

# Full wwPDB X-ray Structure Validation Report (i)

#### Oct 3, 2023 – 04:05 AM EDT

PDB ID	:	6OED
Title	:	CRYSTAL STRUCTURE OF THE RV144 C1-C2 SPECIFIC ANTIBODY
		CH55 FAB
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Deposited on		
Resolution	:	2.46  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 (1)) 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:  $X\hbox{-}RAY\,DIFFRACTION$ 

The reported resolution of this entry is 2.46 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.



#### 60ED

# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9840 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 CH55 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1 U		214	Total	С	Ν	Ο	S	0	0	0
1	11	214	1634	1031	282	313	8	0	0	0
1	1 A	211	Total	С	Ν	0	S	0	0	0
	A	211	1613	1019	278	308	8	0		
1	1 C	211	Total	С	Ν	0	S	0	0	0
L			1613	1019	278	308	8			

• Molecule 2 is a protein called CH55 Fab light chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
	т	213	Total	С	Ν	0	S	0	0	0
		213	1632	1017	280	330	5	0		
2	9 D	213	Total	С	Ν	0	$\mathbf{S}$	0	0	0
	D	213	1632	1017	280	330	5			
0	0 D	213	Total	С	Ν	0	S	0	0	0
			1632	1017	280	330	5			

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	Н	18	Total O 18 18	0	0
3	L	16	Total O   16 16	0	0
3	А	11	Total O   11 11	0	0
3	В	16	Total O 16 16	0	0
3	С	9	Total O 9 9	0	0
3	D	14	Total O   14 14	0	0



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



# 3 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 1	Depositor	
Cell constants	73.99Å 74.03Å 75.93Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$106.84^{\circ}$ $108.43^{\circ}$ $91.78^{\circ}$	Depositor	
Resolution (Å)	42.12 - 2.46	Depositor	
% Data completeness	65.6 (42.12-2.46)	Depositor	
(in resolution range)	· · · · ·	-	
$R_{merge}$	0.09	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$1.56 (at 2.45 \text{\AA})$	Xtriage	
Refinement program	PHENIX (1.13_2998: ???)	Depositor	
$R, R_{free}$	0.256 , $0.312$	Depositor	
Wilson B-factor $(Å^2)$	46.6	Xtriage	
Anisotropy	0.641	Xtriage	
L-test for $twinning^2$	$<  L  > = 0.50, < L^2 > = 0.33$	Xtriage	
Estimated twinning fraction	0.011 for -k,-h,-l	Xtriage	
Total number of atoms	9840	wwPDB-VP	
Average B, all atoms $(Å^2)$	67.0	wwPDB-VP	

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

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.85% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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.

