



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:02 AM GMT

PDB ID : 3MWG
Title : Crystal structure of Staphylococcus aureus SirA
Authors : Grigg, J.C.; Murphy, M.E.P.
Deposited on : 2010-05-05
Resolution : 2.10 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

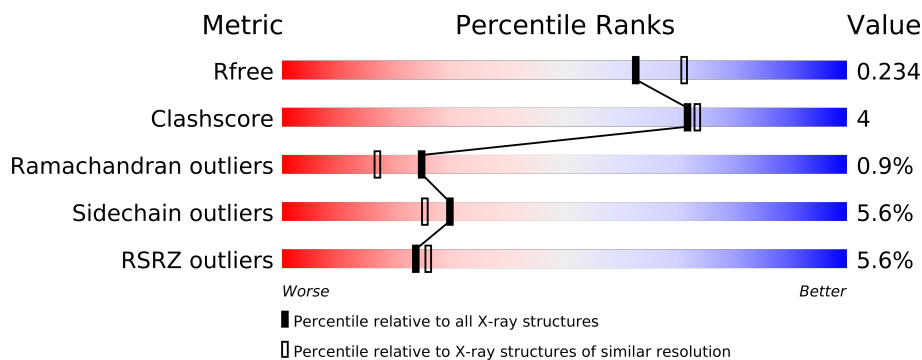
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.10 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}	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	279	
1	B	279	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4597 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Iron-regulated ABC transporter siderophore-binding protein SirA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	Se	0	0	0
			2183	1389	366	426	2			
1	B	274	Total	C	N	O	Se	0	0	0
			2168	1381	363	422	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	GLY	-	EXPRESSION TAG	UNP Q7A869
A	53	SER	-	EXPRESSION TAG	UNP Q7A869
B	52	GLY	-	EXPRESSION TAG	UNP Q7A869
B	53	SER	-	EXPRESSION TAG	UNP Q7A869

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	177	Total	O	0	0
			177	177		
2	B	69	Total	O	0	0
			69	69		

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 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.

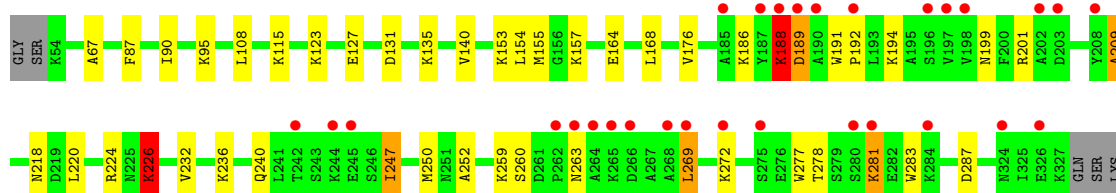
- Molecule 1: Iron-regulated ABC transporter siderophore-binding protein SirA

Chain A: 



- Molecule 1: Iron-regulated ABC transporter siderophore-binding protein SirA

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.14Å 61.51Å 114.65Å 90.00° 100.08° 90.00°	Depositor
Resolution (Å)	31.65 – 2.10 31.65 – 2.09	Depositor EDS
% Data completeness (in resolution range)	99.6 (31.65-2.10) 99.1 (31.65-2.09)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.192 , 0.236 0.192 , 0.234	Depositor DCC
R_{free} test set	1723 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	29.4	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.2	EDS
Estimated twinning fraction	0.033 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 34252 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4597	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.64	0/2217	0.65	0/2985
1	B	0.52	0/2202	0.59	0/2965
All	All	0.58	0/4419	0.62	0/5950

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2183	0	0	3	0
1	B	2168	0	2220	27	0
2	A	177	0	0	2	0
2	B	69	0	0	0	0
All	All	4597	0	2220	29	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (29) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:281:LYS:H	1:B:281:LYS:HD2	1.45	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:188:LYS:O	1:B:189:ASP:HB2	1.85	0.75
1:B:191:TRP:CD2	1:B:192:PRO:HA	2.34	0.62
1:B:153:LYS:O	1:B:157:LYS:HG2	2.00	0.60
1:B:131:ASP:O	1:B:135:LYS:HG3	2.05	0.57
1:B:218:ASN:ND2	1:B:224:ARG:HH22	2.03	0.55
1:B:269:LEU:H	1:B:269:LEU:HD22	1.74	0.52
1:B:247:ILE:O	1:B:250:MSE:HG2	2.09	0.52
1:B:218:ASN:HD22	1:B:224:ARG:HH22	1.59	0.51
1:B:67:ALA:HB2	1:B:155:MSE:HE1	1.92	0.51
1:B:188:LYS:HE2	1:B:191:TRP:HB3	1.93	0.50
1:B:194:LYS:O	1:B:252:ALA:HB1	2.11	0.50
1:B:281:LYS:HD2	1:B:281:LYS:N	2.23	0.47
1:B:123:LYS:O	1:B:127:GLU:HB2	2.14	0.47
1:B:278:THR:HA	1:B:283:TRP:CD1	2.51	0.46
1:A:237:ASP:OD2	2:A:433:HOH:O	2.21	0.46
1:B:278:THR:HG22	1:B:283:TRP:CE2	2.52	0.45
1:A:237:ASP:N	2:A:395:HOH:O	2.49	0.45
1:B:87:PHE:HB2	1:B:90:ILE:HG22	1.99	0.45
1:B:281:LYS:H	1:B:281:LYS:CD	2.25	0.44
1:B:188:LYS:HE2	1:B:188:LYS:HA	2.00	0.43
1:B:226:LYS:HD2	1:B:226:LYS:N	2.34	0.43
1:B:176:VAL:HG13	1:B:220:LEU:HD23	2.01	0.42
1:B:140:VAL:HB	1:B:154:LEU:HD21	2.01	0.42
1:B:209:ALA:HB1	1:B:232:VAL:HG22	2.03	0.41
1:B:199:ASN:OD1	1:B:201:ARG:NE	2.51	0.41
1:A:131:ASP:OD2	1:B:123:LYS:HE2	2.21	0.40
1:B:247:ILE:HD11	1:B:277:TRP:CE3	2.55	0.40
1:B:164:GLU:O	1:B:168:LEU:HG	2.21	0.40

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	274/279 (98%)	268 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	272/279 (98%)	260 (96%)	7 (3%)	5 (2%)	13	5
All	All	546/558 (98%)	528 (97%)	13 (2%)	5 (1%)	25	17

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	189	ASP
1	B	209	ALA
1	B	188	LYS
1	B	226	LYS
1	B	260	SER

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	240/240 (100%)	228 (95%)	12 (5%)	34	30
1	B	238/240 (99%)	223 (94%)	15 (6%)	25	21
All	All	478/480 (100%)	451 (94%)	27 (6%)	30	25

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	LEU
1	A	128	LYS
1	A	157	LYS
1	A	171	LYS
1	A	201	ARG
1	A	226	LYS
1	A	242	THR
1	A	259	LYS
1	A	265	LYS
1	A	269	LEU
1	A	296	ASP
1	A	297	ASP
1	B	95	LYS

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Mol	Chain	Res	Type
1	B	108	LEU
1	B	115	LYS
1	B	186	LYS
1	B	188	LYS
1	B	226	LYS
1	B	236	LYS
1	B	240	GLN
1	B	247	ILE
1	B	259	LYS
1	B	263	ASN
1	B	269	LEU
1	B	272	LYS
1	B	281	LYS
1	B	287	ASP

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

Mol	Chain	Res	Type
1	B	102	GLN
1	B	218	ASN
1	B	285	ASN
1	B	293	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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, 95th 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 ²)	Q<0.9
1	A	276/279 (98%)	-0.17	2 (0%) 84 88	17, 27, 46, 54	0
1	B	274/279 (98%)	0.66	29 (10%) 7 7	20, 49, 85, 90	0
All	All	550/558 (98%)	0.24	31 (5%) 24 26	17, 34, 78, 90	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	266	ASP	5.7
1	B	190	ALA	5.2
1	B	281	LYS	5.0
1	B	202	ALA	4.3
1	B	244	LYS	3.7
1	B	268	ALA	3.6
1	B	197	VAL	3.5
1	B	189	ASP	3.5
1	B	272	LYS	3.5
1	B	284	LYS	3.5
1	B	280	SER	3.4
1	B	245	GLU	3.4
1	B	262	PRO	3.3
1	B	188	LYS	3.2
1	B	265	LYS	3.1
1	B	263	ASN	2.9
1	B	264	ALA	2.8
1	B	208	TYR	2.7
1	B	198	VAL	2.7
1	B	275	SER	2.7
1	B	269	LEU	2.7
1	B	242	THR	2.6
1	B	185	ALA	2.3
1	B	324	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	326	GLU	2.2
1	A	263	ASN	2.2
1	B	192	PRO	2.1
1	B	203	ASP	2.1
1	B	196	SER	2.1
1	A	265	LYS	2.1
1	B	187	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.