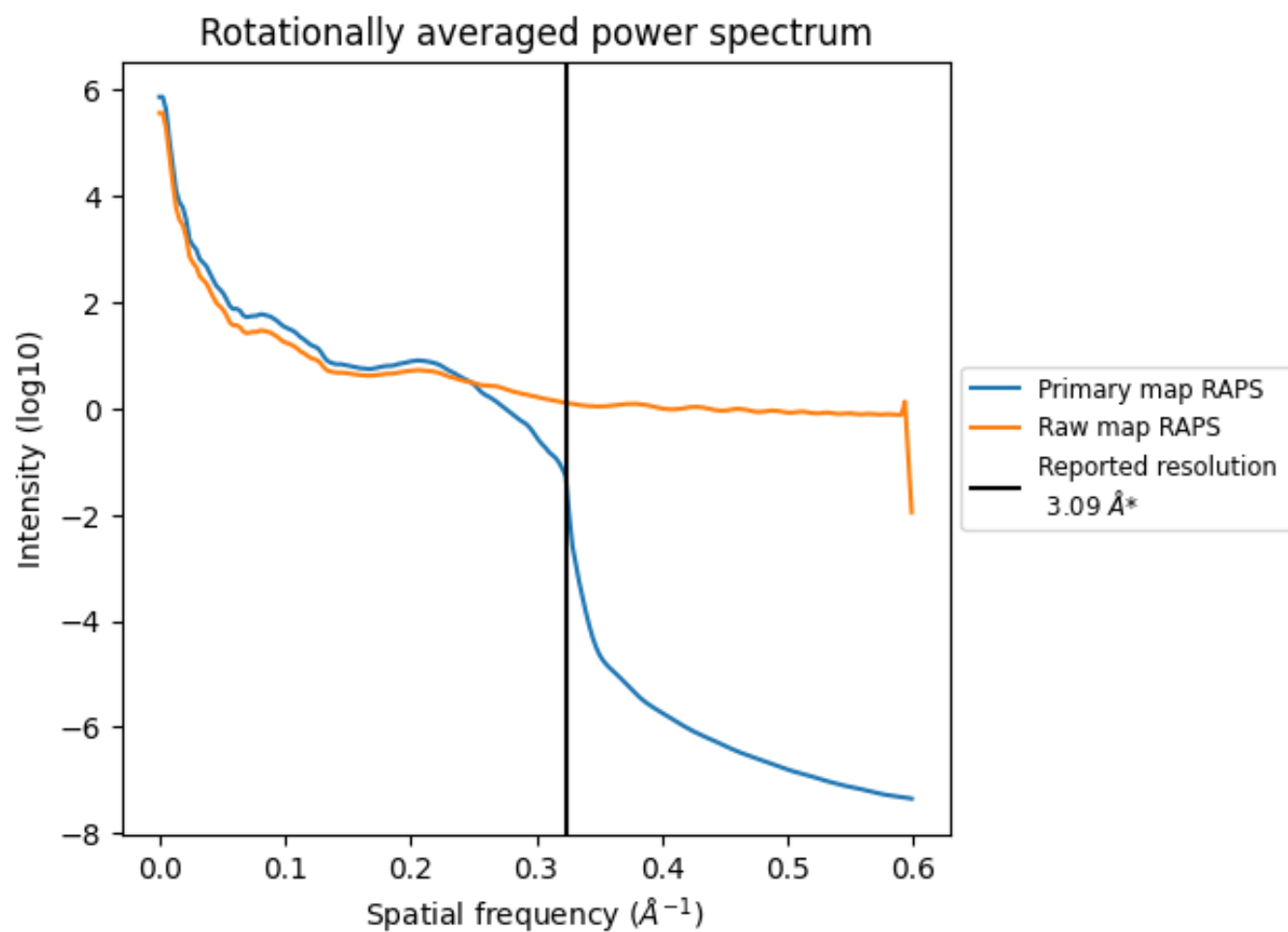
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 709 nm<sup>3</sup>; this corresponds to an approximate mass of 640 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 ⓘ



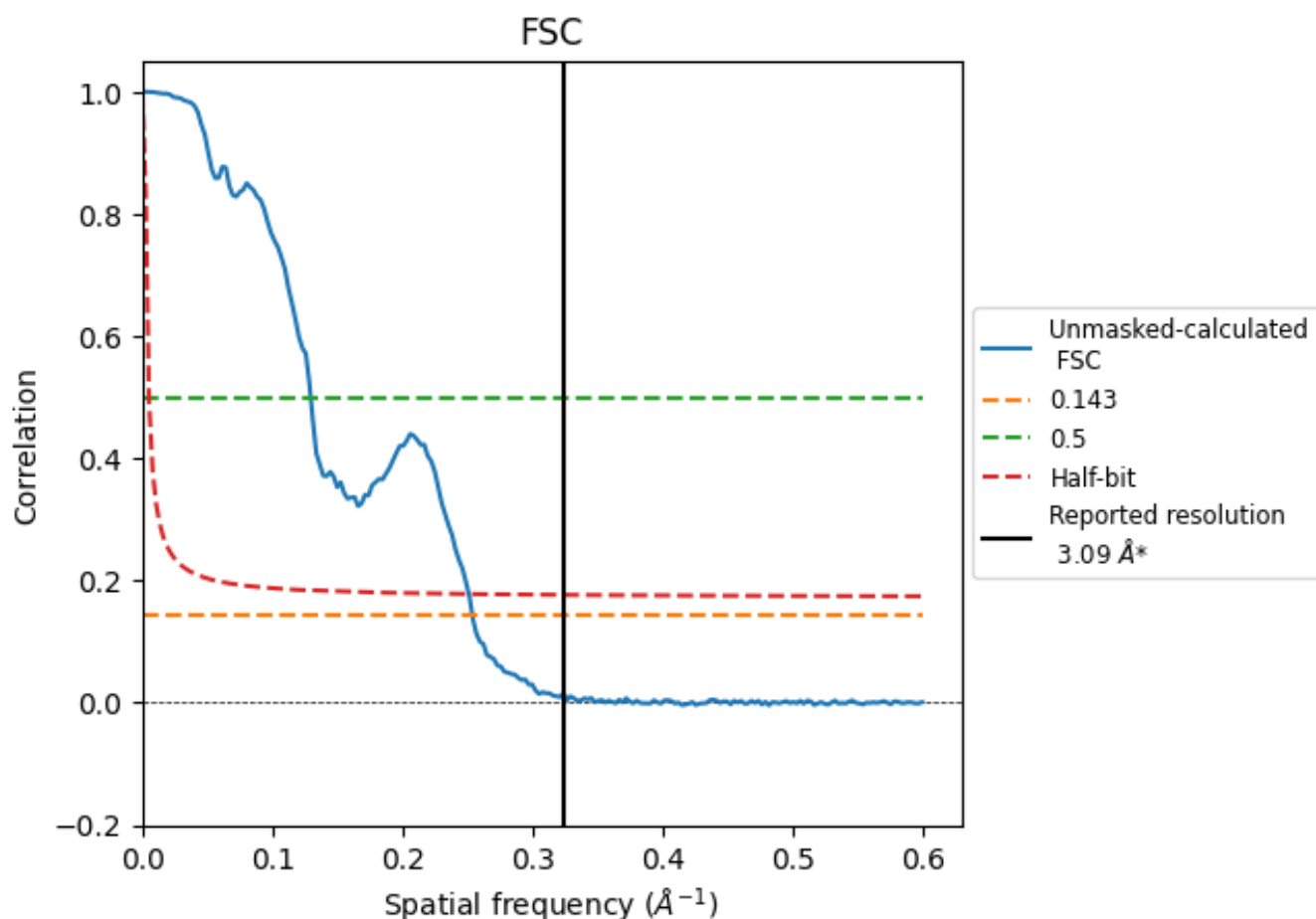
\*Reported resolution corresponds to spatial frequency of 0.324 Å<sup>-1</sup>



## 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  $0.324 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

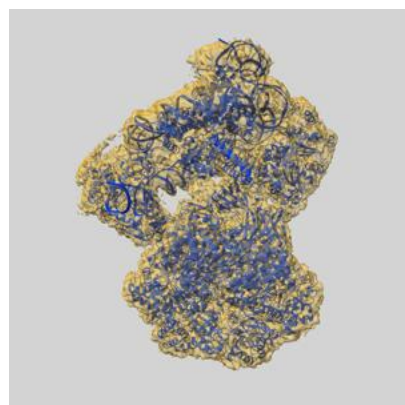
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.95	7.73	3.99

\*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 3.95 differs from the reported value 3.09 by more than 10 %

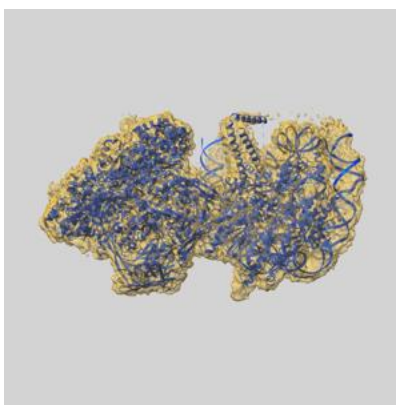
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45369 and PDB model 9C9S. Per-residue inclusion information can be found in section [3](#) on page [7](#).

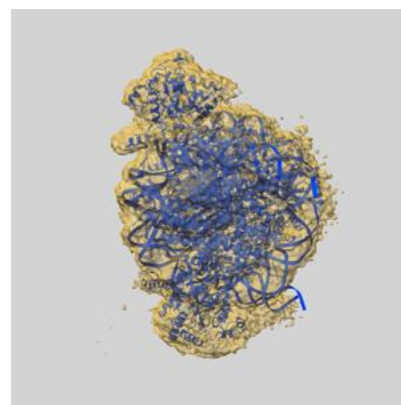
### 9.1 Map-model overlay [i](#)



X



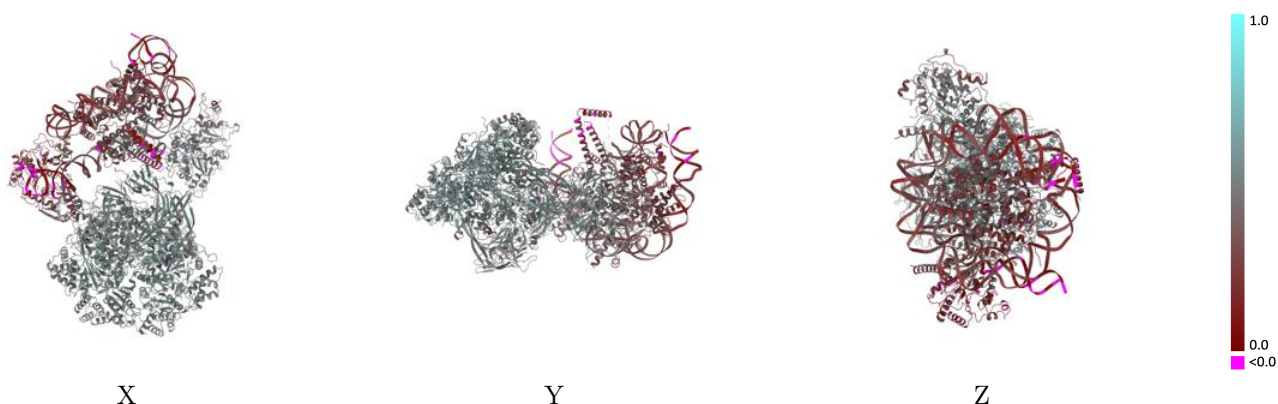
Y



Z

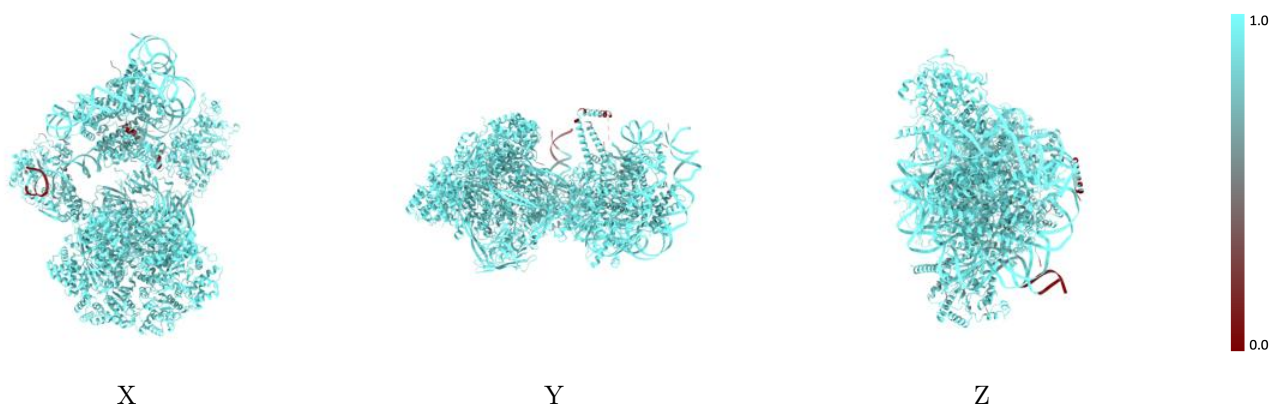
The images above show the 3D surface view of the map at the recommended contour level 0.132 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



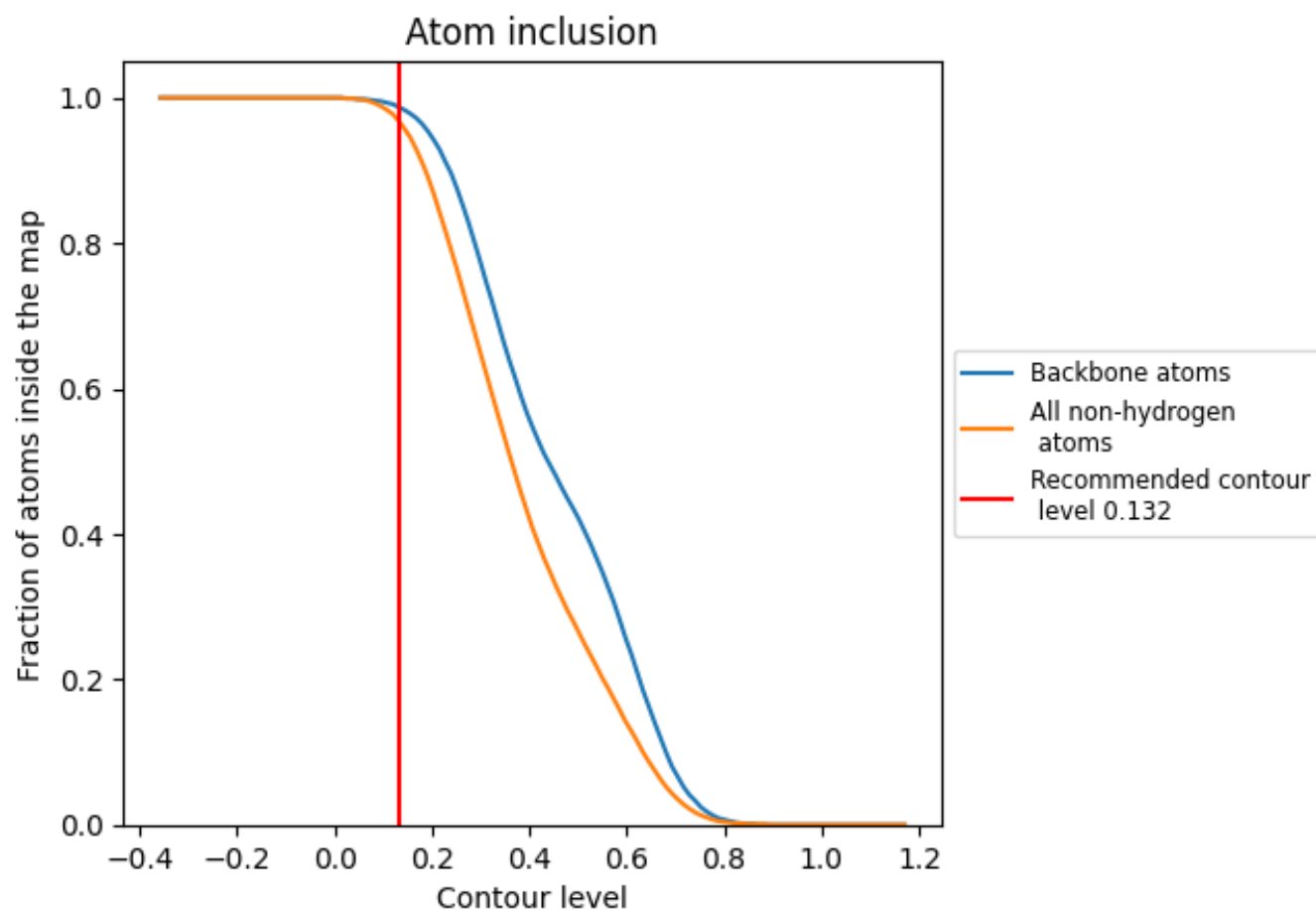
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.132).











































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.132) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9680	 0.4240
A	 0.9590	 0.2840
B	 0.9750	 0.2860
C	 0.9550	 0.3030
D	 0.9790	 0.2950
E	 0.9610	 0.2970
F	 0.9550	 0.3360
G	 0.9330	 0.4090
H	 0.9580	 0.4160
I	 0.9310	 0.2380
J	 0.9510	 0.2330
Q	 0.9460	 0.3580
R	 0.9690	 0.4390
S	 0.9870	 0.4550
T	 0.9860	 0.5260
U	 0.9880	 0.5140
V	 0.9830	 0.5070
W	 0.9890	 0.5210
X	 0.9800	 0.5270
Y	 0.9770	 0.5230
Z	 0.9610	 0.4350

