



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 9, 2024 – 12:46 pm GMT

PDB ID : 8R3X  
Title : Crystal structure of aPKC Iota kinase domain with LLGL2 peptide  
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Deposited on : 2023-11-10  
Resolution : 2.59 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](mailto: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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

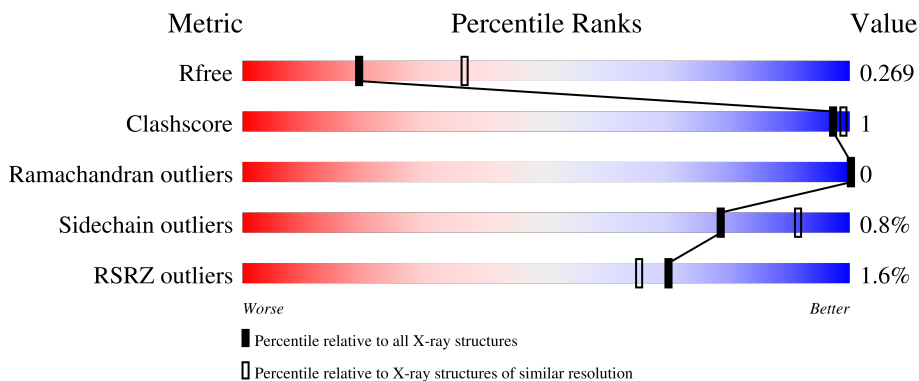
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.59 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))
$R_{free}$	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (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  $\geq 3$ , 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  $\leq 5\%$ . 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	356	 94%
1	B	356	 89% 6% 5%
2	C	20	 5% 45% 5% 50%
2	D	20	 5% 55% 45%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5721 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 kinase C iota type.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
1	A	340	2777	1769	467	526	2	13	0	1	0
1	B	339	2753	1750	463	525	2	13	0	0	0

- Molecule 2 is a protein called LLGL scribble cell polarity complex component 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	10	91	56	22	13	0	0	0
2	D	11	96	59	23	14	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	659	LYS	ARG	conflict	UNP Q6P1M3
D	659	LYS	ARG	conflict	UNP Q6P1M3

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	O	0	0
			2	2		
3	B	1	Total	O	0	0
			1	1		
3	C	1	Total	O	0	0
			1	1		

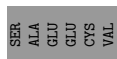
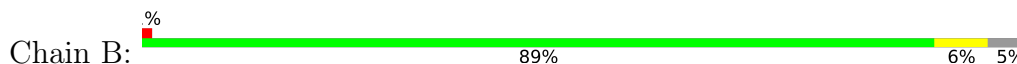
### 3 Residue-property plots [i](#)

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.

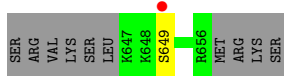
- Molecule 1: Protein kinase C iota type



- Molecule 1: Protein kinase C iota type



- Molecule 2: LLGL scribble cell polarity complex component 2



- Molecule 2: LLGL scribble cell polarity complex component 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.42Å 86.32Å 114.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.00 – 2.59 69.00 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.6 (69.00-2.59) 99.6 (69.00-2.59)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.18 (at 2.58Å)	Xtrriage
Refinement program	REFMAC 5.8.0419	Depositor
R, $R_{free}$	0.232 , 0.269 0.232 , 0.269	Depositor DCC
$R_{free}$ test set	1236 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.9	Xtrriage
Anisotropy	0.305	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 29.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5721	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.16% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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: TPO

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	0.39	0/2824	0.78	0/3813
1	B	0.37	0/2794	0.79	1/3771 (0.0%)
2	C	0.46	0/91	1.05	0/116
2	D	0.45	0/96	0.93	0/123
All	All	0.38	0/5805	0.79	1/7823 (0.0%)

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	B	0	4
2	C	0	1
All	All	0	5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	529	MET	CG-SD-CE	6.87	111.19	100.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	272	ARG	Sidechain
1	B	346	ARG	Sidechain
1	B	372	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	572	ARG	Sidechain
2	C	649	SER	Peptide

## 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	2777	0	2688	2	0
1	B	2753	0	2662	7	0
2	C	91	0	102	0	0
2	D	96	0	104	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
All	All	5721	0	5556	9	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 1.

The worst 5 of 9 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:358:TYR:HB2	1:B:446:MET:HE1	1.86	0.57
1:A:461:ASN:HD22	1:A:464:GLN:NE2	2.03	0.57
1:B:316:VAL:HG21	1:B:395:THR:HG22	1.87	0.55
1:B:301:THR:HG23	1:B:402:GLU:HG2	1.97	0.47
1:B:385:LEU:CD1	1:B:395:THR:HG21	2.45	0.46

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	A	337/356 (95%)	323 (96%)	14 (4%)	0	100	100
1	B	335/356 (94%)	324 (97%)	11 (3%)	0	100	100
2	C	8/20 (40%)	7 (88%)	1 (12%)	0	100	100
2	D	9/20 (45%)	8 (89%)	1 (11%)	0	100	100
All	All	689/752 (92%)	662 (96%)	27 (4%)	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	Outliers	Percentiles	
1	A	304/316 (96%)	304 (100%)	0	100	100
1	B	301/316 (95%)	296 (98%)	5 (2%)	56	78
2	C	10/20 (50%)	10 (100%)	0	100	100
2	D	10/20 (50%)	10 (100%)	0	100	100
All	All	625/672 (93%)	620 (99%)	5 (1%)	79	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	293	ASP
1	B	294	GLU
1	B	305	VAL
1	B	347	GLN
1	B	404	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	464	GLN
1	A	478	GLN
1	B	464	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](#)

4 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	TPO	A	412	1	8,10,11	0.69	0	10,14,16	0.98	1 (10%)
1	TPO	B	564	1	8,10,11	0.74	0	10,14,16	0.92	1 (10%)
1	TPO	B	412	1	8,10,11	0.68	0	10,14,16	0.87	1 (10%)
1	TPO	A	564	1	8,10,11	0.81	0	10,14,16	0.93	1 (10%)

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	TPO	A	412	1	-	1/9/11/13	-
1	TPO	B	564	1	-	1/9/11/13	-
1	TPO	B	412	1	-	1/9/11/13	-
1	TPO	A	564	1	-	0/9/11/13	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	564	TPO	O-C-CA	-2.11	119.25	124.78
1	A	412	TPO	O-C-CA	-2.10	119.28	124.78
1	B	564	TPO	O-C-CA	-2.08	119.34	124.78
1	B	412	TPO	O-C-CA	-2.01	119.51	124.78

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	412	TPO	O-C-CA-CB
1	B	412	TPO	O-C-CA-CB
1	B	564	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	338/356 (94%)	0.20	5 (1%) 71 67	26, 64, 94, 111	1 (0%)
1	B	337/356 (94%)	0.12	4 (1%) 76 72	34, 62, 101, 128	0
2	C	10/20 (50%)	0.87	1 (10%) 14 12	64, 72, 83, 90	0
2	D	11/20 (55%)	0.64	1 (9%) 16 13	62, 71, 80, 82	0
All	All	696/752 (92%)	0.18	11 (1%) 70 65	26, 63, 96, 128	1 (0%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	588	LEU	4.1
1	A	249	LEU	3.6
2	D	657	MET	3.1
1	A	298	TRP	2.5
1	B	587	PRO	2.4

### 6.2 Non-standard residues in protein, DNA, RNA chains [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<sup>th</sup> 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	B-factors(Å <sup>2</sup> )	Q<0.9
1	TPO	A	412	11/12	0.87	0.11	60,63,64,65	0
1	TPO	B	412	11/12	0.88	0.11	56,60,68,69	0
1	TPO	A	564	11/12	0.89	0.09	79,81,86,86	0
1	TPO	B	564	11/12	0.94	0.08	56,59,62,62	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.