



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2016 – 08:04 PM EDT

PDB ID : 4ZDH
Title : Crystal structure of JKA6 TCR
Authors : Singh, N.K.; Hossain, M.; Baker, B.M.
Deposited on : 2015-04-17
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/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
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027457
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

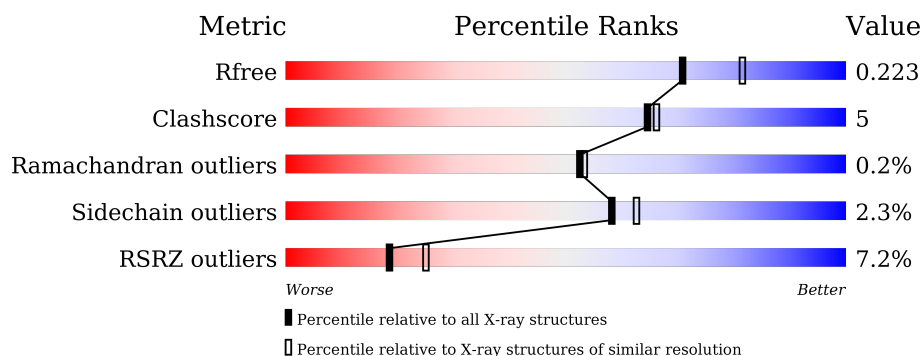
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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. 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 $\leq 5\%$. 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	A	201	<div> <div>10%</div> <div> <div></div> <div>88%</div> <div>10%</div> </div> <div>.</div> </div>
2	B	241	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>14%</div> </div> <div>.</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3641 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 Alpha chain of A6 T-cell receptor,T-cell receptor alpha chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	201	Total	C	N	O	S	0	0	0
			1556	968	255	325	8			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	SER	-	conflict	PDB ?
A	80	ALA	-	conflict	PDB ?
A	93	THR	-	conflict	PDB ?
A	94	THR	-	linker	PDB ?
A	95	ASP	-	linker	PDB ?
A	96	SER	-	linker	PDB ?
A	97	TRP	-	linker	PDB ?
A	98	GLY	-	linker	PDB ?
A	99	LYS	-	linker	PDB ?
A	100	LEU	-	linker	PDB ?
A	101	GLN	-	linker	PDB ?
A	102	PHE	-	linker	PDB ?
A	103	GLY	-	linker	PDB ?
A	104	ALA	-	linker	PDB ?
A	105	GLY	-	linker	PDB ?
A	106	THR	-	linker	PDB ?
A	107	GLN	-	linker	PDB ?
A	108	VAL	-	linker	PDB ?
A	109	VAL	-	linker	PDB ?
A	110	VAL	-	linker	PDB ?
A	111	THR	-	linker	PDB ?
A	112	PRO	-	linker	PDB ?
A	113	ASP	-	linker	PDB ?
A	160	CYS	THR	conflict	UNP P01848

- Molecule 2 is a protein called Beta chain of JKF6 T-cell receptor,Protein TRBV28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	241	Total 1935	C 1228	N 330	O 368	S 9	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	79	ALA	-	conflict	PDB ?
B	84	ASP	-	conflict	PDB ?
B	95	PHE	-	conflict	PDB ?
B	96	LEU	-	linker	PDB ?
B	97	GLY	-	linker	PDB ?
B	98	THR	-	linker	PDB ?
B	99	GLY	-	linker	PDB ?
B	100	VAL	-	linker	PDB ?
B	101	GLU	-	linker	PDB ?
B	102	GLN	-	linker	PDB ?
B	103	TYR	-	linker	PDB ?
B	104	PHE	-	linker	PDB ?
B	105	GLY	-	linker	PDB ?
B	106	PRO	-	linker	PDB ?
B	126	LEU	VAL	conflict	UNP A0A087WZV8
B	150	TYR	PHE	conflict	UNP A0A087WZV8
B	170	CYS	SER	conflict	UNP A0A087WZV8
B	188	ALA	CYS	conflict	UNP A0A087WZV8
B	202	ASP	ASN	conflict	UNP A0A087WZV8
B	219	ALA	ASN	conflict	UNP A0A087WZV8
B	225	ALA	ASP	conflict	UNP A0A087WZV8

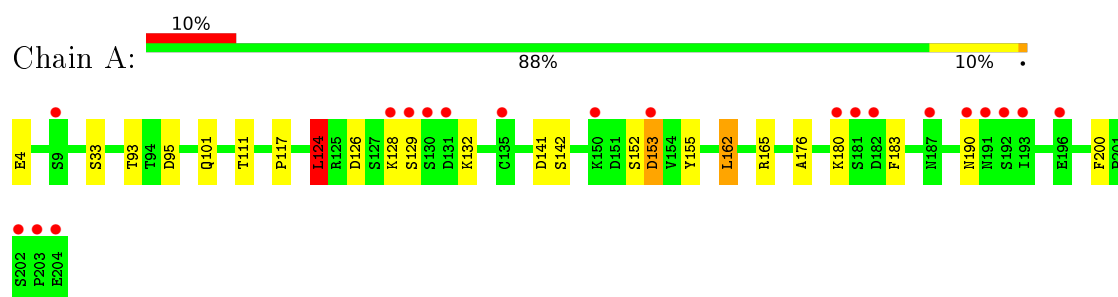
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	60	Total 60	O 60	0	0
3	B	90	Total 90	O 90	0	0

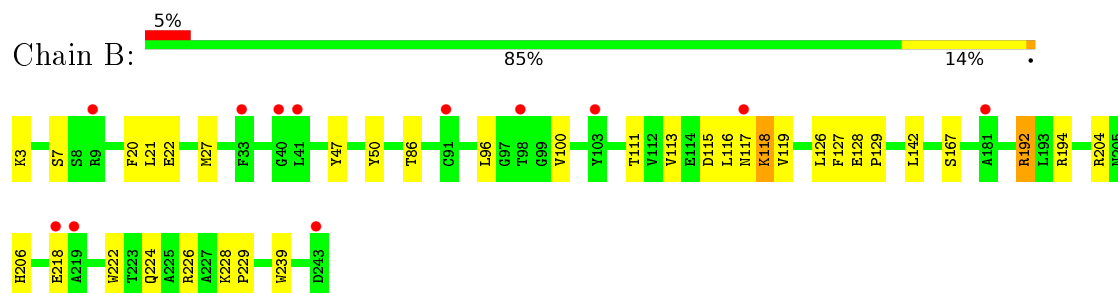
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Alpha chain of A6 T-cell receptor,T-cell receptor alpha chain C region



- Molecule 2: Beta chain of JKF6 T-cell receptor,Protein TRBV28



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.70 Å 60.09 Å 82.46 Å 90.00° 91.75° 90.00°	Depositor
Resolution (Å)	19.49 – 2.10 19.49 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.1 (19.49-2.10) 95.1 (19.49-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.09 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.190 , 0.224 0.188 , 0.223	Depositor DCC
R_{free} test set	1261 reflections (5.16%)	DCC
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.043 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3641	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	A	0.38	0/1590	0.59	2/2160 (0.1%)
2	B	0.42	0/1985	0.57	0/2692
All	All	0.40	0/3575	0.58	2/4852 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	162	LEU	CA-CB-CG	5.78	128.60	115.30
1	A	124	LEU	CA-CB-CG	5.31	127.50	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	A	1556	0	1455	18	0
2	B	1935	0	1863	23	0
3	A	60	0	0	0	0
3	B	90	0	0	1	0
All	All	3641	0	3318	35	0

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 5.

All (35) 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:A:126:ASP:HB3	1:A:129:SER:O	2.02	0.60
1:A:180:LYS:HB2	1:A:183:PHE:HB2	1.90	0.54
1:A:165:ARG:HG3	2:B:167:SER:OG	2.09	0.53
1:A:33:SER:HB2	1:A:93:THR:HG23	1.90	0.53
1:A:132:LYS:HG3	2:B:127:PHE:CE2	2.45	0.53
1:A:33:SER:HB2	1:A:93:THR:CG2	2.40	0.51
2:B:126:LEU:HD21	2:B:142:LEU:HD23	1.94	0.50
1:A:132:LYS:HG3	2:B:127:PHE:HE2	1.75	0.50
2:B:119:VAL:HG12	2:B:229:PRO:HB2	1.95	0.48
1:A:95:ASP:OD2	2:B:50:TYR:OH	2.27	0.48
2:B:218:GLU:HA	2:B:228:LYS:HZ3	1.79	0.47
2:B:3:LYS:HB3	2:B:27:MET:SD	2.54	0.47
2:B:86:THR:HG23	2:B:111:THR:HA	1.98	0.46
1:A:4:GLU:HB3	1:A:101:GLN:OE1	2.15	0.46
2:B:7:SER:HB3	2:B:22:GLU:HB2	1.97	0.46
1:A:153:ASP:OD1	1:A:153:ASP:N	2.50	0.45
2:B:204:ARG:NH1	3:B:312:HOH:O	2.50	0.45
2:B:117:ASN:O	2:B:226:ARG:NH2	2.50	0.44
1:A:155:TYR:O	1:A:176:ALA:HA	2.19	0.43
2:B:115:ASP:O	2:B:118:LYS:HG2	2.18	0.43
1:A:111:THR:HB	1:A:142:SER:HB3	2.00	0.43
2:B:206:HIS:HB2	2:B:239:TRP:CZ3	2.53	0.43
2:B:222:TRP:NE1	2:B:224:GLN:HB2	2.33	0.43
2:B:129:PRO:HD3	2:B:142:LEU:HG	2.00	0.43
1:A:162:LEU:HD11	2:B:194:ARG:HB2	2.01	0.42
1:A:4:GLU:HB2	1:A:101:GLN:HE22	1.83	0.42
2:B:113:VAL:HG21	2:B:118:LYS:HG3	1.99	0.42
1:A:153:ASP:HB2	1:A:180:LYS:NZ	2.34	0.42
2:B:20:PHE:O	2:B:21:LEU:HD23	2.20	0.42
2:B:206:HIS:HB2	2:B:239:TRP:CH2	2.55	0.41
1:A:117:PRO:HG3	1:A:141:ASP:HB3	2.02	0.41
2:B:116:LEU:HA	2:B:116:LEU:HD23	1.92	0.41
1:A:126:ASP:OD2	1:A:128:LYS:HG2	2.21	0.41
1:A:124:LEU:HB3	2:B:128:GLU:O	2.21	0.40
2:B:192:ARG:HD2	2:B:192:ARG:HH21	1.73	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	A	199/201 (99%)	195 (98%)	3 (2%)	1 (0%)	34	30
2	B	239/241 (99%)	234 (98%)	5 (2%)	0	100	100
All	All	438/442 (99%)	429 (98%)	8 (2%)	1 (0%)	52	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	190	ASN

5.3.2 Protein sidechains

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	A	178/178 (100%)	174 (98%)	4 (2%)	60	64
2	B	211/211 (100%)	206 (98%)	5 (2%)	57	61
All	All	389/389 (100%)	380 (98%)	9 (2%)	58	62

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	124	LEU
1	A	152	SER
1	A	153	ASP
1	A	200	PHE
2	B	47	TYR

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Mol	Chain	Res	Type
2	B	96	LEU
2	B	100	VAL
2	B	118	LYS
2	B	192	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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(Å ²)	Q<0.9
1	A	201/201 (100%)	0.45	20 (9%)	9 13	24, 37, 90, 121	1 (0%)
2	B	241/241 (100%)	0.11	12 (4%)	32 41	22, 33, 57, 94	0
All	All	442/442 (100%)	0.27	32 (7%)	18 25	22, 35, 73, 121	1 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	192	SER	9.0
1	A	131	ASP	6.7
1	A	204	GLU	6.5
1	A	182	ASP	5.7
2	B	243	ASP	5.3
1	A	181	SER	5.1
1	A	191	ASN	4.9
1	A	203	PRO	4.6
2	B	219	ALA	4.2
1	A	150	LYS	4.2
1	A	130	SER	4.0
1	A	128	LYS	3.8
1	A	187	ASN	3.6
1	A	129	SER	3.6
2	B	40	GLY	3.5
2	B	181	ALA	3.5
1	A	9	SER	3.4
2	B	98	THR	3.4
1	A	202	SER	3.4
1	A	135	CYS	2.8
1	A	190	ASN	2.8
2	B	103	TYR	2.5
2	B	41	LEU	2.5
1	A	153	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	193	ILE	2.2
2	B	218	GLU	2.2
2	B	9	ARG	2.2
1	A	180	LYS	2.2
1	A	196	GLU	2.1
2	B	91	CYS	2.1
2	B	117	ASN	2.0
2	B	33	PHE	2.0

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.