



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 12:24 PM UTC

PDB ID : 6Z03 / pdb_00006z03
Title : DNA Topoisomerase
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Deposited on : 2020-05-07
Resolution : 2.20 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

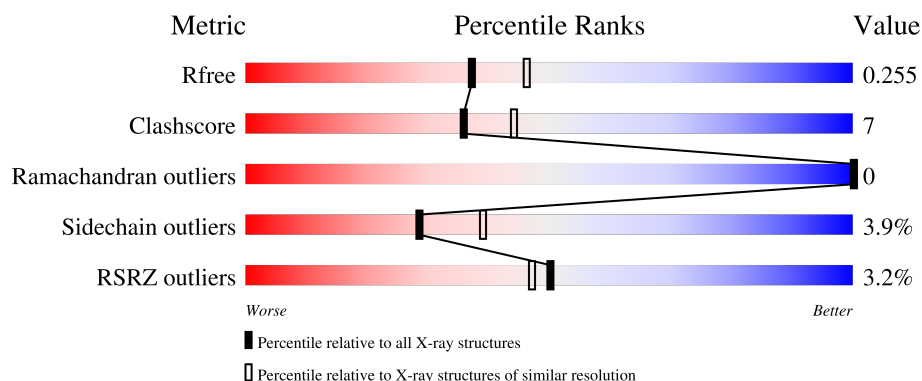
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	539	2% 78% 17% ..
1	B	539	4% 79% 15% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9140 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 topoisomerase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	522	Total	C	N	O	S	0	0	0
			4357	2786	780	781	10			
1	B	521	Total	C	N	O	S	0	0	0
			4350	2781	779	780	10			

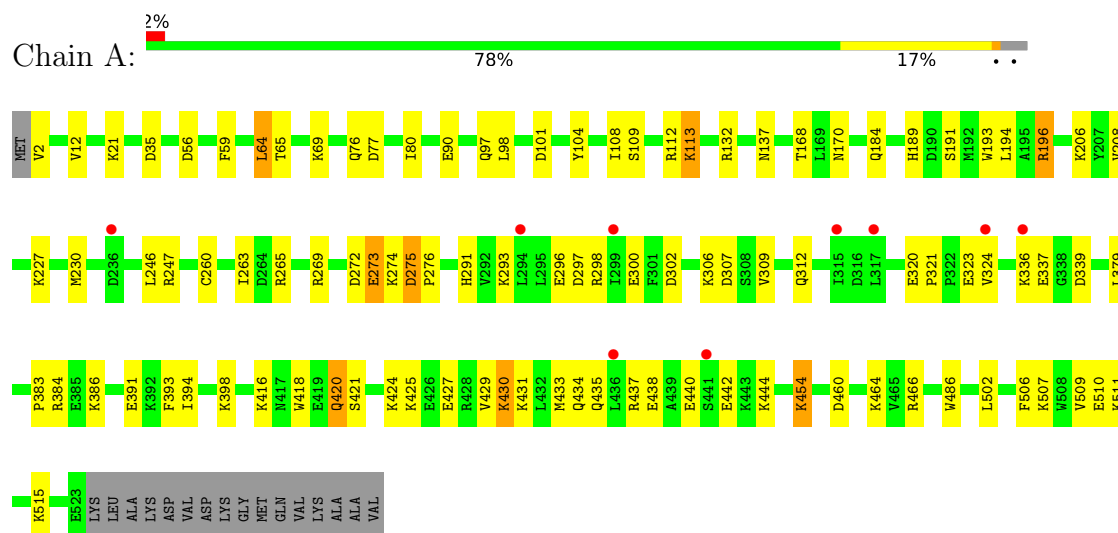
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	209	Total	O	0	0
			209	209		
2	B	224	Total	O	0	0
			224	224		

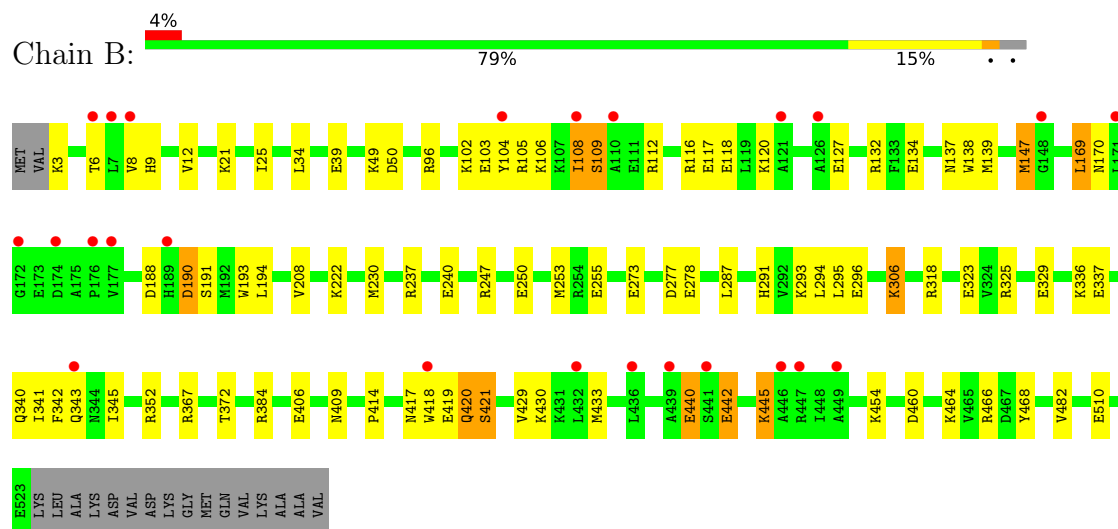
3 Residue-property plots [i](#)

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 topoisomerase I



• Molecule 1: DNA topoisomerase I



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.47Å 94.68Å 92.65Å 90.00° 111.81° 90.00°	Depositor
Resolution (Å)	70.07 – 2.20 70.07 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (70.07-2.20) 99.9 (70.07-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.192 , 0.241 (Not available) , 0.255	Depositor DCC
R_{free} test set	2972 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	42.4	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9140	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% 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	0.16	0/4455	0.35	0/5995
1	B	0.17	0/4448	0.35	0/5985
All	All	0.17	0/8903	0.35	0/11980

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	4357	0	4415	65	0
1	B	4350	0	4406	63	0
2	A	209	0	0	9	0
2	B	224	0	0	15	0
All	All	9140	0	8821	127	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 7.

All (127) 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:76:GLN:O	2:A:601:HOH:O	1.82	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:ARG:NH1	2:A:603:HOH:O	2.02	0.92
1:A:265:ARG:NH2	1:A:320:GLU:OE2	2.02	0.92
1:B:273:GLU:OE2	2:B:601:HOH:O	1.92	0.87
1:A:90:GLU:OE1	2:A:602:HOH:O	1.93	0.85
1:B:247:ARG:HG2	1:B:323:GLU:HG2	1.62	0.81
1:B:296:GLU:OE2	1:B:296:GLU:N	2.13	0.78
1:B:414:PRO:HB3	1:B:466:ARG:HD3	1.64	0.78
1:B:340:GLN:NE2	2:B:603:HOH:O	2.10	0.77
1:A:510:GLU:OE2	2:A:604:HOH:O	2.07	0.72
1:A:507:LYS:O	2:A:605:HOH:O	2.08	0.71
1:A:291:HIS:O	2:A:606:HOH:O	2.11	0.69
1:B:3:LYS:NZ	1:B:190:ASP:O	2.27	0.68
1:B:454:LYS:NZ	2:B:609:HOH:O	2.28	0.66
1:B:240:GLU:O	2:B:604:HOH:O	2.14	0.65
1:A:109:SER:HA	1:A:112:ARG:HG2	1.78	0.65
1:A:383:PRO:HD2	1:A:386:LYS:HD2	1.77	0.65
1:A:273:GLU:OE1	1:A:273:GLU:N	2.22	0.64
1:B:295:LEU:O	1:B:325:ARG:NH2	2.31	0.63
1:A:247:ARG:HG2	1:A:323:GLU:HG2	1.83	0.61
1:A:2:VAL:HG13	1:A:189:HIS:HB3	1.83	0.61
1:A:64:LEU:HD11	1:A:80:ILE:HD13	1.81	0.61
1:A:273:GLU:H	1:A:273:GLU:CD	2.08	0.61
1:B:109:SER:HA	1:B:112:ARG:HG2	1.83	0.61
1:A:296:GLU:H	1:A:296:GLU:CD	2.09	0.60
1:B:336:LYS:HD2	1:B:337:GLU:H	1.66	0.60
1:A:269:ARG:HD2	1:A:273:GLU:OE2	2.01	0.60
1:B:429:VAL:HG12	1:B:433:MET:HE2	1.84	0.59
1:B:247:ARG:CG	1:B:323:GLU:HG2	2.33	0.59
1:A:515:LYS:NZ	2:A:615:HOH:O	2.36	0.57
1:A:336:LYS:HD3	1:A:337:GLU:H	1.69	0.57
1:B:419:GLU:OE1	2:B:605:HOH:O	2.18	0.56
1:A:391:GLU:H	1:A:391:GLU:CD	2.13	0.56
1:A:306:LYS:O	1:A:309:VAL:HG12	2.06	0.55
1:A:101:ASP:OD1	1:A:104:TYR:N	2.40	0.55
1:A:434:GLN:O	1:A:438:GLU:HG2	2.07	0.55
1:B:237:ARG:NH1	2:B:621:HOH:O	2.40	0.55
1:B:418:TRP:CE2	1:B:466:ARG:HG3	2.42	0.54
1:B:409:ASN:HA	2:B:703:HOH:O	2.06	0.54
1:A:431:LYS:O	1:A:435:GLN:HG3	2.08	0.53
1:B:430:LYS:HA	1:B:433:MET:HE3	1.89	0.53
1:B:255:GLU:OE1	1:B:343:GLN:N	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:ASN:HB2	1:A:193:TRP:CZ3	2.45	0.52
1:B:318:ARG:HD2	2:B:608:HOH:O	2.07	0.52
1:B:417:ASN:O	1:B:421:SER:OG	2.26	0.52
1:B:105:ARG:NH2	1:B:352:ARG:HD2	2.24	0.52
1:A:302:ASP:OD1	1:A:312:GLN:HG2	2.09	0.51
1:A:442:GLU:OE2	1:A:442:GLU:HA	2.11	0.51
1:B:296:GLU:H	1:B:296:GLU:CD	2.05	0.51
1:A:321:PRO:O	1:A:324:VAL:HG12	2.10	0.51
1:B:104:TYR:O	1:B:108:ILE:HB	2.10	0.51
1:B:50:ASP:OD2	1:B:96:ARG:NH2	2.42	0.51
1:A:65:THR:O	1:A:69:LYS:HG3	2.11	0.51
1:A:460:ASP:OD2	1:A:464:LYS:NZ	2.43	0.50
1:A:246:LEU:HB3	1:A:323:GLU:HB3	1.93	0.49
1:B:132:ARG:NE	2:B:602:HOH:O	2.00	0.49
1:A:272:ASP:N	1:A:273:GLU:OE1	2.46	0.49
1:A:420:GLN:O	1:A:424:LYS:HG2	2.12	0.49
1:A:97:GLN:NE2	2:A:620:HOH:O	2.46	0.48
1:B:191:SER:HB3	1:B:193:TRP:CD1	2.48	0.48
1:B:440:GLU:H	1:B:440:GLU:CD	2.21	0.48
1:A:511:LYS:HG2	1:B:510:GLU:HB3	1.96	0.47
1:B:460:ASP:O	1:B:464:LYS:HG3	2.14	0.47
1:B:406:GLU:HG2	1:B:468:TYR:CZ	2.50	0.47
1:A:98:LEU:HD13	1:A:104:TYR:CZ	2.49	0.47
1:B:325:ARG:NH1	2:B:616:HOH:O	2.36	0.47
1:A:227:LYS:HA	1:A:230:MET:HE3	1.97	0.47
1:B:342:PHE:CD1	1:B:345:ILE:HG13	2.50	0.47
1:B:103:GLU:HA	1:B:106:LYS:HD3	1.96	0.47
1:B:418:TRP:CD2	1:B:466:ARG:HG3	2.50	0.46
1:B:188:ASP:C	1:B:188:ASP:OD1	2.58	0.46
1:B:120:LYS:NZ	1:B:134:GLU:OE2	2.41	0.46
1:B:250:GLU:OE2	1:B:253:MET:N	2.47	0.46
1:A:434:GLN:HA	1:A:437:ARG:HG2	1.98	0.46
1:B:277:ASP:OD2	1:B:278:GLU:N	2.49	0.46
1:B:9:HIS:HE1	1:B:169:LEU:HG	1.82	0.45
1:B:12:VAL:HG11	1:B:208:VAL:HG21	1.97	0.45
1:B:147:MET:HB2	1:B:147:MET:HE3	1.62	0.45
1:A:379:LEU:HD22	1:A:486:TRP:CE2	2.51	0.45
1:A:418:TRP:CE2	1:A:466:ARG:HG3	2.51	0.45
1:B:406:GLU:HG2	1:B:468:TYR:CE1	2.51	0.45
1:A:12:VAL:HG11	1:A:208:VAL:HG21	1.98	0.45
1:A:391:GLU:HG3	1:A:454:LYS:HE2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:VAL:HG12	1:B:127:GLU:HB2	1.98	0.44
1:A:425:LYS:O	1:A:429:VAL:HG12	2.16	0.44
1:A:274:LYS:HD2	1:A:274:LYS:H	1.82	0.44
1:B:287:LEU:HB3	1:B:341:ILE:HD12	1.99	0.44
1:A:196:ARG:HA	1:A:206:LYS:O	2.17	0.44
1:B:442:GLU:OE2	1:B:445:LYS:HE2	2.18	0.44
1:A:191:SER:HB3	1:A:193:TRP:CD1	2.52	0.44
1:A:444:LYS:HD2	1:A:444:LYS:H	1.82	0.44
1:A:437:ARG:NH2	2:A:622:HOH:O	2.50	0.44
1:B:429:VAL:O	1:B:433:MET:HG3	2.18	0.44
1:A:298:ARG:HD3	1:A:300:GLU:OE2	2.18	0.43
1:B:306:LYS:HB2	1:B:306:LYS:HE2	1.87	0.43
1:B:230:MET:HG3	2:B:648:HOH:O	2.18	0.43
1:A:56:ASP:HB3	1:A:59:PHE:HB2	2.01	0.43
1:B:138:TRP:CZ3	1:B:139:MET:HG2	2.53	0.43
1:A:430:LYS:HA	1:A:430:LYS:HD3	1.82	0.43
1:A:137:ASN:OD1	1:A:137:ASN:N	2.51	0.43
1:A:168:THR:HG23	1:A:184:GLN:HG3	2.01	0.43
1:B:372:THR:HG23	1:B:482:VAL:HG21	2.00	0.42
1:B:49:LYS:O	2:B:606:HOH:O	2.21	0.42
1:A:424:LYS:O	1:A:427:GLU:HG3	2.18	0.42
1:B:21:LYS:N	1:B:39:GLU:OE1	2.47	0.42
1:B:342:PHE:HB3	1:B:345:ILE:HG13	2.01	0.42
1:B:25:ILE:HG23	1:B:34:LEU:HD11	2.01	0.42
1:A:502:LEU:HD23	1:A:502:LEU:HA	1.87	0.42
1:B:222:LYS:NZ	2:B:632:HOH:O	2.51	0.42
1:A:293:LYS:HE2	1:A:300:GLU:HB2	2.02	0.42
1:A:394:ILE:HG22	1:A:398:LYS:HD2	2.01	0.41
1:A:416:LYS:HA	1:A:416:LYS:HD3	1.74	0.41
1:A:393:PHE:CE1	1:A:486:TRP:CD1	3.07	0.41
1:B:170:ASN:HB2	1:B:193:TRP:CZ3	2.56	0.41
1:A:275:ASP:HA	1:A:276:PRO:HD3	1.86	0.41
1:A:306:LYS:HE2	1:A:307:ASP:OD2	2.21	0.41
1:A:433:MET:HE3	1:A:433:MET:HB3	1.78	0.41
1:A:506:PHE:O	1:A:509:VAL:HG12	2.20	0.41
1:B:420:GLN:HG3	1:B:421:SER:N	2.36	0.41
1:B:108:ILE:HD13	1:B:108:ILE:HA	1.86	0.41
1:B:294:LEU:HD21	1:B:329:GLU:HG3	2.02	0.41
1:B:291:HIS:NE2	2:B:613:HOH:O	2.30	0.41
1:B:137:ASN:OD1	1:B:137:ASN:N	2.54	0.41
1:A:113:LYS:HE2	1:A:113:LYS:C	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:CYS:HA	1:A:263:ILE:HD12	2.02	0.40
1:B:367:ARG:HD3	2:B:691:HOH:O	2.20	0.40
1:A:336:LYS:O	1:A:339:ASP:HB2	2.21	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	520/539 (96%)	513 (99%)	7 (1%)	0	100	100
1	B	519/539 (96%)	513 (99%)	6 (1%)	0	100	100
All	All	1039/1078 (96%)	1026 (99%)	13 (1%)	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	460/473 (97%)	443 (96%)	17 (4%)	30	41
1	B	459/473 (97%)	440 (96%)	19 (4%)	27	37
All	All	919/946 (97%)	883 (96%)	36 (4%)	28	39

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LYS
1	A	35	ASP
1	A	64	LEU
1	A	77	ASP
1	A	108	ILE
1	A	113	LYS
1	A	194	LEU
1	A	196	ARG
1	A	273	GLU
1	A	275	ASP
1	A	297	ASP
1	A	384	ARG
1	A	420	GLN
1	A	421	SER
1	A	430	LYS
1	A	440	GLU
1	A	454	LYS
1	B	6	THR
1	B	102	LYS
1	B	108	ILE
1	B	109	SER
1	B	116	ARG
1	B	117	GLU
1	B	118	GLU
1	B	147	MET
1	B	169	LEU
1	B	190	ASP
1	B	194	LEU
1	B	293	LYS
1	B	306	LYS
1	B	384	ARG
1	B	420	GLN
1	B	421	SER
1	B	440	GLU
1	B	442	GLU
1	B	445	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN
1	A	151	ASN
1	A	344	ASN

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Mol	Chain	Res	Type
1	A	349	HIS
1	A	401	ASN
1	A	417	ASN
1	A	420	GLN
1	A	458	ASN
1	A	476	ASN
1	B	76	GLN
1	B	184	GLN
1	B	435	GLN
1	B	476	ASN

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	522/539 (96%)	0.24	9 (1%) 69 66	29, 51, 86, 107	0
1	B	521/539 (96%)	0.28	24 (4%) 37 34	27, 49, 99, 137	0
All	All	1043/1078 (96%)	0.26	33 (3%) 50 47	27, 50, 92, 137	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	446	ALA	4.2
1	B	176	PRO	3.6
1	B	436	LEU	3.4
1	B	343	GLN	3.1
1	B	108	ILE	3.1
1	A	294	LEU	3.1
1	B	171	LEU	2.8
1	B	110	ALA	2.8
1	A	441	SER	2.7
1	B	104	TYR	2.7
1	B	439	ALA	2.7
1	B	449	ALA	2.7
1	A	299	ILE	2.7
1	B	172	GLY	2.4
1	B	177	VAL	2.4
1	B	8	VAL	2.3
1	A	315	ILE	2.3
1	A	317	LEU	2.3
1	B	7	LEU	2.2
1	B	432	LEU	2.2
1	A	436	LEU	2.1
1	B	6	THR	2.1
1	B	121	ALA	2.1
1	B	447	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	126	ALA	2.1
1	A	236	ASP	2.1
1	B	174	ASP	2.1
1	B	418	TRP	2.1
1	B	441	SER	2.1
1	A	324	VAL	2.1
1	B	189	HIS	2.0
1	B	148	GLY	2.0
1	A	336	LYS	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.