



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:48 PM UTC

PDB ID : 1C8N / pdb_00001c8n
Title : TOBACCO NECROSIS VIRUS
Authors : Oda, Y.; Fukuyama, K.
Deposited on : 2000-05-20
Resolution : 2.25 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

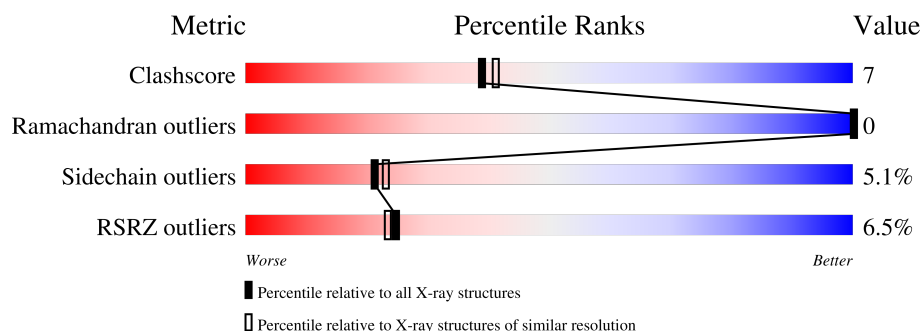
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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))
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	276	4% 54% 13% • 32%
1	B	276	6% 51% 16% • 32%
1	C	276	4% 62% 17% 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4724 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 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	189	Total	C	N	O	S	0	0	0
			1435	926	229	274	6			
1	B	189	Total	C	N	O	S	0	0	0
			1439	928	230	275	6			
1	C	219	Total	C	N	O	S	0	0	0
			1653	1062	273	310	8			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	conflict	UNP Q9IPS9
A	2	ASN	-	conflict	UNP Q9IPS9
A	3	ILE	-	conflict	UNP Q9IPS9
A	4	ASN	-	conflict	UNP Q9IPS9
A	5	ASP	-	conflict	UNP Q9IPS9
A	6	LYS	-	conflict	UNP Q9IPS9
A	7	ARG	-	conflict	UNP Q9IPS9
B	1	ALA	-	conflict	UNP Q9IPS9
B	2	ASN	-	conflict	UNP Q9IPS9
B	3	ILE	-	conflict	UNP Q9IPS9
B	4	ASN	-	conflict	UNP Q9IPS9
B	5	ASP	-	conflict	UNP Q9IPS9
B	6	LYS	-	conflict	UNP Q9IPS9
B	7	ARG	-	conflict	UNP Q9IPS9
C	1	ALA	-	conflict	UNP Q9IPS9
C	2	ASN	-	conflict	UNP Q9IPS9
C	3	ILE	-	conflict	UNP Q9IPS9
C	4	ASN	-	conflict	UNP Q9IPS9
C	5	ASP	-	conflict	UNP Q9IPS9
C	6	LYS	-	conflict	UNP Q9IPS9
C	7	ARG	-	conflict	UNP Q9IPS9

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

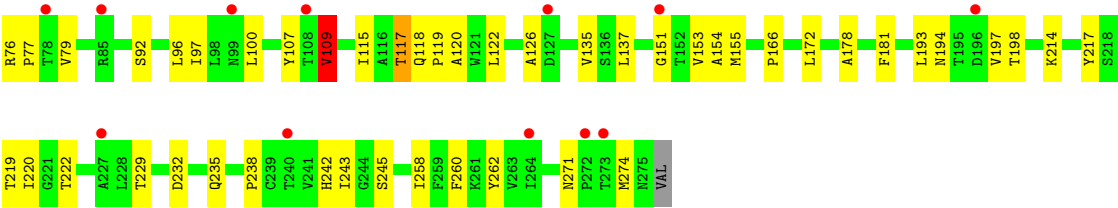
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Ca 2 2	0	0
2	B	2	Total Ca 2 2	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	52	Total O 52 52	0	0
3	B	62	Total O 62 62	0	0
3	C	78	Total O 78 78	0	0

- Molecule 1: COAT PROTEIN





4 Data and refinement statistics

Property	Value	Source
Space group	P 42 3 2	Depositor
Cell constants a, b, c, α , β , γ	336.40Å 336.40Å 336.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.25 8.00 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.0 (8.00-2.25) 95.5 (8.00-2.25)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.25Å)	Xtriage
Refinement program	X-PLOR 3.0	Depositor
R, R_{free}	0.253 , 0.273 0.277 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	18.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.56 , 80.9	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	0.41	EDS
Total number of atoms	4724	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.24% 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.68	0/1475	1.05	9/2030 (0.4%)
1	B	0.71	1/1479 (0.1%)	0.98	6/2036 (0.3%)
1	C	0.67	0/1698	1.03	8/2333 (0.3%)
All	All	0.68	1/4652 (0.0%)	1.02	23/6399 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	89	THR	CB-OG1	5.18	1.52	1.43

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	135	VAL	N-CA-C	-6.80	104.37	111.58
1	C	96	LEU	N-CA-C	-6.65	99.98	109.96
1	B	135	VAL	N-CA-C	-6.60	104.58	111.58
1	C	74	VAL	N-CA-C	-6.60	98.00	107.77
1	A	215	ALA	N-CA-C	6.51	118.46	111.36
1	B	263	VAL	N-CA-C	-6.08	98.78	107.77
1	B	261	LYS	N-CA-C	-6.04	98.57	108.41
1	A	145	CYS	CA-C-N	5.91	125.88	120.03
1	A	145	CYS	C-N-CA	5.91	125.88	120.03
1	A	262	TYR	N-CA-C	5.90	117.93	109.14
1	A	263	VAL	N-CA-C	-5.89	99.00	107.78
1	A	254	PRO	N-CA-C	-5.82	103.60	110.70
1	C	109	VAL	CB-CA-C	-5.63	100.78	110.30
1	C	229	THR	N-CA-C	-5.63	102.95	110.55
1	A	229	THR	N-CA-C	-5.51	103.11	110.55
1	B	254	PRO	N-CA-C	-5.47	104.03	110.70
1	B	99	ASN	N-CA-C	-5.43	100.33	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	SER	N-CA-C	-5.38	101.01	109.50
1	C	120	ALA	N-CA-C	5.35	117.53	111.11
1	C	262	TYR	N-CA-C	5.18	117.06	109.24
1	B	262	TYR	N-CA-C	5.16	117.52	109.52
1	A	261	LYS	N-CA-C	-5.15	100.13	108.52
1	C	151	GLY	N-CA-C	5.04	118.15	111.70

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	1435	0	1401	19	0
1	B	1439	0	1410	22	0
1	C	1653	0	1635	22	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
3	A	52	0	0	1	0
3	B	62	0	0	3	0
3	C	78	0	0	0	0
All	All	4724	0	4446	61	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 (61) 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:C:117:THR:HG23	1:C:222:THR:HG23	1.65	0.79
1:A:167:GLY:H	1:A:171:GLN:NE2	1.93	0.67
1:C:115:ILE:HD12	1:C:117:THR:HG22	1.77	0.66
1:A:117:THR:CG2	1:A:222:THR:HG23	2.25	0.65
1:A:117:THR:HG22	1:A:222:THR:HG23	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:PRO:HD3	1:C:274:MET:HE3	1.80	0.64
1:B:155:MET:O	1:B:178:ALA:HA	1.98	0.63
1:C:107:TYR:CE2	1:C:109:VAL:HG22	2.34	0.62
1:A:88:SER:HB3	1:A:267:ILE:HG22	1.85	0.59
1:B:107:TYR:CE2	1:B:109:VAL:HG22	2.39	0.58
1:A:107:TYR:HA	1:A:245:SER:O	2.02	0.58
1:C:117:THR:HG21	1:C:220:ILE:O	2.04	0.58
1:C:155:MET:O	1:C:178:ALA:HA	2.04	0.57
1:B:217:TYR:CZ	1:B:238:PRO:HB3	2.40	0.57
1:A:155:MET:O	1:A:178:ALA:HA	2.04	0.56
1:C:76:ARG:H	1:C:194:ASN:ND2	2.04	0.55
1:B:232:ASP:O	1:B:235:GLN:HG2	2.06	0.55
1:A:107:TYR:CE2	1:A:109:VAL:HG22	2.43	0.54
1:B:107:TYR:HA	1:B:245:SER:O	2.07	0.54
1:C:232:ASP:O	1:C:235:GLN:HG2	2.07	0.54
1:B:144:LYS:HG2	1:B:256:GLY:HA2	1.90	0.53
1:A:144:LYS:HG2	1:A:256:GLY:HA2	1.91	0.53
1:B:235:GLN:HB3	3:B:864:HOH:O	2.10	0.51
1:A:170:VAL:HG23	3:A:459:HOH:O	2.10	0.51
1:A:217:TYR:CZ	1:A:238:PRO:HB3	2.47	0.50
1:B:108:THR:O	1:B:244:GLY:HA2	2.12	0.50
1:C:107:TYR:HA	1:C:245:SER:O	2.13	0.49
1:A:94:SER:HA	1:A:260:PHE:O	2.12	0.49
1:C:153:VAL:HB	1:C:181:PHE:CE1	2.47	0.49
1:A:255:PRO:HG2	1:A:256:GLY:H	1.78	0.48
1:C:76:ARG:HG2	1:C:77:PRO:N	2.28	0.48
1:B:94:SER:HA	1:B:260:PHE:O	2.14	0.48
1:B:117:THR:HG21	1:B:220:ILE:O	2.14	0.48
1:B:169:ARG:O	1:B:173:SER:HB2	2.14	0.48
1:C:100:LEU:HD21	1:C:243:ILE:HG21	1.96	0.48
1:A:274:MET:HE3	1:C:166:PRO:HD3	1.95	0.47
1:C:197:VAL:HG12	1:C:198:THR:N	2.30	0.46
1:A:118:GLN:HB3	1:A:119:PRO:HD3	1.98	0.45
1:A:271:ASN:OD1	1:A:273:THR:HB	2.17	0.45
1:B:276:VAL:HA	3:B:671:HOH:O	2.17	0.44
1:B:118:GLN:HB3	1:B:119:PRO:HD3	1.99	0.44
1:A:97:ILE:HG13	1:A:260:PHE:CG	2.53	0.44
1:C:155:MET:HA	1:C:242:HIS:O	2.16	0.44
1:B:103:ILE:HG22	1:B:253:VAL:O	2.18	0.43
1:B:182:PRO:HB2	1:B:184:TYR:CE2	2.53	0.43
1:B:182:PRO:HG2	1:B:185:ALA:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:ILE:HG13	1:A:260:PHE:CD1	2.54	0.42
1:A:102:PRO:HB2	1:A:252:ALA:HB1	2.01	0.42
1:A:113:PRO:HG2	1:A:118:GLN:HE21	1.85	0.42
1:B:176:TYR:OH	1:B:211:ARG:NH2	2.53	0.42
1:C:97:ILE:HG13	1:C:260:PHE:CG	2.55	0.42
1:C:118:GLN:HB3	1:C:119:PRO:HD3	2.01	0.42
1:C:154:ALA:HB1	1:C:172:LEU:HD22	2.02	0.42
1:C:271:ASN:HB3	1:C:274:MET:SD	2.59	0.41
1:B:192:ILE:HB	1:B:199:PRO:HD2	2.03	0.41
1:C:97:ILE:HG13	1:C:260:PHE:CD1	2.56	0.41
1:C:217:TYR:CZ	1:C:238:PRO:HB3	2.55	0.41
1:B:253:VAL:HA	3:B:667:HOH:O	2.21	0.40
1:B:97:ILE:HG13	1:B:260:PHE:CG	2.57	0.40
1:C:126:ALA:O	1:C:219:THR:HG21	2.22	0.40
1:B:195:THR:OG1	1:B:197:VAL:HG12	2.22	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	187/276 (68%)	184 (98%)	3 (2%)	0	100	100
1	B	187/276 (68%)	182 (97%)	5 (3%)	0	100	100
1	C	217/276 (79%)	211 (97%)	6 (3%)	0	100	100
All	All	591/828 (71%)	577 (98%)	14 (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	156/225 (69%)	150 (96%)	6 (4%)	29	36
1	B	158/225 (70%)	148 (94%)	10 (6%)	16	16
1	C	179/225 (80%)	170 (95%)	9 (5%)	22	24
All	All	493/675 (73%)	468 (95%)	25 (5%)	21	23

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	THR
1	A	109	VAL
1	A	117	THR
1	A	122	LEU
1	A	137	LEU
1	A	209	VAL
1	B	105	LEU
1	B	108	THR
1	B	109	VAL
1	B	117	THR
1	B	122	LEU
1	B	124	THR
1	B	188	ASP
1	B	197	VAL
1	B	209	VAL
1	B	222	THR
1	C	79	VAL
1	C	92	SER
1	C	109	VAL
1	C	117	THR
1	C	122	LEU
1	C	137	LEU
1	C	193	LEU
1	C	214	LYS
1	C	258	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	ASN
1	A	118	GLN
1	A	162	ASN
1	A	171	GLN
1	B	162	ASN
1	C	118	GLN
1	C	162	ASN
1	C	194	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	189/276 (68%)	0.85	10 (5%) 32 30	7, 13, 20, 34	0
1	B	189/276 (68%)	0.92	17 (8%) 15 14	7, 13, 19, 32	0
1	C	219/276 (79%)	0.88	12 (5%) 30 29	8, 13, 20, 32	0
All	All	597/828 (72%)	0.88	39 (6%) 25 23	7, 13, 20, 34	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	250	ALA	3.9
1	C	78	THR	3.5
1	C	127	ASP	3.1
1	C	240	THR	3.0
1	B	209	VAL	2.9
1	C	99	ASN	2.9
1	C	227	ALA	2.9
1	B	178	ALA	2.8
1	A	87	ASN	2.8
1	A	108	THR	2.8
1	A	89	THR	2.7
1	B	276	VAL	2.6
1	C	151	GLY	2.5
1	A	92	SER	2.5
1	B	273	THR	2.4
1	B	275	ASN	2.4
1	A	102	PRO	2.4
1	B	190	ALA	2.4
1	B	230	ALA	2.4
1	B	100	LEU	2.4
1	B	173	SER	2.3
1	A	88	SER	2.3
1	C	264	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	105	LEU	2.3
1	A	227	ALA	2.2
1	B	201	SER	2.2
1	B	224	ALA	2.2
1	B	272	PRO	2.2
1	B	187	TYR	2.2
1	A	209	VAL	2.1
1	C	85	ARG	2.1
1	A	113	PRO	2.1
1	A	252	ALA	2.1
1	C	273	THR	2.1
1	B	225	PHE	2.1
1	C	108	THR	2.0
1	C	196	ASP	2.0
1	B	232	ASP	2.0
1	C	272	PRO	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	A	303	1/1	0.95	0.12	13,13,13,13	0
2	CA	B	304	1/1	0.95	0.12	19,19,19,19	0
2	CA	C	301	1/1	0.95	0.07	19,19,19,19	0
2	CA	B	302	1/1	0.97	0.08	18,18,18,18	0
2	CA	A	305	1/1	0.99	0.11	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.