



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:47 am GMT

PDB ID : 5HRM
Title : Crystal structure of phosphotriesterase from *Sphingobium* sp. TCM1
Authors : Mabanglo, M.F.; Raushel, F.M.
Deposited on : 2016-01-23
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

<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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
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)	:	recalc28949

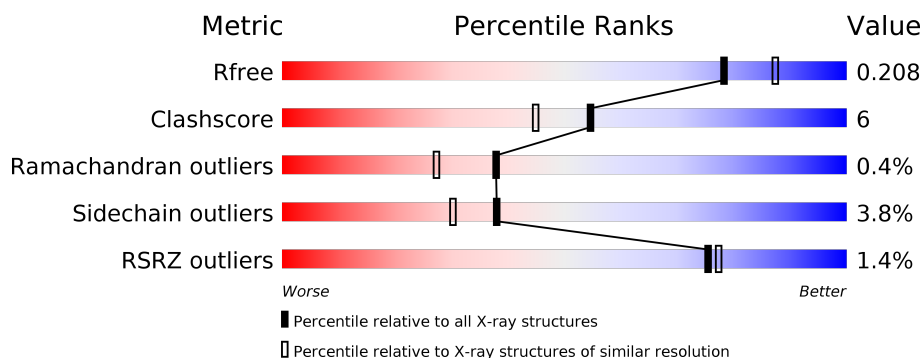
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2028 (2.08-2.04)
Clashscore	112137	2143 (2.08-2.04)
Ramachandran outliers	110173	2126 (2.08-2.04)
Sidechain outliers	110143	2126 (2.08-2.04)
RSRZ outliers	101464	2035 (2.08-2.04)

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 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	A	504	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 87% 10% .. </div> </div>
1	B	504	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 82% 15% .. </div> </div>
1	C	504	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 84% 13% .. </div> </div>
1	D	504	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 86% 12% .. </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MN	A	602	-	-	-	X
2	MN	B	601	-	-	-	X
2	MN	B	602	-	-	-	X
2	MN	C	601	-	-	-	X
2	MN	D	602	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15957 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 Haloalkylphosphorus hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	0	0	0
			3744	2354	680	698	12			
1	B	495	Total	C	N	O	S	0	0	0
			3753	2361	681	699	12			
1	C	494	Total	C	N	O	S	0	1	0
			3750	2357	681	699	13			
1	D	495	Total	C	N	O	S	0	1	0
			3756	2363	681	699	13			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	584	LEU	-	expression tag	UNP A0A077JBW9
A	585	GLU	-	expression tag	UNP A0A077JBW9
A	586	HIS	-	expression tag	UNP A0A077JBW9
A	587	HIS	-	expression tag	UNP A0A077JBW9
A	588	HIS	-	expression tag	UNP A0A077JBW9
A	589	HIS	-	expression tag	UNP A0A077JBW9
A	590	HIS	-	expression tag	UNP A0A077JBW9
A	591	HIS	-	expression tag	UNP A0A077JBW9
B	584	LEU	-	expression tag	UNP A0A077JBW9
B	585	GLU	-	expression tag	UNP A0A077JBW9
B	586	HIS	-	expression tag	UNP A0A077JBW9
B	587	HIS	-	expression tag	UNP A0A077JBW9
B	588	HIS	-	expression tag	UNP A0A077JBW9
B	589	HIS	-	expression tag	UNP A0A077JBW9
B	590	HIS	-	expression tag	UNP A0A077JBW9
B	591	HIS	-	expression tag	UNP A0A077JBW9
C	584	LEU	-	expression tag	UNP A0A077JBW9
C	585	GLU	-	expression tag	UNP A0A077JBW9
C	586	HIS	-	expression tag	UNP A0A077JBW9
C	587	HIS	-	expression tag	UNP A0A077JBW9
C	588	HIS	-	expression tag	UNP A0A077JBW9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	589	HIS	-	expression tag	UNP A0A077JBW9
C	590	HIS	-	expression tag	UNP A0A077JBW9
C	591	HIS	-	expression tag	UNP A0A077JBW9
D	584	LEU	-	expression tag	UNP A0A077JBW9
D	585	GLU	-	expression tag	UNP A0A077JBW9
D	586	HIS	-	expression tag	UNP A0A077JBW9
D	587	HIS	-	expression tag	UNP A0A077JBW9
D	588	HIS	-	expression tag	UNP A0A077JBW9
D	589	HIS	-	expression tag	UNP A0A077JBW9
D	590	HIS	-	expression tag	UNP A0A077JBW9
D	591	HIS	-	expression tag	UNP A0A077JBW9

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total 2	Mn 2	0	0
2	A	2	Total 2	Mn 2	0	0
2	D	2	Total 2	Mn 2	0	0
2	C	2	Total 2	Mn 2	0	0

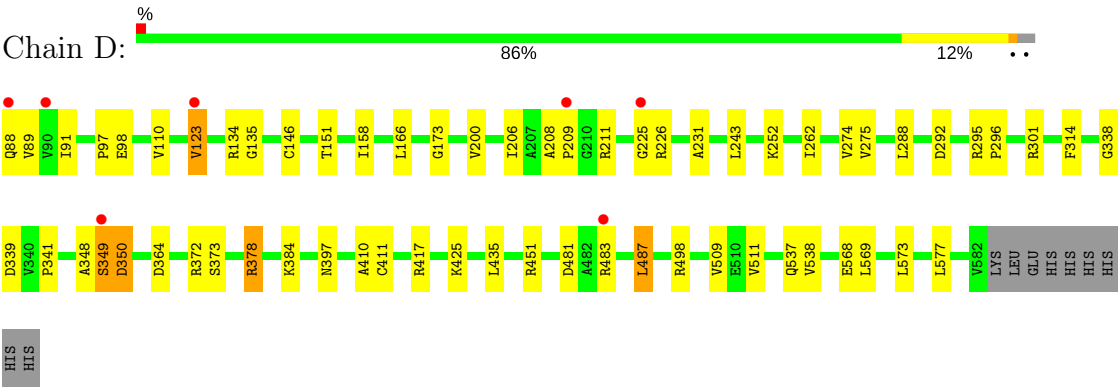
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	255	Total 255	O 255	0	0
3	B	273	Total 273	O 273	0	0
3	C	230	Total 230	O 230	0	0
3	D	188	Total 188	O 188	0	0

- Molecule 1: Haloalkylphosphorus hydrolase



● Molecule 1: Haloalkylphosphorus hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.98Å 91.27Å 96.33Å 78.90° 73.60° 89.86°	Depositor
Resolution (Å)	28.93 – 2.05 49.80 – 2.05	Depositor EDS
% Data completeness (in resolution range)	97.2 (28.93-2.05) 89.1 (49.80-2.05)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.03 (at 2.05Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.173 , 0.209 0.173 , 0.208	Depositor DCC
R_{free} test set	1997 reflections (1.68%)	DCC
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for h,-k,h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15957	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.74% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.52	0/3833	0.65	4/5218 (0.1%)
1	B	0.55	0/3843	0.67	1/5233 (0.0%)
1	C	0.55	0/3839	0.67	3/5226 (0.1%)
1	D	0.54	0/3849	0.63	1/5241 (0.0%)
All	All	0.54	0/15364	0.66	9/20918 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	351	GLY	C-N-CA	8.65	143.31	121.70
1	C	351	GLY	O-C-N	-8.09	109.75	122.70
1	A	339	ASP	CB-CG-OD1	-6.49	112.46	118.30
1	A	339	ASP	CB-CG-OD2	6.04	123.74	118.30
1	C	351	GLY	CA-C-N	5.96	130.32	117.20

There are no chirality outliers.

There are no planarity outliers.

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	A	3744	0	3700	33	4
1	B	3753	0	3713	53	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3750	0	3703	46	4
1	D	3756	0	3720	50	1
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	255	0	0	1	0
3	B	273	0	0	4	0
3	C	230	0	0	6	0
3	D	188	0	0	1	0
All	All	15957	0	14836	170	5

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 170 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:D:350:ASP:HB3	1:D:451:ARG:HH12	1.06	1.10
1:D:350:ASP:HB3	1:D:451:ARG:NH1	1.73	1.03
1:D:350:ASP:CB	1:D:451:ARG:HH12	1.84	0.90
1:D:208:ALA:HB1	1:D:209:PRO:HD2	1.52	0.90
1:C:128:ARG:NH1	3:C:701:HOH:O	2.06	0.87

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:VAL:CG2	1:C:96:ARG:NH1[1_465]	1.97	0.23
1:A:88:GLN:OE1	1:C:117:LEU:CD2[1_465]	1.97	0.23
1:B:117:LEU:CD1	1:D:88:GLN:OE1[1_455]	2.11	0.09
1:A:88:GLN:OE1	1:C:117:LEU:CG[1_465]	2.14	0.06
1:A:88:GLN:OE1	1:C:117:LEU:CD1[1_465]	2.17	0.03

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	
1	A	492/504 (98%)	473 (96%)	18 (4%)	1 (0%)	51	42
1	B	493/504 (98%)	473 (96%)	17 (3%)	3 (1%)	28	17
1	C	493/504 (98%)	471 (96%)	20 (4%)	2 (0%)	38	27
1	D	494/504 (98%)	470 (95%)	23 (5%)	1 (0%)	51	42
All	All	1972/2016 (98%)	1887 (96%)	78 (4%)	7 (0%)	38	27

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	352	ASP
1	C	226	ARG
1	A	200	VAL
1	B	200	VAL
1	B	351	GLY

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	
1	A	397/408 (97%)	384 (97%)	13 (3%)	43	36
1	B	399/408 (98%)	379 (95%)	20 (5%)	28	19
1	C	398/408 (98%)	383 (96%)	15 (4%)	38	30
1	D	400/408 (98%)	388 (97%)	12 (3%)	46	40
All	All	1594/1632 (98%)	1534 (96%)	60 (4%)	38	30

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	417	ARG
1	C	134	ARG
1	D	378	ARG
1	B	477	ASN
1	C	206	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	244	ASN
1	B	88	GLN
1	C	244	ASN
1	C	565	HIS

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](#)

Of 8 ligands modelled in this entry, 8 are 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 [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	A	494/504 (98%)	-0.26	6 (1%) 79 80	28, 38, 52, 79	0
1	B	495/504 (98%)	-0.23	7 (1%) 75 77	25, 36, 54, 99	0
1	C	494/504 (98%)	-0.10	7 (1%) 75 77	29, 40, 59, 93	0
1	D	495/504 (98%)	-0.06	7 (1%) 75 77	31, 42, 62, 79	0
All	All	1978/2016 (98%)	-0.16	27 (1%) 75 77	25, 39, 59, 99	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	349	SER	8.1
1	D	88	GLN	7.1
1	B	582	VAL	5.6
1	C	352	ASP	4.9
1	C	350	ASP	4.8

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. 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
2	MN	A	602	1/1	0.99	0.14	4.72	30,30,30,30	0
2	MN	D	602	1/1	0.99	0.16	4.42	35,35,35,35	0
2	MN	C	601	1/1	0.97	0.14	4.39	30,30,30,30	0
2	MN	B	601	1/1	0.98	0.17	2.75	28,28,28,28	0
2	MN	B	602	1/1	0.97	0.16	2.26	31,31,31,31	0
2	MN	C	602	1/1	0.99	0.16	-	30,30,30,30	0
2	MN	D	601	1/1	0.99	0.15	-	35,35,35,35	0
2	MN	A	601	1/1	1.00	0.13	-	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.