



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:29 PM UTC

PDB ID : 3S1A / pdb_00003s1a
Title : Crystal structure of the phosphorylation-site double mutant S431E/T432E of the KaiC circadian clock protein
Authors : Pattanayek, R.; Williams, D.W.; Rossi, G.; Weigand, S.; Mori, T.; Johnson, C.H.; Stewart, P.L.; Egli, M.
Deposited on : 2011-05-14
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

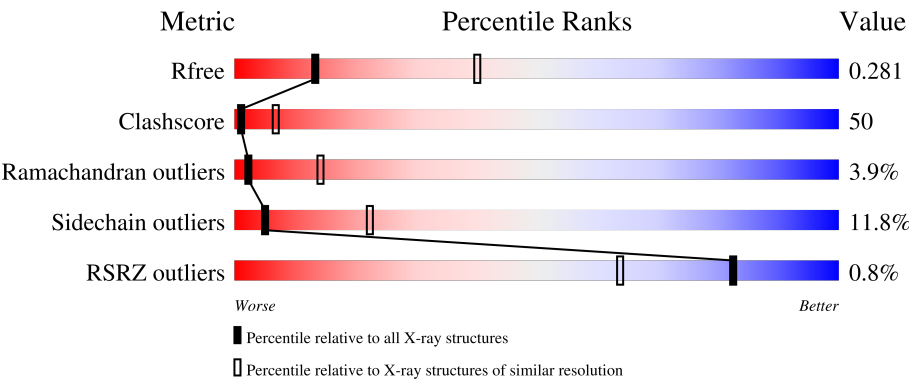
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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:
X-RAY DIFFRACTION

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	525	2% 30%54%11% . .
1	F	525	% 35%49%11% . .
2	B	525	% 28%53%11% . 6%
2	C	525	32%50%10%7%

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Mol	Chain	Length	Quality of chain
2	D	525	
2	E	525	

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
1	SEP	A	320	-	-	X	-
1	SEP	F	320	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23898 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Circadian clock protein kinase kaiC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	506	Total	C	N	O	P	S	0	0	0
			3994	2512	701	765	1	15			
1	F	506	Total	C	N	O	P	S	0	0	0
			3994	2512	701	765	1	15			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	431	GLU	SER	engineered mutation	UNP Q79PF4
A	432	GLU	THR	engineered mutation	UNP Q79PF4
A	520	HIS	-	expression tag	UNP Q79PF4
A	521	HIS	-	expression tag	UNP Q79PF4
A	522	HIS	-	expression tag	UNP Q79PF4
A	523	HIS	-	expression tag	UNP Q79PF4
A	524	HIS	-	expression tag	UNP Q79PF4
A	525	HIS	-	expression tag	UNP Q79PF4
F	431	GLU	SER	engineered mutation	UNP Q79PF4
F	432	GLU	THR	engineered mutation	UNP Q79PF4
F	520	HIS	-	expression tag	UNP Q79PF4
F	521	HIS	-	expression tag	UNP Q79PF4
F	522	HIS	-	expression tag	UNP Q79PF4
F	523	HIS	-	expression tag	UNP Q79PF4
F	524	HIS	-	expression tag	UNP Q79PF4
F	525	HIS	-	expression tag	UNP Q79PF4

- Molecule 2 is a protein called Circadian clock protein kinase kaiC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	491	Total	C	N	O	S		0	0	0
			3875	2442	678	740	15				
2	C	488	Total	C	N	O	S		0	0	0
			3851	2428	674	734	15				

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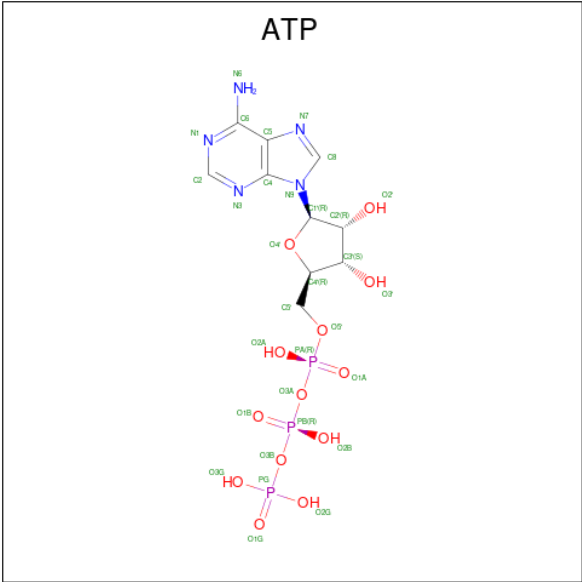
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	485	Total	C	N	O	S	0	0	0
			3827	2414	671	727	15			
2	E	492	Total	C	N	O	S	0	0	0
			3883	2448	679	741	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	431	GLU	SER	engineered mutation	UNP Q79PF4
B	432	GLU	THR	engineered mutation	UNP Q79PF4
B	520	HIS	-	expression tag	UNP Q79PF4
B	521	HIS	-	expression tag	UNP Q79PF4
B	522	HIS	-	expression tag	UNP Q79PF4
B	523	HIS	-	expression tag	UNP Q79PF4
B	524	HIS	-	expression tag	UNP Q79PF4
B	525	HIS	-	expression tag	UNP Q79PF4
C	431	GLU	SER	engineered mutation	UNP Q79PF4
C	432	GLU	THR	engineered mutation	UNP Q79PF4
C	520	HIS	-	expression tag	UNP Q79PF4
C	521	HIS	-	expression tag	UNP Q79PF4
C	522	HIS	-	expression tag	UNP Q79PF4
C	523	HIS	-	expression tag	UNP Q79PF4
C	524	HIS	-	expression tag	UNP Q79PF4
C	525	HIS	-	expression tag	UNP Q79PF4
D	431	GLU	SER	engineered mutation	UNP Q79PF4
D	432	GLU	THR	engineered mutation	UNP Q79PF4
D	520	HIS	-	expression tag	UNP Q79PF4
D	521	HIS	-	expression tag	UNP Q79PF4
D	522	HIS	-	expression tag	UNP Q79PF4
D	523	HIS	-	expression tag	UNP Q79PF4
D	524	HIS	-	expression tag	UNP Q79PF4
D	525	HIS	-	expression tag	UNP Q79PF4
E	431	GLU	SER	engineered mutation	UNP Q79PF4
E	432	GLU	THR	engineered mutation	UNP Q79PF4
E	520	HIS	-	expression tag	UNP Q79PF4
E	521	HIS	-	expression tag	UNP Q79PF4
E	522	HIS	-	expression tag	UNP Q79PF4
E	523	HIS	-	expression tag	UNP Q79PF4
E	524	HIS	-	expression tag	UNP Q79PF4
E	525	HIS	-	expression tag	UNP Q79PF4

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total 4 Mg 4 4	0	0
4	B	4	Total 4 Mg 4 4	0	0
4	C	4	Total 4 Mg 4 4	0	0
4	D	4	Total 4 Mg 4 4	0	0
4	E	2	Total 2 Mg 2 2	0	0
4	F	3	Total 3 Mg 3 3	0	0

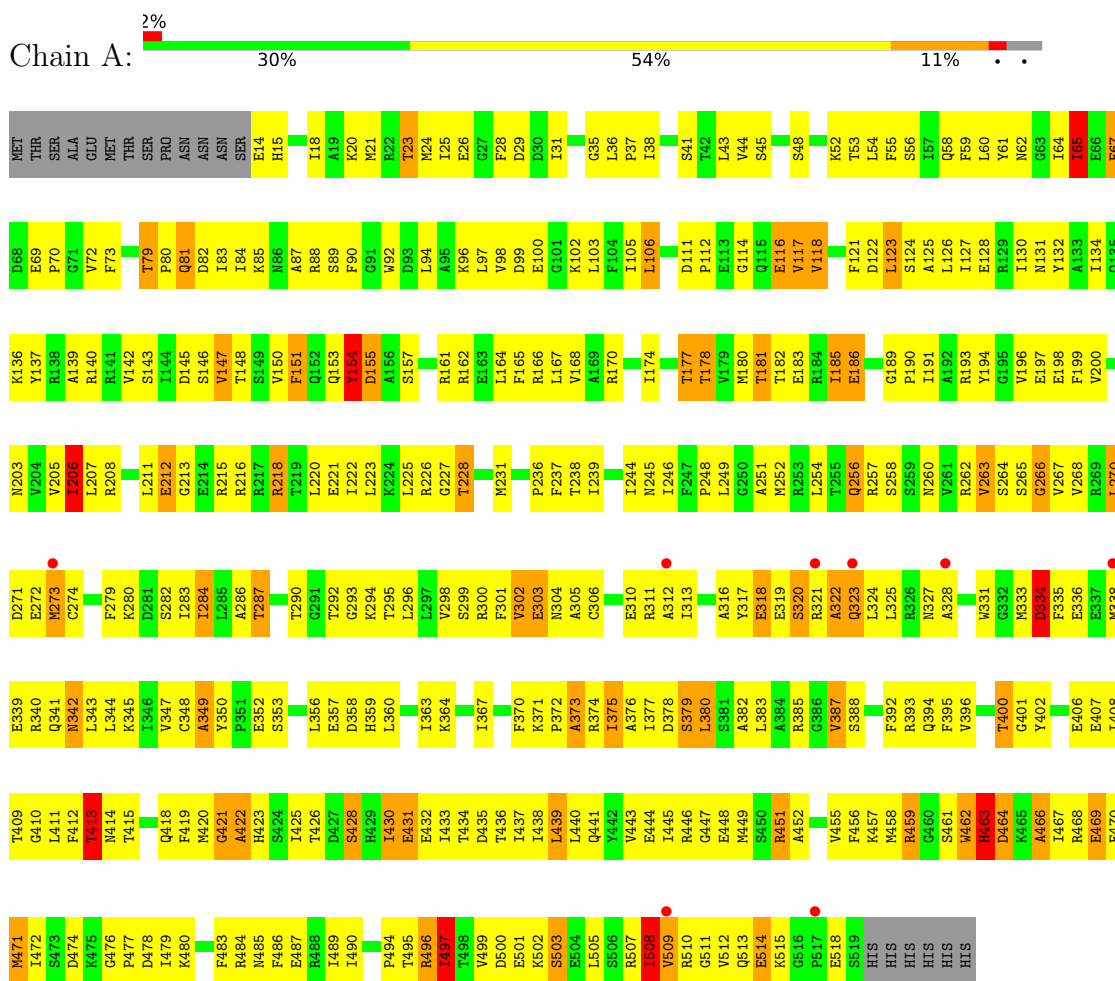
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	5	Total 5 O 5 5	0	0
5	B	6	Total 6 O 6 6	0	0
5	C	10	Total 10 O 10 10	0	0
5	D	32	Total 32 O 32 32	0	0
5	E	16	Total 16 O 16 16	0	0
5	F	12	Total 12 O 12 12	0	0

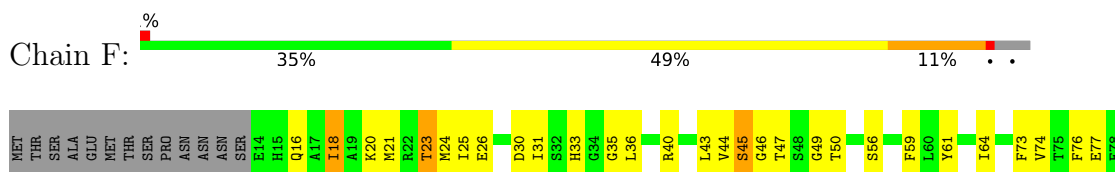
3 Residue-property plots

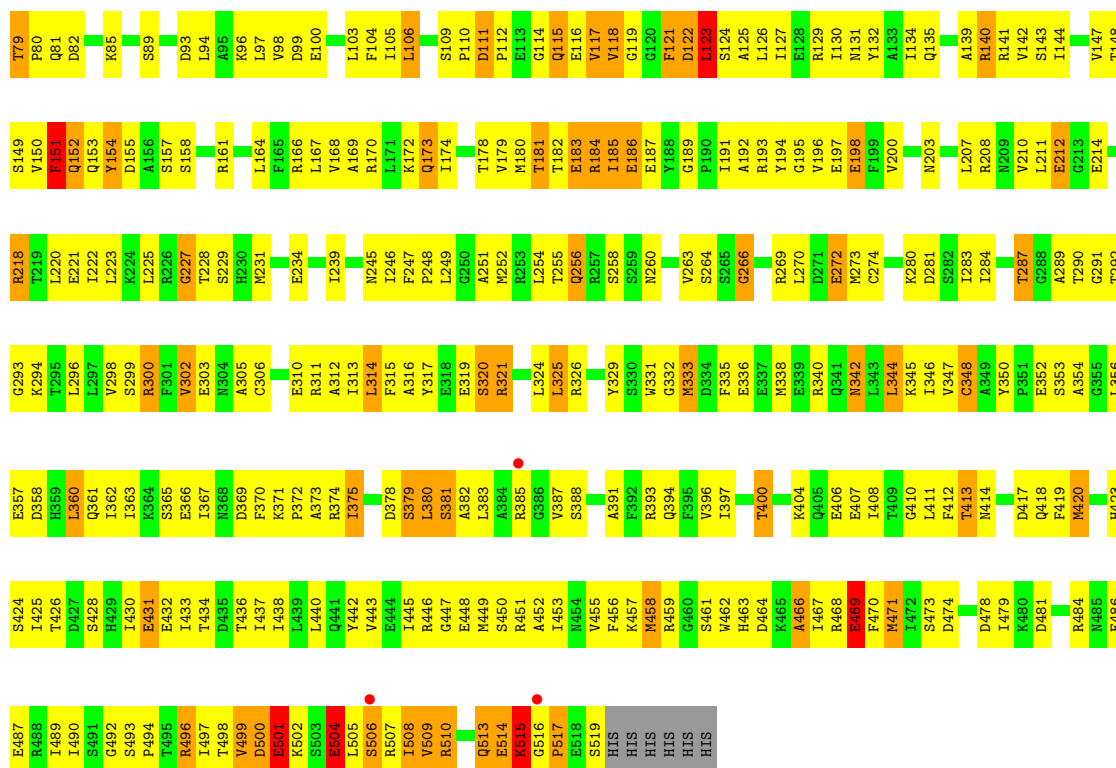
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Circadian clock protein kinase kaiC

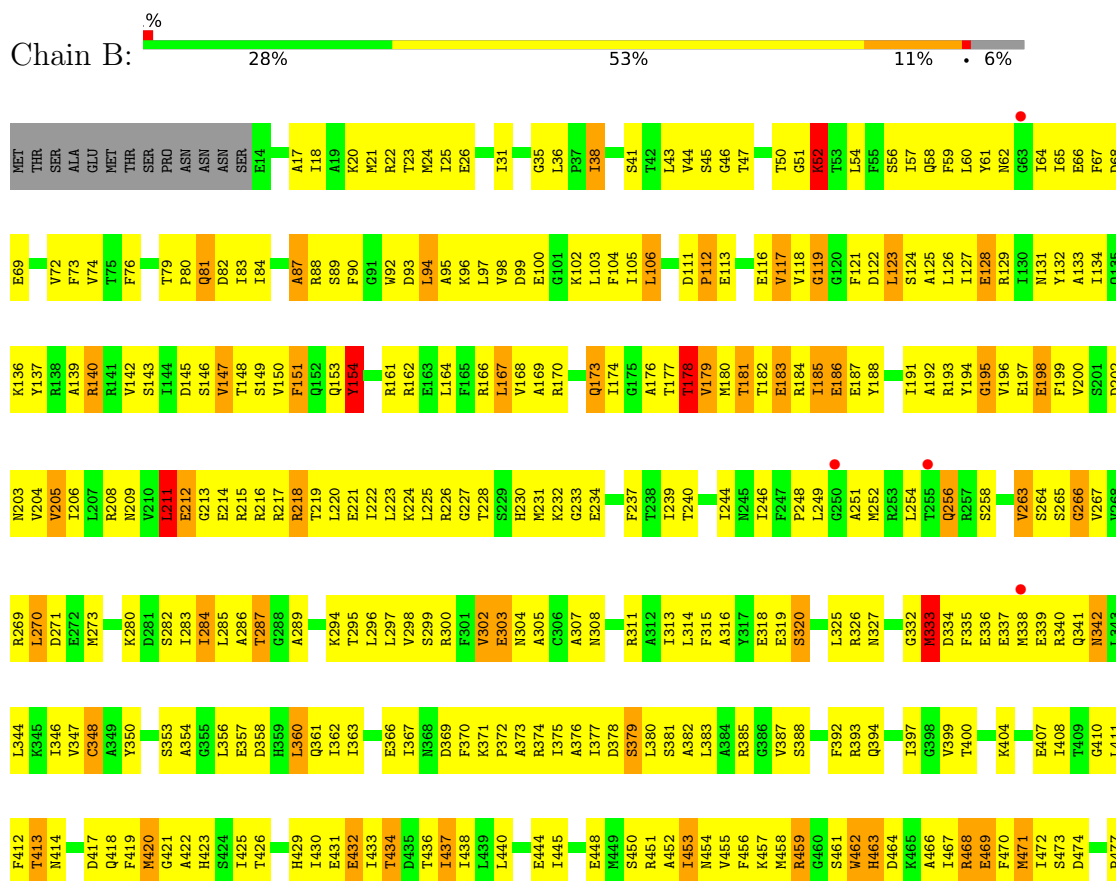


• Molecule 1: Circadian clock protein kinase kaiC



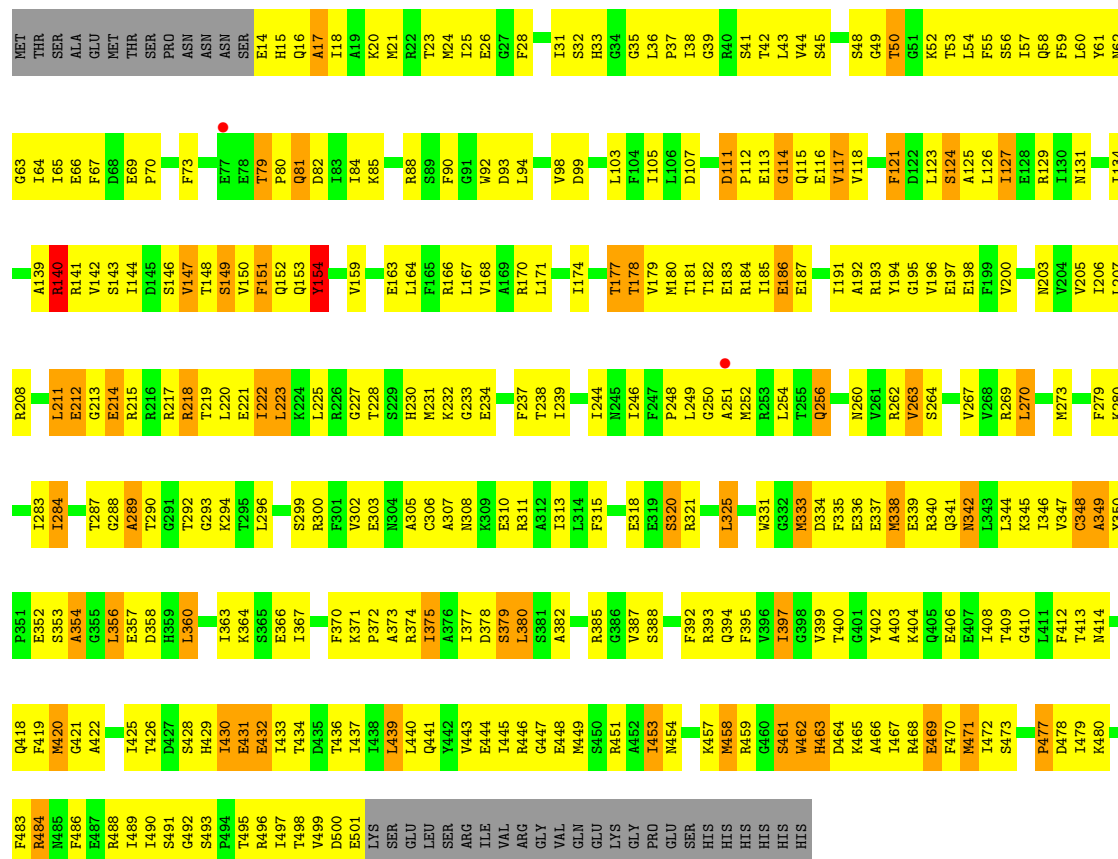


• Molecule 2: Circadian clock protein kinase kaiC

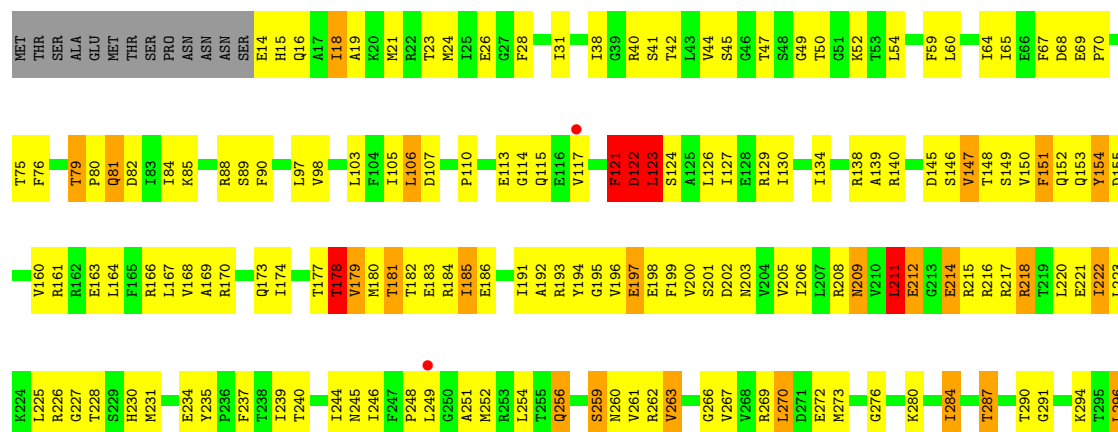


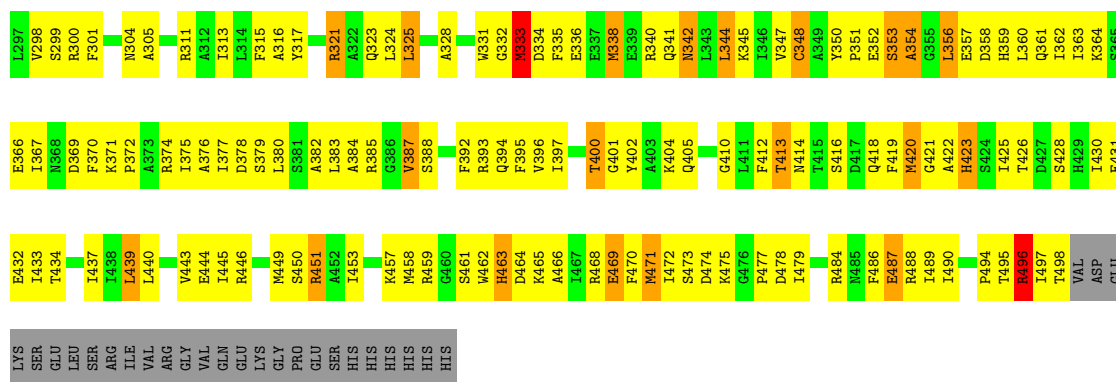


• Molecule 2: Circadian clock protein kinase kaiC



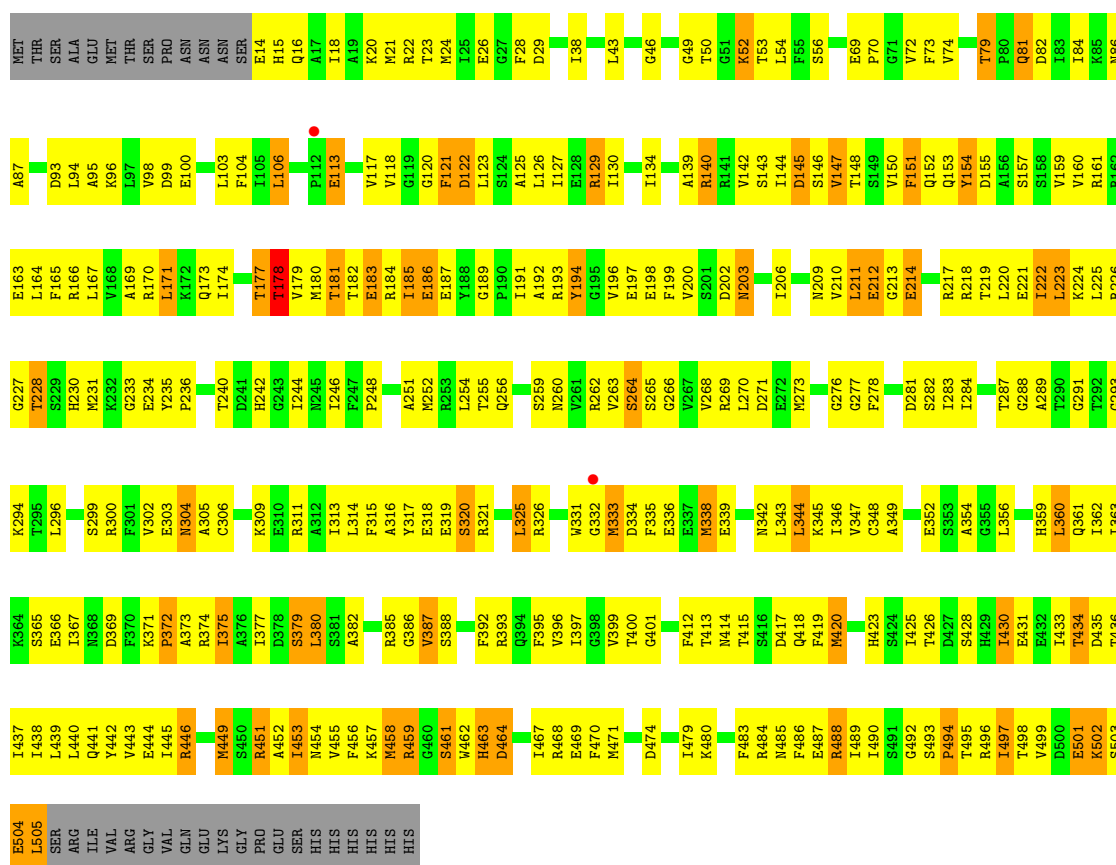
• Molecule 2: Circadian clock protein kinase kaiC





• Molecule 2: Circadian clock protein kinase kaiC

Chain E: 35% 47% 11% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	132.67Å 135.49Å 204.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.00 – 3.00 17.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (17.00-3.00) 93.9 (17.00-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.75 (at 2.87Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.242 , 0.288 0.239 , 0.281	Depositor DCC
R_{free} test set	6459 reflections (7.95%)	wwPDB-VP
Wilson B-factor (Å ²)	65.1	Xtriage
Anisotropy	0.584	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	23898	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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, SEP, 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	0.53	2/4049 (0.0%)	1.10	26/5453 (0.5%)
1	F	0.56	0/4049	1.13	35/5453 (0.6%)
2	B	0.47	0/3940	1.03	22/5309 (0.4%)
2	C	0.51	0/3916	1.03	15/5278 (0.3%)
2	D	0.63	1/3892 (0.0%)	1.07	12/5245 (0.2%)
2	E	0.61	0/3948	1.11	27/5320 (0.5%)
All	All	0.55	3/23794 (0.0%)	1.08	137/32058 (0.4%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	299	SER	CA-C	6.13	1.60	1.52
1	A	334	ASP	CA-C	5.72	1.60	1.52
1	A	206	ILE	CA-CB	5.24	1.60	1.54

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	LEU	N-CA-C	-13.82	96.88	113.88
2	B	502	LYS	N-CA-C	-10.95	98.90	114.12
1	F	380	LEU	N-CA-C	-10.30	100.02	111.14
2	D	380	LEU	N-CA-C	-9.90	99.51	111.69
2	E	380	LEU	N-CA-C	-9.62	99.08	112.45

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	A	3994	0	3985	480	0
1	F	3994	0	3984	421	0
2	B	3875	0	3863	460	0
2	C	3851	0	3839	398	0
2	D	3827	0	3819	377	0
2	E	3883	0	3875	370	0
3	A	62	0	24	7	0
3	B	62	0	24	8	0
3	C	62	0	24	5	0
3	D	62	0	24	8	0
3	E	62	0	24	12	0
3	F	62	0	24	6	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	0	0
4	E	2	0	0	0	0
4	F	3	0	0	0	0
5	A	5	0	0	1	0
5	B	6	0	0	1	0
5	C	10	0	0	2	0
5	D	32	0	0	13	0
5	E	16	0	0	0	0
5	F	12	0	0	1	0
All	All	23898	0	23509	2347	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 50.

The worst 5 of 2347 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:A:455:VAL:HG12	1:A:463:HIS:CD2	1.63	1.30
1:A:320:SEP:HB2	2:B:254:LEU:O	1.42	1.17
1:A:254:LEU:CD2	1:F:320:SEP:HA	1.74	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ARG:O	1:A:324:LEU:HB2	1.45	1.14
1:F:263:VAL:HG12	1:F:374:ARG:HH21	1.10	1.14

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 X-ray entries followed by that with respect to entries of similar resolution.

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	503/525 (96%)	406 (81%)	76 (15%)	21 (4%)	2	13
1	F	503/525 (96%)	422 (84%)	61 (12%)	20 (4%)	2	14
2	B	489/525 (93%)	389 (80%)	82 (17%)	18 (4%)	2	15
2	C	486/525 (93%)	419 (86%)	45 (9%)	22 (4%)	2	12
2	D	483/525 (92%)	415 (86%)	52 (11%)	16 (3%)	3	17
2	E	490/525 (93%)	402 (82%)	69 (14%)	19 (4%)	2	14
All	All	2954/3150 (94%)	2453 (83%)	385 (13%)	116 (4%)	2	14

5 of 116 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	TYR
1	A	334	ASP
1	A	462	TRP
1	A	463	HIS
1	A	503	SER

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

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	431/449 (96%)	385 (89%)	46 (11%)	6	26
1	F	431/449 (96%)	383 (89%)	48 (11%)	6	25
2	B	419/450 (93%)	368 (88%)	51 (12%)	5	21
2	C	416/450 (92%)	364 (88%)	52 (12%)	4	20
2	D	413/450 (92%)	357 (86%)	56 (14%)	3	17
2	E	420/450 (93%)	374 (89%)	46 (11%)	6	25
All	All	2530/2698 (94%)	2231 (88%)	299 (12%)	5	22

5 of 299 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	325	LEU
1	F	375	ILE
2	E	369	ASP
1	F	135	GLN
2	C	15	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	454	ASN
1	F	33	HIS
1	F	260	ASN
2	C	33	HIS
2	B	429	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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
1	SEP	A	320	1	8,9,10	1.96	1 (12%)	7,12,14	2.56	2 (28%)
1	SEP	F	320	1	8,9,10	2.20	3 (37%)	7,12,14	2.75	2 (28%)

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
1	SEP	A	320	1	-	3/6/8/10	-
1	SEP	F	320	1	-	1/6/8/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	SEP	P-O1P	5.03	1.66	1.50
1	F	320	SEP	P-O1P	4.67	1.65	1.50
1	F	320	SEP	P-O2P	2.74	1.65	1.54
1	F	320	SEP	CB-CA	2.72	1.59	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	320	SEP	OG-CB-CA	6.04	114.02	108.14
1	F	320	SEP	OG-CB-CA	-5.44	102.85	108.14
1	F	320	SEP	O3P-P-OG	4.10	117.36	106.67
1	A	320	SEP	O2P-P-OG	2.03	111.97	106.67

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	320	SEP	N-CA-CB-OG
1	A	320	SEP	C-CA-CB-OG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
1	A	320	SEP	CA-CB-OG-P
1	F	320	SEP	CA-CB-OG-P

There are no ring outliers.

2 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	320	SEP	16	0
1	F	320	SEP	12	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 21 are monoatomic - leaving 12 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	E	903	-	32,33,33	1.20	4 (12%)	48,52,52	2.06	14 (29%)
3	ATP	F	901	4	32,33,33	1.21	5 (15%)	48,52,52	2.02	13 (27%)
3	ATP	D	903	4	32,33,33	1.32	3 (9%)	48,52,52	2.12	15 (31%)
3	ATP	B	903	4	32,33,33	1.21	5 (15%)	48,52,52	2.02	12 (25%)
3	ATP	C	901	4	32,33,33	1.13	2 (6%)	48,52,52	2.09	13 (27%)
3	ATP	C	903	4	32,33,33	1.10	2 (6%)	48,52,52	2.09	12 (25%)
3	ATP	A	901	4	32,33,33	1.19	4 (12%)	48,52,52	2.05	11 (22%)
3	ATP	E	901	4	32,33,33	1.31	4 (12%)	48,52,52	2.10	14 (29%)
3	ATP	F	903	4	32,33,33	1.29	2 (6%)	48,52,52	2.05	13 (27%)
3	ATP	D	901	4	32,33,33	1.20	2 (6%)	48,52,52	2.03	12 (25%)
3	ATP	B	901	4	32,33,33	1.24	5 (15%)	48,52,52	1.98	12 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ATP	A	903	4	32,33,33	1.27	4 (12%)	48,52,52	1.96	12 (25%)

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	E	903	-	-	9/22/38/38	0/3/3/3
3	ATP	F	901	4	-	5/22/38/38	0/3/3/3
3	ATP	D	903	4	-	8/22/38/38	0/3/3/3
3	ATP	B	903	4	-	8/22/38/38	0/3/3/3
3	ATP	C	901	4	-	6/22/38/38	0/3/3/3
3	ATP	C	903	4	-	8/22/38/38	0/3/3/3
3	ATP	A	901	4	-	8/22/38/38	0/3/3/3
3	ATP	E	901	4	-	6/22/38/38	0/3/3/3
3	ATP	F	903	4	-	7/22/38/38	0/3/3/3
3	ATP	D	901	4	-	10/22/38/38	0/3/3/3
3	ATP	B	901	4	-	7/22/38/38	0/3/3/3
3	ATP	A	903	4	-	9/22/38/38	0/3/3/3

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	903	ATP	PB-O3A	-4.12	1.55	1.59
3	F	903	ATP	C2-N3	3.31	1.39	1.33
3	E	901	ATP	PA-O3A	3.09	1.62	1.59
3	C	901	ATP	C2-N3	2.99	1.39	1.33
3	E	901	ATP	C2-N3	2.84	1.39	1.33

The worst 5 of 153 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	901	ATP	N3-C2-N1	-5.88	119.69	128.58
3	C	903	ATP	N3-C2-N1	-5.86	119.71	128.58
3	C	901	ATP	N3-C2-N1	-5.69	119.97	128.58
3	B	903	ATP	N3-C2-N1	-5.63	120.06	128.58
3	B	901	ATP	N3-C2-N1	-5.62	120.08	128.58

There are no chirality outliers.

5 of 91 torsion outliers are listed below:

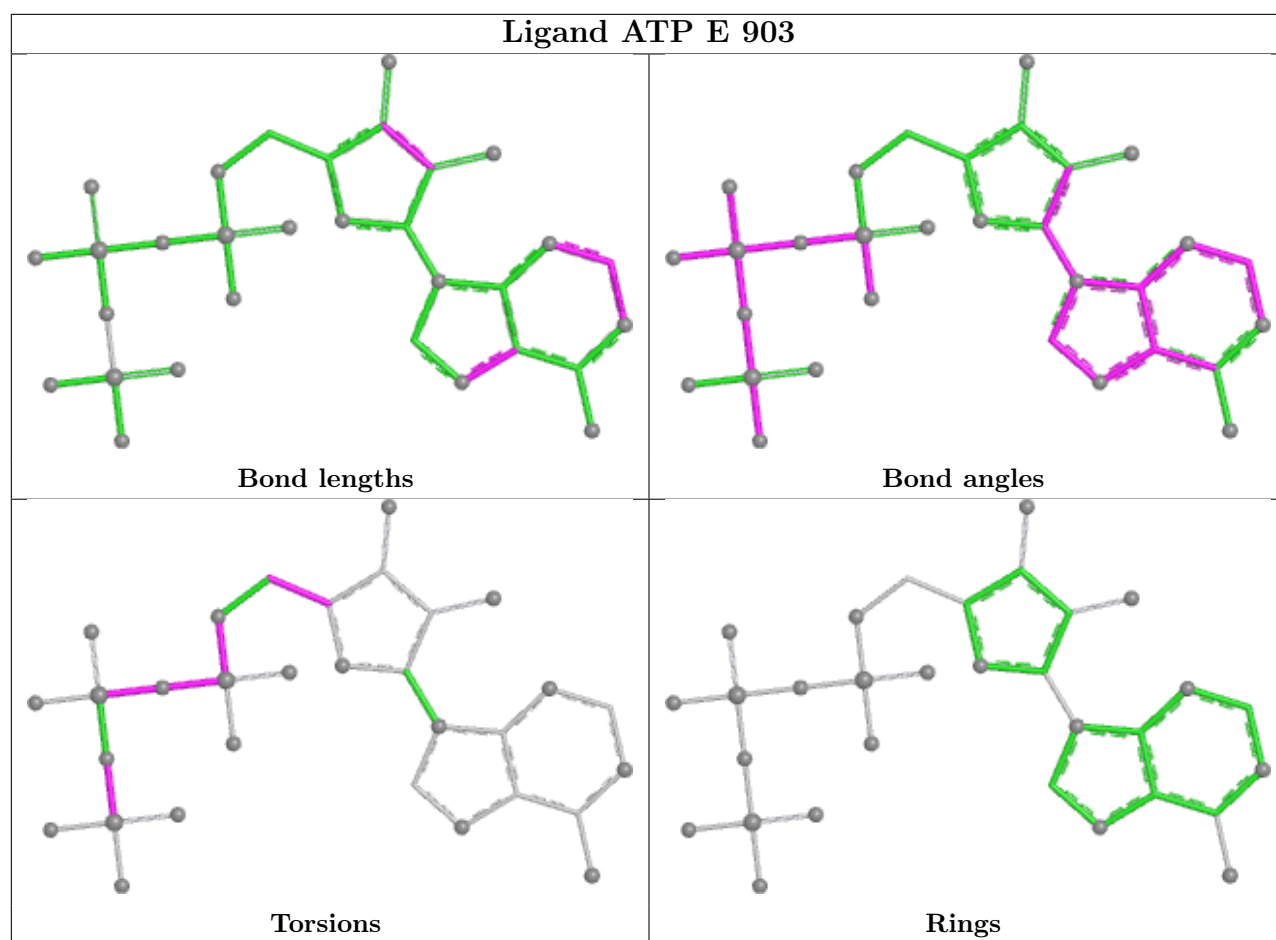
Mol	Chain	Res	Type	Atoms
3	A	901	ATP	C5'-O5'-PA-O1A
3	A	901	ATP	C5'-O5'-PA-O3A
3	A	901	ATP	C3'-C4'-C5'-O5'
3	A	903	ATP	PB-O3B-PG-O3G
3	A	903	ATP	C3'-C4'-C5'-O5'

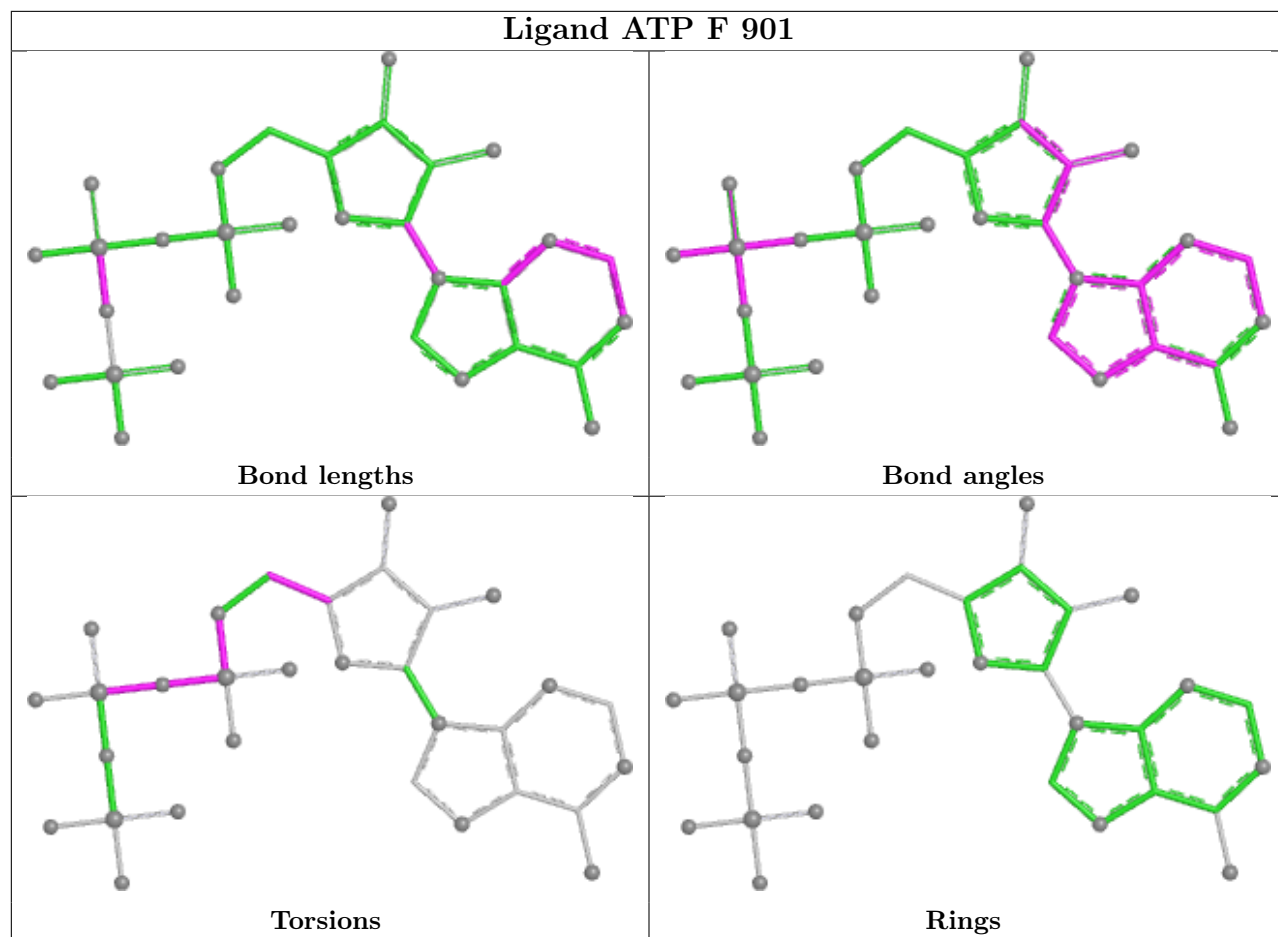
There are no ring outliers.

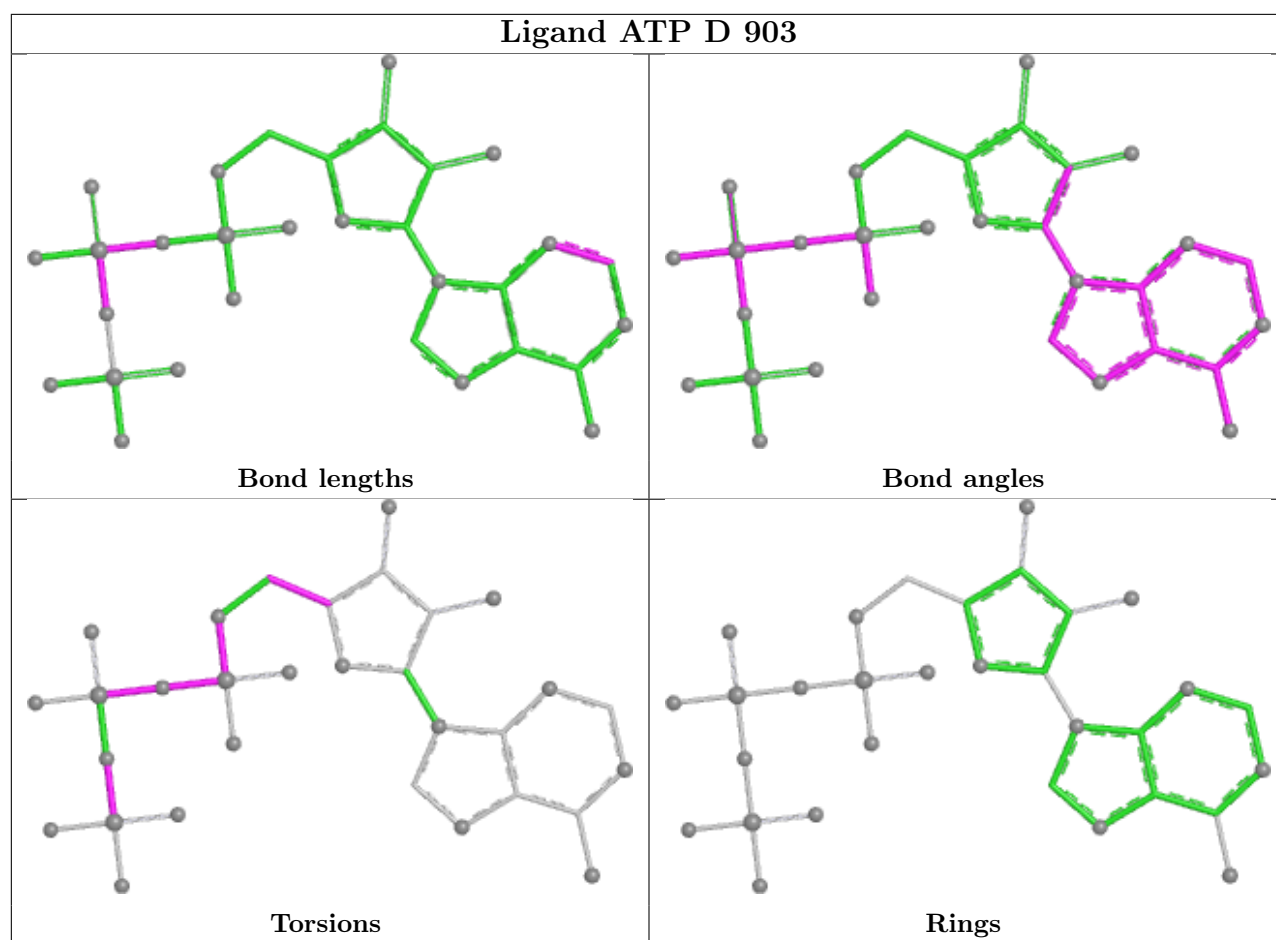
12 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	903	ATP	5	0
3	F	901	ATP	4	0
3	D	903	ATP	4	0
3	B	903	ATP	5	0
3	C	901	ATP	3	0
3	C	903	ATP	2	0
3	A	901	ATP	6	0
3	E	901	ATP	7	0
3	F	903	ATP	2	0
3	D	901	ATP	4	0
3	B	901	ATP	3	0
3	A	903	ATP	1	0

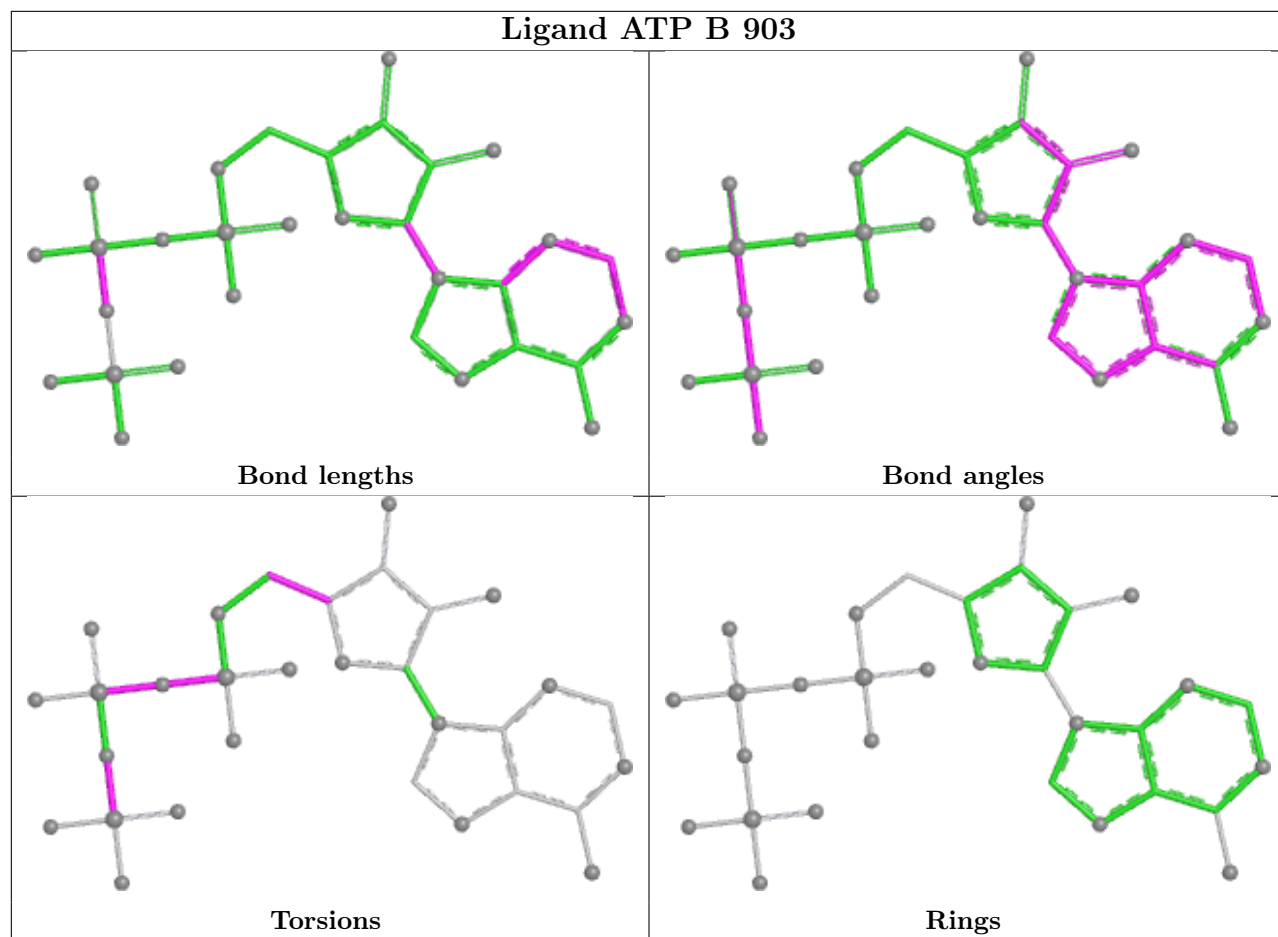
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

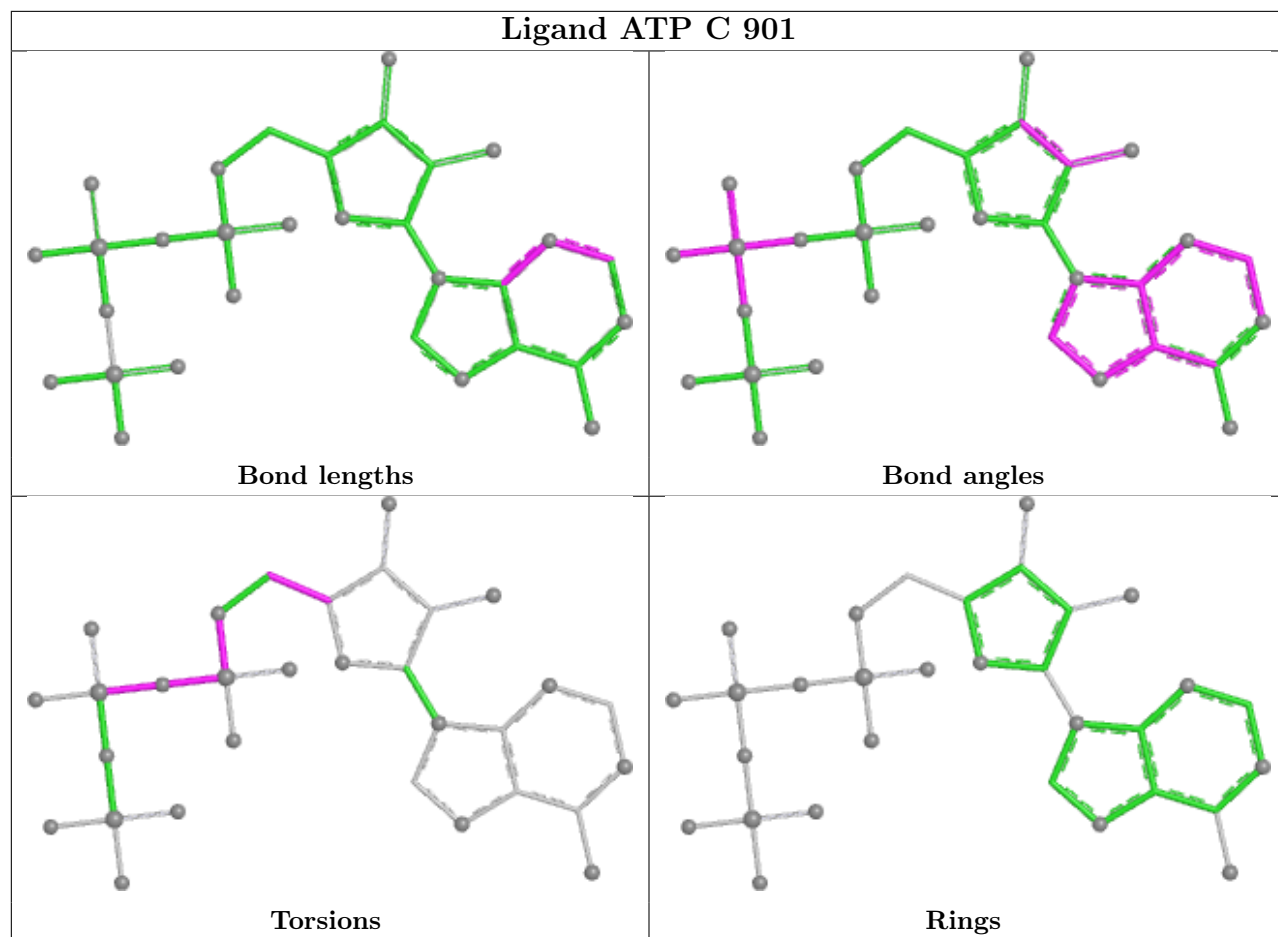




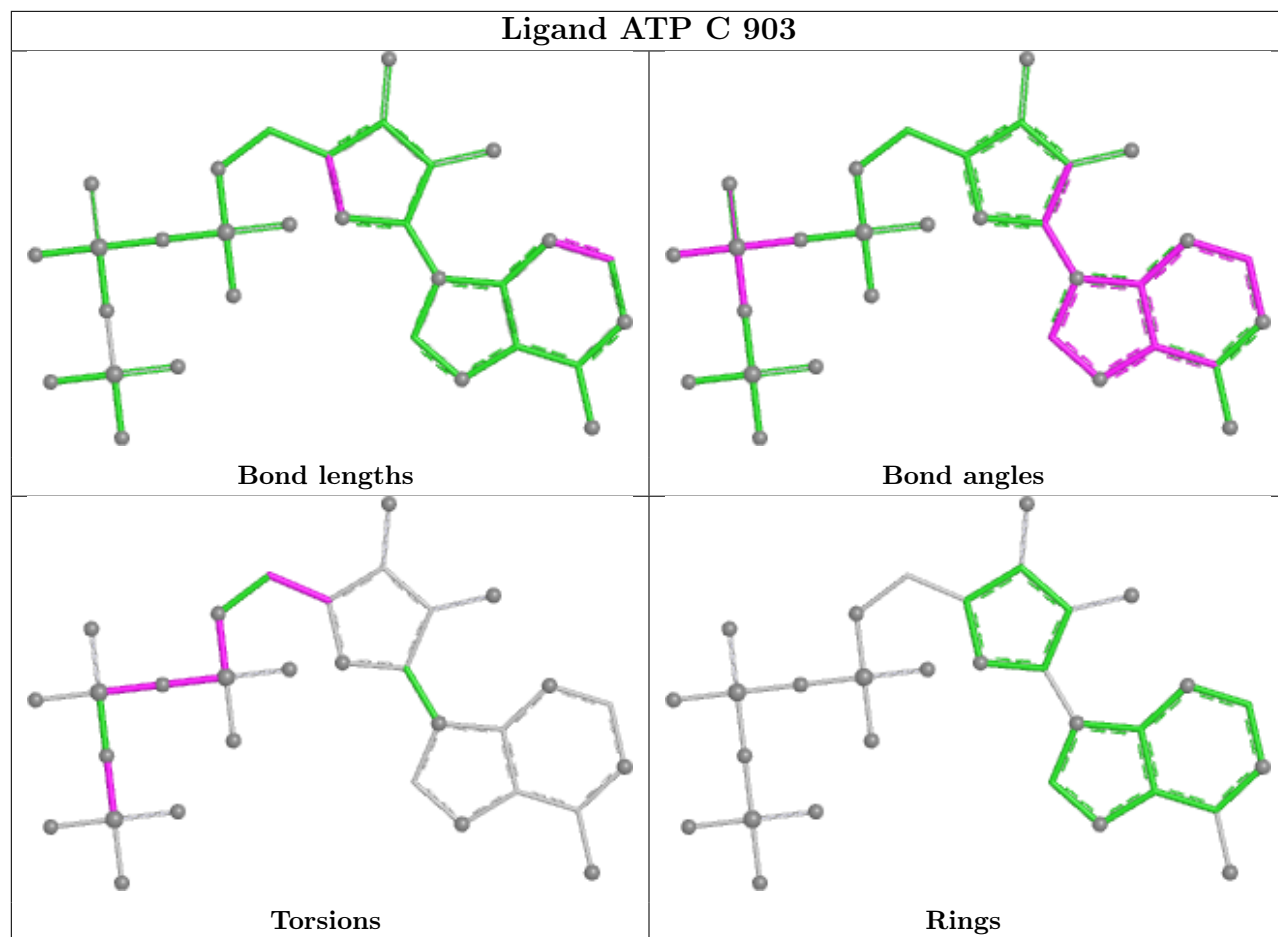


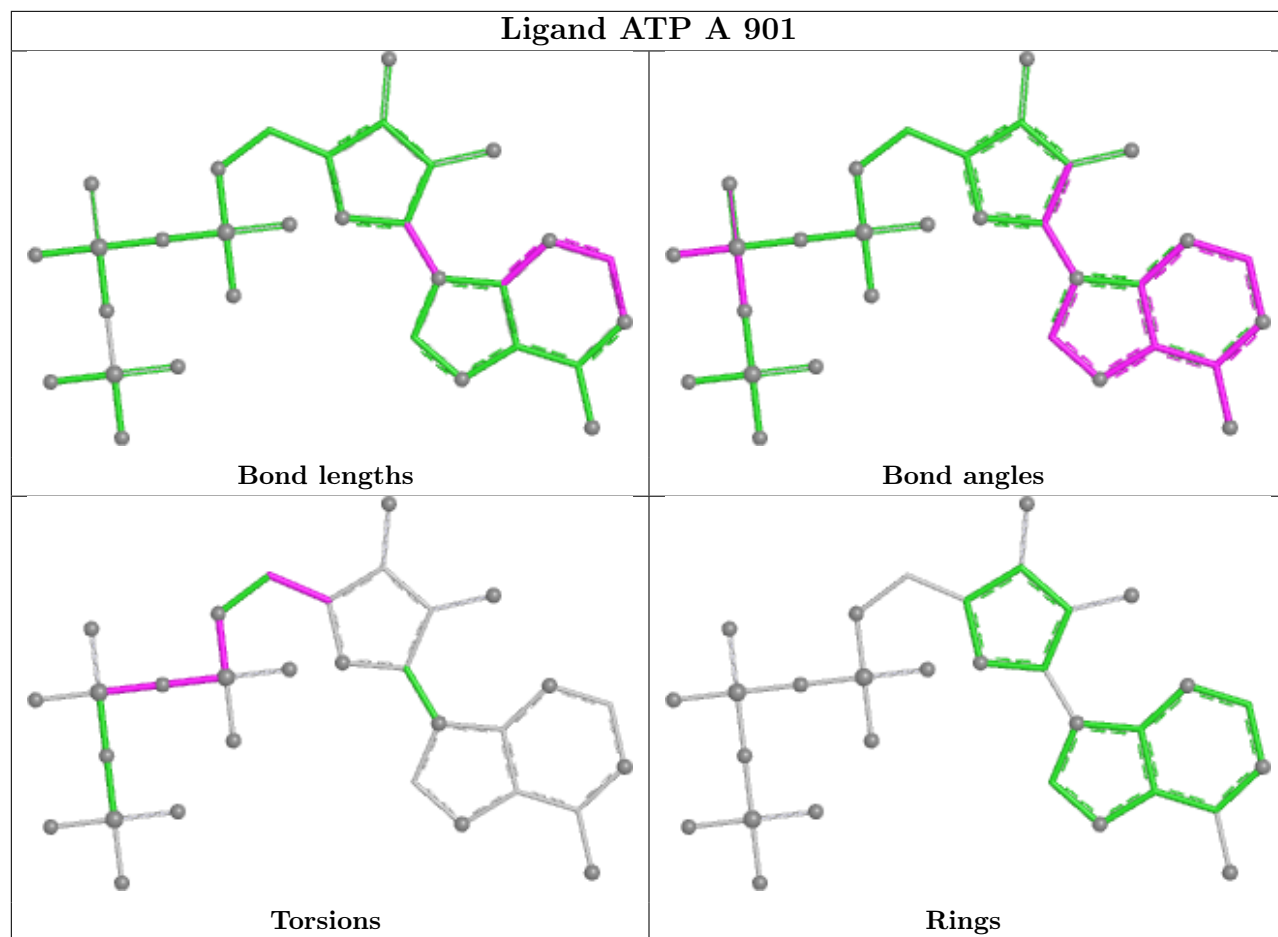
Ligand ATP B 903



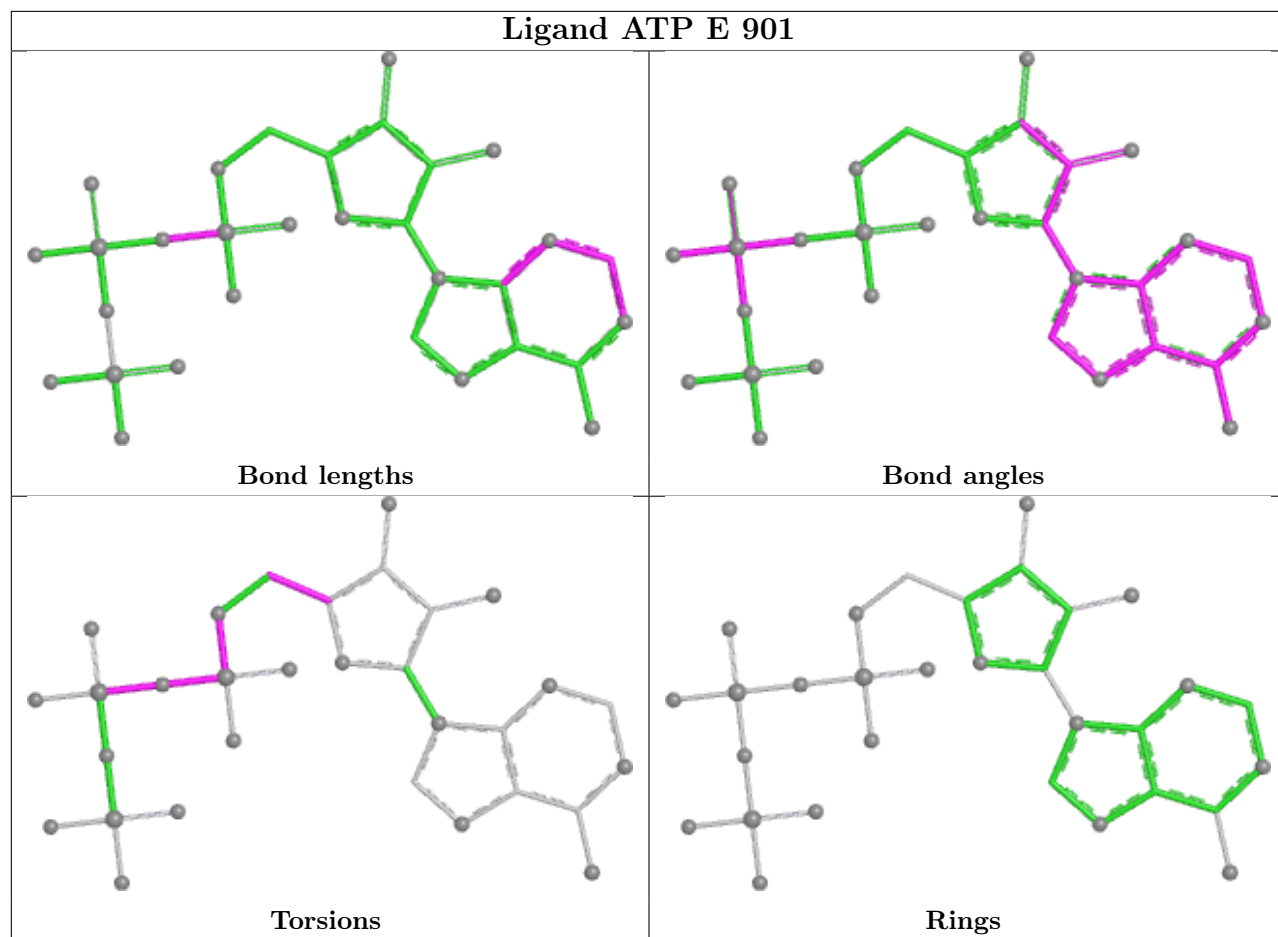


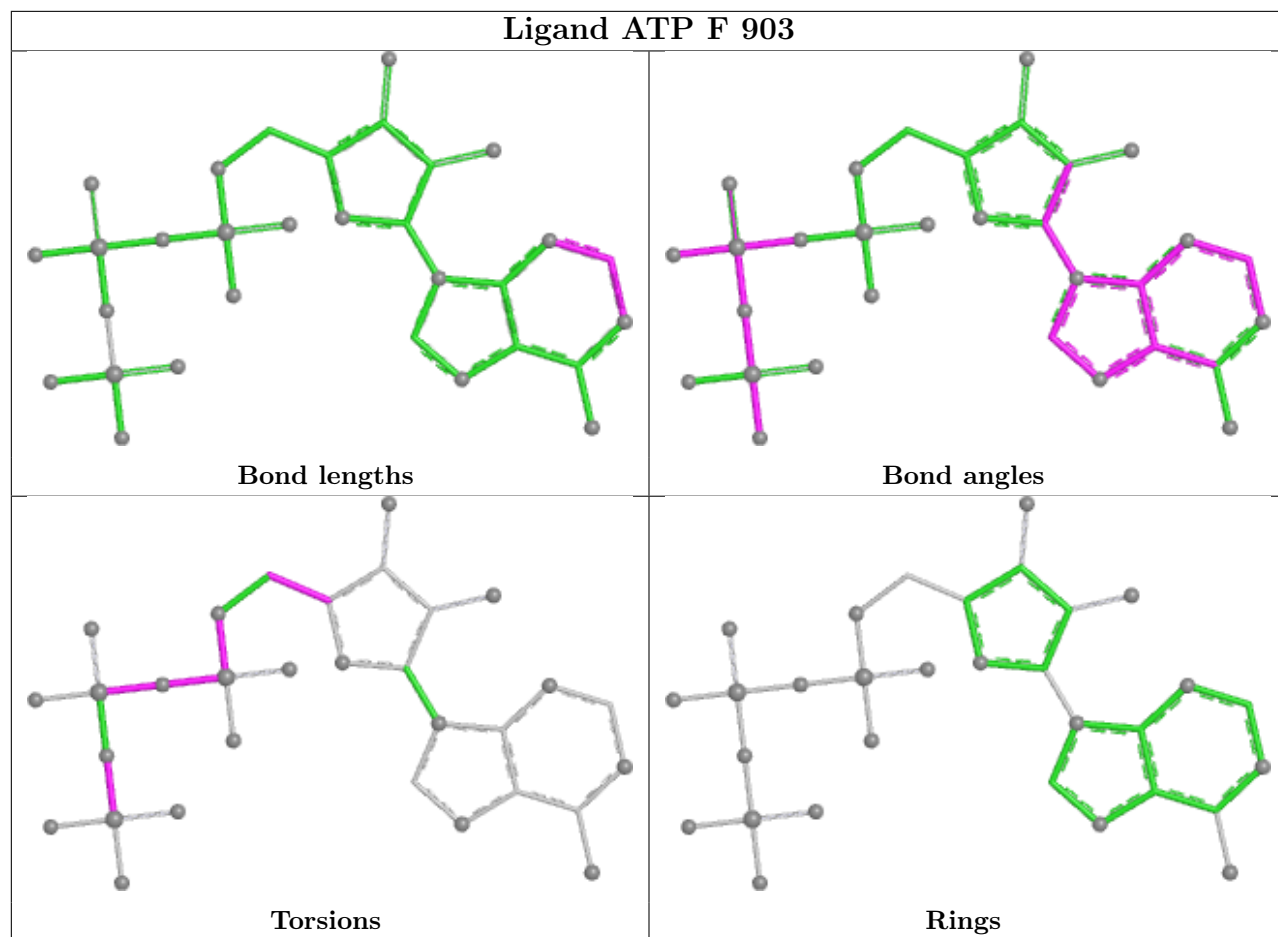
Ligand ATP C 903

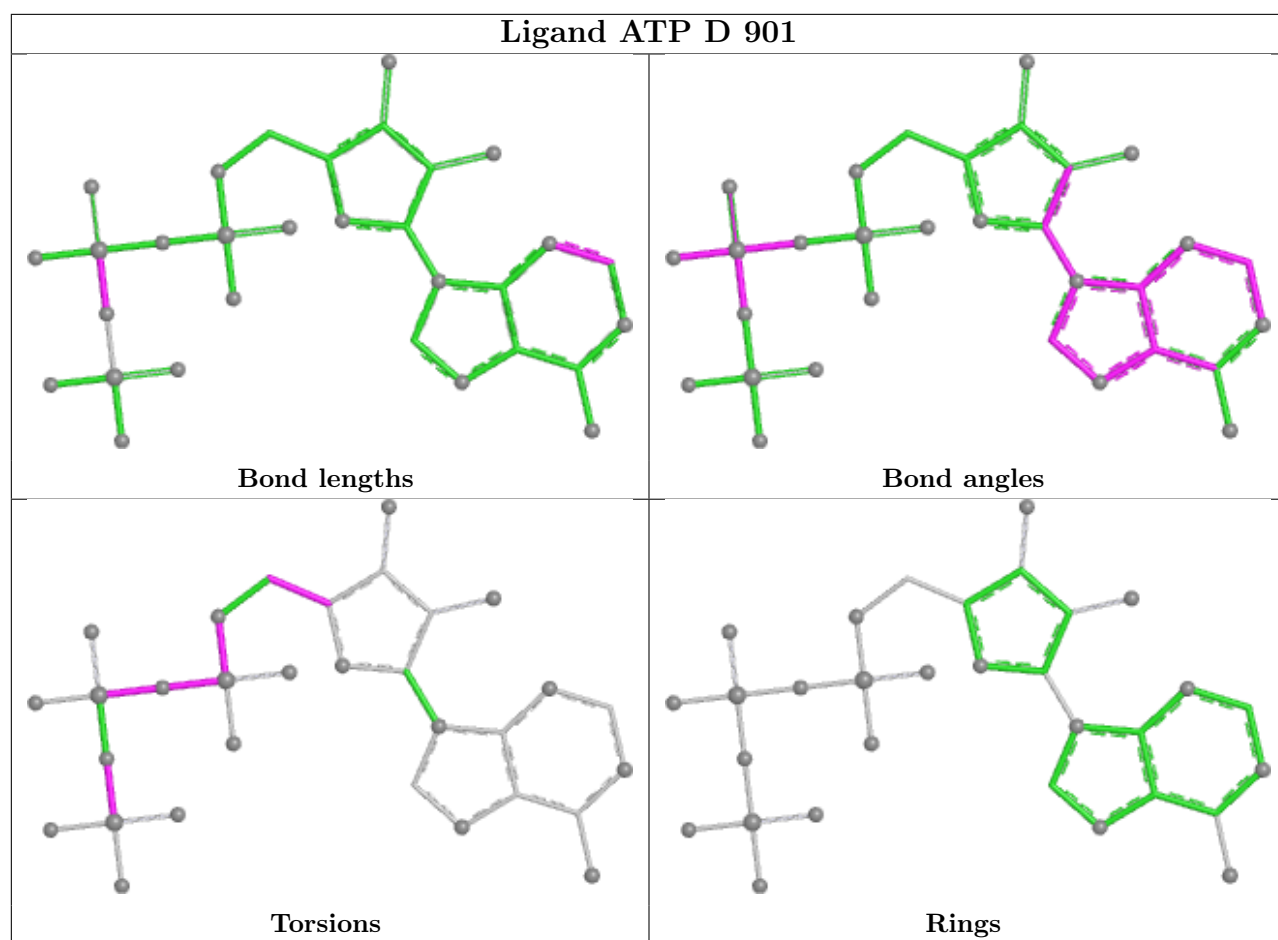




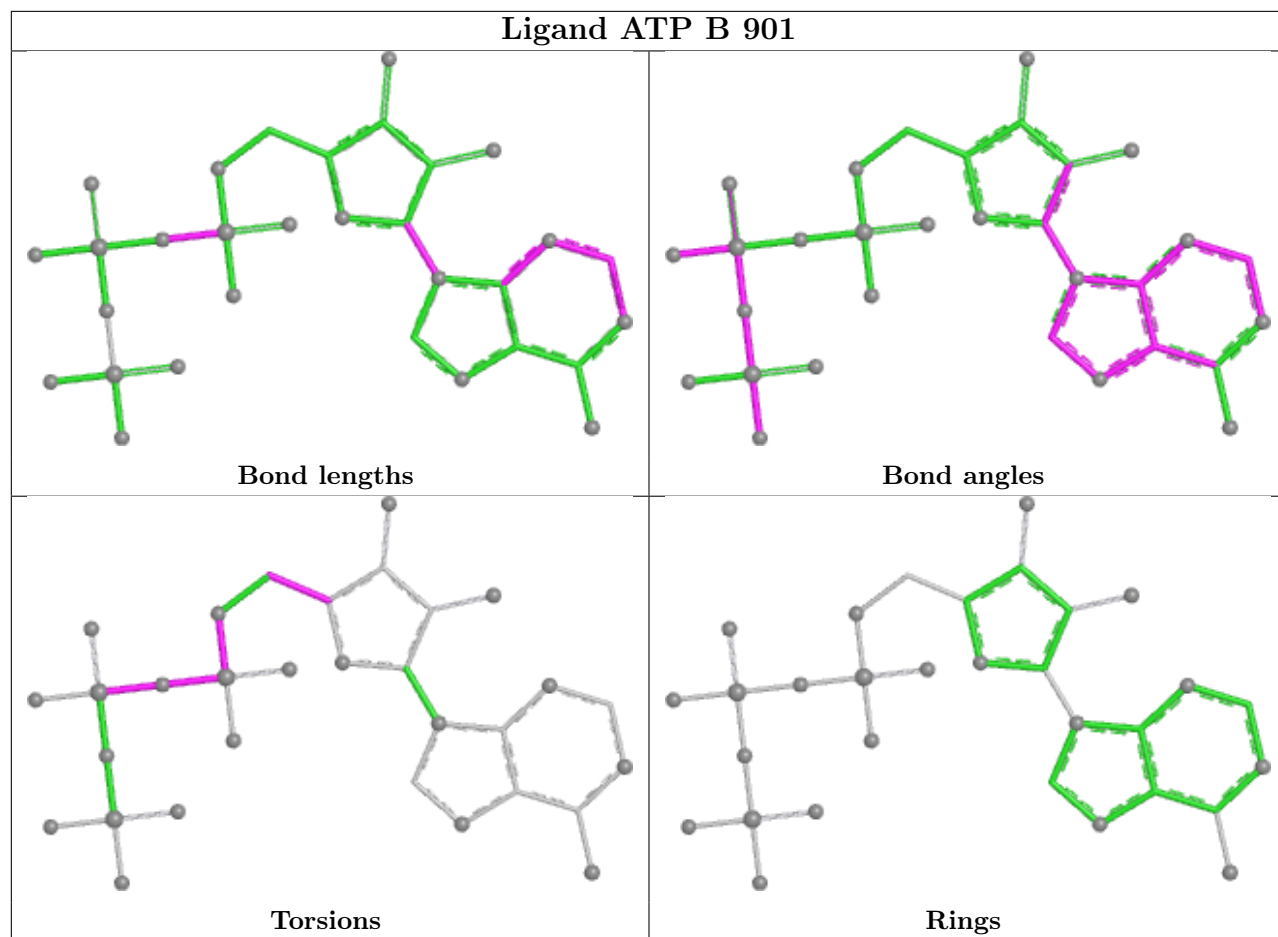
Ligand ATP E 901

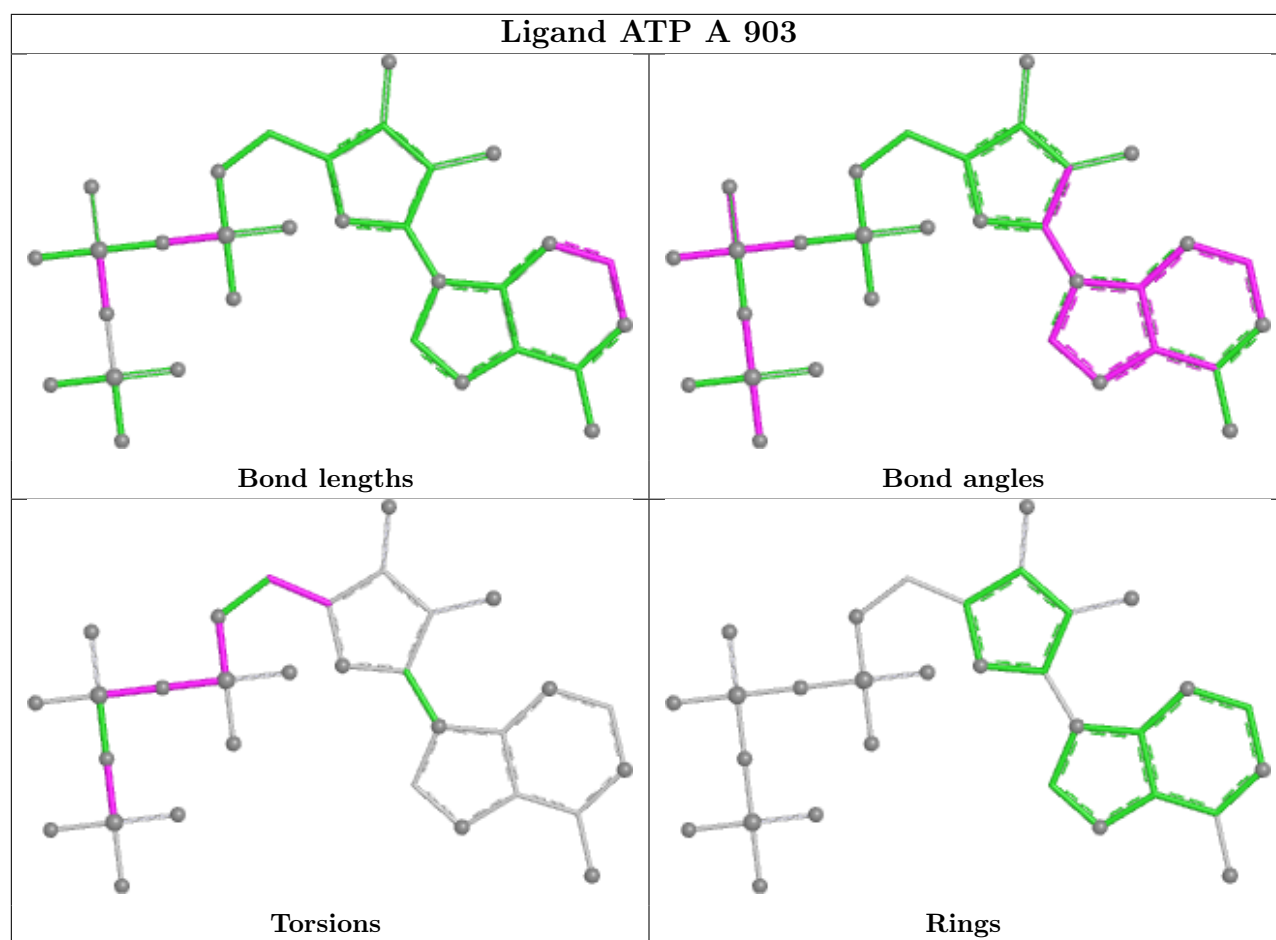






Ligand ATP B 901





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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	505/525 (96%)	0.18	8 (1%)	70 47	31, 77, 121, 154	0
1	F	505/525 (96%)	-0.11	3 (0%)	85 69	18, 66, 113, 145	0
2	B	491/525 (93%)	0.21	7 (1%)	73 51	43, 82, 126, 158	0
2	C	488/525 (92%)	-0.06	2 (0%)	88 76	30, 69, 122, 160	0
2	D	485/525 (92%)	-0.28	2 (0%)	88 76	20, 53, 106, 152	0
2	E	492/525 (93%)	-0.17	2 (0%)	88 76	15, 59, 104, 148	0
All	All	2966/3150 (94%)	-0.04	24 (0%)	82 64	15, 69, 117, 160	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	509	VAL	3.2
1	A	338	MET	2.9
2	B	250	GLY	2.7
2	B	500	ASP	2.6
2	E	332	GLY	2.5

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
1	SEP	A	320	10/11	0.48	0.30	49,59,66,68	0
1	SEP	F	320	10/11	0.52	0.24	45,57,63,66	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MG	B	702	1/1	0.74	0.15	79,79,79,79	0
4	MG	A	526	1/1	0.75	0.23	58,58,58,58	0
4	MG	B	801	1/1	0.82	0.07	45,45,45,45	0
4	MG	D	701	1/1	0.82	0.14	59,59,59,59	0
4	MG	D	801	1/1	0.86	0.27	44,44,44,44	0
4	MG	C	701	1/1	0.86	0.09	70,70,70,70	0
3	ATP	B	903	31/31	0.87	0.12	77,81,94,95	0
4	MG	A	701	1/1	0.89	0.13	63,63,63,63	0
4	MG	C	702	1/1	0.89	0.21	65,65,65,65	0
4	MG	E	801	1/1	0.89	0.14	38,38,38,38	0
4	MG	B	701	1/1	0.90	0.05	58,58,58,58	0
3	ATP	F	901	31/31	0.90	0.12	74,83,88,89	0
3	ATP	A	903	31/31	0.90	0.11	61,66,76,77	0
3	ATP	B	901	31/31	0.90	0.10	67,70,85,87	0
3	ATP	A	901	31/31	0.90	0.11	84,86,89,90	0
3	ATP	C	903	31/31	0.90	0.12	42,52,85,85	0
4	MG	F	701	1/1	0.91	0.14	45,45,45,45	0
4	MG	F	702	1/1	0.91	0.11	68,68,68,68	0
4	MG	A	802	1/1	0.92	0.26	82,82,82,82	0
3	ATP	E	901	31/31	0.93	0.10	65,72,81,81	0
4	MG	E	802	1/1	0.93	0.14	46,46,46,46	0
4	MG	A	801	1/1	0.93	0.09	46,46,46,46	0
4	MG	D	702	1/1	0.93	0.14	49,49,49,49	0
3	ATP	D	903	31/31	0.94	0.09	26,35,60,62	0
3	ATP	F	903	31/31	0.94	0.08	44,48,62,62	0
3	ATP	E	903	31/31	0.94	0.08	22,28,60,62	0
4	MG	F	802	1/1	0.94	0.14	53,53,53,53	0
3	ATP	C	901	31/31	0.95	0.09	36,47,56,56	0
3	ATP	D	901	31/31	0.95	0.09	50,54,60,62	0
4	MG	B	802	1/1	0.96	0.10	64,64,64,64	0
4	MG	C	802	1/1	0.97	0.09	41,41,41,41	0
4	MG	C	801	1/1	0.97	0.06	25,25,25,25	0

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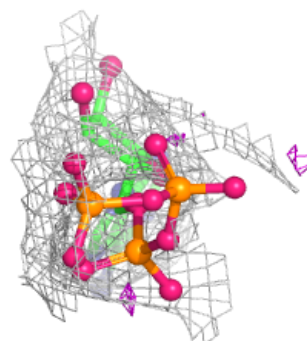
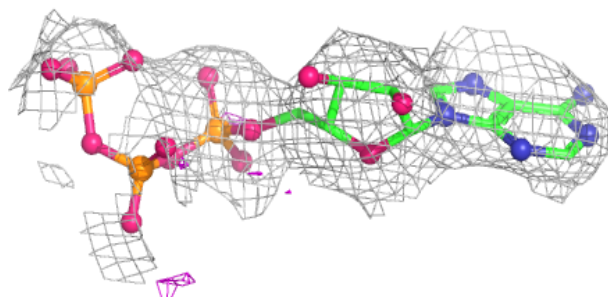
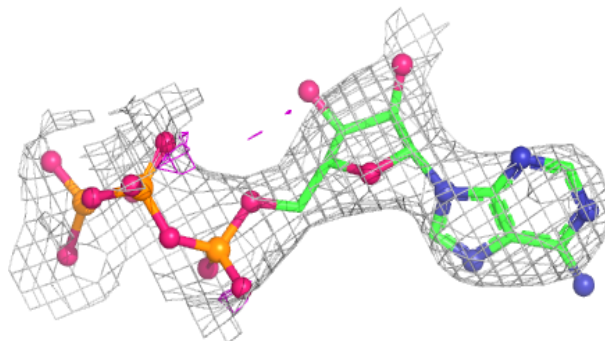
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	D	802	1/1	0.98	0.06	17,17,17,17	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

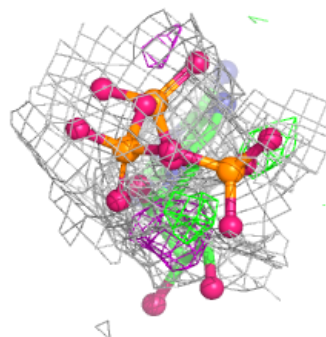
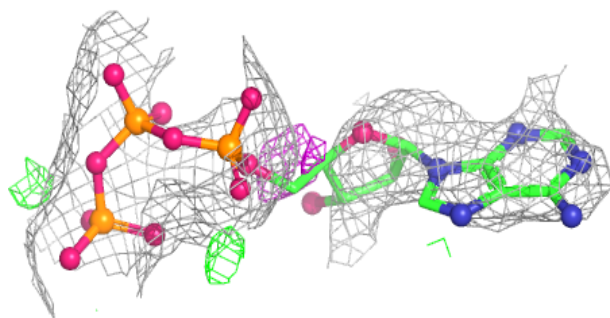
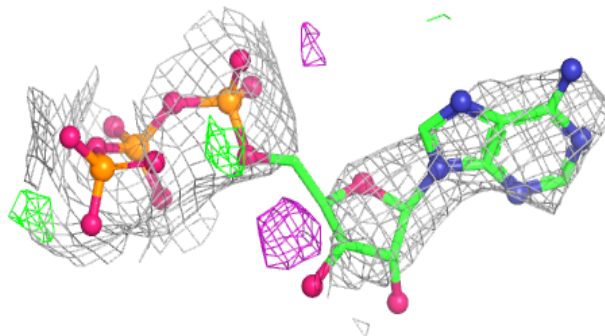
Electron density around ATP B 903:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

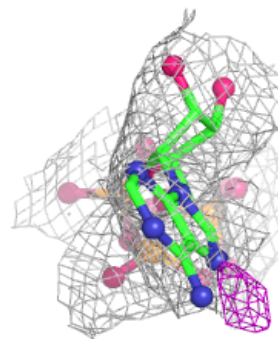
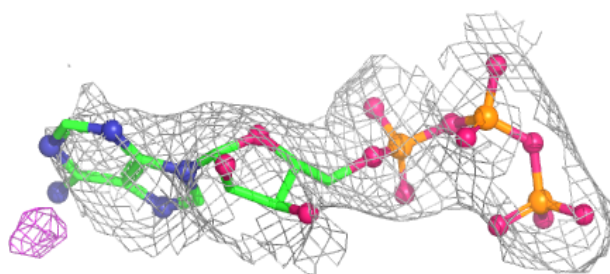
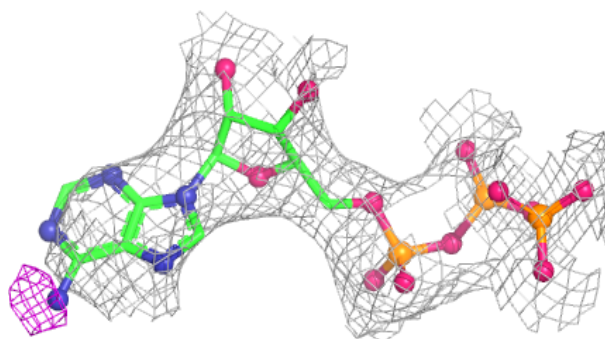


Electron density around ATP F 901:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

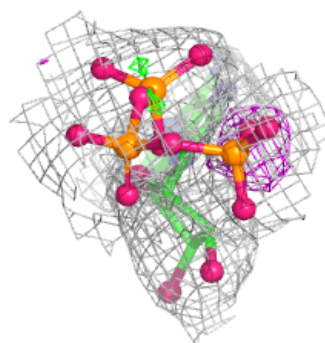
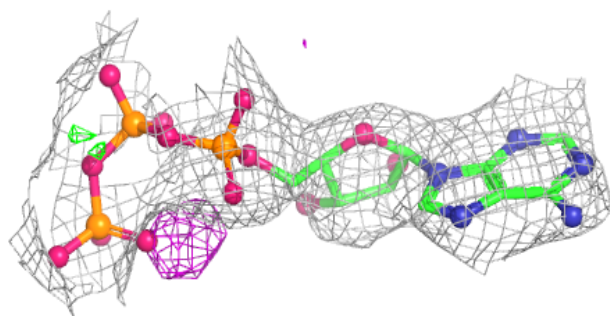
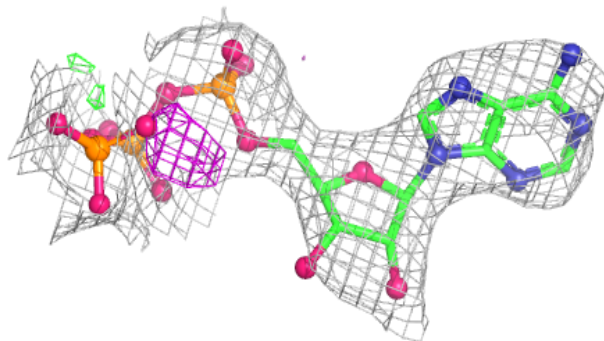
**Electron density around ATP A 903:**

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and green (positive)

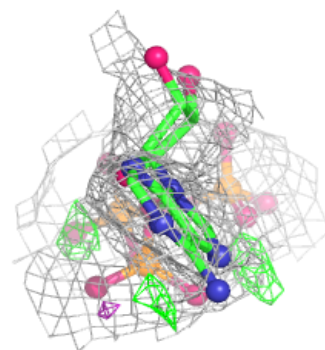
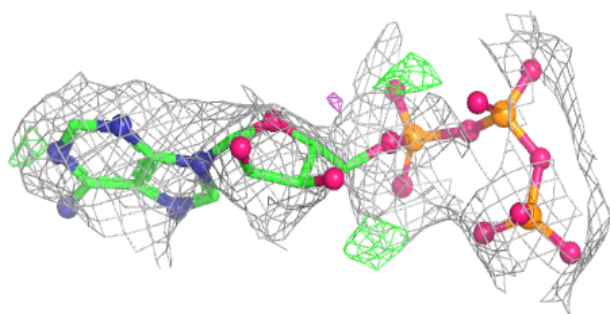
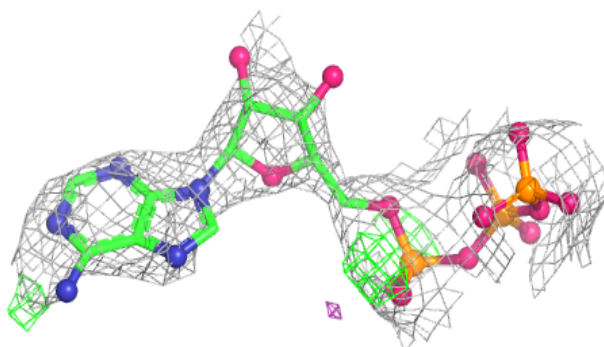


Electron density around ATP B 901:

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and green (positive)

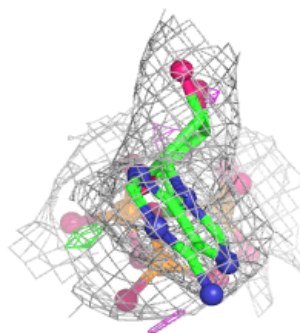
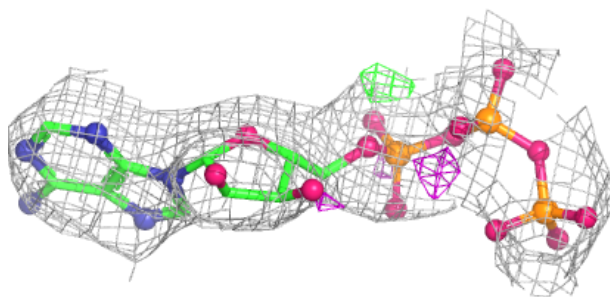
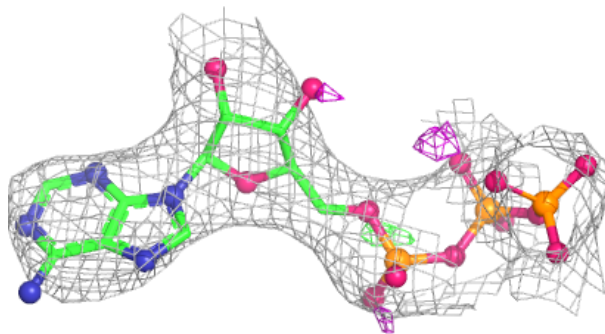
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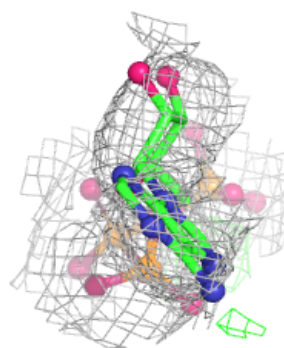
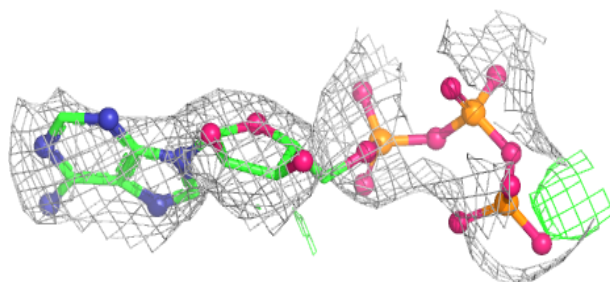
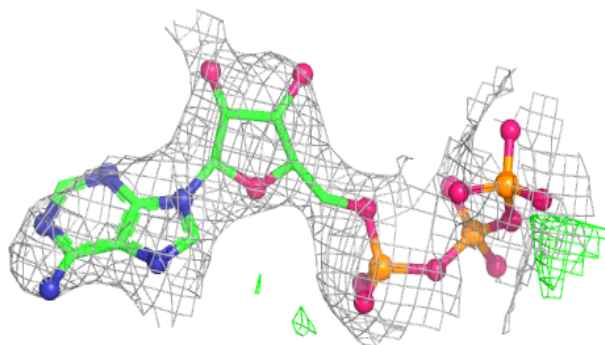


Electron density around ATP C 903:

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and green (positive)

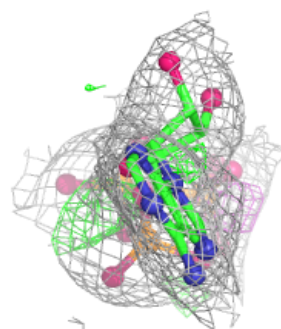
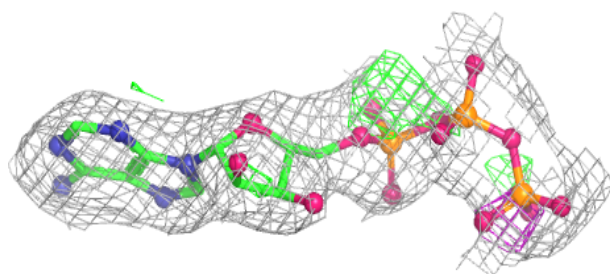
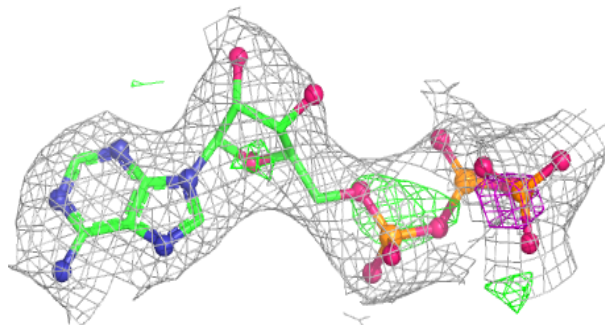
**Electron density around ATP E 901:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

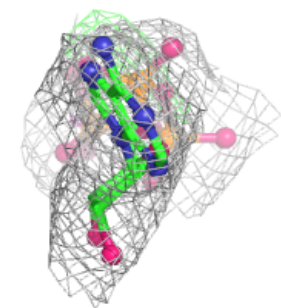
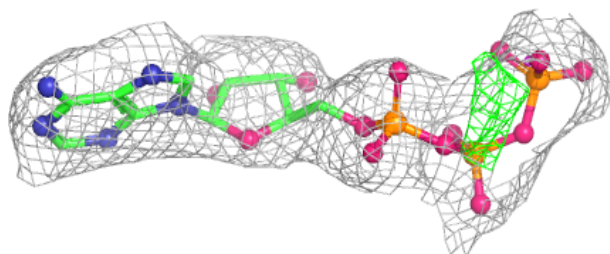
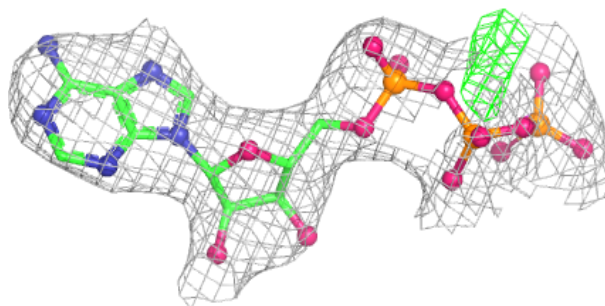


Electron density around ATP D 903:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

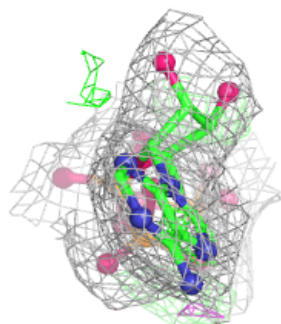
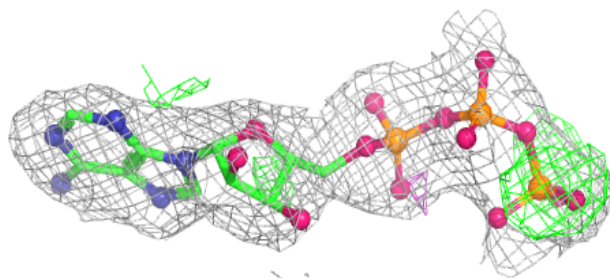
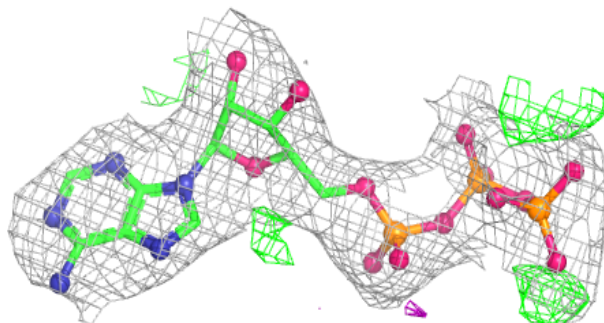
**Electron density around ATP F 903:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

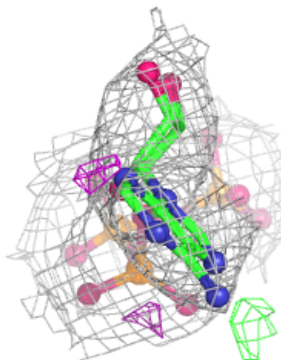
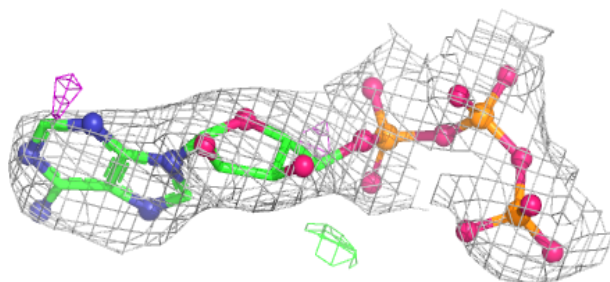
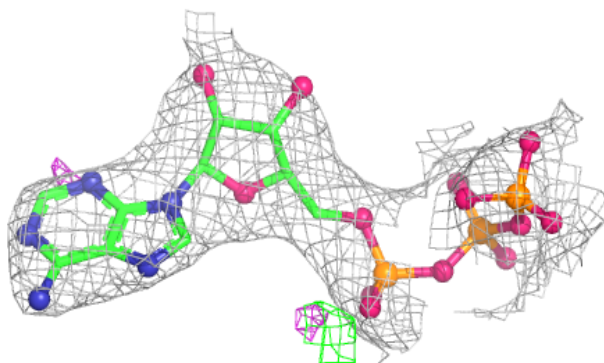


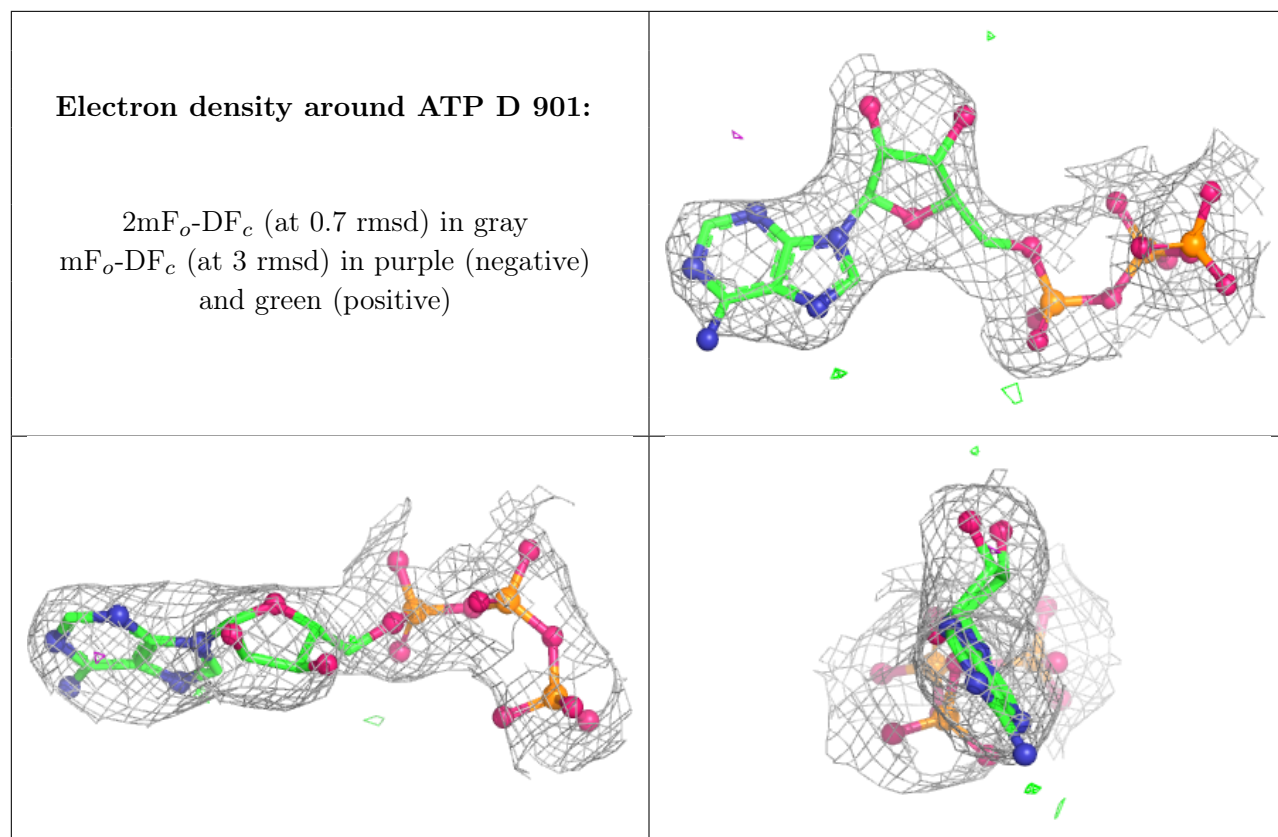
Electron density around ATP E 903:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around ATP C 901:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.