



## wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 05:59 AM EST

PDB ID : 6W20  
EMDB ID : EMD-21520  
Title : ClpAP Disengaged State bound to RepA-GFP  
Authors : Lopez, K.L.; Rizo, A.N.; Tse, E.; Lin, J.; Scull, N.W.; Thwin, A.C.; Lucius, A.L.; Shorter, J.; Southworth, D.R.  
Deposited on : 2020-03-04  
Resolution : 3.00 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)

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<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.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

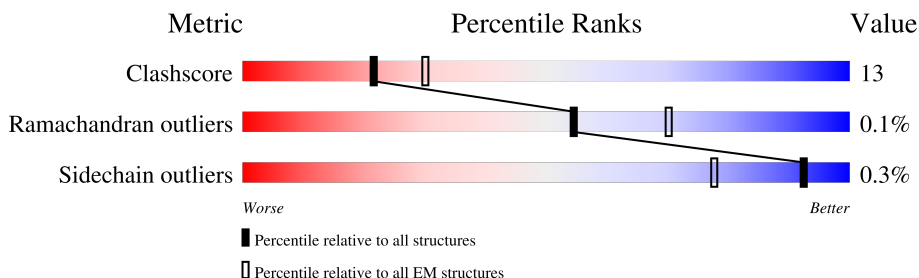
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.






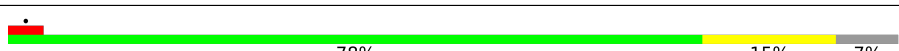
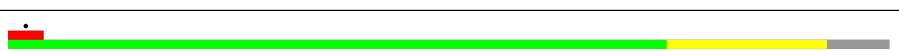
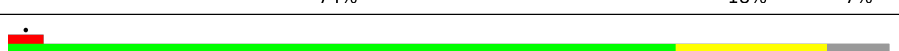

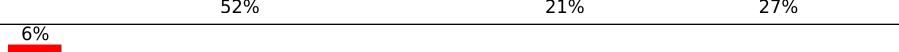

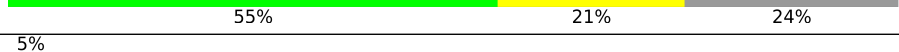



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	G	207	
1	H	207	
1	I	207	
1	J	207	
1	K	207	
1	L	207	
1	M	207	
1	N	207	

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Mol	Chain	Length	Quality of chain
1	O	207	
1	P	207	
1	Q	207	
1	R	207	
1	S	207	
1	T	207	
2	A	758	
2	B	758	
2	C	758	
2	D	758	
2	E	758	
2	F	758	
3	X	24	

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
4	ADP	F	801	-	-	X	-
5	ATP	B	801	-	-	X	-
5	ATP	C	801	-	-	X	-
5	ATP	C	802	-	-	X	-
5	ATP	D	802	-	-	X	-
5	ATP	E	801	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 48206 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 ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	H	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	I	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	J	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	K	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	L	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	M	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	N	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	O	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	P	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	Q	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	R	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	S	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		
1	T	192	Total	C	N	O	S	0	0
			1500	946	260	282	12		

- Molecule 2 is a protein called ATP-dependent Clp protease ATP-binding subunit ClpA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	552	Total	C	N	O	S	0	0
			4321	2730	767	810	14		

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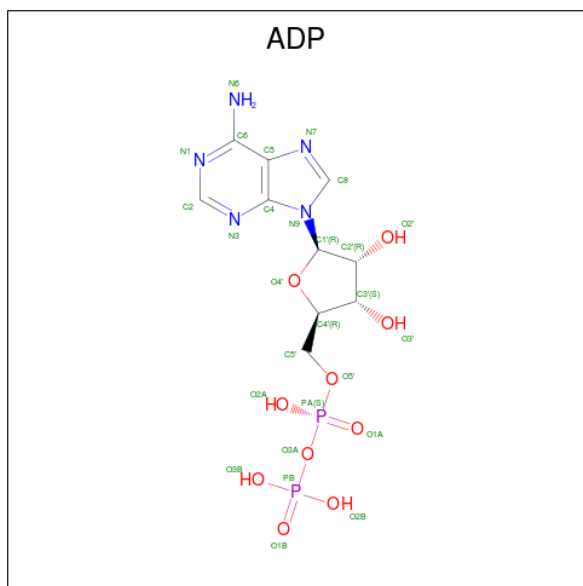
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	578	Total	C	N	O	S	0	0
			4510	2841	805	850	14		
2	C	578	Total	C	N	O	S	0	0
			4510	2841	805	850	14		
2	D	578	Total	C	N	O	S	0	0
			4510	2841	805	850	14		
2	E	568	Total	C	N	O	S	0	0
			4453	2809	794	836	14		
2	F	568	Total	C	N	O	S	0	0
			4453	2809	794	836	14		

- Molecule 3 is a protein called RepA, green fluorescent protein fusion.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	X	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			54	20	10	20	4	
4	A	1	Total	C	N	O	P	0
			54	20	10	20	4	
4	F	1	Total	C	N	O	P	0
			27	10	5	10	2	


- 
- The image displays the chemical structure of Adenosine Triphosphate (ATP). It consists of an adenine base (a purine ring system with an amino group at N6) attached to a ribose sugar (a five-membered ring with hydroxyl groups at C2' and C3'). The ribose is linked to a chain of three phosphate groups (O=P(O)(O)O) via phosphodiester bonds. The structure is labeled with atom names (N1, N3, N6, C2, C4, C6, C8, C5', C6', C3', C2', C1', O1A, O1B, O1C, O2A, O2B, O2C, O3A, O3B, O3C) and shows the spatial arrangement of atoms and bonds, including stereochemistry (wedges and dashes).

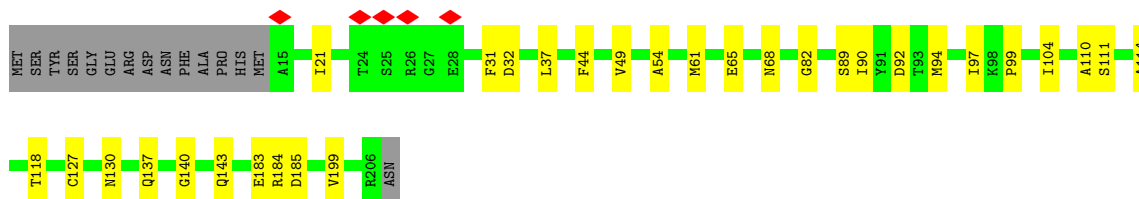


### 3 Residue-property plots


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.

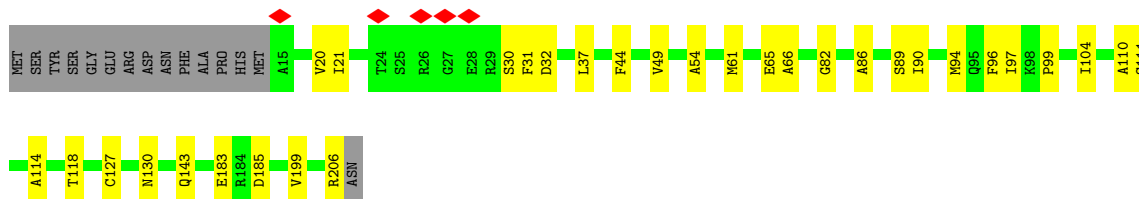
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain G: 




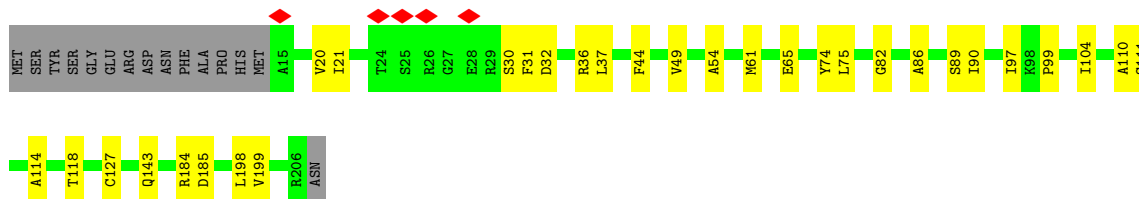
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain H: 




- Molecule 1: ATP-dependent Clp protease proteolytic subunit

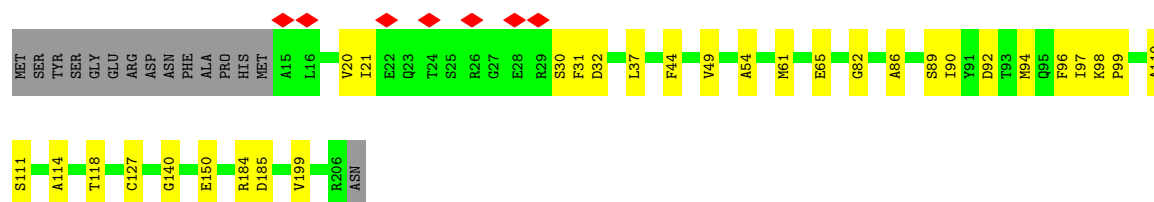
Chain I: 



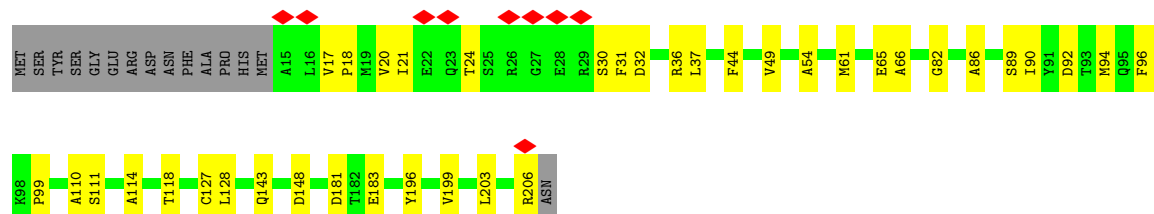
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain J: 

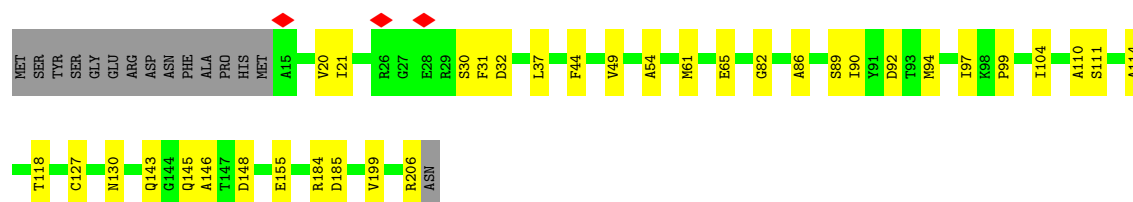
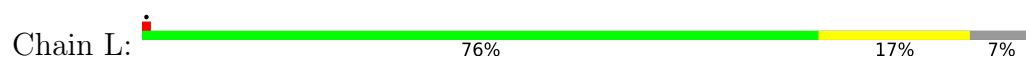




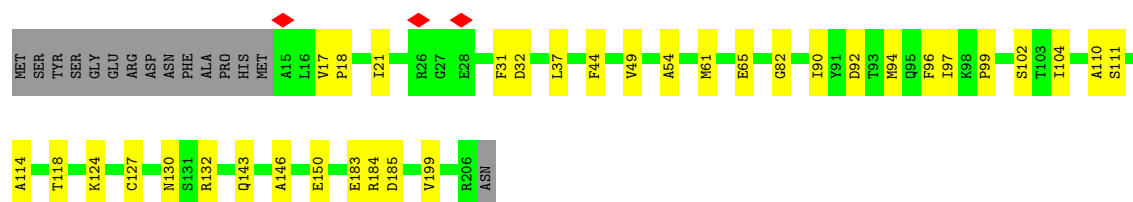
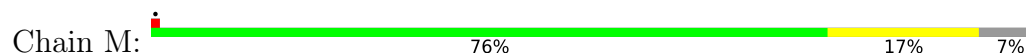
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



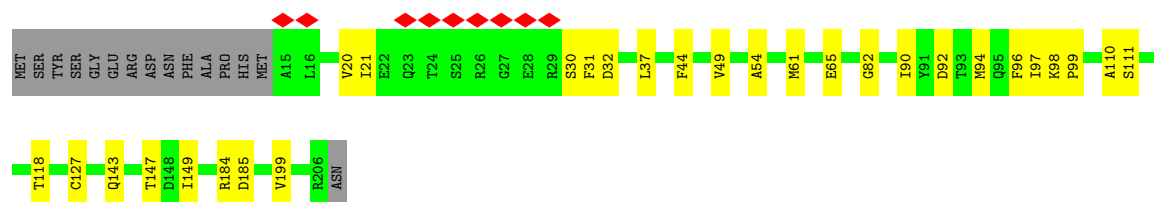
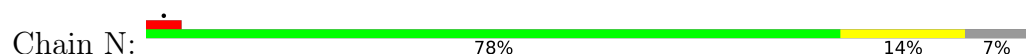
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit




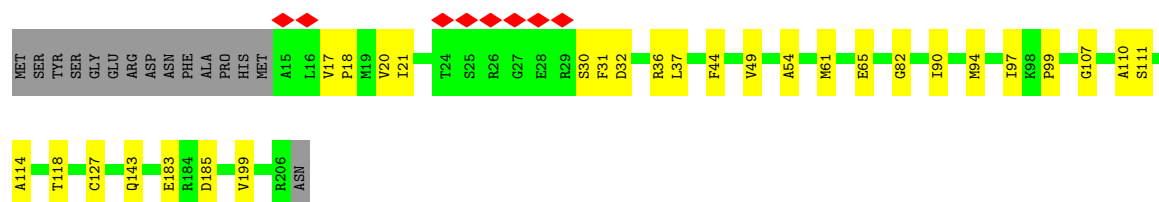
- Molecule 1: ATP-dependent Clp protease proteolytic subunit






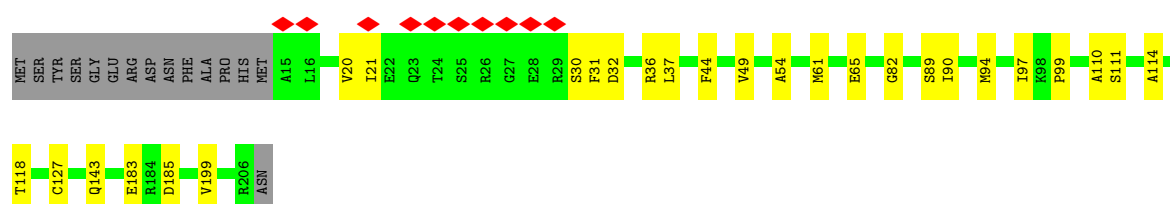
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain O: 




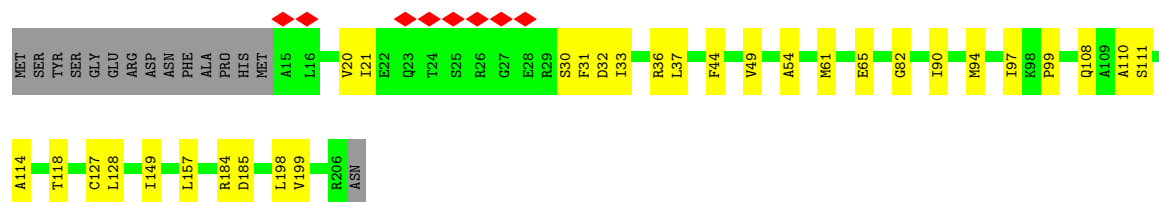
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain P: 




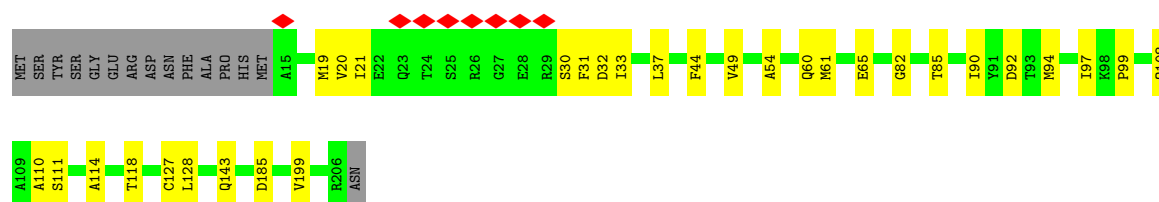
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

Chain Q: 



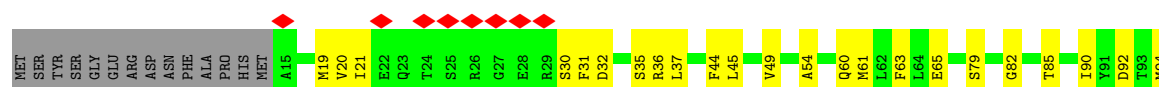
- Molecule 1: ATP-dependent Clp protease proteolytic subunit

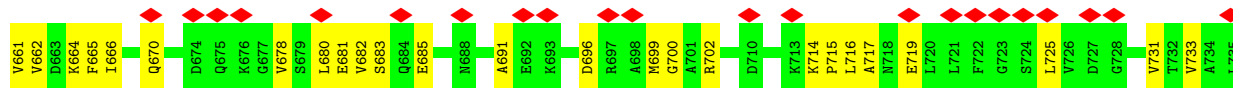
Chain R: 

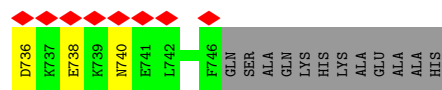


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

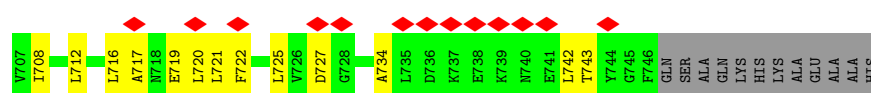
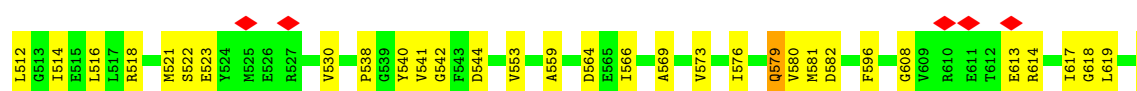
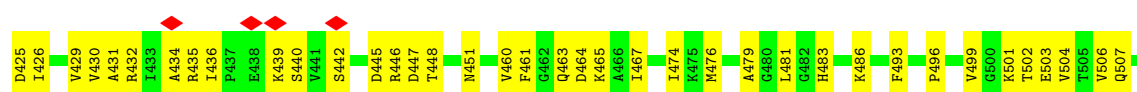
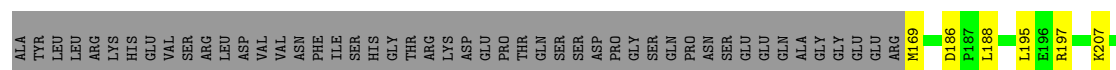
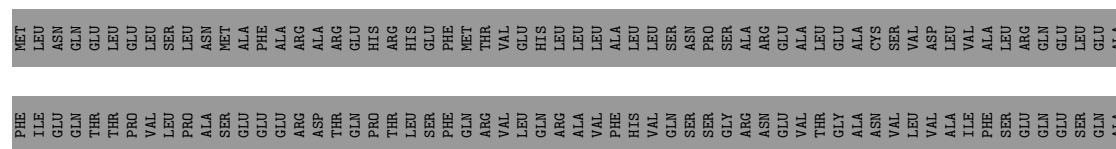
Chain S: 



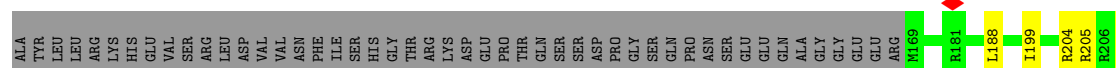
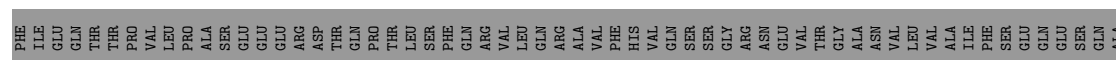
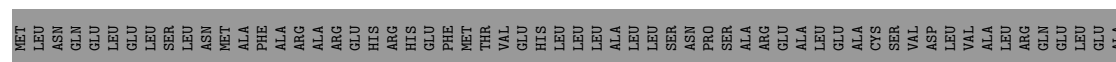


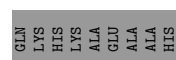


• Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpA



• Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpA

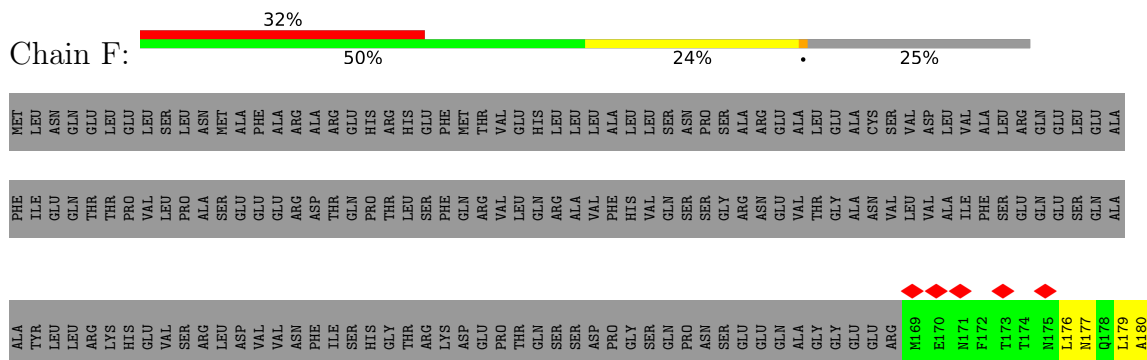


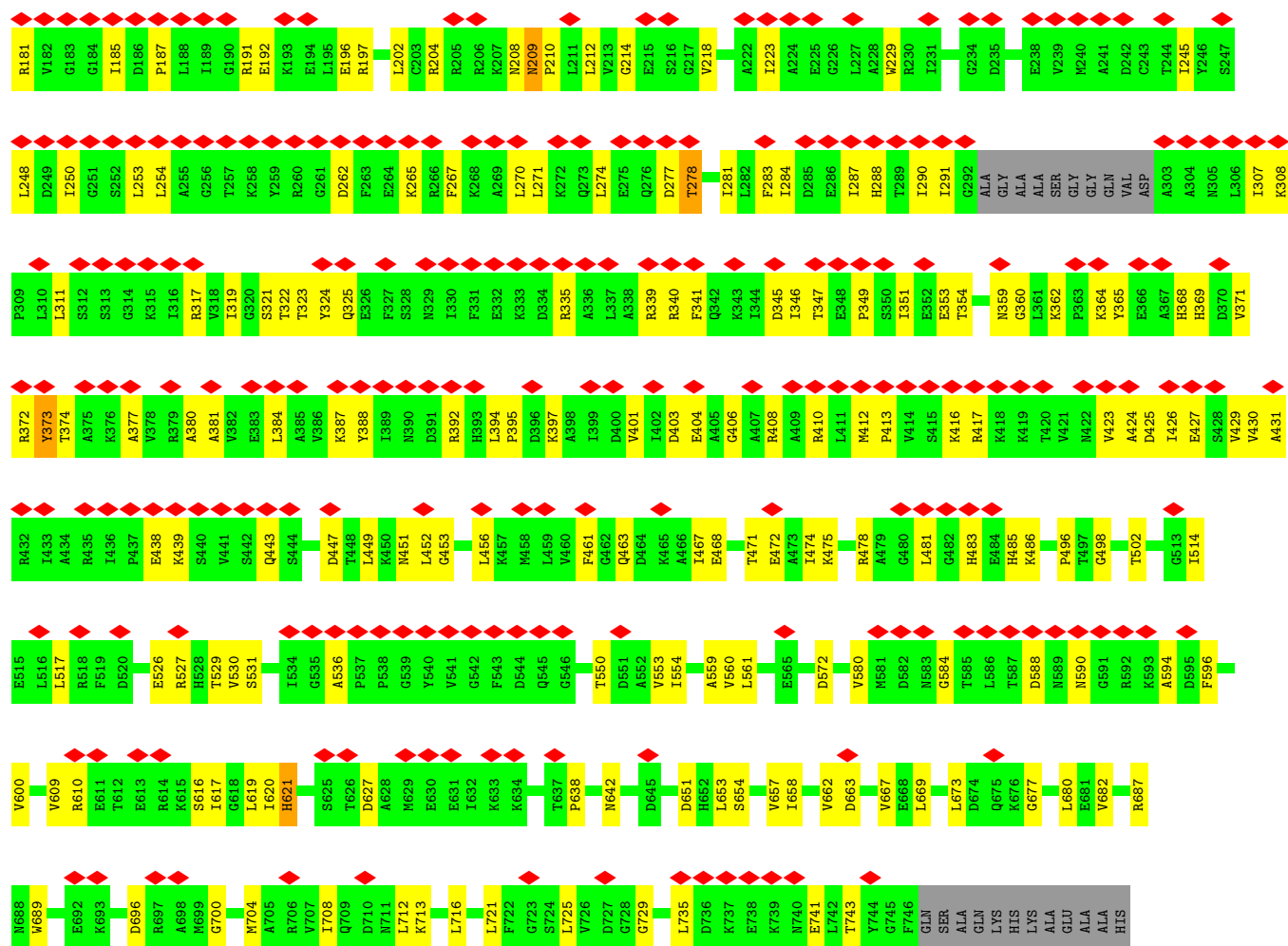


Chain E:

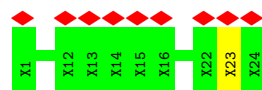
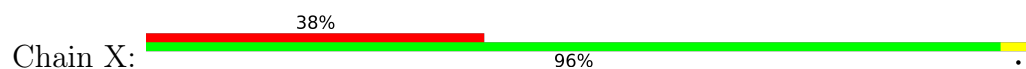


## Chain F:





• Molecule 3: RepA, green fluorescent protein fusion



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	57848	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	69	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	58616	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.142	Depositor
Minimum map value	-0.738	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.058	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	500.4, 500.4, 500.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.834, 0.834, 0.834	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	G	0.28	0/1524	0.42	0/2054
1	H	0.28	0/1524	0.42	0/2054
1	I	0.28	0/1524	0.42	0/2054
1	J	0.28	0/1524	0.42	0/2054
1	K	0.28	0/1524	0.42	0/2054
1	L	0.28	0/1524	0.42	0/2054
1	M	0.28	0/1524	0.42	0/2054
1	N	0.28	0/1524	0.42	0/2054
1	O	0.28	0/1524	0.42	0/2054
1	P	0.28	0/1524	0.42	0/2054
1	Q	0.28	0/1524	0.42	0/2054
1	R	0.28	0/1524	0.42	0/2054
1	S	0.28	0/1524	0.42	0/2054
1	T	0.28	0/1524	0.42	0/2054
2	A	0.35	0/4384	0.45	0/5914
2	B	0.36	0/4576	0.45	0/6175
2	C	0.40	0/4576	0.47	0/6175
2	D	0.37	0/4576	0.45	0/6175
2	E	0.35	0/4518	0.44	0/6095
2	F	0.35	0/4518	0.45	0/6095
All	All	0.33	0/48484	0.44	0/65385

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 ⓘ

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	G	1500	0	1512	38	0
1	H	1500	0	1512	40	0
1	I	1500	0	1512	35	0
1	J	1500	0	1512	34	0
1	K	1500	0	1512	37	0
1	L	1500	0	1512	36	0
1	M	1500	0	1512	40	0
1	N	1500	0	1512	39	0
1	O	1500	0	1512	36	0
1	P	1500	0	1512	32	0
1	Q	1500	0	1512	37	0
1	R	1500	0	1512	37	0
1	S	1500	0	1512	47	0
1	T	1500	0	1512	47	0
2	A	4321	0	4424	145	0
2	B	4510	0	4609	180	0
2	C	4510	0	4609	163	0
2	D	4510	0	4609	151	0
2	E	4453	0	4558	188	0
2	F	4453	0	4558	153	0
3	X	120	0	27	1	0
4	A	54	0	24	12	0
4	F	27	0	12	15	0
5	B	62	0	24	21	0
5	C	62	0	24	30	0
5	D	62	0	24	18	0
5	E	62	0	24	25	0
All	All	48206	0	48694	1257	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 13.

The worst 5 of 1257 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)
2:C:357:ILE:HG23	5:C:801:ATP:C2	1.71	1.23
2:E:361:LEU:CD1	5:E:801:ATP:H1'	1.72	1.19
2:D:502:THR:HG23	5:D:802:ATP:O2B	1.40	1.18
2:C:219:GLY:HA2	5:C:801:ATP:O2A	1.45	1.16
2:E:188:LEU:HD21	2:E:191:ARG:HB2	1.15	1.11

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	G	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	H	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	I	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	J	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	K	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	L	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	M	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	N	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	O	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	P	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	Q	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	R	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	S	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
1	T	190/207 (92%)	187 (98%)	3 (2%)	0	100	100
2	A	546/758 (72%)	528 (97%)	18 (3%)	0	100	100
2	B	576/758 (76%)	550 (96%)	25 (4%)	1 (0%)	47	82

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	576/758 (76%)	542 (94%)	33 (6%)	1 (0%)	47	82
2	D	576/758 (76%)	555 (96%)	21 (4%)	0	100	100
2	E	564/758 (74%)	534 (95%)	29 (5%)	1 (0%)	47	82
2	F	564/758 (74%)	545 (97%)	18 (3%)	1 (0%)	47	82
All	All	6062/7446 (81%)	5872 (97%)	186 (3%)	4 (0%)	54	85

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	278	THR
2	C	349	PRO
2	E	538	PRO
2	B	638	PRO

### 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	G	162/175 (93%)	161 (99%)	1 (1%)	86	95
1	H	162/175 (93%)	162 (100%)	0	100	100
1	I	162/175 (93%)	162 (100%)	0	100	100
1	J	162/175 (93%)	162 (100%)	0	100	100
1	K	162/175 (93%)	162 (100%)	0	100	100
1	L	162/175 (93%)	162 (100%)	0	100	100
1	M	162/175 (93%)	162 (100%)	0	100	100
1	N	162/175 (93%)	162 (100%)	0	100	100
1	O	162/175 (93%)	162 (100%)	0	100	100
1	P	162/175 (93%)	162 (100%)	0	100	100
1	Q	162/175 (93%)	162 (100%)	0	100	100
1	R	162/175 (93%)	162 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	162/175 (93%)	162 (100%)	0	100	100
1	T	162/175 (93%)	162 (100%)	0	100	100
2	A	466/639 (73%)	462 (99%)	4 (1%)	78	92
2	B	485/639 (76%)	484 (100%)	1 (0%)	93	98
2	C	485/639 (76%)	483 (100%)	2 (0%)	91	97
2	D	485/639 (76%)	485 (100%)	0	100	100
2	E	481/639 (75%)	478 (99%)	3 (1%)	86	95
2	F	481/639 (75%)	476 (99%)	5 (1%)	76	91
All	All	5151/6284 (82%)	5135 (100%)	16 (0%)	92	97

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	388	TYR
2	F	373	TYR
2	E	177	ASN
2	F	325	GLN
2	C	642	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
1	S	173	GLN
1	T	60	GLN
2	D	606	ASN
1	M	55	ASN
1	L	173	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

11 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
5	ATP	C	802	-	26,33,33	3.93	9 (34%)	31,52,52	1.78	7 (22%)
5	ATP	B	802	-	26,33,33	3.93	9 (34%)	31,52,52	1.83	7 (22%)
5	ATP	D	802	-	26,33,33	3.92	9 (34%)	31,52,52	1.78	7 (22%)
5	ATP	E	802	-	26,33,33	3.93	9 (34%)	31,52,52	1.79	7 (22%)
5	ATP	D	801	-	26,33,33	3.92	9 (34%)	31,52,52	1.80	7 (22%)
5	ATP	B	801	-	26,33,33	3.91	9 (34%)	31,52,52	1.78	7 (22%)
5	ATP	C	801	-	26,33,33	3.91	9 (34%)	31,52,52	1.79	7 (22%)
5	ATP	E	801	-	26,33,33	3.92	9 (34%)	31,52,52	1.79	7 (22%)
4	ADP	F	801	-	24,29,29	3.75	6 (25%)	29,45,45	1.40	4 (13%)
4	ADP	A	801	-	24,29,29	3.74	6 (25%)	29,45,45	1.41	4 (13%)
4	ADP	A	802	-	24,29,29	3.74	6 (25%)	29,45,45	1.39	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
5	ATP	C	802	-	-	2/18/38/38	0/3/3/3
5	ATP	B	802	-	-	5/18/38/38	0/3/3/3
5	ATP	D	802	-	-	2/18/38/38	0/3/3/3
5	ATP	E	802	-	-	2/18/38/38	0/3/3/3
5	ATP	D	801	-	-	2/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ATP	B	801	-	-	1/18/38/38	0/3/3/3
5	ATP	C	801	-	-	5/18/38/38	0/3/3/3
5	ATP	E	801	-	-	4/18/38/38	0/3/3/3
4	ADP	F	801	-	-	8/12/32/32	0/3/3/3
4	ADP	A	801	-	-	4/12/32/32	0/3/3/3
4	ADP	A	802	-	-	2/12/32/32	0/3/3/3

The worst 5 of 90 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	802	ATP	C8-N7	-12.08	1.13	1.34
5	B	801	ATP	C8-N7	-12.04	1.13	1.34
5	E	802	ATP	C8-N7	-12.03	1.13	1.34
5	D	802	ATP	C8-N7	-12.01	1.13	1.34
5	C	801	ATP	C8-N7	-11.98	1.13	1.34

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	802	ATP	C3'-C2'-C1'	5.04	108.57	100.98
5	D	801	ATP	C3'-C2'-C1'	4.90	108.36	100.98
5	D	801	ATP	C4-C5-N7	-4.79	104.41	109.40
5	D	802	ATP	C4-C5-N7	-4.79	104.41	109.40
5	B	802	ATP	C4-C5-N7	-4.77	104.43	109.40

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	801	ADP	C5'-O5'-PA-O1A
4	A	801	ADP	C5'-O5'-PA-O2A
4	A	802	ADP	O4'-C4'-C5'-O5'
4	A	802	ADP	C3'-C4'-C5'-O5'
4	F	801	ADP	PA-O3A-PB-O2B

There are no ring outliers.

11 monomers are involved in 121 short contacts:

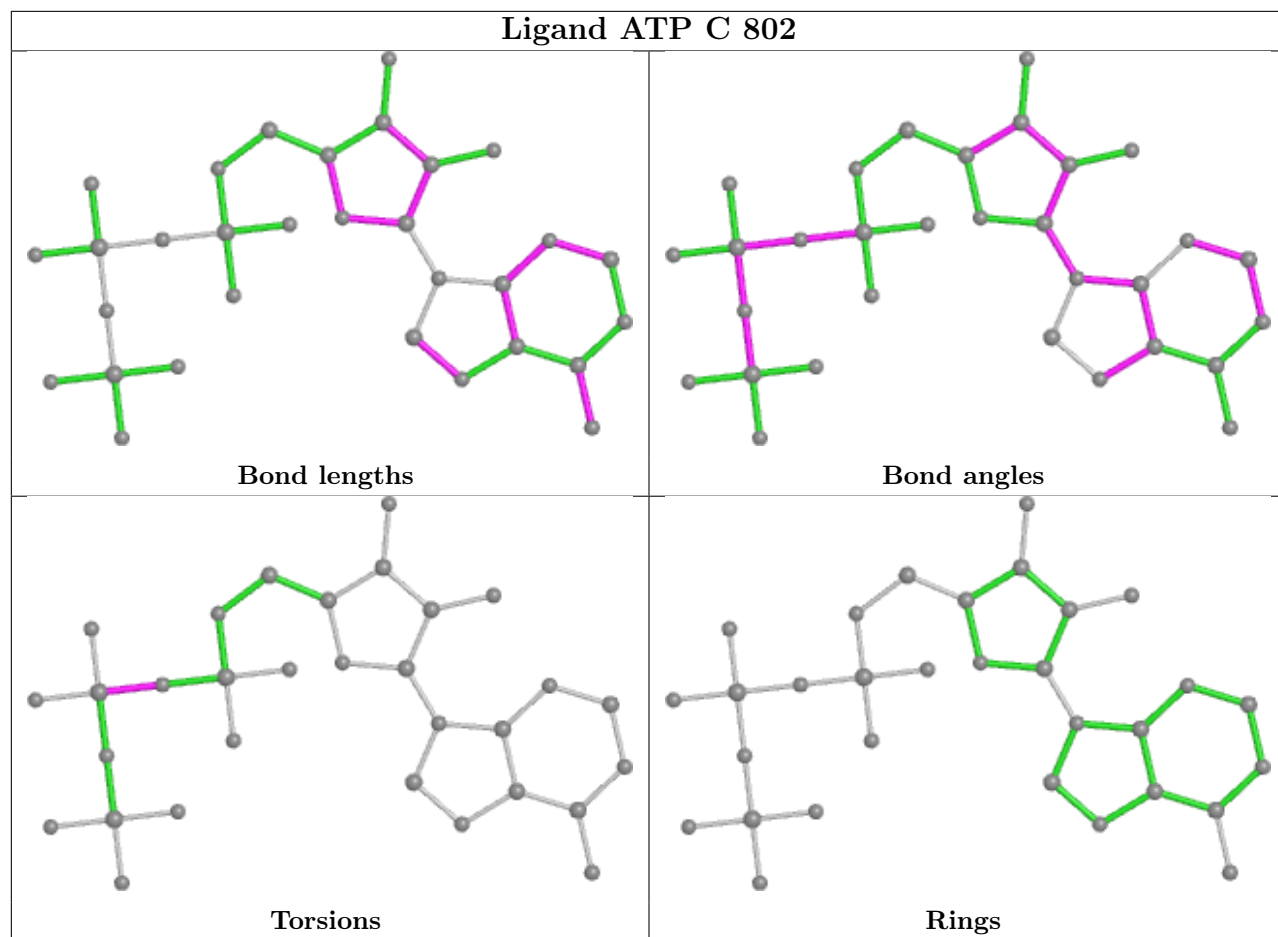
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	802	ATP	15	0

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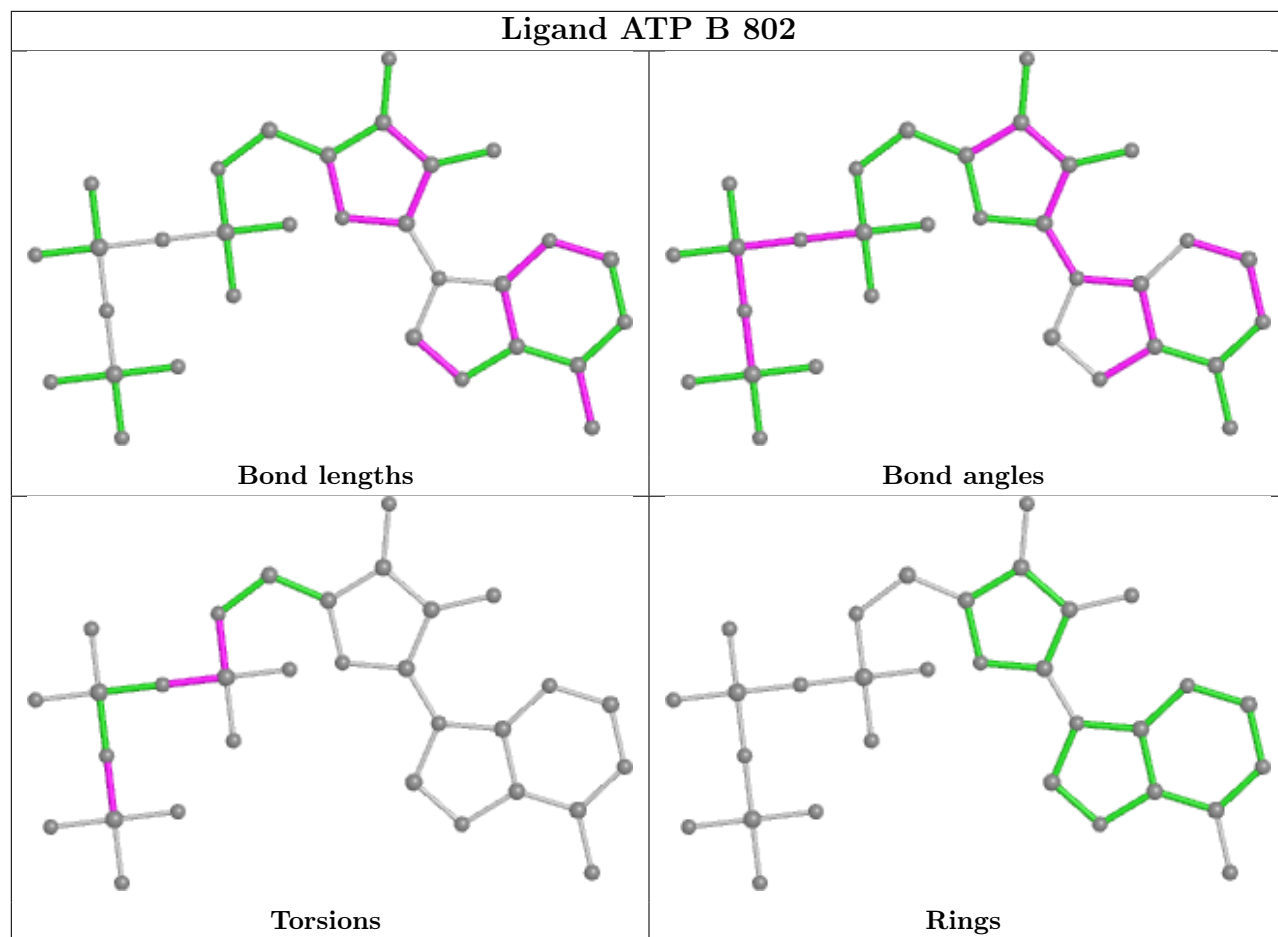
*Continued from previous page...*

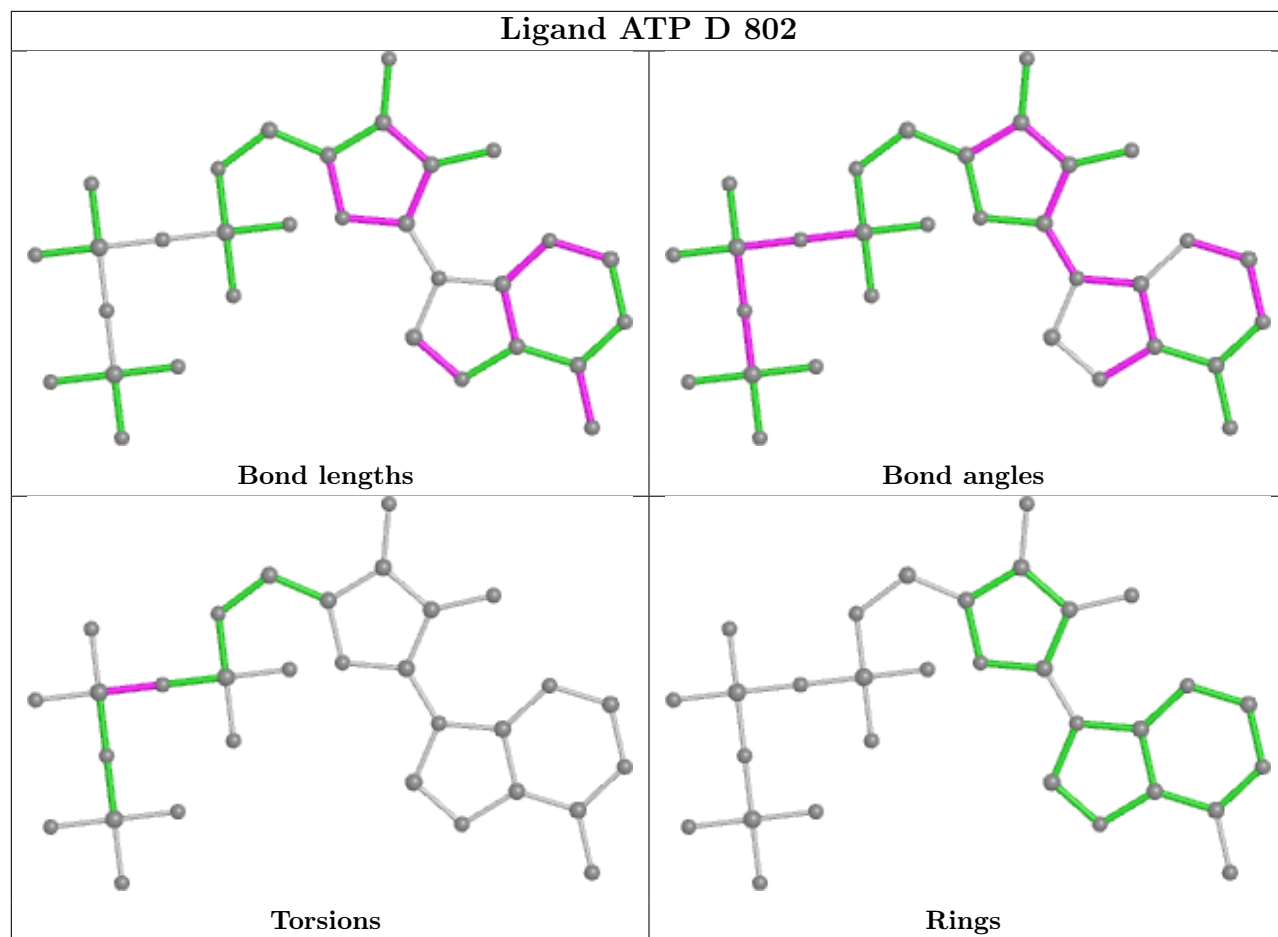
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	802	ATP	4	0
5	D	802	ATP	10	0
5	E	802	ATP	6	0
5	D	801	ATP	8	0
5	B	801	ATP	17	0
5	C	801	ATP	15	0
5	E	801	ATP	19	0
4	F	801	ADP	15	0
4	A	801	ADP	7	0
4	A	802	ADP	5	0

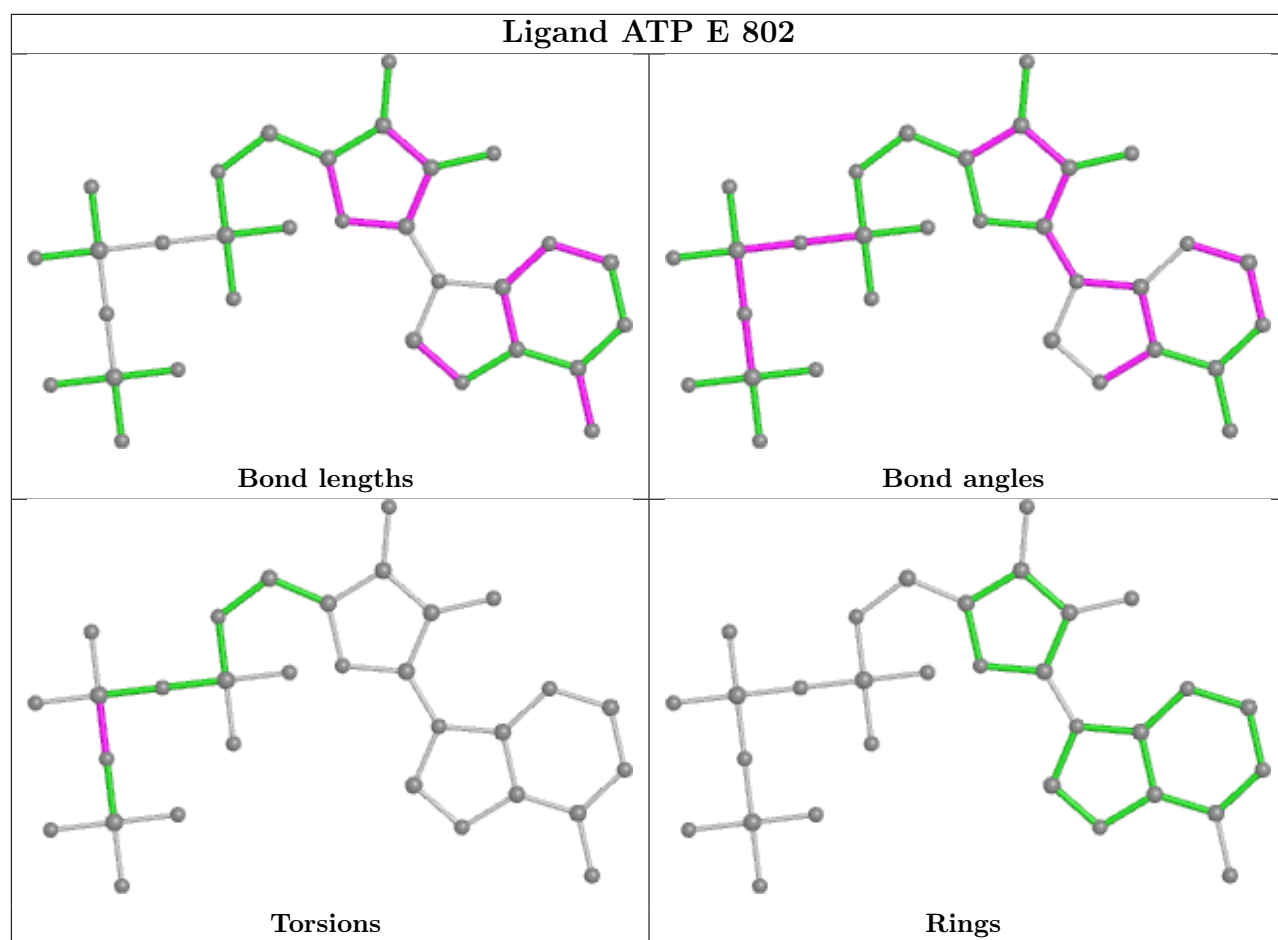
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

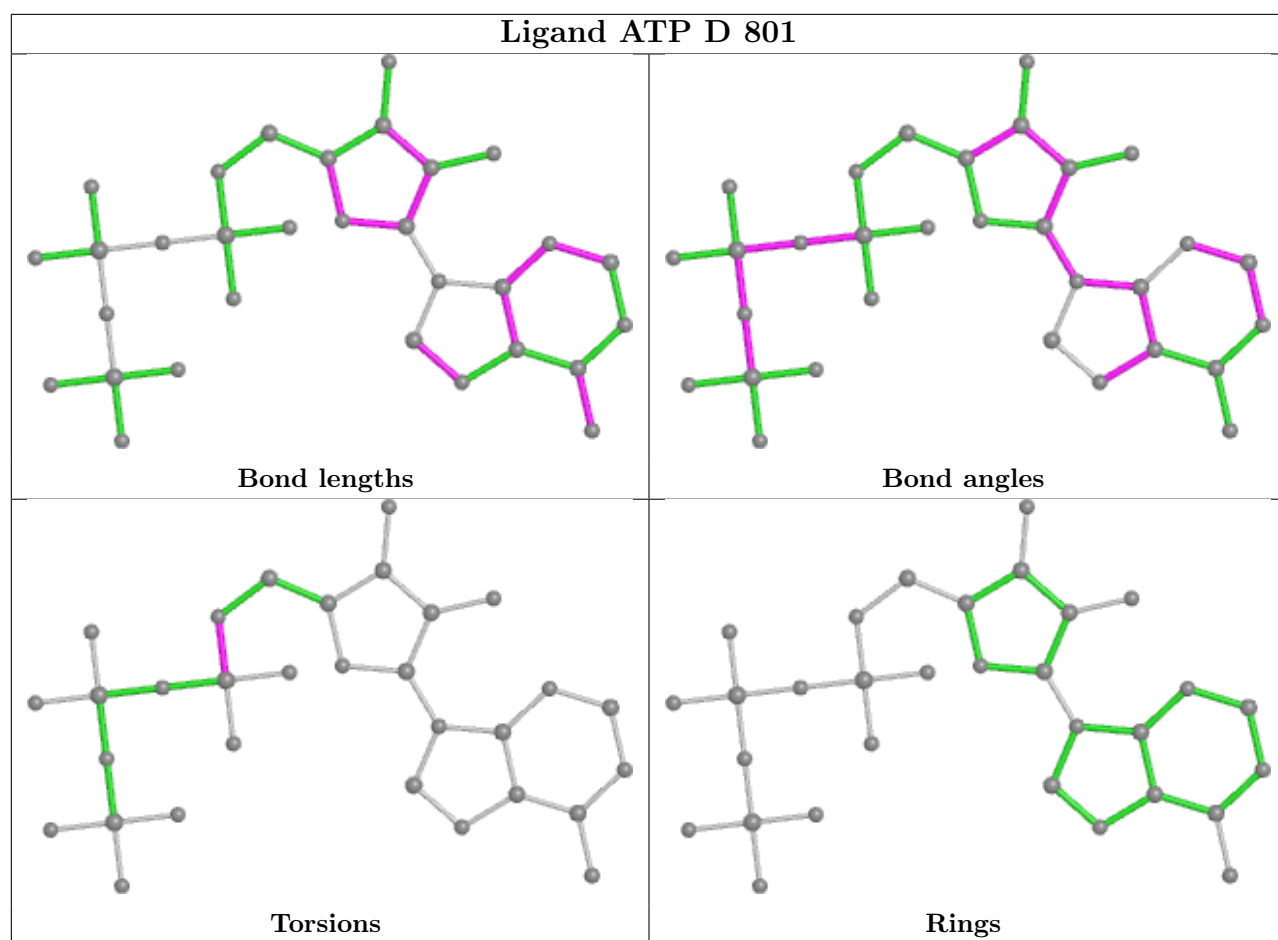


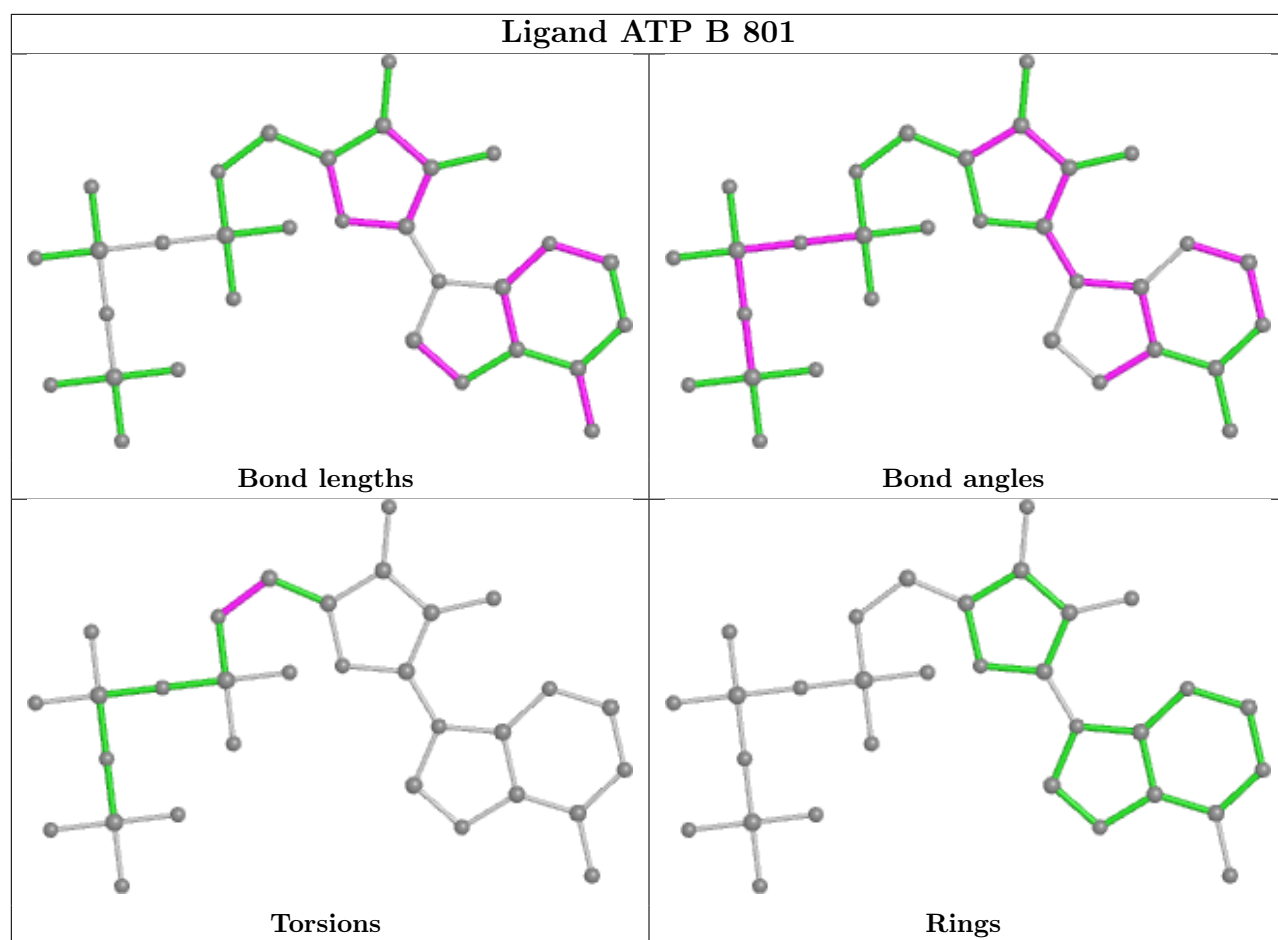


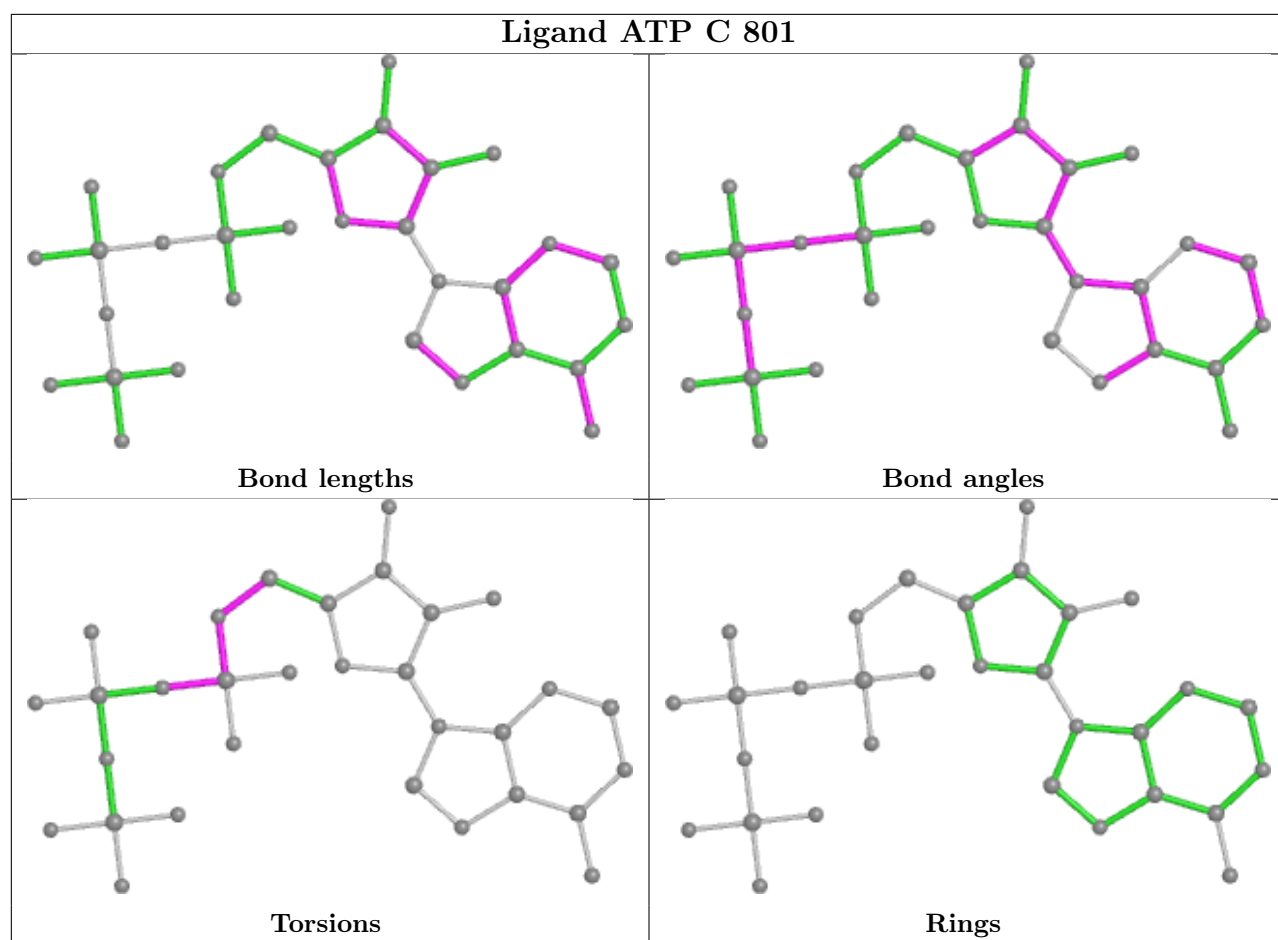




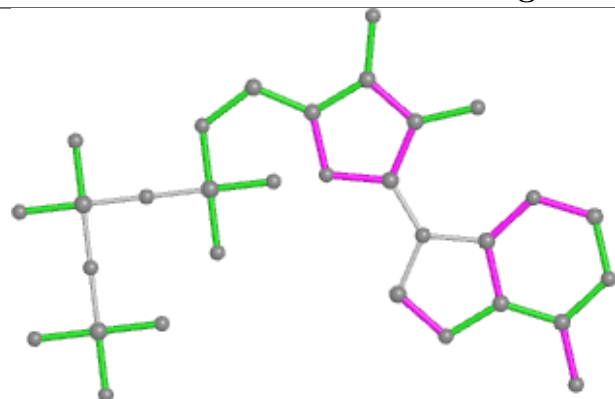




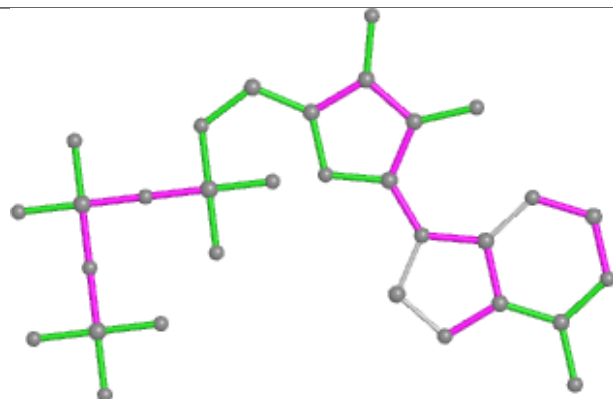




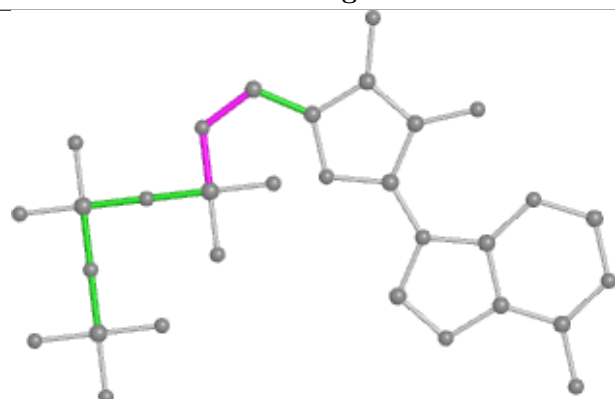
## Ligand ATP E 801



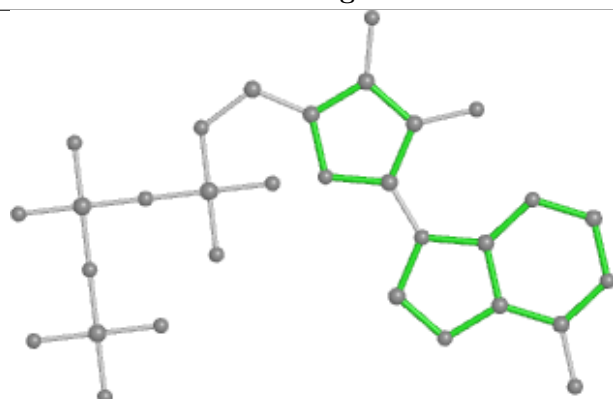
Bond lengths



Bond angles

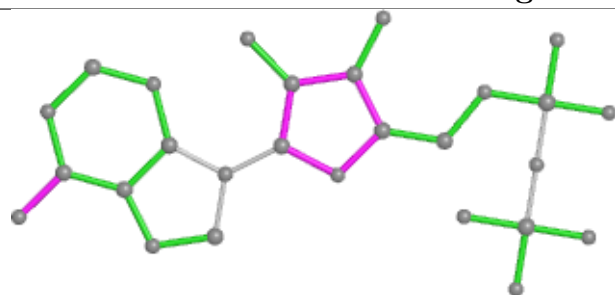


Torsions

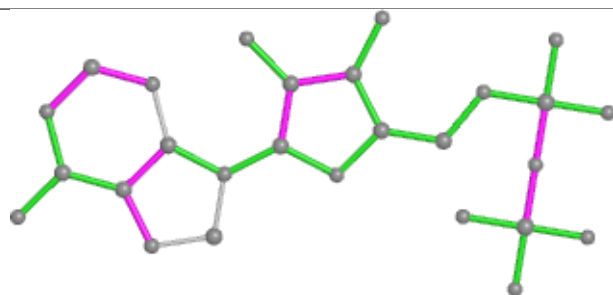


Rings

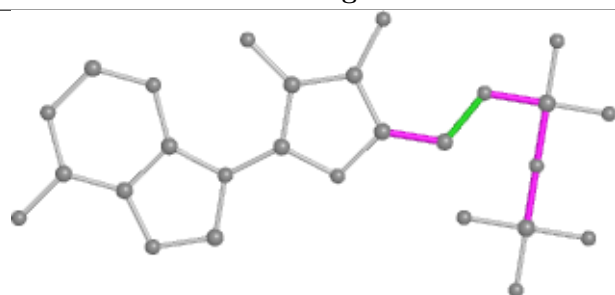
## Ligand ADP F 801



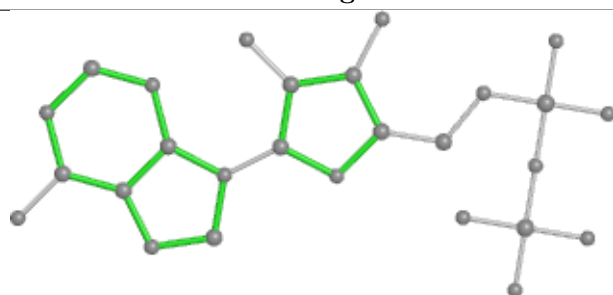
Bond lengths



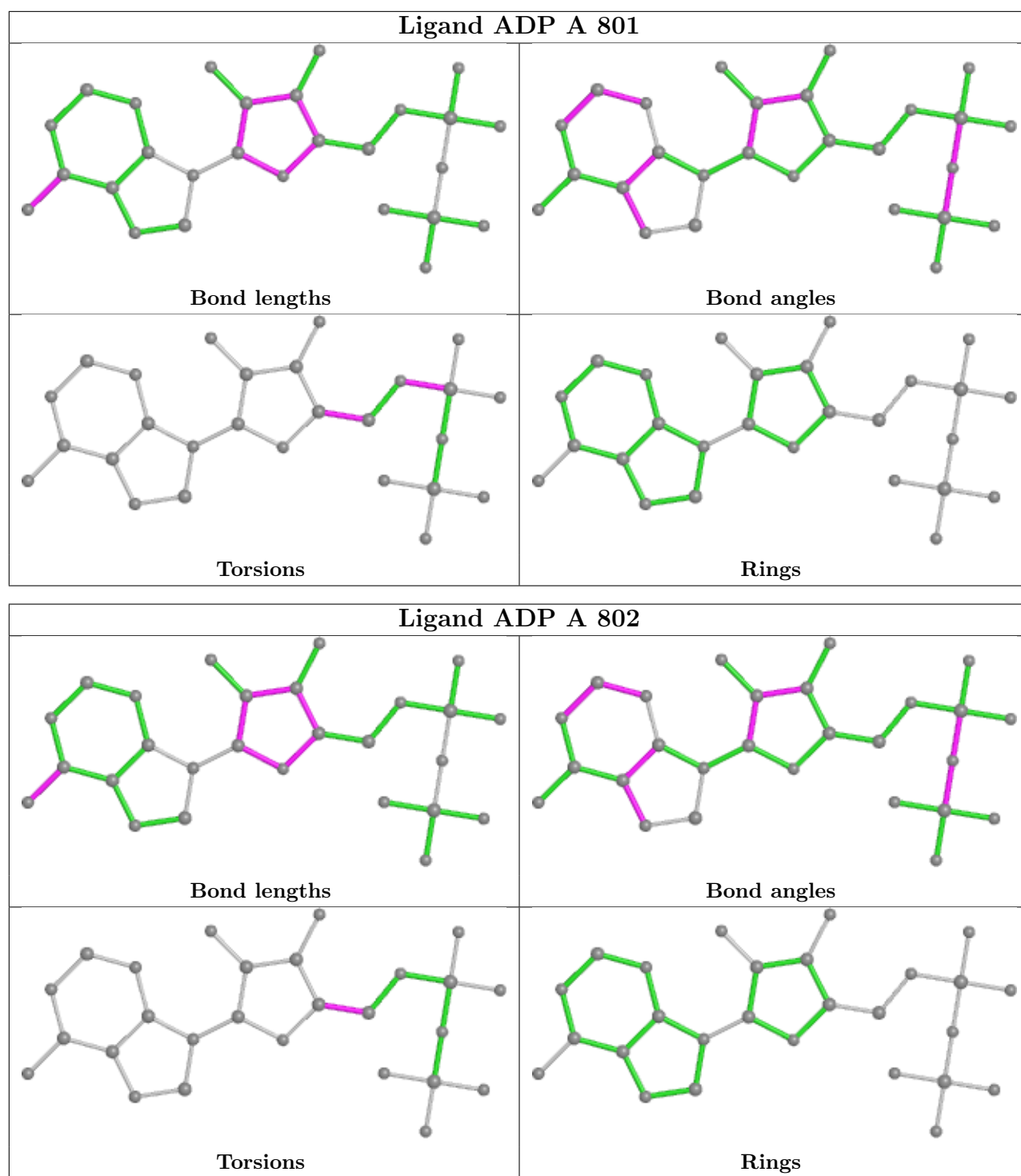
Bond angles



Torsions



Rings



## 5.7 Other polymers ⓘ

There are no such residues in this entry.



## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

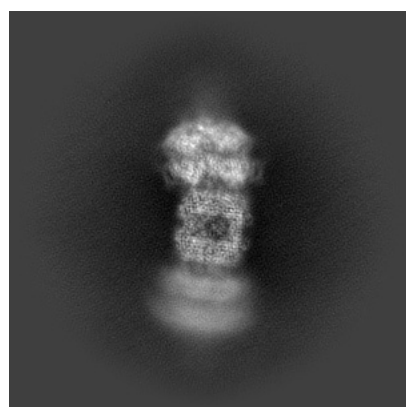
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21520. These allow visual inspection of the internal detail of the map and identification of artifacts.

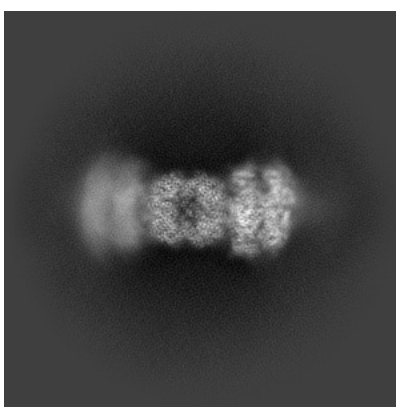
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

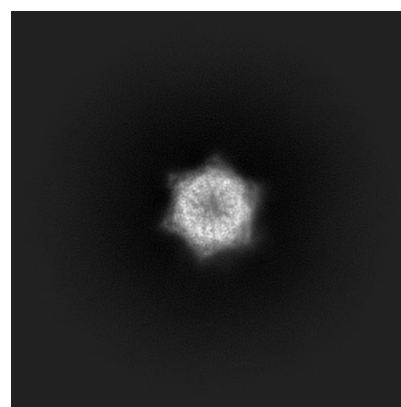
#### 6.1.1 Primary map



X



Y

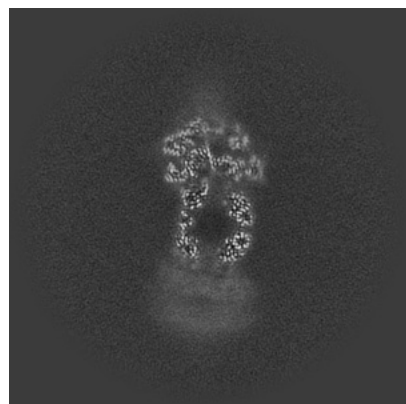


Z

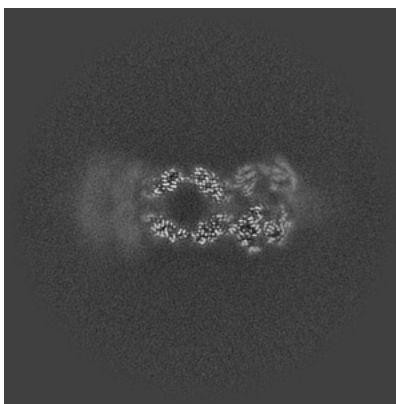
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

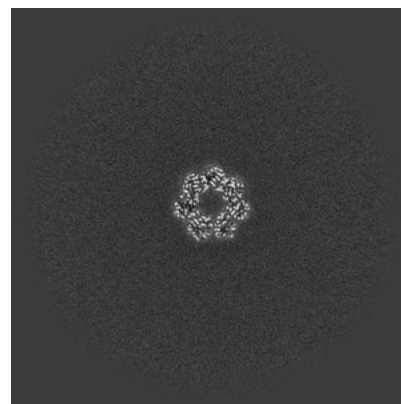
#### 6.2.1 Primary map



X Index: 300



Y Index: 300

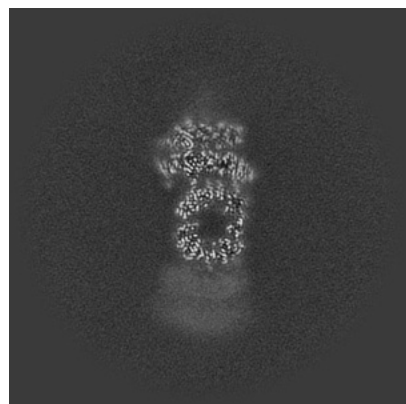


Z Index: 300

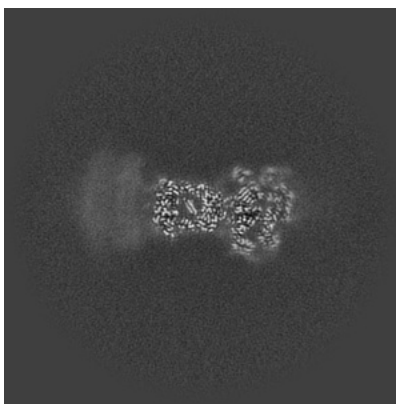
The images above show central slices of the map in three orthogonal directions.

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

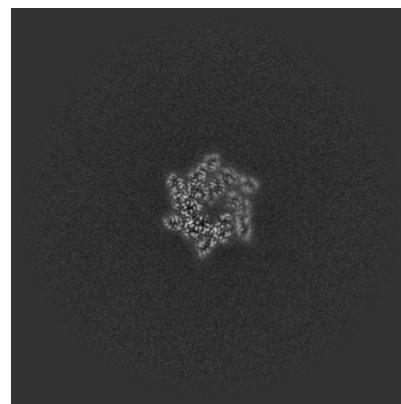
### 6.3.1 Primary map



X Index: 283



Y Index: 273

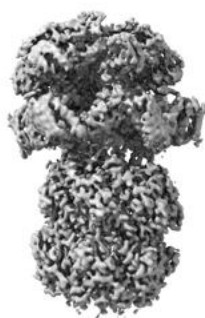


Z Index: 356

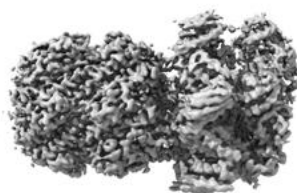
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

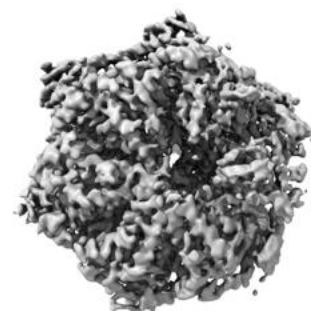
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

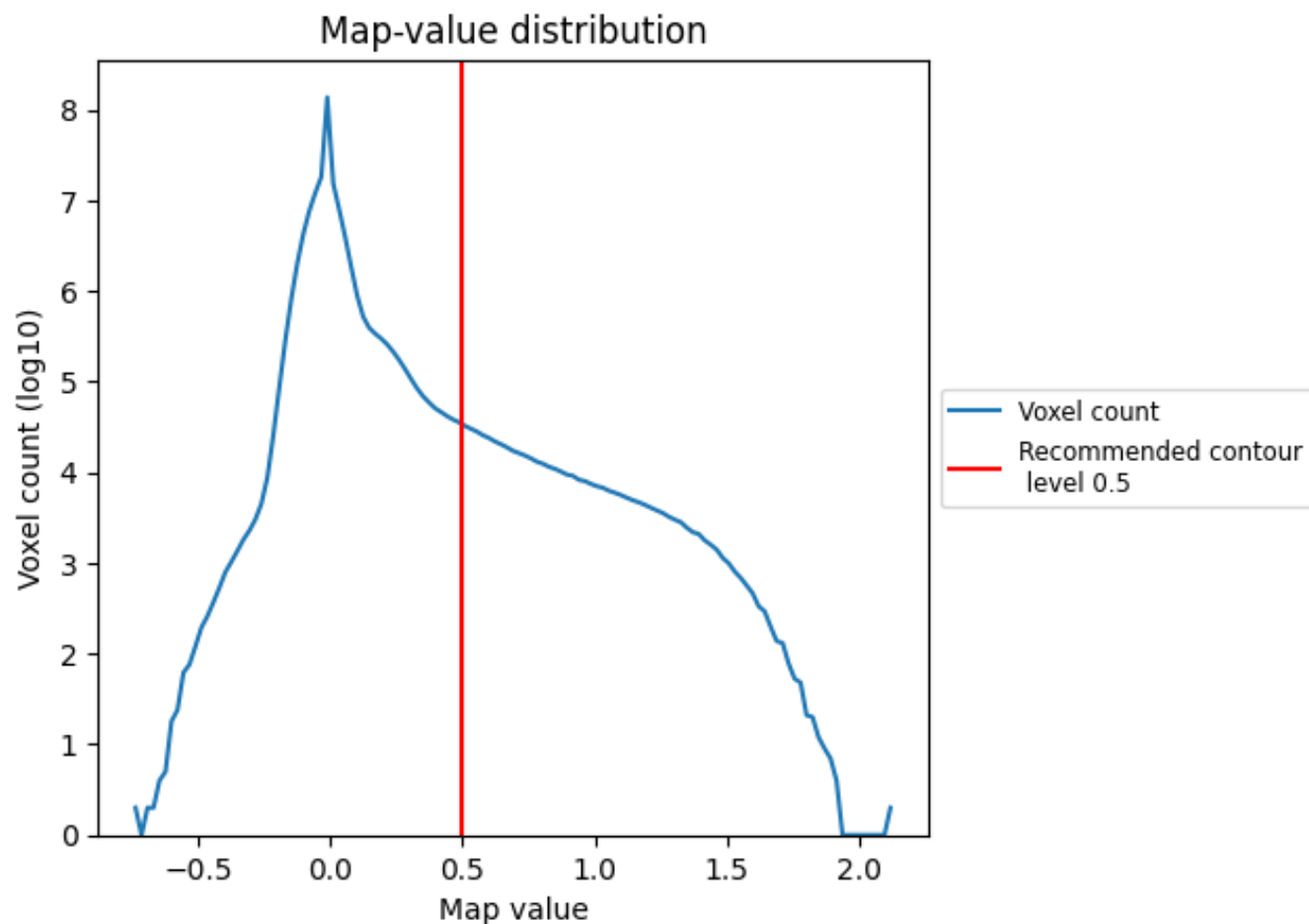
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

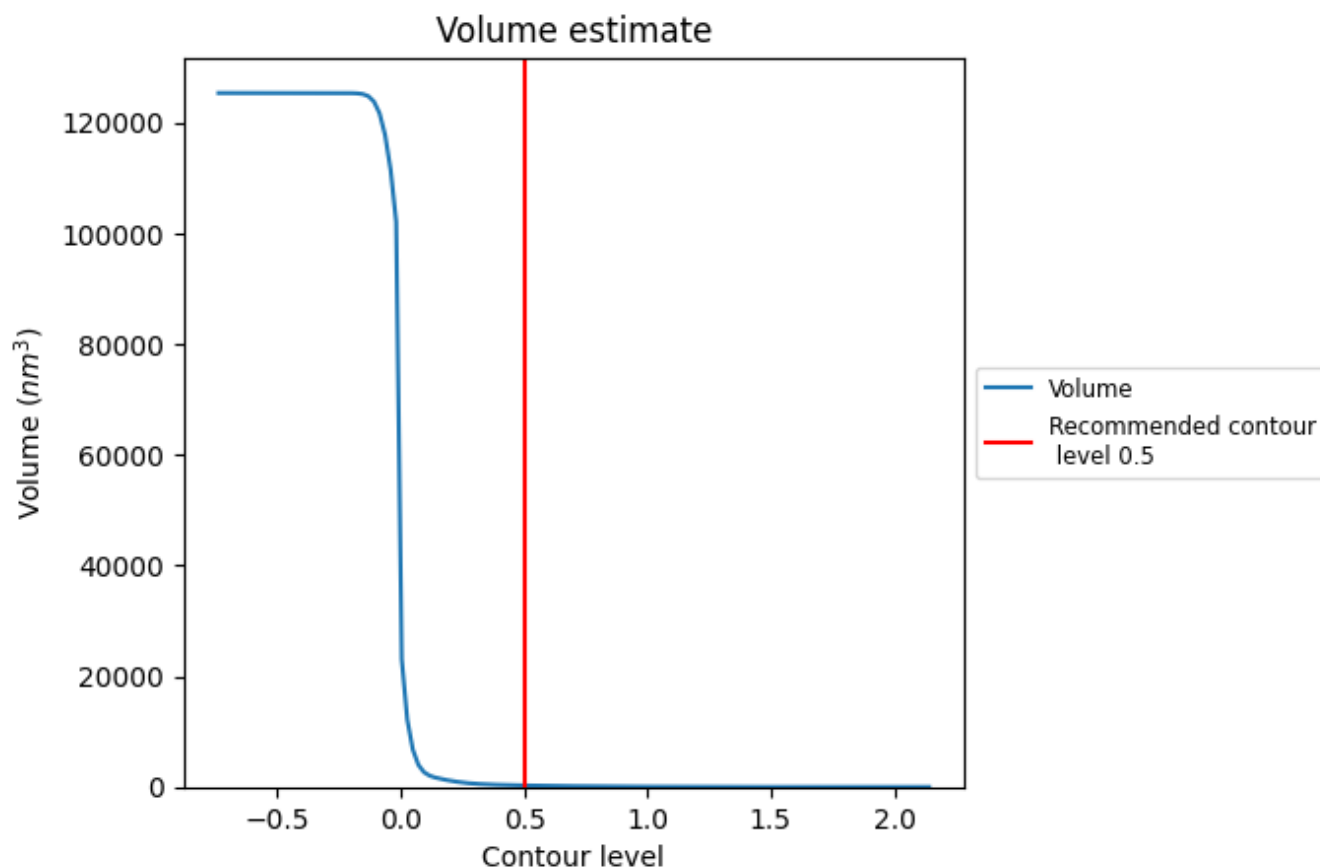
This section contains the results of statistical analysis of the map.

### 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.

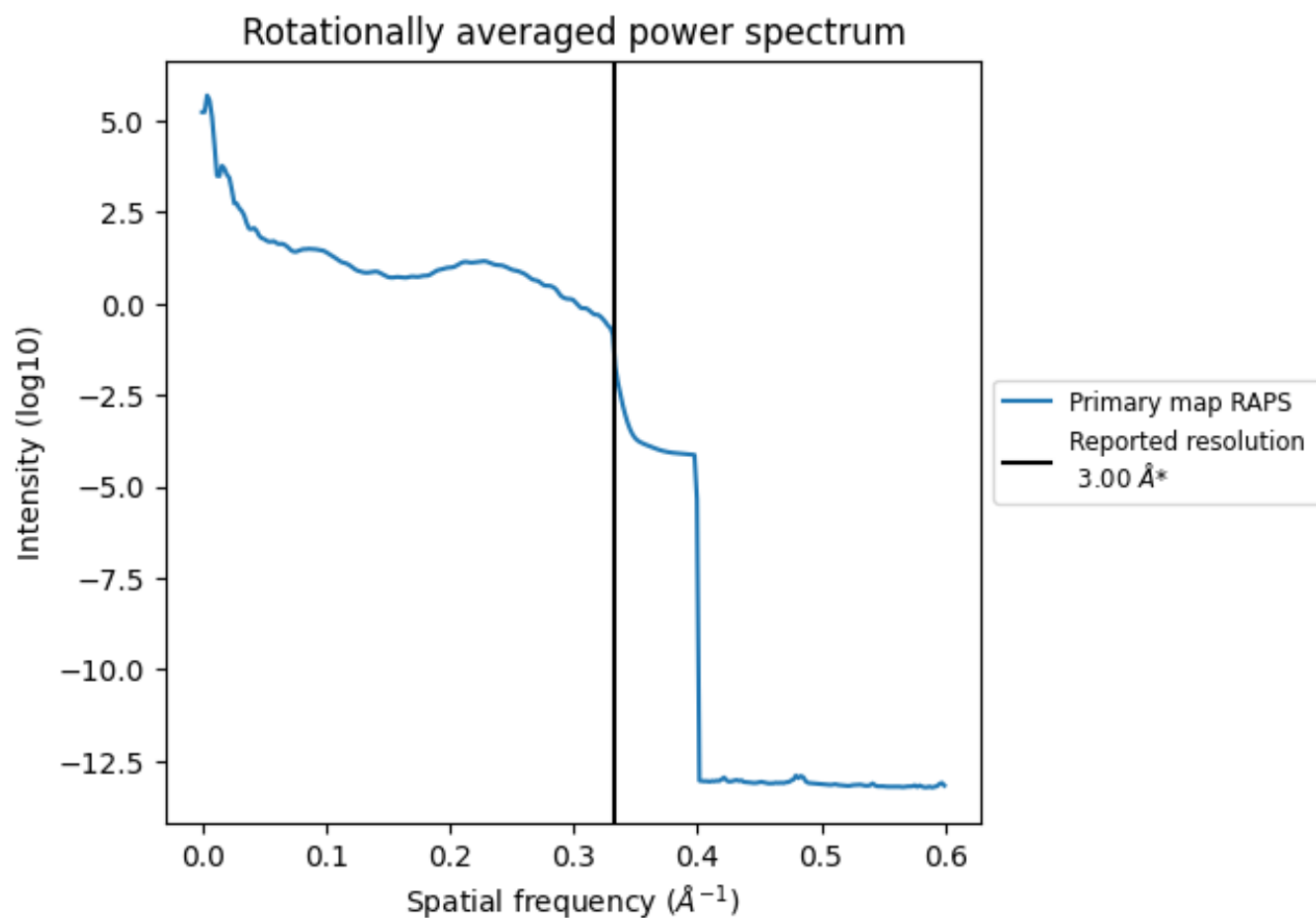
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 272 nm<sup>3</sup>; this corresponds to an approximate mass of 246 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 0.333 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

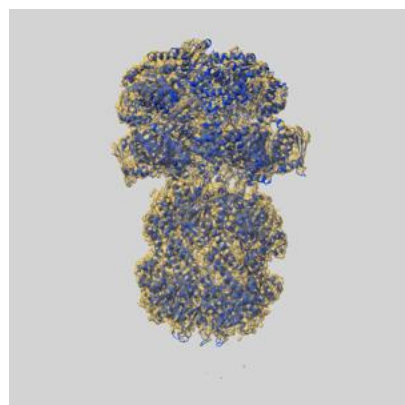
This section was not generated. No FSC curve or half-maps provided.



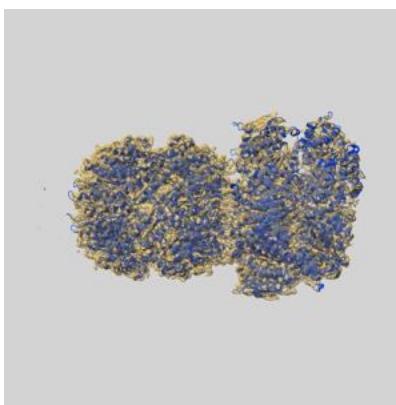
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21520 and PDB model 6W20. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

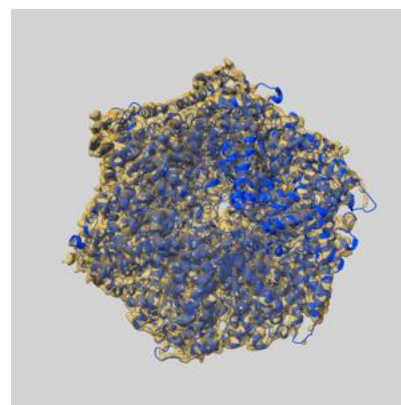
### 9.1 Map-model overlay [i](#)



X



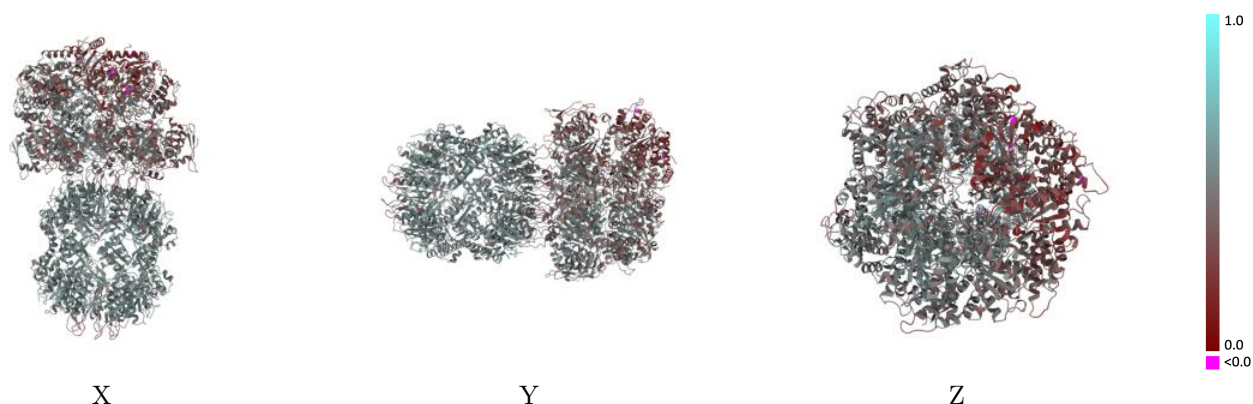
Y



Z

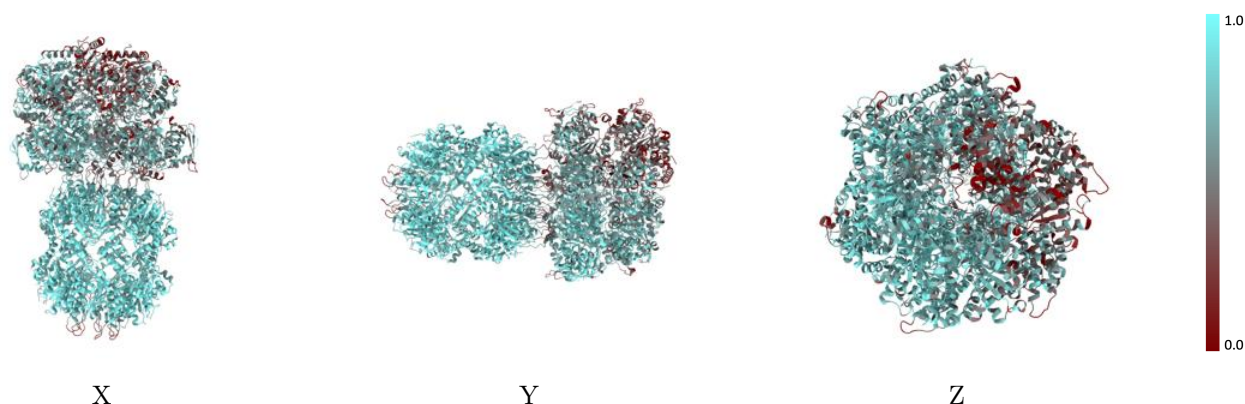
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



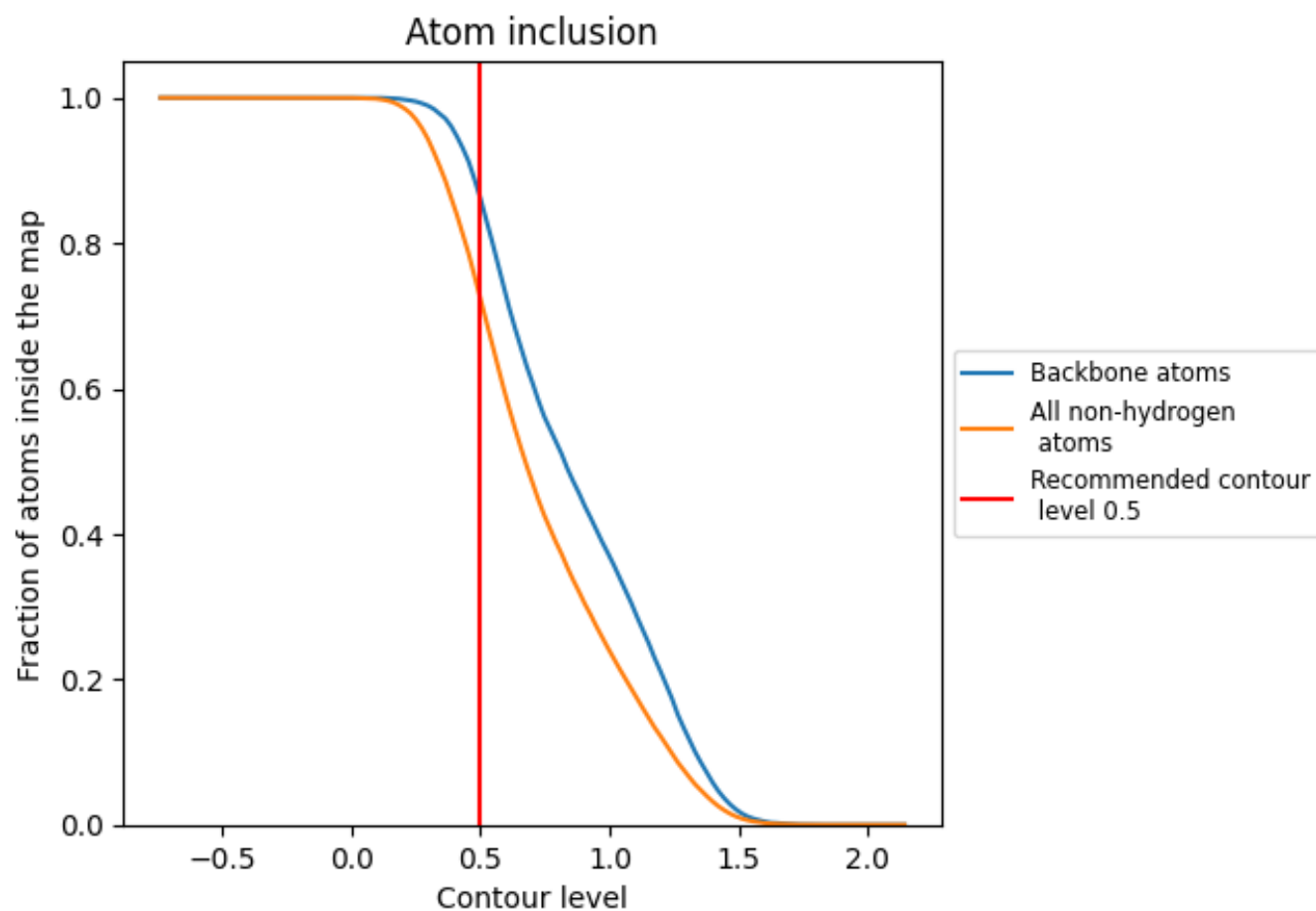
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).













































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7243	 0.4740
A	 0.5888	 0.4220
B	 0.7110	 0.4630
C	 0.7686	 0.4970
D	 0.7414	 0.4850
E	 0.5811	 0.4090
F	 0.4330	 0.3500
G	 0.8347	 0.5190
H	 0.8490	 0.5240
I	 0.8415	 0.5220
J	 0.8327	 0.5180
K	 0.8286	 0.5150
L	 0.8395	 0.5170
M	 0.8469	 0.5210
N	 0.8361	 0.5170
O	 0.8401	 0.5320
P	 0.8245	 0.5200
Q	 0.8238	 0.5210
R	 0.8279	 0.5180
S	 0.8415	 0.5230
T	 0.8367	 0.5200
X	 0.5750	 0.4440

