



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 04:13 PM UTC

PDB ID : 3WQ1 / pdb_00003wq1
Title : Structure of hyperthermophilic family 12 endocellulase from *Pyrococcus furiosus* in complex with cello-oligosaccharide
Authors : Kataoka, M.; Ishikawa, K.
Deposited on : 2014-01-21
Resolution : 1.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

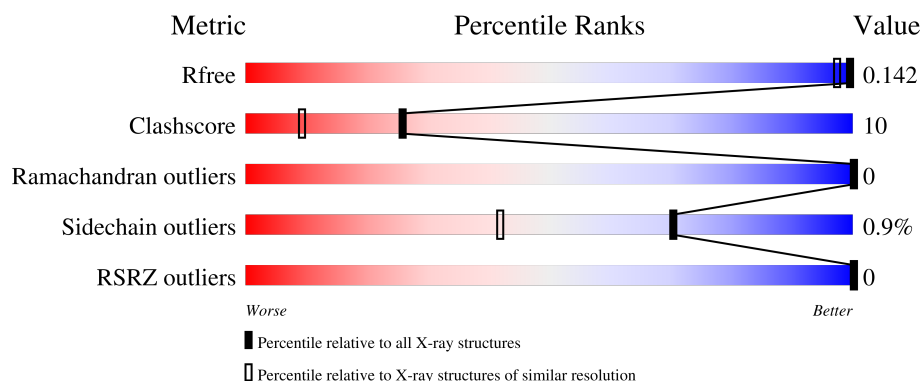
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

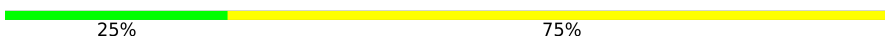
The reported resolution of this entry is 1.30 Å.

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}	180053	1553 (1.30-1.30)
Clashscore	190562	1595 (1.30-1.30)
Ramachandran outliers	187476	1551 (1.30-1.30)
Sidechain outliers	187428	1551 (1.30-1.30)
RSRZ outliers	180081	1549 (1.30-1.30)

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 $\leq 5\%$. 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	319	 71% 12% 15%
2	B	4	 25% 75%

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
4	NHE	A	406	-	X	-	-
4	NHE	A	407	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2760 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 Endoglucanase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	270	Total	C	N	O	S	0	24	0
			2350	1525	375	446	4			

- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.

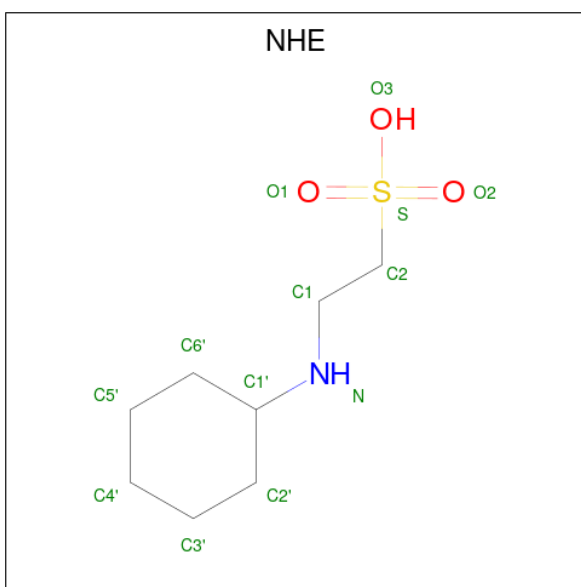


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	B	4	Total	C	O	0	0	0
			45	24	21			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

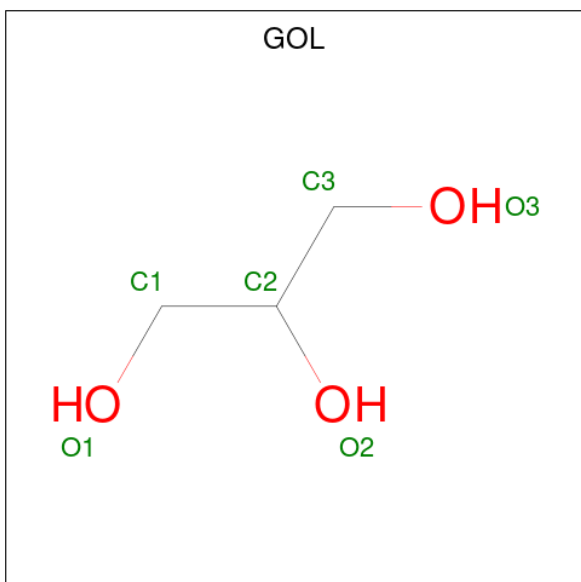
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		

- Molecule 4 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (CCD ID: NHE) (formula: C₈H₁₇NO₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).

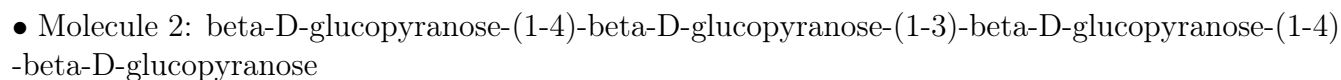


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 6	C 3	O 3	0	0
5	A	1	Total 6	C 3	O 3	0	0
5	A	1	Total 6	C 3	O 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	257	Total 280	O 280	0	23

- Molecule 1: Endoglucanase A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	58.14Å 118.42Å 46.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.91 – 1.30 17.91 – 1.30	Depositor EDS
% Data completeness (in resolution range)	98.1 (17.91-1.30) 98.1 (17.91-1.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.09 (at 1.30Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.112 , 0.139 (Not available) , 0.142	Depositor DCC
R_{free} test set	3956 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	8.1	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	2760	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: NHE, BGC, CA, GOL

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	1.28	7/2420 (0.3%)	1.15	6/3319 (0.2%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	293	THR	CA-C	-9.68	1.43	1.52
1	A	109	GLN	CA-C	-7.46	1.44	1.53
1	A	133	LYS	C-N	6.15	1.39	1.33
1	A	204	TYR	CE2-CZ	5.44	1.51	1.38
1	A	204	TYR	CD2-CE2	5.42	1.54	1.38

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	313	LEU	CA-C-N	-7.13	112.14	122.06
1	A	313	LEU	C-N-CA	-7.13	112.14	122.06
1	A	150	LYS	CG-CD-CE	-6.90	95.42	111.30
1	A	99	LEU	O-C-N	-5.09	115.61	122.43
1	A	69	LYS	CD-CE-NZ	5.08	128.16	111.90

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	2350	0	2270	39	0
2	B	45	0	38	0	0
3	A	2	0	0	0	0
4	A	65	0	84	12	0
5	A	18	0	24	6	0
6	A	280	0	0	19	0
All	All	2760	0	2416	47	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 10.

The worst 5 of 47 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)
5:A:410:GOL:H31	6:A:741:HOH:O	1.12	1.26
4:A:407:NHE:C2	6:A:757:HOH:O	1.86	1.22
1:A:204:TYR:CE2	6:A:737:HOH:O	1.99	1.14
1:A:307[B]:ASN:OD1	6:A:513:HOH:O	1.64	1.14
1:A:97[B]:TYR:HE1	4:A:407:NHE:H4'1	1.15	1.11

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	292/319 (92%)	285 (98%)	7 (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
1	A	257/284 (90%)	255 (99%)	2 (1%)	73 45

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LYS
1	A	69	LYS

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

Mol	Chain	Res	Type
1	A	208	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](#)

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	B	1	2	12,12,12	1.46	2 (16%)	17,17,17	1.80	3 (17%)
2	BGC	B	2	2	11,11,12	1.41	2 (18%)	15,15,17	1.29	2 (13%)
2	BGC	B	3	2	11,11,12	1.16	0	15,15,17	1.02	0
2	BGC	B	4	2	11,11,12	0.82	0	15,15,17	0.99	1 (6%)

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
2	BGC	B	3	2	-	0/2/19/22	0/1/1/1
2	BGC	B	4	2	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	BGC	C2-C3	3.34	1.57	1.52
2	B	1	BGC	O5-C1	3.33	1.51	1.42
2	B	1	BGC	C1-C2	2.80	1.58	1.52
2	B	2	BGC	C4-C5	-2.02	1.48	1.53

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	BGC	O5-C1-C2	-5.99	99.76	110.30
2	B	2	BGC	C3-C4-C5	2.66	115.06	110.23
2	B	1	BGC	O1-C1-O5	-2.56	102.82	110.41
2	B	4	BGC	C1-C2-C3	-2.15	106.51	109.64
2	B	1	BGC	O2-C2-C1	-2.15	104.27	109.25

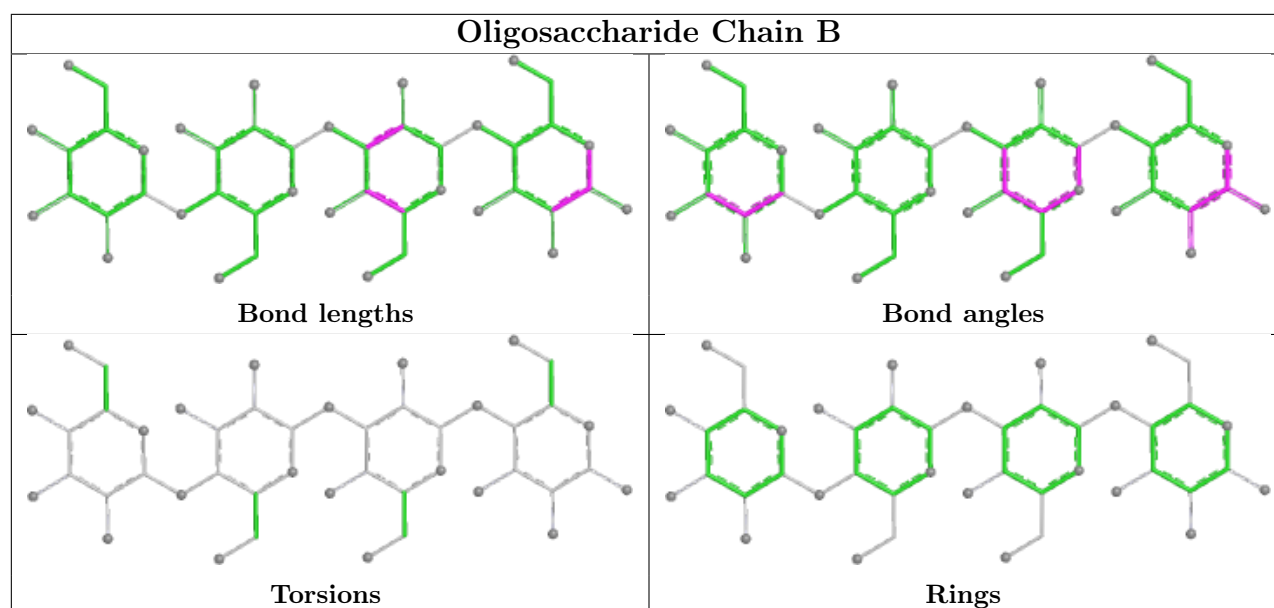
There are no chirality outliers.

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.



5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	NHE	A	404	-	13,13,13	1.84	3 (23%)	16,17,17	1.95	6 (37%)
4	NHE	A	405	-	13,13,13	1.76	3 (23%)	16,17,17	1.94	4 (25%)
4	NHE	A	407	-	13,13,13	1.51	2 (15%)	16,17,17	2.69	7 (43%)
4	NHE	A	403	-	13,13,13	3.02	2 (15%)	16,17,17	1.34	2 (12%)
5	GOL	A	409	-	5,5,5	0.92	0	5,5,5	1.18	0
5	GOL	A	410	-	5,5,5	0.71	0	5,5,5	1.49	1 (20%)
5	GOL	A	408	-	5,5,5	0.40	0	5,5,5	1.15	0
4	NHE	A	406	-	13,13,13	2.81	3 (23%)	16,17,17	4.60	13 (81%)

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	NHE	A	404	-	-	1/7/15/15	0/1/1/1
4	NHE	A	405	-	-	0/7/15/15	0/1/1/1
4	NHE	A	407	-	-	0/7/15/15	0/1/1/1
4	NHE	A	403	-	-	4/7/15/15	0/1/1/1
5	GOL	A	409	-	-	2/4/4/4	-
5	GOL	A	410	-	-	2/4/4/4	-
5	GOL	A	408	-	-	4/4/4/4	-
4	NHE	A	406	-	-	4/7/15/15	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	403	NHE	C2-S	-8.95	1.65	1.77
4	A	406	NHE	C2-S	-7.59	1.67	1.77
4	A	403	NHE	O3-S	5.66	1.68	1.47
4	A	406	NHE	O1-S	-5.20	1.30	1.45
4	A	405	NHE	C2-S	-4.40	1.71	1.77

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	406	NHE	O1-S-C2	11.70	124.42	106.73
4	A	407	NHE	O2-S-C2	7.50	118.06	106.73
4	A	406	NHE	C1-N-C1'	7.15	127.95	114.18
4	A	406	NHE	C6'-C1'-C2'	6.08	121.30	110.80
4	A	406	NHE	O2-S-C2	-4.68	99.66	106.73

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	404	NHE	C2'-C1'-N-C1
4	A	406	NHE	C2'-C1'-N-C1
5	A	408	GOL	O1-C1-C2-C3
5	A	408	GOL	C1-C2-C3-O3
5	A	409	GOL	O1-C1-C2-C3

There are no ring outliers.

5 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	407	NHE	11	0
5	A	409	GOL	1	0
5	A	410	GOL	2	0
5	A	408	GOL	3	0
4	A	406	NHE	1	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	270/319 (84%)	-0.73	0 100 100	4, 9, 19, 48	24 (8%)

There are no RSRZ outliers to report.

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

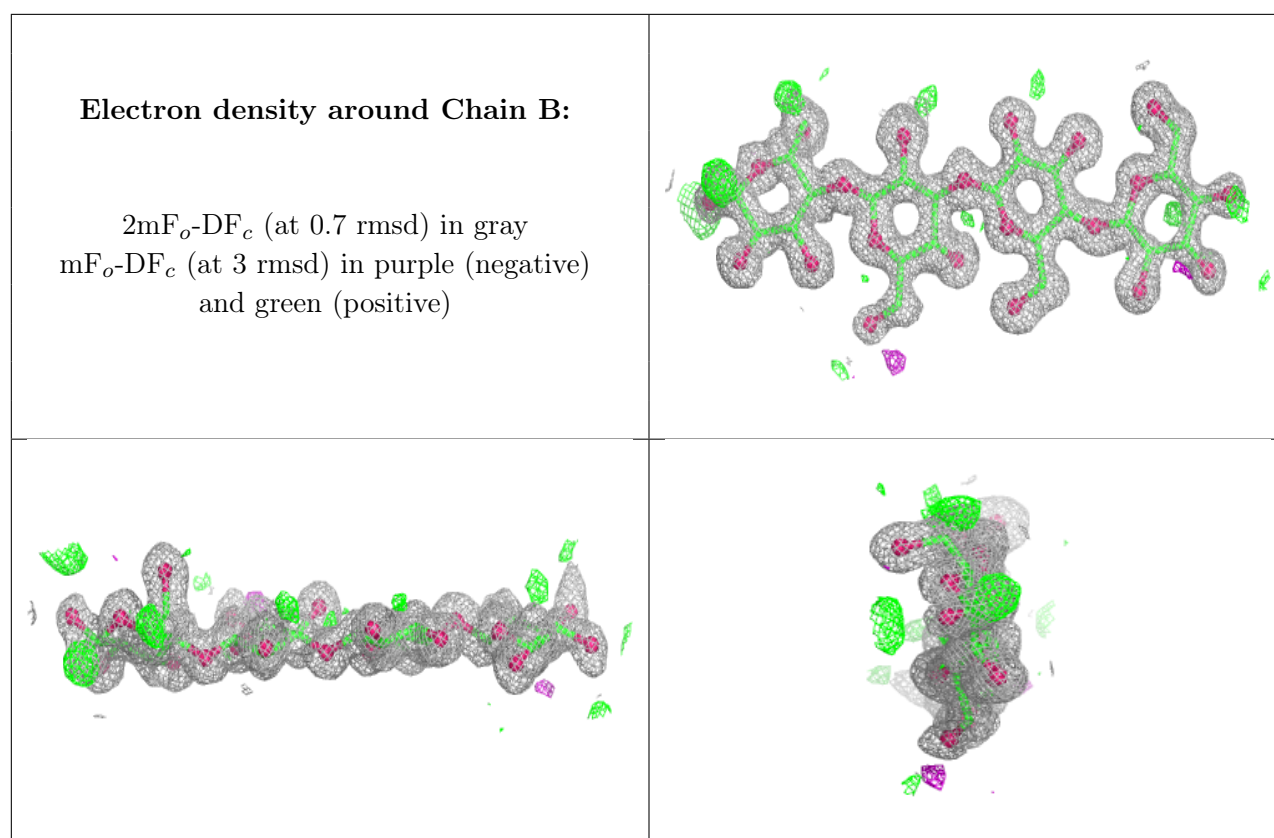
There are no non-standard protein/DNA/RNA residues in this entry.

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	0.98	0.04	6,9,14,22	12
2	BGC	B	4	11/12	0.98	0.06	11,12,20,22	11
2	BGC	B	3	11/12	0.99	0.04	8,8,11,13	11
2	BGC	B	2	11/12	0.99	0.04	6,8,12,20	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($\text{\AA}^2$)	Q<0.9
4	NHE	A	407	13/13	0.88	0.13	13,15,28,30	13
5	GOL	A	410	6/6	0.88	0.12	17,22,25,27	6
4	NHE	A	403	13/13	0.94	0.09	15,17,70,85	0
5	GOL	A	409	6/6	0.94	0.12	20,38,51,56	6
4	NHE	A	405	13/13	0.94	0.10	14,16,19,26	13
4	NHE	A	406	13/13	0.96	0.10	11,16,20,27	13
5	GOL	A	408	6/6	0.97	0.08	16,38,40,47	6
4	NHE	A	404	13/13	0.98	0.07	12,14,21,27	13
3	CA	A	401	1/1	1.00	0.02	8,8,8,8	0
3	CA	A	402	1/1	1.00	0.02	6,6,6,6	1

6.5 Other polymers [i](#)

There are no such residues in this entry.