Full wwPDB X-ray Structure Validation Report (i)

Sep 19, 2023 – 03:57 AM EDT

PDB ID	:	5BV9
Title	:	The Structure of Bacillus pumilus GH48 in complex with cellobiose
Authors	:	Alahuhta, P.M.; Lunin, V.V.
Deposited on	:	2015-06-04
Resolution	:	1.93 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:

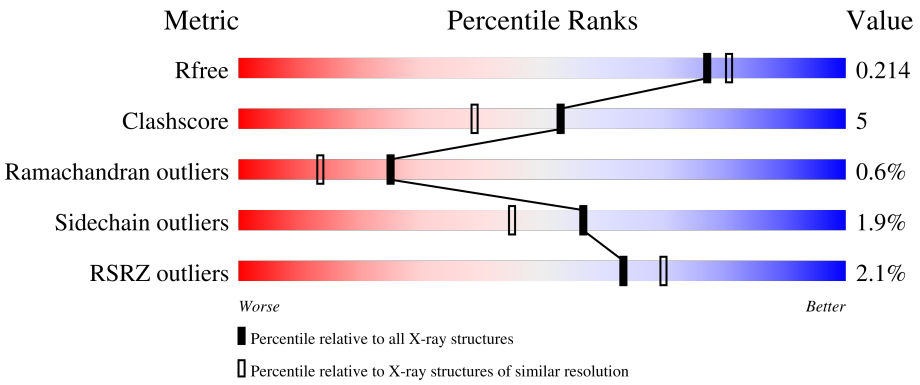
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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	709	2% 89% 9% ••
2	B	2	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	ACT	A	810	-	-	X	-
6	ACT	A	814	-	-	X	-
7	GOL	A	816	-	X	-	-
7	GOL	A	817	-	X	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 6829 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 Cellulose 1,4-beta-cellobiosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	701	5692	3613	950	1111	18	0	14	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	702	LEU	-	expression tag	UNP A8FDC4
A	703	GLU	-	expression tag	UNP A8FDC4
A	704	HIS	-	expression tag	UNP A8FDC4
A	705	HIS	-	expression tag	UNP A8FDC4
A	706	HIS	-	expression tag	UNP A8FDC4
A	707	HIS	-	expression tag	UNP A8FDC4
A	708	HIS	-	expression tag	UNP A8FDC4
A	709	HIS	-	expression tag	UNP A8FDC4

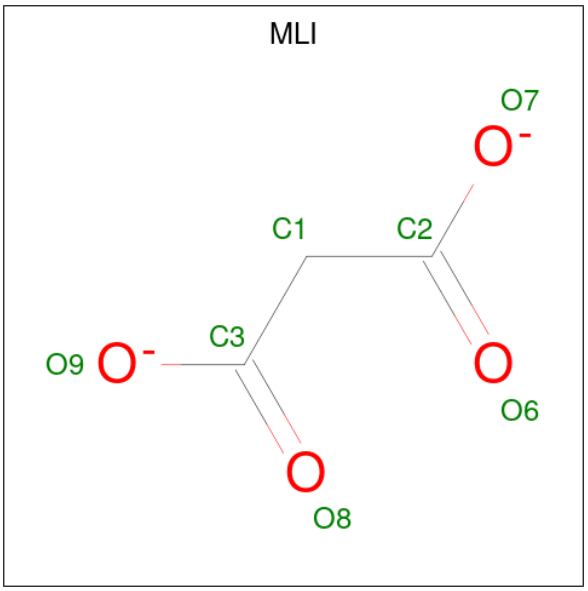
- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.

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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

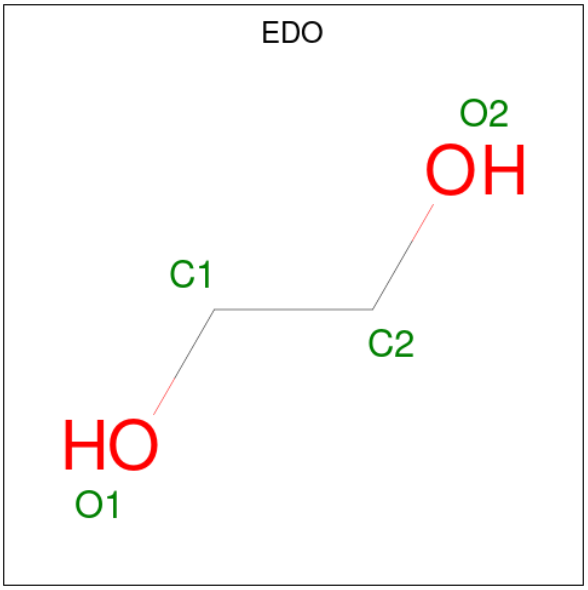
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	3	3	3	0	0

- Molecule 4 is MALONATE ION (three-letter code: MLI) (formula: $C_3H_2O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	7	3	4	0	0
			Total	C	O		
4	A	1	7	3	4	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	4	2	2	0	0
			Total	C	O		
5	A	1	4	2	2	0	0

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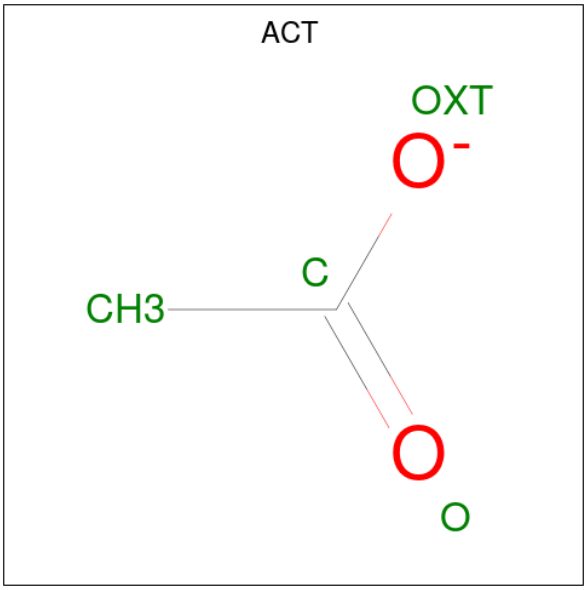
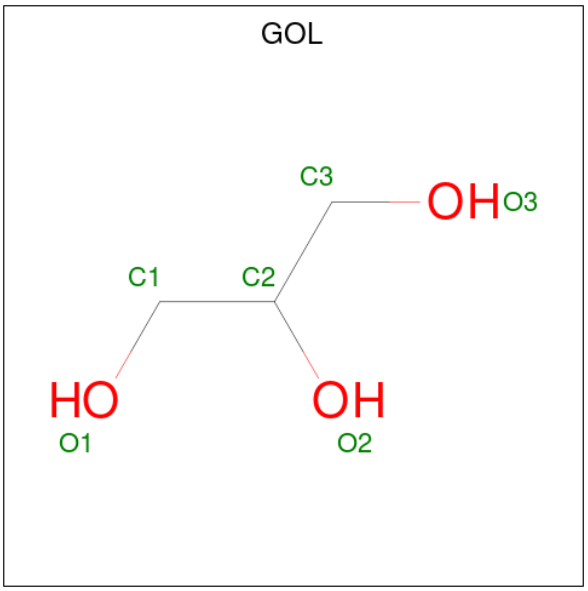
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	4	2	2	0	0

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0
			Total	C	O		
6	A	1	4	2	2	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	6	3	3	0	0
			Total	C	O		
7	A	1	6	3	3	0	0
			Total	C	O		
7	A	1	12	6	6	0	1

- Molecule 8 is water.

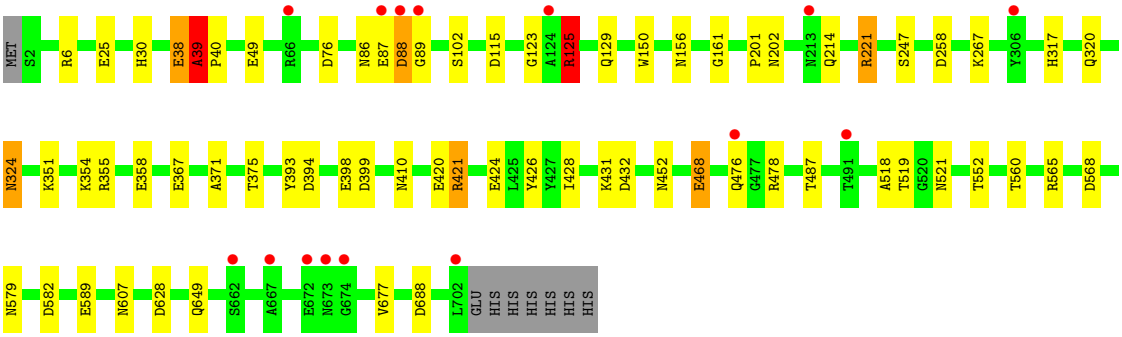
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	950	1037	1037	0	87

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.

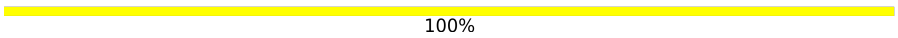
• Molecule 1: Cellulose 1,4-beta-cellobiosidase

Chain A:



• Molecule 2: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	97.29Å 97.29Å 218.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.93 42.73 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.3 (50.00-1.93) 99.3 (42.73-1.93)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$< I/\sigma(I) >$ [1]	1.65 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.8.0123	Depositor
R, R_{free}	0.161 , 0.207 0.170 , 0.214	Depositor DCC
R_{free} test set	3971 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	14.7	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 58.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6829	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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: EDO, CA, ACT, GOL, MLI, 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	1.03	4/5876 (0.1%)	0.99	16/8006 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	421	ARG	CD-NE	-6.41	1.35	1.46
1	A	468	GLU	CG-CD	6.33	1.61	1.51
1	A	247	SER	CB-OG	-5.29	1.35	1.42
1	A	426	TYR	CG-CD1	5.01	1.45	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	421	ARG	NE-CZ-NH2	-23.50	108.55	120.30
1	A	421	ARG	NE-CZ-NH1	11.33	125.97	120.30
1	A	355	ARG	NE-CZ-NH1	10.29	125.45	120.30
1	A	125	ARG	NE-CZ-NH1	10.21	125.41	120.30
1	A	125	ARG	NE-CZ-NH2	-9.14	115.73	120.30
1	A	565	ARG	NE-CZ-NH2	-7.76	116.42	120.30
1	A	399	ASP	CB-CG-OD1	7.13	124.72	118.30
1	A	628	ASP	CB-CG-OD2	-6.62	112.35	118.30
1	A	355	ARG	NE-CZ-NH2	-6.43	117.08	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	421	ARG	CD-NE-CZ	6.23	132.32	123.60
1	A	582	ASP	CB-CG-OD1	6.13	123.81	118.30
1	A	6	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	A	358	GLU	OE1-CD-OE2	-5.68	116.49	123.30
1	A	76	ASP	CB-CG-OD2	-5.59	113.27	118.30
1	A	628	ASP	CB-CG-OD1	5.46	123.22	118.30
1	A	568	ASP	CB-CG-OD1	5.17	122.95	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	39	ALA	Peptide

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	5692	0	5227	59	0
2	B	23	0	21	0	0
3	A	3	0	0	0	0
4	A	14	0	4	2	0
5	A	12	0	18	0	0
6	A	24	0	18	8	0
7	A	24	0	32	8	0
8	A	1037	0	0	24	0
All	All	6829	0	5320	60	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 5.

All (60) 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:25[B]:GLU:OE1	8:A:903:HOH:O	1.53	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49[B]:GLU:CD	8:A:907:HOH:O	1.77	1.20
1:A:49[B]:GLU:CG	8:A:907:HOH:O	1.93	1.11
1:A:202[B]:ASN:OD1	8:A:905:HOH:O	1.74	1.05
1:A:431:LYS:HB3	6:A:810:ACT:H2	1.38	1.05
1:A:25[B]:GLU:OE2	8:A:906:HOH:O	1.79	0.97
1:A:49[B]:GLU:OE2	8:A:907:HOH:O	1.80	0.91
1:A:49[B]:GLU:HG3	8:A:907:HOH:O	1.64	0.88
1:A:521:ASN:OD1	7:A:817:GOL:H32	1.76	0.83
1:A:431:LYS:HB3	6:A:810:ACT:CH3	2.10	0.81
1:A:156:ASN:HD21	1:A:161:GLY:H	1.30	0.77
1:A:393:TYR:CZ	7:A:816:GOL:H2	2.19	0.77
1:A:150:TRP:CE2	6:A:814:ACT:H3	2.19	0.77
1:A:221[A]:ARG:NH1	8:A:904:HOH:O	1.67	0.76
1:A:579[B]:ASN:HD22	1:A:579[B]:ASN:C	1.91	0.73
1:A:431:LYS:CB	6:A:810:ACT:H2	2.19	0.70
1:A:221[A]:ARG:NH2	8:A:904:HOH:O	2.27	0.67
1:A:521:ASN:CG	7:A:817:GOL:H32	2.19	0.63
1:A:579[B]:ASN:ND2	8:A:911:HOH:O	2.33	0.61
1:A:354:LYS:HE2	8:A:1708:HOH:O	2.01	0.61
1:A:393:TYR:CE2	7:A:816:GOL:H2	2.34	0.61
1:A:317:HIS:HD2	1:A:375:THR:OG1	1.84	0.59
1:A:221[A]:ARG:NH1	8:A:914:HOH:O	2.35	0.59
1:A:30:HIS:HD2	8:A:977:HOH:O	1.86	0.58
1:A:579[B]:ASN:C	1:A:579[B]:ASN:ND2	2.55	0.58
1:A:267:LYS:NZ	8:A:920:HOH:O	2.38	0.56
1:A:476:GLN:OE1	1:A:478:ARG:NH2	2.38	0.55
1:A:351:LYS:HE3	8:A:1696:HOH:O	2.08	0.54
1:A:150:TRP:CE2	6:A:814:ACT:CH3	2.91	0.54
1:A:518:ALA:HB1	7:A:817:GOL:H2	1.90	0.53
1:A:521:ASN:OD1	7:A:817:GOL:C3	2.54	0.53
1:A:150:TRP:CD2	6:A:814:ACT:CH3	2.92	0.52
1:A:432:ASP:OD1	6:A:810:ACT:H1	2.10	0.52
1:A:398:GLU:OE2	4:A:805:MLI:O9	2.28	0.51
1:A:87:GLU:O	1:A:88:ASP:CB	2.58	0.51
1:A:324:ASN:C	1:A:324:ASN:HD22	2.14	0.50
1:A:123:GLY:HA2	8:A:1239:HOH:O	2.11	0.50
1:A:649:GLN:NE2	8:A:933:HOH:O	2.46	0.48
1:A:468:GLU:H	1:A:468:GLU:CD	2.16	0.48
1:A:125:ARG:NH2	8:A:918:HOH:O	2.37	0.48
1:A:428:ILE:HA	6:A:810:ACT:H3	1.95	0.48
1:A:552:THR:HB	1:A:560:THR:HG23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:HIS:HE1	1:A:38:GLU:OE1	1.98	0.46
1:A:320:GLN:HG2	1:A:371:ALA:O	2.16	0.46
1:A:421:ARG:HD2	8:A:1251:HOH:O	2.15	0.46
1:A:589:GLU:HG2	1:A:677:VAL:HG13	1.98	0.45
1:A:410:ASN:HD21	7:A:818[A]:GOL:H2	1.82	0.45
1:A:519:THR:H	7:A:817:GOL:H31	1.82	0.44
1:A:317:HIS:CD2	1:A:375:THR:OG1	2.67	0.44
1:A:589:GLU:CD	1:A:677:VAL:HG11	2.37	0.44
1:A:129[B]:GLN:HG3	8:A:1564:HOH:O	2.17	0.43
1:A:589:GLU:CG	1:A:677:VAL:CG1	2.96	0.43
1:A:452:ASN:ND2	8:A:927:HOH:O	2.43	0.42
1:A:221[A]:ARG:CZ	8:A:904:HOH:O	2.26	0.42
1:A:607:ASN:CG	8:A:1067:HOH:O	2.58	0.41
1:A:420:GLU:OE2	1:A:424:GLU:OE2	2.38	0.41
4:A:806:MLI:O9	4:A:806:MLI:O7	2.37	0.41
1:A:39:ALA:HB3	1:A:40:PRO:CD	2.51	0.41
1:A:487:THR:HG21	8:A:1578:HOH:O	2.20	0.41
1:A:201:PRO:O	1:A:202[A]:ASN:HB2	2.19	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	713/709 (101%)	693 (97%)	16 (2%)	4 (1%)	25 13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	ASP
1	A	89	GLY
1	A	39	ALA

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Mol	Chain	Res	Type
1	A	38	GLU

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	586/580 (101%)	574 (98%)	12 (2%)	55 42

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	ASN
1	A	102	SER
1	A	115	ASP
1	A	125	ARG
1	A	214	GLN
1	A	221[A]	ARG
1	A	221[B]	ARG
1	A	258	ASP
1	A	324	ASN
1	A	367	GLU
1	A	394	ASP
1	A	688	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	30	HIS
1	A	86	ASN
1	A	120	GLN
1	A	156	ASN
1	A	317	HIS
1	A	324	ASN
1	A	379	ASN

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Mol	Chain	Res	Type
1	A	410	ASN
1	A	439	ASN
1	A	516	GLN
1	A	581	ASN
1	A	649	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

2 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	B	1	2	12,12,12	1.44	3 (25%)	17,17,17	2.94	10 (58%)
2	BGC	B	2	2	11,11,12	0.81	0	15,15,17	1.39	3 (20%)

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	B	1	2	-	0/2/22/22	0/1/1/1
2	BGC	B	2	2	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	BGC	C4-C5	2.94	1.59	1.53
2	B	1	BGC	C4-C3	2.21	1.58	1.52
2	B	1	BGC	O2-C2	2.15	1.48	1.43

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	BGC	C1-O5-C5	-7.25	99.99	113.66
2	B	1	BGC	C1-C2-C3	-5.01	99.92	110.31
2	B	1	BGC	O2-C2-C1	3.80	117.96	109.16
2	B	1	BGC	O1-C1-C2	3.23	118.12	109.03
2	B	1	BGC	O2-C2-C3	2.63	116.42	110.35
2	B	1	BGC	O1-C1-O5	2.53	117.96	110.38
2	B	2	BGC	O2-C2-C3	2.52	115.19	110.14
2	B	2	BGC	O3-C3-C2	2.40	114.60	109.99
2	B	1	BGC	O5-C1-C2	-2.33	106.12	110.28
2	B	1	BGC	O6-C6-C5	2.28	119.11	111.29
2	B	1	BGC	C6-C5-C4	2.24	118.24	113.00
2	B	2	BGC	O5-C1-C2	2.23	114.21	110.77
2	B	1	BGC	C3-C4-C5	2.16	114.08	110.24

There are no chirality outliers.

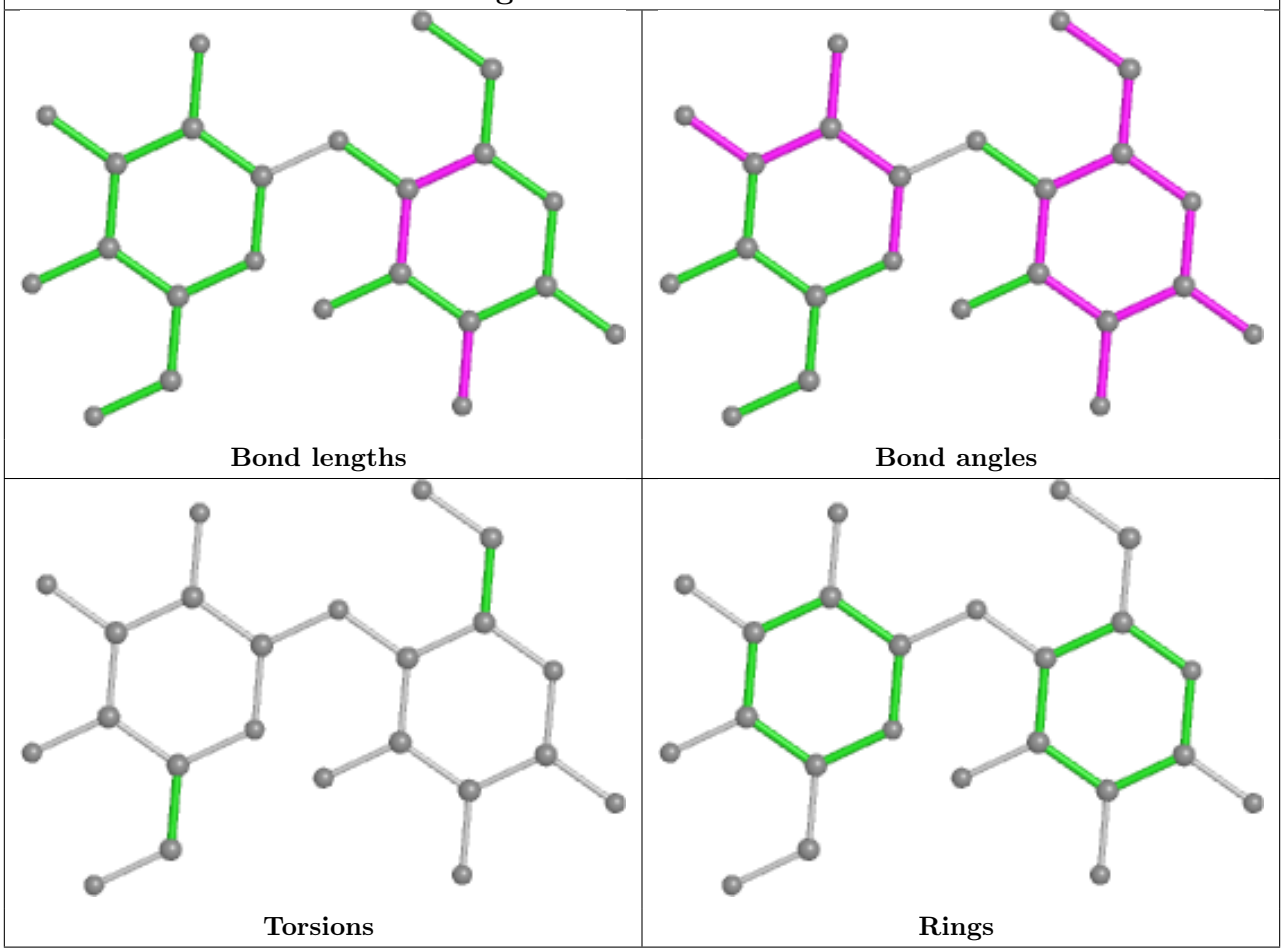
There are no torsion outliers.

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 B



5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 3 are monoatomic - leaving 15 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	$\#\|Z\| > 2$
6	ACT	A	814	-	3,3,3	1.24	0	3,3,3	2.81	1 (33%)
5	EDO	A	808	-	3,3,3	1.10	0	2,2,2	0.85	0
5	EDO	A	807	-	3,3,3	0.32	0	2,2,2	0.17	0
6	ACT	A	810	-	3,3,3	1.27	0	3,3,3	1.61	1 (33%)
6	ACT	A	815	-	3,3,3	1.47	0	3,3,3	1.02	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	MLI	A	806	-	6,6,6	1.59	2 (33%)	7,7,7	1.63	2 (28%)
5	EDO	A	809	-	3,3,3	0.41	0	2,2,2	1.37	0
6	ACT	A	811	-	3,3,3	0.86	0	3,3,3	0.70	0
6	ACT	A	813	-	3,3,3	1.04	0	3,3,3	0.54	0
7	GOL	A	817	-	5,5,5	1.43	1 (20%)	5,5,5	2.45	3 (60%)
7	GOL	A	818[A]	-	5,5,5	0.85	0	5,5,5	0.95	0
4	MLI	A	805	-	6,6,6	1.64	1 (16%)	7,7,7	1.53	1 (14%)
7	GOL	A	818[B]	-	5,5,5	0.75	0	5,5,5	1.48	1 (20%)
6	ACT	A	812	-	3,3,3	0.90	0	3,3,3	0.66	0
7	GOL	A	816	-	5,5,5	1.23	1 (20%)	5,5,5	1.97	2 (40%)

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
5	EDO	A	808	-	-	0/1/1/1	-
5	EDO	A	807	-	-	0/1/1/1	-
4	MLI	A	806	-	-	0/4/4/4	-
5	EDO	A	809	-	-	1/1/1/1	-
7	GOL	A	817	-	-	4/4/4/4	-
7	GOL	A	818[A]	-	-	3/4/4/4	-
4	MLI	A	805	-	-	2/4/4/4	-
7	GOL	A	818[B]	-	-	3/4/4/4	-
7	GOL	A	816	-	-	3/4/4/4	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	805	MLI	O7-C2	-3.07	1.20	1.30
4	A	806	MLI	O8-C3	2.86	1.31	1.22
4	A	806	MLI	O6-C2	2.33	1.29	1.22
7	A	817	GOL	O3-C3	2.25	1.51	1.42
7	A	816	GOL	C1-C2	2.03	1.60	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	814	ACT	OXT-C-O	4.11	137.22	122.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	817	GOL	O3-C3-C2	3.80	128.42	110.20
4	A	805	MLI	C3-C1-C2	-3.21	101.62	112.87
7	A	817	GOL	C3-C2-C1	2.74	122.36	111.70
7	A	818[B]	GOL	O2-C2-C1	2.61	120.63	109.12
7	A	816	GOL	O3-C3-C2	2.55	122.44	110.20
4	A	806	MLI	O8-C3-C1	-2.51	114.75	122.08
4	A	806	MLI	O9-C3-O8	2.48	129.47	123.30
7	A	816	GOL	O1-C1-C2	2.45	121.95	110.20
6	A	810	ACT	OXT-C-O	2.16	130.03	122.05
7	A	817	GOL	O2-C2-C1	-2.03	100.19	109.12

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	816	GOL	C1-C2-C3-O3
7	A	817	GOL	O1-C1-C2-C3
7	A	817	GOL	C1-C2-C3-O3
7	A	818[A]	GOL	O1-C1-C2-O2
7	A	818[A]	GOL	O1-C1-C2-C3
7	A	818[B]	GOL	O1-C1-C2-C3
7	A	816	GOL	O2-C2-C3-O3
7	A	817	GOL	O1-C1-C2-O2
7	A	817	GOL	O2-C2-C3-O3
7	A	818[B]	GOL	O2-C2-C3-O3
4	A	805	MLI	C3-C1-C2-O7
7	A	816	GOL	O1-C1-C2-O2
4	A	805	MLI	C3-C1-C2-O6
7	A	818[B]	GOL	O1-C1-C2-O2
5	A	809	EDO	O1-C1-C2-O2
7	A	818[A]	GOL	O2-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	814	ACT	3	0
6	A	810	ACT	5	0
4	A	806	MLI	1	0
7	A	817	GOL	5	0
7	A	818[A]	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	805	MLI	1	0
7	A	816	GOL	2	0

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	701/709 (98%)	-0.26	15 (2%) 63 70	7, 14, 32, 77	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	88	ASP	6.2
1	A	306	TYR	4.7
1	A	87	GLU	3.2
1	A	702	LEU	3.1
1	A	66	ARG	2.9
1	A	213[A]	ASN	2.7
1	A	667	ALA	2.6
1	A	89	GLY	2.5
1	A	124	ALA	2.2
1	A	673	ASN	2.2
1	A	491	THR	2.2
1	A	662	SER	2.2
1	A	672	GLU	2.1
1	A	476	GLN	2.1
1	A	674	GLY	2.0

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

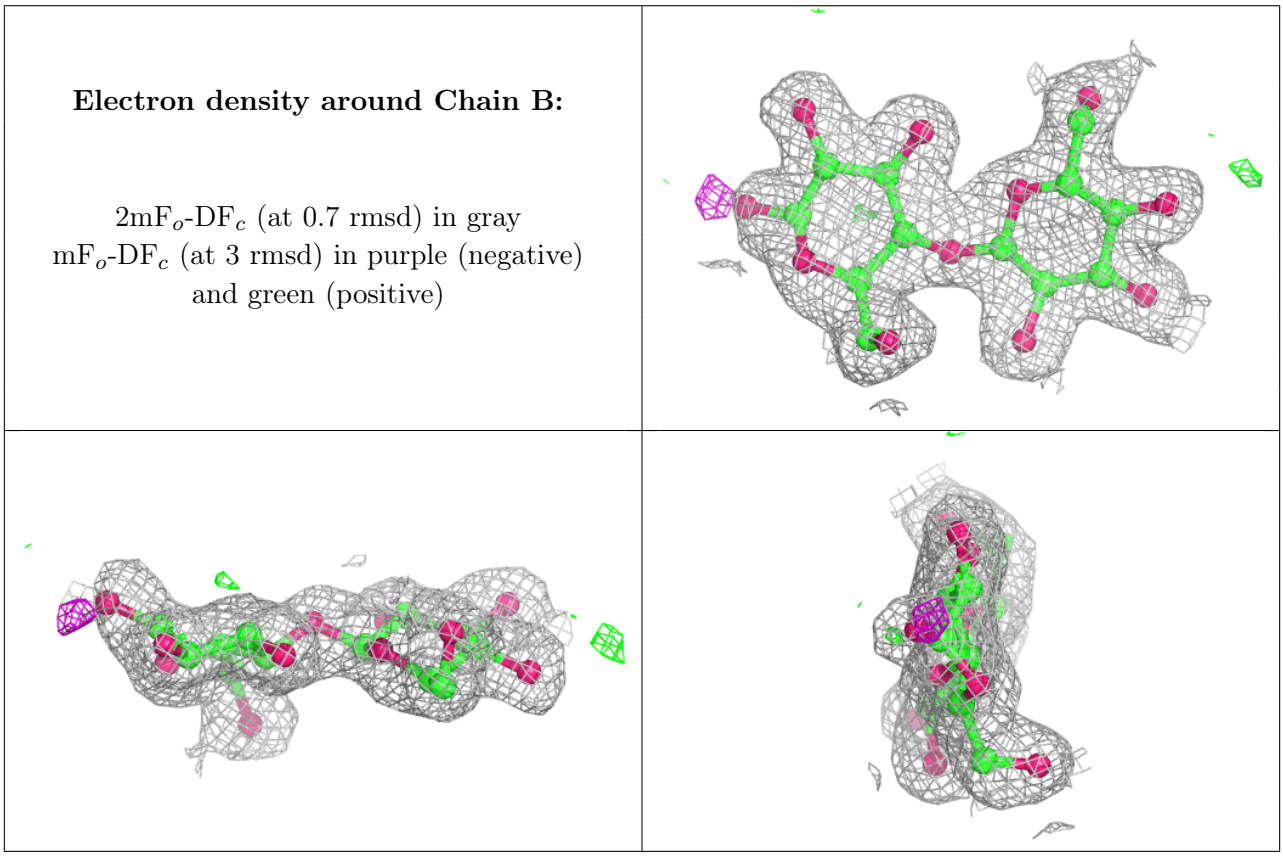
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

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	B	1	12/12	0.94	0.12	24,28,33,42	0
2	BGC	B	2	11/12	0.96	0.12	17,23,26,27	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.



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	ACT	A	815	4/4	0.61	0.38	50,52,53,55	0
7	GOL	A	817	6/6	0.81	0.30	15,17,20,20	6
3	CA	A	803	1/1	0.84	0.36	30,30,30,30	1
5	EDO	A	809	4/4	0.84	0.19	32,33,33,38	4
6	ACT	A	812	4/4	0.85	0.30	43,44,49,50	4
7	GOL	A	818[A]	6/6	0.85	0.34	23,39,42,47	6
7	GOL	A	818[B]	6/6	0.85	0.34	13,17,17,17	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	ACT	A	810	4/4	0.86	0.19	42,44,45,46	0
7	GOL	A	816	6/6	0.87	0.16	25,29,33,36	0
6	ACT	A	813	4/4	0.87	0.20	41,44,44,45	0
6	ACT	A	811	4/4	0.88	0.14	39,39,43,45	0
6	ACT	A	814	4/4	0.89	0.31	32,37,42,45	0
4	MLI	A	806	7/7	0.89	0.14	17,21,28,29	7
4	MLI	A	805	7/7	0.94	0.12	20,21,24,24	7
5	EDO	A	808	4/4	0.95	0.10	26,28,30,31	0
3	CA	A	802	1/1	0.97	0.06	35,35,35,35	1
5	EDO	A	807	4/4	0.97	0.09	15,15,15,16	0
3	CA	A	801	1/1	0.99	0.04	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.