



# wwPDB X-ray Structure Validation Summary Report

Feb 19, 2016 – 07:38 PM GMT

PDB ID : 4RVP  
Title : Crystal structure of superoxide dismutase from sedum alfredii  
Authors : Qiu, R.; Li, C.; Zhai, J.; Tang, L.; Zhang, H.; Yuan, M.; Hu, X.  
Deposited on : 2014-11-27  
Resolution : 2.60 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-20026982  
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-20026982

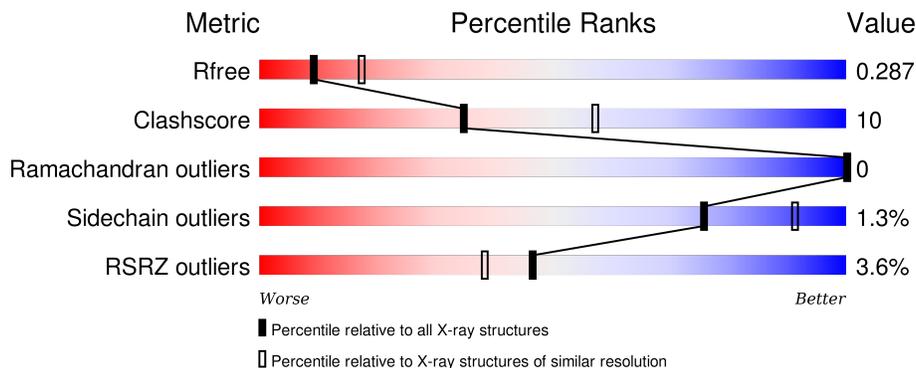
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	158	 3% 80% 16% ..
1	B	158	 2% 84% 11% ..
1	C	158	 8% 75% 17% ..
1	D	158	 3% 73% 25% .
1	E	158	 3% 82% 15% ..

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Mol	Chain	Length	Quality of chain
1	F	158	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into three segments: a small red segment on the left labeled '3%', a large green segment in the middle labeled '77%', and a yellow segment on the right labeled '20%'. A small grey dot is visible at the far right end of the bar.</p>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6704 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	153	1098	678	198	220	2	0	0	0
1	B	153	1095	676	197	220	2	0	0	0
1	C	153	1095	676	197	220	2	0	0	0
1	D	158	1129	699	202	225	3	0	0	0
1	E	153	1095	676	197	220	2	0	0	0
1	F	153	1096	677	197	220	2	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		

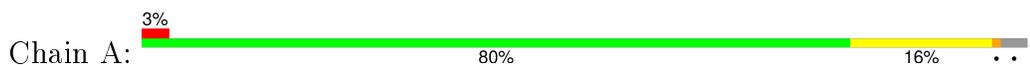
- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	A	11	Total 11	O 11	0	0
3	B	31	Total 31	O 31	0	0
3	C	11	Total 11	O 11	0	0
3	D	10	Total 10	O 10	0	0
3	E	17	Total 17	O 17	0	0
3	F	10	Total 10	O 10	0	0

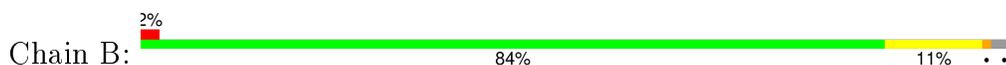
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

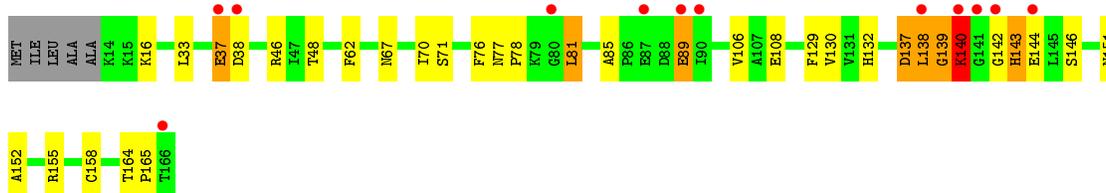
- Molecule 1: superoxide dismutase



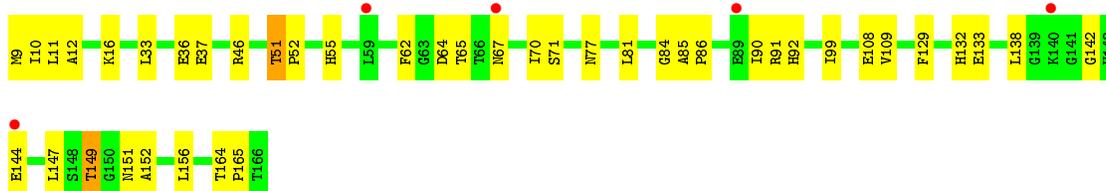
- Molecule 1: superoxide dismutase



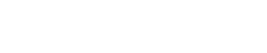
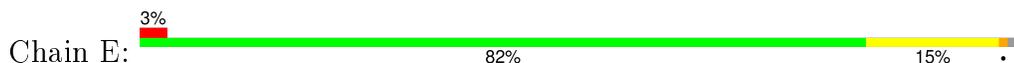
- Molecule 1: superoxide dismutase



- Molecule 1: superoxide dismutase

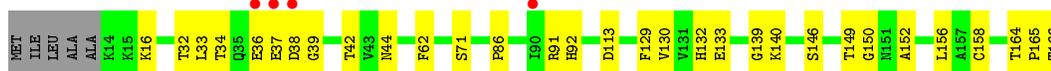
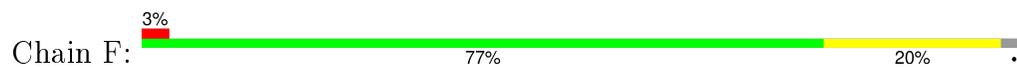


- Molecule 1: superoxide dismutase





- Molecule 1: superoxide dismutase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.98Å 85.78Å 105.31Å 90.00° 99.84° 90.00°	Depositor
Resolution (Å)	25.07 – 2.60 25.07 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (25.07-2.60) 91.1 (25.07-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 2.60Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.224 , 0.290 0.222 , 0.287	Depositor DCC
$R_{free}$ test set	1220 reflections (4.95%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.8	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 39.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	2 of 27073 reflections (0.007%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6704	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.80 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.7241e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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:  
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	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.54	0/1118	0.74	2/1522 (0.1%)
1	B	0.59	1/1115 (0.1%)	0.78	2/1519 (0.1%)
1	C	0.56	0/1115	1.17	9/1519 (0.6%)
1	D	0.59	1/1149 (0.1%)	0.80	2/1565 (0.1%)
1	E	0.57	0/1115	0.78	1/1519 (0.1%)
1	F	0.50	0/1116	0.77	1/1521 (0.1%)
All	All	0.56	2/6728 (0.0%)	0.85	17/9165 (0.2%)

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	C	0	2
1	E	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	52	PRO	N-CD	5.29	1.55	1.47
1	D	52	PRO	N-CD	5.04	1.54	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	140	LYS	CB-CA-C	-19.50	71.39	110.40
1	C	139	GLY	N-CA-C	-14.11	77.82	113.10
1	C	140	LYS	C-N-CA	13.55	150.75	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	140	LYS	N-CA-C	13.21	146.66	111.00
1	C	142	GLY	N-CA-C	11.13	140.92	113.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	137	ASP	Mainchain
1	C	140	LYS	Peptide
1	E	89	GLU	Peptide

## 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	1098	0	1071	22	0
1	B	1095	0	1062	14	0
1	C	1095	0	1061	25	1
1	D	1129	0	1103	34	1
1	E	1095	0	1062	19	0
1	F	1096	0	1066	22	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	11	0	0	0	0
3	B	31	0	0	1	0
3	C	11	0	0	0	0
3	D	10	0	0	1	0
3	E	17	0	0	0	0
3	F	10	0	0	1	0
All	All	6704	0	6425	129	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 10.

The worst 5 of 129 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:37:GLU:HG2	1:C:38:ASP:H	1.20	1.01
1:F:34:THR:HG21	3:F:308:HOH:O	1.62	0.99
1:E:37:GLU:CG	1:E:38:ASP:H	1.82	0.93
1:A:141:GLY:H	1:A:142:GLY:HA2	1.42	0.85
1:C:139:GLY:O	1:C:140:LYS:HB2	1.79	0.81

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:C:155:ARG:NH2	1:D:144:GLU:OE1[1_655]	2.02	0.18

## 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	151/158 (96%)	143 (95%)	8 (5%)	0	100	100
1	B	151/158 (96%)	142 (94%)	9 (6%)	0	100	100
1	C	151/158 (96%)	142 (94%)	9 (6%)	0	100	100
1	D	156/158 (99%)	147 (94%)	9 (6%)	0	100	100
1	E	151/158 (96%)	142 (94%)	9 (6%)	0	100	100
1	F	151/158 (96%)	141 (93%)	10 (7%)	0	100	100
All	All	911/948 (96%)	857 (94%)	54 (6%)	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	117/120 (98%)	116 (99%)	1 (1%)	84	95
1	B	116/120 (97%)	115 (99%)	1 (1%)	84	95
1	C	116/120 (97%)	112 (97%)	4 (3%)	44	72
1	D	119/120 (99%)	118 (99%)	1 (1%)	86	95
1	E	116/120 (97%)	116 (100%)	0	100	100
1	F	116/120 (97%)	114 (98%)	2 (2%)	68	88
All	All	700/720 (97%)	691 (99%)	9 (1%)	76	91

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	137	ASP
1	F	140	LYS
1	D	149	THR
1	C	81	LEU
1	C	140	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	75	HIS
1	F	151	ASN
1	C	77	ASN
1	C	44	ASN
1	C	151	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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 [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	153/158 (96%)	0.07	4 (2%) 59 53	19, 36, 54, 100	0
1	B	153/158 (96%)	-0.25	3 (1%) 68 63	16, 27, 41, 69	0
1	C	153/158 (96%)	0.52	12 (7%) 16 11	23, 44, 76, 86	0
1	D	158/158 (100%)	0.19	5 (3%) 51 44	23, 37, 59, 72	0
1	E	153/158 (96%)	-0.01	5 (3%) 50 43	17, 34, 52, 73	0
1	F	153/158 (96%)	0.11	4 (2%) 59 53	23, 42, 60, 97	0
All	All	923/948 (97%)	0.10	33 (3%) 46 38	16, 37, 64, 100	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	37	GLU	4.4
1	F	36	GLU	4.3
1	C	140	LYS	4.2
1	E	166	THR	3.5
1	C	142	GLY	3.4

### 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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	C	201	1/1	0.97	0.15	-2.68	67,67,67,67	0
2	ZN	B	201	1/1	0.96	0.07	-3.39	29,29,29,29	0
2	ZN	E	201	1/1	0.99	0.07	-3.62	35,35,35,35	0
2	ZN	D	201	1/1	0.98	0.09	-3.86	54,54,54,54	0
2	ZN	F	201	1/1	0.99	0.06	-4.02	41,41,41,41	0
2	ZN	A	201	1/1	0.98	0.10	-5.61	40,40,40,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.