W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 02:40 pm BST

PDB ID	:	6AT6
Title	:	Crystal structure of the KFJ5 TCR
Authors	:	Gully, B.S.; Rossjohn, J.
Deposited on	:	2017-08-28
Resolution	:	1.42 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 following versions of software and data (see references ⓘ) were used in the production of this report:

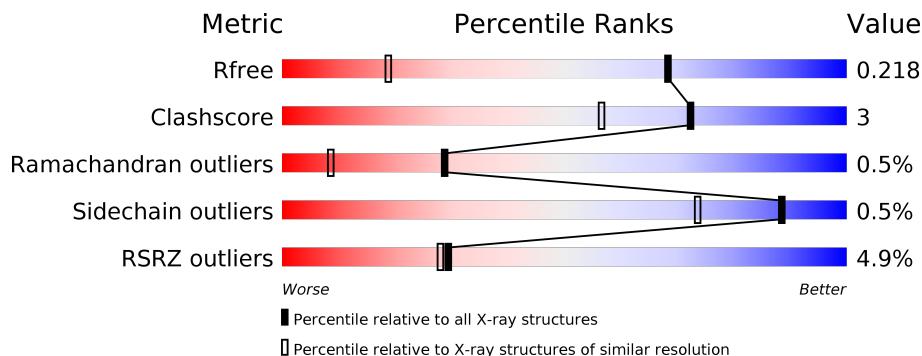|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.42 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	Percentile Ranks	Value
Rfree		0.218
Clashscore		3
Ramachandran outliers		0.5%
Sidechain outliers		0.5%
RSRZ outliers		4.9%

Worse　　　　　　　　　　　　　　*Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	2579 (1.44-1.40)
Clashscore	141614	2696 (1.44-1.40)
Ramachandran outliers	138981	2632 (1.44-1.40)
Sidechain outliers	138945	2631 (1.44-1.40)
RSRZ outliers	127900	2528 (1.44-1.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	245	% / 93% / · ·
2	A	208	9% / 84% / 7% / 9%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4066 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 T-cell receptor beta variable 28, Human nkt tcr beta chain chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	240	1952	1231	340	372	9	0	1	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	HIS	-	expression tag	UNP A0A5B6
B	4	MET	-	expression tag	UNP A0A5B6
B	99	GLN	-	linker	UNP A0A5B6
B	100	ARG	-	linker	UNP A0A5B6
B	101	GLN	-	linker	UNP A0A5B6
B	102	GLU	-	linker	UNP A0A5B6
B	103	GLY	-	linker	UNP A0A5B6
B	104	ASP	-	linker	UNP A0A5B6
B	105	THR	-	linker	UNP A0A5B6
B	106	GLN	-	linker	UNP A0A5B6
B	107	TYR	-	linker	UNP A0A5B6
B	108	PHE	-	linker	UNP A0A5B6
B	109	GLY	-	linker	UNP A0A5B6
B	110	PRO	-	linker	UNP A0A5B6
B	111	GLY	-	linker	UNP A0A5B6
B	112	THR	-	linker	UNP A0A5B6
B	113	ARG	-	linker	UNP A0A5B6
B	114	LEU	-	linker	UNP A0A5B6
B	115	THR	-	linker	UNP A0A5B6
B	116	VAL	-	linker	UNP A0A5B6
B	117	LEU	-	linker	UNP A0A5B6

- Molecule 2 is a protein called T-cell receptor alpha variable 4, T-cell receptor, sp3.4 alpha chain chimera.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	190	1496	940	247	301	8	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	9	HIS	-	expression tag	UNP A0A0B4J268
A	10	MET	-	expression tag	UNP A0A0B4J268
A	102	GLU	-	linker	UNP A0A0B4J268
A	103	ILE	-	linker	UNP A0A0B4J268
A	104	LEU	-	linker	UNP A0A0B4J268
A	105	ASP	-	linker	UNP A0A0B4J268
A	106	ASN	-	linker	UNP A0A0B4J268
A	107	PHE	-	linker	UNP A0A0B4J268
A	108	ASN	-	linker	UNP A0A0B4J268
A	109	LYS	-	linker	UNP A0A0B4J268
A	110	PHE	-	linker	UNP A0A0B4J268
A	111	TYR	-	linker	UNP A0A0B4J268
A	112	PHE	-	linker	UNP A0A0B4J268
A	113	GLY	-	linker	UNP A0A0B4J268
A	114	SER	-	linker	UNP A0A0B4J268
A	115	GLY	-	linker	UNP A0A0B4J268
A	116	THR	-	linker	UNP A0A0B4J268
A	117	LYS	-	linker	UNP A0A0B4J268
A	118	LEU	-	linker	UNP A0A0B4J268
A	119	ASN	-	linker	UNP A0A0B4J268
A	120	VAL	-	linker	UNP A0A0B4J268
A	121	LYS	-	linker	UNP A0A0B4J268
A	122	PRO	-	linker	UNP A0A0B4J268
A	123	ASN	-	linker	UNP A0A0B4J268

- Molecule 3 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	B	309	309	309	0	0
3	A	309	309	309	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: T-cell receptor beta variable 28, Human nkt tcr beta chain chimera
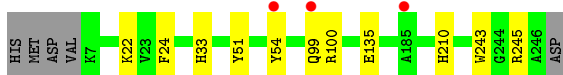
- Molecule 2: T-cell receptor alpha variable 4, T-cell receptor, sp3.4 alpha chain chimera
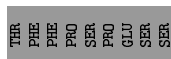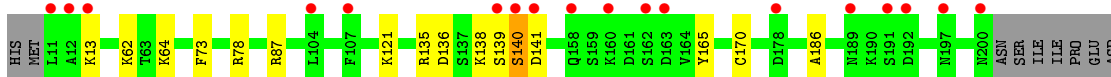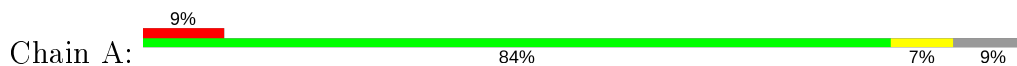
4   Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	49.90Å 73.36Å 123.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.12 – 1.42 39.12 – 1.42	Depositor EDS
% Data completeness (in resolution range)	99.2 (39.12-1.42) 99.2 (39.12-1.42)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.55 (at 1.42Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.198 , 0.218 0.199 , 0.218	Depositor DCC
R_{free} test set	4245 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	12.3	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 44.9	EDS
L-test for twinning[2]	$<|L|> = 0.47, <L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4066	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[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.

5 Model quality (i)

5.1 Standard geometry (i)

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 $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z| > 5$	RMSZ	#$|Z| > 5$
1	B	0.36	0/2004	0.55	0/2715
2	A	0.37	0/1528	0.58	0/2074
All	All	0.36	0/3532	0.57	0/4789

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1952	0	1878	12	0
2	A	1496	0	1433	11	0
3	A	309	0	0	3	1
3	B	309	0	0	4	0
All	All	4066	0	3311	23	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 23 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:ARG:NH2	3:B:301:HOH:O	2.17	0.78

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:62:LYS:HG2	2:A:78:ARG:HD3	1.73	0.71
1:B:33:HIS:HA	1:B:99:GLN:HE22	1.56	0.69
1:B:33:HIS:HA	1:B:99:GLN:NE2	2.10	0.67
1:B:33:HIS:CD2	1:B:99:GLN:HE21	2.15	0.64

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:316:HOH:O	3:A:337:HOH:O[4_555]	2.12	0.08

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	239/245 (98%)	236 (99%)	3 (1%)	0	100	100
2	A	188/208 (90%)	180 (96%)	6 (3%)	2 (1%)	14	2
All	All	427/453 (94%)	416 (97%)	9 (2%)	2 (0%)	29	8

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	87	ARG
2	A	140	SER

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	215/219 (98%)	214 (100%)	1 (0%)	88	73
2	A	173/191 (91%)	172 (99%)	1 (1%)	86	69
All	All	388/410 (95%)	386 (100%)	2 (0%)	88	73

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	51	TYR
2	A	170	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	99	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 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(Å²)	Q<0.9
1	B	240/245 (97%)	0.13	3 (1%)	77 75	7, 14, 29, 37	0
2	A	190/208 (91%)	0.37	18 (9%)	8 7	7, 13, 40, 50	0
All	All	430/453 (94%)	0.23	21 (4%)	29 28	7, 13, 35, 50	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	141	ASP	4.4
2	A	160	LYS	4.4
2	A	200	ASN	4.4
2	A	140	SER	3.8
1	B	54	TYR	3.5

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.