



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 21, 2018 – 12:10 AM EDT

PDB ID : 6C9D  
Title : Crystal structure of KA1-autoinhibited MARK1 kinase  
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Deposited on : 2018-01-26  
Resolution : 2.50 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.

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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  
Xtriage (Phenix) : 1.13  
EDS : rb-20031172  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031172

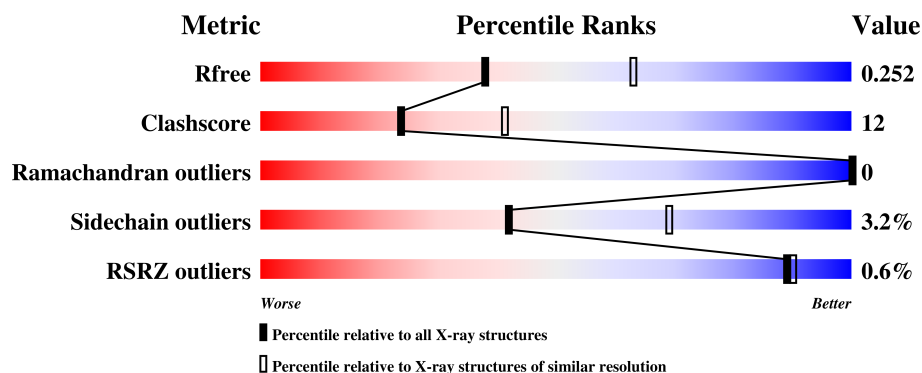
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	111664	4155 (2.50-2.50)
Clashscore	122126	4827 (2.50-2.50)
Ramachandran outliers	120053	4735 (2.50-2.50)
Sidechain outliers	120020	4737 (2.50-2.50)
RSRZ outliers	108989	4058 (2.50-2.50)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	459	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;">%</div> <div style="position: absolute; top: 10px; left: 0; width: 100%;">73% 18% • 7%</div> </div> </div>
1	B	459	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: 10px; left: 0; width: 100%;">67% 23% • 8%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6702 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 Serine/threonine-protein kinase MARK1, Serine/threonine-protein kinase MARK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	425	Total	C	N	O	S	0	4	0
			3353	2149	568	615	21			
1	B	422	Total	C	N	O	S	0	1	0
			3281	2089	557	615	20			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	38	MET	-	expression tag	UNP Q9P0L2
A	39	HIS	-	expression tag	UNP Q9P0L2
A	40	HIS	-	expression tag	UNP Q9P0L2
A	41	HIS	-	expression tag	UNP Q9P0L2
A	42	HIS	-	expression tag	UNP Q9P0L2
A	43	HIS	-	expression tag	UNP Q9P0L2
A	44	HIS	-	expression tag	UNP Q9P0L2
A	215	GLU	THR	engineered mutation	UNP Q9P0L2
A	761	SER	LYS	engineered mutation	UNP Q9P0L2
A	764	SER	ARG	engineered mutation	UNP Q9P0L2
B	38	MET	-	expression tag	UNP Q9P0L2
B	39	HIS	-	expression tag	UNP Q9P0L2
B	40	HIS	-	expression tag	UNP Q9P0L2
B	41	HIS	-	expression tag	UNP Q9P0L2
B	42	HIS	-	expression tag	UNP Q9P0L2
B	43	HIS	-	expression tag	UNP Q9P0L2
B	44	HIS	-	expression tag	UNP Q9P0L2
B	215	GLU	THR	engineered mutation	UNP Q9P0L2
B	761	SER	LYS	engineered mutation	UNP Q9P0L2
B	764	SER	ARG	engineered mutation	UNP Q9P0L2

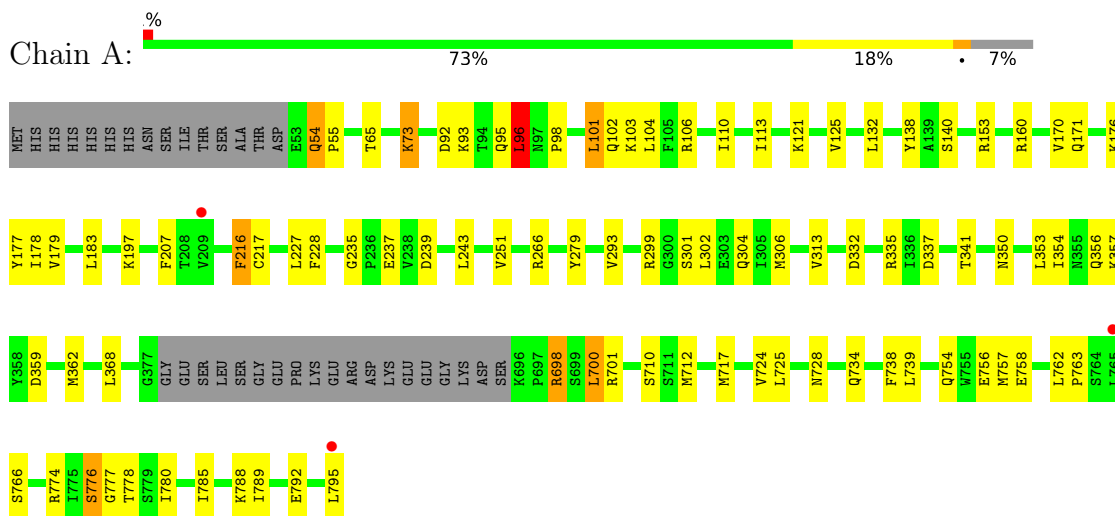
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	39	Total 39	O 39	0	0
2	B	29	Total 29	O 29	0	0

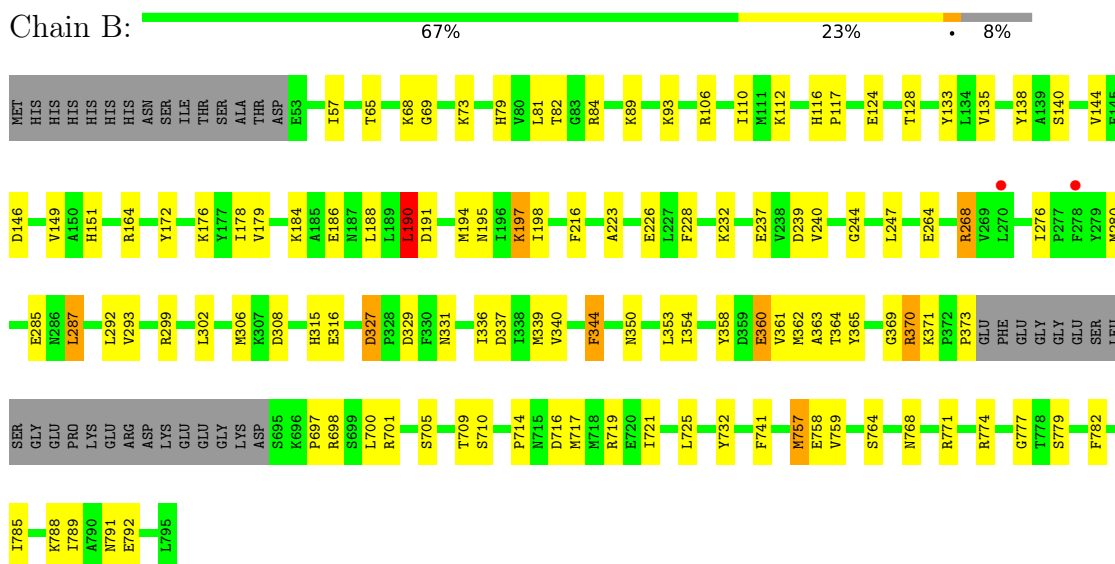
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Serine/threonine-protein kinase MARK1, Serine/threonine-protein kinase MARK1



- Molecule 1: Serine/threonine-protein kinase MARK1, Serine/threonine-protein kinase MARK1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.99Å 69.58Å 104.00Å 90.00° 124.30° 90.00°	Depositor
Resolution (Å)	45.35 – 2.50 45.35 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.6 (45.35-2.50) 98.6 (45.35-2.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.19 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, $R_{free}$	0.203 , 0.251 0.202 , 0.252	Depositor DCC
$R_{free}$ test set	1995 reflections (5.78%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	62.1	Xtriage
Anisotropy	0.661	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 47.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6702	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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

### 5.1 Standard geometry

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	0.50	3/3432 (0.1%)	0.75	6/4636 (0.1%)
1	B	0.47	1/3348 (0.0%)	0.73	2/4534 (0.0%)
All	All	0.48	4/6780 (0.1%)	0.74	8/9170 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	360	GLU	CD-OE2	-6.97	1.18	1.25
1	A	776	SER	CB-OG	-6.53	1.33	1.42
1	A	125	VAL	CB-CG2	-5.77	1.40	1.52
1	A	766	SER	CB-OG	-5.34	1.35	1.42

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	698	ARG	NE-CZ-NH2	11.04	125.82	120.30
1	A	698	ARG	NE-CZ-NH1	-10.62	114.99	120.30
1	A	700	LEU	CB-CG-CD1	-8.85	95.95	111.00
1	A	698	ARG	CD-NE-CZ	-6.46	114.55	123.60
1	A	332	ASP	CB-CG-OD2	5.77	123.49	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	3353	0	3303	65	0
1	B	3281	0	3184	95	0
2	A	39	0	0	1	0
2	B	29	0	0	4	0
All	All	6702	0	6487	157	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 12.

The worst 5 of 157 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:344:PHE:CE1	1:B:361:VAL:HG12	1.91	1.04
1:B:344:PHE:HE1	1:B:361:VAL:HG12	1.23	1.01
1:B:350:ASN:O	1:B:354:ILE:HD12	1.65	0.96
1:B:371:LYS:O	1:B:373:PRO:HD3	1.69	0.90
1:A:698:ARG:HD3	1:A:758:GLU:OE2	1.80	0.80

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	425/459 (93%)	411 (97%)	14 (3%)	0	100	100
1	B	419/459 (91%)	399 (95%)	20 (5%)	0	100	100
All	All	844/918 (92%)	810 (96%)	34 (4%)	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	354/410 (86%)	345 (98%)	9 (2%)	50	77
1	B	346/410 (84%)	332 (96%)	14 (4%)	34	60
All	All	700/820 (85%)	677 (97%)	23 (3%)	42	68

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	164	ARG
1	B	197	LYS
1	B	710	SER
1	B	190	LEU
1	B	216	PHE

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

Mol	Chain	Res	Type
1	A	304	GLN
1	A	754	GLN
1	B	754	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates 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	425/459 (92%)	-0.21	3 (0%) 87 88	54, 74, 96, 112	0
1	B	422/459 (91%)	-0.27	2 (0%) 90 91	61, 79, 105, 121	0
All	All	847/918 (92%)	-0.24	5 (0%) 89 90	54, 77, 101, 121	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	VAL	3.9
1	A	765	LEU	3.7
1	B	278	PHE	2.3
1	B	270	LEU	2.2
1	A	795	LEU	2.2

### 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 carbohydrates 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.