

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

#### Aug 29, 2023 – 10:16 AM EDT

PDB ID	:	3O9X
Title	:	Structure of the E. coli antitoxin MqsA (YgiT/b $3021$ ) in complex with its gene
		promoter
Authors	:	Brown, B.L.; Peti, W.; Page, R.
Deposited on		
Resolution	:	2.10 Å(reported)
Deposited on	:	Brown, B.L.; Peti, W.; Page, R.

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 (1)) were used in the production of this report:

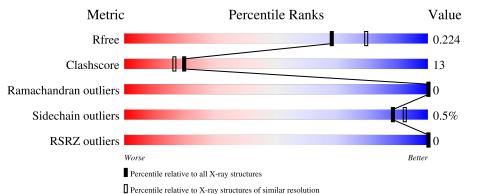
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal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

# 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 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (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 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	133			85%		14%	•	
1	В	133			84%		14%	••	
2	F	26		58%		31%	12%	6	
3	Е	26	19%		65%		15%		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	В	133	-	-	Х	-



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3396 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 HTH-type transcriptional regulator ygiT.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	132	Total	С	Ν	0	S	0	0	0
	A	152	1027	649	184	186	8	0	0	0
1	В	132	Total	С	Ν	0	S	0	0	0
	D	152	1010	640	177	185	8	0		U

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-1	GLY	-	expression tag	UNP Q46864
А	0	HIS	-	expression tag	UNP Q46864
В	-1	GLY	-	expression tag	UNP Q46864
В	0	HIS	-	expression tag	UNP Q46864

• Molecule 2 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	F	26	Total 528	C 257	N 88	O 158	Р 25	0	0	0

• Molecule 3 is a DNA chain called DNA (26-MER).

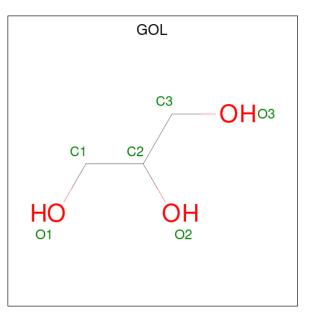
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	Е	26	Total 532	$\begin{array}{c} \mathrm{C} \\ 257 \end{array}$	N 100	O 150	Р 25	0	0	0

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Zn 1 1	0	0
4	В	1	Total Zn 1 1	0	0



• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
5	Е	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	110	Total O 110 110	0	0
6	В	103	Total O 103 103	0	0
6	F	35	Total         O           35         35	0	0
6	Е	37	$\begin{array}{cc} \text{Total} & \text{O} \\ 37 & 37 \end{array}$	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 HTH-type transcriptional regulator ygiT

Chain A:	85%		14% •
GLY M1 M1 M1 17 17 17 850 850 850 850 850 850 850 870 870	F71 F72 775 775 786 889 889 889 889 889 889 889 792 792 792 792 792 792 792 792 7108	I	
• Molecule 1: Uncharacter	ized HTH-type transcrip	otional regulator	ygiT
Chain B:	84%		14% ••
GLY HD M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M6 M6 M6 M6 M6 M6 M7 M1 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2	710 771 773 775 775 777 777 777 777 776 776 776 776	R1 31	
• Molecule 2: DNA (26-M	ER)		
Chain F:	58%	31%	12%
11 62 13 14 48 48 48 61 113 113 113 113 113 113			
• Molecule 3: DNA (26-M	ER)		
Chain E: 19%	65%		15%
A1 62 73 73 75 74 75 76 71 71 11 71 11 719 719 719 719 719 719	122 123 026 <b>026</b> <b>026</b>		



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants	61.00Å 61.00Å 148.61Å	Deneiten
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.15 - 2.10	Depositor
Resolution (A)	$47.15 \ - \ 2.10$	EDS
% Data completeness	99.3 (47.15-2.10)	Depositor
(in resolution range)	97.2 (47.15-2.10)	EDS
R <sub>merge</sub>	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$< I/\sigma(I) > 1$	$2.54 (at 2.10 \text{\AA})$	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.2_432)	Depositor
D D	0.176 , $0.228$	Depositor
$R, R_{free}$	0.173 , $0.224$	DCC
$R_{free}$ test set	2942 reflections $(9.38%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	27.6	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.28 , 21.9	EDS
L-test for $twinning^2$	$< L >=0.40, < L^2>=0.23$	Xtriage
Estimated twinning fraction	0.359 for h,-k,-l	Xtriage
Reported twinning fraction	0.372 for h,-k,-l	Depositor
Outliers	1  of  31367  reflections  (0.003%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3396	wwPDB-VP
Average B, all atoms $(Å^2)$	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.01% 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: GOL, 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	
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.34	0/1047	0.50	0/1407
1	В	0.34	0/1030	0.50	0/1388
2	F	0.61	0/590	1.46	6/909~(0.7%)
3	Е	0.68	0/598	1.52	11/921~(1.2%)
All	All	0.47	0/3265	1.01	17/4625~(0.4%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	Е	15	DA	O4'-C1'-N9	-11.98	99.62	108.00
2	F	16	DA	O4'-C1'-N9	-11.89	99.68	108.00
3	Е	25	DC	C3'-C2'-C1'	-8.92	91.79	102.50
3	Е	25	DC	O4'-C1'-N1	7.73	113.41	108.00
2	F	17	DG	O4'-C1'-N9	7.68	113.38	108.00

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	1027	0	1027	13	0
1	В	1010	0	987	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	528	0	300	14	0
3	Ε	532	0	296	30	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
5	В	6	0	8	7	0
5	Ε	6	0	8	3	0
6	А	110	0	0	2	0
6	В	103	0	0	3	0
6	Ε	37	0	0	1	0
6	F	35	0	0	0	0
All	All	3396	0	2626	72	0

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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 13.

The worst 5 of 72 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)
3:E:8:DA:H2"	3:E:9:DC:O5'	1.51	1.10
1:B:23:ARG:HH21	5:B:133:GOL:H31	1.32	0.94
3:E:24:DA:H2"	3:E:25:DC:H2'	1.50	0.92
3:E:1:DA:HO5'	3:E:1:DA:H8	1.17	0.88
1:B:23:ARG:NH2	5:B:133:GOL:H31	1.98	0.79

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	Percer	ntiles
1	А	130/133~(98%)	124 (95%)	6~(5%)	0	100	100
1	В	130/133~(98%)	126 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	260/266~(98%)	250~(96%)	10 (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	А	110/114~(96%)	110 (100%)	0	100 100
1	В	105/114~(92%)	104 (99%)	1 (1%)	76 82
All	All	215/228~(94%)	214 (100%)	1 (0%)	88 92

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	2	LYS

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

Mol	Chain	Res	Type
1	А	56	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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Dec	Link	B	ond leng	ths Bond angles		gles	
			$\operatorname{Res}$	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
5	GOL	В	133	-	$5,\!5,\!5$	0.35	0	$5,\!5,\!5$	0.29	0
5	GOL	Е	27	-	5,5,5	0.27	0	$5,\!5,\!5$	0.45	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	В	133	-	-	4/4/4/4	-
5	GOL	Е	27	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	В	133	GOL	C1-C2-C3-O3
5	В	133	GOL	O1-C1-C2-C3
5	Е	27	GOL	C1-C2-C3-O3
5	Е	27	GOL	O2-C2-C3-O3
5	В	133	GOL	O2-C2-C3-O3

There are no ring outliers.



Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	В	133	GOL	7	0
5	Е	27	GOL	3	0

2 monomers are involved in 10 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	<RSRZ $>$	#RSRZ>2		Z>2	$OWAB(Å^2)$	Q<0.9
1	А	132/133~(99%)	0.07	0	100	100	18, 27, 36, 54	0
1	В	132/133~(99%)	0.08	0	100	100	18, 27, 36, 48	0
2	F	26/26~(100%)	-0.03	0	100	100	19, 36, 59, 61	0
3	Е	26/26~(100%)	-0.09	0	100	100	21, 34, 58, 63	0
All	All	316/318~(99%)	0.05	0	100	100	18, 28, 47, 63	0

There are no RSRZ outliers to report.

### 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	$B-factors(Å^2)$	Q < 0.9
5	GOL	В	133	6/6	0.83	0.29	24,31,34,39	0
5	GOL	Е	27	6/6	0.95	0.20	27,29,31,31	0
4	ZN	А	132	1/1	0.99	0.12	31,31,31,31	0
4	ZN	В	132	1/1	0.99	0.07	33,33,33,33	0



### 6.5 Other polymers (i)

There are no such residues in this entry.

