Full wwPDB X-ray Structure Validation Report (i)

Oct 2, 2023 – 02:38 PM EDT

PDB ID	:	6NKL
Title	:	2.2 A resolution structure of VapBC-1 from nontypeable Haemophilus influenzae
Authors	:	Lovell, S.; Kashipathy, M.M.; Battaile, K.P.; Molinaro, A.L.; Daines, D.A.
Deposited on	:	2019-01-07
Resolution	:	2.20 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity	:	FAILED
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.20 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3246 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 Ribonuclease VapC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	134	1040	674	174	187	5	0	0	0
1	B	135	1063	693	175	189	6	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	135	LEU	-	expression tag	UNP A0A2R3FUY7
A	136	LEU	-	expression tag	UNP A0A2R3FUY7
A	137	GLU	-	expression tag	UNP A0A2R3FUY7
A	138	HIS	-	expression tag	UNP A0A2R3FUY7
A	139	HIS	-	expression tag	UNP A0A2R3FUY7
A	140	HIS	-	expression tag	UNP A0A2R3FUY7
A	141	HIS	-	expression tag	UNP A0A2R3FUY7
A	142	HIS	-	expression tag	UNP A0A2R3FUY7
A	143	HIS	-	expression tag	UNP A0A2R3FUY7
B	135	LEU	-	expression tag	UNP A0A2R3FUY7
B	136	LEU	-	expression tag	UNP A0A2R3FUY7
B	137	GLU	-	expression tag	UNP A0A2R3FUY7
B	138	HIS	-	expression tag	UNP A0A2R3FUY7
B	139	HIS	-	expression tag	UNP A0A2R3FUY7
B	140	HIS	-	expression tag	UNP A0A2R3FUY7
B	141	HIS	-	expression tag	UNP A0A2R3FUY7
B	142	HIS	-	expression tag	UNP A0A2R3FUY7
B	143	HIS	-	expression tag	UNP A0A2R3FUY7

- Molecule 2 is a protein called Antitoxin VapB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	74	551	355	85	109	2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	70	534	343	88	102	1	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-17	MET	-	initiating methionine	UNP A0A2S9RDZ4
C	-16	ALA	-	expression tag	UNP A0A2S9RDZ4
C	-15	SER	-	expression tag	UNP A0A2S9RDZ4
C	-14	MET	-	expression tag	UNP A0A2S9RDZ4
C	-13	THR	-	expression tag	UNP A0A2S9RDZ4
C	-12	GLY	-	expression tag	UNP A0A2S9RDZ4
C	-11	GLY	-	expression tag	UNP A0A2S9RDZ4
C	-10	GLN	-	expression tag	UNP A0A2S9RDZ4
C	-9	GLN	-	expression tag	UNP A0A2S9RDZ4
C	-8	MET	-	expression tag	UNP A0A2S9RDZ4
C	-7	GLY	-	expression tag	UNP A0A2S9RDZ4
C	-6	ARG	-	expression tag	UNP A0A2S9RDZ4
C	-5	ASP	-	expression tag	UNP A0A2S9RDZ4
C	-4	PRO	-	expression tag	UNP A0A2S9RDZ4
C	-3	ASN	-	expression tag	UNP A0A2S9RDZ4
C	-2	SER	-	expression tag	UNP A0A2S9RDZ4
C	-1	SER	-	expression tag	UNP A0A2S9RDZ4
C	0	SER	-	expression tag	UNP A0A2S9RDZ4
D	-17	MET	-	initiating methionine	UNP A0A2S9RDZ4
D	-16	ALA	-	expression tag	UNP A0A2S9RDZ4
D	-15	SER	-	expression tag	UNP A0A2S9RDZ4
D	-14	MET	-	expression tag	UNP A0A2S9RDZ4
D	-13	THR	-	expression tag	UNP A0A2S9RDZ4
D	-12	GLY	-	expression tag	UNP A0A2S9RDZ4
D	-11	GLY	-	expression tag	UNP A0A2S9RDZ4
D	-10	GLN	-	expression tag	UNP A0A2S9RDZ4
D	-9	GLN	-	expression tag	UNP A0A2S9RDZ4
D	-8	MET	-	expression tag	UNP A0A2S9RDZ4
D	-7	GLY	-	expression tag	UNP A0A2S9RDZ4
D	-6	ARG	-	expression tag	UNP A0A2S9RDZ4
D	-5	ASP	-	expression tag	UNP A0A2S9RDZ4
D	-4	PRO	-	expression tag	UNP A0A2S9RDZ4
D	-3	ASN	-	expression tag	UNP A0A2S9RDZ4
D	-2	SER	-	expression tag	UNP A0A2S9RDZ4
D	-1	SER	-	expression tag	UNP A0A2S9RDZ4
D	0	SER	-	expression tag	UNP A0A2S9RDZ4

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	12	12	12	0	0
			Total	O		
3	B	27	27	27	0	0
			Total	O		
3	C	6	6	6	0	0
			Total	O		
3	D	13	13	13	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	43.88Å 57.33Å 175.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.01 – 2.20	Depositor
% Data completeness (in resolution range)	99.9 (48.01-2.20)	Depositor
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.10 (at 2.20Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.186 , 0.234	Depositor
Wilson B-factor (Å^2)	37.1	Xtriage
Anisotropy	0.468	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3246	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.