



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 11:32 am BST

PDB ID : 6VDC
Title : POL domain of Pol1 from *M. smegmatis*
Authors : Shuman, S.; Goldgur, Y.; Ghosh, S.
Deposited on : 2019-12-24
Resolution : 2.40 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

<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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

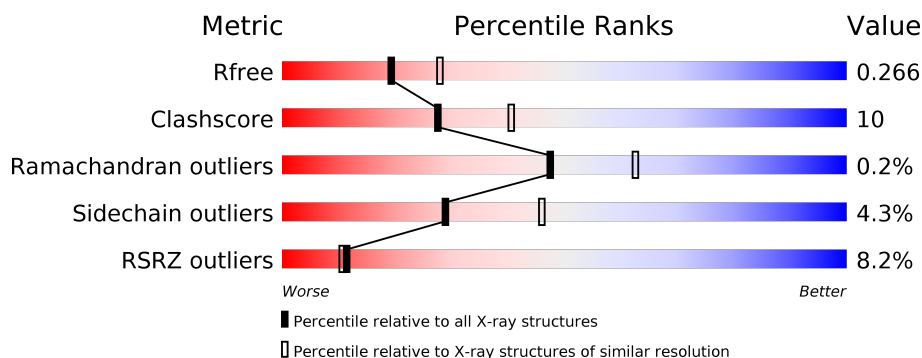
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 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 $\leq 5\%$. 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	A	605	<div> <div>7%</div> <div>65%</div> <div>16%</div> <div>18%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3920 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 DNA polymerase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	0	0
			3838	2386	697	743	12			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	81	Total	O	0	0
			81	81		

- Molecule 1: DNA polymerase I



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	62.59Å 150.95Å 150.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.83 – 2.40 45.83 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (45.83-2.40) 93.3 (45.83-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.219 , 0.266 0.219 , 0.266	Depositor DCC
R_{free} test set	1993 reflections (7.13%)	wwPDB-VP
Wilson B-factor (Å ²)	50.5	Xtriage
Anisotropy	0.410	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3920	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 4.70% 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: MN

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	0.46	1/3896 (0.0%)	0.62	2/5274 (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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	401	GLU	CD-OE2	5.83	1.32	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	878	LEU	CA-CB-CG	6.55	130.36	115.30
1	A	880	ARG	NE-CZ-NH2	-5.17	117.72	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	859	VAL	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	A	3838	0	3788	76	0
2	A	1	0	0	0	0
3	A	81	0	0	1	0
All	All	3920	0	3788	76	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 10.

All (76) 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:A:719:ARG:HB3	1:A:773:ARG:HH12	1.08	1.14
1:A:719:ARG:HB3	1:A:773:ARG:NH1	1.66	1.11
1:A:352:LYS:HE2	1:A:354:TYR:O	1.56	1.06
1:A:781:LEU:HD12	1:A:823:LEU:HD23	1.57	0.84
1:A:729:THR:HG22	1:A:731:GLU:H	1.46	0.80
1:A:771:PHE:CD2	1:A:778:ARG:HB3	2.25	0.71
1:A:766:GLN:HA	1:A:769:GLN:HB2	1.72	0.71
1:A:659:ILE:HG13	1:A:660:ARG:HG3	1.72	0.70
1:A:719:ARG:CB	1:A:773:ARG:HH12	1.98	0.69
1:A:659:ILE:HA	1:A:668:ARG:HH22	1.57	0.68
1:A:717:ALA:HB2	1:A:736:VAL:HG11	1.77	0.66
1:A:781:LEU:HD12	1:A:823:LEU:CD2	2.25	0.66
1:A:650:THR:HG22	1:A:651:GLU:HG3	1.78	0.65
1:A:798:LEU:HD13	1:A:833:ASP:HB3	1.79	0.64
1:A:764:LYS:HA	1:A:767:MET:HG3	1.80	0.63
1:A:352:LYS:NZ	1:A:355:ASP:HB2	2.14	0.62
1:A:713:HIS:O	1:A:736:VAL:HG21	2.00	0.61
1:A:498:ARG:NE	1:A:498:ARG:HA	2.15	0.61
1:A:719:ARG:HD3	1:A:773:ARG:HH22	1.66	0.61
1:A:723:VAL:CG1	1:A:728:VAL:HG12	2.32	0.60
1:A:718:SER:HB2	1:A:728:VAL:HG11	1.84	0.60
1:A:719:ARG:HD3	1:A:773:ARG:NH2	2.17	0.59
1:A:768:GLU:O	1:A:772:ASP:HB2	2.04	0.58
1:A:719:ARG:HH11	1:A:773:ARG:HH22	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:798:LEU:CD1	1:A:833:ASP:HB3	2.33	0.57
1:A:723:VAL:HG12	1:A:728:VAL:HG12	1.87	0.57
1:A:352:LYS:HZ1	1:A:355:ASP:HB2	1.69	0.57
1:A:719:ARG:O	1:A:773:ARG:NH1	2.39	0.56
1:A:699:ASP:O	1:A:703:ILE:HG13	2.06	0.56
1:A:736:VAL:O	1:A:740:SER:OG	2.25	0.55
1:A:342:ARG:HD3	1:A:398:ALA:HB2	1.88	0.55
1:A:352:LYS:CE	1:A:354:TYR:O	2.44	0.55
1:A:512:VAL:HG21	1:A:836:LYS:HB3	1.89	0.54
1:A:723:VAL:HB	1:A:728:VAL:HG12	1.90	0.53
1:A:381:GLU:CD	1:A:381:GLU:H	2.12	0.53
1:A:719:ARG:CB	1:A:773:ARG:NH1	2.58	0.52
1:A:737:LYS:HE3	1:A:741:TYR:HE2	1.75	0.52
1:A:844:GLN:NE2	1:A:848:ASP:OD1	2.43	0.52
1:A:352:LYS:NZ	1:A:355:ASP:CB	2.73	0.51
1:A:723:VAL:HG11	1:A:728:VAL:HA	1.92	0.51
1:A:512:VAL:HG23	1:A:840:ILE:HD11	1.93	0.51
1:A:766:GLN:N	1:A:766:GLN:OE1	2.44	0.50
1:A:538:PHE:CE1	1:A:616:LEU:HB3	2.47	0.50
1:A:473:GLN:HG2	1:A:474:ALA:N	2.28	0.49
1:A:811:ASN:O	1:A:814:VAL:HG12	2.12	0.49
1:A:669:ASP:HA	1:A:902:SER:OG	2.12	0.49
1:A:434:GLN:HB3	1:A:437:PHE:CE2	2.47	0.49
1:A:662:GLU:O	1:A:666:ARG:HG3	2.12	0.49
1:A:342:ARG:NH2	3:A:1108:HOH:O	2.45	0.48
1:A:641:ILE:HG21	1:A:648:SER:OG	2.14	0.48
1:A:723:VAL:CB	1:A:728:VAL:HG12	2.45	0.47
1:A:889:LEU:HB2	1:A:891:VAL:O	2.13	0.47
1:A:811:ASN:HA	1:A:812:ARG:NH1	2.30	0.46
1:A:449:ARG:HG2	1:A:450:GLU:O	2.14	0.46
1:A:538:PHE:CD1	1:A:616:LEU:HB3	2.51	0.45
1:A:733:ARG:HA	1:A:736:VAL:HG22	1.98	0.45
1:A:737:LYS:HE3	1:A:741:TYR:CE2	2.51	0.45
1:A:533:GLN:NE2	1:A:537:GLU:OE1	2.39	0.45
1:A:716:VAL:HG13	1:A:774:PHE:CE2	2.52	0.45
1:A:719:ARG:CD	1:A:773:ARG:HH22	2.29	0.45
1:A:714:SER:HB2	1:A:728:VAL:HG21	1.98	0.45
1:A:876:GLU:O	1:A:880:ARG:HG3	2.17	0.45
1:A:538:PHE:CE2	1:A:616:LEU:HD23	2.53	0.43
1:A:719:ARG:CD	1:A:773:ARG:HH12	2.31	0.43
1:A:612:ASP:O	1:A:616:LEU:HD13	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:716:VAL:O	1:A:720:ALA:HB3	2.19	0.43
1:A:544:ASP:OD2	1:A:544:ASP:N	2.50	0.42
1:A:525:ALA:HB3	1:A:672:VAL:O	2.20	0.42
1:A:734:ARG:HE	1:A:734:ARG:HB2	1.67	0.42
1:A:761:GLU:N	1:A:764:LYS:HD3	2.35	0.42
1:A:744:ALA:H	1:A:820:ARG:HH12	1.67	0.42
1:A:812:ARG:O	1:A:816:GLU:HG3	2.20	0.41
1:A:659:ILE:HG13	1:A:660:ARG:H	1.85	0.41
1:A:381:GLU:HG2	1:A:382:ASP:N	2.36	0.41
1:A:813:GLN:H	1:A:813:GLN:HG3	1.72	0.40
1:A:610:HIS:CD2	1:A:611:ARG:HG3	2.57	0.40

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	487/605 (80%)	464 (95%)	22 (4%)	1 (0%)	47 62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	860	HIS

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	396/487 (81%)	379 (96%)	17 (4%)	29	46

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	412	ARG
1	A	435	ARG
1	A	436	SER
1	A	498	ARG
1	A	533	GLN
1	A	543	ARG
1	A	617	LYS
1	A	735	ARG
1	A	762	GLU
1	A	772	ASP
1	A	802	ARG
1	A	812	ARG
1	A	815	ARG
1	A	899	TYR
1	A	901	ARG
1	A	902	SER
1	A	908	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	769	GLN
1	A	828	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	A	497/605 (82%)	0.48	41 (8%) 11 10	40, 61, 121, 134	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	765	VAL	8.9
1	A	603	PHE	8.2
1	A	607	LEU	7.4
1	A	724	PRO	7.4
1	A	732	LEU	6.6
1	A	770	TYR	6.0
1	A	602	PRO	5.6
1	A	542	ILE	5.6
1	A	763	ALA	4.8
1	A	470	VAL	4.7
1	A	762	GLU	4.2
1	A	733	ARG	3.9
1	A	469	GLY	3.8
1	A	606	HIS	3.6
1	A	769	GLN	3.5
1	A	452	ARG	3.0
1	A	766	GLN	2.8
1	A	736	VAL	2.8
1	A	739	MET	2.7
1	A	768	GLU	2.6
1	A	610	HIS	2.6
1	A	712	LEU	2.6
1	A	660	ARG	2.5
1	A	721	PHE	2.5
1	A	604	LEU	2.5
1	A	707	ASN	2.5
1	A	538	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	735	ARG	2.4
1	A	714	SER	2.4
1	A	715	PHE	2.4
1	A	609	ALA	2.4
1	A	611	ARG	2.4
1	A	722	SER	2.2
1	A	741	TYR	2.2
1	A	471	ASP	2.1
1	A	820	ARG	2.1
1	A	716	VAL	2.1
1	A	776	GLY	2.1
1	A	498	ARG	2.1
1	A	730	PRO	2.0
1	A	743	LEU	2.0

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 carbohydrates 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, 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	B-factors(\AA^2)	Q<0.9
2	MN	A	1001	1/1	0.98	0.08	75,75,75,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.