



wwPDB X-ray Structure Validation Summary Report i

Feb 26, 2014 – 03:34 PM GMT

PDB ID : 1EZ2
Title : THREE-DIMENSIONAL STRUCTURE OF THE ZINC-CONTAINING PHOSPHOTRIESTERASE WITH BOUND SUBSTRATE ANALOG DIISOPROPYLMETHYL PHOSPHONATE.
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Deposited on : 2000-05-09
Resolution : 1.90 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

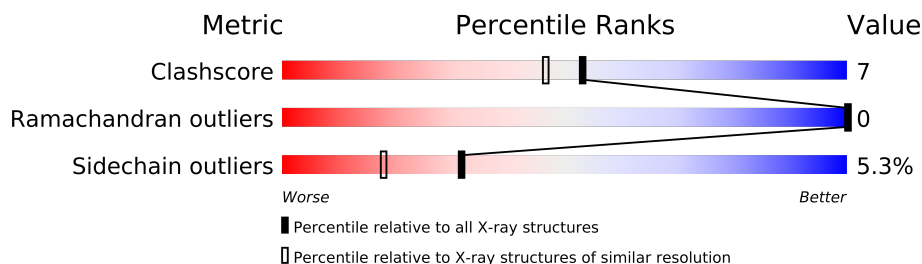
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.90 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))
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	331	
1	B	331	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5344 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PHOSPHOTRIESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	0	0	0
			2511	1590	446	468	7			
1	B	329	Total	C	N	O	S	0	2	0
			2521	1599	446	469	7			

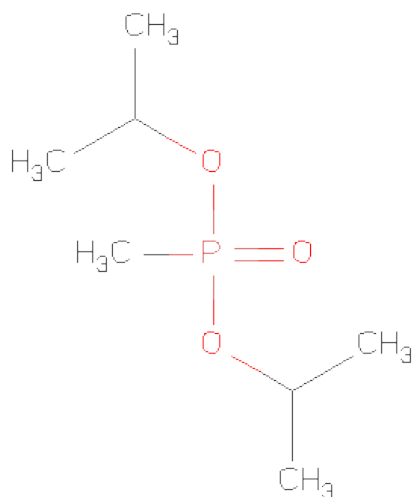
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	KCX	LYS	MODIFIED RESIDUE	UNP P0A434
B	169	KCX	LYS	MODIFIED RESIDUE	UNP P0A434

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is METHYLPHOSPHONIC ACID DIISOPROPYL ESTER (three-letter code: DII) (formula: C₇H₁₇O₃P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			11	7	3	1		
3	B	1	Total	C	O	P	0	0
			11	7	3	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	140	Total	O	0	0
			140	140		
4	B	146	Total	O	0	0
			146	146		

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	129.40Å 91.00Å 69.20Å 90.00° 91.60° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90	Depositor
% Data completeness (in resolution range)	92.0 (20.00-1.90)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT V. 5-E	Depositor
R, R_{free}	0.183 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5344	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

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: ZN, DII, KCX

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	0.95	10/2546 (0.4%)	1.29	37/3458 (1.1%)
1	B	0.91	10/2566 (0.4%)	1.32	42/3486 (1.2%)
All	All	0.93	20/5112 (0.4%)	1.30	79/6944 (1.1%)

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	344	GLU	CD-OE2	6.94	1.33	1.25
1	A	338	GLU	CD-OE2	6.49	1.32	1.25
1	A	263	GLU	CD-OE2	6.16	1.32	1.25
1	A	181	GLU	CD-OE2	6.12	1.32	1.25
1	B	344	GLU	CD-OE2	6.07	1.32	1.25

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	89	ARG	NE-CZ-NH2	-9.61	115.50	120.30
1	B	156[A]	TYR	CB-CG-CD2	-8.47	115.92	121.00
1	B	156[B]	TYR	CB-CG-CD2	-8.47	115.92	121.00
1	A	139	ARG	NE-CZ-NH1	8.06	124.33	120.30
1	B	156[A]	TYR	CB-CG-CD1	8.00	125.80	121.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2511	0	2527	33	0
1	B	2521	0	2537	37	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	11	0	17	0	0
3	B	11	0	17	1	0
4	A	140	0	0	1	0
4	B	146	0	0	3	0
All	All	5344	0	5098	71	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

The worst 5 of 71 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:96:ARG:HH11	1:B:96:ARG:CG	2.02	0.71
1:A:248:TYR:O	1:A:295:GLN:HG2	1.90	0.71
1:B:333:ILE:HB	1:B:334:PRO:HD3	1.73	0.69
1:B:35:ASP:N	4:B:2588:HOH:O	2.26	0.68
1:B:96:ARG:HH11	1:B:96:ARG:HG2	1.58	0.67

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	
1	A	326/331 (98%)	313 (96%)	13 (4%)	0	100	100
1	B	328/331 (99%)	321 (98%)	7 (2%)	0	100	100
All	All	654/662 (99%)	634 (97%)	20 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	262/265 (99%)	246 (94%)	16 (6%)	26	13
1	B	264/265 (100%)	252 (96%)	12 (4%)	38	24
All	All	526/530 (99%)	498 (95%)	28 (5%)	32	18

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	314	MET
1	A	362	LEU
1	B	319	ARG
1	A	337	ARG
1	A	344	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	212	GLN
1	A	290	GLN
1	A	295	GLN
1	B	212	GLN
1	B	290	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

2 non-standard protein/DNA/RNA residues 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	KCX	A	169	1,2	11,11,12	7.13	4 (36%)	10,12,14	2.05	2 (20%)
1	KCX	B	169	1,2	11,11,12	7.62	3 (27%)	10,12,14	2.21	4 (40%)

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
1	KCX	A	169	1,2	-	0/8/10/12	0/0/0/0
1	KCX	B	169	1,2	-	0/8/10/12	0/0/0/0

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	169	KCX	O-C	20.27	1.25	1.11
1	A	169	KCX	O-C	17.66	1.23	1.11
1	A	169	KCX	CX-NZ	15.32	1.47	1.32
1	B	169	KCX	CX-NZ	14.83	1.47	1.32
1	A	169	KCX	CA-C	2.56	1.53	1.48

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	KCX	OQ2-CX-NZ	-5.21	109.84	116.33
1	B	169	KCX	OQ2-CX-NZ	-4.20	111.10	116.33
1	B	169	KCX	CE-NZ-CX	-4.20	114.35	121.99
1	A	169	KCX	OQ2-CX-OQ1	2.99	125.89	122.17
1	B	169	KCX	OQ2-CX-OQ1	2.66	125.48	122.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	DII	A	1403	2	10,10,10	1.45	2 (20%)	14,14,14	1.00	0
3	DII	B	2403	2	10,10,10	1.33	1 (10%)	14,14,14	1.31	1 (7%)

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	DII	A	1403	2	-	0/10/10/10	0/0/0/0
3	DII	B	2403	2	-	0/10/10/10	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1403	DII	P1-C7	-3.61	1.64	1.77
3	B	2403	DII	P1-C7	-3.51	1.64	1.77
3	A	1403	DII	P1-O1	2.32	1.51	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2403	DII	P1-O3-C4	-2.43	116.56	123.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.