



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 11:11 am GMT

PDB ID : 2W1K  
Title : CRYSTAL STRUCTURE OF SORTASE C-3 (SRTC-3) FROM STREPTOCOCCUS PNEUMONIAE  
Authors : Manzano, C.; Contreras-Martel, C.; El Mortaji, L.; Izore, T.; Fenel, D.; Vernet, T.; Schoehn, G.; Di Guilmi, A.M.; Dessen, A.  
Deposited on : 2008-10-17  
Resolution : 2.14 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.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

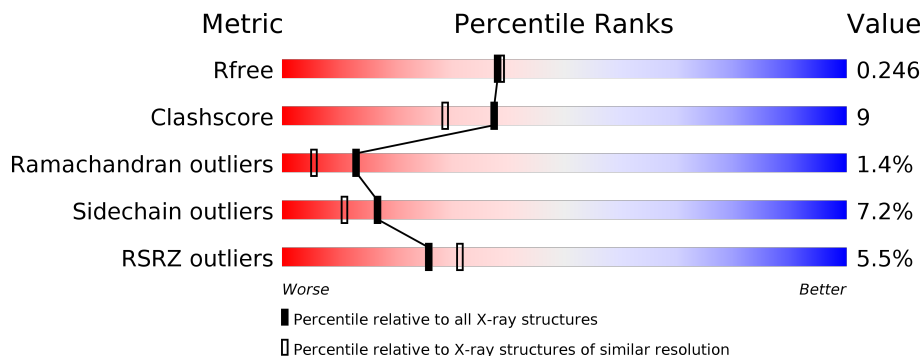
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.14 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))
$R_{free}$	100719	1915 (2.16-2.12)
Clashscore	112137	2047 (2.16-2.12)
Ramachandran outliers	110173	2020 (2.16-2.12)
Sidechain outliers	110143	2019 (2.16-2.12)
RSRZ outliers	101464	1921 (2.16-2.12)

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	252	<div> <div>4%</div> <div> <div></div> <div>64%</div> <div>16%</div> <div>••</div> <div>17%</div> </div> </div>
1	B	252	<div> <div>5%</div> <div> <div></div> <div>64%</div> <div>15%</div> <div>••</div> <div>17%</div> </div> </div>

## 2 Entry composition [i](#)

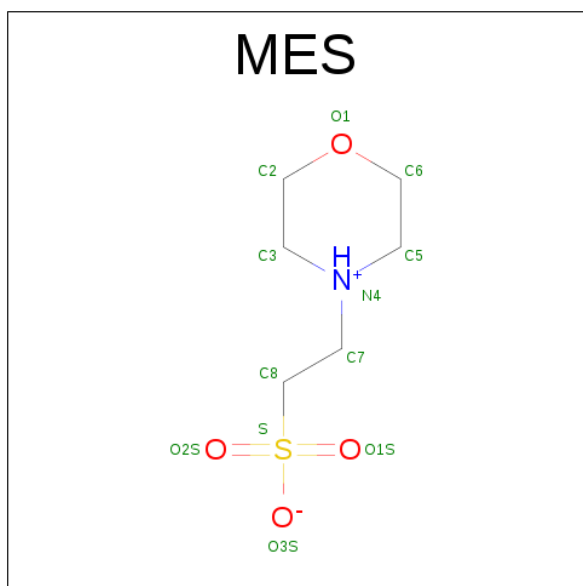
There are 3 unique types of molecules in this entry. The entry contains 3845 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SORTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	2	1
			1658	1053	277	318	10			
1	B	209	Total	C	N	O	S	0	2	1
			1658	1053	277	318	10			

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	266	Total 266	O 266	0	0
3	B	239	Total 239	O 239	0	0



• Molecule 1: PUTATIVE SORTASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	122.64Å 122.64Å 122.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.35 – 2.14 40.88 – 2.14	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.35-2.14) 98.9 (40.88-2.14)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
R, $R_{free}$	0.180 , 0.241 0.186 , 0.246	Depositor DCC
$R_{free}$ test set	1674 reflections (5.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 53.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.468 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3845	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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: MES

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	1.33	2/1703 (0.1%)	1.15	9/2315 (0.4%)
1	B	1.34	10/1703 (0.6%)	1.13	7/2315 (0.3%)
All	All	1.34	12/3406 (0.4%)	1.14	16/4630 (0.3%)

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	A	1	1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	190	GLU	CG-CD	6.69	1.61	1.51
1	B	115	TYR	CD1-CE1	6.08	1.48	1.39
1	B	166	TYR	CD1-CE1	-5.93	1.30	1.39
1	B	193	GLU	CB-CG	-5.87	1.41	1.52
1	B	85	TYR	CE1-CZ	5.66	1.46	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	77	LEU	CA-CB-CG	-8.95	94.70	115.30
1	B	230	ASP	CB-CG-OD1	8.89	126.31	118.30
1	A	145	ARG	NE-CZ-NH2	-7.80	116.40	120.30
1	A	47	MET	CG-SD-CE	7.72	112.56	100.20
1	A	145	ARG	NE-CZ-NH1	7.13	123.86	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	77	LEU	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	77	LEU	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	1658	0	1611	26	0
1	B	1658	0	1611	32	0
2	A	12	0	12	0	0
2	B	12	0	12	0	0
3	A	266	0	0	5	1
3	B	239	0	0	7	1
All	All	3845	0	3246	58	2

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 9.

The worst 5 of 58 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:B:177:GLN:HG3	1:B:179[A]:MET:HE3	1.39	1.02
1:A:76:PHE:O	1:A:77:LEU:HD12	1.59	1.01
1:A:45:LYS:HD3	1:A:45:LYS:O	1.74	0.87
1:A:38:LYS:O	1:A:42:THR:HG23	1.75	0.87
1:B:115:TYR:OH	3:B:2113:HOH:O	1.96	0.82

All (2) 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)
3:A:2059:HOH:O	3:A:2084:HOH:O[8_555]	2.05	0.15
3:B:2062:HOH:O	3:B:2237:HOH:O[6_665]	2.16	0.04

## 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	209/252 (83%)	193 (92%)	14 (7%)	2 (1%)	18	10
1	B	209/252 (83%)	198 (95%)	7 (3%)	4 (2%)	9	3
All	All	418/504 (83%)	391 (94%)	21 (5%)	6 (1%)	13	5

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	78	ALA
1	B	78	ALA
1	B	81	TYR
1	A	79	GLU
1	B	47	MET

### 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	182/217 (84%)	168 (92%)	14 (8%)	15	9
1	B	182/217 (84%)	170 (93%)	12 (7%)	19	13

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	364/434 (84%)	338 (93%)	26 (7%)	17	11

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

Mol	Chain	Res	Type
1	A	210	PRO
1	B	42	THR
1	B	210	PRO
1	A	217	LEU
1	A	242	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	GLN
1	A	177	GLN
1	A	232	GLN
1	B	69	GLN
1	B	171	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](#)

2 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	MES	A	1243	-	12,12,12	1.36	2 (16%)	14,16,16	2.31	5 (35%)
2	MES	B	1243	-	12,12,12	1.45	2 (16%)	14,16,16	3.82	8 (57%)

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	MES	A	1243	-	-	0/6/14/14	0/1/1/1
2	MES	B	1243	-	-	0/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1243	MES	C8-S	-3.37	1.72	1.77
2	B	1243	MES	C8-S	-2.62	1.73	1.77
2	A	1243	MES	O2S-S	2.09	1.51	1.45
2	B	1243	MES	C7-N4	2.49	1.53	1.47

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1243	MES	O1S-S-C8	-8.12	99.82	106.79
2	B	1243	MES	O1-C2-C3	-3.73	103.48	111.83
2	B	1243	MES	O2S-S-C8	-2.35	104.78	106.79
2	B	1243	MES	O3S-S-O1S	2.34	116.74	111.37
2	B	1243	MES	C7-N4-C3	2.38	117.37	111.26

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	209/252 (82%)	-0.21	11 (5%) 27 33	25, 33, 60, 79	0
1	B	209/252 (82%)	-0.24	12 (5%) 24 30	25, 33, 58, 73	0
All	All	418/504 (82%)	-0.23	23 (5%) 26 31	25, 33, 59, 79	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	78	ALA	18.2
1	B	78	ALA	15.4
1	B	81	TYR	6.3
1	A	81	TYR	6.0
1	B	77	LEU	4.4

### 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( $\text{\AA}^2$ )	Q<0.9
2	MES	B	1243	12/12	0.99	0.10	0.49	27,34,35,35	0
2	MES	A	1243	12/12	0.99	0.07	-0.61	30,34,35,38	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.