



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2017 – 10:13 PM EDT

PDB ID : 2H7F
Title : Structure of variola topoisomerase covalently bound to DNA
Authors : Perry, K.; Hwang, Y.; Bushman, F.D.; Van Duyne, G.D.
Deposited on : unknown
Resolution : 2.70 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

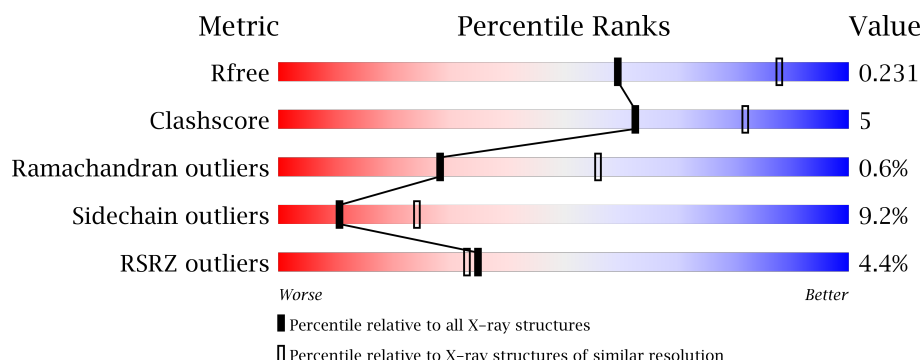
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
R_{free}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Y	11	
2	Z	14	
3	X	314	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3165 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 5'-D(*TP*TP*GP*TP*CP*GP*CP*CP*CP*TP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Y	11	Total	C	N	O	P	0	0	0
			216	106	32	68	10			

- Molecule 2 is a DNA chain called 5'-D(*TP*AP*AP*TP*AP*AP*GP*GP*GP*CP*GP*AP*CP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Z	14	Total	C	N	O	P	0	1	0
			310	148	65	83	14			

- Molecule 3 is a protein called DNA topoisomerase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	X	314	Total	C	N	O	P	S	0	0	0
			2585	1669	439	467	1	9			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	100	SER	CYS	ENGINEERED	UNP P32989
X	211	SER	CYS	ENGINEERED	UNP P32989
X	274	PTR	TYR	MODIFIED RESIDUE	UNP P32989

- Molecule 4 is water.

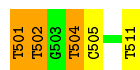
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	Y	4	Total	O	0	0
			4	4		
4	Z	1	Total	O	0	0
			1	1		
4	X	49	Total	O	0	0
			49	49		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

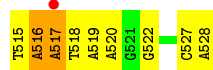
- Molecule 1: 5'-D(*TP*TP*GP*TP*CP*GP*CP*CP*CP*TP*T)-3'

Chain Y: 




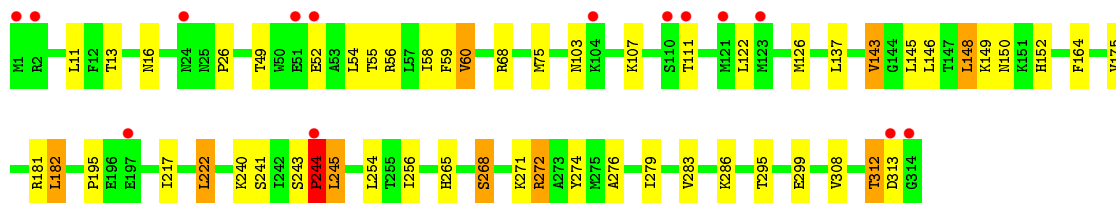
- Molecule 2: 5'-D(*TP*AP*AP*TP*AP*AP*GP*GP*GP*CP*GP*AP*CP*A)-3'

Chain Z: 



- Molecule 3: DNA topoisomerase 1

Chain X: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	68.52Å 138.23Å 113.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 19.66 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.70) 96.6 (19.66-2.91)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	19.54 (at 2.93Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.191 , 0.237 0.202 , 0.231	Depositor DCC
R_{free} test set	598 reflections (5.41%)	DCC
Wilson B-factor (Å ²)	71.1	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3165	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.94% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	Y	1.05	0/239	1.74	4/366 (1.1%)
2	Z	1.03	0/350	1.85	12/539 (2.2%)
3	X	0.57	1/2623 (0.0%)	0.67	1/3530 (0.0%)
All	All	0.68	1/3212 (0.0%)	1.01	17/4435 (0.4%)

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
3	X	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	X	13	THR	C-O	5.56	1.33	1.23

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Z	520	DA	O4'-C1'-N9	9.07	114.35	108.00
1	Y	501	DT	O4'-C1'-N1	8.04	113.63	108.00
1	Y	504	DT	O4'-C1'-N1	8.02	113.62	108.00
2	Z	522	DG	C5-C6-N1	7.52	115.26	111.50
2	Z	516	DA	O4'-C1'-N9	-6.71	103.30	108.00
2	Z	522	DG	C2-N3-C4	6.50	115.15	111.90
2	Z	519	DA	O4'-C1'-N9	-6.35	103.56	108.00
2	Z	528	DA	O4'-C1'-N9	6.13	112.29	108.00
2	Z	517[A]	DA	P-O3'-C3'	6.00	126.89	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Z	517[B]	DA	P-O3'-C3'	6.00	126.89	119.70
2	Z	516	DA	N1-C6-N6	-5.85	115.09	118.60
2	Z	519	DA	P-O3'-C3'	5.76	126.61	119.70
2	Z	527	DC	P-O3'-C3'	5.63	126.45	119.70
2	Z	515	DT	C6-C5-C7	-5.48	119.61	122.90
3	X	148	LEU	CA-CB-CG	5.41	127.75	115.30
1	Y	502	DT	C4-C5-C7	5.27	122.16	119.00
1	Y	504	DT	C6-N1-C2	-5.17	118.71	121.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	X	243	SER	Peptide

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	Y	216	0	126	7	0
2	Z	310	0	169	2	0
3	X	2585	0	2647	25	0
4	X	49	0	0	0	0
4	Y	4	0	0	0	0
4	Z	1	0	0	0	0
All	All	3165	0	2942	29	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 5.

All (29) 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)
3:X:149:LYS:H	3:X:152:HIS:HD2	1.04	0.97
3:X:244:PRO:O	3:X:245:LEU:HG	1.77	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:X:149:LYS:H	3:X:152:HIS:CD2	1.95	0.82
1:Y:501:DT:H2''	1:Y:502:DT:OP2	1.98	0.63
1:Y:511:DT:C2'	3:X:274:PTR:O3P	2.48	0.62
3:X:217:ILE:HD12	3:X:222:LEU:HD13	1.83	0.61
3:X:295:THR:HB	3:X:299:GLU:HG3	1.82	0.60
1:Y:511:DT:C4'	3:X:274:PTR:O3P	2.52	0.57
2:Z:516:DA:H2''	2:Z:517[B]:DA:OP2	2.08	0.53
3:X:103:ASN:OD1	3:X:181:ARG:NH1	2.43	0.51
3:X:143:VAL:HG22	3:X:164:PHE:CD2	2.45	0.51
3:X:58:ILE:HG22	3:X:59:PHE:HD2	1.74	0.51
1:Y:511:DT:H4'	3:X:274:PTR:P	2.50	0.50
3:X:244:PRO:O	3:X:245:LEU:CG	2.55	0.50
2:Z:517[A]:DA:H2''	2:Z:518:DT:O5'	2.10	0.49
3:X:55:THR:HA	3:X:75:MET:HB3	1.94	0.49
3:X:276:ALA:HB3	3:X:279:ILE:HD12	1.96	0.48
3:X:122:LEU:HD23	3:X:182:LEU:HD23	1.96	0.47
3:X:268:SER:O	3:X:272:ARG:HB2	2.14	0.47
3:X:308:VAL:O	3:X:312:THR:HB	2.15	0.46
3:X:26:PRO:HB3	3:X:49:THR:HG22	1.97	0.46
3:X:312:THR:O	3:X:312:THR:HG23	2.16	0.45
3:X:256:ILE:HD13	3:X:271:LYS:HB2	1.99	0.45
3:X:122:LEU:O	3:X:126:MET:HB2	2.17	0.45
3:X:150:ASN:HB2	3:X:195:PRO:HA	1.99	0.44
1:Y:504:DT:H2''	1:Y:505:DC:O5'	2.18	0.43
1:Y:511:DT:H4'	3:X:274:PTR:O3P	2.19	0.43
1:Y:511:DT:H2''	3:X:274:PTR:O3P	2.19	0.43
3:X:60:VAL:HG22	3:X:68:ARG:NH2	2.34	0.43

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	X	311/314 (99%)	295 (95%)	14 (4%)	2 (1%)	28	56

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	X	244	PRO
3	X	245	LEU

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	
3	X	292/292 (100%)	265 (91%)	27 (9%)	11	24

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	X	11	LEU
3	X	16	ASN
3	X	52	GLU
3	X	54	LEU
3	X	56	ARG
3	X	60	VAL
3	X	107	LYS
3	X	111	THR
3	X	137	LEU
3	X	143	VAL
3	X	145	LEU
3	X	146	LEU
3	X	148	LEU
3	X	175	VAL
3	X	182	LEU
3	X	222	LEU
3	X	240	LYS
3	X	241	SER
3	X	244	PRO

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Mol	Chain	Res	Type
3	X	254	LEU
3	X	265	HIS
3	X	268	SER
3	X	272	ARG
3	X	283	VAL
3	X	286	LYS
3	X	312	THR
3	X	313	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
3	X	15	ASN
3	X	16	ASN
3	X	32	GLN
3	X	33	HIS
3	X	78	GLN
3	X	150	ASN
3	X	152	HIS
3	X	307	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	$\# Z > 2$
3	PTR	X	274	1,3	15,16,17	1.88	1 (6%)	19,22,24	1.03	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	PTR	X	274	1,3	-	0/9/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	X	274	PTR	OH-CZ	-6.74	1.25	1.40

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	X	274	PTR	5	0

5.5 Carbohydrates [i](#)

There are no carbohydrates 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	Y	11/11 (100%)	0.13	0 100 100	65, 71, 84, 97	0
2	Z	14/14 (100%)	0.31	1 (7%) 17 14	61, 67, 71, 72	0
3	X	313/314 (99%)	0.37	14 (4%) 34 32	57, 68, 80, 92	0
All	All	338/339 (99%)	0.36	15 (4%) 35 33	57, 68, 80, 97	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	X	313	ASP	4.4
3	X	314	GLY	4.2
3	X	110	SER	3.4
3	X	51	GLU	3.2
3	X	24	ASN	2.9
3	X	1	MET	2.5
3	X	2	ARG	2.5
3	X	52	GLU	2.4
3	X	111	THR	2.2
3	X	123	MET	2.2
3	X	104	LYS	2.1
3	X	244	PRO	2.1
3	X	121	MET	2.1
3	X	197	GLU	2.1
2	Z	517[A]	DA	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	PTR	X	274	16/17	0.96	0.15	-	62,67,68,68	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.