wwPDB X-ray Structure Validation Summary Report (i)

May 26, 2020 – 12:30 pm BST

PDB ID	:	6F3Z
Title	:	Complex of E. coli LolA and periplasmic domain of LolC
Authors	:	Kaplan, E.
Deposited on	:	2017-11-29
Resolution	:	2.00 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 following versions of software and data (see references (1)) were used in the production of this report:

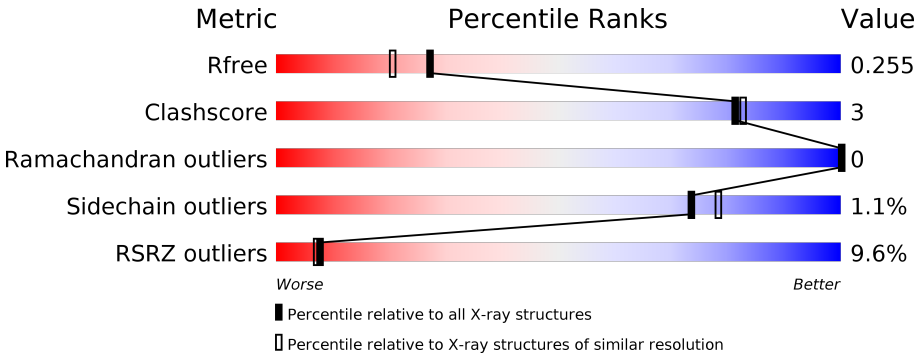
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	230	10% 91% 9%
1	C	230	11% 91% 7% •
2	B	206	7% 79% 11% • 9%
2	D	206	8% 82% 8% • 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6688 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 Lipoprotein-releasing system transmembrane protein LolC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	1	0
			1806	1131	327	339	9			
1	C	225	Total	C	N	O	S	0	0	0
			1748	1097	310	332	9			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	267	ALA	-	expression tag	UNP P0ADC3
A	268	ALA	-	expression tag	UNP P0ADC3
A	269	ALA	-	expression tag	UNP P0ADC3
A	270	LEU	-	expression tag	UNP P0ADC3
A	271	GLU	-	expression tag	UNP P0ADC3
A	272	HIS	-	expression tag	UNP P0ADC3
A	273	HIS	-	expression tag	UNP P0ADC3
A	274	HIS	-	expression tag	UNP P0ADC3
A	275	HIS	-	expression tag	UNP P0ADC3
A	276	HIS	-	expression tag	UNP P0ADC3
A	277	HIS	-	expression tag	UNP P0ADC3
C	267	ALA	-	expression tag	UNP P0ADC3
C	268	ALA	-	expression tag	UNP P0ADC3
C	269	ALA	-	expression tag	UNP P0ADC3
C	270	LEU	-	expression tag	UNP P0ADC3
C	271	GLU	-	expression tag	UNP P0ADC3
C	272	HIS	-	expression tag	UNP P0ADC3
C	273	HIS	-	expression tag	UNP P0ADC3
C	274	HIS	-	expression tag	UNP P0ADC3
C	275	HIS	-	expression tag	UNP P0ADC3
C	276	HIS	-	expression tag	UNP P0ADC3
C	277	HIS	-	expression tag	UNP P0ADC3

- Molecule 2 is a protein called Outer-membrane lipoprotein carrier protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	188	Total	C	N	O	S	0	2	0
			1494	929	263	298	4			
2	D	188	Total	C	N	O	S	0	1	0
			1488	926	262	296	4			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-23	MET	-	initiating methionine	UNP P61316
B	-22	GLY	-	expression tag	UNP P61316
B	-21	SER	-	expression tag	UNP P61316
B	-20	SER	-	expression tag	UNP P61316
B	-19	HIS	-	expression tag	UNP P61316
B	-18	HIS	-	expression tag	UNP P61316
B	-17	HIS	-	expression tag	UNP P61316
B	-16	HIS	-	expression tag	UNP P61316
B	-15	HIS	-	expression tag	UNP P61316
B	-14	HIS	-	expression tag	UNP P61316
B	-13	SER	-	expression tag	UNP P61316
B	-12	SER	-	expression tag	UNP P61316
B	-11	GLY	-	expression tag	UNP P61316
B	-10	LEU	-	expression tag	UNP P61316
B	-9	VAL	-	expression tag	UNP P61316
B	-8	PRO	-	expression tag	UNP P61316
B	-7	ARG	-	expression tag	UNP P61316
B	-6	GLY	-	expression tag	UNP P61316
B	-5	SER	-	expression tag	UNP P61316
B	-4	HIS	-	expression tag	UNP P61316
B	-3	MET	-	expression tag	UNP P61316
B	-2	ALA	-	expression tag	UNP P61316
B	-1	SER	-	expression tag	UNP P61316
B	0	MET	-	expression tag	UNP P61316
D	-23	MET	-	initiating methionine	UNP P61316
D	-22	GLY	-	expression tag	UNP P61316
D	-21	SER	-	expression tag	UNP P61316
D	-20	SER	-	expression tag	UNP P61316
D	-19	HIS	-	expression tag	UNP P61316
D	-18	HIS	-	expression tag	UNP P61316
D	-17	HIS	-	expression tag	UNP P61316
D	-16	HIS	-	expression tag	UNP P61316
D	-15	HIS	-	expression tag	UNP P61316
D	-14	HIS	-	expression tag	UNP P61316
D	-13	SER	-	expression tag	UNP P61316

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-12	SER	-	expression tag	UNP P61316
D	-11	GLY	-	expression tag	UNP P61316
D	-10	LEU	-	expression tag	UNP P61316
D	-9	VAL	-	expression tag	UNP P61316
D	-8	PRO	-	expression tag	UNP P61316
D	-7	ARG	-	expression tag	UNP P61316
D	-6	GLY	-	expression tag	UNP P61316
D	-5	SER	-	expression tag	UNP P61316
D	-4	HIS	-	expression tag	UNP P61316
D	-3	MET	-	expression tag	UNP P61316
D	-2	ALA	-	expression tag	UNP P61316
D	-1	SER	-	expression tag	UNP P61316
D	0	MET	-	expression tag	UNP P61316

- Molecule 3 is water.

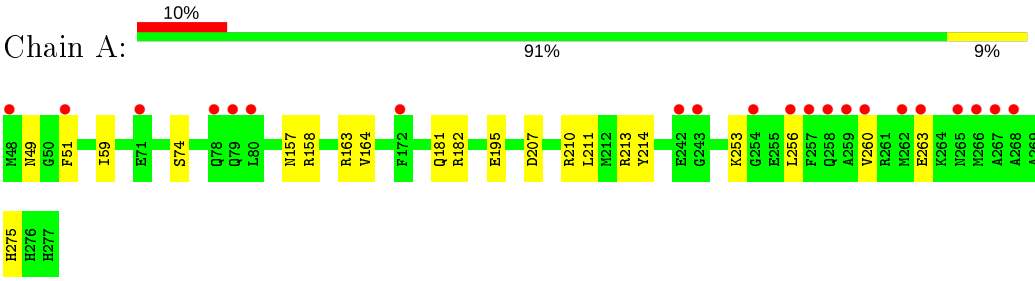
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	34	Total O 34 34	0	0
3	B	42	Total O 42 42	0	0
3	C	34	Total O 34 34	0	0
3	D	42	Total O 42 42	0	0

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.

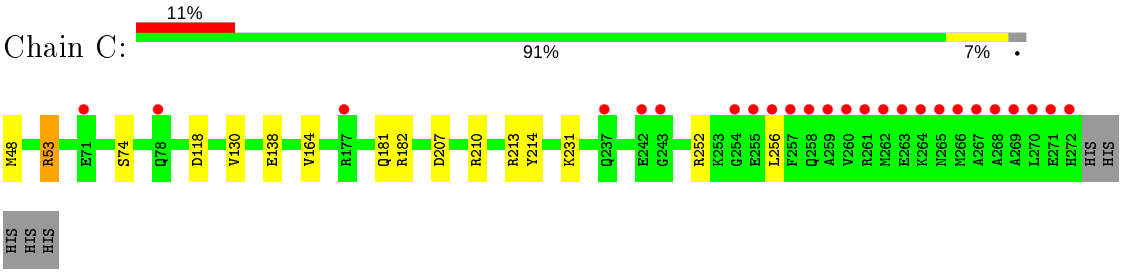
• Molecule 1: Lipoprotein-releasing system transmembrane protein LolC

Chain A:



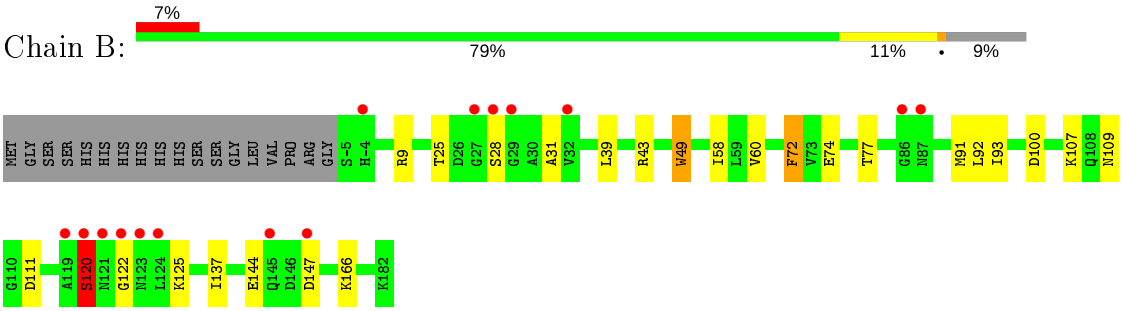
• Molecule 1: Lipoprotein-releasing system transmembrane protein LolC

Chain C:



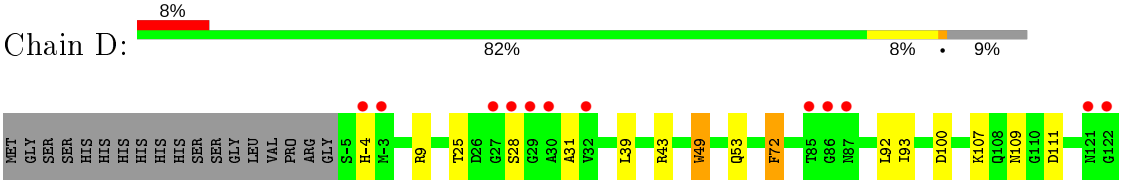
• Molecule 2: Outer-membrane lipoprotein carrier protein

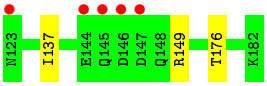
Chain B:



• Molecule 2: Outer-membrane lipoprotein carrier protein

Chain D:




N123
I137
E144
Q145
D146
D147
Q148
R149
T176
K182

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	146.01Å 68.23Å 94.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.01 – 2.00 61.81 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.2 (73.01-2.00) 95.2 (61.81-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.79 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.202 , 0.249 0.211 , 0.255	Depositor DCC
R_{free} test set	3124 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	31.0	Xtriage
Anisotropy	0.738	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 50.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6688	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.93 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2308e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

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	0.90	0/1843	0.97	8/2500 (0.3%)
1	C	0.87	0/1780	0.94	6/2414 (0.2%)
2	B	1.02	1/1528 (0.1%)	0.97	5/2070 (0.2%)
2	D	1.01	1/1522 (0.1%)	0.98	5/2062 (0.2%)
All	All	0.94	2/6673 (0.0%)	0.96	24/9046 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	49	TRP	CB-CG	-9.18	1.33	1.50
2	B	49	TRP	CB-CG	-8.19	1.35	1.50

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	43	ARG	NE-CZ-NH1	9.32	124.96	120.30
2	B	43	ARG	NE-CZ-NH1	7.71	124.15	120.30
1	A	213	ARG	NE-CZ-NH1	7.30	123.95	120.30
2	D	111	ASP	CB-CG-OD1	6.90	124.51	118.30
1	A	163	ARG	NE-CZ-NH1	6.67	123.63	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	120	SER	Peptide

5.2 Too-close contacts

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	1806	0	1793	8	1
1	C	1748	0	1753	7	1
2	B	1494	0	1414	12	0
2	D	1488	0	1410	9	1
3	A	34	0	0	0	0
3	B	42	0	0	2	0
3	C	34	0	0	1	0
3	D	42	0	0	2	0
All	All	6688	0	6370	34	2

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 3.

The worst 5 of 34 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)
2:B:120:SER:OG	2:B:122:GLY:O	2.15	0.65
2:D:-4:HIS:NE2	3:D:201:HOH:O	2.26	0.60
2:B:107:LYS:HE2	2:B:109[A]:ASN:HD21	1.68	0.59
2:B:74:GLU:OE1	3:B:201:HOH:O	2.17	0.58
1:C:130:VAL:O	3:C:301:HOH:O	2.17	0.57

All (2) 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)
2:D:53:GLN:NE2	2:D:53:GLN:NE2[2_565]	1.55	0.65
1:A:275:HIS:NE2	1:C:138:GLU:OE1[4_556]	2.18	0.02

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	229/230 (100%)	221 (96%)	8 (4%)	0	100	100
1	C	223/230 (97%)	217 (97%)	6 (3%)	0	100	100
2	B	188/206 (91%)	181 (96%)	7 (4%)	0	100	100
2	D	187/206 (91%)	178 (95%)	9 (5%)	0	100	100
All	All	827/872 (95%)	797 (96%)	30 (4%)	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	197/196 (100%)	195 (99%)	2 (1%)	76	81
1	C	191/196 (97%)	190 (100%)	1 (0%)	88	92
2	B	163/176 (93%)	159 (98%)	4 (2%)	47	49
2	D	162/176 (92%)	160 (99%)	2 (1%)	71	76
All	All	713/744 (96%)	704 (99%)	9 (1%)	73	74

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	120	SER
2	D	72	PHE
1	C	231	LYS

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Mol	Chain	Res	Type
2	B	28	SER
2	B	147	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
2	B	148	GLN
1	C	258	GLN
2	D	53	GLN
2	D	153	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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, 95^{th} 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	230/230 (100%)	0.35	23 (10%)	7 6	22, 41, 85, 96	0
1	C	225/230 (97%)	0.60	25 (11%)	5 4	26, 42, 121, 140	0
2	B	188/206 (91%)	0.34	15 (7%)	12 11	20, 38, 91, 118	0
2	D	188/206 (91%)	0.42	17 (9%)	9 8	24, 39, 99, 112	0
All	All	831/872 (95%)	0.43	80 (9%)	8 7	20, 40, 95, 140	0

The worst 5 of 80 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	257	PHE	15.1
1	C	262	MET	10.5
1	C	260	VAL	10.0
1	C	268	ALA	8.4
1	C	256	LEU	8.4

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.