wwPDB X-ray Structure Validation Summary Report (i)

Jun 12, 2024 – 05:50 PM EDT

PDB ID	:	3X1S
Title	:	Crystal structure of the nucleosome core particle
Authors	:	Sivaraman, P.; Kumarevel, T.S.
Deposited on	:	2014-11-27
Resolution	:	2.81 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

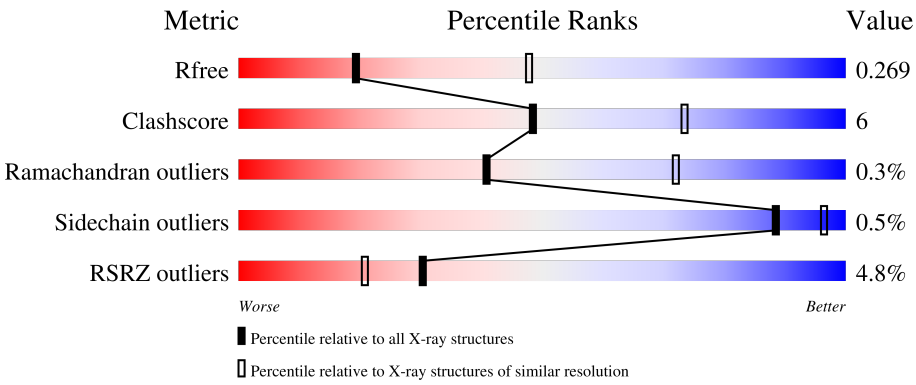
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.81 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 <=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	135	2%, 61%, 10%, •, 29%
1	E	135	65%, 7%, 27%
2	B	102	5%, 64%, 13%, 24%
2	F	102	%, 70%, 13%, 18%
3	C	129	73%, 9%, 19%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	G	129	5% 67% 12% • 19%
4	D	125	66% 9% 25%
4	H	125	66% 8% 26%
5	I	146	12% 64% 36%
5	J	146	12% 66% 34%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 11971 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 Histone H3.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	96	794	500	154	136	4	0	0	0
1	E	98	807	508	156	139	4	0	0	0

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	78	619	391	120	107	1	0	0	0
2	F	84	673	424	133	115	1	0	0	0

- Molecule 3 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	105	810	511	158	141	0	0	0
3	G	104	805	508	157	140	0	0	0

- Molecule 4 is a protein called Histone H2B type 1-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	94	737	462	134	139	2	0	0	0
4	H	92	727	458	131	136	2	0	1	0

- Molecule 5 is a DNA chain called DNA (146-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	I	146	2990	1431	540	874	145	0	0	0
5	J	146	2990	1431	540	874	145	0	0	0

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
6	D	2	2	2	0	0
6	G	1	1	1	0	0
6	I	3	3	3	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
7	I	1	1	1	0	0
7	J	1	1	1	0	0

- Molecule 8 is water.

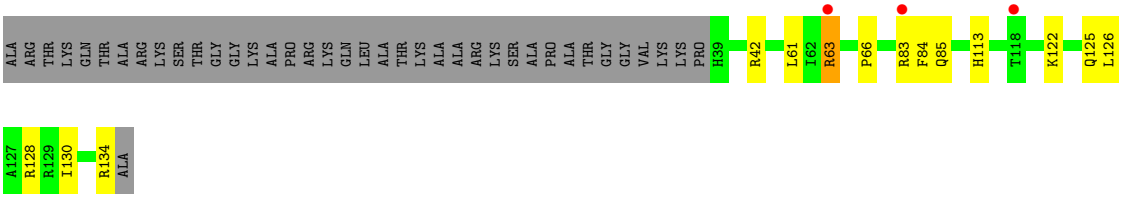
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	1	1	1	0	0
8	C	2	2	2	0	0
8	E	3	3	3	0	0
8	I	3	3	3	0	0
8	J	2	2	2	0	0

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.

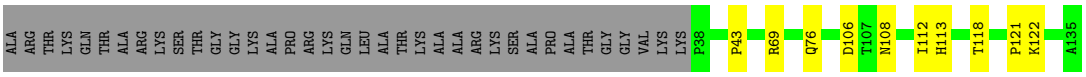
- Molecule 1: Histone H3.1

Chain A:



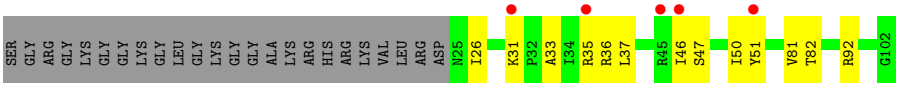
- Molecule 1: Histone H3.1

Chain E:



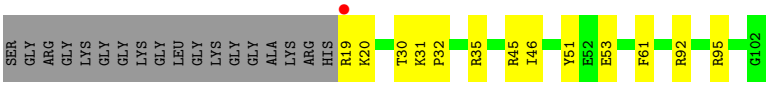
- Molecule 2: Histone H4

Chain B:



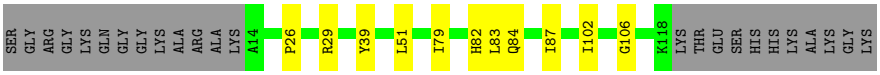
- Molecule 2: Histone H4

Chain F:



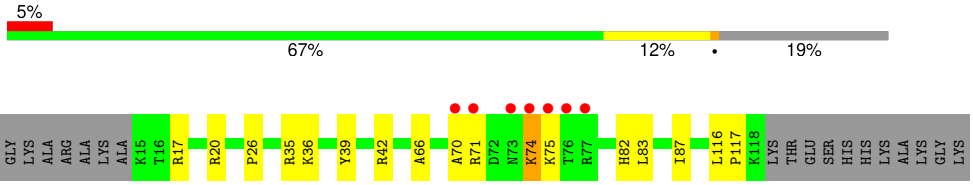
- Molecule 3: Histone H2A type 1-B/E

Chain C:



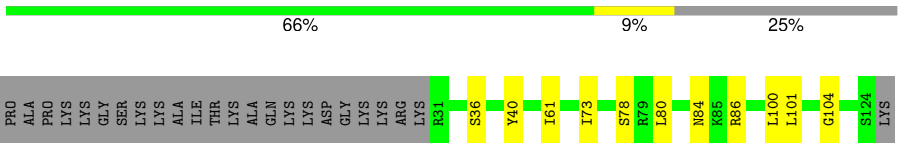
• Molecule 3: Histone H2A type 1-B/E

Chain G:



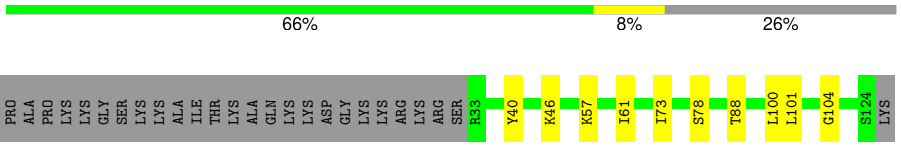
• Molecule 4: Histone H2B type 1-B

Chain D:



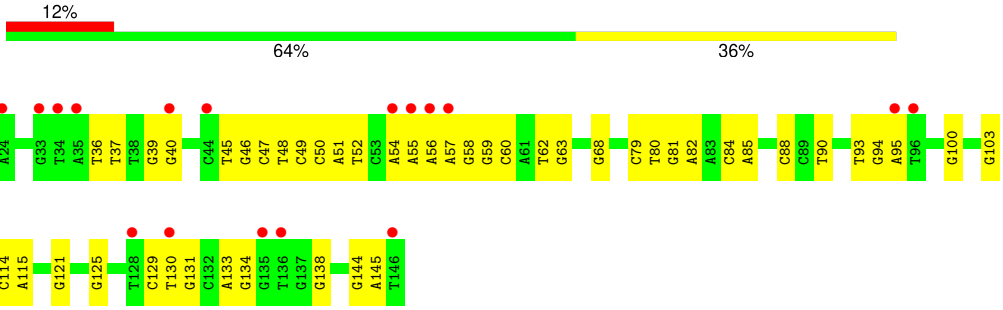
• Molecule 4: Histone H2B type 1-B

Chain H:



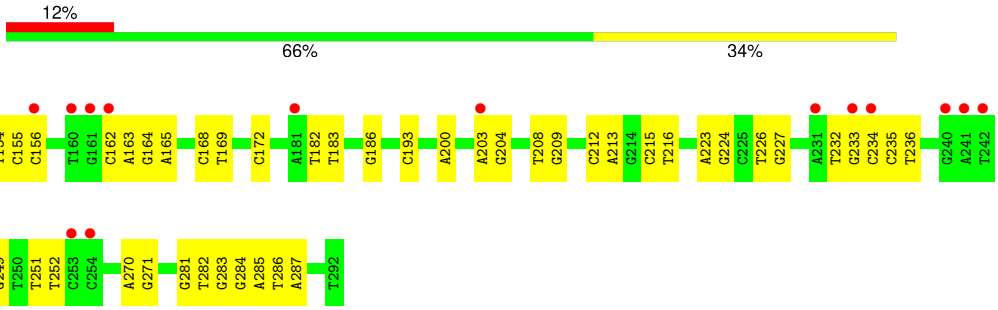
• Molecule 5: DNA (146-MER)

Chain I:



• Molecule 5: DNA (146-MER)

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	105.38Å 109.36Å 175.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.83 – 2.81 39.96 – 2.81	Depositor EDS
% Data completeness (in resolution range)	91.7 (34.83-2.81) 91.8 (39.96-2.81)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.89 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.221 , 0.270 0.224 , 0.269	Depositor DCC
R_{free} test set	2339 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	66.3	Xtriage
Anisotropy	0.727	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 58.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.032 for k,h,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	11971	wwPDB-VP
Average B, all atoms (Å^2)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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)

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

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	0.24	0/805	0.41	0/1079
1	E	0.22	0/819	0.37	0/1097
2	B	0.22	0/626	0.40	0/837
2	F	0.22	0/680	0.44	0/908
3	C	0.20	0/820	0.37	0/1107
3	G	0.31	0/815	0.49	0/1100
4	D	0.21	0/748	0.39	0/1005
4	H	0.21	0/742	0.38	0/998
5	I	0.49	0/3354	0.93	0/5175
5	J	0.48	0/3354	0.93	0/5175
All	All	0.39	0/12763	0.74	0/18481

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	794	0	831	21	0
1	E	807	0	844	11	0
2	B	619	0	659	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	673	0	722	12	0
3	C	810	0	866	8	0
3	G	805	0	861	13	0
4	D	737	0	758	8	0
4	H	727	0	747	9	0
5	I	2990	0	1652	40	0
5	J	2990	0	1652	38	0
6	D	2	0	0	0	0
6	G	1	0	0	0	0
6	I	3	0	0	0	0
7	I	1	0	0	0	0
7	J	1	0	0	0	0
8	A	1	0	0	0	0
8	C	2	0	0	0	0
8	E	3	0	0	0	0
8	I	3	0	0	0	0
8	J	2	0	0	0	0
All	All	11971	0	9592	125	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.

The worst 5 of 125 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:128:ARG:HB2	1:A:134:ARG:HH21	1.33	0.94
1:E:69:ARG:NH2	5:I:90:DT:OP2	2.17	0.76
5:I:121:DG:N2	5:J:172:DC:N3	2.35	0.75
5:I:100:DG:N2	5:J:193:DC:N3	2.38	0.71
1:A:128:ARG:HB2	1:A:134:ARG:NH2	2.06	0.69

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	94/135 (70%)	93 (99%)	1 (1%)	0	100	100
1	E	96/135 (71%)	93 (97%)	3 (3%)	0	100	100
2	B	76/102 (74%)	74 (97%)	2 (3%)	0	100	100
2	F	82/102 (80%)	80 (98%)	2 (2%)	0	100	100
3	C	103/129 (80%)	102 (99%)	1 (1%)	0	100	100
3	G	102/129 (79%)	96 (94%)	6 (6%)	0	100	100
4	D	92/125 (74%)	91 (99%)	0	1 (1%)	14	41
4	H	91/125 (73%)	89 (98%)	1 (1%)	1 (1%)	14	41
All	All	736/982 (75%)	718 (98%)	16 (2%)	2 (0%)	41	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	104	GLY
4	H	104	GLY

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	84/110 (76%)	83 (99%)	1 (1%)	71	92
1	E	85/110 (77%)	85 (100%)	0	100	100
2	B	63/78 (81%)	63 (100%)	0	100	100
2	F	69/78 (88%)	69 (100%)	0	100	100
3	C	83/99 (84%)	83 (100%)	0	100	100
3	G	83/99 (84%)	82 (99%)	1 (1%)	71	92
4	D	81/106 (76%)	80 (99%)	1 (1%)	71	92
4	H	80/106 (76%)	80 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	628/786 (80%)	625 (100%)	3 (0%)	88 96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	ARG
4	D	80	LEU
3	G	74	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

Of 8 ligands modelled in this entry, 8 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 (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 (i)

6.1 Protein, DNA and RNA chains (i)

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	96/135 (71%)	0.50	3 (3%) 49 39	54, 77, 107, 121	0
1	E	98/135 (72%)	0.16	0 100 100	38, 52, 79, 98	0
2	B	78/102 (76%)	0.52	5 (6%) 19 12	52, 70, 87, 94	0
2	F	84/102 (82%)	0.26	1 (1%) 79 73	38, 50, 68, 93	0
3	C	105/129 (81%)	0.07	0 100 100	39, 54, 78, 93	0
3	G	104/129 (80%)	0.47	7 (6%) 17 10	54, 69, 108, 118	0
4	D	94/125 (75%)	0.18	0 100 100	41, 58, 90, 116	0
4	H	92/125 (73%)	0.25	0 100 100	48, 69, 94, 110	0
5	I	146/146 (100%)	0.84	17 (11%) 4 2	71, 118, 157, 170	0
5	J	146/146 (100%)	0.80	17 (11%) 4 2	73, 119, 154, 167	0
All	All	1043/1274 (81%)	0.44	50 (4%) 30 21	38, 71, 143, 170	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	I	146	DT	9.4
5	I	56	DA	7.7
5	I	55	DA	7.0
3	G	73	ASN	5.7
5	J	161	DG	5.5

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)

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(Å^2)	Q<0.9
6	MN	I	201	1/1	0.47	0.16	133,133,133,133	0
7	CL	I	204	1/1	0.52	0.19	124,124,124,124	0
6	MN	I	203	1/1	0.59	0.12	143,143,143,143	0
6	MN	G	201	1/1	0.78	0.16	99,99,99,99	0
7	CL	J	301	1/1	0.78	0.21	140,140,140,140	0
6	MN	I	202	1/1	0.89	0.08	121,121,121,121	0
6	MN	D	201	1/1	0.98	0.17	68,68,68,68	0
6	MN	D	202	1/1	0.99	0.19	68,68,68,68	0

6.5 Other polymers (i)

There are no such residues in this entry.