



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:15 PM UTC

PDB ID : 4LMO / pdb_00004lmo
Title : Structure of a vertebrate RNA binding domain of telomerase (TRBD)
Authors : Harkisheimer, M.; Mason, M.; Shuvaeva, E.; Skordalakes, E.
Deposited on : 2013-07-10
Resolution : 2.37 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

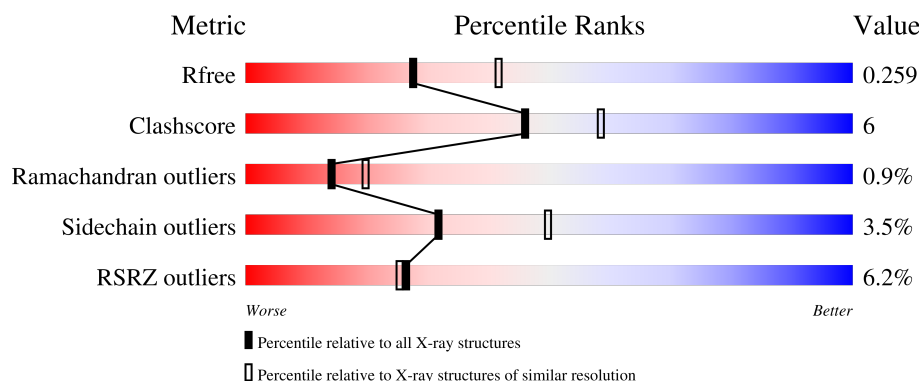
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	254	6% 86% 12% .
1	B	254	7% 86% 11% ..
1	C	254	4% 82% 13% ..
1	D	254	8% 83% 16% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8456 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 Telomerase reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			
1	B	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			
1	C	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			
1	D	251	Total	C	N	O	S	0	0	0
			2078	1348	383	336	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	291	SER	-	expression tag	UNP Q4KTA7
A	292	ASN	-	expression tag	UNP Q4KTA7
A	293	ALA	-	expression tag	UNP Q4KTA7
B	291	SER	-	expression tag	UNP Q4KTA7
B	292	ASN	-	expression tag	UNP Q4KTA7
B	293	ALA	-	expression tag	UNP Q4KTA7
C	291	SER	-	expression tag	UNP Q4KTA7
C	292	ASN	-	expression tag	UNP Q4KTA7
C	293	ALA	-	expression tag	UNP Q4KTA7
D	291	SER	-	expression tag	UNP Q4KTA7
D	292	ASN	-	expression tag	UNP Q4KTA7
D	293	ALA	-	expression tag	UNP Q4KTA7

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	30	Total	O	0	0
			30	30		
2	B	37	Total	O	0	0
			37	37		

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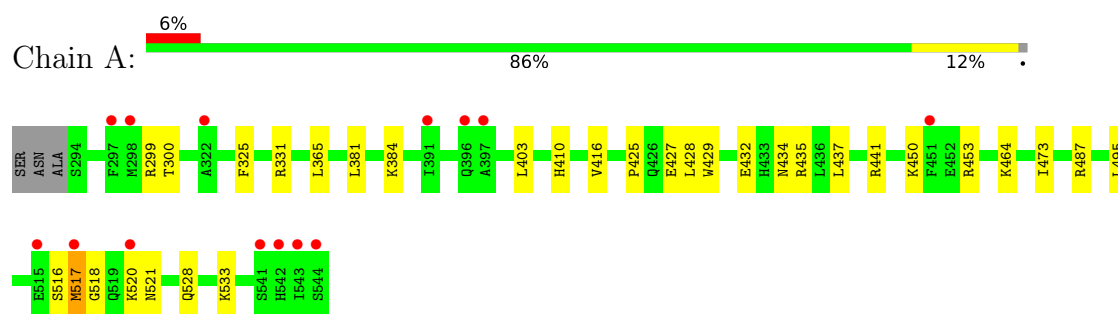
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	38	Total	O	0	0
			38	38		
2	D	39	Total	O	0	0
			39	39		

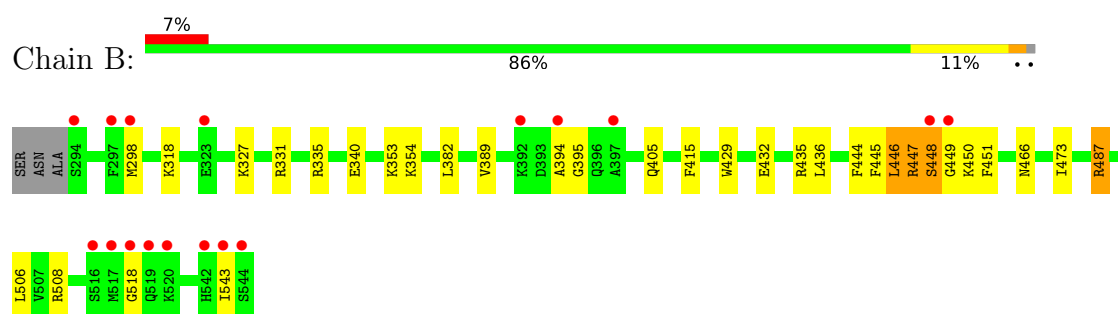
3 Residue-property plots [i](#)

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.

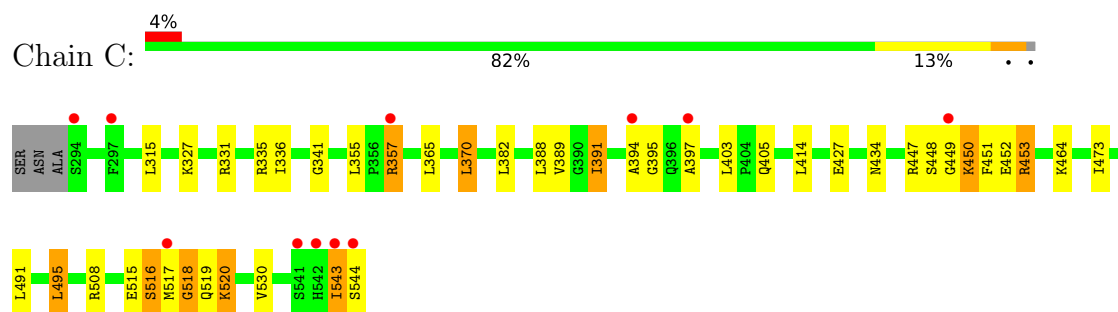
- Molecule 1: Telomerase reverse transcriptase



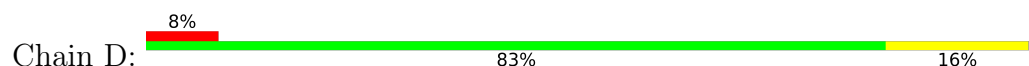
- Molecule 1: Telomerase reverse transcriptase

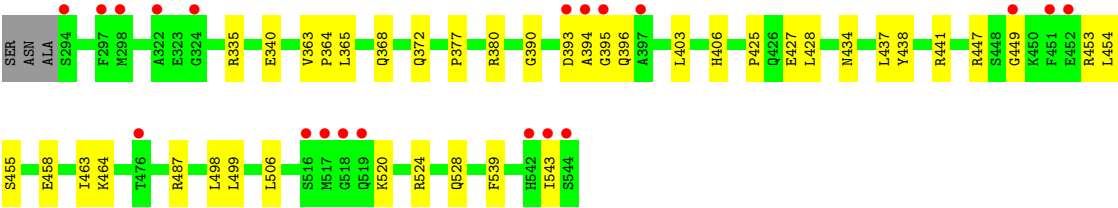


- Molecule 1: Telomerase reverse transcriptase



- Molecule 1: Telomerase reverse transcriptase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.63Å 84.51Å 137.17Å 90.00° 94.31° 90.00°	Depositor
Resolution (Å)	20.00 – 2.37 20.00 – 2.37	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-2.37) 98.5 (20.00-2.37)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.220 , 0.259 0.220 , 0.259	Depositor DCC
R_{free} test set	2865 reflections (3.82%)	wwPDB-VP
Wilson B-factor (Å ²)	33.0	Xtriage
Anisotropy	0.574	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 32.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8456	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.51% 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	0.55	0/2129	0.81	0/2858
1	B	0.55	0/2129	0.81	0/2858
1	C	0.55	0/2129	0.82	0/2858
1	D	0.54	0/2129	0.81	2/2858 (0.1%)
All	All	0.55	0/8516	0.81	2/11432 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	403	LEU	CA-C-N	-5.05	114.84	120.45
1	D	403	LEU	C-N-CA	-5.05	114.84	120.45

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	2078	0	2140	22	0
1	B	2078	0	2140	29	0
1	C	2078	0	2140	33	0
1	D	2078	0	2140	19	0
2	A	30	0	0	0	0
2	B	37	0	0	0	0
2	C	38	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	39	0	0	0	0
All	All	8456	0	8560	98	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 (98) 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:516:SER:CB	1:A:517:MET:HA	1.70	1.18
1:C:448:SER:HB3	1:C:452:GLU:HG3	1.27	1.15
1:B:394:ALA:CB	1:B:395:GLY:HA2	1.71	1.14
1:A:516:SER:HB3	1:A:517:MET:HA	1.18	1.10
1:C:394:ALA:H	1:C:395:GLY:HA2	0.89	1.03
1:B:394:ALA:HB1	1:B:395:GLY:CA	1.90	1.01
1:C:394:ALA:N	1:C:395:GLY:HA2	1.73	1.01
1:C:394:ALA:H	1:C:395:GLY:CA	1.76	0.98
1:B:394:ALA:HB1	1:B:395:GLY:HA2	0.95	0.95
1:B:447:ARG:C	1:B:449:GLY:HA2	1.97	0.89
1:A:516:SER:HB3	1:A:517:MET:CA	2.05	0.82
1:C:448:SER:HB3	1:C:452:GLU:CG	2.09	0.79
1:C:434:ASN:HD21	1:C:464:LYS:H	1.30	0.79
1:B:394:ALA:CB	1:B:395:GLY:CA	2.55	0.73
1:C:448:SER:CB	1:C:452:GLU:HG3	2.15	0.73
1:D:434:ASN:HD21	1:D:464:LYS:H	1.35	0.73
1:A:516:SER:HB2	1:A:517:MET:HA	1.67	0.72
1:C:357:ARG:HH12	1:C:473:ILE:HG23	1.55	0.70
1:A:516:SER:CB	1:A:517:MET:CA	2.58	0.69
1:C:448:SER:C	1:C:450:LYS:HA	2.18	0.68
1:A:434:ASN:HD21	1:A:464:LYS:H	1.42	0.68
1:B:432:GLU:CD	1:B:435:ARG:HH12	2.01	0.68
1:B:448:SER:N	1:B:449:GLY:HA2	2.13	0.62
1:A:300:THR:HG21	1:D:449:GLY:O	2.01	0.61
1:B:444:PHE:O	1:B:447:ARG:HB2	2.01	0.61
1:C:389:VAL:H	1:C:405:GLN:HE22	1.47	0.61
1:B:389:VAL:H	1:B:405:GLN:NE2	1.98	0.60
1:A:432:GLU:CD	1:A:435:ARG:HH12	2.09	0.60
1:D:390:GLY:HA2	1:D:393:ASP:HB3	1.84	0.60
1:A:365:LEU:HD21	1:A:427:GLU:HG3	1.82	0.60
1:C:389:VAL:H	1:C:405:GLN:NE2	2.00	0.59
1:A:381:LEU:HD23	1:A:384:LYS:HD3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:395:GLY:HA3	1:C:397:ALA:H	1.68	0.59
1:B:445:PHE:CD2	1:B:446:LEU:HD13	2.39	0.57
1:B:445:PHE:HD2	1:B:446:LEU:HD13	1.69	0.57
1:B:318:LYS:HE2	1:B:327:LYS:HE3	1.87	0.56
1:D:377:PRO:HB2	1:D:380:ARG:HB2	1.86	0.55
1:C:336:ILE:O	1:C:341:GLY:HA2	2.06	0.55
1:C:515:GLU:O	1:C:517:MET:N	2.40	0.54
1:B:508:ARG:HH21	1:C:508:ARG:NH1	2.04	0.54
1:B:447:ARG:O	1:B:448:SER:HB2	2.08	0.54
1:A:517:MET:HB2	1:A:518:GLY:HA3	1.90	0.54
1:D:455:SER:HB3	1:D:458:GLU:HB2	1.90	0.53
1:B:331:ARG:HH12	1:B:354:LYS:HA	1.72	0.53
1:B:331:ARG:NH1	1:B:353:LYS:O	2.41	0.53
1:B:447:ARG:O	1:B:448:SER:CB	2.56	0.53
1:A:516:SER:HB2	1:A:517:MET:HE2	1.91	0.51
1:C:391:ILE:HD11	1:C:530:VAL:HG22	1.91	0.51
1:B:543:ILE:HD11	1:C:403:LEU:HD12	1.92	0.51
1:D:425:PRO:HD2	1:D:428:LEU:HD12	1.93	0.50
1:A:437:LEU:O	1:A:441:ARG:HG2	2.11	0.50
1:A:425:PRO:HD2	1:A:428:LEU:HD12	1.94	0.49
1:B:447:ARG:O	1:B:449:GLY:HA2	2.10	0.49
1:C:449:GLY:N	1:C:450:LYS:HA	2.26	0.49
1:D:539:PHE:O	1:D:543:ILE:HG22	2.12	0.49
1:D:454:LEU:HD22	1:D:499:LEU:HD23	1.95	0.48
1:A:429:TRP:CE2	1:A:435:ARG:HG3	2.49	0.48
1:D:365:LEU:HD21	1:D:427:GLU:CG	2.44	0.48
1:D:368:GLN:HE21	1:D:372:GLN:NE2	2.12	0.48
1:B:450:LYS:O	1:B:451:PHE:C	2.57	0.48
1:C:518:GLY:C	1:C:520:LYS:H	2.22	0.48
1:C:388:LEU:HB3	1:C:391:ILE:HD13	1.95	0.48
1:A:450:LYS:HD3	1:A:453:ARG:HD2	1.97	0.47
1:C:394:ALA:N	1:C:395:GLY:CA	2.52	0.47
1:D:394:ALA:HA	1:D:395:GLY:HA3	1.77	0.46
1:A:365:LEU:HD21	1:A:427:GLU:CG	2.45	0.46
1:A:403:LEU:HD13	1:D:543:ILE:HD12	1.97	0.46
1:C:516:SER:O	1:C:517:MET:HB2	2.15	0.46
1:D:437:LEU:O	1:D:441:ARG:HG2	2.16	0.46
1:B:429:TRP:CD2	1:B:435:ARG:HG3	2.50	0.45
1:B:335:ARG:HD3	1:B:340:GLU:OE1	2.15	0.45
1:A:517:MET:H	1:A:518:GLY:HA3	1.81	0.45
1:B:389:VAL:H	1:B:405:GLN:HE22	1.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:450:LYS:HB2	1:C:451:PHE:CD2	2.51	0.45
1:C:448:SER:O	1:C:450:LYS:HA	2.17	0.45
1:A:410:HIS:H	1:A:410:HIS:CD2	2.35	0.44
1:B:429:TRP:CE2	1:B:435:ARG:HG3	2.53	0.44
1:C:365:LEU:HD21	1:C:427:GLU:CG	2.48	0.43
1:D:438:TYR:OH	1:D:498:LEU:HB3	2.18	0.43
1:C:434:ASN:ND2	1:C:464:LYS:H	2.06	0.43
1:A:520:LYS:HA	1:A:521:ASN:HA	1.59	0.43
1:B:382:LEU:HG	1:B:415:PHE:CE1	2.53	0.43
1:C:452:GLU:O	1:C:453:ARG:C	2.61	0.43
1:D:335:ARG:HD3	1:D:340:GLU:OE1	2.19	0.43
1:C:543:ILE:O	1:C:543:ILE:HG22	2.18	0.42
1:C:491:LEU:O	1:C:495:LEU:HB2	2.19	0.42
1:C:543:ILE:HA	1:C:544:SER:HA	1.69	0.42
1:C:315:LEU:HD22	1:C:370:LEU:HD11	2.02	0.42
1:A:325:PHE:CE1	1:D:453:ARG:HG2	2.55	0.42
1:C:331:ARG:HG3	1:C:355:LEU:HD11	2.02	0.41
1:D:406:HIS:CD2	1:D:524:ARG:HD3	2.56	0.41
1:B:448:SER:HB2	1:B:449:GLY:C	2.45	0.41
1:D:363:VAL:HB	1:D:364:PRO:HD3	2.01	0.41
1:C:331:ARG:O	1:C:335:ARG:HG2	2.20	0.41
1:B:445:PHE:CD2	1:B:446:LEU:CD1	3.04	0.40
1:B:448:SER:HB2	1:B:450:LYS:HG3	2.04	0.40
1:B:466:ASN:ND2	1:B:487:ARG:HH21	2.19	0.40
1:D:434:ASN:ND2	1:D:464:LYS:H	2.11	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	249/254 (98%)	237 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	249/254 (98%)	233 (94%)	14 (6%)	2 (1%)	16	23
1	C	249/254 (98%)	231 (93%)	13 (5%)	5 (2%)	6	6
1	D	249/254 (98%)	239 (96%)	8 (3%)	2 (1%)	16	23
All	All	996/1016 (98%)	940 (94%)	47 (5%)	9 (1%)	14	20

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	448	SER
1	C	516	SER
1	C	520	LYS
1	B	518	GLY
1	C	518	GLY
1	C	453	ARG
1	D	520	LYS
1	D	396	GLN
1	C	519	GLN

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	221/223 (99%)	212 (96%)	9 (4%)	27	43
1	B	221/223 (99%)	214 (97%)	7 (3%)	34	53
1	C	221/223 (99%)	211 (96%)	10 (4%)	24	39
1	D	221/223 (99%)	216 (98%)	5 (2%)	44	64
All	All	884/892 (99%)	853 (96%)	31 (4%)	32	50

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	299	ARG
1	A	331	ARG

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Mol	Chain	Res	Type
1	A	416	VAL
1	A	473	ILE
1	A	487	ARG
1	A	495	LEU
1	A	517	MET
1	A	528	GLN
1	A	533	LYS
1	B	298	MET
1	B	436	LEU
1	B	446	LEU
1	B	447	ARG
1	B	473	ILE
1	B	487	ARG
1	B	506	LEU
1	C	327	LYS
1	C	357	ARG
1	C	370	LEU
1	C	382	LEU
1	C	391	ILE
1	C	414	LEU
1	C	447	ARG
1	C	450	LYS
1	C	495	LEU
1	C	543	ILE
1	D	447	ARG
1	D	463	ILE
1	D	487	ARG
1	D	506	LEU
1	D	528	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	361	ASN
1	A	405	GLN
1	A	410	HIS
1	A	426	GLN
1	A	433	HIS
1	A	434	ASN
1	A	521	ASN
1	B	295	GLN
1	B	361	ASN

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Mol	Chain	Res	Type
1	B	405	GLN
1	B	410	HIS
1	B	466	ASN
1	B	493	GLN
1	B	542	HIS
1	C	361	ASN
1	C	368	GLN
1	C	372	GLN
1	C	405	GLN
1	C	410	HIS
1	C	433	HIS
1	C	434	ASN
1	C	466	ASN
1	C	542	HIS
1	D	361	ASN
1	D	372	GLN
1	D	406	HIS
1	D	433	HIS
1	D	434	ASN
1	D	466	ASN
1	D	467	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	251/254 (98%)	0.21	14 (5%) 30 29	25, 40, 87, 107	0
1	B	251/254 (98%)	0.16	17 (6%) 23 22	27, 39, 90, 119	0
1	C	251/254 (98%)	0.26	11 (4%) 39 38	27, 43, 93, 112	0
1	D	251/254 (98%)	0.30	20 (7%) 18 17	25, 42, 87, 111	0
All	All	1004/1016 (98%)	0.23	62 (6%) 26 25	25, 41, 90, 119	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	543	ILE	6.0
1	B	543	ILE	5.9
1	B	544	SER	4.0
1	D	543	ILE	4.0
1	B	518	GLY	3.9
1	D	518	GLY	3.9
1	C	542	HIS	3.9
1	C	297	PHE	3.7
1	D	297	PHE	3.7
1	D	544	SER	3.7
1	A	543	ILE	3.6
1	B	449	GLY	3.4
1	C	449	GLY	3.3
1	C	544	SER	3.3
1	A	544	SER	3.2
1	A	515	GLU	3.2
1	D	449	GLY	3.1
1	A	297	PHE	3.0
1	B	294	SER	3.0
1	B	297	PHE	3.0
1	B	517	MET	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	394	ALA	2.8
1	D	397	ALA	2.8
1	C	541	SER	2.7
1	B	397	ALA	2.7
1	B	448	SER	2.7
1	B	298	MET	2.7
1	D	294	SER	2.7
1	A	397	ALA	2.6
1	D	395	GLY	2.6
1	A	517	MET	2.6
1	D	516	SER	2.6
1	B	542	HIS	2.6
1	D	517	MET	2.6
1	C	397	ALA	2.5
1	D	519	GLN	2.5
1	A	542	HIS	2.5
1	A	298	MET	2.5
1	C	517	MET	2.5
1	D	451	PHE	2.4
1	A	541	SER	2.4
1	A	391	ILE	2.3
1	D	324	GLY	2.2
1	A	322	ALA	2.2
1	C	357	ARG	2.2
1	C	394	ALA	2.2
1	B	516	SER	2.2
1	D	452	GLU	2.2
1	D	298	MET	2.2
1	A	396	GLN	2.2
1	D	322	ALA	2.2
1	D	542	HIS	2.1
1	D	476	THR	2.1
1	D	394	ALA	2.1
1	B	323	GLU	2.1
1	B	519	GLN	2.1
1	A	520	LYS	2.1
1	A	451	PHE	2.0
1	B	392	LYS	2.0
1	B	520	LYS	2.0
1	C	294	SER	2.0
1	D	393	ASP	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.