



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 23, 2021 – 01:57 PM EDT

PDB ID : 1A35
Title : HUMAN TOPOISOMERASE I/DNA COMPLEX
Authors : Redinbo, M.R.; Stewart, L.; Kuhn, P.; Champoux, J.J.; Hol, W.G.
Deposited on : 1998-01-29
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 ⓘ symbol.

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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
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) : 2.23.2

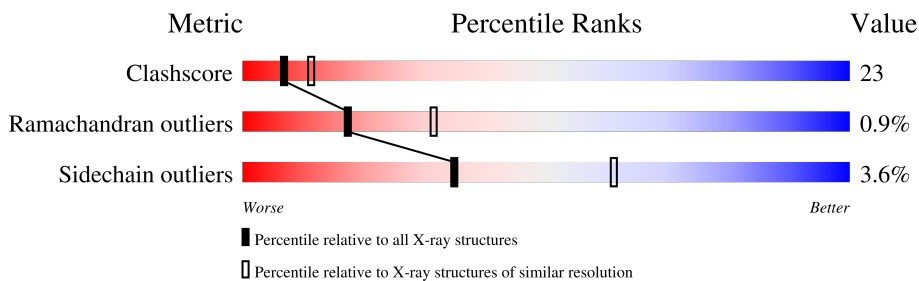
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	22	36% 50% 9% 5%
2	D	22	18% 64% 18%
3	A	591	50% 29% 20%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4947 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 DNA chain called DNA (5'-D(*AP*AP*AP*AP*AP*GP*AP*CP*TP*TP*AP*GP*AP*AP*AP*AP*AP*(BRU)P*(BRU)P*TP*TP*T)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	Br	C	N	O	P			
1	C	22	452	2	217	87	125	21	0	0	0

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*AP*AP*AP*AP*TP*+UP*+UP*+UP*+UP*CP*+UP*AP*AP*GP*TP*CP*TP*TP*TP*+UP*T)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	Br	C	N	O	P			
2	D	22	444	6	212	70	135	21	0	0	0

- Molecule 3 is a protein called PROTEIN (DNA TOPOISOMERASE I).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	474	3778	2431	662	663	22	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	723	PHE	TYR	engineered mutation	UNP P11387

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	23	Total	O	0	0
			23	23		
4	D	44	Total	O	0	0
			44	44		
4	A	206	Total	O	0	0
			206	206		

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: DNA (5'-D(*AP*AP*AP*AP*AP*GP*AP*CP*TP*TP*AP*GP*AP*AP*AP*AP*AP*(BRU)P*(BRU)P*TP*TP*T)-3')

Chain C: 



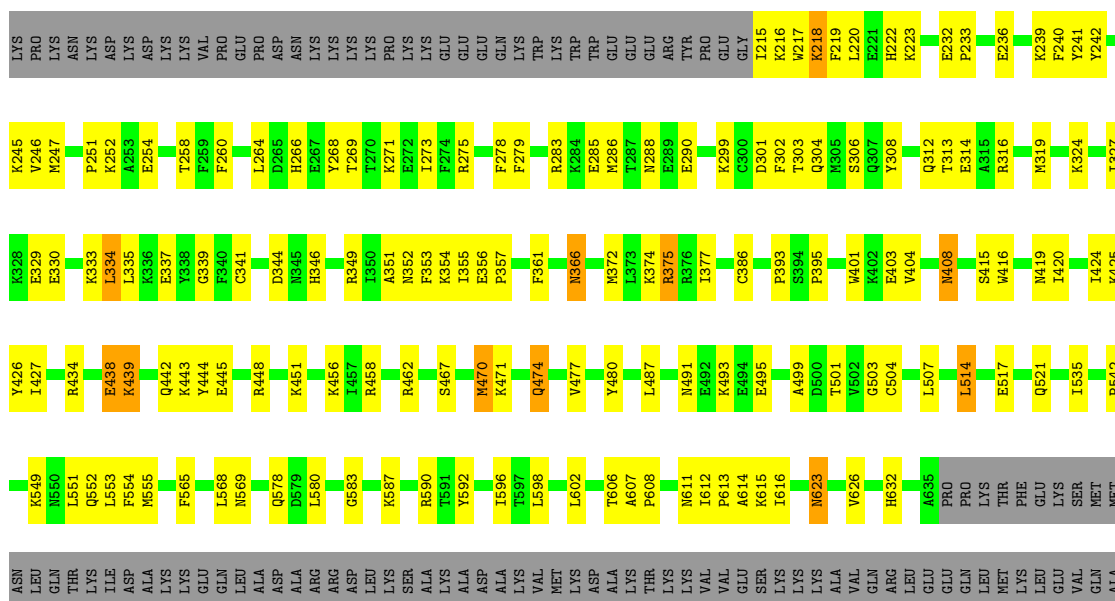
- Molecule 2: DNA (5'-D(*AP*AP*AP*AP*AP*TP*+UP*+UP*+UP*+UP*CP*+UP*AP*AP*GP*TP*CP*TP*TP*TP*+UP*T)-3')

Chain D: 



- Molecule 3: PROTEIN (DNA TOPOISOMERASE I)

Chain A: 



THR	ASP	ARG	GLU	GLU	ASN	LYS	Q713	I714	A715	L716	G717	T718	S719	K720	L721	N722	F723	L724		R727	I728		A731	W732		K735	W736		I743	Y744	N745	K746	I747	Q748	R749	E750	G751	F752	A753	W754	A755	I756	D757	M758	A759	D760	E761	D762		F765
-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	--	------	------	--	------	------	--	------	------	--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	--	------

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.80Å 66.30Å 71.80Å 90.00° 98.40° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	87.0 (20.00-2.50)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.209 , 0.308	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4947	wwPDB-VP
Average B, all atoms (Å ²)	41.0	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: BRU

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	C	0.69	0/464	0.89	1/712 (0.1%)
2	D	0.89	0/360	0.96	0/546
3	A	0.57	0/3868	0.72	0/5222
All	All	0.61	0/4692	0.76	1/6480 (0.0%)

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	C	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	8	DC	C1'-O4'-C4'	-5.94	104.16	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	8	DC	Sidechain

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	C	452	0	245	27	0
2	D	444	0	238	34	0
3	A	3778	0	3713	156	0
4	A	206	0	0	36	0
4	C	23	0	0	3	0
4	D	44	0	0	12	0
All	All	4947	0	4196	203	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 23.

The worst 5 of 203 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)
2:D:105:DA:H2''	2:D:106:DT:C5'	1.85	1.06
2:D:105:DA:H2''	2:D:106:DT:H5'	1.38	1.03
1:C:8:DC:H2''	1:C:9:DT:C7	1.88	1.03
1:C:8:DC:C2'	1:C:9:DT:H71	1.87	1.02
3:A:623:ASN:HD21	3:A:716:LEU:HB3	1.28	0.97

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
3	A	470/591 (80%)	445 (95%)	21 (4%)	4 (1%)	17 31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	761	GLU
3	A	495	GLU
3	A	351	ALA
3	A	714	ILE

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
3	A	388/535 (72%)	374 (96%)	14 (4%)	35 61

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	438	GLU
3	A	439	LYS
3	A	623	ASN
3	A	474	GLN
3	A	514	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	748	GLN
3	A	623	ASN
3	A	421	GLN
3	A	408	ASN
3	A	474	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](#)

8 non-standard protein/DNA/RNA residues 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
2	BRU	D	107	2,1	15,21,22	2.21	3 (20%)	17,30,33	4.15	6 (35%)
2	BRU	D	110	2,1	15,21,22	2.43	4 (26%)	17,30,33	3.90	4 (23%)
2	BRU	D	121	2,1	15,21,22	2.66	4 (26%)	17,30,33	4.07	4 (23%)
1	BRU	C	18	2,1	15,21,22	2.57	4 (26%)	17,30,33	4.03	4 (23%)
2	BRU	D	108	2,1	15,21,22	2.32	3 (20%)	17,30,33	3.99	6 (35%)
1	BRU	C	19	2,1	15,21,22	2.49	4 (26%)	17,30,33	4.13	4 (23%)
2	BRU	D	109	2,1	15,21,22	2.49	3 (20%)	17,30,33	4.05	4 (23%)
2	BRU	D	112	2,1	15,21,22	2.23	4 (26%)	17,30,33	4.03	4 (23%)

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	BRU	D	107	2,1	-	2/4/21/22	0/2/2/2
2	BRU	D	110	2,1	-	1/4/21/22	0/2/2/2
2	BRU	D	121	2,1	-	1/4/21/22	0/2/2/2
1	BRU	C	18	2,1	-	1/4/21/22	0/2/2/2
2	BRU	D	108	2,1	-	1/4/21/22	0/2/2/2
1	BRU	C	19	2,1	-	2/4/21/22	0/2/2/2
2	BRU	D	109	2,1	-	2/4/21/22	0/2/2/2
2	BRU	D	112	2,1	-	1/4/21/22	0/2/2/2

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	19	BRU	BR-C5	7.08	2.10	1.90
2	D	121	BRU	BR-C5	7.00	2.10	1.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	18	BRU	BR-C5	6.87	2.10	1.90
2	D	110	BRU	BR-C5	6.85	2.10	1.90
2	D	109	BRU	BR-C5	6.77	2.09	1.90

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	19	BRU	C4-N3-C2	14.91	127.73	115.14
2	D	107	BRU	C4-N3-C2	14.56	127.44	115.14
2	D	121	BRU	C4-N3-C2	14.49	127.38	115.14
1	C	18	BRU	C4-N3-C2	14.46	127.35	115.14
2	D	109	BRU	C4-N3-C2	14.35	127.26	115.14

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	18	BRU	O4'-C1'-N1-C6
1	C	19	BRU	O4'-C1'-N1-C6
2	D	107	BRU	O4'-C1'-N1-C6
2	D	108	BRU	O4'-C1'-N1-C6
2	D	109	BRU	O4'-C1'-N1-C6

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	107	BRU	1	0
2	D	110	BRU	3	0
2	D	121	BRU	1	0
1	C	18	BRU	2	0
1	C	19	BRU	3	0
2	D	112	BRU	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.