



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:48 PM UTC

PDB ID : 2FJW / pdb_00002fjw
Title : d(CTTGAATGCATTCAAG) in complex with MMLV RT catalytic fragment
Authors : Goodwin, K.D.; Georgiadis, M.M.
Deposited on : 2006-01-03
Resolution : 1.95 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

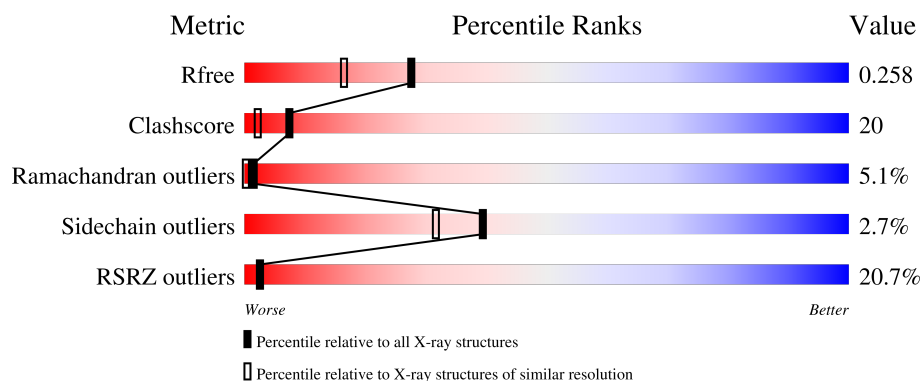
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	B	8	25% 25% 75%
2	G	8	38% 100%
3	A	255	20% 69% 25% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2579 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 DNA chain called 5'-D(*CP*TP*TP*GP*AP*AP*TP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	8	Total	C	N	O	P	0	0	0
			162	79	29	47	7			

- Molecule 2 is a DNA chain called 5'-D(P*CP*AP*TP*TP*CP*AP*AP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	8	Total	C	N	O	P	0	0	0
			163	78	30	47	8			

- Molecule 3 is a protein called Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	255	Total	C	N	O	S	0	0	0
			2041	1311	356	367	7			

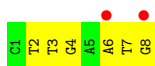
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	4	Total	O	0	0
			4	4		
4	A	209	Total	O	0	0
			209	209		

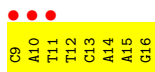
3 Residue-property plots [i](#)

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.

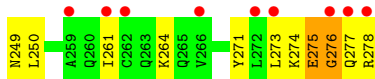
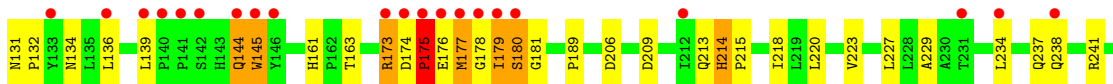
- Molecule 1: 5'-D(*CP*TP*TP*GP*AP*AP*TP*G)-3'



- Molecule 2: 5'-D(P*CP*AP*TP*TP*CP*AP*AP*G)-3'



- Molecule 3: Reverse transcriptase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	54.95Å 145.65Å 46.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.95 50.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-1.95) 96.2 (50.00-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 1.95Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.237 , 0.256 0.237 , 0.258	Depositor DCC
R_{free} test set	1361 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.7	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	0.93	EDS
Total number of atoms	2579	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% 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	B	0.26	0/181	0.61	0/278
2	G	0.26	0/182	0.57	0/278
3	A	0.37	0/2097	0.88	8/2858 (0.3%)
All	All	0.36	0/2460	0.83	8/3414 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	214	HIS	CA-C-N	7.30	127.65	119.32
3	A	214	HIS	C-N-CA	7.30	127.65	119.32
3	A	264	LYS	N-CA-C	-5.54	106.48	113.18
3	A	261	ILE	N-CA-C	5.36	116.03	108.36
3	A	189	PRO	N-CA-C	5.27	120.57	111.77
3	A	91	GLN	N-CA-C	-5.09	99.99	108.34
3	A	54	ALA	N-CA-C	5.03	117.49	111.71
3	A	56	SER	N-CA-C	5.03	117.52	110.23

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	B	162	0	93	8	1
2	G	163	0	91	17	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	2041	0	2056	70	1
4	A	209	0	0	6	0
4	G	4	0	0	1	0
All	All	2579	0	2240	94	2

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 20.

All (94) 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)
3:A:74:ILE:HG23	3:A:111:PRO:HG3	1.49	0.93
3:A:234:LEU:HG	3:A:238:GLN:HE21	1.34	0.90
1:B:7:DT:H2''	1:B:8:DG:H5'	1.57	0.85
3:A:139:LEU:HD13	3:A:278:ARG:OXT	1.78	0.84
3:A:102:LYS:HD3	3:A:106:THR:HA	1.62	0.81
3:A:173:ARG:HA	3:A:173:ARG:HE	1.47	0.79
3:A:103:LYS:HB2	3:A:104:PRO:HD3	1.65	0.78
3:A:174:ASP:HB3	3:A:178:GLY:HA2	1.65	0.77
3:A:161:HIS:HD2	3:A:163:THR:H	1.29	0.77
3:A:71:ARG:NH1	3:A:175:PRO:HG3	2.00	0.77
3:A:179:ILE:HG22	3:A:180:SER:H	1.49	0.76
3:A:274:LYS:HG2	3:A:275:GLU:HG3	1.67	0.76
3:A:234:LEU:HG	3:A:238:GLN:NE2	2.02	0.75
2:G:11:DT:H2''	2:G:12:DT:H5'	1.70	0.73
2:G:12:DT:H2''	2:G:13:DC:H5'	1.70	0.72
3:A:61:ILE:HD11	3:A:117:GLU:HG3	1.73	0.70
1:B:7:DT:H2''	1:B:8:DG:C5'	2.24	0.68
3:A:68:GLN:O	3:A:72:LEU:HD13	1.94	0.67
3:A:179:ILE:HG22	3:A:180:SER:N	2.09	0.67
3:A:234:LEU:O	3:A:237:GLN:HG2	1.96	0.66
3:A:70:ALA:HB1	3:A:100:PRO:HB3	1.78	0.65
2:G:11:DT:H2''	2:G:12:DT:C5'	2.28	0.64
3:A:218:ILE:HB	3:A:229:ALA:HB3	1.81	0.63
3:A:161:HIS:CD2	3:A:163:THR:H	2.15	0.62
3:A:26:LEU:HD23	3:A:26:LEU:O	1.99	0.62
3:A:66:MET:HE2	3:A:100:PRO:HG3	1.82	0.60
3:A:249:ASN:HB2	4:A:479:HOH:O	2.01	0.60
2:G:10:DA:H2''	2:G:11:DT:C5'	2.32	0.60
1:B:6:DA:H2''	1:B:7:DT:H5''	1.83	0.59
3:A:103:LYS:NZ	3:A:110:ARG:HE	2.01	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:71:ARG:HH11	3:A:175:PRO:HG3	1.70	0.57
1:B:6:DA:H2''	1:B:7:DT:C5'	2.35	0.57
1:B:6:DA:C2'	1:B:7:DT:H5''	2.35	0.57
2:G:10:DA:H2''	2:G:11:DT:H5''	1.86	0.56
3:A:80:ARG:NH1	4:A:329:HOH:O	2.38	0.56
2:G:15:DA:H1'	4:G:164:HOH:O	2.06	0.56
2:G:16:DG:C2	3:A:99:LEU:HD21	2.41	0.56
3:A:131:ASN:HD21	3:A:134:ASN:ND2	2.05	0.55
1:B:2:DT:H2''	1:B:3:DT:H5'	1.91	0.53
3:A:277:GLN:HB2	4:A:394:HOH:O	2.09	0.53
3:A:139:LEU:HD13	3:A:278:ARG:C	2.33	0.52
3:A:275:GLU:O	3:A:277:GLN:HG2	2.10	0.52
3:A:213:GLN:C	3:A:215:PRO:HD3	2.35	0.51
3:A:71:ARG:HD3	4:A:352:HOH:O	2.09	0.51
3:A:139:LEU:HD11	3:A:227:LEU:CD2	2.40	0.51
2:G:10:DA:C2'	2:G:11:DT:H5''	2.39	0.50
3:A:174:ASP:O	3:A:175:PRO:C	2.54	0.50
3:A:144:GLN:O	3:A:145:TRP:C	2.55	0.50
2:G:12:DT:H1'	2:G:13:DC:H5''	1.93	0.50
2:G:10:DA:H1'	2:G:11:DT:H5''	1.93	0.50
3:A:80:ARG:HG2	3:A:80:ARG:HH11	1.77	0.49
3:A:132:PRO:O	3:A:136:LEU:HD23	2.12	0.49
2:G:11:DT:H2'	2:G:12:DT:H72	1.94	0.49
3:A:174:ASP:CG	3:A:175:PRO:HD2	2.37	0.49
3:A:139:LEU:HD11	3:A:227:LEU:HD23	1.94	0.49
1:B:6:DA:H1'	1:B:7:DT:H5''	1.95	0.48
3:A:214:HIS:N	3:A:215:PRO:HD3	2.29	0.47
3:A:273:LEU:HG	3:A:278:ARG:HB3	1.95	0.47
3:A:273:LEU:HG	3:A:278:ARG:CB	2.44	0.47
3:A:49:ILE:O	3:A:51:PRO:HD3	2.14	0.46
3:A:99:LEU:HA	3:A:100:PRO:HD3	1.76	0.46
2:G:11:DT:H1'	2:G:12:DT:H5''	1.98	0.46
3:A:61:ILE:HD11	3:A:117:GLU:CG	2.44	0.46
3:A:275:GLU:O	3:A:276:GLY:C	2.57	0.45
3:A:179:ILE:CG2	3:A:180:SER:H	2.23	0.45
3:A:274:LYS:O	3:A:277:GLN:HG2	2.17	0.45
3:A:26:LEU:HD23	3:A:26:LEU:C	2.41	0.44
3:A:98:LEU:C	3:A:99:LEU:HD12	2.42	0.44
3:A:213:GLN:NE2	3:A:213:GLN:HA	2.32	0.44
3:A:273:LEU:HG	3:A:278:ARG:OXT	2.18	0.44
3:A:237:GLN:O	3:A:241:ARG:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:14:DA:H1'	2:G:15:DA:H5''	1.99	0.44
3:A:206:ASP:HB3	3:A:250:LEU:HD13	2.00	0.44
3:A:104:PRO:HD2	3:A:107:ASN:O	2.18	0.43
1:B:3:DT:H2''	1:B:4:DG:C8	2.53	0.43
3:A:99:LEU:HD12	3:A:99:LEU:N	2.34	0.43
2:G:15:DA:H2''	2:G:16:DG:C8	2.54	0.43
2:G:14:DA:H2''	2:G:15:DA:H5'	1.99	0.42
3:A:144:GLN:HB3	3:A:145:TRP:H	1.61	0.42
3:A:75:LYS:HB3	3:A:76:PRO:HD3	2.02	0.42
2:G:12:DT:H2''	2:G:13:DC:C5'	2.44	0.41
3:A:173:ARG:NH2	3:A:179:ILE:O	2.52	0.41
3:A:41:LEU:C	3:A:41:LEU:HD23	2.45	0.41
3:A:71:ARG:HH12	3:A:175:PRO:HG3	1.77	0.41
3:A:120:LYS:HG3	4:A:435:HOH:O	2.20	0.41
3:A:126:HIS:HA	3:A:127:PRO:HD3	1.97	0.41
2:G:12:DT:H1'	2:G:13:DC:C5'	2.51	0.41
3:A:177:MET:SD	3:A:177:MET:C	3.04	0.41
3:A:209:ASP:O	3:A:213:GLN:HG2	2.21	0.41
3:A:234:LEU:O	3:A:238:GLN:HG3	2.20	0.40
3:A:220:LEU:HD22	3:A:227:LEU:HD23	2.02	0.40
3:A:274:LYS:HE2	3:A:275:GLU:OE1	2.21	0.40
3:A:144:GLN:HE21	3:A:145:TRP:N	2.19	0.40
3:A:127:PRO:HG3	4:A:389:HOH:O	2.21	0.40

All (2) 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)
1:B:8:DG:O3'	2:G:9:DC:P[2_765]	1.61	0.59
3:A:271:TYR:OH	3:A:271:TYR:OH[2_665]	2.19	0.01

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
3	A	253/255 (99%)	233 (92%)	7 (3%)	13 (5%)	1 0

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	175	PRO
3	A	180	SER
3	A	104	PRO
3	A	145	TRP
3	A	275	GLU
3	A	276	GLY
3	A	106	THR
3	A	108	ASP
3	A	181	GLY
3	A	223	VAL
3	A	103	LYS
3	A	179	ILE
3	A	105	GLY

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
3	A	224/224 (100%)	218 (97%)	6 (3%)	39 32

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	64	TYR
3	A	144	GLN
3	A	173	ARG
3	A	175	PRO
3	A	176	GLU
3	A	177	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	31	GLN
3	A	77	HIS
3	A	79	GLN
3	A	126	HIS
3	A	134	ASN
3	A	144	GLN
3	A	161	HIS
3	A	213	GLN
3	A	238	GLN
3	A	245	GLN
3	A	277	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	B	8/8 (100%)	1.54	2 (25%) 2 1	44, 60, 64, 68	0
2	G	8/8 (100%)	1.47	3 (37%) 1 0	31, 66, 72, 73	0
3	A	255/255 (100%)	1.10	51 (20%) 3 3	18, 32, 77, 95	0
All	All	271/271 (100%)	1.13	56 (20%) 2 2	18, 33, 75, 95	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	278	ARG	9.0
3	A	276	GLY	9.0
3	A	106	THR	8.9
3	A	179	ILE	8.1
3	A	175	PRO	7.2
3	A	100	PRO	7.0
3	A	104	PRO	6.7
3	A	101	VAL	6.6
3	A	144	GLN	6.4
3	A	107	ASN	6.1
3	A	99	LEU	6.1
3	A	277	GLN	5.7
3	A	139	LEU	5.3
3	A	180	SER	4.8
3	A	105	GLY	4.6
3	A	108	ASP	4.6
3	A	26	LEU	4.3
3	A	234	LEU	4.2
3	A	173	ARG	4.1
3	A	231	THR	4.0
3	A	64	TYR	3.8
3	A	30	PRO	3.7
3	A	24	THR	3.7

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Mol	Chain	Res	Type	RSRZ
3	A	25	TRP	3.6
3	A	273	LEU	3.6
3	A	146	TYR	3.6
3	A	145	TRP	3.5
3	A	103	LYS	3.5
3	A	176	GLU	3.2
3	A	109	TYR	3.1
3	A	142	SER	3.1
3	A	178	GLY	3.1
3	A	272	LEU	2.9
3	A	174	ASP	2.9
3	A	29	PHE	2.9
3	A	177	MET	2.9
3	A	102	LYS	2.8
3	A	262	CYS	2.7
1	B	8	DG	2.6
3	A	238	GLN	2.6
3	A	111	PRO	2.6
3	A	141	PRO	2.5
3	A	110	ARG	2.5
2	G	9	DC	2.5
3	A	133	TYR	2.4
3	A	140	PRO	2.4
3	A	261	ILE	2.3
3	A	112	VAL	2.3
3	A	259	ALA	2.2
3	A	212	ILE	2.2
3	A	266	VAL	2.2
1	B	6	DA	2.2
3	A	66	MET	2.1
3	A	136	LEU	2.1
2	G	10	DA	2.0
2	G	11	DT	2.0

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

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

6.3 Carbohydrates ⓘ

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.