wwPDB EM Validation Summary Report (i)

May 13, 2024 – 10:29 pm BST

PDB ID	:	6T17
EMDB ID	:	EMD-10362
Title	:	Cryo-EM structure of the wild-type flagellar filament of the Firmicute Kurthia
Authors	:	Blum, T.B.; Abrahams, J.P.
Deposited on	:	2019-10-03
Resolution	:	2.80 Å(reported)

This is a wwPDB EM Validation Summary 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/EMValidationReportHelp
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 (i)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
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 (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

There are no overall percentile quality scores available for this entry.

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 181940 atoms, of which 91432 are hydrogens and 0 are deuteriums.

In the tables below, 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 Flagellin.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	B	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	C	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	D	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	E	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	F	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	G	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	H	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	I	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	J	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	K	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	L	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	M	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	N	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	O	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	P	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	Q	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	S	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	T	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	U	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	V	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	W	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	X	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	Y	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	Z	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	a	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	b	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	c	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	d	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	e	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	f	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	g	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	h	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	i	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	j	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	k	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	l	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	m	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	n	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	o	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	p	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	q	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		
1	r	276	Total	C	H	N	O	S	0	0
			4135	1236	2078	386	424	11		

SEQUENCE-PLOTS INFOmissingINFO

3 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=65.45°, rise=4.83 Å, axial sym=C1	Depositor
Number of segments used	9270	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	86	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

4 Model quality

4.1 Standard geometry

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles

4.3.1 Protein backbone

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

There are no ligands in this entry.

4.7 Other polymers

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Map visualisation

This section contains visualisations of the EMDB entry EMD-10362. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections

This section was not generated.

5.2 Central slices

This section was not generated.

5.3 Largest variance slices

This section was not generated.

5.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

5.5 Orthogonal surface views

This section was not generated.

5.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

6 Map analysis

This section contains the results of statistical analysis of the map.

6.1 Map-value distribution

This section was not generated.

6.2 Volume estimate versus contour level

This section was not generated.

6.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

7 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

8 Map-model fit

This section was not generated.