



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 25, 2016 – 11:39 AM GMT

PDB ID : 4YIP  
Title : X-ray structure of the iron/manganese cambialistic superoxide dismutase from Streptococcus mutans  
Authors : Russo Krauss, I.; Merlino, A.; Pica, A.; Sica, F.  
Deposited on : 2015-03-02  
Resolution : 2.15 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	:	<b>FAILED</b>
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

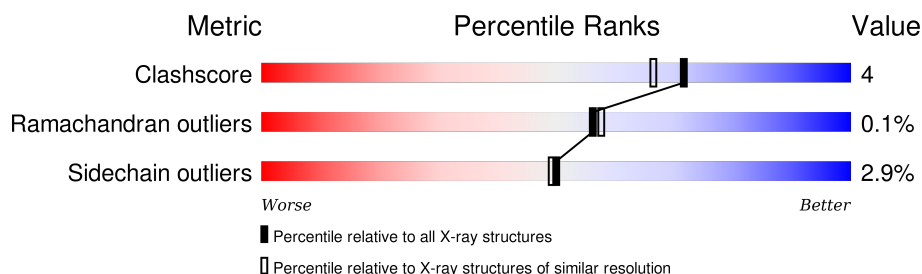
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)

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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	210	
1	B	210	
1	C	210	
1	D	210	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6699 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 Superoxide dismutase [Mn/Fe].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	2	0
			1615	1042	266	306	1			
1	B	203	Total	C	N	O	S	0	1	0
			1607	1036	265	305	1			
1	C	201	Total	C	N	O	S	0	0	0
			1586	1022	263	300	1			
1	D	203	Total	C	N	O	S	0	1	0
			1609	1037	265	306	1			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	LEU	-	expression tag	UNP P09738
A	203	GLU	-	expression tag	UNP P09738
A	204	HIS	-	expression tag	UNP P09738
A	205	HIS	-	expression tag	UNP P09738
A	206	HIS	-	expression tag	UNP P09738
A	207	HIS	-	expression tag	UNP P09738
A	208	HIS	-	expression tag	UNP P09738
A	209	HIS	-	expression tag	UNP P09738
B	202	LEU	-	expression tag	UNP P09738
B	203	GLU	-	expression tag	UNP P09738
B	204	HIS	-	expression tag	UNP P09738
B	205	HIS	-	expression tag	UNP P09738
B	206	HIS	-	expression tag	UNP P09738
B	207	HIS	-	expression tag	UNP P09738
B	208	HIS	-	expression tag	UNP P09738
B	209	HIS	-	expression tag	UNP P09738
C	202	LEU	-	expression tag	UNP P09738
C	203	GLU	-	expression tag	UNP P09738
C	204	HIS	-	expression tag	UNP P09738
C	205	HIS	-	expression tag	UNP P09738
C	206	HIS	-	expression tag	UNP P09738

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Chain	Residue	Modelled	Actual	Comment	Reference
C	207	HIS	-	expression tag	UNP P09738
C	208	HIS	-	expression tag	UNP P09738
C	209	HIS	-	expression tag	UNP P09738
D	202	LEU	-	expression tag	UNP P09738
D	203	GLU	-	expression tag	UNP P09738
D	204	HIS	-	expression tag	UNP P09738
D	205	HIS	-	expression tag	UNP P09738
D	206	HIS	-	expression tag	UNP P09738
D	207	HIS	-	expression tag	UNP P09738
D	208	HIS	-	expression tag	UNP P09738
D	209	HIS	-	expression tag	UNP P09738

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Fe 1 1	0	0
2	A	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0

- Molecule 3 is water.

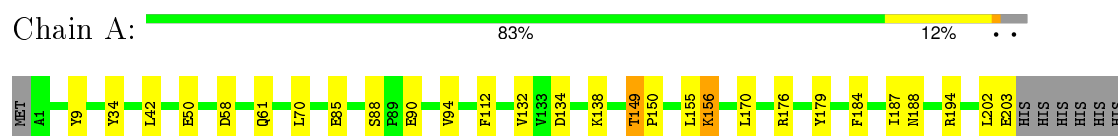
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	71	Total O 72 72	0	1
3	B	70	Total O 70 70	0	0
3	C	65	Total O 65 65	0	0
3	D	71	Total O 71 71	0	0

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

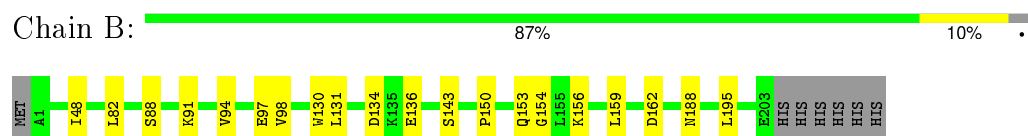
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ( $\text{RSRZ} > 2$ ). 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.

Note EDS failed to run properly.

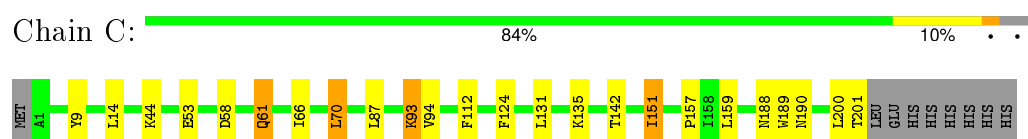
- Molecule 1: Superoxide dismutase [Mn/Fe]



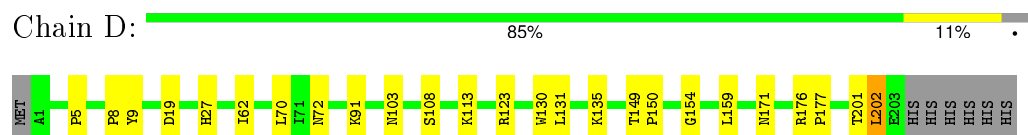
- Molecule 1: Superoxide dismutase [Mn/Fe]



- Molecule 1: Superoxide dismutase [Mn/Fe]



- Molecule 1: Superoxide dismutase [Mn/Fe]



## 4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.96Å 82.88Å 72.78Å 90.00° 94.25° 90.00°	Depositor
Resolution (Å)	31.39 – 2.15	Depositor
% Data completeness (in resolution range)	99.0 (31.39-2.15)	Depositor
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.193 , 0.259	Depositor
Wilson B-factor (Å <sup>2</sup> )	26.6	Xtriage
Anisotropy	0.304	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 43442 reflections	Xtriage
Total number of atoms	6699	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.53% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: FE

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	0.75	0/1664	0.83	0/2275
1	B	0.78	0/1653	0.88	1/2262 (0.0%)
1	C	0.76	0/1629	0.81	0/2229
1	D	0.78	0/1655	0.83	1/2264 (0.0%)
All	All	0.77	0/6601	0.84	2/9030 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	162	ASP	CB-CG-OD1	7.56	125.10	118.30
1	D	123	ARG	NE-CZ-NH1	5.29	122.95	120.30

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	1615	0	1570	15	0
1	B	1607	0	1558	9	0
1	C	1586	0	1534	20	0
1	D	1609	0	1557	11	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	72	0	0	2	0
3	B	70	0	0	3	0
3	C	65	0	0	4	0
3	D	71	0	0	0	0
All	All	6699	0	6219	54	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 54 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:C:200:LEU:O	1:C:201:THR:HB	1.79	0.80
1:C:142:THR:HG22	3:C:426:HOH:O	1.90	0.71
1:B:88:SER:HB2	1:B:188:ASN:HB2	1.71	0.71
1:A:88:SER:HB2	1:A:188:ASN:HB2	1.73	0.70
1:A:134:ASP:HB2	1:A:138:LYS:H	1.58	0.67

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	203/210 (97%)	190 (94%)	13 (6%)	0	100	100
1	B	202/210 (96%)	194 (96%)	8 (4%)	0	100	100
1	C	199/210 (95%)	192 (96%)	7 (4%)	0	100	100
1	D	202/210 (96%)	192 (95%)	9 (4%)	1 (0%)	34	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	806/840 (96%)	768 (95%)	37 (5%)	1 (0%)	56	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	202	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	166/171 (97%)	161 (97%)	5 (3%)	48	48
1	B	165/171 (96%)	161 (98%)	4 (2%)	57	60
1	C	162/171 (95%)	155 (96%)	7 (4%)	35	32
1	D	165/171 (96%)	162 (98%)	3 (2%)	66	71
All	All	658/684 (96%)	639 (97%)	19 (3%)	50	49

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	153	GLN
1	C	61	GLN
1	C	151	ILE
1	B	143	SER
1	D	91	LYS

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 [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 [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 ⓘ

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.