



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:22 PM UTC

PDB ID : 1JVS / pdb_00001jvs
Title : Crystal structure of 1-deoxy-D-xylulose 5-phosphate reductoisomerase; a target enzyme for antimalarial drugs
Authors : Yajima, S.; Nonaka, T.; Kuzuyama, T.; Seto, H.; Ohsawa, K.
Deposited on : 2001-08-31
Resolution : 2.20 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 ⓘ 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

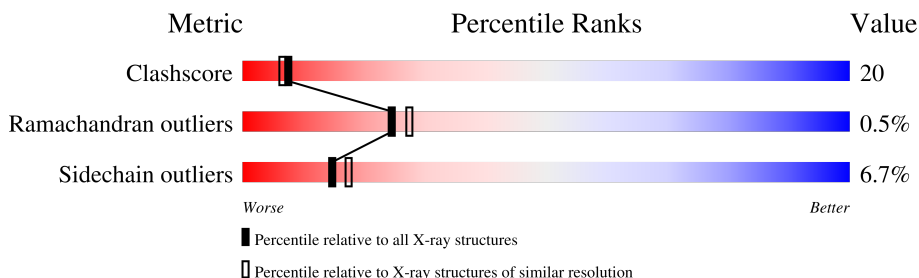
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	400	
1	B	400	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6446 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	Se	0	0	0
			3037	1895	536	580	8	18			
1	B	398	Total	C	N	O	S	Se	0	0	0
			3025	1889	534	576	8	18			

There are 42 discrepancies between the modelled and reference sequences:

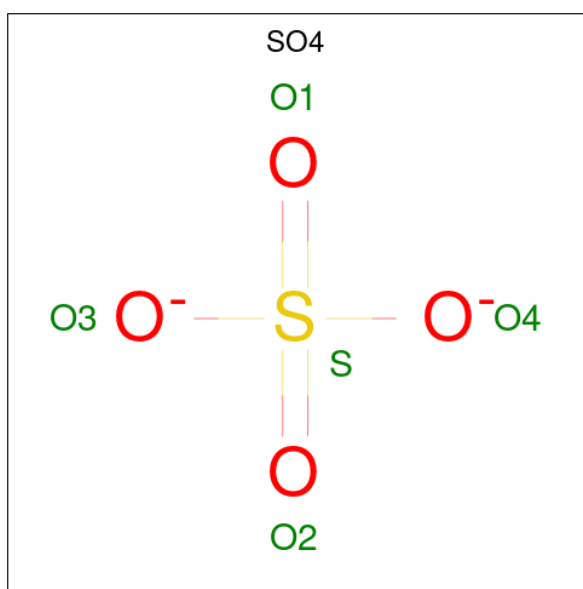
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	cloning artifact	UNP P45568
A	41	MSE	MET	modified residue	UNP P45568
A	55	MSE	MET	modified residue	UNP P45568
A	67	MSE	MET	modified residue	UNP P45568
A	87	MSE	MET	modified residue	UNP P45568
A	97	MSE	MET	modified residue	UNP P45568
A	135	MSE	MET	modified residue	UNP P45568
A	200	MSE	MET	modified residue	UNP P45568
A	213	MSE	MET	modified residue	UNP P45568
A	224	MSE	MET	modified residue	UNP P45568
A	225	MSE	MET	modified residue	UNP P45568
A	245	MSE	MET	modified residue	UNP P45568
A	258	MSE	MET	modified residue	UNP P45568
A	275	MSE	MET	modified residue	UNP P45568
A	283	MSE	MET	modified residue	UNP P45568
A	321	MSE	MET	modified residue	UNP P45568
A	366	MSE	MET	modified residue	UNP P45568
A	368	MSE	MET	modified residue	UNP P45568
A	393	MSE	MET	modified residue	UNP P45568
A	398	SER	-	cloning artifact	UNP P45568
A	399	ALA	-	cloning artifact	UNP P45568
B	0	GLY	-	cloning artifact	UNP P45568
B	41	MSE	MET	modified residue	UNP P45568
B	55	MSE	MET	modified residue	UNP P45568
B	67	MSE	MET	modified residue	UNP P45568

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Chain	Residue	Modelled	Actual	Comment	Reference
B	87	MSE	MET	modified residue	UNP P45568
B	97	MSE	MET	modified residue	UNP P45568
B	135	MSE	MET	modified residue	UNP P45568
B	200	MSE	MET	modified residue	UNP P45568
B	213	MSE	MET	modified residue	UNP P45568
B	224	MSE	MET	modified residue	UNP P45568
B	225	MSE	MET	modified residue	UNP P45568
B	245	MSE	MET	modified residue	UNP P45568
B	258	MSE	MET	modified residue	UNP P45568
B	275	MSE	MET	modified residue	UNP P45568
B	283	MSE	MET	modified residue	UNP P45568
B	321	MSE	MET	modified residue	UNP P45568
B	366	MSE	MET	modified residue	UNP P45568
B	368	MSE	MET	modified residue	UNP P45568
B	393	MSE	MET	modified residue	UNP P45568
B	398	SER	-	cloning artifact	UNP P45568
B	399	ALA	-	cloning artifact	UNP P45568

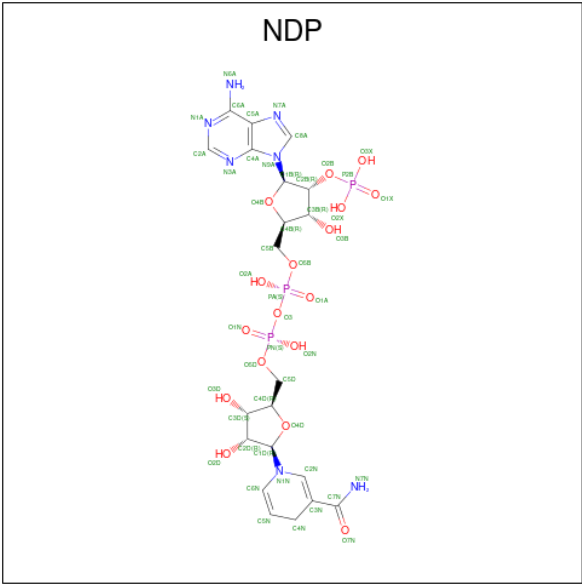
- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE

PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is water.

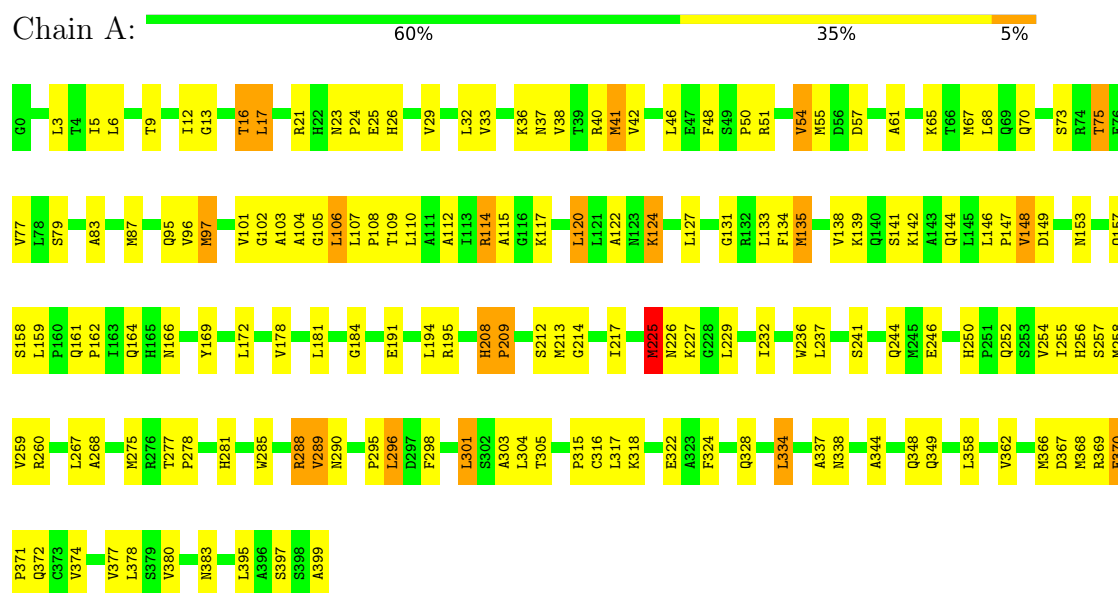
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	148	Total	O	0	0
			148	148		
4	B	130	Total	O	0	0
			130	130		

3 Residue-property plots

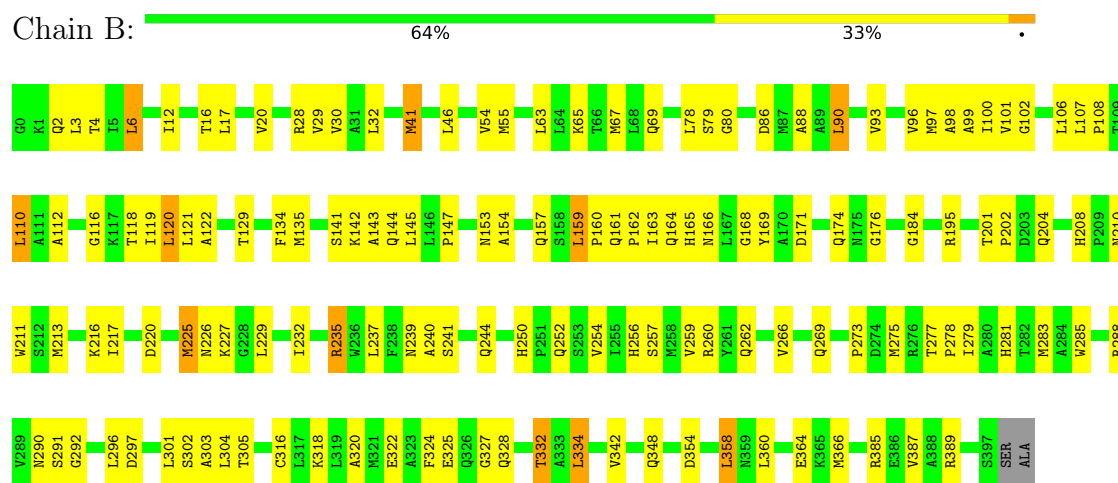
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



- Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	182.16Å 59.19Å 87.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (100.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.213 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6446	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, SO4

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	0.40	0/3067	0.92	12/4127 (0.3%)
1	B	0.39	0/3055	0.90	11/4112 (0.3%)
All	All	0.39	0/6122	0.91	23/8239 (0.3%)

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	HIS	CA-C-N	7.88	129.69	119.84
1	A	208	HIS	C-N-CA	7.88	129.69	119.84
1	B	225	MSE	N-CA-C	-6.94	103.77	111.82
1	B	254	VAL	N-CA-C	-6.51	105.40	111.45
1	B	250	HIS	CA-C-N	6.31	126.51	119.32

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3037	0	3059	144	0
1	B	3025	0	3049	117	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	48	0	26	2	0
3	B	48	0	26	1	0
4	A	148	0	0	8	0
4	B	130	0	0	6	0
All	All	6446	0	6160	250	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 20.

The worst 5 of 250 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:366:MSE:HE1	1:B:387:VAL:HG21	1.39	1.02
1:A:296:LEU:HD11	1:B:266:VAL:HG21	1.45	0.97
1:A:337:ALA:HB2	1:A:362:VAL:HG21	1.53	0.90
1:B:12:ILE:O	1:B:16:THR:HG23	1.72	0.88
1:B:328:GLN:O	1:B:332:THR:HG23	1.74	0.88

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	398/400 (100%)	382 (96%)	13 (3%)	3 (1%)	16	16
1	B	396/400 (99%)	387 (98%)	8 (2%)	1 (0%)	36	42
All	All	794/800 (99%)	769 (97%)	21 (3%)	4 (0%)	24	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	SER
1	B	257	SER
1	A	397	SER
1	A	370	GLU

5.3.2 Protein sidechains ⓘ

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	328/310 (106%)	297 (90%)	31 (10%)	8	8
1	B	327/310 (106%)	314 (96%)	13 (4%)	28	38
All	All	655/620 (106%)	611 (93%)	44 (7%)	15	17

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	372	GLN
1	B	110	LEU
1	A	377	VAL
1	B	41	MSE
1	B	144	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	175	ASN
1	B	290	ASN
1	B	210	ASN
1	B	256	HIS
1	B	372	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 ligands are 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	$\# Z > 2$
3	NDP	A	2001	-	51,52,52	1.56	9 (17%)	71,80,80	1.08	4 (5%)
2	SO4	B	1002	-	4,4,4	0.35	0	6,6,6	0.05	0
3	NDP	B	2002	-	51,52,52	1.55	9 (17%)	71,80,80	1.08	4 (5%)
2	SO4	A	1001	-	4,4,4	0.35	0	6,6,6	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
3	NDP	A	2001	-	-	16/34/77/77	0/5/5/5
3	NDP	B	2002	-	-	15/34/77/77	0/5/5/5

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2001	NDP	C4N-C5N	-5.02	1.36	1.49
3	B	2002	NDP	C4N-C5N	-4.95	1.36	1.49
3	A	2001	NDP	C4N-C3N	-4.49	1.41	1.50
3	B	2002	NDP	C4N-C3N	-4.44	1.41	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2002	NDP	C2N-C3N	3.71	1.45	1.35

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2001	NDP	C3N-C2N-N1N	-4.22	117.01	123.20
3	B	2002	NDP	C3N-C2N-N1N	-4.08	117.22	123.20
3	B	2002	NDP	O7N-C7N-N7N	-2.84	116.53	122.89
3	A	2001	NDP	O7N-C7N-N7N	-2.71	116.82	122.89
3	B	2002	NDP	N3A-C2A-N1A	-2.31	125.09	128.58

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

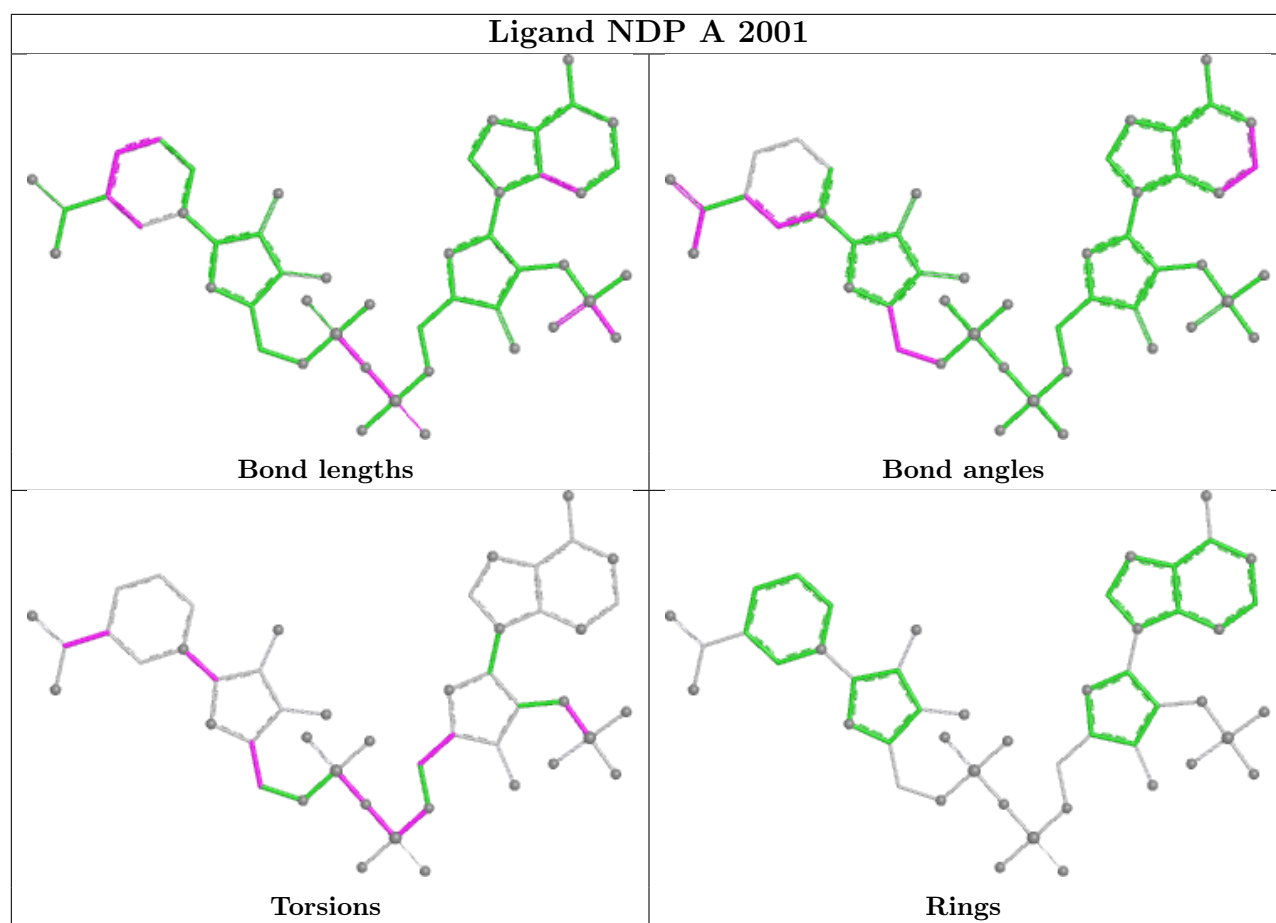
Mol	Chain	Res	Type	Atoms
3	A	2001	NDP	C5B-O5B-PA-O1A
3	A	2001	NDP	C5B-O5B-PA-O2A
3	A	2001	NDP	C5B-O5B-PA-O3
3	A	2001	NDP	PN-O3-PA-O5B
3	B	2002	NDP	C5B-O5B-PA-O1A

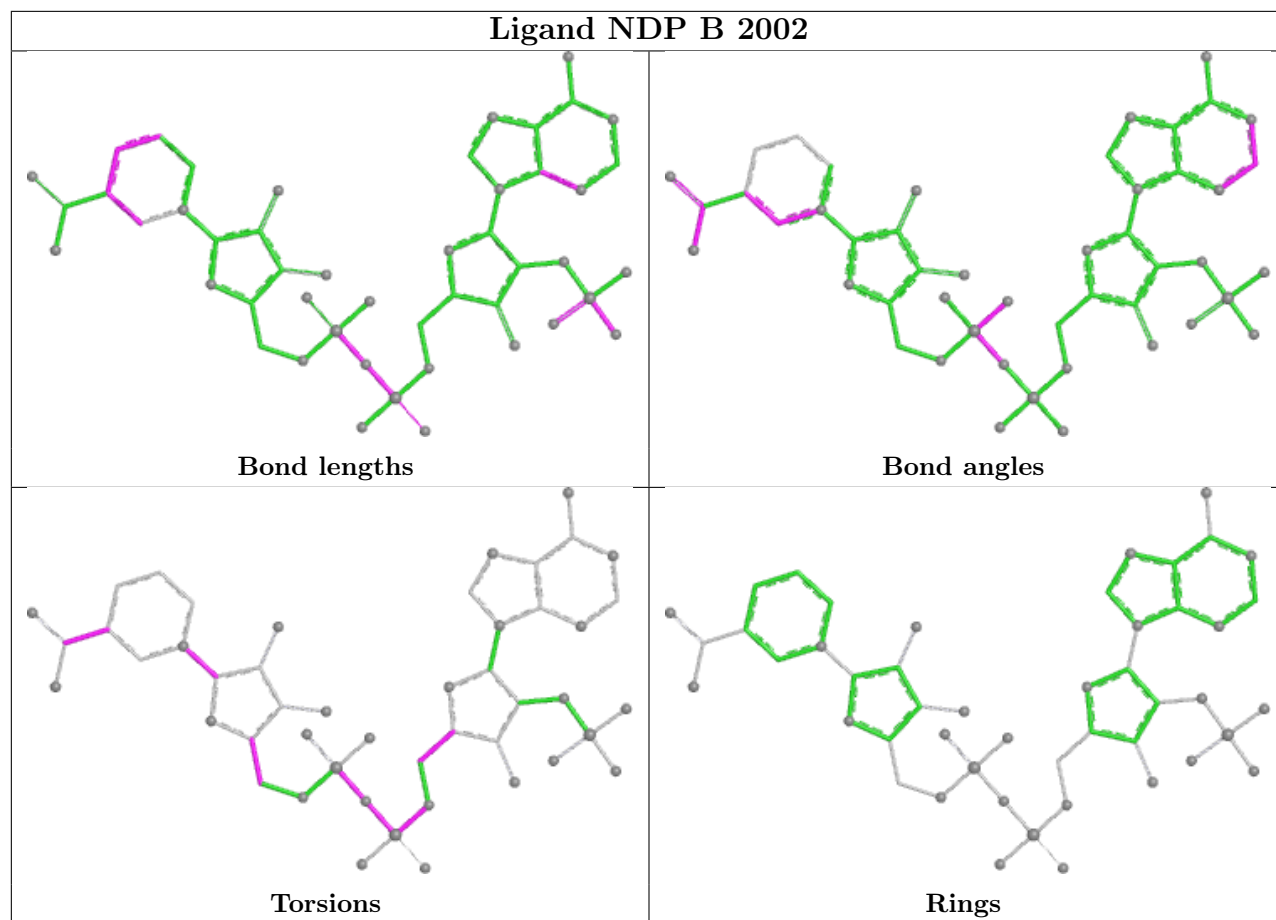
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2001	NDP	2	0
3	B	2002	NDP	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 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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.