



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:35 PM UTC

PDB ID : 6K5S / pdb_00006k5s
Title : Crystal structure of the Helical domain of S. pombe Tbf1
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Deposited on : 2019-05-31
Resolution : 1.90 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

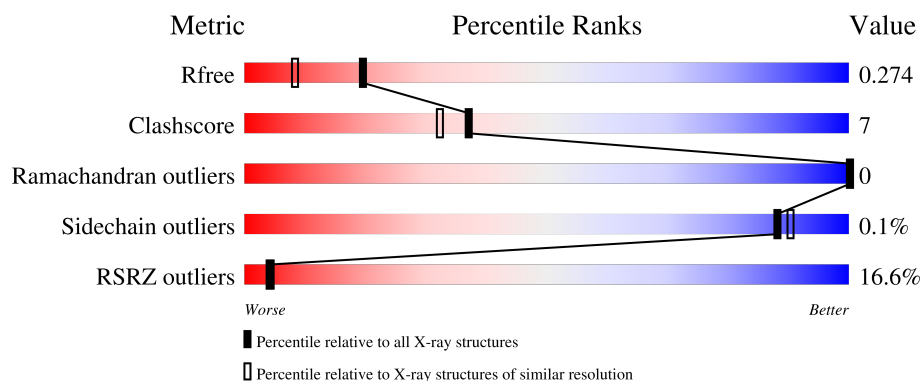
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	227	9% 86% 11% .
1	B	227	2% 85% 10% 5%
1	C	227	31% 81% 15% .
1	D	227	21% 81% 13% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7380 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 Telomeric DNA-binding factor trf1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1740	1110	296	323	11			
1	B	216	Total	C	N	O	S	0	0	0
			1712	1092	292	317	11			
1	C	219	Total	C	N	O	S	0	0	0
			1731	1105	295	320	11			
1	D	215	Total	C	N	O	S	0	0	0
			1707	1091	290	315	11			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	93	GLY	-	expression tag	UNP Q6E434
A	94	PRO	-	expression tag	UNP Q6E434
A	95	LEU	-	expression tag	UNP Q6E434
A	96	GLY	-	expression tag	UNP Q6E434
A	97	SER	-	expression tag	UNP Q6E434
B	93	GLY	-	expression tag	UNP Q6E434
B	94	PRO	-	expression tag	UNP Q6E434
B	95	LEU	-	expression tag	UNP Q6E434
B	96	GLY	-	expression tag	UNP Q6E434
B	97	SER	-	expression tag	UNP Q6E434
C	93	GLY	-	expression tag	UNP Q6E434
C	94	PRO	-	expression tag	UNP Q6E434
C	95	LEU	-	expression tag	UNP Q6E434
C	96	GLY	-	expression tag	UNP Q6E434
C	97	SER	-	expression tag	UNP Q6E434
D	93	GLY	-	expression tag	UNP Q6E434
D	94	PRO	-	expression tag	UNP Q6E434
D	95	LEU	-	expression tag	UNP Q6E434
D	96	GLY	-	expression tag	UNP Q6E434
D	97	SER	-	expression tag	UNP Q6E434

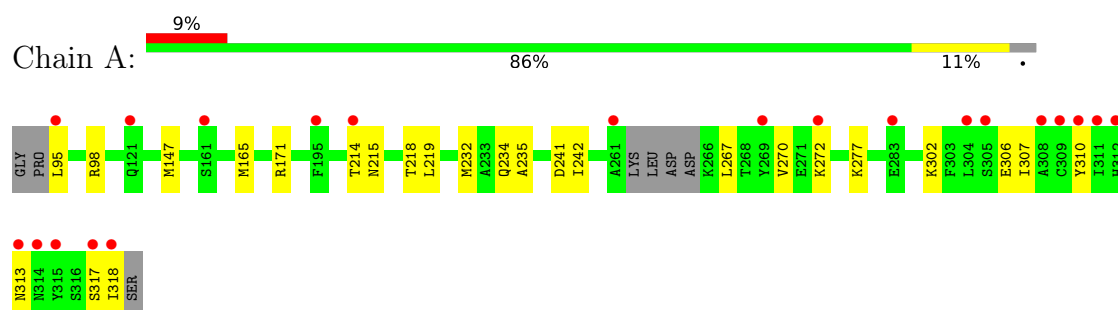
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	153	Total 153	O 153	0	0
2	B	174	Total 174	O 174	0	0
2	C	72	Total 72	O 72	0	0
2	D	91	Total 91	O 91	0	0

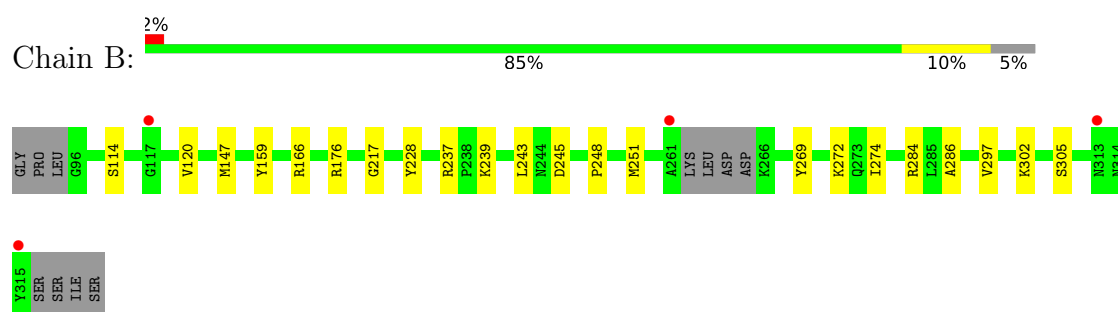
3 Residue-property plots [i](#)

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.

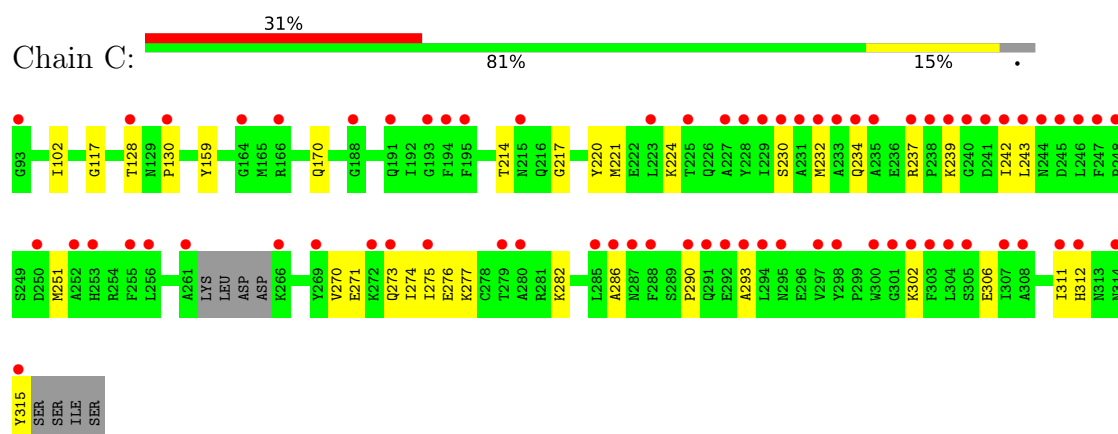
- Molecule 1: Telomeric DNA-binding factor trf1



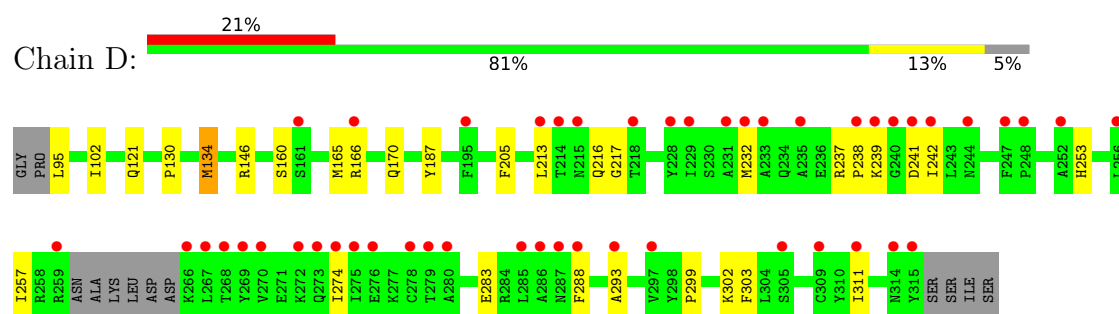
- Molecule 1: Telomeric DNA-binding factor trf1



- Molecule 1: Telomeric DNA-binding factor trf1



- Molecule 1: Telomeric DNA-binding factor trf1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.50Å 80.64Å 77.37Å 111.45° 94.64° 92.05°	Depositor
Resolution (Å)	38.30 – 1.90 38.30 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.1 (38.30-1.90) 92.1 (38.30-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.57 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.221 , 0.275 0.222 , 0.274	Depositor DCC
R_{free} test set	3070 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7380	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 79.73 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.2300e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.35	0/1773	0.53	0/2395
1	B	0.36	0/1745	0.51	0/2357
1	C	0.29	0/1765	0.46	0/2385
1	D	0.29	0/1740	0.46	0/2350
All	All	0.33	0/7023	0.49	0/9487

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	1740	0	1750	25	0
1	B	1712	0	1718	16	0
1	C	1731	0	1739	25	0
1	D	1707	0	1718	39	0
2	A	153	0	0	3	1
2	B	174	0	0	5	0
2	C	72	0	0	2	1
2	D	91	0	0	6	0
All	All	7380	0	6925	98	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 7.

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:219:LEU:HD21	1:A:307:ILE:HD12	1.31	1.11
1:A:234:GLN:HE22	1:D:166:ARG:NH2	1.79	0.80
1:B:166:ARG:NH2	2:B:402:HOH:O	2.13	0.79
1:A:219:LEU:HD21	1:A:307:ILE:CD1	2.12	0.78
1:C:214:THR:HG21	1:D:130:PRO:HG2	1.67	0.77
1:A:232:MET:HE3	1:A:242:ILE:HD12	1.66	0.76
1:A:318:ILE:O	2:A:401:HOH:O	2.04	0.73
1:D:205:PHE:CE2	1:D:311:ILE:HD11	2.26	0.70
1:D:237:ARG:HG3	1:D:242:ILE:HD11	1.74	0.70
1:D:288:PHE:HE2	1:D:293:ALA:HB3	1.58	0.68
1:D:146:ARG:NH1	2:D:404:HOH:O	2.27	0.68
1:D:237:ARG:HD3	1:D:241:ASP:CB	2.26	0.66
1:B:159:TYR:OH	2:B:401:HOH:O	2.12	0.66
1:C:290:PRO:HG2	1:C:293:ALA:HB2	1.77	0.65
1:C:232:MET:HE3	1:C:242:ILE:HD12	1.78	0.65
1:C:117:GLY:HA2	1:C:312:HIS:NE2	2.13	0.64
1:D:237:ARG:HD3	1:D:241:ASP:HB2	1.79	0.64
1:B:147:MET:HG2	2:D:471:HOH:O	1.97	0.64
1:D:237:ARG:HD2	1:D:242:ILE:HG13	1.80	0.63
1:A:219:LEU:CD2	1:A:307:ILE:HD12	2.19	0.62
1:C:117:GLY:HA2	1:C:312:HIS:CE1	2.35	0.62
1:C:273:GLN:HE22	1:D:130:PRO:HG3	1.66	0.61
1:C:159:TYR:OH	2:C:401:HOH:O	2.15	0.61
1:A:214:THR:HG23	1:A:270:VAL:HG22	1.82	0.60
1:D:121:GLN:NE2	2:D:405:HOH:O	2.35	0.59
1:C:239:LYS:HE3	1:C:286:ALA:HA	1.84	0.59
1:A:302:LYS:O	1:A:306:GLU:HG2	2.04	0.58
1:D:299:PRO:HG2	1:D:302:LYS:HG3	1.85	0.57
1:D:160:SER:HB2	1:D:165:MET:HB2	1.87	0.56
1:D:213:LEU:HB2	1:D:216:GLN:HG3	1.88	0.56
1:D:217:GLY:HA3	1:D:274:ILE:HG12	1.87	0.56
1:C:251:MET:HE2	1:C:275:ILE:HG12	1.88	0.56
1:D:237:ARG:HG3	1:D:242:ILE:CD1	2.37	0.54
1:C:217:GLY:HA3	1:C:274:ILE:HD13	1.90	0.53
1:A:215:ASN:ND2	2:A:409:HOH:O	2.41	0.53
1:B:284:ARG:HH12	1:B:297:VAL:HG11	1.74	0.52
1:C:270:VAL:HA	1:C:273:GLN:HE21	1.74	0.52
1:D:205:PHE:CZ	1:D:311:ILE:HD11	2.45	0.52
1:D:237:ARG:HD3	1:D:241:ASP:HB3	1.92	0.52
1:C:220:TYR:CE1	1:C:224:LYS:HE2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:MET:CE	1:A:242:ILE:HD12	2.38	0.51
1:B:120:VAL:HG21	1:B:305:SER:OG	2.10	0.51
1:A:95:LEU:HD23	1:A:98:ARG:H	1.76	0.51
1:D:165:MET:HB3	1:D:170:GLN:HB3	1.93	0.50
1:D:232:MET:SD	1:D:239:LYS:HG2	2.52	0.50
1:D:102:ILE:HG13	1:D:170:GLN:HG2	1.93	0.50
1:D:232:MET:CE	1:D:242:ILE:HD13	2.41	0.50
1:D:187:TYR:OH	2:D:401:HOH:O	2.15	0.49
1:C:311:ILE:O	1:C:315:TYR:HD2	1.96	0.49
1:A:317:SER:O	1:A:318:ILE:HB	2.13	0.48
1:B:269:TYR:HA	1:B:272:LYS:HZ3	1.79	0.48
1:B:302:LYS:HE3	2:B:552:HOH:O	2.13	0.48
1:D:232:MET:HA	1:D:232:MET:HE2	1.96	0.47
1:D:232:MET:HE3	1:D:242:ILE:HD13	1.97	0.47
1:A:235:ALA:HB1	1:D:95:LEU:HD13	1.95	0.47
1:B:114:SER:OG	1:D:95:LEU:HD11	2.15	0.47
1:C:243:LEU:HD22	1:C:282:LYS:HG3	1.96	0.47
1:D:238:PRO:O	1:D:242:ILE:HD12	2.15	0.47
1:A:218:THR:OG1	1:A:277:LYS:NZ	2.48	0.47
1:B:239:LYS:NZ	1:B:286:ALA:O	2.48	0.47
1:B:228:TYR:CE1	1:B:243:LEU:HG	2.50	0.46
1:C:230:SER:O	1:C:234:GLN:HG3	2.15	0.46
1:C:302:LYS:HG2	1:C:306:GLU:OE1	2.15	0.46
1:D:205:PHE:CE2	1:D:311:ILE:CD1	2.98	0.46
1:B:248:PRO:HD2	1:B:251:MET:HG3	1.97	0.45
1:D:253:HIS:O	1:D:257:ILE:HG13	2.16	0.45
1:C:224:LYS:NZ	2:C:411:HOH:O	2.48	0.45
1:A:171:ARG:NE	2:A:406:HOH:O	2.38	0.45
1:C:232:MET:HA	1:C:232:MET:HE2	1.98	0.45
1:D:239:LYS:HE2	1:D:239:LYS:HB2	1.82	0.45
1:A:232:MET:HA	1:A:232:MET:HE2	1.99	0.45
1:C:237:ARG:NH2	1:C:242:ILE:HA	2.31	0.44
1:D:303:PHE:HB2	2:D:445:HOH:O	2.18	0.44
1:A:234:GLN:NE2	1:D:166:ARG:NH2	2.58	0.44
1:B:269:TYR:HA	1:B:272:LYS:NZ	2.33	0.44
1:C:273:GLN:O	1:C:276:GLU:HG3	2.18	0.44
1:C:128:THR:O	1:C:130:PRO:HD3	2.17	0.44
1:C:273:GLN:HA	1:C:276:GLU:HG2	2.00	0.44
1:D:253:HIS:CD2	1:D:257:ILE:HD11	2.52	0.44
1:A:232:MET:HE3	1:A:242:ILE:CD1	2.40	0.43
1:B:217:GLY:HA3	1:B:274:ILE:HG12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:271:GLU:O	1:C:275:ILE:HG13	2.18	0.43
1:C:102:ILE:HG13	1:C:170:GLN:HG2	2.02	0.42
1:C:221:MET:HE1	1:C:277:LYS:NZ	2.33	0.42
1:B:245:ASP:HB3	2:B:546:HOH:O	2.19	0.42
1:D:134:MET:HE2	1:D:134:MET:HB3	1.88	0.42
1:D:283:GLU:OE1	2:D:403:HOH:O	2.22	0.42
1:A:95:LEU:HD22	1:A:98:ARG:HG3	2.01	0.42
1:B:237:ARG:HD2	2:B:474:HOH:O	2.19	0.42
1:A:98:ARG:HB3	1:A:165:MET:HE3	2.02	0.42
1:A:147:MET:HB3	1:A:147:MET:HE2	1.62	0.42
1:D:232:MET:HE1	1:D:239:LYS:HA	2.02	0.42
1:A:267:LEU:HD23	1:A:272:LYS:HG2	2.02	0.41
1:A:241:ASP:CG	1:B:176:ARG:HH22	2.27	0.41
1:A:313:ASN:OD1	1:A:313:ASN:N	2.54	0.41
1:D:95:LEU:HD12	1:D:95:LEU:HA	1.90	0.41
1:A:310:TYR:CD1	1:A:310:TYR:C	2.99	0.40
1:D:237:ARG:HB2	1:D:238:PRO:HD2	2.03	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)
2:A:530:HOH:O	2:C:471:HOH:O[1_665]	2.18	0.02

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	216/227 (95%)	212 (98%)	4 (2%)	0	100	100
1	B	212/227 (93%)	210 (99%)	2 (1%)	0	100	100
1	C	215/227 (95%)	211 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	211/227 (93%)	208 (99%)	3 (1%)	0	100	100
All	All	854/908 (94%)	841 (98%)	13 (2%)	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	189/195 (97%)	189 (100%)	0	100	100
1	B	185/195 (95%)	185 (100%)	0	100	100
1	C	187/195 (96%)	187 (100%)	0	100	100
1	D	185/195 (95%)	184 (100%)	1 (0%)	81	84
All	All	746/780 (96%)	745 (100%)	1 (0%)	88	90

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	134	MET

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	129	ASN
1	A	226	GLN
1	A	234	GLN
1	A	314	ASN
1	B	200	ASN
1	B	314	ASN
1	C	129	ASN
1	C	200	ASN
1	C	211	ASN
1	C	273	GLN

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Mol	Chain	Res	Type
1	D	170	GLN
1	D	196	HIS
1	D	226	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	220/227 (96%)	0.45	21 (9%) 14 14	7, 20, 35, 47	0
1	B	216/227 (95%)	0.20	4 (1%) 66 70	7, 19, 31, 37	0
1	C	219/227 (96%)	1.55	71 (32%) 1 1	9, 33, 56, 60	0
1	D	215/227 (94%)	1.20	48 (22%) 2 2	8, 30, 52, 58	0
All	All	870/908 (95%)	0.85	144 (16%) 4 4	7, 24, 50, 60	0

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	231	ALA	6.5
1	C	242	ILE	5.8
1	D	269	TYR	5.6
1	C	269	TYR	4.8
1	C	279	THR	4.7
1	C	240	GLY	4.6
1	C	285	LEU	4.6
1	A	315	TYR	4.4
1	D	286	ALA	4.4
1	C	286	ALA	4.3
1	D	235	ALA	4.3
1	A	313	ASN	4.2
1	C	275	ILE	4.1
1	A	318	ILE	4.0
1	D	275	ILE	4.0
1	C	303	PHE	4.0
1	D	272	LYS	3.8
1	C	238	PRO	3.8
1	C	295	ASN	3.8
1	C	288	PHE	3.8
1	C	300	TRP	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	294	LEU	3.7
1	C	291	GLN	3.7
1	C	297	VAL	3.7
1	C	280	ALA	3.5
1	C	246	LEU	3.3
1	D	195	PHE	3.3
1	C	292	GLU	3.3
1	D	305	SER	3.3
1	C	261	ALA	3.3
1	D	218	THR	3.3
1	C	315	TYR	3.2
1	A	272	LYS	3.1
1	C	215	ASN	3.1
1	C	235	ALA	3.1
1	D	213	LEU	3.1
1	C	307	ILE	3.1
1	C	234	GLN	3.1
1	A	314	ASN	3.1
1	C	255	PHE	3.1
1	D	279	THR	3.1
1	C	298	TYR	3.0
1	A	309	CYS	3.0
1	A	312	HIS	3.0
1	C	128	THR	3.0
1	C	228	TYR	2.9
1	C	301	GLY	2.9
1	C	232	MET	2.9
1	A	311	ILE	2.9
1	B	315	TYR	2.9
1	D	242	ILE	2.9
1	C	290	PRO	2.8
1	C	243	LEU	2.8
1	D	285	LEU	2.8
1	C	273	GLN	2.8
1	C	239	LYS	2.8
1	A	308	ALA	2.8
1	C	225	THR	2.8
1	D	214	THR	2.8
1	D	297	VAL	2.8
1	D	280	ALA	2.8
1	C	195	PHE	2.8
1	D	309	CYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	312	HIS	2.8
1	D	268	THR	2.7
1	A	305	SER	2.7
1	C	237	ARG	2.7
1	D	244	ASN	2.7
1	C	241	ASP	2.7
1	D	166	ARG	2.7
1	D	228	TYR	2.7
1	C	250	ASP	2.7
1	C	244	ASN	2.7
1	C	308	ALA	2.6
1	D	278	CYS	2.6
1	C	166	ARG	2.6
1	D	266	LYS	2.6
1	C	248	PRO	2.6
1	C	256	LEU	2.6
1	C	304	LEU	2.6
1	C	227	ALA	2.6
1	C	253	HIS	2.6
1	D	259	ARG	2.6
1	B	313	ASN	2.6
1	C	287	ASN	2.6
1	D	239	LYS	2.5
1	D	315	TYR	2.5
1	C	311	ILE	2.5
1	C	230	SER	2.5
1	C	293	ALA	2.5
1	D	273	GLN	2.5
1	B	117	GLY	2.4
1	D	276	GLU	2.4
1	D	274	ILE	2.4
1	D	311	ILE	2.4
1	C	233	ALA	2.4
1	D	270	VAL	2.4
1	D	215	ASN	2.4
1	D	240	GLY	2.4
1	A	121	GLN	2.4
1	D	256	LEU	2.4
1	D	229	ILE	2.4
1	C	229	ILE	2.4
1	C	266	LYS	2.3
1	D	241	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	304	LEU	2.3
1	B	261	ALA	2.3
1	C	272	LYS	2.3
1	D	287	ASN	2.3
1	D	231	ALA	2.3
1	D	293	ALA	2.3
1	C	188	GLY	2.3
1	A	195	PHE	2.2
1	A	269	TYR	2.2
1	D	247	PHE	2.2
1	D	248	PRO	2.2
1	C	314	ASN	2.2
1	D	314	ASN	2.2
1	C	193	GLY	2.2
1	C	247	PHE	2.2
1	A	95	LEU	2.2
1	D	267	LEU	2.2
1	C	245	ASP	2.2
1	C	305	SER	2.2
1	D	238	PRO	2.2
1	A	310	TYR	2.2
1	D	288	PHE	2.2
1	A	261	ALA	2.2
1	C	252	ALA	2.2
1	D	233	ALA	2.2
1	D	232	MET	2.1
1	A	317	SER	2.1
1	D	252	ALA	2.1
1	C	194	PHE	2.1
1	A	214	THR	2.1
1	C	93	GLY	2.1
1	C	164	GLY	2.1
1	A	283	GLU	2.1
1	A	161	SER	2.1
1	C	302	LYS	2.1
1	C	130	PRO	2.1
1	C	223	LEU	2.1
1	C	191	GLN	2.0
1	D	161	SER	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.