

# Full wwPDB X-ray Structure Validation Report (i)

#### Sep 7, 2023 – 03:01 AM EDT

:	4F2U
:	Structure of the N254Y/H258Y double mutant of the Phosphatidylinositol-S
	pecific Phospholipase C from S.aureus
:	Cheng, J.; Goldstein, R.; Stec, B.; Gershenson, A.; Roberts, M.F.
	2012-05-08
:	2.19  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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

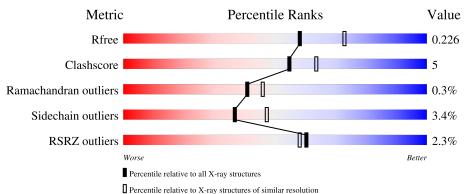
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

# 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 2.19 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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% 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	
			2%	
1	А	310	88%	8% ••



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2759 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 1-phosphatidylinositol phosphodiesterase.

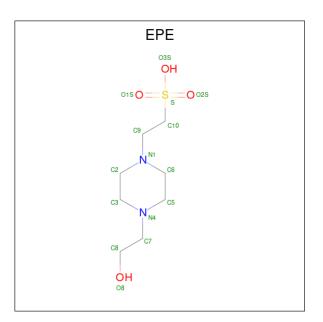
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	304	Total 2436	C 1549	N 400	O 480	${ m S} 7$	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

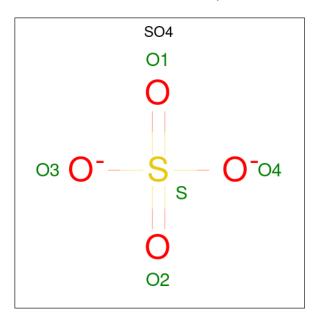
Chain	Residue	Modelled	Actual	Comment	Reference
А	254	TYR	ASN	engineered mutation	UNP P45723
А	258	TYR	HIS	engineered mutation	UNP P45723
А	303	LEU	-	expression tag	UNP P45723
А	304	GLU	-	expression tag	UNP P45723
А	305	HIS	-	expression tag	UNP P45723
А	306	HIS	-	expression tag	UNP P45723
А	307	HIS	-	expression tag	UNP P45723
А	308	HIS	-	expression tag	UNP P45723
А	309	HIS	-	expression tag	UNP P45723
А	310	HIS	-	expression tag	UNP P45723

• Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula:  $C_8H_{18}N_2O_4S$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
0	٨	1	Total	С	Ν	Ο	S	0	0
	Z A	1	15	8	2	4	1	0	0
0	2 A	1	Total	С	Ν	0	S	0	0
		1	15	8	2	4	1	0	U



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total 5	0 4	S 1	0	0

• Molecule 4 is water.



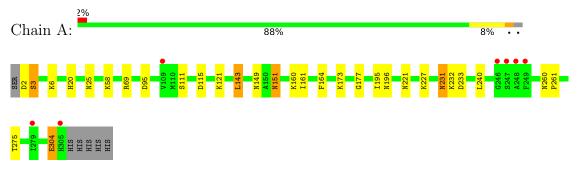
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	А	288	Total 288	O 288	0	0



# 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 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: 1-phosphatidylinositol phosphodiesterase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	86.22Å 56.12Å 61.71Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	30.85 - 2.19	Depositor
Resolution (A)	30.85 - 2.19	EDS
% Data completeness	99.5 (30.85-2.19)	Depositor
(in resolution range)	99.5 (30.85 - 2.19)	EDS
R <sub>merge</sub>	0.12	Depositor
R <sub>sym</sub>	0.12	Depositor
$< I/\sigma(I) > 1$	$3.66 (at 2.20 \text{\AA})$	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
B B.	0.158 , $0.236$	Depositor
$R, R_{free}$	0.154 , $0.226$	DCC
$R_{free}$ test set	795 reflections $(5.00\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	33.1	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31, 32.7	EDS
L-test for twinning <sup>2</sup>	$< L >=0.47, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2759	wwPDB-VP
Average B, all atoms $(Å^2)$	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.11% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: EPE,  $\mathrm{SO4}$ 

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		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.92	0/2495	0.82	2/3373~(0.1%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	95	ASP	CB-CG-OD1	5.41	123.17	118.30
1	А	240	LEU	CB-CG-CD2	5.01	119.51	111.00

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	А	2436	0	2343	23	0
2	А	30	0	35	2	0
3	А	5	0	0	0	0
4	А	288	0	0	11	0
All	All	2759	0	2378	25	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 5.



A. 1		Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
1:A:2:ASP:HA	4:A:651:HOH:O	1.73	0.88
1:A:149:ASN:HB2	4:A:763:HOH:O	1.82	0.78
1:A:2:ASP:N	4:A:721:HOH:O	2.29	0.64
1:A:3:SER:HB3	1:A:6:LYS:HG2	1.82	0.60
1:A:231:ASN:ND2	1:A:233:ASP:H	1.99	0.60
1:A:231:ASN:HD22	1:A:231:ASN:C	2.05	0.57
1:A:195:ILE:HG13	1:A:196:ASN:HD22	1.70	0.56
1:A:177:GLY:H	1:A:196:ASN:HD21	1.54	0.56
1:A:20:HIS:HD2	1:A:151:ASN:O	1.91	0.53
1:A:173:LYS:HE3	4:A:598:HOH:O	2.10	0.51
1:A:260:ASN:HB2	1:A:261:PRO:HD3	1.91	0.51
1:A:2:ASP:HB3	4:A:740:HOH:O	2.10	0.51
1:A:304:GLU:HG3	4:A:697:HOH:O	2.10	0.50
1:A:177:GLY:H	1:A:196:ASN:ND2	2.10	0.50
1:A:111:SER:HA	1:A:164:PHE:HB3	1.94	0.49
1:A:3:SER:HB2	4:A:787:HOH:O	2.11	0.49
1:A:227:LYS:HE3	4:A:750:HOH:O	2.11	0.49
1:A:231:ASN:HD22	1:A:233:ASP:H	1.61	0.49
1:A:25:ASN:HB3	1:A:275:THR:OG1	2.14	0.48
1:A:143:LEU:HD13	1:A:161:ILE:HD12	1.95	0.47
1:A:231:ASN:HD22	1:A:232:LYS:N	2.13	0.46
1:A:160:LYS:HE3	4:A:739:HOH:O	2.18	0.42
2:A:401:EPE:H82	2:A:401:EPE:H31	1.73	0.42
1:A:232:LYS:HG2	4:A:526:HOH:O	2.21	0.40
2:A:402:EPE:H91	4:A:726:HOH:O	2.21	0.40

All (25) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	302/310~(97%)	296~(98%)	5(2%)	1 (0%)	41 46	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	3	SER

#### 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.

N	Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
	1	А	264/270~(98%)	255~(97%)	9~(3%)	37 47	

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	58	LYS
1	А	69	ARG
1	А	115	ASP
1	А	121	LYS
1	А	143	LEU
1	А	151	ASN
1	А	221	ASN
1	А	231	ASN
1	А	304	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	20	HIS
1	А	56	GLN
1	А	79	HIS
1	А	80	HIS
1	А	139	GLN
1	А	151	ASN

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	v	-	1 0
Mol	Chain	$\mathbf{Res}$	Type
1	А	196	ASN
1	А	221	ASN
1	А	231	ASN
1	А	250	ASN
1	А	270	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 monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

3 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 C	Chain	Res	Link	Bo	Bond lengths			Bond angles		
10101	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	SO4	А	403	-	4,4,4	0.15	0	6,6,6	0.34	0
2	EPE	А	402	-	$15,\!15,\!15$	0.74	1 (6%)	18,20,20	2.83	8 (44%)
2	EPE	А	401	-	$15,\!15,\!15$	0.90	1 (6%)	18,20,20	1.97	4 (22%)

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
2	EPE	А	402	-	-	4/9/19/19	0/1/1/1
2	EPE	А	401	-	-	5/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	401	EPE	C10-S	3.08	1.81	1.77
2	А	402	EPE	C10-S	2.35	1.80	1.77

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	402	EPE	O3S-S-C10	6.05	115.55	105.77
2	А	402	EPE	C5-N4-C3	5.72	121.70	108.83
2	А	401	EPE	C5-N4-C3	5.23	120.60	108.83
2	А	402	EPE	C7-N4-C3	4.02	121.50	111.23
2	А	401	EPE	C7-N4-C3	3.92	121.27	111.23
2	А	402	EPE	C2-C3-N4	3.61	118.05	110.64
2	А	402	EPE	C3-C2-N1	3.52	117.87	110.64
2	А	402	EPE	C6-N1-C2	2.89	115.33	108.83
2	А	402	EPE	C9-N1-C2	-2.65	104.45	111.23
2	А	401	EPE	C7-N4-C5	2.62	117.94	111.23
2	А	402	EPE	C7-N4-C5	2.11	116.63	111.23
2	А	401	EPE	O1S-S-C10	2.09	109.43	106.92

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	401	EPE	C8-C7-N4-C3
2	А	401	EPE	C9-C10-S-O1S
2	А	402	EPE	C8-C7-N4-C3
2	А	402	EPE	C9-C10-S-O1S
2	А	402	EPE	C9-C10-S-O3S
2	А	401	EPE	C9-C10-S-O3S
2	А	401	EPE	N4-C7-C8-O8
2	А	401	EPE	C9-C10-S-O2S
2	А	402	EPE	C9-C10-S-O2S

There are no ring outliers.

2 monomers are involved in 2 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	402	EPE	1	0
2	А	401	EPE	1	0

## 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,  $95^{th}$  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		$\mathbf{OWAB}(\mathbf{A}^2)$	Q < 0.9	
1	А	304/310~(98%)	-0.44	7 (2%)	60	58	23, 31, 46, 67	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	248	ALA	5.5
1	А	247	SER	4.5
1	А	305	HIS	3.6
1	А	246	GLY	3.5
1	А	109	VAL	2.1
1	А	249	PHE	2.0
1	А	279	ILE	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 monosaccharides 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q < 0.9
2	EPE	А	401	15/15	0.83	0.17	$45,\!50,\!75,\!79$	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	SO4	А	403	5/5	0.97	0.16	$45,\!46,\!52,\!55$	0
2	EPE	А	402	15/15	0.98	0.09	$37,\!43,\!50,\!53$	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

