



wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 07:53 PM EDT

PDB ID : 7SXO
EMDB ID : EMD-25502
Title : Yeast Lon (PIM1) with endogenous substrate
Authors : Yang, J.; Song, A.S.; Wiseman, R.L.; Lander, G.C.
Deposited on : 2021-11-24
Resolution : 3.30 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.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)	:	2.39

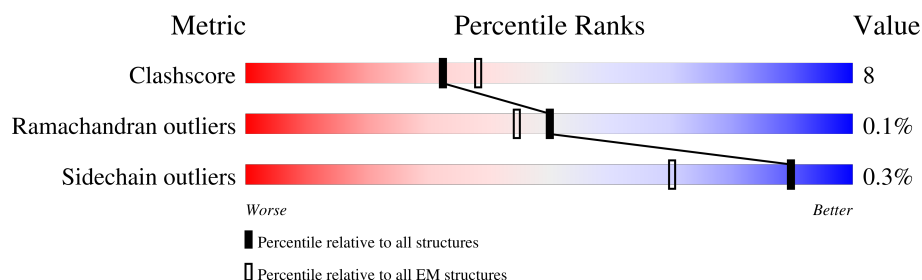
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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 ≥ 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	968	<div> <div>7%</div> <div>44%</div> <div>12%</div> <div>44%</div> </div>
1	B	968	<div> <div>14%</div> <div>39%</div> <div>11%</div> <div>50%</div> </div>
1	C	968	<div> <div>12%</div> <div>39%</div> <div>11%</div> <div>50%</div> </div>
1	D	968	<div> <div>9%</div> <div>43%</div> <div>13%</div> <div>43%</div> </div>
1	E	968	<div> <div>•</div> <div>46%</div> <div>10%</div> <div>44%</div> </div>
1	F	968	<div> <div>•</div> <div>45%</div> <div>11%</div> <div>43%</div> </div>
2	G	12	<div> <div>58%</div> <div>75%</div> <div>25%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24894 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 Lon protease homolog, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	544	Total	C	N	O	S	0	0
			4256	2721	720	797	18		
1	B	487	Total	C	N	O	S	0	0
			3793	2421	643	711	18		
1	C	487	Total	C	N	O	S	0	0
			3786	2416	645	708	17		
1	D	547	Total	C	N	O	S	0	0
			4262	2725	718	801	18		
1	E	546	Total	C	N	O	S	0	0
			4278	2734	725	801	18		
1	F	549	Total	C	N	O	S	0	0
			4292	2745	726	802	19		

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	MET	-	expression tag	UNP P36775
A	167	ASN	-	expression tag	UNP P36775
A	168	HIS	-	expression tag	UNP P36775
A	169	LYS	-	expression tag	UNP P36775
A	170	VAL	-	expression tag	UNP P36775
A	171	SER	-	expression tag	UNP P36775
A	172	SER	-	expression tag	UNP P36775
A	173	HIS	-	expression tag	UNP P36775
A	174	HIS	-	expression tag	UNP P36775
A	175	HIS	-	expression tag	UNP P36775
A	176	HIS	-	expression tag	UNP P36775
A	177	HIS	-	expression tag	UNP P36775
A	178	HIS	-	expression tag	UNP P36775
A	179	SER	-	expression tag	UNP P36775
A	180	ALA	-	expression tag	UNP P36775
A	181	GLY	-	expression tag	UNP P36775
B	166	MET	-	expression tag	UNP P36775
B	167	ASN	-	expression tag	UNP P36775

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Chain	Residue	Modelled	Actual	Comment	Reference
B	168	HIS	-	expression tag	UNP P36775
B	169	LYS	-	expression tag	UNP P36775
B	170	VAL	-	expression tag	UNP P36775
B	171	SER	-	expression tag	UNP P36775
B	172	SER	-	expression tag	UNP P36775
B	173	HIS	-	expression tag	UNP P36775
B	174	HIS	-	expression tag	UNP P36775
B	175	HIS	-	expression tag	UNP P36775
B	176	HIS	-	expression tag	UNP P36775
B	177	HIS	-	expression tag	UNP P36775
B	178	HIS	-	expression tag	UNP P36775
B	179	SER	-	expression tag	UNP P36775
B	180	ALA	-	expression tag	UNP P36775
B	181	GLY	-	expression tag	UNP P36775
C	166	MET	-	expression tag	UNP P36775
C	167	ASN	-	expression tag	UNP P36775
C	168	HIS	-	expression tag	UNP P36775
C	169	LYS	-	expression tag	UNP P36775
C	170	VAL	-	expression tag	UNP P36775
C	171	SER	-	expression tag	UNP P36775
C	172	SER	-	expression tag	UNP P36775
C	173	HIS	-	expression tag	UNP P36775
C	174	HIS	-	expression tag	UNP P36775
C	175	HIS	-	expression tag	UNP P36775
C	176	HIS	-	expression tag	UNP P36775
C	177	HIS	-	expression tag	UNP P36775
C	178	HIS	-	expression tag	UNP P36775
C	179	SER	-	expression tag	UNP P36775
C	180	ALA	-	expression tag	UNP P36775
C	181	GLY	-	expression tag	UNP P36775
D	166	MET	-	expression tag	UNP P36775
D	167	ASN	-	expression tag	UNP P36775
D	168	HIS	-	expression tag	UNP P36775
D	169	LYS	-	expression tag	UNP P36775
D	170	VAL	-	expression tag	UNP P36775
D	171	SER	-	expression tag	UNP P36775
D	172	SER	-	expression tag	UNP P36775
D	173	HIS	-	expression tag	UNP P36775
D	174	HIS	-	expression tag	UNP P36775
D	175	HIS	-	expression tag	UNP P36775
D	176	HIS	-	expression tag	UNP P36775
D	177	HIS	-	expression tag	UNP P36775

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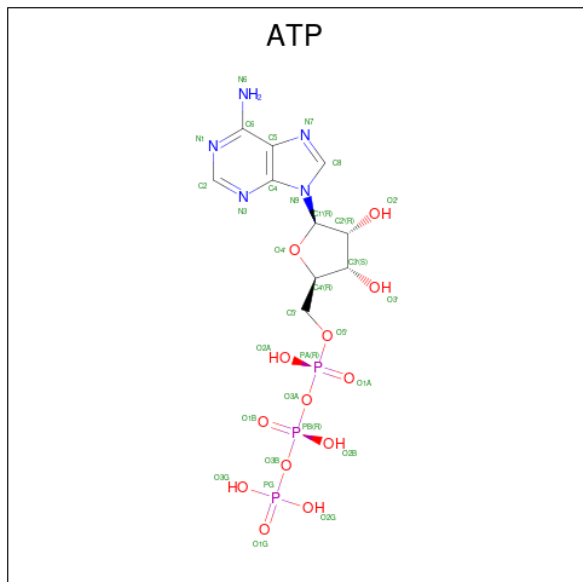
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Chain	Residue	Modelled	Actual	Comment	Reference
D	178	HIS	-	expression tag	UNP P36775
D	179	SER	-	expression tag	UNP P36775
D	180	ALA	-	expression tag	UNP P36775
D	181	GLY	-	expression tag	UNP P36775
E	166	MET	-	expression tag	UNP P36775
E	167	ASN	-	expression tag	UNP P36775
E	168	HIS	-	expression tag	UNP P36775
E	169	LYS	-	expression tag	UNP P36775
E	170	VAL	-	expression tag	UNP P36775
E	171	SER	-	expression tag	UNP P36775
E	172	SER	-	expression tag	UNP P36775
E	173	HIS	-	expression tag	UNP P36775
E	174	HIS	-	expression tag	UNP P36775
E	175	HIS	-	expression tag	UNP P36775
E	176	HIS	-	expression tag	UNP P36775
E	177	HIS	-	expression tag	UNP P36775
E	178	HIS	-	expression tag	UNP P36775
E	179	SER	-	expression tag	UNP P36775
E	180	ALA	-	expression tag	UNP P36775
E	181	GLY	-	expression tag	UNP P36775
F	166	MET	-	expression tag	UNP P36775
F	167	ASN	-	expression tag	UNP P36775
F	168	HIS	-	expression tag	UNP P36775
F	169	LYS	-	expression tag	UNP P36775
F	170	VAL	-	expression tag	UNP P36775
F	171	SER	-	expression tag	UNP P36775
F	172	SER	-	expression tag	UNP P36775
F	173	HIS	-	expression tag	UNP P36775
F	174	HIS	-	expression tag	UNP P36775
F	175	HIS	-	expression tag	UNP P36775
F	176	HIS	-	expression tag	UNP P36775
F	177	HIS	-	expression tag	UNP P36775
F	178	HIS	-	expression tag	UNP P36775
F	179	SER	-	expression tag	UNP P36775
F	180	ALA	-	expression tag	UNP P36775
F	181	GLY	-	expression tag	UNP P36775

- Molecule 2 is a protein called endogenous substrate.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	Mg	0
			1	1	
4	D	1	Total	Mg	0
			1	1	
4	E	2	Total	Mg	0
			2	2	

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

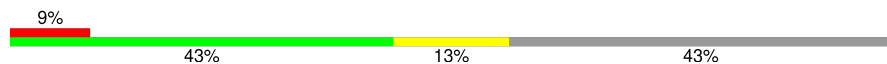


Mol	Chain	Residues	Atoms					AltConf
5	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
5	C	1	Total	C	N	O	P	0
			27	10	5	10	2	

Chain C:

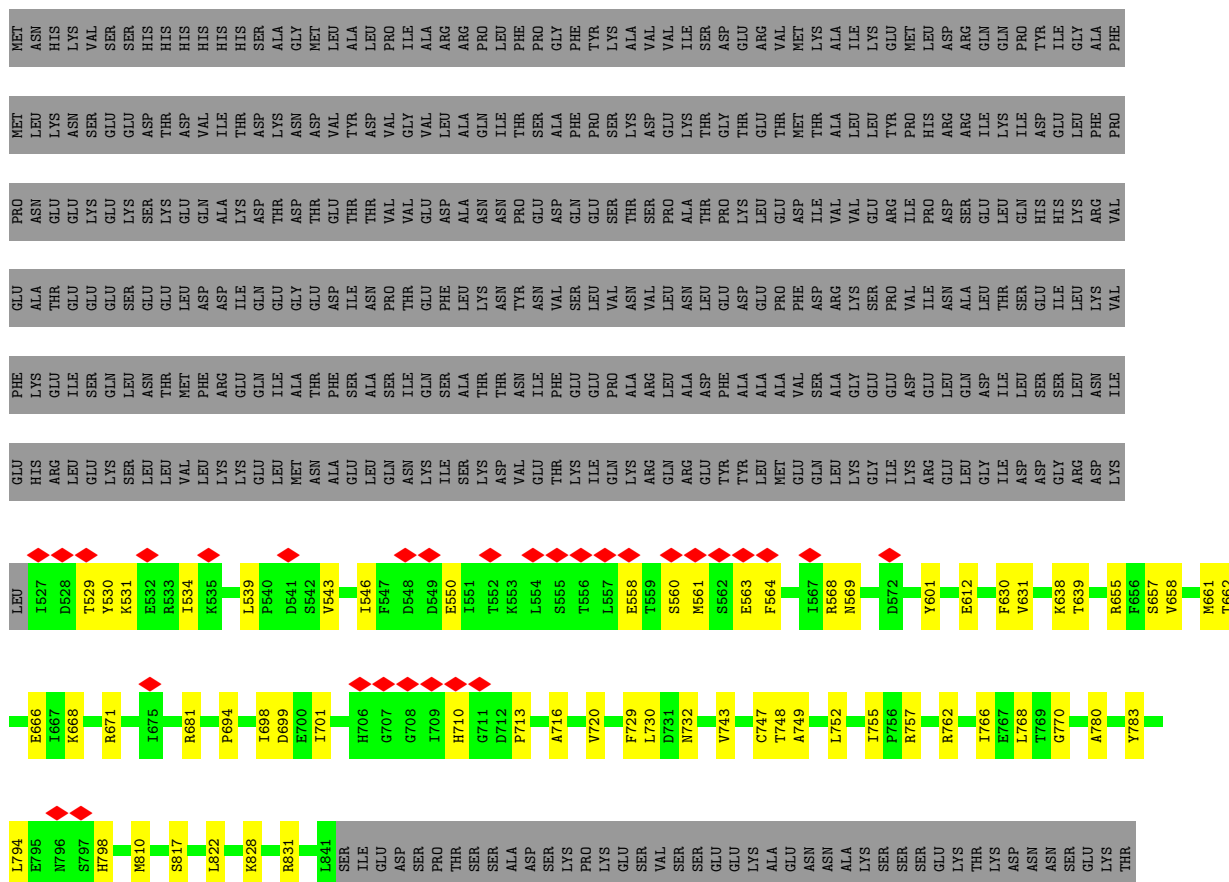
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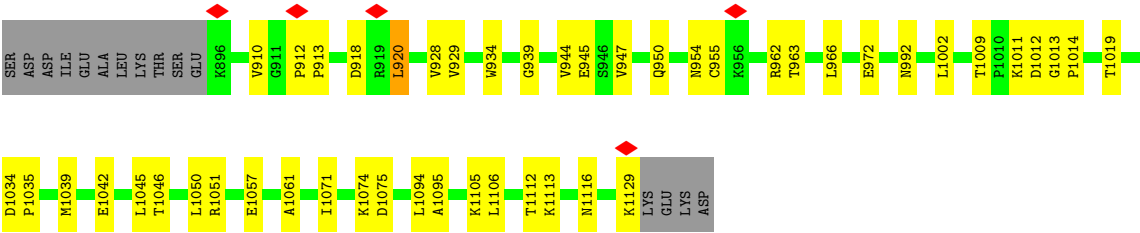
Chain D:



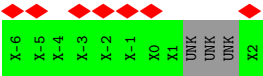
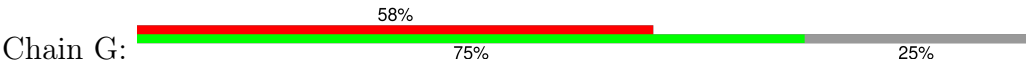
MET	ASN	ASN	LVS	LVS	VAL	SER	SER	HIS	HIS	HIS	HIS	HIS	ALA	ALA	LEU	LEU	ARG	ARG	PRO	PRO	LEU	PHE	PRO	GLY	PHE	LVS	LYS	VAL	VAL	ILE	ILE	ASP	SER	GLU	ARG	VAL	MET	MET	LEU	LEU	ASP	ARG	ARG	GLN	GLN	PRO	PRO	TYR	ILE	GLY	ALA	PHE
MET	LEU	LVS	ASN	SER	GLU	GLU	ASP	THR	THR	THR	THR	ILE	VAL	VAL	VAL	LEU	LEU	ALA	ALA	GLN	ILE	THR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







• Molecule 2: endogenous substrate



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81945	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.754	Depositor
Minimum map value	-0.843	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.224	Depositor
Map size (\AA)	294.4, 294.4, 294.4	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.15, 1.15, 1.15	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.25	0/4339	0.47	0/5862
1	B	0.25	0/3864	0.48	0/5221
1	C	0.25	0/3857	0.47	0/5212
1	D	0.25	0/4345	0.48	0/5873
1	E	0.24	0/4362	0.48	1/5893 (0.0%)
1	F	0.25	0/4377	0.54	2/5915 (0.0%)
All	All	0.25	0/25144	0.49	3/33976 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	920	LEU	CB-CA-C	-13.68	84.20	110.20
1	F	920	LEU	N-CA-C	13.57	147.63	111.00
1	E	958	PRO	N-CA-CB	6.85	111.52	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4256	0	4325	76	0
1	B	3793	0	3861	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3786	0	3854	67	0
1	D	4262	0	4324	90	0
1	E	4278	0	4351	71	0
1	F	4292	0	4369	75	0
2	G	45	0	13	0	0
3	A	31	0	12	1	0
3	D	31	0	12	2	0
3	E	31	0	12	1	0
3	F	31	0	11	1	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
4	E	2	0	0	0	0
5	B	27	0	11	2	0
5	C	27	0	12	1	0
All	All	24894	0	25167	413	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 8.

The worst 5 of 413 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:C:651:ARG:NH1	1:C:692:GLN:O	2.14	0.79
1:D:809:LEU:O	1:D:813:TYR:HB2	1.87	0.75
1:D:576:SER:HB3	1:D:687:LYS:HG3	1.71	0.72
1:E:1026:SER:HB2	1:E:1033:ILE:HD11	1.70	0.72
1:C:638:LYS:HD2	1:C:748:THR:HG23	1.70	0.72

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	536/968 (55%)	508 (95%)	27 (5%)	1 (0%)	44	71
1	B	481/968 (50%)	463 (96%)	18 (4%)	0	100	100
1	C	481/968 (50%)	459 (95%)	21 (4%)	1 (0%)	44	71
1	D	543/968 (56%)	512 (94%)	30 (6%)	1 (0%)	44	71
1	E	542/968 (56%)	514 (95%)	27 (5%)	1 (0%)	44	71
1	F	545/968 (56%)	511 (94%)	34 (6%)	0	100	100
All	All	3128/5808 (54%)	2967 (95%)	157 (5%)	4 (0%)	50	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	1120	LYS
1	D	955	CYS
1	E	958	PRO
1	A	623	VAL

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	466/855 (54%)	465 (100%)	1 (0%)	92	95
1	B	414/855 (48%)	411 (99%)	3 (1%)	81	88
1	C	412/855 (48%)	411 (100%)	1 (0%)	92	95
1	D	464/855 (54%)	463 (100%)	1 (0%)	92	95
1	E	468/855 (55%)	467 (100%)	1 (0%)	92	95
1	F	470/855 (55%)	468 (100%)	2 (0%)	89	93
All	All	2694/5130 (52%)	2685 (100%)	9 (0%)	90	94

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	569	ASN

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Mol	Chain	Res	Type
1	F	1129	LYS
1	B	919	ARG
1	C	1120	LYS
1	D	907	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	750	ASN
1	B	954	ASN
1	D	693	ASN
1	F	987	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	ATP	F	1200	-	28,33,33	0.62	0	34,52,52	0.60	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ADP	C	1200	-	24,29,29	0.90	0	29,45,45	1.20	2 (6%)
3	ATP	D	1200	4	28,33,33	0.62	0	34,52,52	0.60	1 (2%)
3	ATP	A	1200	-	28,33,33	0.62	0	34,52,52	0.61	1 (2%)
3	ATP	E	1201	-	28,33,33	0.64	0	34,52,52	0.59	1 (2%)
5	ADP	B	1200	-	24,29,29	0.93	1 (4%)	29,45,45	1.42	4 (13%)

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	F	1200	-	-	1/18/38/38	0/3/3/3
5	ADP	C	1200	-	-	0/12/32/32	0/3/3/3
3	ATP	D	1200	4	-	8/18/38/38	0/3/3/3
3	ATP	A	1200	-	-	2/18/38/38	0/3/3/3
3	ATP	E	1201	-	-	2/18/38/38	0/3/3/3
5	ADP	B	1200	-	-	7/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1200	ADP	O4'-C1'	2.08	1.43	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1200	ADP	O4'-C1'-N9	4.14	114.23	108.75
5	C	1200	ADP	N3-C2-N1	-3.65	123.72	128.67
5	B	1200	ADP	N3-C2-N1	-3.14	124.41	128.67
5	B	1200	ADP	C4-C5-N7	-2.81	106.37	109.34
5	C	1200	ADP	C4-C5-N7	-2.56	106.63	109.34

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1200	ATP	C5'-O5'-PA-O1A
3	D	1200	ATP	C5'-O5'-PA-O3A

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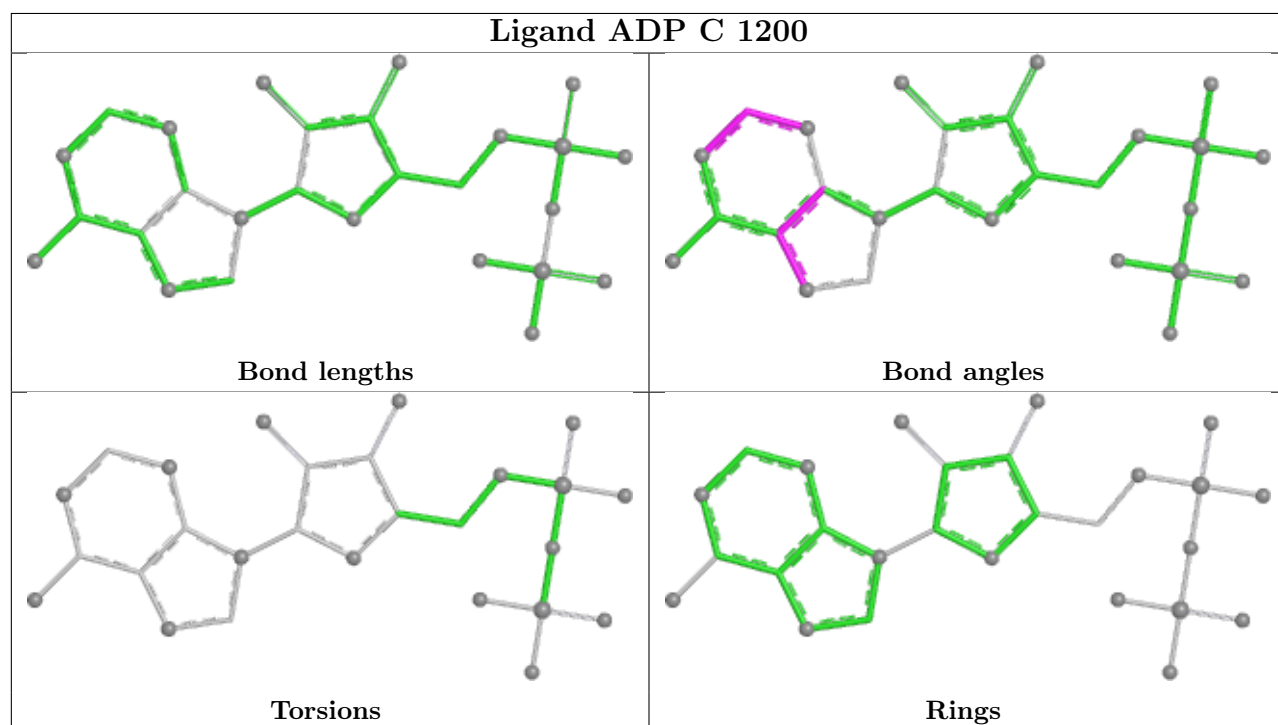
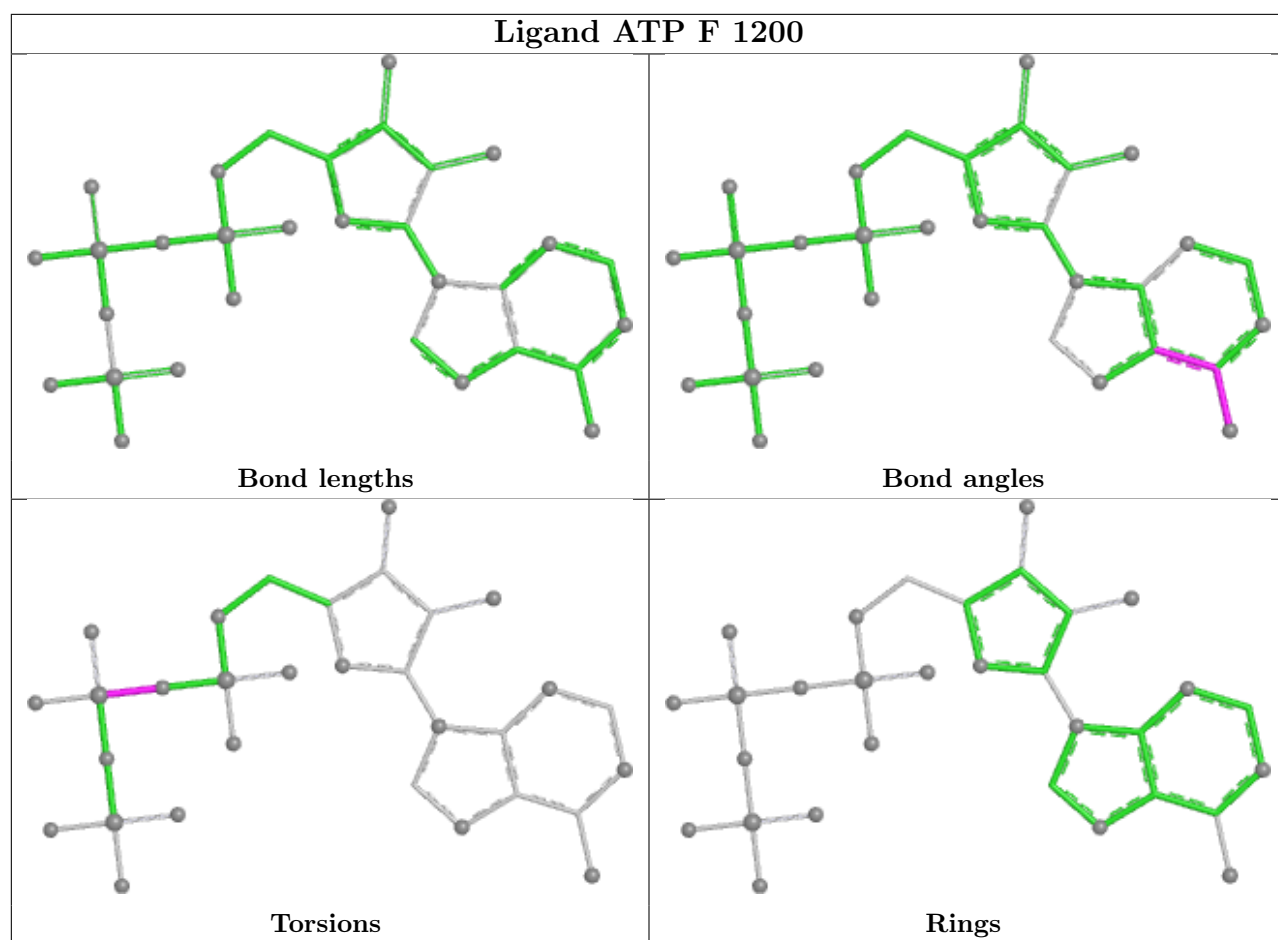
Mol	Chain	Res	Type	Atoms
5	B	1200	ADP	C5'-O5'-PA-O1A
5	B	1200	ADP	C5'-O5'-PA-O2A
3	E	1201	ATP	O4'-C4'-C5'-O5'

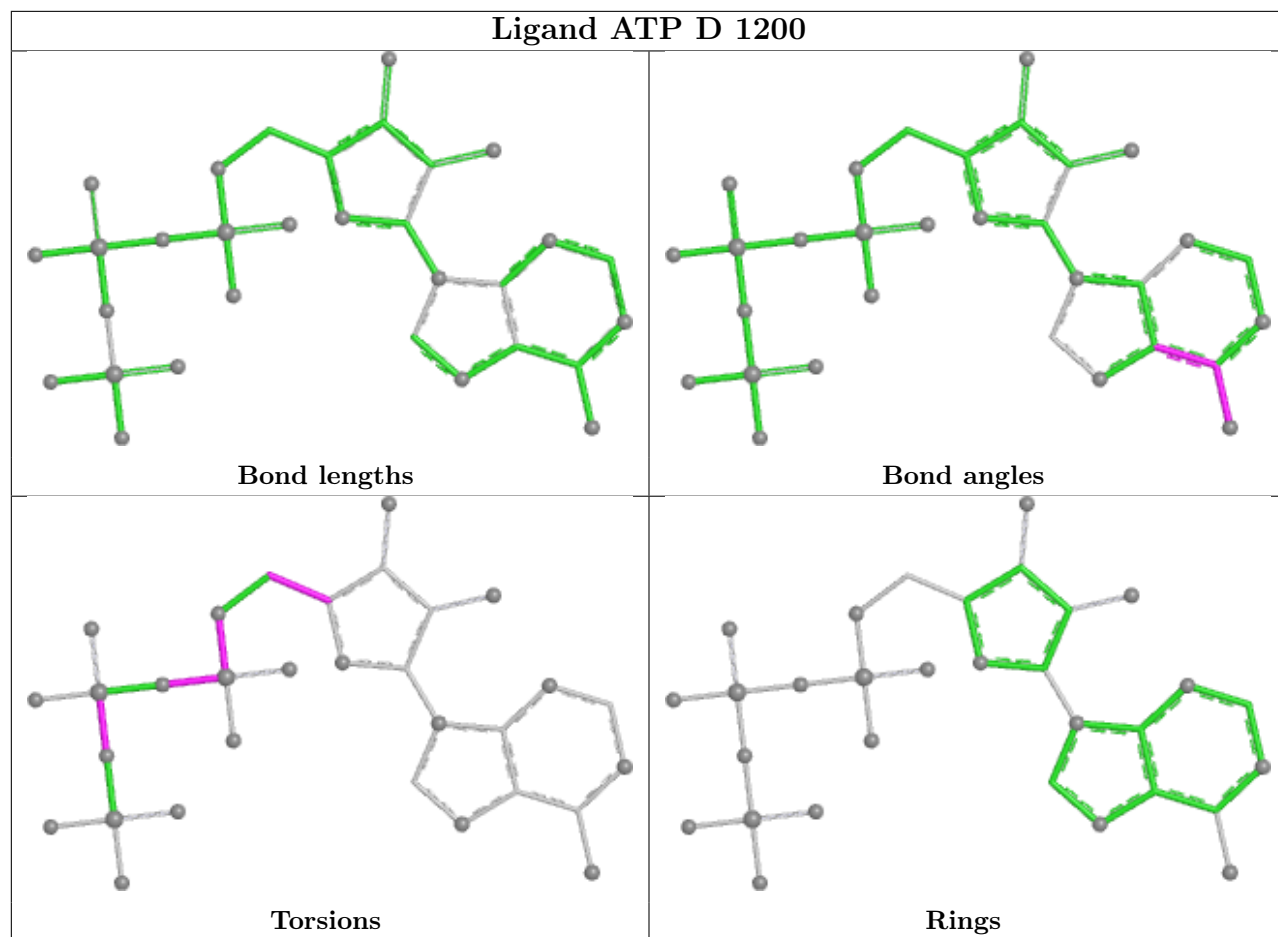
There are no ring outliers.

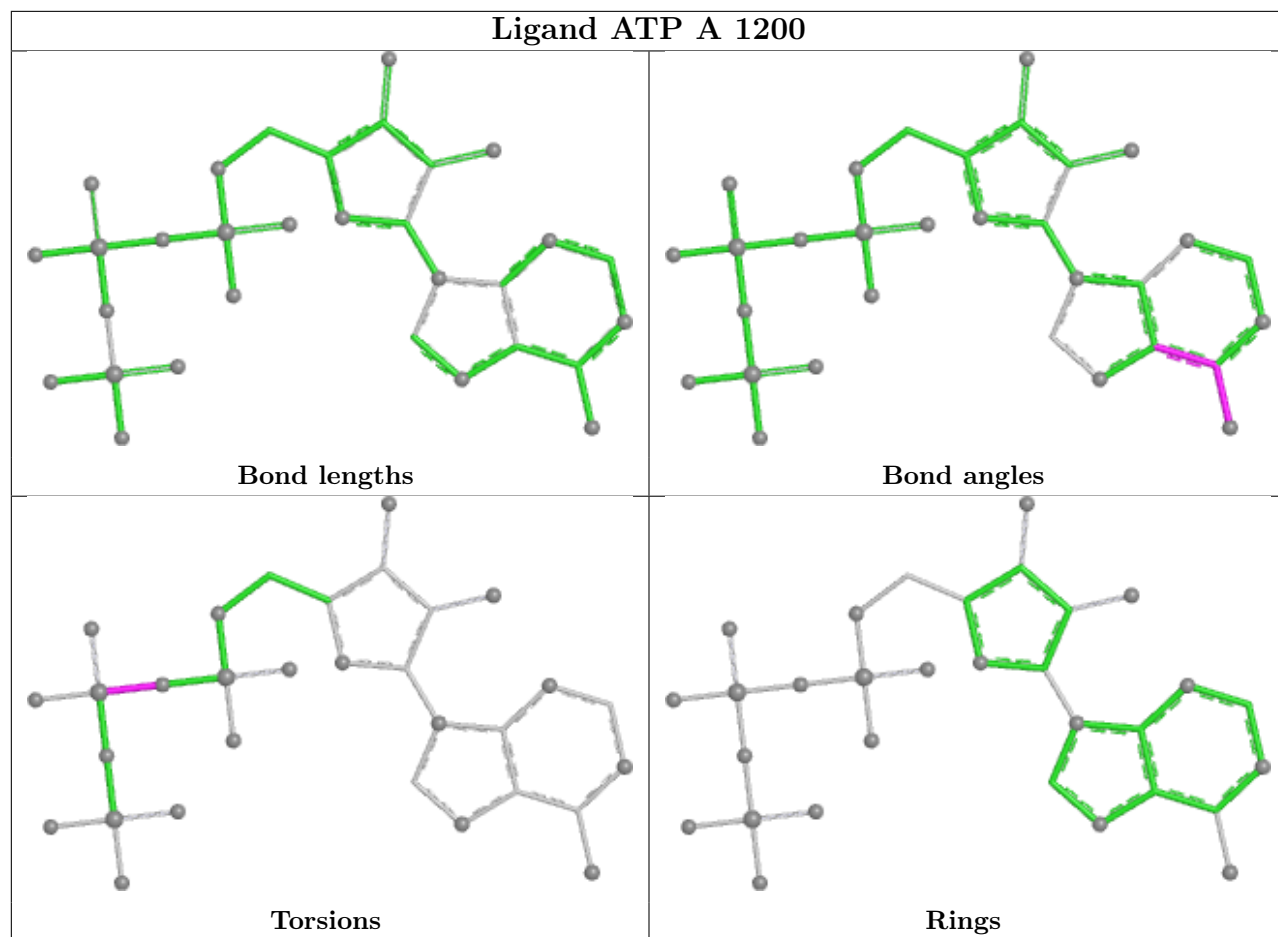
6 monomers are involved in 8 short contacts:

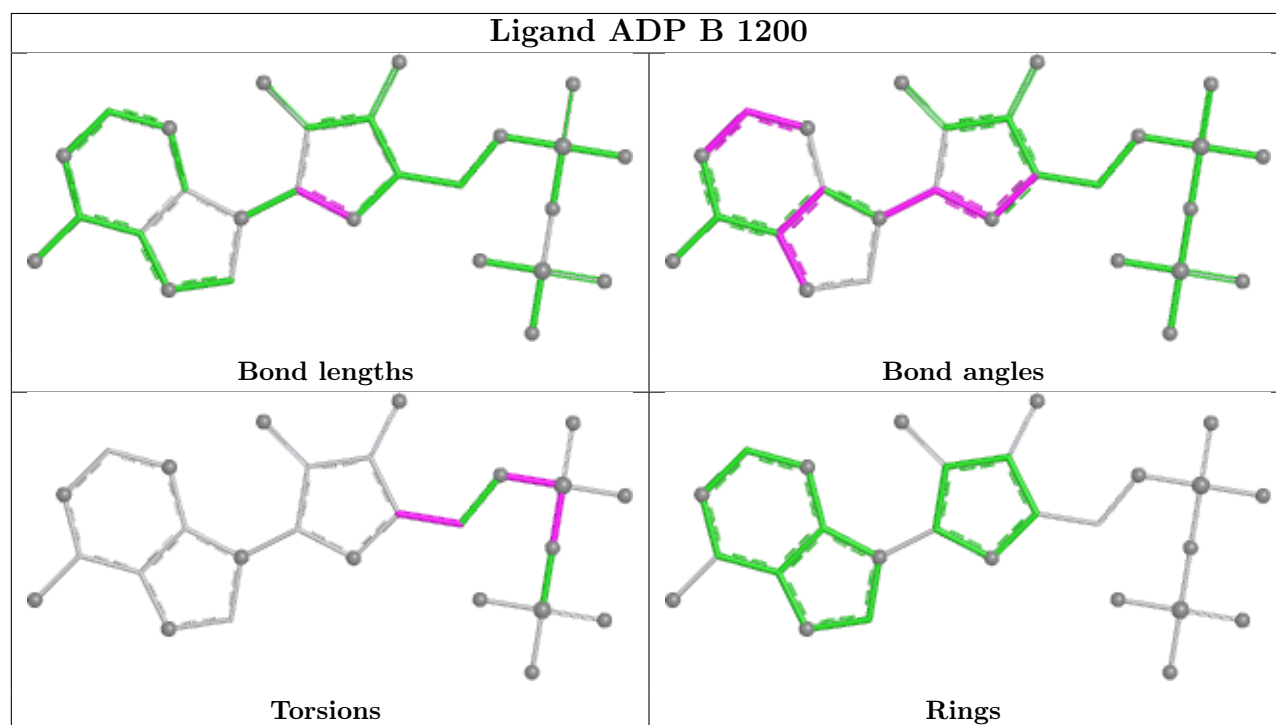
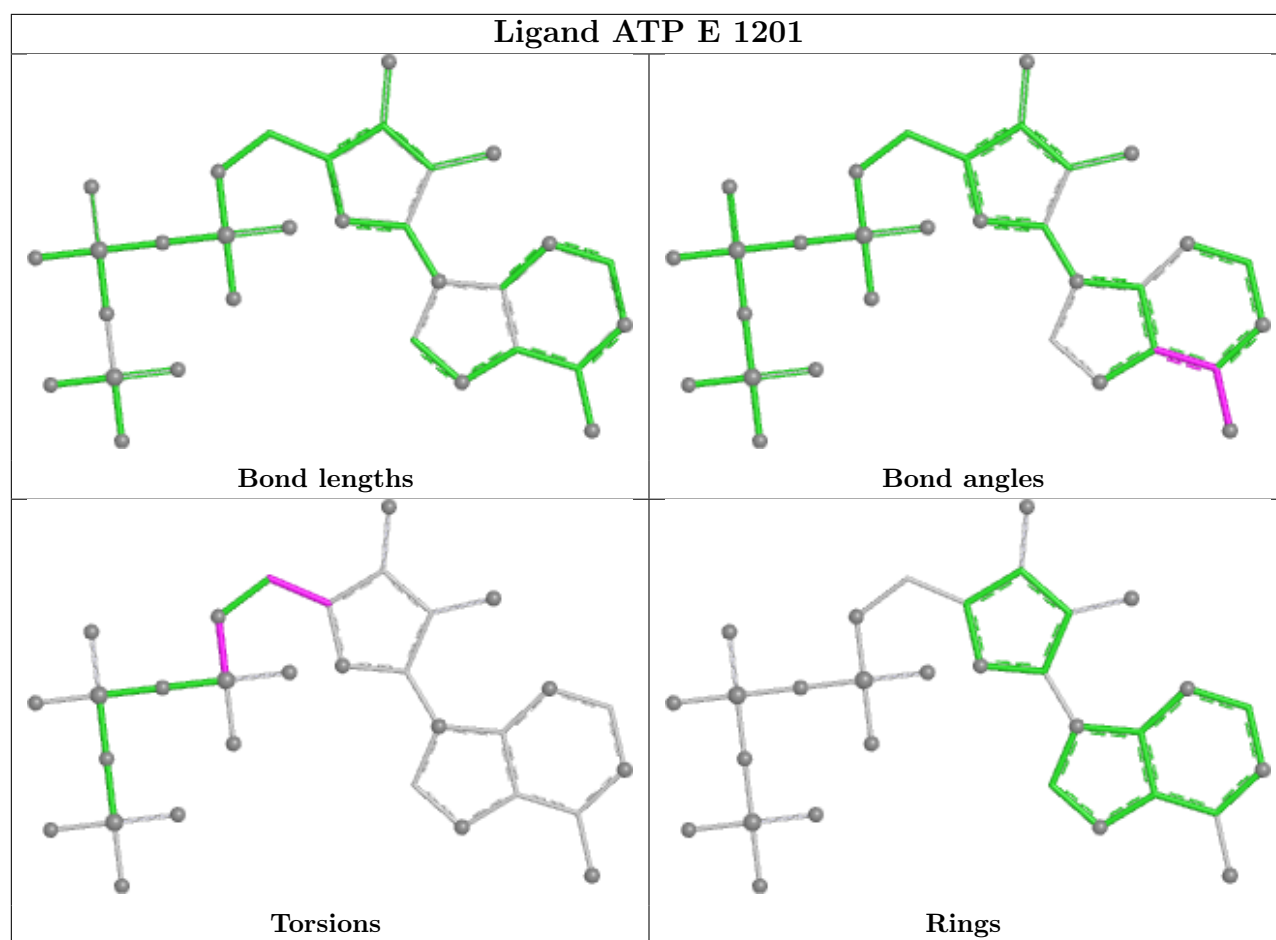
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1200	ATP	1	0
5	C	1200	ADP	1	0
3	D	1200	ATP	2	0
3	A	1200	ATP	1	0
3	E	1201	ATP	1	0
5	B	1200	ADP	2	0

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

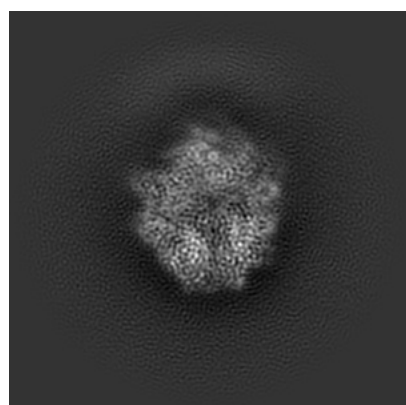
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25502. These allow visual inspection of the internal detail of the map and identification of artifacts.

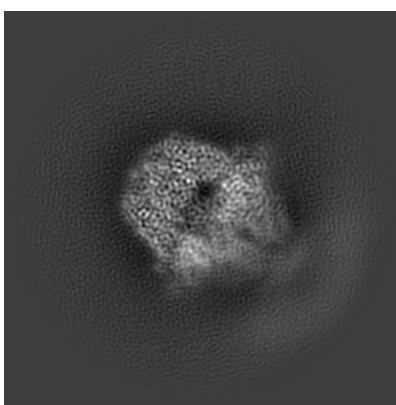
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

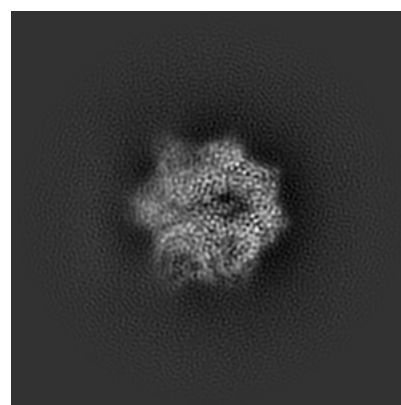
6.1.1 Primary map



X



Y

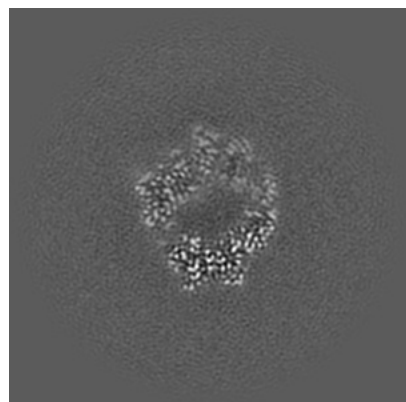


Z

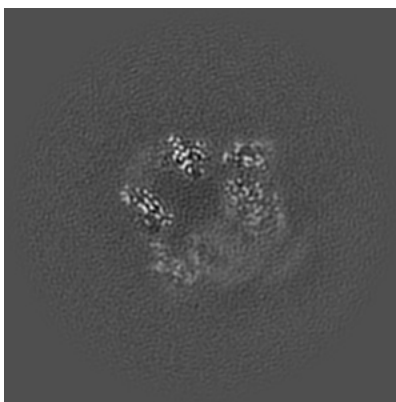
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

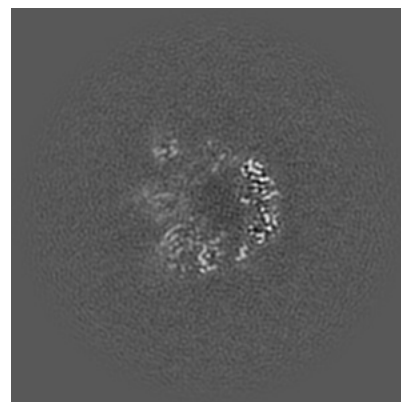
6.2.1 Primary map



X Index: 128



Y Index: 128

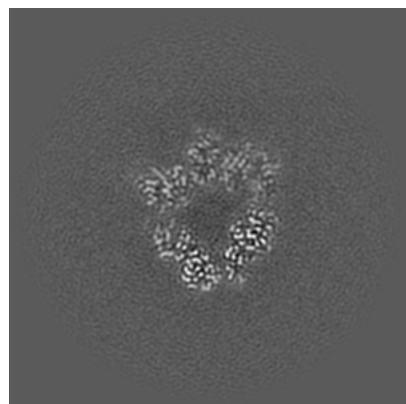


Z Index: 128

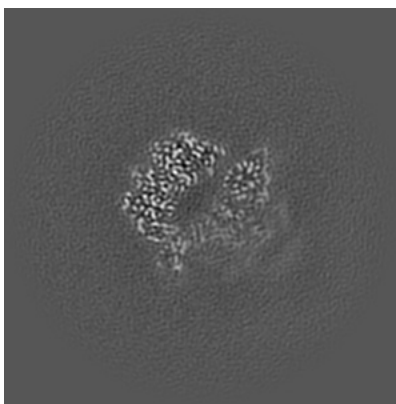
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

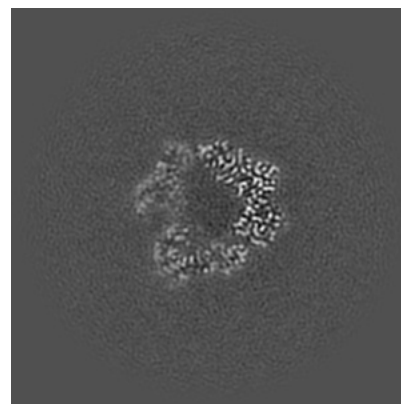
6.3.1 Primary map



X Index: 133



Y Index: 117

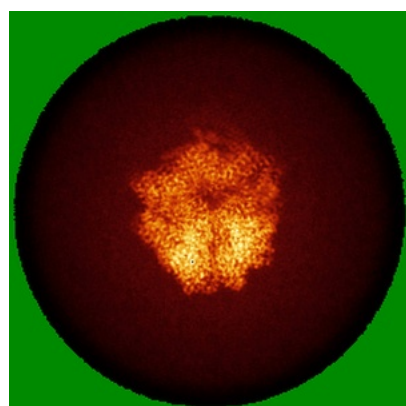


Z Index: 118

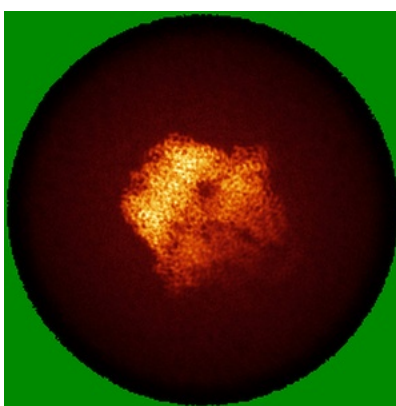
The images above show the largest variance slices of the map in three orthogonal directions.

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

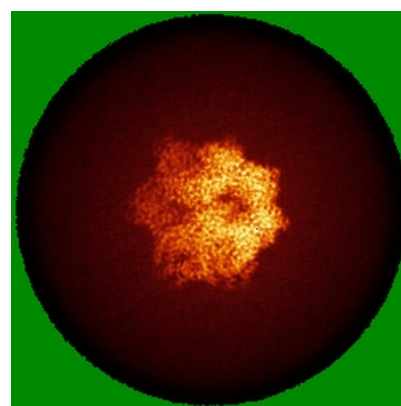
6.4.1 Primary map



X



Y

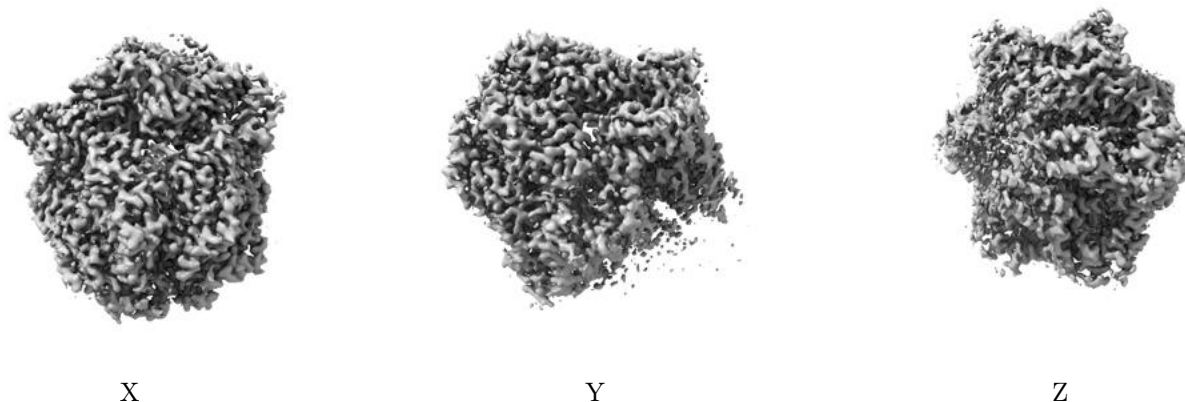


Z

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 0.224. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

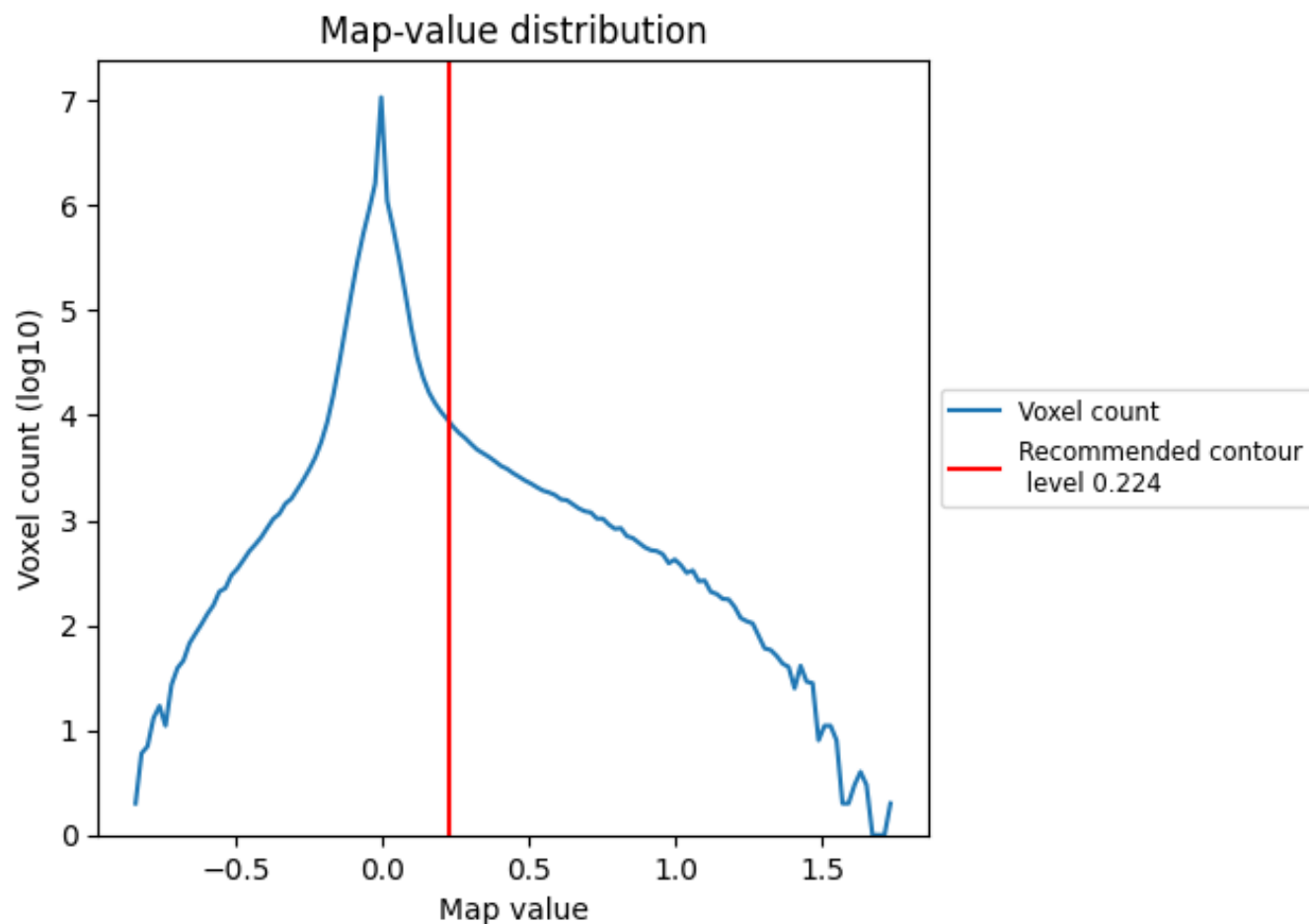
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

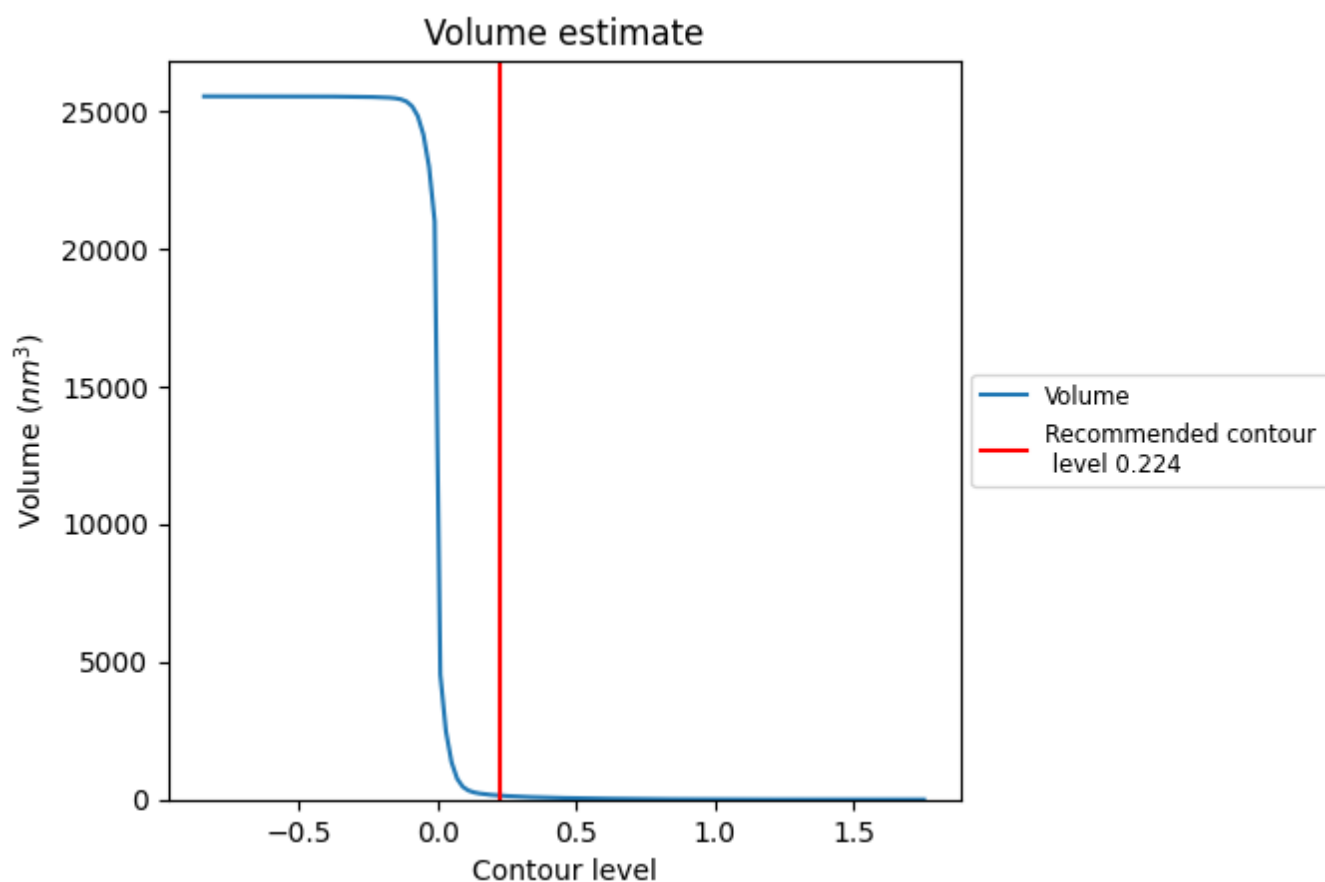
This section contains the results of statistical analysis of the map.

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.

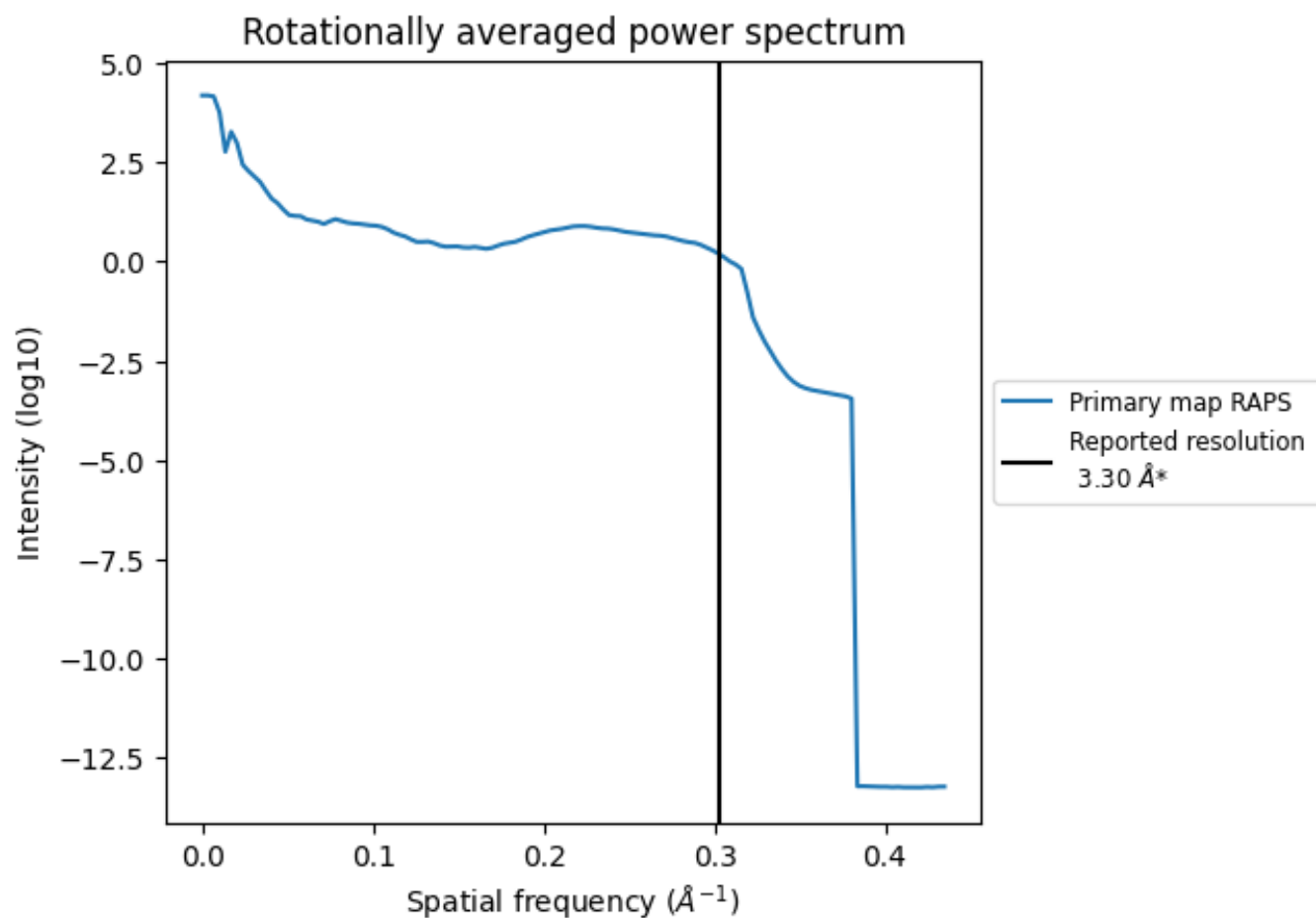
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 145 nm^3 ; this corresponds to an approximate mass of 131 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 0.303 Å⁻¹

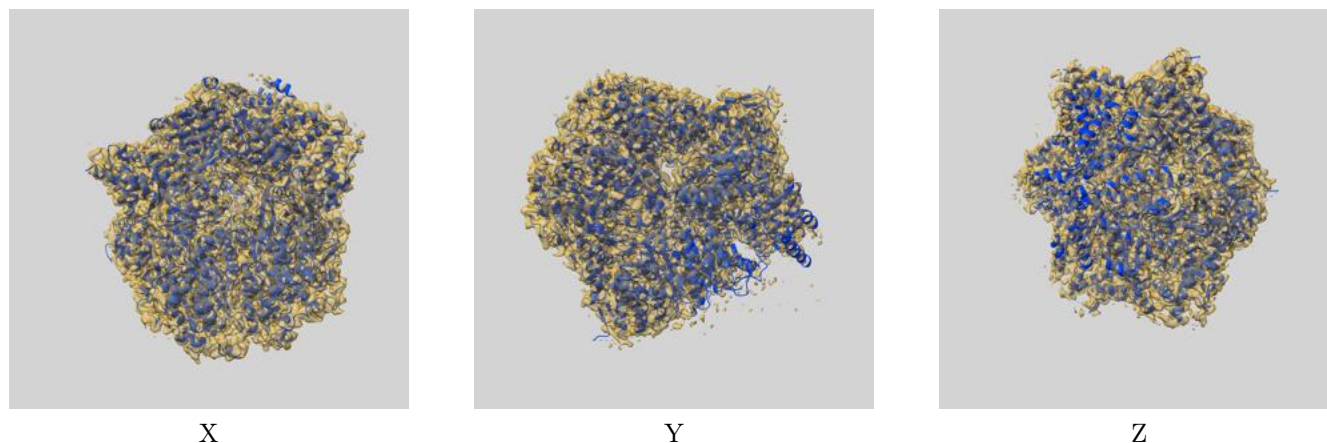
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

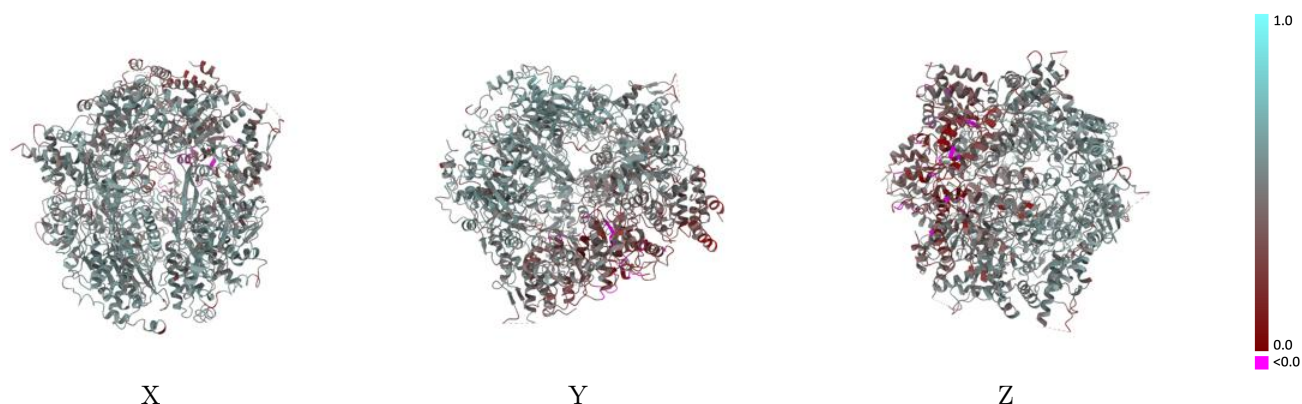
This section contains information regarding the fit between EMDB map EMD-25502 and PDB model 7SXO. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



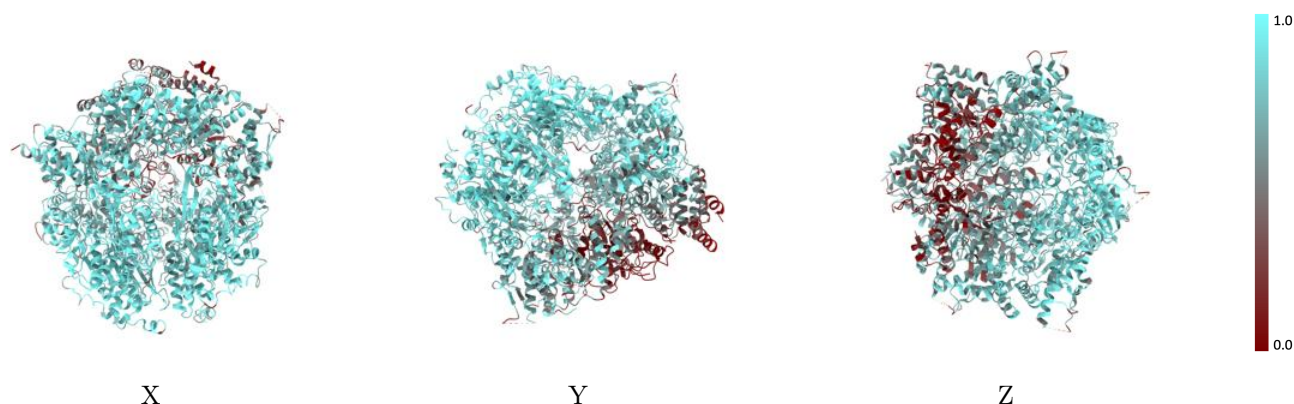
The images above show the 3D surface view of the map at the recommended contour level 0.224 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



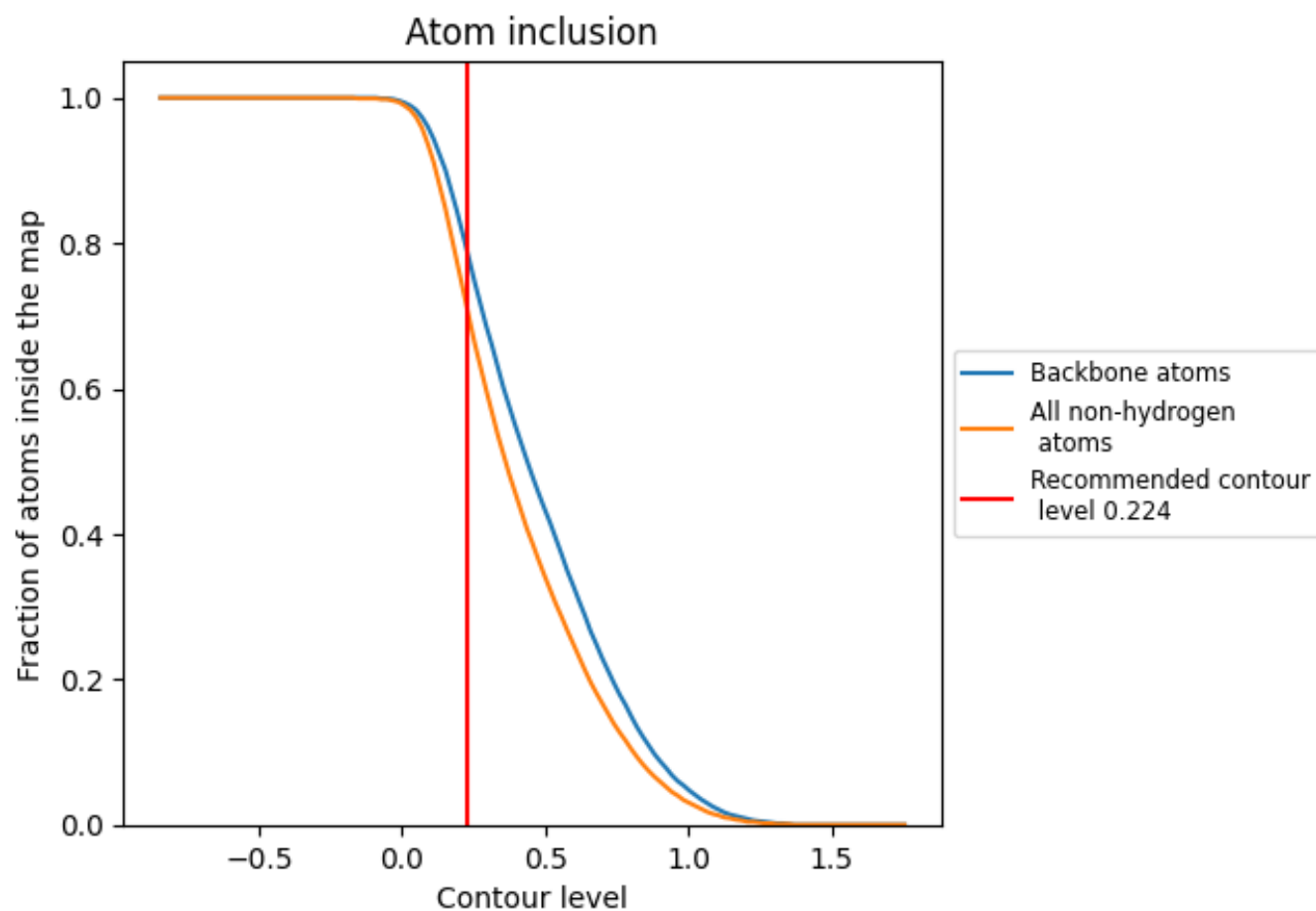
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.224).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 72% 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 (0.224) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.7150</div>	<div><div></div>0.4710</div>
A	<div><div></div>0.7420</div>	<div><div></div>0.4880</div>
B	<div><div></div>0.6080</div>	<div><div></div>0.4190</div>
C	<div><div></div>0.6400</div>	<div><div></div>0.4220</div>
D	<div><div></div>0.6990</div>	<div><div></div>0.4670</div>
E	<div><div></div>0.7800</div>	<div><div></div>0.5080</div>
F	<div><div></div>0.8030</div>	<div><div></div>0.5140</div>
G	<div><div></div>0.2440</div>	<div><div></div>0.3400</div>

1.0

0.0

<0.0