



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 3, 2021 – 02:28 AM EDT

PDB ID : 3K0A
Title : Crystal structure of the phosphorylation-site mutant S431A of the KaiC circadian clock protein
Authors : Pattanayek, R.; Egli, M.; Pattanayek, S.
Deposited on : 2009-09-24
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

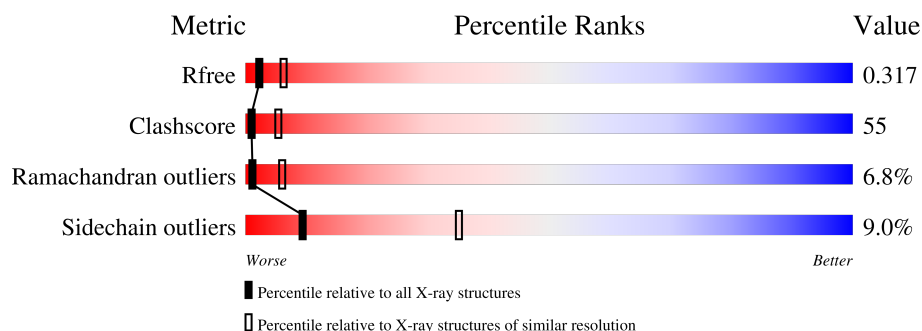
1 Overall quality at a glance ⓘ

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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	519	31% 56% 10% . .
2	B	519	30% 56% 8% . 5%
2	C	519	28% 56% 9% 6%
2	D	519	29% 56% 8% . 7%
2	E	519	29% 56% 9% 5%
2	F	519	28% 56% 13% . .

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	TPO	A	426	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23921 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
			3992	2509	701	765	2	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	431	ALA	SER	engineered mutation	UNP Q79PF4

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

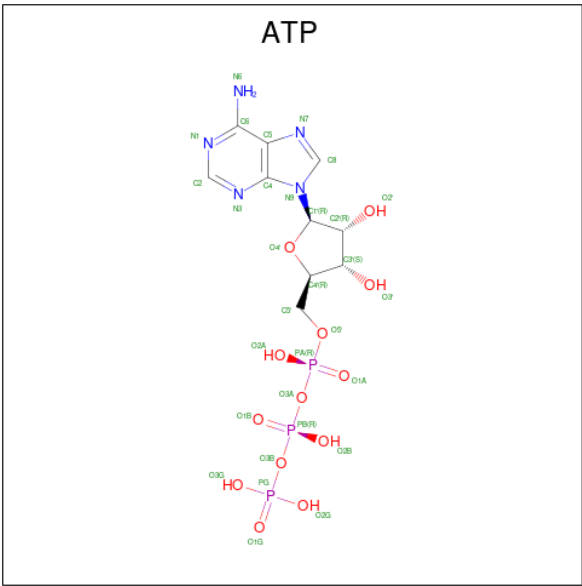
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	491	Total	C	N	O	P	S	0	0	0
			3873	2439	678	740	1	15			
2	C	488	Total	C	N	O	P	S	0	0	0
			3849	2425	674	734	1	15			
2	D	485	Total	C	N	O	P	S	0	0	0
			3825	2411	671	727	1	15			
2	E	492	Total	C	N	O	P	S	0	0	0
			3881	2445	679	741	1	15			
2	F	506	Total	C	N	O	P	S	0	0	0
			3988	2509	701	762	1	15			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	431	ALA	SER	engineered mutation	UNP Q79PF4
C	431	ALA	SER	engineered mutation	UNP Q79PF4
D	431	ALA	SER	engineered mutation	UNP Q79PF4
E	431	ALA	SER	engineered mutation	UNP Q79PF4
F	431	ALA	SER	engineered mutation	UNP Q79PF4

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: 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 (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	6	Total Mg 6 6	0	0
4	B	3	Total Mg 3 3	0	0
4	C	4	Total Mg 4 4	0	0
4	D	2	Total Mg 2 2	0	0
4	E	4	Total Mg 4 4	0	0
4	F	3	Total Mg 3 3	0	0

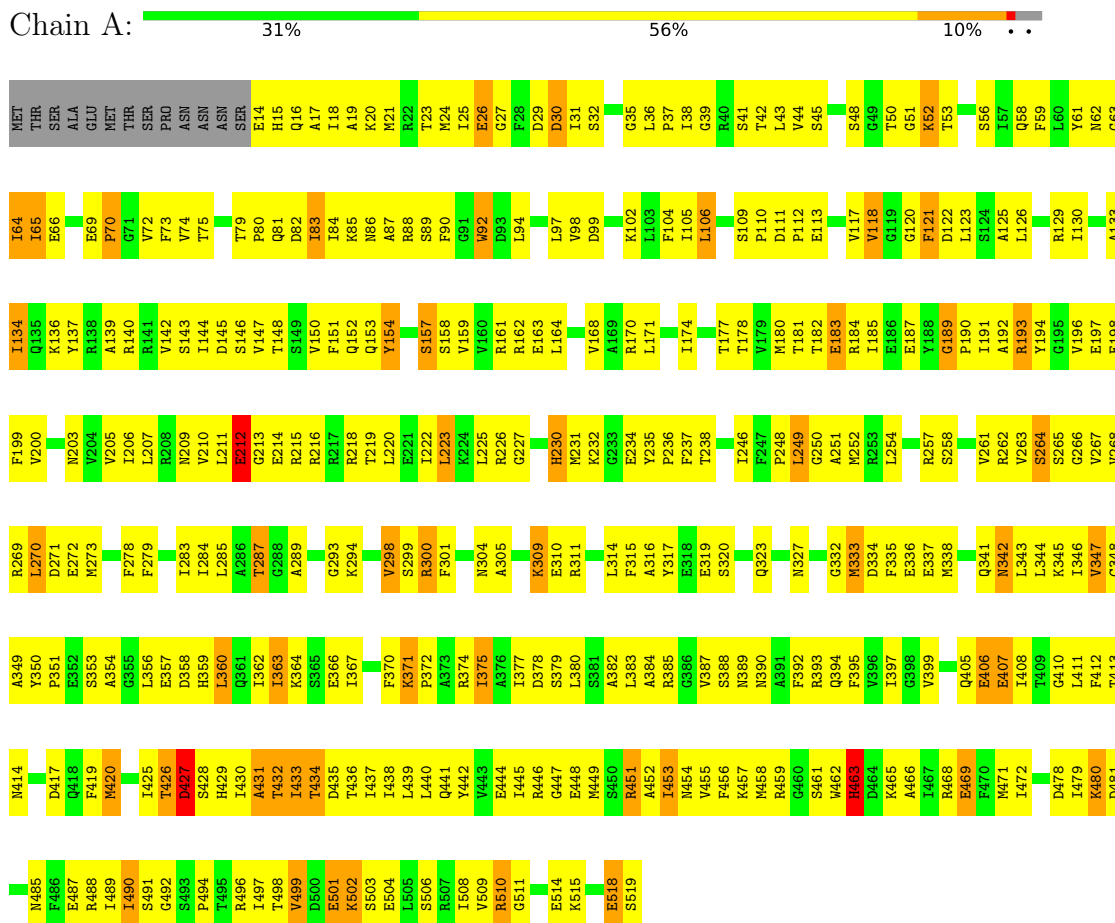
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	14	Total O 14 14	0	0
5	B	20	Total O 20 20	0	0
5	C	23	Total O 23 23	0	0
5	D	28	Total O 28 28	0	0
5	E	15	Total O 15 15	0	0
5	F	19	Total O 19 19	0	0

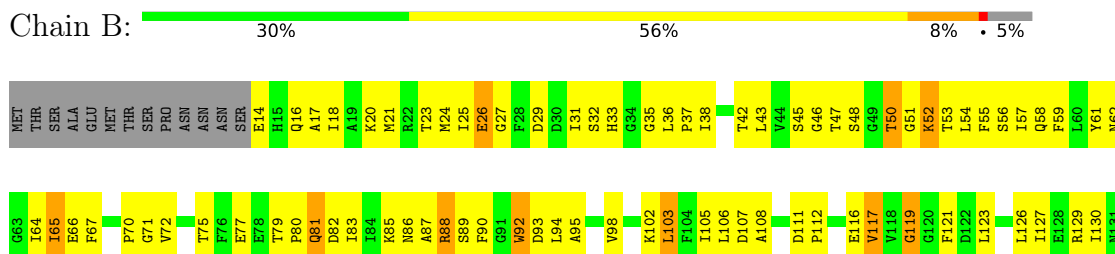
3 Residue-property plots

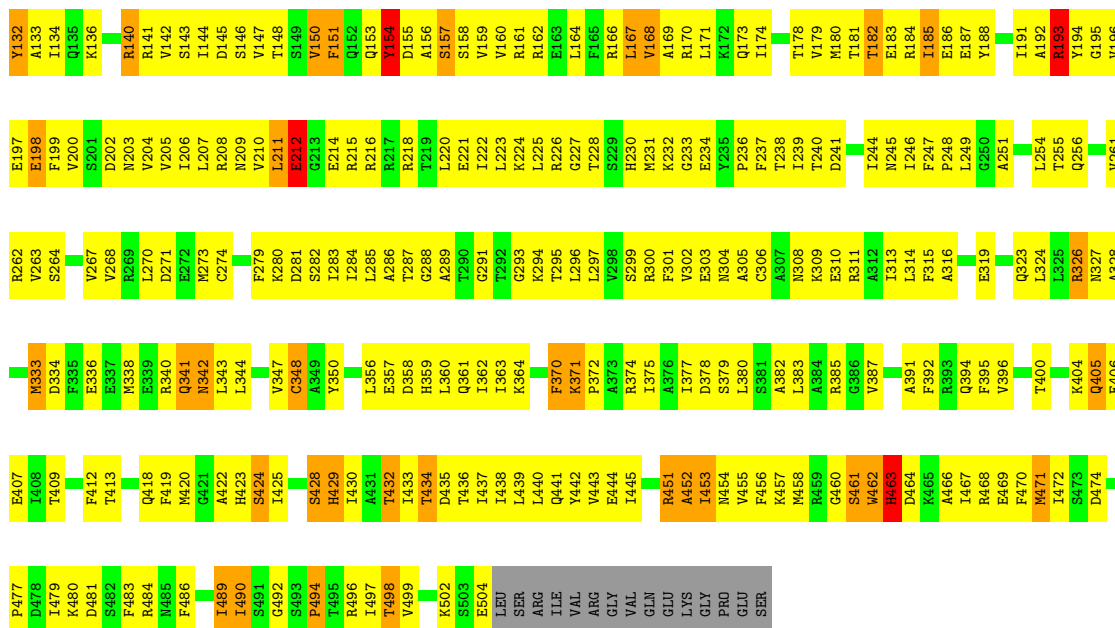
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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



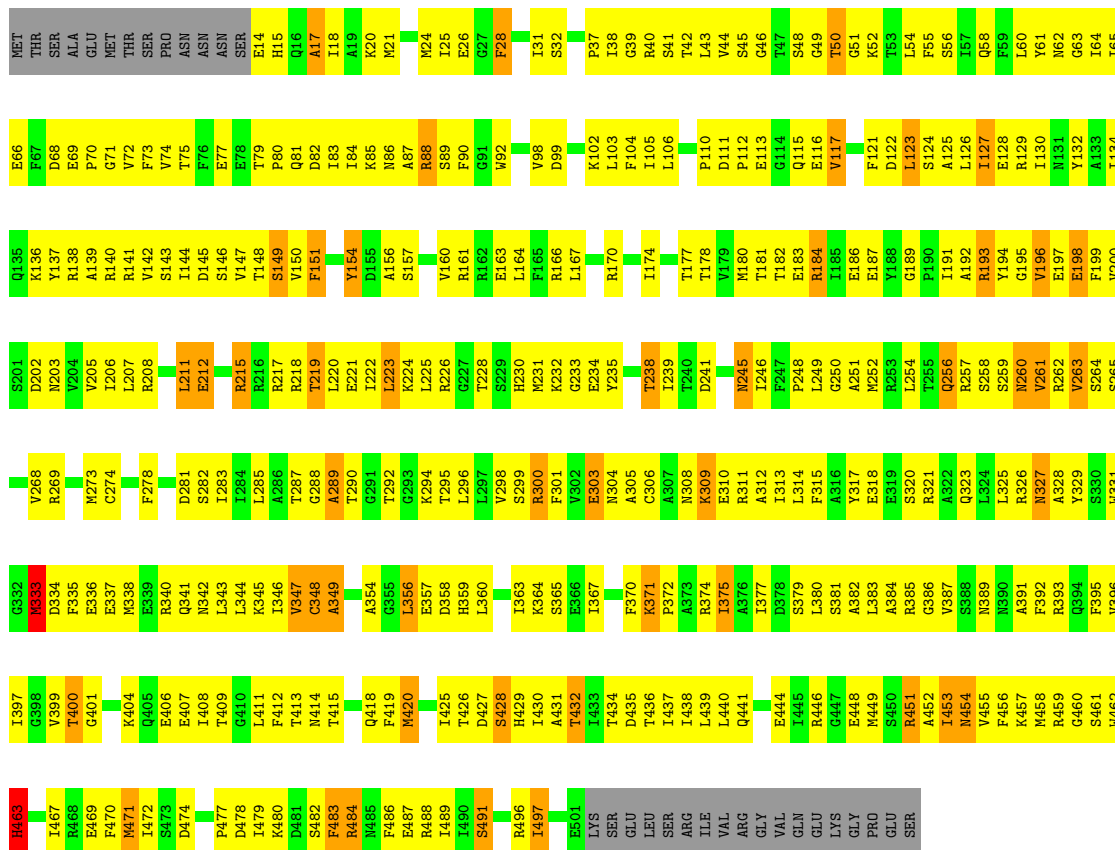
• Molecule 2: Circadian clock protein kinase KaiC






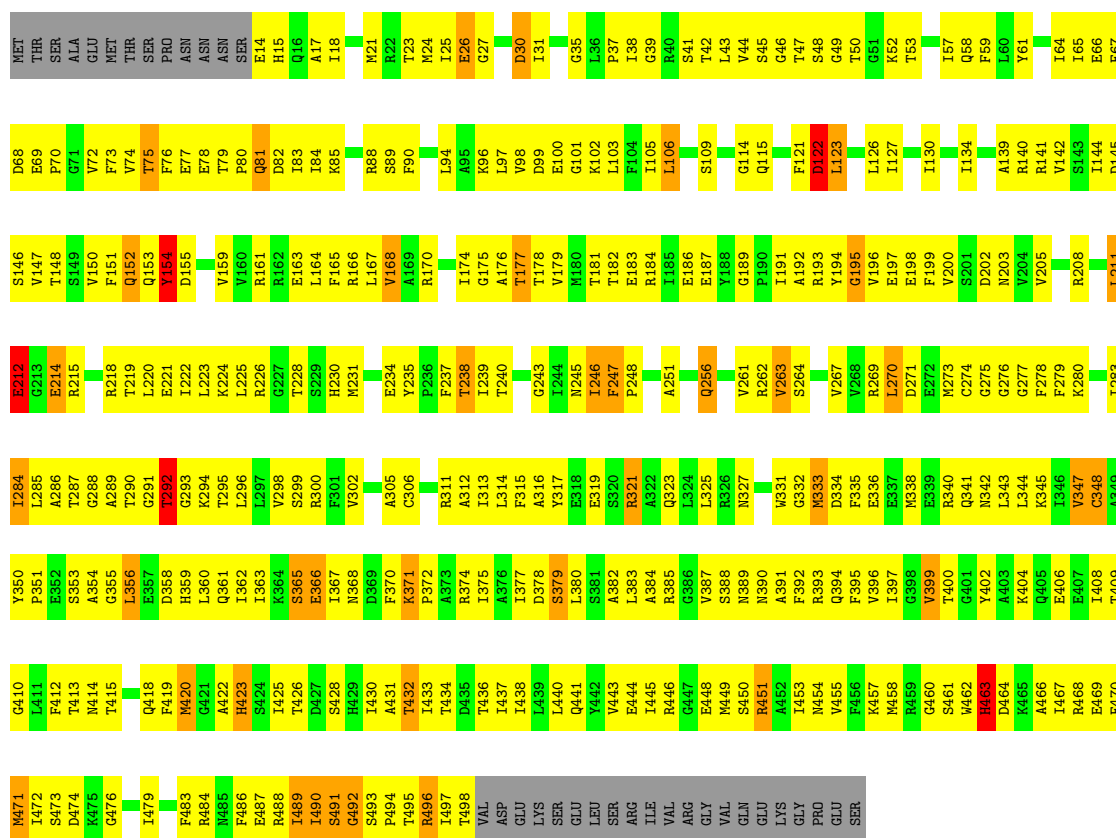
• Molecule 2: Circadian clock protein kinase KaiC

Chain C: 28% 56% 9% 6%



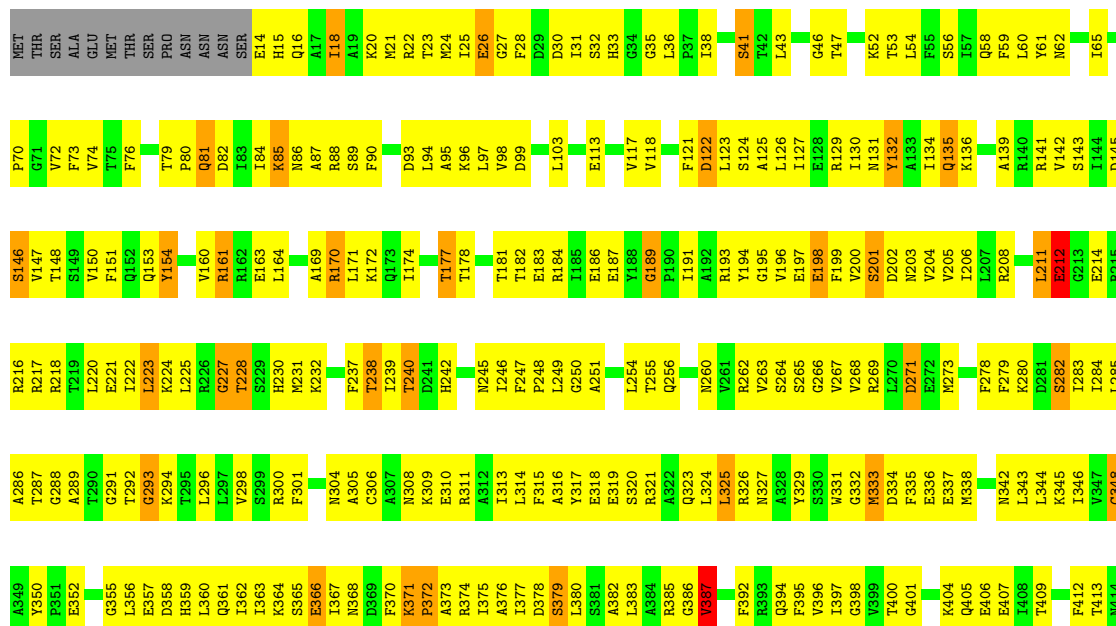
• Molecule 2: Circadian clock protein kinase KaiC

Chain D:  29% 56% 8% 7%



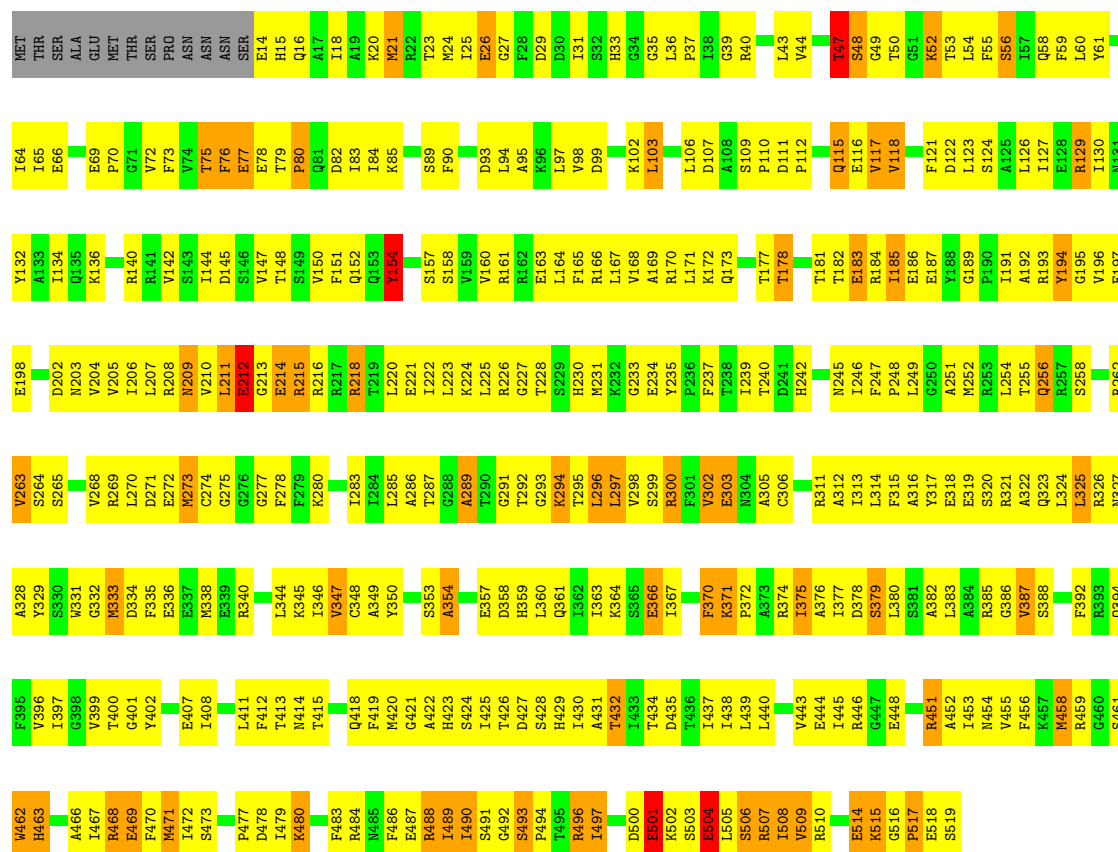
● Molecule 2: Circadian clock protein kinase KaiC

Chain E:  29% 56% 9% 5%





● Molecule 2: Circadian clock protein kinase KaiC



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	133.23Å 134.96Å 204.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.00 48.00 – 2.99	Depositor EDS
% Data completeness (in resolution range)	65.4 (30.00-3.00) 64.8 (48.00-2.99)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.242 , 0.307 0.300 , 0.317	Depositor DCC
R_{free} test set	4953 reflections (9.05%)	wwPDB-VP
Wilson B-factor (Å ²)	62.9	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	23921	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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: TPO, MG, 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	0.43	0/4034	0.67	0/5431
2	B	0.40	0/3926	0.65	0/5289
2	C	0.44	0/3902	0.70	0/5258
2	D	0.50	0/3878	0.74	0/5225
2	E	0.49	0/3934	0.73	1/5300 (0.0%)
2	F	0.51	1/4042 (0.0%)	0.73	0/5444
All	All	0.46	1/23716 (0.0%)	0.71	1/31947 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	21	MET	CG-SD	5.15	1.94	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	208	ARG	NE-CZ-NH1	5.56	123.08	120.30

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	3992	0	3983	439	0
2	B	3873	0	3862	437	0
2	C	3849	0	3838	462	0
2	D	3825	0	3820	445	0
2	E	3881	0	3873	448	0
2	F	3988	0	3983	492	0
3	A	62	0	24	8	0
3	B	62	0	24	8	0
3	C	62	0	24	5	0
3	D	62	0	24	13	0
3	E	62	0	24	6	0
3	F	62	0	24	7	0
4	A	6	0	0	0	0
4	B	3	0	0	0	0
4	C	4	0	0	0	0
4	D	2	0	0	0	0
4	E	4	0	0	0	0
4	F	3	0	0	0	0
5	A	14	0	0	4	0
5	B	20	0	0	4	0
5	C	23	0	0	5	0
5	D	28	0	0	7	0
5	E	15	0	0	5	0
5	F	19	0	0	4	0
All	All	23921	0	23503	2588	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 55.

The worst 5 of 2588 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:D:379:SER:H	2:D:413:THR:HB	1.13	1.13
2:E:283:ILE:HG13	2:E:400:THR:HG23	1.26	1.13
2:F:25:ILE:HD12	2:F:58:GLN:HE21	1.12	1.13
2:E:164:LEU:HD11	2:E:197:GLU:HG3	1.32	1.12
1:A:72:VAL:HG21	1:A:134:ILE:HD12	1.34	1.09

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	502/519 (97%)	364 (72%)	98 (20%)	40 (8%)	1	4
2	B	488/519 (94%)	368 (75%)	86 (18%)	34 (7%)	1	6
2	C	485/519 (93%)	371 (76%)	80 (16%)	34 (7%)	1	6
2	D	482/519 (93%)	378 (78%)	83 (17%)	21 (4%)	2	15
2	E	489/519 (94%)	374 (76%)	86 (18%)	29 (6%)	1	9
2	F	503/519 (97%)	384 (76%)	75 (15%)	44 (9%)	1	3
All	All	2949/3114 (95%)	2239 (76%)	508 (17%)	202 (7%)	1	6

5 of 202 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	LYS
1	A	65	ILE
1	A	154	TYR
1	A	193	ARG
1	A	212	GLU

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 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	429/441 (97%)	397 (92%)	32 (8%)	13	43
2	B	417/442 (94%)	383 (92%)	34 (8%)	11	39
2	C	414/442 (94%)	377 (91%)	37 (9%)	9	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	411/442 (93%)	367 (89%)	44 (11%)	6	26
2	E	418/442 (95%)	383 (92%)	35 (8%)	11	38
2	F	430/442 (97%)	385 (90%)	45 (10%)	7	27
All	All	2519/2651 (95%)	2292 (91%)	227 (9%)	9	35

5 of 227 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	212	GLU
2	F	493	SER
2	D	490	ILE
2	F	469	GLU
2	F	186	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	418	GLN
2	E	33	HIS
2	F	245	ASN
2	D	33	HIS
2	D	418	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

7 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	TPO	A	432	1	8,10,11	1.64	3 (37%)	10,14,16	2.57	1 (10%)
1	TPO	A	426	1	8,10,11	1.24	1 (12%)	10,14,16	1.32	1 (10%)
2	TPO	C	432	2	8,10,11	3.68	5 (62%)	10,14,16	1.97	4 (40%)
2	TPO	F	432	2	8,10,11	1.87	2 (25%)	10,14,16	2.17	1 (10%)
2	TPO	E	432	2	8,10,11	1.87	2 (25%)	10,14,16	2.44	1 (10%)
2	TPO	D	432	2	8,10,11	1.27	1 (12%)	10,14,16	1.98	1 (10%)
2	TPO	B	432	2	8,10,11	1.19	2 (25%)	10,14,16	2.10	2 (20%)

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	TPO	A	432	1	-	4/9/11/13	-
1	TPO	A	426	1	-	1/9/11/13	-
2	TPO	C	432	2	-	1/9/11/13	-
2	TPO	F	432	2	-	0/9/11/13	-
2	TPO	E	432	2	-	4/9/11/13	-
2	TPO	D	432	2	-	0/9/11/13	-
2	TPO	B	432	2	-	1/9/11/13	-

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	432	TPO	P-O2P	6.67	1.80	1.54
2	C	432	TPO	CB-CA	6.23	1.67	1.53
2	F	432	TPO	CG2-CB	-3.90	1.42	1.51
2	E	432	TPO	CG2-CB	-3.74	1.42	1.51
2	C	432	TPO	P-O1P	-2.79	1.41	1.50

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	432	TPO	P-OG1-CB	-7.28	101.22	123.21
2	E	432	TPO	P-OG1-CB	-6.69	102.99	123.21
2	F	432	TPO	P-OG1-CB	-5.84	105.56	123.21
2	B	432	TPO	P-OG1-CB	-5.59	106.32	123.21
2	D	432	TPO	P-OG1-CB	-5.36	107.03	123.21

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	426	TPO	CG2-CB-OG1-P
1	A	432	TPO	N-CA-CB-CG2
1	A	432	TPO	N-CA-CB-OG1
1	A	432	TPO	C-CA-CB-CG2
1	A	432	TPO	O-C-CA-CB

There are no ring outliers.

6 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	432	TPO	2	0
1	A	426	TPO	7	0
2	C	432	TPO	5	0
2	F	432	TPO	3	0
2	D	432	TPO	3	0
2	B	432	TPO	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 22 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	901	4	26,33,33	1.28	2 (7%)	31,52,52	1.80	6 (19%)
3	ATP	C	903	4	26,33,33	1.15	2 (7%)	31,52,52	1.82	5 (16%)
3	ATP	F	901	4	26,33,33	1.31	3 (11%)	31,52,52	1.85	6 (19%)
3	ATP	B	901	4	26,33,33	1.29	3 (11%)	31,52,52	1.73	5 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ATP	D	903	4	26,33,33	1.24	2 (7%)	31,52,52	1.80	6 (19%)
3	ATP	A	903	4	26,33,33	1.27	2 (7%)	31,52,52	1.63	4 (12%)
3	ATP	D	901	4	26,33,33	1.45	4 (15%)	31,52,52	1.71	4 (12%)
3	ATP	C	901	4	26,33,33	1.41	4 (15%)	31,52,52	1.76	7 (22%)
3	ATP	E	903	4	26,33,33	1.20	1 (3%)	31,52,52	1.85	8 (25%)
3	ATP	A	901	4	26,33,33	1.30	3 (11%)	31,52,52	1.71	4 (12%)
3	ATP	B	903	4	26,33,33	1.30	2 (7%)	31,52,52	1.80	7 (22%)
3	ATP	F	903	4	26,33,33	1.37	3 (11%)	31,52,52	1.70	5 (16%)

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	901	4	-	6/18/38/38	0/3/3/3
3	ATP	C	903	4	-	6/18/38/38	0/3/3/3
3	ATP	F	901	4	-	6/18/38/38	0/3/3/3
3	ATP	B	901	4	-	7/18/38/38	0/3/3/3
3	ATP	D	903	4	-	9/18/38/38	0/3/3/3
3	ATP	A	903	4	-	8/18/38/38	0/3/3/3
3	ATP	D	901	4	-	6/18/38/38	0/3/3/3
3	ATP	C	901	4	-	10/18/38/38	0/3/3/3
3	ATP	E	903	4	-	7/18/38/38	0/3/3/3
3	ATP	A	901	4	-	6/18/38/38	0/3/3/3
3	ATP	B	903	4	-	9/18/38/38	0/3/3/3
3	ATP	F	903	4	-	8/18/38/38	0/3/3/3

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	901	ATP	C2-N3	4.42	1.39	1.32
3	C	901	ATP	C2-N3	4.39	1.39	1.32
3	F	903	ATP	C2-N3	4.37	1.39	1.32
3	D	901	ATP	C2-N3	4.16	1.38	1.32
3	F	901	ATP	C2-N3	4.15	1.38	1.32

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	903	ATP	N3-C2-N1	-5.70	119.76	128.68
3	F	901	ATP	N3-C2-N1	-5.64	119.86	128.68
3	D	901	ATP	N3-C2-N1	-5.60	119.92	128.68
3	C	903	ATP	N3-C2-N1	-5.54	120.03	128.68
3	B	901	ATP	N3-C2-N1	-5.52	120.05	128.68

There are no chirality outliers.

5 of 88 torsion outliers are listed below:

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

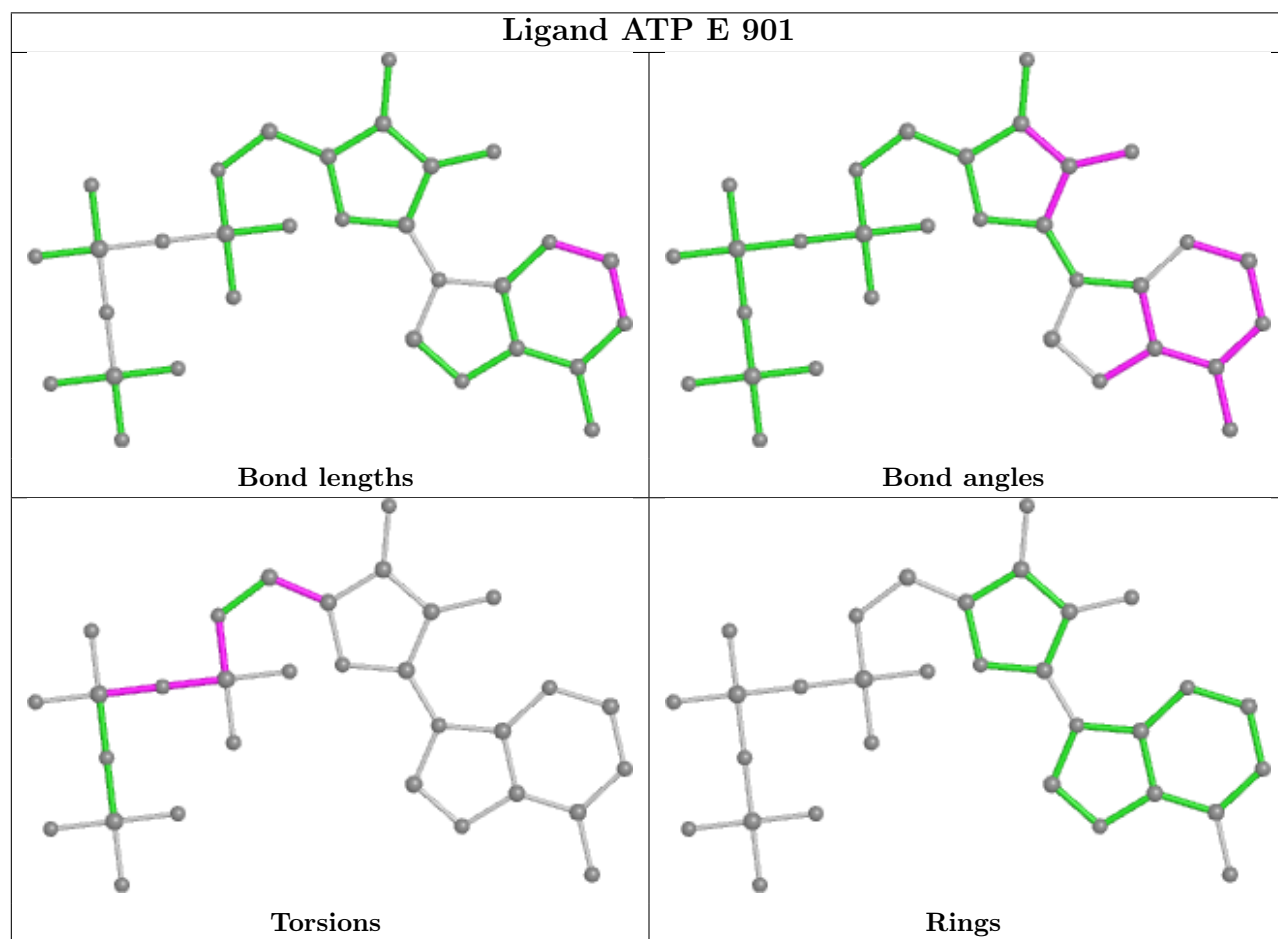
There are no ring outliers.

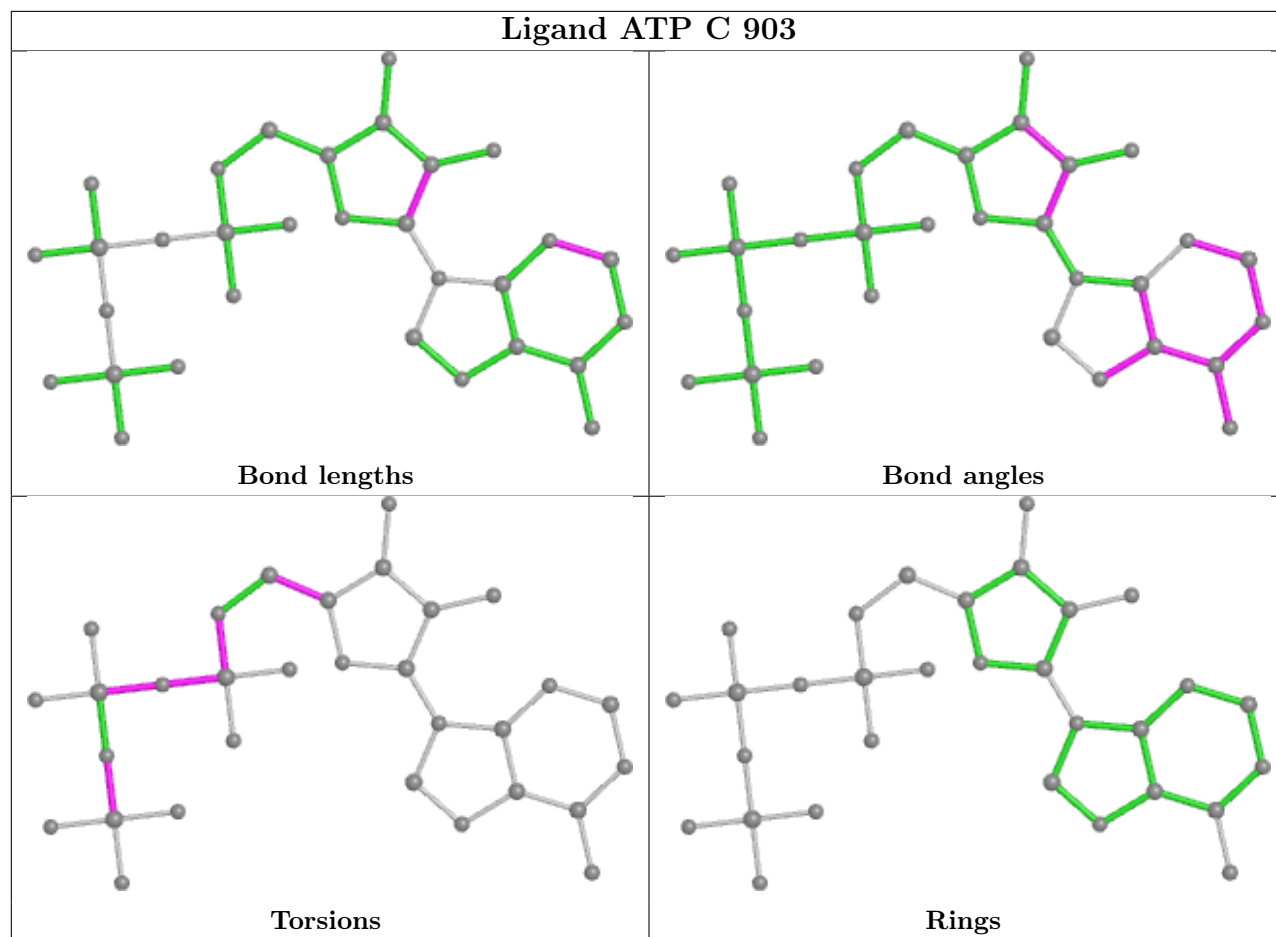
12 monomers are involved in 47 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	901	ATP	3	0
3	C	903	ATP	2	0
3	F	901	ATP	4	0
3	B	901	ATP	4	0
3	D	903	ATP	5	0
3	A	903	ATP	3	0
3	D	901	ATP	8	0
3	C	901	ATP	3	0
3	E	903	ATP	3	0
3	A	901	ATP	5	0
3	B	903	ATP	4	0
3	F	903	ATP	3	0

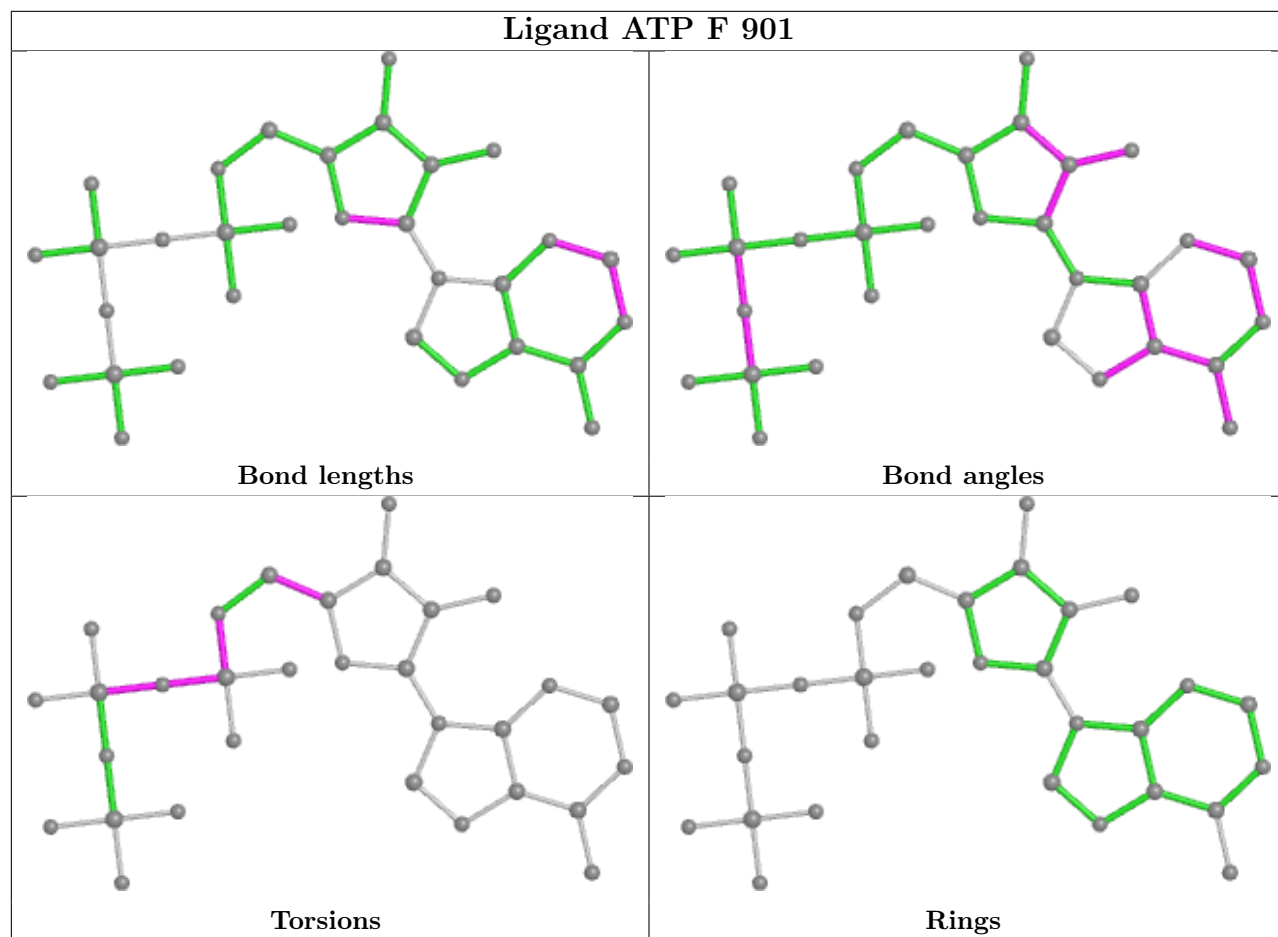
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

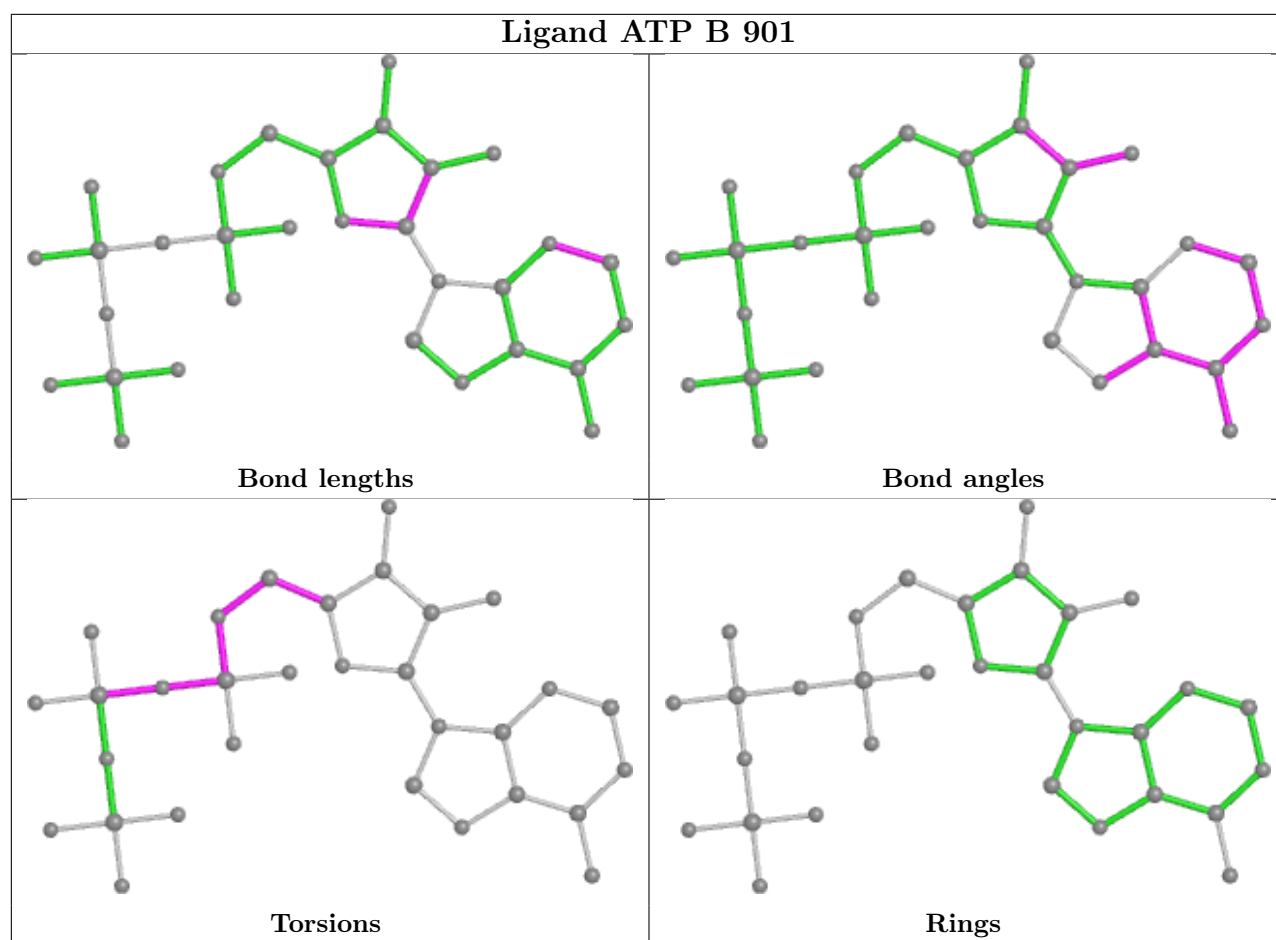
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

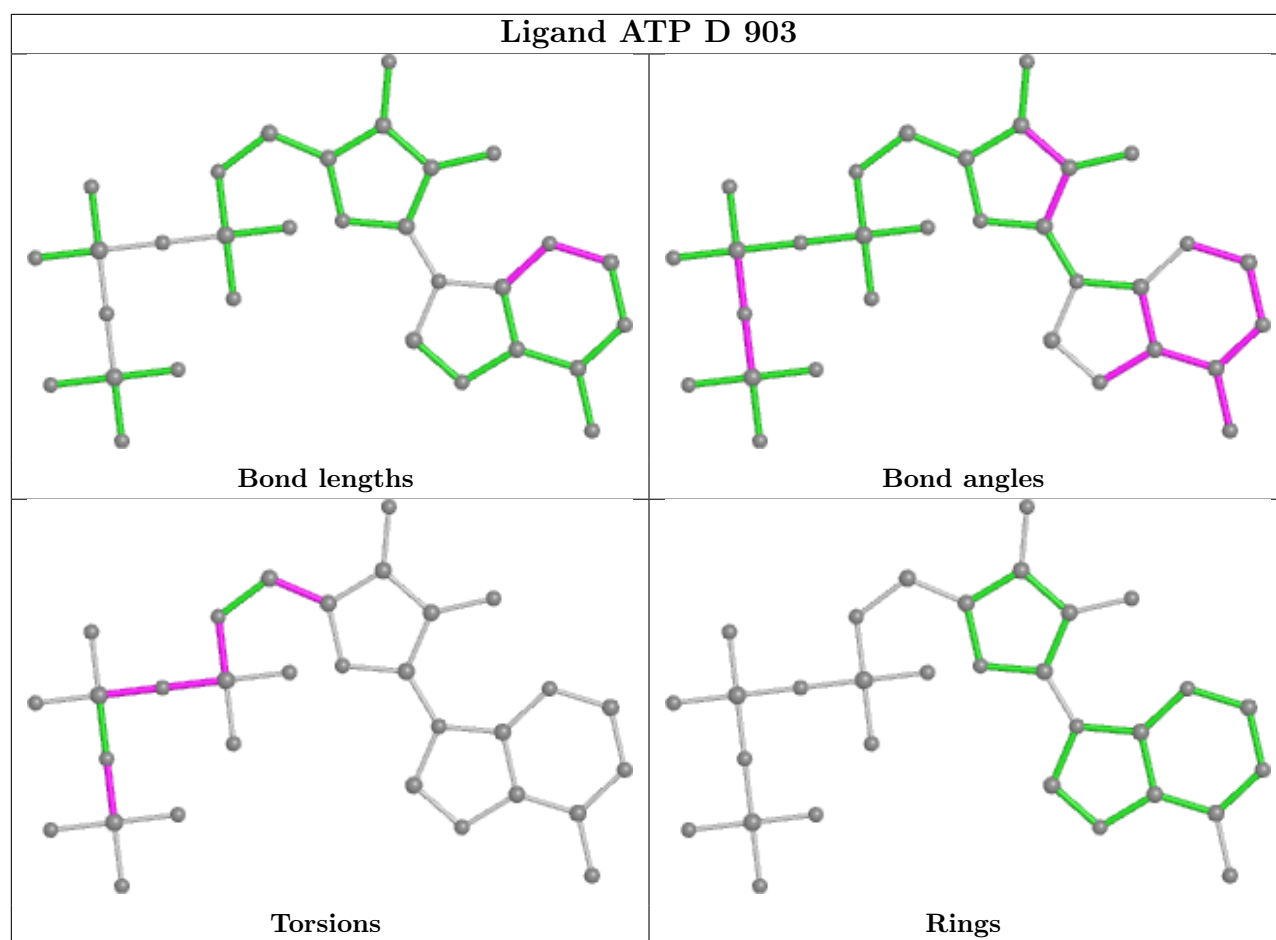


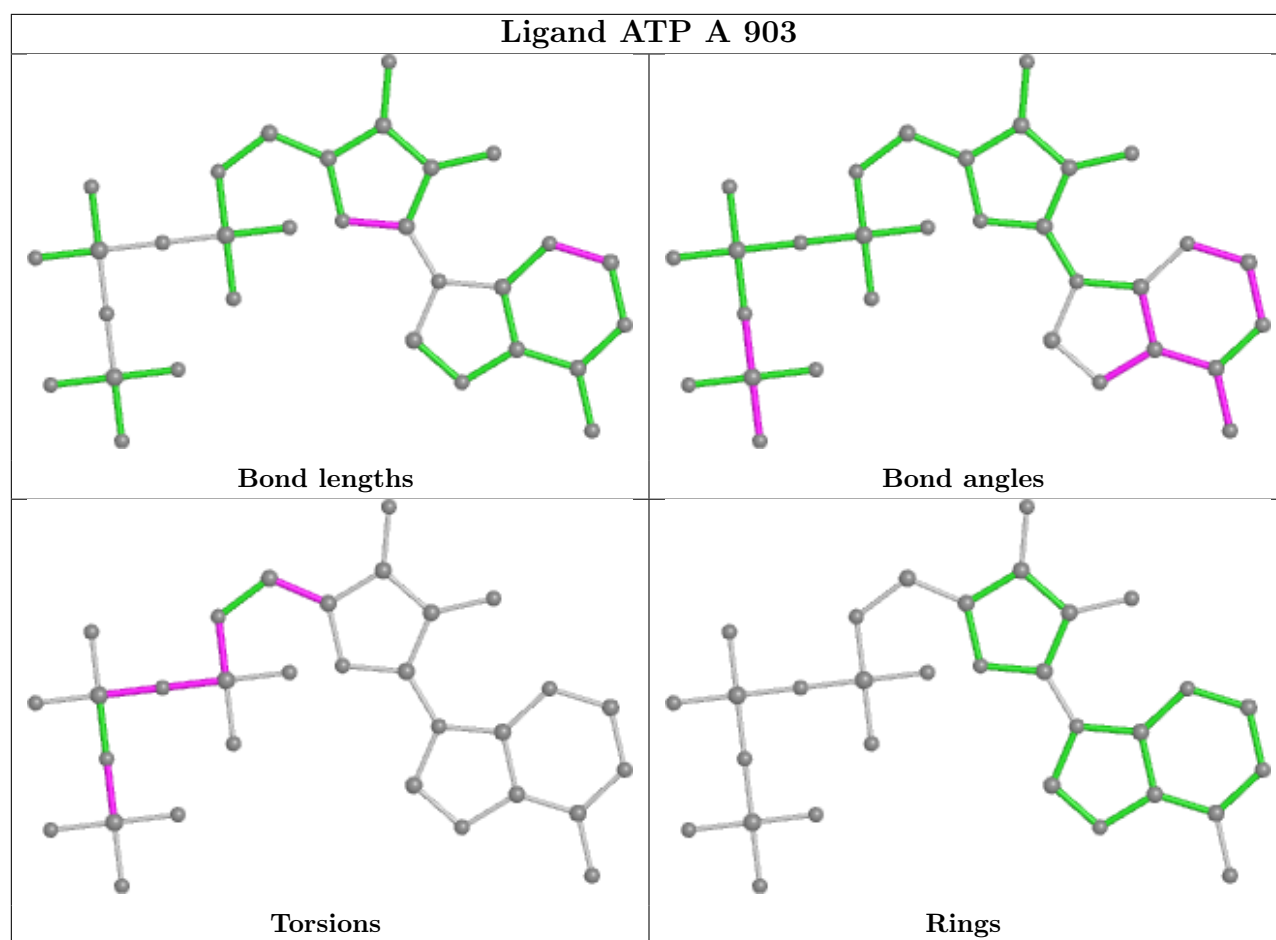


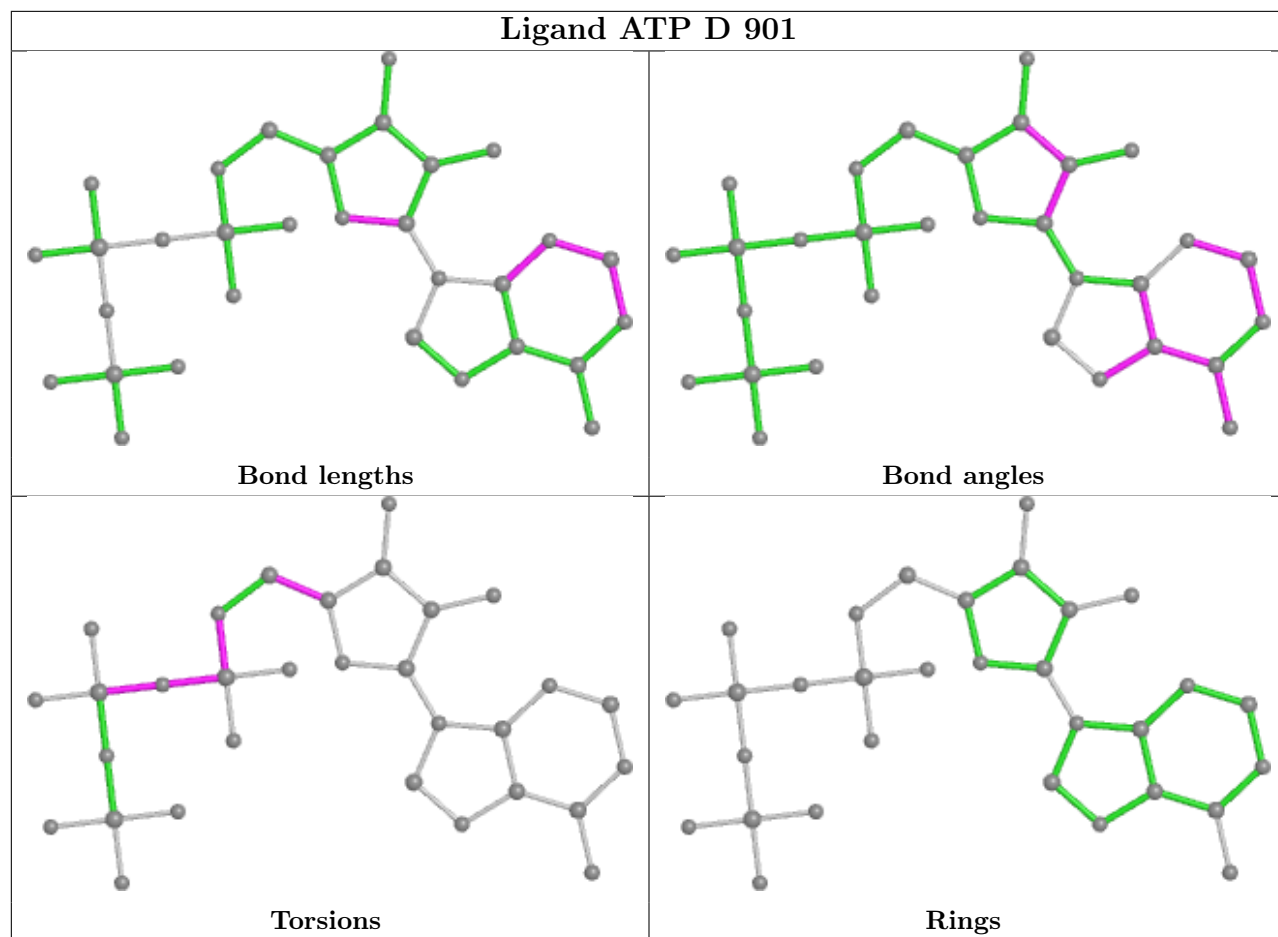
Ligand ATP F 901

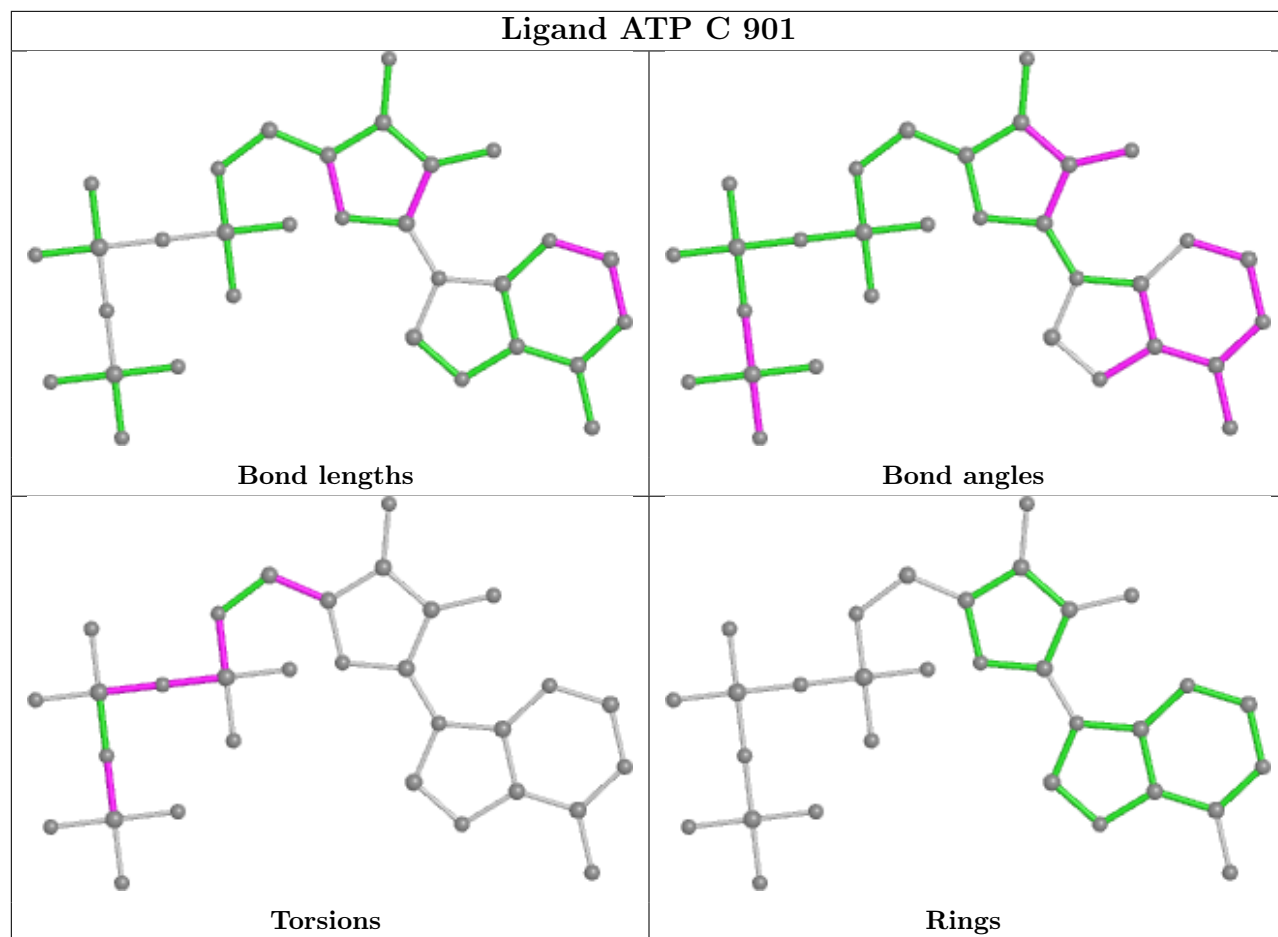




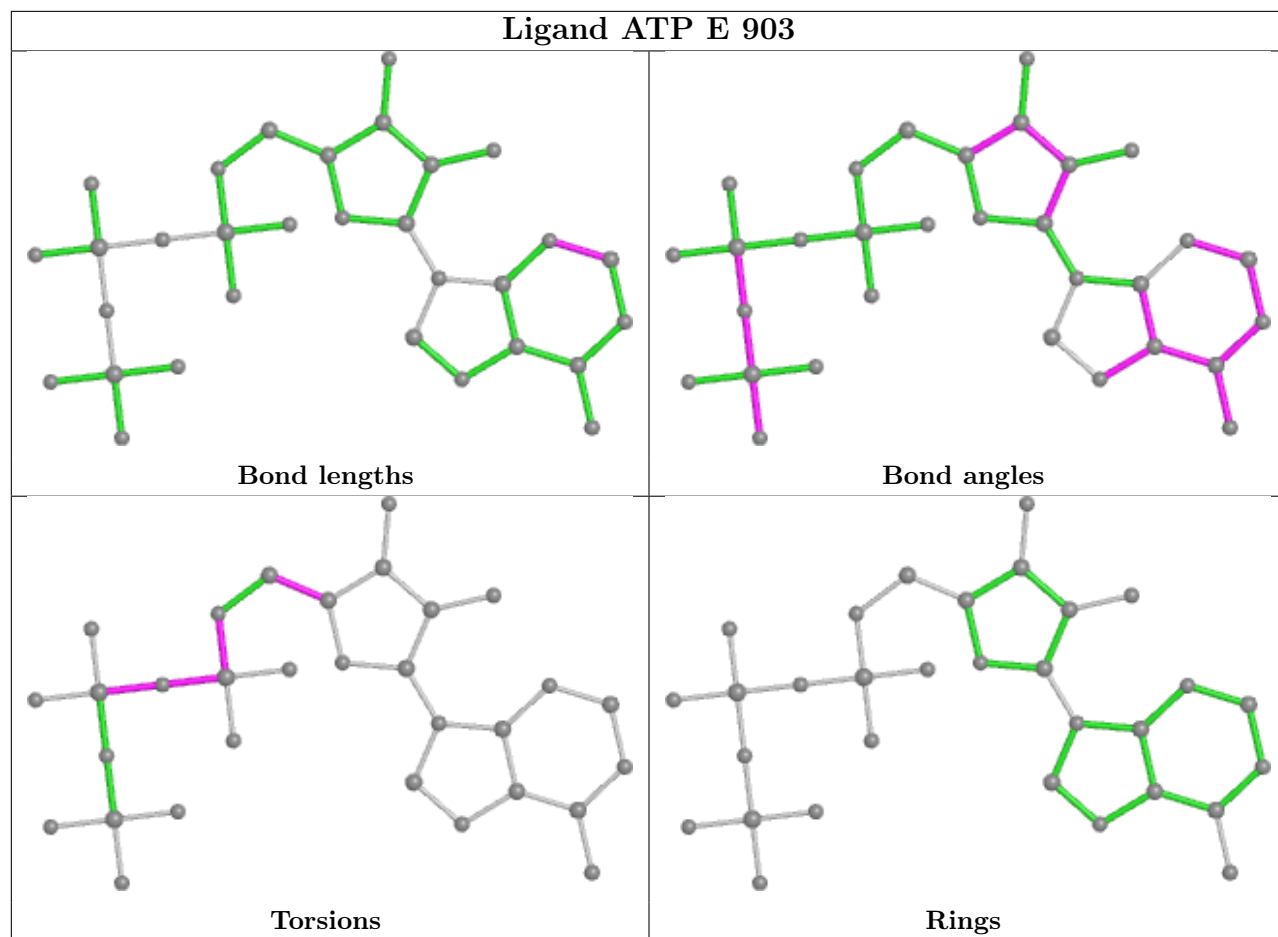


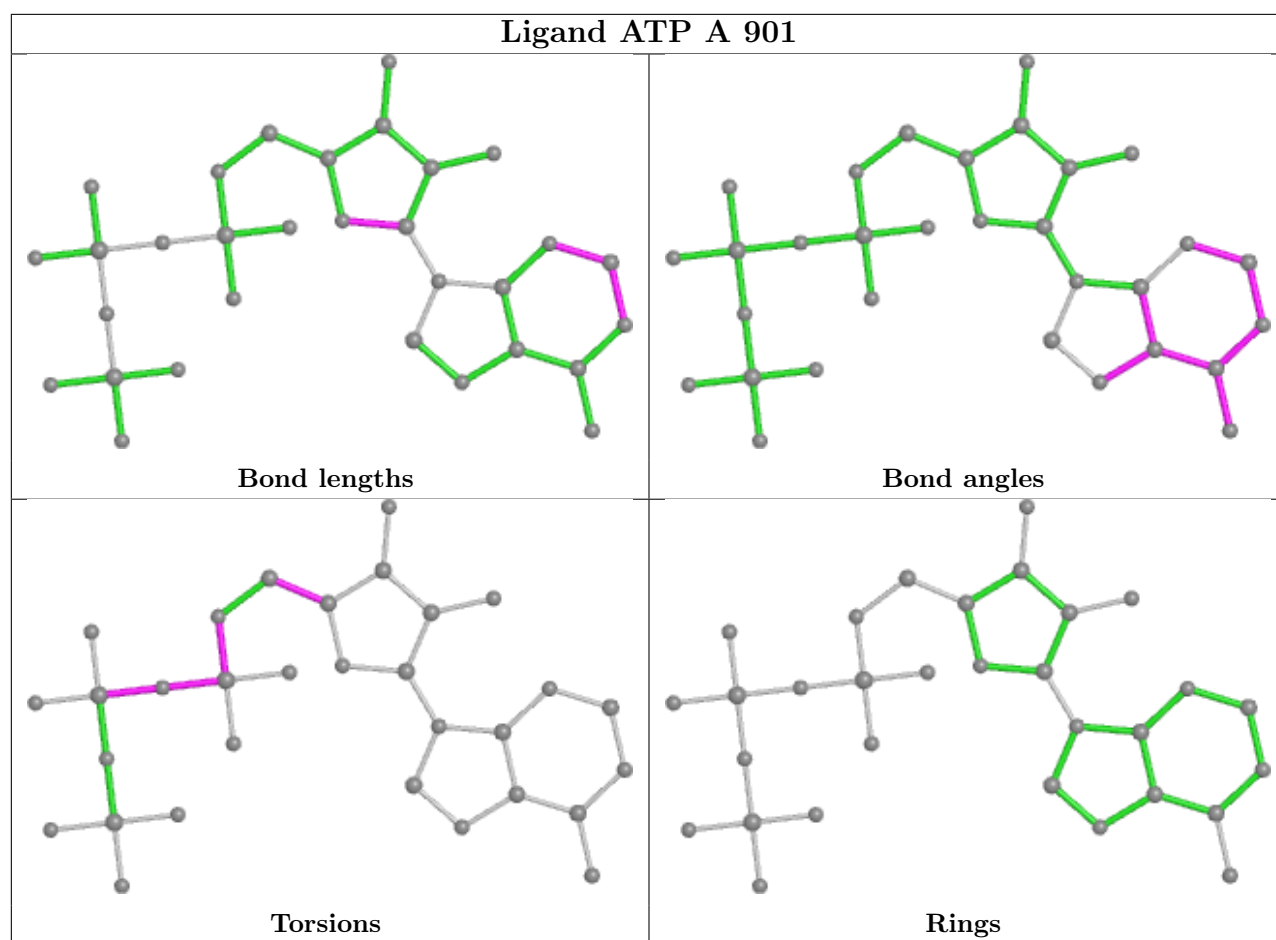


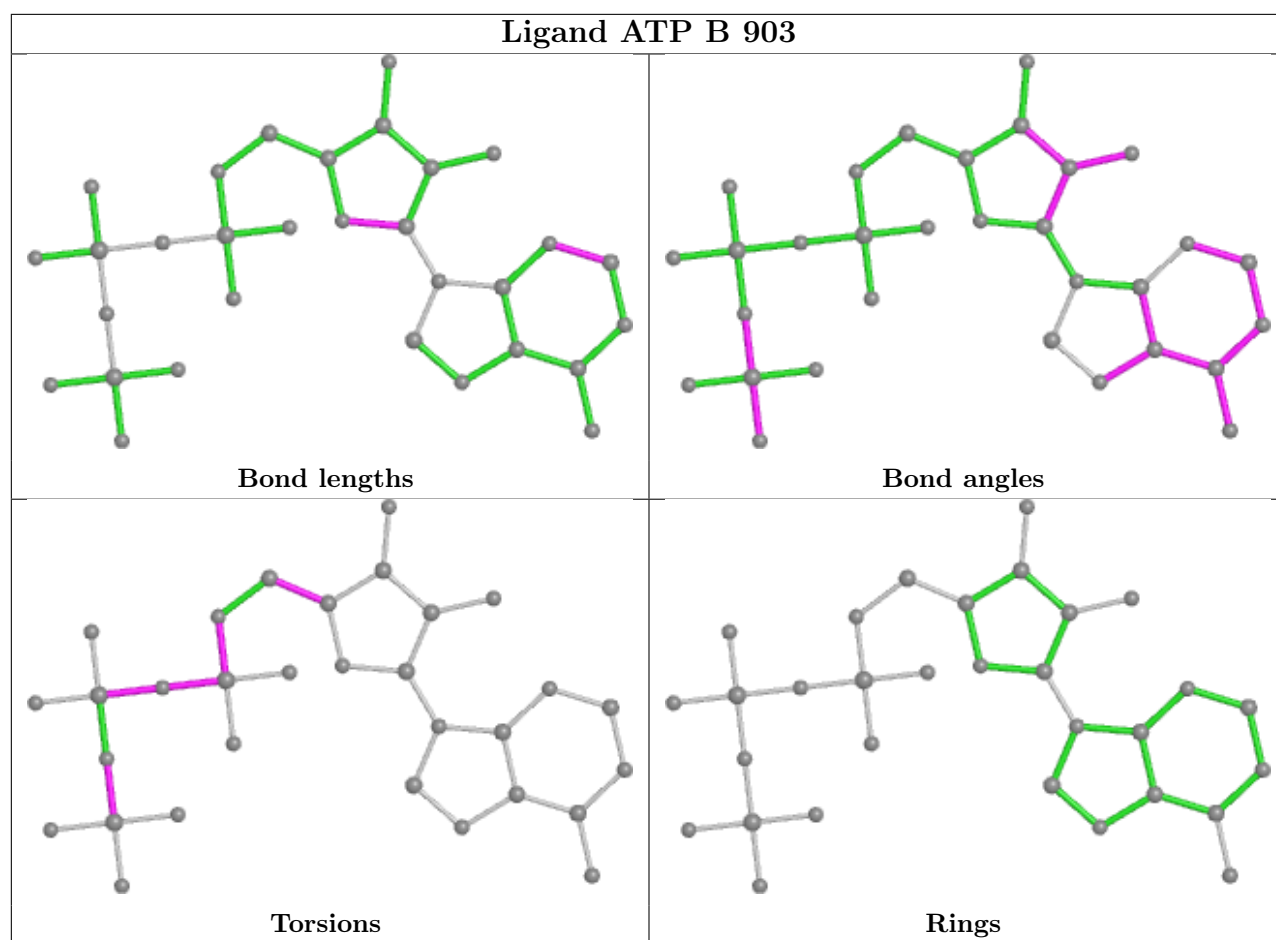


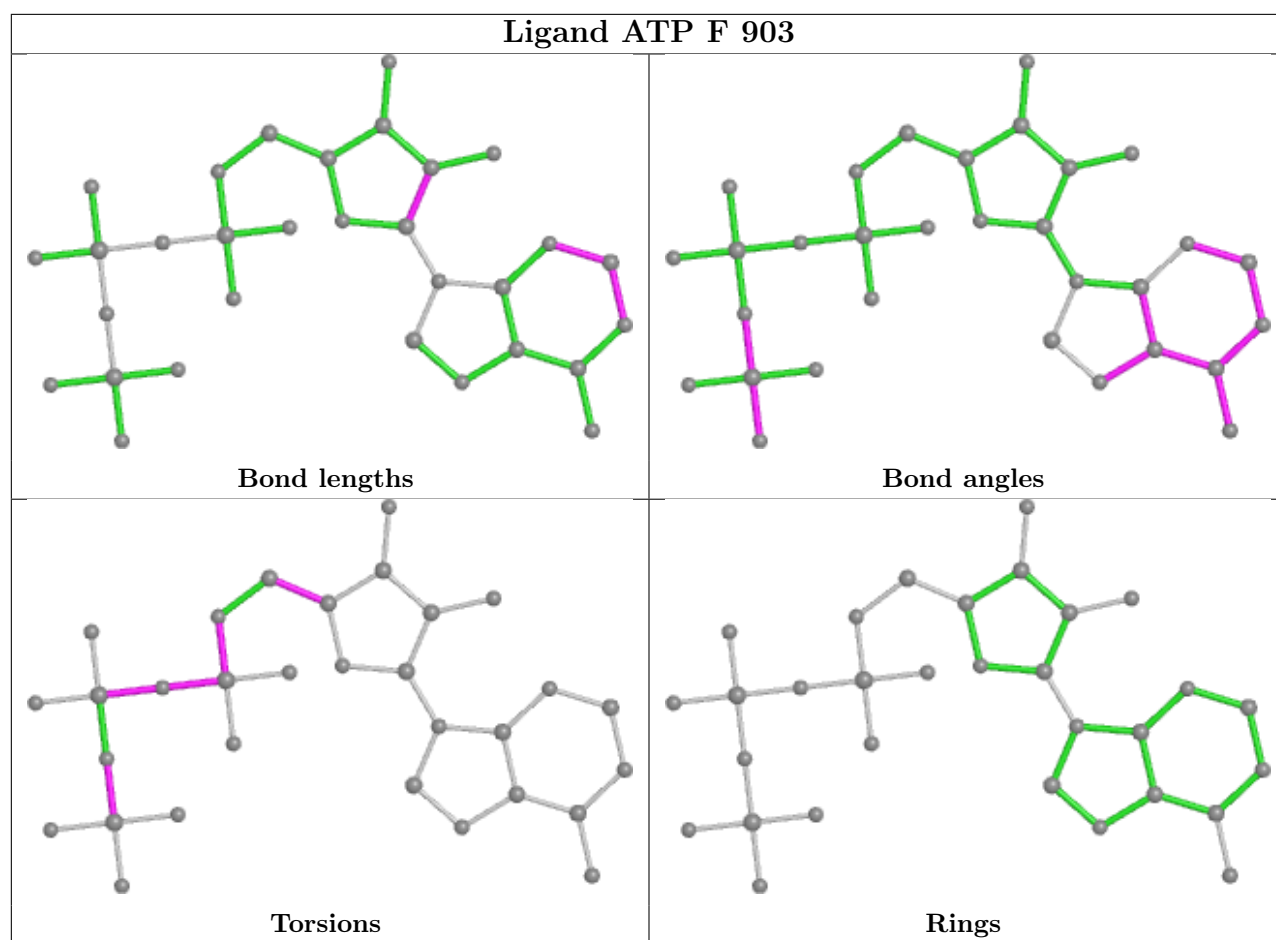


Ligand ATP E 903









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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

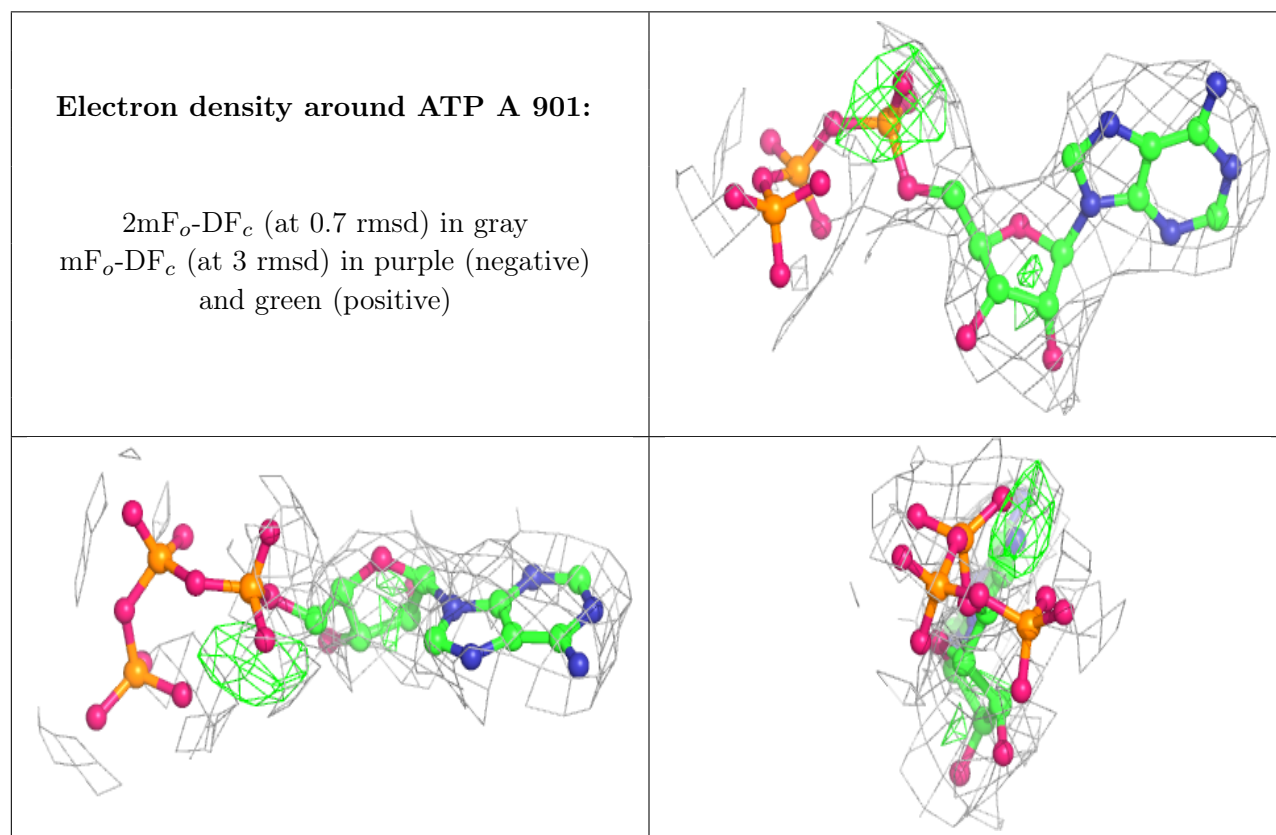
6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

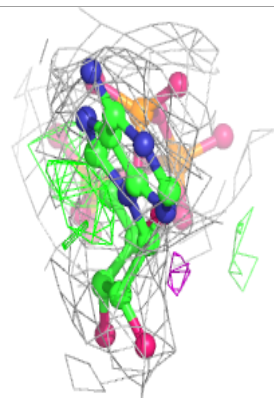
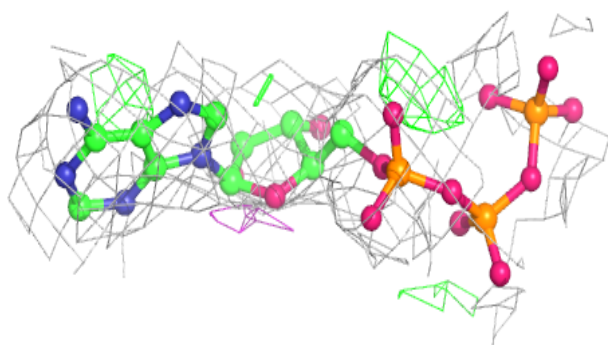
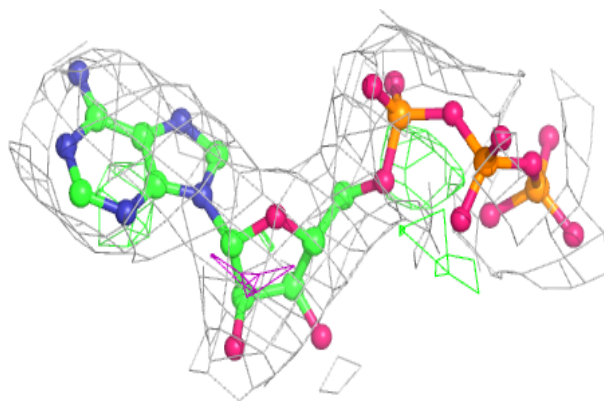
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

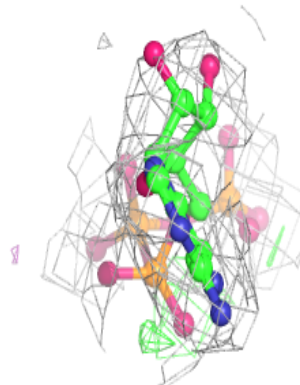
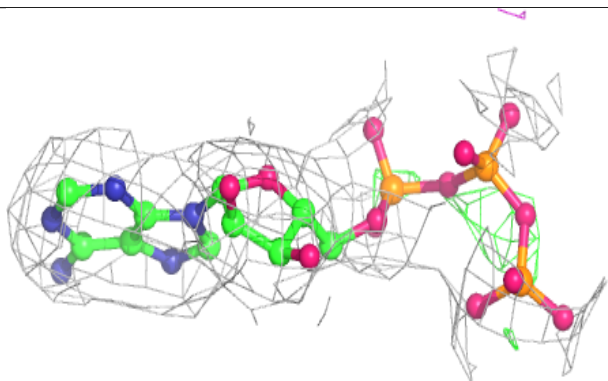
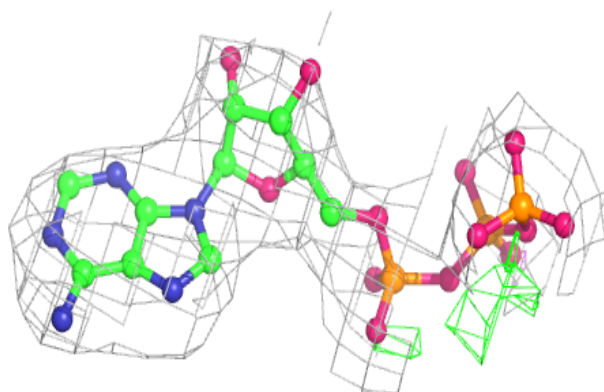


Electron density around ATP A 903:

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

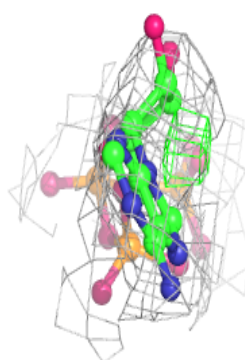
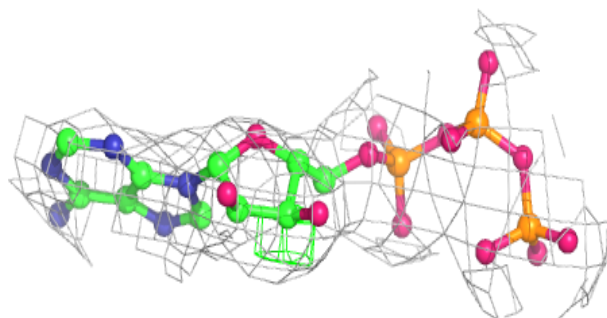
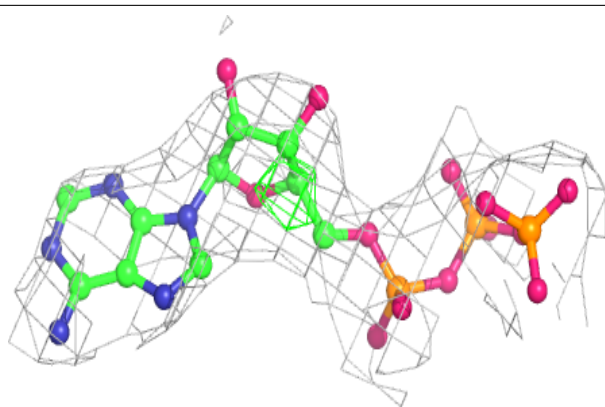
**Electron density around ATP B 901:**

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

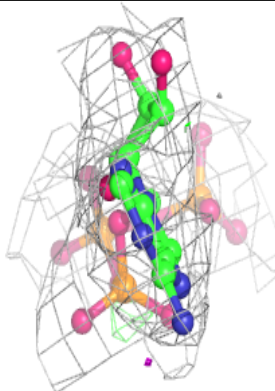
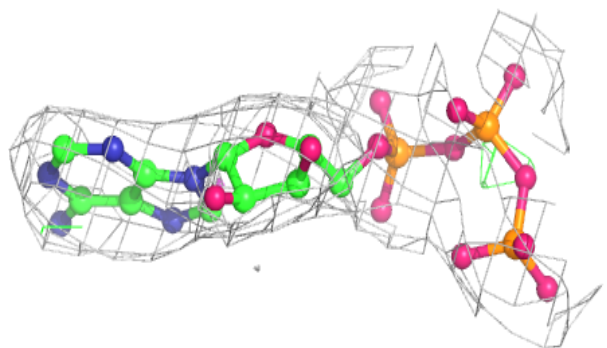
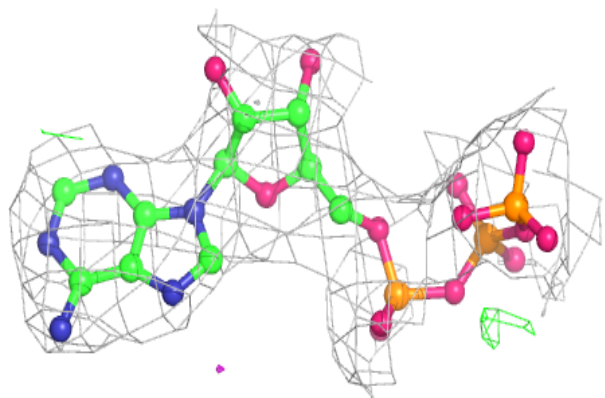


Electron density around ATP B 903:

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

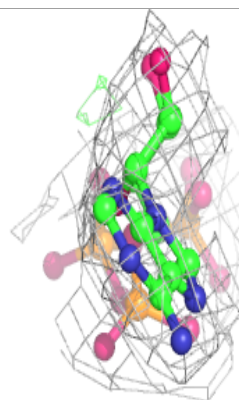
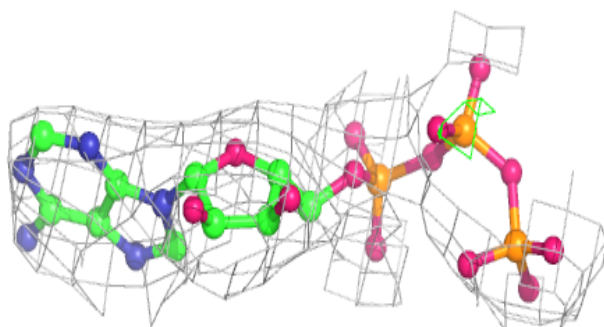
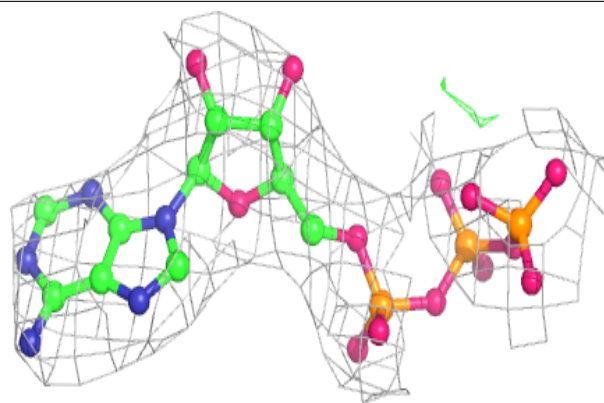
**Electron density around ATP C 901:**

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

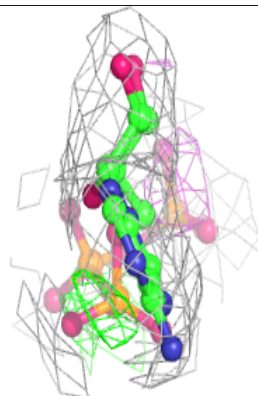
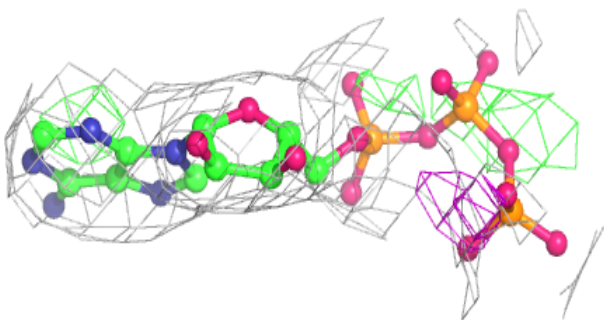
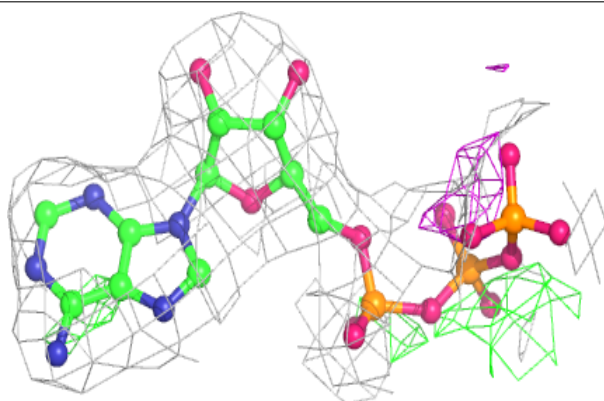


Electron density around ATP C 903:

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

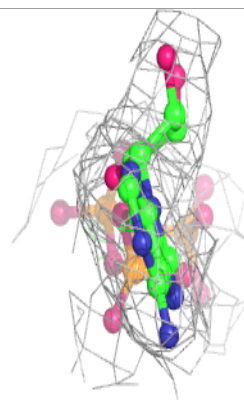
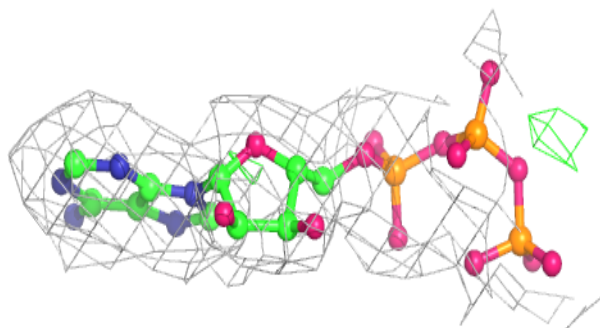
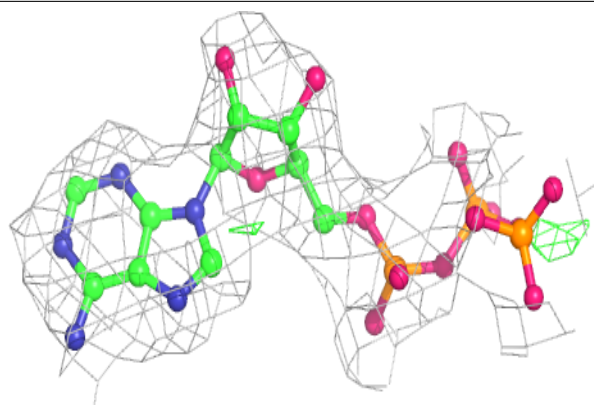
**Electron density around ATP D 901:**

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

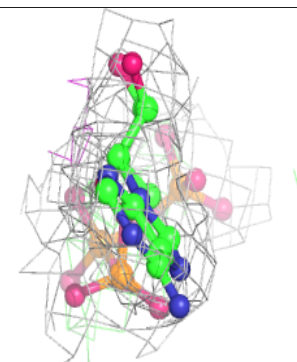
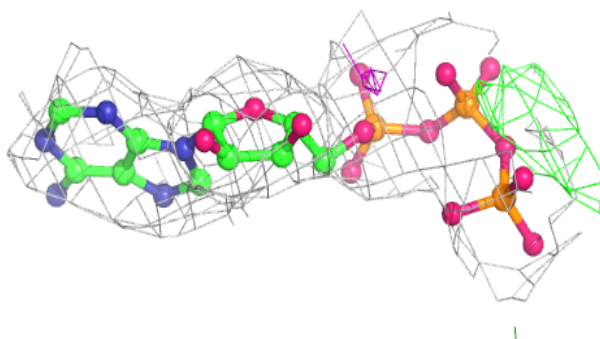
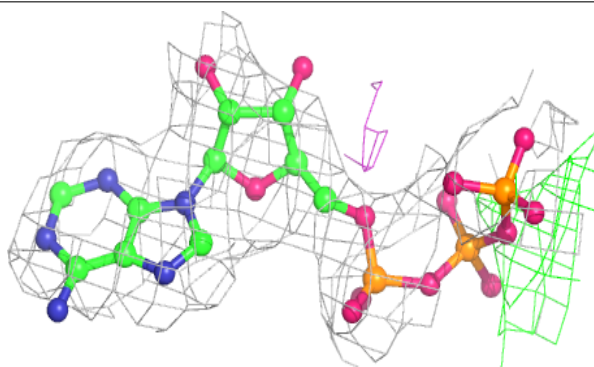


Electron density around ATP D 903:

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

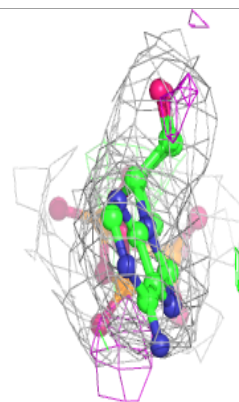
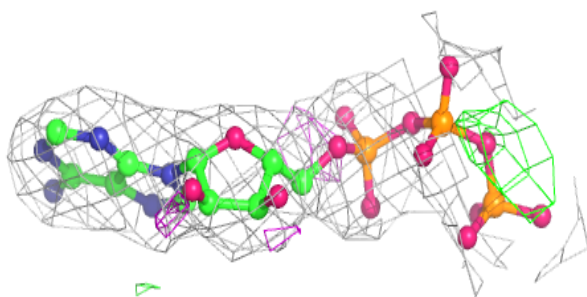
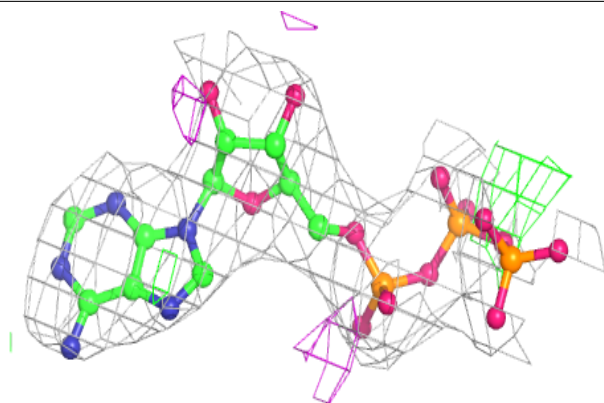
**Electron density around ATP E 901:**

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

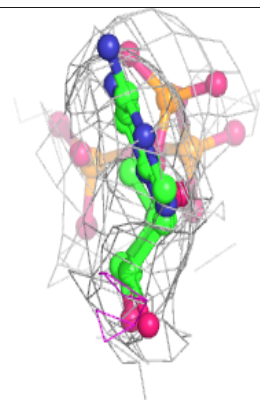
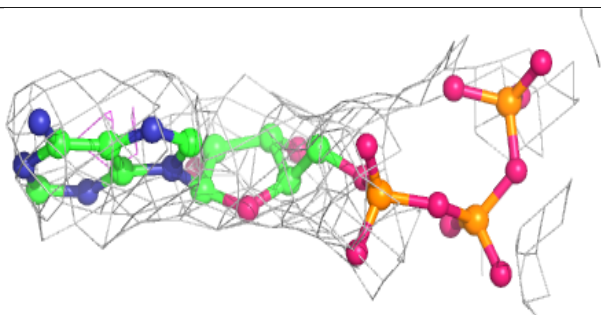
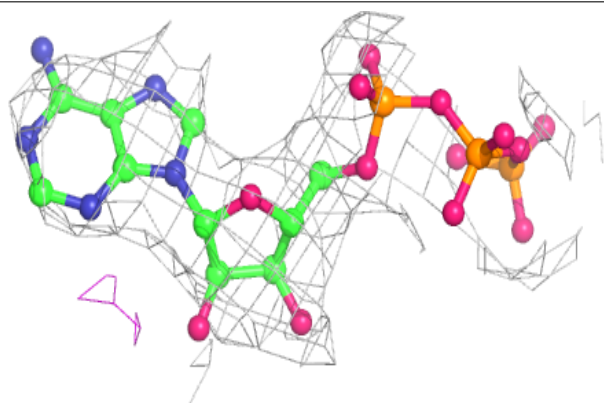


Electron density around ATP E 903:

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

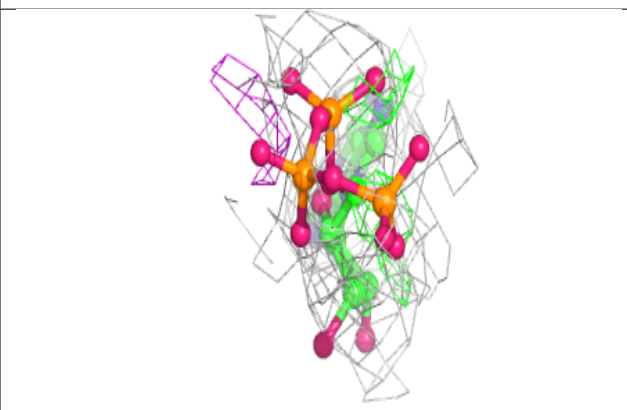
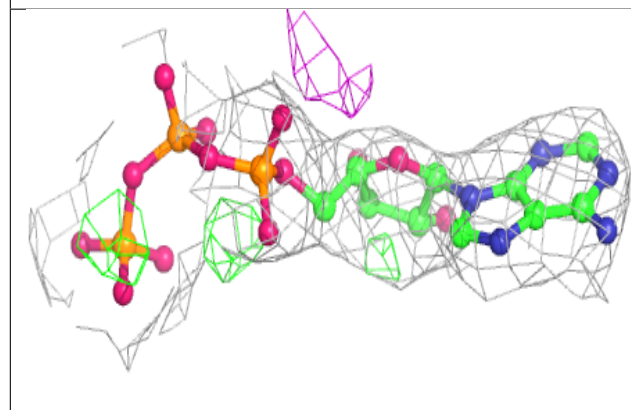
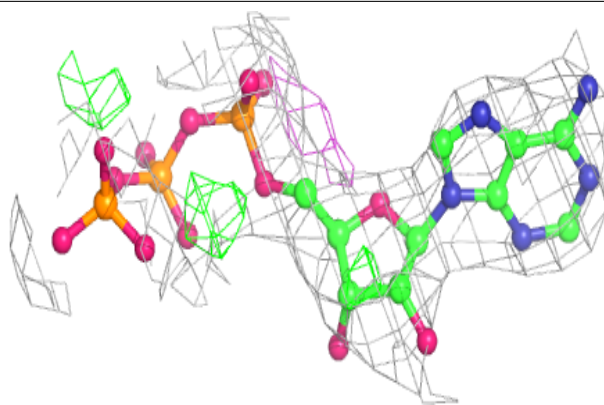
**Electron density around ATP F 901:**

$2mF_o-DF_c$ (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)



6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.