



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:00 AM UTC

PDB ID : 5VU5 / pdb_00005vu5
Title : TNA polymerase, apo
Authors : Chim, N.; Chaput, J.C.
Deposited on : 2017-05-18
Resolution : 2.80 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

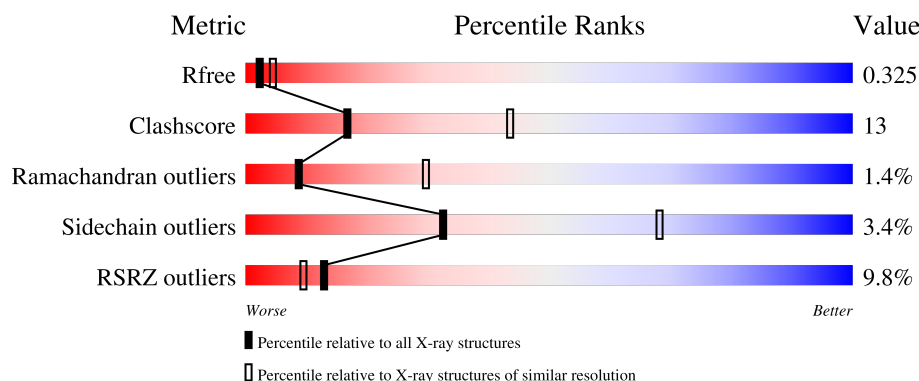
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	774	9% 64% 25% 9%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5738 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 DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	707	Total	C	N	O	S	0	0	0
			5738	3696	967	1059	16			

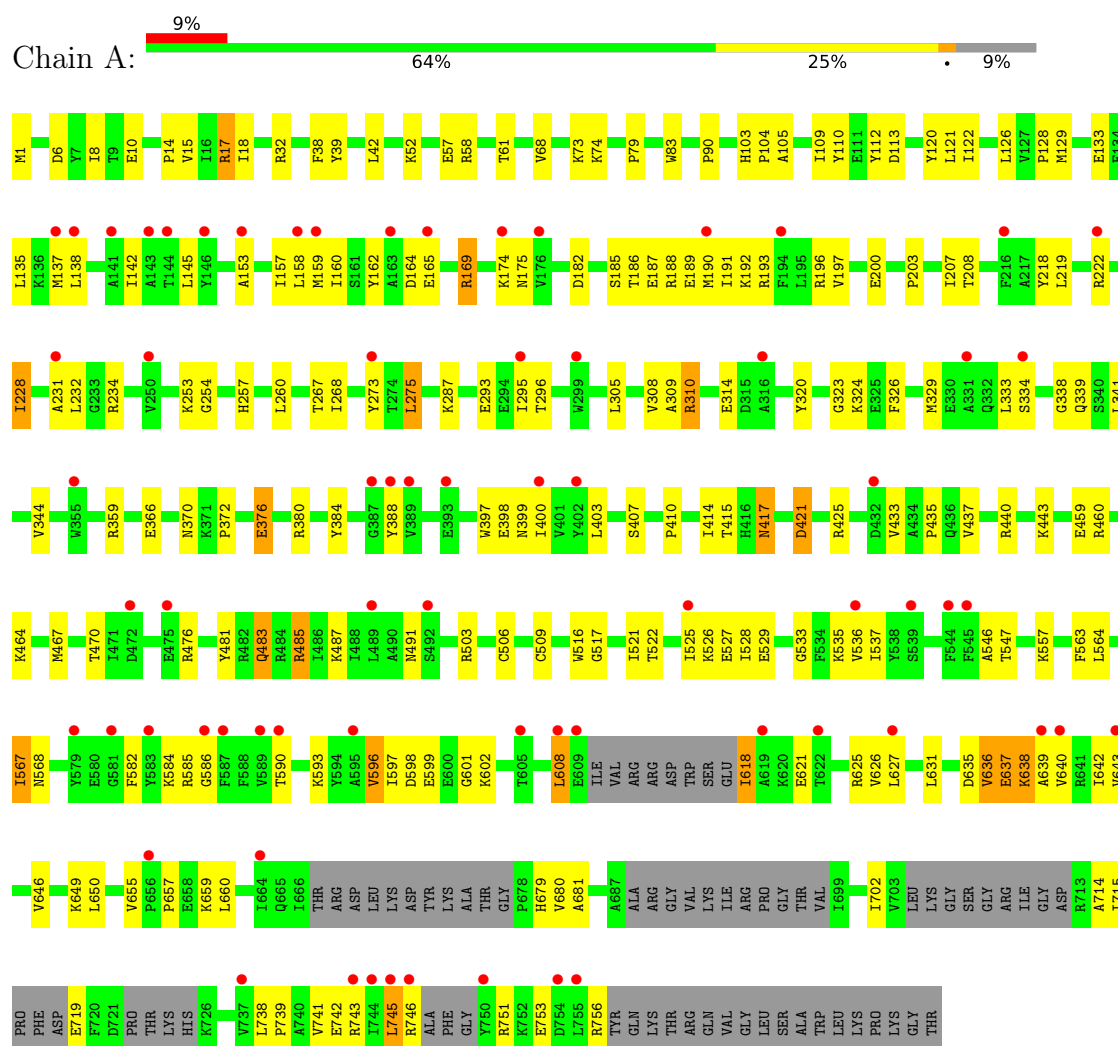
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ALA	ASP	engineered mutation	UNP D0VWU9
A	143	ALA	GLU	engineered mutation	UNP D0VWU9
A	147	HIS	GLU	engineered mutation	UNP D0VWU9
A	485	ARG	ALA	engineered mutation	UNP D0VWU9
A	584	LYS	GLU	engineered mutation	UNP D0VWU9
A	664	ILE	GLU	engineered mutation	UNP D0VWU9

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: DNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.82Å 110.62Å 111.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	55.31 – 2.80 55.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	86.4 (55.31-2.80) 75.2 (55.31-2.80)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.268 , 0.317 0.285 , 0.325	Depositor DCC
R_{free} test set	1989 reflections (7.22%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	0.488	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.022 for -h,l,k	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5738	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.95% 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 [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	A	0.12	0/5860	0.36	0/7906

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	A	5738	0	5661	146	0
All	All	5738	0	5661	146	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 13.

All (146) 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:267:THR:HG23	1:A:268:ILE:HG13	1.70	0.73
1:A:384:TYR:OH	1:A:388:TYR:OH	2.07	0.70
1:A:169:ARG:NH1	1:A:182:ASP:OD1	2.26	0.69
1:A:521:ILE:O	1:A:525:ILE:N	2.26	0.68
1:A:529:GLU:HA	1:A:533:GLY:O	1.93	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:586:GLY:HA3	1:A:596:VAL:HG13	1.76	0.67
1:A:593:LYS:HD3	1:A:608:LEU:HD13	1.77	0.66
1:A:460:ARG:HE	1:A:483:GLN:HG2	1.61	0.66
1:A:638:LYS:O	1:A:642:ILE:N	2.29	0.65
1:A:643:VAL:HG11	1:A:741:VAL:HG21	1.78	0.65
1:A:126:LEU:O	1:A:359:ARG:NH2	2.30	0.65
1:A:626:VAL:HG13	1:A:639:ALA:HB1	1.78	0.65
1:A:376:GLU:OE2	1:A:380:ARG:NE	2.29	0.65
1:A:333:LEU:HD13	1:A:485:ARG:HD2	1.79	0.64
1:A:751:ARG:HG3	1:A:753:GLU:H	1.61	0.64
1:A:464:LYS:HG2	1:A:467:MET:HE2	1.79	0.64
1:A:608:LEU:HD11	1:A:743:ARG:HB3	1.81	0.63
1:A:338:GLY:O	1:A:359:ARG:NH1	2.32	0.62
1:A:109:ILE:O	1:A:370:ASN:ND2	2.31	0.61
1:A:397:TRP:HB2	1:A:400:ILE:HD11	1.82	0.61
1:A:526:LYS:C	1:A:528:ILE:H	2.08	0.61
1:A:159:MET:HA	1:A:190:MET:HE1	1.82	0.61
1:A:39:TYR:HB2	1:A:110:TYR:HB2	1.83	0.60
1:A:596:VAL:HG12	1:A:597:ILE:H	1.67	0.59
1:A:203:PRO:O	1:A:234:ARG:NH1	2.35	0.59
1:A:164:ASP:OD1	1:A:165:GLU:N	2.35	0.59
1:A:590:THR:OG1	1:A:746:ARG:NH1	2.35	0.59
1:A:129:MET:HE1	1:A:135:LEU:HD11	1.85	0.59
1:A:157:ILE:HD12	1:A:222:ARG:HH21	1.67	0.59
1:A:464:LYS:HG3	1:A:483:GLN:HG3	1.85	0.58
1:A:537:ILE:HD11	1:A:547:THR:HG22	1.83	0.58
1:A:417:ASN:HB2	1:A:443:LYS:HE3	1.85	0.58
1:A:6:ASP:OD2	1:A:253:LYS:NZ	2.31	0.58
1:A:8:ILE:HG13	1:A:17:ARG:HD3	1.85	0.58
1:A:169:ARG:HH11	1:A:169:ARG:HB3	1.69	0.57
1:A:137:MET:HE2	1:A:207:ILE:HD11	1.86	0.57
1:A:10:GLU:OE1	1:A:32:ARG:NH2	2.38	0.56
1:A:415:THR:O	1:A:443:LYS:NZ	2.37	0.56
1:A:637:GLU:O	1:A:639:ALA:N	2.39	0.56
1:A:186:THR:OG1	1:A:187:GLU:N	2.38	0.55
1:A:208:THR:OG1	1:A:257:HIS:NE2	2.36	0.55
1:A:287:LYS:HE2	1:A:314:GLU:HG2	1.88	0.55
1:A:470:THR:O	1:A:476:ARG:NH1	2.35	0.55
1:A:421:ASP:OD1	1:A:421:ASP:N	2.23	0.55
1:A:741:VAL:O	1:A:745:LEU:N	2.36	0.54
1:A:142:ILE:HD13	1:A:219:LEU:HG	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:SER:HB3	1:A:410:PRO:HG2	1.90	0.54
1:A:557:LYS:HE2	1:A:582:PHE:CG	2.43	0.54
1:A:74:LYS:HE3	1:A:366:GLU:HG2	1.89	0.53
1:A:598:ASP:OD1	1:A:599:GLU:N	2.32	0.52
1:A:165:GLU:HG3	1:A:320:TYR:OH	2.10	0.52
1:A:74:LYS:HA	1:A:79:PRO:HA	1.92	0.52
1:A:121:LEU:O	1:A:359:ARG:NH2	2.43	0.52
1:A:679:HIS:C	1:A:681:ALA:H	2.19	0.51
1:A:196:ARG:O	1:A:200:GLU:HG2	2.10	0.51
1:A:188:ARG:HE	1:A:192:LYS:HD3	1.75	0.51
1:A:529:GLU:OE1	1:A:535:LYS:NZ	2.44	0.51
1:A:590:THR:HG1	1:A:746:ARG:NH1	2.09	0.51
1:A:122:ILE:HG23	1:A:359:ARG:HA	1.93	0.50
1:A:739:PRO:HA	1:A:743:ARG:HG2	1.93	0.50
1:A:753:GLU:HA	1:A:756:ARG:HG3	1.94	0.50
1:A:113:ASP:OD1	1:A:503:ARG:NH2	2.39	0.49
1:A:174:LYS:HG3	1:A:175:ASN:H	1.76	0.49
1:A:719:GLU:N	1:A:719:GLU:OE1	2.45	0.49
1:A:525:ILE:HG23	1:A:536:VAL:HG21	1.93	0.49
1:A:372:PRO:HG3	1:A:380:ARG:NH1	2.27	0.49
1:A:585:ARG:HD2	1:A:631:LEU:O	2.11	0.49
1:A:646:VAL:O	1:A:650:LEU:N	2.39	0.49
1:A:38:PHE:HE1	1:A:109:ILE:HD12	1.78	0.49
1:A:334:SER:HA	1:A:344:VAL:HG21	1.95	0.49
1:A:397:TRP:O	1:A:586:GLY:N	2.40	0.49
1:A:597:ILE:HG12	1:A:598:ASP:H	1.76	0.49
1:A:460:ARG:HH21	1:A:483:GLN:HE21	1.60	0.48
1:A:1:MET:HG3	1:A:133:GLU:HB2	1.95	0.48
1:A:57:GLU:OE2	1:A:61:THR:N	2.47	0.48
1:A:129:MET:HE2	1:A:341:LEU:HD12	1.94	0.48
1:A:153:ALA:HA	1:A:218:TYR:CZ	2.49	0.48
1:A:109:ILE:HG22	1:A:112:TYR:CD2	2.49	0.48
1:A:142:ILE:HG22	1:A:160:ILE:HG12	1.95	0.48
1:A:637:GLU:HG2	1:A:638:LYS:H	1.78	0.48
1:A:57:GLU:OE2	1:A:58:ARG:N	2.47	0.47
1:A:751:ARG:HG3	1:A:753:GLU:N	2.29	0.47
1:A:295:ILE:HG13	1:A:308:VAL:HG23	1.97	0.47
1:A:506:CYS:SG	1:A:509:CYS:N	2.86	0.47
1:A:526:LYS:HA	1:A:529:GLU:HG2	1.97	0.46
1:A:14:PRO:HG3	1:A:90:PRO:HD3	1.97	0.46
1:A:517:GLY:O	1:A:521:ILE:HG12	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:679:HIS:O	1:A:681:ALA:N	2.49	0.46
1:A:526:LYS:C	1:A:528:ILE:N	2.74	0.46
1:A:267:THR:HG21	1:A:326:PHE:HE2	1.80	0.46
1:A:267:THR:HG21	1:A:326:PHE:CE2	2.50	0.46
1:A:597:ILE:HD11	1:A:601:GLY:HA2	1.98	0.45
1:A:618:ILE:HD13	1:A:660:LEU:HA	1.98	0.45
1:A:649:LYS:O	1:A:655:VAL:N	2.49	0.45
1:A:268:ILE:O	1:A:273:TYR:OH	2.26	0.45
1:A:260:LEU:HD21	1:A:323:GLY:HA2	1.99	0.45
1:A:738:LEU:O	1:A:742:GLU:N	2.46	0.45
1:A:103:HIS:CE1	1:A:105:ALA:HB3	2.51	0.45
1:A:192:LYS:HG2	1:A:228:ILE:HD12	1.99	0.45
1:A:536:VAL:HG12	1:A:546:ALA:HB2	1.99	0.45
1:A:637:GLU:O	1:A:640:VAL:N	2.48	0.44
1:A:191:ILE:HD11	1:A:222:ARG:NH2	2.32	0.44
1:A:738:LEU:HB3	1:A:739:PRO:HD3	2.00	0.44
1:A:234:ARG:NH2	1:A:254:GLY:O	2.43	0.44
1:A:403:LEU:HD22	1:A:564:LEU:HD21	2.00	0.44
1:A:433:VAL:HG22	1:A:440:ARG:HG3	1.99	0.44
1:A:563:PHE:O	1:A:567:ILE:HG13	2.17	0.44
1:A:15:VAL:HG22	1:A:32:ARG:HG2	1.99	0.43
1:A:186:THR:HG23	1:A:188:ARG:H	1.83	0.43
1:A:145:LEU:HB2	1:A:158:LEU:HD11	1.99	0.43
1:A:398:GLU:HA	1:A:584:LYS:O	2.18	0.43
1:A:158:LEU:HB3	1:A:159:MET:HE2	2.00	0.42
1:A:702:ILE:O	1:A:714:ALA:HB3	2.19	0.42
1:A:309:ALA:O	1:A:310:ARG:HB2	2.19	0.42
1:A:329:MET:H	1:A:329:MET:HG2	1.71	0.42
1:A:526:LYS:O	1:A:528:ILE:N	2.45	0.42
1:A:18:ILE:HD11	1:A:120:TYR:HE2	1.85	0.42
1:A:160:ILE:H	1:A:190:MET:HE1	1.85	0.42
1:A:187:GLU:OE1	1:A:222:ARG:HD2	2.19	0.42
1:A:275:LEU:HD23	1:A:275:LEU:HA	1.92	0.42
1:A:399:ASN:HA	1:A:582:PHE:CZ	2.54	0.42
1:A:621:GLU:O	1:A:625:ARG:HG3	2.20	0.42
1:A:567:ILE:HD12	1:A:568:ASN:N	2.35	0.42
1:A:103:HIS:CD2	1:A:104:PRO:HD2	2.55	0.42
1:A:329:MET:HE2	1:A:481:TYR:CE2	2.55	0.41
1:A:190:MET:HB2	1:A:190:MET:HE3	1.82	0.41
1:A:305:LEU:HA	1:A:308:VAL:HG12	2.02	0.41
1:A:138:LEU:HD21	1:A:162:TYR:HB2	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:TYR:CE2	1:A:169:ARG:HB2	2.55	0.41
1:A:435:PRO:O	1:A:437:VAL:N	2.43	0.41
1:A:637:GLU:O	1:A:638:LYS:C	2.64	0.41
1:A:618:ILE:HG23	1:A:659:LYS:C	2.45	0.41
1:A:39:TYR:CZ	1:A:73:LYS:HE3	2.56	0.41
1:A:635:ASP:OD1	1:A:636:VAL:N	2.53	0.41
1:A:193:ARG:O	1:A:197:VAL:HG23	2.20	0.41
1:A:293:GLU:HA	1:A:296:THR:HG22	2.02	0.41
1:A:679:HIS:C	1:A:681:ALA:N	2.78	0.41
1:A:715:ILE:H	1:A:719:GLU:HB2	1.86	0.41
1:A:68:VAL:HG22	1:A:83:TRP:HE3	1.85	0.41
1:A:128:PRO:HG2	1:A:339:GLN:C	2.46	0.40
1:A:232:LEU:HD23	1:A:232:LEU:HA	1.90	0.40
1:A:52:LYS:HD3	1:A:68:VAL:HG11	2.03	0.40
1:A:324:LYS:HE2	1:A:324:LYS:HB3	1.96	0.40
1:A:522:THR:HA	1:A:525:ILE:HB	2.03	0.40
1:A:487:LYS:O	1:A:491:ASN:ND2	2.35	0.40
1:A:657:PRO:C	1:A:659:LYS:H	2.29	0.40

There are no symmetry-related clashes.

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	691/774 (89%)	636 (92%)	45 (6%)	10 (1%)	9	30

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	638	LYS
1	A	185	SER
1	A	310	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	459	GLU
1	A	636	VAL
1	A	680	VAL
1	A	231	ALA
1	A	602	LYS
1	A	608	LEU
1	A	527	GLU

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	592/673 (88%)	572 (97%)	20 (3%)	32	68

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	42	LEU
1	A	169	ARG
1	A	189	GLU
1	A	228	ILE
1	A	275	LEU
1	A	376	GLU
1	A	414	ILE
1	A	417	ASN
1	A	421	ASP
1	A	425	ARG
1	A	483	GLN
1	A	485	ARG
1	A	516	TRP
1	A	567	ILE
1	A	596	VAL
1	A	618	ILE
1	A	627	LEU
1	A	637	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	745	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	339	GLN
1	A	399	ASN
1	A	483	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	707/774 (91%)	0.74	69 (9%) 13 9	45, 102, 206, 264	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	579	TYR	4.9
1	A	222	ARG	4.7
1	A	587	PHE	4.6
1	A	137	MET	4.4
1	A	627	LEU	4.0
1	A	190	MET	3.8
1	A	545	PHE	3.8
1	A	609	GLU	3.7
1	A	299	TRP	3.6
1	A	295	ILE	3.5
1	A	608	LEU	3.4
1	A	639	ALA	3.4
1	A	643	VAL	3.3
1	A	158	LEU	3.3
1	A	640	VAL	3.2
1	A	159	MET	3.2
1	A	432	ASP	3.2
1	A	525	ILE	3.2
1	A	581	GLY	3.0
1	A	146	TYR	3.0
1	A	746	ARG	3.0
1	A	754	ASP	2.9
1	A	144	THR	2.9
1	A	273	TYR	2.9
1	A	539	SER	2.9
1	A	331	ALA	2.9
1	A	536	VAL	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	389	VAL	2.8
1	A	387	GLY	2.8
1	A	586	GLY	2.7
1	A	194	PHE	2.6
1	A	595	ALA	2.6
1	A	589	VAL	2.6
1	A	231	ALA	2.6
1	A	619	ALA	2.6
1	A	743	ARG	2.5
1	A	250	VAL	2.5
1	A	472	ASP	2.5
1	A	622	THR	2.5
1	A	165	GLU	2.5
1	A	489	LEU	2.4
1	A	153	ALA	2.4
1	A	744	ILE	2.4
1	A	750	TYR	2.4
1	A	755	LEU	2.4
1	A	174	LYS	2.3
1	A	138	LEU	2.3
1	A	583	TYR	2.3
1	A	656	PRO	2.3
1	A	737	VAL	2.3
1	A	141	ALA	2.2
1	A	393	GLU	2.2
1	A	492	SER	2.2
1	A	745	LEU	2.2
1	A	163	ALA	2.2
1	A	316	ALA	2.2
1	A	400	ILE	2.2
1	A	664	ILE	2.2
1	A	388	TYR	2.2
1	A	605	THR	2.1
1	A	216	PHE	2.1
1	A	590	THR	2.1
1	A	475	GLU	2.1
1	A	143	ALA	2.1
1	A	402	TYR	2.1
1	A	355	TRP	2.0
1	A	176	VAL	2.0
1	A	334	SER	2.0
1	A	544	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 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.