Full wwPDB X-ray Structure Validation Report

Aug 8, 2020 – 02:07 AM BST

PDB ID	:	3T7D
Title	:	Vall from streptomyces hygroscopicus in complex with trehalose
Authors	:	Zhang, H.; Zheng, L.; Qian, H.; Chen, J.
Deposited on	:	2011-07-29
Resolution	:	1.70 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 following versions of software and data (see references (1)) were used in the production of this report:

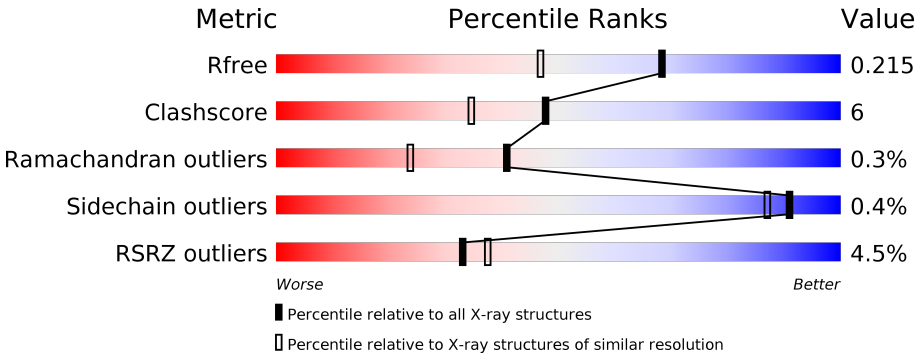
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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	497	5%, 83%, 10%, 8%
1	B	497	3%, 79%, 12%, 9%
2	C	2	100%
2	D	2	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7882 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.

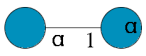
- Molecule 1 is a protein called Putative glycosyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	Se	0	1	0
			3613	2262	668	671	4	8			
1	B	454	Total	C	N	O	S	Se	0	0	0
			3568	2235	658	663	4	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	PHE	-	expression tag	UNP Q15JG1
B	1	PHE	-	expression tag	UNP Q15JG1

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

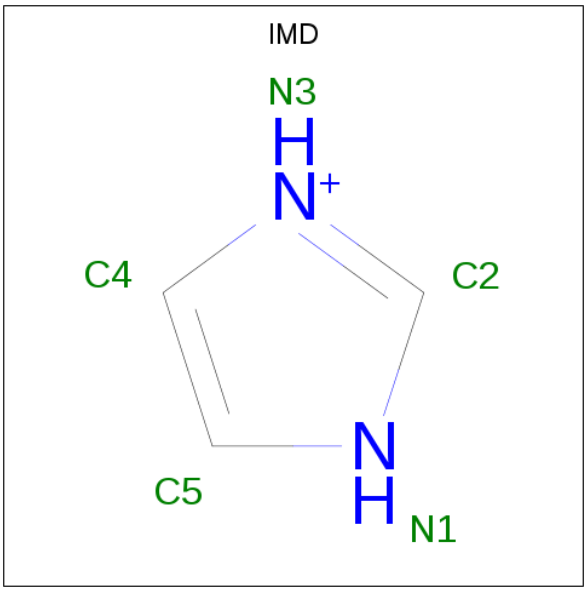


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	O		0	0	0
			23	12	11				
2	D	2	Total	C	O		0	0	0
			23	12	11				

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	8	Total	Mg	0	0
			8	8		
3	A	10	Total	Mg	0	0
			10	10		

- Molecule 4 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N 5 3 2	0	0
4	B	1	Total C N 5 3 2	0	0

- Molecule 5 is water.

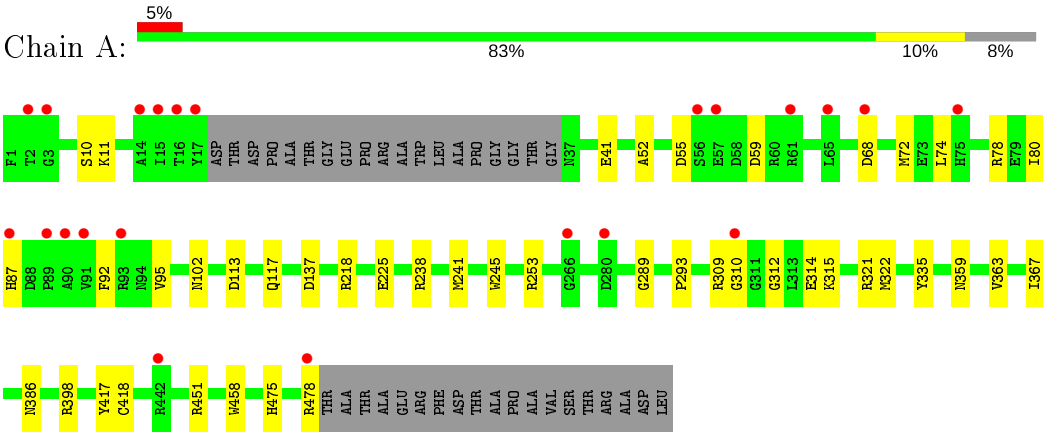
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	329	Total O 329 329	0	0
5	B	298	Total O 298 298	0	0

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.

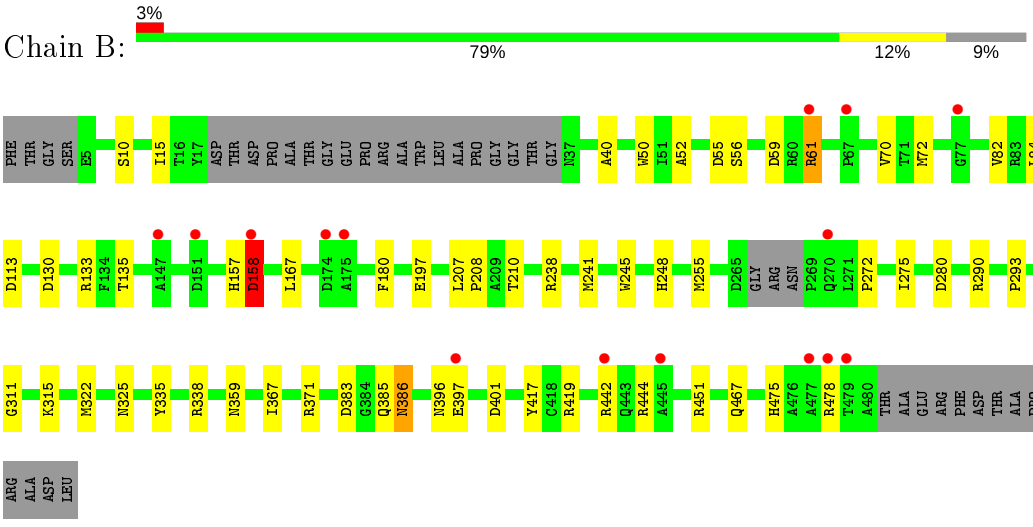
- Molecule 1: Putative glycosyltransferase

Chain A:



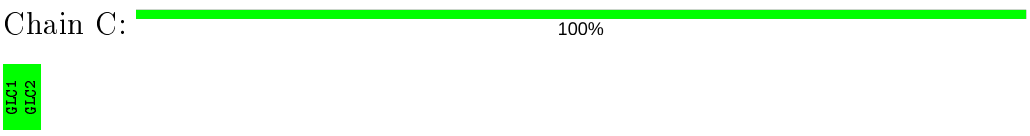
- Molecule 1: Putative glycosyltransferase

Chain B:



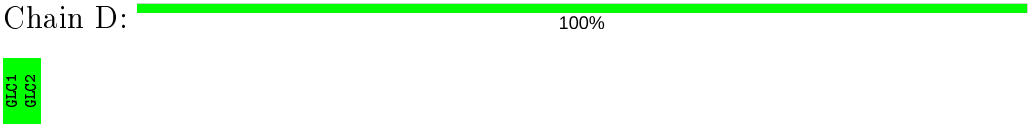
- Molecule 2: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose

Chain C:



- Molecule 2: alpha-D-glucopyranose-(1-1)-alpha-D-glucopyranose

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	79.66Å 45.82Å 115.03Å 90.00° 107.36° 90.00°	Depositor
Resolution (Å)	39.78 – 1.70 39.78 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (39.78-1.70) 99.0 (39.78-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.162 , 0.214 0.166 , 0.215	Depositor DCC
R_{free} test set	4373 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	23.6	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 49.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.014 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7882	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.20 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9214e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GLC, IMD

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	0.65	2/3690 (0.1%)	0.76	3/5012 (0.1%)
1	B	0.64	2/3640 (0.1%)	0.71	0/4943
All	All	0.64	4/7330 (0.1%)	0.73	3/9955 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	245	TRP	CD2-CE2	5.69	1.48	1.41
1	B	245	TRP	CD2-CE2	5.64	1.48	1.41
1	A	458	TRP	CD2-CE2	5.46	1.47	1.41
1	B	112	TRP	CD2-CE2	5.07	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	253	ARG	NE-CZ-NH1	5.51	123.05	120.30
1	A	253	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	218	ARG	NE-CZ-NH1	5.17	122.89	120.30

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	3613	0	3515	36	0
1	B	3568	0	3471	52	0
2	C	23	0	21	0	0
2	D	23	0	21	0	0
3	A	10	0	0	0	0
3	B	8	0	0	0	0
4	B	10	0	10	0	0
5	A	329	0	0	9	0
5	B	298	0	0	12	0
All	All	7882	0	7038	87	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 (87) 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:B:157:HIS:O	1:B:158:ASP:HB2	1.55	1.04
1:A:72:MSE:HE2	1:A:80:ILE:HD11	1.48	0.94
1:A:315:LYS:HE2	5:A:670:HOH:O	1.68	0.92
1:A:72:MSE:CE	1:A:80:ILE:HD11	2.05	0.86
1:B:248:HIS:HB3	1:B:478:ARG:HH12	1.40	0.86
1:B:180:PHE:CE1	1:B:255:MSE:HE3	2.12	0.83
1:A:137:ASP:HB3	5:A:809:HOH:O	1.84	0.78
1:B:478:ARG:HG2	5:B:587:HOH:O	1.84	0.77
1:B:315:LYS:HG2	1:B:315:LYS:O	1.84	0.76
1:B:157:HIS:O	1:B:158:ASP:CB	2.35	0.75
1:B:475:HIS:HD2	5:B:587:HOH:O	1.71	0.74
1:B:158:ASP:CB	5:B:536:HOH:O	2.35	0.73
1:B:158:ASP:HB3	5:B:536:HOH:O	1.90	0.72
1:B:180:PHE:HE1	1:B:255:MSE:HE3	1.53	0.72
1:B:272:PRO:HB2	1:B:275:ILE:HD13	1.78	0.66
1:A:87:HIS:ND1	5:A:809:HOH:O	2.27	0.65
1:B:180:PHE:CD1	1:B:255:MSE:HE3	2.32	0.64
1:B:210:THR:HA	1:B:478:ARG:HD3	1.81	0.63
1:A:321:ARG:HD3	1:A:369:CYS:SG	2.40	0.62
1:B:197:GLU:HG3	5:B:576:HOH:O	2.00	0.61
1:A:87:HIS:CE1	5:A:809:HOH:O	2.53	0.60
1:B:70:VAL:HG23	1:B:82:VAL:HG13	1.83	0.60
1:A:398:ARG:NH2	5:A:537:HOH:O	2.34	0.59
1:B:417:TYR:O	1:B:451:ARG:HD3	2.02	0.59
1:B:367:ILE:O	1:B:371:ARG:HG3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ARG:O	1:A:241:MSE:SE	2.73	0.57
1:A:225:GLU:OE2	1:A:238:ARG:NH1	2.37	0.57
1:B:290:ARG:HH21	1:B:325:ASN:HB2	1.69	0.57
1:A:11:LYS:NZ	1:A:92:PHE:CE1	2.68	0.56
1:A:321:ARG:CD	1:A:369:CYS:SG	2.93	0.56
1:B:238:ARG:O	1:B:241:MSE:SE	2.74	0.55
1:B:305:VAL:O	1:B:309:ARG:HG2	2.06	0.55
1:A:72:MSE:HE3	1:A:74:LEU:HD21	1.89	0.55
1:A:95:VAL:HG12	5:A:711:HOH:O	2.07	0.54
1:A:312:GLY:H	1:A:314:GLU:CD	2.11	0.54
1:B:335:TYR:HD1	1:B:338:ARG:NH2	2.06	0.54
1:B:371:ARG:NE	5:B:780:HOH:O	2.29	0.52
1:B:385:GLN:O	1:B:386:ASN:CB	2.56	0.52
1:B:158:ASP:HB2	5:B:536:HOH:O	2.08	0.51
1:A:117[B]:GLN:NE2	5:A:726:HOH:O	2.41	0.50
1:B:55:ASP:OD1	1:B:59:ASP:OD1	2.29	0.50
1:B:248:HIS:HB3	1:B:478:ARG:NH1	2.20	0.50
1:A:68:ASP:O	1:A:83:ARG:HG2	2.10	0.50
1:B:315:LYS:O	1:B:315:LYS:CG	2.59	0.49
1:B:371:ARG:NH1	1:B:397:GLU:OE2	2.46	0.48
1:A:41:GLU:OE2	1:A:78:ARG:HD2	2.13	0.48
1:A:309:ARG:HA	1:A:310:GLY:HA2	1.66	0.48
1:A:417:TYR:O	1:A:451:ARG:HD3	2.13	0.48
1:A:117[A]:GLN:NE2	5:A:726:HOH:O	2.47	0.47
1:B:70:VAL:CG2	1:B:82:VAL:HG13	2.44	0.47
1:B:15:ILE:HG12	1:B:72:MSE:SE	2.65	0.47
1:A:113:ASP:HB3	1:B:113:ASP:HB3	1.96	0.46
1:B:371:ARG:HA	1:B:396:ASN:HA	1.97	0.46
1:A:321:ARG:HD2	1:A:369:CYS:SG	2.56	0.45
1:A:72:MSE:HE2	1:A:80:ILE:CD1	2.32	0.45
1:B:272:PRO:HB2	1:B:275:ILE:CD1	2.44	0.45
1:B:59:ASP:HB3	1:B:84:LEU:HD13	1.99	0.45
1:A:55:ASP:N	1:A:59:ASP:OD2	2.48	0.45
1:B:130:ASP:OD1	1:B:133:ARG:NH1	2.51	0.44
1:A:315:LYS:CE	5:A:670:HOH:O	2.42	0.44
1:A:322:MSE:O	1:A:359:ASN:HA	2.17	0.44
1:A:363:VAL:O	1:A:367:ILE:HG12	2.17	0.44
1:A:72:MSE:HE3	1:A:74:LEU:CD2	2.48	0.44
1:B:255:MSE:SE	1:B:467:GLN:HA	2.68	0.44
1:B:444:ARG:HD2	5:B:615:HOH:O	2.16	0.44
1:B:61:ARG:NH1	5:B:736:HOH:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:PRO:HA	1:B:335:TYR:CD1	2.53	0.43
1:A:418:CYS:SG	1:A:451:ARG:HD2	2.58	0.43
1:B:322:MSE:O	1:B:359:ASN:HA	2.18	0.43
1:B:207:LEU:N	1:B:208:PRO:CD	2.82	0.43
1:B:10:SER:O	1:B:52:ALA:HA	2.19	0.43
1:B:478:ARG:HB2	5:B:550:HOH:O	2.18	0.43
1:B:401:ASP:OD2	1:B:419:ARG:NH1	2.45	0.42
1:A:293:PRO:HA	1:A:335:TYR:CD1	2.55	0.42
1:B:335:TYR:HD1	1:B:338:ARG:HH22	1.68	0.41
1:A:371:ARG:NH1	1:A:371:ARG:HB2	2.36	0.41
1:B:280:ASP:N	5:B:589:HOH:O	2.54	0.41
1:B:442:ARG:HB2	5:B:779:HOH:O	2.19	0.41
1:A:475:HIS:O	1:A:478:ARG:HG3	2.21	0.41
1:B:40:ALA:HB2	1:B:50:TRP:CZ3	2.56	0.41
1:B:135:THR:HG22	1:B:167:LEU:HD22	2.03	0.41
1:A:289:GLY:O	1:A:322:MSE:HA	2.21	0.40
1:B:241:MSE:HB3	1:B:241:MSE:HE3	1.89	0.40
1:B:55:ASP:OD1	1:B:56:SER:N	2.55	0.40
1:A:102:ASN:C	1:A:102:ASN:OD1	2.59	0.40
1:A:10:SER:O	1:A:52:ALA:HA	2.21	0.40
1:B:310:GLY:HA2	1:B:311:GLY:HA2	1.52	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
1	A	456/497 (92%)	440 (96%)	15 (3%)	1 (0%)	47 30
1	B	448/497 (90%)	434 (97%)	12 (3%)	2 (0%)	34 18
All	All	904/994 (91%)	874 (97%)	27 (3%)	3 (0%)	41 24

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	158	ASP
1	B	386	ASN
1	A	386	ASN

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	370/387 (96%)	370 (100%)	0	100	100
1	B	365/387 (94%)	362 (99%)	3 (1%)	81	74
All	All	735/774 (95%)	732 (100%)	3 (0%)	91	87

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

Mol	Chain	Res	Type
1	B	61	ARG
1	B	158	ASP
1	B	383	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	204	HIS

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 (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	GLC	C	1	2	11,11,12	0.26	0	15,15,17	0.64	0
2	GLC	C	2	2	12,12,12	0.41	0	17,17,17	0.53	0
2	GLC	D	1	2	11,11,12	0.27	0	15,15,17	0.64	0
2	GLC	D	2	2	12,12,12	0.41	0	17,17,17	0.53	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
2	GLC	C	1	2	-	0/2/19/22	0/1/1/1
2	GLC	C	2	2	-	0/2/22/22	0/1/1/1
2	GLC	D	1	2	-	0/2/19/22	0/1/1/1
2	GLC	D	2	2	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

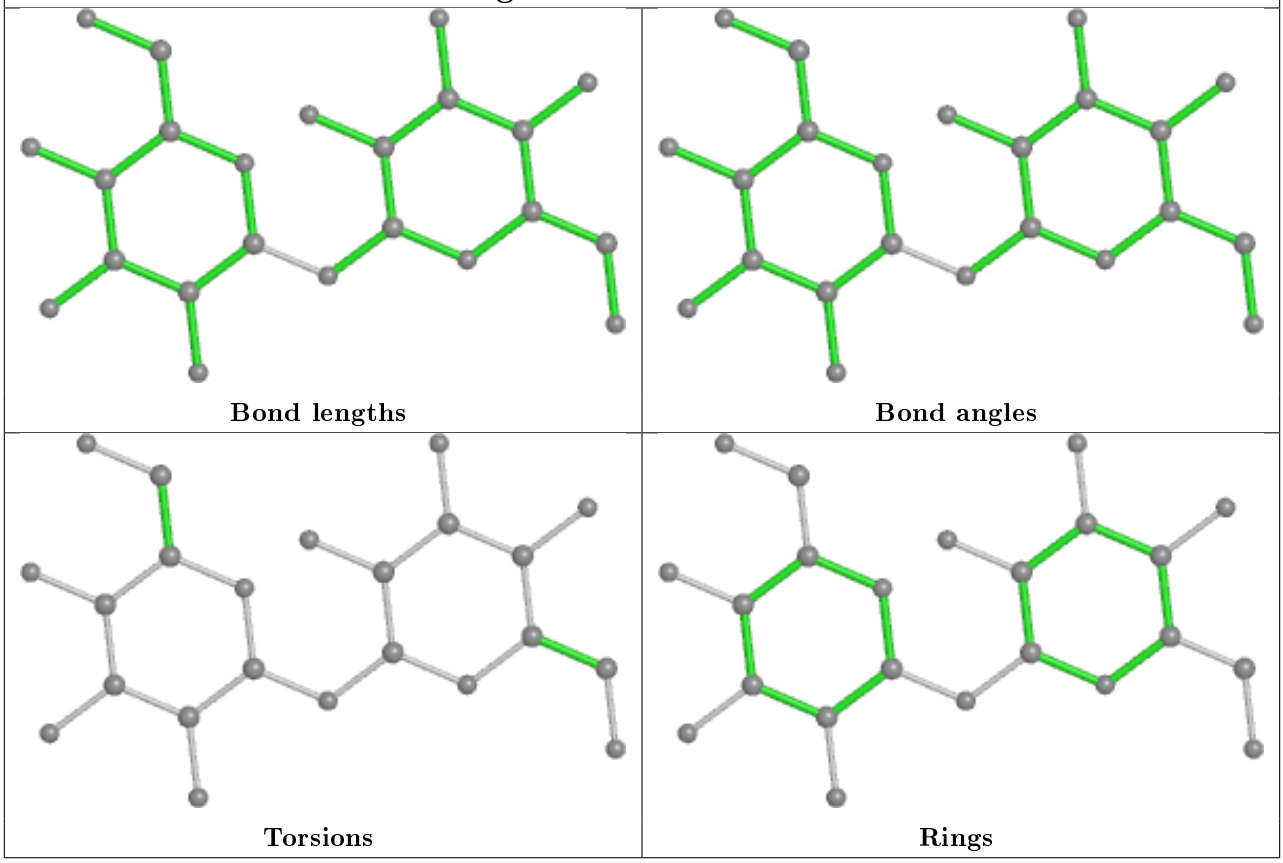
There are no torsion outliers.

There are no ring outliers.

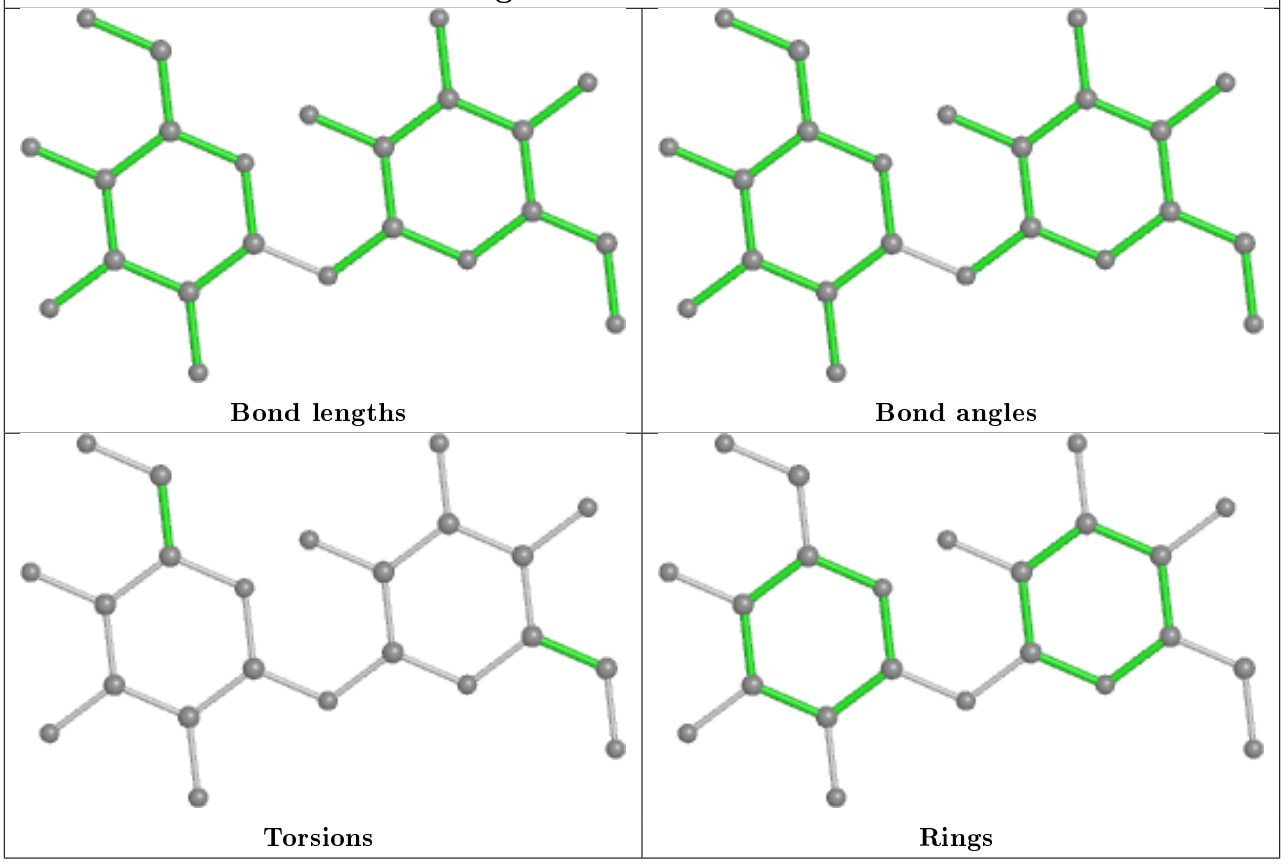
No monomer is involved in short contacts.

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



Oligosaccharide Chain D



5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 18 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
4	IMD	B	499	-	3,5,5	0.36	0	4,5,5	0.57	0
4	IMD	B	500	-	3,5,5	0.36	0	4,5,5	0.56	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
4	IMD	B	499	-	-	-	0/1/1/1
4	IMD	B	500	-	-	-	0/1/1/1

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

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	A	451/497 (90%)	0.09	23 (5%)	28	31	11, 27, 55, 90	0
1	B	446/497 (89%)	0.04	17 (3%)	40	45	12, 28, 56, 70	0
All	All	897/994 (90%)	0.06	40 (4%)	33	37	11, 28, 56, 90	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	57	GLU	6.5
1	A	310	GLY	6.1
1	A	65	LEU	5.4
1	A	75	HIS	5.0
1	A	68	ASP	4.6
1	A	16	THR	4.4
1	B	158	ASP	4.4
1	A	61	ARG	4.4
1	B	477	ALA	4.0
1	B	67	PRO	3.8
1	B	310	GLY	3.8
1	A	86	ARG	3.8
1	A	14	ALA	3.5
1	A	89	PRO	3.5
1	A	56	SER	3.4
1	A	90	ALA	3.4
1	B	478	ARG	3.3
1	A	2	THR	3.2
1	B	174	ASP	3.2
1	B	61	ARG	3.0
1	A	93	ARG	3.0
1	A	266	GLY	2.9
1	B	479	THR	2.9
1	B	151	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	3	GLY	2.8
1	B	270	GLN	2.7
1	A	17	TYR	2.7
1	A	478	ARG	2.6
1	B	93	ARG	2.6
1	A	91	VAL	2.6
1	B	397	GLU	2.5
1	B	147	ALA	2.5
1	A	442	ARG	2.4
1	A	87	HIS	2.4
1	B	442	ARG	2.2
1	A	280	ASP	2.2
1	B	77	GLY	2.2
1	B	175	ALA	2.2
1	B	445	ALA	2.1
1	A	15	ILE	2.1

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)

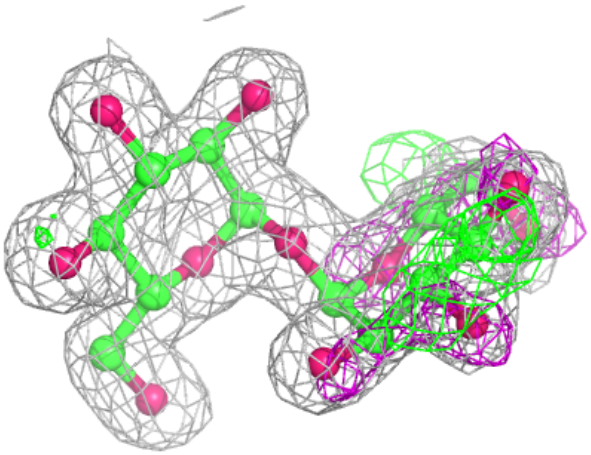
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

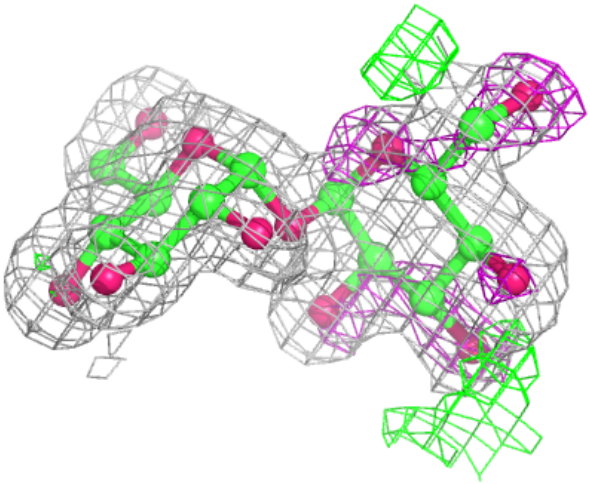
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GLC	D	2	12/12	0.89	0.12	20,21,22,22	0
2	GLC	C	2	12/12	0.90	0.13	21,21,23,23	0
2	GLC	D	1	11/12	0.94	0.11	20,20,20,21	0
2	GLC	C	1	11/12	0.95	0.07	20,21,21,21	0

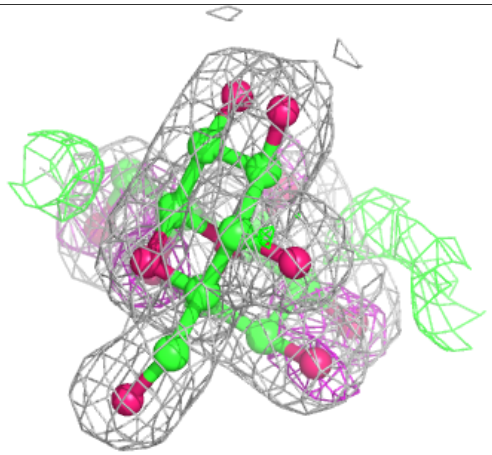
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

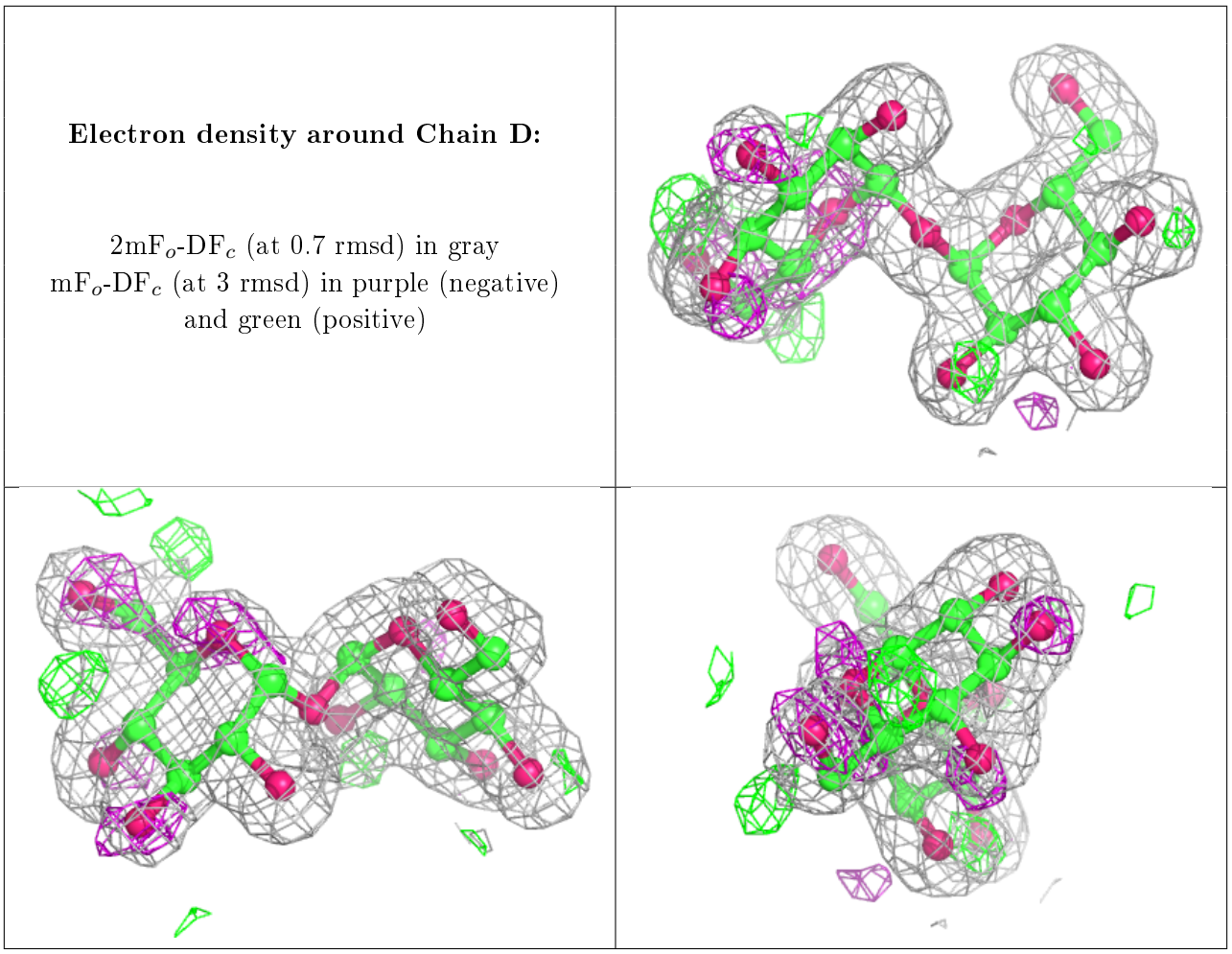






Electron density around Chain D:

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



6.4 Ligands

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, 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	B-factors(Å^2)	Q<0.9
4	IMD	B	500	5/5	0.86	0.14	48,53,65,67	0
4	IMD	B	499	5/5	0.90	0.14	44,46,50,54	0
3	MG	A	508	1/1	0.92	0.22	35,35,35,35	0
3	MG	B	508	1/1	0.93	0.44	54,54,54,54	0
3	MG	B	506	1/1	0.94	0.10	54,54,54,54	0
3	MG	B	507	1/1	0.95	0.35	49,49,49,49	0
3	MG	A	501	1/1	0.95	0.16	48,48,48,48	0
3	MG	A	505	1/1	0.96	0.08	37,37,37,37	0
3	MG	A	500	1/1	0.97	0.08	47,47,47,47	0
3	MG	A	507	1/1	0.98	0.09	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	A	504	1/1	0.98	0.04	39,39,39,39	0
3	MG	A	503	1/1	0.98	0.10	33,33,33,33	0
3	MG	A	506	1/1	0.98	0.05	51,51,51,51	0
3	MG	B	503	1/1	0.98	0.22	35,35,35,35	0
3	MG	B	504	1/1	0.99	0.08	41,41,41,41	0
3	MG	A	502	1/1	0.99	0.09	33,33,33,33	0
3	MG	B	501	1/1	0.99	0.07	34,34,34,34	0
3	MG	B	502	1/1	0.99	0.10	40,40,40,40	0
3	MG	B	505	1/1	0.99	0.07	35,35,35,35	0
3	MG	A	499	1/1	1.00	0.08	29,29,29,29	0

6.5 Other polymers (i)

There are no such residues in this entry.