



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1ORJ
Title : FLAGELLAR EXPORT CHAPERONE
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Deposited on : 2003-03-13
Resolution : 2.25 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
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

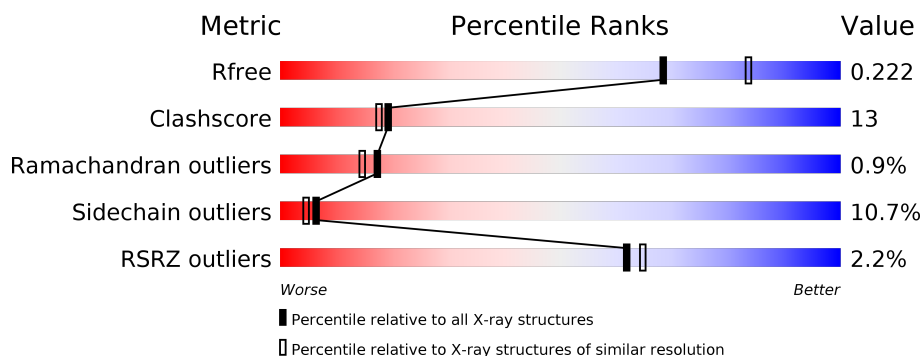
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 $\leq 5\%$. 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	130	<div> <div>3%</div> <div> <div></div> <div>66%</div> <div>23%</div> <div>7%</div> <div>••</div> </div> </div>
1	B	130	<div> <div>2%</div> <div> <div></div> <div>62%</div> <div>14%</div> <div>5%</div> <div>19%</div> </div> </div>
1	C	130	<div> <div>2%</div> <div> <div></div> <div>55%</div> <div>20%</div> <div>5%</div> <div>20%</div> </div> </div>
1	D	130	<div> <div>2%</div> <div> <div></div> <div>63%</div> <div>27%</div> <div>6%</div> <div>•</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4130 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 protein FlhS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	126	Total	C	N	O	S	0	0	0
			1054	676	175	201	2			
1	B	105	Total	C	N	O	S	0	0	0
			879	567	141	170	1			
1	C	104	Total	C	N	O	S	0	0	0
			870	561	139	169	1			
1	D	125	Total	C	N	O	S	0	0	0
			1044	670	172	200	2			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1125	HIS	-	EXPRESSION TAG	UNP O67806
A	1126	HIS	-	EXPRESSION TAG	UNP O67806
A	1127	HIS	-	EXPRESSION TAG	UNP O67806
A	1128	HIS	-	EXPRESSION TAG	UNP O67806
A	1129	HIS	-	EXPRESSION TAG	UNP O67806
A	1130	HIS	-	EXPRESSION TAG	UNP O67806
B	2125	HIS	-	EXPRESSION TAG	UNP O67806
B	2126	HIS	-	EXPRESSION TAG	UNP O67806
B	2127	HIS	-	EXPRESSION TAG	UNP O67806
B	2128	HIS	-	EXPRESSION TAG	UNP O67806
B	2129	HIS	-	EXPRESSION TAG	UNP O67806
B	2130	HIS	-	EXPRESSION TAG	UNP O67806
C	3125	HIS	-	EXPRESSION TAG	UNP O67806
C	3126	HIS	-	EXPRESSION TAG	UNP O67806
C	3127	HIS	-	EXPRESSION TAG	UNP O67806
C	3128	HIS	-	EXPRESSION TAG	UNP O67806
C	3129	HIS	-	EXPRESSION TAG	UNP O67806
C	3130	HIS	-	EXPRESSION TAG	UNP O67806
D	4125	HIS	-	EXPRESSION TAG	UNP O67806
D	4126	HIS	-	EXPRESSION TAG	UNP O67806
D	4127	HIS	-	EXPRESSION TAG	UNP O67806

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Chain	Residue	Modelled	Actual	Comment	Reference
D	4128	HIS	-	EXPRESSION TAG	UNP O67806
D	4129	HIS	-	EXPRESSION TAG	UNP O67806
D	4130	HIS	-	EXPRESSION TAG	UNP O67806

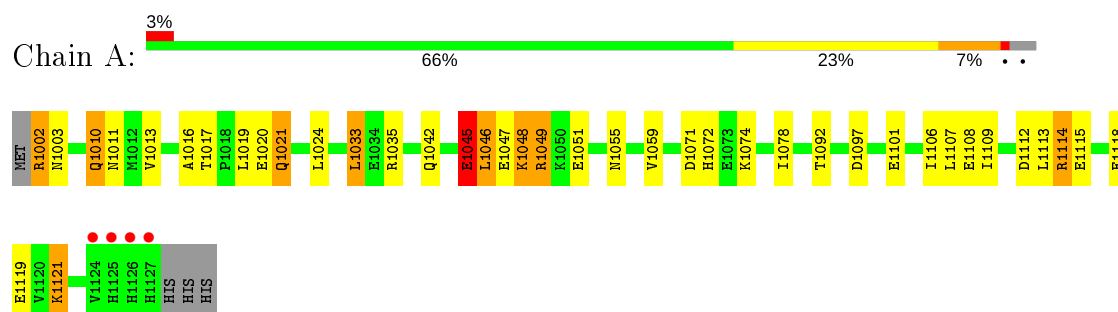
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	77	Total 77	O 77	0	0
2	B	69	Total 69	O 69	0	0
2	C	56	Total 56	O 56	0	0
2	D	81	Total 81	O 81	0	0

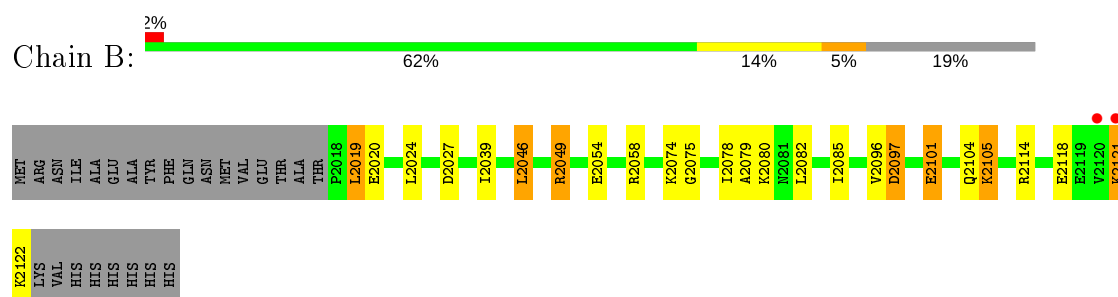
3 Residue-property plots [i](#)

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.

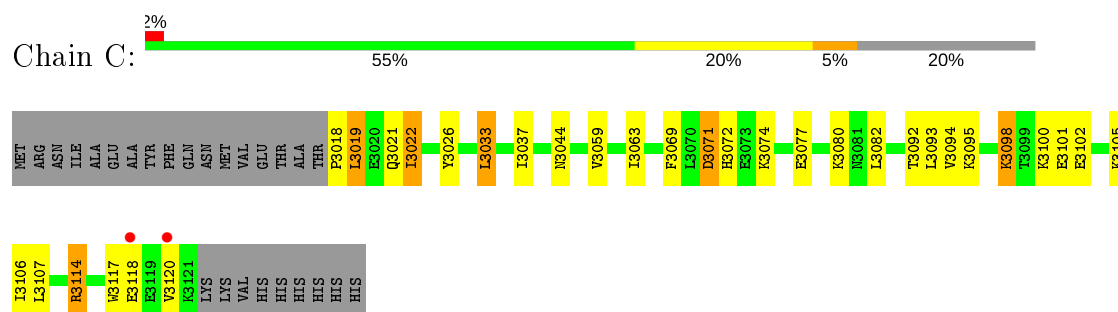
• Molecule 1: flagellar protein FliS



• Molecule 1: flagellar protein FliS

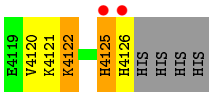
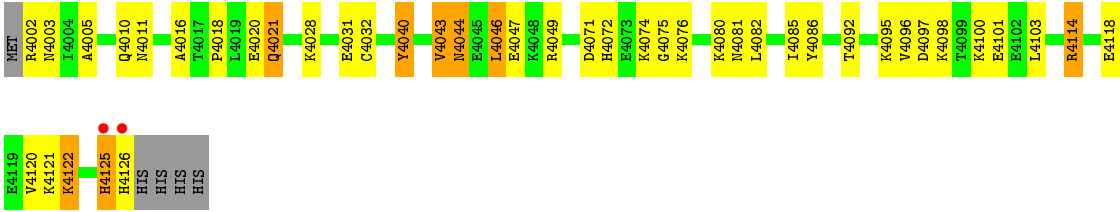


• Molecule 1: flagellar protein FliS



• Molecule 1: flagellar protein FliS





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	87.07Å 131.76Å 74.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.00 – 2.25 43.01 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.2 (43.00-2.25) 95.0 (43.01-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.1.19, SHELXL	Depositor
R, R_{free}	0.189 , 0.247 0.203 , 0.222	Depositor DCC
R_{free} test set	2120 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.634	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 101.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4130	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.43% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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	0.36	0/1068	0.85	0/1437
1	B	0.35	0/888	0.99	4/1192 (0.3%)
1	C	0.36	0/879	0.92	2/1181 (0.2%)
1	D	0.33	0/1057	0.88	2/1422 (0.1%)
All	All	0.35	0/3892	0.91	8/5232 (0.2%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2049	ARG	NE-CZ-NH2	-11.50	114.55	120.30
1	B	2049	ARG	CD-NE-CZ	7.31	133.83	123.60
1	B	2049	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	C	3074	LYS	C-N-CA	-5.86	109.99	122.30
1	D	4040	TYR	CB-CG-CD1	5.75	124.45	121.00

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	1054	0	1084	27	0
1	B	879	0	921	17	0
1	C	870	0	908	22	1
1	D	1044	0	1077	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	77	0	0	4	0
2	B	69	0	0	3	1
2	C	56	0	0	3	0
2	D	81	0	0	9	0
All	All	4130	0	3990	101	1

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 13.

The worst 5 of 101 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:1114:ARG:HD3	1:A:1118:GLU:OE2	1.80	0.81
1:D:4016:ALA:O	1:D:4020:GLU:HG3	1.85	0.78
1:B:2049:ARG:HD3	2:B:5059:HOH:O	1.84	0.76
1:D:4044:ASN:H	1:D:4044:ASN:HD22	1.35	0.75
1:A:1109:ILE:O	1:A:1112:ASP:OD1	2.04	0.74

All (1) 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:3077:GLU:OE2	2:B:5174:HOH:O[2_554]	2.17	0.03

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	124/130 (95%)	118 (95%)	3 (2%)	3 (2%)	6 3
1	B	103/130 (79%)	100 (97%)	3 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	102/130 (78%)	99 (97%)	3 (3%)	0	100	100
1	D	123/130 (95%)	119 (97%)	3 (2%)	1 (1%)	19	17
All	All	452/520 (87%)	436 (96%)	12 (3%)	4 (1%)	17	14

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1003	ASN
1	A	1011	ASN
1	A	1045	GLU
1	D	4003	ASN

5.3.2 Protein sidechains ⓘ

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	117/121 (97%)	101 (86%)	16 (14%)	3	2
1	B	99/121 (82%)	90 (91%)	9 (9%)	9	7
1	C	98/121 (81%)	88 (90%)	10 (10%)	7	5
1	D	116/121 (96%)	105 (90%)	11 (10%)	8	6
All	All	430/484 (89%)	384 (89%)	46 (11%)	6	4

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	2097	ASP
1	C	3019	LEU
1	D	4114	ARG
1	B	2101	GLU
1	B	2121	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	4010	GLN
1	D	4081	ASN
1	D	4044	ASN
1	A	1072	HIS
1	D	4072	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](#)

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	126/130 (96%)	0.06	4 (3%) 47 50	20, 42, 77, 117	0
1	B	105/130 (80%)	-0.17	2 (1%) 66 69	22, 38, 72, 108	0
1	C	104/130 (80%)	-0.19	2 (1%) 66 69	20, 41, 73, 89	0
1	D	125/130 (96%)	-0.04	2 (1%) 72 74	21, 38, 63, 110	0
All	All	460/520 (88%)	-0.08	10 (2%) 62 65	20, 40, 73, 117	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2121	LYS	4.4
1	A	1126	HIS	4.0
1	B	2120	VAL	3.5
1	D	4126	HIS	3.3
1	A	1125	HIS	3.2

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.