

wwPDB X-ray Structure Validation Summary Report (i)

Oct 17, 2021 – 03:17 AM EDT

PDB ID	:	1MU9
Title	:	Crystal Structure of a Human Tyrosyl-DNA Phosphodiesterase (Tdp1)-
		Vanadate Complex
Authors	:	Davies, D.R.; Interthal, H.; Champoux, J.J.; Hol, W.G.J.
Deposited on		
Resolution	:	2.05 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 following versions of software and data (see references (1)) were used in the production of this report:

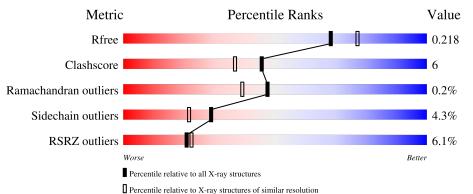
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.05 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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% 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	А	485	6% 75%	11%	•	12%
1	В	485	5% 74%	15%		• 11%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7146 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.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	425	Total	С	Ν	0	\mathbf{S}	0	0	0
	А	420	3393	2208	573	601	11	0		
1	В	434	Total	С	Ν	0	S	0	0	0
	D	434	3452	2242	584	615	11	0		0

• Molecule 1 is a protein called Tyrosyl-DNA Phosphodiesterase.

Chain	Residue	Modelled	Actual	Comment	Reference
А	124	MET	-	cloning artifact	GB 20127586
А	125	GLY	-	cloning artifact	GB 20127586
А	126	SER	-	cloning artifact	GB 20127586
А	127	SER	-	cloning artifact	GB 20127586
А	128	HIS	-	cloning artifact	GB 20127586
А	129	HIS	-	cloning artifact	GB 20127586
А	130	HIS	-	cloning artifact	GB 20127586
А	131	HIS	-	cloning artifact	GB 20127586
А	132	HIS	-	cloning artifact	GB 20127586
А	133	HIS	-	cloning artifact	GB 20127586
А	134	SER	-	cloning artifact	GB 20127586
А	135	SER	-	cloning artifact	GB 20127586
А	136	GLY	-	cloning artifact	GB 20127586
А	137	LEU	-	cloning artifact	GB 20127586
А	138	VAL	-	cloning artifact	GB 20127586
А	139	PRO	-	cloning artifact	GB 20127586
А	140	ARG	-	cloning artifact	GB 20127586
А	141	GLY	-	cloning artifact	GB 20127586
А	142	SER	-	cloning artifact	GB 20127586
А	143	HIS	-	cloning artifact	GB 20127586
А	144	MET	-	cloning artifact	GB 20127586
А	145	LEU	-	cloning artifact	GB 20127586
А	146	GLU	-	cloning artifact	GB 20127586
А	147	ASP	-	cloning artifact	GB 20127586
А	148	PRO	-	cloning artifact	GB 20127586

There are 56 discrepancies between the modelled and reference sequences:

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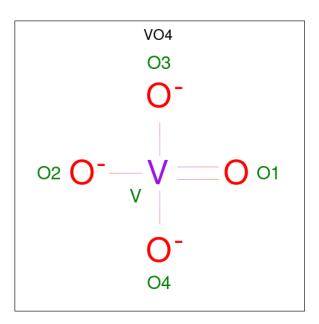


Chain	Residue	Modelled	Actual	Comment	Reference
А	322	ASN	ASP	engineered mutation	GB 20127586
А	328	THR	MET	engineered mutation	GB 20127586
А	548	LEU	PHE	engineered mutation	GB 20127586
В	124	MET	-	cloning artifact	GB 20127586
В	125	GLY	-	cloning artifact	GB 20127586
В	126	SER	-	cloning artifact	GB 20127586
В	127	SER	-	cloning artifact	GB 20127586
В	128	HIS	-	cloning artifact	GB 20127586
В	129	HIS	-	cloning artifact	GB 20127586
В	130	HIS	-	cloning artifact	GB 20127586
В	131	HIS	-	cloning artifact	GB 20127586
В	132	HIS	-	cloning artifact	GB 20127586
В	133	HIS	-	cloning artifact	GB 20127586
В	134	SER	-	cloning artifact	GB 20127586
В	135	SER	-	cloning artifact	GB 20127586
В	136	GLY	-	cloning artifact	GB 20127586
В	137	LEU	-	cloning artifact	GB 20127586
В	138	VAL	-	cloning artifact	GB 20127586
В	139	PRO	-	cloning artifact	GB 20127586
В	140	ARG	-	cloning artifact	GB 20127586
В	141	GLY	-	cloning artifact	GB 20127586
В	142	SER	-	cloning artifact	GB 20127586
В	143	HIS	-	cloning artifact	GB 20127586
В	144	MET	-	cloning artifact	GB 20127586
В	145	LEU	-	cloning artifact	GB 20127586
В	146	GLU	-	cloning artifact	GB 20127586
В	147	ASP	-	cloning artifact	GB 20127586
В	148	PRO	-	cloning artifact	GB 20127586
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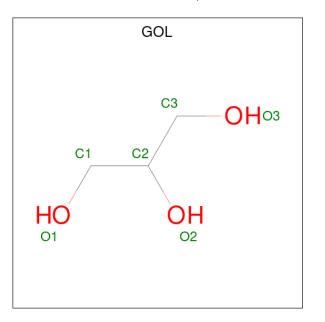
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• Molecule 2 is VANADATE ION (three-letter code: VO4) (formula: O_4V).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total O V 3 2 1	0	0
2	В	1	Total O V 3 2 1	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0



• Molecule 4 is water.

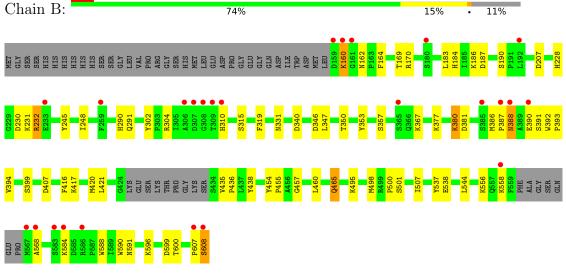
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	136	Total O 136 136	0	0
4	В	147	Total O 147 147	0	0



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 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.

- Chain A: 75% 11% 12%
- Molecule 1: Tyrosyl-DNA Phosphodiesterase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	50.03Å 104.98Å 194.30Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.97 - 2.05	Depositor
Resolution (A)	19.97 - 2.05	EDS
% Data completeness	99.8 (19.97-2.05)	Depositor
(in resolution range)	99.7 (19.97 - 2.05)	EDS
R _{merge}	0.10	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$4.46 (at 2.06 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
D D.	0.199 , 0.214	Depositor
R, R_{free}	0.203 , 0.218	DCC
R_{free} test set	3291 reflections $(5.06%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	25.8	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 57.3	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7146	wwPDB-VP
Average B, all atoms $(Å^2)$	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.26% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: GOL, $\rm VO4$

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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.58	0/3504	0.82	6/4765~(0.1%)	
1	В	0.63	0/3565	0.82	5/4849~(0.1%)	
All	All	0.61	0/7069	0.82	11/9614~(0.1%)	

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	А	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	407	ASP	CB-CG-OD2	7.37	124.93	118.30
1	А	209	ASP	CB-CG-OD2	6.65	124.28	118.30
1	А	599	ASP	CB-CG-OD2	6.51	124.16	118.30
1	В	207	ASP	CB-CG-OD2	6.06	123.75	118.30
1	А	340	ASP	CB-CG-OD2	6.00	123.70	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	307	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	А	3393	0	3330	32	0
1	В	3452	0	3377	55	0
2	А	3	0	0	0	0
2	В	3	0	0	0	0
3	А	6	0	6	0	0
3	В	6	0	6	0	0
4	А	136	0	0	2	0
4	В	147	0	0	2	0
All	All	7146	0	6719	87	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 6.

The worst 5 of 87 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:498:MET:CE	1:B:507:ILE:HG21	1.64	1.26
1:A:607:PRO:O	1:A:608:SER:HB2	1.40	1.13
1:B:498:MET:HE1	1:B:507:ILE:HG21	1.30	1.07
1:B:607:PRO:O	1:B:608:SER:HB2	1.50	1.06
1:B:160:LYS:HG3	1:B:160:LYS:O	1.53	1.04

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	А	417/485~(86%)	401 (96%)	15~(4%)	1 (0%)	47	39
1	В	428/485 (88%)	408 (95%)	19 (4%)	1 (0%)	47	39
All	All	845/970~(87%)	809 (96%)	34 (4%)	2(0%)	47	39

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	307	ASP
1	В	160	LYS

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	Percentiles		
1	А	366/421~(87%)	349~(95%)	17~(5%)	27 19	
1	В	371/421 (88%)	356~(96%)	15 (4%)	31 24	
All	All	737/842~(88%)	705~(96%)	32 (4%)	29 22	

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	В	584	LYS
1	В	590	TRP
1	А	500	PRO
1	А	495	LYS
1	В	600	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	228	HIS
1	В	310	HIS
1	В	528	ASN
1	В	397	GLN

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Mol	Chain	Res	Type
1	В	465	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)

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	Turne	Type Chain R	Chain Res	Link	Bond lengths			Bond angles		
	Type		nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	GOL	В	610	2	$5,\!5,\!5$	0.75	0	$5,\!5,\!5$	1.17	0
2	VO4	А	609	3,1	0,2,4	-	-	-		
2	VO4	В	609	3,1	0,2,4	-	-	-		
3	GOL	А	610	2	$5,\!5,\!5$	0.61	0	$5,\!5,\!5$	2.25	1 (20%)

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	GOL	В	610	2	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	А	610	2	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	rpe Atoms		$Observed(^{o})$	$Ideal(^{o})$
3	А	610	GOL	C3-C2-C1	4.47	129.10	111.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95^{th} 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	$\langle RSRZ \rangle$	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	А	425/485~(87%)	0.43	27 (6%) 19 21	17, 31, 52, 69	0
1	В	434/485~(89%)	0.21	25 (5%) 23 25	12, 24, 42, 66	0
All	All	859/970~(88%)	0.32	52 (6%) 21 22	12, 27, 48, 69	0

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	608	SER	7.4
1	В	307	ASP	6.6
1	А	528	ASN	6.1
1	А	608	SER	5.3
1	В	308	GLY	5.3

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (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. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	GOL	А	610	6/6	0.95	0.13	$27,\!31,\!34,\!38$	0
3	GOL	В	610	6/6	0.95	0.12	20,24,30,34	0
2	VO4	А	609	3/5	0.99	0.08	27,27,28,29	0
2	VO4	В	609	3/5	0.99	0.07	21,21,23,23	0

6.5 Other polymers (i)

There are no such residues in this entry.

