

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

#### Aug 27, 2023 – 07:57 AM EDT

PDB ID	:	3IDU
Title	:	Crystal Structure of the CARDB domain of the PF1109 protein in complex
		with di-metal ions from Pyrococcus furiosus, Northeast Structural Genomics
		Consortium Target PfR193A
Authors	:	Forouhar, F.; Neely, H.; Seetharaman, J.; Mao, M.; Xiao, R.; Ciccosanti, C.;
		Lee, D.; Everett, J.K.; Nair, R.; Acton, T.B.; Rost, B.; Montelione, G.T.;
		Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2009-07-21
Resolution	:	1.70 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 (i)) were used in the production of this report:

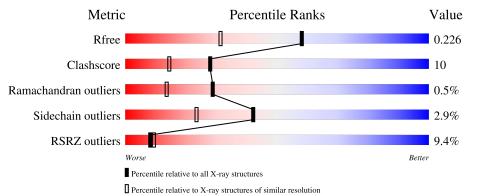
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal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

# 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 1.70 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	$\begin{array}{l} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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				
1	А	127	72%	20	%	9%	
1	В	127	6%	20%	•	13%	

Validation Pipeline (wwPDB-VP) : 2.35



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1995 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	116	Total	С	Ν	0	Se	0	0	0
		110	916	584	147	184	1	0	0	0
1	В	110	Total	С	Ν	Ο	Se	0	0	0
	D	110	866	553	139	173	1	0	0	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	422	MSE	-	initiating methionine	UNP Q8U1U6
А	541	LEU	-	expression tag	UNP Q8U1U6
А	542	GLU	-	expression tag	UNP Q8U1U6
A	543	HIS	-	expression tag	UNP Q8U1U6
А	544	HIS	-	expression tag	UNP Q8U1U6
A	545	HIS	-	expression tag	UNP Q8U1U6
А	546	HIS	-	expression tag	UNP Q8U1U6
А	547	HIS	-	expression tag	UNP Q8U1U6
А	548	HIS	-	expression tag	UNP Q8U1U6
В	422	MSE	-	initiating methionine	UNP Q8U1U6
В	541	LEU	-	expression tag	UNP Q8U1U6
В	542	GLU	-	expression tag	UNP Q8U1U6
В	543	HIS	-	expression tag	UNP Q8U1U6
В	544	HIS	-	expression tag	UNP Q8U1U6
В	545	HIS	-	expression tag	UNP Q8U1U6
В	546	HIS	-	expression tag	UNP Q8U1U6
В	547	HIS	-	expression tag	UNP Q8U1U6
В	548	HIS	-	expression tag	UNP Q8U1U6

There are 18 discrepancies between the modelled and reference sequences:

• Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	2	Total Mn 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	2	Total Mn 2 2	0	0

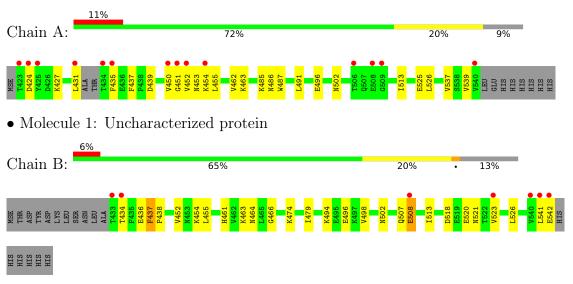
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	103	Total O 103 103	0	0
3	В	106	Total O 106 106	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: Uncharacterized protein



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	24.55Å $72.67$ Å $58.46$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $93.44^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	19.49 - 1.70	Depositor
Resolution (A)	24.51 - 1.69	EDS
% Data completeness	84.8 (19.49-1.70)	Depositor
(in resolution range)	95.7(24.51-1.69)	EDS
R <sub>merge</sub>	0.06	Depositor
R <sub>sym</sub>	0.04	Depositor
$< I/\sigma(I) > 1$	7.69 (at 1.69 Å)	Xtriage
Refinement program	CNS 1.2 & XtalView, REFMAC	Depositor
D D	0.190 , $0.212$	Depositor
$R, R_{free}$	0.205 , $0.226$	DCC
$R_{free}$ test set	2143 reflections $(4.98%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	13.1	Xtriage
Anisotropy	0.884	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.34,48.0	EDS
L-test for twinning <sup>2</sup>	$ L  > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	1995	wwPDB-VP
Average B, all atoms $(Å^2)$	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.59% 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: MN

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		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.31	0/932	0.60	0/1270	
1	В	0.33	0/882	0.62	0/1204	
All	All	0.32	0/1814	0.61	0/2474	

There are no bond length outliers.

There are no bond angle outliers.

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	916	0	898	19	0
1	В	866	0	853	16	0
2	А	2	0	0	0	0
2	В	2	0	0	0	0
3	А	103	0	0	3	0
3	В	106	0	0	1	0
All	All	1995	0	1751	35	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 10.

The worst 5 of 35 close contacts within the same asymmetric unit are listed below, sorted by their



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:463:LYS:HG2	1:B:496:GLU:HG3	1.52	0.92
1:A:463:LYS:HG2	1:A:496:GLU:HG3	1.74	0.69
1:B:479:ILE:CD1	1:B:513:ILE:HG13	2.31	0.60
1:B:479:ILE:HD12	1:B:513:ILE:HG13	1.85	0.58
1:B:513:ILE:HD12	1:B:513:ILE:N	2.19	0.58

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	Perce	ntiles
1	А	112/127~(88%)	111 (99%)	1 (1%)	0	100	100
1	В	108/127~(85%)	106 (98%)	1 (1%)	1 (1%)	17	5
All	All	220/254~(87%)	217 (99%)	2(1%)	1 (0%)	29	13

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	436	GLU

#### 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	А	105/113~(93%)	103~(98%)	2(2%)	57 41	
1	В	99/113~(88%)	95~(96%)	4 (4%)	31 13	
All	All	204/226~(90%)	198~(97%)	6 (3%)	42 23	

5 of 6 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	В	507	GLN
1	В	508	GLU
1	В	523	VAL
1	А	427	LYS
1	А	424	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	453	ASN
1	В	502	ASN
1	В	507	GLN
1	В	514	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)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

#### 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	115/127~(90%)	0.58	14 (12%) 4 4	8, 16, 41, 53	0
1	В	109/127~(85%)	0.26	7 (6%) 19 21	7, 16, 31, 49	0
All	All	224/254~(88%)	0.42	21 (9%) 8 9	7, 16, 38, 53	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	434	THR	6.6
1	А	423	THR	5.4
1	В	433	THR	5.4
1	В	541	LEU	5.0
1	А	540	VAL	4.7

### 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	MN	В	601	1/1	0.99	0.05	$13,\!13,\!13,\!13$	0
2	MN	В	602	1/1	0.99	0.05	12,12,12,12	0
2	MN	А	601	1/1	1.00	0.03	9,9,9,9	0
2	MN	А	602	1/1	1.00	0.04	12,12,12,12	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

