



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2022 – 01:10 pm BST

PDB ID : 7OT4  
Title : Crystal structure of MsrA variant C198C206 from Escherichia coli, oxidized  
Authors : Napolitano, S.; Glockshuber, R.  
Deposited on : 2021-06-09  
Resolution : 2.19 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 : 2.28.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.28.1

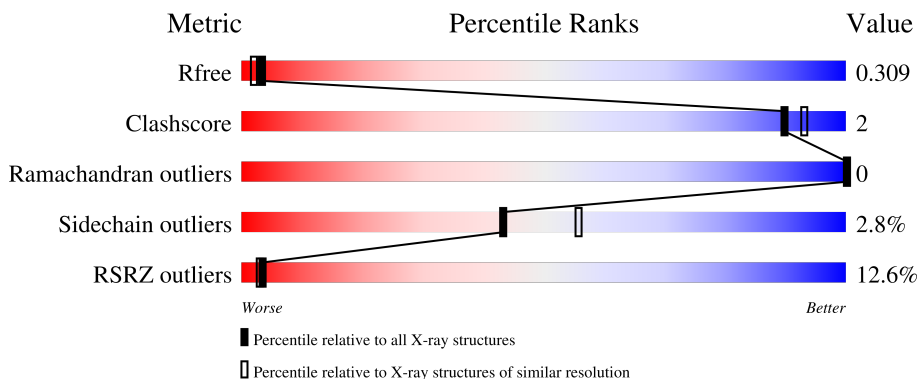
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.19 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	212	
1	B	212	

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
2	K	B	301	-	-	-	X

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3135 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 Peptide methionine sulfoxide reductase MsrA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	202	1557	983	267	299	8	0	0	0
1	B	203	1566	988	268	302	8	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	SER	CYS	engineered mutation	UNP J7RCD1
A	86	ALA	CYS	engineered mutation	UNP J7RCD1
B	51	SER	CYS	engineered mutation	UNP J7RCD1
B	86	ALA	CYS	engineered mutation	UNP J7RCD1

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total K 1 1	0	0

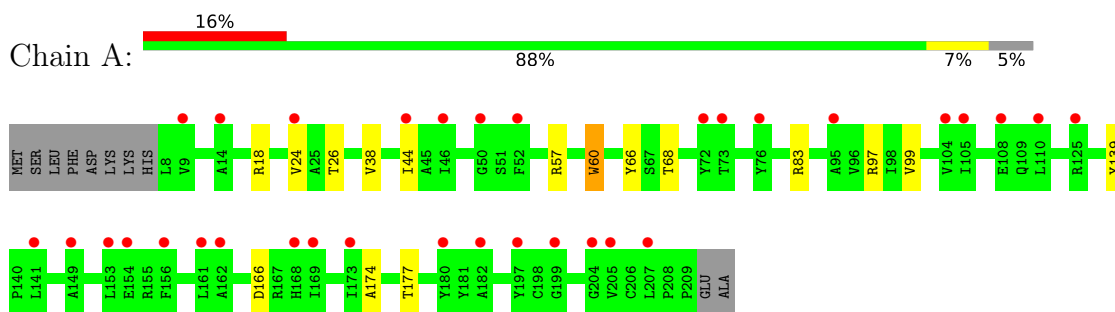
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	7	Total O 7 7	0	0
3	B	4	Total O 4 4	0	0

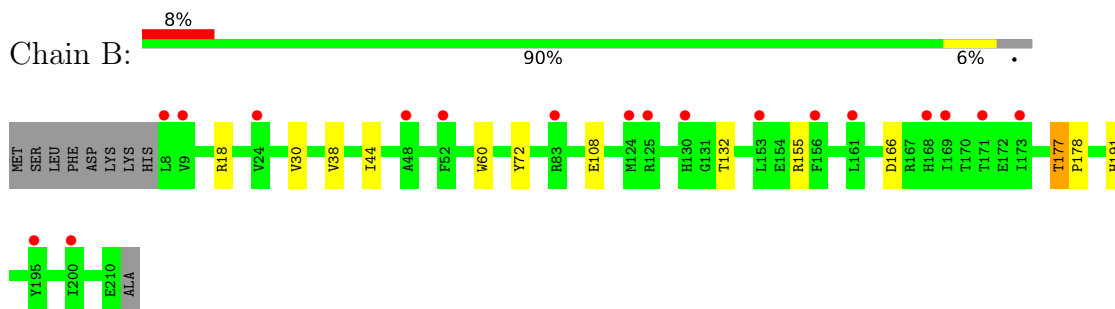
### 3 Residue-property plots [i](#)

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: Peptide methionine sulfoxide reductase MsrA



- Molecule 1: Peptide methionine sulfoxide reductase MsrA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.21Å 128.21Å 118.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.48 – 2.19 43.48 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.4 (43.48-2.19) 99.9 (43.48-2.19)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.19rc5_4047	Depositor
R, $R_{free}$	0.286 , 0.308 0.291 , 0.309	Depositor DCC
$R_{free}$ test set	1503 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.5	Xtriage
Anisotropy	0.455	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3135	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.43% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.26	0/1605	0.49	0/2197
1	B	0.26	0/1614	0.49	0/2209
All	All	0.26	0/3219	0.49	0/4406

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	A	1557	0	1448	6	1
1	B	1566	0	1454	5	0
2	B	1	0	0	0	0
3	A	7	0	0	0	0
3	B	4	0	0	0	0
All	All	3135	0	2902	11	1

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 2.

All (11) 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:38:VAL:HG21	1:A:44:ILE:HD11	1.83	0.60
1:B:38:VAL:HG21	1:B:44:ILE:HD11	1.87	0.56
1:B:108:GLU:OE2	1:B:155:ARG:NH2	2.48	0.47
1:B:30:VAL:HG22	1:B:191:HIS:CG	2.51	0.45
1:B:166:ASP:OD1	1:B:166:ASP:N	2.46	0.44
1:A:139:TYR:HA	1:A:174:ALA:O	2.16	0.44
1:A:57:ARG:HA	1:A:60:TRP:CD2	2.55	0.42
1:B:177:THR:HG22	1:B:178:PRO:HD2	2.03	0.41
1:A:68:THR:HA	1:A:97:ARG:O	2.21	0.41
1:A:166:ASP:OD1	1:A:166:ASP:N	2.54	0.41
1:A:66:TYR:N	1:A:99:VAL:O	2.54	0.40

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:VAL:O	1:A:26:THR:OG1[11_654]	2.00	0.20

## 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	200/212 (94%)	198 (99%)	2 (1%)	0	100	100
1	B	201/212 (95%)	199 (99%)	2 (1%)	0	100	100
All	All	401/424 (95%)	397 (99%)	4 (1%)	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	159/168 (95%)	155 (98%)	4 (2%)	47	60
1	B	160/168 (95%)	155 (97%)	5 (3%)	40	51
All	All	319/336 (95%)	310 (97%)	9 (3%)	43	56

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ARG
1	A	60	TRP
1	A	83	ARG
1	A	177	THR
1	B	18	ARG
1	B	60	TRP
1	B	72	TYR
1	B	132	THR
1	B	177	THR

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

### 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 1 ligands modelled in this entry, 1 is 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

### 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	202/212 (95%)	1.08	33 (16%) <b>1</b> <b>1</b>	75, 100, 125, 145	0
1	B	203/212 (95%)	0.69	18 (8%) <b>9</b> <b>8</b>	54, 87, 133, 167	0
All	All	405/424 (95%)	0.89	51 (12%) <b>3</b> <b>3</b>	54, 97, 130, 167	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	168	HIS	6.5
1	A	173	ILE	5.3
1	B	125	ARG	4.6
1	A	141	LEU	4.3
1	A	76	TYR	4.2
1	A	204	GLY	3.9
1	B	130	HIS	3.7
1	B	169	ILE	3.6
1	A	44	ILE	3.5
1	A	110	LEU	3.5
1	A	72	TYR	3.5
1	A	207	LEU	3.3
1	A	9	VAL	3.3
1	B	156	PHE	3.2
1	A	169	ILE	3.1
1	A	73	THR	3.1
1	B	24	VAL	3.0
1	B	195	TYR	3.0
1	B	8	LEU	2.9
1	B	48	ALA	2.7
1	B	124	MET	2.6
1	A	153	LEU	2.6
1	A	168	HIS	2.6
1	B	161	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	125	ARG	2.6
1	A	156	PHE	2.6
1	A	95	ALA	2.4
1	B	83	ARG	2.4
1	A	52	PHE	2.4
1	A	105	ILE	2.3
1	B	200	ILE	2.3
1	B	173	ILE	2.2
1	B	153	LEU	2.2
1	A	46	ILE	2.2
1	A	154	GLU	2.2
1	A	199	GLY	2.2
1	A	182	ALA	2.2
1	A	14	ALA	2.2
1	B	171	THR	2.2
1	A	161	LEU	2.1
1	A	104	VAL	2.1
1	A	180	TYR	2.1
1	A	197	TYR	2.1
1	B	52	PHE	2.1
1	A	108	GLU	2.1
1	A	149	ALA	2.1
1	B	9	VAL	2.1
1	A	205	VAL	2.1
1	A	24	VAL	2.0
1	A	162	ALA	2.0
1	A	50	GLY	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	K	B	301	1/1	0.68	0.47	167,167,167,167	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.