wwPDB X-ray Structure Validation Summary Report (i)

Aug 2, 2023 – 09:02 AM EDT

PDB ID	:	1B6S
Title	:	STRUCTURE OF N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE
Authors	:	Thoden, J.B.; Kappock, T.J.; Stubbe, J.; Holden, H.M.
Deposited on	:	1999-01-18
Resolution	:	2.50 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 (1)) were used in the production of this report:

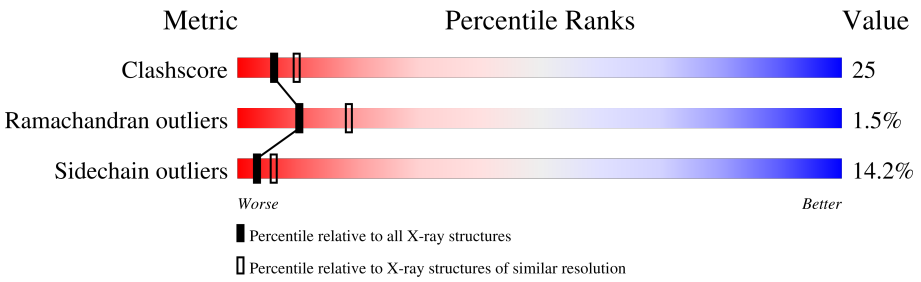
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

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	355	46% 41% 10% ••
1	B	355	50% 38% 12% •
1	C	355	46% 37% 13% • •
1	D	355	49% 38% 11% ••

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11632 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 PROTEIN (N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	351	2751	1752	487	501	11	0	0	0
1	B	355	2784	1772	493	508	11	0	0	0
1	C	350	2747	1750	486	500	11	0	0	0
1	D	350	2747	1750	486	500	11	0	0	0

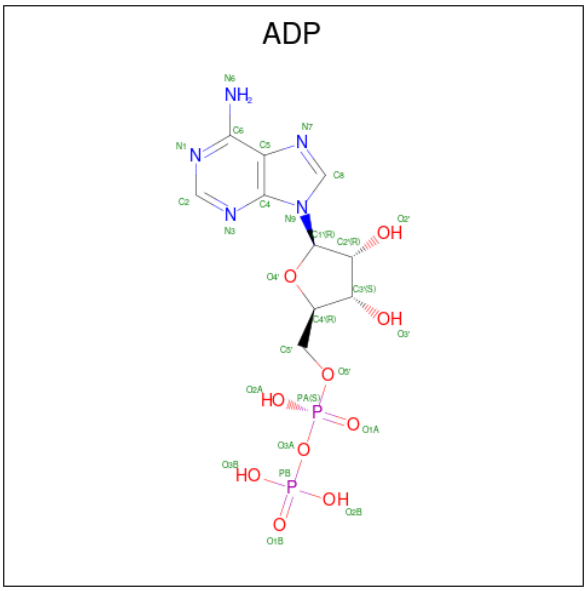
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	ARG	GLN	conflict	UNP P09029
B	205	ARG	GLN	conflict	UNP P09029
C	205	ARG	GLN	conflict	UNP P09029
D	205	ARG	GLN	conflict	UNP P09029

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
2	A	1	1	1	0	0
2	B	1	1	1	0	0
2	C	1	1	1	0	0
2	D	1	1	1	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	107	Total	O	0	0
			107	107		
4	B	121	Total	O	0	0
			121	121		
4	C	136	Total	O	0	0
			136	136		
4	D	127	Total	O	0	0
			127	127		

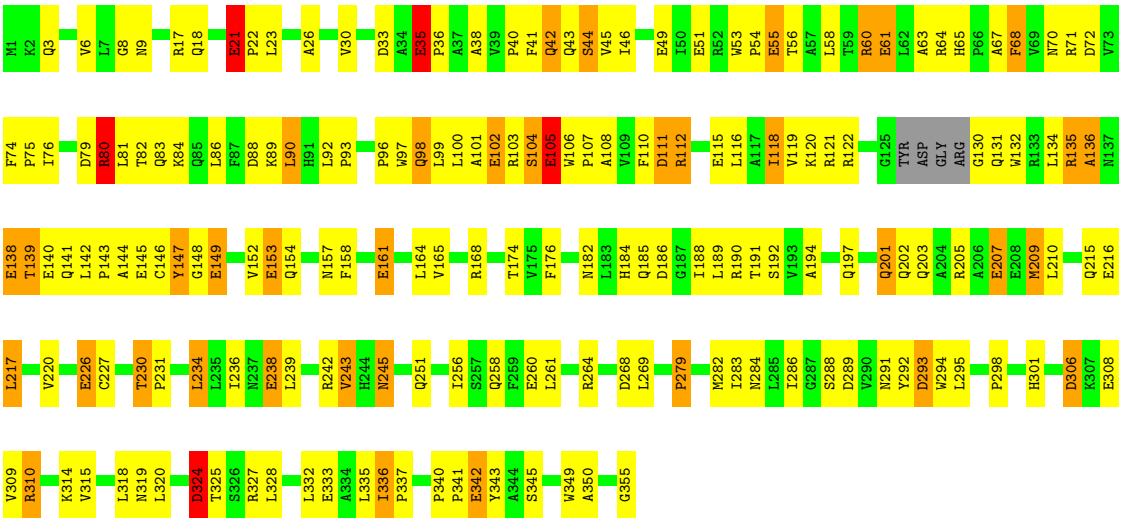
3 Residue-property plots (i)

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.

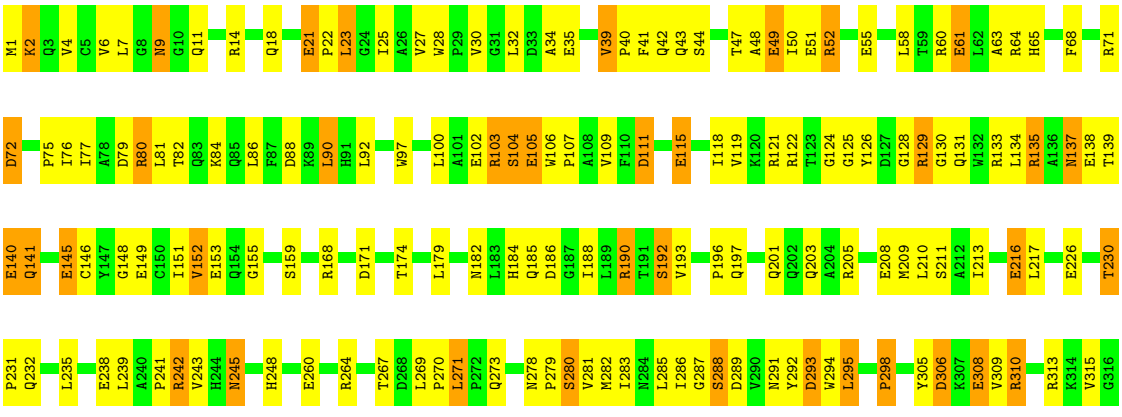
• Molecule 1: PROTEIN (N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE)

Chain A: 46% 41% 10% ••



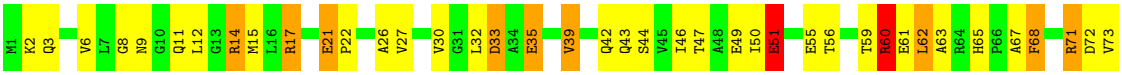
• Molecule 1: PROTEIN (N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE)

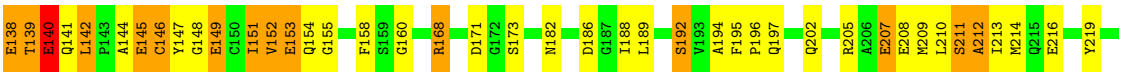
Chain B: 50% 38% 12% •

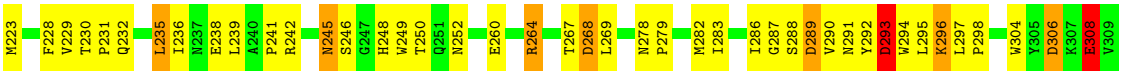


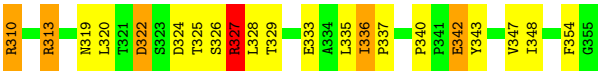
• Molecule 1: PROTEIN (N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE)

Chain C:



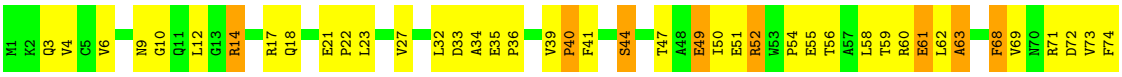


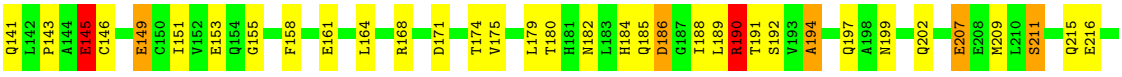


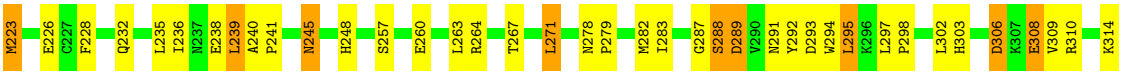


• Molecule 1: PROTEIN (N5-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE SYNTHETASE)

Chain D:







4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	60.60Å 92.10Å 102.60Å 66.10° 82.70° 81.80°	Depositor
Resolution (Å)	30.00 – 2.50	Depositor
% Data completeness (in resolution range)	95.7 (30.00-2.50)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.72	Depositor
Refinement program	TNT 5D	Depositor
R, R_{free}	0.185 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11632	wwPDB-VP
Average B, all atoms (Å^2)	32.0	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: MG, ADP

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	1.01	24/2819 (0.9%)	1.34	28/3841 (0.7%)
1	B	1.00	18/2853 (0.6%)	1.31	24/3888 (0.6%)
1	C	0.99	18/2815 (0.6%)	1.40	40/3836 (1.0%)
1	D	0.98	19/2815 (0.7%)	1.37	31/3836 (0.8%)
All	All	1.00	79/11302 (0.7%)	1.35	123/15401 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

The worst 5 of 79 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	324	ASP	CG-OD1	10.12	1.48	1.25
1	A	324	ASP	C-O	-9.72	1.04	1.23
1	B	260	GLU	CD-OE1	9.49	1.36	1.25
1	D	102	GLU	CD-OE1	9.12	1.35	1.25
1	B	65	HIS	CG-CD2	-8.89	1.20	1.35

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	147	TYR	CG-CD1-CE1	10.92	130.04	121.30
1	A	324	ASP	CA-C-N	-10.04	95.12	117.20
1	D	72	ASP	CB-CG-OD1	-9.82	109.46	118.30
1	C	327	ARG	NE-CZ-NH1	8.61	124.60	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	324	ASP	CB-CG-OD1	-8.42	110.72	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	324	ASP	Mainchain

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	2751	0	2732	158	0
1	B	2784	0	2759	114	0
1	C	2747	0	2729	159	0
1	D	2747	0	2729	131	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	27	0	12	0	0
3	B	27	0	12	1	0
3	C	27	0	12	0	0
3	D	27	0	12	0	0
4	A	107	0	0	4	1
4	B	121	0	0	5	0
4	C	136	0	0	4	0
4	D	127	0	0	5	1
All	All	11632	0	10997	547	1

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 25.

The worst 5 of 547 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:93:PRO:HB2	1:D:235:LEU:HD23	1.46	0.96
1:B:119:VAL:HG22	1:B:152:VAL:HG13	1.47	0.94
1:C:8:GLY:HA3	1:C:49:GLU:HG2	1.54	0.90
1:A:42:GLN:NE2	1:A:42:GLN:H	1.73	0.87
1:A:42:GLN:H	1:A:42:GLN:HE21	1.26	0.83

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2439:HOH:O	4:D:2477:HOH:O[1_454]	0.20	2.00

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	347/355 (98%)	329 (95%)	14 (4%)	4 (1%)	13 24
1	B	353/355 (99%)	326 (92%)	21 (6%)	6 (2%)	9 16
1	C	346/355 (98%)	321 (93%)	19 (6%)	6 (2%)	9 16
1	D	346/355 (98%)	331 (96%)	10 (3%)	5 (1%)	11 20
All	All	1392/1420 (98%)	1307 (94%)	64 (5%)	21 (2%)	10 18

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	129	ARG
1	C	146	CYS
1	A	139	THR
1	A	146	CYS
1	C	136	ALA

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	293/296 (99%)	256 (87%)	37 (13%)	4 8
1	B	296/296 (100%)	248 (84%)	48 (16%)	2 4
1	C	293/296 (99%)	249 (85%)	44 (15%)	3 5
1	D	293/296 (99%)	255 (87%)	38 (13%)	4 7
All	All	1175/1184 (99%)	1008 (86%)	167 (14%)	3 6

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	192	SER
1	D	116	LEU
1	C	211	SER
1	D	23	LEU
1	D	149	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	9	ASN
1	C	98	GLN
1	D	185	GLN
1	C	43	GLN
1	C	182	ASN

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	ADP	D	1400	2	24,29,29	1.14	2 (8%)	29,45,45	1.30	4 (13%)
3	ADP	A	1100	2	24,29,29	1.13	3 (12%)	29,45,45	1.69	7 (24%)
3	ADP	C	1300	2	24,29,29	1.12	3 (12%)	29,45,45	1.41	5 (17%)
3	ADP	B	1200	2	24,29,29	1.15	3 (12%)	29,45,45	1.32	3 (10%)

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	ADP	D	1400	2	-	4/12/32/32	0/3/3/3
3	ADP	A	1100	2	-	4/12/32/32	0/3/3/3
3	ADP	C	1300	2	-	6/12/32/32	0/3/3/3
3	ADP	B	1200	2	-	5/12/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1100	ADP	O3'-C3'	3.03	1.50	1.43
3	C	1300	ADP	O2'-C2'	2.93	1.49	1.43
3	A	1100	ADP	O2'-C2'	2.89	1.49	1.43
3	B	1200	ADP	O3'-C3'	2.87	1.49	1.43
3	B	1200	ADP	O2'-C2'	2.85	1.49	1.43

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1100	ADP	O3'-C3'-C2'	4.68	126.94	111.82
3	C	1300	ADP	O3'-C3'-C2'	4.12	125.17	111.82
3	D	1400	ADP	O3'-C3'-C2'	3.63	123.56	111.82
3	B	1200	ADP	C5-C6-N6	3.43	125.56	120.35
3	A	1100	ADP	C2'-C3'-C4'	-3.41	96.02	102.64

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1100	ADP	C5'-O5'-PA-O1A
3	A	1100	ADP	C5'-O5'-PA-O2A
3	A	1100	ADP	C5'-O5'-PA-O3A
3	C	1300	ADP	C5'-O5'-PA-O2A
3	C	1300	ADP	C5'-O5'-PA-O3A

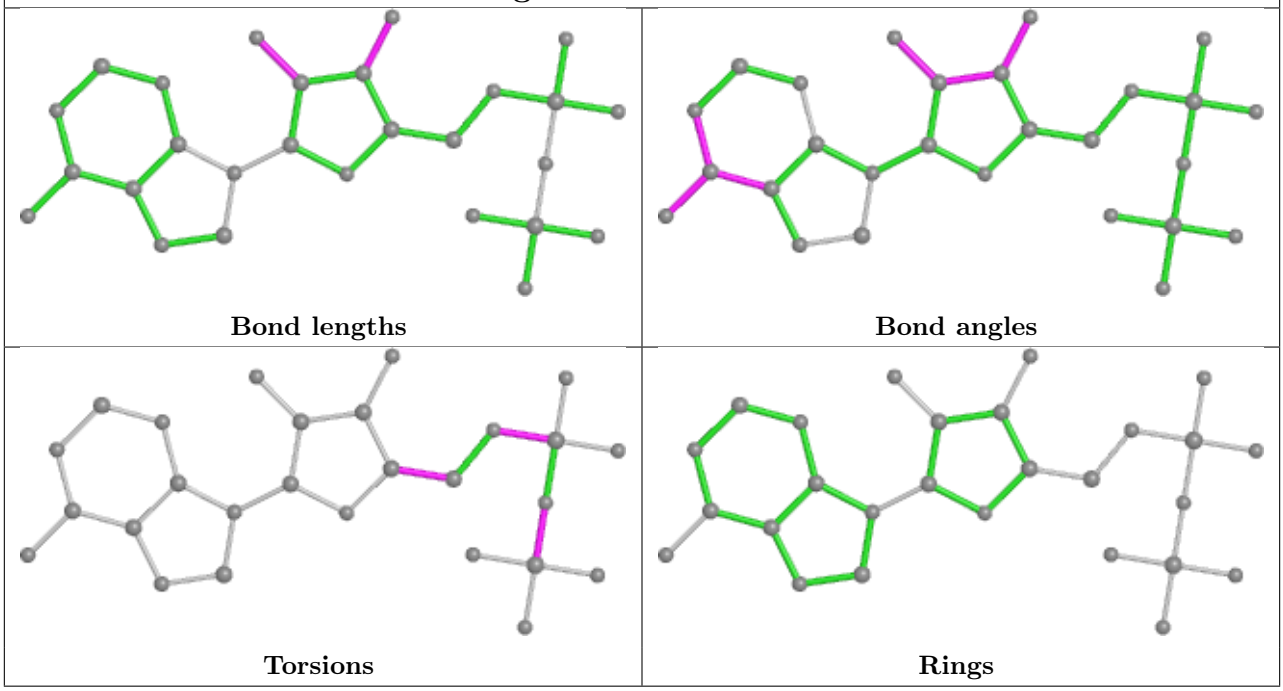
There are no ring outliers.

1 monomer is involved in 1 short contact:

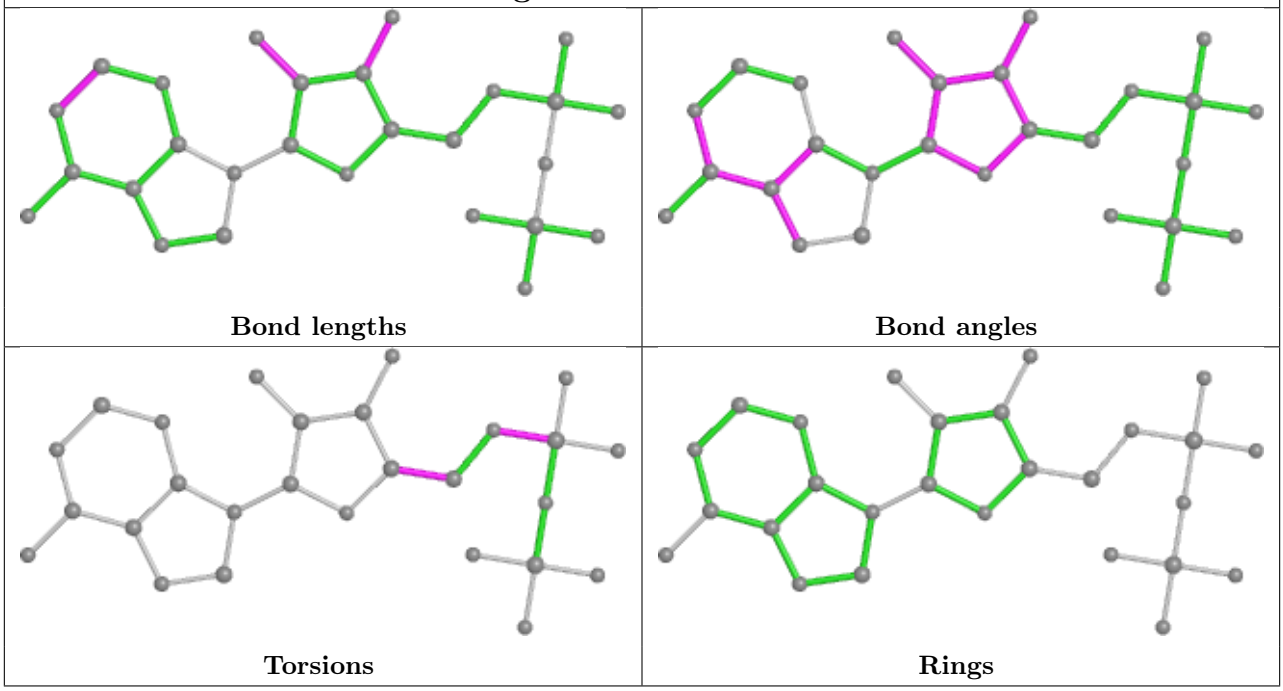
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1200	ADP	1	0

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.

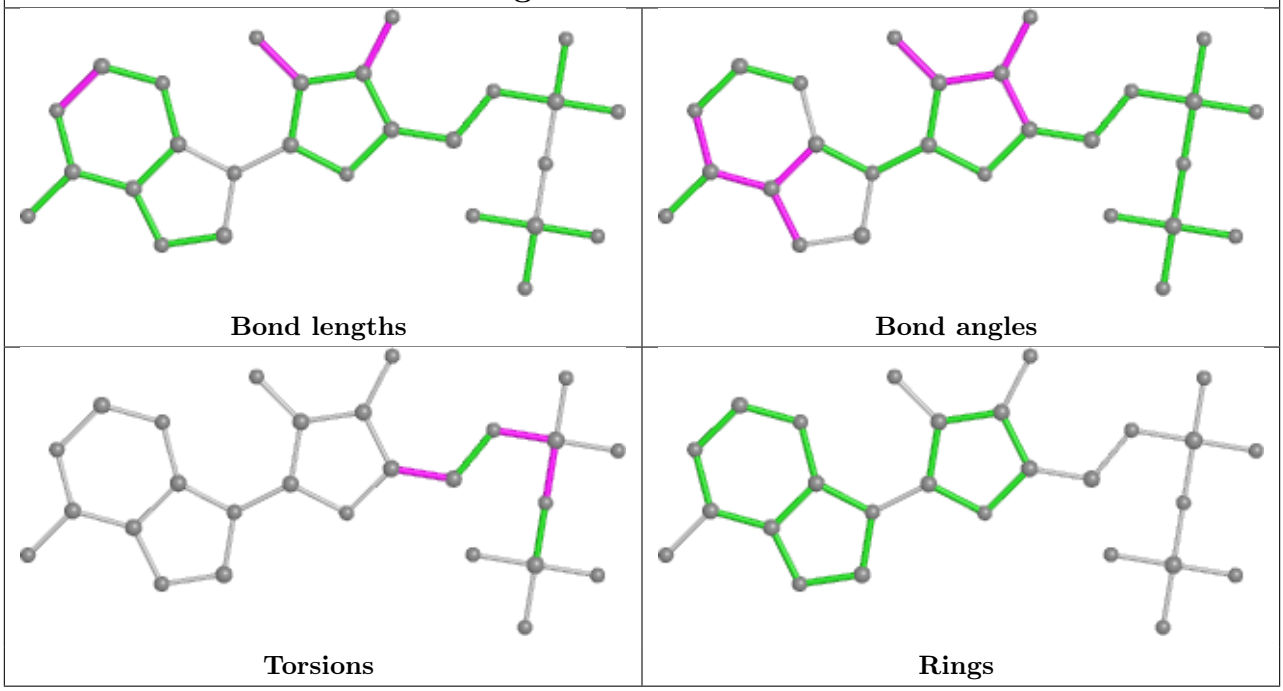
Ligand ADP D 1400



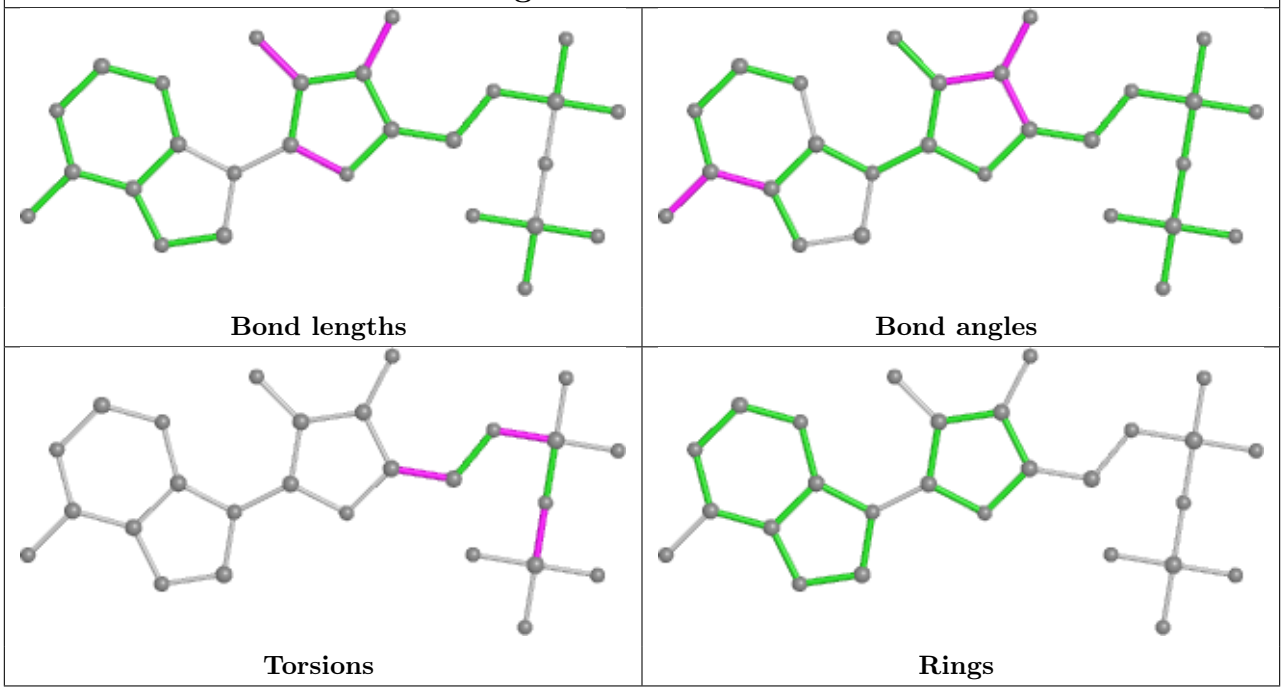
Ligand ADP A 1100



Ligand ADP C 1300



Ligand ADP B 1200



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.