Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 11:15 PM GMT

PDB ID	:	1WTE
Title	:	Crystal structure of type II restrcition endonuclease, EcoO109I complexed with cognate DNA
Authors	:	Hashimoto, H.; Shimizu, T.; Imasaki, T.; Kato, M.; Shichijo, N.; Kita, K.; Sato, M.
Deposited on	:	2004-11-22
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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

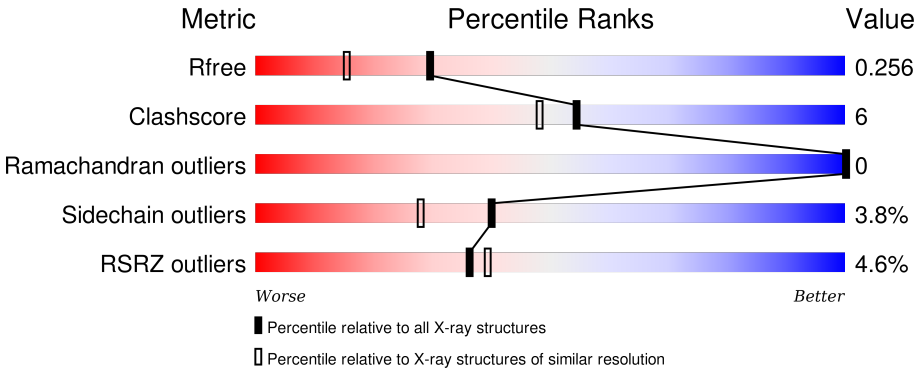
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 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}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	1-X	13	77% 31% 54% 15%
1	2-X	13	77% 15% 38% 46%
2	1-Y	13	85% 38% 46% 15%
2	2-Y	13	85% 15% 46% 38%
3	1-A	272	% 86% 12% ••

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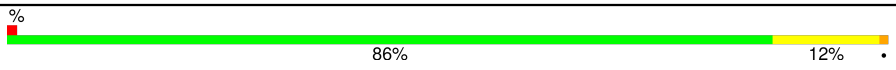
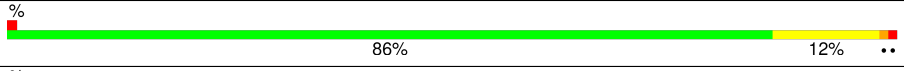
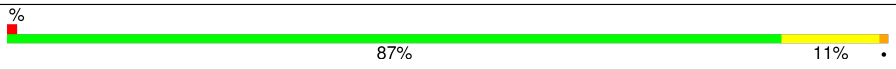
Mol	Chain	Length	Quality of chain
3	1-B	272	
3	2-A	272	
3	2-B	272	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11188 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(*AP*CP*CP*GP*GP*GP*CP*CP*CP*TP*GP*CP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-X	13	Total	C	N	O	P	0	0	0
			259	123	48	76	12			
1	2-X	13	Total	C	N	O	P	0	0	0
			259	123	48	76	12			

- Molecule 2 is a DNA chain called 5'-D(*GP*GP*CP*AP*GP*GP*GP*CP*CP*CP*GP*GP*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1-Y	13	Total	C	N	O	P	0	0	0
			268	126	54	76	12			
2	2-Y	13	Total	C	N	O	P	0	0	0
			268	126	54	76	12			

- Molecule 3 is a protein called EcoO109IR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1-A	272	Total	C	N	O	S	0	0	0
			2219	1422	381	407	9			
3	2-A	272	Total	C	N	O	S	0	0	0
			2219	1422	381	407	9			
3	1-B	272	Total	C	N	O	S	0	0	0
			2219	1422	381	407	9			
3	2-B	272	Total	C	N	O	S	0	0	0
			2219	1422	381	407	9			

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	2-A	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	1-B	1	Total Na 1 1	0	0
4	1-A	1	Total Na 1 1	0	0
4	2-B	1	Total Na 1 1	0	0

- Molecule 5 is water.

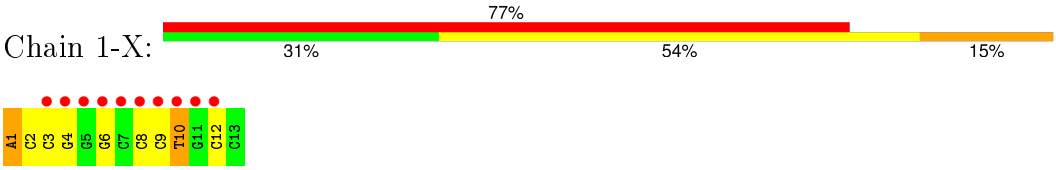
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	1-A	263	Total O 263 263	0	0
5	2-A	263	Total O 263 263	0	0
5	1-B	287	Total O 287 287	0	0
5	2-B	288	Total O 288 288	0	0
5	1-X	41	Total O 41 41	0	0
5	2-X	39	Total O 39 39	0	0
5	1-Y	36	Total O 36 36	0	0
5	2-Y	37	Total O 37 37	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

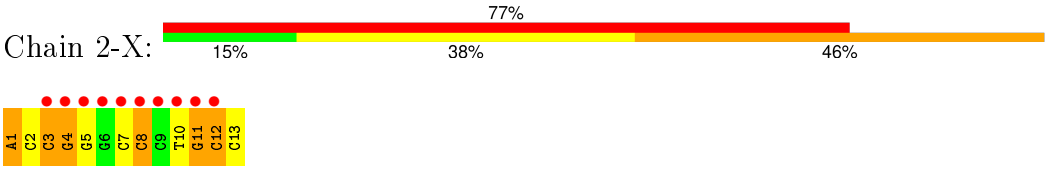
- Molecule 1: 5'-D(*AP*CP*CP*GP*GP*GP*CP*CP*CP*TP*GP*CP*C)-3'

Chain 1-X:



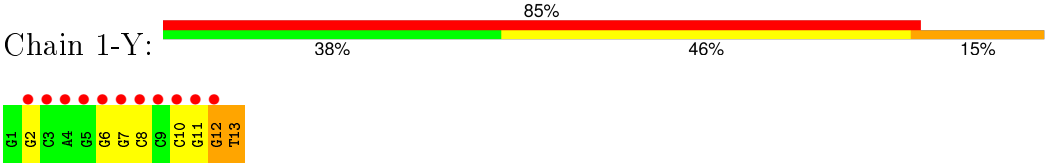
- Molecule 1: 5'-D(*AP*CP*CP*GP*GP*GP*CP*CP*CP*TP*GP*CP*C)-3'

Chain 2-X:



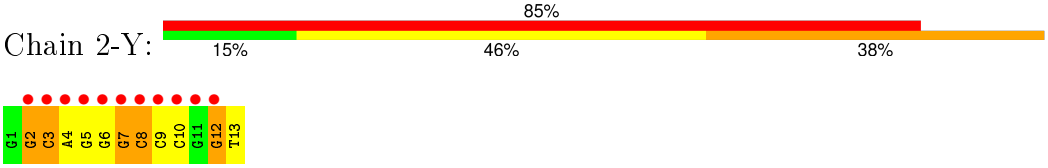
- Molecule 2: 5'-D(*GP*GP*CP*AP*GP*GP*GP*CP*CP*CP*GP*GP*T)-3'

Chain 1-Y:



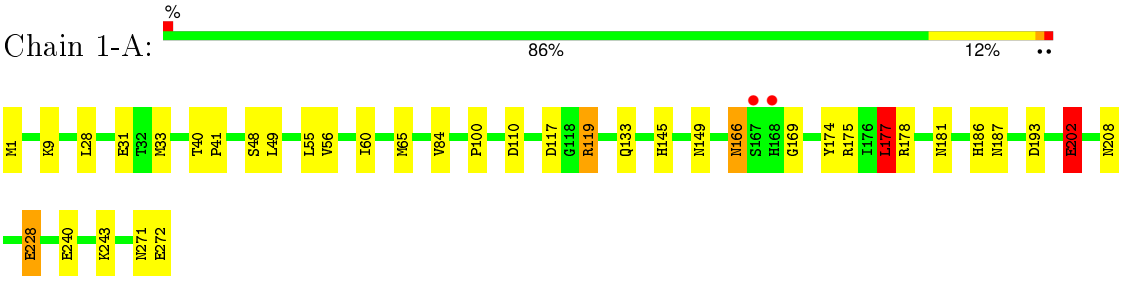
- Molecule 2: 5'-D(*GP*GP*CP*AP*GP*GP*GP*CP*CP*CP*GP*GP*T)-3'

Chain 2-Y:



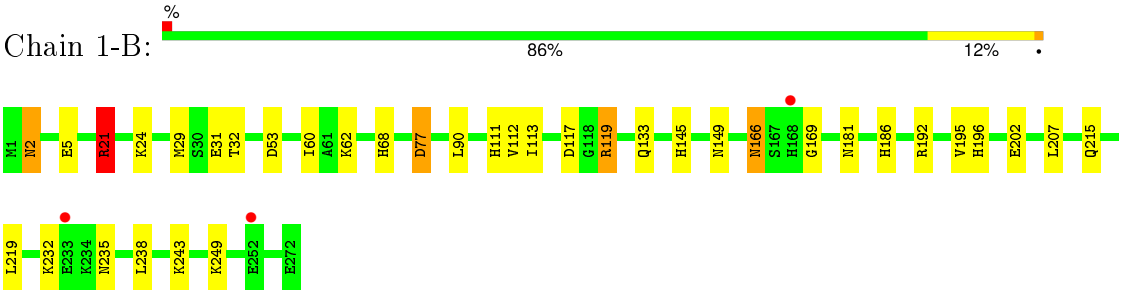
- Molecule 3: EcoO109IR

Chain 1-A:



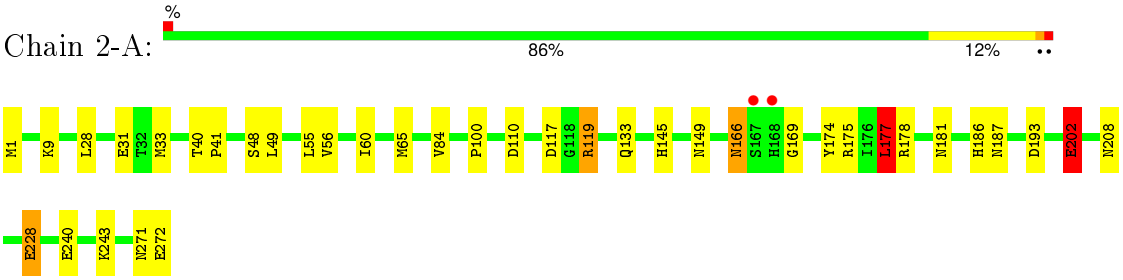
• Molecule 3: EcoO109IR

Chain 1-B:



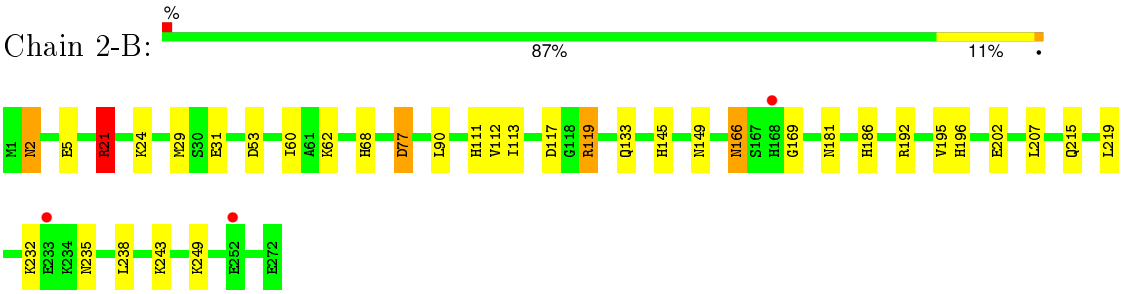
• Molecule 3: EcoO109IR

Chain 2-A:



• Molecule 3: EcoO109IR

Chain 2-B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	49.10Å 71.88Å 203.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.64 – 1.90 23.61 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (23.64-1.90) 97.6 (23.61-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.68 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.171 , 0.223 0.205 , 0.256	Depositor DCC
R_{free} test set	2841 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	18.7	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.75 , 65.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Outliers	1 of 57335 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	11188	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA

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	1-X	1.30	1/289 (0.3%)	1.90	10/443 (2.3%)
1	2-X	1.25	0/289	2.05	14/443 (3.2%)
2	1-Y	1.23	1/301 (0.3%)	1.92	10/464 (2.2%)
2	2-Y	1.23	0/301	1.95	13/464 (2.8%)
3	1-A	0.95	3/2270 (0.1%)	0.90	8/3065 (0.3%)
3	1-B	0.89	0/2270	0.96	8/3065 (0.3%)
3	2-A	0.95	3/2270 (0.1%)	0.90	8/3065 (0.3%)
3	2-B	0.89	0/2270	0.96	8/3065 (0.3%)
All	All	0.97	8/10260 (0.1%)	1.12	79/14074 (0.6%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-A	202	GLU	CD-OE1	7.11	1.33	1.25
3	2-A	202	GLU	CD-OE1	7.11	1.33	1.25
3	1-A	202	GLU	CG-CD	6.18	1.61	1.51
3	2-A	202	GLU	CG-CD	6.18	1.61	1.51
2	1-Y	13	DT	C5-C7	5.18	1.53	1.50
3	1-A	31	GLU	CG-CD	5.14	1.59	1.51
3	2-A	31	GLU	CG-CD	5.14	1.59	1.51
1	1-X	1	DA	C3'-O3'	-5.03	1.37	1.44

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	1-B	21	ARG	NE-CZ-NH1	15.42	128.01	120.30
3	2-B	21	ARG	NE-CZ-NH1	15.42	128.01	120.30
3	1-B	21	ARG	NE-CZ-NH2	-15.11	112.75	120.30
3	2-B	21	ARG	NE-CZ-NH2	-15.11	112.75	120.30
1	2-X	8	DC	O4'-C1'-N1	12.94	117.06	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2-Y	8	DC	O4'-C1'-N1	12.72	116.91	108.00
1	1-X	12	DC	O4'-C1'-N1	12.36	116.65	108.00
1	1-X	8	DC	O4'-C1'-N1	11.64	116.15	108.00
2	1-Y	8	DC	O4'-C1'-N1	11.45	116.02	108.00
2	1-Y	10	DC	O4'-C1'-N1	-10.24	100.83	108.00
3	1-A	178	ARG	NE-CZ-NH1	10.14	125.37	120.30
3	2-A	178	ARG	NE-CZ-NH1	10.14	125.37	120.30
3	1-A	119	ARG	NE-CZ-NH2	-9.26	115.67	120.30
3	2-A	119	ARG	NE-CZ-NH2	-9.26	115.67	120.30
2	2-Y	3	DC	P-O3'-C3'	8.90	130.38	119.70
3	1-B	119	ARG	NE-CZ-NH1	8.48	124.54	120.30
3	2-B	119	ARG	NE-CZ-NH1	8.48	124.54	120.30
3	1-A	178	ARG	NE-CZ-NH2	-8.46	116.07	120.30
3	2-A	178	ARG	NE-CZ-NH2	-8.46	116.07	120.30
3	1-B	119	ARG	NE-CZ-NH2	-8.34	116.13	120.30
3	2-B	119	ARG	NE-CZ-NH2	-8.34	116.13	120.30
1	1-X	4	DG	O4'-C1'-N9	8.23	113.76	108.00
3	1-A	177	LEU	CA-CB-CG	8.10	133.93	115.30
3	2-A	177	LEU	CA-CB-CG	8.10	133.93	115.30
2	1-Y	12	DG	O4'-C1'-N9	7.92	113.55	108.00
1	2-X	7	DC	O4'-C1'-N1	7.87	113.51	108.00
1	2-X	10	DT	O4'-C1'-N1	-7.69	102.62	108.00
2	2-Y	2	DG	O4'-C1'-N9	-7.42	102.81	108.00
3	1-A	177	LEU	CB-CG-CD2	7.39	123.56	111.00
3	2-A	177	LEU	CB-CG-CD2	7.39	123.56	111.00
2	1-Y	7	DG	O4'-C1'-N9	7.34	113.14	108.00
1	1-X	10	DT	O4'-C1'-N1	-7.12	103.02	108.00
3	1-A	175	ARG	NE-CZ-NH2	-6.65	116.97	120.30
3	2-A	175	ARG	NE-CZ-NH2	-6.65	116.97	120.30
3	1-A	119	ARG	NE-CZ-NH1	6.46	123.53	120.30
3	2-A	119	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	2-X	12	DC	C1'-O4'-C4'	-6.41	103.69	110.10
2	2-Y	12	DG	C1'-O4'-C4'	-6.37	103.73	110.10
1	2-X	11	DG	O4'-C1'-N9	-6.29	103.59	108.00
2	1-Y	6	DG	O4'-C4'-C3'	-6.18	102.03	104.50
2	1-Y	11	DG	C1'-O4'-C4'	-6.11	103.99	110.10
1	2-X	5	DG	O4'-C1'-N9	6.08	112.26	108.00
3	1-B	21	ARG	CD-NE-CZ	6.05	132.06	123.60
3	2-B	21	ARG	CD-NE-CZ	6.05	132.06	123.60
3	1-B	53	ASP	CB-CG-OD1	6.04	123.74	118.30
3	2-B	53	ASP	CB-CG-OD1	6.04	123.74	118.30
2	2-Y	7	DG	O4'-C1'-N9	5.83	112.08	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1-X	8	DC	P-O3'-C3'	5.78	126.64	119.70
2	1-Y	7	DG	C4'-C3'-C2'	-5.78	97.89	103.10
1	1-X	6	DG	C4'-C3'-C2'	-5.74	97.93	103.10
3	1-A	110	ASP	CB-CG-OD1	-5.70	113.17	118.30
3	2-A	110	ASP	CB-CG-OD1	-5.70	113.17	118.30
1	2-X	4	DG	P-O3'-C3'	5.68	126.51	119.70
2	1-Y	13	DT	C1'-O4'-C4'	-5.61	104.49	110.10
3	1-B	77	ASP	CB-CG-OD2	5.50	123.25	118.30
3	2-B	77	ASP	CB-CG-OD2	5.50	123.25	118.30
1	1-X	4	DG	O4'-C1'-C2'	-5.47	101.52	105.90
1	2-X	3	DC	C2-N3-C4	5.47	122.64	119.90
1	2-X	13	DC	C1'-O4'-C4'	-5.47	104.63	110.10
1	2-X	10	DT	C4-C5-C7	5.44	122.26	119.00
1	2-X	1	DA	O4'-C4'-C3'	-5.36	102.36	104.50
2	1-Y	6	DG	O4'-C1'-N9	5.36	111.75	108.00
2	2-Y	7	DG	C4-C5-N7	-5.34	108.66	110.80
2	2-Y	8	DC	O5'-P-OP2	-5.33	100.91	105.70
1	1-X	3	DC	C3'-C2'-C1'	-5.28	96.16	102.50
1	1-X	9	DC	C6-N1-C2	-5.28	118.19	120.30
1	2-X	10	DT	C6-C5-C7	-5.26	119.74	122.90
2	2-Y	10	DC	C6-N1-C2	-5.17	118.23	120.30
2	1-Y	2	DG	C2-N3-C4	5.14	114.47	111.90
3	1-B	192	ARG	NE-CZ-NH2	-5.13	117.73	120.30
3	2-B	192	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	2-X	7	DC	C4'-C3'-C2'	-5.12	98.49	103.10
2	2-Y	12	DG	O4'-C1'-N9	-5.09	104.43	108.00
1	2-X	3	DC	N1-C2-O2	5.07	121.94	118.90
2	2-Y	12	DG	N9-C4-C5	-5.07	103.37	105.40
1	1-X	3	DC	C1'-O4'-C4'	-5.05	105.05	110.10
2	2-Y	6	DG	O4'-C1'-N9	5.05	111.53	108.00
2	2-Y	10	DC	C2-N1-C1'	5.04	124.35	118.80
2	2-Y	10	DC	O4'-C1'-N1	-5.04	104.47	108.00

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	1-X	259	0	146	5	0
1	2-X	259	0	146	5	0
2	1-Y	268	0	146	1	0
2	2-Y	268	0	146	9	0
3	1-A	2219	0	2196	31	0
3	1-B	2219	0	2196	28	0
3	2-A	2219	0	2196	31	0
3	2-B	2219	0	2196	27	0
4	1-A	1	0	0	0	0
4	1-B	1	0	0	0	0
4	2-A	1	0	0	0	0
4	2-B	1	0	0	0	0
5	1-A	263	0	0	6	0
5	1-B	287	0	0	4	0
5	1-X	41	0	0	1	0
5	1-Y	36	0	0	0	0
5	2-A	263	0	0	6	0
5	2-B	288	0	0	4	0
5	2-X	39	0	0	1	0
5	2-Y	37	0	0	0	0
All	All	11188	0	9368	121	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.

All (121) 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:272:GLU:HG2	5:A:1231:HOH:O	1.69	0.91
3:A:272:GLU:HG2	5:A:1232:HOH:O	1.69	0.91
3:A:65:MET:HB3	3:B:62:LYS:HE2	1.59	0.84
3:A:65:MET:HB3	3:B:62:LYS:HE2	1.59	0.84
2:Y:2:DG:H2"	2:Y:3:DC:O5'	1.77	0.83
1:X:1:DA:H1'	1:X:2:DC:H5'	1.61	0.82
3:B:181:ASN:HD21	3:B:186:HIS:H	1.30	0.79
3:B:181:ASN:HD21	3:B:186:HIS:H	1.30	0.79
1:X:12:DC:H5	5:X:453:HOH:O	1.69	0.76
3:A:181:ASN:HD21	3:A:186:HIS:H	1.30	0.75
3:A:181:ASN:HD21	3:A:186:HIS:H	1.30	0.75
2:Y:12:DG:H2"	2:Y:13:DT:O5'	1.91	0.69
3:A:1:MET:N	3:A:208:ASN:HD21	1.91	0.69
3:A:1:MET:N	3:A:208:ASN:HD21	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:117:ASP:OD2	3:A:119:ARG:HD3	1.94	0.66
3:A:117:ASP:OD2	3:A:119:ARG:HD3	1.94	0.66
3:A:202:GLU:HB2	5:A:1228:HOH:O	1.95	0.65
3:A:202:GLU:HB2	5:A:1229:HOH:O	1.95	0.65
1:X:2:DC:H5	5:X:50:HOH:O	1.80	0.64
1:X:1:DA:H2"	1:X:2:DC:OP2	1.96	0.64
3:A:1:MET:H3	3:A:208:ASN:HD21	1.46	0.63
3:A:1:MET:H3	3:A:208:ASN:HD21	1.46	0.63
3:A:193:ASP:HB2	5:A:1245:HOH:O	1.99	0.63
3:A:193:ASP:HB2	5:A:1245:HOH:O	1.99	0.63
3:A:60:ILE:CD1	3:A:243:LYS:HA	2.29	0.61
3:A:60:ILE:CD1	3:A:243:LYS:HA	2.29	0.61
2:Y:4:DA:H2"	2:Y:5:DG:O4'	2.00	0.61
3:A:166:ASN:ND2	3:A:169:GLY:H	2.00	0.59
3:A:166:ASN:ND2	3:A:169:GLY:H	2.00	0.59
2:Y:2:DG:C2'	2:Y:3:DC:O5'	2.49	0.57
3:B:181:ASN:ND2	3:B:186:HIS:H	2.02	0.57
3:B:181:ASN:ND2	3:B:186:HIS:H	2.02	0.57
3:A:271:ASN:HB3	3:B:215:GLN:HE22	1.70	0.57
3:A:271:ASN:HB3	3:B:215:GLN:HE22	1.70	0.57
2:Y:4:DA:OP2	3:B:186:HIS:NE2	2.32	0.56
3:A:9:LYS:HD2	5:A:1142:HOH:O	2.06	0.56
3:A:9:LYS:HD2	5:A:1143:HOH:O	2.06	0.56
3:A:60:ILE:HD13	3:A:243:LYS:HA	1.89	0.54
3:A:40:THR:OG1	3:A:41:PRO:HD3	2.07	0.54
1:X:10:DT:H71	3:B:32:THR:HG21	1.89	0.54
3:A:60:ILE:HD13	3:A:243:LYS:HA	1.89	0.54
3:A:40:THR:OG1	3:A:41:PRO:HD3	2.07	0.54
3:A:166:ASN:HD22	3:A:169:GLY:H	1.54	0.54
3:A:166:ASN:HD22	3:A:169:GLY:H	1.54	0.54
1:X:10:DT:C7	3:B:32:THR:HG21	2.38	0.54
3:A:181:ASN:ND2	3:A:186:HIS:H	2.04	0.53
3:A:181:ASN:ND2	3:A:186:HIS:H	2.04	0.53
3:A:186:HIS:O	3:A:187:ASN:HB2	2.10	0.52
3:A:186:HIS:O	3:A:187:ASN:HB2	2.10	0.52
3:B:24:LYS:HA	3:B:29:MET:HE3	1.92	0.52
3:B:24:LYS:HA	3:B:29:MET:HE3	1.92	0.52
3:A:271:ASN:HD22	3:B:215:GLN:NE2	2.08	0.51
3:A:271:ASN:HD22	3:B:215:GLN:NE2	2.08	0.51
3:B:90:LEU:HD11	3:B:112:VAL:HG23	1.93	0.50
3:B:90:LEU:HD11	3:B:112:VAL:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:21:ARG:HD3	3:B:68:HIS:ND1	2.26	0.50
3:B:21:ARG:HD3	3:B:68:HIS:ND1	2.26	0.50
3:A:49:LEU:HD13	3:A:55:LEU:HA	1.94	0.50
3:A:49:LEU:HD13	3:A:55:LEU:HA	1.94	0.50
2:Y:3:DC:H2"	2:Y:4:DA:C8	2.48	0.49
2:Y:3:DC:H4'	2:Y:4:DA:OP1	2.12	0.48
2:Y:12:DG:H2"	2:Y:13:DT:O5'	2.13	0.48
1:X:11:DG:H2"	1:X:12:DC:O5'	2.13	0.48
3:B:145:HIS:CD2	3:B:149:ASN:ND2	2.82	0.46
3:B:145:HIS:CD2	3:B:149:ASN:ND2	2.82	0.46
3:B:2:ASN:ND2	3:B:5:GLU:HG3	2.30	0.46
3:B:2:ASN:ND2	3:B:5:GLU:HG3	2.30	0.46
3:B:117:ASP:OD2	3:B:119:ARG:HD3	2.15	0.46
3:B:117:ASP:OD2	3:B:119:ARG:HD3	2.15	0.46
3:A:271:ASN:CB	3:B:215:GLN:HE22	2.28	0.45
3:A:271:ASN:CB	3:B:215:GLN:HE22	2.28	0.45
3:A:174:TYR:HA	3:A:177:LEU:HD13	1.98	0.45
3:A:174:TYR:HA	3:A:177:LEU:HD13	1.98	0.45
3:A:33:MET:HG3	5:A:1085:HOH:O	2.16	0.45
3:A:33:MET:HG3	5:A:1086:HOH:O	2.16	0.45
3:B:232:LYS:NZ	5:B:1232:HOH:O	2.49	0.45
3:B:232:LYS:NZ	5:B:1233:HOH:O	2.49	0.45
3:B:2:ASN:HD22	3:B:2:ASN:C	2.21	0.44
3:B:2:ASN:HD22	3:B:2:ASN:C	2.21	0.44
3:A:117:ASP:CG	3:A:119:ARG:HD3	2.37	0.44
3:B:31:GLU:HG2	5:B:1287:HOH:O	2.17	0.44
3:A:117:ASP:CG	3:A:119:ARG:HD3	2.37	0.44
3:B:31:GLU:HG2	5:B:1288:HOH:O	2.17	0.44
1:X:8:DC:N3	2:Y:7:DG:C2	2.86	0.43
1:X:1:DA:C2'	1:X:2:DC:OP2	2.66	0.43
3:A:9:LYS:HB3	3:A:84:VAL:HG22	2.00	0.43
3:A:9:LYS:HB3	3:A:84:VAL:HG22	2.00	0.43
1:X:3:DC:H2"	1:X:4:DG:C8	2.54	0.43
3:A:56:VAL:HG12	3:A:60:ILE:HD12	2.01	0.43
3:A:56:VAL:HG12	3:A:60:ILE:HD12	2.01	0.43
3:B:2:ASN:HB3	5:B:1267:HOH:O	2.19	0.42
3:B:2:ASN:HB3	5:B:1268:HOH:O	2.19	0.42
3:B:60:ILE:CD1	3:B:243:LYS:HA	2.49	0.42
3:B:60:ILE:CD1	3:B:243:LYS:HA	2.49	0.42
3:A:228:GLU:HG2	5:A:1241:HOH:O	2.20	0.42
3:A:228:GLU:HG2	5:A:1242:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:48:SER:HA	3:B:232:LYS:HG3	2.01	0.42
3:A:48:SER:HA	3:B:232:LYS:HG3	2.01	0.42
3:A:166:ASN:HD22	3:A:166:ASN:C	2.23	0.41
3:B:21:ARG:CD	3:B:68:HIS:ND1	2.83	0.41
3:B:166:ASN:ND2	3:B:169:GLY:H	2.19	0.41
3:A:166:ASN:C	3:A:166:ASN:HD22	2.23	0.41
3:B:21:ARG:CD	3:B:68:HIS:ND1	2.83	0.41
3:B:166:ASN:ND2	3:B:169:GLY:H	2.19	0.41
2:Y:8:DC:C2	2:Y:9:DC:C5	3.09	0.41
3:B:249:LYS:HD3	5:B:1271:HOH:O	2.21	0.41
3:B:249:LYS:HD3	5:B:1272:HOH:O	2.21	0.41
3:B:195:VAL:O	3:B:196:HIS:HD2	2.03	0.41
3:B:195:VAL:O	3:B:196:HIS:HD2	2.03	0.41
3:A:145:HIS:CD2	3:A:149:ASN:ND2	2.89	0.41
3:A:145:HIS:CD2	3:A:149:ASN:ND2	2.89	0.41
3:A:271:ASN:HD22	3:B:215:GLN:HE21	1.68	0.40
3:B:24:LYS:HA	3:B:29:MET:CE	2.50	0.40
3:A:271:ASN:HD22	3:B:215:GLN:HE21	1.68	0.40
3:B:24:LYS:HA	3:B:29:MET:CE	2.50	0.40
3:B:2:ASN:ND2	3:B:5:GLU:H	2.19	0.40
3:B:2:ASN:ND2	3:B:5:GLU:H	2.19	0.40
3:B:77:ASP:O	3:B:111:HIS:HE1	2.04	0.40
3:B:77:ASP:O	3:B:111:HIS:HE1	2.04	0.40
3:A:181:ASN:HD21	3:A:186:HIS:N	2.08	0.40
3:A:181:ASN:HD21	3:A:186:HIS:N	2.08	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	
3	1-A	270/272 (99%)	264 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1-B	270/272 (99%)	267 (99%)	3 (1%)	0	100	100
3	2-A	270/272 (99%)	264 (98%)	6 (2%)	0	100	100
3	2-B	270/272 (99%)	267 (99%)	3 (1%)	0	100	100
All	All	1080/1088 (99%)	1062 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
3	1-A	237/237 (100%)	229 (97%)	8 (3%)	44	33
3	1-B	237/237 (100%)	227 (96%)	10 (4%)	36	24
3	2-A	237/237 (100%)	229 (97%)	8 (3%)	44	33
3	2-B	237/237 (100%)	227 (96%)	10 (4%)	36	24
All	All	948/948 (100%)	912 (96%)	36 (4%)	40	28

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1-A	28	LEU
3	1-A	100	PRO
3	1-A	133	GLN
3	1-A	166	ASN
3	1-A	177	LEU
3	1-A	202	GLU
3	1-A	228	GLU
3	1-A	240	GLU
3	1-B	2	ASN
3	1-B	21	ARG
3	1-B	113	ILE
3	1-B	133	GLN
3	1-B	166	ASN

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Mol	Chain	Res	Type
3	1-B	202	GLU
3	1-B	207	LEU
3	1-B	219	LEU
3	1-B	235	ASN
3	1-B	238	LEU
3	2-A	28	LEU
3	2-A	100	PRO
3	2-A	133	GLN
3	2-A	166	ASN
3	2-A	177	LEU
3	2-A	202	GLU
3	2-A	228	GLU
3	2-A	240	GLU
3	2-B	2	ASN
3	2-B	21	ARG
3	2-B	113	ILE
3	2-B	133	GLN
3	2-B	166	ASN
3	2-B	202	GLU
3	2-B	207	LEU
3	2-B	219	LEU
3	2-B	235	ASN
3	2-B	238	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
3	1-A	4	GLN
3	1-A	103	HIS
3	1-A	139	GLN
3	1-A	149	ASN
3	1-A	150	ASN
3	1-A	166	ASN
3	1-A	181	ASN
3	1-A	185	ASN
3	1-A	187	ASN
3	1-A	208	ASN
3	1-B	2	ASN
3	1-B	22	GLN
3	1-B	111	HIS
3	1-B	114	GLN
3	1-B	139	GLN

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Mol	Chain	Res	Type
3	1-B	149	ASN
3	1-B	150	ASN
3	1-B	166	ASN
3	1-B	181	ASN
3	1-B	185	ASN
3	1-B	196	HIS
3	1-B	215	GLN
3	1-B	235	ASN
3	1-B	245	HIS
3	1-B	251	ASN
3	1-B	262	GLN
3	2-A	4	GLN
3	2-A	103	HIS
3	2-A	139	GLN
3	2-A	149	ASN
3	2-A	150	ASN
3	2-A	166	ASN
3	2-A	181	ASN
3	2-A	185	ASN
3	2-A	187	ASN
3	2-A	208	ASN
3	2-B	2	ASN
3	2-B	22	GLN
3	2-B	111	HIS
3	2-B	114	GLN
3	2-B	139	GLN
3	2-B	149	ASN
3	2-B	150	ASN
3	2-B	166	ASN
3	2-B	181	ASN
3	2-B	185	ASN
3	2-B	196	HIS
3	2-B	215	GLN
3	2-B	235	ASN
3	2-B	245	HIS
3	2-B	251	ASN
3	2-B	262	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 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, 95^{th} 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	1-X	13/13 (100%)	3.30	10 (76%)	0	0	11, 14, 22, 24	13 (100%)
1	2-X	13/13 (100%)	3.30	10 (76%)	0	0	11, 14, 22, 24	13 (100%)
2	1-Y	13/13 (100%)	3.56	11 (84%)	0	0	8, 13, 30, 32	13 (100%)
2	2-Y	13/13 (100%)	3.56	11 (84%)	0	0	8, 13, 30, 32	13 (100%)
3	1-A	272/272 (100%)	-0.02	2 (0%)	89	90	12, 19, 30, 39	0
3	1-B	272/272 (100%)	-0.02	3 (1%)	82	84	11, 19, 30, 35	0
3	2-A	272/272 (100%)	-0.02	2 (0%)	89	90	12, 19, 30, 39	0
3	2-B	272/272 (100%)	-0.02	3 (1%)	82	84	11, 19, 30, 35	0
All	All	1140/1140 (100%)	0.14	52 (4%)	36	39	8, 19, 30, 39	52 (4%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	1-Y	5	DG	5.3
2	2-Y	5	DG	5.3
1	1-X	5	DG	5.3
1	2-X	5	DG	5.3
2	1-Y	6	DG	5.1
2	2-Y	6	DG	5.1
1	1-X	6	DG	4.8
1	2-X	6	DG	4.8
1	1-X	4	DG	4.5
1	2-X	4	DG	4.5
2	1-Y	7	DG	4.4
2	2-Y	7	DG	4.4
2	1-Y	10	DC	4.1
2	2-Y	10	DC	4.1
2	1-Y	8	DC	4.1
2	2-Y	8	DC	4.1

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Mol	Chain	Res	Type	RSRZ
1	1-X	10	DT	4.0
1	2-X	10	DT	4.0
2	1-Y	9	DC	4.0
2	2-Y	9	DC	4.0
1	1-X	7	DC	3.8
1	2-X	7	DC	3.8
2	1-Y	4	DA	3.8
2	2-Y	4	DA	3.8
1	1-X	9	DC	3.7
1	2-X	9	DC	3.7
1	1-X	11	DG	3.6
1	2-X	11	DG	3.6
2	1-Y	11	DG	3.6
2	2-Y	11	DG	3.6
3	1-A	168	HIS	3.5
3	2-A	168	HIS	3.5
2	1-Y	3	DC	3.3
2	2-Y	3	DC	3.3
1	1-X	8	DC	3.3
1	2-X	8	DC	3.3
1	1-X	3	DC	3.2
1	2-X	3	DC	3.2
2	1-Y	12	DG	2.5
2	2-Y	12	DG	2.5
3	1-A	167	SER	2.5
3	2-A	167	SER	2.5
3	1-B	168	HIS	2.3
3	2-B	168	HIS	2.3
2	1-Y	2	DG	2.3
2	2-Y	2	DG	2.3
3	1-B	252	GLU	2.2
3	2-B	252	GLU	2.2
3	1-B	233	GLU	2.0
3	2-B	233	GLU	2.0
1	1-X	12	DC	2.0
1	2-X	12	DC	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
4	NA	1-B	1002	1/1	0.98	0.05	-0.99	11,11,11,11	0
4	NA	2-B	1002	1/1	0.98	0.05	-0.99	11,11,11,11	0
4	NA	2-A	1001	1/1	0.99	0.03	-1.11	10,10,10,10	0
4	NA	1-A	1001	1/1	0.99	0.03	-1.13	10,10,10,10	0

6.5 Other polymers (i)

There are no such residues in this entry.