



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2018 – 03:30 pm GMT

PDB ID : 4PW3  
Title : Crystal structure of the sulfite dehydrogenase SorT from Sinorhizobium meliloti  
Authors : McGrath, A.P.; Maher, M.J.  
Deposited on : 2014-03-18  
Resolution : 2.35 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.

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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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

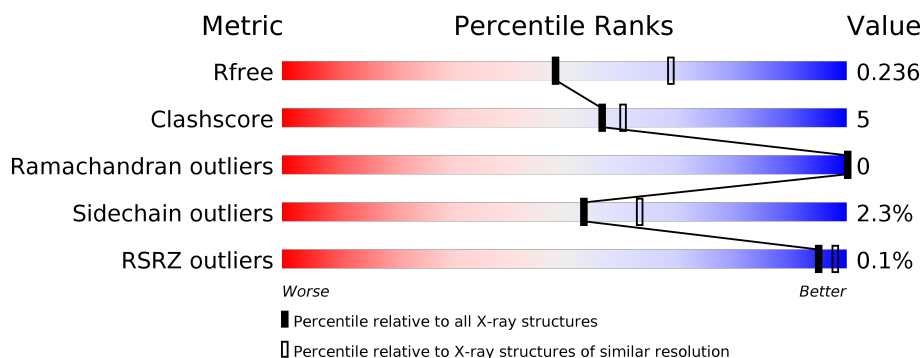
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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))
$R_{free}$	111664	1015 (2.36-2.36)
Clashscore	122126	1081 (2.36-2.36)
Ramachandran outliers	120053	1066 (2.36-2.36)
Sidechain outliers	120020	1067 (2.36-2.36)
RSRZ outliers	108989	1002 (2.36-2.36)

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	369	 89% 9% ..
1	B	369	 86% 11% .
1	C	369	 89% 10% ..
1	D	369	 87% 12% .

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11378 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.

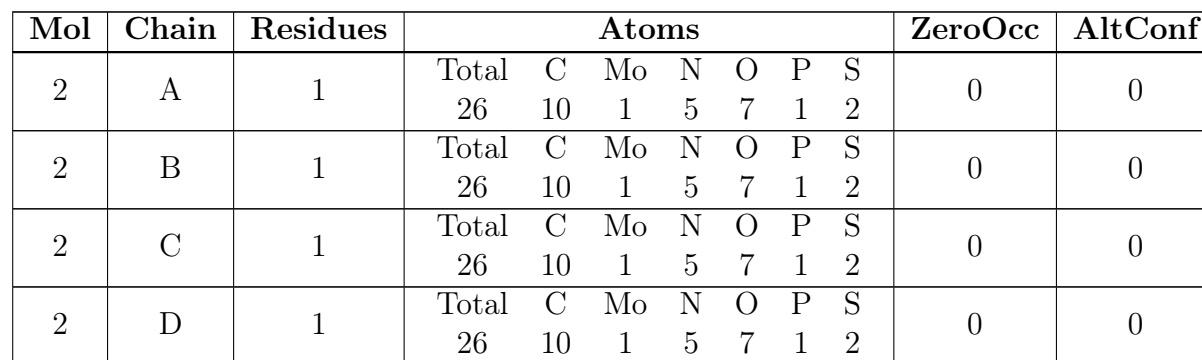
- Molecule 1 is a protein called Putative sulfite oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	0	0
			2730	1722	472	527	9			
1	B	363	Total	C	N	O	S	0	0	0
			2707	1710	467	521	9			
1	C	365	Total	C	N	O	S	0	0	0
			2721	1720	469	523	9			
1	D	365	Total	C	N	O	S	0	0	0
			2732	1726	470	527	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	SER	-	EXPRESSION TAG	UNP Q92M24
B	31	SER	-	EXPRESSION TAG	UNP Q92M24
C	31	SER	-	EXPRESSION TAG	UNP Q92M24
D	31	SER	-	EXPRESSION TAG	UNP Q92M24

- Molecule 2 is (MOLYBDOPTERIN-S,S)-OXO-MOLYBDENUM (three-letter code: MSS) (formula:  $C_{10}H_{12}MoN_5O_7PS_2$ ).



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- Chemical structure of EDO (Ethane-1,2-diol) is shown. The structure consists of two carbon atoms (C1 and C2) connected by a single bond. Each carbon atom is bonded to a hydroxyl group (OH). The oxygen atoms are labeled O1 and O2. The structure is drawn in a zig-zag conformation.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		

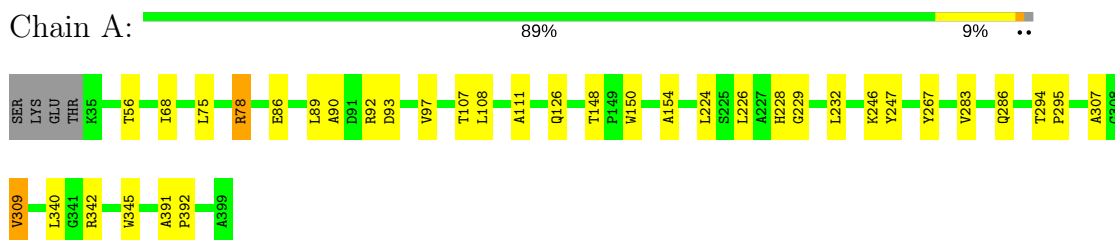
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	102	Total	O	0	0
			102	102		
4	B	85	Total	O	0	0
			85	85		
4	C	103	Total	O	0	0
			103	103		
4	D	86	Total	O	0	0
			86	86		

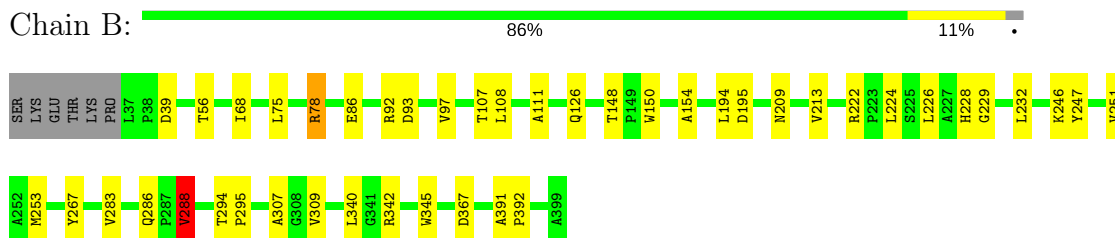
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

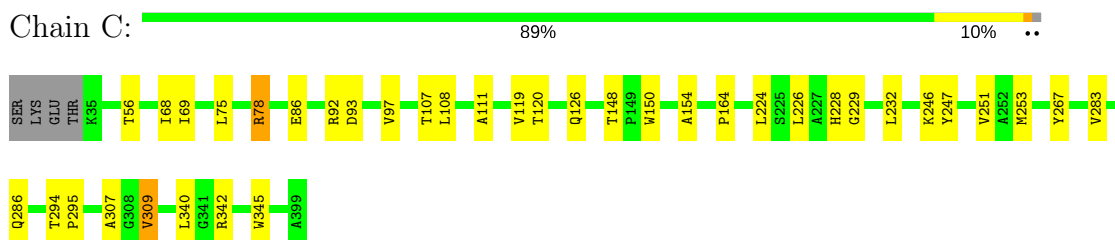
- Molecule 1: Putative sulfite oxidase



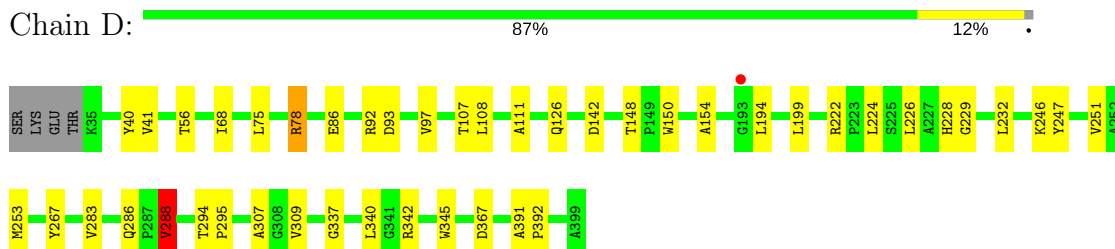
- Molecule 1: Putative sulfite oxidase



- Molecule 1: Putative sulfite oxidase



- Molecule 1: Putative sulfite oxidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.06Å 92.22Å 109.43Å 90.00° 89.74° 90.00°	Depositor
Resolution (Å)	47.64 – 2.35 47.64 – 2.35	Depositor EDS
% Data completeness (in resolution range)	97.2 (47.64-2.35) 97.3 (47.64-2.35)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.208 , 0.240 0.209 , 0.236	Depositor DCC
$R_{free}$ test set	3905 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.6	Xtriage
Anisotropy	0.888	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 14.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -k,-h,-l 0.000 for k,h,-l 0.427 for h,-k,-l	Xtriage
Reported twinning fraction	0.495 for H, K, L 0.505 for -h,-k,l	Depositor
Outliers	0 of 77952 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11378	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	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 24.97 % 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 3.4630e-03. 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

### 5.1 Standard geometry

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

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	0.44	1/2791 (0.0%)	0.56	1/3806 (0.0%)
1	B	0.43	1/2767 (0.0%)	0.57	2/3774 (0.1%)
1	C	0.43	1/2782 (0.0%)	0.56	1/3795 (0.0%)
1	D	0.44	2/2793 (0.1%)	0.57	2/3808 (0.1%)
All	All	0.44	5/11133 (0.0%)	0.57	6/15183 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	309	VAL	CB-CG2	-13.13	1.25	1.52
1	D	309	VAL	CB-CG1	-12.62	1.26	1.52
1	C	309	VAL	CB-CG2	-12.38	1.26	1.52
1	B	309	VAL	CB-CG1	-12.16	1.27	1.52
1	D	309	VAL	CB-CG2	-5.37	1.41	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	309	VAL	CG1-CB-CG2	-9.29	96.03	110.90
1	B	309	VAL	CG1-CB-CG2	-9.00	96.49	110.90
1	C	309	VAL	CG1-CB-CG2	-8.72	96.95	110.90
1	A	309	VAL	CG1-CB-CG2	-8.64	97.08	110.90
1	D	288	VAL	CG1-CB-CG2	6.18	120.79	110.90

There are no chirality outliers.

There are no planarity outliers.



## 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	2730	0	2684	26	0
1	B	2707	0	2665	31	0
1	C	2721	0	2678	27	0
1	D	2732	0	2695	32	0
2	A	26	0	10	2	0
2	B	26	0	10	2	0
2	C	26	0	10	2	0
2	D	26	0	10	2	0
3	B	4	0	6	1	0
3	C	4	0	6	2	0
4	A	102	0	0	0	0
4	B	85	0	0	1	0
4	C	103	0	0	0	0
4	D	86	0	0	0	0
All	All	11378	0	10774	117	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 5.

The worst 5 of 117 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:C:402:EDO:H22	1:D:222:ARG:HH12	1.43	0.83
1:D:56:THR:HG23	1:D:150:TRP:CH2	2.17	0.79
1:A:56:THR:HG23	1:A:150:TRP:CH2	2.20	0.77
1:C:56:THR:HG23	1:C:150:TRP:CH2	2.20	0.76
1:B:56:THR:HG23	1:B:150:TRP:CH2	2.21	0.75

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	363/369 (98%)	352 (97%)	11 (3%)	0	100	100
1	B	361/369 (98%)	350 (97%)	11 (3%)	0	100	100
1	C	363/369 (98%)	352 (97%)	11 (3%)	0	100	100
1	D	363/369 (98%)	352 (97%)	11 (3%)	0	100	100
All	All	1450/1476 (98%)	1406 (97%)	44 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	284/294 (97%)	278 (98%)	6 (2%)	56	67
1	B	281/294 (96%)	274 (98%)	7 (2%)	50	60
1	C	282/294 (96%)	276 (98%)	6 (2%)	56	67
1	D	285/294 (97%)	278 (98%)	7 (2%)	50	60
All	All	1132/1176 (96%)	1106 (98%)	26 (2%)	53	63

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	342	ARG
1	C	247	TYR
1	D	342	ARG

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Mol	Chain	Res	Type
1	B	345	TRP
1	C	78	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	286	GLN
1	B	286	GLN
1	C	286	GLN
1	D	286	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MSS	A	401	1	23,29,29	2.34	5 (21%)	20,45,45	1.76	2 (10%)
2	MSS	B	401	1	23,29,29	2.30	5 (21%)	20,45,45	1.77	5 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	B	402	-	3,3,3	0.55	0	2,2,2	0.15	0
2	MSS	C	401	1	23,29,29	2.31	5 (21%)	20,45,45	1.82	5 (25%)
3	EDO	C	402	-	3,3,3	0.52	0	2,2,2	0.31	0
2	MSS	D	401	1	23,29,29	2.31	5 (21%)	20,45,45	1.75	4 (20%)

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
2	MSS	A	401	1	-	0/6/42/42	0/4/4/4
2	MSS	B	401	1	-	0/6/42/42	0/4/4/4
3	EDO	B	402	-	-	0/1/1/1	0/0/0/0
2	MSS	C	401	1	-	0/6/42/42	0/4/4/4
3	EDO	C	402	-	-	0/1/1/1	0/0/0/0
2	MSS	D	401	1	-	0/6/42/42	0/4/4/4

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	MSS	C1'-S1'	-5.04	1.66	1.76
2	C	401	MSS	C1'-S1'	-4.95	1.66	1.76
2	B	401	MSS	C1'-S1'	-4.90	1.66	1.76
2	D	401	MSS	C1'-S1'	-4.72	1.66	1.76
2	C	401	MSS	C2'-S2'	-4.55	1.67	1.76

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	MSS	C9-C4-N3	-2.06	117.84	123.91
2	B	401	MSS	C9-C4-N3	-2.05	117.88	123.91
2	B	401	MSS	C4-C9-C10	2.00	116.38	114.56
2	B	401	MSS	C2'-C1'-S1'	2.10	121.34	120.15
2	D	401	MSS	C4-C9-C10	2.31	116.65	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	MSS	2	0
2	B	401	MSS	2	0
3	B	402	EDO	1	0
2	C	401	MSS	2	0
3	C	402	EDO	2	0
2	D	401	MSS	2	0

## 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(Å²)	Q<0.9
1	A	365/369 (98%)	-0.43	0	100100	23, 31, 46, 57	0
1	B	363/369 (98%)	-0.44	0	100100	23, 31, 46, 57	0
1	C	365/369 (98%)	-0.43	0	100100	23, 31, 46, 57	0
1	D	365/369 (98%)	-0.43	1 (0%)	9397	23, 31, 46, 57	0
All	All	1458/1476 (98%)	-0.43	1 (0%)	9598	23, 31, 46, 57	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	193	GLY	2.1

### 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. 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
3	EDO	B	402	4/4	0.92	0.17	39,39,39,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	C	402	4/4	0.94	0.14	28,29,29,30	0
2	MSS	A	401	26/26	0.99	0.11	25,28,30,33	0
2	MSS	B	401	26/26	0.99	0.11	28,31,32,34	0
2	MSS	C	401	26/26	0.99	0.10	28,34,37,38	0
2	MSS	D	401	26/26	0.99	0.10	31,32,33,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.