Full wwPDB X-ray Structure Validation Report ⓘ

Nov 3, 2026 – 12:15 PM JST

PDB ID	:	9UP8 / pdb_00009up8
Title	:	Tacheng tick virus 1 nucleoprotein
Authors	:	Li, Z.; Sun, L.
Deposited on	:	2025-04-27
Resolution	:	2.52 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:

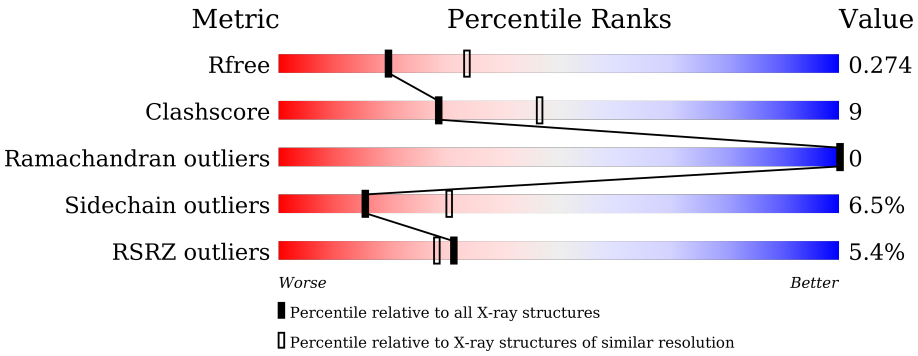
MolProbity	:	4-5-2 with Phenix2.2
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.52 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	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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	490	7% 73% 19% · 5%
1	B	490	3% 73% 20% · ·

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 7351 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	466	Total	C	N	O	S	0	0	0
			3669	2341	621	687	20			
1	B	468	Total	C	N	O	S	0	0	0
			3682	2350	623	689	20			

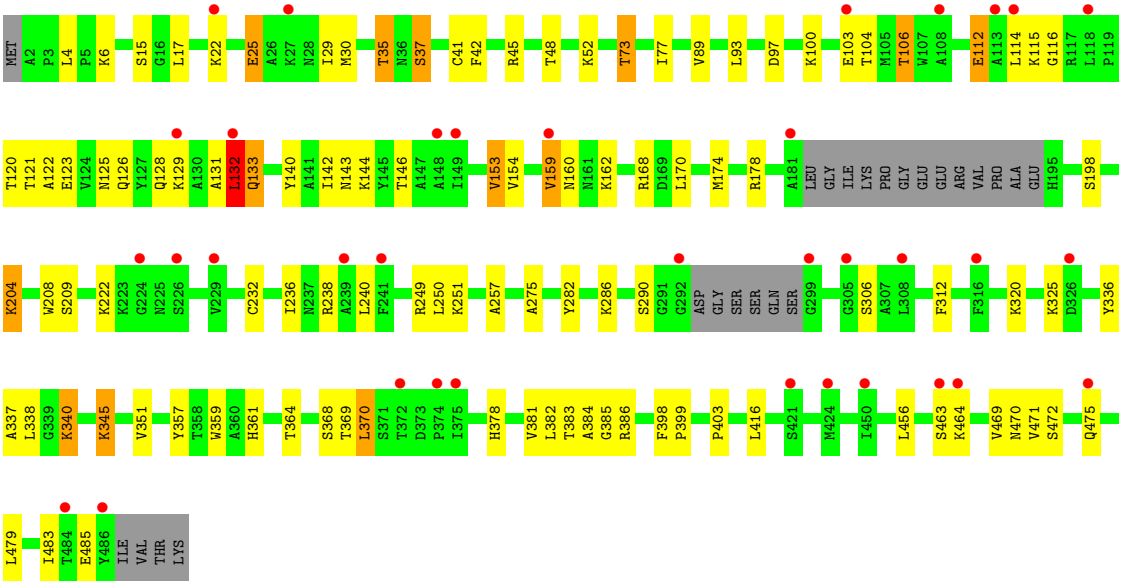
3 Residue-property plots (i)

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: Nucleoprotein

Chain A:

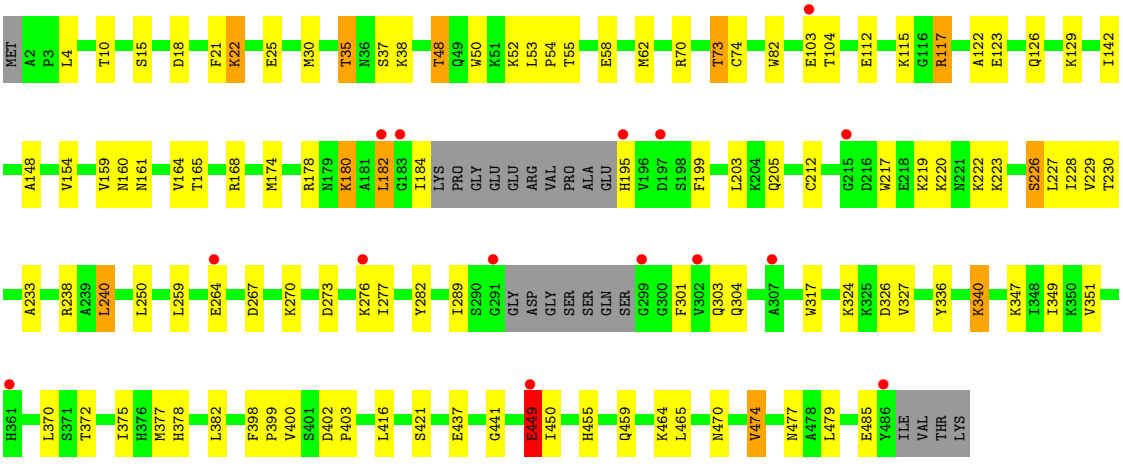




• Molecule 1: Nucleoprotein

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	154.56Å 78.75Å 92.64Å 90.00° 107.60° 90.00°	Depositor
Resolution (Å)	50.00 – 2.52 50.00 – 2.52	Depositor EDS
% Data completeness (in resolution range)	98.9 (50.00-2.52) 98.9 (50.00-2.52)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.04 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158, PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.223 , 0.273 0.224 , 0.274	Depositor DCC
R_{free} test set	1741 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å^2)	54.5	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7351	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.01% 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	0.44	1/3757 (0.0%)	0.69	4/5085 (0.1%)
1	B	0.45	0/3770	0.64	1/5103 (0.0%)
All	All	0.44	1/7527 (0.0%)	0.67	5/10188 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	133	GLN	CB-CG	-7.03	1.31	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	132	LEU	CA-C-N	-12.76	101.49	122.54
1	A	132	LEU	C-N-CA	-12.76	101.49	122.54
1	B	449	GLU	CB-CG-CD	6.35	123.39	112.60
1	A	133	GLN	CA-CB-CG	5.24	124.58	114.10
1	A	340	LYS	CA-CB-CG	5.09	124.27	114.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	449	GLU	Sidechain

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	A	3669	0	3631	59	0
1	B	3682	0	3644	69	1
All	All	7351	0	7275	128	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 9.

All (128) 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:449:GLU:HB3	1:B:450:ILE:HG13	1.52	0.92
1:A:336:TYR:CE2	1:A:340:LYS:HE3	2.18	0.77
1:B:53:LEU:HD12	1:B:58:GLU:HB3	1.68	0.76
1:A:170:LEU:O	1:A:174:MET:HG3	1.87	0.73
1:A:361:HIS:O	1:A:364:THR:HG22	1.89	0.73
1:B:154:VAL:HG22	1:B:464:LYS:HE2	1.70	0.71
1:B:50:TRP:CE3	1:B:62:MET:HG2	2.26	0.70
1:B:303:GLN:NE2	1:B:304:GLN:OE1	2.27	0.68
1:A:338:LEU:HD21	1:A:351:VAL:HG21	1.73	0.68
1:A:463:SER:HB3	1:A:471:VAL:HG11	1.76	0.68
1:B:219:LYS:HD2	1:B:220:LYS:H	1.57	0.68
1:A:337:ALA:HA	1:A:340:LYS:HD2	1.75	0.67
1:B:227:LEU:HD12	1:B:227:LEU:H	1.59	0.66
1:A:378:HIS:O	1:A:381:VAL:HG12	1.95	0.65
1:B:238:ARG:O	1:B:240:LEU:N	2.29	0.65
1:B:233:ALA:HB1	1:B:289:ILE:HD11	1.79	0.64
1:B:223:LYS:HE2	1:B:372:THR:O	1.99	0.62
1:A:97:ASP:HA	1:A:100:LYS:HE3	1.82	0.61
1:B:455:HIS:O	1:B:459:GLN:HG3	2.00	0.60
1:A:160:ASN:OD1	1:A:162:LYS:HG3	2.01	0.60
1:A:128:GLN:O	1:A:132:LEU:HD12	2.01	0.59
1:A:178:ARG:HG3	1:A:479:LEU:HD13	1.84	0.59
1:B:324:LYS:HD2	1:B:326:ASP:HB2	1.84	0.59
1:B:55:THR:HG23	1:B:58:GLU:H	1.66	0.59
1:A:168:ARG:NH1	1:A:483:ILE:O	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:ALA:O	1:B:126:GLN:HG3	2.04	0.58
1:B:70:ARG:NH2	1:B:437:GLU:OE2	2.36	0.57
1:B:250:LEU:HD12	1:B:282:TYR:HB2	1.84	0.57
1:A:383:THR:CG2	1:A:386:ARG:H	2.18	0.57
1:B:54:PRO:HD2	1:B:58:GLU:OE1	2.05	0.57
1:A:383:THR:HG22	1:A:386:ARG:H	1.69	0.57
1:B:195:HIS:CD2	1:B:227:LEU:HD23	2.40	0.56
1:A:345:LYS:HE2	1:A:384:ALA:HB3	1.87	0.56
1:B:104:THR:HA	1:B:126:GLN:HB3	1.86	0.56
1:B:304:GLN:HE21	1:B:474:VAL:HG12	1.71	0.56
1:B:161:ASN:O	1:B:164:VAL:HG12	2.07	0.55
1:A:232:CYS:O	1:A:236:ILE:HG13	2.06	0.55
1:B:264:GLU:HA	1:B:264:GLU:OE1	2.07	0.54
1:A:116:GLY:HA2	1:A:370:LEU:HD23	1.90	0.53
1:B:4:LEU:HD11	1:B:327:VAL:HG12	1.88	0.53
1:B:52:LYS:NZ	1:B:441:GLY:O	2.42	0.53
1:B:273:ASP:O	1:B:277:ILE:HG13	2.09	0.53
1:A:116:GLY:HA2	1:A:370:LEU:CD2	2.39	0.53
1:B:212:CYS:HB2	1:B:217:TRP:CE2	2.44	0.53
1:B:219:LYS:HD2	1:B:220:LYS:N	2.23	0.52
1:B:217:TRP:CE3	1:B:228:ILE:HD12	2.45	0.52
1:B:18:ASP:O	1:B:22:LYS:HG2	2.09	0.52
1:B:347:LYS:O	1:B:351:VAL:HG23	2.10	0.52
1:B:164:VAL:O	1:B:168:ARG:HG3	2.11	0.51
1:A:257:ALA:HB3	1:A:275:ALA:HB2	1.93	0.51
1:B:55:THR:HG22	1:B:58:GLU:OE1	2.11	0.51
1:B:174:MET:HG2	1:B:301:PHE:CZ	2.45	0.51
1:B:199:PHE:CZ	1:B:203:LEU:HD11	2.47	0.50
1:A:463:SER:HB3	1:A:471:VAL:CG1	2.41	0.50
1:B:336:TYR:CZ	1:B:340:LYS:HD2	2.47	0.49
1:B:370:LEU:HD21	1:B:372:THR:OG1	2.12	0.49
1:A:238:ARG:O	1:A:240:LEU:N	2.44	0.49
1:A:383:THR:HG23	1:A:385:GLY:N	2.28	0.49
1:B:267:ASP:OD2	1:B:270:LYS:HD2	2.11	0.49
1:B:222:LYS:HD2	1:B:222:LYS:N	2.28	0.49
1:A:475:GLN:HA	1:A:475:GLN:OE1	2.13	0.48
1:A:159:VAL:HG23	1:A:160:ASN:O	2.14	0.48
1:B:70:ARG:HH21	1:B:437:GLU:CD	2.21	0.48
1:A:121:THR:O	1:A:125:ASN:ND2	2.47	0.47
1:A:153:VAL:HG23	1:A:154:VAL:O	2.15	0.47
1:B:273:ASP:O	1:B:276:LYS:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:TYR:CD2	1:B:399:PRO:HG3	2.49	0.47
1:A:29:ILE:HG22	1:A:42:PHE:CZ	2.49	0.47
1:B:180:LYS:HG3	1:B:180:LYS:O	2.14	0.47
1:A:238:ARG:O	1:A:240:LEU:HD12	2.15	0.47
1:A:122:ALA:O	1:A:126:GLN:HG3	2.15	0.47
1:A:45:ARG:HH21	1:A:48:THR:HG21	1.80	0.46
1:B:73:THR:HG22	1:B:74:CYS:SG	2.55	0.46
1:B:10:THR:O	1:B:10:THR:OG1	2.29	0.46
1:B:212:CYS:HB2	1:B:217:TRP:CD2	2.50	0.46
1:B:112:GLU:HA	1:B:115:LYS:HD3	1.97	0.46
1:A:89:VAL:HG13	1:A:93:LEU:HD13	1.97	0.46
1:A:120:THR:HG23	1:A:123:GLU:OE1	2.16	0.45
1:B:199:PHE:O	1:B:203:LEU:HD12	2.16	0.45
1:A:35:THR:HG23	1:A:37:SER:O	2.16	0.45
1:B:55:THR:HG22	1:B:58:GLU:CD	2.40	0.45
1:B:178:ARG:HE	1:B:178:ARG:HB3	1.56	0.45
1:A:41:CYS:HA	1:A:73:THR:HG23	1.97	0.45
1:B:21:PHE:CZ	1:B:30:MET:HE1	2.52	0.45
1:B:159:VAL:HG23	1:B:160:ASN:O	2.17	0.44
1:A:208:TRP:CE2	1:A:209:SER:HB3	2.51	0.44
1:A:336:TYR:CG	1:A:399:PRO:HD3	2.53	0.44
1:A:345:LYS:HG3	1:A:384:ALA:HB2	2.00	0.44
1:A:103:GLU:O	1:A:106:THR:OG1	2.33	0.44
1:B:230:THR:O	1:B:233:ALA:HB3	2.17	0.44
1:A:116:GLY:O	1:A:370:LEU:HD21	2.17	0.44
1:A:470:ASN:OD1	1:A:472:SER:HB3	2.18	0.44
1:A:131:ALA:HA	1:A:312:PHE:CD1	2.53	0.43
1:B:398:PHE:CD1	1:B:403:PRO:HA	2.54	0.43
1:A:357:TYR:HB3	1:A:359:TRP:CD1	2.53	0.43
1:B:25:GLU:OE2	1:B:38:LYS:HE3	2.19	0.43
1:B:82:TRP:CE2	1:B:142:ILE:HD13	2.54	0.43
1:A:140:TYR:O	1:A:142:ILE:HG23	2.19	0.42
1:A:398:PHE:CD1	1:A:403:PRO:HA	2.54	0.42
1:B:22:LYS:HG2	1:B:22:LYS:H	1.70	0.42
1:A:144:LYS:H	1:A:144:LYS:HG2	1.63	0.42
1:A:204:LYS:O	1:A:249:ARG:NH2	2.52	0.42
1:A:22:LYS:HD3	1:A:25:GLU:OE2	2.19	0.42
1:B:48:THR:HG23	1:B:437:GLU:OE2	2.19	0.42
1:A:159:VAL:O	1:A:485:GLU:HA	2.19	0.42
1:A:416:LEU:HD22	1:A:456:LEU:HB3	2.00	0.42
1:B:50:TRP:H	1:B:50:TRP:CD1	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:ALA:HA	1:B:470:ASN:HB3	2.00	0.42
1:B:182:LEU:O	1:B:184:ILE:N	2.49	0.42
1:B:317:TRP:CD2	1:B:382:LEU:HD13	2.55	0.42
1:A:282:TYR:CE2	1:A:286:LYS:HD2	2.55	0.42
1:B:226:SER:HB2	1:B:229:VAL:HG23	2.01	0.41
1:B:35:THR:HG23	1:B:37:SER:O	2.20	0.41
1:B:349:ILE:HD13	1:B:349:ILE:HA	1.80	0.41
1:A:383:THR:HG23	1:A:385:GLY:H	1.85	0.41
1:B:117:ARG:HH12	1:B:123:GLU:CD	2.28	0.41
1:B:377:MET:O	1:B:378:HIS:C	2.63	0.41
1:A:143:ASN:H	1:A:146:THR:HG1	1.68	0.41
1:A:45:ARG:HH21	1:A:48:THR:CG2	2.34	0.41
1:A:112:GLU:OE2	1:A:115:LYS:HD3	2.20	0.41
1:B:375:ILE:HD12	1:B:455:HIS:NE2	2.35	0.41
1:A:250:LEU:HD23	1:A:250:LEU:HA	1.88	0.41
1:B:159:VAL:O	1:B:485:GLU:HA	2.20	0.41
1:A:123:GLU:HA	1:A:126:GLN:NE2	2.36	0.40
1:A:30:MET:HE3	1:A:77:ILE:HG13	2.04	0.40
1:A:104:THR:HG22	1:A:129:LYS:HG2	2.03	0.40
1:B:479:LEU:HD23	1:B:479:LEU:HA	1.87	0.40
1:A:114:LEU:HD13	1:A:378:HIS:CG	2.57	0.40

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)
1:B:205:GLN:NE2	1:B:402:ASP:OD2[2_655]	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	A	460/490 (94%)	444 (96%)	16 (4%)	0	100	100
1	B	462/490 (94%)	447 (97%)	15 (3%)	0	100	100
All	All	922/980 (94%)	891 (97%)	31 (3%)	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	393/413 (95%)	363 (92%)	30 (8%)	12	24
1	B	394/413 (95%)	373 (95%)	21 (5%)	20	39
All	All	787/826 (95%)	736 (94%)	51 (6%)	15	30

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	6	LYS
1	A	15	SER
1	A	17	LEU
1	A	25	GLU
1	A	35	THR
1	A	37	SER
1	A	52	LYS
1	A	73	THR
1	A	106	THR
1	A	112	GLU
1	A	132	LEU
1	A	133	GLN
1	A	153	VAL
1	A	159	VAL
1	A	198	SER
1	A	204	LYS
1	A	222	LYS

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Mol	Chain	Res	Type
1	A	251	LYS
1	A	290	SER
1	A	306	SER
1	A	320	LYS
1	A	325	LYS
1	A	345	LYS
1	A	368	SER
1	A	369	THR
1	A	370	LEU
1	A	382	LEU
1	A	464	LYS
1	A	469	VAL
1	B	15	SER
1	B	22	LYS
1	B	35	THR
1	B	48	THR
1	B	73	THR
1	B	103	GLU
1	B	117	ARG
1	B	129	LYS
1	B	165	THR
1	B	180	LYS
1	B	182	LEU
1	B	226	SER
1	B	240	LEU
1	B	259	LEU
1	B	340	LYS
1	B	400	VAL
1	B	416	LEU
1	B	421	SER
1	B	465	LEU
1	B	474	VAL
1	B	477	ASN

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

Mol	Chain	Res	Type
1	A	28	ASN
1	A	49	GLN
1	A	125	ASN
1	A	161	ASN
1	B	28	ASN

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Mol	Chain	Res	Type
1	B	65	GLN
1	B	125	ASN
1	B	361	HIS

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, 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	466/490 (95%)	0.71	35 (7%)	20	18	36, 64, 95, 137	0
1	B	468/490 (95%)	0.45	15 (3%)	50	47	36, 57, 82, 111	0
All	All	934/980 (95%)	0.58	50 (5%)	31	28	36, 59, 91, 137	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	449	GLU	4.4
1	A	486	TYR	3.9
1	B	215	GLY	3.6
1	B	276	LYS	3.5
1	A	372	THR	3.4
1	B	182	LEU	2.9
1	B	183	GLY	2.8
1	B	291	GLY	2.8
1	A	305	GLY	2.7
1	B	299	GLY	2.7
1	A	421	SER	2.7
1	A	181	ALA	2.7
1	A	374	PRO	2.6
1	A	375	ILE	2.6
1	A	22	LYS	2.6
1	A	299	GLY	2.6
1	A	326	ASP	2.6
1	A	241	PHE	2.5
1	B	361	HIS	2.5
1	A	148	ALA	2.5
1	A	224	GLY	2.4
1	A	27	LYS	2.4
1	B	486	TYR	2.4
1	A	108	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	239	ALA	2.4
1	A	424	MET	2.3
1	B	302	VAL	2.3
1	A	159	VAL	2.3
1	A	103	GLU	2.3
1	B	103	GLU	2.3
1	A	226	SER	2.3
1	A	114	LEU	2.3
1	A	484	THR	2.3
1	A	118	LEU	2.3
1	A	229	VAL	2.2
1	B	195	HIS	2.2
1	A	316	PHE	2.2
1	A	308	LEU	2.2
1	A	464	LYS	2.2
1	B	307	ALA	2.1
1	B	264	GLU	2.1
1	A	129	LYS	2.1
1	A	113	ALA	2.1
1	A	463	SER	2.1
1	A	475	GLN	2.1
1	A	132	LEU	2.1
1	B	197	ASP	2.1
1	A	149	ILE	2.0
1	A	292	GLY	2.0
1	A	450	ILE	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.