

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

#### May 13, 2020 – 03:48 pm BST

PDB ID	:	5LNM
Title	:	Crystal structure of D1050E mutant of the receiver domain of the histidine
		kinase CKI1 from Arabidopsis thaliana
Authors	:	Otrusinova, O.; Demo, G.; Kaderavek, P.; Jansen, S.; Jasenakova, Z.;
		Pekarova, B.; Janda, L.; Wimmerova, M.; Hejatko, J.; Zidek, L.
Deposited on	:	2016-08-05
Resolution	:	1.95  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 following versions of software and data (see references (1)) were used in the production of this report:

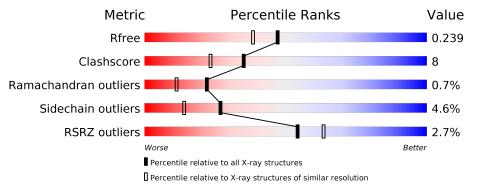
MolProbity Xtriage (Phenix) EDS		
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
$R_{free}$	130704	2580 (1.96-1.96)
Clashscore	141614	2705(1.96-1.96)
Ramachandran outliers	138981	2678(1.96-1.96)
Sidechain outliers	138945	2678(1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 >=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 c	f chain	
1	А	206	2% <b>5</b> 5%	17%	27%



#### 5LNM

# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1294 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 Histidine kinase CKI1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	150	Total 1200	C 745	N 211	О 237	S 7	0	7	0

Chain	Residue	Modelled	Actual	Comment	Reference
A	925	GLY	_	expression tag	UNP 022267
A	926	SER	_	expression tag	UNP 022267
A	927	SER	_	expression tag	UNP 022267
A	928	HIS	_	expression tag	UNP 022267
A	929	HIS	_	expression tag	UNP 022267
A	930	HIS	-	expression tag	UNP 022267
A	931	HIS	-	expression tag	UNP 022267
A	932	HIS	-	expression tag	UNP 022267
A	933	HIS	-	expression tag	UNP 022267
A	934	SER	-	expression tag	UNP 022267
A	935	SER	-	expression tag	UNP 022267
A	936	GLY	-	expression tag	UNP 022267
A	937	LEU	-	expression tag	UNP 022267
A	938	VAL	-	expression tag	UNP 022267
A	939	PRO	-	expression tag	UNP 022267
A	940	ARG	-	expression tag	UNP 022267
A	941	GLY	-	expression tag	UNP 022267
А	942	SER	-	expression tag	UNP 022267
A	943	HIS	-	expression tag	UNP 022267
A	1050	GLU	ASP	engineered mutation	UNP 022267
A	1123	LEU	-	expression tag	UNP 022267
А	1124	GLU	-	expression tag	UNP 022267
A	1125	HIS	-	expression tag	UNP 022267
А	1126	HIS	-	expression tag	UNP 022267
А	1127	HIS	-	expression tag	UNP 022267
A	1128	HIS	-	expression tag	UNP 022267
A	1129	HIS	-	expression tag	UNP 022267

There are 28 discrepancies between the modelled and reference sequences:

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Chain	Residue	Modelled	Actual	Comment	Reference
А	1130	HIS	-	expression tag	UNP 022267

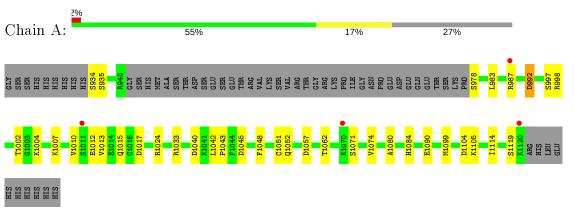
• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	94	Total O 94 94	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: Histidine kinase CKI1



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	54.34Å 98.73Å 79.90Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	42.37 - 1.95	Depositor
Resolution (A)	42.00 - 1.95	EDS
% Data completeness	86.1 (42.37-1.95)	Depositor
(in resolution range)	$86.1 \ (42.00-1.95)$	EDS
R <sub>merge</sub>	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.26 (at 1.95 Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
D D	0.207 , $0.234$	Depositor
$R, R_{free}$	0.216 , $0.239$	DCC
R <sub>free</sub> test set	696 reflections $(5.04\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	30.8	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.37 , 46.6	EDS
L-test for $twinning^2$	$< L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.026 for $1/2$ *h- $1/2$ *k,- $3/2$ *h- $1/2$ *k,-l	Xtriage
Estimated twinning fraction	0.037 for $1/2$ *h+ $1/2$ *k, $3/2$ *h- $1/2$ *k,-l	Attrage
$\mathbf{F}_{o}, \mathbf{F}_{c}$ correlation	0.94	EDS
Total number of atoms	1294	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 9.94% 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)

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	0.97	0/1245	1.12	7/1665~(0.4%)	

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	998	ARG	NE-CZ-NH2	8.19	124.40	120.30
1	А	998	ARG	NE-CZ-NH1	-6.84	116.88	120.30
1	А	1024	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	А	992	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	А	1045	ASP	CB-CG-OD2	5.77	123.49	118.30
1	А	1017	ASP	CB-CG-OD2	-5.32	113.52	118.30
1	А	1057	ASP	CB-CG-OD2	-5.19	113.63	118.30

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	1200	0	1215	20	0
2	А	94	0	0	3	1
All	All	1294	0	1215	20	1

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 8.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1010[A]:VAL:HG11	1:A:1013:VAL:CG2	2.29	0.63
1:A:1052:GLN:NE2	2:A:1201:HOH:O	2.28	0.60
1:A:1004:LYS:O	1:A:1007[B]:LYS:HG2	2.06	0.56
1:A:1084:HIS:HE1	1:A:1090:GLU:OE2	1.88	0.55
1:A:1062:THR:HG21	1:A:1099:MET:HG3	1.89	0.54
1:A:987[A]:ARG:HD3	1:A:1043:PRO:O	2.10	0.51
1:A:1052:GLN:HG2	2:A:1220:HOH:O	2.14	0.47
1:A:987[A]:ARG:HG2	1:A:1012:GLU:HB2	1.96	0.47
1:A:992:ASP:OD2	1:A:997:SER:HB2	2.16	0.46
1:A:987[B]:ARG:NH1	1:A:1040:ASP:OD2	2.49	0.46
1:A:1002:THR:HG21	1:A:1015:GLN:HE21	1.81	0.45
1:A:1040:ASP:HB3	2:A:1255:HOH:O	2.18	0.44
1:A:987[B]:ARG:HD2	1:A:1033:ARG:HH22	1.83	0.44
1:A:983[B]:LEU:HB3	1:A:1010[B]:VAL:HG22	2.00	0.44
1:A:1010[A]:VAL:CG1	1:A:1013:VAL:HG23	2.47	0.43
1:A:1010[A]:VAL:HG11	1:A:1013:VAL:HG22	1.99	0.42
1:A:1051:CYS:SG	1:A:1080:ALA:HB1	2.60	0.42
1:A:1042:LEU:HD21	1:A:1074:VAL:HB	2.00	0.42
1:A:1048:PHE:HZ	1:A:1114:ILE:HD11	1.84	0.42
1:A:1010[A]:VAL:CG1	1:A:1013:VAL:CG2	2.99	0.40

All (20) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1205:HOH:O	2:A:1244:HOH:O[3_654]	2.14	0.06

## 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	153/206~(74%)	148 (97%)	4 (3%)	1 (1%)	22 11

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	935	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.

M	ol	Chain	Analysed	Rotameric	Outliers	Percentiles	
]	L	А	137/181~(76%)	131~(96%)	6 (4%)	28 15	

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	934	SER
1	А	978	SER
1	А	1071	SER
1	А	1104	ASP
1	А	1105	LYS
1	А	1119	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	1084	HIS

#### 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 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	$<$ <b>RSRZ</b> $>$	# <b>RS</b>	$\mathbf{RZ}$	>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	А	150/206~(72%)	0.39	4 (2%)	54	63	18, 32, 54, 72	1 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	1070	LYS	2.7
1	А	1011	SER	2.1
1	А	987[A]	ARG	2.1
1	А	1120	LYS	2.1

#### 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.

