Full wwPDB X-ray Structure Validation Report ⓘ

Oct 19, 2026 – 11:36 PM JST

PDB ID	:	9X9I / pdb_00009x9i
Title	:	complex of TCR1414_2-TGFbetaR2(-1)-HLA-DR4, a TGFbetaR2(-1)-HLA-DR4, with a TGFbetaR2(-1) specific TCR1414_2
Authors	:	Shi, J.L.; Wu, D.C.
Deposited on	:	2025-10-20
Resolution	:	1.90 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 ⓘ 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 ⓘ) were used in the production of this report:

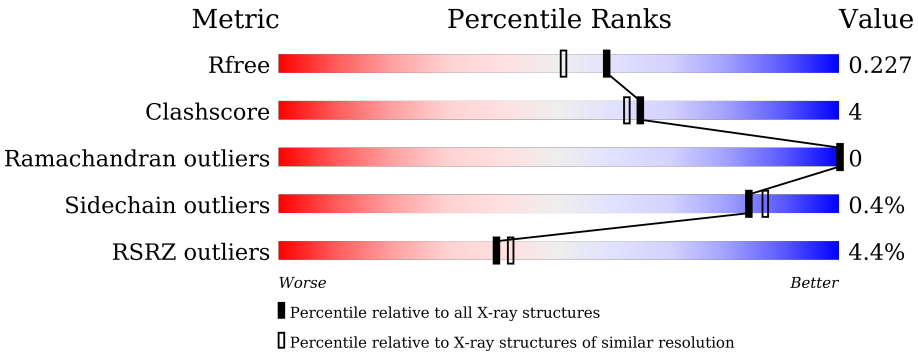
MolProbity	:	4-5-2 with Phenix2.2
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 1.90 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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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 of 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	A	181	2% 88% 10% ••
2	B	189	9% 88% 9% •
3	C	16	88% 12%
4	D	203	5% 86% 11% •
5	E	243	2% 91% 8% •

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7434 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 II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	0	0
			1473	954	239	275	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen DR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	184	Total	C	N	O	S	0	0	0
			1528	967	271	285	5			

- Molecule 3 is a protein called mutant human TGFbetaR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	14	Total	C	N	O	S	0	0	0
			97	58	16	21	2			

- Molecule 4 is a protein called TCR1414_2 alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	199	Total	C	N	O	S	0	0	0
			1540	963	258	312	7			

- Molecule 5 is a protein called TCR1414_2 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	241	Total	C	N	O	S	0	0	0
			1936	1222	336	369	9			

- Molecule 6 is water.

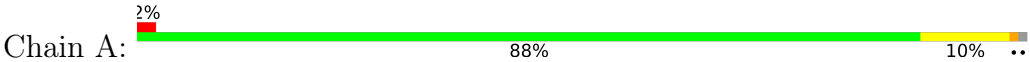
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	202	Total O 202 202	0	0
6	B	201	Total O 201 201	0	0
6	C	12	Total O 12 12	0	0
6	D	185	Total O 185 185	0	0
6	E	260	Total O 260 260	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: HLA class II histocompatibility antigen, DR alpha chain

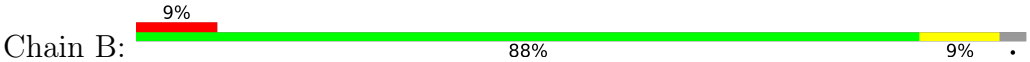
Chain A:

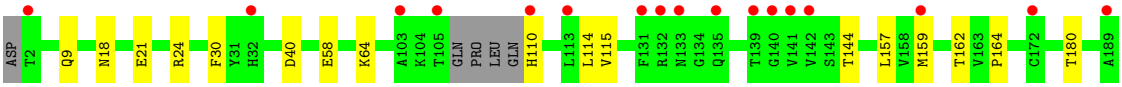




• Molecule 2: HLA class II histocompatibility antigen DR beta chain

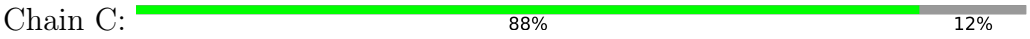
Chain B:





• Molecule 3: mutant human TGFbetaR2

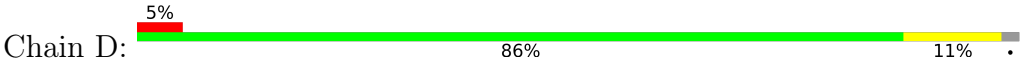
Chain C:

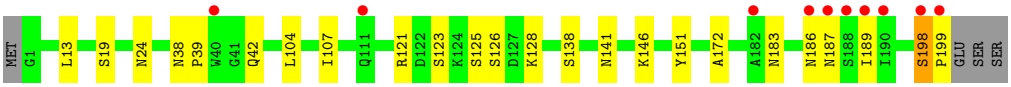




• Molecule 4: TCR1414_2 alpha

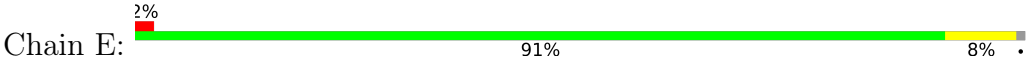
Chain D:

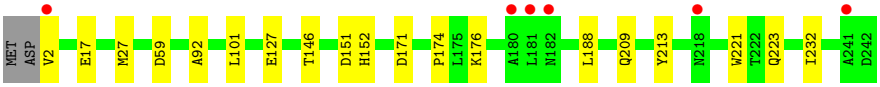




• Molecule 5: TCR1414_2 beta

Chain E:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	65.20Å 71.75Å 191.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.60 – 1.90 32.60 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.7 (32.60-1.90) 98.7 (32.60-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.75 (at 1.89Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.185 , 0.227 0.186 , 0.227	Depositor DCC
R_{free} test set	3568 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	21.2	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 54.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7434	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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

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	0.28	0/1518	0.53	0/2070
2	B	0.27	0/1570	0.46	0/2132
3	C	0.25	0/96	0.55	0/127
4	D	0.24	0/1575	0.48	0/2145
5	E	0.25	0/1983	0.50	0/2687
All	All	0.26	0/6742	0.49	0/9161

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

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	1473	0	1407	14	0
2	B	1528	0	1439	11	0
3	C	97	0	105	0	0
4	D	1540	0	1464	14	0
5	E	1936	0	1871	13	0
6	A	202	0	0	3	1
6	B	201	0	0	3	2
6	C	12	0	0	0	0
6	D	185	0	0	1	0
6	E	260	0	0	2	0
All	All	7434	0	6286	50	2

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 4.

All (50) 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:49:ARG:NH1	6:A:201:HOH:O	1.77	1.10
1:A:37:LYS:NZ	6:A:202:HOH:O	2.11	0.72
1:A:140:GLU:OE2	6:A:203:HOH:O	2.15	0.64
5:E:2:VAL:HA	5:E:27:MET:SD	2.39	0.62
2:B:180:THR:OG1	6:B:201:HOH:O	2.16	0.60
1:A:37:LYS:HB2	1:A:39:GLU:HG2	1.85	0.58
5:E:17:GLU:OE1	6:E:301:HOH:O	2.17	0.57
2:B:162:THR:HG23	2:B:164:PRO:HD3	1.86	0.57
5:E:92:ALA:HB1	5:E:101:LEU:HG	1.88	0.54
1:A:179:PHE:O	1:A:180:ASP:HB2	2.09	0.53
2:B:24:ARG:NH2	2:B:40:ASP:OD2	2.39	0.53
2:B:18:ASN:ND2	2:B:21:GLU:OE1	2.42	0.53
2:B:115:VAL:HG22	2:B:159:MET:HG3	1.91	0.52
4:D:121:ARG:HB3	5:E:127:GLU:HB2	1.91	0.52
4:D:38:ASN:HB2	4:D:39:PRO:HD2	1.91	0.52
4:D:107:ILE:HG23	4:D:138:SER:HB3	1.93	0.51
5:E:59:ASP:OD2	6:E:302:HOH:O	2.20	0.51
4:D:141:ASN:H	4:D:189:ILE:HD11	1.75	0.50
4:D:13:LEU:HD21	4:D:19:SER:HB2	1.93	0.49
5:E:221:TRP:CE2	5:E:223:GLN:HB2	2.49	0.48
4:D:13:LEU:HD12	4:D:104:LEU:HD11	1.95	0.48
5:E:171:ASP:HB2	5:E:188:LEU:HD12	1.96	0.47
5:E:152:HIS:HB3	5:E:213:TYR:HB2	1.96	0.47
1:A:117:ASN:HB3	1:A:165:GLU:HB2	1.96	0.47
2:B:144:THR:HG23	2:B:157:LEU:O	2.15	0.47
4:D:24:ASN:ND2	6:D:313:HOH:O	2.46	0.47
1:A:93:ASN:HB3	1:A:105:ILE:HD11	1.96	0.47
4:D:151:TYR:O	4:D:172:ALA:HA	2.15	0.47
2:B:58:GLU:HG3	6:B:249:HOH:O	2.15	0.46
2:B:9:GLN:HB2	2:B:30:PHE:HB2	1.98	0.46
4:D:198:SER:OG	4:D:199:PRO:HD3	2.16	0.45
5:E:151:ASP:CG	5:E:174:PRO:HG3	2.41	0.45
5:E:209:GLN:HG3	5:E:232:ILE:HG23	1.99	0.45
1:A:155:SER:OG	1:A:158:ASP:OD2	2.35	0.44
1:A:161:ASP:HB3	1:A:174:LEU:HD22	1.99	0.44
4:D:146:LYS:HD2	4:D:187:ASN:OD1	2.18	0.43
1:A:99:ARG:HG3	1:A:99:ARG:NH1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:183:ASN:O	4:D:186:ASN:ND2	2.52	0.43
1:A:99:ARG:HG3	1:A:99:ARG:HH11	1.84	0.42
2:B:110:HIS:N	6:B:217:HOH:O	2.52	0.42
1:A:137:LEU:HB2	1:A:145:ARG:HG2	2.02	0.41
4:D:123:SER:HB3	4:D:126:SER:HB3	2.02	0.41
2:B:114:LEU:HD12	2:B:114:LEU:HA	1.82	0.41
4:D:128:LYS:HE2	5:E:146:THR:HG21	2.02	0.41
5:E:176:LYS:H	5:E:176:LYS:HD3	1.86	0.41
1:A:62:ILE:HD12	1:A:62:ILE:HA	1.90	0.41
4:D:38:ASN:ND2	4:D:42:GLN:HB3	2.35	0.41
5:E:209:GLN:HG3	5:E:232:ILE:CG2	2.51	0.41
2:B:64:LYS:O	2:B:64:LYS:HD2	2.21	0.40
1:A:134:THR:HG23	1:A:147:PHE:HB2	2.03	0.40

All (2) 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)
6:B:292:HOH:O	6:B:352:HOH:O[4_545]	2.12	0.08
6:A:373:HOH:O	6:B:249:HOH:O[4_545]	2.18	0.02

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	A	177/181 (98%)	174 (98%)	3 (2%)	0	100	100
2	B	180/189 (95%)	177 (98%)	3 (2%)	0	100	100
3	C	12/16 (75%)	12 (100%)	0	0	100	100
4	D	197/203 (97%)	190 (96%)	7 (4%)	0	100	100
5	E	239/243 (98%)	235 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	805/832 (97%)	788 (98%)	17 (2%)	0	100 100

There are no Ramachandran outliers to report.

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	A	164/166 (99%)	163 (99%)	1 (1%)	78 81
2	B	166/171 (97%)	166 (100%)	0	100 100
3	C	12/14 (86%)	12 (100%)	0	100 100
4	D	178/182 (98%)	176 (99%)	2 (1%)	65 67
5	E	213/215 (99%)	213 (100%)	0	100 100
All	All	733/748 (98%)	730 (100%)	3 (0%)	84 87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	ILE
4	D	125	SER
4	D	198	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	155	GLN
3	C	13	GLN
4	D	37	GLN
4	D	55	GLN
4	D	93	ASN
4	D	119	GLN
5	E	37	GLN
5	E	99	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	179/181 (98%)	-0.04	3 (1%) 69 72	12, 21, 40, 75	0
2	B	184/189 (97%)	0.27	17 (9%) 14 15	13, 24, 52, 65	0
3	C	14/16 (87%)	-0.04	0 100 100	13, 15, 45, 61	0
4	D	199/203 (98%)	0.35	10 (5%) 34 36	12, 26, 52, 82	0
5	E	241/243 (99%)	0.02	6 (2%) 58 62	12, 22, 48, 71	0
All	All	817/832 (98%)	0.14	36 (4%) 39 41	12, 23, 50, 82	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	199	PRO	6.0
4	D	189	ILE	4.6
5	E	181	LEU	4.1
2	B	139	THR	3.9
1	A	179	PHE	3.5
4	D	40	TRP	3.2
5	E	218	ASN	3.1
2	B	110	HIS	3.1
5	E	180	ALA	3.0
2	B	113	LEU	2.9
2	B	172	CYS	2.6
4	D	187	ASN	2.6
2	B	159	MET	2.6
5	E	2	VAL	2.6
2	B	135	GLN	2.6
2	B	142	VAL	2.6
2	B	140	GLY	2.5
2	B	133	ASN	2.4
2	B	105	THR	2.4
1	A	180	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
4	D	198	SER	2.4
1	A	156	THR	2.4
4	D	190	ILE	2.4
2	B	103	ALA	2.2
4	D	188	SER	2.2
5	E	241	ALA	2.2
2	B	131	PHE	2.2
2	B	132	ARG	2.2
4	D	186	ASN	2.1
4	D	182	ALA	2.1
2	B	2	THR	2.1
2	B	32	HIS	2.1
2	B	189	ALA	2.1
2	B	141	VAL	2.0
4	D	111	GLN	2.0
5	E	182	ASN	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 oligosaccharides 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.