

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

#### Jan 27, 2024 - 11:07 PM EST

PDB ID	:	1DJG
Title	:	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-DELTA1 FROM
		RAT COMPLEXED WITH LANTHANUM
Authors	:	Essen, LO.; Perisic, O.; Williams, R.L.
Deposited on	:	1996-09-25
Resolution	:	2.60  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 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)	:	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)	:	2.36

# 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 2.60 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455(2.60-2.60)

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	624	49%	28%	·	18%
1	В	624	52%	32%		5%• 10%

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACT	А	5	-	-	Х	-



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9246 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 PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, ISOZYME DELTA1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	513	Total 4057	$\begin{array}{c} \mathrm{C} \\ 2565 \end{array}$	N 709	О 761	S 22	86	0	0
1	В	561	Total 4465	C 2818	N 776	0 847	S 24	101	0	0

• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 3 is LANTHANUM (III) ION (three-letter code: LA) (formula: La).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	4	Total La 4 4	0	0
3	В	4	Total La 4 4	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	335	Total O 335 335	0	0
4	В	373	Total O 373 373	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.

 Chain A:
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• Molecule 1: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, ISOZYME DELTA1



Note EDS was not executed.

• Molecule 1: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, ISOZYME DELTA1





# 4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	F 41 3 2	Depositor	
Cell constants	397.92Å 397.92Å 397.92Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	10.00 - 2.60	Depositor	
% Data completeness	98.5 (10.00-2.60)	Depositor	
(in resolution range)	56.5 (10.00 2.00)	Depositor	
$R_{merge}$	0.04	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	TNT 5E	Depositor	
$R, R_{free}$	0.210 , $0.270$	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	9246	wwPDB-VP	
Average B, all atoms $(Å^2)$	38.0	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: LA, ACT

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).

Mal	Chain	Bo	nd lengths	Bond angles		
	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.98	29/4152~(0.7%)	0.88	4/5624~(0.1%)	
1	В	1.00	31/4565~(0.7%)	0.90	8/6174~(0.1%)	
All	All	0.99	60/8717~(0.7%)	0.89	12/11798~(0.1%)	

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
1	В	1	0
All	All	1	1

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	В	730	TYR	CE2-CZ	-10.49	1.25	1.38
1	А	358	TYR	CE1-CZ	-9.51	1.26	1.38
1	А	314	TYR	CE2-CZ	-9.42	1.26	1.38
1	А	551	TYR	CE2-CZ	-9.34	1.26	1.38
1	В	314	TYR	CE1-CZ	-8.98	1.26	1.38

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	393	CYS	CA-CB-SG	8.09	128.56	114.00
1	А	406	ARG	NE-CZ-NH1	-6.75	116.93	120.30
1	В	393	CYS	N-CA-C	6.06	127.35	111.00
1	А	509	SER	N-CA-C	5.79	126.63	111.00

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	173	ASN	CB-CA-C	5.50	121.39	110.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	В	393	CYS	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	691	GLU	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	4057	0	3972	173	0
1	В	4465	0	4375	208	0
2	А	4	0	3	2	0
2	В	4	0	3	0	0
3	А	4	0	0	0	0
3	В	4	0	0	0	0
4	А	335	0	0	11	0
4	В	373	0	0	18	0
All	All	9246	0	8353	370	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 23.

The worst 5 of 370 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:B:161:ASN:H	1:B:164:GLU:HG3	1.18	1.07
1:A:613:THR:HG22	1:A:615:PHE:H	1.23	1.02
1:A:504:PHE:HB3	1:A:527:ARG:HH22	1.24	1.01
1:B:438:LYS:HD2	1:B:520:MET:HE1	1.46	0.98

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Atom-1 Atom-2		Interatomic distance (Å)	Clash overlap (Å)
1:B:728:GLN:NE2	1:B:754:ILE:H	1.64	0.94

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	Perc	entiles
1	А	509/624~(82%)	471 (92%)	31~(6%)	7(1%)	11	22
1	В	557/624~(89%)	511 (92%)	35~(6%)	11 (2%)	7	14
All	All	1066/1248~(85%)	982 (92%)	66~(6%)	18 (2%)	9	18

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	515	GLN
1	В	175	GLN
1	В	176	VAL
1	В	177	ASP
1	В	510	PRO

#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Analysed Rotameric		Percentiles	
1	А	444/545~(82%)	404 (91%)	40 (9%)	9 18	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	В	492/545~(90%)	436 (89%)	56 (11%)	5 10
All	All	936/1090~(86%)	840 (90%)	96 (10%)	7 13

 $5~{\rm of}~96$  residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	В	310	SER
1	В	539	PHE
1	В	406	ARG
1	В	484	ASP
1	В	607	PHE

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such side chains are listed below:

Mol	Chain	Res	Type
1	В	661	HIS
1	В	755	GLN
1	В	728	GLN
1	А	734	HIS
1	В	594	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)

Of 10 ligands modelled in this entry, 8 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).

Mal Trma (	Chain	Dec	s Link	Bond lengths			Bond angles			
	Mol Type Chain K	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
2	ACT	А	5	-	3,3,3	0.87	0	3,3,3	0.59	0
2	ACT	В	5	-	3,3,3	0.77	0	3,3,3	0.86	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	5	ACT	2	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)

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.

