wwPDB X-ray Structure Validation Summary Report (i)

Feb 19, 2016 – 07:54 PM GMT

PDB ID	:	4X2E
Title	:	Clostridium difficile wild type Fic protein
Authors	:	Jorgensen, R.; Dedic, E.
Deposited on	:	2014-11-26
Resolution	:	3.10 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
A user guide is available at
http://wwpdb.org/validation/2016/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:

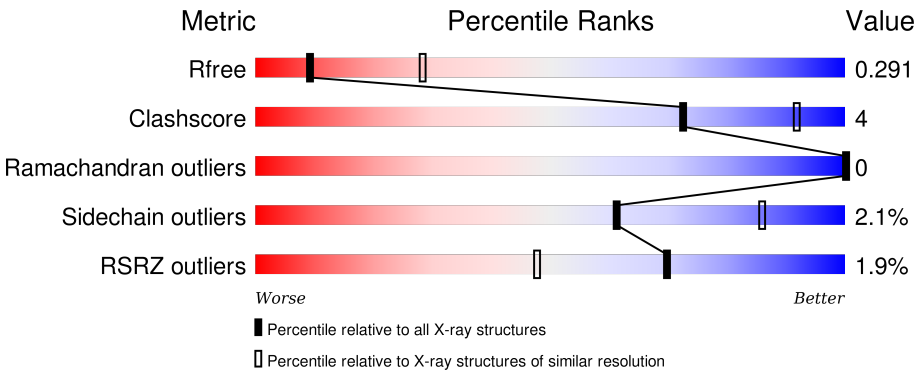
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

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 3.10 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}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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. 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	235	76% 9% 14%
1	B	235	71% 15% 14%
1	C	235	2% 74% 11% • 15%
1	D	235	5% 71% 11% 18%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 6561 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 Fic family protein putative filamentation induced by cAMP protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	201	1663	1069	272	318	4	0	0	0
1	B	203	1673	1080	273	316	4	0	0	0
1	C	200	1653	1065	269	316	3	0	0	0
1	D	193	1572	1007	258	304	3	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

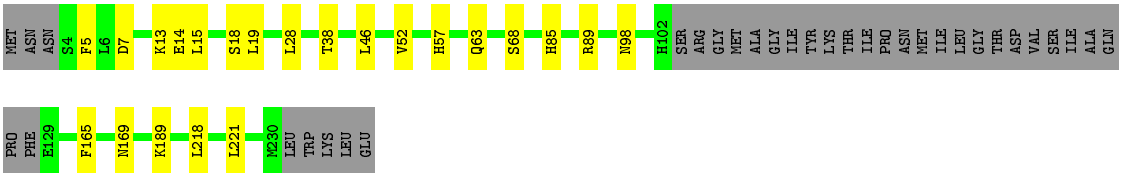
Chain	Residue	Modelled	Actual	Comment	Reference
A	234	LEU	-	expression tag	UNP C9YJ22
A	235	GLU	-	expression tag	UNP C9YJ22
B	234	LEU	-	expression tag	UNP C9YJ22
B	235	GLU	-	expression tag	UNP C9YJ22
C	234	LEU	-	expression tag	UNP C9YJ22
C	235	GLU	-	expression tag	UNP C9YJ22
D	234	LEU	-	expression tag	UNP C9YJ22
D	235	GLU	-	expression tag	UNP C9YJ22

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 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.

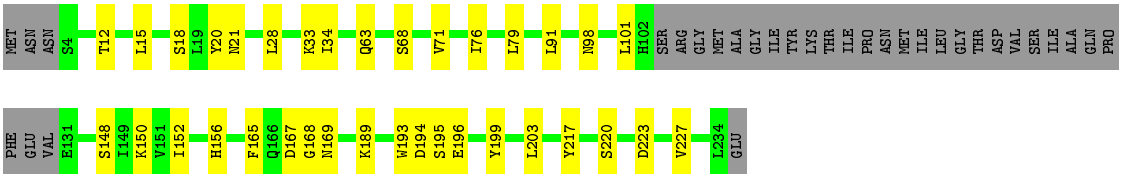
- Molecule 1: Fic family protein putative filamentation induced by cAMP protein

Chain A:



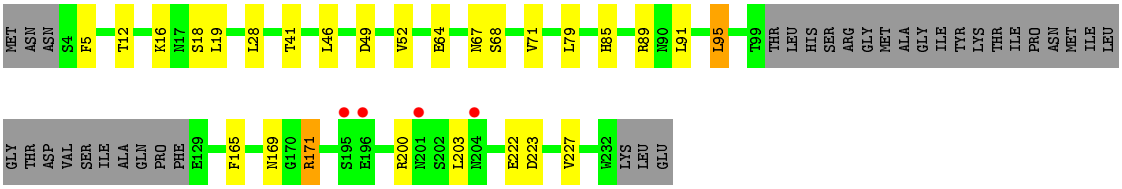
- Molecule 1: Fic family protein putative filamentation induced by cAMP protein

Chain B:



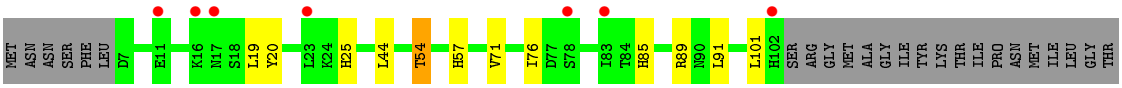
- Molecule 1: Fic family protein putative filamentation induced by cAMP protein

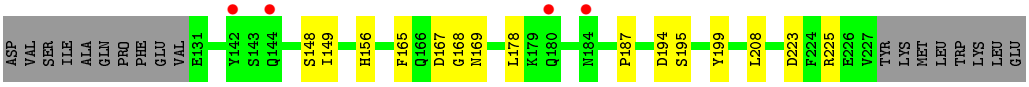
Chain C:



- Molecule 1: Fic family protein putative filamentation induced by cAMP protein

Chain D:




ASP
VAL
SER
ILE
ALA
GLN
PRO
PHE
GLU
VAL
E131
Y142
S143
Q144
S148
I149
H156
F165
Q166
D167
G168
N169
L178
K179
Q180
N184
P187
D194
S195
Y199
L208
D223
F224
R225
E226
V227
TYR
LYS
MET
LEU
TRP
LYS
LEU
GLU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	57.42Å 157.37Å 262.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 – 3.10 45.93 – 3.10	Depositor EDS
% Data completeness (in resolution range)	92.9 (19.95-3.10) 93.0 (45.93-3.10)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.85 (at 3.12Å)	Xtriage
Refinement program	phenix	Depositor
R, R_{free}	0.243 , 0.286 0.242 , 0.291	Depositor DCC
R_{free} test set	1031 reflections (5.02%)	DCC
Wilson B-factor (Å^2)	51.9	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 37.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Outliers	1 of 20550 reflections (0.005%)	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	6561	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.25	0/1698	0.41	0/2297
1	B	0.24	0/1709	0.42	0/2314
1	C	0.24	0/1689	0.41	0/2288
1	D	0.24	0/1604	0.42	0/2176
All	All	0.24	0/6700	0.42	0/9075

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 (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	1663	0	1639	11	0
1	B	1673	0	1649	19	0
1	C	1653	0	1617	13	0
1	D	1572	0	1526	12	0
All	All	6561	0	6431	55	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 4.

The worst 5 of 55 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:150:LYS:H	1:B:150:LYS:HD2	1.58	0.69
1:D:71:VAL:HG13	1:D:91:LEU:HD22	1.77	0.67
1:D:20:TYR:HE2	1:D:76:ILE:HG21	1.62	0.63
1:B:217:TYR:O	1:B:220:SER:OG	2.17	0.62
1:B:195:SER:HG	1:B:217:TYR:HE1	1.50	0.60

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	197/235 (84%)	194 (98%)	3 (2%)	0	100	100
1	B	199/235 (85%)	195 (98%)	4 (2%)	0	100	100
1	C	196/235 (83%)	195 (100%)	1 (0%)	0	100	100
1	D	189/235 (80%)	186 (98%)	3 (2%)	0	100	100
All	All	781/940 (83%)	770 (99%)	11 (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	192/221 (87%)	191 (100%)	1 (0%)	92	96
1	B	191/221 (86%)	187 (98%)	4 (2%)	61	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	189/221 (86%)	183 (97%)	6 (3%)	46	79
1	D	179/221 (81%)	174 (97%)	5 (3%)	51	82
All	All	751/884 (85%)	735 (98%)	16 (2%)	61	86

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	171	ARG
1	C	200	ARG
1	D	54	THR
1	C	95	LEU
1	D	101	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

There are no ligands in this entry.

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, 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	201/235 (85%)	-0.03	0	100	100	19, 41, 78, 98	0
1	B	203/235 (86%)	-0.05	0	100	100	21, 49, 75, 97	0
1	C	200/235 (85%)	0.12	4 (2%)	68	46	31, 55, 87, 125	0
1	D	193/235 (82%)	0.40	11 (5%)	27	11	48, 71, 109, 131	0
All	All	797/940 (84%)	0.11	15 (1%)	70	48	19, 55, 96, 131	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	196	GLU	3.5
1	D	78	SER	3.4
1	D	144	GLN	3.1
1	C	195	SER	3.0
1	D	184	ASN	2.7

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.