



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 8, 2021 – 06:01 PM EDT

PDB ID : 6WNZ  
Title : Structure of a dimer of the Sulfolobus solfataricus MCM N-terminal domain reveals potential role in MCM ring opening  
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Deposited on : 2020-04-23  
Resolution : 2.00 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](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 : 2.20  
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)  
Validation Pipeline (wwPDB-VP) : 2.20

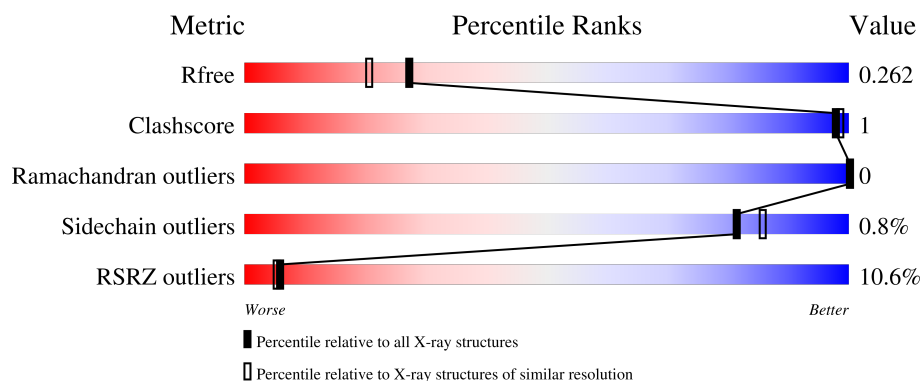
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	270	<div> <div>9%</div> <div>93%</div> <div>.</div> <div>.</div> </div>
1	B	270	<div> <div>11%</div> <div>93%</div> <div>.</div> <div>.</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4311 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 Minichromosome maintenance protein MCM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	261	Total	C	N	O	S	0	0	0
			2132	1368	361	396	7			
1	A	258	Total	C	N	O	S	0	0	0
			2107	1352	356	392	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	expression tag	UNP Q9UXG1
A	0	SER	-	expression tag	UNP Q9UXG1

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

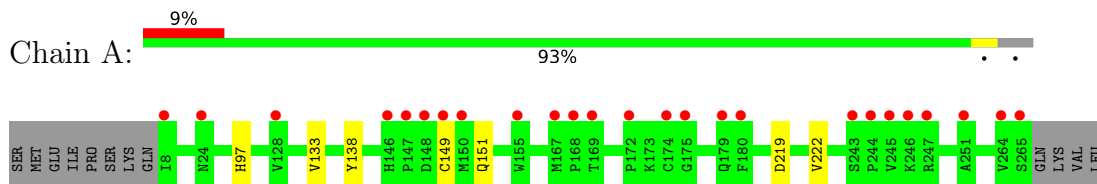
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	37	Total	O	0	0
			37	37		
3	A	33	Total	O	0	0
			33	33		



- Molecule 1: Minichromosome maintenance protein MCM



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.23Å 102.45Å 128.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 40.01 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (50.00-2.00) 99.1 (40.01-2.00)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.233 , 0.255 0.237 , 0.262	Depositor DCC
$R_{free}$ test set	2506 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.1	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 42.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4311	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.30	0/2147	0.56	0/2905
1	B	0.32	0/2172	0.56	0/2938
All	All	0.31	0/4319	0.56	0/5843

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

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	2107	0	2165	3	0
1	B	2132	0	2195	3	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	33	0	0	0	0
3	B	37	0	0	0	0
All	All	4311	0	4360	6	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.

All (6) 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:A:97:HIS:HE1	1:A:219:ASP:OD2	1.89	0.56
1:A:149:CYS:O	1:A:151:GLN:NE2	2.42	0.53
1:A:133:VAL:HG22	1:A:222:VAL:CG1	2.39	0.53
1:B:67:THR:HG23	1:B:71:LEU:HD23	1.99	0.45
1:B:65:ASN:OD1	1:B:105:ARG:NH2	2.51	0.42
1:B:240:LYS:HE2	1:B:254:ASP:HA	2.01	0.41

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	256/270 (95%)	247 (96%)	9 (4%)	0	100	100
1	B	259/270 (96%)	247 (95%)	12 (5%)	0	100	100
All	All	515/540 (95%)	494 (96%)	21 (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	240/252 (95%)	239 (100%)	1 (0%)	91	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	243/252 (96%)	240 (99%)	3 (1%)	71	76
All	All	483/504 (96%)	479 (99%)	4 (1%)	81	86

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	161	MET
1	B	163	GLU
1	B	165	LEU
1	A	138	TYR

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

Mol	Chain	Res	Type
1	B	193	GLN
1	A	97	HIS
1	A	151	GLN
1	A	193	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 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	258/270 (95%)	0.44	25 (9%) <b>7</b> <b>7</b>	30, 50, 108, 141	0
1	B	261/270 (96%)	0.67	30 (11%) <b>4</b> <b>4</b>	31, 47, 113, 172	0
All	All	519/540 (96%)	0.56	55 (10%) <b>6</b> <b>5</b>	30, 49, 109, 172	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	245	VAL	11.5
1	B	253	PHE	9.0
1	B	244	PRO	8.8
1	B	243	SER	8.5
1	B	249	SER	8.3
1	B	246	LYS	7.1
1	B	247	ARG	6.1
1	A	244	PRO	5.7
1	A	243	SER	5.5
1	B	242	ASP	5.5
1	B	162	PRO	5.5
1	B	252	VAL	4.9
1	A	167	MET	4.7
1	B	250	ARG	4.6
1	B	165	LEU	4.6
1	A	148	ASP	4.6
1	B	163	GLU	4.2
1	A	245	VAL	4.1
1	B	160	GLU	4.0
1	B	251	ALA	4.0
1	B	248	GLY	3.8
1	B	8	ILE	3.7
1	A	8	ILE	3.7
1	A	169	THR	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	24	ASN	3.6
1	A	174	CYS	3.4
1	A	179	GLN	3.4
1	B	164	VAL	3.3
1	B	241	GLN	3.2
1	A	251	ALA	3.1
1	B	158	ASP	3.0
1	B	24	ASN	2.9
1	B	157	GLU	2.9
1	A	172	PRO	2.9
1	A	247	ARG	2.8
1	B	174	CYS	2.8
1	A	149	CYS	2.7
1	B	179	GLN	2.7
1	A	128	VAL	2.7
1	A	168	PRO	2.4
1	A	175	GLY	2.4
1	B	167	MET	2.4
1	B	148	ASP	2.3
1	B	172	PRO	2.3
1	B	239	ILE	2.3
1	B	161	MET	2.3
1	A	147	PRO	2.3
1	A	264	VAL	2.2
1	B	166	GLU	2.2
1	A	180	PHE	2.2
1	A	246	LYS	2.1
1	A	265	SER	2.1
1	A	150	MET	2.1
1	A	146	HIS	2.0
1	A	155	TRP	2.0

## 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<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
2	ZN	A	301	1/1	0.84	0.07	82,82,82,82	0
2	ZN	B	301	1/1	0.94	0.06	58,58,58,58	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.