wwPDB X-ray Structure Validation Summary Report (i)

Nov 16, 2023 – 08:55 AM JST

PDB ID	:	6LEA
Title	:	Structure of FliS chaperone in complex with flagellin and HP1076
Authors	:	Au, S.W.; Lam, W.W.
Deposited on	:	2019-11-25
Resolution	:	2.95 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
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 (1)) were used in the production of this report:

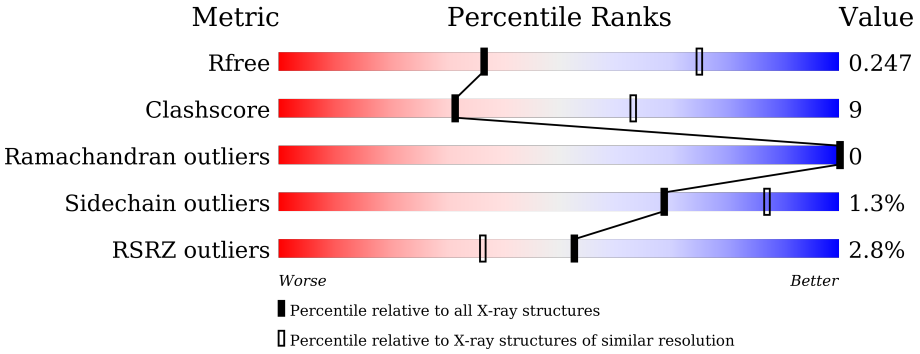
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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% 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	131	2%; 65%; 15%; 20%
1	B	131	2%; 68%; 12%; 20%
2	C	177	2%; 55%; 16%; 29%
2	D	177	3%; 47%; 21%; •; 31%
3	E	105	%; 35%; •; 63%
3	F	105	26%; 11%; 63%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4283 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 Flagellar secretion chaperone FliS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	105	851	544	141	164	2	0	0	0
1	B	105	851	544	141	164	2	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP I9NY49
A	-3	PRO	-	expression tag	UNP I9NY49
A	-2	LEU	-	expression tag	UNP I9NY49
A	-1	GLY	-	expression tag	UNP I9NY49
A	0	SER	-	expression tag	UNP I9NY49
B	-4	GLY	-	expression tag	UNP I9NY49
B	-3	PRO	-	expression tag	UNP I9NY49
B	-2	LEU	-	expression tag	UNP I9NY49
B	-1	GLY	-	expression tag	UNP I9NY49
B	0	SER	-	expression tag	UNP I9NY49

- Molecule 2 is a protein called Uncharacterized protein HP_1076.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	126	997	633	161	198	5	0	0	0
2	D	123	973	618	157	193	5	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	HIS	-	expression tag	UNP O25709
C	-4	HIS	-	expression tag	UNP O25709

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	HIS	-	expression tag	UNP O25709
C	-2	HIS	-	expression tag	UNP O25709
C	-1	HIS	-	expression tag	UNP O25709
C	0	HIS	-	expression tag	UNP O25709
D	-5	HIS	-	expression tag	UNP O25709
D	-4	HIS	-	expression tag	UNP O25709
D	-3	HIS	-	expression tag	UNP O25709
D	-2	HIS	-	expression tag	UNP O25709
D	-1	HIS	-	expression tag	UNP O25709
D	0	HIS	-	expression tag	UNP O25709

- Molecule 3 is a protein called Flagellin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	39	300	188	52	59	1	0	0	0
			Total	C	N	O	S			
3	F	39	300	188	52	59	1	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	410	HIS	-	expression tag	UNP A0A1Q2QRN0
E	411	HIS	-	expression tag	UNP A0A1Q2QRN0
E	412	HIS	-	expression tag	UNP A0A1Q2QRN0
E	413	HIS	-	expression tag	UNP A0A1Q2QRN0
E	414	HIS	-	expression tag	UNP A0A1Q2QRN0
E	415	HIS	-	expression tag	UNP A0A1Q2QRN0
F	410	HIS	-	expression tag	UNP A0A1Q2QRN0
F	411	HIS	-	expression tag	UNP A0A1Q2QRN0
F	412	HIS	-	expression tag	UNP A0A1Q2QRN0
F	413	HIS	-	expression tag	UNP A0A1Q2QRN0
F	414	HIS	-	expression tag	UNP A0A1Q2QRN0
F	415	HIS	-	expression tag	UNP A0A1Q2QRN0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	4	4	4	0	0
			Total	O		
4	B	3	3	3	0	0

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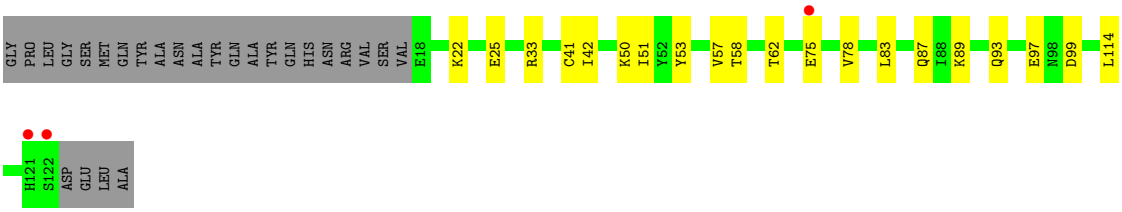
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total O 1 1	0	0
4	D	1	Total O 1 1	0	0
4	E	1	Total O 1 1	0	0
4	F	1	Total O 1 1	0	0

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 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: Flagellar secretion chaperone FliS

Chain A:

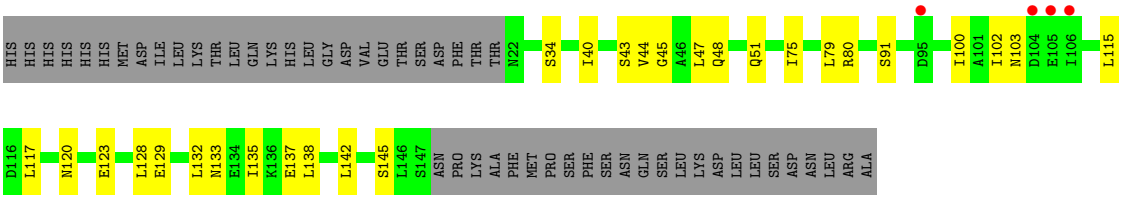


• Molecule 1: Flagellar secretion chaperone FliS

Chain B:

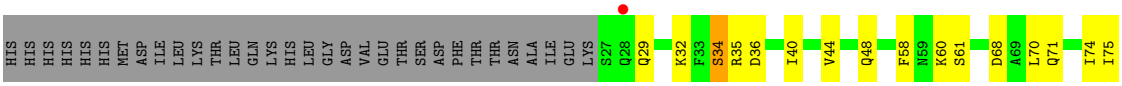
• Molecule 2: Uncharacterized protein HP_1076

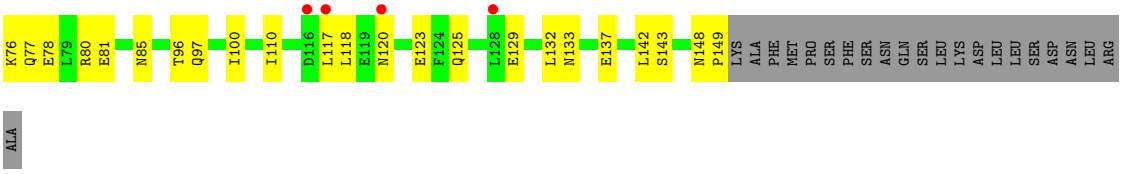
Chain C:



• Molecule 2: Uncharacterized protein HP_1076

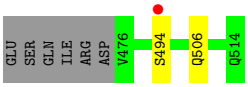
Chain D:





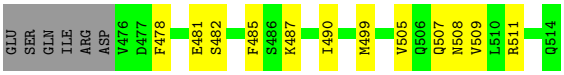
- Molecule 3: Flagellin

Chain E:



- Molecule 3: Flagellin

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	103.33Å 103.33Å 144.21Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.62 – 2.95 30.62 – 2.95	Depositor EDS
% Data completeness (in resolution range)	87.6 (30.62-2.95) 87.5 (30.62-2.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.40 (at 2.95Å)	Xtriage
Refinement program	PHENIX 1.17rc1_3605	Depositor
R, R_{free}	0.190 , 0.247 0.189 , 0.247	Depositor DCC
R_{free} test set	1658 reflections (9.92%)	wwPDB-VP
Wilson B-factor (Å^2)	56.3	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 31.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.054 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4283	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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 (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	0.37	0/863	0.54	0/1166
1	B	0.41	0/863	0.53	0/1166
2	C	0.36	0/1006	0.57	1/1352 (0.1%)
2	D	0.37	0/983	0.61	1/1323 (0.1%)
3	E	0.34	0/303	0.46	0/408
3	F	0.47	0/303	0.77	1/408 (0.2%)
All	All	0.38	0/4321	0.57	3/5823 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	117	LEU	CA-CB-CG	5.96	129.01	115.30
3	F	511	ARG	NE-CZ-NH1	5.86	123.23	120.30
2	C	117	LEU	CB-CG-CD1	-5.48	101.68	111.00

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	851	0	861	19	0
1	B	851	0	861	16	0
2	C	997	0	1016	19	0
2	D	973	0	988	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	300	0	290	2	0
3	F	300	0	290	12	0
4	A	4	0	0	0	0
4	B	3	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	1	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
All	All	4283	0	4306	77	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 9.

The worst 5 of 77 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:119:GLU:OE2	3:F:487:LYS:HE2	1.51	1.09
3:E:506:GLN:HE22	3:F:507:GLN:HG2	1.29	0.97
2:D:60:LYS:HE2	2:D:75:ILE:HG12	1.53	0.91
2:D:129:GLU:HA	2:D:132:LEU:HB2	1.55	0.88
1:B:119:GLU:OE2	3:F:487:LYS:CE	2.21	0.88

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	103/131 (79%)	102 (99%)	1 (1%)	0	100 100
1	B	103/131 (79%)	101 (98%)	2 (2%)	0	100 100
2	C	124/177 (70%)	120 (97%)	4 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	121/177 (68%)	118 (98%)	3 (2%)	0	100	100
3	E	37/105 (35%)	33 (89%)	4 (11%)	0	100	100
3	F	37/105 (35%)	35 (95%)	2 (5%)	0	100	100
All	All	525/826 (64%)	509 (97%)	16 (3%)	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	93/113 (82%)	93 (100%)	0	100	100
1	B	93/113 (82%)	93 (100%)	0	100	100
2	C	113/161 (70%)	112 (99%)	1 (1%)	78	91
2	D	111/161 (69%)	107 (96%)	4 (4%)	35	67
3	E	31/88 (35%)	30 (97%)	1 (3%)	39	71
3	F	31/88 (35%)	31 (100%)	0	100	100
All	All	472/724 (65%)	466 (99%)	6 (1%)	69	87

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	61	SER
2	D	143	SER
3	E	494	SER
2	D	34	SER
2	C	91	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	506	GLN
3	F	506	GLN
3	F	508	ASN
2	D	120	ASN
2	C	120	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)

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	105/131 (80%)	-0.02	3 (2%)	51	35	31, 45, 79, 104	0
1	B	105/131 (80%)	-0.10	2 (1%)	66	49	32, 49, 96, 117	0
2	C	126/177 (71%)	0.06	4 (3%)	47	31	39, 63, 88, 115	0
2	D	123/177 (69%)	0.24	5 (4%)	37	24	48, 71, 111, 146	0
3	E	39/105 (37%)	-0.27	1 (2%)	56	39	36, 57, 90, 101	0
3	F	39/105 (37%)	-0.21	0	100	100	42, 59, 85, 109	0
All	All	537/826 (65%)	0.01	15 (2%)	53	36	31, 59, 97, 146	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	28	GLN	3.8
1	A	75	GLU	2.9
2	C	106	ILE	2.8
2	C	105	GLU	2.6
2	D	117	LEU	2.5

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 monosaccharides 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.