wwPDB X-ray Structure Validation Summary Report (i)

Jan 14, 2024 – 05:29 am GMT

PDB ID	:	6S5N
Title	:	Non-square conformations of KtrA E125Q mutant rings with bound ATP
Authors	:	Teixeira-Duarte, C.M.; Fonseca, F.; Morais-Cabral, J.H.
Deposited on	:	2019-07-02
Resolution	:	4.09 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 (i) 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 (i)) were used in the production of this report:

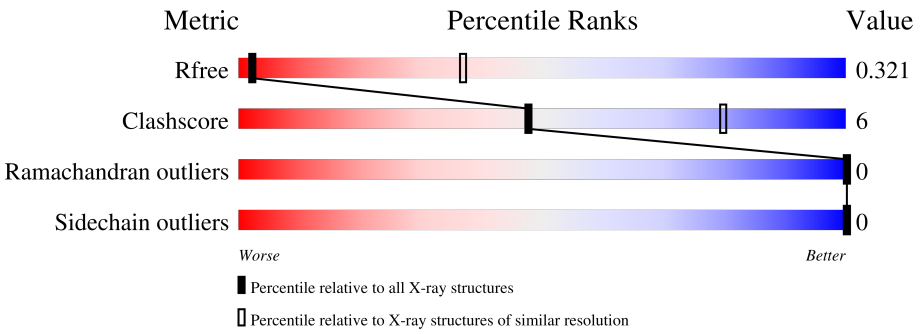
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 4.09 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	1193 (4.50-3.70)
Clashscore	141614	1003 (4.44-3.76)
Ramachandran outliers	138981	1005 (4.48-3.72)
Sidechain outliers	138945	1199 (4.50-3.70)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	222	83% 14% •
1	B	222	84% 14% •
1	C	222	83% 14% •
1	D	222	84% 14% •
1	E	222	81% 17% •
1	F	222	85% 13% •
1	G	222	51% 9% 39%

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Mol	Chain	Length	Quality of chain
1	H	222	51% 9% 39%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 12594 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 Ktr system potassium uptake protein A.

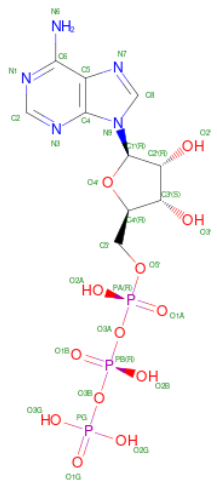
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	217	1706	1081	295	322	8	29	0	0
1	B	217	1706	1081	295	322	8	29	0	0
1	C	217	1706	1081	295	322	8	39	0	0
1	D	217	1706	1081	295	322	8	24	0	0
1	E	217	1706	1081	295	322	8	24	0	0
1	F	217	1706	1081	295	322	8	31	0	0
1	G	135	1055	670	184	198	3	0	0	0
1	H	135	1055	670	184	198	3	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	125	GLN	GLU	engineered mutation	UNP O32080
B	125	GLN	GLU	engineered mutation	UNP O32080
C	125	GLN	GLU	engineered mutation	UNP O32080
D	125	GLN	GLU	engineered mutation	UNP O32080
E	125	GLN	GLU	engineered mutation	UNP O32080
F	125	GLN	GLU	engineered mutation	UNP O32080
G	125	GLN	GLU	engineered mutation	UNP O32080
H	125	GLN	GLU	engineered mutation	UNP O32080

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

ATP



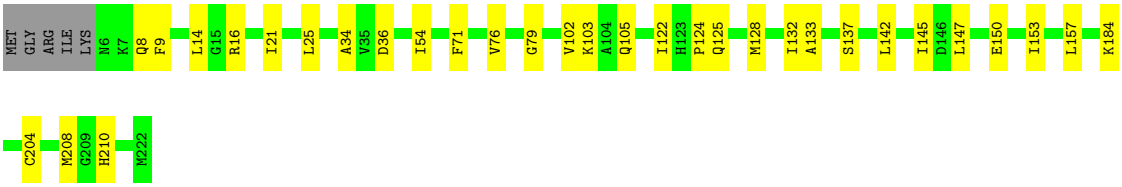
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	31	10	5	13	3	0	0
2	B	1	31	10	5	13	3	0	0
2	C	1	31	10	5	13	3	0	0
2	D	1	31	10	5	13	3	0	0
2	E	1	31	10	5	13	3	0	0
2	F	1	31	10	5	13	3	0	0
2	G	1	31	10	5	13	3	0	0
2	H	1	31	10	5	13	3	0	0

3 Residue-property plots (i)

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.

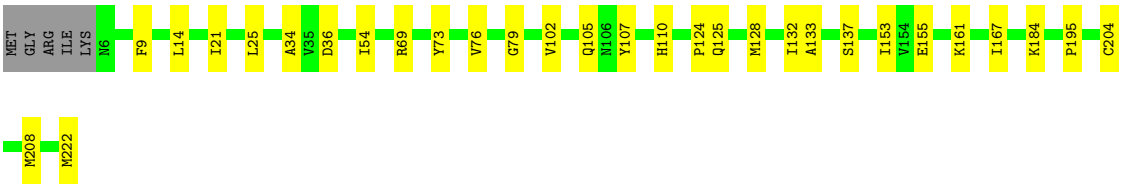
• Molecule 1: Ktr system potassium uptake protein A

Chain A:



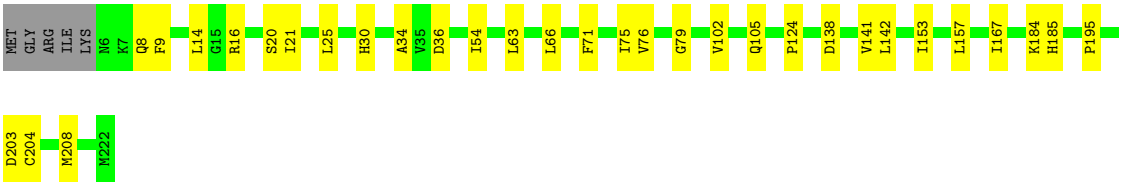
• Molecule 1: Ktr system potassium uptake protein A

Chain B:



• Molecule 1: Ktr system potassium uptake protein A

Chain C:

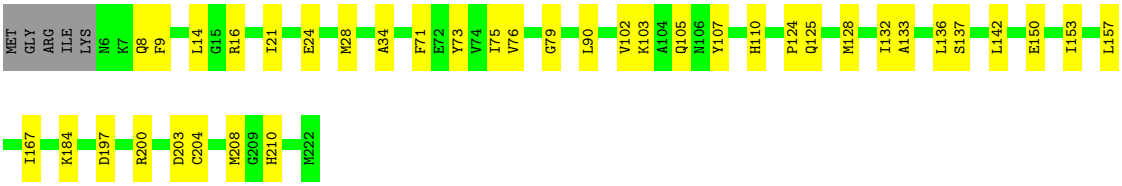


• Molecule 1: Ktr system potassium uptake protein A

Chain D:

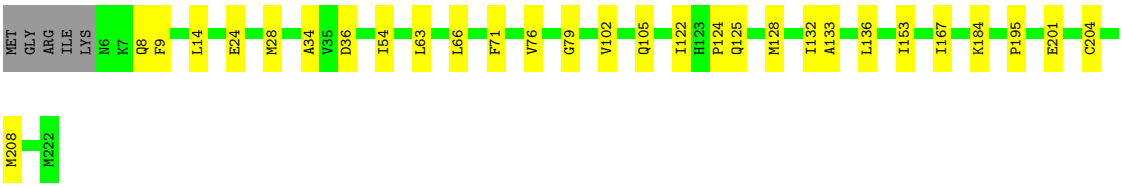
• Molecule 1: Ktr system potassium uptake protein A

Chain E:



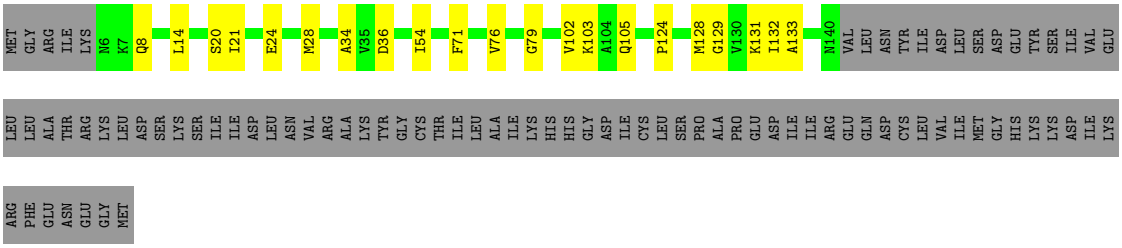
• Molecule 1: Ktr system potassium uptake protein A

Chain F:



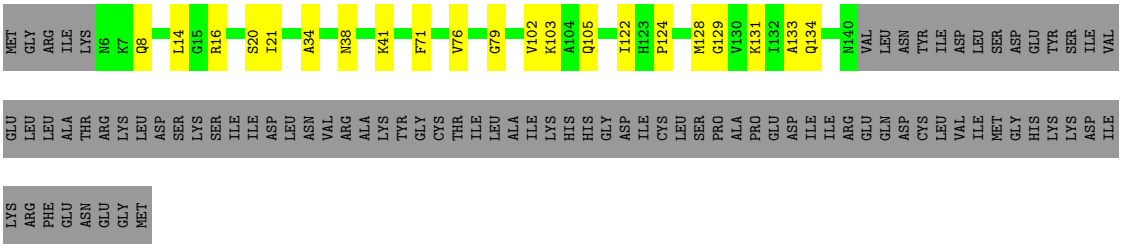
• Molecule 1: Ktr system potassium uptake protein A

Chain G:



• Molecule 1: Ktr system potassium uptake protein A

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	109.11Å 156.53Å 286.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.24 – 4.09 48.24 – 4.09	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.24-4.09) 99.7 (48.24-4.09)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.79 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.279 , 0.320 0.281 , 0.321	Depositor DCC
R_{free} test set	2010 reflections (10.22%)	wwPDB-VP
Wilson B-factor (Å^2)	183.9	Xtriage
Anisotropy	0.471	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 87.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	12594	wwPDB-VP
Average B, all atoms (Å^2)	155.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 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	0.22	0/1732	0.42	0/2339
1	B	0.23	0/1732	0.44	0/2339
1	C	0.22	0/1732	0.43	0/2339
1	D	0.22	0/1732	0.43	0/2339
1	E	0.22	0/1732	0.44	0/2339
1	F	0.22	0/1732	0.42	0/2339
1	G	0.22	0/1072	0.41	0/1450
1	H	0.22	0/1072	0.41	0/1450
All	All	0.22	0/12536	0.43	0/16934

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1706	0	1732	26	0
1	B	1706	0	1732	26	0
1	C	1706	0	1732	21	0
1	D	1706	0	1732	26	0
1	E	1706	0	1732	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1706	0	1732	20	0
1	G	1055	0	1064	25	0
1	H	1055	0	1064	23	0
2	A	31	0	12	1	0
2	B	31	0	12	0	0
2	C	31	0	12	1	0
2	D	31	0	12	1	0
2	E	31	0	12	2	0
2	F	31	0	12	0	0
2	G	31	0	12	0	0
2	H	31	0	12	2	0
All	All	12594	0	12616	152	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 6.

The worst 5 of 152 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:E:21:ILE:HA	1:F:133:ALA:HB2	1.57	0.86
1:B:184:LYS:HB3	1:B:204:CYS:HB2	1.58	0.86
1:D:184:LYS:HB3	1:D:204:CYS:HB2	1.58	0.85
1:E:184:LYS:HB3	1:E:204:CYS:HB2	1.58	0.84
1:C:184:LYS:HB3	1:C:204:CYS:HB2	1.59	0.83

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	215/222 (97%)	211 (98%)	4 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	215/222 (97%)	211 (98%)	4 (2%)	0	100	100
1	C	215/222 (97%)	211 (98%)	4 (2%)	0	100	100
1	D	215/222 (97%)	210 (98%)	5 (2%)	0	100	100
1	E	215/222 (97%)	211 (98%)	4 (2%)	0	100	100
1	F	215/222 (97%)	212 (99%)	3 (1%)	0	100	100
1	G	133/222 (60%)	131 (98%)	2 (2%)	0	100	100
1	H	133/222 (60%)	131 (98%)	2 (2%)	0	100	100
All	All	1556/1776 (88%)	1528 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	186/190 (98%)	186 (100%)	0	100	100
1	B	186/190 (98%)	186 (100%)	0	100	100
1	C	186/190 (98%)	186 (100%)	0	100	100
1	D	186/190 (98%)	186 (100%)	0	100	100
1	E	186/190 (98%)	186 (100%)	0	100	100
1	F	186/190 (98%)	186 (100%)	0	100	100
1	G	112/190 (59%)	112 (100%)	0	100	100
1	H	112/190 (59%)	112 (100%)	0	100	100
All	All	1340/1520 (88%)	1340 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	$\#\|Z\| > 2$
2	ATP	C	601	-	26,33,33	0.92	1 (3%)	31,52,52	1.45	5 (16%)
2	ATP	A	601	-	26,33,33	0.93	1 (3%)	31,52,52	1.47	5 (16%)
2	ATP	F	601	-	26,33,33	0.92	1 (3%)	31,52,52	1.48	5 (16%)
2	ATP	E	601	-	26,33,33	0.93	1 (3%)	31,52,52	1.46	5 (16%)
2	ATP	B	601	-	26,33,33	0.92	1 (3%)	31,52,52	1.47	5 (16%)
2	ATP	D	601	-	26,33,33	0.92	1 (3%)	31,52,52	1.44	5 (16%)
2	ATP	G	601	-	26,33,33	0.91	1 (3%)	31,52,52	1.47	5 (16%)
2	ATP	H	601	-	26,33,33	0.92	1 (3%)	31,52,52	1.60	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
2	ATP	C	601	-	-	8/18/38/38	0/3/3/3
2	ATP	A	601	-	-	8/18/38/38	0/3/3/3
2	ATP	F	601	-	-	7/18/38/38	0/3/3/3
2	ATP	E	601	-	-	6/18/38/38	0/3/3/3
2	ATP	B	601	-	-	8/18/38/38	0/3/3/3
2	ATP	D	601	-	-	11/18/38/38	0/3/3/3
2	ATP	G	601	-	-	8/18/38/38	0/3/3/3
2	ATP	H	601	-	-	4/18/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	ATP	C5-C4	2.50	1.47	1.40
2	F	601	ATP	C5-C4	2.49	1.47	1.40
2	E	601	ATP	C5-C4	2.49	1.47	1.40
2	C	601	ATP	C5-C4	2.48	1.47	1.40
2	B	601	ATP	C5-C4	2.48	1.47	1.40

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	601	ATP	PA-O3A-PB	-3.94	119.30	132.83
2	H	601	ATP	PB-O3B-PG	-3.67	120.22	132.83
2	G	601	ATP	N3-C2-N1	-3.26	123.58	128.68
2	C	601	ATP	N3-C2-N1	-3.25	123.60	128.68
2	H	601	ATP	N3-C2-N1	-3.23	123.62	128.68

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	ATP	PB-O3B-PG-O2G
2	A	601	ATP	PB-O3B-PG-O3G
2	A	601	ATP	PB-O3A-PA-O5'
2	A	601	ATP	C5'-O5'-PA-O1A
2	A	601	ATP	C5'-O5'-PA-O2A

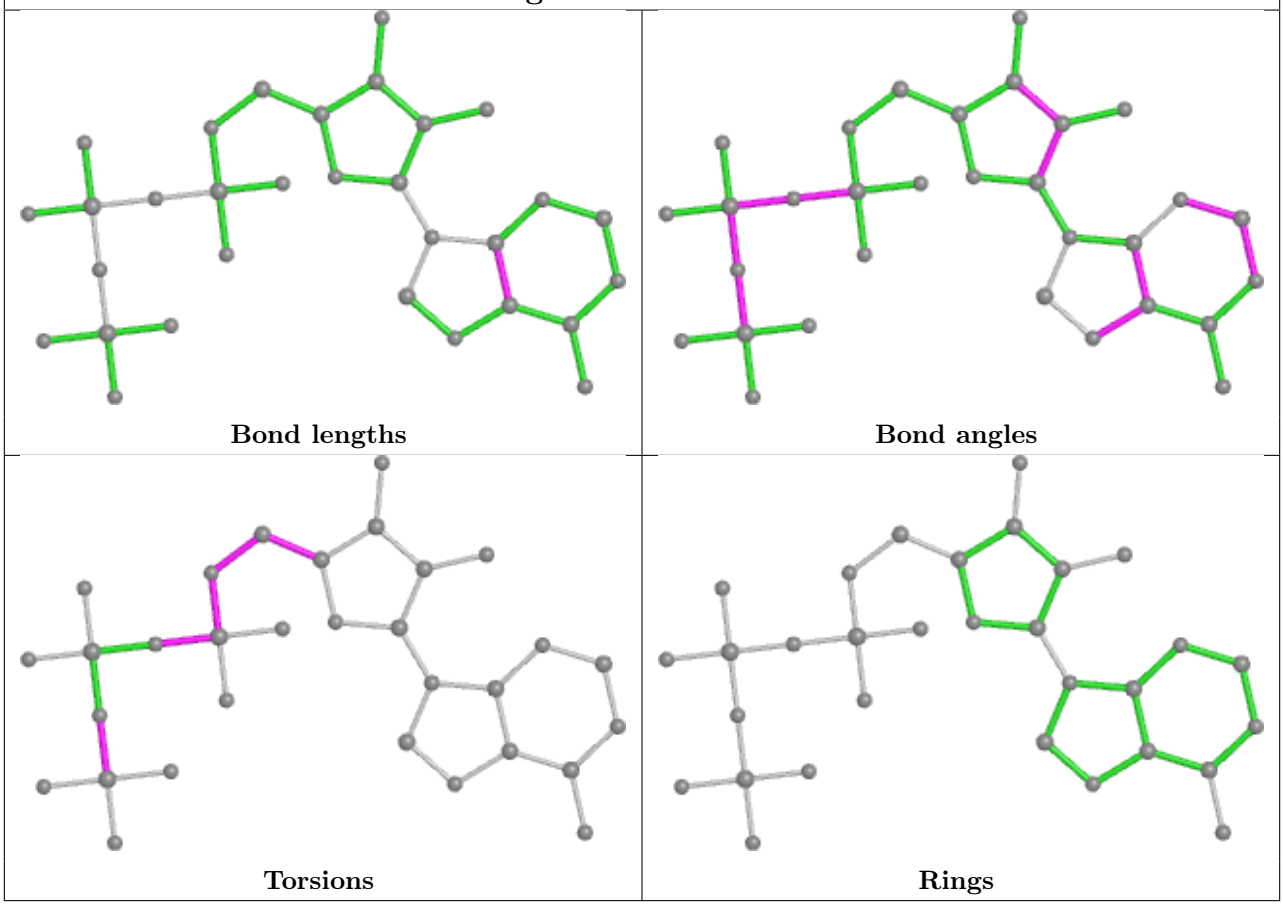
There are no ring outliers.

5 monomers are involved in 7 short contacts:

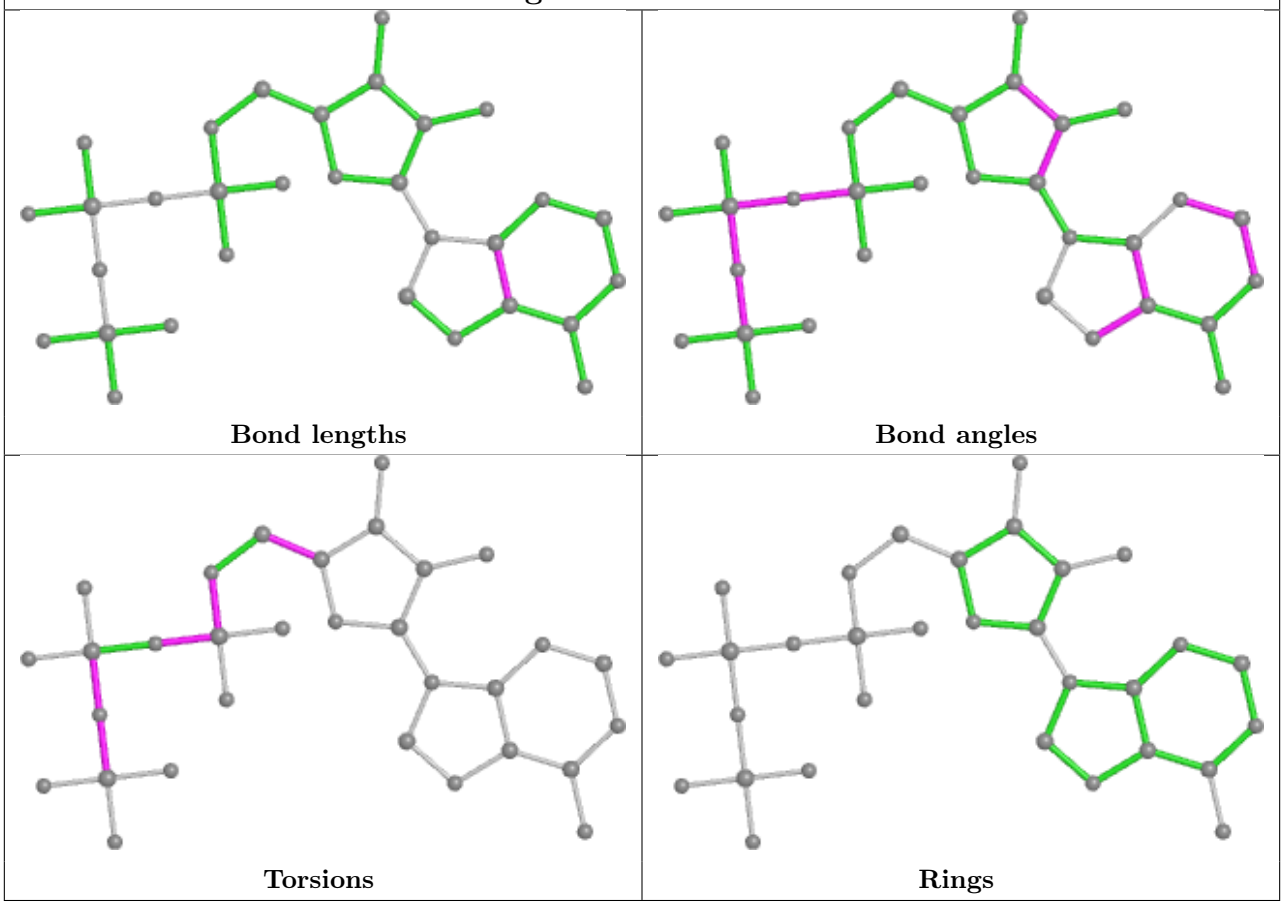
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	601	ATP	1	0
2	A	601	ATP	1	0
2	E	601	ATP	2	0
2	D	601	ATP	1	0
2	H	601	ATP	2	0

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

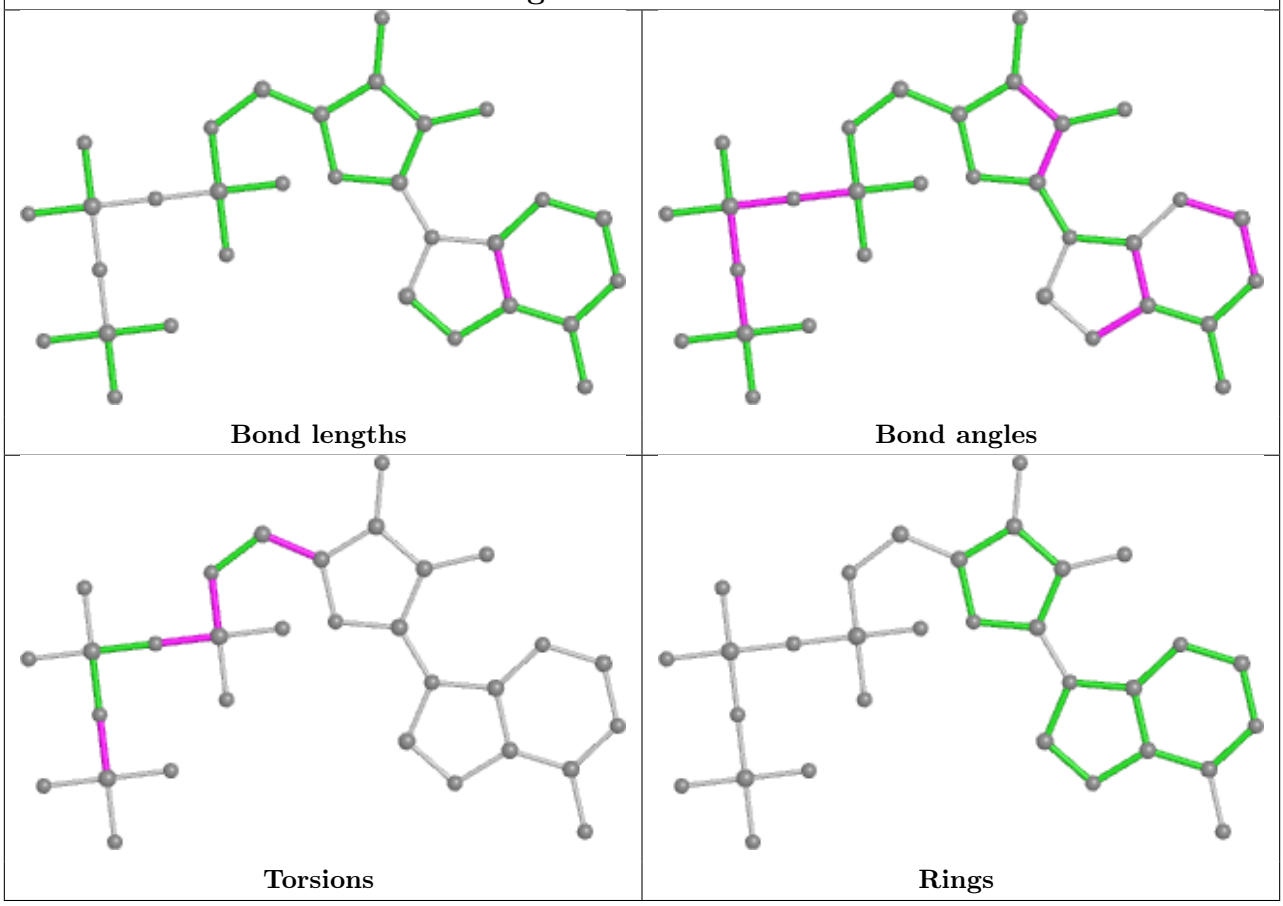
Ligand ATP C 601



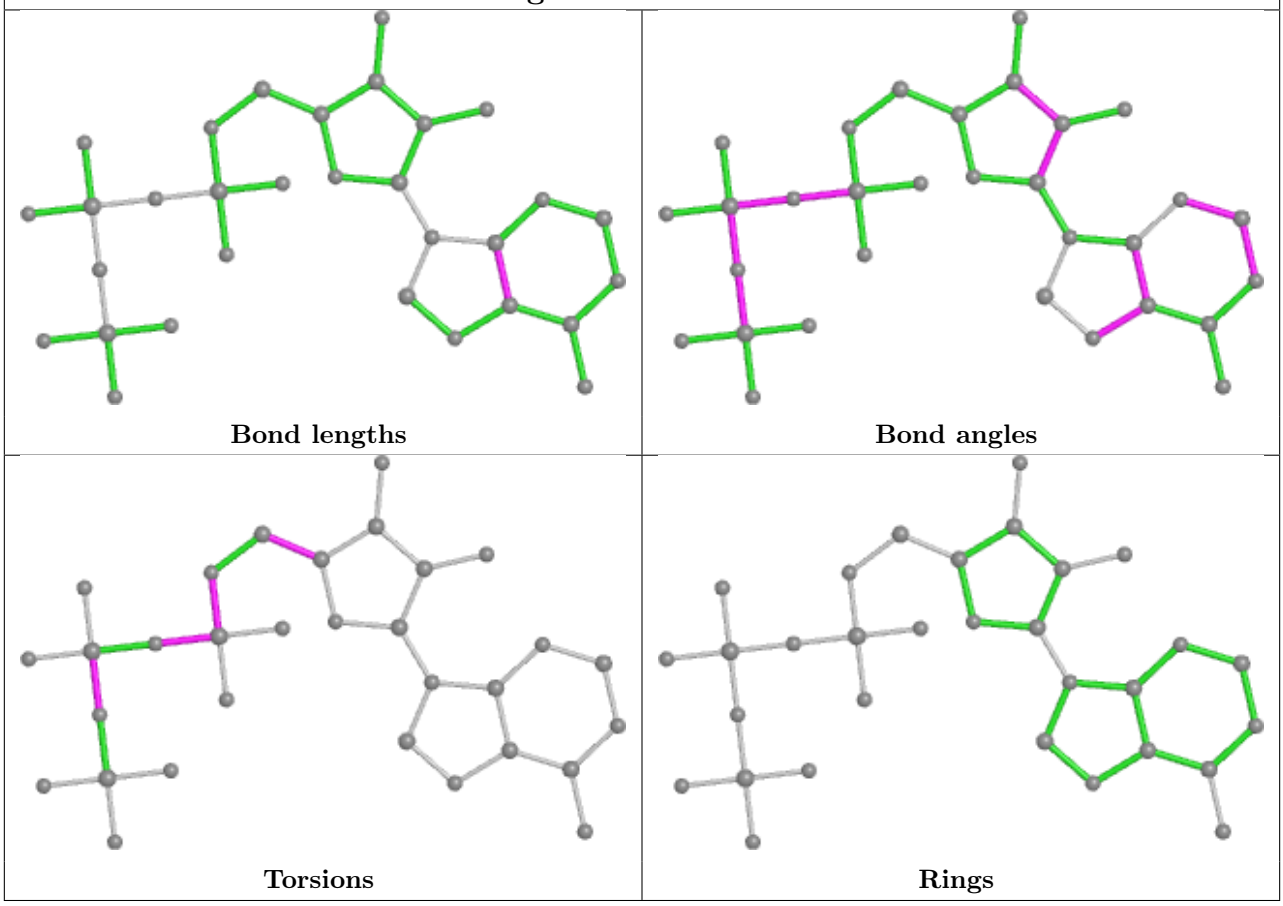
Ligand ATP A 601



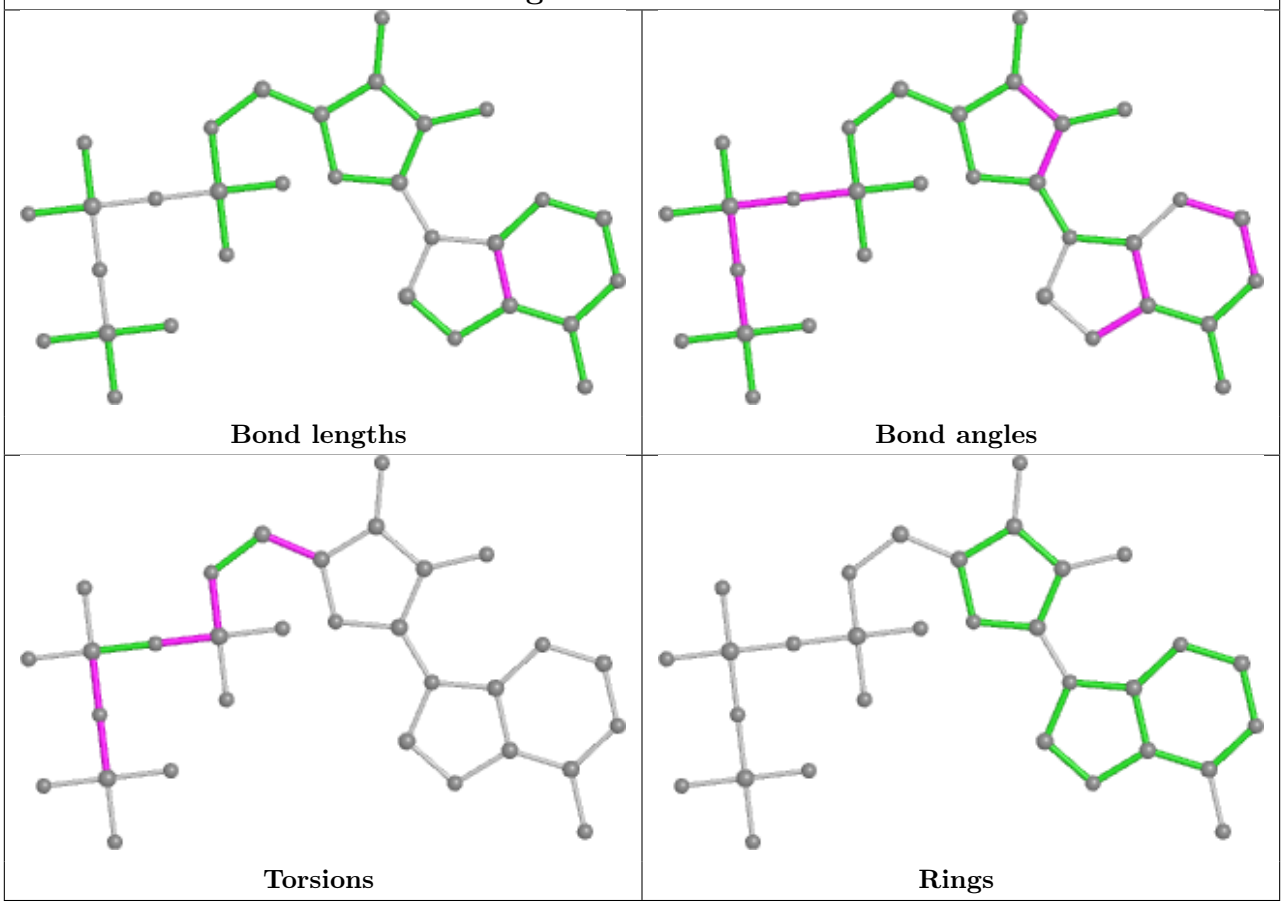
Ligand ATP F 601



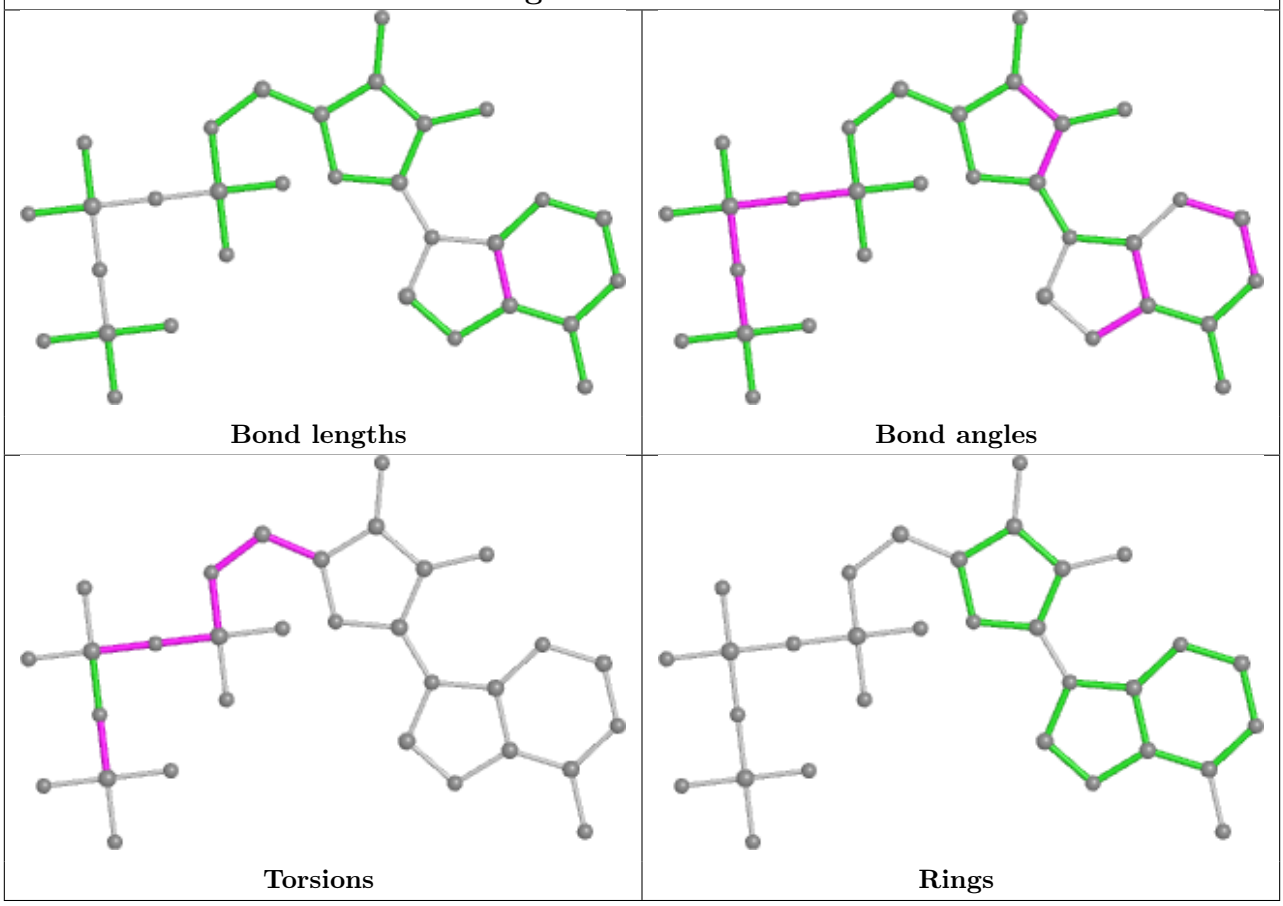
Ligand ATP E 601



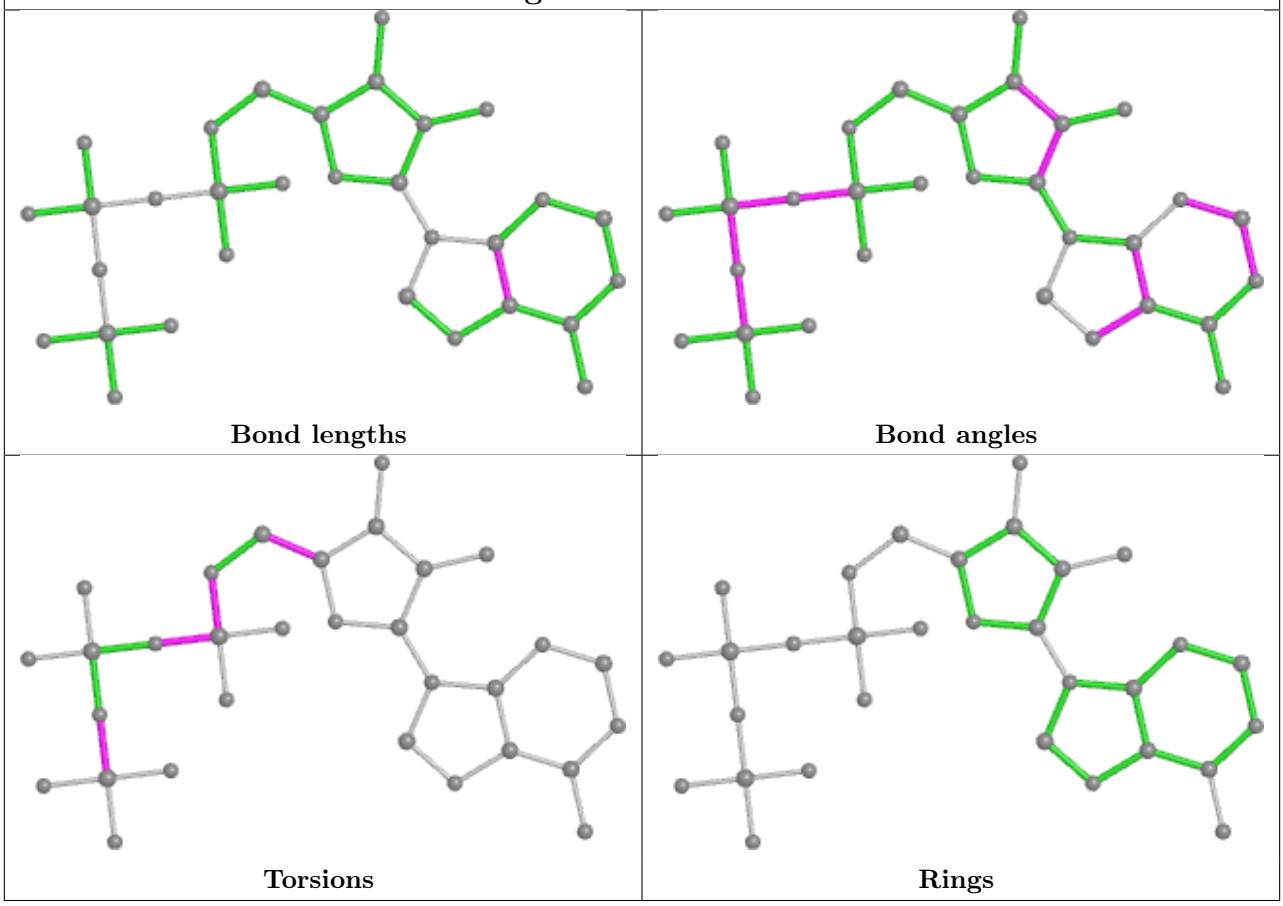
Ligand ATP B 601



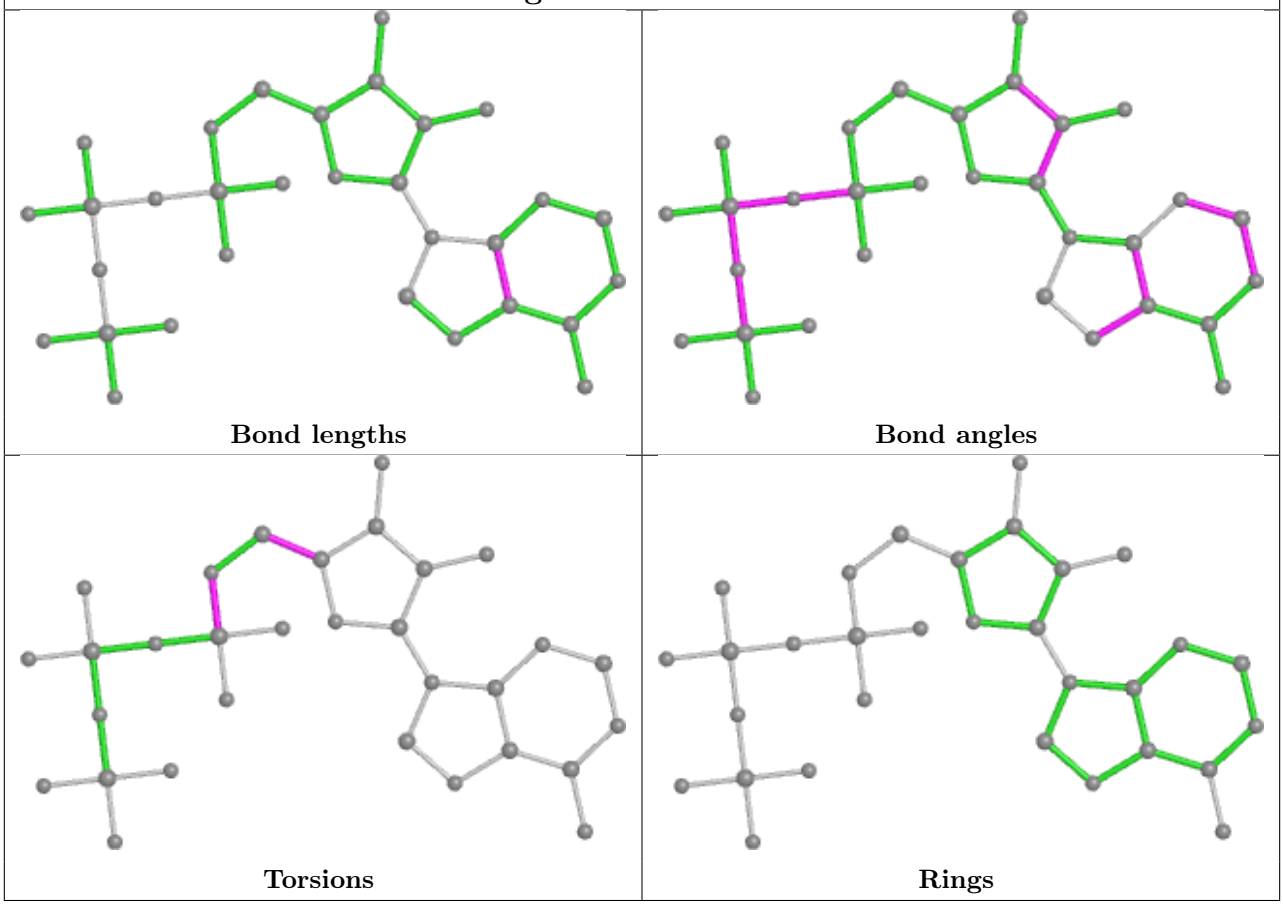
Ligand ATP D 601



Ligand ATP G 601



Ligand ATP H 601



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)

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

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

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

6.3 Carbohydrates (i)

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

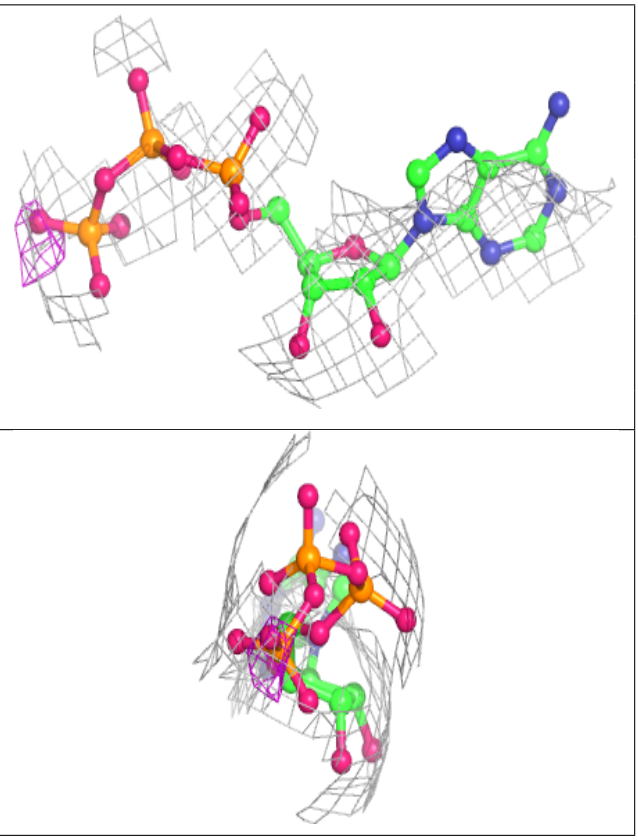
6.4 Ligands (i)

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.

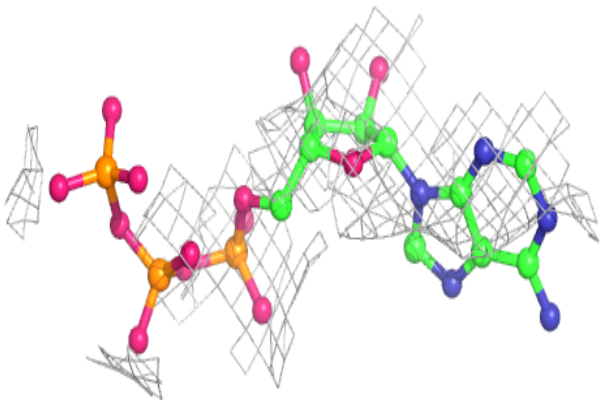
Electron density around ATP A 601:

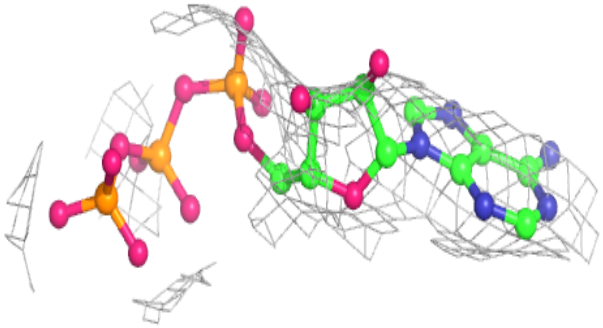
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

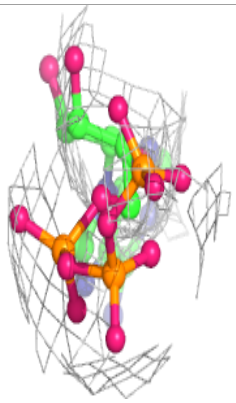


Electron density around ATP B 601:

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

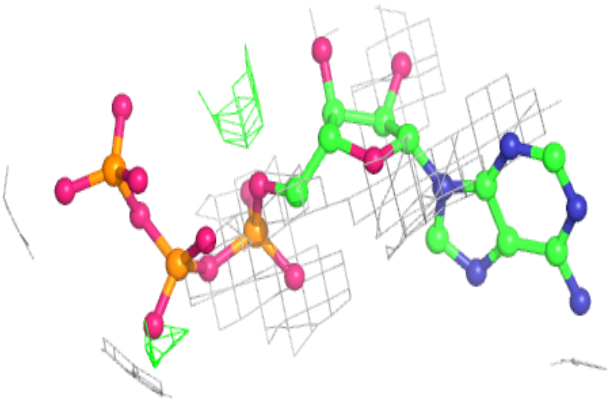


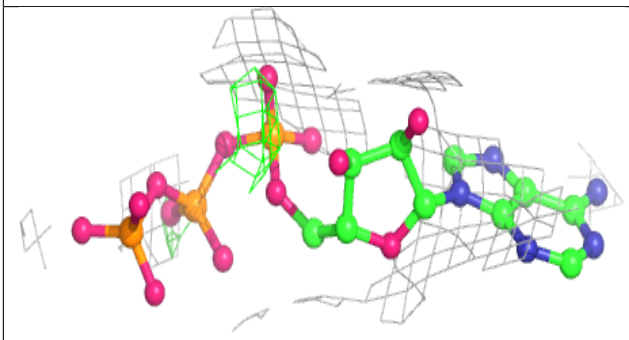


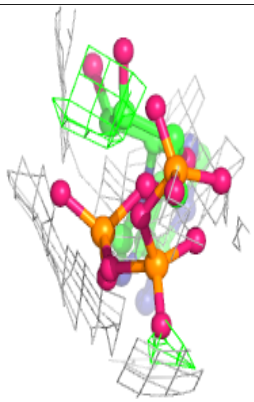


Electron density around ATP C 601:

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

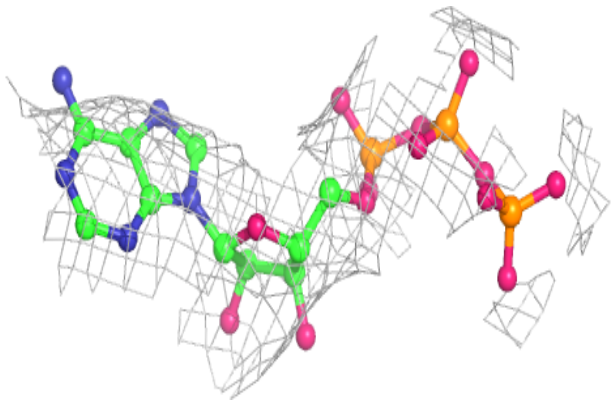


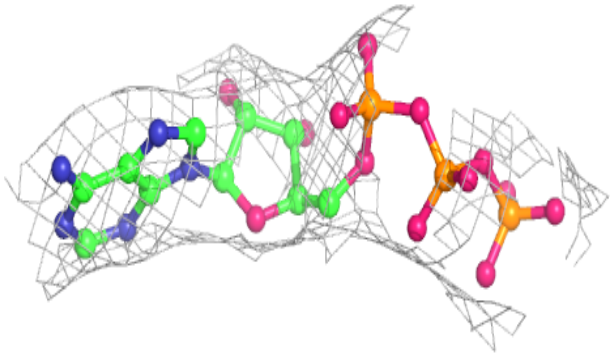


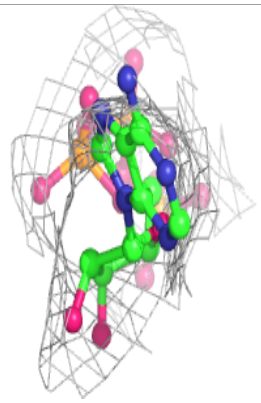


Electron density around ATP D 601:

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

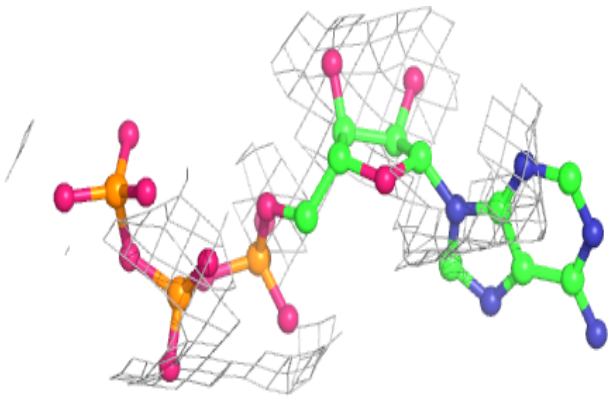


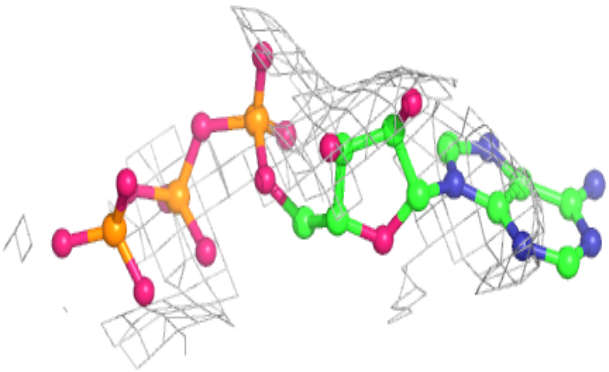


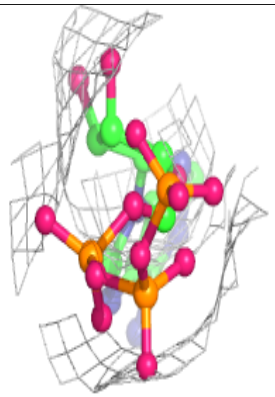


Electron density around ATP E 601:

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

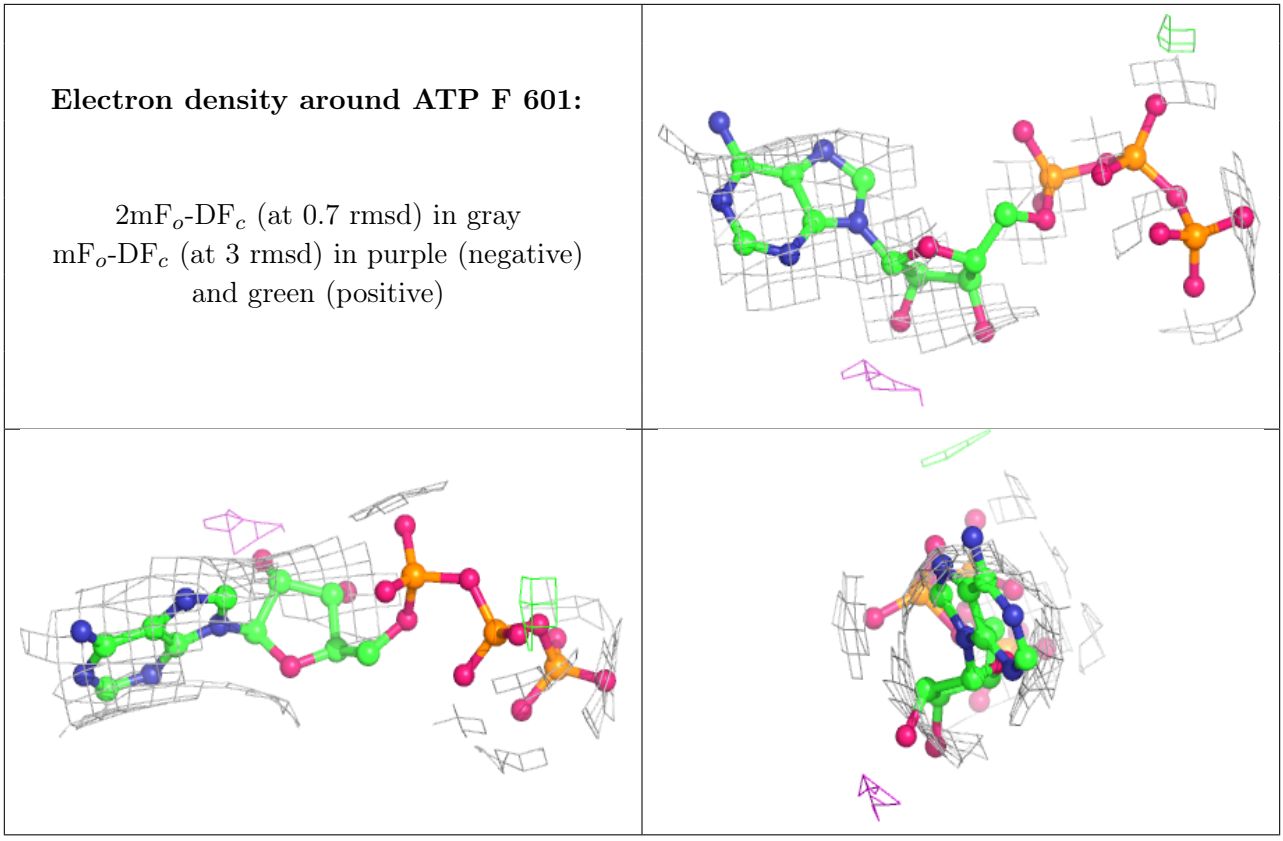






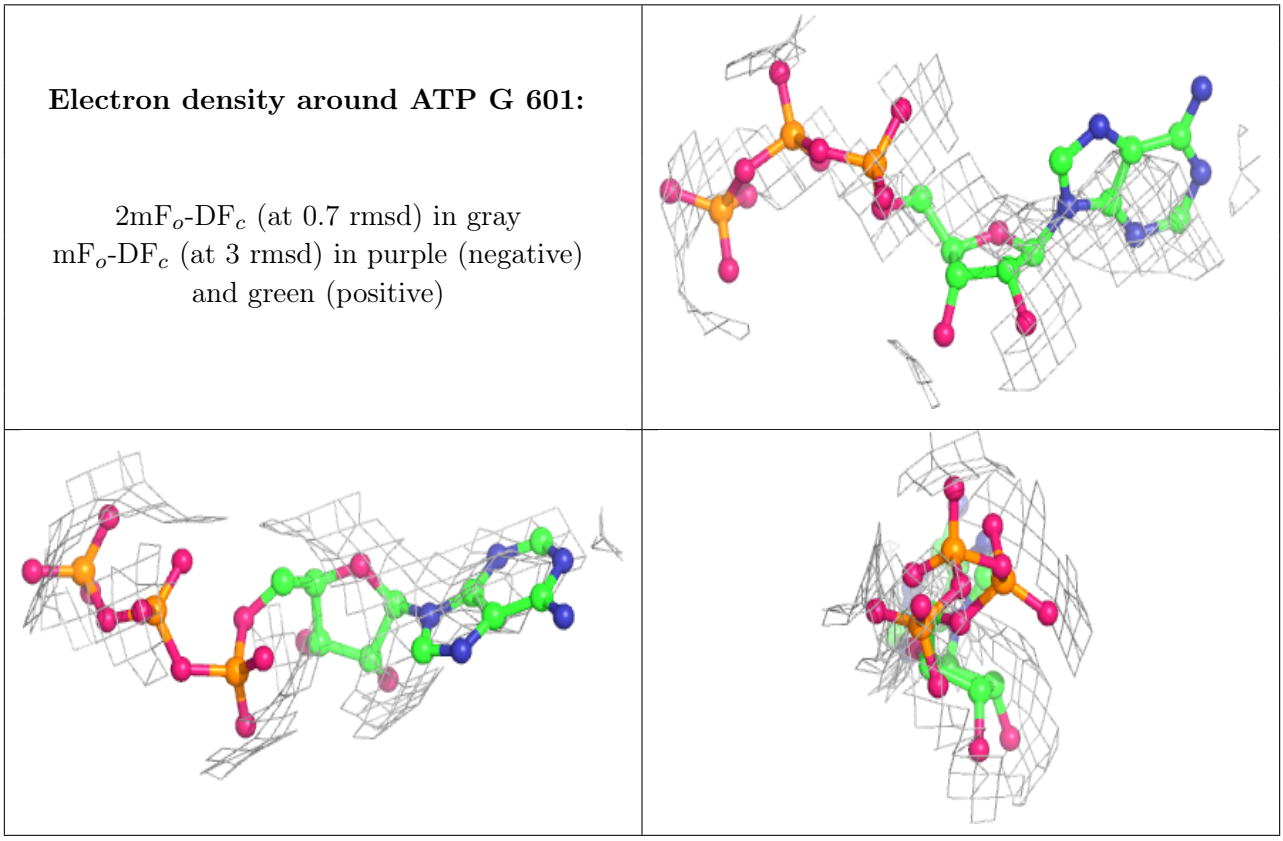
Electron density around ATP F 601:

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



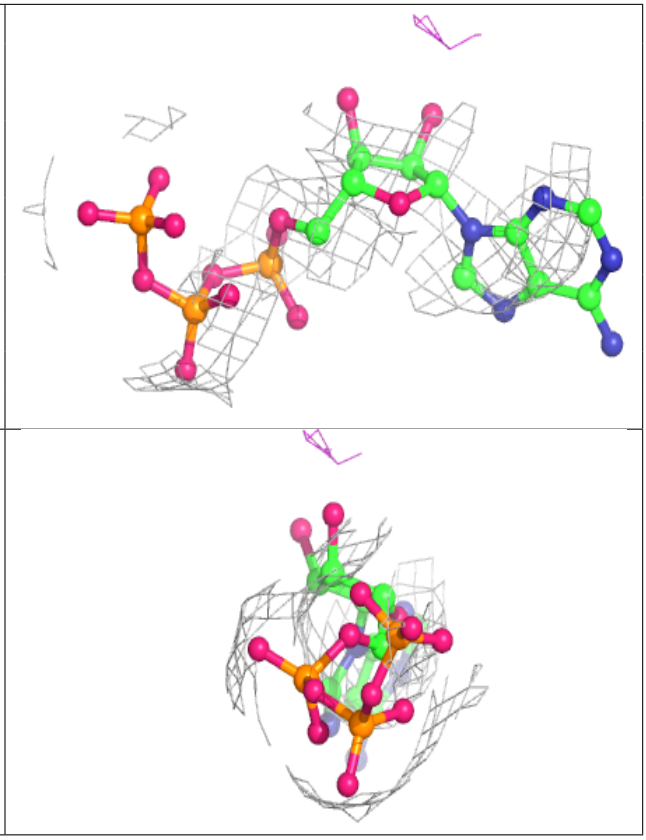
Electron density around ATP G 601:

$2mF_o$-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 H 601:

$2mF_o$-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.