Full wwPDB X-ray Structure Validation Report (i)

Nov 7, 2023 – 02:35 PM JST

PDB ID	:	5H40
Title	:	Crystal Structure of 1,2-beta-oligoglucan phosphorylase from Lachnoclostridium phytofermentans in complex with sophorose
Authors	:	Nakajima, M.; Tanaka, N.; Furukawa, N.; Nihira, T.; Kodutsumi, Y.; Takahashi, Y.; Sugimoto, N.; Miyanaga, A.; Fushinobu, S.; Taguchi, H.; Nakai, H.
Deposited on	:	2016-10-28
Resolution	:	2.20 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 (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 (i)) were used in the production of this report:

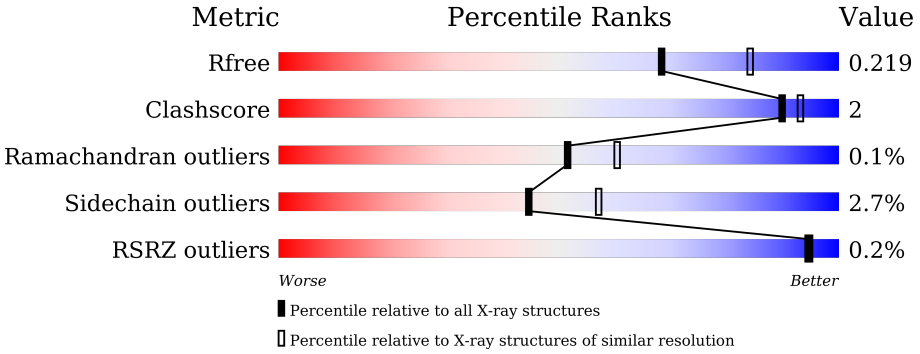
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	1122	91% 8% •
1	B	1122	92% 7% •
2	C	2	100%
2	D	2	100%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 18677 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.

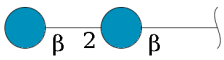
- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	1113	8918	5712	1483	1691	14	18	0	0	0
1	B	1113	8926	5717	1484	1692	14	19	0	1	0

There are 20 discrepancies between the modelled and reference sequences:

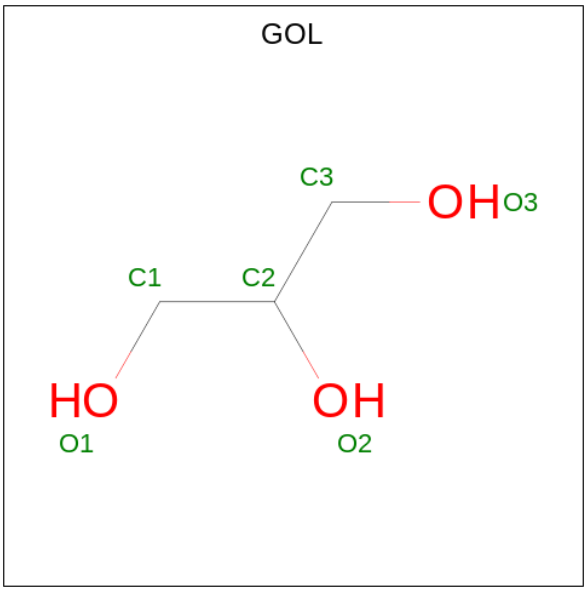
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MSE	-	expression tag	UNP A9KJS6
A	1	GLY	-	expression tag	UNP A9KJS6
A	1114	LEU	-	expression tag	UNP A9KJS6
A	1115	GLU	-	expression tag	UNP A9KJS6
A	1116	HIS	-	expression tag	UNP A9KJS6
A	1117	HIS	-	expression tag	UNP A9KJS6
A	1118	HIS	-	expression tag	UNP A9KJS6
A	1119	HIS	-	expression tag	UNP A9KJS6
A	1120	HIS	-	expression tag	UNP A9KJS6
A	1121	HIS	-	expression tag	UNP A9KJS6
B	0	MSE	-	expression tag	UNP A9KJS6
B	1	GLY	-	expression tag	UNP A9KJS6
B	1114	LEU	-	expression tag	UNP A9KJS6
B	1115	GLU	-	expression tag	UNP A9KJS6
B	1116	HIS	-	expression tag	UNP A9KJS6
B	1117	HIS	-	expression tag	UNP A9KJS6
B	1118	HIS	-	expression tag	UNP A9KJS6
B	1119	HIS	-	expression tag	UNP A9KJS6
B	1120	HIS	-	expression tag	UNP A9KJS6
B	1121	HIS	-	expression tag	UNP A9KJS6

- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-2)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	C	2	23	12	11	0	0	0
			Total	C	O			
2	D	2	23	12	11	0	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	A	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0
			Total	C	O		
3	B	1	6	3	3	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is water.

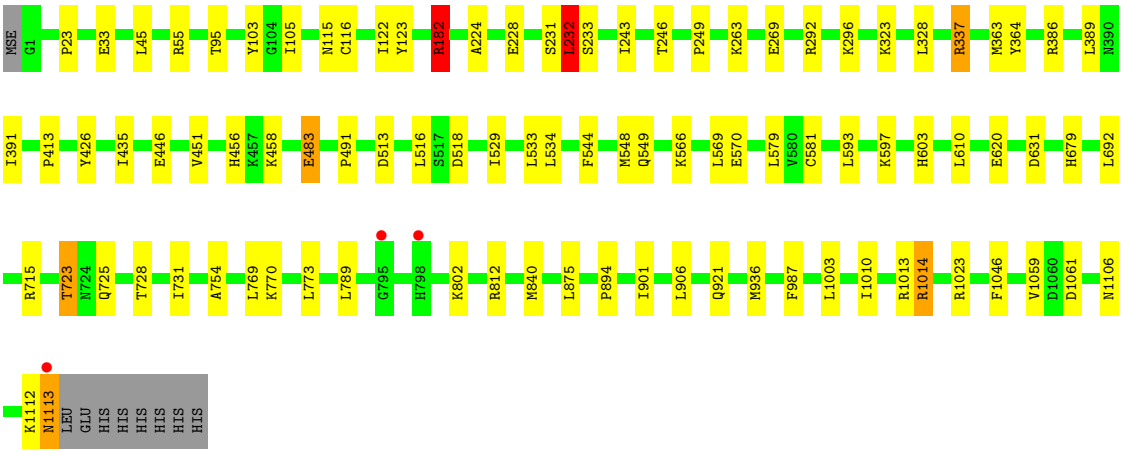
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	374	374	374	0	0
5	B	369	369	369	0	0

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.

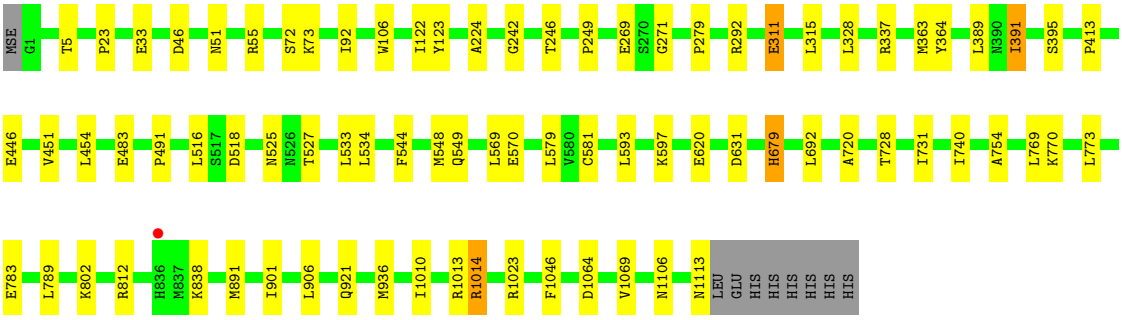
• Molecule 1: Uncharacterized protein

Chain A:



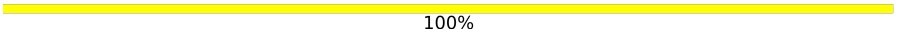
• Molecule 1: Uncharacterized protein

Chain B:



• Molecule 2: beta-D-glucopyranose-(1-2)-beta-D-glucopyranose

Chain C:



• Molecule 2: beta-D-glucopyranose-(1-2)-beta-D-glucopyranose

Chain D: 100%

BGC1
BGC2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	86.78Å 94.33Å 156.92Å 90.00° 97.60° 90.00°	Depositor
Resolution (Å)	86.02 – 2.20 86.02 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.9 (86.02-2.20) 96.9 (86.02-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.12 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.179 , 0.211 0.188 , 0.219	Depositor DCC
R_{free} test set	6103 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	24.9	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	18677	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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: GOL, CA, BGC

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	0.85	0/9125	0.88	12/12366 (0.1%)
1	B	0.84	1/9133 (0.0%)	0.88	12/12376 (0.1%)
All	All	0.85	1/18258 (0.0%)	0.88	24/24742 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	395	SER	CB-OG	-5.29	1.35	1.42

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1023	ARG	NE-CZ-NH1	7.92	124.26	120.30
1	B	936	MSE	CA-CB-CG	-7.09	101.25	113.30
1	A	1013	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	B	1013	ARG	NE-CZ-NH2	-6.70	116.95	120.30
1	A	337	ARG	NE-CZ-NH2	-6.31	117.15	120.30
1	B	1023	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	A	936	MSE	CA-CB-CG	-6.10	102.93	113.30
1	B	1064	ASP	CB-CG-OD1	5.71	123.44	118.30
1	A	812	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	A	182	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	1013	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	B	1023	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	B	271	GLY	N-CA-C	-5.44	99.50	113.10
1	B	1013	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	A	1023	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	B	311	GLU	OE1-CD-OE2	-5.36	116.87	123.30
1	B	812	ARG	NE-CZ-NH2	-5.23	117.68	120.30
1	A	386	ARG	NE-CZ-NH1	5.22	122.91	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	337	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	A	232	LEU	CA-CB-CG	5.17	127.19	115.30
1	B	812	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	B	46	ASP	CB-CG-OD1	5.03	122.83	118.30
1	B	391	ILE	CG1-CB-CG2	-5.02	100.36	111.40
1	A	715	ARG	NE-CZ-NH2	-5.01	117.80	120.30

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	8918	0	8675	33	0
1	B	8926	0	8683	30	0
2	C	23	0	21	0	0
2	D	23	0	21	0	0
3	A	18	0	24	0	0
3	B	24	0	32	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	374	0	0	1	1
5	B	369	0	0	5	1
All	All	18677	0	17456	63	1

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 2.

All (63) 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:548:MSE:HE3	5:A:1611:HOH:O	1.96	0.64
1:B:525:ASN:HB2	1:B:527:THR:H	1.65	0.62
1:B:548:MSE:HE3	5:B:1546:HOH:O	2.01	0.61
1:A:103:TYR:CE1	1:A:263:LYS:HE3	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:518:ASP:HA	1:B:533:LEU:O	2.04	0.58
1:A:518:ASP:HA	1:A:533:LEU:O	2.04	0.57
1:A:728:THR:OG1	1:A:731:ILE:HD12	2.05	0.57
1:B:23:PRO:HB2	1:B:279:PRO:HD3	1.86	0.56
1:B:728:THR:OG1	1:B:731:ILE:HD12	2.05	0.56
1:B:491:PRO:HA	5:B:1385:HOH:O	2.11	0.51
1:B:5:THR:HG22	5:B:1527:HOH:O	2.12	0.50
1:A:603:HIS:H	1:A:603:HIS:CD2	2.30	0.48
1:B:33:GLU:HB2	1:B:246:THR:HG21	1.97	0.47
1:A:451:VAL:HG21	1:A:544:PHE:CZ	2.50	0.47
1:A:446:GLU:HG2	1:A:549:GLN:HG2	1.97	0.47
1:B:315:LEU:O	1:B:328:LEU:HD12	2.15	0.46
1:A:516:LEU:HD11	1:A:534:LEU:HD11	1.97	0.46
1:A:1061:ASP:HA	1:A:1112:LYS:HB2	1.98	0.46
1:A:33:GLU:HB2	1:A:246:THR:HG21	1.98	0.46
1:B:754:ALA:O	1:B:770:LYS:HG3	2.16	0.46
1:B:446:GLU:HG2	1:B:549:GLN:HG2	1.97	0.46
1:B:106:TRP:CZ2	1:B:242:GLY:HA3	2.51	0.46
1:A:337:ARG:HD3	1:A:620:GLU:OE2	2.16	0.45
1:A:769:LEU:O	1:A:773:LEU:HB2	2.16	0.45
1:B:1010:ILE:O	1:B:1014:ARG:HD2	2.17	0.45
1:A:723:THR:HG23	1:A:725:GLN:HG3	1.99	0.45
1:A:579:LEU:HD11	1:A:610:LEU:HD22	1.99	0.44
1:A:182:ARG:NH1	1:A:228:GLU:OE1	2.50	0.44
1:A:754:ALA:O	1:A:770:LYS:HG3	2.16	0.44
1:B:123:TYR:O	1:B:224:ALA:HA	2.18	0.44
1:A:483:GLU:O	1:A:483:GLU:HG2	2.18	0.44
1:B:55:ARG:CZ	1:B:122:ILE:HD11	2.49	0.43
1:A:328:LEU:HD22	1:A:328:LEU:N	2.33	0.43
1:B:451:VAL:HG21	1:B:544:PHE:CZ	2.54	0.43
1:A:1059:VAL:CG1	1:A:1113:ASN:OD1	2.67	0.43
1:A:1010:ILE:O	1:A:1014:ARG:HD2	2.18	0.43
1:B:769:LEU:O	1:B:773:LEU:HB2	2.19	0.43
1:A:323:LYS:HB3	1:A:603:HIS:CE1	2.54	0.43
1:A:593:LEU:HG	1:A:597:LYS:HE3	2.01	0.43
1:B:783:GLU:OE1	5:B:1301:HOH:O	2.21	0.43
1:A:363:MSE:O	1:A:413:PRO:HD3	2.19	0.42
1:A:581:CYS:HB2	1:A:1046:PHE:CE1	2.53	0.42
1:B:249:PRO:O	1:B:901:ILE:HD11	2.19	0.42
1:A:389:LEU:HB2	1:A:391:ILE:CD1	2.49	0.42
1:B:516:LEU:HD11	1:B:534:LEU:HD11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:894:PRO:HD3	1:A:987:PHE:CD1	2.55	0.42
1:B:593:LEU:HG	1:B:597:LYS:HE3	2.02	0.42
1:B:581:CYS:HB2	1:B:1046:PHE:CE1	2.54	0.42
1:B:525:ASN:HB3	1:B:527:THR:OG1	2.20	0.42
1:B:337:ARG:HD3	1:B:620:GLU:OE2	2.19	0.41
1:B:363:MSE:O	1:B:413:PRO:HD3	2.20	0.41
1:A:426:TYR:CD2	1:A:435:ILE:HD12	2.56	0.41
1:B:891:MSE:HG3	5:B:1663:HOH:O	2.20	0.41
1:B:389:LEU:HB2	1:B:391:ILE:CD1	2.50	0.41
1:A:55:ARG:CZ	1:A:122:ILE:HD11	2.51	0.41
1:A:249:PRO:O	1:A:901:ILE:HD11	2.20	0.41
1:B:679:HIS:CE1	1:B:720:ALA:HA	2.55	0.41
1:A:23:PRO:HG2	1:A:529:ILE:HD13	2.03	0.41
1:A:123:TYR:O	1:A:224:ALA:HA	2.20	0.41
1:A:115:ASN:HA	1:A:232:LEU:O	2.21	0.41
1:A:105:ILE:HG12	1:A:243:ILE:HG12	2.03	0.41
1:B:72:SER:O	1:B:73:LYS:HB2	2.20	0.40
1:B:483:GLU:HG2	1:B:483:GLU:O	2.21	0.40

All (1) 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)
5:A:1305:HOH:O	5:B:1490:HOH:O[1_545]	1.17	1.03

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	1111/1122 (99%)	1068 (96%)	41 (4%)	2 (0%)	47 55
1	B	1112/1122 (99%)	1071 (96%)	40 (4%)	1 (0%)	51 60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2223/2244 (99%)	2139 (96%)	81 (4%)	3 (0%)	51 60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	906	LEU
1	A	906	LEU
1	A	1003	LEU

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	975/965 (101%)	944 (97%)	31 (3%)	39 50
1	B	976/965 (101%)	954 (98%)	22 (2%)	50 63
All	All	1951/1930 (101%)	1898 (97%)	53 (3%)	44 57

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	LEU
1	A	95	THR
1	A	116	CYS
1	A	182	ARG
1	A	231	SER
1	A	232	LEU
1	A	233	SER
1	A	269	GLU
1	A	292	ARG
1	A	296	LYS
1	A	364	TYR
1	A	456	HIS
1	A	458	LYS
1	A	483	GLU
1	A	491	PRO

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Mol	Chain	Res	Type
1	A	513	ASP
1	A	566	LYS
1	A	569	LEU
1	A	570	GLU
1	A	631	ASP
1	A	679	HIS
1	A	692	LEU
1	A	723	THR
1	A	789	LEU
1	A	802	LYS
1	A	840	MSE
1	A	875	LEU
1	A	921	GLN
1	A	1014	ARG
1	A	1106	ASN
1	A	1113	ASN
1	B	51	ASN
1	B	92	ILE
1	B	269	GLU
1	B	292	ARG
1	B	311	GLU
1	B	364	TYR
1	B	454	LEU
1	B	569	LEU
1	B	570	GLU
1	B	579	LEU
1	B	631	ASP
1	B	679	HIS
1	B	692	LEU
1	B	740	ILE
1	B	789	LEU
1	B	802	LYS
1	B	838	LYS
1	B	921	GLN
1	B	1014	ARG
1	B	1069	VAL
1	B	1106	ASN
1	B	1113	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	397	GLN
1	A	603	HIS
1	B	397	GLN
1	B	1113	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)

4 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	BGC	C	1	2	12,12,12	1.39	3 (25%)	17,17,17	0.60	0
2	BGC	C	2	2	11,11,12	1.85	2 (18%)	15,15,17	1.40	2 (13%)
2	BGC	D	1	2	12,12,12	1.31	3 (25%)	17,17,17	0.96	0
2	BGC	D	2	2	11,11,12	1.45	1 (9%)	15,15,17	1.90	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	C	1	2	-	0/2/22/22	0/1/1/1
2	BGC	C	2	2	-	0/2/19/22	0/1/1/1
2	BGC	D	1	2	-	0/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	D	2	2	-	0/2/19/22	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	BGC	O5-C1	4.70	1.51	1.43
2	D	2	BGC	O3-C3	3.58	1.51	1.43
2	C	1	BGC	O3-C3	2.51	1.48	1.43
2	C	2	BGC	O5-C5	-2.39	1.38	1.43
2	D	1	BGC	O1-C1	2.38	1.47	1.39
2	D	1	BGC	C4-C3	2.32	1.58	1.52
2	C	1	BGC	C3-C2	2.25	1.58	1.52
2	C	1	BGC	O5-C1	2.17	1.48	1.42
2	D	1	BGC	O4-C4	2.15	1.48	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	2	BGC	O5-C5-C6	5.39	115.65	107.20
2	C	2	BGC	O5-C5-C6	3.73	113.05	107.20
2	D	2	BGC	O4-C4-C3	-3.01	103.40	110.35
2	C	2	BGC	C6-C5-C4	-2.01	108.30	113.00

There are no chirality outliers.

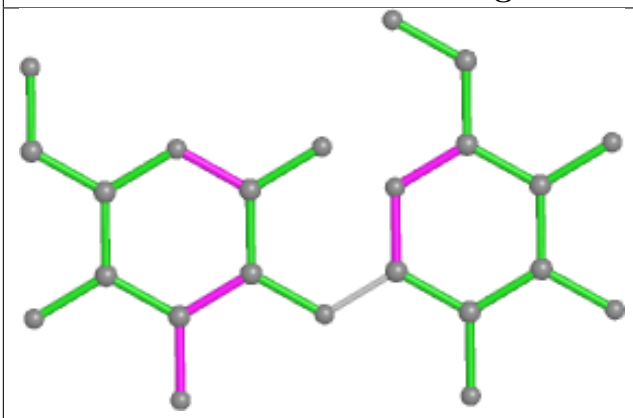
There are no torsion outliers.

There are no ring outliers.

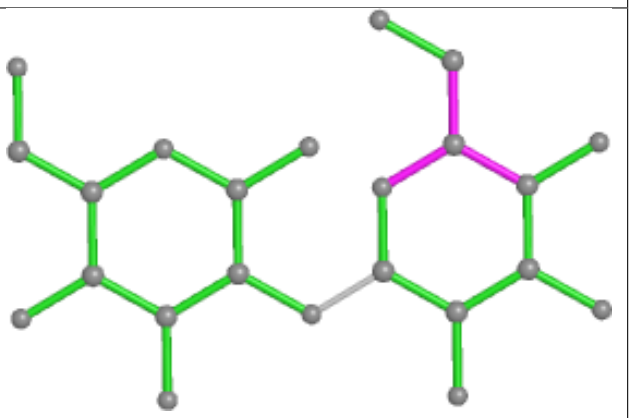
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

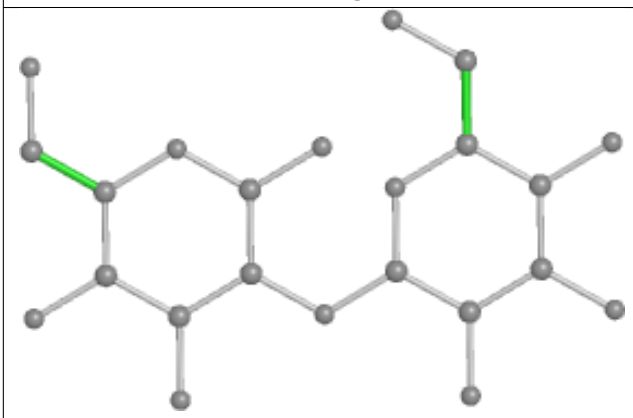
Oligosaccharide Chain C



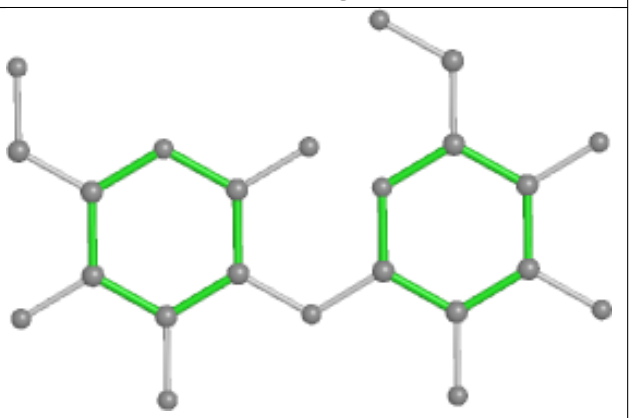
Bond lengths



Bond angles

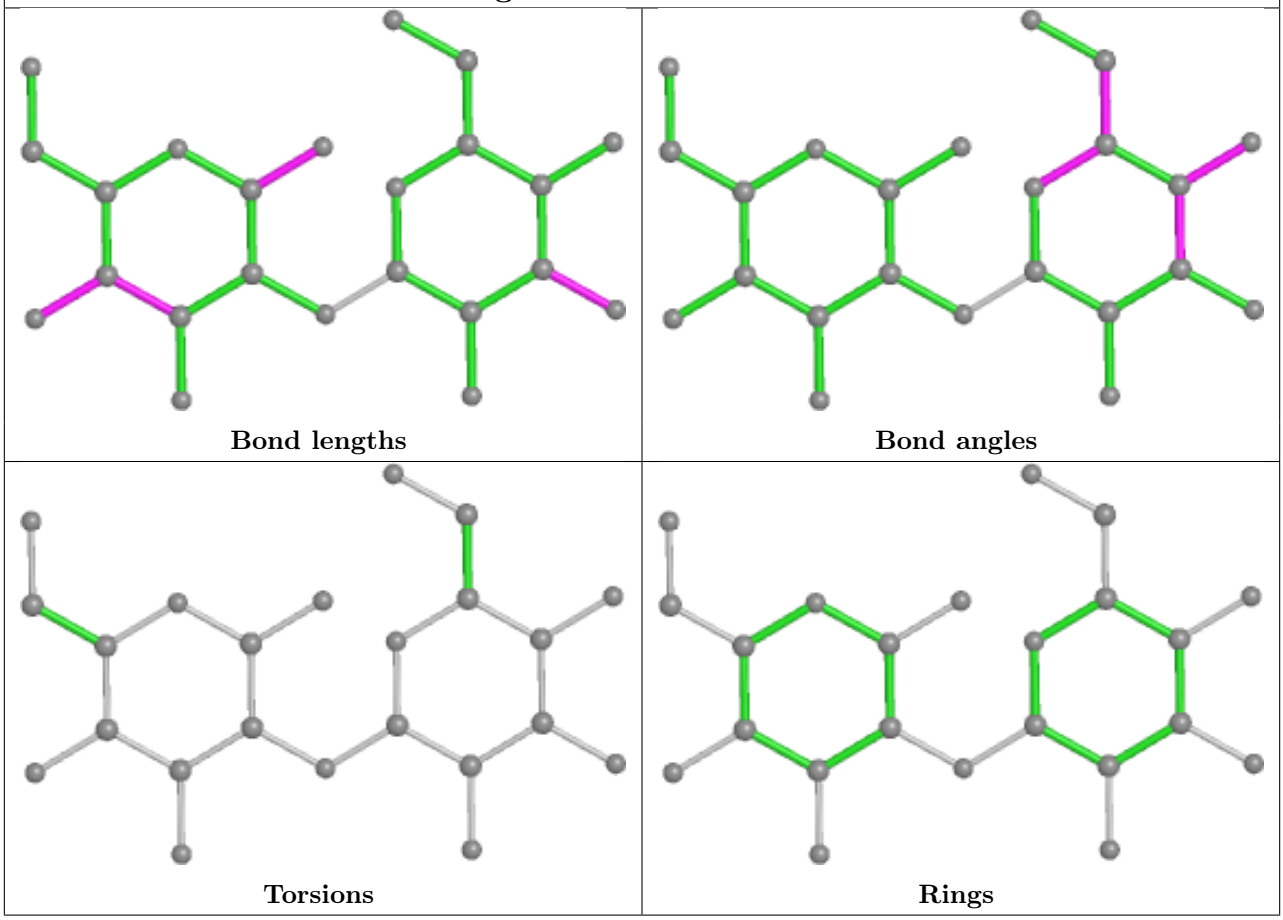


Torsions



Rings

Oligosaccharide Chain D



5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	A	1201	-	5,5,5	0.59	0	5,5,5	0.54	0
3	GOL	B	1202	-	5,5,5	0.54	0	5,5,5	0.40	0
3	GOL	B	1201	-	5,5,5	0.85	0	5,5,5	0.60	0
3	GOL	B	1204	-	5,5,5	0.64	0	5,5,5	0.75	0
3	GOL	A	1203	-	5,5,5	0.64	0	5,5,5	0.64	0
3	GOL	B	1203	-	5,5,5	0.32	0	5,5,5	0.24	0
3	GOL	A	1202	-	5,5,5	0.53	0	5,5,5	0.70	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1201	-	-	0/4/4/4	-
3	GOL	B	1202	-	-	0/4/4/4	-
3	GOL	B	1201	-	-	0/4/4/4	-
3	GOL	B	1204	-	-	0/4/4/4	-
3	GOL	A	1203	-	-	4/4/4/4	-
3	GOL	B	1203	-	-	2/4/4/4	-
3	GOL	A	1202	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1203	GOL	O1-C1-C2-C3
3	A	1203	GOL	C1-C2-C3-O3
3	B	1203	GOL	O1-C1-C2-O2
3	B	1203	GOL	O1-C1-C2-C3
3	A	1203	GOL	O1-C1-C2-O2
3	A	1203	GOL	O2-C2-C3-O3

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	1095/1122 (97%)	-0.08	3 (0%)	94	93	14, 26, 45, 72	0
1	B	1095/1122 (97%)	-0.10	1 (0%)	95	95	14, 26, 46, 75	0
All	All	2190/2244 (97%)	-0.09	4 (0%)	95	94	14, 26, 46, 75	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	795	GLY	4.2
1	A	798	HIS	3.1
1	A	1113	ASN	2.8
1	B	836	HIS	2.5

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

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

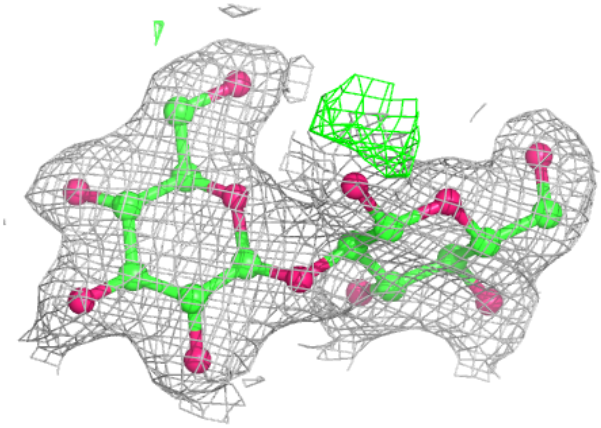
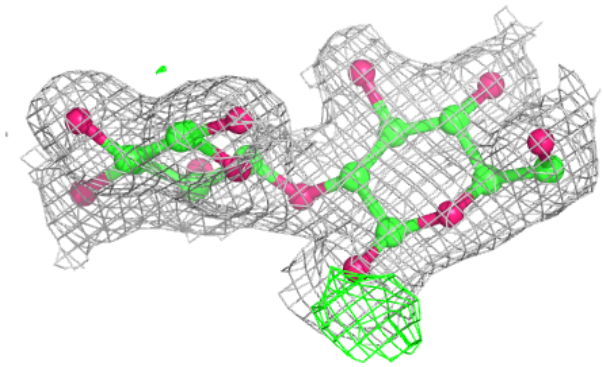
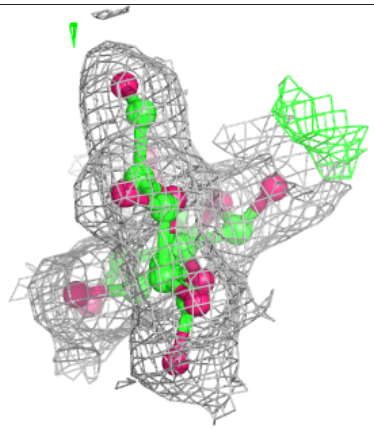
6.3 Carbohydrates (i)

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
2	BGC	D	1	12/12	0.95	0.15	20,23,27,29	0
2	BGC	C	1	12/12	0.96	0.12	16,18,21,22	0
2	BGC	D	2	11/12	0.97	0.13	17,19,20,21	0
2	BGC	C	2	11/12	0.98	0.11	16,19,20,21	0

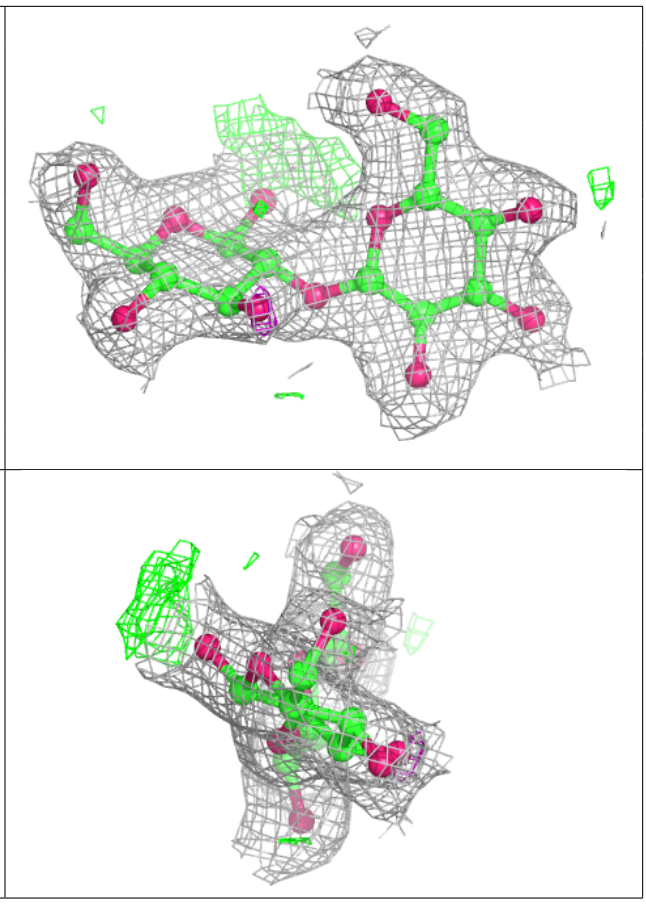
The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C: 2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)	
	

Electron density around Chain D:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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
3	GOL	B	1203	6/6	0.91	0.17	35,42,48,52	0
3	GOL	B	1201	6/6	0.92	0.14	20,22,24,26	0
3	GOL	A	1203	6/6	0.93	0.18	34,44,45,48	0
3	GOL	B	1204	6/6	0.94	0.20	39,42,44,45	0
3	GOL	A	1201	6/6	0.95	0.11	20,21,22,22	0
3	GOL	A	1202	6/6	0.96	0.15	28,29,32,34	0
3	GOL	B	1202	6/6	0.96	0.18	24,29,29,30	0
4	CA	A	1204	1/1	0.97	0.05	36,36,36,36	0
4	CA	B	1205	1/1	0.98	0.07	33,33,33,33	0

6.5 Other polymers (i)

There are no such residues in this entry.