



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 08:39 AM UTC

PDB ID : 6AS3 / pdb_00006as3
Title : Structure of a phage anti-CRISPR protein
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Deposited on : 2017-08-23
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 ⓘ 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

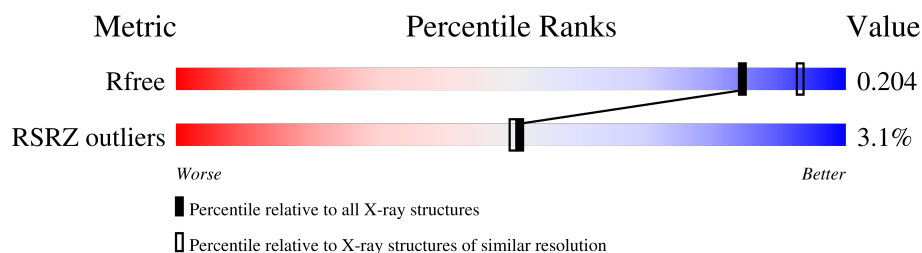
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3066 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 NHis AcrE1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	95	Total	C	N	O	S	0	5	0
			779	491	134	150	4			
1	1-B	94	Total	C	N	O	S	0	3	0
			755	473	131	148	3			
1	1-C	65	Total	C	N	O		0	4	0
			521	329	87	105				
1	?-C	1	Total	S				0	0	1
			1	1						
1	1-D	64	Total	C	N	O	S	0	5	0
			531	333	90	105	3			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP L7P7L6
A	-4	HIS	-	expression tag	UNP L7P7L6
A	-3	HIS	-	expression tag	UNP L7P7L6
A	-2	HIS	-	expression tag	UNP L7P7L6
A	-1	HIS	-	expression tag	UNP L7P7L6
A	0	HIS	-	expression tag	UNP L7P7L6
A	86	TYR	HIS	engineered mutation	UNP L7P7L6
B	-5	HIS	-	expression tag	UNP L7P7L6
B	-4	HIS	-	expression tag	UNP L7P7L6
B	-3	HIS	-	expression tag	UNP L7P7L6
B	-2	HIS	-	expression tag	UNP L7P7L6
B	-1	HIS	-	expression tag	UNP L7P7L6
B	0	HIS	-	expression tag	UNP L7P7L6
B	86	TYR	HIS	engineered mutation	UNP L7P7L6
C	-5	HIS	-	expression tag	UNP L7P7L6
C	-4	HIS	-	expression tag	UNP L7P7L6
C	-3	HIS	-	expression tag	UNP L7P7L6
C	-2	HIS	-	expression tag	UNP L7P7L6
C	-1	HIS	-	expression tag	UNP L7P7L6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP L7P7L6
C	86	TYR	HIS	engineered mutation	UNP L7P7L6
D	-5	HIS	-	expression tag	UNP L7P7L6
D	-4	HIS	-	expression tag	UNP L7P7L6
D	-3	HIS	-	expression tag	UNP L7P7L6
D	-2	HIS	-	expression tag	UNP L7P7L6
D	-1	HIS	-	expression tag	UNP L7P7L6
D	0	HIS	-	expression tag	UNP L7P7L6
D	86	TYR	HIS	engineered mutation	UNP L7P7L6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	103	Total O 103 103	0	0
2	1-B	115	Total O 115 115	0	0
2	1-C	106	Total O 106 106	0	0
2	1-D	108	Total O 108 108	0	0

SEQUENCE-PLOTS INFOmissingINFO

3 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.80Å 87.46Å 91.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	63.09 – 2.00 63.09 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (63.09-2.00) 96.4 (63.09-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.60 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.164 , 0.214 (Not available) , 0.204	Depositor DCC
R_{free} test set	1743 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	0.571	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3066	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.26% 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](#)

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 oligosaccharides 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](#)

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	1-A	95/106 (89%)	-0.22	4 (4%)	40	39	8, 24, 60, 96	5 (5%)
1	1-B	94/106 (88%)	-0.30	3 (3%)	50	49	10, 22, 53, 94	3 (3%)
1	1-C	65/106 (61%)	-0.19	2 (3%)	51	50	12, 26, 55, 88	4 (6%)
1	?-C	0/106	-	-			-	-
1	1-D	64/106 (60%)	-0.21	1 (1%)	70	70	12, 24, 48, 75	5 (7%)
All	All	318/530 (60%)	-0.24	10 (3%)	51	50	8, 24, 55, 96	17 (5%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	2	GLU	4.1
1	1-D	96	ASP	3.6
1	1-A	94	ALA	3.4
1	1-B	94	ALA	3.4
1	1-B	3	LYS	3.2

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

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

5.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.4 Ligands [i](#)

There are no ligands in this entry.

5.5 Other polymers [i](#)

There are no such residues in this entry.