



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 20, 2024 – 04:03 pm GMT

PDB ID : 7B4P  
Title : A Bacteroidetes bacterium CuZn-superoxide dismutase with CuZn metalation  
Authors : Wright, G.S.A.  
Deposited on : 2020-12-02  
Resolution : 2.70 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.36  
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) : 2.36

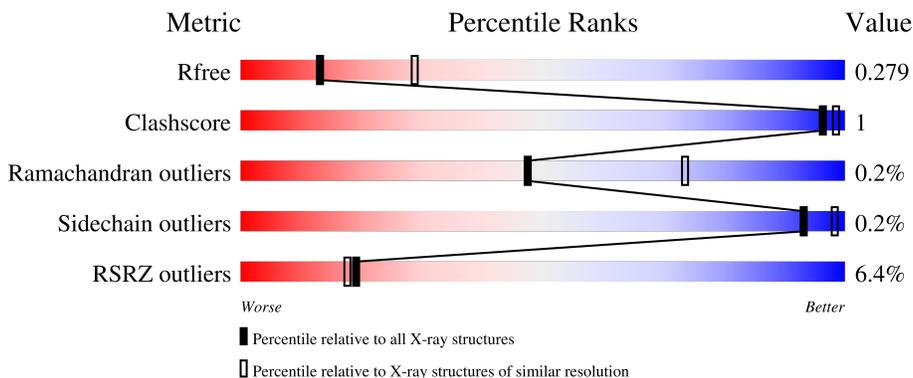
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	AAA	153	 5% (poor fit), 96% (0-3 outliers), 3% (4+ outliers), 2% (not modelled)
1	BBB	153	 6% (poor fit), 92% (0-3 outliers), 2% (4+ outliers), 0% (not modelled)
1	CCC	153	 7% (poor fit), 95% (0-3 outliers), 1% (4+ outliers), 7% (not modelled)
1	DDD	153	 8% (poor fit), 95% (0-3 outliers), 1% (4+ outliers), 6% (not modelled)

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8768 atoms, of which 4312 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 [Cu-Zn].

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	AAA	151	2207	688	1088	199	224	8	41	0	0
1	BBB	148	2162	675	1066	195	218	8	41	0	0
1	CCC	149	2185	681	1079	197	220	8	41	0	0
1	DDD	149	2185	681	1079	197	220	8	41	0	0

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	1	Total	Cu	0	0
			1	1		
2	BBB	1	Total	Cu	0	0
			1	1		
2	CCC	1	Total	Cu	0	0
			1	1		
2	DDD	1	Total	Cu	0	0
			1	1		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total	Zn	0	0
			1	1		
3	BBB	1	Total	Zn	0	0
			1	1		
3	CCC	1	Total	Zn	0	0
			1	1		
3	DDD	1	Total	Zn	0	0
			1	1		

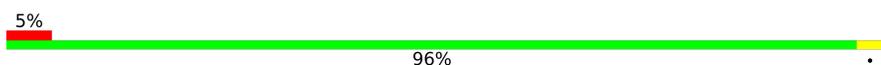
- Molecule 4 is water.

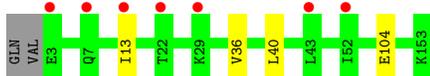
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
4	AAA	7	Total O 7 7	0	0
4	BBB	4	Total O 4 4	0	0
4	CCC	4	Total O 4 4	0	0
4	DDD	6	Total O 6 6	0	0

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

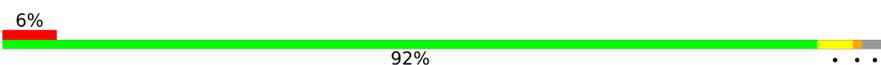
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

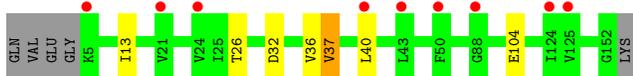
- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain AAA:  5% 96%



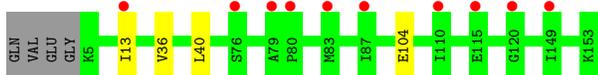
- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain BBB:  6% 92%

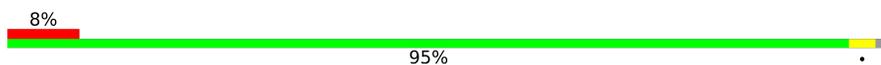


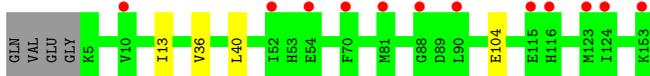
- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain CCC:  7% 95%



- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain DDD:  8% 95%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.79Å 109.59Å 122.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	81.70 – 2.70 81.71 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (81.70-2.70) 100.0 (81.71-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.03 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.240 , 0.278 0.247 , 0.279	Depositor DCC
$R_{free}$ test set	803 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	78.0	Xtrriage
Anisotropy	0.169	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8768	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.68 % 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 6.2487e-05. 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, 0.333 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: ZN, CU

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	AAA	0.66	0/1139	0.73	0/1532
1	BBB	0.67	0/1116	0.74	0/1504
1	CCC	0.66	0/1126	0.73	0/1515
1	DDD	0.67	0/1126	0.73	0/1515
All	All	0.67	0/4507	0.73	0/6066

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	AAA	1119	1088	1078	2	0
1	BBB	1096	1066	1056	3	0
1	CCC	1106	1079	1069	2	0
1	DDD	1106	1079	1069	2	0
2	AAA	1	0	0	0	0
2	BBB	1	0	0	0	0
2	CCC	1	0	0	0	0
2	DDD	1	0	0	0	0
3	AAA	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BBB	1	0	0	0	0
3	CCC	1	0	0	0	0
3	DDD	1	0	0	0	0
4	AAA	7	0	0	0	0
4	BBB	4	0	0	0	0
4	CCC	4	0	0	0	0
4	DDD	6	0	0	0	0
All	All	4456	4312	4272	9	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 1.

The worst 5 of 9 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:BBB:36:VAL:O	1:BBB:104:GLU:HA	2.05	0.57
1:CCC:36:VAL:O	1:CCC:104:GLU:HA	2.07	0.55
1:DDD:13:ILE:HD11	1:DDD:40:LEU:HG	1.88	0.55
1:AAA:36:VAL:O	1:AAA:104:GLU:HA	2.07	0.55
1:DDD:36:VAL:O	1:DDD:104:GLU:HA	2.07	0.55

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	AAA	149/153 (97%)	144 (97%)	5 (3%)	0	100	100
1	BBB	146/153 (95%)	141 (97%)	4 (3%)	1 (1%)	22	46
1	CCC	147/153 (96%)	142 (97%)	5 (3%)	0	100	100
1	DDD	147/153 (96%)	142 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	589/612 (96%)	569 (97%)	19 (3%)	1 (0%)	47 73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	32	ASP

### 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	AAA	120/122 (98%)	120 (100%)	0	100 100
1	BBB	118/122 (97%)	117 (99%)	1 (1%)	81 93
1	CCC	119/122 (98%)	119 (100%)	0	100 100
1	DDD	119/122 (98%)	119 (100%)	0	100 100
All	All	476/488 (98%)	475 (100%)	1 (0%)	93 98

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

Mol	Chain	Res	Type
1	BBB	37	VAL

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 8 ligands modelled in this entry, 8 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	AAA	151/153 (98%)	0.52	7 (4%) 32 31	66, 87, 123, 141	11 (7%)
1	BBB	148/153 (96%)	0.45	9 (6%) 21 20	68, 98, 128, 149	12 (8%)
1	CCC	149/153 (97%)	0.57	10 (6%) 17 16	65, 86, 129, 149	7 (4%)
1	DDD	149/153 (97%)	0.61	12 (8%) 12 10	67, 102, 139, 169	16 (10%)
All	All	597/612 (97%)	0.54	38 (6%) 19 18	65, 92, 133, 169	46 (7%)

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	CCC	83	MET	4.3
1	DDD	124	ILE	4.0
1	DDD	116	HIS	3.7
1	CCC	80	PRO	3.7
1	DDD	88	GLY	3.5

### 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( $\text{\AA}^2$ )	Q<0.9
3	ZN	DDD	202	1/1	0.95	0.11	102,102,102,102	0
3	ZN	AAA	202	1/1	0.96	0.08	119,119,119,119	0
3	ZN	CCC	202	1/1	0.97	0.09	123,123,123,123	0
2	CU	BBB	201	1/1	0.97	0.15	78,78,78,78	0
2	CU	DDD	201	1/1	0.98	0.14	85,85,85,85	0
3	ZN	BBB	202	1/1	0.99	0.08	103,103,103,103	0
2	CU	AAA	201	1/1	0.99	0.17	90,90,90,90	0
2	CU	CCC	201	1/1	0.99	0.19	80,80,80,80	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.