Full wwPDB X-ray Structure Validation Report (i)

May 21, 2020 – 06:01 am BST

PDB ID	:	6H2E
Title	:	Structure of the soluble AhlC of the tripartite alpha-pore forming toxin, AHL, from Aeromonas hydrophila.
Authors	:	Churchill-Angus, A.M.; Wilson, J.S.; Baker, P.J.
Deposited on	:	2018-07-13
Resolution	:	2.35 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
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:

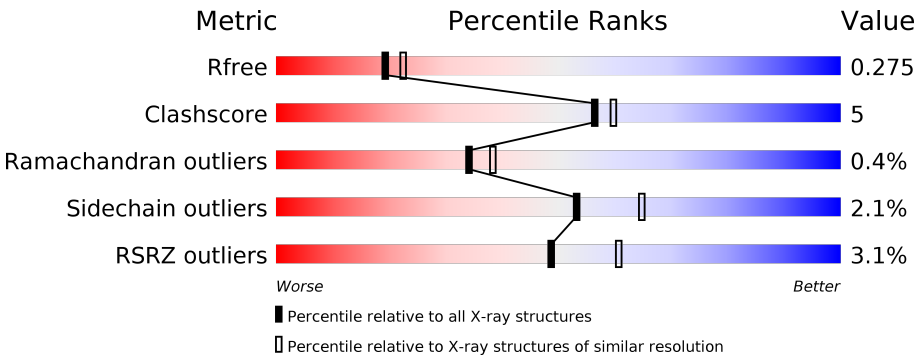
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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	P	274	2% 81% 10% • 7%
1	Q	274	4% 84% 10% • 5%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 3866 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 AhlC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	P	254	1908	1193	335	378	2	0	0	0
1	Q	259	1958	1218	348	390	2	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

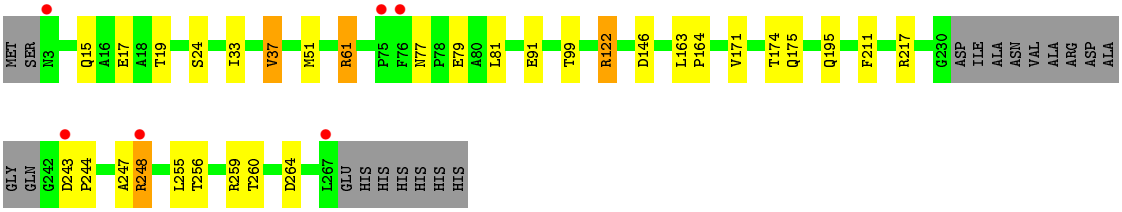
Chain	Residue	Modelled	Actual	Comment	Reference
P	267	LEU	-	expression tag	UNP A0A1U6XZ15
P	268	GLU	-	expression tag	UNP A0A1U6XZ15
P	269	HIS	-	expression tag	UNP A0A1U6XZ15
P	270	HIS	-	expression tag	UNP A0A1U6XZ15
P	271	HIS	-	expression tag	UNP A0A1U6XZ15
P	272	HIS	-	expression tag	UNP A0A1U6XZ15
P	273	HIS	-	expression tag	UNP A0A1U6XZ15
P	274	HIS	-	expression tag	UNP A0A1U6XZ15
Q	267	LEU	-	expression tag	UNP A0A1U6XZ15
Q	268	GLU	-	expression tag	UNP A0A1U6XZ15
Q	269	HIS	-	expression tag	UNP A0A1U6XZ15
Q	270	HIS	-	expression tag	UNP A0A1U6XZ15
Q	271	HIS	-	expression tag	UNP A0A1U6XZ15
Q	272	HIS	-	expression tag	UNP A0A1U6XZ15
Q	273	HIS	-	expression tag	UNP A0A1U6XZ15
Q	274	HIS	-	expression tag	UNP A0A1U6XZ15

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.

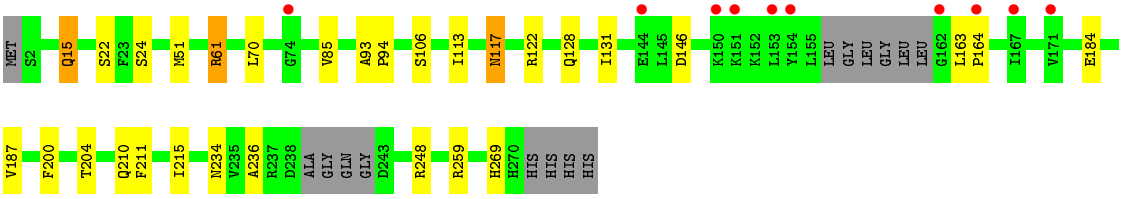
- Molecule 1: AhlC

Chain P:



- Molecule 1: AhlC

Chain Q:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	134.71Å 134.71Å 145.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	58.33 – 2.35 58.33 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.7 (58.33-2.35) 99.8 (58.33-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.86 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.227 , 0.274 0.229 , 0.275	Depositor DCC
R_{free} test set	1589 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å^2)	62.7	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 34.2	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	0.95	EDS
Total number of atoms	3866	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.30% 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	P	0.67	0/1923	0.74	1/2609 (0.0%)
1	Q	0.66	0/1974	0.76	1/2678 (0.0%)
All	All	0.66	0/3897	0.75	2/5287 (0.0%)

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
1	P	0	2
1	Q	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	P	122	ARG	NE-CZ-NH1	-5.54	117.53	120.30
1	Q	259	ARG	NE-CZ-NH2	-5.38	117.61	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	P	248	ARG	Sidechain
1	P	61	ARG	Sidechain
1	Q	61	ARG	Sidechain

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	P	1908	0	1956	25	0
1	Q	1958	0	1981	20	0
All	All	3866	0	3937	39	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 5.

All (39) 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:P:15:GLN:HE22	1:Q:24:SER:H	1.27	0.81
1:P:51:MET:HE2	1:P:99:THR:HA	1.74	0.69
1:P:195:GLN:HE22	1:Q:210:GLN:HE21	1.38	0.69
1:P:122:ARG:HG2	1:P:122:ARG:HH11	1.59	0.68
1:P:51:MET:CE	1:P:99:THR:HA	2.23	0.67
1:P:19:THR:HG22	1:Q:22:SER:OG	1.96	0.66
1:Q:85:VAL:HG11	1:Q:236:ALA:HB2	1.77	0.66
1:P:247:ALA:O	1:P:248:ARG:C	2.33	0.64
1:Q:106:SER:HB3	1:Q:215:ILE:CD1	2.31	0.60
1:Q:163:LEU:N	1:Q:164:PRO:CD	2.67	0.58
1:P:256:THR:O	1:P:260:THR:HG23	2.04	0.57
1:P:33:ILE:O	1:P:37:VAL:HB	2.07	0.55
1:Q:106:SER:HB3	1:Q:215:ILE:HD11	1.88	0.55
1:P:217:ARG:HD2	1:P:264:ASP:O	2.08	0.53
1:P:24:SER:H	1:Q:15:GLN:HE22	1.54	0.53
1:Q:200:PHE:O	1:Q:204:THR:HG23	2.11	0.51
1:Q:61:ARG:HG3	1:Q:61:ARG:HH11	1.76	0.51
1:Q:163:LEU:N	1:Q:164:PRO:HD2	2.27	0.50
1:P:163:LEU:HB3	1:P:164:PRO:HD3	1.94	0.50
1:P:17:GLU:HG2	1:P:37:VAL:HG13	1.93	0.50
1:P:243:ASP:HB2	1:P:244:PRO:HD2	1.92	0.49
1:P:195:GLN:NE2	1:Q:210:GLN:HE21	2.07	0.49
1:P:163:LEU:HD21	1:Q:248:ARG:HG2	1.95	0.48
1:P:77:ASN:OD1	1:P:79:GLU:HB2	2.14	0.47
1:P:122:ARG:CG	1:P:122:ARG:HH11	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:113:ILE:O	1:Q:117:ASN:HB2	2.15	0.46
1:Q:70:LEU:CD2	1:Q:248:ARG:HD3	2.46	0.46
1:Q:184:GLU:O	1:Q:187:VAL:HG22	2.16	0.46
1:Q:122:ARG:HH11	1:Q:122:ARG:HG2	1.82	0.45
1:Q:128:GLN:HA	1:Q:131:ILE:HG12	1.99	0.44
1:Q:93:ALA:N	1:Q:94:PRO:HD2	2.32	0.44
1:P:171:VAL:HG12	1:P:175:GLN:NE2	2.33	0.43
1:P:255:LEU:HD21	1:P:259:ARG:NH1	2.34	0.43
1:Q:106:SER:CB	1:Q:215:ILE:HD12	2.49	0.43
1:P:81:LEU:HD23	1:P:81:LEU:N	2.35	0.41
1:P:17:GLU:CG	1:P:37:VAL:HG13	2.51	0.41
1:P:61:ARG:NH2	1:P:91:GLU:OE1	2.54	0.41
1:P:51:MET:HE3	1:P:99:THR:HA	2.01	0.40
1:P:17:GLU:HG2	1:P:37:VAL:CG1	2.52	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	P	250/274 (91%)	241 (96%)	9 (4%)	0	100 100
1	Q	253/274 (92%)	242 (96%)	9 (4%)	2 (1%)	19 20
All	All	503/548 (92%)	483 (96%)	18 (4%)	2 (0%)	34 38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Q	234	ASN
1	Q	269	HIS

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	P	207/223 (93%)	203 (98%)	4 (2%)	57	68
1	Q	212/223 (95%)	207 (98%)	5 (2%)	49	59
All	All	419/446 (94%)	410 (98%)	9 (2%)	53	65

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	37	VAL
1	P	146	ASP
1	P	174	THR
1	P	211	PHE
1	Q	15	GLN
1	Q	51	MET
1	Q	117	ASN
1	Q	146	ASP
1	Q	211	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	P	15	GLN
1	P	175	GLN
1	P	195	GLN
1	Q	15	GLN
1	Q	54	GLN
1	Q	115	GLN
1	Q	195	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 (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	P	254/274 (92%)	0.06	6 (2%)	59	68	46, 61, 108, 144	0
1	Q	259/274 (94%)	0.17	10 (3%)	39	52	46, 62, 111, 163	0
All	All	513/548 (93%)	0.11	16 (3%)	49	61	46, 62, 111, 163	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	153	LEU	7.1
1	Q	154	TYR	5.5
1	Q	167	ILE	4.3
1	Q	164	PRO	3.3
1	P	267	LEU	2.7
1	P	76	PHE	2.5
1	Q	150	LYS	2.4
1	Q	144	GLU	2.4
1	P	75	PRO	2.3
1	Q	74	GLY	2.3
1	P	243	ASP	2.2
1	Q	151	LYS	2.2
1	P	248	ARG	2.2
1	Q	171	VAL	2.2
1	P	3	ASN	2.0
1	Q	162	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.