

wwPDB X-ray Structure Validation Summary Report (i)

Oct 23, 2021 – 11:58 AM EDT

PDB ID	:	1C0E
Title	:	Active Site S19A Mutant of Bovine Heart Phosphotyrosyl Phosphatase
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Deposited on		
Resolution	:	2.20 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:

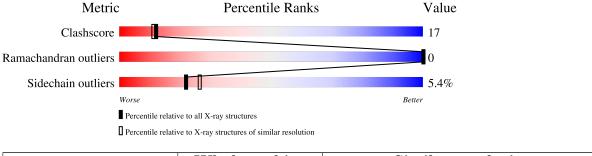
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (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 2.20 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	Similar resolution
Metric	$(\# {\rm Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain									
1	А	157	72%	24%	••							
1	В	157	66%	30%	•••							



1C0E

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2572 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.

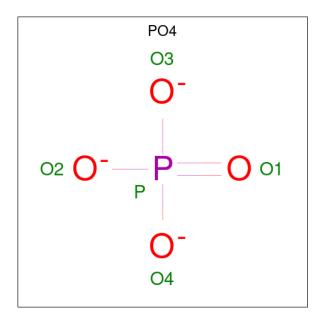
• Molecule 1 is a protein called PROTEIN (TYROSINE PHOSPHATASE (ORTHOPHOS-PHORIC MONOESTER PHOSPHOHYDROLASE)).

Mol	Chain	Residues		oms			ZeroOcc	AltConf	Trace	
1	А	154	Total			0	\mathbf{S}	0	0	0
-		101	1232	767	223	233	9	Ŭ	Ŭ	Ŭ
1	Р	154	Total	С	Ν	Ο	\mathbf{S}	0	0	0
	D	104	1232	767	223	233	9	0	0	0

There is a discrepancy between the modelled and reference sequences:

ſ	Chain	Residue	Modelled	Actual	Comment	Reference
	А	19	ALA	SER	engineered mutation	UNP P11064

• Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
2	А	1	Total 5	0 4	Р 1	0	0

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Mol	Chain	Residues	Ato	oms	ZeroOcc	AltConf	
2	В	1	Total 5	0 4	Р 1	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf					
3	А	55	$\begin{array}{cc} \text{Total} & \text{O} \\ 55 & 55 \end{array}$	0	0					
3	В	43	Total O 43 43	0	0					

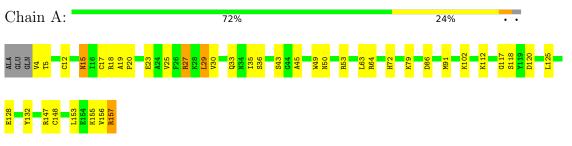


3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: PROTEIN (TYROSINE PHOSPHATASE (ORTHOPHOSPHORIC MONOESTER PHOSPHOHYDROLASE))



• Molecule 1: PROTEIN (TYROSINE PHOSPHATASE (ORTHOPHOSPHORIC MONOESTER PHOSPHOHYDROLASE))

Cha	in	E	3:									6	6%	, D														30	9%						•	•			
ALA GLU GLN	V204 #005	1205 K206	S207		7170	N215		A219 P220	R227	V230	8236	W239 V240	1241	D242	S243	6244 A245		R253	L263	R264	N269	H272 K973	A274	E280	D281	F282	V283	F285		7.870	N295	L296	R297 D298	6671	N300	R301	S303	N304	Q305
K312	L315	L316 C317	S318	Y319	P321	<mark>q322</mark>	K323	4324 L325	E328	Y332	D337	T340 V341		Q344	1 700	n n	-	F352	V356	R357																			



4 Data and refinement statistics (i)

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

Property	Value	Source				
Space group	P 21 21 21	Depositor				
Cell constants	43.32Å 55.47Å 131.45Å	Depositor				
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor				
Resolution (Å)	20.00 - 2.20	Depositor				
% Data completeness	(Not available) (20.00-2.20)	Depositor				
(in resolution range)	(100 available) (20.00 2.20)	Depositor				
R_{merge}	0.06	Depositor				
R _{sym}	(Not available)	Depositor				
Refinement program	CNS	Depositor				
R, R_{free}	0.191 , 0.244	Depositor				
Estimated twinning fraction	No twinning to report.	Xtriage				
Total number of atoms	2572	wwPDB-VP				
Average B, all atoms $(Å^2)$	37.0	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: PO4

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
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.45	0/1253	0.69	0/1694
1	В	0.48	0/1253	0.72	0/1694
All	All	0.47	0/2506	0.70	0/3388

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.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	27	ARG	Sidechain

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	1232	0	1215	36	0
1	В	1232	0	1215	52	0
2	А	5	0	0	0	0
2	В	5	0	0	0	0
3	А	55	0	0	1	0
3	В	43	0	0	2	0
All	All	2572	0	2430	84	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 17.

The worst 5 of 84 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:30:VAL:HG13	1:A:35:ILE:HG13	1.41	1.02
1:B:317:GLY:C	1:B:325:LEU:HD12	1.84	0.98
1:A:15:ASN:HB2	1:A:45:ALA:HB2	1.57	0.86
1:B:318:SER:N	1:B:325:LEU:CD1	2.40	0.85
1:B:215:ASN:HB2	1:B:245:ALA:HB2	1.59	0.84

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	\mathbf{s}
1	А	152/157~(97%)	142 (93%)	10 (7%)	0	100 100	
1	В	152/157~(97%)	139 (91%)	13 (9%)	0	100 100	
All	All	304/314~(97%)	281 (92%)	23 (8%)	0	100 100	

There are no Ramachandran outliers to report.



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	138/140~(99%)	131~(95%)	7 (5%)	24 29
1	В	138/140~(99%)	130 (94%)	8 (6%)	20 23
All	All	276/280~(99%)	261~(95%)	15~(5%)	22 26

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	227	ARG
1	В	328	GLU
1	В	263	LEU
1	В	357	ARG
1	В	297	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such side chains are listed below:

Mol	Chain	Res	Type
1	А	122	GLN
1	В	343	GLN
1	А	143	GLN
1	В	344	GLN
1	В	305	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)

2 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 Type		Chain Res	Link	Bond lengths		Bond angles				
	туре	Chain	Res		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	PO4	А	158	-	4,4,4	1.36	0	$6,\!6,\!6$	0.50	0
2	PO4	В	358	-	4,4,4	1.29	0	$6,\!6,\!6$	0.43	0

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

