

Full wwPDB X-ray Structure Validation Report (i)

Oct 5, 2023 – 08:44 AM EDT

PDB ID : 6VMX

Title: Structure of HD14 TCR in complex with HLA-B7 presenting an EBV epitope

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Deposited on : 2020-01-28

Resolution : 3.10 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

Mogul : 1.8.5 (274361), CSD as541be (2020)

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 3.10 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 8 unique types of molecules in this entry. The entry contains 13564 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 HLA class I histocompatibility antigen, B-7 alpha chain.

Mol	Chain	Residues		Atoms					AltConf	Trace
1	A	276	Total 2287	C 1417	11	O 446	S 6	0	3	0
1	F	267	Total 2201	C 1363	N 403	O 429	S 6	0	2	0

• Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	В	100	Total 845	C 539		O 160	S 4	0	1	0
2	G	100	Total 845	C 539	N 142	O 160	S 4	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	0	MET	-	initiating methionine	UNP P61769
G	0	MET	-	initiating methionine	UNP P61769

• Molecule 3 is a protein called Epstein-Barr nuclear antigen 3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	С	0	Total	С	N	О	0	0	0
3		9	83	55	18	10	0	U	U
2	П	0	Total	С	N	О	0	0	0
3	11	9	83	55	18	10	0	U	U

• Molecule 4 is a protein called HD14 alpha chain.

Mol	Chain	Residues		Atoms					AltConf	Trace
4	D	203	Total 1591	C 998	N 260	O 324	S 9	0	0	0

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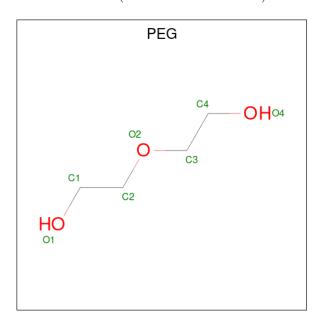
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Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
4	I	203	Total 1591	C 998	N 260	O 324	S 9	0	0	0

• Molecule 5 is a protein called HD14 beta chain.

Mol	Chain	Residues		Atoms					AltConf	Trace
5	E	243	Total 1943	C 1228	N 334	O 370	S 11	0	0	0
5	J	242	Total 1935	C 1224	N 333	O 367	S 11	0	0	0

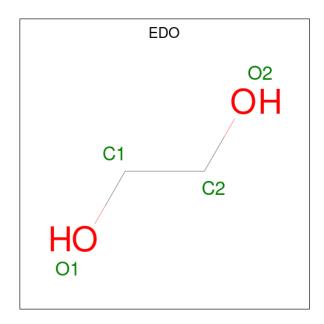
 $\bullet \ \ Molecule \ 6 \ is \ DI(HYDROXYETHYL)ETHER \ (three-letter \ code: \ PEG) \ (formula: \ C_4H_{10}O_3).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 7 4 3	0	0
6	F	1	Total C O 7 4 3	0	0
6	J	1	Total C O 7 4 3	0	0

• Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0

• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	17	Total O 17 17	0	0
8	В	5	Total O 5 5	0	0
8	D	9	Total O 9 9	0	0
8	Е	33	Total O 33 33	0	0
8	F	19	Total O 19 19	0	0
8	G	5	Total O 5 5	0	0
8	I	17	Total O 17 17	0	0
8	J	22	Total O 22 22	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 2 2 21	Depositor		
Cell constants	165.46Å 181.09Å 190.29Å	Depositor		
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor		
Resolution (Å)	48.71 - 3.10	Depositor		
% Data completeness	100.0 (48.71-3.10)	Depositor		
(in resolution range)	,	-		
R_{merge}	0.10	Depositor		
R_{sym}	(Not available)	Depositor		
$< I/\sigma(I) > 1$	2.12 (at 3.12Å)	Xtriage		
Refinement program	BUSTER 2.10.3	Depositor		
R, R_{free}	0.221 , 0.242	Depositor		
Wilson B-factor (\mathring{A}^2)	40.8	Xtriage		
Anisotropy	0.717	Xtriage		
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage		
Estimated twinning fraction	No twinning to report.	Xtriage		
Total number of atoms	13564	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 2.80% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond



length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Trme	Chain	Res	Link	B	ond leng	$_{ m gths}$	В	ond ang	gles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
7	EDO	Е	302	-	3,3,3	0.63	0	2,2,2	0.24	0
6	PEG	F	301	-	6,6,6	0.07	0	5,5,5	0.04	0
6	PEG	J	301	-	6,6,6	0.09	0	5,5,5	0.02	0
6	PEG	A	301	-	6,6,6	0.08	0	5,5,5	0.02	0
7	EDO	A	302	-	3,3,3	0.60	0	2,2,2	0.31	0
7	EDO	Е	301	-	3,3,3	0.58	0	2,2,2	0.33	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	Ε	302	-	=	0/1/1/1	-
6	PEG	F	301	-	-	1/4/4/4	-
6	PEG	J	301	-	-	1/4/4/4	-
6	PEG	A	301	-	-	2/4/4/4	ı
7	EDO	A	302	-	-	0/1/1/1	-
7	EDO	Ε	301	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	301	PEG	C4-C3-O2-C2
6	F	301	PEG	C1-C2-O2-C3
6	A	301	PEG	C1-C2-O2-C3
6	J	301	PEG	C4-C3-O2-C2

There are no ring outliers.

No monomer is involved in short contacts.



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.

