



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 07:21 PM UTC

PDB ID : 8IUC / pdb_00008iuc
Title : Crystal structure of GH65 alpha-1,2-glucosidase from *Flavobacterium johnsoniae* in complex with isomaltose
Authors : Nakamura, S.; Miyazaki, T.
Deposited on : 2023-03-24
Resolution : 1.56 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 ⓘ 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

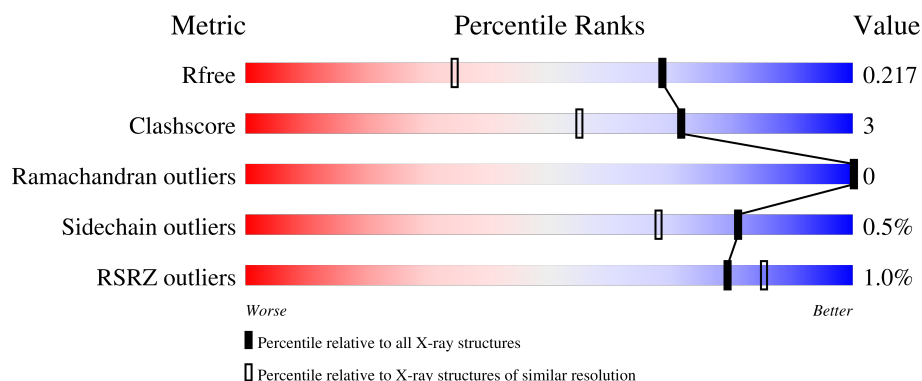
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.56 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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	678	% 89% 8% .
1	B	678	% 87% 9% ..
1	C	678	% 88% 9% .
2	D	2	50% 50%
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	 50%50%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 33574 atoms, of which 15978 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 Candidate alpha glycoside phosphorylase Glycoside hydrolase family 65.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	659	Total	C	H	N	O	S	160	12	0
			10555	3392	5233	891	1017	22			
1	B	659	Total	C	H	N	O	S	159	12	0
			10545	3389	5229	889	1015	23			
1	C	659	Total	C	H	N	O	S	158	15	0
			10622	3411	5267	899	1022	23			

There are 60 discrepancies between the modelled and reference sequences:

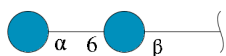
Chain	Residue	Modelled	Actual	Comment	Reference
A	4	MET	-	initiating methionine	UNP A5FBJ5
A	5	GLY	-	expression tag	UNP A5FBJ5
A	6	SER	-	expression tag	UNP A5FBJ5
A	7	SER	-	expression tag	UNP A5FBJ5
A	8	HIS	-	expression tag	UNP A5FBJ5
A	9	HIS	-	expression tag	UNP A5FBJ5
A	10	HIS	-	expression tag	UNP A5FBJ5
A	11	HIS	-	expression tag	UNP A5FBJ5
A	12	HIS	-	expression tag	UNP A5FBJ5
A	13	HIS	-	expression tag	UNP A5FBJ5
A	14	SER	-	expression tag	UNP A5FBJ5
A	15	SER	-	expression tag	UNP A5FBJ5
A	16	GLY	-	expression tag	UNP A5FBJ5
A	17	LEU	-	expression tag	UNP A5FBJ5
A	18	VAL	-	expression tag	UNP A5FBJ5
A	19	PRO	-	expression tag	UNP A5FBJ5
A	20	ARG	-	expression tag	UNP A5FBJ5
A	21	GLY	-	expression tag	UNP A5FBJ5
A	22	SER	-	expression tag	UNP A5FBJ5
A	23	HIS	-	expression tag	UNP A5FBJ5
B	4	MET	-	initiating methionine	UNP A5FBJ5
B	5	GLY	-	expression tag	UNP A5FBJ5

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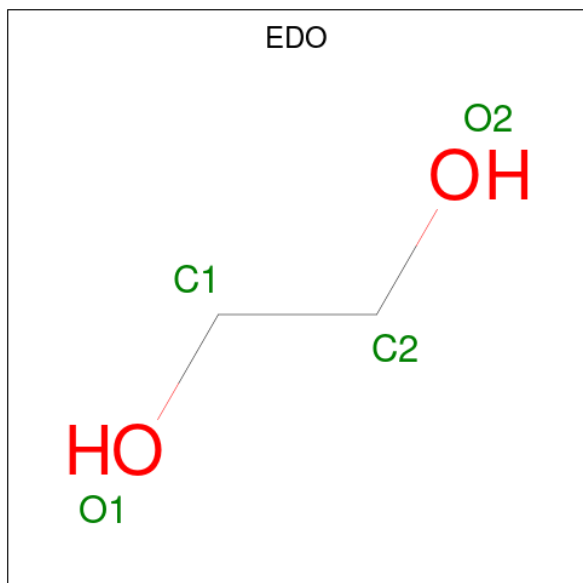
Chain	Residue	Modelled	Actual	Comment	Reference
B	6	SER	-	expression tag	UNP A5FBJ5
B	7	SER	-	expression tag	UNP A5FBJ5
B	8	HIS	-	expression tag	UNP A5FBJ5
B	9	HIS	-	expression tag	UNP A5FBJ5
B	10	HIS	-	expression tag	UNP A5FBJ5
B	11	HIS	-	expression tag	UNP A5FBJ5
B	12	HIS	-	expression tag	UNP A5FBJ5
B	13	HIS	-	expression tag	UNP A5FBJ5
B	14	SER	-	expression tag	UNP A5FBJ5
B	15	SER	-	expression tag	UNP A5FBJ5
B	16	GLY	-	expression tag	UNP A5FBJ5
B	17	LEU	-	expression tag	UNP A5FBJ5
B	18	VAL	-	expression tag	UNP A5FBJ5
B	19	PRO	-	expression tag	UNP A5FBJ5
B	20	ARG	-	expression tag	UNP A5FBJ5
B	21	GLY	-	expression tag	UNP A5FBJ5
B	22	SER	-	expression tag	UNP A5FBJ5
B	23	HIS	-	expression tag	UNP A5FBJ5
C	4	MET	-	initiating methionine	UNP A5FBJ5
C	5	GLY	-	expression tag	UNP A5FBJ5
C	6	SER	-	expression tag	UNP A5FBJ5
C	7	SER	-	expression tag	UNP A5FBJ5
C	8	HIS	-	expression tag	UNP A5FBJ5
C	9	HIS	-	expression tag	UNP A5FBJ5
C	10	HIS	-	expression tag	UNP A5FBJ5
C	11	HIS	-	expression tag	UNP A5FBJ5
C	12	HIS	-	expression tag	UNP A5FBJ5
C	13	HIS	-	expression tag	UNP A5FBJ5
C	14	SER	-	expression tag	UNP A5FBJ5
C	15	SER	-	expression tag	UNP A5FBJ5
C	16	GLY	-	expression tag	UNP A5FBJ5
C	17	LEU	-	expression tag	UNP A5FBJ5
C	18	VAL	-	expression tag	UNP A5FBJ5
C	19	PRO	-	expression tag	UNP A5FBJ5
C	20	ARG	-	expression tag	UNP A5FBJ5
C	21	GLY	-	expression tag	UNP A5FBJ5
C	22	SER	-	expression tag	UNP A5FBJ5
C	23	HIS	-	expression tag	UNP A5FBJ5

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-6)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	2	Total	C	H	O	8	0	0
			46	12	23	11			
2	E	2	Total	C	H	O	8	0	0
			46	12	23	11			
2	F	2	Total	C	H	O	8	0	0
			46	12	23	11			

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	A	1	Total	C	H	O	1	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	A	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	B	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		
3	C	1	Total	C	H	O	1	0
			10	2	6	2		

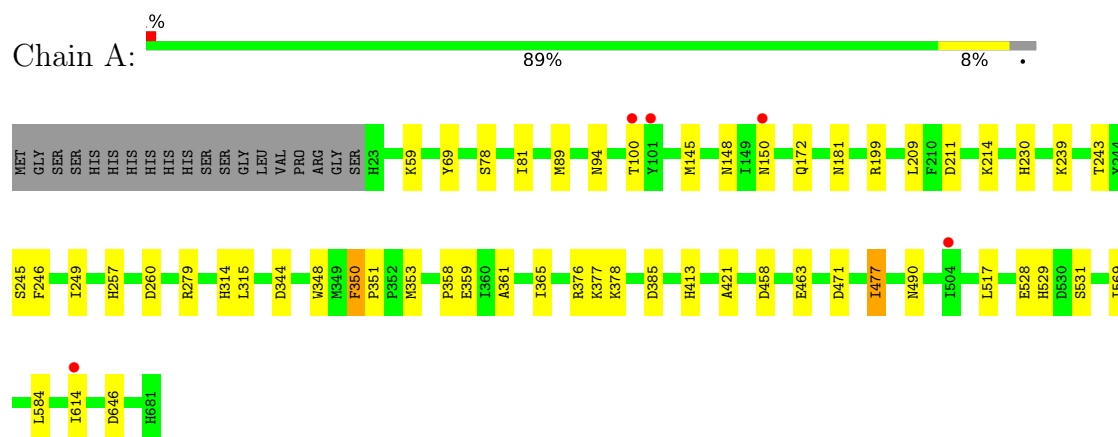
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	480	Total	O	0	0
			480	480		
4	B	425	Total	O	0	0
			425	425		
4	C	509	Total	O	0	0
			509	509		

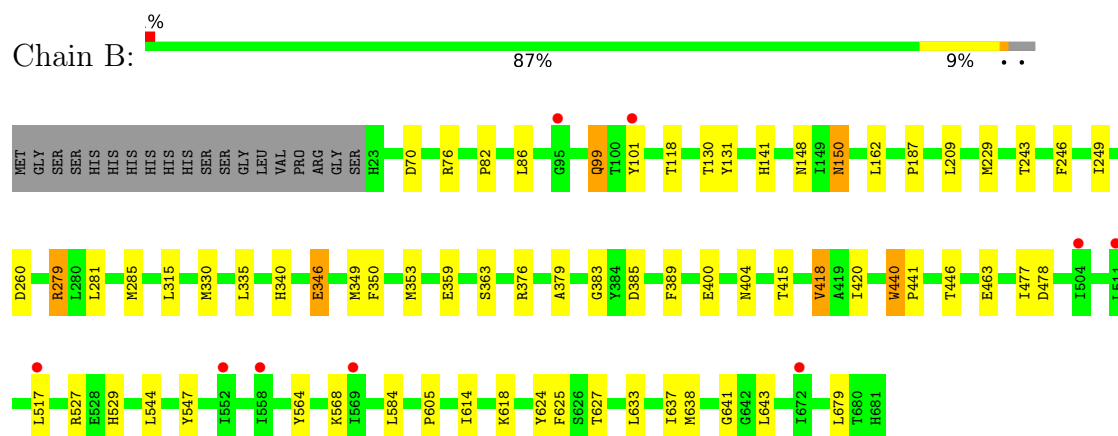
3 Residue-property plots [i](#)

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.

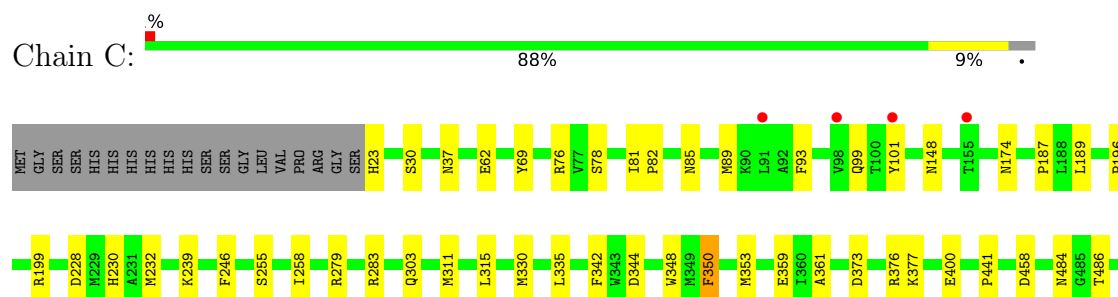
- Molecule 1: Candidate alpha glycoside phosphorylase Glycoside hydrolase family 65

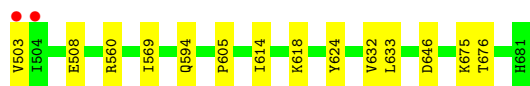


- Molecule 1: Candidate alpha glycoside phosphorylase Glycoside hydrolase family 65



- Molecule 1: Candidate alpha glycoside phosphorylase Glycoside hydrolase family 65





- Molecule 2: alpha-D-glucopyranose-(1-6)-beta-D-glucopyranose

Chain D: 50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-6)-beta-D-glucopyranose

Chain E: 50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-6)-beta-D-glucopyranose

Chain F: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.94Å 194.09Å 111.88Å 90.00° 116.35° 90.00°	Depositor
Resolution (Å)	44.71 – 1.56 44.71 – 1.56	Depositor EDS
% Data completeness (in resolution range)	98.3 (44.71-1.56) 98.3 (44.71-1.56)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 1.56Å)	Xtriage
Refinement program	REFMAC 5.8.0405	Depositor
R, R_{free}	0.187 , 0.211 0.193 , 0.217	Depositor DCC
R_{free} test set	16344 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	20.0	Xtriage
Anisotropy	0.518	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 39.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	33574	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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: BGC, GLC, EDO

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	0.95	4/5463 (0.1%)	1.23	12/7412 (0.2%)
1	B	0.96	6/5463 (0.1%)	1.27	15/7412 (0.2%)
1	C	0.95	1/5505 (0.0%)	1.26	16/7467 (0.2%)
All	All	0.95	11/16431 (0.1%)	1.25	43/22291 (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	2
1	B	0	2
1	C	0	1
All	All	0	5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	230	HIS	CG-CD2	-6.96	1.28	1.35
1	B	400	GLU	CD-OE1	6.12	1.36	1.25
1	B	340	HIS	ND1-CE1	5.94	1.38	1.32
1	A	257	HIS	CE1-NE2	5.67	1.38	1.32
1	B	346	GLU	C-O	5.39	1.30	1.24
1	B	363	SER	CA-CB	-5.32	1.45	1.53
1	A	385	ASP	CG-OD2	5.25	1.35	1.25
1	B	379	ALA	N-CA	-5.24	1.40	1.46
1	A	314	HIS	CG-CD2	-5.12	1.30	1.35
1	C	81	ILE	CA-C	5.08	1.56	1.52
1	B	141	HIS	CG-CD2	5.05	1.41	1.35

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	646	ASP	CA-CB-CG	9.54	122.14	112.60
1	A	350	PHE	CA-CB-CG	7.89	121.69	113.80
1	C	342	PHE	CA-CB-CG	7.66	121.46	113.80
1	B	359	GLU	CB-CG-CD	7.63	125.57	112.60
1	A	260	ASP	CA-CB-CG	6.90	119.50	112.60
1	B	187	PRO	N-CD-CG	-6.89	92.86	103.20
1	A	458	ASP	CB-CA-C	-6.86	95.85	110.32
1	C	569	ILE	CA-C-O	6.13	123.91	119.25
1	C	350	PHE	CA-CB-CG	6.13	119.93	113.80
1	C	359	GLU	CB-CG-CD	6.13	123.02	112.60
1	B	70	ASP	CA-CB-CG	6.08	118.68	112.60
1	A	359	GLU	CB-CG-CD	5.97	122.75	112.60
1	B	385	ASP	CA-CB-CG	5.91	118.51	112.60
1	C	484	ASN	N-CA-C	-5.82	105.02	111.71
1	A	172	GLN	OE1-CD-NE2	-5.70	116.91	122.60
1	C	569	ILE	O-C-N	-5.67	117.80	121.37
1	A	239	LYS	CB-CA-C	5.65	118.86	109.53
1	B	350	PHE	CA-CB-CG	5.59	119.39	113.80
1	B	420	ILE	O-C-N	-5.56	116.46	121.91
1	B	440	TRP	O-C-N	-5.56	115.27	120.55
1	A	646	ASP	CA-CB-CG	5.55	118.15	112.60
1	C	228	ASP	CB-CA-C	-5.50	102.58	111.28
1	B	376	ARG	NE-CZ-NH2	-5.50	114.25	119.20
1	B	260	ASP	CA-CB-CG	5.49	118.09	112.60
1	A	94	ASN	CB-CA-C	-5.41	103.83	111.95
1	B	420	ILE	CA-C-O	5.35	126.84	121.17
1	B	389	PHE	CA-CB-CG	-5.34	108.46	113.80
1	A	413	HIS	CB-CG-CD2	-5.33	124.27	131.20
1	A	351	PRO	O-C-N	-5.32	115.18	121.46
1	C	508	GLU	CB-CG-CD	5.32	121.64	112.60
1	C	187	PRO	N-CD-CG	-5.31	95.23	103.20
1	C	37	ASN	CA-CB-CG	-5.29	107.31	112.60
1	A	569	ILE	CA-C-O	5.25	122.06	119.12
1	C	93	PHE	CB-CA-C	-5.22	101.49	110.16
1	C	400	GLU	CB-CA-C	-5.20	101.69	110.64
1	C	458	ASP	CB-CA-C	-5.12	101.15	110.63
1	C	486	THR	N-CA-CB	5.12	118.22	110.28
1	C	81	ILE	O-C-N	-5.09	115.97	121.11
1	B	99	GLN	CB-CA-C	-5.08	100.24	110.30
1	B	150	ASN	CA-CB-CG	-5.07	107.53	112.60
1	B	418	VAL	CA-C-O	-5.06	115.79	121.05
1	A	490	ASN	CA-CB-CG	5.04	117.64	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	478	ASP	CA-CB-CG	5.02	117.62	112.60

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	376	ARG	Sidechain
1	A	81	ILE	Mainchain
1	B	279	ARG	Sidechain
1	B	76	ARG	Sidechain
1	C	76	ARG	Sidechain

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	5322	5233	5212	31	0
1	B	5316	5229	5212	43	0
1	C	5355	5267	5249	29	0
2	D	23	23	21	1	0
2	E	23	23	21	1	0
2	F	23	23	21	1	0
3	A	40	60	60	6	0
3	B	40	60	60	6	0
3	C	40	60	60	2	0
4	A	480	0	0	3	1
4	B	425	0	0	6	1
4	C	509	0	0	6	0
All	All	17596	15978	15916	105	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (105) 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:148:ASN:OD1	1:A:245[B]:SER:OG	1.86	0.91
1:A:614:ILE:HD11	3:A:707:EDO:H21	1.60	0.84
1:A:209:LEU:HD11	1:A:249:ILE:HD11	1.63	0.79
1:A:209:LEU:HD11	1:A:249:ILE:CD1	2.15	0.76
1:B:209:LEU:HD11	1:B:249:ILE:CD1	2.16	0.75
1:B:130[B]:THR:HG21	4:B:1138:HOH:O	1.88	0.73
1:B:209:LEU:HD11	1:B:249:ILE:HD12	1.71	0.72
4:A:934:HOH:O	1:C:377:LYS:HD3	1.91	0.71
1:B:148:ASN:ND2	4:B:802:HOH:O	2.23	0.69
1:A:358:PRO:HG3	4:A:1028:HOH:O	1.92	0.68
1:C:246:PHE:HA	3:C:704:EDO:H11	1.78	0.65
1:A:377:LYS:HD3	4:B:945:HOH:O	1.99	0.62
1:B:315[B]:LEU:HD12	1:B:633:LEU:HD12	1.81	0.61
1:C:303:GLN:HG2	4:C:1240:HOH:O	2.00	0.61
1:B:614:ILE:HD11	3:B:708:EDO:H21	1.84	0.60
1:A:614:ILE:HG13	3:A:707:EDO:H22	1.84	0.59
1:A:150:ASN:OD1	1:A:243:THR:OG1	2.16	0.57
1:C:315:LEU:HD22	1:C:633:LEU:HD12	1.86	0.57
1:B:209:LEU:HD11	1:B:249:ILE:HD11	1.86	0.57
1:C:560:ARG:HD3	4:C:1262:HOH:O	2.04	0.56
1:A:89[A]:MET:HE3	1:A:145:MET:CE	2.35	0.56
1:C:23:HIS:HD2	1:C:30:SER:OG	1.88	0.56
1:C:614:ILE:HD11	3:C:705:EDO:H21	1.88	0.56
1:C:99:GLN:HG3	1:C:101:TYR:CE2	2.42	0.55
4:C:805:HOH:O	2:D:1:BGC:H6C1	2.06	0.55
1:C:62:GLU:HA	1:C:85:ASN:HD21	1.72	0.54
1:B:315[B]:LEU:HD12	1:B:633:LEU:CD1	2.37	0.54
1:C:189:LEU:HD22	1:C:232:MET:HG2	1.90	0.54
1:B:82:PRO:HD3	1:B:335:LEU:HD21	1.88	0.54
1:A:365[B]:ILE:HD11	1:A:421:ALA:HB1	1.91	0.53
1:B:86:LEU:H	1:B:86:LEU:HD23	1.74	0.53
1:B:463:GLU:HG2	1:B:517:LEU:HD12	1.91	0.53
1:B:605:PRO:HB2	1:B:618:LYS:HG2	1.91	0.53
1:A:463:GLU:HG2	1:A:517:LEU:HD12	1.90	0.52
1:B:330:MET:HA	1:B:624:TYR:O	2.11	0.51
1:A:584:LEU:HD23	1:A:584:LEU:C	2.37	0.50
1:C:315:LEU:HD23	1:C:353:MET:HE3	1.94	0.49
1:A:89[A]:MET:HE3	1:A:145:MET:HE3	1.95	0.49
1:B:162:LEU:HD23	1:B:229[B]:MET:SD	2.52	0.49
1:B:246:PHE:HA	3:B:707:EDO:H22	1.93	0.49
1:B:150:ASN:OD1	1:B:243:THR:OG1	2.16	0.49
1:C:69:TYR:HB3	1:C:78:SER:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:PRO:HG3	1:C:335[B]:LEU:HD11	1.94	0.49
1:B:315[B]:LEU:HD13	1:B:353:MET:HE3	1.94	0.48
1:C:605:PRO:HB2	1:C:618:LYS:HG2	1.95	0.47
1:B:477:ILE:C	1:B:477:ILE:HD12	2.40	0.47
1:A:209:LEU:HD11	1:A:249:ILE:HD12	1.94	0.47
1:C:350:PHE:CE2	1:C:361:ALA:HB1	2.49	0.47
1:A:614:ILE:CD1	3:A:707:EDO:H21	2.39	0.46
1:A:315:LEU:HD23	1:A:353:MET:HE3	1.98	0.46
1:B:86:LEU:H	1:B:86:LEU:CD2	2.28	0.46
1:C:148:ASN:ND2	4:C:815:HOH:O	2.48	0.46
1:C:311:MET:HE1	1:C:632:VAL:HG11	1.98	0.46
1:B:130[B]:THR:HG22	4:B:1078:HOH:O	2.15	0.45
1:B:86:LEU:HD23	1:B:86:LEU:N	2.31	0.45
1:B:130[A]:THR:HG23	4:B:1078:HOH:O	2.15	0.45
1:C:239:LYS:HE3	1:C:239:LYS:HB2	1.67	0.45
1:C:199:ARG:HG2	4:C:838:HOH:O	2.17	0.45
1:A:471:ASP:OD2	1:A:528:GLU:OE1	2.35	0.45
1:C:344:ASP:O	1:C:348:TRP:HB2	2.16	0.45
1:A:89[A]:MET:CE	1:A:145:MET:HE3	2.47	0.44
1:B:547:TYR:C	1:B:547:TYR:CD1	2.94	0.44
1:B:99:GLN:HG3	1:B:101:TYR:CE2	2.52	0.44
1:A:378:LYS:HE3	4:B:1031:HOH:O	2.17	0.44
1:C:89:MET:HE3	1:C:89:MET:HB3	1.82	0.44
1:A:350:PHE:CE2	1:A:361:ALA:HB1	2.53	0.43
1:B:625:PHE:CZ	1:B:627:THR:HB	2.53	0.43
1:B:637:ILE:HG23	1:B:643:LEU:HD12	2.00	0.43
1:A:199:ARG:HG2	4:A:824:HOH:O	2.18	0.43
1:A:477:ILE:HD12	1:A:477:ILE:C	2.43	0.43
1:C:330:MET:HA	1:C:624:TYR:O	2.18	0.43
1:B:638:MET:HG3	1:B:643:LEU:O	2.19	0.43
1:C:174:ASN:HB3	1:C:230:HIS:CG	2.54	0.43
1:B:564:TYR:CE2	1:B:568:LYS:HE3	2.53	0.43
1:B:440:TRP:O	1:B:441:PRO:C	2.59	0.43
1:A:344:ASP:O	1:A:348:TRP:HB2	2.19	0.42
1:B:544:LEU:HA	1:B:547:TYR:O	2.19	0.42
1:B:527:ARG:HG2	1:B:529:HIS:O	2.19	0.42
1:A:529:HIS:CE1	1:A:531:SER:HB2	2.54	0.42
1:B:614:ILE:HD11	3:B:708:EDO:C2	2.47	0.42
1:C:315:LEU:HD22	1:C:633:LEU:CD1	2.48	0.42
1:A:69:TYR:HB3	1:A:78:SER:HB2	2.01	0.42
3:A:705:EDO:H11	2:E:2:GLC:H62	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:614:ILE:HG13	3:B:708:EDO:H22	2.02	0.42
1:B:346:GLU:HG2	1:B:418:VAL:HA	2.01	0.42
1:B:383:GLY:O	1:C:283[A]:ARG:NH2	2.52	0.41
1:A:246:PHE:HA	3:A:706:EDO:H11	2.02	0.41
1:B:118:THR:HA	1:B:131:TYR:O	2.21	0.41
1:C:373[B]:ASP:HA	1:C:376[B]:ARG:HH11	1.85	0.41
1:C:675:LYS:HG3	1:C:676:THR:N	2.34	0.41
1:B:404:ASN:ND2	3:B:705:EDO:H12	2.35	0.41
1:A:181:ASN:O	1:A:214:LYS:NZ	2.50	0.41
3:B:705:EDO:H11	2:F:2:GLC:H62	2.02	0.41
1:B:415:THR:HG23	1:B:446:THR:HG22	2.03	0.41
1:B:641:GLY:HA2	1:B:679:LEU:HD13	2.03	0.41
1:C:594:GLN:NE2	4:C:807:HOH:O	2.41	0.41
1:B:281:LEU:O	1:B:285[A]:MET:HG2	2.21	0.40
1:C:255:SER:HA	1:C:258:ILE:O	2.20	0.40
1:A:148:ASN:OD1	1:A:245[A]:SER:HB2	2.20	0.40
1:A:211:ASP:OD2	3:A:706:EDO:H12	2.22	0.40
1:A:477:ILE:C	1:A:477:ILE:CD1	2.94	0.40
1:B:315[B]:LEU:HD21	1:B:349:MET:HG2	2.04	0.40
1:B:315[B]:LEU:HD23	1:B:315[B]:LEU:HA	1.96	0.40
1:B:584:LEU:HD23	1:B:584:LEU:C	2.47	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1126:HOH:O	4:B:1088:HOH:O[2_555]	2.18	0.02

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	669/678 (99%)	645 (96%)	24 (4%)	0	100	100
1	B	669/678 (99%)	645 (96%)	24 (4%)	0	100	100
1	C	673/678 (99%)	654 (97%)	19 (3%)	0	100	100
All	All	2011/2034 (99%)	1944 (97%)	67 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	577/581 (99%)	574 (100%)	3 (0%)	81	68
1	B	577/581 (99%)	576 (100%)	1 (0%)	87	79
1	C	581/581 (100%)	577 (99%)	4 (1%)	76	59
All	All	1735/1743 (100%)	1727 (100%)	8 (0%)	81	68

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	THR
1	A	279	ARG
1	A	477	ILE
1	B	279	ARG
1	C	196	PRO
1	C	279	ARG
1	C	441	PRO
1	C	503	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	85	ASN

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Mol	Chain	Res	Type
1	A	105	ASN
1	A	108	GLN
1	A	122	GLN
1	A	178	ASN
1	A	183	HIS
1	A	185	ASN
1	A	259	ASN
1	A	476	ASN
1	A	539	GLN
1	A	571	GLN
1	A	608	ASN
1	B	85	ASN
1	B	108	GLN
1	B	178	ASN
1	B	183	HIS
1	B	185	ASN
1	B	206	ASN
1	B	286	GLN
1	B	539	GLN
1	B	571	GLN
1	B	594	GLN
1	B	608	ASN
1	C	23	HIS
1	C	24	GLN
1	C	85	ASN
1	C	108	GLN
1	C	150	ASN
1	C	171	ASN
1	C	178	ASN
1	C	185	ASN
1	C	539	GLN
1	C	566	GLN
1	C	571	GLN
1	C	608	ASN
1	C	681	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 ⓘ

6 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	D	1	2	12,12,12	1.50	2 (16%)	17,17,17	1.38	3 (17%)
2	GLC	D	2	2	11,11,12	0.92	0	15,15,17	1.14	1 (6%)
2	BGC	E	1	2	12,12,12	1.84	4 (33%)	17,17,17	1.61	3 (17%)
2	GLC	E	2	2	11,11,12	2.47	1 (9%)	15,15,17	1.35	1 (6%)
2	BGC	F	1	2	12,12,12	1.24	2 (16%)	17,17,17	1.70	6 (35%)
2	GLC	F	2	2	11,11,12	1.35	1 (9%)	15,15,17	1.34	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	D	1	2	-	0/2/22/22	0/1/1/1
2	GLC	D	2	2	-	0/2/19/22	0/1/1/1
2	BGC	E	1	2	-	0/2/22/22	0/1/1/1
2	GLC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	F	1	2	-	0/2/22/22	0/1/1/1
2	GLC	F	2	2	-	0/2/19/22	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2	GLC	C2-C3	-7.81	1.40	1.52
2	E	1	BGC	C4-C5	4.11	1.61	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	BGC	C4-C5	3.76	1.61	1.53
2	F	2	GLC	O5-C1	2.75	1.48	1.43
2	E	1	BGC	C4-C3	2.72	1.59	1.52
2	F	1	BGC	C4-C5	2.30	1.57	1.53
2	D	1	BGC	O5-C1	2.23	1.48	1.42
2	E	1	BGC	C1-C2	2.18	1.57	1.52
2	E	1	BGC	O3-C3	2.18	1.48	1.43
2	F	1	BGC	C4-C3	2.13	1.57	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	2	GLC	C1-O5-C5	4.31	117.97	112.19
2	E	2	GLC	C1-O5-C5	3.57	116.97	112.19
2	F	1	BGC	O5-C1-C2	3.41	116.30	110.30
2	E	1	BGC	O3-C3-C4	3.06	117.58	110.38
2	F	1	BGC	O4-C4-C5	-2.97	102.02	109.32
2	D	1	BGC	O4-C4-C5	-2.84	102.33	109.32
2	D	1	BGC	O5-C1-C2	2.73	115.09	110.30
2	F	1	BGC	O3-C3-C4	2.54	116.36	110.38
2	E	1	BGC	O5-C1-C2	2.35	114.43	110.30
2	F	1	BGC	C1-C2-C3	2.27	114.98	110.36
2	D	2	GLC	O5-C5-C6	-2.22	103.35	107.66
2	D	1	BGC	O1-C1-O5	-2.12	104.10	110.41
2	F	1	BGC	O1-C1-O5	-2.11	104.14	110.41
2	E	1	BGC	O2-C2-C1	2.07	114.02	109.25
2	F	1	BGC	O3-C3-C2	-2.01	105.64	110.38

There are no chirality outliers.

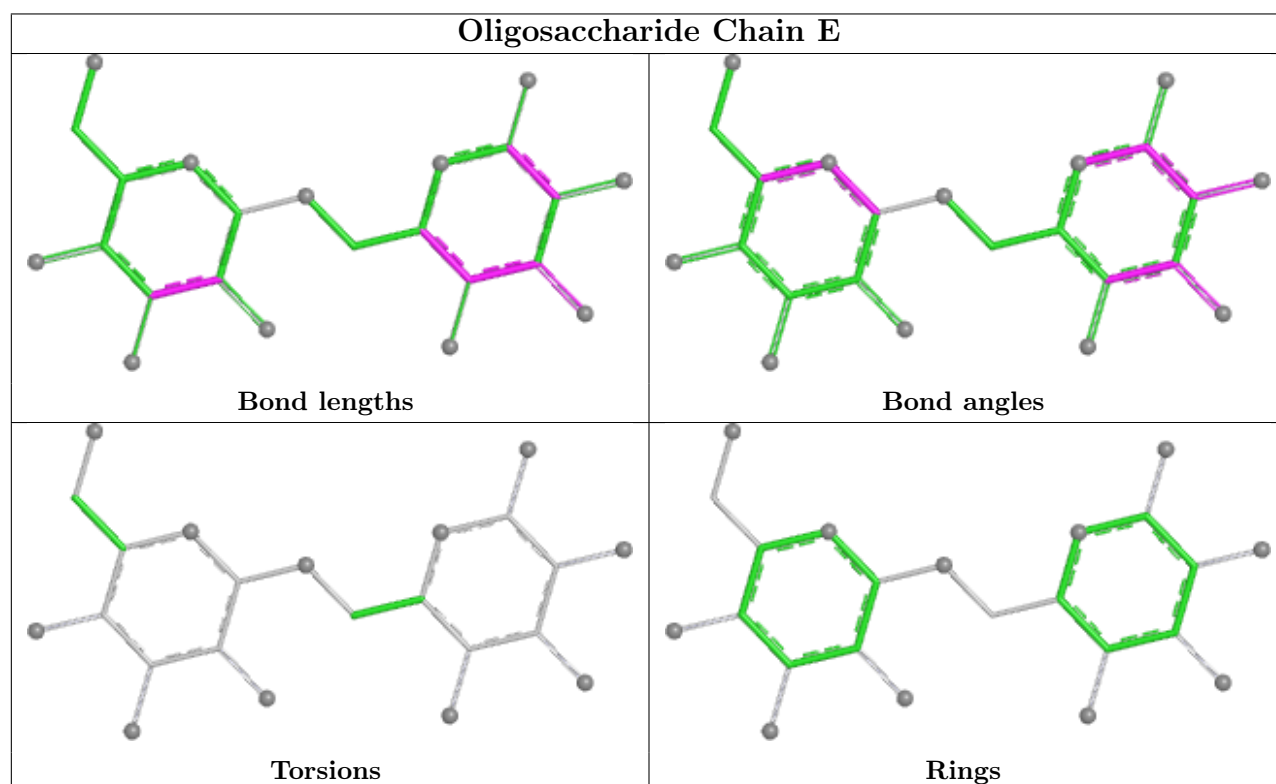
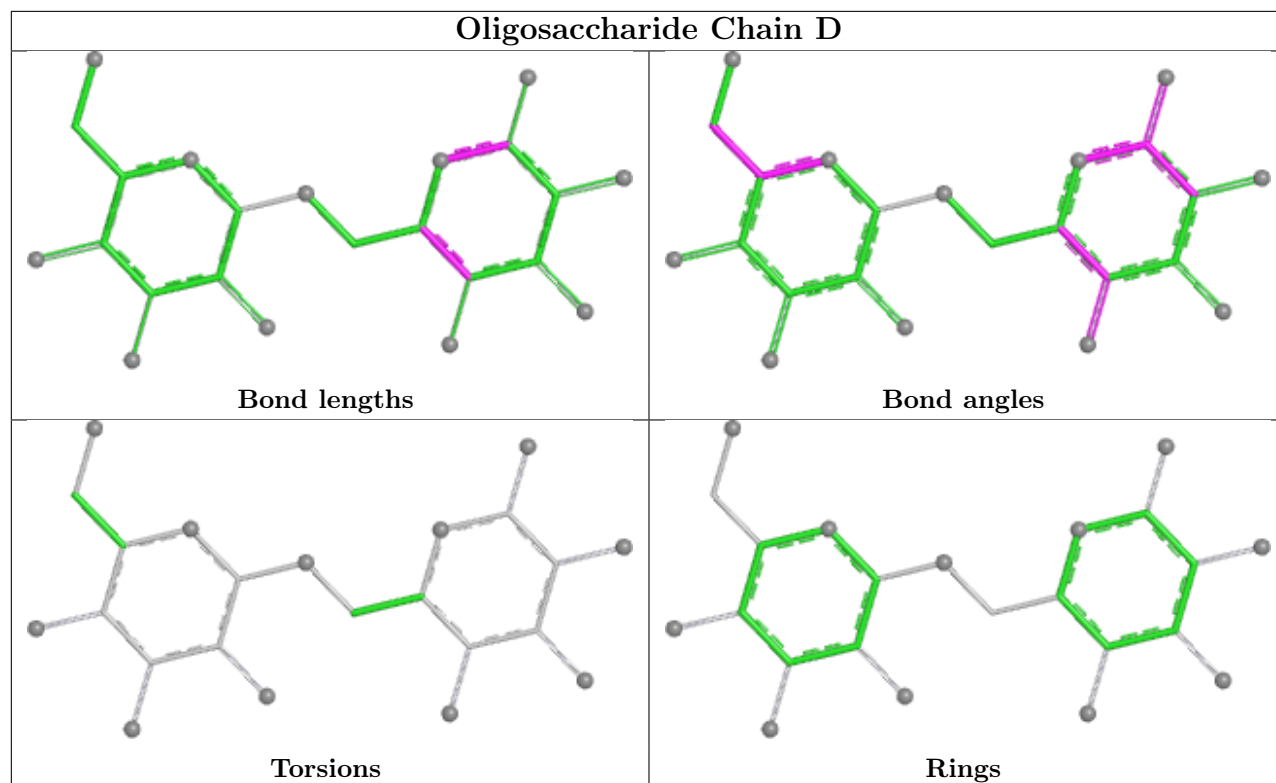
There are no torsion outliers.

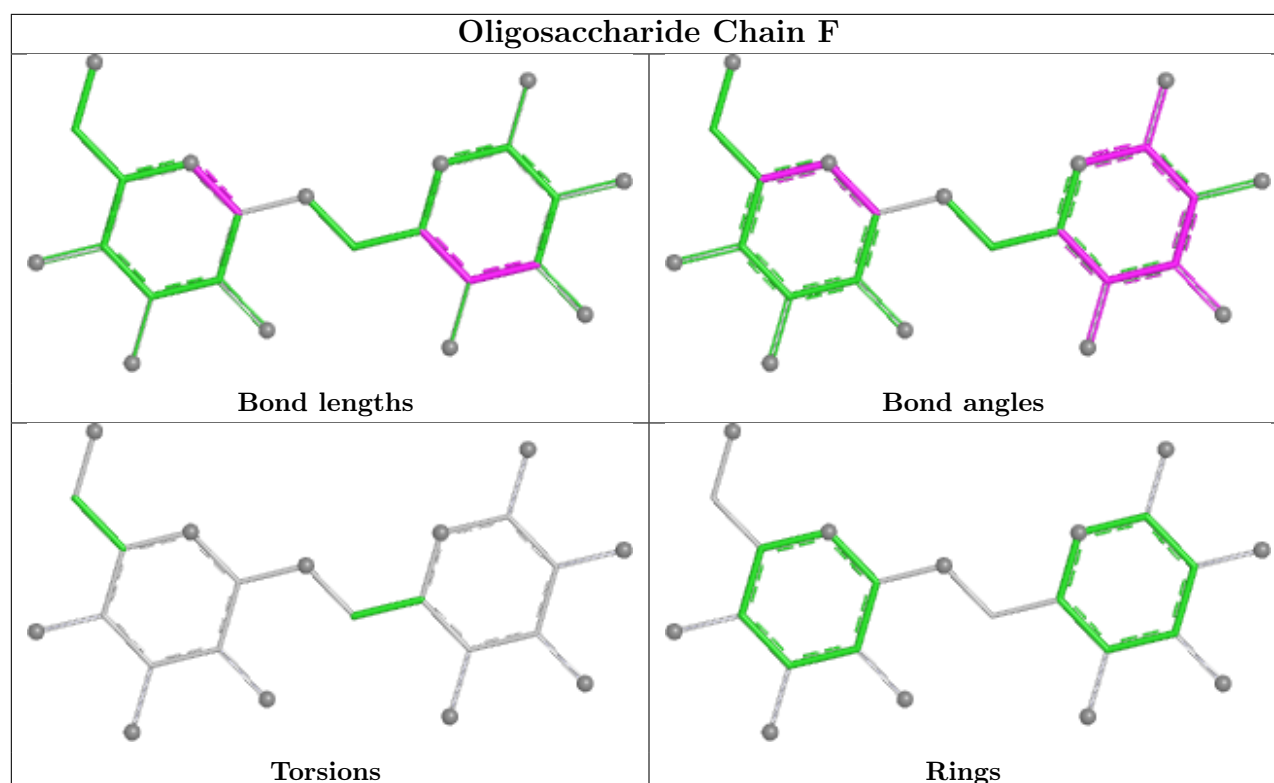
There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	BGC	1	0
2	F	2	GLC	1	0
2	E	2	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](#)

30 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	$\# Z > 2$
3	EDO	A	711	-	3,3,3	0.12	0	2,2,2	0.76	0
3	EDO	A	707	-	3,3,3	0.94	0	2,2,2	0.97	0
3	EDO	B	704	-	3,3,3	0.25	0	2,2,2	0.48	0
3	EDO	A	706	-	3,3,3	0.87	0	2,2,2	0.20	0
3	EDO	B	707	-	3,3,3	0.84	0	2,2,2	0.40	0
3	EDO	B	711	-	3,3,3	0.30	0	2,2,2	0.71	0
3	EDO	C	707	-	3,3,3	0.35	0	2,2,2	0.09	0
3	EDO	C	708	-	3,3,3	0.19	0	2,2,2	0.16	0
3	EDO	A	705	-	3,3,3	0.53	0	2,2,2	0.42	0
3	EDO	B	706	-	3,3,3	1.13	0	2,2,2	0.52	0
3	EDO	A	709	-	3,3,3	0.35	0	2,2,2	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	704	-	3,3,3	0.54	0	2,2,2	0.62	0
3	EDO	C	701	-	3,3,3	0.48	0	2,2,2	0.35	0
3	EDO	C	703	-	3,3,3	0.47	0	2,2,2	0.45	0
3	EDO	A	712	-	3,3,3	0.93	0	2,2,2	0.90	0
3	EDO	C	704	-	3,3,3	0.54	0	2,2,2	0.32	0
3	EDO	B	708	-	3,3,3	1.00	0	2,2,2	0.41	0
3	EDO	C	705	-	3,3,3	0.82	0	2,2,2	0.54	0
3	EDO	B	705	-	3,3,3	0.63	0	2,2,2	0.52	0
3	EDO	A	710	-	3,3,3	0.32	0	2,2,2	0.41	0
3	EDO	B	710	-	3,3,3	0.30	0	2,2,2	0.63	0
3	EDO	A	703	-	3,3,3	0.38	0	2,2,2	0.46	0
3	EDO	C	710	-	3,3,3	0.17	0	2,2,2	0.33	0
3	EDO	C	709	-	3,3,3	0.18	0	2,2,2	0.86	0
3	EDO	B	712	-	3,3,3	0.30	0	2,2,2	1.07	0
3	EDO	C	702	-	3,3,3	0.37	0	2,2,2	0.34	0
3	EDO	B	703	-	3,3,3	0.47	0	2,2,2	0.84	0
3	EDO	B	709	-	3,3,3	0.53	0	2,2,2	0.31	0
3	EDO	C	706	-	3,3,3	0.41	0	2,2,2	0.32	0
3	EDO	A	708	-	3,3,3	0.36	0	2,2,2	0.16	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	711	-	-	1/1/1/1	-
3	EDO	A	707	-	-	0/1/1/1	-
3	EDO	B	704	-	-	0/1/1/1	-
3	EDO	A	706	-	-	1/1/1/1	-
3	EDO	B	707	-	-	0/1/1/1	-
3	EDO	B	711	-	-	1/1/1/1	-
3	EDO	C	707	-	-	0/1/1/1	-
3	EDO	C	708	-	-	0/1/1/1	-
3	EDO	A	705	-	-	1/1/1/1	-
3	EDO	B	706	-	-	1/1/1/1	-
3	EDO	A	709	-	-	1/1/1/1	-
3	EDO	A	704	-	-	0/1/1/1	-
3	EDO	C	701	-	-	0/1/1/1	-
3	EDO	C	703	-	-	0/1/1/1	-
3	EDO	A	712	-	-	1/1/1/1	-
3	EDO	C	704	-	-	0/1/1/1	-
3	EDO	B	708	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	705	-	-	0/1/1/1	-
3	EDO	B	705	-	-	1/1/1/1	-
3	EDO	A	710	-	-	0/1/1/1	-
3	EDO	B	710	-	-	0/1/1/1	-
3	EDO	A	703	-	-	0/1/1/1	-
3	EDO	C	710	-	-	1/1/1/1	-
3	EDO	C	709	-	-	1/1/1/1	-
3	EDO	B	712	-	-	1/1/1/1	-
3	EDO	C	702	-	-	0/1/1/1	-
3	EDO	B	703	-	-	0/1/1/1	-
3	EDO	B	709	-	-	1/1/1/1	-
3	EDO	C	706	-	-	1/1/1/1	-
3	EDO	A	708	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	705	EDO	O1-C1-C2-O2
3	A	711	EDO	O1-C1-C2-O2
3	A	709	EDO	O1-C1-C2-O2
3	B	705	EDO	O1-C1-C2-O2
3	C	709	EDO	O1-C1-C2-O2
3	A	712	EDO	O1-C1-C2-O2
3	B	711	EDO	O1-C1-C2-O2
3	C	706	EDO	O1-C1-C2-O2
3	B	706	EDO	O1-C1-C2-O2
3	B	712	EDO	O1-C1-C2-O2
3	A	706	EDO	O1-C1-C2-O2
3	B	709	EDO	O1-C1-C2-O2
3	C	710	EDO	O1-C1-C2-O2

There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	707	EDO	3	0
3	A	706	EDO	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	707	EDO	1	0
3	A	705	EDO	1	0
3	C	704	EDO	1	0
3	B	708	EDO	3	0
3	C	705	EDO	1	0
3	B	705	EDO	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

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, 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	659/678 (97%)	0.04	5 (0%) 82 87	9, 25, 47, 69	12 (1%)
1	B	659/678 (97%)	0.24	9 (1%) 73 80	10, 28, 50, 74	12 (1%)
1	C	659/678 (97%)	0.01	6 (0%) 81 86	9, 24, 42, 61	15 (2%)
All	All	1977/2034 (97%)	0.10	20 (1%) 79 85	9, 26, 47, 74	39 (1%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	101	TYR	3.8
1	C	504	ILE	3.7
1	A	100	THR	3.7
1	B	672	ILE	3.1
1	B	95	GLY	3.0
1	B	569	ILE	2.8
1	A	150	ASN	2.6
1	B	504	ILE	2.6
1	B	101	TYR	2.6
1	A	504	ILE	2.5
1	B	558	ILE	2.4
1	B	517	LEU	2.4
1	C	101	TYR	2.3
1	B	511	LEU	2.3
1	C	503	VAL	2.2
1	A	614	ILE	2.2
1	B	552	ILE	2.1
1	C	98	VAL	2.1
1	C	155	THR	2.1
1	C	91	LEU	2.0

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

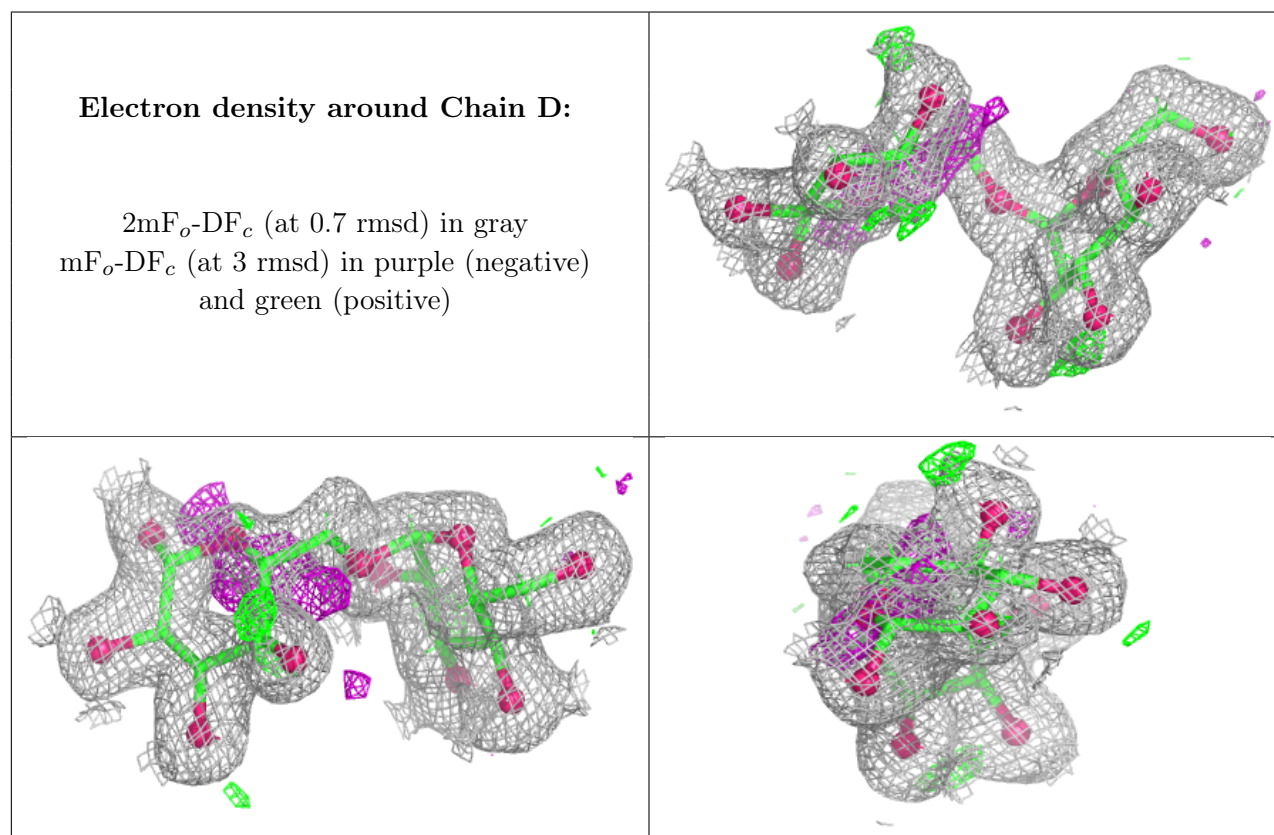
There are no non-standard protein/DNA/RNA residues in this entry.

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.

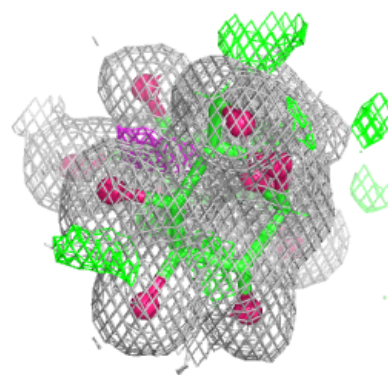
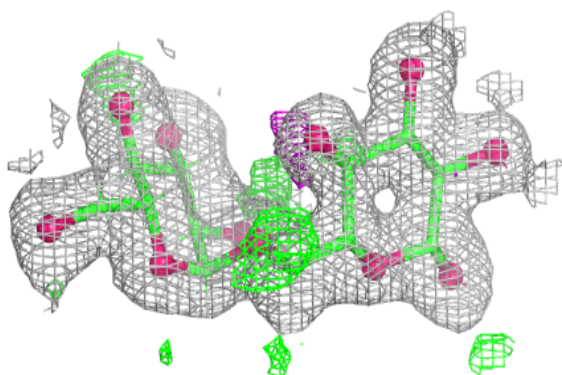
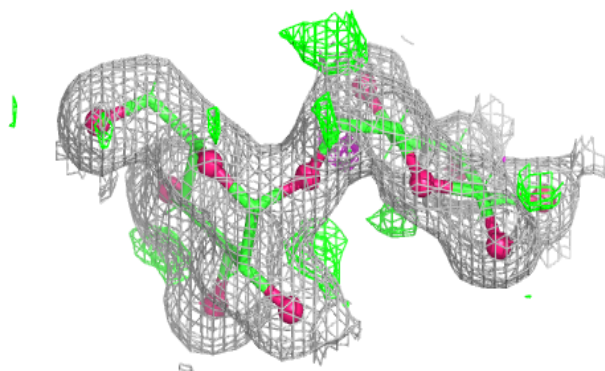
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BGC	F	1	12/12	0.84	0.13	34,43,45,48	4
2	BGC	D	1	12/12	0.89	0.12	26,34,43,43	4
2	BGC	E	1	12/12	0.92	0.10	27,33,43,43	4
2	GLC	F	2	11/12	0.95	0.07	21,24,43,43	4
2	GLC	D	2	11/12	0.97	0.07	18,20,43,43	4
2	GLC	E	2	11/12	0.97	0.07	17,20,43,43	4

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.

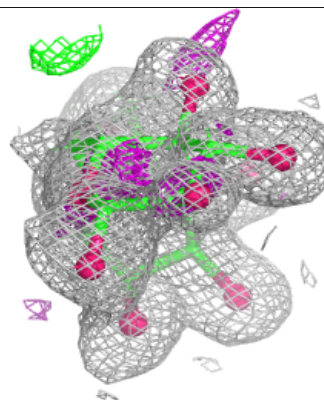
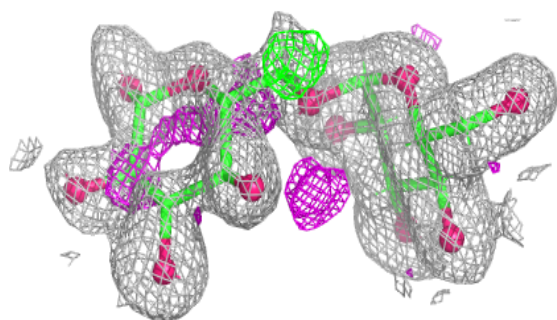
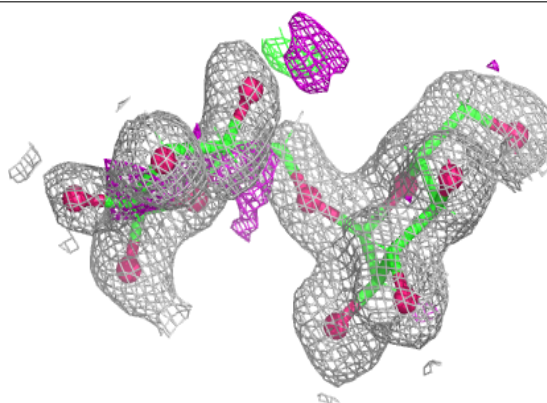


Electron density around Chain E:

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

**Electron density around Chain F:**

$2mF_o-DF_c$ (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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	EDO	B	706	4/4	0.76	0.17	43,45,46,47	1
3	EDO	A	712	4/4	0.82	0.15	43,52,52,53	1
3	EDO	A	711	4/4	0.85	0.14	40,41,46,51	1
3	EDO	B	708	4/4	0.86	0.14	31,36,38,43	1
3	EDO	B	712	4/4	0.88	0.14	43,52,54,54	1
3	EDO	C	708	4/4	0.88	0.12	43,51,54,55	1
3	EDO	C	709	4/4	0.88	0.14	43,49,56,59	1
3	EDO	C	710	4/4	0.88	0.15	43,48,53,59	1
3	EDO	B	710	4/4	0.89	0.11	37,43,47,50	1
3	EDO	B	705	4/4	0.91	0.10	33,34,43,46	1
3	EDO	A	705	4/4	0.91	0.12	29,31,43,45	1
3	EDO	B	707	4/4	0.92	0.09	33,34,35,43	1
3	EDO	C	704	4/4	0.93	0.09	34,36,42,43	1
3	EDO	C	707	4/4	0.93	0.09	37,39,41,43	1
3	EDO	A	710	4/4	0.93	0.08	34,39,42,43	1
3	EDO	A	708	4/4	0.93	0.09	34,39,41,43	1
3	EDO	A	709	4/4	0.93	0.09	29,42,43,44	1
3	EDO	B	711	4/4	0.94	0.08	33,38,43,43	1
3	EDO	C	705	4/4	0.95	0.10	25,31,35,43	1
3	EDO	C	706	4/4	0.95	0.07	33,37,38,43	1
3	EDO	B	703	4/4	0.95	0.08	24,26,31,43	1
3	EDO	A	707	4/4	0.95	0.12	24,31,37,43	1
3	EDO	C	703	4/4	0.95	0.08	29,37,40,43	1
3	EDO	A	706	4/4	0.95	0.09	35,39,43,44	1
3	EDO	B	709	4/4	0.96	0.07	36,37,38,43	1
3	EDO	C	702	4/4	0.97	0.06	21,26,28,43	1
3	EDO	A	704	4/4	0.97	0.07	20,23,27,43	1
3	EDO	A	703	4/4	0.97	0.06	19,20,22,43	1
3	EDO	C	701	4/4	0.98	0.04	20,23,25,43	1
3	EDO	B	704	4/4	0.98	0.05	25,26,27,43	1

6.5 Other polymers

There are no such residues in this entry.