



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 07:05 AM GMT

PDB ID : 3CRA  
Title : Crystal Structure of Escherichia coli MazG, the Regulator of Nutritional Stress Response  
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Deposited on : 2008-04-05  
Resolution : 2.10 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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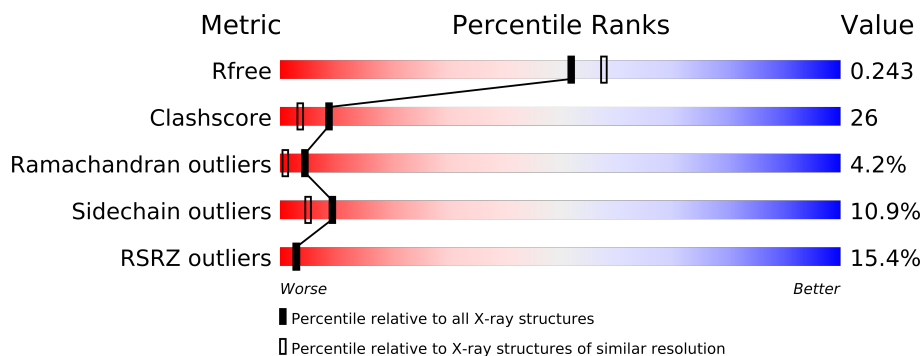
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.10 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))
$R_{free}$	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	265	
1	B	265	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3870 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Protein mazG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	0	0	0
			1956	1223	345	378	10			
1	B	222	Total	C	N	O	S	0	0	0
			1806	1135	312	350	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P0AEY3
A	0	HIS	-	EXPRESSION TAG	UNP P0AEY3
B	-1	GLY	-	EXPRESSION TAG	UNP P0AEY3
B	0	HIS	-	EXPRESSION TAG	UNP P0AEY3

- Molecule 2 is water.

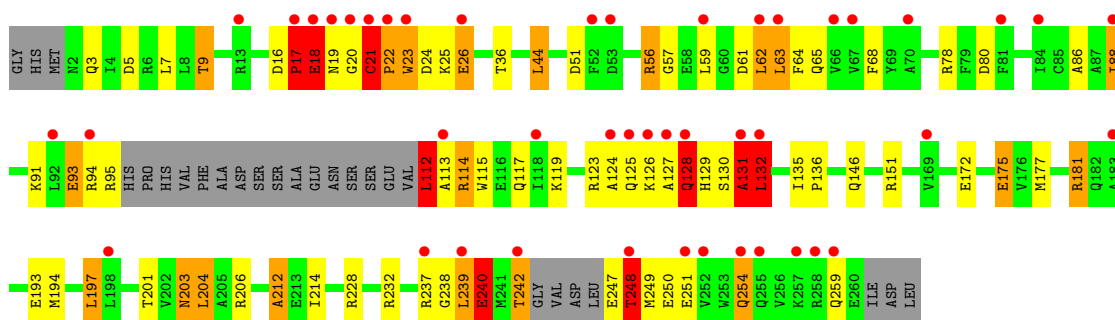
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total	O	0	0
			44	44		
2	B	64	Total	O	0	0
			64	64		

### 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.

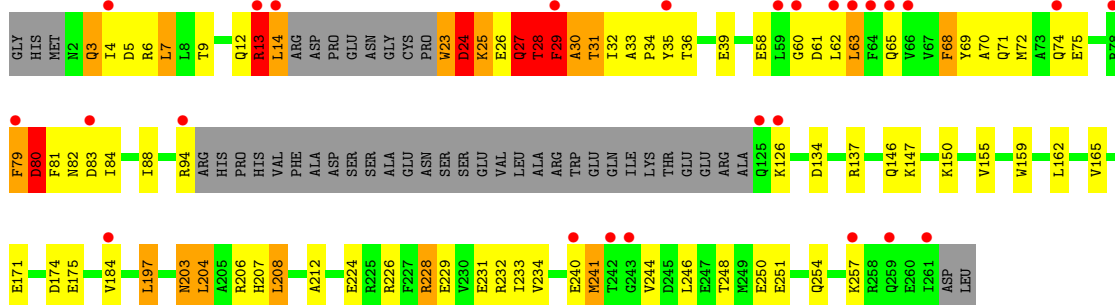
#### • Molecule 1: Protein mazG

Chain A: 



#### • Molecule 1: Protein mazG

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.79Å 67.57Å 140.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.47 – 2.10 32.85 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.2 (28.47-2.10) 93.5 (32.85-2.00)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.69 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.226 , 0.284 0.241 , 0.243	Depositor DCC
$R_{free}$ test set	1923 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.1	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 45.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 38465 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3870	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.73% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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	1.12	3/1984 (0.2%)	1.12	17/2671 (0.6%)
1	B	1.11	1/1830 (0.1%)	1.09	13/2464 (0.5%)
All	All	1.11	4/3814 (0.1%)	1.10	30/5135 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	6
All	All	0	11

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	175	GLU	CB-CG	-11.57	1.30	1.52
1	A	212	ALA	CA-CB	6.06	1.65	1.52
1	A	172	GLU	CD-OE2	-5.51	1.19	1.25
1	B	147	LYS	CD-CE	5.50	1.65	1.51

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	228	ARG	NE-CZ-NH1	9.75	125.17	120.30
1	A	228	ARG	NE-CZ-NH2	-8.37	116.11	120.30
1	A	21	CYS	C-N-CD	-8.34	102.24	120.60
1	B	174	ASP	CB-CG-OD1	7.19	124.77	118.30
1	B	197	LEU	CB-CG-CD2	7.14	123.14	111.00

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	LEU	Peptide
1	A	131	ALA	Peptide
1	A	17	PRO	Peptide
1	A	240	GLU	Peptide
1	A	248	THR	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1956	0	1919	109	5
1	B	1806	0	1779	113	5
2	A	44	0	0	4	0
2	B	64	0	0	9	0
All	All	3870	0	3698	191	5

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 26.

The worst 5 of 191 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:112:LEU:HB3	1:B:14:LEU:CD2	1.12	1.54
1:A:112:LEU:CB	1:B:14:LEU:HD21	1.33	1.50
1:B:74:GLN:CG	1:B:80:ASP:HB2	1.49	1.40
1:A:112:LEU:CB	1:B:14:LEU:CD2	1.95	1.35
1:A:132:LEU:HD22	2:A:307:HOH:O	1.27	1.29

All (5) 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	Distance(Å)	Clash(Å)
1:A:239:LEU:CD2	1:B:254:GLN:NE2[4_456]	1.24	0.96
1:A:239:LEU:CD2	1:B:254:GLN:CD[4_456]	1.55	0.65
1:A:239:LEU:CG	1:B:254:GLN:NE2[4_456]	2.08	0.12

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:242:THR:OG1	1:B:250:GLU:OE1[4.456]	2.10	0.10
1:A:239:LEU:CD2	1:B:254:GLN:OE1[4.456]	2.13	0.07

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	233/265 (88%)	206 (88%)	14 (6%)	13 (6%)	3	0
1	B	216/265 (82%)	203 (94%)	7 (3%)	6 (3%)	8	2
All	All	449/530 (85%)	409 (91%)	21 (5%)	19 (4%)	4	1

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	PRO
1	A	18	GLU
1	A	21	CYS
1	A	22	PRO
1	A	239	LEU

### 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	205/227 (90%)	182 (89%)	23 (11%)	9	4
1	B	190/227 (84%)	170 (90%)	20 (10%)	10	5
All	All	395/454 (87%)	352 (89%)	43 (11%)	9	5

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	237	ARG
1	B	7	LEU
1	B	197	LEU
1	A	240	GLU
1	A	242	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	259	GLN
1	B	65	GLN
1	B	146	GLN
1	A	203	ASN
1	B	129	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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	239/265 (90%)	0.99	45 (18%)	2 2	22, 44, 78, 89	0
1	B	222/265 (83%)	0.71	26 (11%)	5 6	20, 41, 73, 89	0
All	All	461/530 (86%)	0.86	71 (15%)	3 3	20, 42, 76, 89	0

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	79	PHE	8.9
1	B	125	GLN	8.8
1	A	239	LEU	7.7
1	B	261	ILE	7.0
1	A	124	ALA	7.0

### 6.2 Non-standard residues in protein, DNA, RNA chains

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

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

There are no ligands in this entry.

### 6.5 Other polymers

There are no such residues in this entry.