

Full wwPDB X-ray Structure Validation Report (i)

May 21, 2020 - 07:32 am BST

PDB ID	:	1V0R
Title	:	Tungstate-inhibited phospholipase D from Streptomyces sp. strain PMF
Authors	:	Leiros, I.; McSweeney, S.; Hough, E.
Deposited on		
Resolution	:	1.70 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 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:

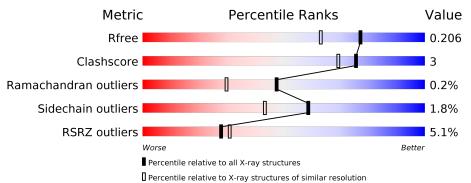
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25 th 2019)
Refmac	:	5.8.0158
CCP4	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	$egin{array}{c} \mathbf{Whole \ archive} \ (\#\mathbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695(1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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					
			5%					
1	A	506	89%	7% • •				



2 Entry composition (i)

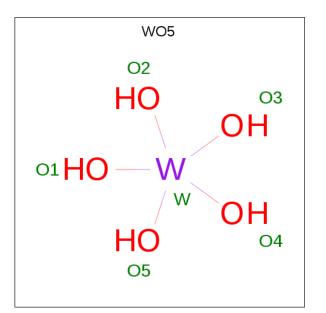
There are 3 unique types of molecules in this entry. The entry contains 4250 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PHOSPHOLIPASE D.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	40.3	Total	С	Ν	Ο	\mathbf{S}	52	0	0
		493	3700	2308	651	727	14	52		

• Molecule 2 is TUNGSTATE(VI) ION (three-letter code: WO5) (formula: H₅O₅W).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 6	O 5	W 1	0	0

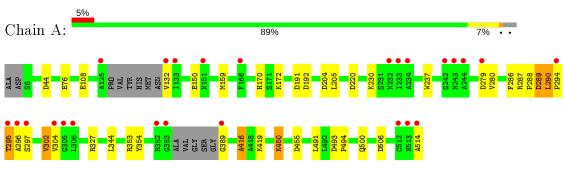
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	544	Total O 544 544	0	0



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: PHOSPHOLIPASE D



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	57.61\AA 56.90\AA 68.95\AA	Depositor
a, b, c, α , β , γ	90.00° 93.67° 90.00°	Depositor
Resolution (Å)	69.01 - 1.70	Depositor
Resolution (A)	22.94 - 1.70	EDS
% Data completeness	99.6(69.01-1.70)	Depositor
(in resolution range)	99.7(22.94-1.70)	EDS
R _{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.89 (at 1.70 \text{\AA})$	Xtriage
Refinement program	REFMAC $5.1.24$	Depositor
R R.	0.155 , 0.198	Depositor
R, R_{free}	0.168 , 0.206	DCC
R_{free} test set	2485 reflections $(5.08%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	18.4	Xtriage
Anisotropy	0.534	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34 , 50.1	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4250	wwPDB-VP
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.67% 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: $\rm WO5$

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	Bo	nd lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.16	8/3775~(0.2%)	1.09	22/5141~(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
1	А	1	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	290	LEU	C-N	32.05	1.95	1.34
1	А	150	GLU	CB-CG	-22.19	1.09	1.52
1	А	295	THR	CA-CB	-21.15	0.98	1.53
1	А	302	VAL	C-N	17.00	1.73	1.34
1	А	416	ALA	C-N	8.46	1.53	1.34
1	А	132	VAL	CA-CB	-6.84	1.40	1.54
1	А	170	HIS	CD2-NE2	-6.59	1.23	1.38
1	A	170	HIS	CG-CD2	-6.34	1.25	1.35

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
1	А	295	THR	N-CA-CB	29.42	166.20	110.30
1	А	295	THR	CA-CB-CG2	14.88	133.24	112.40
1	А	295	THR	CB-CA-C	-11.27	81.17	111.60
1	А	150	GLU	CA-CB-CG	10.06	135.53	113.40
1	А	170	HIS	CG-CD2-NE2	9.36	126.98	109.20

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	327	ARG	NE-CZ-NH1	7.83	124.21	120.30
1	А	220	ASP	CB-CG-OD1	7.49	125.04	118.30
1	А	290	LEU	CA-C-N	-7.20	96.93	117.10
1	А	290	LEU	O-C-N	-6.95	107.90	121.10
1	А	302	VAL	O-C-N	-6.59	112.16	122.70
1	А	237	TRP	CD1-CG-CD2	6.52	111.51	106.30
1	А	192	ASP	CB-CG-OD2	6.48	124.14	118.30
1	А	204	ASP	CB-CG-OD1	6.24	123.92	118.30
1	А	191	ASP	CB-CG-OD2	6.16	123.84	118.30
1	А	506	ASP	CB-CG-OD2	6.13	123.82	118.30
1	А	44	ASP	CB-CG-OD1	5.89	123.60	118.30
1	А	455	ASP	CB-CG-OD2	5.83	123.55	118.30
1	А	170	HIS	ND1-CG-CD2	-5.77	97.92	106.00
1	А	289	ASP	CB-CG-OD2	5.72	123.45	118.30
1	А	327	ARG	NE-CZ-NH2	-5.39	117.60	120.30
1	А	353	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	А	132	VAL	N-CA-CB	5.21	122.95	111.50

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All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	А	295	THR	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	416	ALA	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	3700	0	3630	21	0
2	А	6	0	0	3	0
3	А	544	0	0	7	0
All	All	4250	0	3630	22	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 3.

All (22) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom D	Interatomic	Clash
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)
1:A:302:VAL:C	1:A:304:VAL:N	1.73	1.41
1:A:290:LEU:C	1:A:294:PRO:N	1.95	1.19
1:A:290:LEU:C	1:A:294:PRO:CA	2.65	0.64
1:A:290:LEU:CA	1:A:294:PRO:N	2.61	0.64
1:A:76:GLU:CG	3:A:2156:HOH:O	2.47	0.62
1:A:108:GLU:HG2	3:A:2211:HOH:O	2.02	0.57
1:A:389:GLY:N	3:A:2435:HOH:O	2.39	0.56
1:A:297:SER:HB2	1:A:354:TYR:OH	2.05	0.55
1:A:279:ASP:OD2	1:A:280:VAL:HG12	2.08	0.53
1:A:294:PRO:HG3	3:A:2419:HOH:O	2.08	0.52
1:A:450:LYS:NZ	2:A:600:WO5:O2	2.43	0.52
1:A:230:LYS:HE3	3:A:2322:HOH:O	2.12	0.49
1:A:302:VAL:C	1:A:304:VAL:CA	2.75	0.49
1:A:491:LEU:HD23	1:A:491:LEU:C	2.34	0.48
1:A:290:LEU:HA	1:A:294:PRO:N	2.30	0.46
1:A:286:PHE:CZ	1:A:288:PRO:HB3	2.51	0.45
1:A:286:PHE:O	1:A:287:ARG:HD3	2.18	0.44
1:A:419:LYS:NZ	1:A:514:ALA:O	2.50	0.43
1:A:500:GLN:NE2	3:A:2534:HOH:O	2.52	0.42
1:A:450:LYS:CE	2:A:600:WO5:O2	2.68	0.42
1:A:493:ASP:HB2	1:A:494:PRO:HD3	2.01	0.41
2:A:600:WO5:O3	3:A:2544:HOH:O	2.22	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	А	487/506~(96%)	473 (97%)	13 (3%)	1 (0%)	47 30

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	296	ALA

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	395/406~(97%)	388~(98%)	7(2%)	59 43

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	159	MET
1	А	172	LYS
1	А	205	LEU
1	А	289	ASP
1	А	295	THR
1	А	344	LEU
1	А	450	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	20	GLN
1	А	309	ASN
1	А	409	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand 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).

ſ	Mol	Type	Chain	Res	Link	B	ond leng	gths	В	ond ang	gles
	IVIOI	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
	2	WO5	A	600	1	0,5,5	0.00	-	-		

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.

1 monomer is involved in 3 short contacts:

N	Лоl	Chain	\mathbf{Res}	Type	Clashes	Symm-Clashes
	2	А	600	WO5	3	0

5.7 Other polymers (i)

There are no such residues in this entry.



5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	А	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	А	290:LEU	С	294:PRO	Ν	1.95
1	А	302:VAL	С	304:VAL	Ν	1.73



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 >	$\# RSRZ {>}2$		$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	А	493/506~(97%)	0.01	25 (5%) 28	31	12, 20, 36, 50	14 (2%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	А	296	ALA	8.6	
1	А	132	VAL	8.0	
1	А	383	GLY	6.5	
1	А	242	GLY	4.7	
1	А	233	ILE	4.7	
1	А	125	ALA	4.6	
1	А	244	ALA	4.0	
1	А	297	SER	3.9	
1	А	382	ARG	3.8	
1	А	243	ASN	3.7	
1	А	304	VAL	3.4	
1	А	166	PHE	3.2	
1	А	389	GLY	3.1	
1	А	279	ASP	3.1	
1	А	133	ILE	2.8	
1	А	513	ASN	2.7	
1	А	306	LEU	2.7	
1	А	512	CYS	2.6	
1	А	151	ASN	2.5	
1	А	232	ASN	2.5	
1	А	295	THR	2.4	
1	А	305	GLY	2.4	
1	А	514	ALA	2.4	
1	А	234	ALA	2.2	
1	А	294	PRO	2.2	



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, 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	${f B} ext{-factors}({f A}^2)$	$Q{<}0.9$
2	WO5	А	600	6/6	0.99	0.08	$17,\!22,\!24,\!26$	0

6.5 Other polymers (i)

There are no such residues in this entry.

