



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 10:06 AM UTC

PDB ID : 5E24 / pdb\_00005e24  
Title : Structure of the Su(H)-Hairless-DNA Repressor Complex  
Authors : Kovall, R.A.; Yuan, Z.  
Deposited on : 2015-09-30  
Resolution : 2.14 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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>.

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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

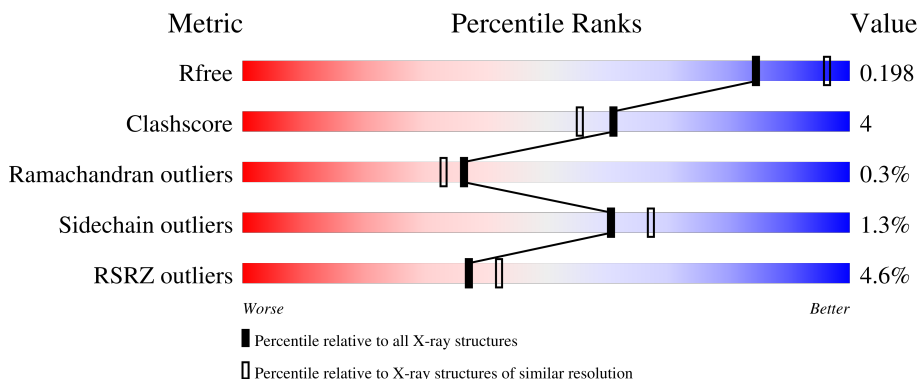
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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  $\geq 3$ , 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	370	
1	C	370	
2	B	38	
2	D	38	
3	E	424	

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Mol	Chain	Length	Quality of chain
3	F	424	
4	G	15	
5	H	15	
6	I	4	
6	J	4	

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
7	EDO	E	623	-	-	X	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 14968 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 Maltose-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	370	Total	C	N	O	S	0	5	0
			2876	1849	470	551	6			
1	C	370	Total	C	N	O	S	0	2	0
			2851	1835	466	544	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	ALA	ASP	engineered mutation	UNP P0AEY0
A	83	ALA	LYS	engineered mutation	UNP P0AEY0
A	172	ALA	GLU	engineered mutation	UNP P0AEY0
A	173	ALA	ASN	engineered mutation	UNP P0AEY0
A	239	ALA	LYS	engineered mutation	UNP P0AEY0
A	367	ASN	ARG	engineered mutation	UNP P0AEY0
C	82	ALA	ASP	engineered mutation	UNP P0AEY0
C	83	ALA	LYS	engineered mutation	UNP P0AEY0
C	172	ALA	GLU	engineered mutation	UNP P0AEY0
C	173	ALA	ASN	engineered mutation	UNP P0AEY0
C	239	ALA	LYS	engineered mutation	UNP P0AEY0
C	367	ASN	ARG	engineered mutation	UNP P0AEY0

- Molecule 2 is a protein called Protein hairless.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	38	Total	C	N	O	0	0	0
			292	189	55	48			
2	D	38	Total	C	N	O	0	0	0
			292	189	55	48			

- Molecule 3 is a protein called Suppressor of hairless protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	424	3445	2180	595	641	29	0	11	0
3	F	422	3392	2146	583	634	29	0	5	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	155	THR	ARG	engineered mutation	UNP P28159
E	281	GLY	ASN	engineered mutation	UNP P28159
F	155	THR	ARG	engineered mutation	UNP P28159
F	281	GLY	ASN	engineered mutation	UNP P28159

- Molecule 4 is a DNA chain called DNA (5'-D(\*AP\*AP\*TP\*CP\*TP\*TP\*TP\*CP\*CP\*CP\*AP\*CP\*AP\*GP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	G	15	298	145	50	89	14	0	0	0

- Molecule 5 is a DNA chain called DNA (5'-D(\*TP\*TP\*AP\*CP\*TP\*GP\*TP\*GP\*GP\*GP\*AP\*AP\*AP\*GP\*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	H	15	311	149	61	87	14	0	0	0

- Molecule 6 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
6	I	4	45	24	21	0	0	0
6	J	4	45	24	21	0	0	0

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	D	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0
7	E	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		

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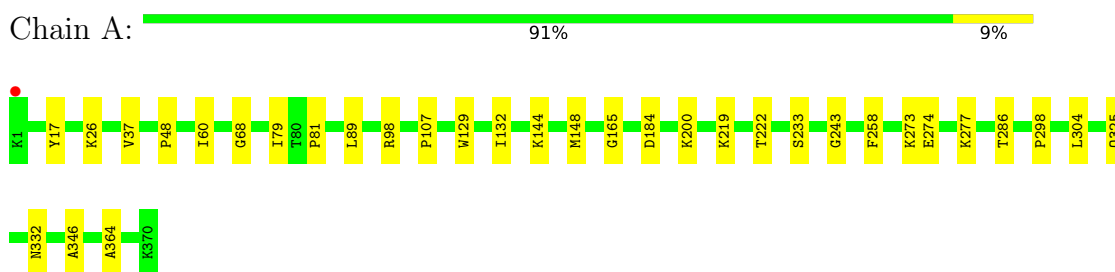
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
8	E	174	Total 174	O 174	0	0
8	F	80	Total 80	O 80	0	0
8	G	6	Total 6	O 6	0	0
8	H	13	Total 13	O 13	0	0

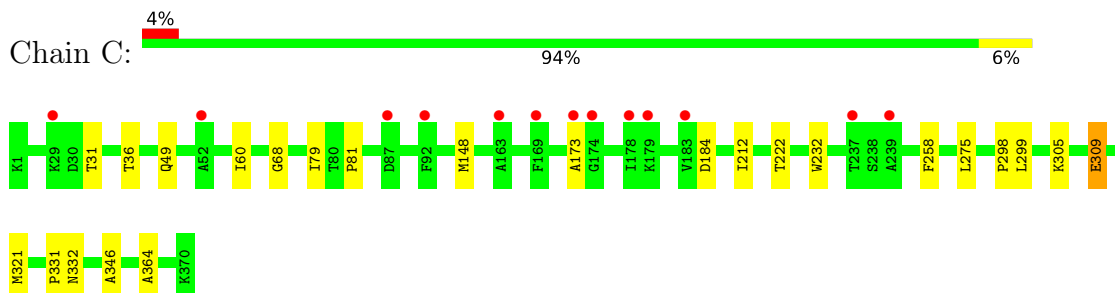
### 3 Residue-property plots [i](#)

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.

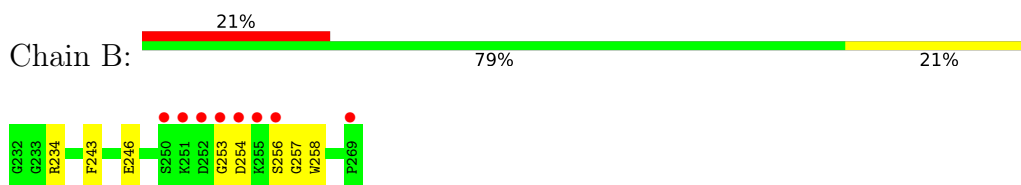
- Molecule 1: Maltose-binding periplasmic protein



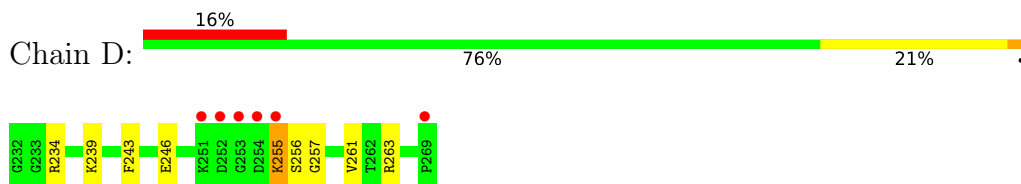
- Molecule 1: Maltose-binding periplasmic protein



- Molecule 2: Protein hairless

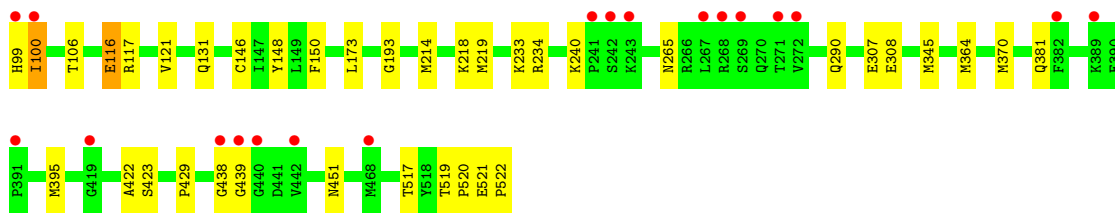


- Molecule 2: Protein hairless

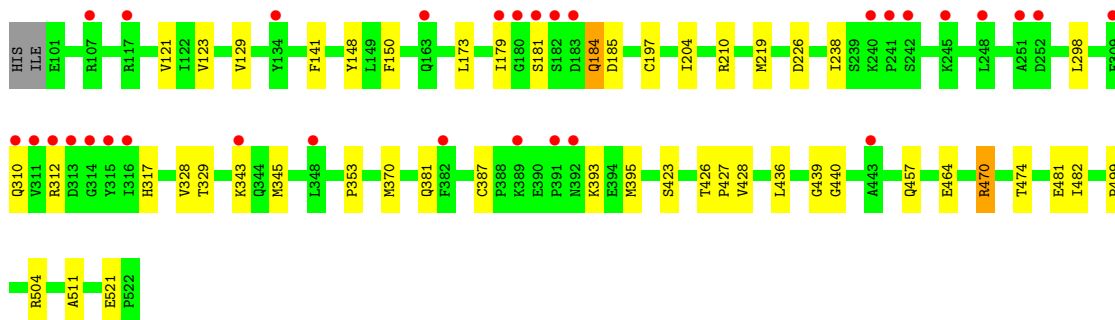
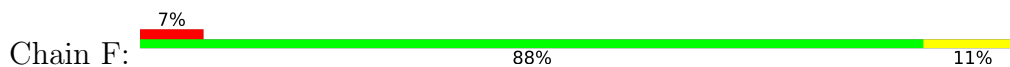


- Molecule 3: Suppressor of hairless protein

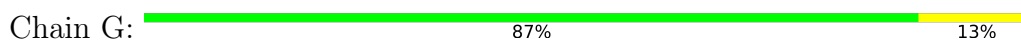




• Molecule 3: Suppressor of hairless protein



• Molecule 4: DNA (5'-D(\*AP\*AP\*TP\*CP\*TP\*TP\*TP\*CP\*CP\*CP\*AP\*CP\*AP\*GP\*T)-3')

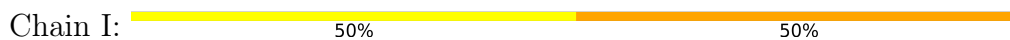


• Molecule 5: DNA (5'-D(\*TP\*TP\*AP\*CP\*TP\*GP\*TP\*GP\*GP\*GP\*AP\*AP\*AP\*GP\*A)-3')

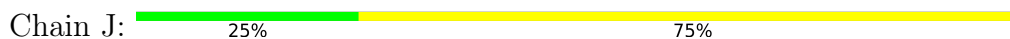


There are no outlier residues recorded for this chain.

• Molecule 6: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



• Molecule 6: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



GLC1  
GLC2  
GLC3  
GLC4

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	177.71Å 93.89Å 154.39Å 90.00° 109.83° 90.00°	Depositor
Resolution (Å)	31.30 – 2.14 31.30 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.6 (31.30-2.14) 100.0 (31.30-2.14)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 2.14Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, $R_{free}$	0.173 , 0.193 0.175 , 0.198	Depositor DCC
$R_{free}$ test set	6595 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.2	Xtrriage
Anisotropy	0.122	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 49.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14968	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.92	0/2945	1.11	1/4004 (0.0%)
1	C	0.82	0/2920	1.18	2/3971 (0.1%)
2	B	0.72	0/299	1.06	0/400
2	D	0.77	0/299	1.15	2/400 (0.5%)
3	E	0.76	0/3525	1.05	0/4763
3	F	0.76	0/3467	1.10	6/4684 (0.1%)
4	G	0.48	0/332	0.65	0/509
5	H	0.50	0/350	0.64	0/540
All	All	0.80	0/14137	1.09	11/19271 (0.1%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	255	LYS	CA-C-N	7.48	135.17	121.70
2	D	255	LYS	C-N-CA	7.48	135.17	121.70
3	F	184	GLN	CA-C-N	6.16	133.31	121.54
3	F	184	GLN	C-N-CA	6.16	133.31	121.54
3	F	310	GLN	N-CA-C	5.63	117.59	110.33

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	2876	0	2819	27	0
1	C	2851	0	2797	16	0
2	B	292	0	287	5	0
2	D	292	0	287	7	0
3	E	3445	0	3383	30	0
3	F	3392	0	3342	27	0
4	G	298	0	172	3	0
5	H	311	0	171	0	0
6	I	45	0	39	2	0
6	J	45	0	39	0	0
7	A	192	0	288	23	0
7	C	56	0	84	10	0
7	D	8	0	12	1	0
7	E	96	0	144	18	0
7	F	100	0	150	10	0
8	A	283	0	0	0	0
8	B	8	0	0	0	0
8	C	96	0	0	0	0
8	D	9	0	0	0	0
8	E	174	0	0	0	0
8	F	80	0	0	1	0
8	G	6	0	0	0	0
8	H	13	0	0	0	0
All	All	14968	0	14014	118	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 4.

The worst 5 of 118 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:290:GLN:HA	7:E:623:EDO:H12	1.42	0.99
4:G:1:DA:H2''	4:G:2:DA:H5''	1.46	0.95
3:F:345:MET:HE1	3:F:387:CYS:HB2	1.51	0.92
3:E:146[B]:CYS:SG	7:E:623:EDO:H11	2.18	0.84
1:C:299:LEU:HD23	7:C:403:EDO:H22	1.60	0.83

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	373/370 (101%)	369 (99%)	4 (1%)	0	100	100
1	C	370/370 (100%)	362 (98%)	7 (2%)	1 (0%)	36	33
2	B	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
2	D	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
3	E	433/424 (102%)	422 (98%)	10 (2%)	1 (0%)	43	42
3	F	425/424 (100%)	415 (98%)	7 (2%)	3 (1%)	18	13
All	All	1673/1664 (100%)	1632 (98%)	36 (2%)	5 (0%)	36	33

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	185	ASP
1	C	173	ALA
3	E	100	ILE
3	F	343	LYS
3	F	439	GLY

### 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	291/292 (100%)	289 (99%)	2 (1%)	76	81
1	C	287/292 (98%)	284 (99%)	3 (1%)	68	74
2	B	28/32 (88%)	27 (96%)	1 (4%)	31	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	28/32 (88%)	27 (96%)	1 (4%)	31	30
3	E	378/370 (102%)	373 (99%)	5 (1%)	61	67
3	F	373/370 (101%)	366 (98%)	7 (2%)	50	55
All	All	1385/1388 (100%)	1366 (99%)	19 (1%)	61	65

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	226	ASP
3	F	470[B]	ARG
3	F	521	GLU
3	F	470[A]	ARG
3	E	240	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	392	ASN
3	F	265	ASN
3	F	437	ASN
1	C	72	GLN
3	E	131	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](#)

8 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
6	GLC	I	1	6	12,12,12	0.70	0	17,17,17	1.00	1 (5%)
6	GLC	I	2	6	11,11,12	1.13	1 (9%)	15,15,17	1.06	2 (13%)
6	GLC	I	3	6	11,11,12	0.71	0	15,15,17	1.23	1 (6%)
6	GLC	I	4	6	11,11,12	0.63	0	15,15,17	1.28	2 (13%)
6	GLC	J	1	6	12,12,12	0.61	0	17,17,17	1.01	0
6	GLC	J	2	6	11,11,12	0.98	0	15,15,17	1.10	1 (6%)
6	GLC	J	3	6	11,11,12	0.70	0	15,15,17	1.13	1 (6%)
6	GLC	J	4	6	11,11,12	0.53	0	15,15,17	1.21	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
6	GLC	I	1	6	-	0/2/22/22	0/1/1/1
6	GLC	I	2	6	-	0/2/19/22	0/1/1/1
6	GLC	I	3	6	-	0/2/19/22	0/1/1/1
6	GLC	I	4	6	-	2/2/19/22	0/1/1/1
6	GLC	J	1	6	-	0/2/22/22	0/1/1/1
6	GLC	J	2	6	-	0/2/19/22	0/1/1/1
6	GLC	J	3	6	-	0/2/19/22	0/1/1/1
6	GLC	J	4	6	-	2/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	I	2	GLC	C2-C3	2.01	1.55	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	I	3	GLC	C6-C5-C4	-2.91	105.88	113.02
6	J	3	GLC	C6-C5-C4	-2.71	106.37	113.02
6	J	4	GLC	C2-C3-C4	-2.67	106.16	110.86
6	I	4	GLC	O5-C5-C6	-2.60	102.60	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	4	GLC	O5-C5-C6	-2.56	102.69	107.66

There are no chirality outliers.

All (4) torsion outliers are listed below:

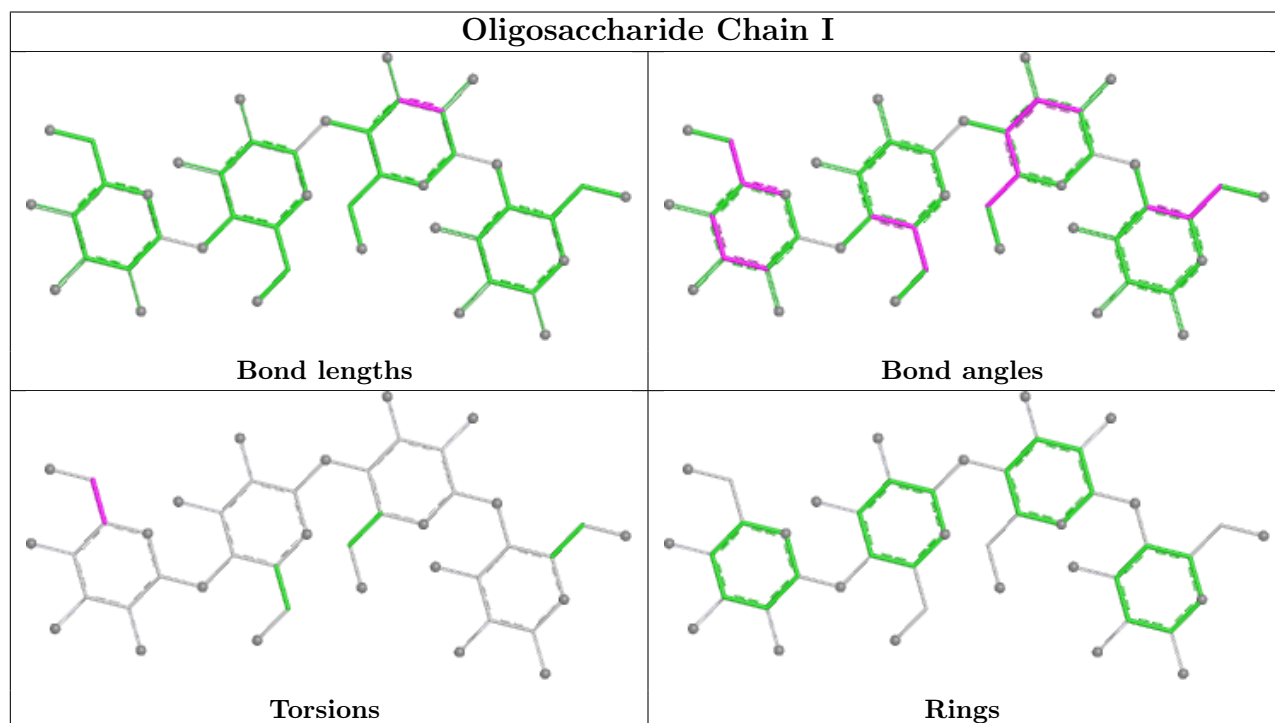
Mol	Chain	Res	Type	Atoms
6	I	4	GLC	C4-C5-C6-O6
6	J	4	GLC	C4-C5-C6-O6
6	J	4	GLC	O5-C5-C6-O6
6	I	4	GLC	O5-C5-C6-O6

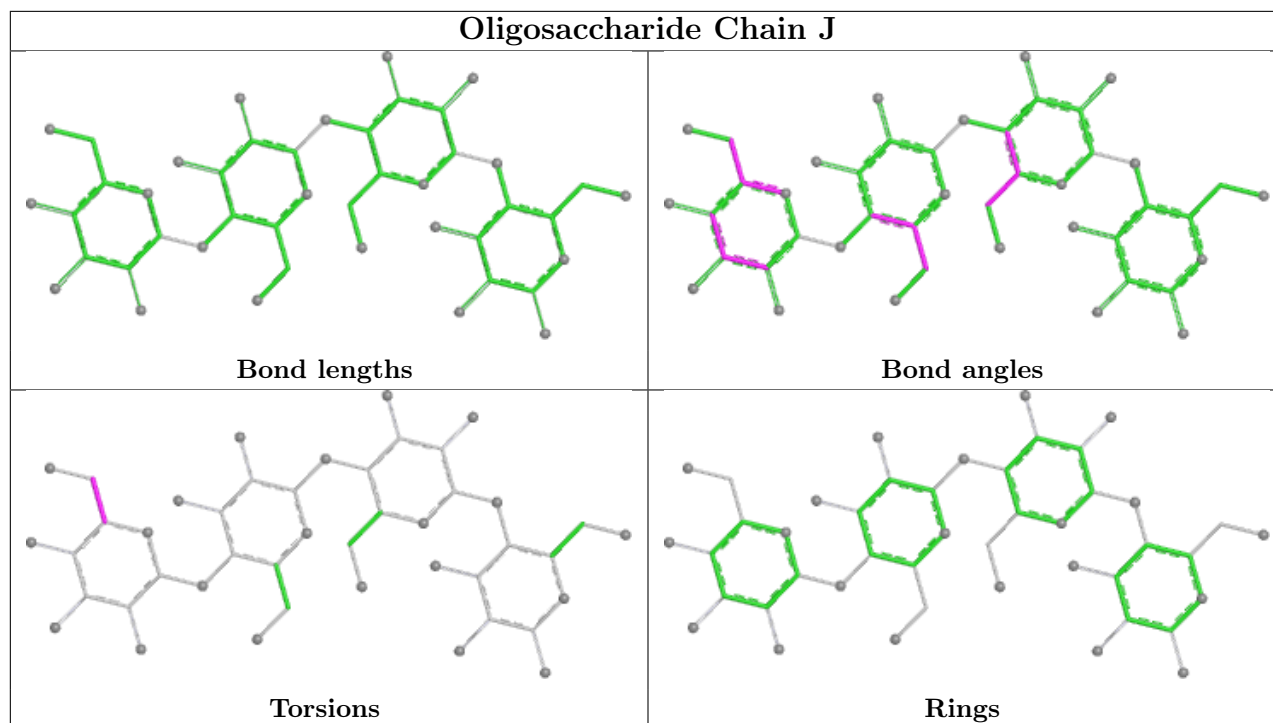
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	I	3	GLC	2	0
6	I	4	GLC	1	0

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](#)

113 ligands 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	$\# Z  > 2$
7	EDO	C	404	-	3,3,3	0.43	0	2,2,2	0.53	0
7	EDO	A	419	-	3,3,3	0.56	0	2,2,2	0.24	0
7	EDO	C	411	-	3,3,3	0.58	0	2,2,2	0.32	0
7	EDO	A	409	-	3,3,3	0.46	0	2,2,2	0.33	0
7	EDO	A	401	-	3,3,3	0.45	0	2,2,2	0.25	0
7	EDO	A	408	-	3,3,3	0.46	0	2,2,2	0.73	0
7	EDO	A	444	-	3,3,3	0.59	0	2,2,2	0.14	0
7	EDO	A	411	-	3,3,3	0.51	0	2,2,2	0.32	0
7	EDO	A	415	-	3,3,3	0.49	0	2,2,2	0.40	0
7	EDO	A	421	-	3,3,3	0.49	0	2,2,2	0.46	0
7	EDO	E	604	-	3,3,3	0.44	0	2,2,2	0.38	0
7	EDO	A	405	-	3,3,3	0.55	0	2,2,2	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	EDO	C	406	-	3,3,3	0.57	0	2,2,2	0.30	0
7	EDO	A	437	-	3,3,3	0.37	0	2,2,2	0.46	0
7	EDO	E	612	-	3,3,3	0.55	0	2,2,2	0.25	0
7	EDO	E	623	-	3,3,3	0.61	0	2,2,2	0.03	0
7	EDO	F	621	-	3,3,3	0.53	0	2,2,2	0.28	0
7	EDO	A	404	-	3,3,3	0.39	0	2,2,2	0.55	0
7	EDO	F	612	-	3,3,3	0.45	0	2,2,2	0.48	0
7	EDO	E	615	-	3,3,3	0.62	0	2,2,2	0.25	0
7	EDO	A	423	-	3,3,3	0.49	0	2,2,2	0.20	0
7	EDO	C	401	-	3,3,3	0.46	0	2,2,2	0.33	0
7	EDO	C	402	-	3,3,3	0.55	0	2,2,2	0.34	0
7	EDO	D	302	-	3,3,3	0.51	0	2,2,2	0.34	0
7	EDO	A	418	-	3,3,3	0.49	0	2,2,2	0.44	0
7	EDO	A	445	-	3,3,3	0.53	0	2,2,2	0.37	0
7	EDO	A	417	-	3,3,3	0.80	0	2,2,2	0.13	0
7	EDO	F	602	-	3,3,3	0.57	0	2,2,2	0.45	0
7	EDO	E	618	-	3,3,3	0.41	0	2,2,2	0.25	0
7	EDO	E	609	-	3,3,3	0.48	0	2,2,2	0.36	0
7	EDO	A	427	-	3,3,3	0.41	0	2,2,2	0.54	0
7	EDO	E	617	-	3,3,3	0.54	0	2,2,2	0.26	0
7	EDO	F	617	-	3,3,3	0.47	0	2,2,2	0.35	0
7	EDO	C	410	-	3,3,3	0.54	0	2,2,2	0.17	0
7	EDO	E	613	-	3,3,3	0.42	0	2,2,2	0.48	0
7	EDO	A	433	-	3,3,3	0.49	0	2,2,2	0.29	0
7	EDO	E	605	-	3,3,3	0.41	0	2,2,2	0.53	0
7	EDO	A	439	-	3,3,3	0.57	0	2,2,2	0.18	0
7	EDO	C	408	-	3,3,3	0.59	0	2,2,2	0.26	0
7	EDO	E	619	-	3,3,3	0.51	0	2,2,2	0.34	0
7	EDO	A	435	-	3,3,3	0.46	0	2,2,2	0.28	0
7	EDO	F	613	-	3,3,3	0.53	0	2,2,2	0.24	0
7	EDO	E	610	-	3,3,3	0.41	0	2,2,2	0.45	0
7	EDO	F	607	-	3,3,3	0.43	0	2,2,2	0.65	0
7	EDO	F	625	-	3,3,3	0.50	0	2,2,2	0.41	0
7	EDO	F	604	-	3,3,3	0.50	0	2,2,2	0.38	0
7	EDO	A	422	-	3,3,3	0.63	0	2,2,2	0.19	0
7	EDO	C	409	-	3,3,3	0.55	0	2,2,2	0.35	0
7	EDO	F	605	-	3,3,3	0.58	0	2,2,2	0.16	0
7	EDO	A	403	-	3,3,3	0.53	0	2,2,2	0.84	0
7	EDO	F	614	-	3,3,3	0.52	0	2,2,2	0.17	0
7	EDO	A	425	-	3,3,3	0.59	0	2,2,2	0.43	0
7	EDO	A	424	-	3,3,3	0.63	0	2,2,2	0.02	0
7	EDO	A	441	-	3,3,3	0.48	0	2,2,2	0.24	0
7	EDO	A	440	-	3,3,3	0.50	0	2,2,2	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	EDO	A	416	-	3,3,3	0.61	0	2,2,2	0.23	0
7	EDO	F	615	-	3,3,3	0.51	0	2,2,2	0.34	0
7	EDO	A	426	-	3,3,3	0.62	0	2,2,2	0.29	0
7	EDO	C	412	-	3,3,3	0.54	0	2,2,2	0.30	0
7	EDO	A	414	-	3,3,3	0.57	0	2,2,2	0.19	0
7	EDO	F	618	-	3,3,3	0.51	0	2,2,2	0.28	0
7	EDO	F	609	-	3,3,3	0.58	0	2,2,2	0.25	0
7	EDO	F	624	-	3,3,3	0.42	0	2,2,2	0.67	0
7	EDO	A	446	-	3,3,3	0.55	0	2,2,2	0.42	0
7	EDO	C	407	-	3,3,3	0.59	0	2,2,2	0.28	0
7	EDO	E	607	-	3,3,3	0.52	0	2,2,2	0.29	0
7	EDO	A	429	-	3,3,3	0.67	0	2,2,2	0.35	0
7	EDO	E	614	-	3,3,3	0.51	0	2,2,2	0.42	0
7	EDO	F	606	-	3,3,3	0.50	0	2,2,2	0.37	0
7	EDO	A	430	-	3,3,3	0.33	0	2,2,2	0.60	0
7	EDO	C	413	-	3,3,3	0.50	0	2,2,2	0.62	0
7	EDO	A	402	-	3,3,3	0.38	0	2,2,2	0.60	0
7	EDO	E	621	-	3,3,3	0.51	0	2,2,2	0.54	0
7	EDO	E	616	-	3,3,3	0.44	0	2,2,2	0.51	0
7	EDO	F	622	-	3,3,3	0.64	0	2,2,2	0.17	0
7	EDO	C	414	-	3,3,3	0.51	0	2,2,2	0.41	0
7	EDO	A	420	-	3,3,3	0.45	0	2,2,2	0.49	0
7	EDO	A	443	-	3,3,3	0.47	0	2,2,2	0.46	0
7	EDO	A	432	-	3,3,3	0.53	0	2,2,2	0.13	0
7	EDO	A	410	-	3,3,3	0.50	0	2,2,2	0.26	0
7	EDO	E	603	-	3,3,3	0.52	0	2,2,2	0.29	0
7	EDO	F	619	-	3,3,3	0.51	0	2,2,2	0.28	0
7	EDO	A	431	-	3,3,3	0.47	0	2,2,2	0.29	0
7	EDO	F	611	-	3,3,3	0.57	0	2,2,2	0.29	0
7	EDO	D	301	-	3,3,3	0.49	0	2,2,2	0.37	0
7	EDO	A	413	-	3,3,3	0.43	0	2,2,2	0.33	0
7	EDO	F	610	-	3,3,3	0.62	0	2,2,2	0.45	0
7	EDO	E	608	-	3,3,3	0.52	0	2,2,2	0.48	0
7	EDO	F	616	-	3,3,3	0.42	0	2,2,2	0.28	0
7	EDO	E	620	-	3,3,3	0.41	0	2,2,2	0.56	0
7	EDO	A	436	-	3,3,3	0.31	0	2,2,2	0.48	0
7	EDO	A	412	-	3,3,3	0.48	0	2,2,2	0.47	0
7	EDO	E	624	-	3,3,3	0.57	0	2,2,2	0.28	0
7	EDO	F	601	-	3,3,3	0.52	0	2,2,2	0.39	0
7	EDO	F	603	-	3,3,3	0.52	0	2,2,2	0.32	0
7	EDO	F	623	-	3,3,3	0.50	0	2,2,2	0.36	0
7	EDO	E	611	-	3,3,3	0.60	0	2,2,2	0.21	0
7	EDO	F	620	-	3,3,3	0.50	0	2,2,2	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	EDO	A	438	-	3,3,3	0.68	0	2,2,2	0.14	0
7	EDO	A	428	-	3,3,3	0.53	0	2,2,2	0.26	0
7	EDO	A	407	-	3,3,3	0.59	0	2,2,2	0.30	0
7	EDO	E	606	-	3,3,3	0.47	0	2,2,2	0.46	0
7	EDO	C	403	-	3,3,3	0.36	0	2,2,2	0.43	0
7	EDO	E	602	-	3,3,3	0.50	0	2,2,2	0.45	0
7	EDO	F	608	-	3,3,3	0.52	0	2,2,2	0.46	0
7	EDO	C	405	-	3,3,3	0.43	0	2,2,2	0.53	0
7	EDO	A	448	-	3,3,3	0.49	0	2,2,2	0.34	0
7	EDO	A	442	-	3,3,3	0.56	0	2,2,2	0.37	0
7	EDO	A	434	-	3,3,3	0.57	0	2,2,2	0.62	0
7	EDO	A	406	-	3,3,3	0.37	0	2,2,2	0.44	0
7	EDO	A	447	-	3,3,3	0.46	0	2,2,2	0.41	0
7	EDO	E	622	-	3,3,3	0.45	0	2,2,2	0.40	0
7	EDO	E	601	-	3,3,3	0.60	0	2,2,2	0.36	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
7	EDO	C	404	-	-	0/1/1/1	-
7	EDO	A	419	-	-	1/1/1/1	-
7	EDO	C	411	-	-	1/1/1/1	-
7	EDO	A	409	-	-	1/1/1/1	-
7	EDO	A	401	-	-	0/1/1/1	-
7	EDO	A	408	-	-	0/1/1/1	-
7	EDO	A	444	-	-	0/1/1/1	-
7	EDO	A	411	-	-	0/1/1/1	-
7	EDO	A	415	-	-	0/1/1/1	-
7	EDO	A	421	-	-	0/1/1/1	-
7	EDO	E	604	-	-	0/1/1/1	-
7	EDO	A	405	-	-	0/1/1/1	-
7	EDO	C	406	-	-	1/1/1/1	-
7	EDO	A	437	-	-	1/1/1/1	-
7	EDO	E	612	-	-	1/1/1/1	-
7	EDO	E	623	-	-	1/1/1/1	-
7	EDO	F	621	-	-	0/1/1/1	-
7	EDO	A	404	-	-	1/1/1/1	-
7	EDO	F	612	-	-	0/1/1/1	-
7	EDO	E	615	-	-	0/1/1/1	-
7	EDO	A	423	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	C	401	-	-	0/1/1/1	-
7	EDO	C	402	-	-	0/1/1/1	-
7	EDO	D	302	-	-	1/1/1/1	-
7	EDO	A	418	-	-	0/1/1/1	-
7	EDO	A	445	-	-	0/1/1/1	-
7	EDO	A	417	-	-	1/1/1/1	-
7	EDO	F	602	-	-	0/1/1/1	-
7	EDO	E	618	-	-	0/1/1/1	-
7	EDO	E	609	-	-	1/1/1/1	-
7	EDO	A	427	-	-	1/1/1/1	-
7	EDO	E	617	-	-	0/1/1/1	-
7	EDO	F	617	-	-	1/1/1/1	-
7	EDO	C	410	-	-	1/1/1/1	-
7	EDO	E	613	-	-	0/1/1/1	-
7	EDO	A	433	-	-	0/1/1/1	-
7	EDO	E	605	-	-	0/1/1/1	-
7	EDO	A	439	-	-	0/1/1/1	-
7	EDO	C	408	-	-	0/1/1/1	-
7	EDO	E	619	-	-	0/1/1/1	-
7	EDO	A	435	-	-	0/1/1/1	-
7	EDO	F	613	-	-	0/1/1/1	-
7	EDO	E	610	-	-	0/1/1/1	-
7	EDO	F	607	-	-	0/1/1/1	-
7	EDO	F	625	-	-	0/1/1/1	-
7	EDO	F	604	-	-	0/1/1/1	-
7	EDO	A	422	-	-	0/1/1/1	-
7	EDO	C	409	-	-	0/1/1/1	-
7	EDO	F	605	-	-	0/1/1/1	-
7	EDO	A	403	-	-	0/1/1/1	-
7	EDO	F	614	-	-	1/1/1/1	-
7	EDO	A	425	-	-	1/1/1/1	-
7	EDO	A	424	-	-	1/1/1/1	-
7	EDO	A	441	-	-	0/1/1/1	-
7	EDO	A	440	-	-	0/1/1/1	-
7	EDO	A	416	-	-	1/1/1/1	-
7	EDO	F	615	-	-	1/1/1/1	-
7	EDO	A	426	-	-	0/1/1/1	-
7	EDO	C	412	-	-	0/1/1/1	-
7	EDO	A	414	-	-	1/1/1/1	-
7	EDO	F	618	-	-	0/1/1/1	-
7	EDO	F	609	-	-	0/1/1/1	-
7	EDO	F	624	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	A	446	-	-	1/1/1/1	-
7	EDO	C	407	-	-	0/1/1/1	-
7	EDO	E	607	-	-	1/1/1/1	-
7	EDO	A	429	-	-	1/1/1/1	-
7	EDO	E	614	-	-	0/1/1/1	-
7	EDO	F	606	-	-	0/1/1/1	-
7	EDO	A	430	-	-	1/1/1/1	-
7	EDO	C	413	-	-	0/1/1/1	-
7	EDO	A	402	-	-	0/1/1/1	-
7	EDO	E	621	-	-	0/1/1/1	-
7	EDO	E	616	-	-	1/1/1/1	-
7	EDO	F	622	-	-	1/1/1/1	-
7	EDO	C	414	-	-	0/1/1/1	-
7	EDO	A	420	-	-	0/1/1/1	-
7	EDO	A	443	-	-	0/1/1/1	-
7	EDO	A	432	-	-	1/1/1/1	-
7	EDO	A	410	-	-	1/1/1/1	-
7	EDO	E	603	-	-	0/1/1/1	-
7	EDO	F	619	-	-	0/1/1/1	-
7	EDO	A	431	-	-	0/1/1/1	-
7	EDO	F	611	-	-	0/1/1/1	-
7	EDO	D	301	-	-	0/1/1/1	-
7	EDO	A	413	-	-	1/1/1/1	-
7	EDO	F	610	-	-	1/1/1/1	-
7	EDO	E	608	-	-	0/1/1/1	-
7	EDO	F	616	-	-	0/1/1/1	-
7	EDO	E	620	-	-	0/1/1/1	-
7	EDO	A	436	-	-	1/1/1/1	-
7	EDO	A	412	-	-	0/1/1/1	-
7	EDO	E	624	-	-	1/1/1/1	-
7	EDO	F	601	-	-	0/1/1/1	-
7	EDO	F	603	-	-	0/1/1/1	-
7	EDO	F	623	-	-	1/1/1/1	-
7	EDO	E	611	-	-	1/1/1/1	-
7	EDO	F	620	-	-	0/1/1/1	-
7	EDO	A	438	-	-	1/1/1/1	-
7	EDO	A	428	-	-	0/1/1/1	-
7	EDO	A	407	-	-	0/1/1/1	-
7	EDO	E	606	-	-	0/1/1/1	-
7	EDO	C	403	-	-	0/1/1/1	-
7	EDO	E	602	-	-	1/1/1/1	-
7	EDO	F	608	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	C	405	-	-	0/1/1/1	-
7	EDO	A	448	-	-	0/1/1/1	-
7	EDO	A	442	-	-	0/1/1/1	-
7	EDO	A	434	-	-	0/1/1/1	-
7	EDO	A	406	-	-	1/1/1/1	-
7	EDO	A	447	-	-	0/1/1/1	-
7	EDO	E	622	-	-	1/1/1/1	-
7	EDO	E	601	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	410	EDO	O1-C1-C2-O2
7	A	429	EDO	O1-C1-C2-O2
7	A	436	EDO	O1-C1-C2-O2
7	F	617	EDO	O1-C1-C2-O2
7	A	413	EDO	O1-C1-C2-O2

There are no ring outliers.

45 monomers are involved in 62 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	404	EDO	1	0
7	A	401	EDO	1	0
7	A	421	EDO	1	0
7	E	604	EDO	1	0
7	A	405	EDO	1	0
7	C	406	EDO	1	0
7	A	437	EDO	1	0
7	E	612	EDO	1	0
7	E	623	EDO	6	0
7	A	404	EDO	2	0
7	C	402	EDO	1	0
7	D	302	EDO	1	0
7	E	618	EDO	1	0
7	E	609	EDO	1	0
7	E	617	EDO	1	0
7	E	613	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	433	EDO	1	0
7	E	605	EDO	1	0
7	C	408	EDO	1	0
7	E	619	EDO	1	0
7	F	607	EDO	1	0
7	C	409	EDO	1	0
7	A	425	EDO	3	0
7	F	609	EDO	2	0
7	F	624	EDO	2	0
7	C	407	EDO	2	0
7	E	607	EDO	1	0
7	A	429	EDO	1	0
7	A	430	EDO	2	0
7	F	622	EDO	1	0
7	F	611	EDO	2	0
7	F	610	EDO	1	0
7	E	608	EDO	2	0
7	F	616	EDO	1	0
7	E	620	EDO	1	0
7	A	436	EDO	1	0
7	A	412	EDO	1	0
7	A	438	EDO	1	0
7	A	428	EDO	2	0
7	C	403	EDO	3	0
7	E	602	EDO	1	0
7	A	448	EDO	2	0
7	A	442	EDO	1	0
7	A	434	EDO	3	0
7	A	447	EDO	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	370/370 (100%)	-0.66	1 (0%) 90 92	13, 30, 51, 82	5 (1%)
1	C	370/370 (100%)	0.36	13 (3%) 47 51	18, 59, 99, 123	2 (0%)
2	B	38/38 (100%)	0.77	8 (21%) 2 3	36, 58, 118, 122	0
2	D	38/38 (100%)	0.75	6 (15%) 5 6	38, 56, 114, 116	0
3	E	424/424 (100%)	0.00	19 (4%) 38 43	16, 44, 83, 122	11 (2%)
3	F	422/424 (99%)	0.54	31 (7%) 21 24	17, 59, 115, 161	5 (1%)
4	G	15/15 (100%)	-0.24	0 100 100	47, 60, 72, 75	0
5	H	15/15 (100%)	-0.41	0 100 100	38, 57, 70, 73	0
All	All	1692/1694 (99%)	0.10	78 (4%) 37 42	13, 49, 98, 161	23 (1%)

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	311	VAL	7.0
3	F	181	SER	5.3
3	F	248	LEU	5.0
3	F	251	ALA	4.2
3	F	117[A]	ARG	3.9

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

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

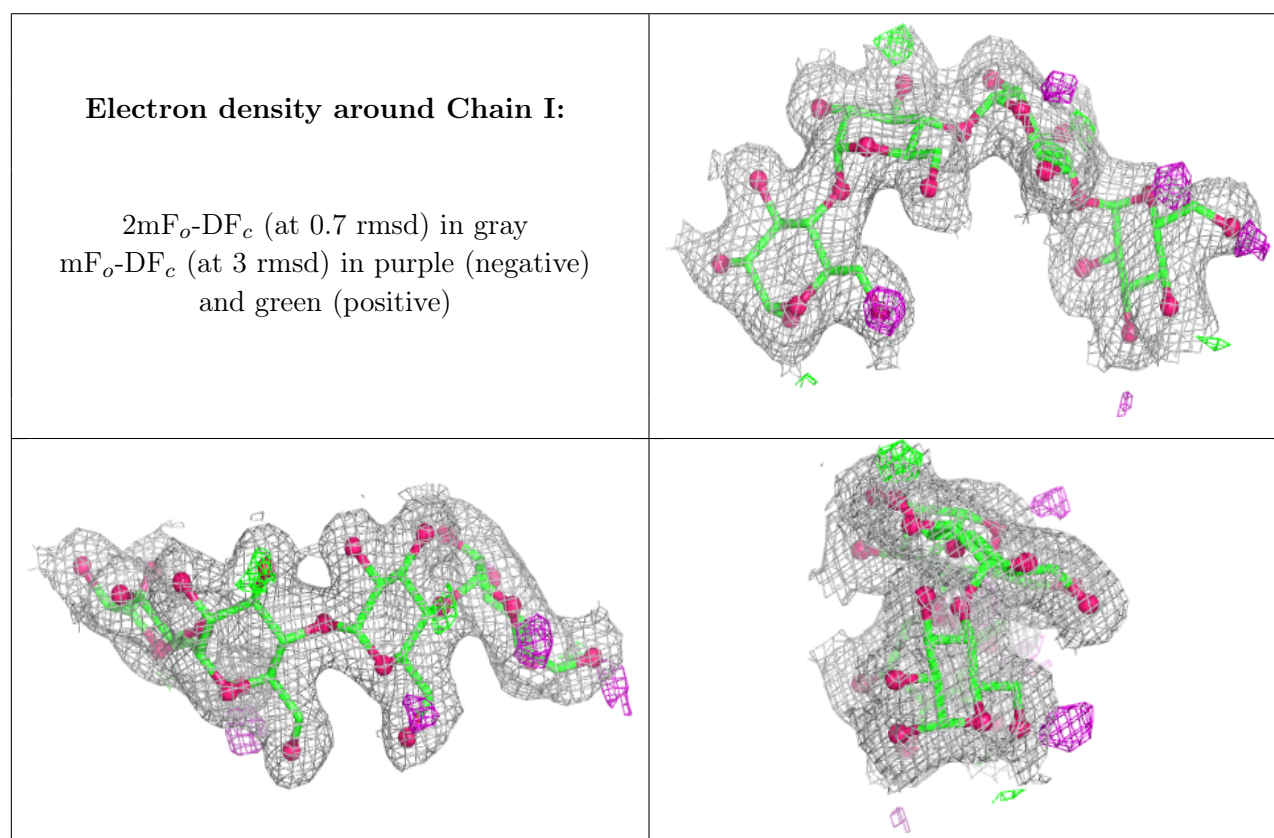
### 6.3 Carbohydrates [i](#)

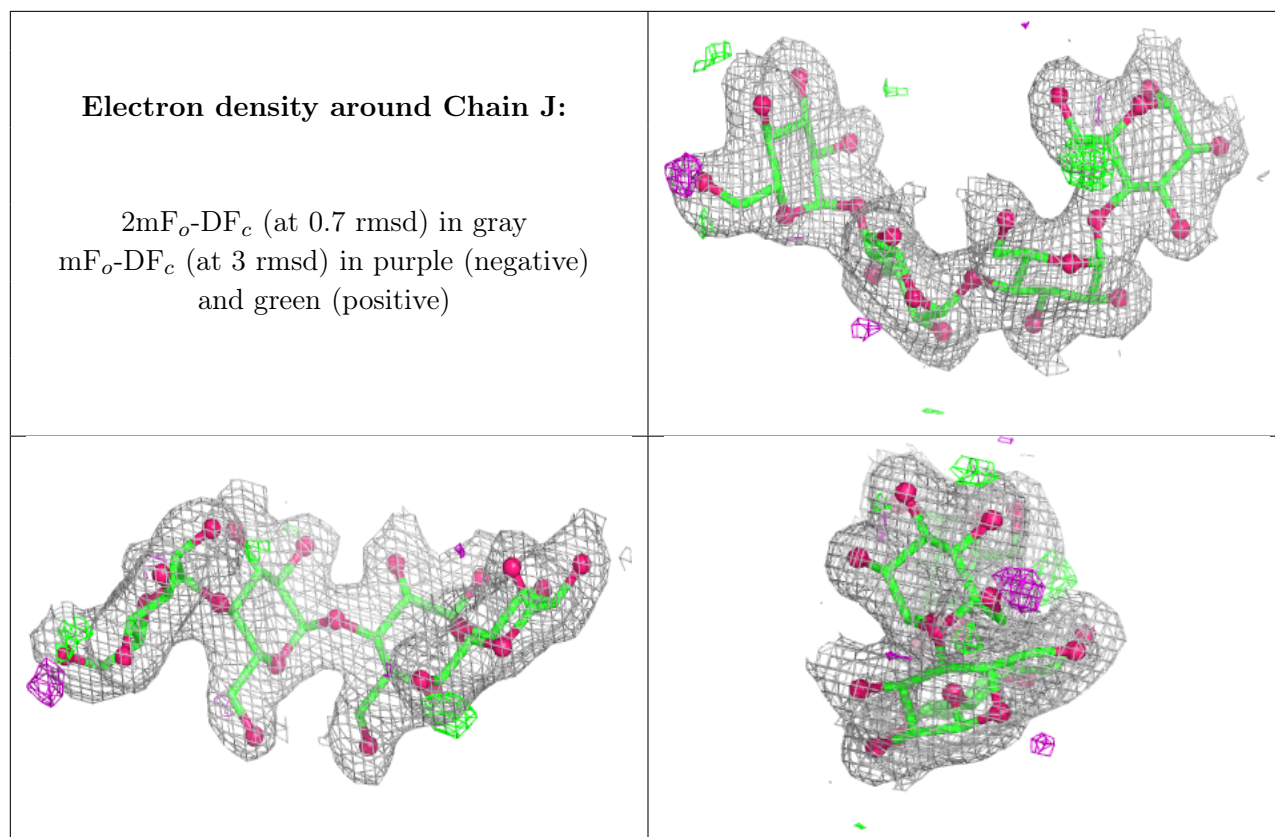
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	GLC	J	4	11/12	0.93	0.08	34,36,38,42	0
6	GLC	J	1	12/12	0.94	0.07	33,39,41,42	0
6	GLC	I	4	11/12	0.94	0.08	29,32,40,42	0
6	GLC	J	2	11/12	0.96	0.06	33,36,37,37	0
6	GLC	J	3	11/12	0.97	0.06	34,36,42,45	0
6	GLC	I	3	11/12	0.97	0.05	23,25,29,34	0
6	GLC	I	1	12/12	0.98	0.05	20,22,25,26	0
6	GLC	I	2	11/12	0.98	0.04	18,21,22,24	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
7	EDO	C	408	4/4	0.62	0.24	77,77,78,79	0
7	EDO	F	621	4/4	0.65	0.18	83,84,84,84	0
7	EDO	E	617	4/4	0.66	0.29	89,89,90,90	0
7	EDO	C	407	4/4	0.70	0.22	70,72,73,74	0
7	EDO	A	422	4/4	0.72	0.23	68,70,73,75	0
7	EDO	C	412	4/4	0.72	0.22	75,76,77,77	0
7	EDO	A	440	4/4	0.73	0.17	77,77,78,79	0
7	EDO	F	622	4/4	0.73	0.27	64,66,66,67	0
7	EDO	E	609	4/4	0.74	0.22	79,81,83,84	0
7	EDO	A	437	4/4	0.74	0.26	82,82,82,82	0
7	EDO	F	625	4/4	0.74	0.15	78,78,78,79	0
7	EDO	C	414	4/4	0.75	0.13	79,80,81,82	0
7	EDO	A	446	4/4	0.75	0.26	66,67,68,68	0
7	EDO	F	603	4/4	0.76	0.17	72,73,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	EDO	D	302	4/4	0.76	0.16	79,80,81,81	0
7	EDO	C	411	4/4	0.77	0.16	76,76,77,77	0
7	EDO	E	611	4/4	0.77	0.25	65,67,68,68	0
7	EDO	F	619	4/4	0.77	0.20	79,80,81,81	0
7	EDO	A	445	4/4	0.78	0.24	71,72,72,73	0
7	EDO	F	613	4/4	0.78	0.22	67,70,72,74	0
7	EDO	C	409	4/4	0.79	0.27	68,69,69,69	0
7	EDO	E	619	4/4	0.79	0.18	73,74,74,74	0
7	EDO	C	410	4/4	0.79	0.16	64,67,68,69	0
7	EDO	E	615	4/4	0.79	0.17	69,71,71,71	0
7	EDO	A	434	4/4	0.80	0.26	42,47,52,54	0
7	EDO	C	405	4/4	0.80	0.21	75,76,77,78	0
7	EDO	F	624	4/4	0.80	0.27	47,51,54,56	0
7	EDO	A	416	4/4	0.80	0.23	65,67,70,73	0
7	EDO	A	413	4/4	0.81	0.20	79,80,80,81	0
7	EDO	A	411	4/4	0.81	0.17	65,67,68,69	0
7	EDO	E	613	4/4	0.81	0.20	59,60,63,66	0
7	EDO	A	417	4/4	0.81	0.18	50,51,52,53	0
7	EDO	A	439	4/4	0.81	0.21	68,69,69,70	0
7	EDO	E	606	4/4	0.81	0.20	64,65,66,68	0
7	EDO	E	624	4/4	0.81	0.23	68,69,69,70	0
7	EDO	C	406	4/4	0.82	0.21	69,69,69,69	0
7	EDO	C	402	4/4	0.82	0.17	62,63,63,64	0
7	EDO	C	401	4/4	0.82	0.16	80,80,81,81	0
7	EDO	A	420	4/4	0.83	0.20	72,73,76,78	0
7	EDO	A	441	4/4	0.83	0.18	67,68,68,69	0
7	EDO	F	614	4/4	0.83	0.29	76,77,78,78	0
7	EDO	A	436	4/4	0.83	0.18	53,56,60,61	0
7	EDO	A	407	4/4	0.83	0.16	63,64,65,65	0
7	EDO	D	301	4/4	0.83	0.20	84,85,86,86	0
7	EDO	A	447	4/4	0.83	0.20	63,65,68,71	0
7	EDO	A	433	4/4	0.83	0.24	54,58,58,59	0
7	EDO	E	612	4/4	0.84	0.26	51,55,58,59	0
7	EDO	E	622	4/4	0.84	0.19	65,65,66,68	0
7	EDO	A	444	4/4	0.84	0.23	57,62,65,68	0
7	EDO	E	610	4/4	0.84	0.18	72,72,73,73	0
7	EDO	F	608	4/4	0.84	0.18	61,64,67,69	0
7	EDO	C	413	4/4	0.84	0.24	56,60,63,64	0
7	EDO	F	617	4/4	0.85	0.20	76,77,77,77	0
7	EDO	E	602	4/4	0.85	0.15	55,57,58,59	0
7	EDO	A	424	4/4	0.85	0.17	59,63,66,66	0
7	EDO	E	623	4/4	0.85	0.25	47,52,59,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	EDO	A	418	4/4	0.85	0.18	73,73,73,74	0
7	EDO	F	615	4/4	0.85	0.23	65,65,65,67	0
7	EDO	A	425	4/4	0.86	0.25	43,43,46,49	0
7	EDO	F	620	4/4	0.86	0.13	68,69,71,72	0
7	EDO	E	603	4/4	0.86	0.12	63,63,64,65	0
7	EDO	A	412	4/4	0.86	0.23	50,50,52,54	0
7	EDO	E	608	4/4	0.86	0.21	55,56,56,60	0
7	EDO	F	606	4/4	0.86	0.19	58,59,60,62	0
7	EDO	E	621	4/4	0.87	0.16	63,63,64,64	0
7	EDO	F	611	4/4	0.87	0.33	57,57,57,58	0
7	EDO	F	601	4/4	0.87	0.13	67,67,68,68	0
7	EDO	A	409	4/4	0.87	0.17	63,65,66,67	0
7	EDO	E	605	4/4	0.87	0.18	50,50,52,54	0
7	EDO	F	607	4/4	0.87	0.25	70,70,71,71	0
7	EDO	A	428	4/4	0.88	0.22	62,63,64,64	0
7	EDO	E	618	4/4	0.88	0.26	46,51,52,55	0
7	EDO	A	414	4/4	0.88	0.17	52,56,61,63	0
7	EDO	A	423	4/4	0.88	0.17	73,74,75,77	0
7	EDO	A	427	4/4	0.88	0.20	75,75,77,77	0
7	EDO	F	610	4/4	0.88	0.18	56,58,59,59	0
7	EDO	A	448	4/4	0.88	0.20	42,48,51,57	0
7	EDO	F	612	4/4	0.88	0.16	64,64,65,65	0
7	EDO	A	442	4/4	0.88	0.20	66,66,66,67	0
7	EDO	A	406	4/4	0.89	0.16	56,58,61,63	0
7	EDO	F	618	4/4	0.89	0.16	52,53,57,59	0
7	EDO	A	429	4/4	0.89	0.23	37,45,47,52	0
7	EDO	E	607	4/4	0.89	0.13	66,67,67,68	0
7	EDO	A	432	4/4	0.89	0.19	55,57,58,60	0
7	EDO	A	403	4/4	0.89	0.17	38,41,41,45	0
7	EDO	E	616	4/4	0.89	0.17	69,70,72,73	0
7	EDO	F	616	4/4	0.89	0.20	73,73,73,73	0
7	EDO	E	604	4/4	0.90	0.15	64,64,65,66	0
7	EDO	C	404	4/4	0.90	0.16	59,63,66,70	0
7	EDO	A	438	4/4	0.90	0.16	38,41,43,45	0
7	EDO	E	620	4/4	0.90	0.29	50,55,58,62	0
7	EDO	A	431	4/4	0.90	0.18	58,59,60,60	0
7	EDO	A	421	4/4	0.90	0.13	57,61,65,69	0
7	EDO	A	408	4/4	0.90	0.13	43,43,47,47	0
7	EDO	A	443	4/4	0.91	0.17	60,61,62,64	0
7	EDO	A	430	4/4	0.91	0.34	58,58,61,62	0
7	EDO	A	426	4/4	0.91	0.17	45,51,53,54	0
7	EDO	A	419	4/4	0.91	0.15	46,53,58,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	EDO	F	609	4/4	0.91	0.16	51,56,57,59	0
7	EDO	F	623	4/4	0.92	0.17	71,71,71,71	0
7	EDO	F	604	4/4	0.92	0.10	73,74,75,76	0
7	EDO	C	403	4/4	0.92	0.37	45,47,48,51	0
7	EDO	A	410	4/4	0.93	0.11	46,51,54,57	0
7	EDO	A	401	4/4	0.93	0.12	50,51,51,54	0
7	EDO	E	614	4/4	0.93	0.14	60,61,61,62	0
7	EDO	A	435	4/4	0.93	0.14	40,45,46,47	0
7	EDO	F	605	4/4	0.94	0.12	64,65,66,66	0
7	EDO	A	415	4/4	0.94	0.11	43,45,48,49	0
7	EDO	A	402	4/4	0.94	0.12	47,48,49,53	0
7	EDO	A	404	4/4	0.95	0.10	35,36,37,40	0
7	EDO	A	405	4/4	0.96	0.13	45,48,49,50	0
7	EDO	E	601	4/4	0.97	0.07	34,37,37,38	0
7	EDO	F	602	4/4	0.98	0.05	29,30,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.