

Full wwPDB X-ray Structure Validation Report (i)

Oct 3, 2023 – 12:13 AM EDT

PDB ID : 6PUD

Title : Structure of human MAIT A-F7 TCR in complex with human MR1-5'OH-Pe

ntyl-5-OP-U

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Deposited on : 2019-07-18

Resolution : 1.80 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

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

Xtriage (Phenix) : 1.13

EDS : FAILED

buster-report : 1.1.7 (2018)

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 1.80 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 6 unique types of molecules in this entry. The entry contains 15334 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 Major histocompatibility complex class I-related gene protein.

\mathbf{Mol}	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total 2196	C 1408	N 375	O 399	S 14	0	9	0
1	С	266	Total 2267	C 1458	N 390	O 404	S 15	0	14	0

There are 4 discrepancies between the modelled and reference sequences:

Chain			Actual	Comment	Reference	
A	0 MET -		initiating methionine	UNP Q95460		
A	261	1 SER CYS		conflict	UNP Q95460	
С	0	MET	-	initiating methionine	UNP Q95460	
С	261 SER		CYS	conflict	UNP Q95460	

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	В	98	Total 801	C 513		O 149	S 3	0	1	0
2	F	100	Total 825		N		S	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	
F	0	MET	-	initiating methionine	UNP P61769	

• Molecule 3 is a protein called Human TCR alpha chain.

Mol	Chain	Residues	${f Atoms}$					ZeroOcc	AltConf	Trace
3	D	188	Total	С	N	0	S	0	9	0
			1491	955	233	293	10			

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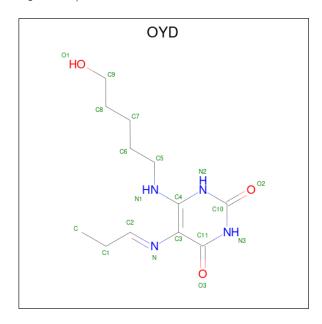
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	201	Total 1642	C 1048	N 256	O 327	S 11	0	18	0

• Molecule 4 is a protein called Human TCR beta chain.

Mol	Chain	Residues		Atoms					AltConf	Trace
4	Е	241	Total 1899	C 1199	N 324	O 364	S 12	0	9	0
4	Н	244	Total 2009	C 1274	N 345	O 377	S 13	0	21	0

• Molecule 5 is 6-[(5-hydroxypentyl)amino]-5-[(E)-propylideneamino]pyrimidine-2,4(1H,3H)-dione (three-letter code: OYD) (formula: $C_{12}H_{20}N_4O_3$) (labeled as "Ligand of Interest" by depositor).



Mo	ol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf
5		A	1	Total 19				0	0
5		С	1	Total 19	C 12		O 3	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	365	Total O 365 365	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	113	Total O 113 113	0	0
6	С	376	Total O 376 376	0	0
6	D	186	Total O 186 186	0	0
6	E	220	Total O 220 220	0	0
6	F	163	Total O 163 163	0	0
6	G	346	Total O 346 346	0	0
6	Н	397	Total O 397 397	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	216.92Å 69.97Å 142.83Å	Depositor	
a, b, c, α , β , γ	90.00° 104.31° 90.00°	Depositor	
Resolution (Å)	47.94 - 1.80	Depositor	
% Data completeness	99.0 (47.94-1.80)	Depositor	
(in resolution range)	, , ,		
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.86 (at 1.79Å)	Xtriage	
Refinement program	PHENIX 1.16_3549	Depositor	
R, R_{free}	0.164 , 0.200	Depositor	
Wilson B-factor (\mathring{A}^2)	24.9	Xtriage	
Anisotropy	0.142	Xtriage	
L-test for twinning ²	$ < L > = 0.47, < L^2> = 0.30$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	15334	wwPDB-VP	
Average B, all atoms $(Å^2)$	33.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.68% 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)

2 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	Trino	e Chain	Res	Link	Вс	ond leng	ths	В	ond ang	les
	IVIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
Ī	5	OYD	A	801	1	18,19,19	1.02	2 (11%)	15,23,23	0.70	0
	5	OYD	С	801	1	18,19,19	1.13	1 (5%)	15,23,23	0.85	1 (6%)

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	Res Link Chirals		Torsions	Rings
Ī	5	OYD	A	801	1	-	0/10/11/11	0/1/1/1
	5	OYD	С	801	1	-	0/10/11/11	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
5	С	801	OYD	C4-N1	4.61	1.38	1.32
5	A	801	OYD	C4-N1	3.33	1.37	1.32
5	A	801	OYD	C1-C2	-2.25	1.46	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	С	801	OYD	C-C1-C2	2.13	117.52	113.75

There are no chirality outliers.

There are no torsion outliers.

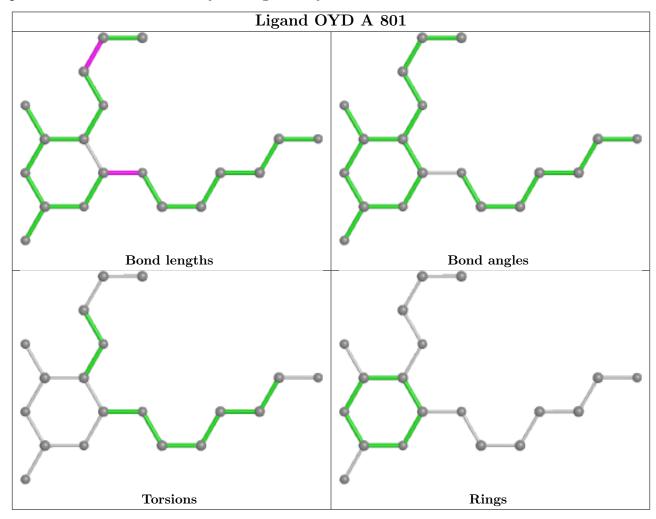
There are no ring outliers.

No monomer is involved in short contacts.

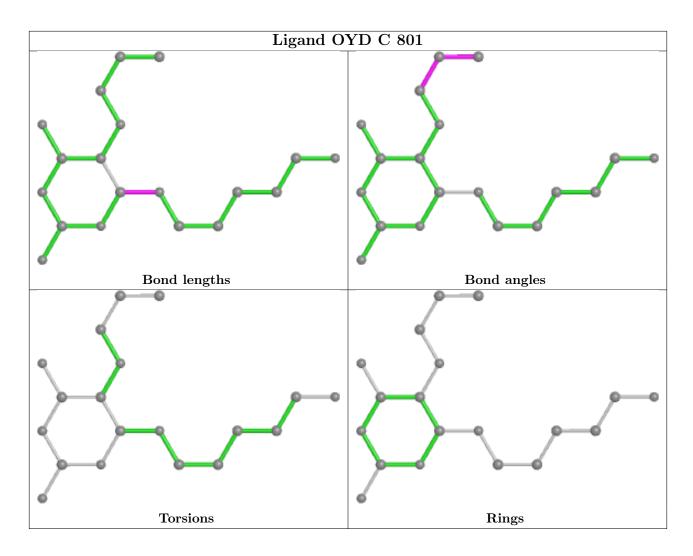
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the



average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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.

