Full wwPDB X-ray Structure Validation Report ⓘ

Jun 11, 2024 – 10:59 PM EDT

PDB ID	:	1JMK
Title	:	Structural Basis for the Cyclization of the Lipopeptide Antibiotic Surfactin by the Thioesterase Domain SrfTE
Authors	:	Bruner, S.D.; Weber, T.; Kohli, R.M.; Schwarzer, D.; Marahiel, M.A.; Walsh, C.T.; Stubbs, M.T.
Deposited on	:	2001-07-18
Resolution	:	1.71 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 ⓘ 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 ⓘ) were used in the production of this report:

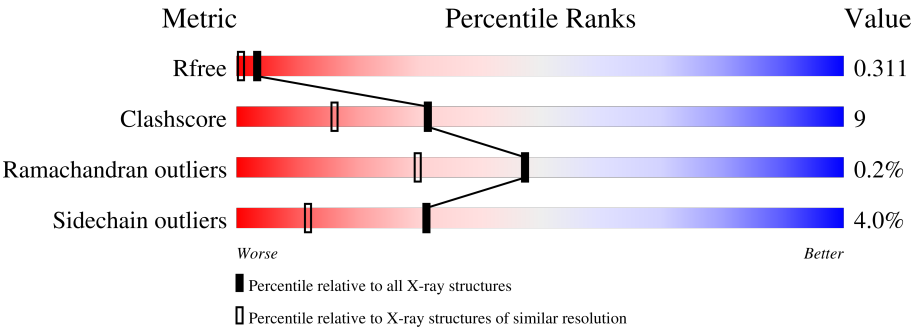
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.71 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	5722 (1.74-1.70)
Clashscore	141614	6152 (1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)

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%

Mol	Chain	Length	Quality of chain
1	C	230	79% 15%
1	O	230	81% 17%

2 Entry composition (i)

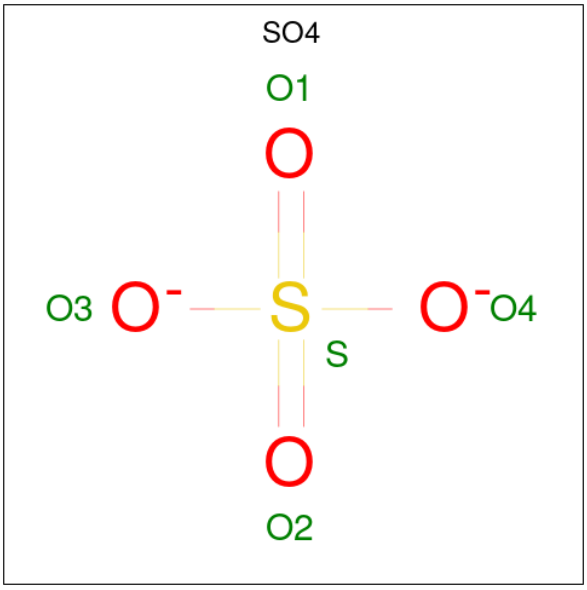
There are 3 unique types of molecules in this entry. The entry contains 3779 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Surfactin Synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	222	Total	C	N	O	S	0	0	0
			1733	1098	289	338	8			
1	O	230	Total	C	N	O	S	0	0	0
			1798	1134	301	355	8			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	O	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

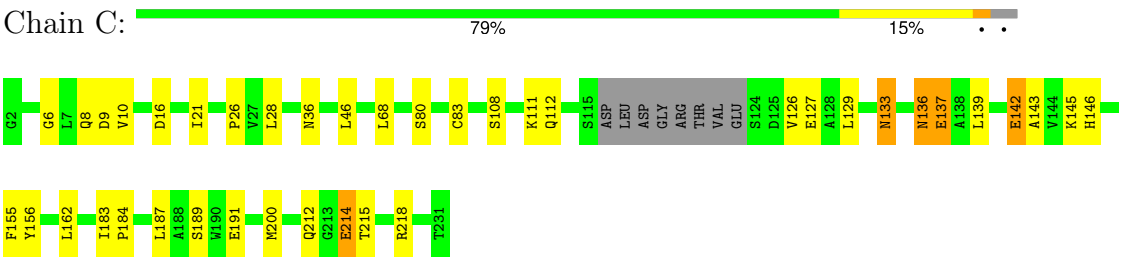
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	141	Total O 141 141	0	0
3	O	97	Total O 97 97	0	0

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. 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. 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.

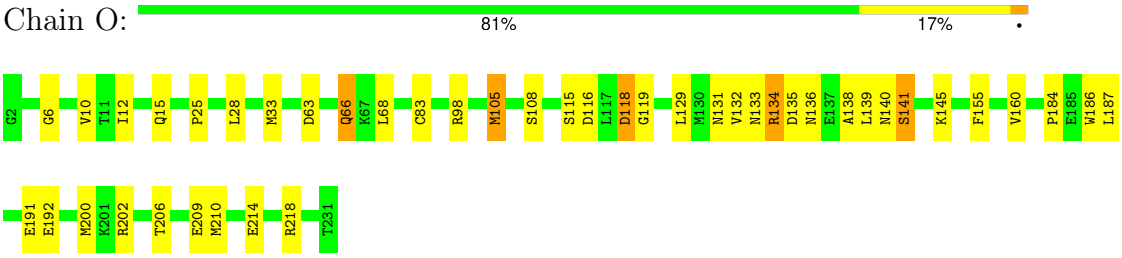
- Molecule 1: Surfactin Synthetase

Chain C:



- Molecule 1: Surfactin Synthetase

Chain O:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	63.01Å 76.37Å 119.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.71 24.90 – 1.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-1.71) 94.6 (24.90-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.56 (at 1.70Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.230 , 0.245 0.305 , 0.311	Depositor DCC
R_{free} test set	6162 reflections (9.85%)	wwPDB-VP
Wilson B-factor (Å^2)	24.0	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	3779	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	C	0.33	0/1764	0.60	0/2380
1	O	0.30	0/1830	0.57	0/2471
All	All	0.32	0/3594	0.59	0/4851

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

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	C	1733	0	1683	32	4
1	O	1798	0	1746	33	4
2	C	5	0	0	0	0
2	O	5	0	0	0	0
3	C	141	0	0	2	1
3	O	97	0	0	1	1
All	All	3779	0	3429	63	5

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.

All (63) 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:O:134:ARG:HE	1:O:135:ASP:H	1.03	0.97
1:C:36:ASN:HD22	1:C:212:GLN:NE2	1.69	0.90
1:C:36:ASN:HD22	1:C:212:GLN:HE22	1.23	0.86
1:O:134:ARG:HE	1:O:135:ASP:N	1.72	0.85
1:O:83:CYS:SG	1:O:105:MET:HG3	2.19	0.83
1:C:28:LEU:HD11	1:C:133:ASN:HD21	1.46	0.80
1:O:134:ARG:NE	1:O:135:ASP:H	1.84	0.73
1:C:28:LEU:HD11	1:C:133:ASN:ND2	2.06	0.71
1:C:215:THR:HG22	1:C:218:ARG:NH1	2.08	0.68
1:C:21:ILE:HB	1:C:46:LEU:HD23	1.76	0.65
1:O:66:GLN:NE2	1:O:98:ARG:HH11	1.94	0.64
1:C:184:PRO:HD2	1:C:187:LEU:HD12	1.80	0.64
1:C:36:ASN:ND2	1:C:212:GLN:NE2	2.43	0.63
1:O:214:GLU:HG3	1:O:218:ARG:NH1	2.13	0.63
1:O:214:GLU:HG3	1:O:218:ARG:HH12	1.68	0.59
1:C:215:THR:HG22	1:C:218:ARG:HH11	1.69	0.58
1:O:140:ASN:HA	1:O:145:LYS:HE3	1.85	0.57
1:O:134:ARG:HA	3:O:592:HOH:O	2.05	0.56
1:O:184:PRO:HD2	1:O:187:LEU:HD12	1.88	0.55
1:C:36:ASN:ND2	1:C:212:GLN:HE22	1.99	0.55
1:C:183:ILE:HD11	1:C:187:LEU:HB3	1.88	0.55
1:O:28:LEU:HD12	1:O:33:MET:CE	2.37	0.54
1:O:131:ASN:O	1:O:134:ARG:HD3	2.07	0.54
1:C:112:GLN:HG3	3:C:581:HOH:O	2.09	0.53
1:O:134:ARG:NE	1:O:134:ARG:N	2.56	0.53
1:O:136:ASN:ND2	1:O:138:ALA:HB3	2.24	0.52
1:O:83:CYS:SG	1:O:108:SER:HB3	2.50	0.52
1:C:142:GLU:HG2	1:C:143:ALA:N	2.27	0.50
1:C:191:GLU:HG3	1:O:200:MET:SD	2.53	0.49
1:C:111:LYS:HG2	1:C:162:LEU:O	2.12	0.49
1:C:28:LEU:CD1	1:C:133:ASN:ND2	2.73	0.49
1:O:12:ILE:HG22	1:O:15:GLN:HG2	1.95	0.49
1:O:66:GLN:HA	1:O:66:GLN:HE21	1.77	0.49
1:C:26:PRO:HA	1:C:80:SER:HB3	1.95	0.48
1:C:136:ASN:HD22	1:C:137:GLU:N	2.12	0.48
1:C:145:LYS:HG3	1:C:146:HIS:N	2.29	0.47
1:O:115:SER:HB2	1:O:160:VAL:HG13	1.97	0.47
1:C:129:LEU:O	1:C:133:ASN:ND2	2.48	0.47
1:C:126:VAL:HG11	1:C:156:TYR:CD1	2.50	0.47
1:C:139:LEU:HD12	1:C:139:LEU:N	2.30	0.46
1:C:183:ILE:O	1:C:183:ILE:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:GLN:O	1:C:9:ASP:HB2	2.16	0.46
1:O:134:ARG:HE	1:O:134:ARG:N	2.13	0.45
1:O:66:GLN:NE2	1:O:98:ARG:NH1	2.62	0.45
1:O:206:THR:O	1:O:210:MET:HG3	2.17	0.45
1:C:83:CYS:SG	1:C:108:SER:HB3	2.57	0.45
1:O:134:ARG:NE	1:O:134:ARG:H	2.14	0.45
1:C:126:VAL:HG23	1:C:127:GLU:N	2.32	0.44
1:C:183:ILE:HD11	1:C:187:LEU:CB	2.48	0.44
1:O:83:CYS:CB	1:O:105:MET:HG3	2.47	0.44
1:O:116:ASP:HB3	1:O:186:TRP:CZ3	2.53	0.43
1:C:111:LYS:CG	1:C:162:LEU:O	2.66	0.43
1:C:214:GLU:N	1:C:214:GLU:OE1	2.51	0.43
1:O:83:CYS:HB3	1:O:105:MET:HG3	2.00	0.42
1:O:129:LEU:O	1:O:132:VAL:HG22	2.19	0.42
1:O:133:ASN:O	1:O:139:LEU:HD12	2.20	0.42
1:O:206:THR:OG1	1:O:209:GLU:HG2	2.20	0.41
1:C:36:ASN:HB2	1:C:212:GLN:HE22	1.84	0.41
1:O:206:THR:H	1:O:209:GLU:CG	2.33	0.41
1:C:200:MET:SD	1:O:191:GLU:HG3	2.61	0.41
1:O:134:ARG:NE	1:O:135:ASP:N	2.54	0.41
1:O:118:ASP:HB3	1:O:119:GLY:H	1.55	0.40
1:C:189:SER:HB2	3:C:633:HOH:O	2.22	0.40

All (5) 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)
1:C:68:LEU:O	1:O:6:GLY:N[2_664]	1.93	0.27
1:C:16:ASP:OD2	1:O:141:SER:OG[2_664]	1.97	0.23
1:C:10:VAL:O	3:O:503:HOH:O[2_664]	2.11	0.09
1:O:10:VAL:O	3:C:538:HOH:O[2_665]	2.11	0.09
1:C:6:GLY:N	1:O:68:LEU:O[2_664]	2.12	0.08

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	C	218/230 (95%)	210 (96%)	8 (4%)	0	100 100
1	O	228/230 (99%)	221 (97%)	6 (3%)	1 (0%)	34 18
All	All	446/460 (97%)	431 (97%)	14 (3%)	1 (0%)	47 30

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O	141	SER

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	C	181/192 (94%)	175 (97%)	6 (3%)	38 17
1	O	190/192 (99%)	181 (95%)	9 (5%)	26 9
All	All	371/384 (97%)	356 (96%)	15 (4%)	31 12

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	133	ASN
1	C	136	ASN
1	C	137	GLU
1	C	142	GLU
1	C	155	PHE
1	C	214	GLU
1	O	25	PRO
1	O	63	ASP
1	O	66	GLN
1	O	105	MET
1	O	118	ASP
1	O	134	ARG

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Mol	Chain	Res	Type
1	O	155	PHE
1	O	192	GLU
1	O	202	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	8	GLN
1	C	14	ASN
1	C	96	GLN
1	C	112	GLN
1	C	133	ASN
1	C	136	ASN
1	C	212	GLN
1	C	228	ASN
1	O	8	GLN
1	O	14	ASN
1	O	36	ASN
1	O	66	GLN
1	O	96	GLN
1	O	101	GLN
1	O	112	GLN
1	O	131	ASN
1	O	133	ASN
1	O	136	ASN
1	O	140	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)

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	SO4	O	501	-	4,4,4	0.59	0	6,6,6	0.97	0
2	SO4	C	502	-	4,4,4	0.59	0	6,6,6	0.97	0

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.