



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 11, 2022 – 01:31 pm BST

PDB ID : 6SAU  
Title : Structural and functional characterisation of three novel fungal amylases with enhanced stability and pH tolerance  
Authors : Roth, C.; Moroz, O.V.; Turkenburg, J.P.; Blagova, E.; Waterman, J.; Ariza, A.; Ming, L.; Tinaqi, S.; Andersen, C.; Davies, G.J.; Wilson, K.S.  
Deposited on : 2019-07-17  
Resolution : 1.35 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.27  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.27

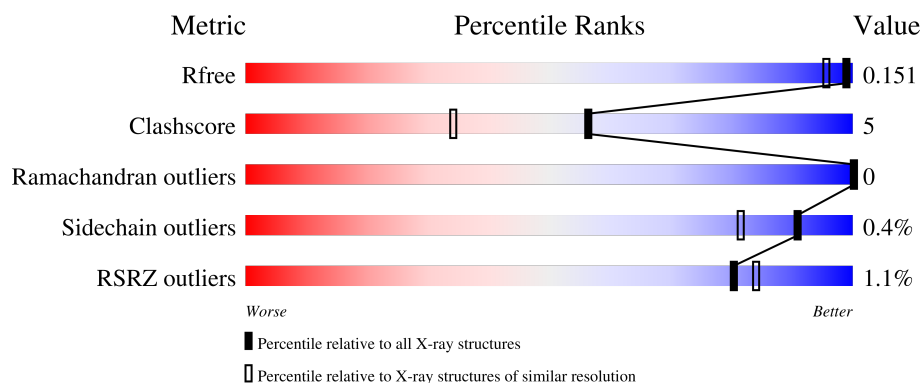
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



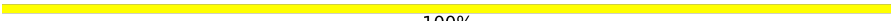
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1509 (1.38-1.34)
Clashscore	141614	1551 (1.38-1.34)
Ramachandran outliers	138981	1530 (1.38-1.34)
Sidechain outliers	138945	1530 (1.38-1.34)
RSRZ outliers	127900	1487 (1.38-1.34)

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	460	 2% 85% 11% .
1	B	460	 % 90% 6% .
2	C	5	 100%
2	E	5	 60% 40%
3	D	2	 100%

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Mol	Chain	Length	Quality of chain
3	F	2	 100%

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8263 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 alpha amylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	6	14	0
			3557	2248	614	679	16			
1	B	442	Total	C	N	O	S	3	20	0
			3609	2280	627	688	14			

- Molecule 2 is an oligosaccharide called 4,6-dideoxy-4-[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-4,6-dideoxy-4-[(1S,4R,5S,6S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	0	0
			76	44	2	30			
2	E	5	Total	C	N	O	0	1	0
			97	57	3	37			

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



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

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Ca 1	0	0
4	B	1	Total 1	Ca 1	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	Na 1	0	0

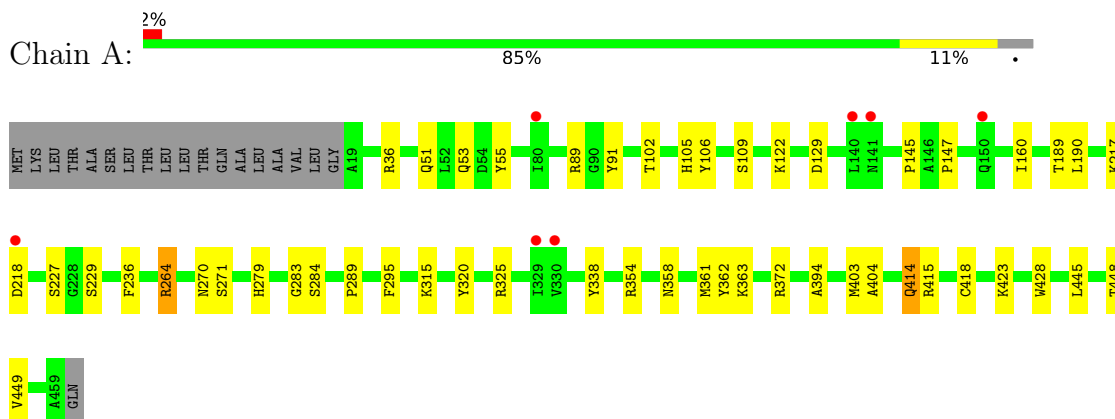
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	432	Total 432	O 432	0	0
6	B	443	Total 443	O 443	0	0

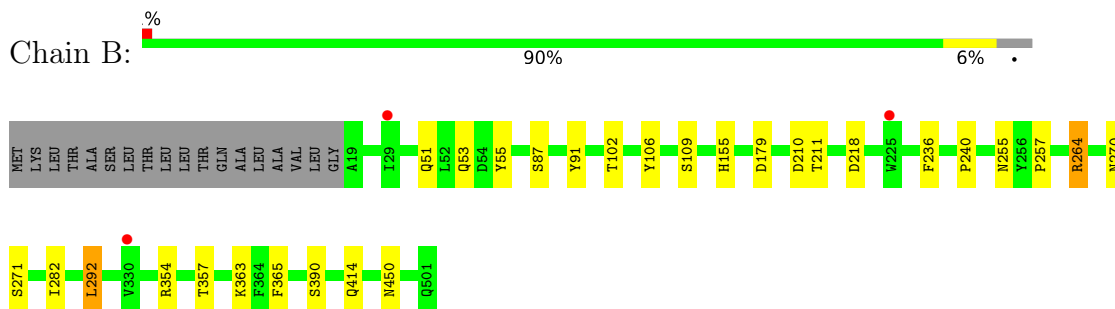
### 3 Residue-property plots

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.

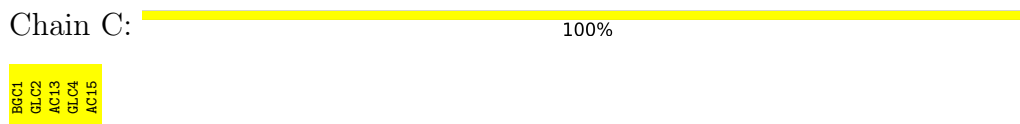
- Molecule 1: alpha amylase



- Molecule 1: alpha amylase



- Molecule 2: 4,6-dideoxy-4- $\{[(1S,4R,5S,6S)-4,5,6$ -trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino $\}$ -alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-4,6-dideoxy-4- $\{[(1S,4R,5S,6S)-4,5,6$ -trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino $\}$ -alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranose



- Molecule 2: 4,6-dideoxy-4- $\{[(1S,4R,5S,6S)-4,5,6$ -trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino $\}$ -alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-4,6-dideoxy-4- $\{[(1S,4R,5S,6S)-4,5,6$ -trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino $\}$ -alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranose

S)-4,5,6-trihydroxy-3-(hydroxymethyl)cyclohex-2-en-1-yl]amino}-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain E:  60% 40%

BGC1  
GLC2  
AC13  
GLC4  
AC15

- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D:  100%

GLC1  
GLC2

- Molecule 3: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain F:  100%

GLC1  
GLC2

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.88Å 61.97Å 70.39Å 79.33° 82.88° 67.99°	Depositor
Resolution (Å)	33.13 – 1.35 33.11 – 1.35	Depositor EDS
% Data completeness (in resolution range)	85.2 (33.13-1.35) 85.3 (33.11-1.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	10.15 (at 1.35Å)	Xtrriage
Refinement program	REFMAC 5.8.0253	Depositor
R, $R_{free}$	0.113 , 0.150 0.114 , 0.151	Depositor DCC
$R_{free}$ test set	8289 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	8.0	Xtrriage
Anisotropy	0.070	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8263	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	10.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% 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: BGC, GLC, CA, NA, AC1

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	0.96	6/3658 (0.2%)	1.16	17/4965 (0.3%)
1	B	0.92	3/3716 (0.1%)	1.06	12/5041 (0.2%)
All	All	0.94	9/7374 (0.1%)	1.11	29/10006 (0.3%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	390	SER	CA-CB	9.26	1.66	1.52
1	A	270	ASN	CB-CG	-7.85	1.32	1.51
1	A	271	SER	CB-OG	6.32	1.50	1.42
1	B	87	SER	CB-OG	-6.16	1.34	1.42
1	A	284	SER	CB-OG	5.79	1.49	1.42
1	A	227[A]	SER	CA-CB	5.66	1.61	1.52
1	A	227[B]	SER	CA-CB	5.66	1.61	1.52
1	B	271	SER	CA-CB	5.19	1.60	1.52
1	A	325	ARG	NE-CZ	5.16	1.39	1.33

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	325	ARG	NE-CZ-NH2	-17.34	111.63	120.30
1	A	325	ARG	NE-CZ-NH1	10.98	125.79	120.30
1	B	264[A]	ARG	CD-NE-CZ	9.64	137.10	123.60
1	B	264[B]	ARG	CD-NE-CZ	9.64	137.10	123.60
1	A	415	ARG	NE-CZ-NH1	9.40	125.00	120.30
1	A	415	ARG	NE-CZ-NH2	-9.11	115.75	120.30
1	A	89	ARG	NE-CZ-NH2	-8.57	116.02	120.30
1	B	106	TYR	CB-CG-CD1	7.32	125.39	121.00
1	A	372	ARG	NE-CZ-NH2	-7.14	116.73	120.30
1	A	89	ARG	NE-CZ-NH1	7.10	123.85	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	264[A]	ARG	NE-CZ-NH1	6.83	123.72	120.30
1	B	264[B]	ARG	NE-CZ-NH1	6.83	123.72	120.30
1	A	36	ARG	NE-CZ-NH1	6.23	123.42	120.30
1	A	354	ARG	CB-CG-CD	6.13	127.53	111.60
1	B	354	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	A	354	ARG	NE-CZ-NH2	-6.05	117.27	120.30
1	B	365	PHE	CB-CG-CD2	6.05	125.04	120.80
1	A	106	TYR	CB-CG-CD1	6.04	124.62	121.00
1	B	53	GLN	CB-CG-CD	5.89	126.92	111.60
1	A	264[A]	ARG	CG-CD-NE	5.79	123.95	111.80
1	A	264[B]	ARG	CG-CD-NE	5.79	123.95	111.80
1	A	129	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	B	51	GLN	CB-CG-CD	5.42	125.69	111.60
1	A	362	TYR	CB-CG-CD1	5.34	124.20	121.00
1	B	106	TYR	CB-CG-CD2	-5.13	117.92	121.00
1	A	338	TYR	CB-CG-CD2	-5.13	117.92	121.00
1	A	295	PHE	CB-CG-CD2	-5.11	117.23	120.80
1	B	292[A]	LEU	CB-CG-CD2	-5.10	102.33	111.00
1	B	292[B]	LEU	CB-CG-CD2	-5.10	102.33	111.00

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	3557	0	3362	38	0
1	B	3609	0	3422	32	0
2	C	76	0	48	0	0
2	E	97	0	56	4	0
3	D	23	0	21	0	0
3	F	23	0	20	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	1	0	0	0	0
6	A	432	0	0	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	443	0	0	12	0
All	All	8263	0	6929	71	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (71) 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:358:ASN:HB3	6:A:694:HOH:O	1.29	1.29
1:B:363[B]:LYS:HE3	6:B:720:HOH:O	1.47	1.13
2:E:2:GLC:O4	2:E:3[B]:AC1:C1	2.00	1.09
1:B:363[B]:LYS:CE	6:B:720:HOH:O	2.03	1.02
1:B:218:ASP:OD1	6:B:701:HOH:O	1.82	0.97
1:B:264[A]:ARG:NE	6:B:702:HOH:O	1.99	0.90
1:B:282[A]:ILE:HD11	6:B:1043:HOH:O	1.73	0.87
1:B:414:GLN:NE2	1:B:450[A]:ASN:OD1	2.07	0.87
1:A:361[A]:MET:HA	1:A:361[A]:MET:CE	2.07	0.84
1:B:264[A]:ARG:CZ	6:B:702:HOH:O	2.26	0.84
1:A:315:LYS:HE3	1:A:361[A]:MET:HE1	1.59	0.84
1:A:218[A]:ASP:OD1	6:A:601:HOH:O	1.94	0.83
1:B:264[A]:ARG:NH2	6:B:702:HOH:O	2.13	0.81
1:B:257:PRO:HB2	1:B:282[A]:ILE:HG21	1.64	0.79
1:A:361[A]:MET:HA	1:A:361[A]:MET:HE2	1.66	0.76
1:B:363[B]:LYS:HD2	6:B:720:HOH:O	1.85	0.76
1:A:51:GLN:HE21	1:A:53:GLN:HE22	1.32	0.75
1:B:240:PRO:HB3	1:B:282[A]:ILE:HG22	1.68	0.73
1:A:315:LYS:CE	1:A:361[A]:MET:HE1	2.21	0.70
1:B:210:ASP:OD1	2:E:3[B]:AC1:HCB1	1.92	0.69
1:A:448[A]:THR:HG21	6:A:656:HOH:O	1.93	0.69
1:B:257:PRO:CB	1:B:282[A]:ILE:HG21	2.24	0.67
1:A:145:PRO:HG2	1:A:190[A]:LEU:HD11	1.79	0.65
1:A:147:PRO:HD2	1:A:190[B]:LEU:HD12	1.79	0.64
1:A:122:LYS:NZ	6:A:604:HOH:O	2.18	0.64
1:A:279:HIS:HD2	1:A:320:TYR:OH	1.81	0.63
1:A:102[A]:THR:OG1	6:A:603:HOH:O	2.16	0.63
1:B:240:PRO:HB3	1:B:282[A]:ILE:CG2	2.29	0.63
1:B:282[A]:ILE:CD1	1:B:292[A]:LEU:HD13	2.29	0.63
1:B:211:THR:HG23	2:E:3[B]:AC1:HC7	1.81	0.63
1:A:229[A]:SER:OG	6:A:602:HOH:O	2.15	0.62
1:A:361[A]:MET:CE	1:A:361[A]:MET:CA	2.77	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:PRO:CB	1:B:282[A]:ILE:HG22	2.31	0.60
1:B:255:ASN:HD21	1:B:282[A]:ILE:HD11	1.68	0.59
1:A:189[A]:THR:HG23	6:A:918:HOH:O	2.04	0.58
1:A:448[A]:THR:HG23	6:A:814:HOH:O	2.05	0.56
1:A:363:LYS:NZ	6:A:606:HOH:O	2.36	0.55
1:A:147:PRO:HD2	1:A:190[B]:LEU:CD1	2.37	0.55
1:B:357:THR:O	1:B:363[B]:LYS:HE2	2.07	0.55
1:B:102[A]:THR:OG1	6:B:703:HOH:O	2.18	0.54
1:A:361[A]:MET:CA	1:A:361[A]:MET:HE3	2.38	0.54
1:B:155:HIS:HE1	6:B:916:HOH:O	1.91	0.53
1:A:217[A]:LYS:NZ	6:A:607:HOH:O	2.37	0.53
1:B:155:HIS:HD2	1:B:179:ASP:OD2	1.93	0.52
1:A:403[A]:MET:HE1	1:A:428:TRP:CZ2	2.46	0.51
1:A:55:TYR:CE1	1:A:91:TYR:HA	2.47	0.50
1:B:210:ASP:OD1	2:E:3[B]:AC1:C1B	2.59	0.50
1:B:282[A]:ILE:CD1	1:B:292[A]:LEU:CD1	2.90	0.49
1:A:358:ASN:CB	6:A:694:HOH:O	2.14	0.49
1:B:55:TYR:CE1	1:B:91:TYR:HA	2.49	0.48
1:B:102[A]:THR:HG21	1:B:109:SER:HA	1.94	0.47
1:B:363[B]:LYS:CD	6:B:720:HOH:O	2.36	0.47
1:A:102[A]:THR:HG22	6:A:665:HOH:O	2.14	0.47
1:A:279:HIS:HE1	6:A:766:HOH:O	1.98	0.47
1:B:264[B]:ARG:NE	1:B:270:ASN:OD1	2.48	0.46
1:A:102[A]:THR:HG21	1:A:109:SER:HA	1.99	0.45
1:A:315:LYS:CE	1:A:361[A]:MET:CE	2.95	0.44
1:B:264[B]:ARG:NH2	1:B:270:ASN:OD1	2.50	0.44
1:B:357:THR:O	1:B:363[B]:LYS:CE	2.66	0.44
1:A:160:ILE:HG21	1:A:160:ILE:HD13	1.64	0.44
1:A:105:HIS:HE1	6:A:968:HOH:O	2.01	0.43
1:A:394:ALA:HA	1:A:404:ALA:O	2.18	0.43
1:B:282[A]:ILE:HD13	1:B:292[A]:LEU:HD13	1.98	0.42
1:A:315:LYS:HE2	1:A:361[A]:MET:CE	2.50	0.42
1:A:414:GLN:HA	1:A:449:VAL:O	2.20	0.42
1:B:264[A]:ARG:HD3	6:B:945:HOH:O	2.20	0.42
1:A:418:CYS:HA	1:A:445:LEU:O	2.20	0.41
1:A:264[A]:ARG:HD3	6:A:940:HOH:O	2.21	0.41
1:A:423:LYS:HE2	6:A:946:HOH:O	2.20	0.40
1:A:283:GLY:HA2	1:A:289:PRO:HB3	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	453/460 (98%)	445 (98%)	8 (2%)	0	100	100
1	B	460/460 (100%)	453 (98%)	7 (2%)	0	100	100
All	All	913/920 (99%)	898 (98%)	15 (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	378/379 (100%)	376 (100%)	2 (0%)	88	74
1	B	385/379 (102%)	384 (100%)	1 (0%)	92	83
All	All	763/758 (101%)	760 (100%)	3 (0%)	91	81

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

Mol	Chain	Res	Type
1	A	236	PHE
1	A	414	GLN
1	B	236	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	GLN
1	A	105	HIS
1	A	150	GLN
1	A	267	GLN
1	A	279	HIS
1	B	22	ASN
1	B	105	HIS
1	B	155	HIS
1	B	163	ASN
1	B	241	ASN
1	B	267	GLN
1	B	414	GLN

### 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 ⓘ

15 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	C	1	2	12,12,12	1.08	1 (8%)	17,17,17	1.54	2 (11%)
2	GLC	C	2	2	11,11,12	0.95	0	15,15,17	1.49	2 (13%)
2	AC1	C	3	2	21,22,23	2.26	5 (23%)	22,32,34	1.73	3 (13%)
2	GLC	C	4	2	11,11,12	1.28	1 (9%)	15,15,17	1.26	2 (13%)
2	AC1	C	5	2	21,22,23	0.86	1 (4%)	22,32,34	1.13	2 (9%)
3	GLC	D	1	3	12,12,12	1.71	4 (33%)	17,17,17	2.19	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GLC	D	2	3	11,11,12	1.40	2 (18%)	15,15,17	1.68	3 (20%)
2	BGC	E	1	2	12,12,12	1.26	0	17,17,17	1.25	2 (11%)
2	GLC	E	2	2	11,11,12	0.97	2 (18%)	15,15,17	0.89	0
2	AC1	E	3[A]	2	21,22,23	2.36	8 (38%)	22,32,34	1.93	7 (31%)
2	AC1	E	3[B]	2	21,22,23	0.93	1 (4%)	22,32,34	1.39	5 (22%)
2	GLC	E	4	2	11,11,12	1.59	2 (18%)	15,15,17	1.42	3 (20%)
2	AC1	E	5	2	21,22,23	1.74	4 (19%)	22,32,34	1.76	8 (36%)
3	GLC	F	1	3	12,12,12	1.28	2 (16%)	17,17,17	1.68	3 (17%)
3	GLC	F	2	3	11,11,12	1.45	3 (27%)	15,15,17	2.01	4 (26%)

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	C	1	2	-	0/2/22/22	0/1/1/1
2	GLC	C	2	2	-	0/2/19/22	0/1/1/1
2	AC1	C	3	2	-	3/6/43/46	0/2/2/2
2	GLC	C	4	2	-	0/2/19/22	0/1/1/1
2	AC1	C	5	2	-	1/6/43/46	0/2/2/2
3	GLC	D	1	3	-	0/2/22/22	0/1/1/1
3	GLC	D	2	3	-	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	AC1	E	3[A]	2	-	2/6/43/46	0/2/2/2
2	AC1	E	3[B]	2	-	2/6/43/46	0/2/2/2
2	GLC	E	4	2	-	0/2/19/22	0/1/1/1
2	AC1	E	5	2	-	1/6/43/46	0/2/2/2
3	GLC	F	1	3	-	0/2/22/22	0/1/1/1
3	GLC	F	2	3	-	0/2/19/22	0/1/1/1

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	3[A]	AC1	C1B-N4A	7.41	1.61	1.47
2	C	3	AC1	C1B-N4A	6.51	1.59	1.47
2	E	5	AC1	C7B-C5B	4.46	1.39	1.32
2	C	3	AC1	C4A-C5B	-4.31	1.47	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	4	GLC	C4-C5	3.56	1.60	1.53
2	E	5	AC1	C1B-N4A	3.50	1.53	1.47
3	D	1	GLC	O4-C4	3.47	1.51	1.43
2	E	3[A]	AC1	C2B-C1B	3.29	1.57	1.52
2	C	3	AC1	O6B-C6B	3.14	1.52	1.41
2	C	3	AC1	O5-C1	-2.92	1.39	1.43
2	E	3[A]	AC1	C4A-C5B	-2.91	1.49	1.51
2	E	5	AC1	O4-C4A	2.89	1.48	1.42
2	E	3[A]	AC1	O4-C4A	2.88	1.48	1.42
2	C	4	GLC	C2-C3	-2.84	1.48	1.52
2	E	3[A]	AC1	O3B-C3B	-2.61	1.36	1.43
3	D	1	GLC	C1-C2	-2.57	1.46	1.52
2	E	4	GLC	O6-C6	2.50	1.53	1.42
3	D	2	GLC	O3-C3	-2.48	1.37	1.43
3	F	2	GLC	C6-C5	2.48	1.60	1.51
2	E	3[A]	AC1	O5-C1	2.47	1.47	1.43
3	D	1	GLC	O2-C2	-2.45	1.37	1.43
2	C	3	AC1	C1B-C7B	2.41	1.53	1.50
3	F	2	GLC	C2-C3	2.29	1.55	1.52
2	E	3[A]	AC1	O3-C3	2.22	1.48	1.43
2	E	5	AC1	C4A-C5B	2.21	1.53	1.51
2	E	3[A]	AC1	C4-N4A	2.19	1.51	1.47
3	F	1	GLC	C1-C2	2.17	1.57	1.52
3	D	1	GLC	C3-C2	2.14	1.57	1.52
3	F	2	GLC	O6-C6	-2.08	1.33	1.42
2	C	5	AC1	C4-N4A	2.06	1.50	1.47
2	E	2	GLC	C4-C5	-2.04	1.48	1.53
2	E	3[B]	AC1	C1B-N4A	2.04	1.51	1.47
3	D	2	GLC	O5-C1	2.02	1.46	1.43
3	F	1	GLC	O5-C5	2.02	1.49	1.44
2	E	2	GLC	C2-C3	-2.02	1.49	1.52
2	C	1	BGC	C4-C5	-2.01	1.48	1.53

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1	GLC	O5-C5-C4	-5.11	100.41	109.69
2	C	3	AC1	O6B-C6B-C5B	-5.07	100.38	112.50
3	D	2	GLC	O2-C2-C1	-4.69	99.56	109.15
3	F	2	GLC	C2-C3-C4	-4.08	103.84	110.89
3	F	2	GLC	C1-C2-C3	4.08	114.68	109.67
3	D	1	GLC	C1-O5-C5	4.07	121.34	113.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	3[A]	AC1	C1-C2-C3	4.05	114.64	109.67
3	D	1	GLC	O5-C5-C6	4.01	116.42	106.44
3	D	1	GLC	O5-C1-C2	-3.92	103.29	110.28
2	C	2	GLC	C1-O5-C5	3.90	117.47	112.19
2	C	1	BGC	O4-C4-C3	-3.84	101.47	110.35
2	E	3[A]	AC1	O2B-C2B-C3B	3.72	118.94	110.35
2	E	5	AC1	C1-C2-C3	-3.63	105.20	109.67
2	E	3[A]	AC1	O3-C3-C4	3.41	116.54	109.66
2	C	3	AC1	O2B-C2B-C3B	3.34	118.06	110.35
2	E	4	GLC	C3-C4-C5	-3.33	104.30	110.24
3	F	1	GLC	O4-C4-C5	3.28	117.44	109.30
3	F	1	GLC	C1-O5-C5	3.27	119.83	113.66
2	C	4	GLC	C3-C4-C5	-3.26	104.42	110.24
2	C	3	AC1	O5-C1-C2	3.25	115.78	110.77
2	E	3[A]	AC1	O6B-C6B-C5B	-3.13	105.02	112.50
2	E	1	BGC	O2-C2-C1	3.08	116.30	109.16
2	E	5	AC1	O5-C5-C6	-2.92	101.05	107.33
2	E	5	AC1	O2B-C2B-C1B	2.89	114.92	109.12
2	C	4	GLC	O3-C3-C2	-2.81	104.62	109.99
2	E	3[A]	AC1	O3-C3-C2	-2.81	104.62	109.99
3	F	1	GLC	O5-C5-C4	-2.78	104.65	109.69
2	E	3[B]	AC1	O3-C3-C4	-2.73	104.15	109.66
2	C	5	AC1	O5-C1-C2	2.64	114.85	110.77
2	E	3[B]	AC1	C1-C2-C3	2.62	112.88	109.67
2	E	5	AC1	O3-C3-C4	2.62	114.94	109.66
3	F	2	GLC	O2-C2-C1	-2.58	103.87	109.15
2	E	3[A]	AC1	O2B-C2B-C1B	-2.58	103.94	109.12
2	C	5	AC1	O3-C3-C4	2.58	114.86	109.66
3	D	2	GLC	C3-C4-C5	-2.52	105.74	110.24
2	C	2	GLC	O5-C5-C6	2.43	111.01	107.20
2	E	3[B]	AC1	O5-C5-C4	-2.41	105.61	110.05
2	C	1	BGC	C3-C4-C5	-2.39	105.98	110.24
3	F	2	GLC	C6-C5-C4	2.36	118.53	113.00
2	E	4	GLC	C1-C2-C3	2.35	112.56	109.67
2	E	5	AC1	O2B-C2B-C3B	-2.19	105.29	110.35
3	D	1	GLC	O2-C2-C1	-2.15	104.17	109.16
3	D	2	GLC	O3-C3-C2	-2.14	105.89	109.99
2	E	3[B]	AC1	C2-C3-C4	2.13	112.50	110.63
2	E	3[A]	AC1	C2-C3-C4	-2.11	108.77	110.63
2	E	1	BGC	O2-C2-C3	-2.10	105.50	110.35
2	E	3[B]	AC1	C7B-C1B-N4A	-2.09	107.54	110.68
2	E	4	GLC	O4-C4-C5	-2.07	104.14	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	5	AC1	O4-C4A-C5B	2.04	114.74	110.82
2	E	5	AC1	C7B-C1B-N4A	2.00	113.69	110.68
2	E	5	AC1	O5-C5-C4	-2.00	106.36	110.05

There are no chirality outliers.

All (9) torsion outliers are listed below:

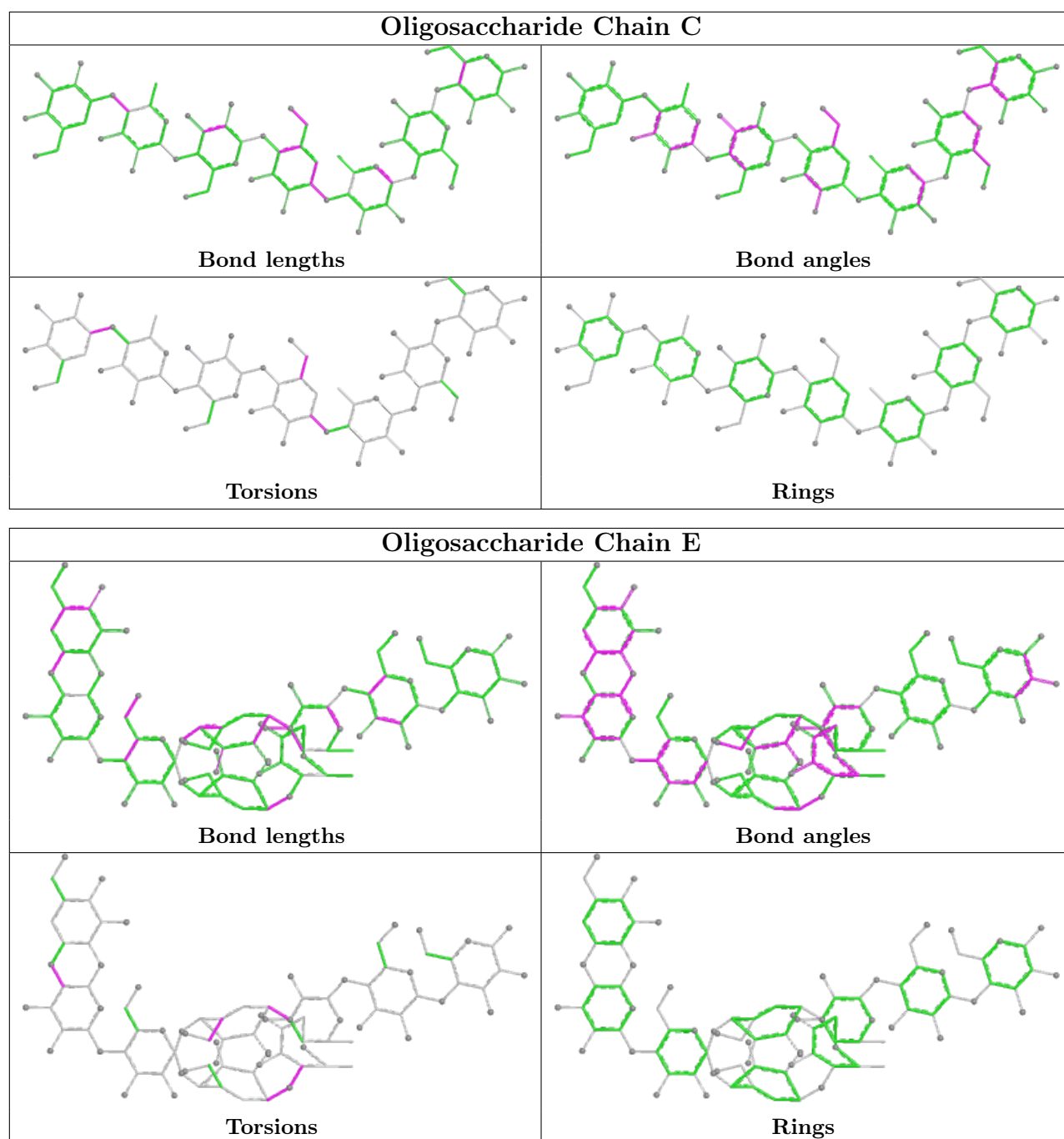
Mol	Chain	Res	Type	Atoms
2	C	3	AC1	C7B-C1B-N4A-C4
2	C	3	AC1	C7B-C5B-C6B-O6B
2	E	3[A]	AC1	C7B-C1B-N4A-C4
2	E	3[B]	AC1	C7B-C1B-N4A-C4
2	C	5	AC1	C2B-C1B-N4A-C4
2	E	3[B]	AC1	C3-C4-N4A-C1B
2	E	5	AC1	C5-C4-N4A-C1B
2	C	3	AC1	C4A-C5B-C6B-O6B
2	E	3[A]	AC1	C7B-C5B-C6B-O6B

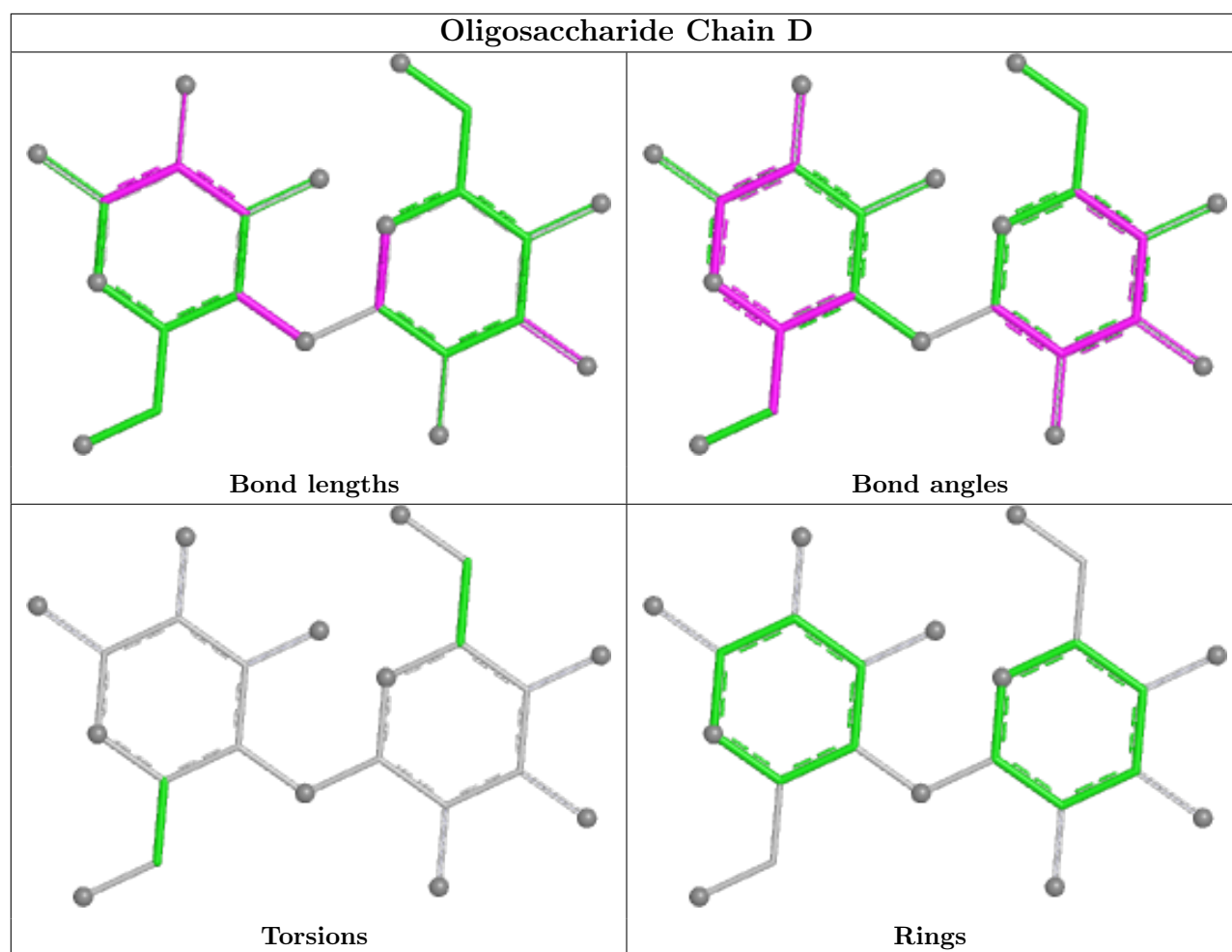
There are no ring outliers.

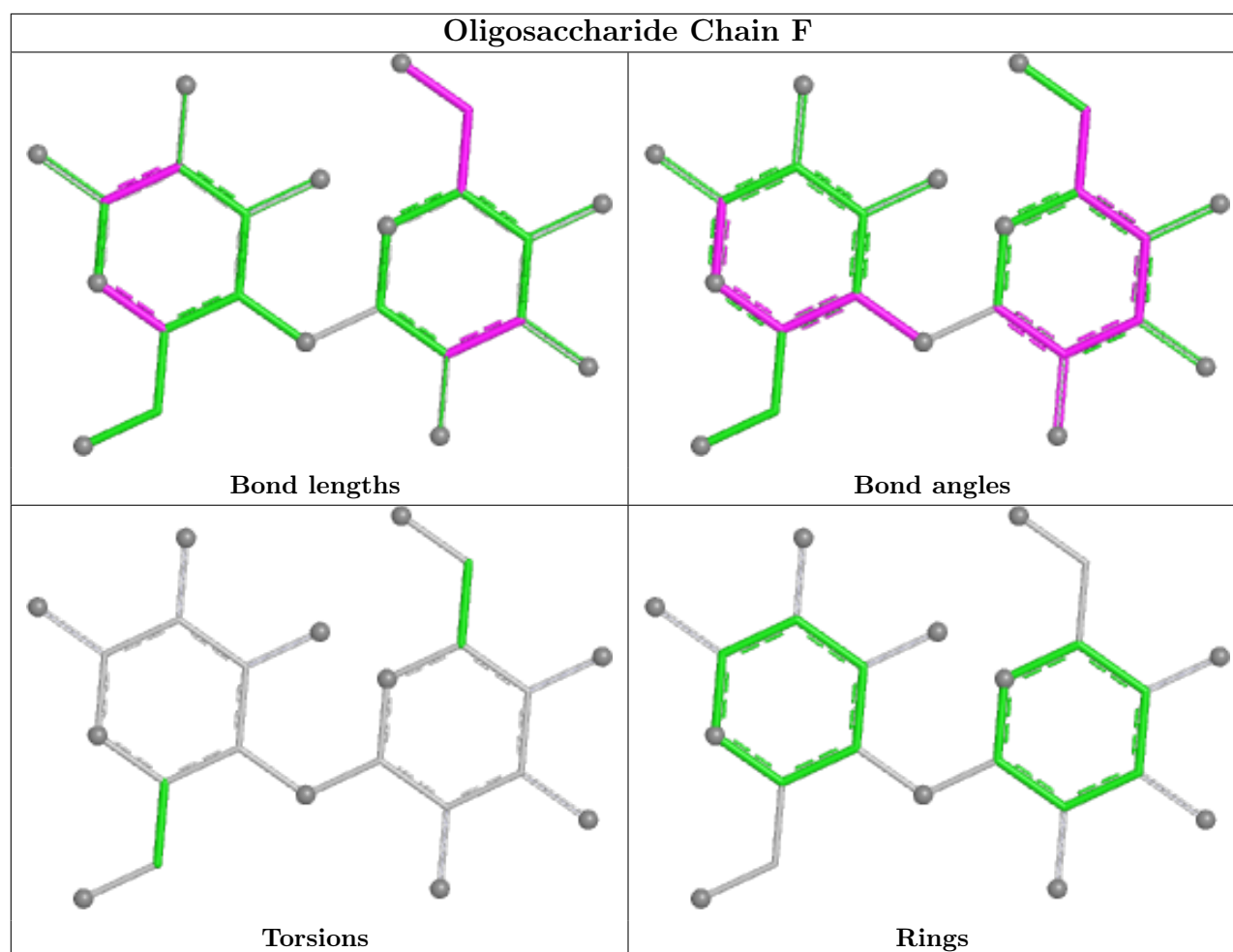
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	3[B]	AC1	4	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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	441/460 (95%)	0.23	7 (1%) 72 76	5, 9, 17, 32	3 (0%)
1	B	442/460 (96%)	0.14	3 (0%) 87 90	4, 8, 16, 23	1 (0%)
All	All	883/920 (95%)	0.18	10 (1%) 80 84	4, 8, 17, 32	4 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	225	TRP	3.2
1	A	330	VAL	2.3
1	A	218[A]	ASP	2.3
1	B	29	ILE	2.3
1	A	329	ILE	2.2
1	A	80	ILE	2.1
1	A	150	GLN	2.1
1	A	140	LEU	2.1
1	B	330	VAL	2.0
1	A	141	ASN	2.0

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

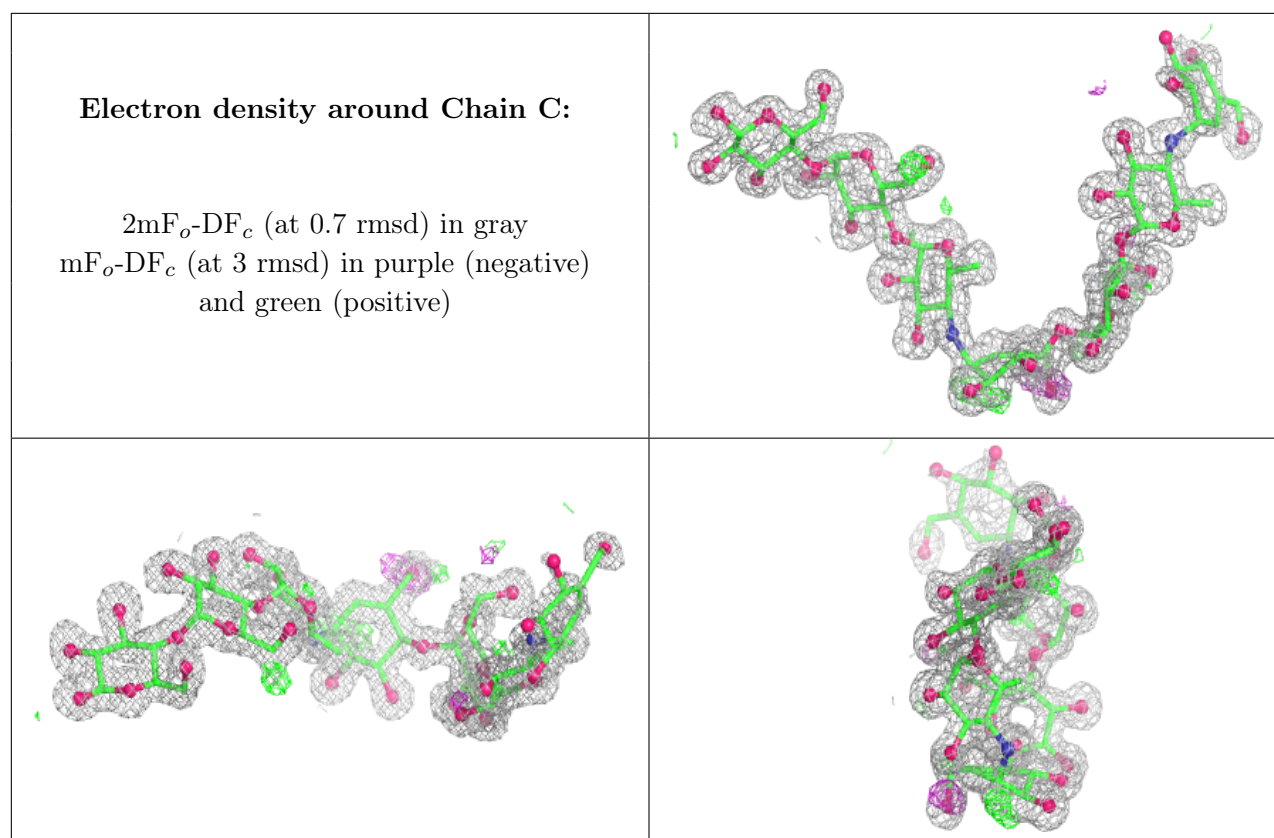
There are no non-standard protein/DNA/RNA residues in this entry.

### 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, 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.

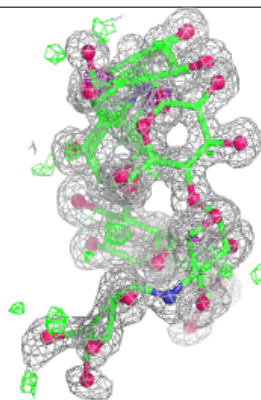
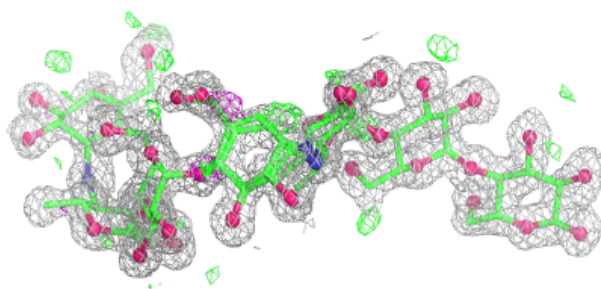
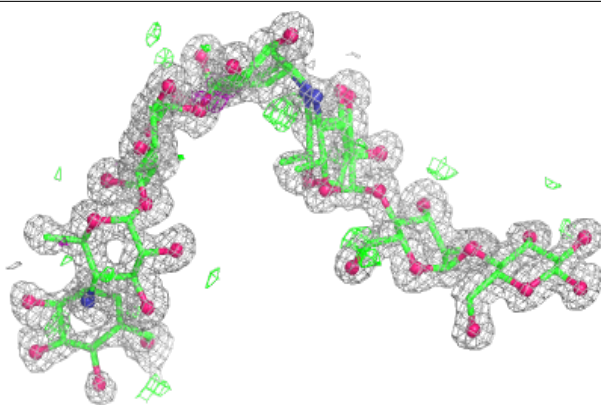
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	AC1	E	5	21/22	0.90	0.20	15,21,26,39	0
3	GLC	F	2	11/12	0.91	0.22	17,25,33,54	0
3	GLC	D	2	11/12	0.92	0.15	22,27,31,32	0
3	GLC	D	1	12/12	0.92	0.13	15,18,22,24	12
2	AC1	C	5	21/22	0.94	0.21	13,22,47,61	0
3	GLC	F	1	12/12	0.95	0.15	15,17,23,28	0
2	BGC	C	1	12/12	0.95	0.14	15,20,27,29	0
2	BGC	E	1	12/12	0.96	0.19	13,21,26,31	0
2	AC1	E	3[A]	21/22	0.96	0.12	5,8,10,12	21
2	AC1	E	3[B]	21/22	0.96	0.12	7,10,13,17	21
2	AC1	C	3	21/22	0.96	0.09	7,10,14,15	0
2	GLC	E	2	11/12	0.97	0.11	10,11,17,25	0
2	GLC	C	2	11/12	0.97	0.09	11,13,17,28	0
2	GLC	E	4	11/12	0.98	0.06	7,8,12,13	0
2	GLC	C	4	11/12	0.98	0.07	6,8,11,12	0

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



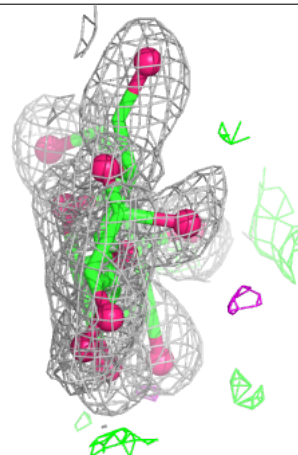
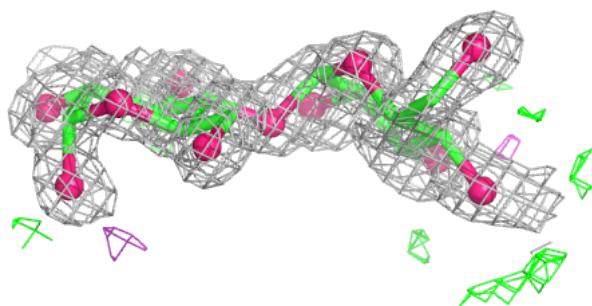
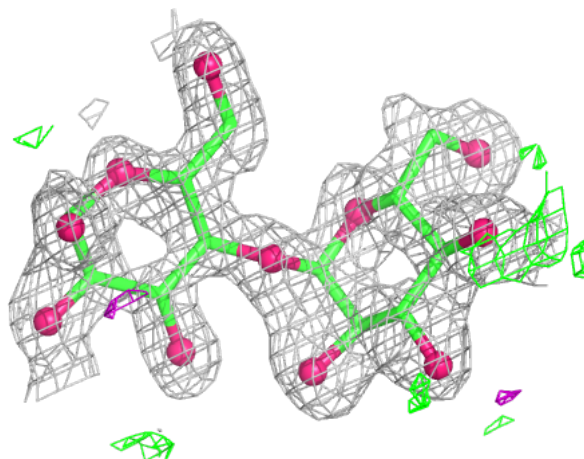
**Electron density around Chain E:**

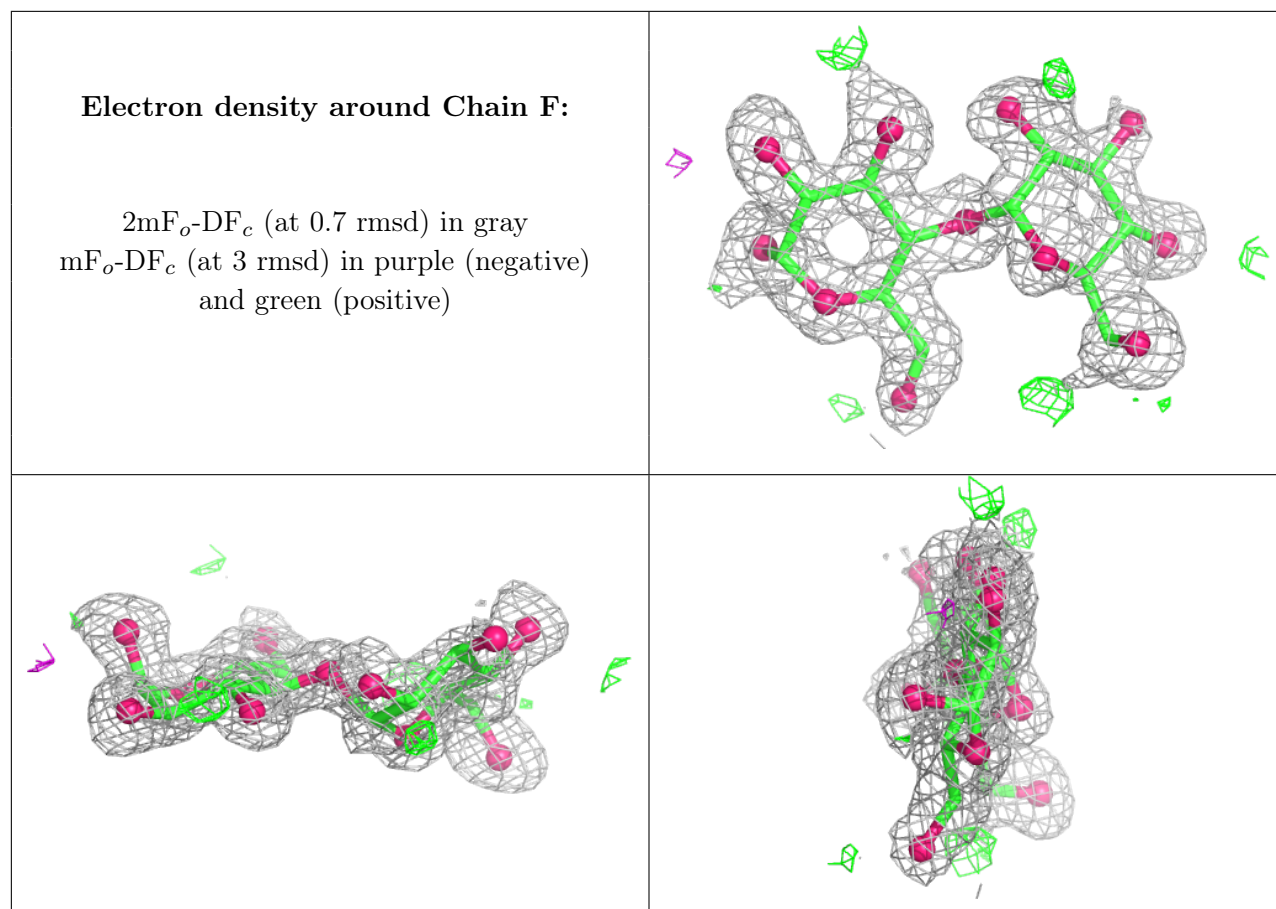
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain D:**

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





## 6.4 Ligands [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( $\text{\AA}^2$ )	Q<0.9
4	CA	A	501	1/1	1.00	0.05	6,6,6,6	0
4	CA	B	601	1/1	1.00	0.05	5,5,5,5	0
5	NA	B	602	1/1	1.00	0.08	10,10,10,10	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.