Full wwPDB X-ray Structure Validation Report (i)

Dec 9, 2023 – 08:53 pm GMT

PDB ID	:	2IXE
Title	:	Crystal structure of the ATPase domain of TAP1 with ATP (D645N mutant)
Authors	:	Procko, E.; Ferrin-O'Connell, I.; Ng, S.-L.; Gaudet, R.
Deposited on	:	2006-07-07
Resolution	:	2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

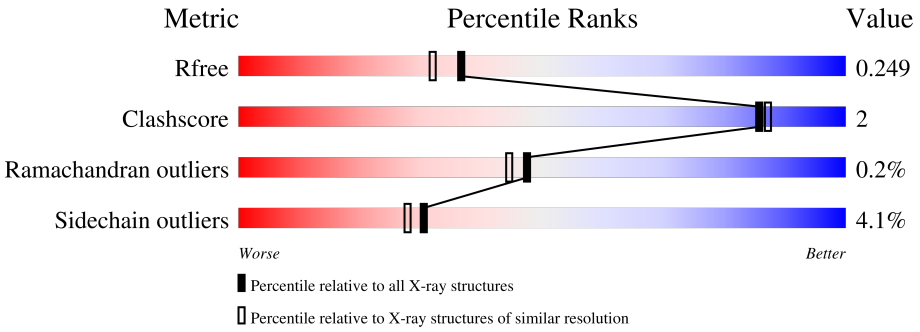
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	271	85% 7% 7%
1	D	271	83% 8% 8%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4203 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.

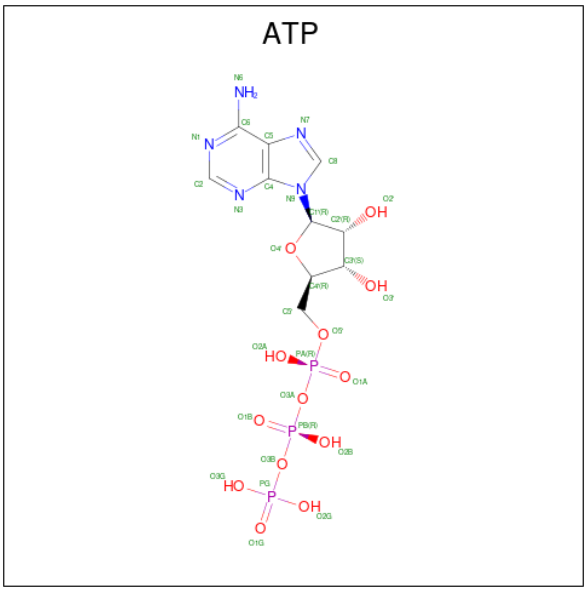
- Molecule 1 is a protein called ANTIGEN PEPTIDE TRANSPORTER 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	251	1902	1203	336	356	7	0	2	0
1	D	248	1900	1205	337	351	7	0	5	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	464	MET	-	expression tag	UNP P36370
A	726	ALA	-	expression tag	UNP P36370
A	727	ALA	-	expression tag	UNP P36370
A	728	ALA	-	expression tag	UNP P36370
A	729	HIS	-	expression tag	UNP P36370
A	730	HIS	-	expression tag	UNP P36370
A	731	HIS	-	expression tag	UNP P36370
A	732	HIS	-	expression tag	UNP P36370
A	733	HIS	-	expression tag	UNP P36370
A	734	HIS	-	expression tag	UNP P36370
A	645	ASN	ASP	engineered mutation	UNP P36370
D	464	MET	-	expression tag	UNP P36370
D	726	ALA	-	expression tag	UNP P36370
D	727	ALA	-	expression tag	UNP P36370
D	728	ALA	-	expression tag	UNP P36370
D	729	HIS	-	expression tag	UNP P36370
D	730	HIS	-	expression tag	UNP P36370
D	731	HIS	-	expression tag	UNP P36370
D	732	HIS	-	expression tag	UNP P36370
D	733	HIS	-	expression tag	UNP P36370
D	734	HIS	-	expression tag	UNP P36370
D	645	ASN	ASP	engineered mutation	UNP P36370

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

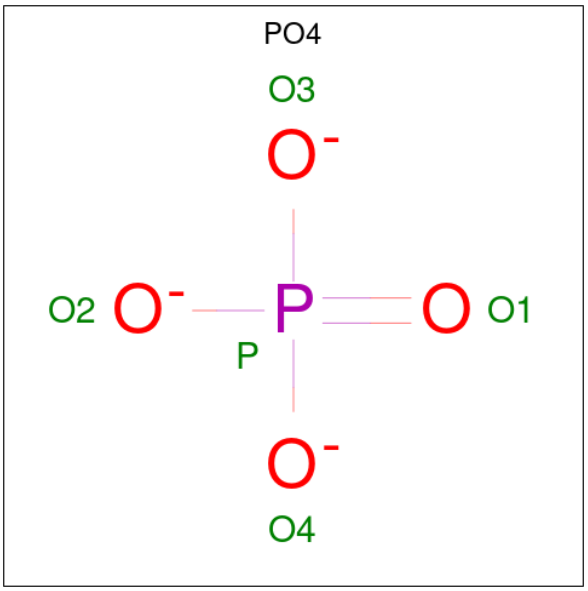


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	31	10	5	13	3	0	0
			Total	C	N	O	P		
2	D	1	31	10	5	13	3	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	1	1	1	0	0
			Total	Mg		
3	D	1	1	1	0	0

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 5 4 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	159	Total O 159 159	0	0
5	D	173	Total O 173 173	0	0

3 Residue-property plots (i)

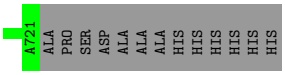
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: ANTIGEN PEPTIDE TRANSPORTER 1

Chain A:

• Molecule 1: ANTIGEN PEPTIDE TRANSPORTER 1

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	80.43Å 80.43Å 168.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.55 – 2.00 37.25 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (72.55-2.00) 99.7 (37.25-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.69 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.199 , 0.241 0.204 , 0.249	Depositor DCC
R_{free} test set	2705 reflections (7.12%)	wwPDB-VP
Wilson B-factor (Å^2)	32.8	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4203	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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: PO4, ATP, MG

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	0.35	0/1946	0.54	0/2648
1	D	0.35	0/1951	0.54	0/2648
All	All	0.35	0/3897	0.54	0/5296

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	1902	0	1875	10	0
1	D	1900	0	1906	7	0
2	A	31	0	12	0	0
2	D	31	0	12	0	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
4	A	5	0	0	0	0
5	A	159	0	0	2	0
5	D	173	0	0	1	0
All	All	4203	0	3805	17	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 2.

All (17) 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:D:478:GLY:O	1:D:672:THR:HG21	1.86	0.76
1:A:570:ARG:HD3	1:A:574:GLU:OE1	1.91	0.71
1:A:618[A]:ASN:HA	1:A:625[A]:ARG:HH21	1.56	0.69
1:A:529:GLN:HB2	1:A:531:LEU:HD13	1.84	0.60
1:D:680:LEU:HD21	1:D:716:MET:HG2	1.86	0.57
1:A:478:GLY:O	1:A:672:THR:HG21	2.07	0.54
1:A:679:GLN:OE1	5:A:2141:HOH:O	2.20	0.48
1:A:567:LEU:O	1:A:616:THR:HA	2.13	0.48
1:A:632:ARG:HD2	5:A:2109:HOH:O	2.14	0.47
1:D:559:ALA:HB3	1:D:638:PRO:HG3	1.98	0.46
1:A:529:GLN:CB	1:A:531:LEU:HD13	2.47	0.45
1:D:480:VAL:HG11	1:D:528:LEU:HD21	1.98	0.44
1:D:645:ASN:ND2	5:D:2112:HOH:O	2.50	0.44
1:D:533:GLN:NE2	1:D:547:VAL:CG1	2.81	0.43
1:D:590:THR:HG23	1:D:599:HIS:CD2	2.56	0.41
1:A:528:LEU:CD1	1:A:674:LEU:HD22	2.52	0.40
1:A:566:LEU:O	1:A:632:ARG:NH2	2.48	0.40

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	251/271 (93%)	248 (99%)	2 (1%)	1 (0%)	34 30
1	D	247/271 (91%)	246 (100%)	1 (0%)	0	100 100
All	All	498/542 (92%)	494 (99%)	3 (1%)	1 (0%)	47 44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	615	GLU

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	198/219 (90%)	192 (97%)	6 (3%)	41	41
1	D	201/219 (92%)	190 (94%)	11 (6%)	21	17
All	All	399/438 (91%)	382 (96%)	17 (4%)	30	26

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	509	LYS
1	A	573	ARG
1	A	581	THR
1	A	640	LEU
1	A	672	THR
1	A	680	LEU
1	D	471	LEU
1	D	474	LEU
1	D	501	LEU
1	D	535[A]	THR
1	D	535[B]	THR
1	D	588	GLU
1	D	607	GLN
1	D	639	ARG
1	D	672	THR
1	D	709	ARG
1	D	718	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	557	GLN

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Mol	Chain	Res	Type
1	A	619	GLN
1	D	494	ASN
1	D	533	GLN
1	D	599	HIS
1	D	607	GLN
1	D	619	GLN
1	D	679	GLN
1	D	700	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
2	ATP	A	1	3	26,33,33	0.91	1 (3%)	31,52,52	1.34	4 (12%)
2	ATP	D	1	3	26,33,33	0.92	1 (3%)	31,52,52	1.35	4 (12%)
4	PO4	A	3	-	4,4,4	0.90	0	6,6,6	0.38	0

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	A	1	3	-	1/18/38/38	0/3/3/3
2	ATP	D	1	3	-	2/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	ATP	C5-C4	2.36	1.47	1.40
2	D	1	ATP	C5-C4	2.29	1.47	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1	ATP	N3-C2-N1	-3.71	122.88	128.68
2	A	1	ATP	N3-C2-N1	-3.61	123.03	128.68
2	A	1	ATP	C4-C5-N7	-2.81	106.47	109.40
2	D	1	ATP	PA-O3A-PB	-2.34	124.79	132.83
2	D	1	ATP	C4-C5-N7	-2.30	107.00	109.40
2	A	1	ATP	PA-O3A-PB	-2.14	125.48	132.83
2	A	1	ATP	O3G-PG-O2G	2.08	115.61	107.64
2	D	1	ATP	C3'-C2'-C1'	2.04	104.05	100.98

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	ATP	PA-O3A-PB-O2B
2	A	1	ATP	PA-O3A-PB-O2B
2	D	1	ATP	PA-O3A-PB-O1B

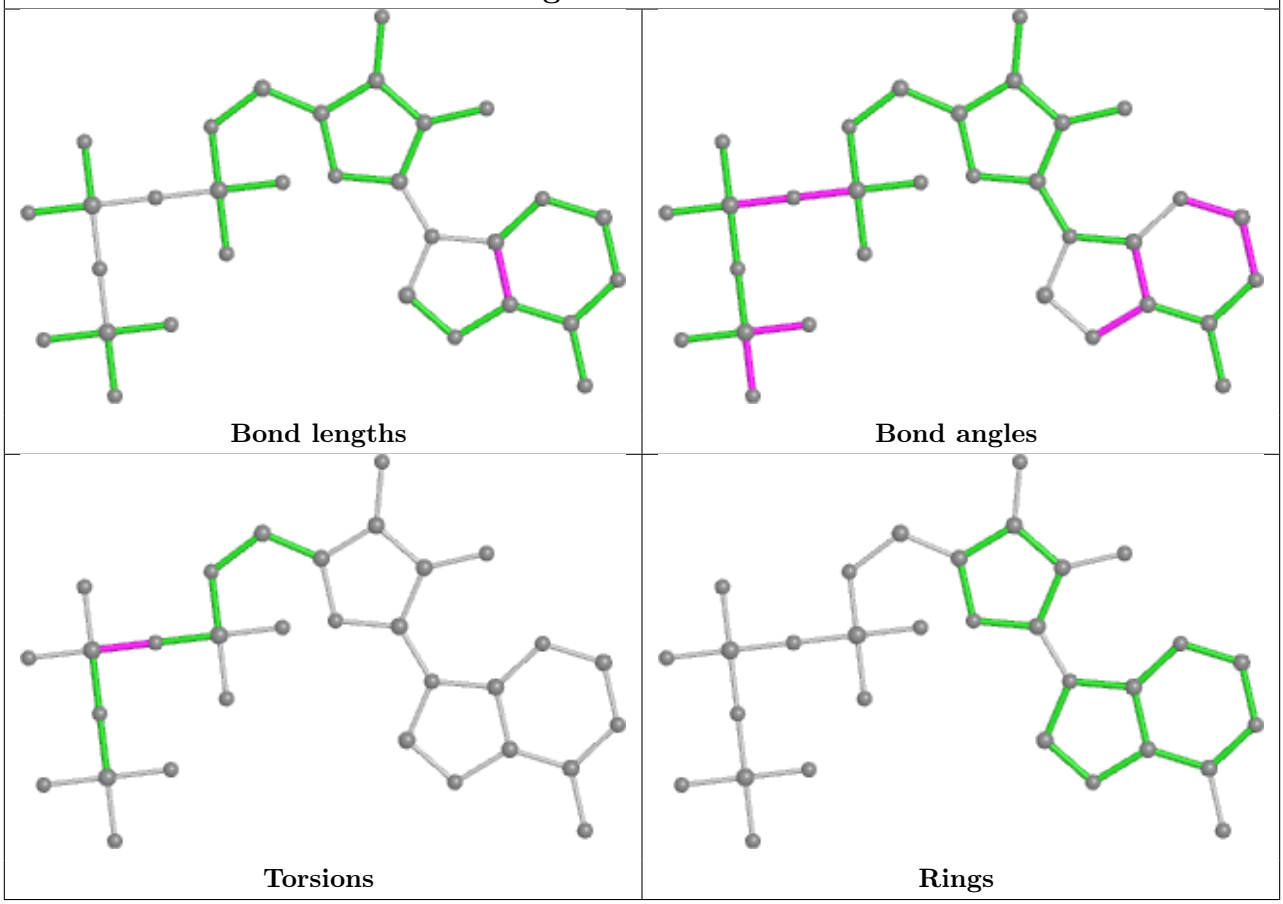
There are no ring outliers.

No monomer is involved in short contacts.

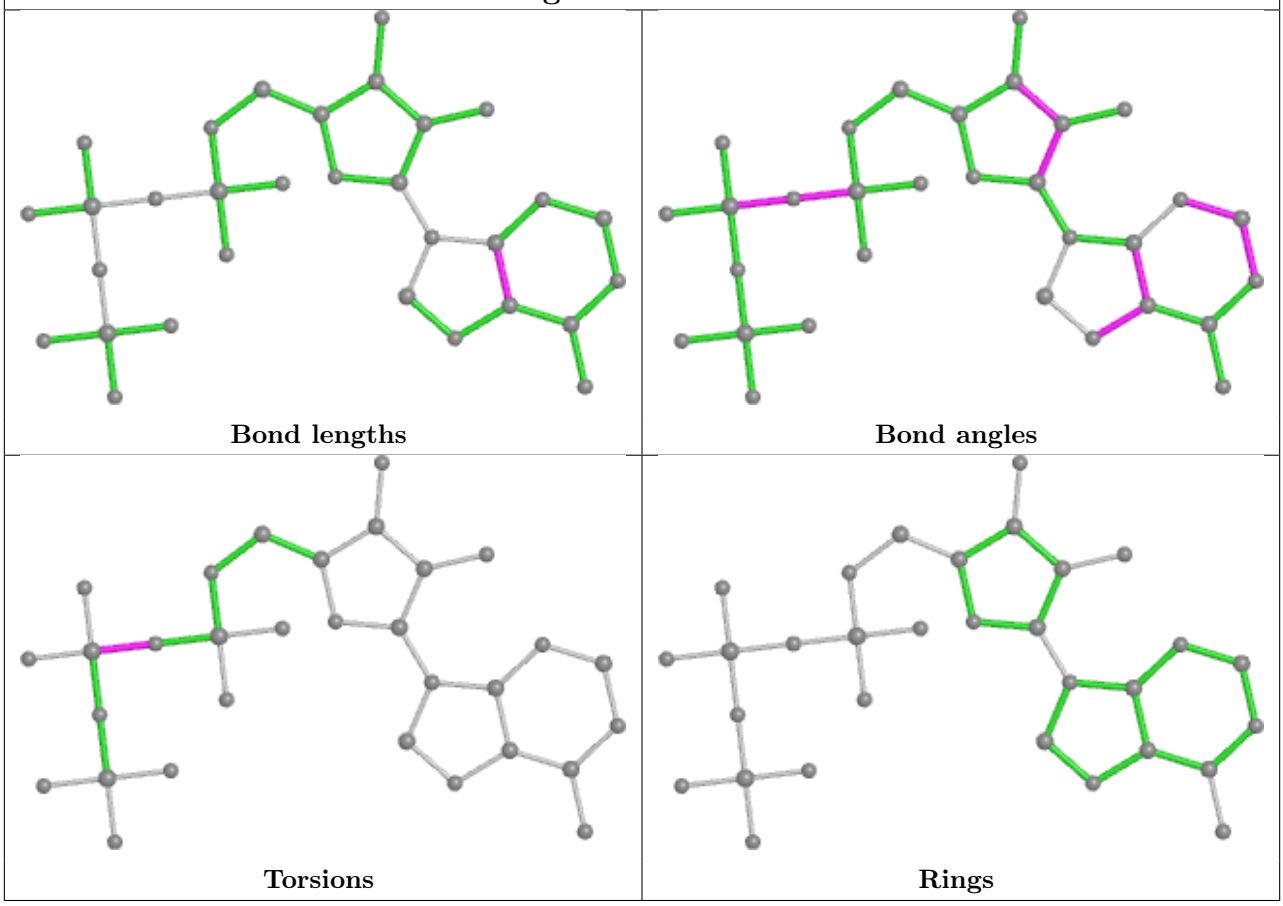
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 A 1



Ligand ATP D 1



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.

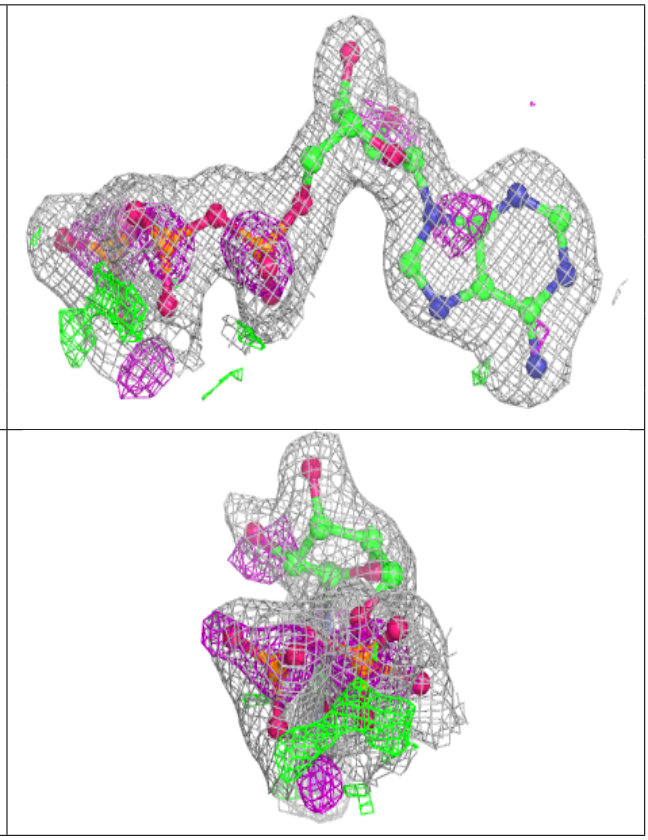
6.4 Ligands (i)

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.

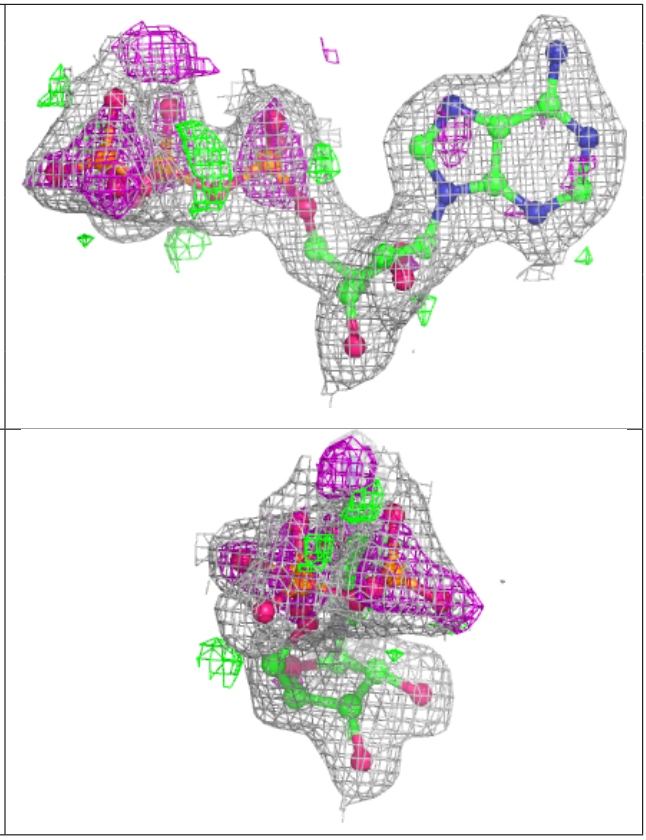
Electron density around ATP A 1:

$2mF_o$-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 1:

$2mF_o$-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.