



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 30, 2017 – 04:11 PM EST

PDB ID : 5F9M  
Title : Crystal structure of native B3275, member of MccF family of enzymes  
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Deposited on : 2015-12-09  
Resolution : 2.40 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

<http://wwpdb.org/validation/2016/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
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

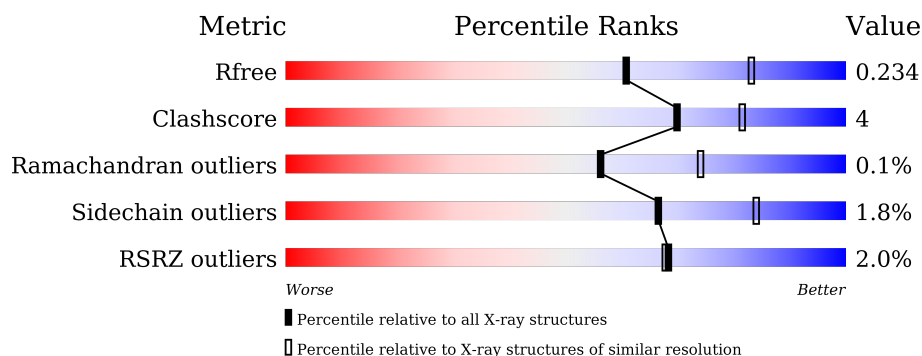
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	344	<div> <div>2%</div> <div>85% 14%</div> </div>
1	B	344	<div> <div>2%</div> <div>87% 13%</div> </div>
1	C	344	<div> <div>3%</div> <div>88% 11%</div> </div>
1	D	344	<div> <div>2%</div> <div>88% 12%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11201 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 MccC family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2760	1769	455	522	14			
1	B	344	Total	C	N	O	S	0	0	0
			2763	1771	456	522	14			
1	C	344	Total	C	N	O	S	0	0	0
			2751	1763	454	520	14			
1	D	344	Total	C	N	O	S	0	0	0
			2767	1773	456	524	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP Q734X3
A	116	ALA	SER	engineered mutation	UNP Q734X3
B	0	ALA	-	expression tag	UNP Q734X3
B	116	ALA	SER	engineered mutation	UNP Q734X3
C	0	ALA	-	expression tag	UNP Q734X3
C	116	ALA	SER	engineered mutation	UNP Q734X3
D	0	ALA	-	expression tag	UNP Q734X3
D	116	ALA	SER	engineered mutation	UNP Q734X3

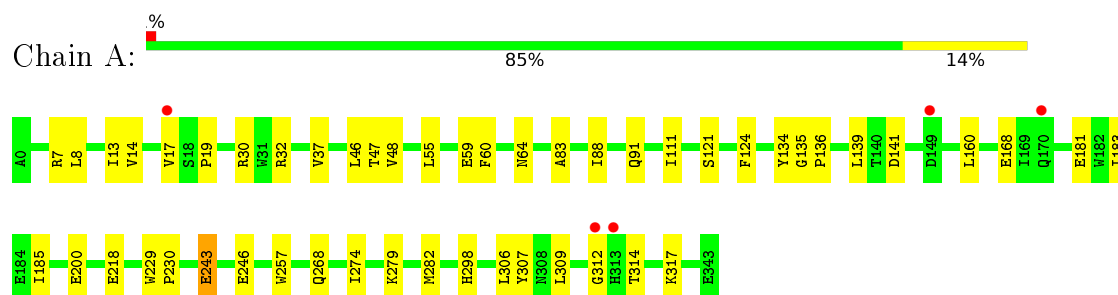
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total	O	0	0
			44	44		
2	B	51	Total	O	0	0
			51	51		
2	C	26	Total	O	0	0
			26	26		
2	D	39	Total	O	0	0
			39	39		

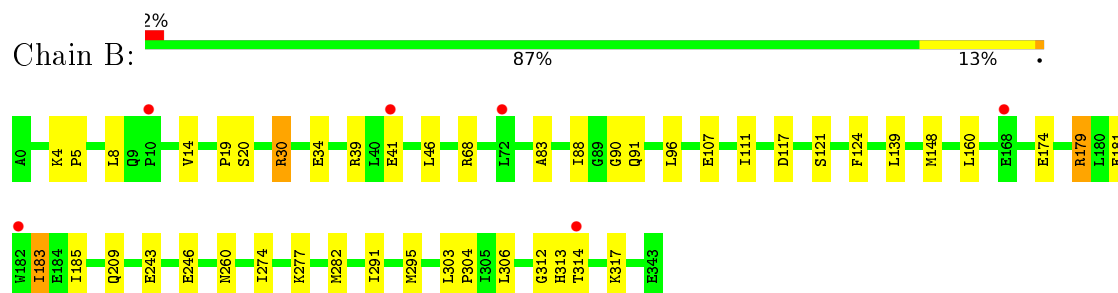
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

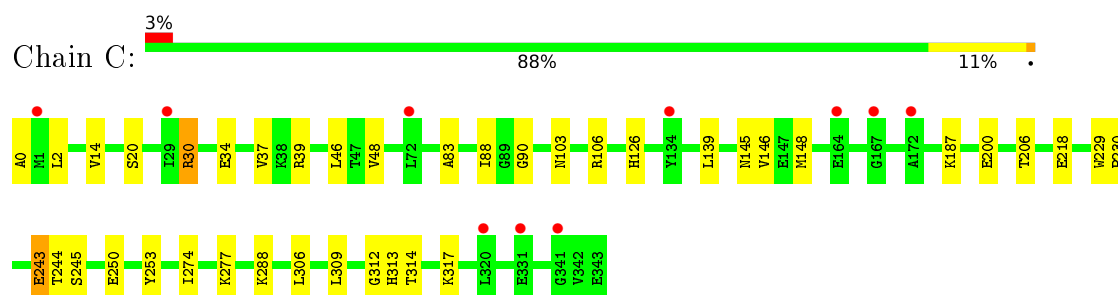
#### • Molecule 1: MccC family protein



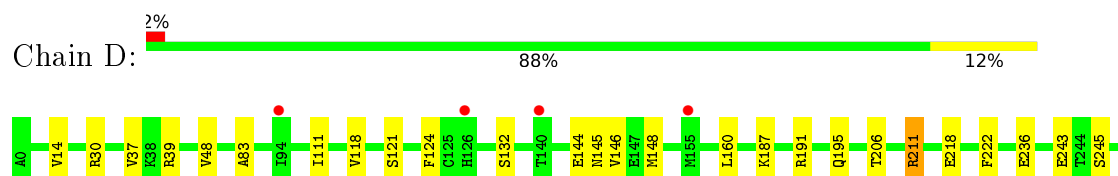
#### • Molecule 1: MccC family protein

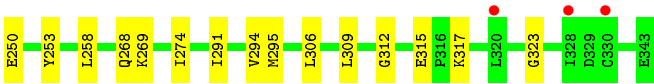


#### • Molecule 1: MccC family protein



#### • Molecule 1: MccC family protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.78Å 70.86Å 85.49Å 92.12° 90.24° 89.87°	Depositor
Resolution (Å)	37.19 – 2.40 38.92 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.8 (37.19-2.40) 64.6 (38.92-2.40)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.71 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1888)	Depositor
R, $R_{free}$	0.187 , 0.227 0.191 , 0.234	Depositor DCC
$R_{free}$ test set	2105 reflections (4.97%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.5	Xtriage
Anisotropy	0.250	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 1.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.417 for h,-k,-l 0.038 for -h,k,-l 0.035 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	11201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	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	0.24	0/2829	0.38	0/3833
1	B	0.25	0/2833	0.38	0/3838
1	C	0.23	0/2821	0.38	0/3825
1	D	0.31	0/2837	0.39	0/3843
All	All	0.26	0/11320	0.38	0/15339

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	2760	0	2683	27	0
1	B	2763	0	2692	27	0
1	C	2751	0	2666	23	0
1	D	2767	0	2696	22	0
2	A	44	0	0	3	0
2	B	51	0	0	4	0
2	C	26	0	0	2	0
2	D	39	0	0	3	0
All	All	11201	0	10737	97	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 4.

The worst 5 of 97 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:246:GLU:OE2	2:B:401:HOH:O	1.99	0.80
1:B:41:GLU:OE2	2:B:402:HOH:O	2.01	0.78
1:A:7:ARG:NH1	2:A:402:HOH:O	2.16	0.78
1:A:30:ARG:NH2	1:B:107:GLU:OE2	2.18	0.76
1:B:274:ILE:HG22	1:B:306:LEU:HB2	1.72	0.71

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	342/344 (99%)	330 (96%)	11 (3%)	1 (0%)	46	63
1	B	342/344 (99%)	330 (96%)	11 (3%)	1 (0%)	46	63
1	C	342/344 (99%)	330 (96%)	12 (4%)	0	100	100
1	D	342/344 (99%)	329 (96%)	13 (4%)	0	100	100
All	All	1368/1376 (99%)	1319 (96%)	47 (3%)	2 (0%)	56	74

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	B	91	GLN

### 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	296/299 (99%)	289 (98%)	7 (2%)	57	76
1	B	297/299 (99%)	291 (98%)	6 (2%)	63	81
1	C	294/299 (98%)	291 (99%)	3 (1%)	82	93
1	D	298/299 (100%)	293 (98%)	5 (2%)	68	85
All	All	1185/1196 (99%)	1164 (98%)	21 (2%)	66	84

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	181	GLU
1	B	209	GLN
1	D	195	GLN
1	B	179	ARG
1	D	206	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

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	344/344 (100%)	0.05	5 (1%) 76 75	19, 35, 55, 66	0
1	B	344/344 (100%)	0.03	6 (1%) 73 72	20, 34, 54, 66	0
1	C	344/344 (100%)	0.15	10 (2%) 55 54	26, 42, 61, 83	0
1	D	344/344 (100%)	0.09	7 (2%) 68 68	25, 41, 61, 86	0
All	All	1376/1376 (100%)	0.08	28 (2%) 68 68	19, 38, 57, 86	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	330	CYS	4.5
1	C	167	GLY	4.4
1	A	312	GLY	4.3
1	B	168	GLU	3.8
1	D	140	THR	3.3

### 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.