



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 8, 2024 – 10:54 AM EST

PDB ID : 2HIX
Title : ATP dependent DNA ligase from *S. solfataricus* bound to ATP
Authors : Pascal, J.M.; Ellenberger, T.
Deposited on : 2006-06-29
Resolution : 2.87 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 ⓘ 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 : 4.02b-467
Mogul : 1.8.5 (274361), 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

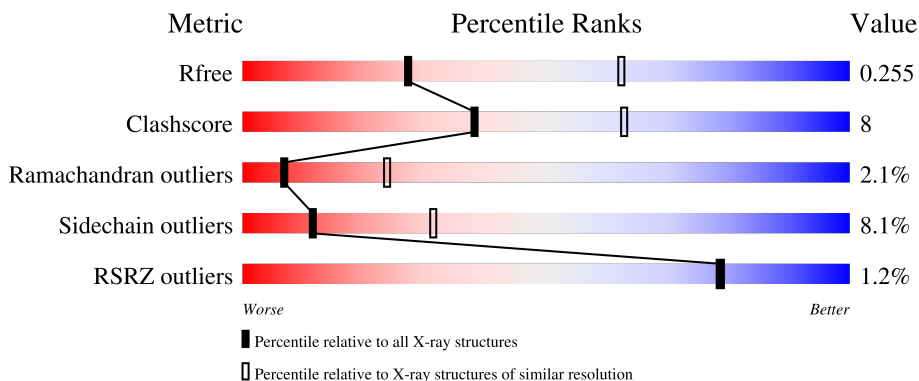
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.87 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	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)

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	621	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4606 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 Thermostable DNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	577	4571	2926	764	866	15	0	1	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	cloning artifact	UNP Q980T8
A	-18	GLY	-	cloning artifact	UNP Q980T8
A	-17	SER	-	cloning artifact	UNP Q980T8
A	-16	SER	-	cloning artifact	UNP Q980T8
A	-15	HIS	-	expression tag	UNP Q980T8
A	-14	HIS	-	expression tag	UNP Q980T8
A	-13	HIS	-	expression tag	UNP Q980T8
A	-12	HIS	-	expression tag	UNP Q980T8
A	-11	HIS	-	expression tag	UNP Q980T8
A	-10	HIS	-	expression tag	UNP Q980T8
A	-9	SER	-	cloning artifact	UNP Q980T8
A	-8	SER	-	cloning artifact	UNP Q980T8
A	-7	GLY	-	cloning artifact	UNP Q980T8
A	-6	LEU	-	cloning artifact	UNP Q980T8
A	-5	VAL	-	cloning artifact	UNP Q980T8
A	-4	PRO	-	cloning artifact	UNP Q980T8
A	-3	ARG	-	cloning artifact	UNP Q980T8
A	-2	GLY	-	cloning artifact	UNP Q980T8
A	-1	SER	-	cloning artifact	UNP Q980T8
A	0	HIS	-	cloning artifact	UNP Q980T8

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

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	119.32Å 171.65Å 78.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.87 47.54 – 2.86	Depositor EDS
% Data completeness (in resolution range)	95.0 (20.00-2.87) 94.6 (47.54-2.86)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 2.86Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.217 , 0.279 0.204 , 0.255	Depositor DCC
R_{free} test set	921 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	68.7	Xtrriage
Anisotropy	0.389	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 57.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4606	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.63% 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: 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	0.58	4/4653 (0.1%)	0.64	4/6271 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	586	LYS	CD-CE	15.91	1.91	1.51
1	A	586	LYS	CE-NZ	7.41	1.67	1.49
1	A	589	LYS	CD-CE	7.35	1.69	1.51
1	A	462	GLY	C-O	6.82	1.34	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	586	LYS	CG-CD-CE	-6.45	92.56	111.90
1	A	352	LEU	CA-CB-CG	6.39	130.00	115.30
1	A	589	LYS	CD-CE-NZ	-5.42	99.23	111.70
1	A	586	LYS	CD-CE-NZ	-5.08	100.01	111.70

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	4571	0	4644	70	0
2	A	31	0	12	4	0
3	A	4	0	0	0	0
All	All	4606	0	4656	70	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 8.

All (70) 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:586:LYS:NZ	1:A:586:LYS:CE	1.67	1.54
1:A:586:LYS:CE	1:A:586:LYS:CD	1.91	1.49
1:A:586:LYS:CE	1:A:586:LYS:CG	2.60	0.80
1:A:332:ARG:HG3	1:A:332:ARG:HH11	1.46	0.79
1:A:242:SER:HB3	1:A:437:ASP:OD2	1.83	0.79
1:A:171:ARG:HD2	1:A:171:ARG:H	1.50	0.74
1:A:96:ARG:HB2	1:A:160:LYS:HB2	1.70	0.74
1:A:436:ARG:O	1:A:439:GLN:HG2	1.88	0.74
1:A:196:ILE:HD12	1:A:219:ILE:HD12	1.73	0.70
1:A:183:MET:HE1	1:A:207:LEU:HD22	1.76	0.68
1:A:332:ARG:HH11	1:A:332:ARG:CG	2.07	0.66
1:A:454:PHE:HB2	1:A:466:SER:HB3	1.81	0.63
1:A:71:SER:HB2	1:A:76:THR:O	1.98	0.63
1:A:536:ILE:H	1:A:587:GLN:HE22	1.48	0.61
1:A:332:ARG:HG3	1:A:332:ARG:NH1	2.10	0.60
1:A:440:SER:O	1:A:441:GLU:HG2	2.01	0.60
1:A:204:ARG:HG2	1:A:231:ILE:HG21	1.84	0.60
1:A:433:LYS:NZ	2:A:602:ATP:O3A	2.35	0.59
1:A:317:GLU:O	1:A:319:GLY:N	2.37	0.57
1:A:335:ASP:HB3	1:A:338:GLU:HB2	1.87	0.56
1:A:260:LYS:HE2	2:A:602:ATP:H5'2	1.87	0.56
1:A:325:GLN:NE2	1:A:328:MET:SD	2.79	0.55
1:A:179:VAL:HB	1:A:207:LEU:HD11	1.87	0.55
1:A:269:HIS:HB2	1:A:276:PHE:HB2	1.89	0.55
1:A:448:LEU:HD12	1:A:531:ILE:HG13	1.89	0.55
1:A:183:MET:HE1	1:A:207:LEU:CD2	2.36	0.54
1:A:171:ARG:O	1:A:173:GLY:N	2.41	0.54
1:A:269:HIS:CD2	1:A:306:ILE:HG23	2.43	0.54
1:A:130:LYS:O	1:A:134:THR:HG22	2.08	0.53
1:A:341:LYS:HG3	1:A:342:GLU:N	2.22	0.53
1:A:296:VAL:HA	1:A:300:ILE:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:LEU:HD21	1:A:166:VAL:HG21	1.93	0.50
1:A:586:LYS:NZ	1:A:586:LYS:CD	2.74	0.50
1:A:280:ARG:NH1	2:A:602:ATP:O1G	2.40	0.49
1:A:181:ASP:O	1:A:185:ILE:HD13	2.12	0.49
1:A:180:LEU:HD22	1:A:197:ILE:HG22	1.94	0.48
1:A:314:ILE:HD13	1:A:346:ASN:HB2	1.95	0.48
1:A:180:LEU:HD23	1:A:207:LEU:HD21	1.95	0.48
1:A:180:LEU:HA	1:A:183:MET:HE2	1.96	0.48
1:A:238:ALA:CB	1:A:412:MET:HE1	2.43	0.48
1:A:41:VAL:O	1:A:45:ILE:HG12	2.14	0.47
1:A:162:LEU:O	1:A:166:VAL:HG23	2.14	0.47
1:A:4:LYS:O	1:A:8:GLU:HG2	2.15	0.46
1:A:270:LYS:O	1:A:304:GLU:HA	2.15	0.46
1:A:385:ALA:O	1:A:387:HIS:HD2	1.97	0.46
1:A:251:MET:CE	1:A:415:ALA:HB2	2.45	0.45
1:A:13:LEU:HD21	1:A:172:VAL:HG13	1.99	0.45
1:A:258:ASP:OD2	1:A:369:ARG:NH2	2.50	0.45
1:A:437:ASP:C	1:A:439:GLN:N	2.70	0.45
1:A:576:THR:O	1:A:580:ILE:HG12	2.17	0.45
1:A:99:LYS:NZ	1:A:151:LEU:O	2.45	0.44
1:A:269:HIS:NE2	1:A:306:ILE:HG23	2.32	0.44
1:A:180:LEU:HA	1:A:183:MET:CE	2.48	0.44
1:A:427:ARG:HH22	2:A:602:ATP:PG	2.41	0.44
1:A:207:LEU:HD23	1:A:207:LEU:HA	1.87	0.44
1:A:170:LEU:HD23	1:A:170:LEU:HA	1.74	0.43
1:A:133:LEU:HD23	1:A:133:LEU:HA	1.91	0.43
1:A:180:LEU:CD2	1:A:207:LEU:HD21	2.49	0.43
1:A:304:GLU:O	1:A:304:GLU:HG3	2.19	0.42
1:A:373:GLU:HG2	1:A:384:ILE:HG13	2.01	0.42
1:A:168:GLY:O	1:A:170:LEU:N	2.51	0.42
1:A:485:VAL:HG21	1:A:531:ILE:HD12	2.02	0.42
1:A:325:GLN:HE22	1:A:328:MET:CE	2.32	0.42
1:A:204:ARG:CG	1:A:231:ILE:HG21	2.49	0.42
1:A:251:MET:HE2	1:A:415:ALA:HB2	2.01	0.41
1:A:59:LEU:HD22	1:A:166:VAL:HG13	2.03	0.41
1:A:251:MET:HE2	1:A:251:MET:HA	2.02	0.41
1:A:254:ASN:HD22	1:A:254:ASN:HA	1.65	0.41
1:A:50:TRP:HB2	1:A:54:LEU:HD12	2.01	0.41
1:A:479:PHE:N	1:A:512:ARG:O	2.46	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	574/621 (92%)	535 (93%)	27 (5%)	12 (2%)	7 24

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	171	ARG
1	A	317	GLU
1	A	318	SER
1	A	437	ASP
1	A	172	VAL
1	A	438	TYR
1	A	137	GLU
1	A	169	ARG
1	A	436	ARG
1	A	272	GLU
1	A	316	PRO
1	A	156	PRO

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	492/536 (92%)	452 (92%)	40 (8%)	11 31

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	18	SER
1	A	22	LEU
1	A	25	LEU
1	A	50	TRP
1	A	59	LEU
1	A	71	SER
1	A	122	ASP
1	A	129	SER
1	A	135	THR
1	A	137	GLU
1	A	155	ASP
1	A	171	ARG
1	A	185	ILE
1	A	207	LEU
1	A	219	ILE
1	A	225	LEU
1	A	245	GLU
1	A	254	ASN
1	A	272	GLU
1	A	280	ARG
1	A	314	ILE
1	A	328	MET
1	A	332	ARG
1	A	352	LEU
1	A	366	GLU
1	A	371	LEU
1	A	393	VAL
1	A	433	LYS
1	A	434	LEU
1	A	440	SER
1	A	459	LYS
1	A	460	ARG
1	A	482	VAL
1	A	494	LEU
1	A	498	GLN
1	A	513	VAL
1	A	514	ASN
1	A	581	LEU
1	A	589	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	254	ASN
1	A	387	HIS
1	A	391	ASN
1	A	542	HIS
1	A	587	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](#)

1 ligand is 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	A	602	-	26,33,33	0.95	1 (3%)	31,52,52	1.73	8 (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
2	ATP	A	602	-	-	3/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	602	ATP	C5-C4	2.60	1.47	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	602	ATP	PA-O3A-PB	-4.25	118.26	132.83
2	A	602	ATP	N3-C2-N1	-3.73	122.84	128.68
2	A	602	ATP	C4-C5-N7	-3.14	106.13	109.40
2	A	602	ATP	PB-O3B-PG	-2.69	123.59	132.83
2	A	602	ATP	C5-C6-N6	2.59	124.28	120.35
2	A	602	ATP	C2-N1-C6	2.38	122.83	118.75
2	A	602	ATP	C1'-N9-C4	-2.27	122.66	126.64
2	A	602	ATP	C5'-C4'-C3'	-2.13	107.21	115.18

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	602	ATP	O4'-C4'-C5'-O5'
2	A	602	ATP	C3'-C4'-C5'-O5'
2	A	602	ATP	PB-O3B-PG-O1G

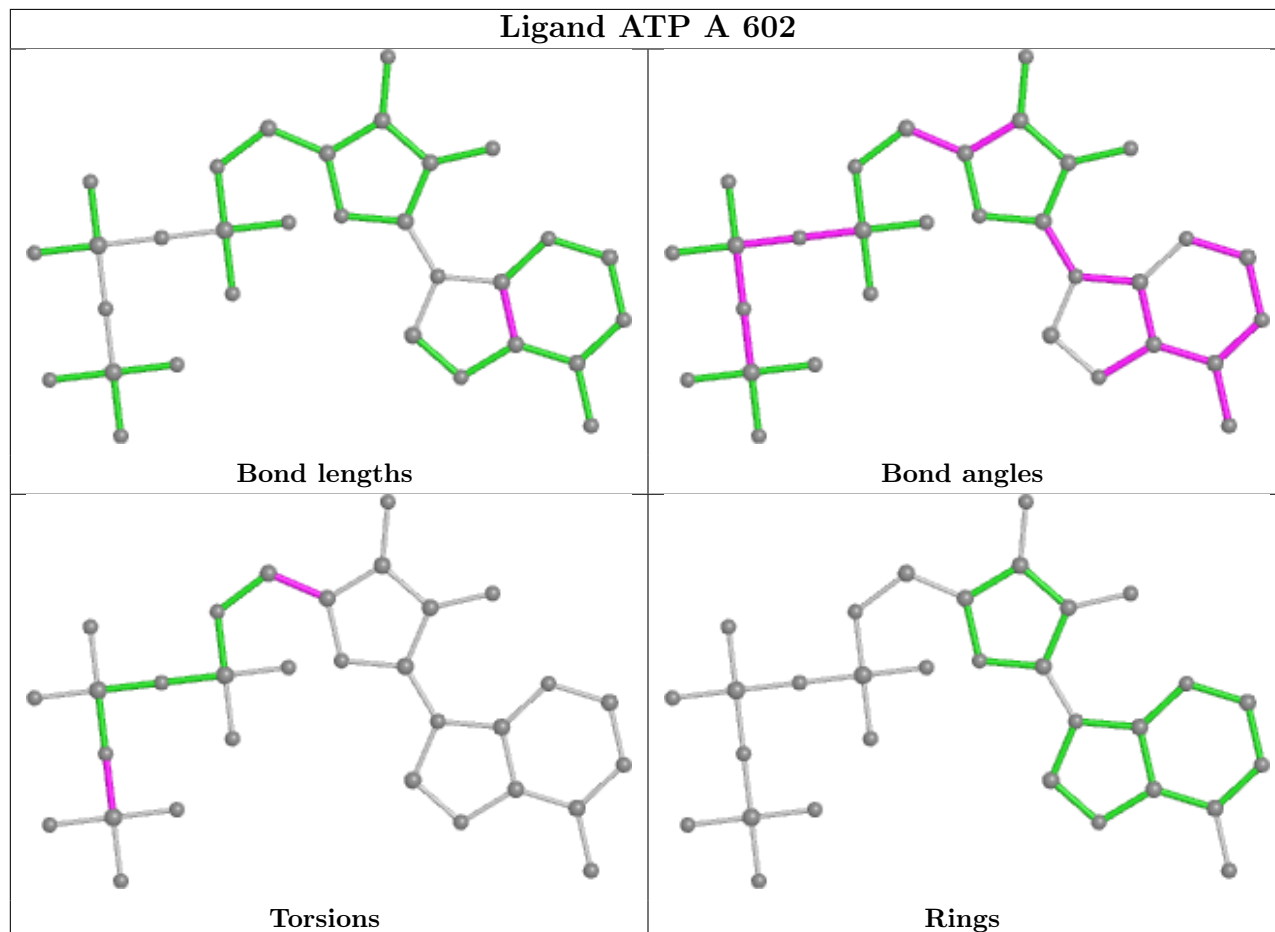
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	602	ATP	4	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.



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	577/621 (92%)	-0.18	7 (1%) 79 78	41, 49, 58, 68	1 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	590	LYS	3.5
1	A	100	SER	3.3
1	A	589	LYS	3.3
1	A	171	ARG	2.8
1	A	459	LYS	2.7
1	A	172	VAL	2.1
1	A	564	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

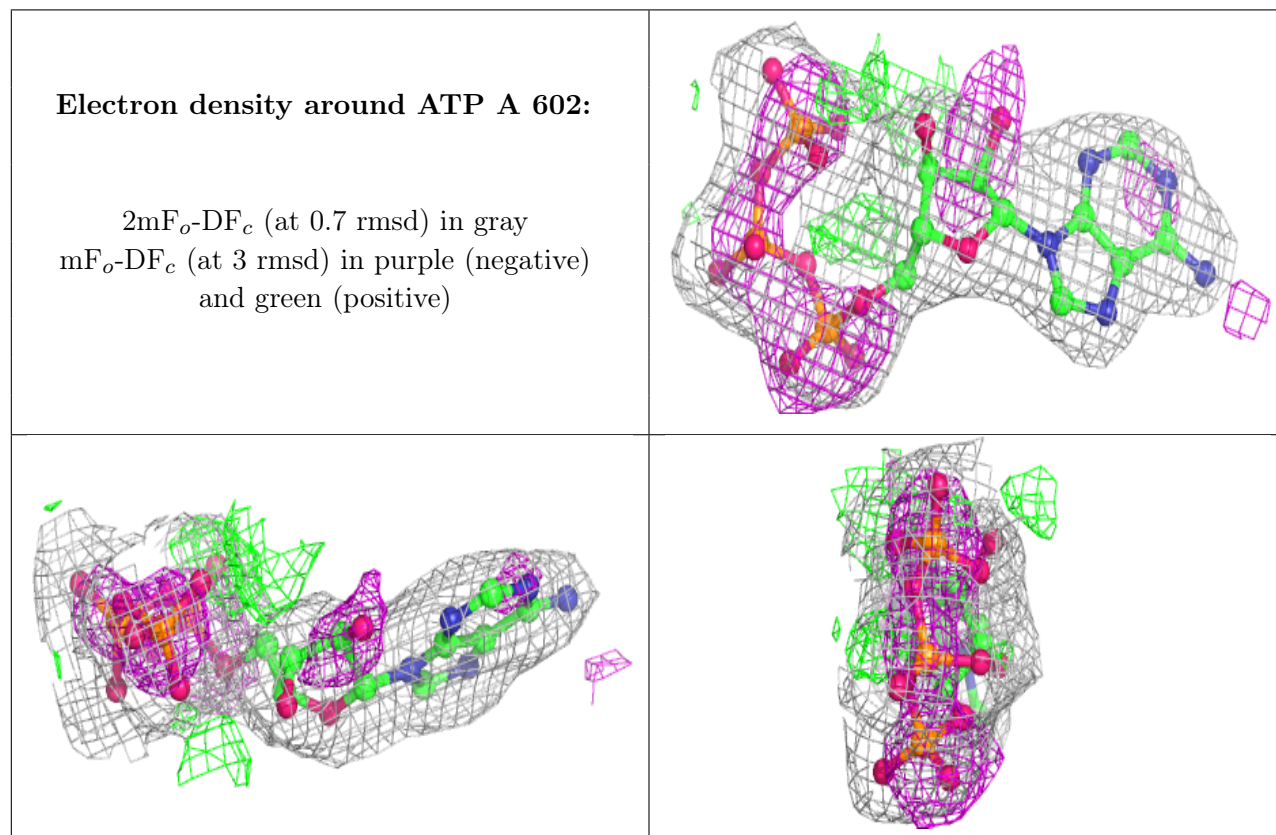
There are no monosaccharides in this entry.

6.4 Ligands [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
2	ATP	A	602	31/31	0.95	0.12	37,45,51,52	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.