



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 27, 2016 – 01:11 PM EDT

PDB ID : 3VJP
Title : Orthorhombic Crystal Structure of Salmonella FlgA in closed form
Authors : Matsunami, H.; Samatey, F.A.; Namba, K.
Deposited on : 2011-10-27
Resolution : 2.70 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
<http://wwpdb.org/validation/2016/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
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
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-20027790

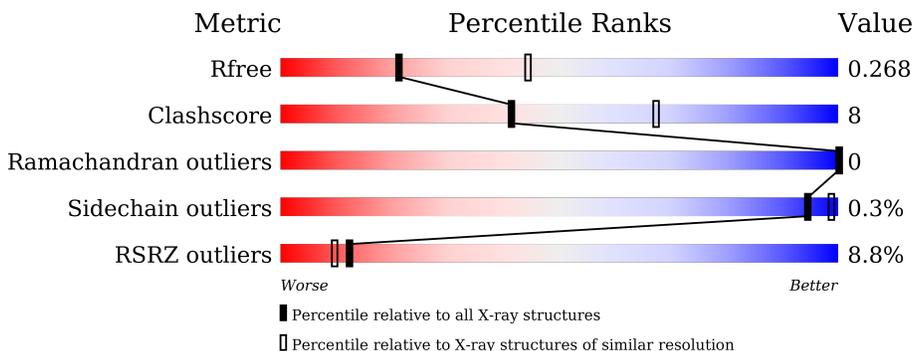
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 $\leq 5\%$. 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	219	 8% 73% 17% 10%
1	B	219	 8% 73% 17% 10%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 3035 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 Flagella basal body P-ring formation protein flgA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	198	1495	925	283	281	2	4	0	0	0
1	B	198	1495	925	283	281	2	4	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	199	ASP	-	EXPRESSION TAG	UNP P40131
A	200	PRO	-	EXPRESSION TAG	UNP P40131
A	201	ASN	-	EXPRESSION TAG	UNP P40131
A	202	SER	-	EXPRESSION TAG	UNP P40131
A	203	SER	-	EXPRESSION TAG	UNP P40131
A	204	SER	-	EXPRESSION TAG	UNP P40131
A	205	VAL	-	EXPRESSION TAG	UNP P40131
A	206	ASP	-	EXPRESSION TAG	UNP P40131
A	207	LYS	-	EXPRESSION TAG	UNP P40131
A	208	LEU	-	EXPRESSION TAG	UNP P40131
A	209	ALA	-	EXPRESSION TAG	UNP P40131
A	210	ALA	-	EXPRESSION TAG	UNP P40131
A	211	ALA	-	EXPRESSION TAG	UNP P40131
A	212	LEU	-	EXPRESSION TAG	UNP P40131
A	213	GLU	-	EXPRESSION TAG	UNP P40131
A	214	HIS	-	EXPRESSION TAG	UNP P40131
A	215	HIS	-	EXPRESSION TAG	UNP P40131
A	216	HIS	-	EXPRESSION TAG	UNP P40131
A	217	HIS	-	EXPRESSION TAG	UNP P40131
A	218	HIS	-	EXPRESSION TAG	UNP P40131
A	219	HIS	-	EXPRESSION TAG	UNP P40131
B	199	ASP	-	EXPRESSION TAG	UNP P40131
B	200	PRO	-	EXPRESSION TAG	UNP P40131
B	201	ASN	-	EXPRESSION TAG	UNP P40131
B	202	SER	-	EXPRESSION TAG	UNP P40131

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Chain	Residue	Modelled	Actual	Comment	Reference
B	203	SER	-	EXPRESSION TAG	UNP P40131
B	204	SER	-	EXPRESSION TAG	UNP P40131
B	205	VAL	-	EXPRESSION TAG	UNP P40131
B	206	ASP	-	EXPRESSION TAG	UNP P40131
B	207	LYS	-	EXPRESSION TAG	UNP P40131
B	208	LEU	-	EXPRESSION TAG	UNP P40131
B	209	ALA	-	EXPRESSION TAG	UNP P40131
B	210	ALA	-	EXPRESSION TAG	UNP P40131
B	211	ALA	-	EXPRESSION TAG	UNP P40131
B	212	LEU	-	EXPRESSION TAG	UNP P40131
B	213	GLU	-	EXPRESSION TAG	UNP P40131
B	214	HIS	-	EXPRESSION TAG	UNP P40131
B	215	HIS	-	EXPRESSION TAG	UNP P40131
B	216	HIS	-	EXPRESSION TAG	UNP P40131
B	217	HIS	-	EXPRESSION TAG	UNP P40131
B	218	HIS	-	EXPRESSION TAG	UNP P40131
B	219	HIS	-	EXPRESSION TAG	UNP P40131

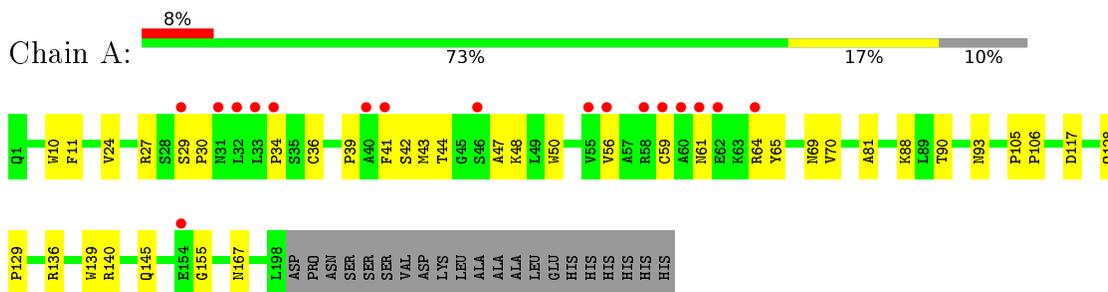
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	33	Total O 33 33	0	0
2	B	12	Total O 12 12	0	0

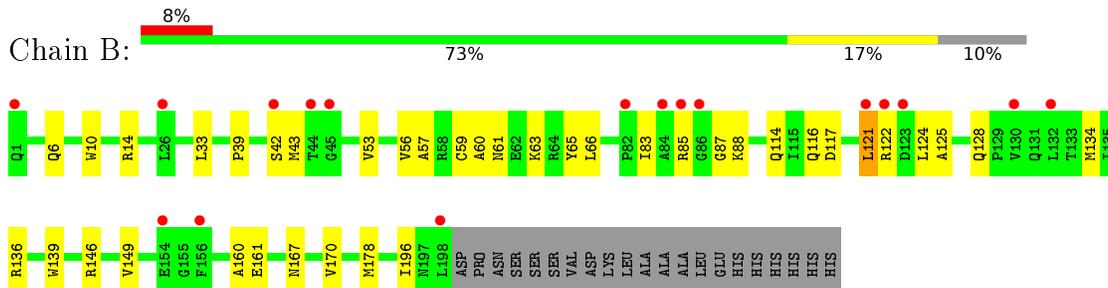
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Flagella basal body P-ring formation protein flgA



- Molecule 1: Flagella basal body P-ring formation protein flgA



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	53.17Å 162.50Å 103.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.55 – 2.70 28.49 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.7 (24.55-2.70) 97.6 (28.49-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 2.72Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.244 , 0.277 0.234 , 0.268	Depositor DCC
R_{free} test set	603 reflections (4.86%)	DCC
Wilson B-factor (Å ²)	55.2	Xtrriage
Anisotropy	0.563	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 63.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3035	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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	0.27	0/1511	0.51	0/2048
1	B	0.26	0/1511	0.52	0/2048
All	All	0.26	0/3022	0.51	0/4096

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	1495	0	1522	27	0
1	B	1495	0	1522	25	0
2	A	33	0	0	4	0
2	B	12	0	0	3	0
All	All	3035	0	3044	51	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 8.

All (51) 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:155:GLY:O	2:A:246:HOH:O	2.01	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:SER:HB2	1:A:56:VAL:HB	1.73	0.71
1:B:87:GLY:O	2:B:229:HOH:O	2.11	0.69
1:B:42:SER:HB2	1:B:56:VAL:HB	1.77	0.67
1:B:85:ARG:O	2:B:229:HOH:O	2.12	0.66
1:A:27:ARG:HD2	1:A:69:ASN:HB2	1.78	0.65
1:A:88:LYS:HE3	1:A:117:ASP:HA	1.78	0.64
1:A:36:CYS:SG	1:A:39:PRO:HB3	2.39	0.63
1:B:43:MSE:HE1	1:B:53:VAL:HG21	1.81	0.63
1:B:122:ARG:HD2	1:B:134:MSE:SE	2.50	0.62
1:B:39:PRO:HB3	1:B:59:CYS:SG	2.43	0.58
1:A:39:PRO:HG2	1:A:41:PHE:CE1	2.39	0.57
1:A:34:PRO:HB2	1:A:59:CYS:SG	2.44	0.57
1:B:88:LYS:HE3	1:B:117:ASP:HA	1.87	0.56
1:B:10:TRP:HH2	1:B:43:MSE:HG2	1.70	0.56
1:A:43:MSE:HE3	1:A:44:THR:H	1.73	0.54
1:A:34:PRO:HD3	1:A:64:ARG:HB2	1.89	0.54
1:B:149:VAL:HG13	1:B:196:ILE:HD13	1.89	0.53
1:B:160:ALA:HB1	1:B:178:MSE:HE1	1.90	0.51
1:A:48:LYS:NZ	2:A:243:HOH:O	2.34	0.50
1:B:6:GLN:OE1	1:B:39:PRO:HD2	2.12	0.50
1:B:125:ALA:O	1:B:128:GLN:HB2	2.12	0.50
1:B:83:ILE:HG21	1:B:87:GLY:HA3	1.93	0.49
1:A:59:CYS:O	1:A:61:ASN:N	2.45	0.48
1:A:47:ALA:O	1:A:48:LYS:HG3	2.12	0.48
1:B:114:GLN:HA	1:B:170:VAL:HG13	1.94	0.48
1:A:136:ARG:HD3	2:A:238:HOH:O	2.14	0.47
1:B:63:LYS:HE2	1:B:65:TYR:CE2	2.49	0.47
1:A:139:TRP:CD2	1:A:167:ASN:HB3	2.50	0.47
1:A:24:VAL:HG22	1:A:70:VAL:HG13	1.96	0.47
1:B:146:ARG:HH22	1:B:161:GLU:HB3	1.80	0.46
1:B:139:TRP:CD2	1:B:167:ASN:HB3	2.51	0.45
1:A:81:ALA:HB3	1:A:93:ASN:HA	1.97	0.45
1:A:140:ARG:NH1	2:A:221:HOH:O	2.39	0.45
1:B:57:ALA:HB2	1:B:66:LEU:HD11	1.99	0.44
1:A:29:SER:HA	1:A:30:PRO:HD2	1.84	0.44
1:A:50:TRP:HA	1:A:70:VAL:HB	2.00	0.44
1:A:145:GLN:HG2	1:B:116:GLN:HE22	1.83	0.44
1:A:10:TRP:CE2	1:A:41:PHE:HB2	2.53	0.43
1:B:124:LEU:HD21	1:B:134:MSE:HB3	2.00	0.42
1:B:60:ALA:O	1:B:61:ASN:HB3	2.20	0.42
1:B:33:LEU:HD23	1:B:66:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:PHE:HB2	1:A:24:VAL:HG21	2.01	0.42
1:B:121:LEU:HD11	1:B:136:ARG:HB2	2.01	0.42
1:A:56:VAL:HG22	1:A:65:TYR:CE1	2.55	0.42
1:A:88:LYS:O	1:A:90:THR:HG23	2.21	0.41
1:B:14:ARG:NH2	2:B:224:HOH:O	2.53	0.41
1:B:10:TRP:CH2	1:B:43:MSE:HG2	2.53	0.41
1:A:128:GLN:HA	1:A:129:PRO:HD3	1.92	0.41
1:A:44:THR:HG23	1:A:44:THR:O	2.21	0.41
1:A:105:PRO:HA	1:A:106:PRO:HD3	1.95	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	196/219 (90%)	188 (96%)	8 (4%)	0	100	100
1	B	196/219 (90%)	185 (94%)	11 (6%)	0	100	100
All	All	392/438 (90%)	373 (95%)	19 (5%)	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	160/174 (92%)	160 (100%)	0	100	100
1	B	160/174 (92%)	159 (99%)	1 (1%)	90	97
All	All	320/348 (92%)	319 (100%)	1 (0%)	94	99

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	121	LEU

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	148	GLN
1	A	193	ASN
1	B	148	GLN

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

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, 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	194/219 (88%)	0.50	17 (8%) 12 10	26, 65, 114, 147	0
1	B	194/219 (88%)	0.57	17 (8%) 12 10	28, 76, 116, 157	0
All	All	388/438 (88%)	0.54	34 (8%) 12 10	26, 71, 115, 157	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	121	LEU	4.9
1	A	31	ASN	4.8
1	A	46	SER	4.6
1	A	32	LEU	4.2
1	A	154	GLU	4.2
1	A	29	SER	4.0
1	B	86	GLY	3.9
1	B	1	GLN	3.7
1	B	154	GLU	3.6
1	A	40	ALA	3.4
1	A	59	CYS	3.3
1	B	85	ARG	3.2
1	A	64	ARG	3.1
1	B	123	ASP	3.0
1	A	56	VAL	2.9
1	A	41	PHE	2.8
1	A	34	PRO	2.8
1	A	58	ARG	2.8
1	B	84	ALA	2.7
1	B	42	SER	2.7
1	B	122	ARG	2.5
1	B	130	VAL	2.5
1	B	198	LEU	2.5
1	A	61	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	132	LEU	2.4
1	A	33	LEU	2.2
1	B	26	LEU	2.2
1	B	82	PRO	2.2
1	A	62	GLU	2.1
1	B	156	PHE	2.1
1	A	60	ALA	2.1
1	B	44	THR	2.1
1	A	55	VAL	2.0
1	B	45	GLY	2.0

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.