



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 4, 2023 – 06:39 pm GMT

PDB ID : 1GXX
Title : SMC hinge domain from *T. maritima* w/o coiled coil, P212121 crystal form
Authors : Lowe, J.; Haering, C.; Nasmyth, K.
Deposited on : 2002-04-07
Resolution : 3.00 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 : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

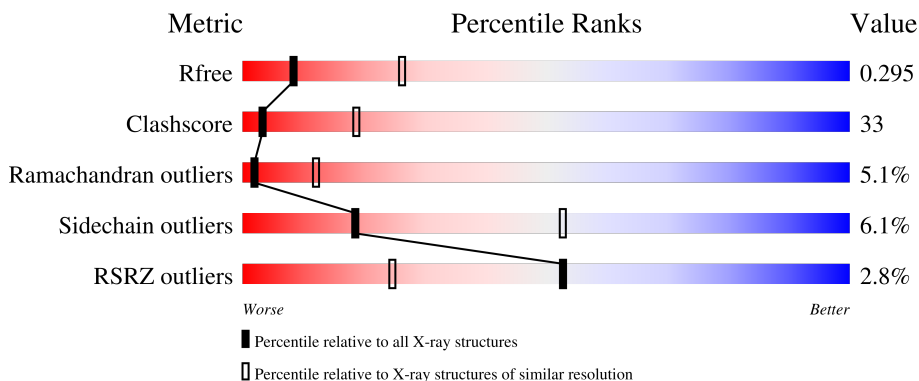
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	186	 5% 41% 38% 15%
1	B	186	 5% 41% 39% 13%
1	C	186	 5% 42% 38% 15%
1	D	186	 5% 44% 35% 16%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4867 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.

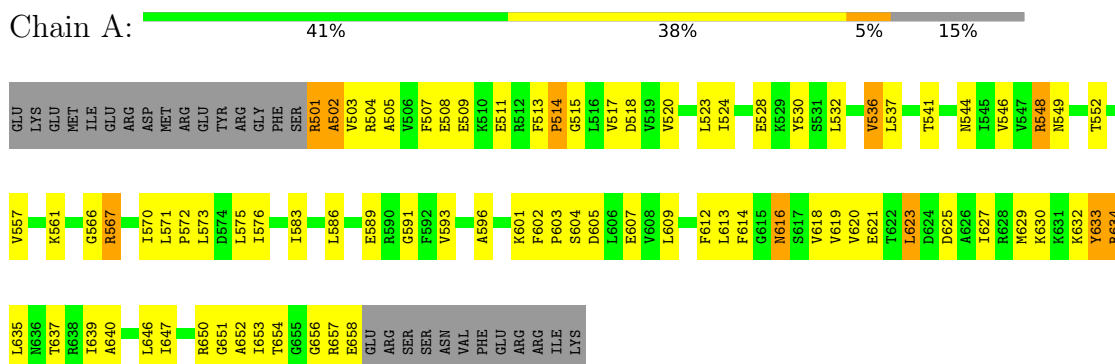
- Molecule 1 is a protein called CHROMOSOME SEGREGATION SMC PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	158	1216	771	212	232	1	0	0	0
1	B	161	1239	786	218	234	1	0	0	0
1	C	158	1216	771	212	232	1	0	0	0
1	D	156	1196	760	207	228	1	0	0	0

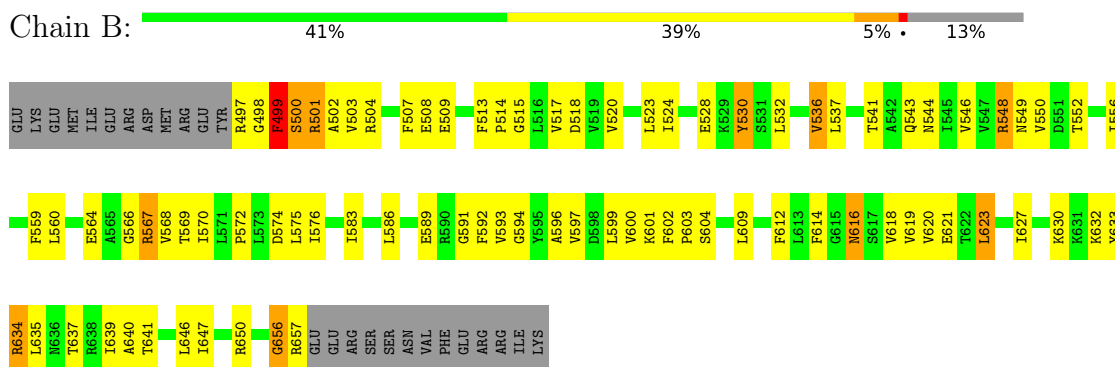
3 Residue-property plots [i](#)

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.

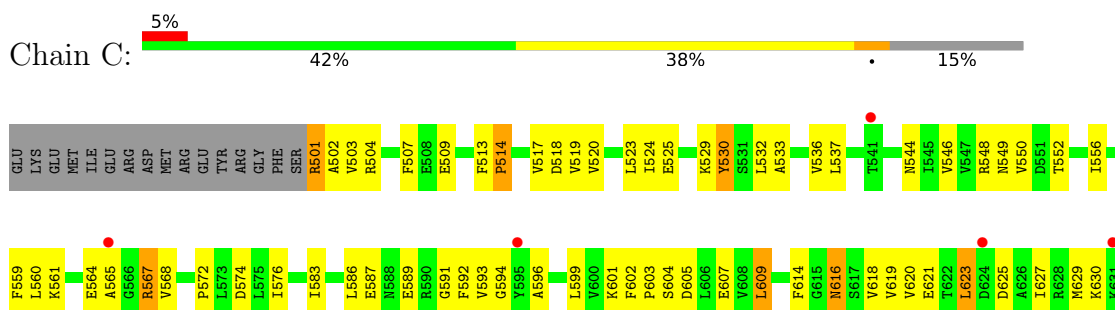
• Molecule 1: CHROMOSOME SEGREGATION SMC PROTEIN

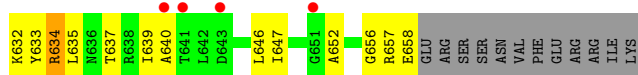


• Molecule 1: CHROMOSOME SEGREGATION SMC PROTEIN

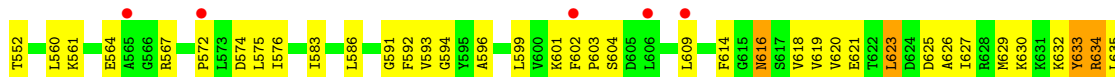
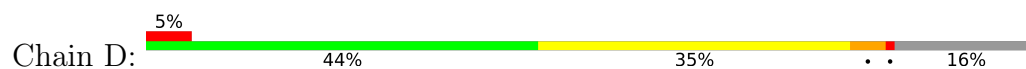


• Molecule 1: CHROMOSOME SEGREGATION SMC PROTEIN





● Molecule 1: CHROMOSOME SEGREGATION SMC PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.90Å 62.21Å 225.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.00 34.05 – 3.00	Depositor EDS
% Data completeness (in resolution range)	83.5 (30.00-3.00) 79.2 (34.05-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.04 (at 3.00Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.253 , 0.298 0.257 , 0.295	Depositor DCC
R_{free} test set	709 reflections (4.47%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtrriage
Anisotropy	0.442	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	4867	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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	0.50	0/1229	0.79	4/1658 (0.2%)
1	B	0.51	0/1253	0.79	4/1689 (0.2%)
1	C	0.47	0/1229	0.75	4/1658 (0.2%)
1	D	0.42	0/1209	0.74	4/1632 (0.2%)
All	All	0.48	0/4920	0.77	16/6637 (0.2%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	567	ARG	NE-CZ-NH2	7.81	124.20	120.30
1	A	548	ARG	NE-CZ-NH2	-7.75	116.42	120.30
1	C	548	ARG	NE-CZ-NH2	-7.68	116.46	120.30
1	C	567	ARG	NE-CZ-NH2	-7.48	116.56	120.30
1	A	567	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	D	567	ARG	NE-CZ-NH2	6.83	123.72	120.30
1	B	567	ARG	NE-CZ-NH1	-6.81	116.89	120.30
1	D	548	ARG	NE-CZ-NH2	6.66	123.63	120.30
1	D	567	ARG	NE-CZ-NH1	-6.61	116.99	120.30
1	D	548	ARG	NE-CZ-NH1	-6.58	117.01	120.30
1	A	567	ARG	NE-CZ-NH1	6.43	123.51	120.30
1	C	567	ARG	NE-CZ-NH1	6.24	123.42	120.30
1	A	548	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	B	548	ARG	NE-CZ-NH1	-6.04	117.28	120.30
1	C	548	ARG	NE-CZ-NH1	5.81	123.21	120.30
1	B	548	ARG	NE-CZ-NH2	5.77	123.19	120.30

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	1216	0	1250	103	0
1	B	1239	0	1274	105	0
1	C	1216	0	1250	72	0
1	D	1196	0	1231	73	0
All	All	4867	0	5005	325	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 33.

All (325) 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:501:ARG:NH1	1:A:505:ALA:H	1.57	1.02
1:C:518:ASP:HB3	1:C:523:LEU:HD23	1.44	0.97
1:B:616:ASN:HD22	1:B:616:ASN:H	1.10	0.97
1:B:616:ASN:H	1:B:616:ASN:ND2	1.63	0.94
1:C:616:ASN:H	1:C:616:ASN:HD22	1.13	0.93
1:A:501:ARG:HH12	1:A:505:ALA:H	1.07	0.93
1:A:501:ARG:HE	1:A:502:ALA:N	1.65	0.93
1:C:616:ASN:H	1:C:616:ASN:ND2	1.63	0.93
1:D:518:ASP:HB3	1:D:523:LEU:HD23	1.52	0.92
1:B:500:SER:OG	1:B:503:VAL:HB	1.70	0.91
1:C:561:LYS:HG3	1:D:656:GLY:O	1.71	0.91
1:D:501:ARG:HB2	1:D:504:ARG:HD2	1.52	0.87
1:A:635:LEU:HB3	1:A:637:THR:HG22	1.57	0.87
1:D:616:ASN:H	1:D:616:ASN:ND2	1.73	0.86
1:A:501:ARG:HE	1:A:501:ARG:C	1.77	0.85
1:B:616:ASN:HD22	1:B:616:ASN:N	1.69	0.85
1:A:634:ARG:HB2	1:A:634:ARG:HH21	1.40	0.84
1:D:501:ARG:HH11	1:D:502:ALA:HA	1.41	0.84
1:C:635:LEU:HB3	1:C:637:THR:HG22	1.59	0.83
1:D:635:LEU:HB3	1:D:637:THR:HG22	1.59	0.83
1:A:616:ASN:H	1:A:616:ASN:ND2	1.76	0.83
1:C:616:ASN:HD22	1:C:616:ASN:N	1.72	0.83
1:A:616:ASN:H	1:A:616:ASN:HD22	1.27	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:568:VAL:O	1:D:654:THR:HG23	1.79	0.82
1:C:609:LEU:H	1:C:609:LEU:HD12	1.45	0.82
1:B:518:ASP:HB3	1:B:523:LEU:HD23	1.62	0.81
1:A:616:ASN:HD22	1:A:616:ASN:N	1.77	0.81
1:D:601:LYS:HD3	1:D:602:PHE:N	1.94	0.80
1:B:635:LEU:HB3	1:B:637:THR:HG22	1.61	0.80
1:D:616:ASN:H	1:D:616:ASN:HD22	1.25	0.80
1:C:501:ARG:HH21	1:C:501:ARG:HB2	1.44	0.80
1:A:566:GLY:HA2	1:B:657:ARG:HG3	1.63	0.80
1:A:501:ARG:HH12	1:A:505:ALA:N	1.79	0.80
1:A:501:ARG:HB2	1:A:504:ARG:HD2	1.62	0.80
1:A:601:LYS:HD3	1:A:602:PHE:N	1.97	0.79
1:D:634:ARG:HH21	1:D:634:ARG:HB2	1.47	0.78
1:C:601:LYS:HD3	1:C:602:PHE:N	1.98	0.77
1:C:634:ARG:HB2	1:C:634:ARG:HH21	1.49	0.77
1:A:518:ASP:HB3	1:A:523:LEU:HD23	1.66	0.77
1:D:618:VAL:HG12	1:D:619:VAL:N	2.01	0.76
1:A:634:ARG:HB2	1:A:634:ARG:NH2	2.00	0.75
1:B:501:ARG:H	1:B:504:ARG:HD2	1.51	0.75
1:C:601:LYS:HD3	1:C:602:PHE:H	1.51	0.75
1:D:616:ASN:HD22	1:D:616:ASN:N	1.78	0.74
1:D:601:LYS:HD3	1:D:602:PHE:H	1.52	0.74
1:A:501:ARG:C	1:A:501:ARG:NE	2.40	0.74
1:B:601:LYS:HD3	1:B:602:PHE:N	2.03	0.73
1:B:634:ARG:HH21	1:B:634:ARG:HB2	1.53	0.73
1:A:601:LYS:HD3	1:A:602:PHE:H	1.53	0.73
1:D:634:ARG:HB2	1:D:634:ARG:NH2	2.03	0.73
1:D:630:LYS:HD2	1:D:647:ILE:HG21	1.71	0.71
1:B:500:SER:CB	1:B:503:VAL:HB	2.21	0.71
1:B:630:LYS:HD2	1:B:647:ILE:HG21	1.73	0.71
1:A:657:ARG:O	1:A:658:GLU:HG2	1.91	0.71
1:A:609:LEU:HD12	1:A:609:LEU:H	1.55	0.71
1:C:634:ARG:HB2	1:C:634:ARG:NH2	2.06	0.70
1:A:501:ARG:HH11	1:A:502:ALA:CA	2.05	0.70
1:C:593:VAL:HG23	1:C:620:VAL:HA	1.73	0.69
1:D:635:LEU:HD12	1:D:639:ILE:HD11	1.75	0.69
1:A:650:ARG:HD3	1:B:612:PHE:CD1	2.28	0.69
1:C:609:LEU:H	1:C:609:LEU:CD1	2.04	0.69
1:C:630:LYS:HD2	1:C:647:ILE:HG21	1.74	0.69
1:B:634:ARG:HB2	1:B:634:ARG:NH2	2.08	0.69
1:A:618:VAL:HG12	1:A:619:VAL:N	2.06	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:653:ILE:O	1:B:570:ILE:N	2.20	0.69
1:B:601:LYS:HD3	1:B:602:PHE:H	1.58	0.68
1:B:501:ARG:N	1:B:504:ARG:HD2	2.08	0.68
1:A:572:PRO:O	1:A:576:ILE:HG23	1.95	0.67
1:D:583:ILE:HB	1:D:586:LEU:HD12	1.77	0.67
1:B:618:VAL:HG12	1:B:619:VAL:N	2.10	0.66
1:B:646:LEU:HD12	1:B:647:ILE:H	1.60	0.66
1:B:501:ARG:HA	1:B:504:ARG:CD	2.25	0.66
1:A:583:ILE:HD12	1:A:586:LEU:HD11	1.76	0.66
1:D:583:ILE:HD12	1:D:586:LEU:HD11	1.77	0.65
1:C:572:PRO:O	1:C:576:ILE:HG23	1.96	0.65
1:A:501:ARG:HH11	1:A:502:ALA:C	2.01	0.65
1:A:630:LYS:HD2	1:A:647:ILE:HG21	1.77	0.65
1:A:635:LEU:HD12	1:A:639:ILE:HD11	1.79	0.65
1:B:499:PHE:O	1:B:499:PHE:HD1	1.80	0.65
1:B:515:GLY:O	1:B:548:ARG:HG3	1.97	0.65
1:D:593:VAL:HG23	1:D:620:VAL:HA	1.79	0.64
1:A:646:LEU:HD12	1:A:647:ILE:H	1.62	0.64
1:B:593:VAL:HG23	1:B:620:VAL:HA	1.79	0.64
1:B:500:SER:HB3	1:B:543:GLN:OE1	1.97	0.64
1:B:532:LEU:O	1:B:536:VAL:HG13	1.97	0.64
1:A:501:ARG:HH11	1:A:502:ALA:HA	1.62	0.64
1:B:583:ILE:HD12	1:B:586:LEU:HD11	1.79	0.64
1:D:515:GLY:O	1:D:548:ARG:HG3	1.97	0.63
1:C:591:GLY:O	1:C:621:GLU:HG2	1.98	0.62
1:B:609:LEU:HD12	1:B:609:LEU:H	1.64	0.62
1:D:609:LEU:HD12	1:D:609:LEU:H	1.63	0.62
1:B:498:GLY:O	1:B:499:PHE:HB3	1.99	0.62
1:D:517:VAL:HB	1:D:546:VAL:O	2.00	0.62
1:B:501:ARG:HA	1:B:504:ARG:HD2	1.81	0.62
1:B:499:PHE:CD1	1:B:499:PHE:C	2.71	0.61
1:C:609:LEU:HD12	1:C:609:LEU:N	2.12	0.61
1:C:618:VAL:HG12	1:C:619:VAL:N	2.15	0.61
1:A:593:VAL:HG23	1:A:620:VAL:HA	1.83	0.61
1:B:501:ARG:CA	1:B:504:ARG:HD2	2.31	0.61
1:A:658:GLU:HG2	1:B:566:GLY:HA2	1.82	0.61
1:D:646:LEU:HD12	1:D:647:ILE:H	1.66	0.60
1:A:501:ARG:NH1	1:A:502:ALA:HA	2.17	0.60
1:A:591:GLY:O	1:A:621:GLU:HG2	2.02	0.60
1:C:517:VAL:HB	1:C:546:VAL:O	2.02	0.60
1:A:609:LEU:H	1:A:609:LEU:CD1	2.13	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:583:ILE:HD12	1:C:586:LEU:HD11	1.85	0.59
1:A:656:GLY:O	1:A:657:ARG:HG2	2.03	0.59
1:B:517:VAL:HB	1:B:546:VAL:O	2.02	0.59
1:D:501:ARG:C	1:D:503:VAL:N	2.56	0.59
1:B:639:ILE:O	1:B:646:LEU:HD12	2.03	0.59
1:A:501:ARG:HH12	1:A:505:ALA:CB	2.15	0.59
1:B:572:PRO:O	1:B:576:ILE:HG23	2.02	0.59
1:B:500:SER:C	1:B:502:ALA:H	2.06	0.58
1:B:499:PHE:HD1	1:B:499:PHE:C	2.06	0.58
1:A:501:ARG:O	1:A:504:ARG:N	2.29	0.58
1:A:630:LYS:HD3	1:B:575:LEU:HD11	1.86	0.58
1:A:591:GLY:HA2	1:A:621:GLU:HG3	1.86	0.58
1:C:635:LEU:HD12	1:C:639:ILE:HD11	1.84	0.58
1:C:591:GLY:HA2	1:C:621:GLU:HG3	1.86	0.57
1:C:621:GLU:HB2	1:C:625:ASP:OD1	2.04	0.57
1:D:618:VAL:HG12	1:D:619:VAL:H	1.68	0.57
1:D:609:LEU:H	1:D:609:LEU:CD1	2.17	0.57
1:D:629:MET:HE2	1:D:639:ILE:HD13	1.86	0.57
1:D:501:ARG:C	1:D:503:VAL:H	2.07	0.57
1:D:618:VAL:CG1	1:D:619:VAL:N	2.67	0.57
1:D:633:TYR:O	1:D:634:ARG:C	2.43	0.57
1:D:592:PHE:CZ	1:D:594:GLY:HA2	2.40	0.57
1:A:654:THR:HA	1:B:568:VAL:O	2.05	0.56
1:A:618:VAL:HG12	1:A:619:VAL:H	1.70	0.56
1:D:518:ASP:HB3	1:D:523:LEU:CD2	2.31	0.56
1:B:609:LEU:H	1:B:609:LEU:CD1	2.18	0.56
1:B:513:PHE:HB3	1:B:552:THR:HG23	1.89	0.55
1:B:499:PHE:O	1:B:504:ARG:HD2	2.07	0.55
1:C:646:LEU:HD12	1:C:647:ILE:H	1.71	0.55
1:B:623:LEU:HD22	1:B:627:ILE:HG13	1.88	0.55
1:A:567:ARG:H	1:B:657:ARG:HH22	1.55	0.55
1:C:619:VAL:HA	1:C:640:ALA:O	2.07	0.55
1:A:532:LEU:O	1:A:536:VAL:HG13	2.05	0.55
1:C:549:ASN:OD1	1:C:552:THR:N	2.36	0.55
1:D:591:GLY:O	1:D:621:GLU:HG2	2.07	0.55
1:A:629:MET:HE2	1:A:639:ILE:HD13	1.89	0.55
1:C:591:GLY:HA2	1:C:621:GLU:CG	2.36	0.55
1:A:621:GLU:HB2	1:A:625:ASP:OD1	2.07	0.54
1:B:609:LEU:HD12	1:B:609:LEU:N	2.22	0.54
1:B:633:TYR:O	1:B:634:ARG:C	2.46	0.54
1:A:501:ARG:HE	1:A:502:ALA:CA	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:623:LEU:HD22	1:A:627:ILE:HG13	1.90	0.54
1:C:583:ILE:HB	1:C:586:LEU:HD12	1.88	0.54
1:B:550:VAL:HG23	1:B:574:ASP:OD2	2.08	0.54
1:B:591:GLY:O	1:B:621:GLU:HG2	2.08	0.54
1:A:650:ARG:HB3	1:B:612:PHE:CE1	2.43	0.53
1:A:650:ARG:HD3	1:B:612:PHE:HD1	1.71	0.53
1:C:518:ASP:HB3	1:C:523:LEU:CD2	2.28	0.53
1:D:549:ASN:OD1	1:D:552:THR:N	2.36	0.53
1:C:623:LEU:HD22	1:C:627:ILE:HG13	1.91	0.53
1:D:591:GLY:HA2	1:D:621:GLU:HG3	1.91	0.52
1:A:567:ARG:H	1:B:657:ARG:NH2	2.06	0.52
1:B:507:PHE:C	1:B:509:GLU:H	2.12	0.52
1:B:500:SER:O	1:B:502:ALA:N	2.39	0.52
1:A:501:ARG:C	1:A:503:VAL:N	2.61	0.52
1:B:549:ASN:OD1	1:B:552:THR:N	2.40	0.52
1:B:635:LEU:HD12	1:B:639:ILE:HD11	1.91	0.52
1:A:609:LEU:HD12	1:A:609:LEU:N	2.21	0.51
1:B:592:PHE:CZ	1:B:594:GLY:HA2	2.46	0.51
1:D:623:LEU:HD22	1:D:627:ILE:HG13	1.93	0.51
1:B:541:THR:HA	1:B:544:ASN:ND2	2.26	0.51
1:A:647:ILE:HA	1:A:652:ALA:O	2.11	0.51
1:B:499:PHE:O	1:B:504:ARG:CD	2.59	0.51
1:D:634:ARG:O	1:D:634:ARG:HG3	2.10	0.51
1:B:583:ILE:HB	1:B:586:LEU:HD12	1.92	0.51
1:C:556:ILE:O	1:C:559:PHE:HB3	2.10	0.51
1:A:532:LEU:HD23	1:A:532:LEU:C	2.31	0.51
1:A:557:VAL:O	1:A:561:LYS:HG3	2.10	0.50
1:A:591:GLY:HA2	1:A:621:GLU:CG	2.40	0.50
1:A:656:GLY:CA	1:B:567:ARG:HG2	2.41	0.50
1:A:634:ARG:O	1:A:634:ARG:NE	2.44	0.50
1:C:520:VAL:HG23	1:C:544:ASN:O	2.11	0.50
1:A:583:ILE:HB	1:A:586:LEU:HD12	1.93	0.50
1:B:618:VAL:CG1	1:B:619:VAL:N	2.75	0.50
1:C:530:TYR:CE1	1:C:599:LEU:HD22	2.47	0.50
1:C:550:VAL:HG23	1:C:574:ASP:OD2	2.12	0.50
1:A:633:TYR:O	1:A:634:ARG:C	2.49	0.50
1:A:561:LYS:HG3	1:B:656:GLY:HA3	1.93	0.50
1:D:609:LEU:HD12	1:D:609:LEU:N	2.26	0.50
1:A:501:ARG:C	1:A:503:VAL:H	2.14	0.50
1:A:634:ARG:O	1:A:634:ARG:CZ	2.60	0.50
1:B:556:ILE:O	1:B:559:PHE:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:ASN:OD1	1:A:552:THR:N	2.33	0.49
1:A:609:LEU:O	1:A:613:LEU:N	2.41	0.49
1:D:501:ARG:NH1	1:D:502:ALA:HA	2.20	0.49
1:C:501:ARG:HG3	1:C:502:ALA:N	2.26	0.49
1:A:507:PHE:C	1:A:509:GLU:H	2.16	0.49
1:D:618:VAL:CG1	1:D:619:VAL:H	2.25	0.49
1:D:532:LEU:O	1:D:536:VAL:HG13	2.13	0.49
1:A:501:ARG:HH12	1:A:505:ALA:HB2	1.77	0.49
1:C:592:PHE:CZ	1:C:594:GLY:HA2	2.48	0.49
1:B:634:ARG:HG3	1:B:634:ARG:O	2.12	0.48
1:A:517:VAL:HB	1:A:546:VAL:O	2.13	0.48
1:C:501:ARG:C	1:C:503:VAL:N	2.67	0.48
1:C:596:ALA:HB3	1:C:614:PHE:HB3	1.93	0.48
1:A:618:VAL:CG1	1:A:619:VAL:N	2.74	0.48
1:B:514:PRO:HG2	1:B:515:GLY:H	1.79	0.48
1:A:501:ARG:O	1:A:503:VAL:N	2.47	0.47
1:B:618:VAL:HG12	1:B:619:VAL:H	1.78	0.47
1:C:618:VAL:HG12	1:C:619:VAL:H	1.76	0.47
1:C:639:ILE:O	1:C:646:LEU:HD12	2.15	0.47
1:D:572:PRO:O	1:D:576:ILE:HG23	2.13	0.47
1:B:500:SER:C	1:B:502:ALA:N	2.67	0.47
1:D:513:PHE:HB3	1:D:552:THR:HG23	1.95	0.47
1:D:591:GLY:HA2	1:D:621:GLU:CG	2.45	0.47
1:B:560:LEU:O	1:B:564:GLU:N	2.47	0.47
1:C:507:PHE:C	1:C:509:GLU:H	2.19	0.47
1:C:560:LEU:O	1:C:564:GLU:N	2.48	0.47
1:D:501:ARG:C	1:D:501:ARG:NE	2.68	0.47
1:C:633:TYR:O	1:C:634:ARG:C	2.54	0.46
1:B:498:GLY:O	1:B:499:PHE:CB	2.63	0.46
1:B:591:GLY:HA2	1:B:621:GLU:HG3	1.98	0.46
1:C:634:ARG:O	1:C:634:ARG:HG3	2.16	0.46
1:A:570:ILE:O	1:A:571:LEU:HD23	2.15	0.46
1:D:550:VAL:HG23	1:D:574:ASP:OD2	2.15	0.46
1:D:583:ILE:HB	1:D:586:LEU:CD1	2.43	0.46
1:B:633:TYR:HD1	1:B:633:TYR:H	1.64	0.46
1:A:520:VAL:HG23	1:A:544:ASN:O	2.16	0.46
1:D:634:ARG:O	1:D:634:ARG:NE	2.49	0.46
1:B:530:TYR:CE1	1:B:599:LEU:HD22	2.51	0.45
1:B:646:LEU:HD12	1:B:647:ILE:N	2.30	0.45
1:C:647:ILE:HA	1:C:652:ALA:O	2.16	0.45
1:A:612:PHE:CD1	1:B:650:ARG:HD3	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:532:LEU:C	1:D:532:LEU:HD23	2.36	0.45
1:A:619:VAL:HA	1:A:640:ALA:O	2.16	0.45
1:A:650:ARG:O	1:B:576:ILE:HA	2.16	0.45
1:A:514:PRO:HG2	1:A:515:GLY:H	1.82	0.45
1:A:646:LEU:HD12	1:A:647:ILE:N	2.30	0.45
1:D:504:ARG:O	1:D:508:GLU:HG2	2.17	0.45
1:C:501:ARG:HB2	1:C:501:ARG:NH2	2.22	0.45
1:C:532:LEU:HD23	1:C:532:LEU:C	2.37	0.44
1:C:618:VAL:CG1	1:C:619:VAL:N	2.81	0.44
1:D:507:PHE:C	1:D:509:GLU:H	2.19	0.44
1:B:596:ALA:HB3	1:B:614:PHE:HB3	1.99	0.44
1:A:572:PRO:HG2	1:A:575:LEU:HB3	2.00	0.44
1:D:501:ARG:HH12	1:D:505:ALA:HB2	1.83	0.44
1:D:583:ILE:HD12	1:D:586:LEU:CD1	2.46	0.44
1:D:634:ARG:O	1:D:634:ARG:CG	2.63	0.44
1:D:630:LYS:HD2	1:D:647:ILE:CG2	2.44	0.44
1:A:627:ILE:HD13	1:B:550:VAL:CG1	2.48	0.44
1:C:587:GLU:HA	1:C:592:PHE:CD2	2.52	0.44
1:C:634:ARG:O	1:C:634:ARG:NE	2.51	0.44
1:A:654:THR:HG23	1:B:568:VAL:O	2.17	0.44
1:D:520:VAL:HG23	1:D:544:ASN:O	2.18	0.44
1:A:605:ASP:C	1:A:607:GLU:H	2.21	0.44
1:B:623:LEU:HD22	1:B:627:ILE:CG1	2.48	0.44
1:D:572:PRO:HG2	1:D:575:LEU:HB3	1.99	0.43
1:B:634:ARG:O	1:B:634:ARG:CG	2.66	0.43
1:A:524:ILE:HB	1:A:602:PHE:HE2	1.84	0.43
1:B:497:ARG:HD3	1:B:497:ARG:HA	1.72	0.43
1:C:513:PHE:HB3	1:C:552:THR:HG23	2.01	0.43
1:A:634:ARG:O	1:A:634:ARG:CG	2.66	0.43
1:A:634:ARG:O	1:A:634:ARG:HG3	2.17	0.43
1:C:550:VAL:HG11	1:D:627:ILE:HD13	2.00	0.43
1:D:647:ILE:HA	1:D:652:ALA:O	2.19	0.43
1:A:567:ARG:HG3	1:B:657:ARG:HB2	2.01	0.43
1:B:513:PHE:HA	1:B:514:PRO:HD2	1.84	0.43
1:B:600:VAL:HG12	1:B:601:LYS:N	2.34	0.43
1:A:657:ARG:O	1:A:658:GLU:CG	2.64	0.43
1:B:634:ARG:O	1:B:634:ARG:NE	2.50	0.43
1:A:650:ARG:HB3	1:B:612:PHE:CD1	2.53	0.43
1:B:591:GLY:HA2	1:B:621:GLU:CG	2.49	0.43
1:D:623:LEU:O	1:D:626:ALA:N	2.52	0.43
1:B:616:ASN:ND2	1:B:616:ASN:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:633:TYR:CD1	1:B:633:TYR:N	2.87	0.42
1:A:586:LEU:HD22	1:A:629:MET:SD	2.59	0.42
1:A:630:LYS:HE2	1:A:651:GLY:HA2	2.02	0.42
1:C:634:ARG:O	1:C:634:ARG:CG	2.67	0.42
1:D:596:ALA:HB3	1:D:614:PHE:HB3	2.00	0.42
1:A:561:LYS:CG	1:B:656:GLY:HA3	2.50	0.42
1:A:618:VAL:CG1	1:A:619:VAL:H	2.31	0.42
1:B:497:ARG:O	1:B:498:GLY:C	2.58	0.42
1:A:586:LEU:O	1:A:589:GLU:HB2	2.19	0.42
1:B:524:ILE:HB	1:B:602:PHE:HE2	1.84	0.42
1:C:532:LEU:O	1:C:536:VAL:HG13	2.20	0.42
1:D:621:GLU:HB2	1:D:625:ASP:OD1	2.20	0.42
1:A:653:ILE:O	1:B:569:THR:HA	2.19	0.42
1:C:501:ARG:O	1:C:504:ARG:N	2.43	0.42
1:D:530:TYR:O	1:D:534:VAL:HG23	2.20	0.42
1:D:643:ASP:HB2	1:D:645:GLU:OE1	2.20	0.42
1:D:520:VAL:O	1:D:521:SER:C	2.58	0.41
1:A:517:VAL:O	1:A:518:ASP:HB2	2.19	0.41
1:A:596:ALA:HB3	1:A:614:PHE:HB3	2.01	0.41
1:A:639:ILE:O	1:A:646:LEU:HD12	2.20	0.41
1:C:501:ARG:C	1:C:503:VAL:H	2.22	0.41
1:C:533:ALA:O	1:C:536:VAL:HG22	2.20	0.41
1:B:501:ARG:HA	1:B:504:ARG:HD3	2.01	0.41
1:D:560:LEU:O	1:D:564:GLU:N	2.53	0.41
1:A:596:ALA:HB1	1:A:614:PHE:CD2	2.56	0.41
1:C:513:PHE:HA	1:C:514:PRO:HD2	1.88	0.41
1:C:616:ASN:ND2	1:C:616:ASN:N	2.34	0.41
1:D:518:ASP:CB	1:D:523:LEU:HD23	2.34	0.41
1:B:619:VAL:HA	1:B:640:ALA:O	2.21	0.41
1:C:520:VAL:O	1:C:524:ILE:HG22	2.20	0.41
1:D:586:LEU:HD22	1:D:629:MET:SD	2.60	0.41
1:A:566:GLY:HA2	1:B:657:ARG:HH21	1.86	0.41
1:B:657:ARG:HG3	1:B:657:ARG:HH21	1.85	0.41
1:C:503:VAL:HG11	1:C:519:VAL:HG11	2.02	0.41
1:B:532:LEU:C	1:B:532:LEU:HD23	2.41	0.41
1:C:629:MET:HE2	1:C:639:ILE:HD13	2.03	0.41
1:B:520:VAL:HG23	1:B:544:ASN:O	2.21	0.41
1:B:549:ASN:HA	1:B:574:ASP:OD1	2.21	0.41
1:D:530:TYR:CE1	1:D:599:LEU:HD22	2.56	0.41
1:B:589:GLU:HG2	1:B:633:TYR:OH	2.21	0.41
1:C:583:ILE:HB	1:C:586:LEU:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:586:LEU:O	1:C:589:GLU:HB2	2.22	0.41
1:A:627:ILE:HD13	1:B:550:VAL:HG11	2.02	0.40
1:B:618:VAL:CG1	1:B:619:VAL:H	2.34	0.40
1:C:567:ARG:HG2	1:D:656:GLY:HA2	2.03	0.40
1:C:587:GLU:HA	1:C:592:PHE:CE2	2.56	0.40
1:C:656:GLY:HA2	1:D:561:LYS:HG3	2.03	0.40
1:D:634:ARG:O	1:D:634:ARG:CZ	2.69	0.40
1:C:525:GLU:OE1	1:C:525:GLU:N	2.55	0.40
1:C:634:ARG:O	1:C:634:ARG:CZ	2.69	0.40
1:A:657:ARG:O	1:B:566:GLY:HA2	2.22	0.40
1:B:623:LEU:HA	1:B:641:THR:HG21	2.03	0.40
1:D:646:LEU:O	1:D:653:ILE:HA	2.22	0.40
1:A:513:PHE:HB3	1:A:552:THR:HG23	2.04	0.40
1:A:548:ARG:HA	1:A:573:LEU:HD12	2.04	0.40
1:C:605:ASP:C	1:C:607:GLU:H	2.25	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	156/186 (84%)	120 (77%)	27 (17%)	9 (6%)	1 10
1	B	159/186 (86%)	120 (76%)	31 (20%)	8 (5%)	2 12
1	C	156/186 (84%)	118 (76%)	30 (19%)	8 (5%)	2 12
1	D	154/186 (83%)	117 (76%)	30 (20%)	7 (4%)	2 14
All	All	625/744 (84%)	475 (76%)	118 (19%)	32 (5%)	2 12

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	604	SER
1	B	499	PHE
1	B	604	SER
1	C	604	SER
1	D	604	SER
1	A	632	LYS
1	B	656	GLY
1	A	502	ALA
1	A	541	THR
1	A	603	PRO
1	B	500	SER
1	B	632	LYS
1	C	603	PRO
1	C	632	LYS
1	D	603	PRO
1	D	632	LYS
1	B	603	PRO
1	D	633	TYR
1	A	508	GLU
1	A	633	TYR
1	B	508	GLU
1	B	528	GLU
1	C	529	LYS
1	C	565	ALA
1	C	609	LEU
1	C	657	ARG
1	D	541	THR
1	A	528	GLU
1	D	529	LYS
1	C	514	PRO
1	A	514	PRO
1	D	520	VAL

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	131/158 (83%)	123 (94%)	8 (6%)	18	53
1	B	133/158 (84%)	124 (93%)	9 (7%)	16	48
1	C	131/158 (83%)	124 (95%)	7 (5%)	22	58
1	D	129/158 (82%)	121 (94%)	8 (6%)	18	52
All	All	524/632 (83%)	492 (94%)	32 (6%)	18	53

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	501	ARG
1	A	511	GLU
1	A	530	TYR
1	A	536	VAL
1	A	537	LEU
1	A	616	ASN
1	A	623	LEU
1	A	634	ARG
1	B	499	PHE
1	B	501	ARG
1	B	530	TYR
1	B	536	VAL
1	B	537	LEU
1	B	597	VAL
1	B	616	ASN
1	B	623	LEU
1	B	634	ARG
1	C	501	ARG
1	C	530	TYR
1	C	537	LEU
1	C	616	ASN
1	C	623	LEU
1	C	634	ARG
1	C	658	GLU
1	D	501	ARG
1	D	530	TYR
1	D	536	VAL
1	D	537	LEU
1	D	548	ARG
1	D	616	ASN
1	D	623	LEU
1	D	634	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	562	GLN
1	A	616	ASN
1	B	562	GLN
1	B	616	ASN
1	C	562	GLN
1	C	616	ASN
1	D	544	ASN
1	D	562	GLN
1	D	616	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 monosaccharides 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	158/186 (84%)	-0.16	0 100 100	7, 34, 68, 86	0
1	B	161/186 (86%)	-0.21	0 100 100	4, 25, 56, 84	0
1	C	158/186 (84%)	0.49	9 (5%) 23 8	11, 60, 85, 110	0
1	D	156/186 (83%)	0.63	9 (5%) 23 7	22, 74, 102, 114	0
All	All	633/744 (85%)	0.18	18 (2%) 53 25	4, 45, 90, 114	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	606	LEU	5.8
1	D	602	PHE	4.7
1	C	640	ALA	4.0
1	D	565	ALA	3.7
1	D	514	PRO	3.2
1	C	641	THR	2.9
1	C	595	TYR	2.8
1	D	506	VAL	2.7
1	D	609	LEU	2.6
1	C	651	GLY	2.6
1	C	624	ASP	2.5
1	C	643	ASP	2.5
1	C	541	THR	2.3
1	D	510	LYS	2.3
1	C	565	ALA	2.2
1	D	511	GLU	2.2
1	C	631	LYS	2.2
1	D	572	PRO	2.1

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 monosaccharides 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.