

Full wwPDB X-ray Structure Validation Report (i)

Sep 24, 2023 – 06:17 PM EDT

PDB ID : 5UTT

Title: SrtA sortase from Actinomyces oris

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Deposited on : 2017-02-15

Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at 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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467 Xtriage (Phenix) : 1.13

EDS : 2.35.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

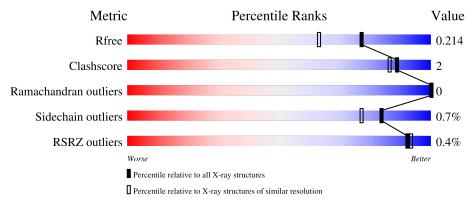
Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 >=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 <=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	190	90%	5%	5%
1	В	190	89%	6%	5%
1	С	190	88%	7%	5%
1	D	190	91%		5%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6188 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 Sortase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	180	Total	С	N	О	S	0	0	0
1	A	100	1405	882	245	272	6	0	U	U
1	В	180	Total	С	N	О	S	0	2	0
1	Ъ	160	1414	888	245	275	6	0	2	U
1	С	180	Total	С	N	О	S	0	0	0
1		100	1405	882	245	272	6	0	U	U
1	D	180	Total	С	N	О	S	0	3	0
1		160	1423	895	249	273	6	U	J	U

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	SER	-	expression tag	UNP A0A0X8K1J2
A	69	ASN	-	expression tag	UNP A0A0X8K1J2
A	70	ALA	-	expression tag	UNP A0A0X8K1J2
В	68	SER	-	expression tag	UNP A0A0X8K1J2
В	69	ASN	-	expression tag	UNP A0A0X8K1J2
В	70	ALA	_	expression tag	UNP A0A0X8K1J2
С	68	SER	-	expression tag	UNP A0A0X8K1J2
С	69	ASN	-	expression tag	UNP A0A0X8K1J2
С	70	ALA	-	expression tag	UNP A0A0X8K1J2
D	68	SER	-	expression tag	UNP A0A0X8K1J2
D	69	ASN	-	expression tag	UNP A0A0X8K1J2
D	70	ALA	_	expression tag	UNP A0A0X8K1J2

• Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total Cl 3 3	0	0
2	В	3	Total Cl 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	С	3	Total Cl 3 3	0	0
2	D	3	Total Cl 3 3	0	0

$\bullet\,$ Molecule 3 is water.

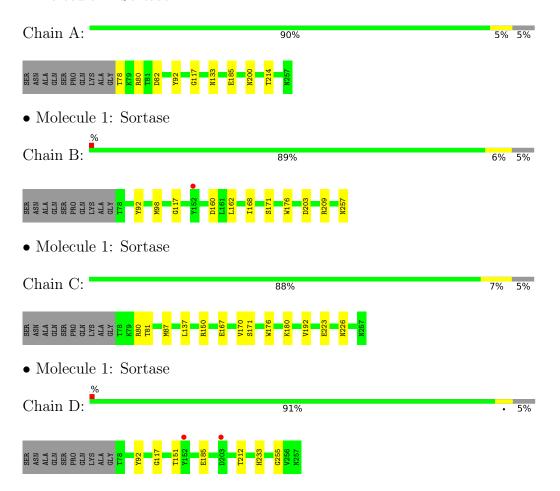
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	128	Total O 128 128	0	0
3	В	140	Total O 140 140	0	0
3	С	135	Total O 135 135	0	0
3	D	126	Total O 126 126	0	0



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: Sortase





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	62.18Å 75.08Å 77.65Å	Depositor	
a, b, c, α , β , γ	90.00° 89.96° 90.00°	Depositor	
Resolution (Å)	37.54 - 1.70	Depositor	
Resolution (A)	37.54 - 1.70	EDS	
% Data completeness	94.7 (37.54-1.70)	Depositor	
(in resolution range)	94.7 (37.54-1.70)	EDS	
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.01 (at 1.70Å)	Xtriage	
Refinement program	REFMAC 5.8.0069	Depositor	
D D.	0.160 , 0.205	Depositor	
R, R_{free}	0.167 , 0.214	DCC	
R_{free} test set	3652 reflections $(4.91%)$	wwPDB-VP	
Wilson B-factor (Å ²)	15.6	Xtriage	
Anisotropy	0.818	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 34.9	EDS	
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.33$	Xtriage	
	0.000 for -h,l,k		
Estimated twinning fraction	0.000 for -h,-l,-k	Xtriage	
	0.459 for h,-k,-l		
Reported twinning fraction	0.524 for H, K, L	Depositor	
	0.476 for -h,-k,l		
Outliers	3 of 74444 reflections (0.004%)	Xtriage	
F_o, F_c correlation	0.97	EDS	
Total number of atoms	6188	wwPDB-VP	
Average B, all atoms (\mathring{A}^2)	19.0	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 22.04 % 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 6.1889e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: CL

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		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.66	0/1440	0.72	0/1962	
1	В	0.66	0/1455	0.75	1/1982 (0.1%)	
1	С	0.60	0/1440	0.72	0/1962	
1	D	0.62	0/1467	0.72	0/1997	
All	All	0.63	0/5802	0.73	1/7903 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	В	160	ASP	CB-CG-OD1	5.31	123.08	118.30

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	1405	0	1347	5	0
1	В	1414	0	1358	6	0
1	С	1405	0	1347	8	0
1	D	1423	0	1380	4	0
2	A	3	0	0	0	0
2	В	3	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	С	3	0	0	0	0
2	D	3	0	0	0	0
3	A	128	0	0	1	0
3	В	140	0	0	0	0
3	С	135	0	0	1	0
3	D	126	0	0	0	0
All	All	6188	0	5432	21	0

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 2.

All (21) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\text{\AA}) \end{array}$	Clash overlap (Å)
1:A:185:GLU:OE2	1:A:200:ASN:ND2	2.10	0.80
1:A:133:ASN:ND2	3:A:601:HOH:O	2.20	0.73
1:A:80:ARG:NH2	1:A:82:ASP:OD2	2.28	0.66
1:A:214:THR:OG1	1:B:257:ASN:ND2	2.34	0.59
1:B:162:LEU:HD13	1:B:168:ILE:HD11	1.84	0.59
1:C:80:ARG:NH1	3:C:604:HOH:O	2.43	0.51
1:C:137:LEU:HD21	1:C:170:VAL:HG11	1.92	0.51
1:B:98:MET:HB3	1:B:171[B]:SER:OG	2.10	0.51
1:C:192:VAL:CG1	1:D:255:GLY:HA2	2.42	0.50
1:B:209:ARG:NH1	2:B:503:CL:CL	2.80	0.48
1:C:150:ARG:HD2	1:C:223:GLU:O	2.15	0.47
1:D:92:TYR:CE2	1:D:117:GLY:HA3	2.50	0.46
1:D:185:GLU:OE2	1:D:233:HIS:HE1	1.97	0.46
1:C:167:GLU:HG2	1:C:180:LYS:HE2	1.98	0.45
1:C:171:SER:HB3	1:C:176:TRP:CZ3	2.51	0.44
1:D:212:THR:OG1	1:D:233:HIS:HD2	2.01	0.44
1:C:226:ASN:OD1	1:C:226:ASN:N	2.52	0.42
1:A:92:TYR:CE2	1:A:117:GLY:HA3	2.56	0.41
1:B:92:TYR:CE2	1:B:117:GLY:HA3	2.56	0.40
1:B:171[A]:SER:HB2	1:B:176:TRP:CZ3	2.56	0.40
1:C:87:MET:HG3	1:C:137:LEU:HB3	2.04	0.40

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	Perce	Percentiles	
1	A	178/190 (94%)	176 (99%)	2 (1%)	0	100	100	
1	В	180/190 (95%)	174 (97%)	6 (3%)	0	100	100	
1	С	178/190 (94%)	174 (98%)	4 (2%)	0	100	100	
1	D	181/190 (95%)	177 (98%)	4 (2%)	0	100	100	
All	All	717/760 (94%)	701 (98%)	16 (2%)	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	150/157~(96%)	149 (99%)	1 (1%)	84 77		
1	В	152/157 (97%)	151 (99%)	1 (1%)	84 77		
1	С	150/157 (96%)	149 (99%)	1 (1%)	84 77		
1	D	153/157 (98%)	152 (99%)	1 (1%)	84 77		
All	All	605/628 (96%)	601 (99%)	4 (1%)	84 77		

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	THR
1	В	203	ASP

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Mol	Chain	Res	Type
1	С	81	THR
1	D	151	THR

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

Mol	Chain	Res	Type
1	В	257	ASN
1	С	257	ASN
1	D	200	ASN
1	D	233	HIS
1	D	257	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 12 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^{th} 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>	$\# \mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	180/190 (94%)	-0.44	0 100 100	9, 16, 25, 35	0
1	В	180/190 (94%)	-0.43	1 (0%) 89 91	10, 17, 27, 41	0
1	С	180/190 (94%)	-0.43	0 100 100	11, 18, 32, 40	0
1	D	180/190 (94%)	-0.37	2 (1%) 80 83	10, 17, 31, 44	0
All	All	720/760 (94%)	-0.42	3 (0%) 92 93	9, 17, 29, 44	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	152	TYR	4.3
1	D	152	TYR	4.1
1	D	203	ASP	2.4

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 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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	CL	В	503	1/1	0.96	0.06	26,26,26,26	0
2	CL	С	503	1/1	0.97	0.14	30,30,30,30	0
2	CL	A	503	1/1	0.98	0.05	22,22,22,22	0
2	CL	D	503	1/1	0.98	0.04	26,26,26,26	0
2	CL	A	502	1/1	0.99	0.04	15,15,15,15	0
2	CL	С	501	1/1	0.99	0.04	20,20,20,20	0
2	CL	С	502	1/1	0.99	0.04	18,18,18,18	0
2	CL	В	501	1/1	0.99	0.03	23,23,23,23	0
2	CL	D	501	1/1	0.99	0.04	26,26,26,26	0
2	CL	D	502	1/1	0.99	0.04	18,18,18,18	0
2	CL	В	502	1/1	0.99	0.05	16,16,16,16	0
2	CL	A	501	1/1	1.00	0.04	24,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.

