wwPDB X-ray Structure Validation Summary Report (i)

Dec 3, 2023 – 09:00 am GMT

PDB ID	:	2V1X
Title	:	Crystal structure of human RECQ-like DNA helicase
Authors	:	Pike, A.C.W.; Shrestha, B.; Burgess-Brown, N.; King, O.; Ugochukwu, E.; Watt, S.; Edwards, A.; Arrowsmith, C.H.; Weigelt, J.; Sundstrom, M.; Gileadi, O.
Deposited on	:	2007-05-30
Resolution	:	2.00 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:

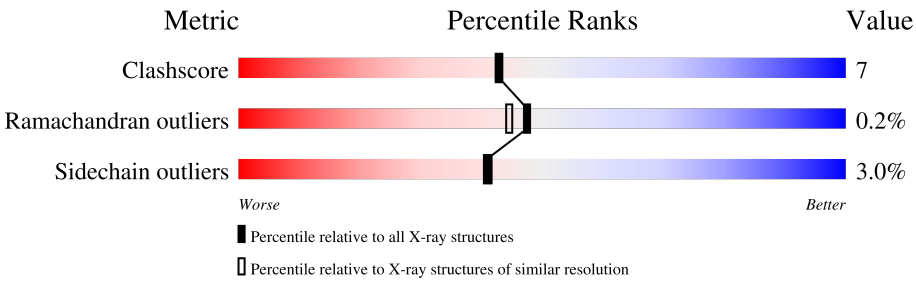
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et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

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))
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%

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	591	74% 15% 11%
1	B	591	74% 14% • 11%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8630 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 ATP-DEPENDENT DNA HELICASE Q1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	527	4101	2626	686	755	34	0	9	0
1	B	527	4139	2648	694	762	35	0	13	0

There are 46 discrepancies between the modelled and reference sequences:

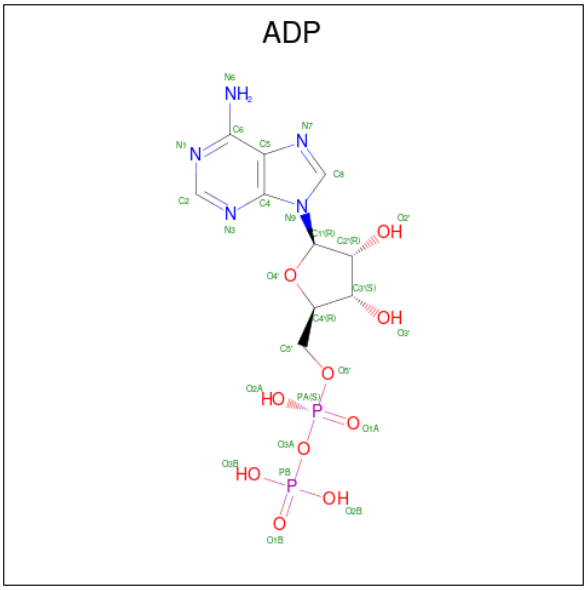
Chain	Residue	Modelled	Actual	Comment	Reference
A	48	MET	-	expression tag	UNP P46063
A	617	ALA	-	expression tag	UNP P46063
A	618	GLU	-	expression tag	UNP P46063
A	619	ASN	-	expression tag	UNP P46063
A	620	LEU	-	expression tag	UNP P46063
A	621	TYR	-	expression tag	UNP P46063
A	622	PHE	-	expression tag	UNP P46063
A	623	GLN	-	expression tag	UNP P46063
A	624	SER	-	expression tag	UNP P46063
A	625	HIS	-	expression tag	UNP P46063
A	626	HIS	-	expression tag	UNP P46063
A	627	HIS	-	expression tag	UNP P46063
A	628	HIS	-	expression tag	UNP P46063
A	629	HIS	-	expression tag	UNP P46063
A	630	HIS	-	expression tag	UNP P46063
A	631	ASP	-	expression tag	UNP P46063
A	632	TYR	-	expression tag	UNP P46063
A	633	LYS	-	expression tag	UNP P46063
A	634	ASP	-	expression tag	UNP P46063
A	635	ASP	-	expression tag	UNP P46063
A	636	ASP	-	expression tag	UNP P46063
A	637	ASP	-	expression tag	UNP P46063
A	638	LYS	-	expression tag	UNP P46063
B	48	MET	-	expression tag	UNP P46063
B	617	ALA	-	expression tag	UNP P46063

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	618	GLU	-	expression tag	UNP P46063
B	619	ASN	-	expression tag	UNP P46063
B	620	LEU	-	expression tag	UNP P46063
B	621	TYR	-	expression tag	UNP P46063
B	622	PHE	-	expression tag	UNP P46063
B	623	GLN	-	expression tag	UNP P46063
B	624	SER	-	expression tag	UNP P46063
B	625	HIS	-	expression tag	UNP P46063
B	626	HIS	-	expression tag	UNP P46063
B	627	HIS	-	expression tag	UNP P46063
B	628	HIS	-	expression tag	UNP P46063
B	629	HIS	-	expression tag	UNP P46063
B	630	HIS	-	expression tag	UNP P46063
B	631	ASP	-	expression tag	UNP P46063
B	632	TYR	-	expression tag	UNP P46063
B	633	LYS	-	expression tag	UNP P46063
B	634	ASP	-	expression tag	UNP P46063
B	635	ASP	-	expression tag	UNP P46063
B	636	ASP	-	expression tag	UNP P46063
B	637	ASP	-	expression tag	UNP P46063
B	638	LYS	-	expression tag	UNP P46063

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

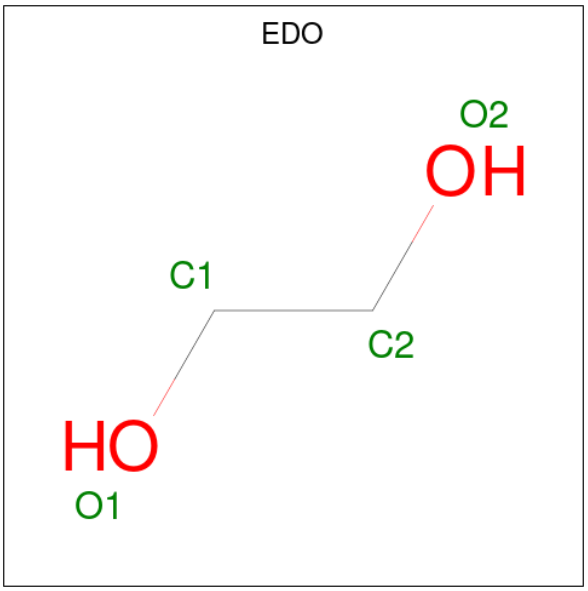
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	1	1	1	0	0
4	B	1	1	1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
5	A	4	4	4	0	0
5	B	5	5	5	0	0

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	B	1	4	2	2	0	0
			Total	C	O		
6	B	1	4	2	2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	146	146	146	0	0
			Total	O		
7	B	169	169	169	0	0

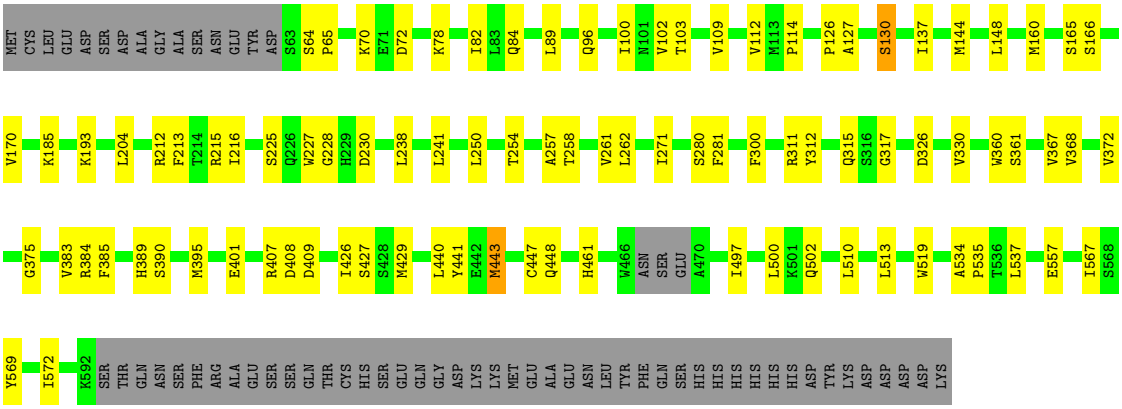
3 Residue-property plots (i)

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 failed to run properly.

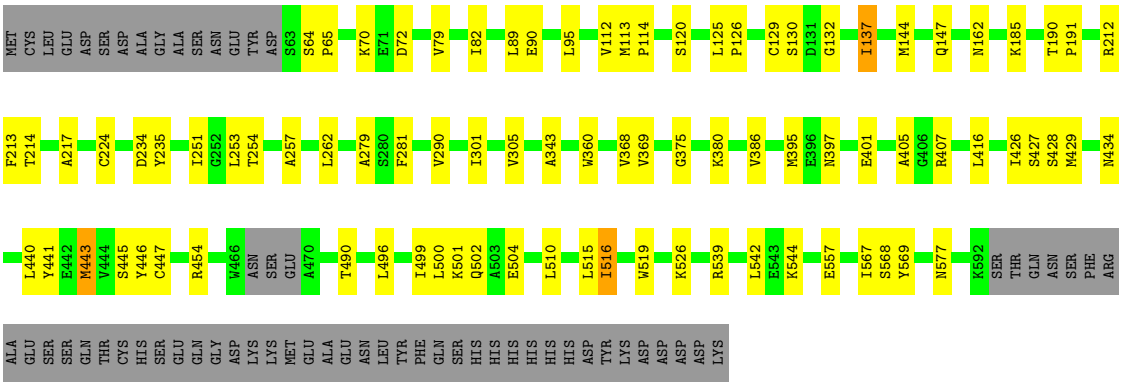
- Molecule 1: ATP-DEPENDENT DNA HELICASE Q1

Chain A:



- Molecule 1: ATP-DEPENDENT DNA HELICASE Q1

Chain B:



4 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	83.23Å 97.65Å 85.85Å 90.00° 104.50° 90.00°	Depositor
Resolution (Å)	45.00 – 2.00	Depositor
% Data completeness (in resolution range)	100.0 (45.00-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.3.0037	Depositor
R, R_{free}	0.232 , 0.278	Depositor
Wilson B-factor (Å^2)	34.3	Xtriage
Anisotropy	0.078	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
Total number of atoms	8630	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.42 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.9456e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: ZN, CL, MG, ADP, EDO

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	0.62	1/4218 (0.0%)	0.70	0/5713
1	B	0.63	1/4276 (0.0%)	0.70	0/5788
All	All	0.63	2/8494 (0.0%)	0.70	0/11501

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	447	CYS	CB-SG	-8.20	1.68	1.82
1	A	447	CYS	CB-SG	-5.81	1.72	1.81

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	4101	0	3969	54	0
1	B	4139	0	4026	56	0
2	A	27	0	12	0	0
2	B	27	0	12	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
5	A	4	0	0	1	0
5	B	5	0	0	0	0
6	B	8	0	12	0	0
7	A	146	0	0	4	0
7	B	169	0	0	2	0
All	All	8630	0	8031	111	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 7.

The worst 5 of 111 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:B:386:VAL:HG23	1:B:405:ALA:HB2	1.64	0.79
1:A:426:ILE:HG21	1:A:440:LEU:HD13	1.67	0.77
1:A:130:SER:O	1:A:185:LYS:NZ	2.18	0.75
1:B:443:MET:HA	1:B:443:MET:HE3	1.69	0.74
1:A:193:LYS:NZ	7:A:2027:HOH:O	2.24	0.71

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	532/591 (90%)	509 (96%)	22 (4%)	1 (0%)	47	44
1	B	536/591 (91%)	523 (98%)	12 (2%)	1 (0%)	47	44
All	All	1068/1182 (90%)	1032 (97%)	34 (3%)	2 (0%)	47	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	375	GLY
1	A	375	GLY

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	425/520 (82%)	410 (96%)	15 (4%)	36	35
1	B	436/520 (84%)	422 (97%)	14 (3%)	39	38
All	All	861/1040 (83%)	832 (97%)	29 (3%)	41	36

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	513	LEU
1	B	516	ILE
1	B	162	ASN
1	B	434	ASN
1	B	137	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	502	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 17 ligands modelled in this entry, 13 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	$\#\|Z\| > 2$
6	EDO	B	1602	-	3,3,3	0.52	0	2,2,2	0.23	0
2	ADP	B	1593	3	24,29,29	1.09	2 (8%)	29,45,45	1.26	3 (10%)
2	ADP	A	1593	3	24,29,29	1.04	2 (8%)	29,45,45	1.34	2 (6%)
6	EDO	B	1601	-	3,3,3	0.55	0	2,2,2	0.09	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
6	EDO	B	1602	-	-	0/1/1/1	-
2	ADP	B	1593	3	-	2/12/32/32	0/3/3/3
2	ADP	A	1593	3	-	2/12/32/32	0/3/3/3
6	EDO	B	1601	-	-	1/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1593	ADP	C5-C4	2.35	1.47	1.40
2	B	1593	ADP	C5-C4	2.30	1.47	1.40
2	B	1593	ADP	O4'-C1'	2.21	1.44	1.41
2	A	1593	ADP	C2-N3	2.10	1.35	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1593	ADP	N3-C2-N1	-3.83	122.69	128.68
2	B	1593	ADP	N3-C2-N1	-3.56	123.11	128.68
2	A	1593	ADP	O3B-PB-O2B	2.47	117.06	107.64
2	B	1593	ADP	O2A-PA-O1A	2.24	123.33	112.24
2	B	1593	ADP	C4-C5-N7	-2.22	107.08	109.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1593	ADP	PA-O3A-PB-O2B
2	B	1593	ADP	PA-O3A-PB-O2B
6	B	1601	EDO	O1-C1-C2-O2
2	A	1593	ADP	PA-O3A-PB-O3B
2	B	1593	ADP	PA-O3A-PB-O3B

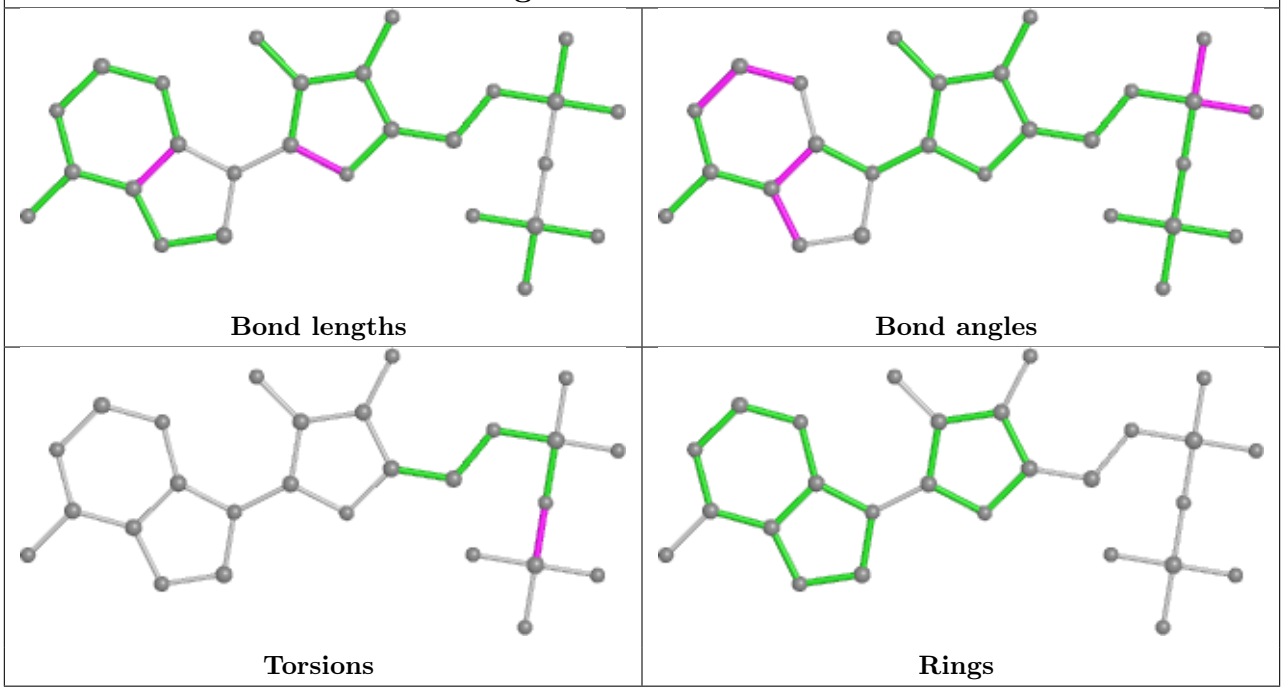
There are no ring outliers.

1 monomer is involved in 1 short contact:

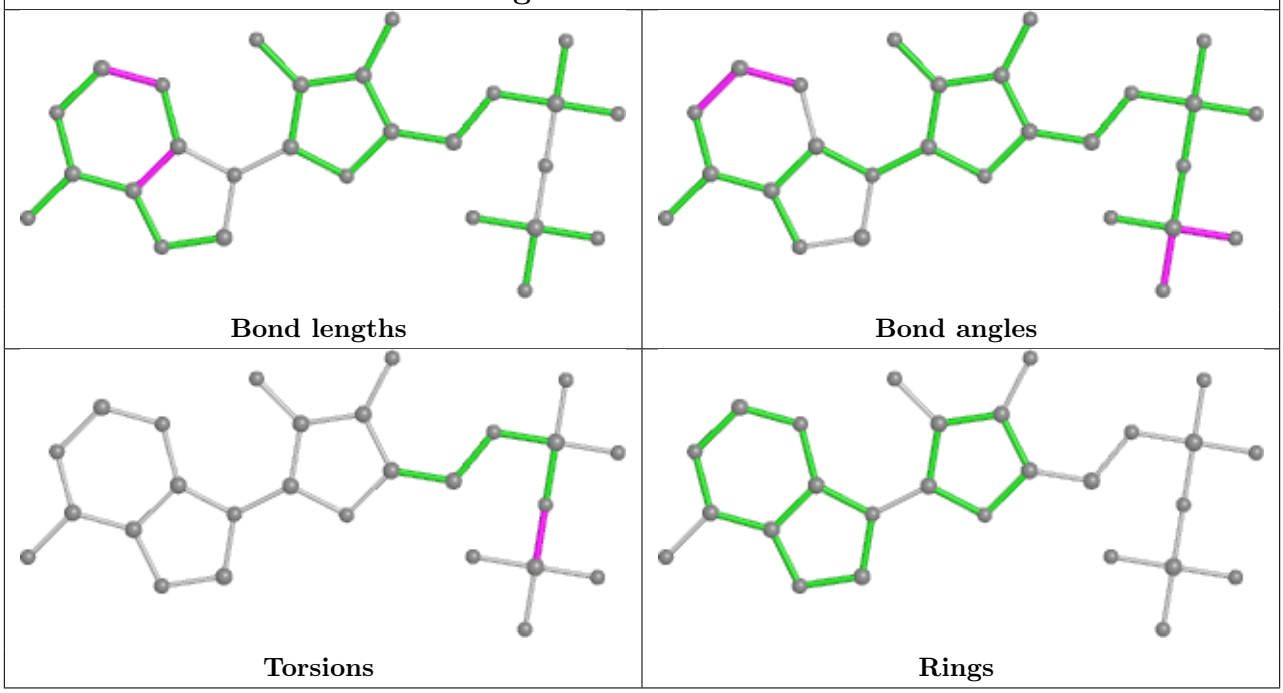
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1593	ADP	1	0

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 B 1593



Ligand ADP A 1593



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 failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

6.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.