



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:34 PM UTC

PDB ID : 3VXQ / pdb_00003vxq
Title : H27-14 TCR specific for HLA-A24-Nef134-10
Authors : Shimizu, A.; Fukai, S.; Yamagata, A.; Iwamoto, A.
Deposited on : 2012-09-20
Resolution : 2.00 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 Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

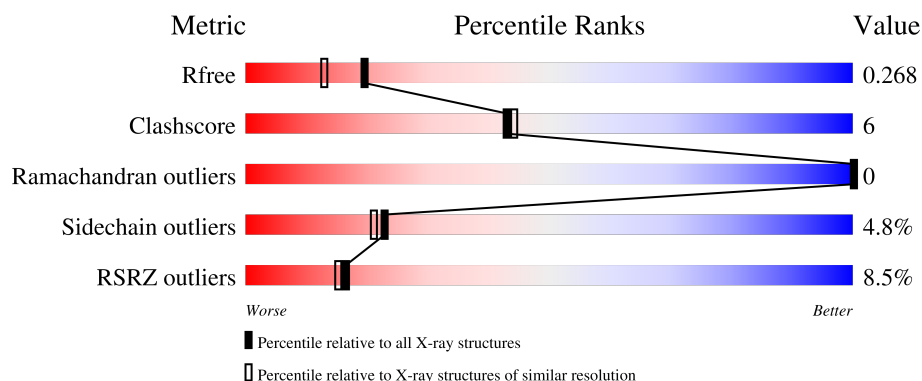
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	205	13% 86% 12% .
1	D	205	6% 86% 11% .
2	B	244	5% 86% 13% .
2	E	244	11% 80% 18% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7672 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 H27-14 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	204	Total	C	N	O	S	0	0	0
			1575	978	266	323	8			
1	A	204	Total	C	N	O	S	0	0	0
			1575	978	266	323	8			

- Molecule 2 is a protein called H27-14 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	242	Total	C	N	O	S	0	0	0
			1954	1226	347	375	6			
2	B	242	Total	C	N	O	S	0	0	0
			1954	1226	347	375	6			

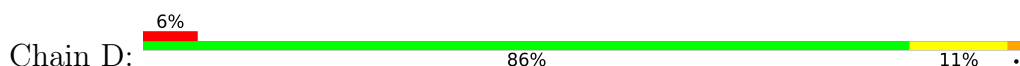
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	158	Total	O	0	0
			158	158		
3	E	185	Total	O	0	0
			185	185		
3	A	130	Total	O	0	0
			130	130		
3	B	141	Total	O	0	0
			141	141		

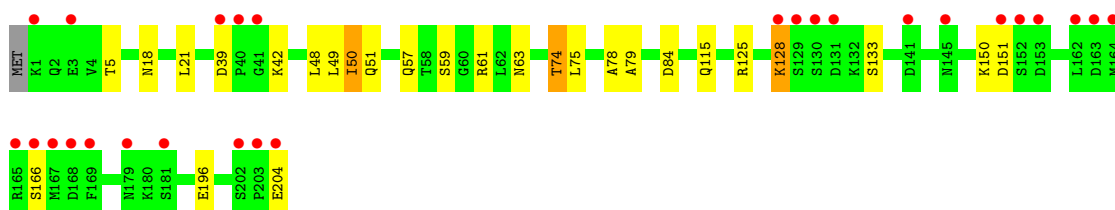
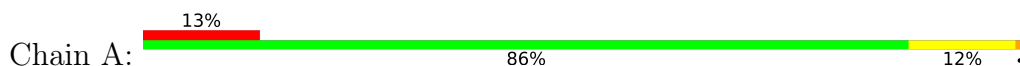
3 Residue-property plots [i](#)

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.

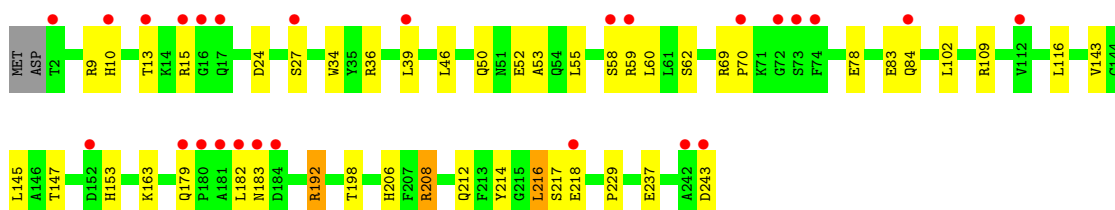
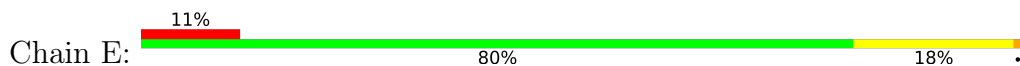
- Molecule 1: H27-14 TCR alpha chain



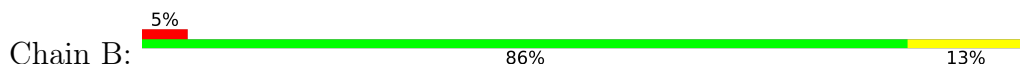
- Molecule 1: H27-14 TCR alpha chain



- Molecule 2: H27-14 TCR beta chain



- Molecule 2: H27-14 TCR beta chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.42Å 159.17Å 68.35Å 90.00° 93.56° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.8 (50.00-2.00) 98.0 (50.00-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.29 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.222 , 0.267 0.222 , 0.268	Depositor DCC
R_{free} test set	3097 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7672	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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, 0.333 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	0.44	0/1604	0.74	2/2175 (0.1%)
1	D	0.44	0/1604	0.74	2/2175 (0.1%)
2	B	0.60	0/2006	0.74	0/2724
2	E	0.63	0/2006	0.74	2/2724 (0.1%)
All	All	0.55	0/7220	0.74	6/9798 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	39	ASP	CA-C-N	5.58	125.89	119.93
1	D	39	ASP	C-N-CA	5.58	125.89	119.93
1	A	39	ASP	CA-C-N	5.55	126.78	119.84
1	A	39	ASP	C-N-CA	5.55	126.78	119.84
2	E	69	ARG	CA-C-N	5.01	124.45	119.24
2	E	69	ARG	C-N-CA	5.01	124.45	119.24

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	1575	0	1522	18	0
1	D	1575	0	1522	22	0
2	B	1954	0	1850	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	1954	0	1850	33	0
3	A	130	0	0	7	0
3	B	141	0	0	5	0
3	D	158	0	0	4	0
3	E	185	0	0	16	0
All	All	7672	0	6744	86	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 6.

All (86) 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:D:202:SER:HB3	1:D:203:PRO:HD2	1.50	0.91
2:E:59:ARG:HH12	2:E:60:LEU:HB3	1.45	0.82
2:E:59:ARG:NH1	2:E:60:LEU:HB3	1.94	0.82
2:E:34:TRP:CZ2	3:E:474:HOH:O	2.32	0.81
1:D:41:GLY:HA3	3:D:368:HOH:O	1.88	0.72
1:D:13:VAL:HG21	1:D:19:LEU:HD22	1.72	0.72
1:D:202:SER:HB3	1:D:203:PRO:CD	2.25	0.67
2:E:34:TRP:HZ2	3:E:474:HOH:O	1.74	0.67
1:D:18:ASN:HD22	1:D:79:ALA:H	1.43	0.67
2:B:179:GLN:HG3	3:B:433:HOH:O	1.96	0.65
2:E:70:PRO:HA	3:E:393:HOH:O	1.98	0.64
1:D:13:VAL:HG21	1:D:19:LEU:CD2	2.28	0.63
1:A:21:LEU:HD12	1:A:75:LEU:HD23	1.82	0.62
2:E:34:TRP:CH2	3:E:474:HOH:O	2.51	0.62
2:E:15:ARG:HE	2:E:84:GLN:HE21	1.48	0.62
2:B:197:ALA:O	2:B:201:GLN:HG3	2.00	0.62
1:D:34:GLN:HE22	2:E:102:LEU:H	1.48	0.62
2:B:7:ASN:HB2	3:B:346:HOH:O	2.00	0.61
1:A:49:LEU:HD12	2:B:101:GLU:HG3	1.82	0.61
1:D:18:ASN:ND2	1:D:79:ALA:H	1.98	0.60
1:D:109:LEU:HD22	1:D:111:ARG:NH2	2.18	0.58
2:E:62:SER:HA	3:E:449:HOH:O	2.02	0.58
2:E:15:ARG:HE	2:E:84:GLN:HG3	1.72	0.55
1:D:204:GLU:H	1:D:204:GLU:CD	2.15	0.55
2:B:21:PHE:HZ	2:B:110:LEU:HB2	1.72	0.54
1:D:173:SER:OG	2:E:192:ARG:HD2	2.07	0.54
1:A:48:LEU:HD21	1:A:59:SER:HB3	1.90	0.54
2:E:50:GLN:HB3	3:E:473:HOH:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:129:PRO:HD3	2:B:142:LEU:HG	1.90	0.53
2:E:217:SER:OG	2:E:218:GLU:N	2.41	0.53
2:E:78:GLU:HG3	3:E:483:HOH:O	2.09	0.52
1:D:202:SER:HA	1:A:166:SER:O	2.10	0.52
2:E:145:LEU:HD13	3:E:365:HOH:O	2.11	0.51
1:A:74:THR:HG22	3:A:326:HOH:O	2.10	0.51
1:D:158:ASP:HB2	3:D:338:HOH:O	2.11	0.51
2:E:143:VAL:HG22	2:E:192:ARG:HG3	1.92	0.50
2:E:53:ALA:HB3	3:E:473:HOH:O	2.11	0.50
1:D:190:ASN:ND2	3:D:374:HOH:O	2.45	0.50
1:A:18:ASN:ND2	1:A:79:ALA:H	2.10	0.50
2:E:15:ARG:NE	2:E:84:GLN:HE21	2.10	0.49
1:A:61:ARG:NH2	1:A:84:ASP:OD1	2.29	0.48
1:A:133:SER:HB3	3:A:340:HOH:O	2.12	0.48
1:D:109:LEU:CD2	1:D:111:ARG:NH2	2.77	0.48
2:E:216:LEU:HD22	2:E:229:PRO:HG2	1.95	0.47
2:B:203:PRO:HA	2:B:240:GLY:O	2.13	0.47
1:A:128:LYS:HD3	3:A:398:HOH:O	2.14	0.47
1:A:18:ASN:HD22	1:A:78:ALA:HA	1.80	0.47
1:A:150:LYS:HD2	3:A:422:HOH:O	2.15	0.47
1:A:50:ILE:CD1	1:A:57:GLN:HB3	2.45	0.47
1:A:125:ARG:HB3	3:A:424:HOH:O	2.14	0.46
1:D:21:LEU:HD22	1:D:106:THR:HG21	1.97	0.46
2:B:152:ASP:HB2	2:B:175:PRO:HG2	1.97	0.46
2:E:10:HIS:HD2	2:E:153:HIS:ND1	2.14	0.46
2:E:163:LYS:HD2	3:E:317:HOH:O	2.14	0.46
1:A:115:GLN:HG2	3:A:427:HOH:O	2.16	0.46
1:A:196:GLU:HG2	3:A:396:HOH:O	2.15	0.46
2:E:55:LEU:HG	3:E:473:HOH:O	2.16	0.46
2:E:198:THR:HG23	3:E:419:HOH:O	2.15	0.45
2:E:52:GLU:H	2:E:52:GLU:CD	2.25	0.45
2:B:218:GLU:HA	2:B:218:GLU:OE2	2.16	0.45
1:D:61:ARG:NH2	1:D:84:ASP:OD1	2.40	0.45
2:E:83:GLU:HB3	3:E:445:HOH:O	2.16	0.45
2:E:145:LEU:HG	2:E:147:THR:HG23	1.99	0.45
1:D:125:ARG:HH22	1:D:204:GLU:CD	2.25	0.44
2:E:36:ARG:HD3	2:E:46:LEU:HD21	1.98	0.44
2:B:148:GLY:O	2:B:186:ARG:HD2	2.17	0.44
1:A:63:ASN:HD22	1:A:63:ASN:C	2.25	0.43
2:E:206:HIS:HE1	2:E:237:GLU:OE2	2.01	0.43
2:E:153:HIS:HB3	2:E:214:TYR:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:83:GLU:HB2	3:B:378:HOH:O	2.17	0.43
2:B:176:LEU:HD12	2:B:188:ALA:HB3	2.00	0.43
1:D:13:VAL:HG11	1:D:19:LEU:HD22	2.00	0.43
2:E:116:LEU:HD22	2:E:216:LEU:HD11	2.01	0.43
1:A:18:ASN:HD22	1:A:79:ALA:H	1.67	0.43
1:A:49:LEU:HD23	1:A:50:ILE:N	2.34	0.42
2:B:129:PRO:HD2	2:B:200:TRP:CZ2	2.55	0.42
2:B:176:LEU:CD1	2:B:188:ALA:HB3	2.49	0.42
2:B:7:ASN:CB	3:B:346:HOH:O	2.64	0.42
2:B:155:GLU:HG3	2:B:214:TYR:HE1	1.84	0.42
2:E:9:ARG:NH1	3:E:364:HOH:O	2.49	0.41
1:D:81:GLN:HG2	3:D:373:HOH:O	2.19	0.41
2:E:208:ARG:HD2	3:E:323:HOH:O	2.20	0.41
1:D:58:THR:HG22	1:D:63:ASN:HD22	1.85	0.40
2:B:31:ARG:HD2	3:B:432:HOH:O	2.21	0.40
2:E:145:LEU:HB2	3:E:365:HOH:O	2.20	0.40
1:D:2:GLN:HB3	1:D:101:ILE:HD13	2.03	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	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
1	D	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
2	B	240/244 (98%)	234 (98%)	6 (2%)	0	100	100
2	E	240/244 (98%)	233 (97%)	7 (3%)	0	100	100
All	All	884/898 (98%)	859 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	182/183 (100%)	174 (96%)	8 (4%)	25	24
1	D	182/183 (100%)	176 (97%)	6 (3%)	33	34
2	B	213/215 (99%)	203 (95%)	10 (5%)	23	22
2	E	213/215 (99%)	199 (93%)	14 (7%)	15	12
All	All	790/796 (99%)	752 (95%)	38 (5%)	23	21

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	19	LEU
1	D	42	LYS
1	D	58	THR
1	D	109	LEU
1	D	111	ARG
1	D	180	LYS
2	E	13	THR
2	E	24	ASP
2	E	27	SER
2	E	39	LEU
2	E	58	SER
2	E	109	ARG
2	E	179	GLN
2	E	182	LEU
2	E	183	ASN
2	E	192	ARG
2	E	208	ARG
2	E	212	GLN
2	E	216	LEU
2	E	243	ASP
1	A	5	THR
1	A	42	LYS
1	A	50	ILE
1	A	51	GLN

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Mol	Chain	Res	Type
1	A	74	THR
1	A	128	LYS
1	A	151	ASP
1	A	204	GLU
2	B	13	THR
2	B	39	LEU
2	B	50	GLN
2	B	84	GLN
2	B	109	ARG
2	B	179	GLN
2	B	192	ARG
2	B	204	ARG
2	B	217	SER
2	B	225	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	18	ASN
1	D	34	GLN
1	D	63	ASN
1	D	115	GLN
1	D	190	ASN
2	E	10	HIS
2	E	41	GLN
2	E	51	ASN
2	E	84	GLN
2	E	118	ASN
2	E	138	GLN
2	E	183	ASN
2	E	206	HIS
2	E	210	GLN
2	E	224	GLN
1	A	18	ASN
1	A	63	ASN
1	A	115	GLN
1	A	179	ASN
1	A	190	ASN
2	B	30	ASN
2	B	51	ASN
2	B	179	GLN
2	B	183	ASN

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Mol	Chain	Res	Type
2	B	212	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 oligosaccharides 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	204/205 (99%)	0.83	27 (13%) 7 6	13, 25, 48, 65	0
1	D	204/205 (99%)	0.42	12 (5%) 28 27	10, 20, 36, 57	0
2	B	242/244 (99%)	0.59	11 (4%) 38 37	12, 25, 41, 61	0
2	E	242/244 (99%)	0.77	26 (10%) 11 10	11, 25, 40, 55	0
All	All	892/898 (99%)	0.65	76 (8%) 16 15	10, 24, 41, 65	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	167	MET	6.2
1	A	169	PHE	5.5
1	A	181	SER	4.6
1	A	40	PRO	4.3
2	B	242	ALA	4.2
1	A	163	ASP	4.2
1	D	203	PRO	4.1
1	A	162	LEU	3.9
1	A	166	SER	3.9
2	B	218	GLU	3.7
2	E	182	LEU	3.6
1	A	165	ARG	3.6
2	E	181	ALA	3.6
2	E	243	ASP	3.5
1	A	153	ASP	3.5
1	D	41	GLY	3.5
2	E	2	THR	3.4
2	B	241	ARG	3.4
2	B	72	GLY	3.4
1	D	96	SER	3.2
1	A	168	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
2	E	16	GLY	3.2
1	A	129	SER	3.1
2	B	223	THR	3.1
2	B	2	THR	3.0
2	E	183	ASN	2.9
2	E	59	ARG	2.8
2	E	10	HIS	2.8
2	E	72	GLY	2.8
1	A	128	LYS	2.8
2	E	58	SER	2.7
1	A	3	GLU	2.7
2	B	97	TRP	2.7
2	E	184	ASP	2.7
1	A	164	MET	2.6
1	D	168	ASP	2.6
1	A	39	ASP	2.6
1	A	41	GLY	2.6
1	D	204	GLU	2.6
1	D	160	CYS	2.6
2	E	218	GLU	2.5
1	A	204	GLU	2.5
2	E	70	PRO	2.4
2	E	15	ARG	2.4
1	A	131	ASP	2.4
2	B	199	PHE	2.4
1	D	202	SER	2.4
2	E	13	THR	2.4
1	D	40	PRO	2.4
1	A	152	SER	2.4
2	E	180	PRO	2.4
2	B	39	LEU	2.3
1	A	202	SER	2.3
1	A	203	PRO	2.3
1	A	141	ASP	2.3
1	D	181	SER	2.3
2	E	27	SER	2.3
2	E	112	VAL	2.3
1	A	130	SER	2.2
1	A	179	ASN	2.2
2	E	39	LEU	2.2
1	A	151	ASP	2.2
2	E	74	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	39	ASP	2.2
2	B	9	ARG	2.2
1	A	1	LYS	2.2
2	E	179	GLN	2.1
1	A	145	ASN	2.1
1	D	182	ASP	2.1
2	E	84	GLN	2.1
2	E	152	ASP	2.1
1	D	42	LYS	2.1
2	E	73	SER	2.1
2	E	17	GLN	2.0
2	E	242	ALA	2.0
2	B	219	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.