



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:03 PM UTC

PDB ID : 8JUY / pdb_00008juy
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

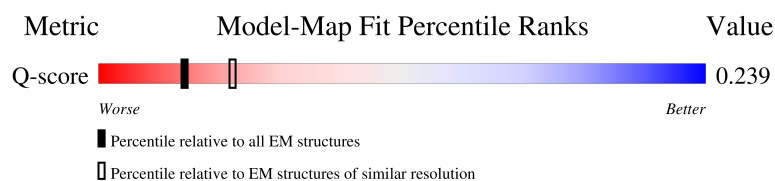
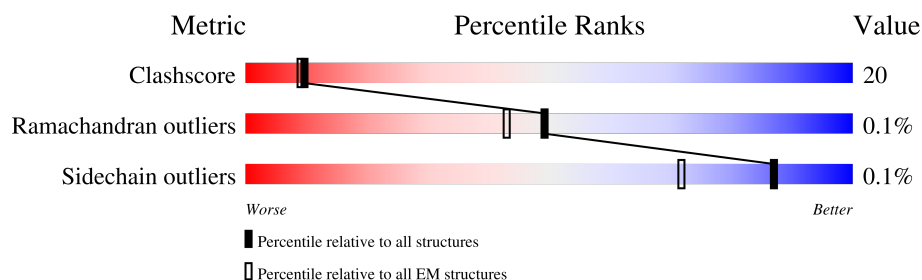
1 Overall quality at a glance i

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.



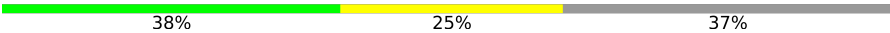
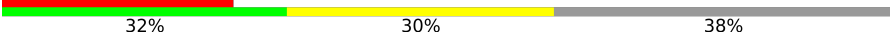
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3836 (3.84 - 4.84)

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	831	44% 33% 20% 47%
1	B	831	9% 41% 23% 37%
1	C	831	43% 21% 37%
1	D	831	42% 21% 36%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	831	 38% 25% 37%
1	F	831	 26% 32% 30% 38%

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.

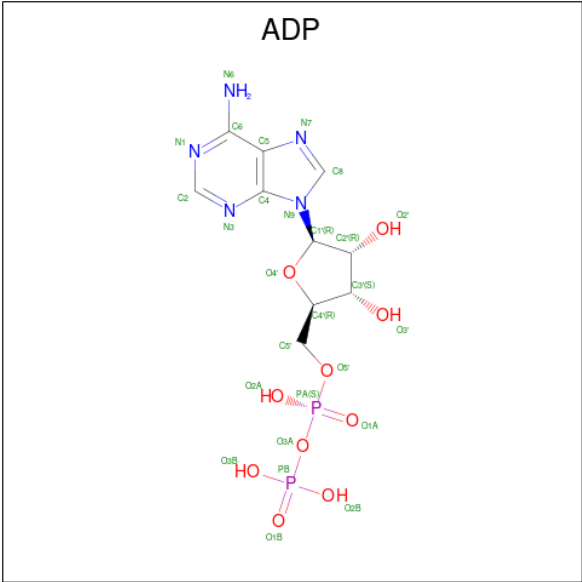
- Molecule 1 is a protein called ATPase family AAA domain-containing protein 2.

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:

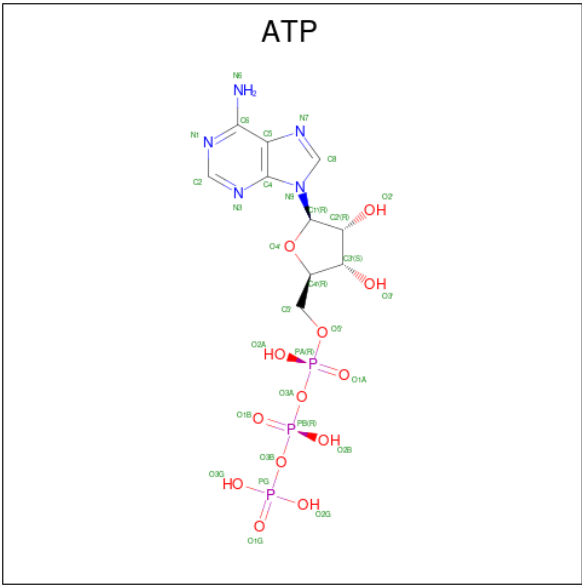
Chain	Residue	Modelled	Actual	Comment	Reference
A	532	GLN	GLU	engineered mutation	UNP Q6PL18
B	532	GLN	GLU	engineered mutation	UNP Q6PL18
C	532	GLN	GLU	engineered mutation	UNP Q6PL18
D	532	GLN	GLU	engineered mutation	UNP Q6PL18
E	532	GLN	GLU	engineered mutation	UNP Q6PL18
F	532	GLN	GLU	engineered mutation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

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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 (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

Continued on next page...

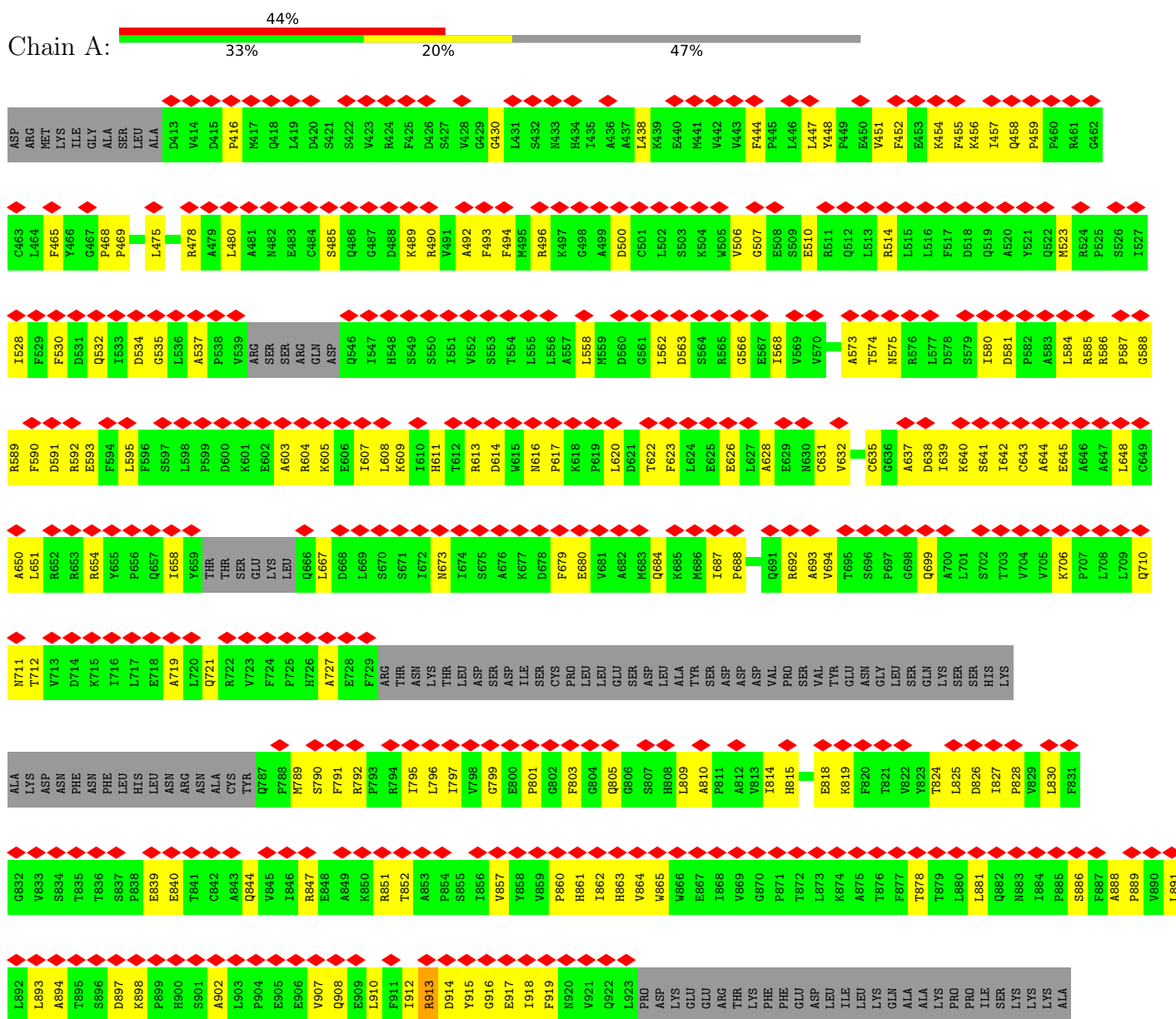
Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
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

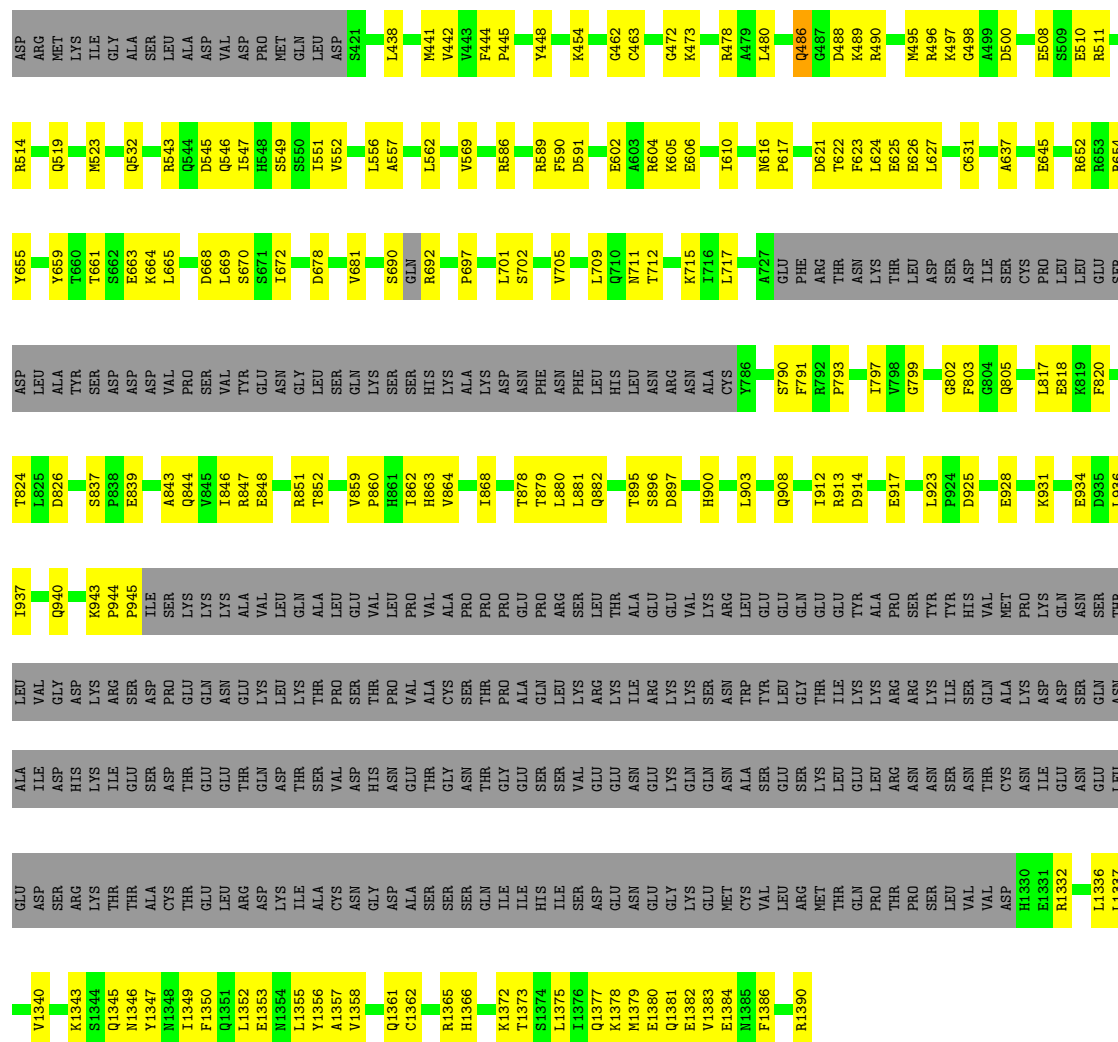






● Molecule 1: ATPase family AAA domain-containing protein 2

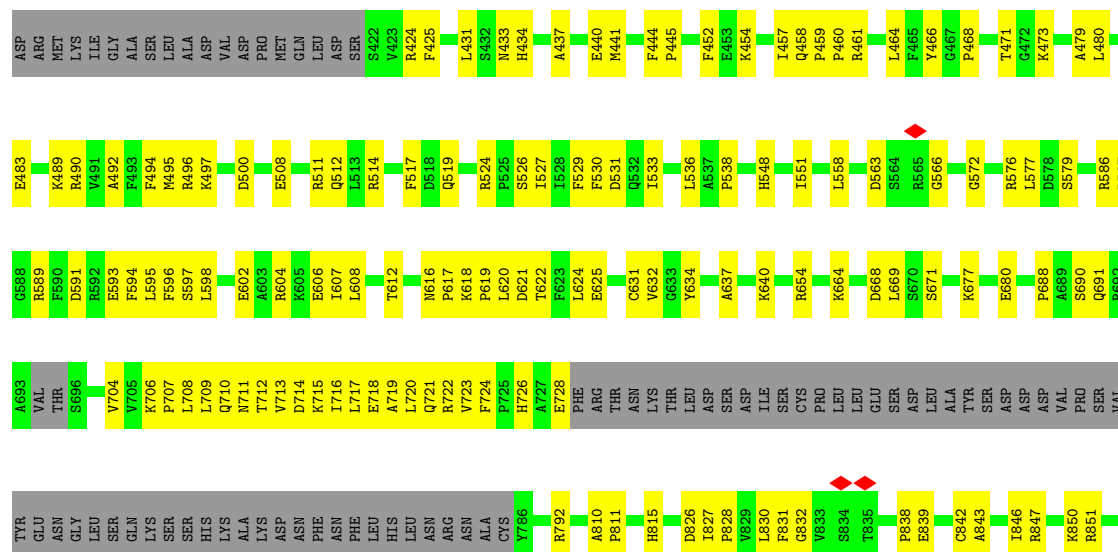
Chain C: 43% 21% 37%



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

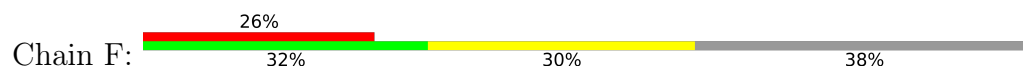
Chain D: 42% 21% 36%





D935	THR	ASN	LEU
L936	LEU	ALA	GLU
I937	VAL	ILE	ASP
L938	GLY	HIS	SER
K939	ASP	LYS	ARG
Q940	LYS	ILE	SER
P945	ARG	ASP	ILE
ILE	SER	THR	LYS
SER	PRO	THR	GLN
LYS	GLN	GLU	LYS
LYS	ASN	THR	ALA
LYS	GLU	THR	VAL
ALA	GLN	ASP	LEU
VAL	LYS	THR	GLN
LEU	LEU	THR	ALA
GLN	THR	VAL	LEU
LEU	SER	ASP	GLU
GLU	THR	VAL	THR
VAL	PRO	HIS	VAL
VAL	PRO	ASN	ASP
LEU	VAL	ASN	THR
PRO	VAL	GLU	PRO
ALA	VAL	GLU	PRO
VAL	ALA	THR	ALA
VAL	CYS	GLY	VAL
ALA	SER	THR	GLY
PRO	SER	ASN	SER
PRO	THR	THR	THR
PRO	PRO	ILE	GLU
GLU	ALA	ILE	GLU
PRO	GLN	SER	GLN
ARG	LEU	SER	VAL
SER	LEU	GLU	ASP
LEU	THR	GLU	THR
ALA	ALA	ASN	ILE
GLU	ARG	GLU	ALA
GLU	LYS	GLN	LYS
VAL	LYS	GLN	VAL
LYS	SER	GLN	LYS
ARG	LYS	ASN	THR
ARG	ARG	ASN	THR
TYR	LYS	ASN	ILE
TYR	ILE	SER	ASN
HIS	ASN	SER	THR
VAL	GLN	THR	VAL
VAL	ALA	CYS	ALA
MET	LYS	ASN	LYS
PRO	ASP	ILE	ASP
LYS	GLN	GLU	ASP
ASN	ASN	GLU	ASN
SER	GLN	GLU	SER

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



ASP	ASP	C463	ASP	P525	R586	PHE	M769	S855	G916
ARG	ARG	L464	ARG	S526	P587	ARG	I856	I856	E917
LYS	MET	F465	LYS	I527	F590	THR	I658	V857	I918
ILE	GLY	V466	ILE	I528	D591	LYS	Y659	Y858	V921
ALA	ALA	G470	ALA	F529	R592	THR	R792	Y859	E927
SER	SER	T471	SER	F530	R593	LEU	R794	P860	E928
LEU	LEU	G472	LEU	D531	F594	ASP	I795	H861	R929
ALA	ALA	K473	ALA	Q532	F595	SER	L796	H862	T930
ASP	ASP	T474	ASP	I533	L475	ILE	H863	H863	K931
VAL	VAL	V475	VAL	I534	F596	LYS	D668	H864	K931
ASP	ASP	V476	ASP	D534	S597	CYS	S670	W865	F932
ASP	ASP	A477	ASP	G535	L598	PRO	S671	W866	F933
MET	MET	R478	MET	L536	PRO	LEU	S675	W867	E934
GLN	GLN	A479	GLN	A537	ASP	LEU	K601	E867	E934
LEU	LEU	L480	LEU	F538	K602	GLU	F679	I868	I937
ASP	ASP	A481	ASP	V539	E602	SER	E680	L938	L938
SER	SER	H482	SER	R540	A603	ASP	P811	P811	P944
S422	V423	E483	S422	S541	R604	LEU	A812	T872	P944
V424	R424	S485	V424	S542	E605	ALA	I812	L873	PRO
P425	P425	Q486	P425	S543	I607	TYR	K874	T874	ILE
D426	D426	Q487	D426	S544	L608	SER	A875	A875	SER
S427	S427	D488	S427	S545	M609	ASP	T876	T876	LYS
V428	V428	R489	V428	S546	H610	ASP	F877	F877	LYS
G429	G429	K490	G429	I547	T611	VAL	T878	T878	ALA
L431	L431	R491	L431	H548	H612	PRO	T879	T879	VAL
S432	S432	V491	S432	S549	D614	SER	L880	L880	LEU
N433	N433	A492	N433	S550	W615	GLN	F820	F820	GLN
H434	H434	F493	H434	I551	K618	ARG	L881	L881	ALA
I435	I435	F494	I435	T554	P619	VAL	T821	T821	LEU
A436	A436	M495	A436	L555	G620	THR	V822	V822	GLU
A437	A437	R496	A437	L556	L621	VAL	W823	W823	VAL
L438	L438	R497	L438	L557	L624	GLY	I824	I824	LEU
R439	R439	G498	R439	A557	E625	LEU	T825	T825	PRO
E440	E440	L558	E440	L558	E626	SER	D826	D826	VAL
M441	M441	A499	M441	M559	E627	LYS	I827	I827	ALA
V442	V442	D500	V442	D560	L628	SER	P828	P828	PRO
F444	F444	C501	F444	G561	A628	HIS	R829	R829	PRO
P445	P445	L502	P445	D562	V705	LYS	L830	L830	GLU
L446	L446	S503	L446	S563	K706	ALA	L831	L831	PRO
L447	L447	K504	L447	S564	P707	LYS	L832	L832	ARG
Y448	Y448	M505	Y448	S565	L708	ASP	G832	G832	SER
P449	P449	V506	P449	G566	L709	ASN	V833	V833	LEU
E450	E450	G507	E450	E567	Y634	THR	S834	S834	THR
V451	V451	E508	V451	I568	C635	PHE	T835	T835	ALA
F452	F452	S509	F452	V569	A637	LEU	T836	T836	GLU
E453	E453	R511	E453	I571	D638	HIS	S837	S837	VAL
K454	K454	O512	K454	G572	L639	LEU	P838	P838	LYS
P455	P455	L513	P455	T574	K640	ASN	E839	E839	ARG
R456	R456	R514	R456	R575	S641	ARG	E840	E840	VAL
I457	I457	L515	I457	R576	T642	THR	T841	T841	GLU
Q458	Q458	F517	Q458	L577	I643	LEU	C842	C842	GLU
P459	P459	D518	P459	S579	C643	ASN	A843	A843	GLN
R460	R460	A520	R460	I580	E644	THR	Q844	Q844	GLU
R461	R461	Y521	R461	D581	E645	LEU	Y786	Y786	TYR
Q462	Q462	O522	Q462	F582	L648	LEU	Q787	Q787	ALA
		R523		L584	L651	HIS	P788	P788	
		L584		R585	R652	LEU			
		R585				THR			
						GLU			



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: ATP, ADP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.18	0/3551	0.49	0/4820
1	B	0.21	0/4289	0.47	0/5806
1	C	0.30	0/4281	0.51	0/5796
1	D	0.31	0/4297	0.48	0/5818
1	E	0.24	0/4279	0.48	0/5792
1	F	0.21	0/4206	0.54	0/5691
All	All	0.25	0/24903	0.49	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	148	0
1	B	4197	0	4255	149	0
1	C	4190	0	4247	131	0
1	D	4206	0	4258	143	0
1	E	4188	0	4245	202	0
1	F	4119	0	4179	257	0
2	A	27	0	11	0	0

Continued on next page...

Continued from previous page...

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	975	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 20.

The worst 5 of 975 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%)	43	77
1	B	519/831 (62%)	478 (92%)	40 (8%)	1 (0%)	43	77
1	C	519/831 (62%)	480 (92%)	38 (7%)	1 (0%)	43	77
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%)	43	77

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3019/4986 (60%)	2752 (91%)	263 (9%)	4 (0%)	49 83

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%)	464 (100%)	0	100 100
1	C	464/742 (62%)	463 (100%)	1 (0%)	87 85
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%)	76 79
All	All	2695/4452 (60%)	2691 (100%)	4 (0%)	87 88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	486	GLN
1	F	717	LEU
1	F	1382	GLU
1	F	1383	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	863	HIS
1	F	1361	GLN
1	E	532	GLN
1	F	863	HIS
1	D	1370	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	B	1401	-	32,33,33	0.48	0	48,52,52	0.42	0
3	ATP	F	1401	-	32,33,33	0.35	0	48,52,52	0.60	0
3	ATP	E	1401	-	32,33,33	0.92	2 (6%)	48,52,52	0.46	0
2	ADP	A	1301	-	28,29,29	1.43	4 (14%)	43,45,45	1.90	8 (18%)
3	ATP	C	1401	-	32,33,33	0.93	1 (3%)	48,52,52	0.52	1 (2%)
3	ATP	C	1402	-	32,33,33	0.83	2 (6%)	48,52,52	0.46	0

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	B	1401	-	-	7/22/38/38	0/3/3/3
3	ATP	F	1401	-	-	11/22/38/38	0/3/3/3
3	ATP	E	1401	-	-	7/22/38/38	0/3/3/3
2	ADP	A	1301	-	-	1/16/32/32	0/3/3/3
3	ATP	C	1401	-	-	7/22/38/38	0/3/3/3
3	ATP	C	1402	-	-	6/22/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1301	ADP	C5-C4	4.81	1.47	1.39
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
2	A	1301	ADP	C5-C6	2.79	1.48	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1301	ADP	C5-C4-N3	-6.27	118.09	126.72
2	A	1301	ADP	N3-C4-N9	5.06	135.77	127.17
2	A	1301	ADP	C2-N3-C4	3.85	121.23	111.83
2	A	1301	ADP	C4-C5-N7	-3.37	106.73	110.58
2	A	1301	ADP	N3-C2-N1	-3.21	123.72	128.58

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

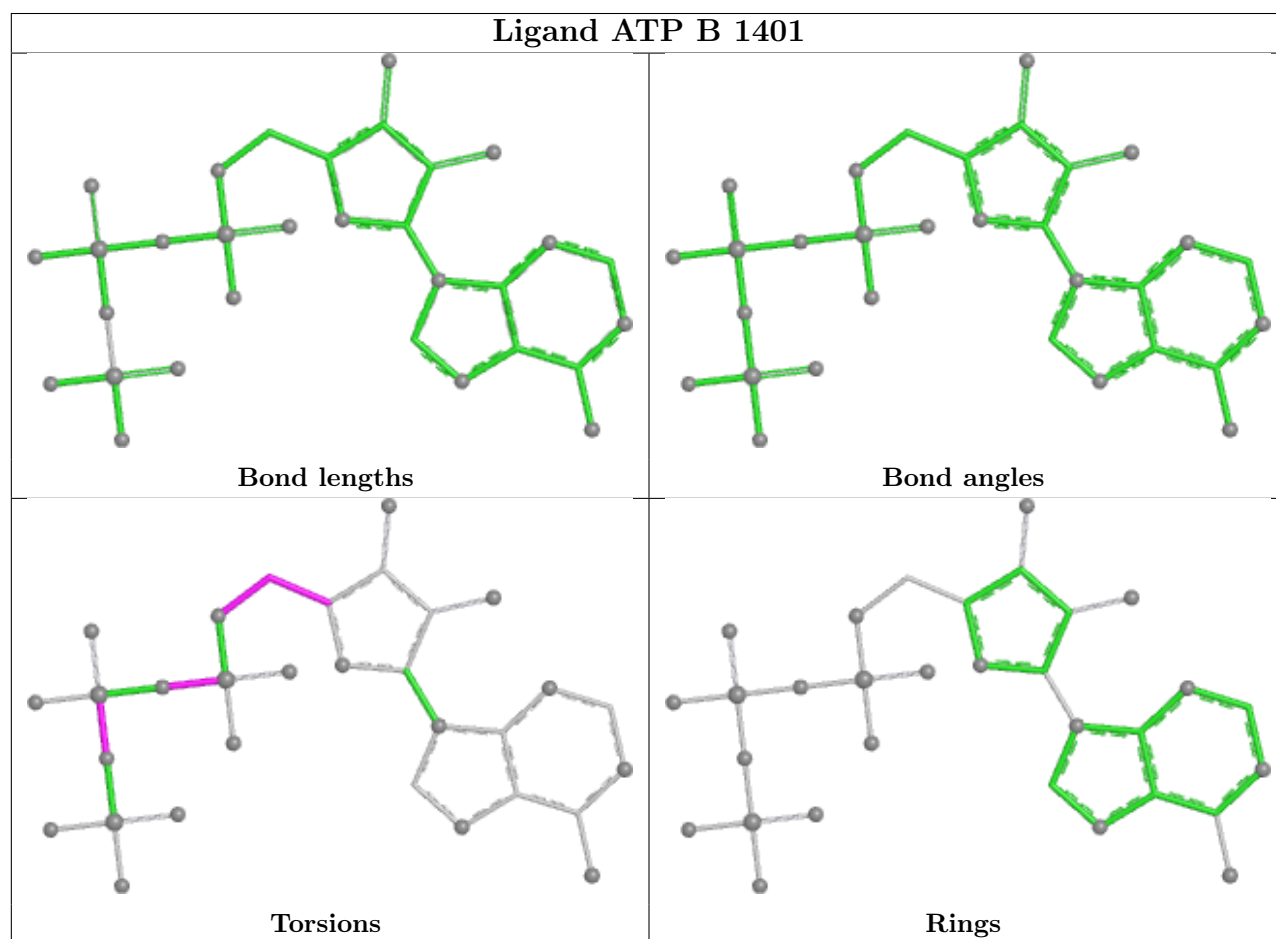
Mol	Chain	Res	Type	Atoms
3	C	1401	ATP	PB-O3B-PG-O3G
3	C	1401	ATP	O4'-C4'-C5'-O5'
3	C	1402	ATP	PB-O3B-PG-O3G
3	C	1402	ATP	O4'-C4'-C5'-O5'
3	C	1402	ATP	C3'-C4'-C5'-O5'

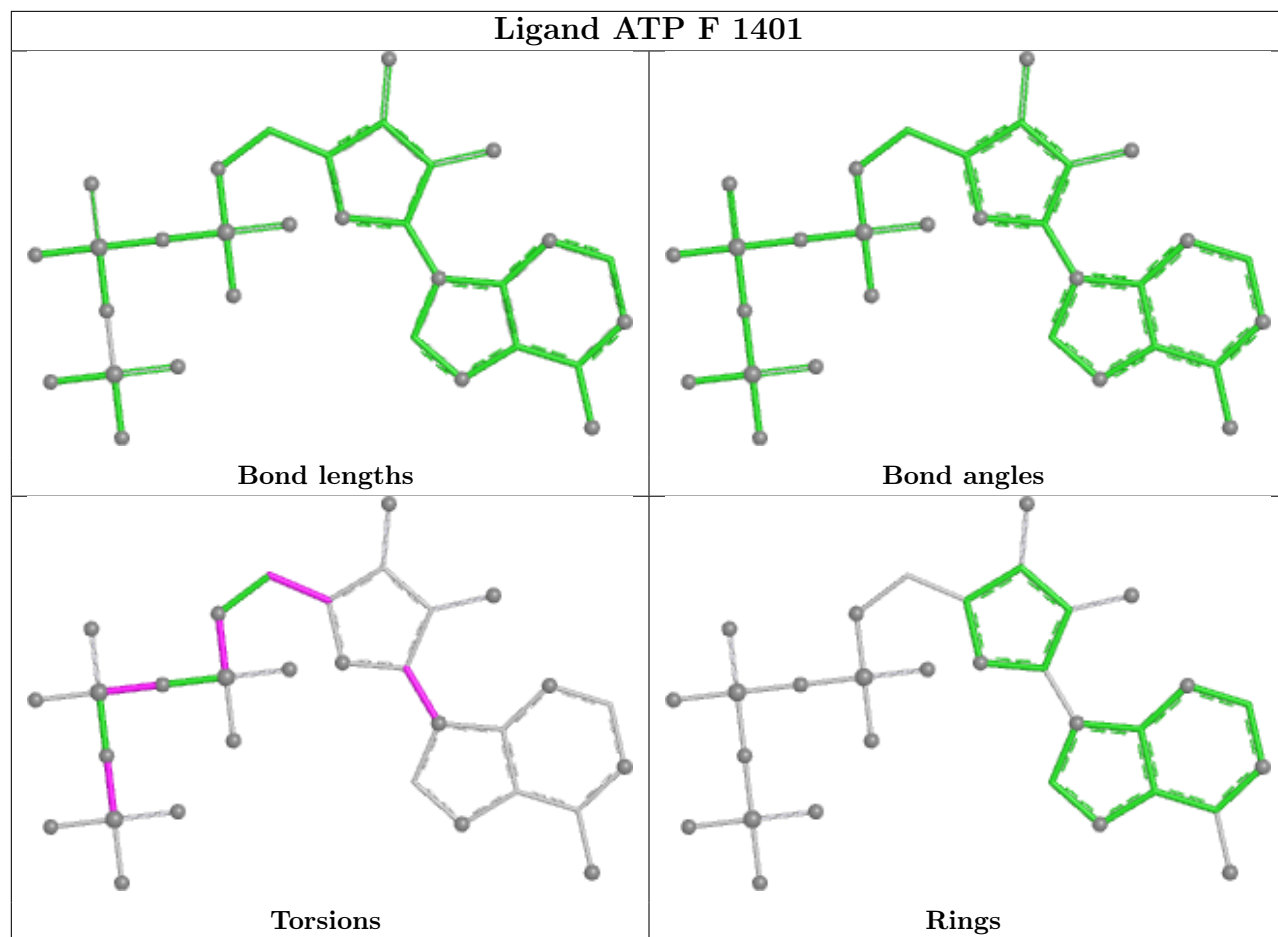
There are no ring outliers.

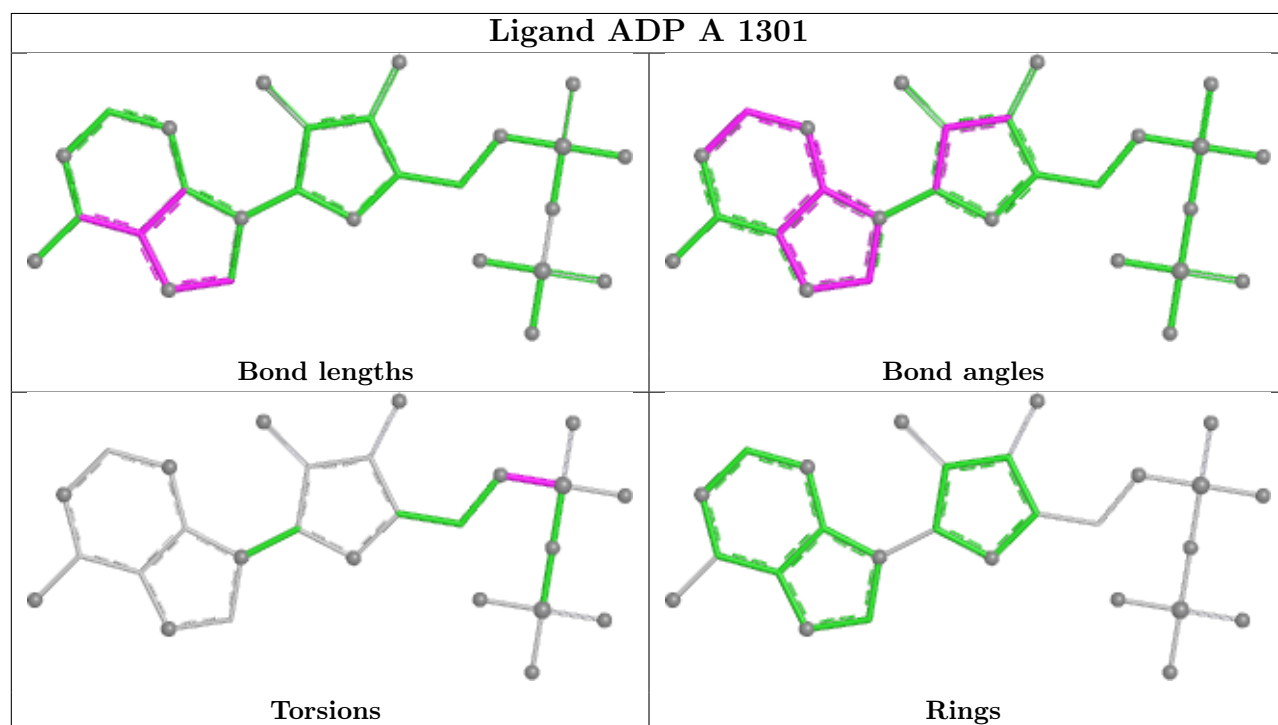
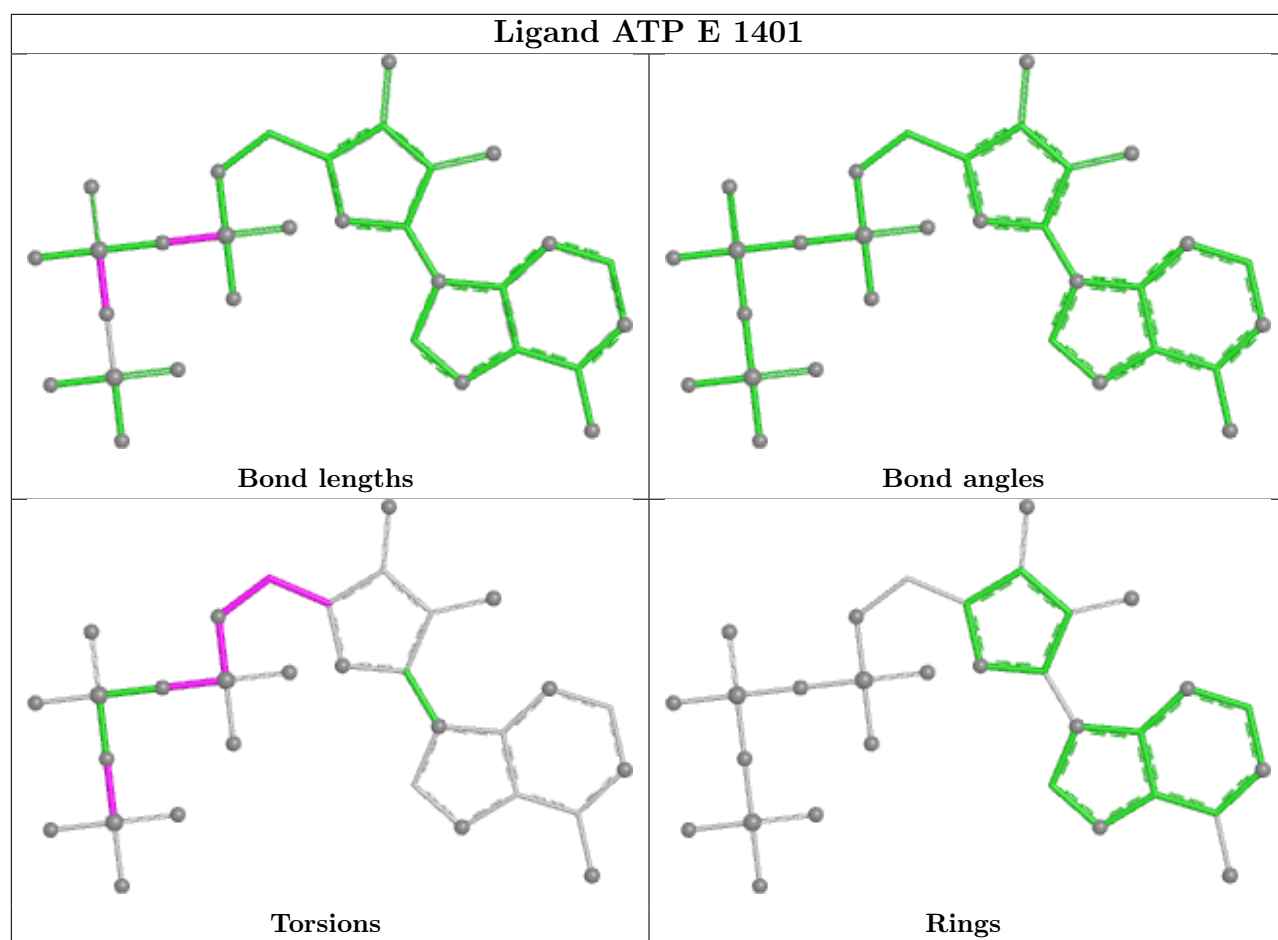
5 monomers are involved in 28 short contacts:

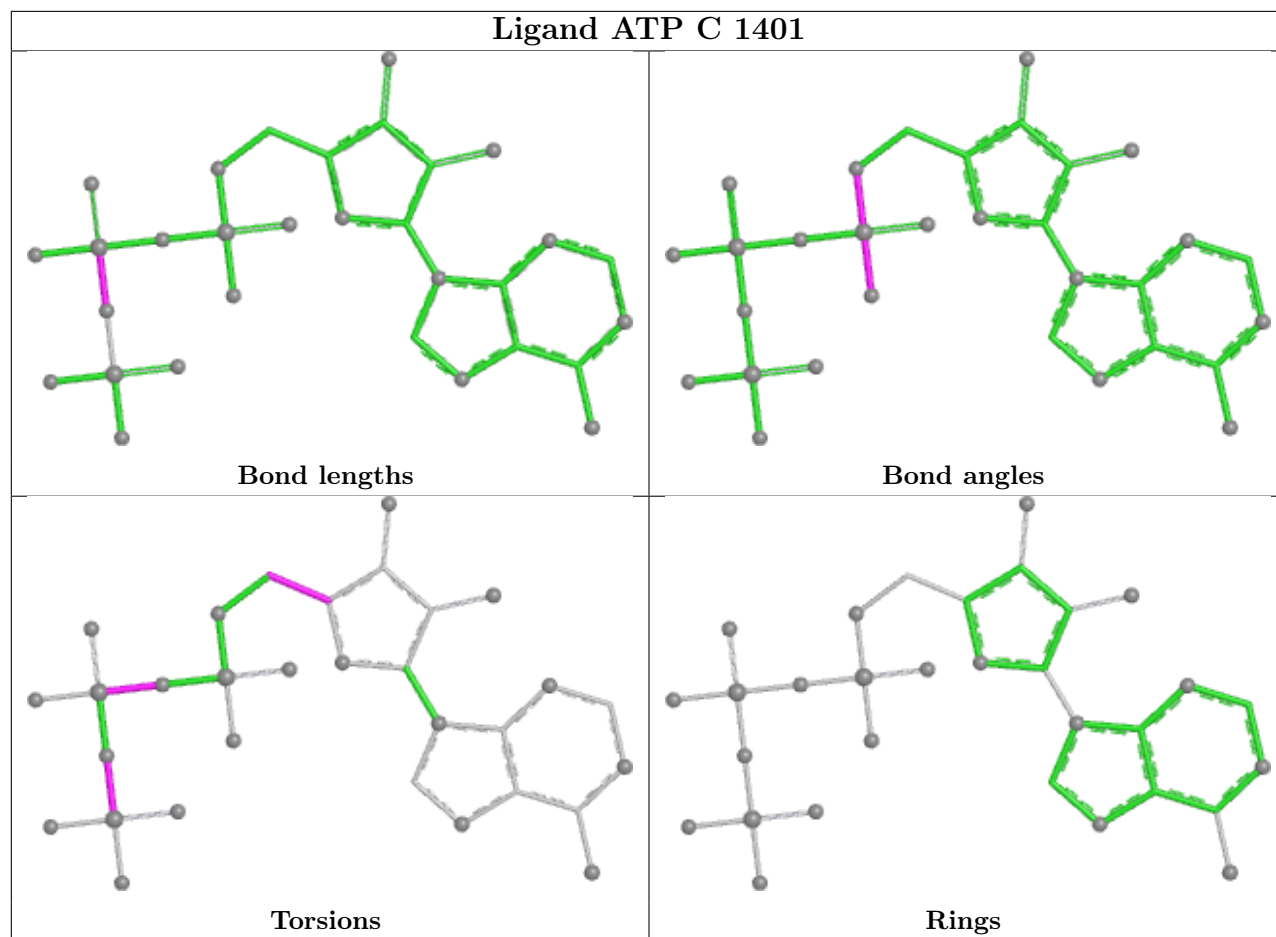
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1401	ATP	4	0
3	F	1401	ATP	14	0
3	E	1401	ATP	3	0
3	C	1401	ATP	3	0
3	C	1402	ATP	4	0

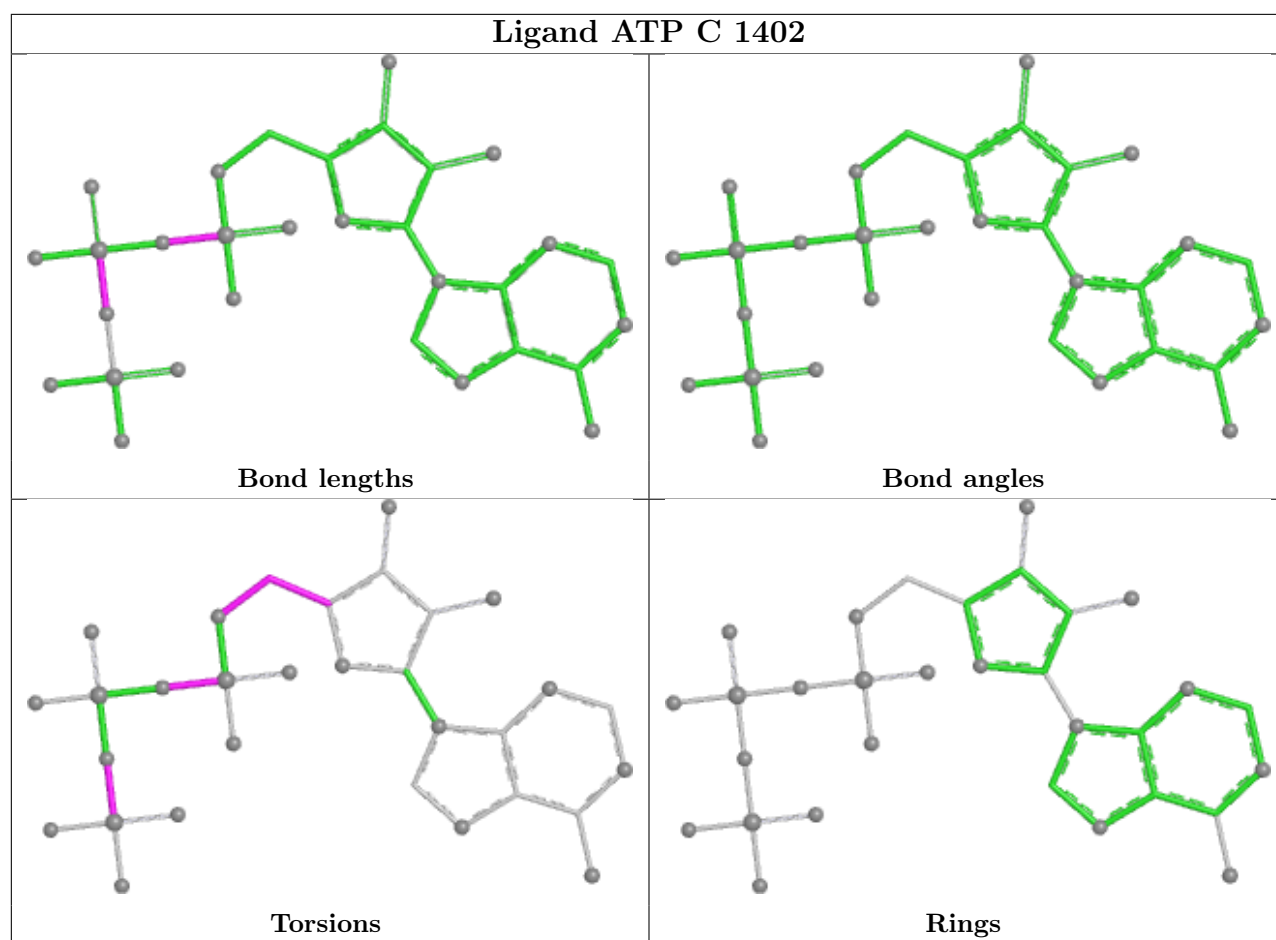
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

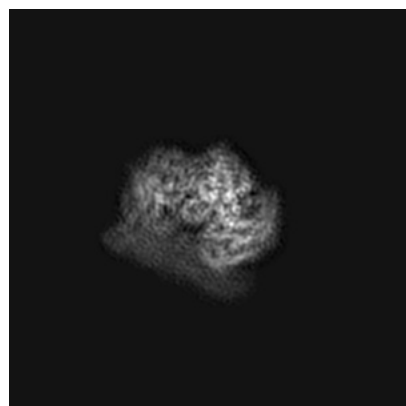
6 Map visualisation [i](#)

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.

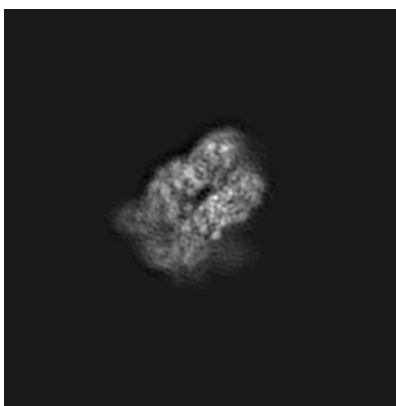
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

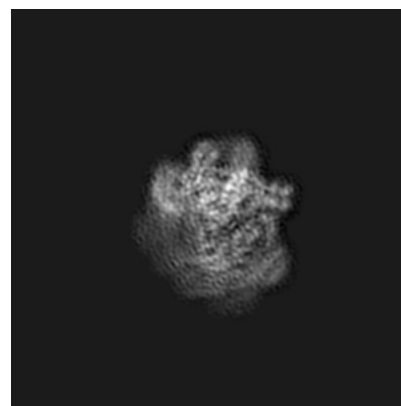
6.1.1 Primary map



X

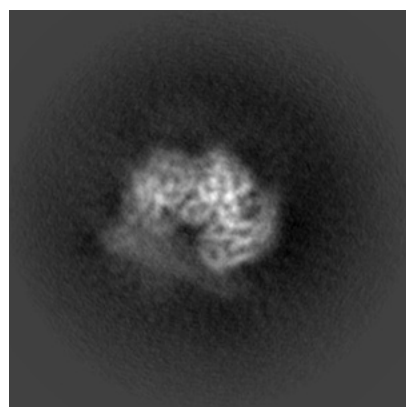


Y

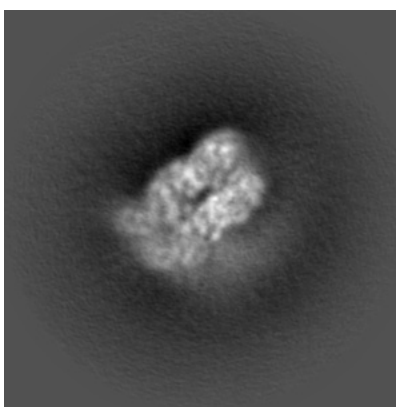


Z

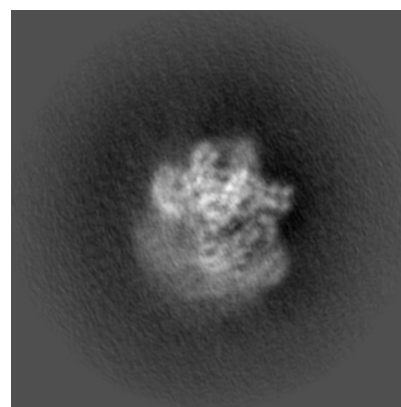
6.1.2 Raw map



X



Y

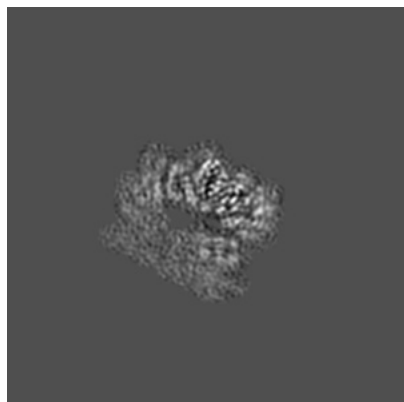


Z

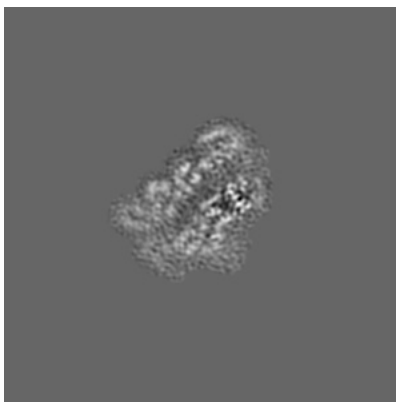
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

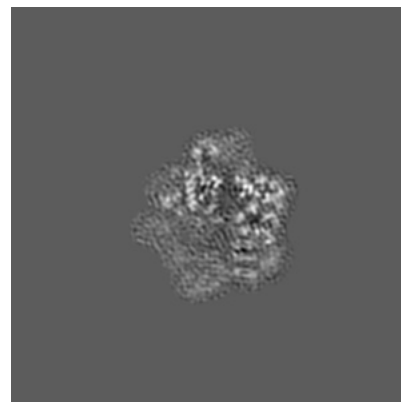
6.2.1 Primary map



X Index: 150

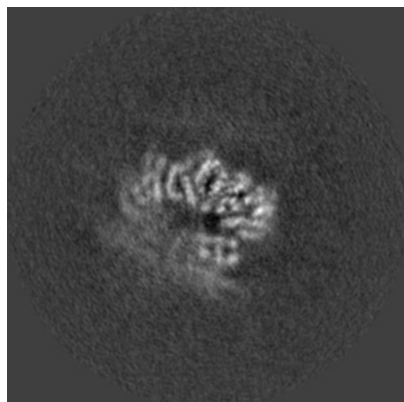


Y Index: 150

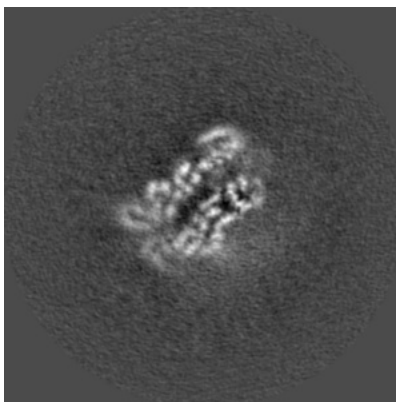


Z Index: 150

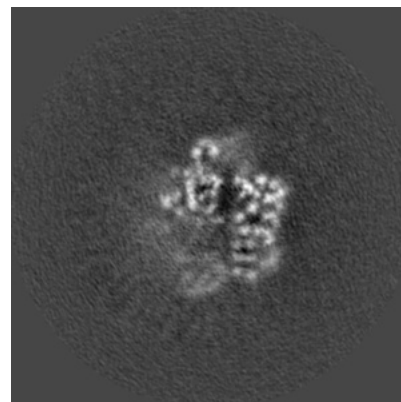
6.2.2 Raw map



X Index: 150



Y Index: 150

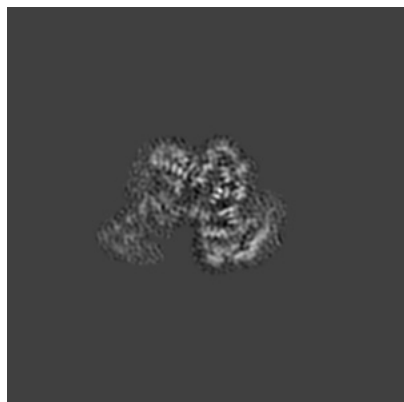


Z Index: 150

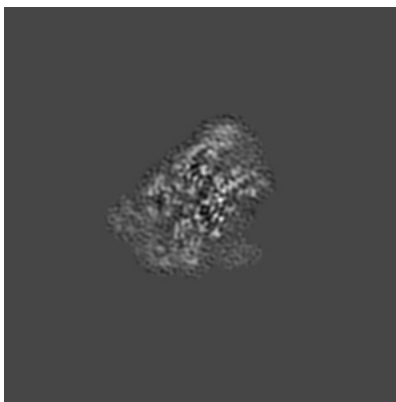
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

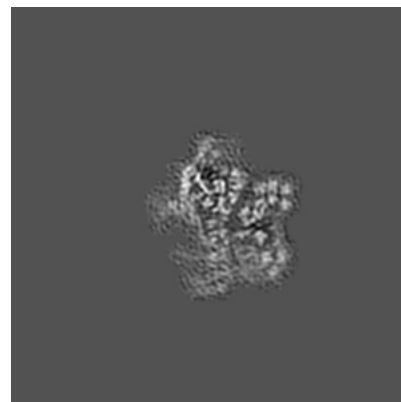
6.3.1 Primary map



X Index: 168

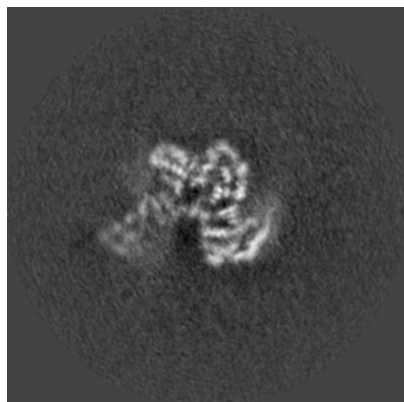


Y Index: 165

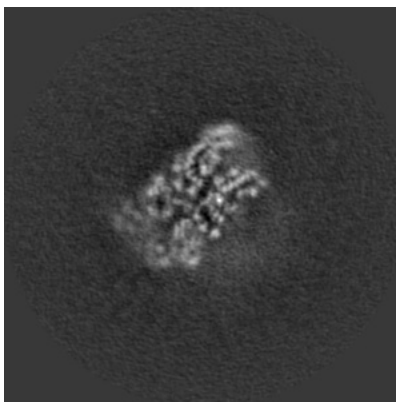


Z Index: 159

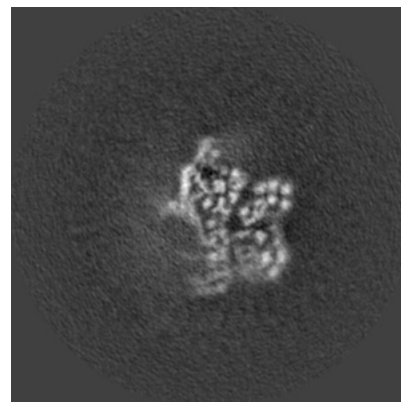
6.3.2 Raw map



X Index: 168



Y Index: 164

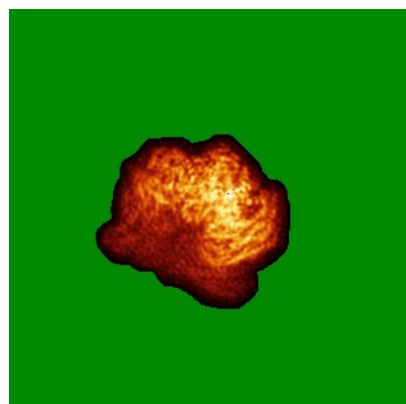


Z Index: 159

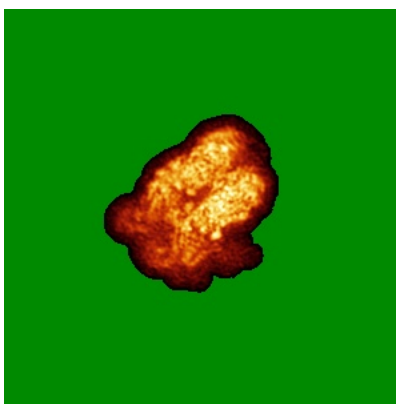
The images above show the largest variance slices of the map in three orthogonal directions.

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

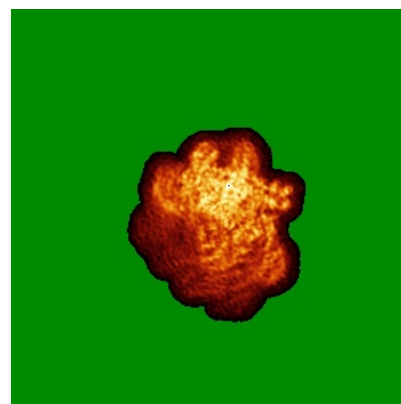
6.4.1 Primary map



X

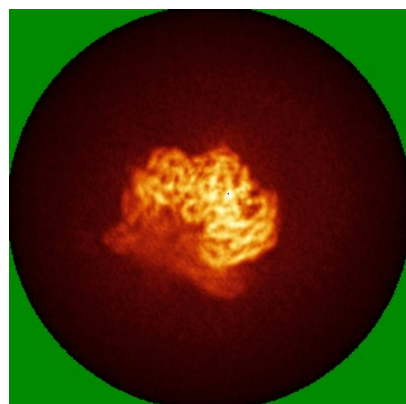


Y

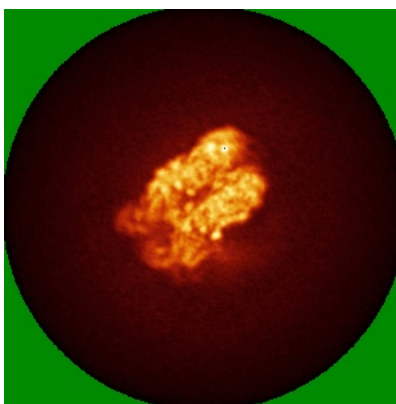


Z

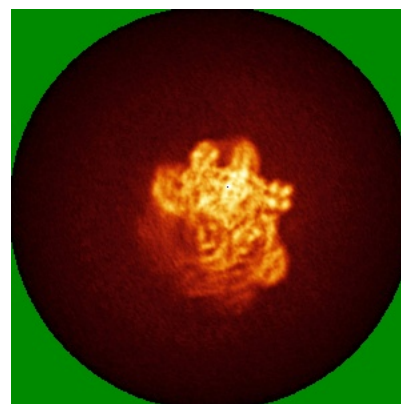
6.4.2 Raw map



X



Y

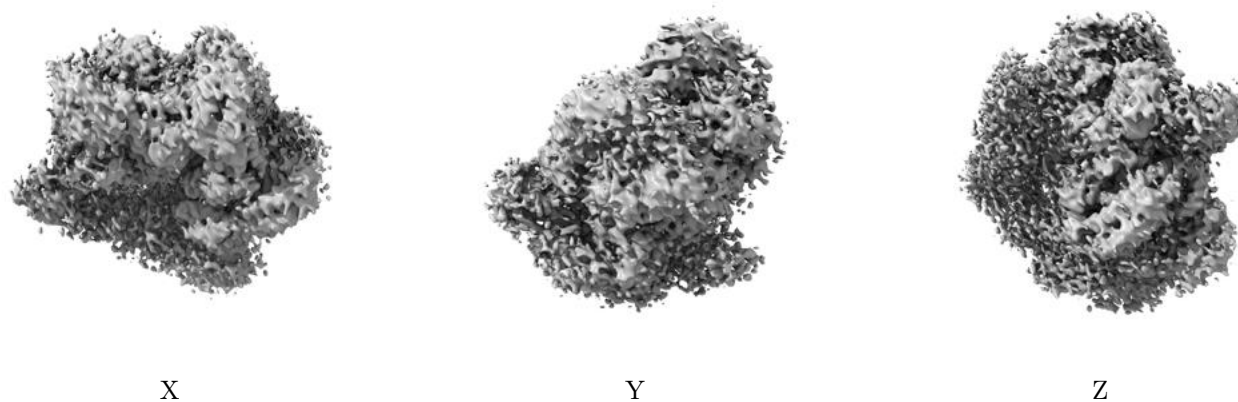


Z

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.

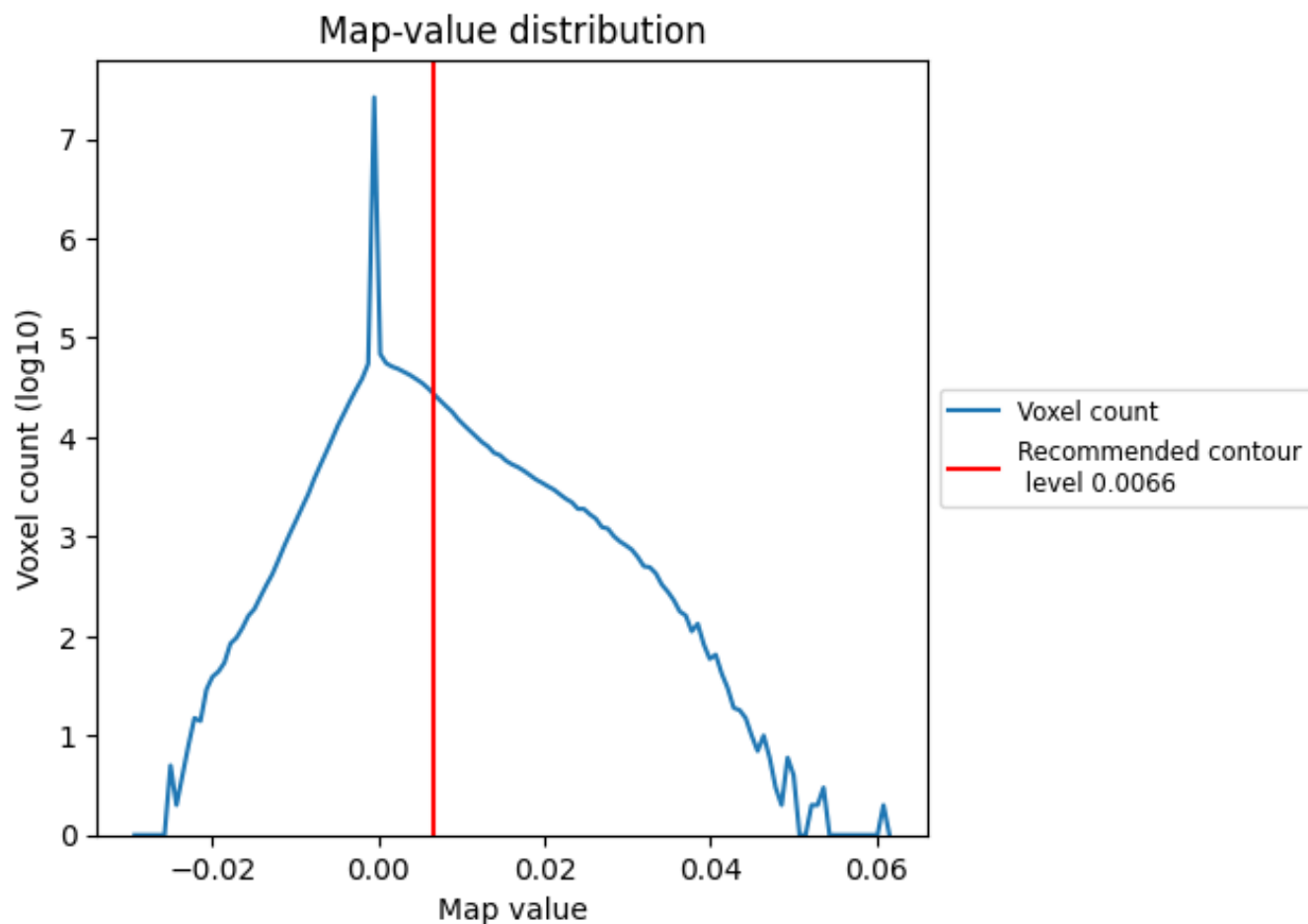
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

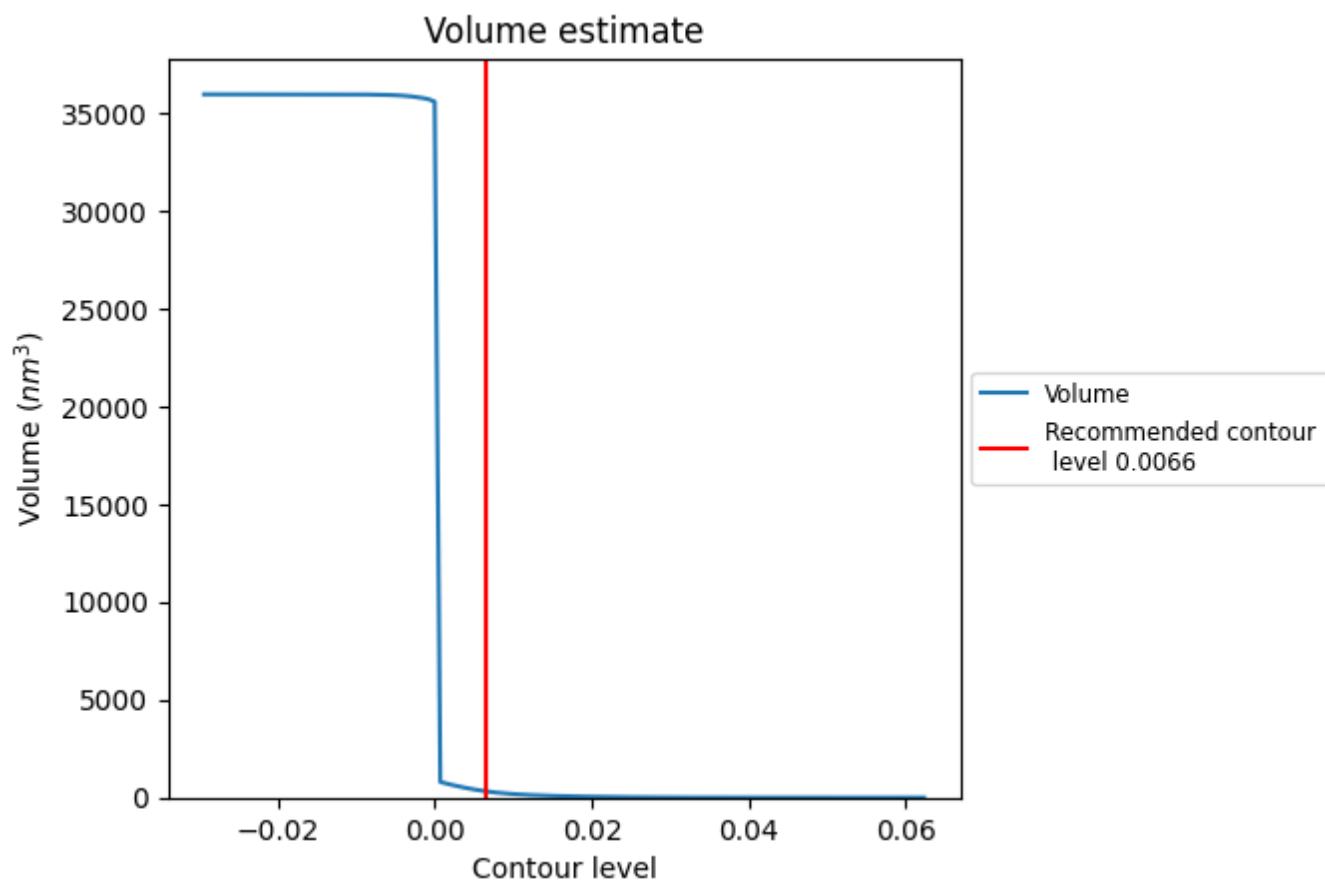
This section contains the results of statistical analysis of the map.

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.

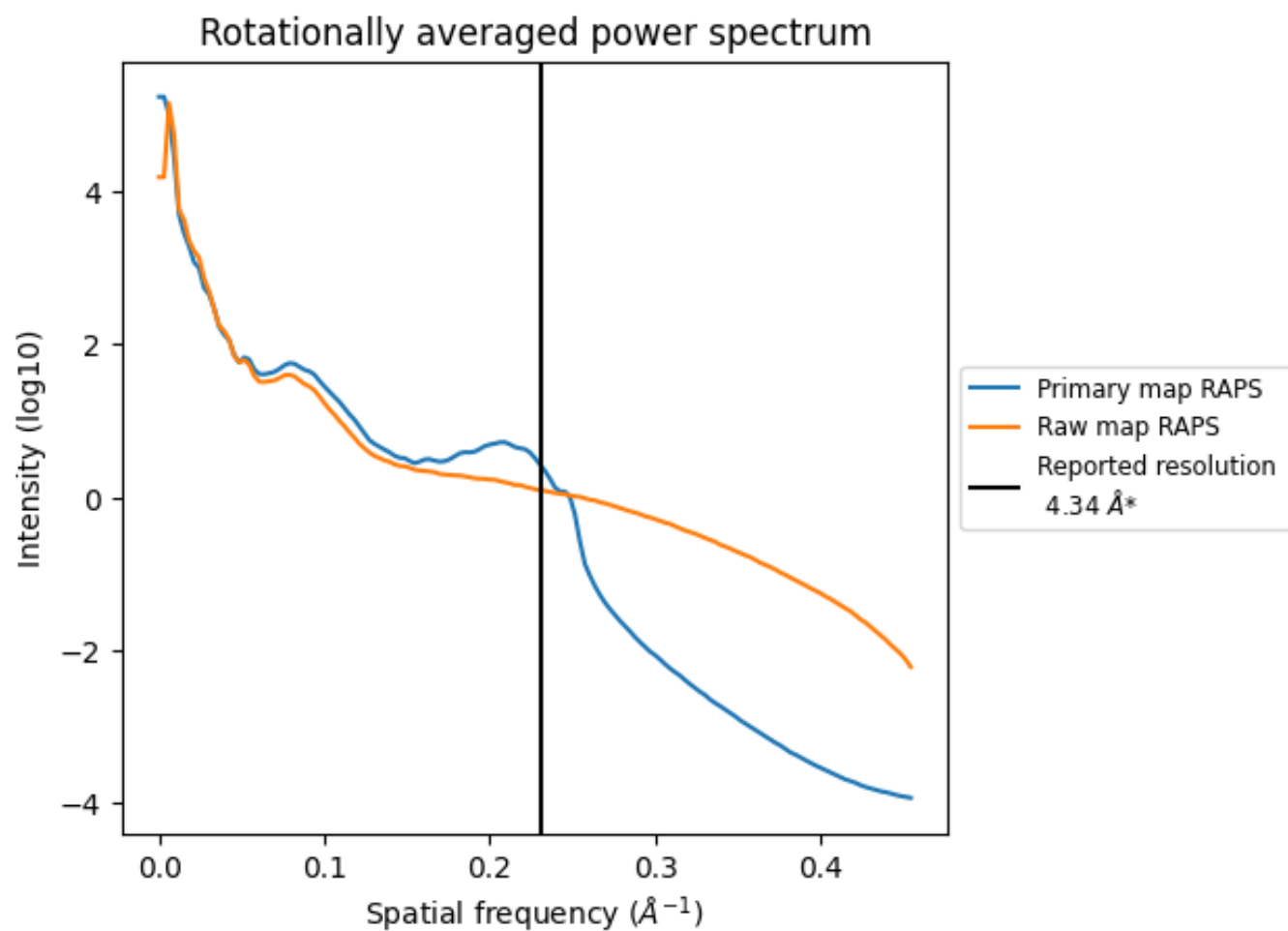
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 315 nm³; 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 ⓘ

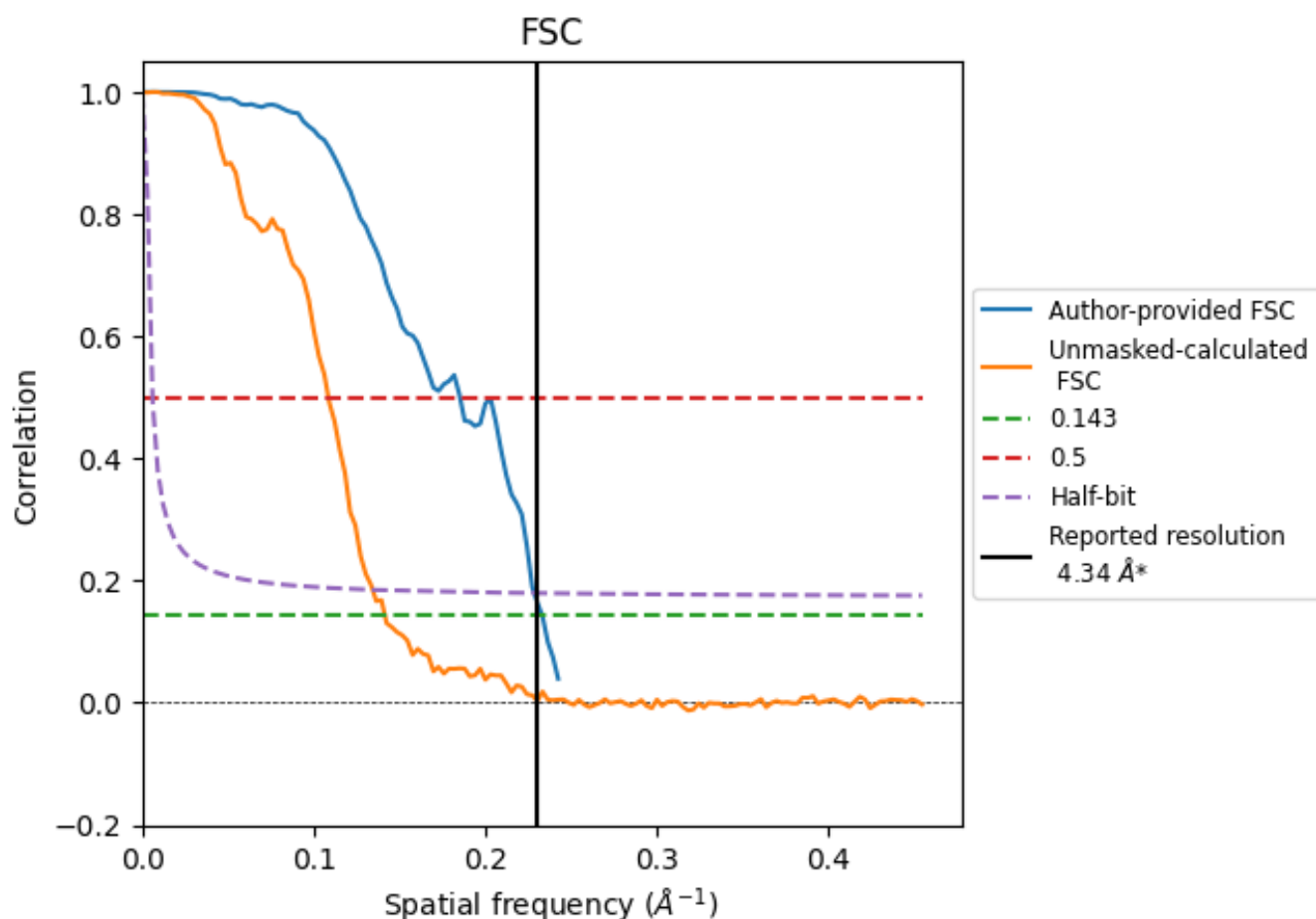


*Reported resolution corresponds to spatial frequency of $0.230 \text{ \AA}^{-1}$

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 0.230 Å⁻¹

8.2 Resolution estimates [i](#)

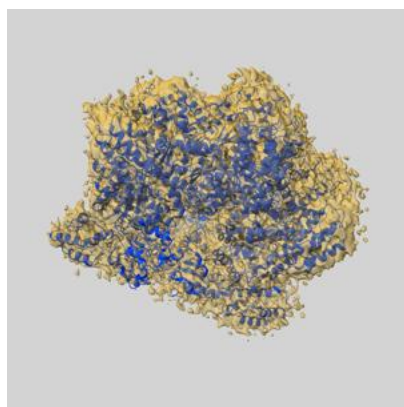
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.34	-	-
Author-provided FSC curve	4.29	5.40	4.38
Unmasked-calculated*	7.07	9.22	7.45

*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 %

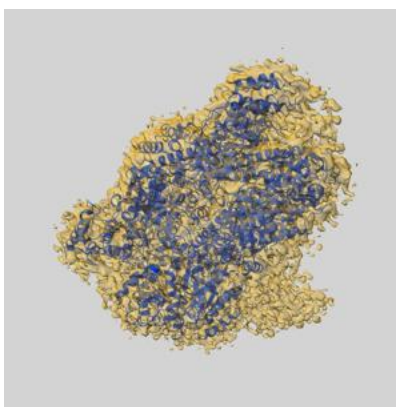
9 Map-model fit [i](#)

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](#).

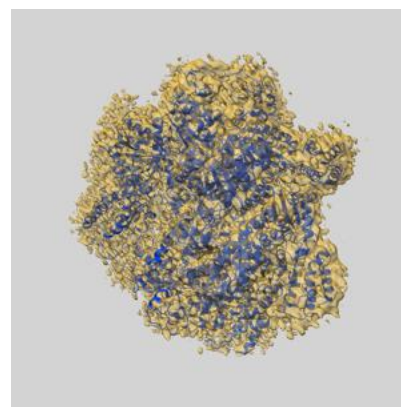
9.1 Map-model overlay [i](#)



X



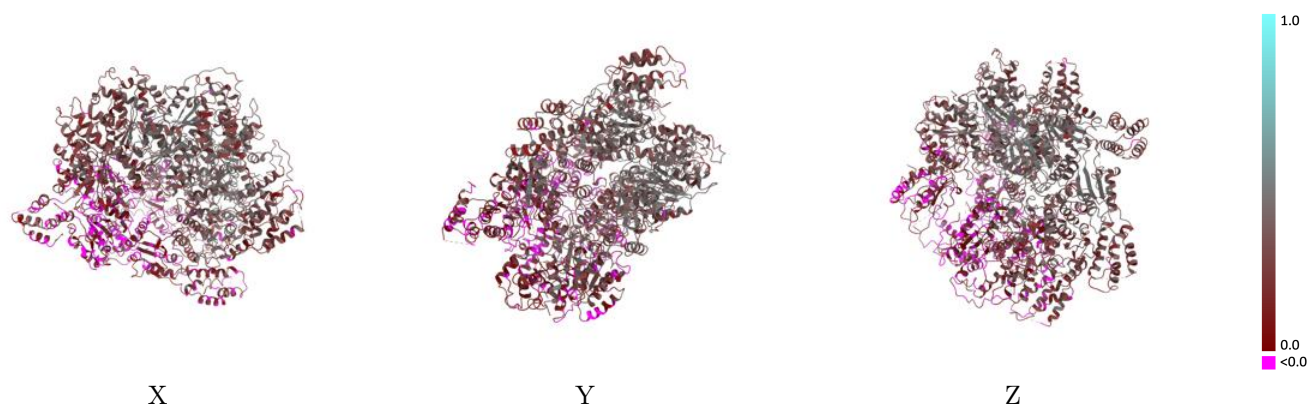
Y



Z

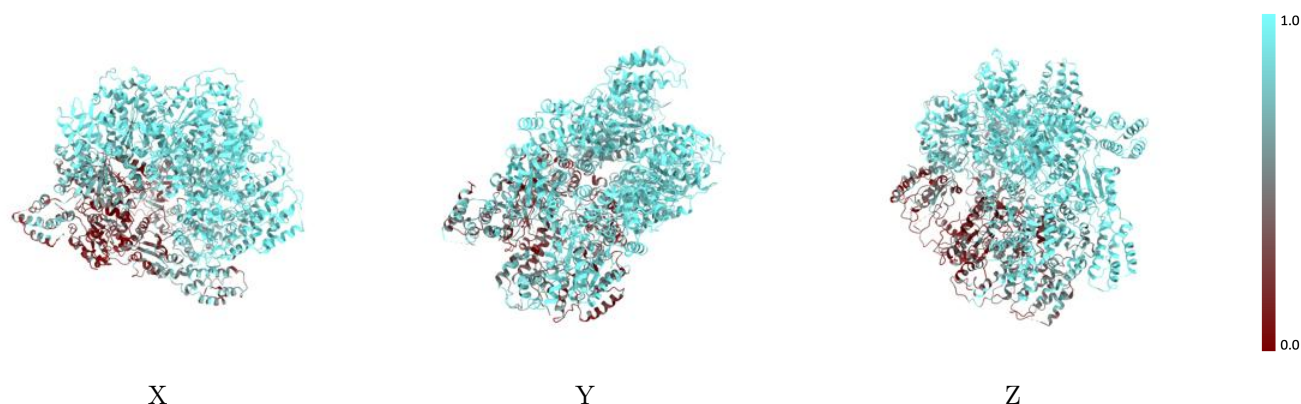
The images above show the 3D surface view of the map at the recommended contour level 0.0066 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



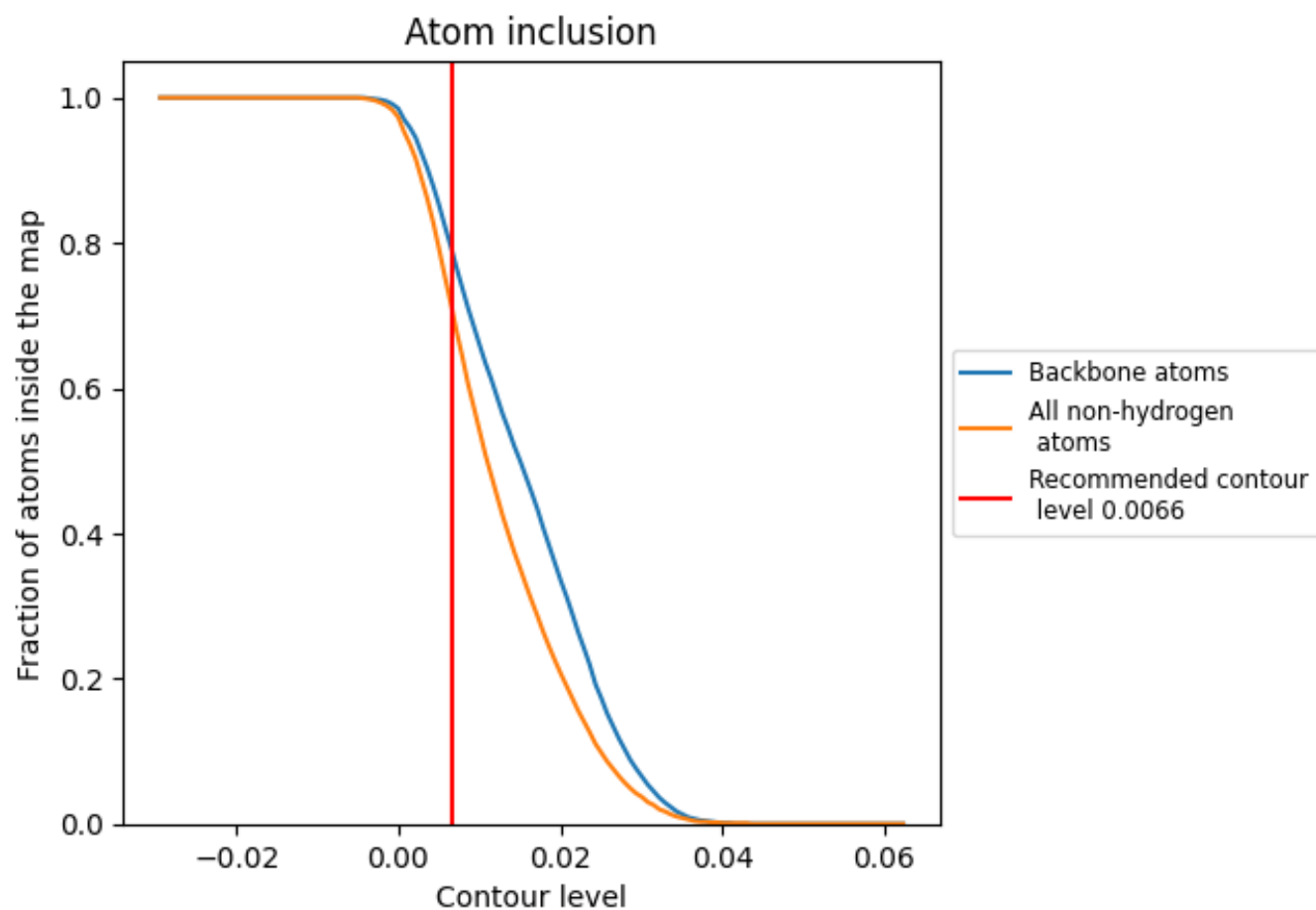
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.7100	0.2390
A	0.2050	0.0560
B	0.7100	0.2430
C	0.9350	0.3590
D	0.9380	0.3700
E	0.9170	0.2840
F	0.4660	0.0860

1.0

0.0

<0.0