



## wwPDB EM Validation Summary Report ⓘ

Dec 31, 2024 – 05:56 PM EST

PDB ID : 8JUY  
EMDB ID : EMD-36666  
Title : Human ATAD2 Walker B mutant-H3/H4K5Q complex, ATP state (Class II)  
Authors : Cho, C.; Song, J.  
Deposited on : 2023-06-27  
Resolution : 4.34 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.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
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)	:	2.40

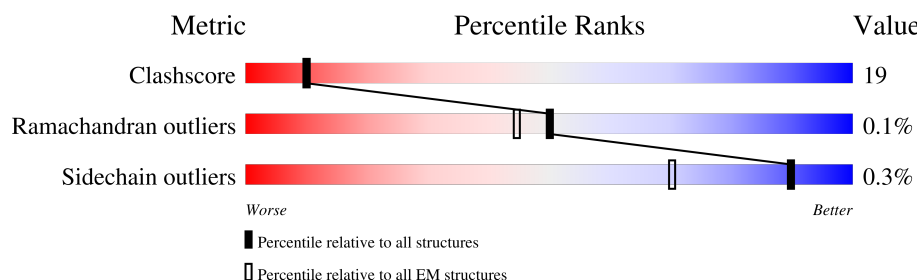
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.34 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	A	831	<div> <div>44%</div> <div> <div>33%</div> <div>20%</div> <div>47%</div> </div> </div>
1	B	831	<div> <div>9%</div> <div>42%</div> <div>22%</div> <div>37%</div> </div>
1	C	831	<div> <div>43%</div> <div>20%</div> <div>37%</div> </div>
1	D	831	<div> <div>43%</div> <div>21%</div> <div>36%</div> </div>
1	E	831	<div> <div>39%</div> <div>24%</div> <div>37%</div> </div>
1	F	831	<div> <div>26%</div> <div>33%</div> <div>29%</div> <div>38%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ATP	F	1401	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24554 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.

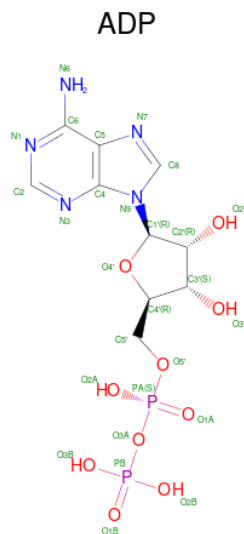
- Molecule 1 is a protein called ATPase family AAA domain-containing protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	442	Total	C	N	O	S	0	0
			3472	2232	592	632	16		
1	B	527	Total	C	N	O	S	0	0
			4197	2691	724	764	18		
1	C	527	Total	C	N	O	S	0	0
			4190	2682	726	764	18		
1	D	529	Total	C	N	O	S	0	0
			4206	2691	726	771	18		
1	E	526	Total	C	N	O	S	0	0
			4188	2680	726	764	18		
1	F	518	Total	C	N	O	S	0	0
			4119	2639	710	751	19		

There are 6 discrepancies between the modelled and reference sequences:

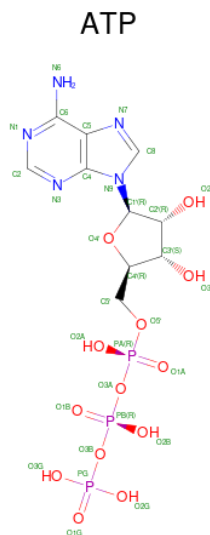
Chain	Residue	Modelled	Actual	Comment	Reference
A	532	GLN	GLU	engineered mutation	UNP Q6PL18
B	532	GLN	GLU	engineered mutation	UNP Q6PL18
C	532	GLN	GLU	engineered mutation	UNP Q6PL18
D	532	GLN	GLU	engineered mutation	UNP Q6PL18
E	532	GLN	GLU	engineered mutation	UNP Q6PL18
F	532	GLN	GLU	engineered mutation	UNP Q6PL18

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



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

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{13}\text{P}_3$ ).



Mol	Chain	Residues	Atoms					AltConf
3	B	1	Total 31	C 10	N 5	O 13	P 3	0
3	C	1	Total 31	C 10	N 5	O 13	P 3	0

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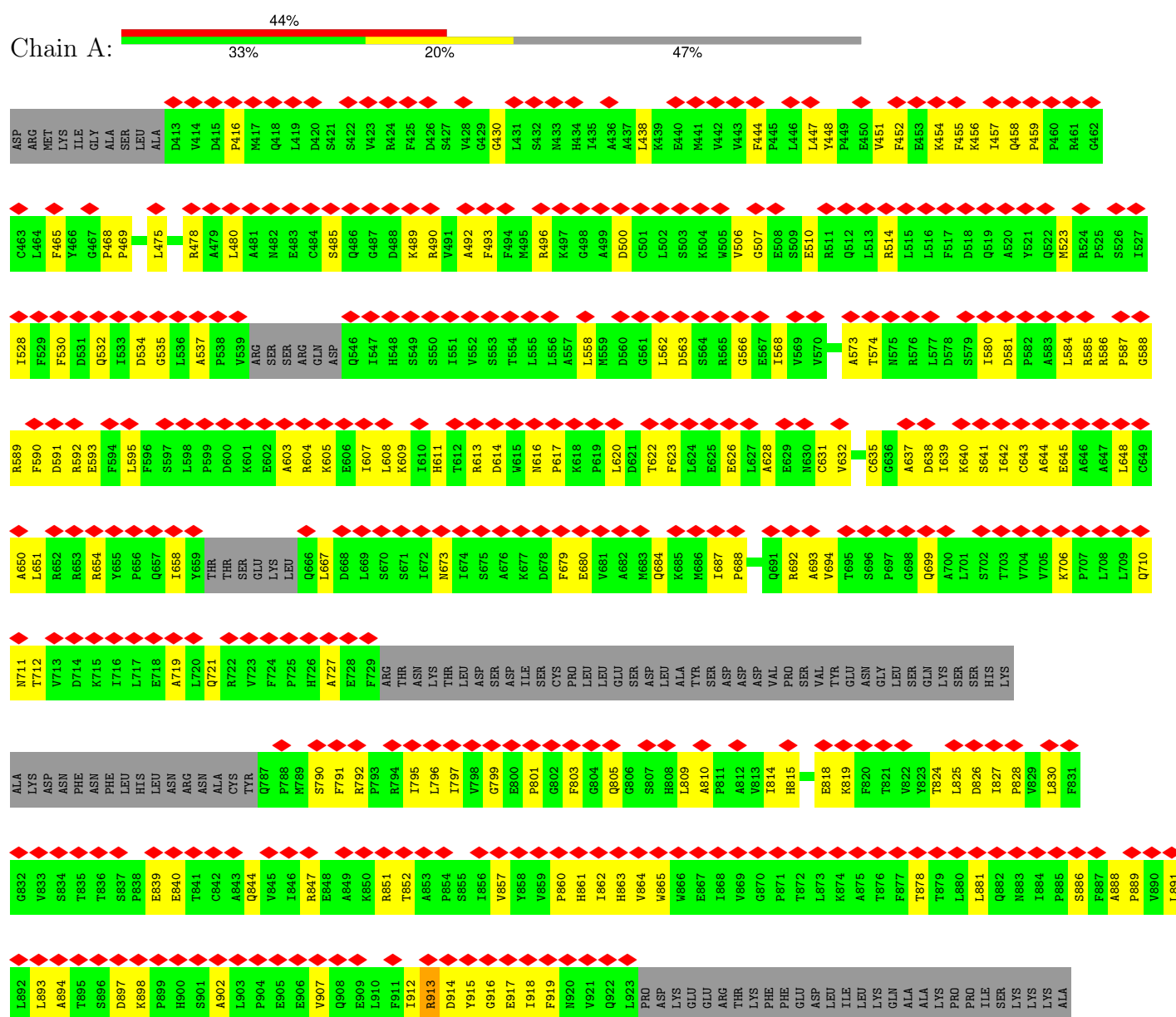
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Mol	Chain	Residues	Atoms					AltConf
3	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
3	F	1	Total	C	N	O	P	0
			31	10	5	13	3	

### 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.

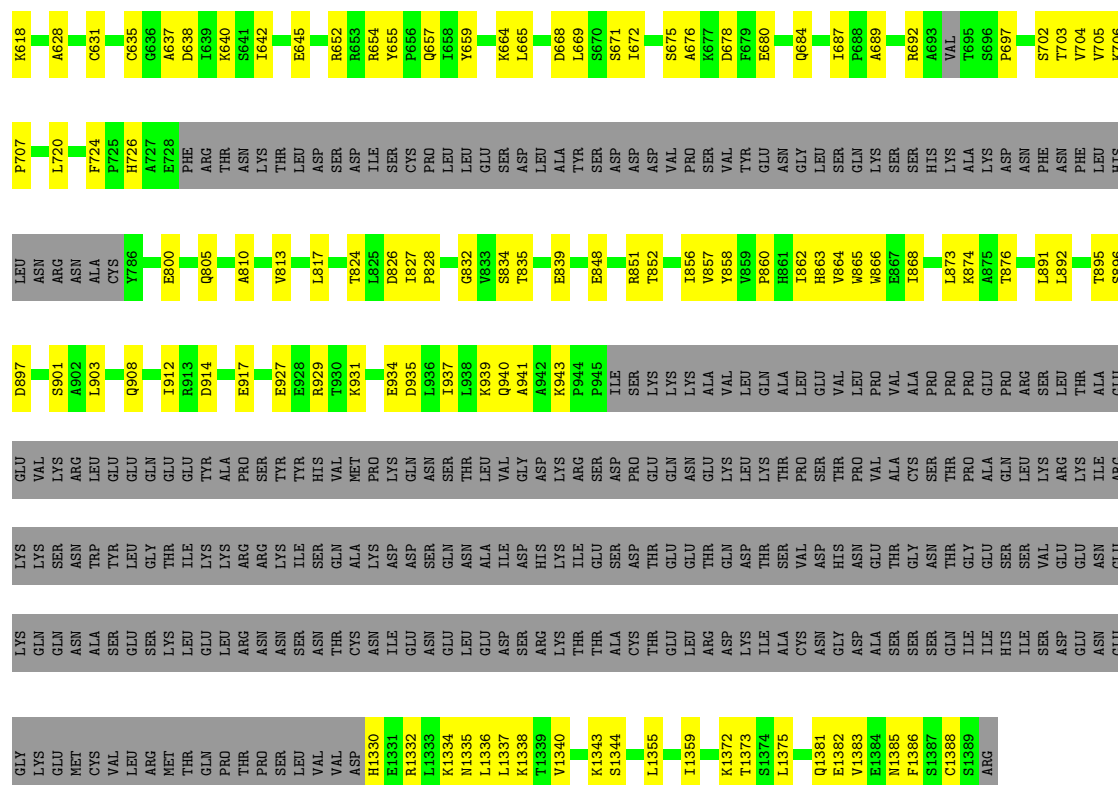
- Molecule 1: ATPase family AAA domain-containing protein 2



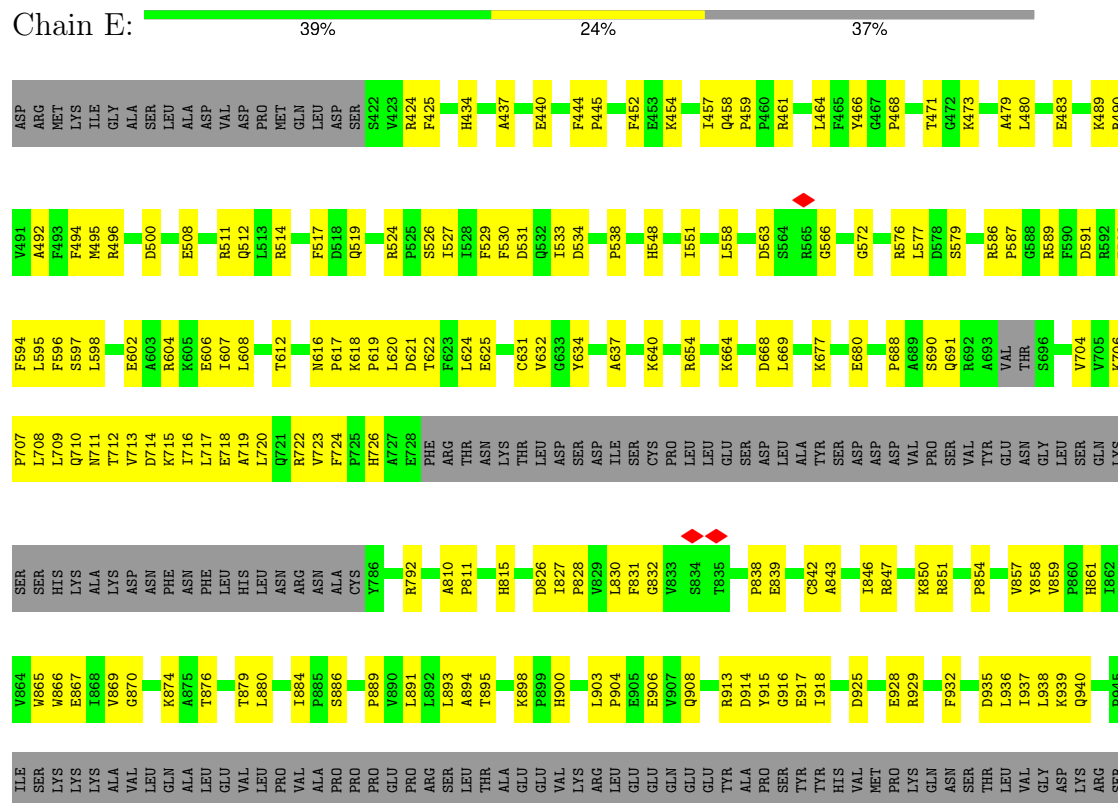


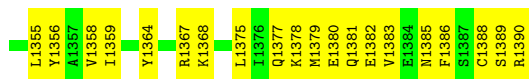






● Molecule 1: ATPase family AAA domain-containing protein 2





- Molecule 1: ATPase family AAA domain-containing protein 2

[illegible]

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

VAL	THR
ASP	CYS
HIS	ILE
E1331	ASN
R1332	GLU
L1333	ASP
K1334	ASN
N1335	GLU
L1336	LEU
L1337	GLU
V1341	ASP
S1344	SER
N1348	ARG
I1349	THR
F1350	GLU
L1355	LEU
V1358	ARG
C1362	ASN
R1365	LYS
H1366	ILE
R1367	ALA
K1368	CYS
D1369	ASN
H1370	SER
D1371	GLN
K1372	ILE
T1373	ILE
S1374	HIS
L1375	ILE
K1378	SER
M1379	ASP
E1380	GLU
Q1381	GLU
E1382	GLY
V1383	LYS
E1384	GLU
N1385	MET
F1386	CYS
S1387	VAL
C1388	SER
S1389	LEU
ARG	ARG

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63298	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0066	Depositor
Map size ( $\text{\AA}$ )	330.0, 330.0, 330.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	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, ATP

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	0.26	0/3551	0.55	0/4820
1	B	0.30	0/4289	0.54	0/5806
1	C	0.37	0/4281	0.56	0/5796
1	D	0.37	0/4297	0.56	0/5818
1	E	0.31	0/4279	0.55	0/5792
1	F	0.28	0/4206	0.56	0/5691
All	All	0.32	0/24903	0.55	0/33723

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	3472	0	3509	142	0
1	B	4197	0	4255	143	0
1	C	4190	0	4247	129	0
1	D	4206	0	4258	135	0
1	E	4188	0	4245	189	0
1	F	4119	0	4179	250	0
2	A	27	0	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	31	0	12	4	0
3	C	62	0	24	7	0
3	E	31	0	12	3	0
3	F	31	0	12	14	0
All	All	24554	0	24764	936	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 19.

The worst 5 of 936 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:1379:MET:O	1:F:1383:VAL:HG22	1.40	1.21
1:A:687:ILE:HB	1:A:688:PRO:HD2	1.34	1.05
1:F:1378:LYS:O	1:F:1382:GLU:HG2	1.64	0.98
1:F:716:ILE:HG21	1:F:813:VAL:HG13	1.51	0.93
1:A:468:PRO:HB2	1:A:694:VAL:HA	1.49	0.91

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	434/831 (52%)	384 (88%)	49 (11%)	1 (0%)	44	78
1	B	519/831 (62%)	478 (92%)	40 (8%)	1 (0%)	44	78
1	C	519/831 (62%)	480 (92%)	38 (7%)	1 (0%)	44	78
1	D	521/831 (63%)	471 (90%)	50 (10%)	0	100	100
1	E	518/831 (62%)	486 (94%)	32 (6%)	0	100	100
1	F	508/831 (61%)	453 (89%)	54 (11%)	1 (0%)	44	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3019/4986 (60%)	2752 (91%)	263 (9%)	4 (0%)	50 82

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	913	ARG
1	A	913	ARG
1	B	913	ARG
1	C	913	ARG

### 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	382/742 (52%)	382 (100%)	0	100 100
1	B	464/742 (62%)	463 (100%)	1 (0%)	92 94
1	C	464/742 (62%)	461 (99%)	3 (1%)	84 88
1	D	466/742 (63%)	466 (100%)	0	100 100
1	E	463/742 (62%)	463 (100%)	0	100 100
1	F	456/742 (62%)	453 (99%)	3 (1%)	81 87
All	All	2695/4452 (60%)	2688 (100%)	7 (0%)	90 92

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	794	ARG
1	F	565	ARG
1	F	1383	VAL
1	F	1382	GLU
1	C	543	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:



Mol	Chain	Res	Type
1	F	482	ASN
1	F	710	GLN
1	F	1385	ASN
1	D	863	HIS
1	A	611	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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	$\# Z  > 2$
3	ATP	C	1402	-	28,33,33	1.07	2 (7%)	34,52,52	0.73	1 (2%)
3	ATP	C	1401	-	28,33,33	1.17	1 (3%)	34,52,52	0.80	2 (5%)
3	ATP	F	1401	-	28,33,33	0.66	0	34,52,52	0.83	1 (2%)
3	ATP	B	1401	-	28,33,33	0.76	0	34,52,52	0.69	1 (2%)
3	ATP	E	1401	-	28,33,33	1.13	2 (7%)	34,52,52	0.88	2 (5%)
2	ADP	A	1301	-	24,29,29	0.93	0	29,45,45	1.25	3 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	C	1402	-	-	6/18/38/38	0/3/3/3
3	ATP	C	1401	-	-	7/18/38/38	0/3/3/3
3	ATP	F	1401	-	-	9/18/38/38	0/3/3/3
3	ATP	B	1401	-	-	7/18/38/38	0/3/3/3
3	ATP	E	1401	-	-	7/18/38/38	0/3/3/3
2	ADP	A	1301	-	-	1/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1401	ATP	PB-O3B	-4.79	1.54	1.59
3	E	1401	ATP	PB-O3B	-3.93	1.55	1.59
3	C	1402	ATP	PA-O3A	-3.51	1.55	1.59
3	E	1401	ATP	PA-O3A	-2.71	1.56	1.59
3	C	1402	ATP	PB-O3B	-2.34	1.57	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1301	ADP	N3-C2-N1	-3.65	123.72	128.67
3	E	1401	ATP	C4'-O4'-C1'	-3.29	106.92	109.92
2	A	1301	ADP	C4-C5-N7	-2.47	106.73	109.34
3	C	1401	ATP	C5-C6-N6	2.38	123.94	120.31
3	C	1402	ATP	C5-C6-N6	2.34	123.87	120.31

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

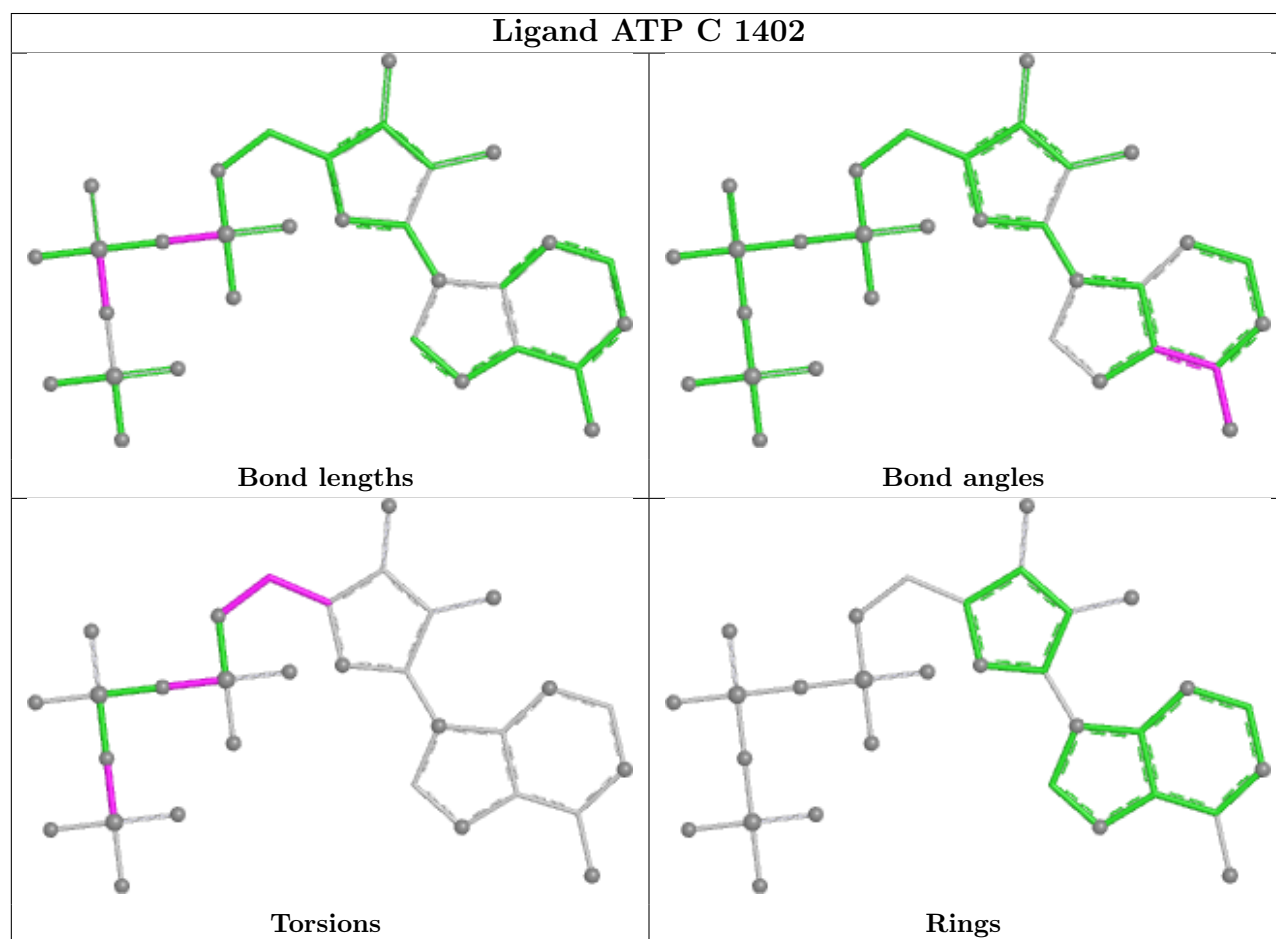
Mol	Chain	Res	Type	Atoms
3	C	1401	ATP	PB-O3B-PG-O3G
3	C	1401	ATP	O4'-C4'-C5'-O5'
3	C	1402	ATP	PB-O3B-PG-O3G
3	C	1402	ATP	O4'-C4'-C5'-O5'
3	C	1402	ATP	C3'-C4'-C5'-O5'

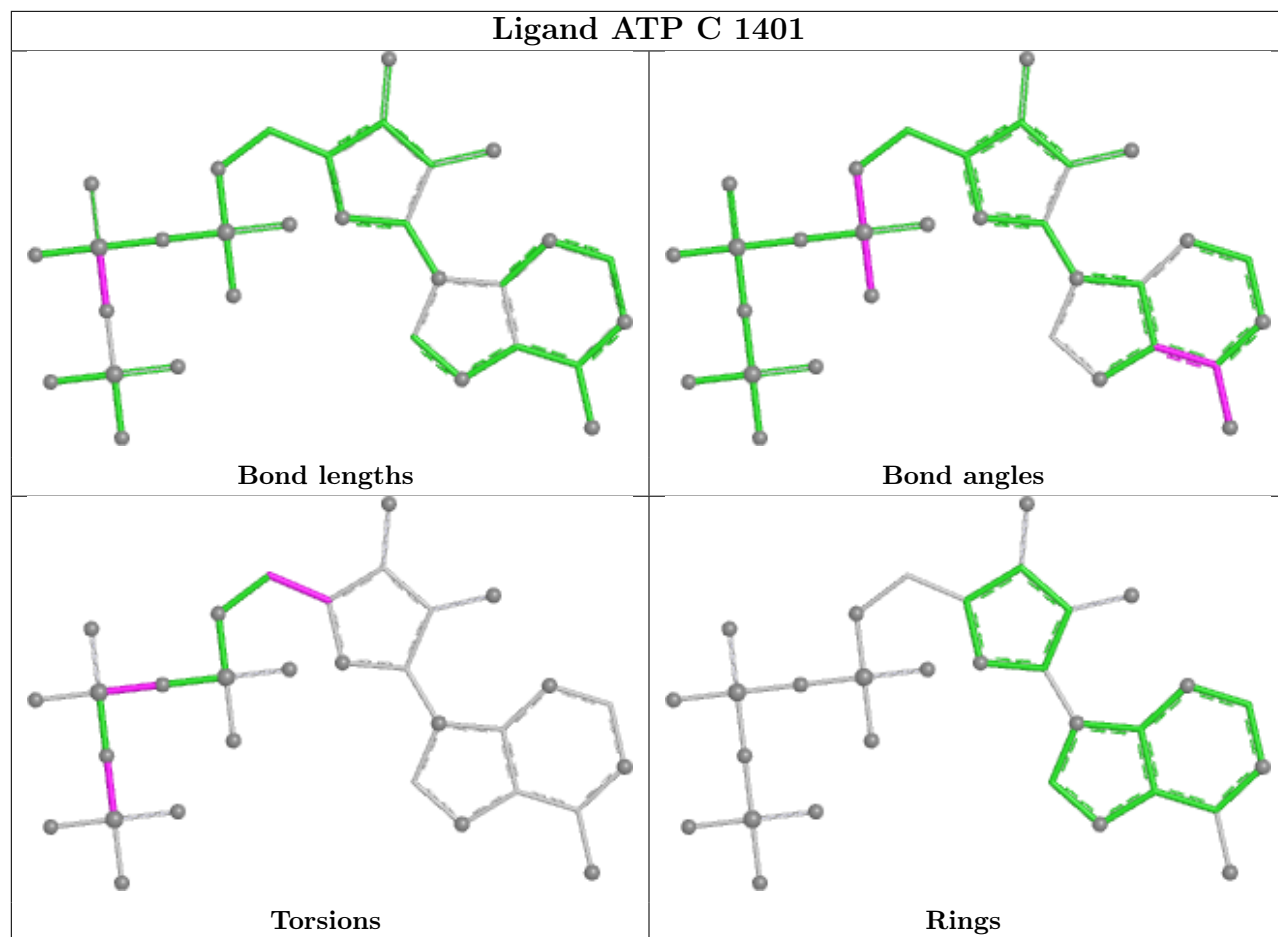
There are no ring outliers.

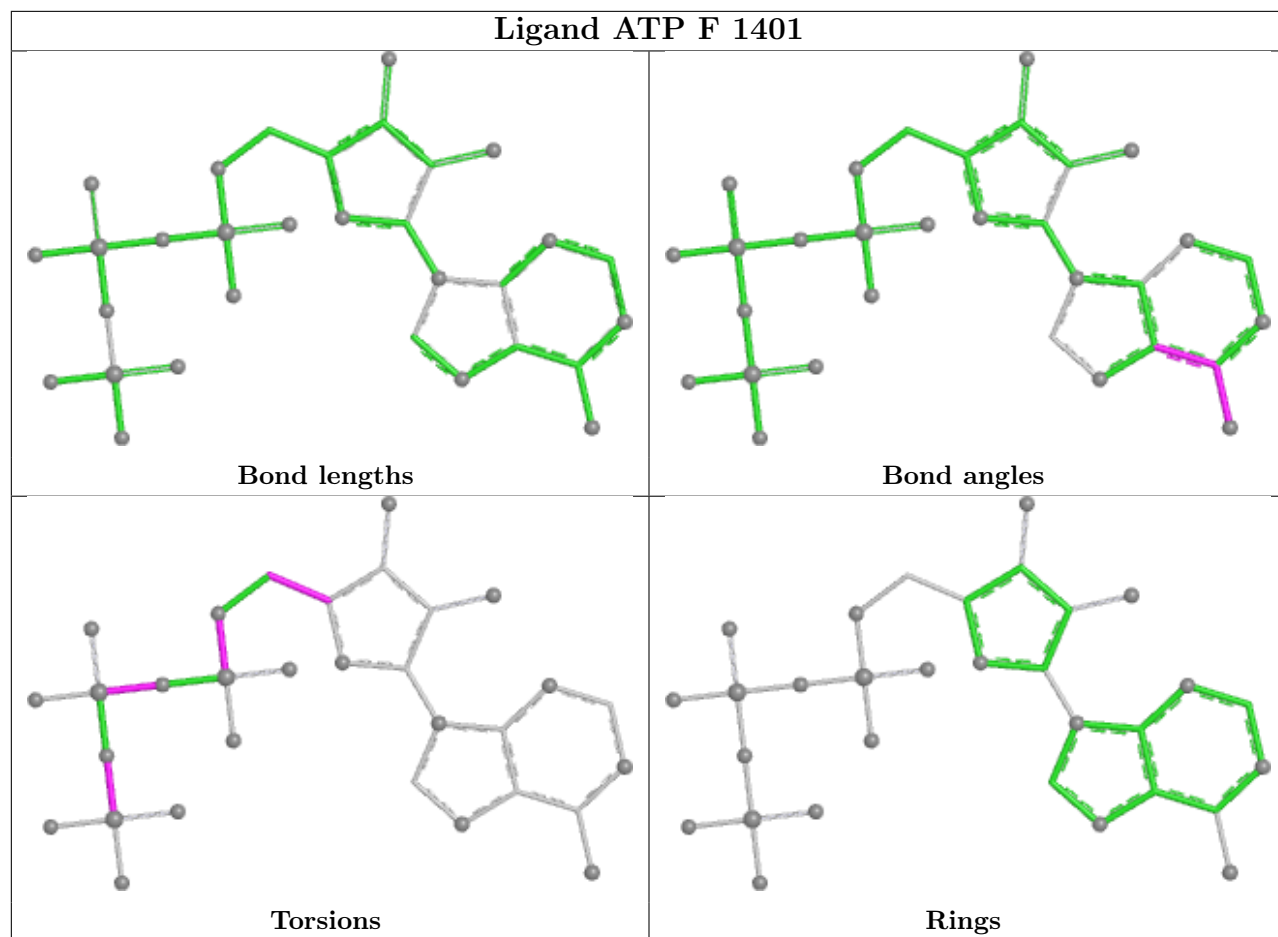
5 monomers are involved in 28 short contacts:

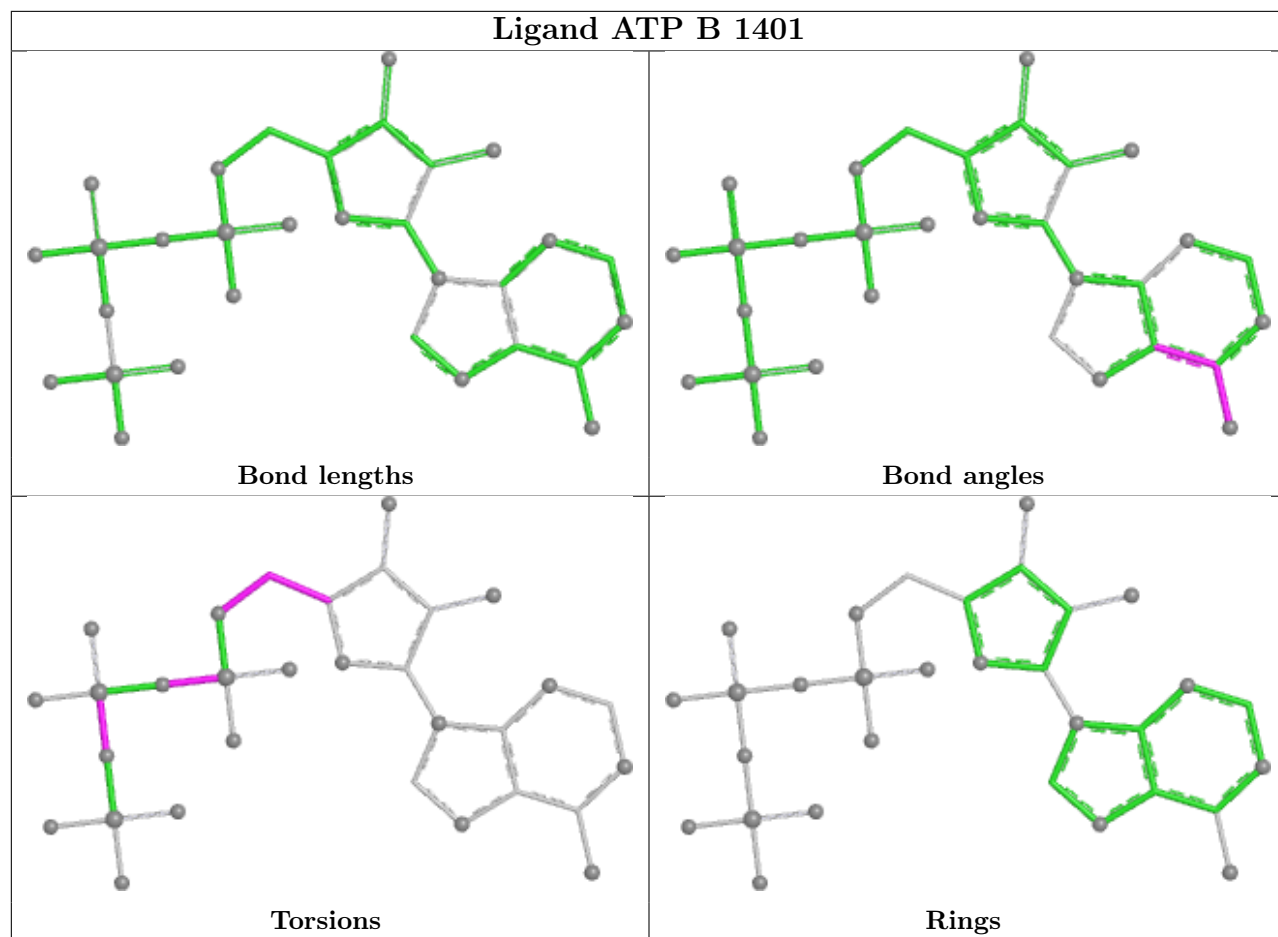
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1402	ATP	4	0
3	C	1401	ATP	3	0
3	F	1401	ATP	14	0
3	B	1401	ATP	4	0
3	E	1401	ATP	3	0

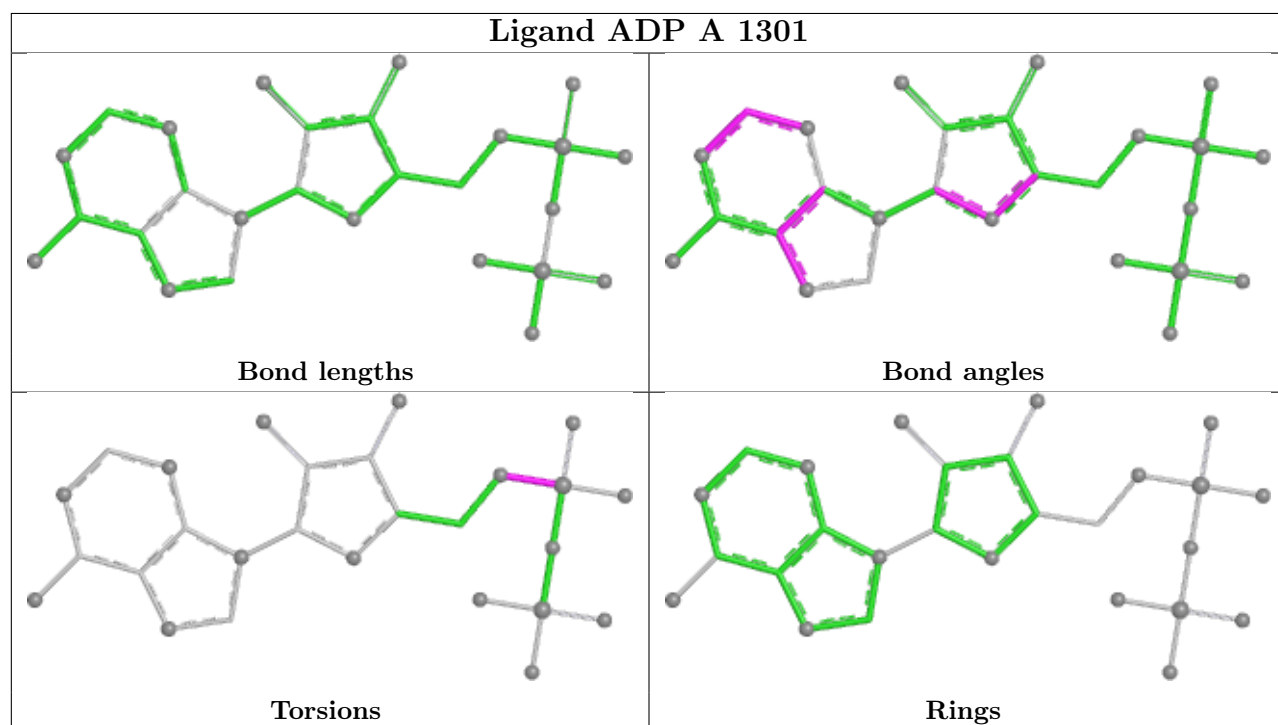
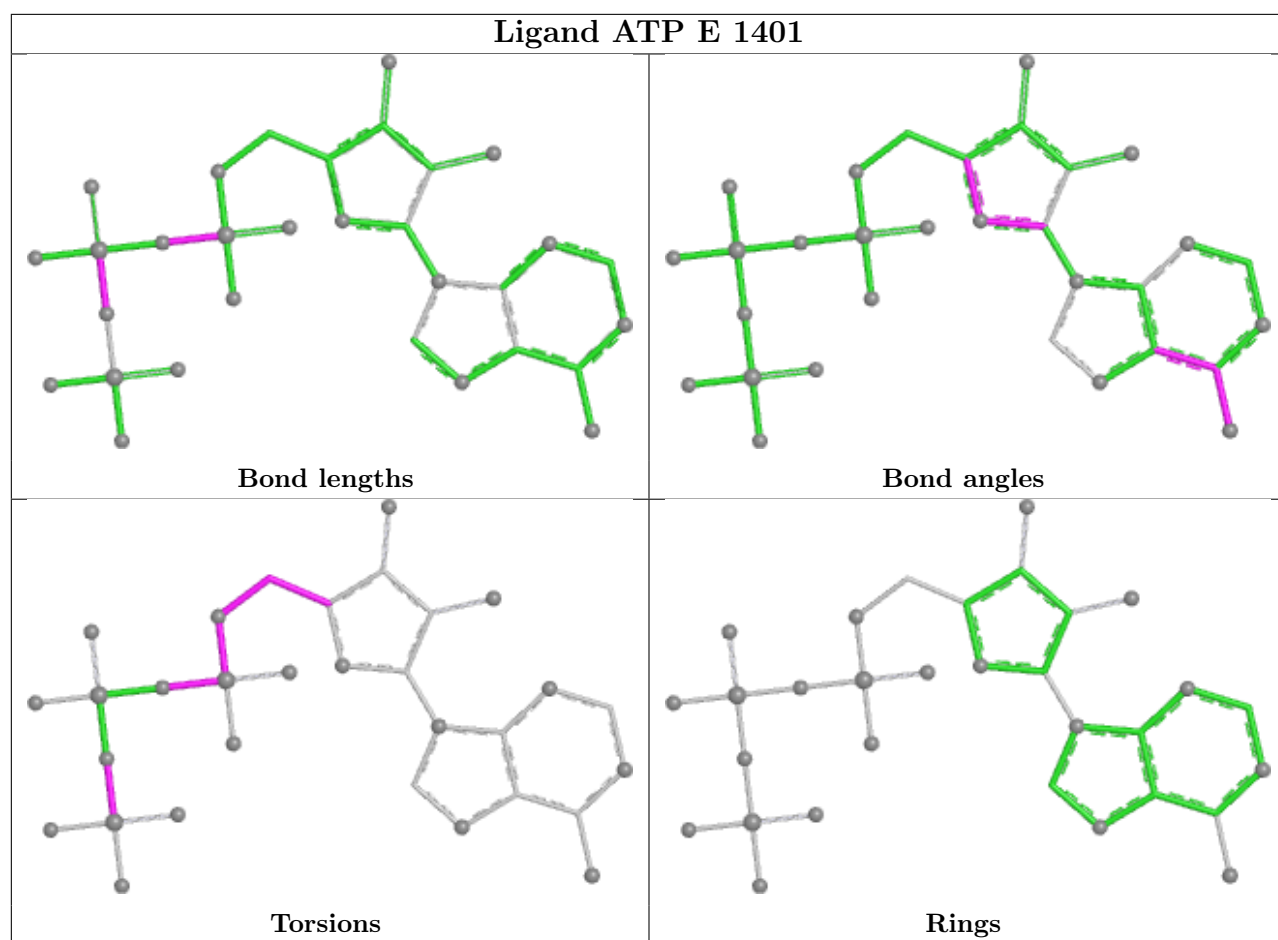
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



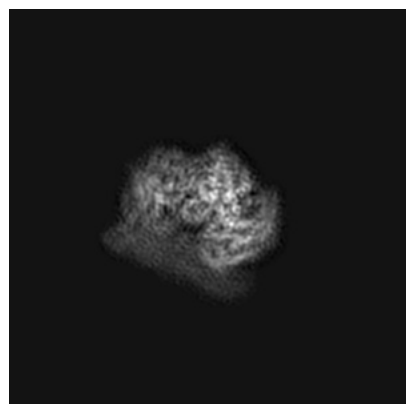
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36666. These allow visual inspection of the internal detail of the map and identification of artifacts.

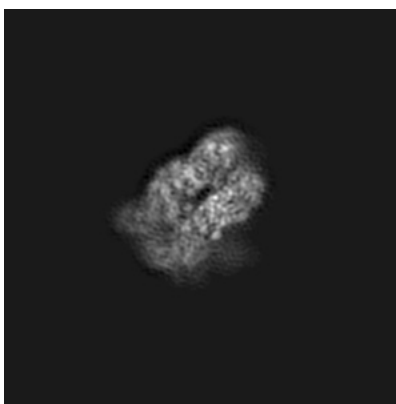
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

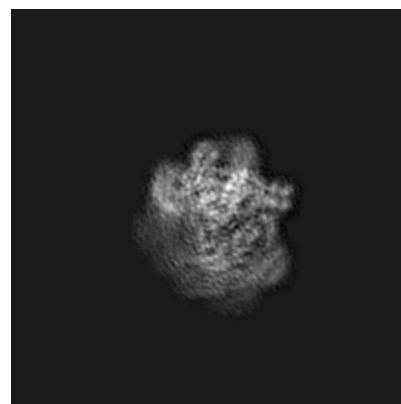
#### 6.1.1 Primary map



X

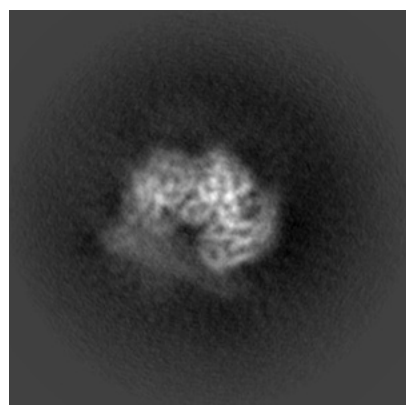


Y

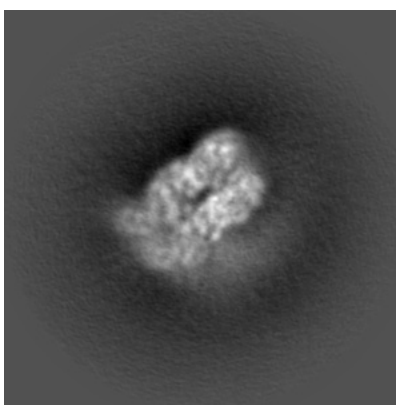


Z

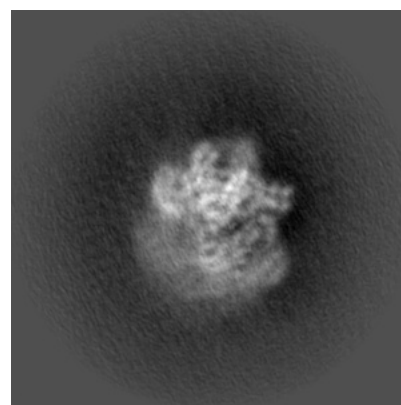
#### 6.1.2 Raw map



X



Y

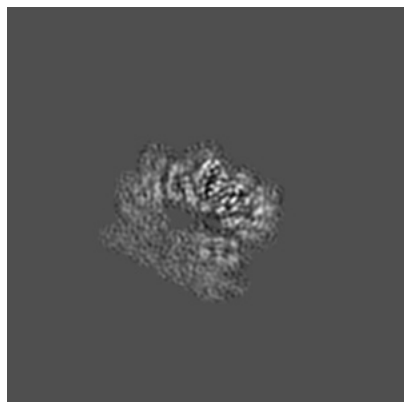


Z

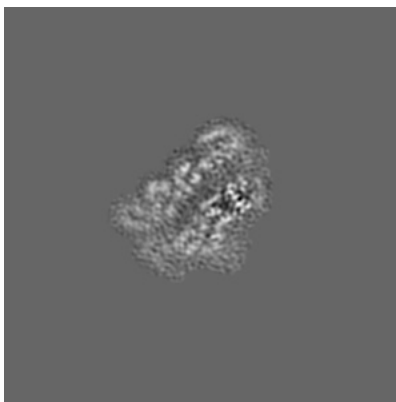
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

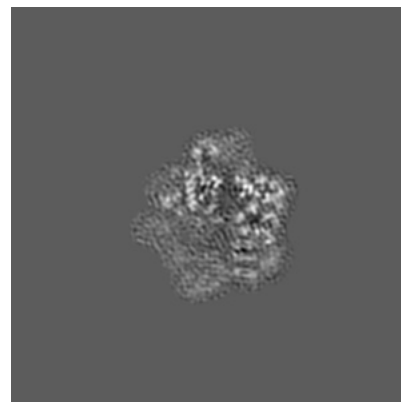
### 6.2.1 Primary map



X Index: 150

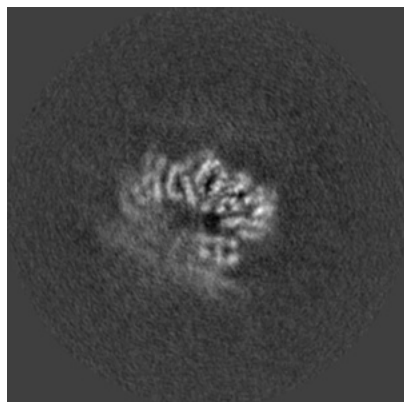


Y Index: 150

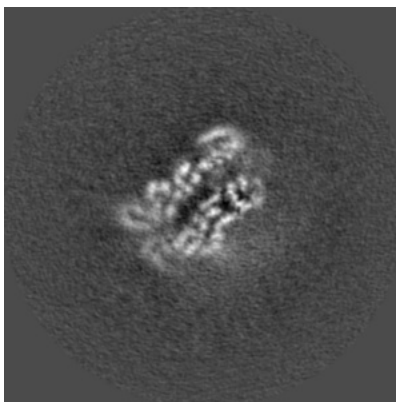


Z Index: 150

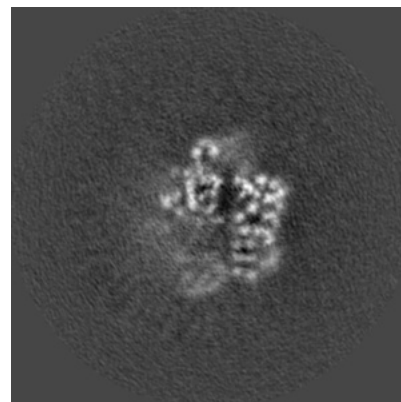
### 6.2.2 Raw map



X Index: 150



Y Index: 150

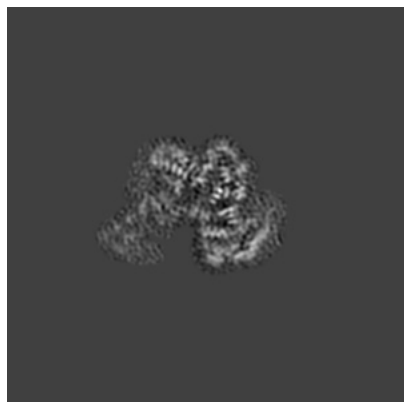


Z Index: 150

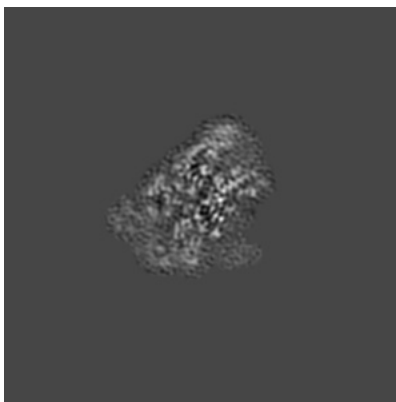
The images above show central slices of the map in three orthogonal directions.

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

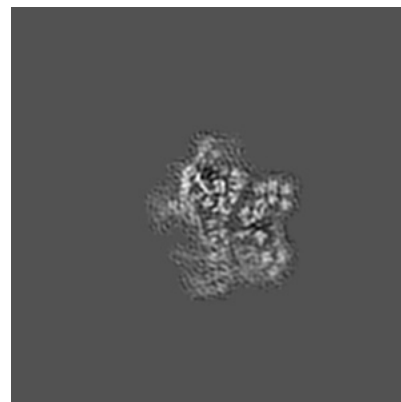
### 6.3.1 Primary map



X Index: 168

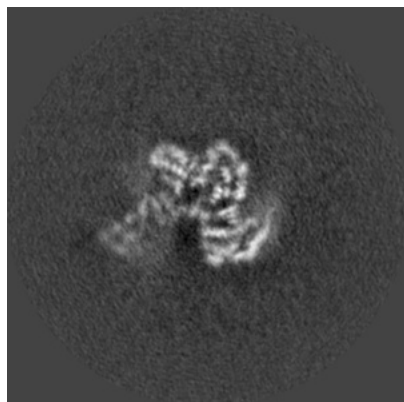


Y Index: 165

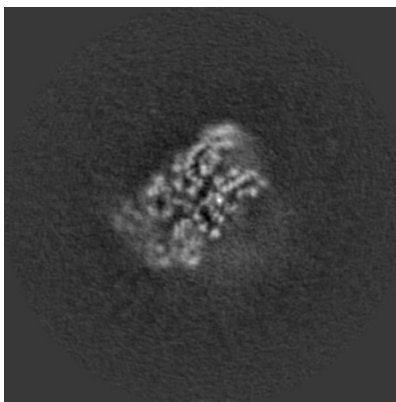


Z Index: 159

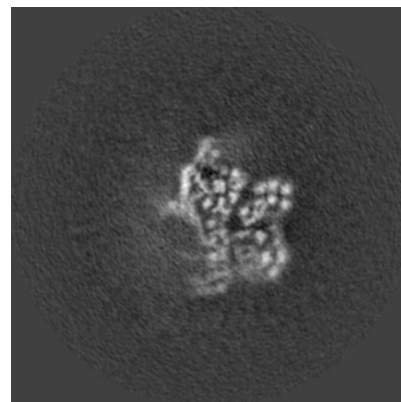
### 6.3.2 Raw map



X Index: 168



Y Index: 164

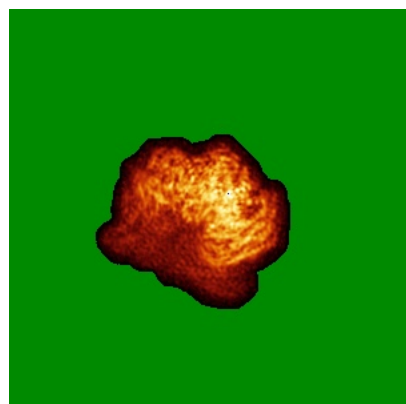


Z Index: 159

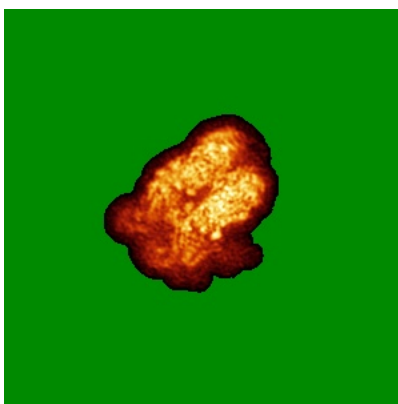
The images above show the largest variance slices of the map in three orthogonal directions.

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

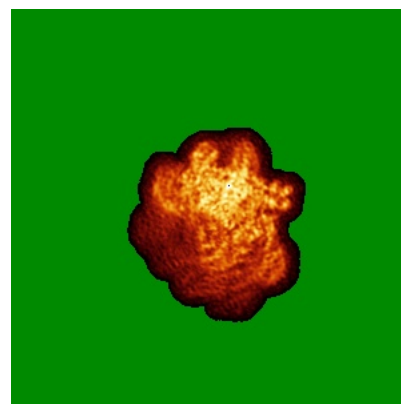
### 6.4.1 Primary map



X

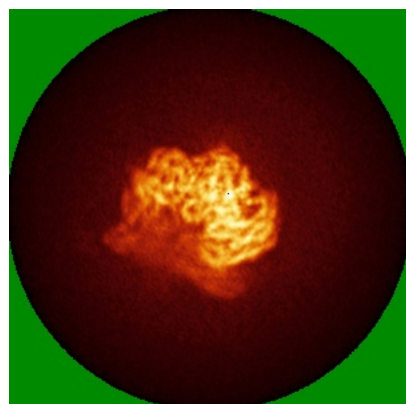


Y

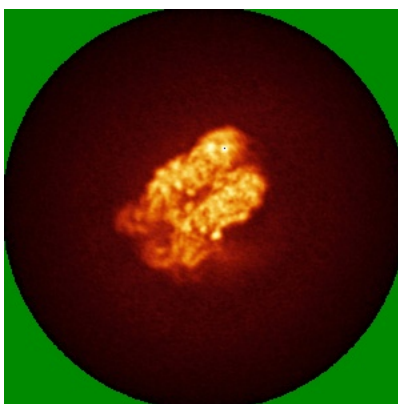


Z

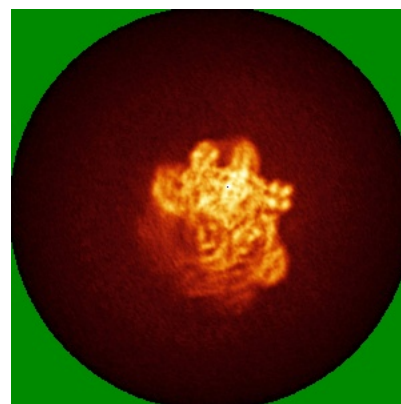
### 6.4.2 Raw map



X



Y

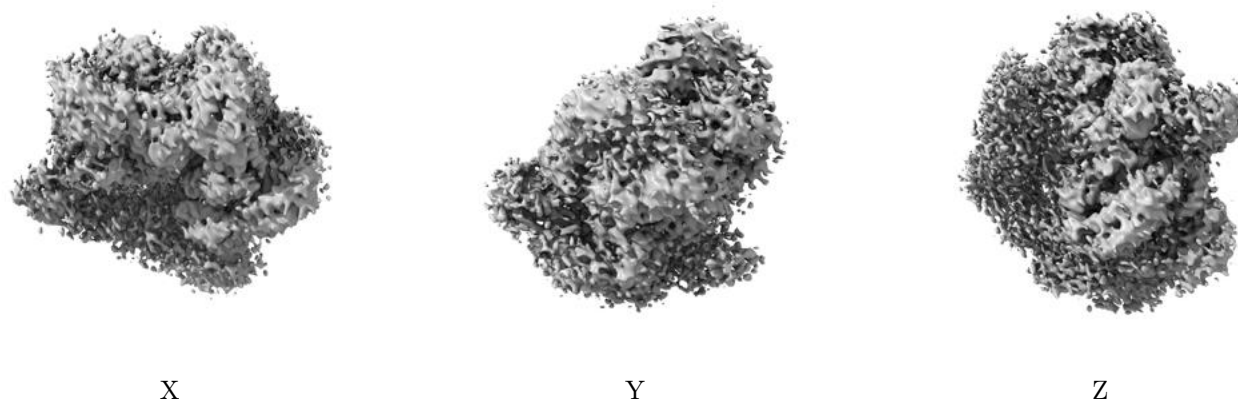


Z

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 0.0066. 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.

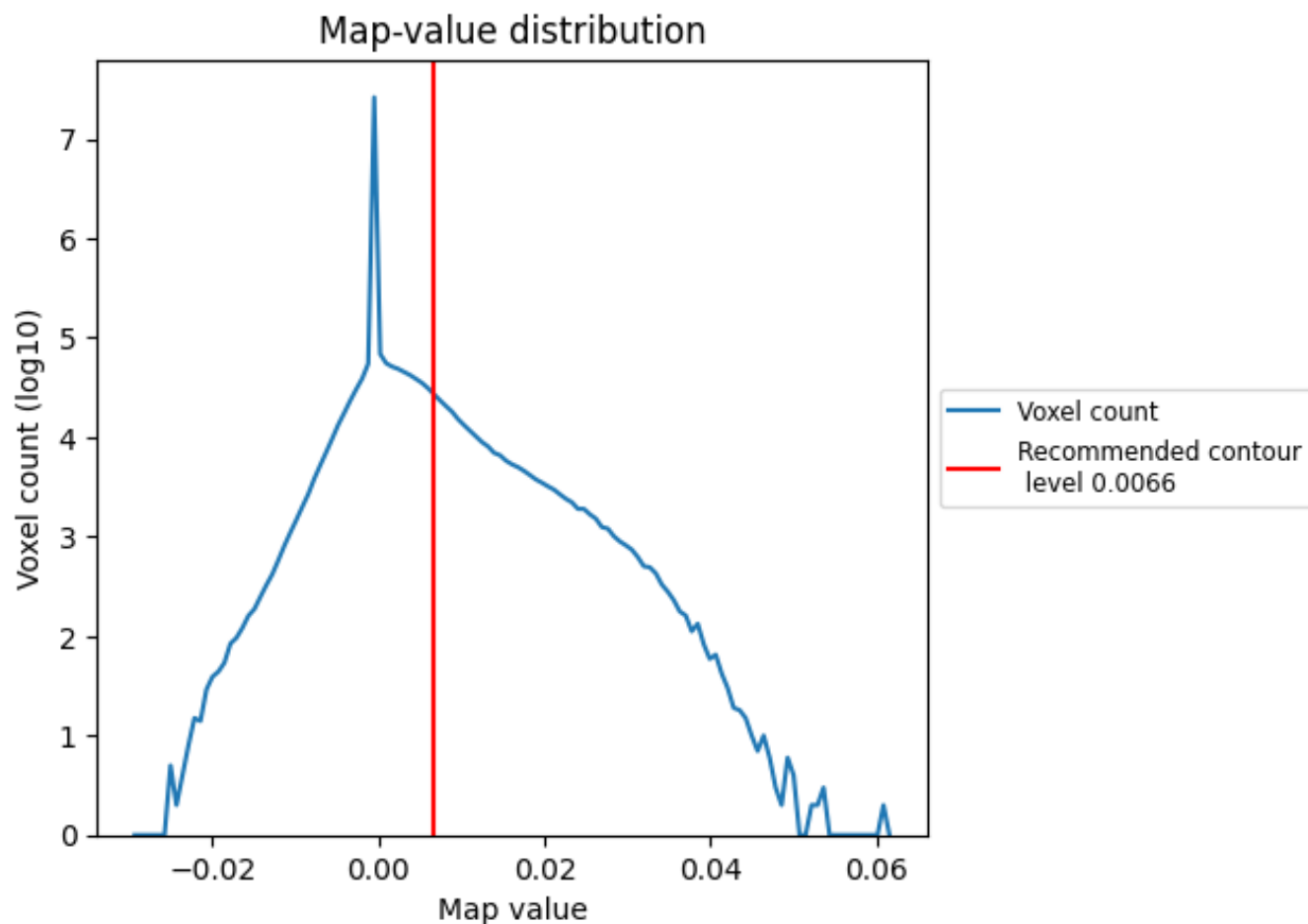
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

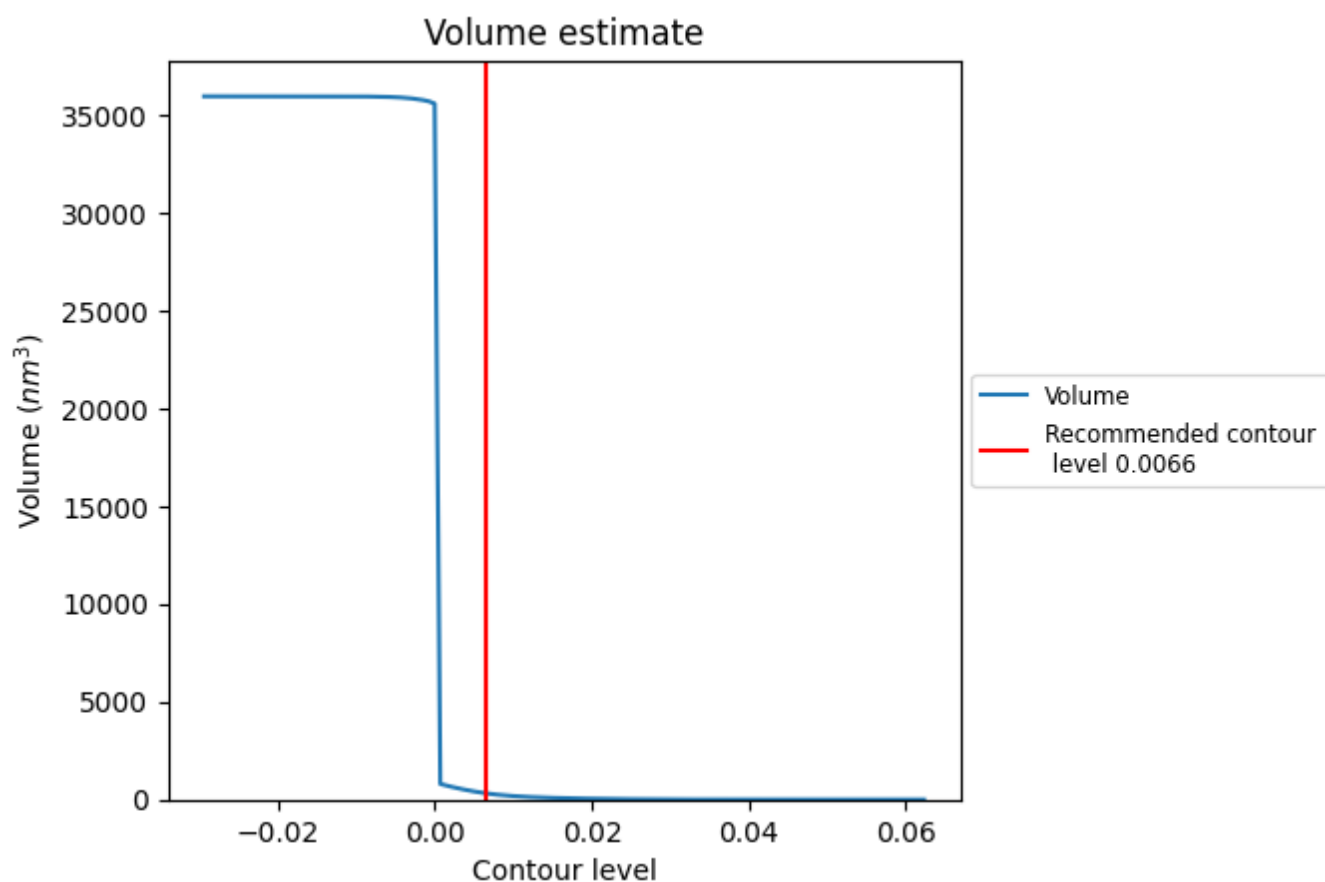
This section contains the results of statistical analysis of the map.

### 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.

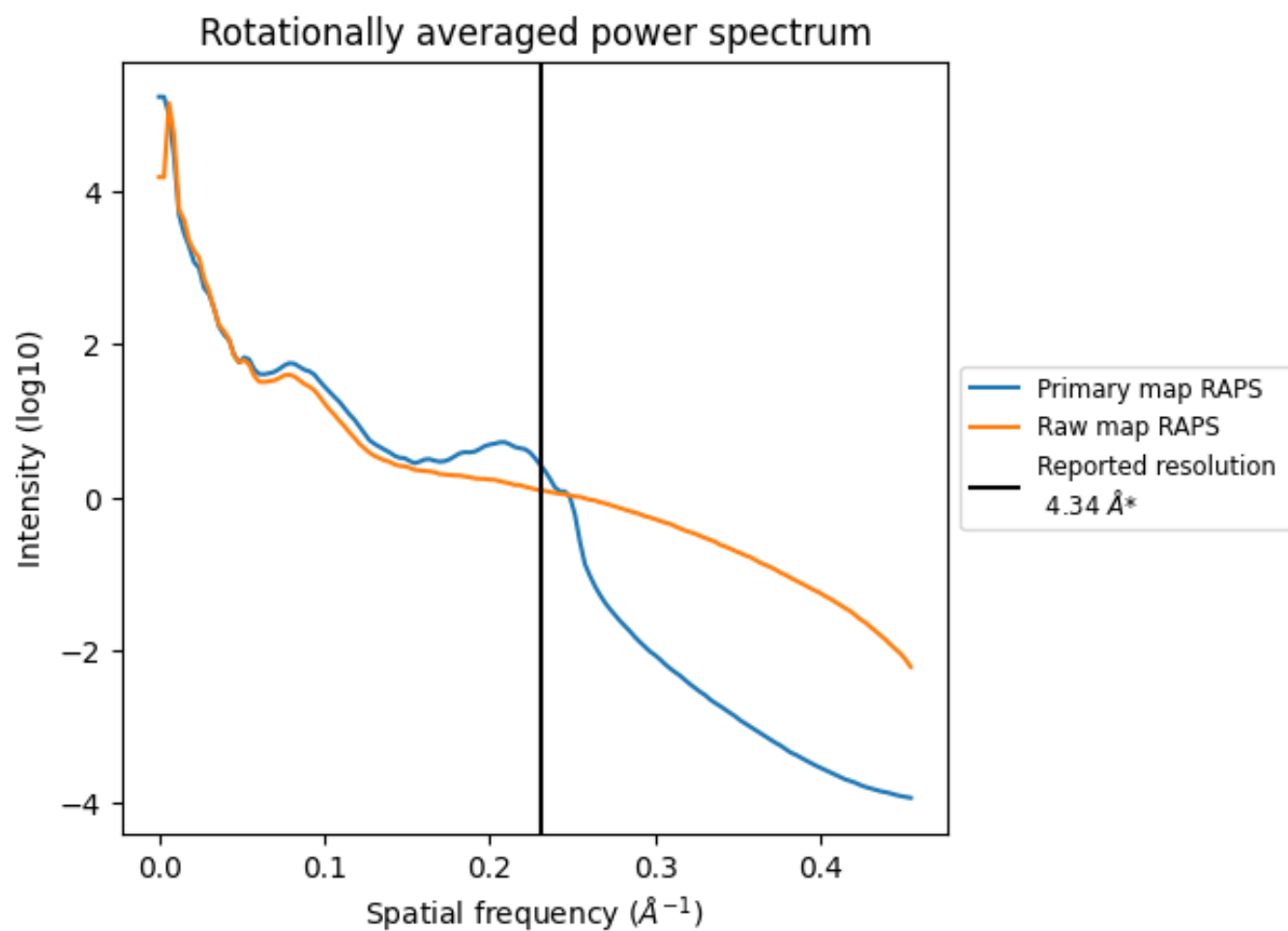
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 315 nm<sup>3</sup>; this corresponds to an approximate mass of 285 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 ⓘ



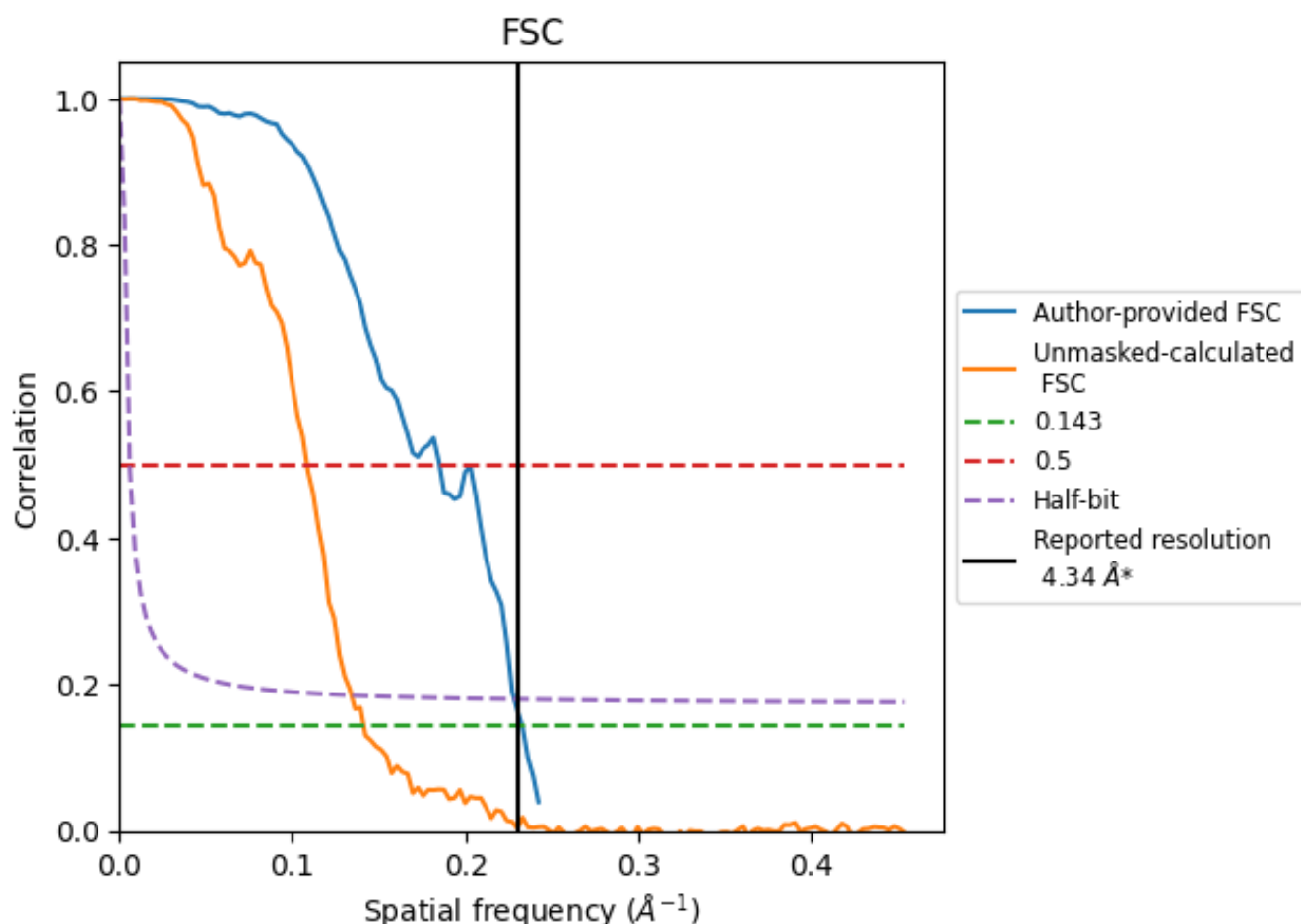
\*Reported resolution corresponds to spatial frequency of 0.230 Å<sup>-1</sup>



## 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 0.230 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

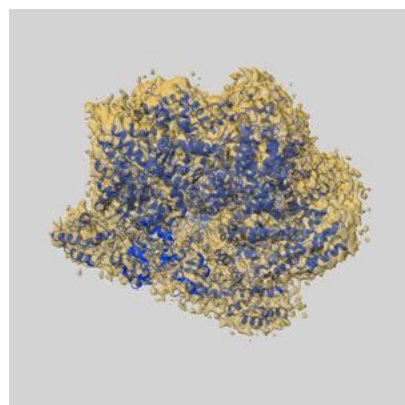
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.34	-	-
Author-provided FSC curve	4.29	5.40	4.38
Unmasked-calculated*	7.07	9.22	7.45

\*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 7.07 differs from the reported value 4.34 by more than 10 %

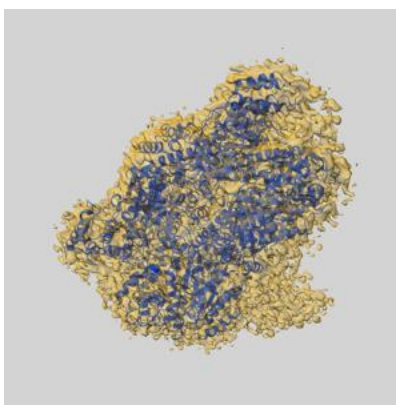
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36666 and PDB model 8JUY. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

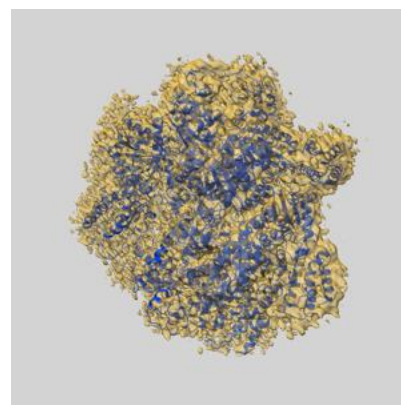
### 9.1 Map-model overlay [i](#)



X



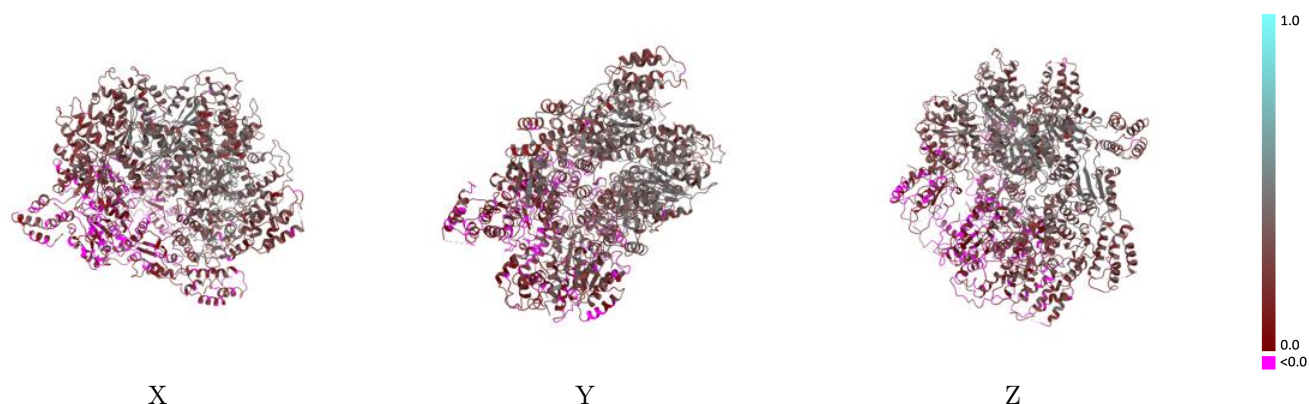
Y



Z

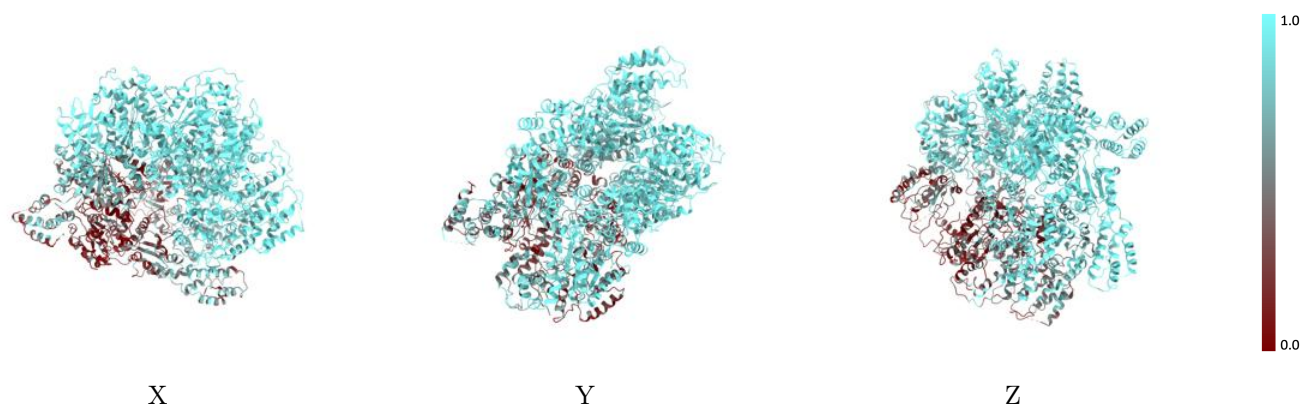
The images above show the 3D surface view of the map at the recommended contour level 0.0066 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



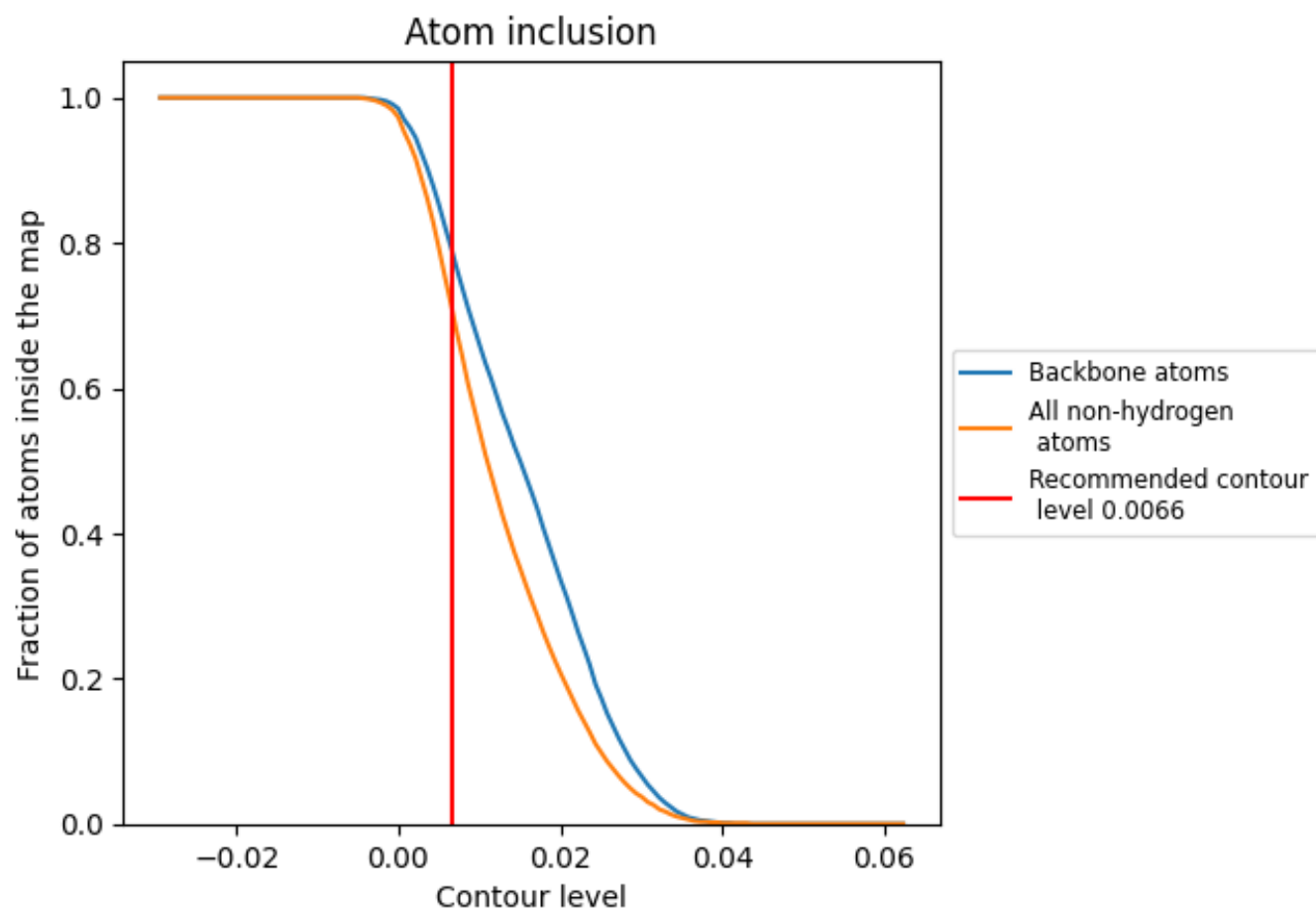
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0066).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 71% 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 (0.0066) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7100	<div></div> 0.2390
A	<div></div> 0.2050	<div></div> 0.0560
B	<div></div> 0.7100	<div></div> 0.2430
C	<div></div> 0.9350	<div></div> 0.3590
D	<div></div> 0.9380	<div></div> 0.3700
E	<div></div> 0.9170	<div></div> 0.2840
F	<div></div> 0.4660	<div></div> 0.0860

1.0

0.0

<0.0