



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 4, 2023 – 09:20 PM EDT

PDB ID : 6V7V
Title : Structure of a phage-encoded quorum sensing anti-activator, Aqs1
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Deposited on : 2019-12-09
Resolution : 2.30 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : **FAILED**
Xtrriage (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

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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 2 unique types of molecules in this entry. The entry contains 2835 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 Quorum sensing anti-activator Aqs1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	62	473	294	83	96	0	0	0
1	B	56	438	274	80	83	1	0	0
1	C	62	482	299	86	96	1	0	0
1	D	55	430	269	79	82	0	0	0
1	E	62	482	299	86	96	1	0	0
1	F	55	430	269	79	82	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	ALA	LYS	engineered mutation	UNP A0SML3
A	25	ALA	GLU	engineered mutation	UNP A0SML3
B	24	ALA	LYS	engineered mutation	UNP A0SML3
B	25	ALA	GLU	engineered mutation	UNP A0SML3
C	24	ALA	LYS	engineered mutation	UNP A0SML3
C	25	ALA	GLU	engineered mutation	UNP A0SML3
D	24	ALA	LYS	engineered mutation	UNP A0SML3
D	25	ALA	GLU	engineered mutation	UNP A0SML3
E	24	ALA	LYS	engineered mutation	UNP A0SML3
E	25	ALA	GLU	engineered mutation	UNP A0SML3
F	24	ALA	LYS	engineered mutation	UNP A0SML3
F	25	ALA	GLU	engineered mutation	UNP A0SML3

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	19	Total O 19 19	0	0
2	B	12	Total O 12 12	0	0
2	C	24	Total O 24 24	0	0
2	D	9	Total O 9 9	0	0
2	E	20	Total O 20 20	0	0
2	F	16	Total O 16 16	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	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	114.73Å 66.12Å 73.21Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	45.17 – 2.30	Depositor
% Data completeness (in resolution range)	98.9 (45.17-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.205 , 0.244	Depositor
Wilson B-factor (Å ²)	29.2	Xtrriage
Anisotropy	0.889	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.036 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.034 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.459 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.457 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.036 for -h,-k,l	Xtrriage
Total number of atoms	2835	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.28% 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.

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](#)

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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

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](#)

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5.3 Carbohydrates [i](#)

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5.4 Ligands [i](#)

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5.5 Other polymers [i](#)

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