WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2023 – 01:52 AM EDT

PDB ID	:	6ME1
Title	:	Crystal structure of the clade B isolate B41 mutant fusion peptide (residues 512-521) in complex with VRC34.01
Authors	:	Kumar, S.; Sarkar, A.; Wilson, I.A.
Deposited on	:	2018-09-05
Resolution	:	1.97 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 ⓘ 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)	:	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 1.97 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 ⓘ

There are 4 unique types of molecules in this entry. The entry contains 7368 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 VRC34.01 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total 1674	C 1054	N 285	O 329	S 6	0	0	0
1	C	223	Total 1674	C 1054	N 285	O 329	S 6	0	0	0

- Molecule 2 is a protein called VRC34.01 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total 1628	C 1024	N 274	O 325	S 5	0	0	0
2	D	212	Total 1634	C 1028	N 274	O 327	S 5	0	1	0

- Molecule 3 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	10	Total 63	C 43	N 10	O 10	0	0	0
3	E	16	Total 123	C 79	N 28	O 16	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	515	LEU	ILE	conflict	UNP P03375
F	518	VAL	LEU	conflict	UNP P03375
F	522	HIS	-	expression tag	UNP P03375
F	523	HIS	-	expression tag	UNP P03375
F	524	HIS	-	expression tag	UNP P03375
F	525	HIS	-	expression tag	UNP P03375
F	526	HIS	-	expression tag	UNP P03375
F	527	HIS	-	expression tag	UNP P03375

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Chain	Residue	Modelled	Actual	Comment	Reference
E	515	LEU	ILE	conflict	UNP P03375
E	518	VAL	LEU	conflict	UNP P03375
E	522	HIS	-	expression tag	UNP P03375
E	523	HIS	-	expression tag	UNP P03375
E	524	HIS	-	expression tag	UNP P03375
E	525	HIS	-	expression tag	UNP P03375
E	526	HIS	-	expression tag	UNP P03375
E	527	HIS	-	expression tag	UNP P03375

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	131	Total 131	O 131	0	0
4	B	151	Total 151	O 151	0	0
4	F	9	Total 9	O 9	0	0
4	C	143	Total 143	O 143	0	0
4	D	126	Total 126	O 126	0	0
4	E	12	Total 12	O 12	0	0

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

3 Data and refinement statistics ⓘ

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	42.42Å 123.67Å 101.25Å 90.00° 90.87° 90.00°	Depositor
Resolution (Å)	38.18 – 1.97	Depositor
% Data completeness (in resolution range)	98.6 (38.18-1.97)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.11 (at 1.97Å)	Xtriage
Refinement program	PHENIX (1.12_2829)	Depositor
R, R_{free}	0.199 , 0.238	Depositor
Wilson B-factor (Å^2)	29.5	Xtriage
Anisotropy	0.487	Xtriage
L-test for twinning[2]	$<|L|> = 0.49, <L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.033 for h,-k,-l	Xtriage
Total number of atoms	7368	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

4.1 Standard geometry ⓘ

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

4.2 Too-close contacts ⓘ

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

4.3 Torsion angles ⓘ

4.3.1 Protein backbone ⓘ

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

4.3.2 Protein sidechains ⓘ

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

4.3.3 RNA ⓘ

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

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

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

4.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

4.6 Ligand geometry ⓘ

There are no ligands in this entry.

4.7 Other polymers ⓘ

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 ⓘ

5.1 Protein, DNA and RNA chains ⓘ

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

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

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

5.3 Carbohydrates ⓘ

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

5.4 Ligands ⓘ

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

5.5 Other polymers ⓘ

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