Full wwPDB X-ray Structure Validation Report (i)

Aug 21, 2023 – 07:22 PM EDT

PDB ID	:	2Q97
Title	:	Complex of mammalian actin with toxofilin from toxoplasma gondii
Authors	:	Lee, S.H.; Dominguez, R.
Deposited on	:	2007-06-12
Resolution	:	2.50 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 (1)) were used in the production of this report:

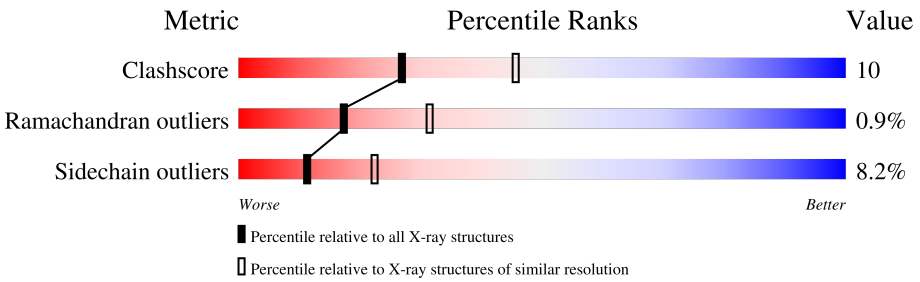
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	375	76% 16% • 6%
2	T	129	55% 23% 6% 16%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3757 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	354	2768	1757	463	530	18	0	0	0

- Molecule 2 is a protein called Toxofilin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	T	109	874	544	162	167	1	0	0	0

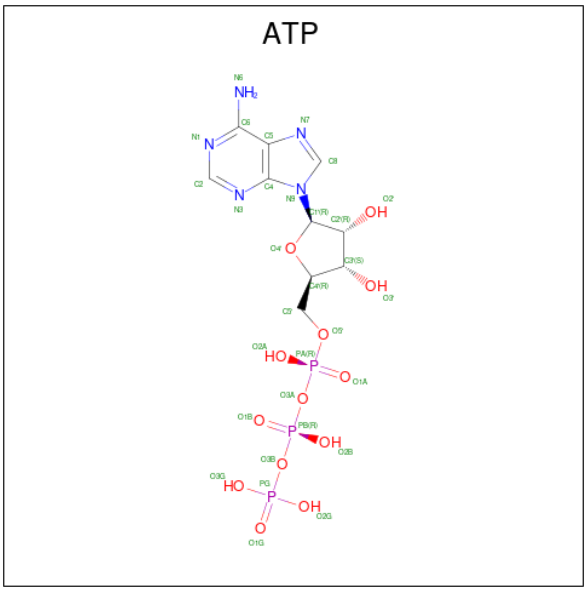
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	68	MET	-	initiating methionine	UNP Q9NG25

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	1	1	1	0	0

- Molecule 4 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		
4	A	1	31	10	5	13	3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	68	68	68	0	0
			Total	O		
5	T	15	15	15	0	0

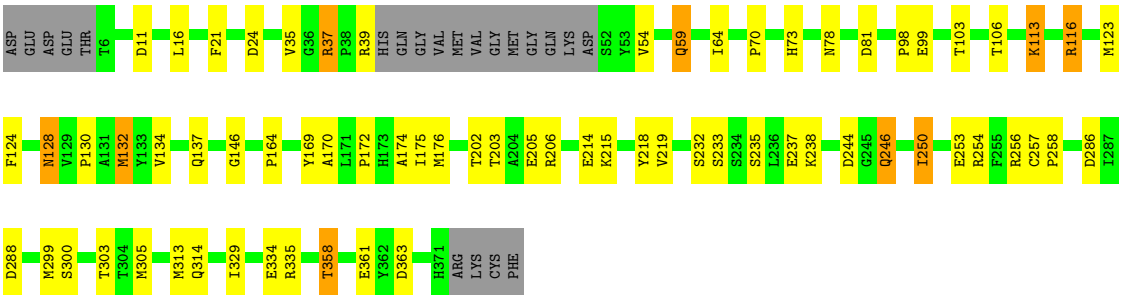
3 Residue-property plots (i)

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.

Note EDS was not executed.

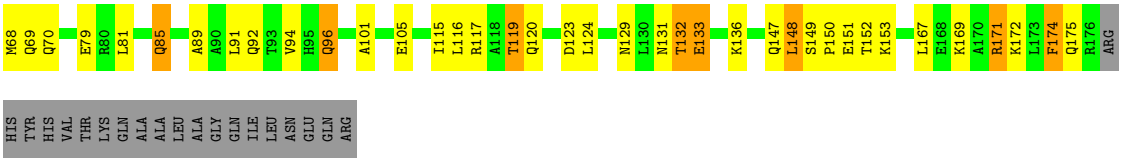
• Molecule 1: Actin, alpha skeletal muscle

Chain A: 76% 16% • 6%



• Molecule 2: Toxofilin

Chain T: 55% 23% 6% 16%



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α, β, γ	54.52Å 54.52Å 363.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50	Depositor
% Data completeness (in resolution range)	99.5 (50.00-2.50)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.229 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3757	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

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: CA, ATP, HIC

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	0.52	0/2815	0.61	0/3816
2	T	0.45	0/880	0.63	0/1182
All	All	0.50	0/3695	0.61	0/4998

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	2768	0	2739	52	0
2	T	874	0	915	25	0
3	A	1	0	0	0	0
4	A	31	0	12	1	0
5	A	68	0	0	5	0
5	T	15	0	0	0	0
All	All	3757	0	3666	75	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 10.

All (75) 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:113:LYS:HD3	1:A:113:LYS:H	1.20	1.06
1:A:113:LYS:HD3	1:A:113:LYS:N	1.81	0.96
2:T:123:ASP:OD2	2:T:124:LEU:N	1.99	0.96
1:A:113:LYS:H	1:A:113:LYS:CD	1.78	0.92
2:T:68:MET:HB3	2:T:70:GLN:HE22	1.46	0.80
1:A:358:THR:HG22	1:A:361:GLU:H	1.47	0.79
1:A:299:MET:CE	1:A:313:MET:HG3	2.15	0.77
2:T:79:GLU:HB3	2:T:81:LEU:HD13	1.68	0.76
2:T:133:GLU:H	2:T:133:GLU:CD	1.88	0.75
1:A:146:GLY:HA2	2:T:119:THR:HG21	1.68	0.74
1:A:305:MET:HE2	5:A:1018:HOH:O	1.91	0.71
2:T:171:ARG:HA	2:T:174:PHE:HB2	1.76	0.68
1:A:257:CYS:HB3	1:A:258:PRO:HD3	1.77	0.66
2:T:85:GLN:HE21	2:T:85:GLN:HA	1.62	0.64
1:A:78:ASN:HD22	1:A:81:ASP:HB2	1.63	0.64
1:A:299:MET:HE2	1:A:313:MET:HG3	1.80	0.63
1:A:244:ASP:HB2	1:A:246:GLN:HB3	1.80	0.62
1:A:286:ASP:HB2	5:A:1033:HOH:O	1.99	0.62
1:A:59:GLN:HA	1:A:59:GLN:HE21	1.64	0.61
1:A:250:ILE:HD13	1:A:254:ARG:HG3	1.83	0.59
1:A:146:GLY:CA	2:T:119:THR:HG21	2.32	0.59
1:A:300:SER:HA	1:A:335:ARG:HB2	1.84	0.58
1:A:11:ASP:OD1	5:A:1003:HOH:O	2.17	0.58
1:A:172:PRO:HA	1:A:175:ILE:HD12	1.89	0.55
2:T:148:LEU:HD22	2:T:152:THR:HG21	1.87	0.55
1:A:170:ALA:O	1:A:172:PRO:HD3	2.06	0.55
2:T:68:MET:HB3	2:T:70:GLN:NE2	2.18	0.55
1:A:358:THR:CG2	1:A:361:GLU:H	2.19	0.55
2:T:133:GLU:CD	2:T:133:GLU:N	2.60	0.54
1:A:37:ARG:NH2	1:A:37:ARG:HB2	2.21	0.54
2:T:132:THR:O	2:T:136:LYS:HG2	2.07	0.54
1:A:219:VAL:HG22	1:A:258:PRO:HB2	1.91	0.53
1:A:21:PHE:O	1:A:24:ASP:HB2	2.09	0.52
1:A:203:THR:HA	1:A:206:ARG:HB2	1.91	0.52
1:A:98:PRO:HD2	1:A:99:GLU:OE2	2.10	0.51
1:A:103:THR:HG21	1:A:123:MET:HE2	1.91	0.51
1:A:169:TYR:HE1	5:A:1064:HOH:O	1.93	0.50
1:A:235:SER:O	1:A:238:LYS:HE3	2.12	0.50
2:T:115:ILE:O	2:T:119:THR:HB	2.10	0.50
2:T:149:SER:O	2:T:151:GLU:N	2.44	0.49
1:A:99:GLU:O	1:A:130:PRO:HD3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:VAL:HG22	1:A:54:VAL:HG22	1.94	0.49
1:A:106:THR:HB	1:A:137:GLN:HG3	1.94	0.49
2:T:92:GLN:CG	2:T:96:GLN:HE22	2.26	0.48
1:A:39:ARG:HB3	1:A:39:ARG:NH1	2.28	0.47
2:T:149:SER:O	2:T:153:LYS:HG2	2.15	0.47
1:A:78:ASN:ND2	1:A:81:ASP:H	2.13	0.47
1:A:164:PRO:HG2	1:A:174:ALA:HB3	1.97	0.46
1:A:214:GLU:HG2	4:A:1001:ATP:C5	2.50	0.46
1:A:70:PRO:HG3	1:A:81:ASP:HB3	1.97	0.46
2:T:85:GLN:HE21	2:T:85:GLN:CA	2.25	0.46
1:A:116:ARG:H	1:A:116:ARG:HG2	1.59	0.45
1:A:303:THR:HG22	1:A:303:THR:O	2.16	0.45
1:A:37:ARG:HB2	1:A:37:ARG:HH21	1.80	0.45
1:A:253:GLU:HA	1:A:256:ARG:HB2	1.99	0.45
1:A:202:THR:HG22	1:A:205:GLU:HG3	1.98	0.45
2:T:85:GLN:HA	2:T:85:GLN:NE2	2.29	0.45
1:A:78:ASN:ND2	1:A:81:ASP:HB2	2.32	0.44
1:A:314:GLN:OE1	1:A:329:ILE:HG12	2.16	0.44
2:T:151:GLU:O	2:T:152:THR:C	2.56	0.44
1:A:250:ILE:CD1	1:A:254:ARG:HG3	2.47	0.44
2:T:117:ARG:O	2:T:120:GLN:HG2	2.17	0.44
1:A:16:LEU:HD11	5:A:1047:HOH:O	2.18	0.43
2:T:117:ARG:C	2:T:119:THR:H	2.22	0.43
1:A:39:ARG:HB3	1:A:39:ARG:HH11	1.83	0.43
2:T:105:GLU:CD	2:T:105:GLU:H	2.22	0.43
1:A:233:SER:C	1:A:235:SER:H	2.22	0.43
1:A:132:MET:HE1	1:A:134:VAL:CG2	2.49	0.43
1:A:286:ASP:OD1	1:A:288:ASP:N	2.31	0.42
2:T:149:SER:C	2:T:151:GLU:H	2.23	0.42
1:A:218:TYR:O	1:A:258:PRO:HG2	2.19	0.42
1:A:215:LYS:HA	1:A:215:LYS:HD3	1.84	0.41
2:T:149:SER:C	2:T:151:GLU:N	2.74	0.41
1:A:124:PHE:O	1:A:128:ASN:HA	2.21	0.40
2:T:89:ALA:HA	2:T:92:GLN:NE2	2.36	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	349/375 (93%)	331 (95%)	18 (5%)	0	100	100
2	T	107/129 (83%)	91 (85%)	12 (11%)	4 (4%)	3	4
All	All	456/504 (90%)	422 (92%)	30 (7%)	4 (1%)	17	31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	T	131	ASN
2	T	101	ALA
2	T	148	LEU
2	T	150	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	299/317 (94%)	284 (95%)	15 (5%)	24	46
2	T	92/108 (85%)	75 (82%)	17 (18%)	1	2
All	All	391/425 (92%)	359 (92%)	32 (8%)	11	22

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	59	GLN

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Mol	Chain	Res	Type
1	A	64	ILE
1	A	113	LYS
1	A	116	ARG
1	A	128	ASN
1	A	132	MET
1	A	176	MET
1	A	232	SER
1	A	237	GLU
1	A	246	GLN
1	A	250	ILE
1	A	334	GLU
1	A	358	THR
1	A	363	ASP
2	T	69	GLN
2	T	85	GLN
2	T	91	LEU
2	T	94	VAL
2	T	96	GLN
2	T	116	LEU
2	T	119	THR
2	T	129	ASN
2	T	132	THR
2	T	133	GLU
2	T	147	GLN
2	T	167	LEU
2	T	169	LYS
2	T	171	ARG
2	T	172	LYS
2	T	174	PHE
2	T	175	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	78	ASN
1	A	92	ASN
1	A	162	ASN
1	A	225	ASN
1	A	246	GLN
1	A	275	HIS
2	T	70	GLN

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Mol	Chain	Res	Type
2	T	85	GLN
2	T	96	GLN
2	T	121	ASN
2	T	129	ASN
2	T	140	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)

1 non-standard protein/DNA/RNA residue 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	$\#\|Z\| > 2$
1	HIC	A	73	1	8,11,12	1.81	2 (25%)	6,14,16	1.44	1 (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
1	HIC	A	73	1	-	1/5/6/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	73	HIC	CD2-NE2	-3.63	1.32	1.38
1	A	73	HIC	CZ-NE2	2.69	1.55	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	73	HIC	CB-CG-CD2	-2.59	122.61	127.95

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	73	HIC	CA-CB-CG-ND1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\#\|Z\| > 2$
4	ATP	A	1001	3	26,33,33	1.02	2 (7%)	31,52,52	1.49	6 (19%)

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
4	ATP	A	1001	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)
4	A	1001	ATP	C2'-C1'	-2.40	1.50	1.53
4	A	1001	ATP	C5-C4	2.01	1.46	1.40

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1001	ATP	N3-C2-N1	-3.46	123.27	128.68
4	A	1001	ATP	O3G-PG-O2G	2.78	118.25	107.64
4	A	1001	ATP	PA-O3A-PB	-2.43	124.48	132.83
4	A	1001	ATP	O2A-PA-O1A	2.38	124.01	112.24
4	A	1001	ATP	C4-C5-N7	-2.29	107.02	109.40
4	A	1001	ATP	C2-N1-C6	2.13	122.39	118.75

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	ATP	PB-O3B-PG-O2G
4	A	1001	ATP	PB-O3B-PG-O1G

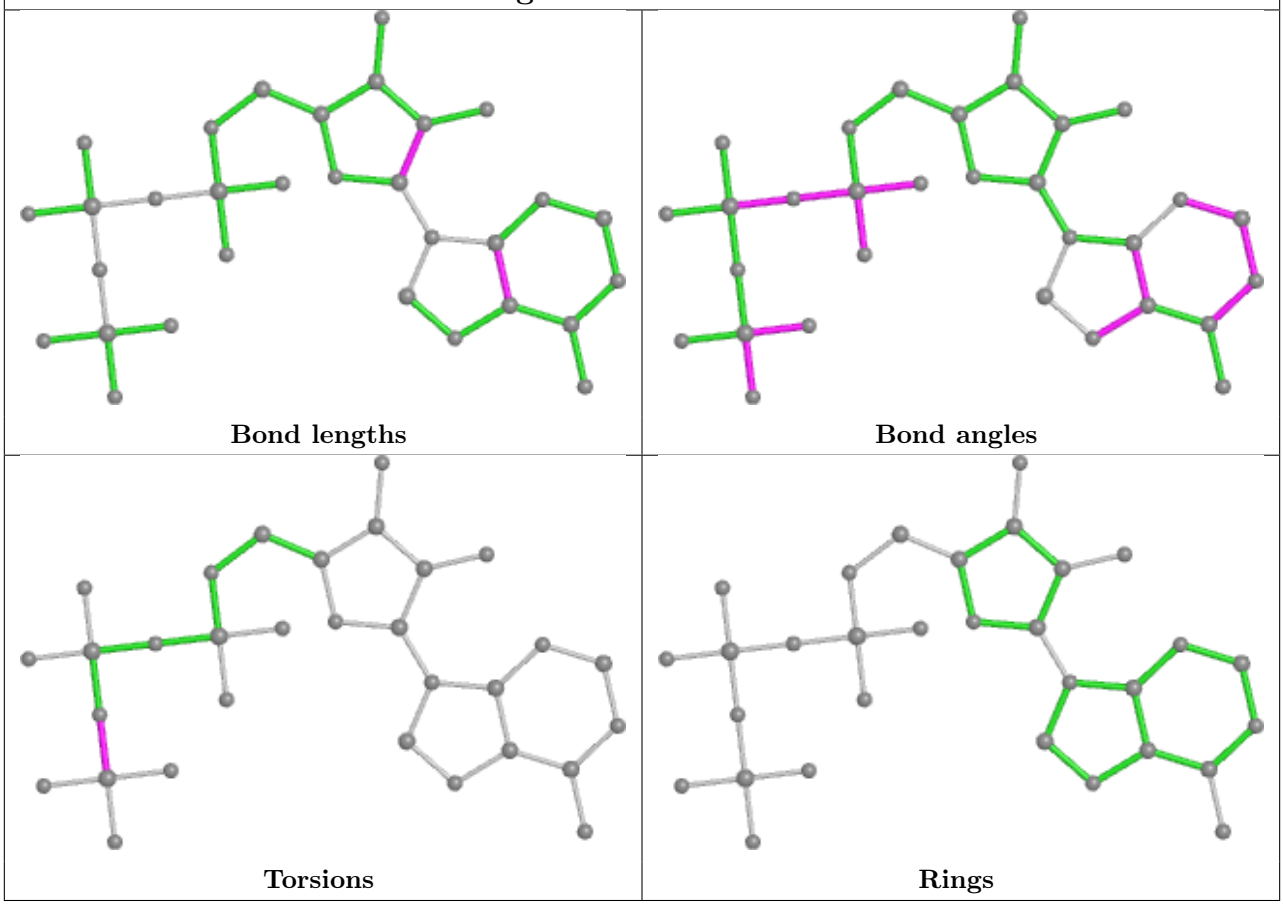
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	ATP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 1001



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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.