Full wwPDB X-ray Structure Validation Report (i)

May 19, 2020 – 04:13 am BST

PDB ID	:	6JBX
Title	:	Crystal structure of Streptococcus pneumoniae FabT in complex with DNA
Authors	:	Zuo, G.; Chen, Z.P.; Li, Q.; Zhou, C.Z.
Deposited on	:	2019-01-27
Resolution	:	2.20 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 following versions of software and data (see references (1)) were used in the production of this report:

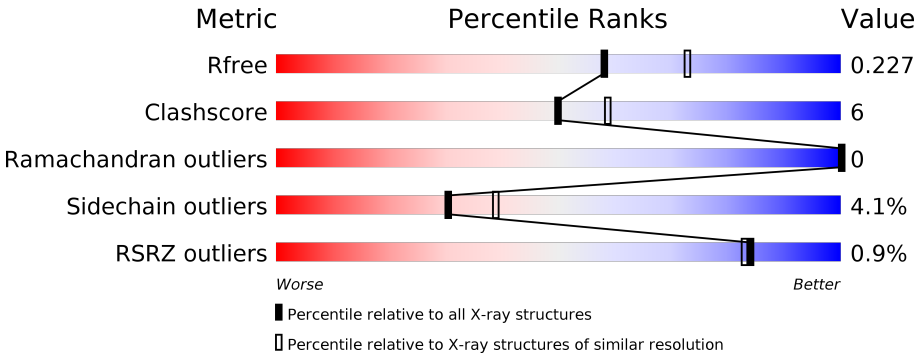
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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	152	% 83% 13% •
1	B	152	% 79% 14% • 6%
2	C	23	57% 35% 9%
3	D	23	78% 13% 9%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3540 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 Fatty acid biosynthesis transcriptional regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	146	Total	C	N	O	S	0	0	0
			1193	751	218	218	6			
1	B	143	Total	C	N	O	S	0	1	0
			1177	743	212	217	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	UNP A0A062WM61
A	-7	GLY	-	expression tag	UNP A0A062WM61
A	-6	HIS	-	expression tag	UNP A0A062WM61
A	-5	HIS	-	expression tag	UNP A0A062WM61
A	-4	HIS	-	expression tag	UNP A0A062WM61
A	-3	HIS	-	expression tag	UNP A0A062WM61
A	-2	HIS	-	expression tag	UNP A0A062WM61
A	-1	HIS	-	expression tag	UNP A0A062WM61
B	-8	MET	-	expression tag	UNP A0A062WM61
B	-7	GLY	-	expression tag	UNP A0A062WM61
B	-6	HIS	-	expression tag	UNP A0A062WM61
B	-5	HIS	-	expression tag	UNP A0A062WM61
B	-4	HIS	-	expression tag	UNP A0A062WM61
B	-3	HIS	-	expression tag	UNP A0A062WM61
B	-2	HIS	-	expression tag	UNP A0A062WM61
B	-1	HIS	-	expression tag	UNP A0A062WM61

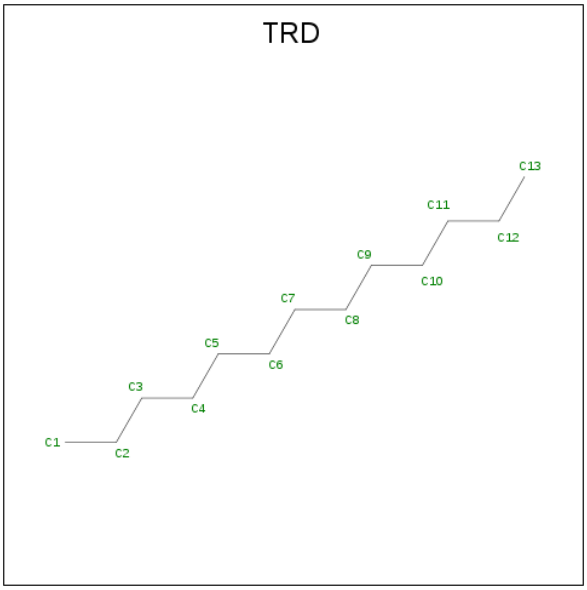
- Molecule 2 is a DNA chain called DNA (5'-D(*AP*AP*TP*AP*GP*TP*TP*TP*GP*AP*CP*TP*GP*TP*CP*AP*AP*AP*TP*TP*AP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	23	Total	C	N	O	P	0	0	0
			470	228	84	136	22			

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*AP*TP*AP*AP*TP*TP*TP*GP*AP*CP*AP*GP*TP*CP*AP*AP*AP*CP*TP*AP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	23	Total	C	N	O	P	0	0	0
			465	226	83	134	22			

- Molecule 4 is TRIDECANE (three-letter code: TRD) (formula: $C_{13}H_{28}$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	C	0	0
			13	13		
4	B	1	Total	C	0	0
			13	13		

- Molecule 5 is water.

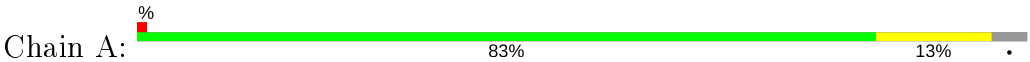
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	71	Total	O	0	0
			71	71		
5	B	84	Total	O	0	0
			84	84		
5	C	26	Total	O	0	0
			26	26		
5	D	28	Total	O	0	0
			28	28		

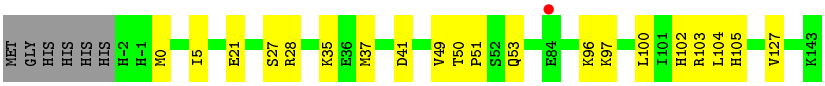
3 Residue-property plots (i)

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: Fatty acid biosynthesis transcriptional regulator

Chain A:





• Molecule 1: Fatty acid biosynthesis transcriptional regulator

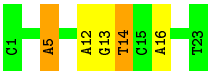
Chain B:

• Molecule 2: DNA (5'-D(*AP*AP*TP*AP*GP*TP*TP*TP*GP*AP*CP*TP*GP*TP*CP*AP *AP*AP*TP*TP*AP*TP*G)-3')

Chain C:

• Molecule 3: DNA (5'-D(*CP*AP*TP*AP*AP*TP*TP*TP*GP*AP*CP*AP*GP*TP*CP*AP *AP*AP*CP*TP*AP*TP*T)-3')

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	73.02Å 60.87Å 74.09Å 90.00° 105.40° 90.00°	Depositor
Resolution (Å)	35.96 – 2.20 35.93 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.6 (35.96-2.20) 98.6 (35.93-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.24 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.188 , 0.221 0.194 , 0.227	Depositor DCC
R_{free} test set	1503 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å^2)	38.0	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 45.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.010 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3540	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.00% 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: TRD

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	0.65	0/1210	0.67	0/1623
1	B	0.65	0/1193	0.66	0/1601
2	C	0.70	0/527	1.01	5/813 (0.6%)
3	D	0.66	0/521	1.00	4/802 (0.5%)
All	All	0.66	0/3451	0.79	9/4839 (0.2%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	5	DA	C1'-O4'-C4'	-6.89	103.21	110.10
2	C	4	DA	O5'-P-OP2	-5.86	100.43	105.70
3	D	14	DT	O5'-P-OP1	-5.75	100.53	105.70
2	C	5	DG	C1'-O4'-C4'	-5.54	104.56	110.10
2	C	15	DC	O5'-P-OP2	-5.45	100.79	105.70
2	C	14	DT	C1'-O4'-C4'	-5.40	104.70	110.10
2	C	11	DC	C1'-O4'-C4'	-5.22	104.88	110.10
3	D	14	DT	C1'-O4'-C4'	-5.07	105.03	110.10
3	D	16	DA	O5'-P-OP2	-5.03	101.17	105.70

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	1193	0	1233	13	0
1	B	1177	0	1218	17	0
2	C	470	0	261	4	0
3	D	465	0	260	5	0
4	B	26	0	56	5	0
5	A	71	0	0	3	0
5	B	84	0	0	5	0
5	C	26	0	0	1	0
5	D	28	0	0	1	0
All	All	3540	0	3028	37	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 6.

All (37) 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:A:103:ARG:NH2	5:A:201:HOH:O	1.80	0.94
1:B:125:ILE:HG23	4:B:202:TRD:H12	1.62	0.81
3:D:12:DA:H2"	3:D:13:DG:O5'	1.81	0.81
1:B:73:GLU:OE2	5:B:301:HOH:O	2.02	0.78
3:D:14:DT:OP2	5:D:101:HOH:O	2.01	0.76
1:B:79:GLU:HB2	1:B:93:HIS:CE1	2.25	0.71
2:C:6:DT:OP1	5:C:101:HOH:O	2.09	0.70
1:A:50:THR:OG1	1:A:53:GLN:HG3	1.95	0.67
1:B:125:ILE:CG2	4:B:202:TRD:H12	2.28	0.64
1:B:79:GLU:OE1	1:B:93:HIS:CE1	2.51	0.64
1:B:112:MET:HE2	4:B:202:TRD:H131	1.80	0.63
1:A:96:LYS:HE3	1:A:100:LEU:HG	1.84	0.59
2:C:15:DC:H2"	2:C:16:DA:C8	2.39	0.58
1:B:112:MET:CE	4:B:202:TRD:H131	2.36	0.56
1:A:49:VAL:CG2	1:A:53:GLN:HB2	2.38	0.53
1:B:105:HIS:CE1	1:B:109:HIS:NE2	2.80	0.49
1:A:0:MET:HE2	1:A:5:ILE:HG12	1.93	0.49
1:B:4:ARG:HH21	1:B:5:ILE:HD13	1.77	0.49
4:B:202:TRD:H11	5:B:358:HOH:O	2.13	0.49
1:B:114:GLU:HA	1:B:114:GLU:OE1	2.13	0.47
1:A:127:VAL:HG12	1:B:127:VAL:HG11	1.96	0.47
1:B:2[A]:TYR:C	1:B:2[A]:TYR:CD1	2.88	0.47
2:C:21:DA:H2"	2:C:22:DT:O5'	2.16	0.46
1:B:143:LYS:NZ	5:B:309:HOH:O	2.49	0.46
1:A:97:LYS:NZ	5:A:204:HOH:O	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:LYS:NZ	5:B:310:HOH:O	2.50	0.45
1:A:35:LYS:NZ	5:A:207:HOH:O	2.50	0.45
1:B:4:ARG:HH21	1:B:5:ILE:CD1	2.30	0.44
3:D:12:DA:C2'	3:D:13:DG:O5'	2.60	0.44
1:A:27:SER:HB2	1:A:104:LEU:HD21	2.01	0.43
3:D:12:DA:H2"	3:D:13:DG:C5'	2.48	0.42
1:B:97:LYS:NZ	5:B:307:HOH:O	2.41	0.42
1:A:51:PRO:HD2	3:D:5:DA:OP1	2.20	0.42
1:A:41:ASP:OD1	1:A:102:HIS:HE1	2.03	0.41
1:A:37:MET:HG3	1:A:105:HIS:CD2	2.55	0.41
1:A:127:VAL:HG11	1:B:123:GLU:HG3	2.02	0.40
2:C:11:DC:C6	2:C:12:DT:H72	2.56	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	Percentiles	
1	A	144/152 (95%)	142 (99%)	2 (1%)	0	100	100
1	B	142/152 (93%)	142 (100%)	0	0	100	100
All	All	286/304 (94%)	284 (99%)	2 (1%)	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	135/140 (96%)	133 (98%)	2 (2%)	65 78
1	B	133/140 (95%)	123 (92%)	10 (8%)	13 14
All	All	268/280 (96%)	256 (96%)	12 (4%)	30 34

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLU
1	A	28	ARG
1	B	2[A]	TYR
1	B	2[B]	TYR
1	B	4	ARG
1	B	20	GLU
1	B	45	LYS
1	B	57	GLU
1	B	62	LEU
1	B	85	GLN
1	B	110	LYS
1	B	115	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	HIS
1	A	105	HIS
1	B	93	HIS

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	$\#\|Z\| > 2$
4	TRD	B	201	-	12,12,12	0.95	0	11,11,11	0.52	0
4	TRD	B	202	-	12,12,12	1.09	0	11,11,11	0.75	0

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
4	TRD	B	201	-	-	6/10/10/10	-
4	TRD	B	202	-	-	5/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	202	TRD	C9-C10-C11-C12
4	B	201	TRD	C2-C3-C4-C5
4	B	202	TRD	C7-C8-C9-C10
4	B	201	TRD	C5-C6-C7-C8
4	B	202	TRD	C11-C10-C9-C8
4	B	201	TRD	C10-C11-C12-C13
4	B	201	TRD	C4-C5-C6-C7
4	B	202	TRD	C2-C3-C4-C5
4	B	202	TRD	C10-C11-C12-C13
4	B	201	TRD	C6-C7-C8-C9
4	B	201	TRD	C9-C10-C11-C12

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	202	TRD	5	0

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, 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>2			OWAB(Å^2)	Q<0.9
1	A	146/152 (96%)	-0.12	1 (0%)	87	86	27, 43, 67, 83	0
1	B	143/152 (94%)	-0.24	2 (1%)	75	73	25, 39, 59, 84	0
2	C	23/23 (100%)	-0.39	0	100	100	30, 46, 72, 76	0
3	D	23/23 (100%)	-0.51	0	100	100	33, 46, 67, 69	0
All	All	335/350 (95%)	-0.21	3 (0%)	84	83	25, 41, 67, 84	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2[A]	TYR	2.9
1	B	93	HIS	2.5
1	A	84	GLU	2.5

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

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	B-factors(Å^2)	Q<0.9
4	TRD	B	201	13/13	0.88	0.30	48,55,61,66	0
4	TRD	B	202	13/13	0.91	0.26	62,65,68,73	0

6.5 Other polymers (i)

There are no such residues in this entry.