



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2022 – 04:05 PM EDT

PDB ID : 7UFL  
Title : Crystal structure of chimeric omicron RBD (strain BA.2) complexed with chimeric mouse ACE2  
Authors : Zhang, W.; Shi, K.; Geng, Q.; Ye, G.; Aihara, H.; Li, F.  
Deposited on : 2022-03-22  
Resolution : 2.84 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)

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>.

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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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

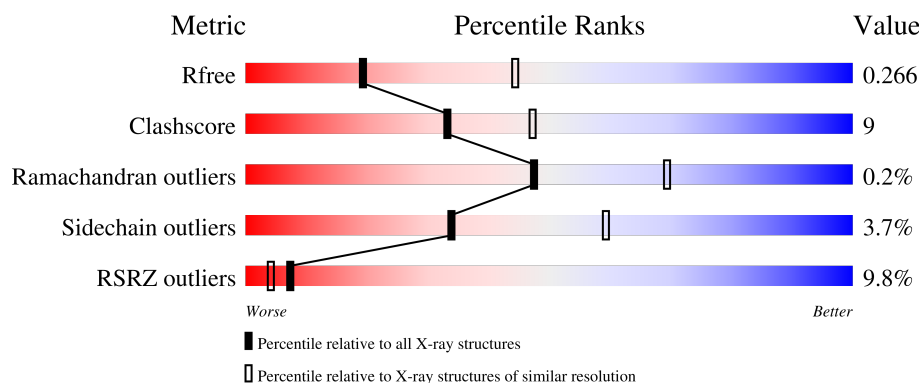
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.84 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	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

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	597	<div> <div>9%</div> <div>73%</div> <div>25%</div> <div>.</div> </div>
1	B	597	<div> <div>8%</div> <div>77%</div> <div>21%</div> <div>..</div> </div>
2	E	217	<div> <div>10%</div> <div>73%</div> <div>12%</div> <div>.</div> <div>13%</div> </div>
2	F	217	<div> <div>14%</div> <div>62%</div> <div>24%</div> <div>.</div> <div>12%</div> </div>
3	C	2	<div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain	
4	D	3		67% 33%
4	J	3		67% 33%

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 12955 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 Angiotensin-converting enzyme 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	1	0
			4860	3103	813	916	28			
1	B	593	Total	C	N	O	S	0	0	0
			4838	3089	809	912	28			

- Molecule 2 is a protein called Spike protein S1.

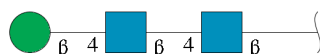
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	188	Total	C	N	O	S	0	1	0
			1504	968	249	277	10			
2	F	190	Total	C	N	O	S	0	0	0
			1517	977	252	279	9			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

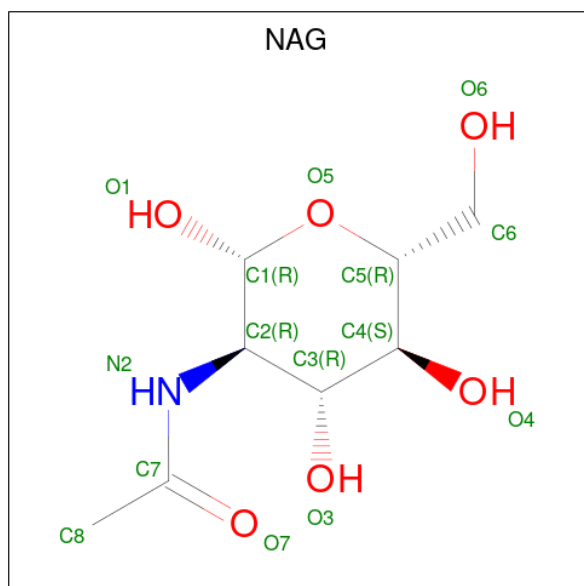
- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		
5	B	1	Total	Zn	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		
6	B	1	Total	Cl	0	0
			1	1		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



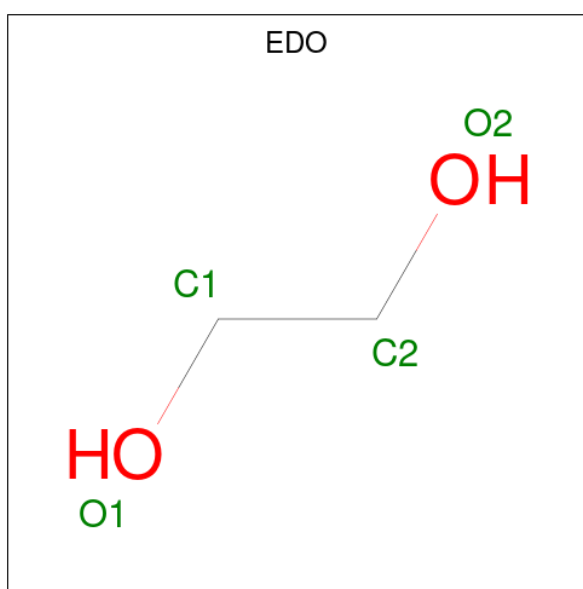
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		
7	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		

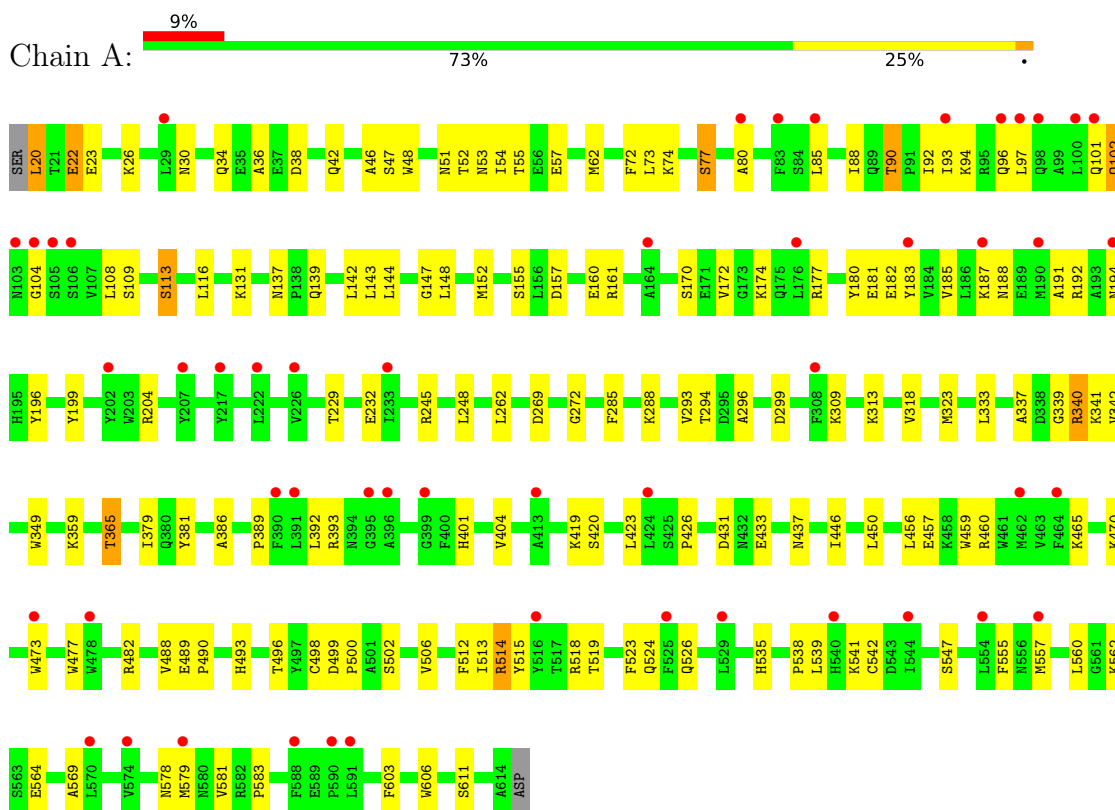
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	9	Total	O	0	0
			9	9		
9	B	9	Total	O	0	0
			9	9		
9	E	1	Total	O	0	0
			1	1		
9	F	1	Total	O	0	0
			1	1		

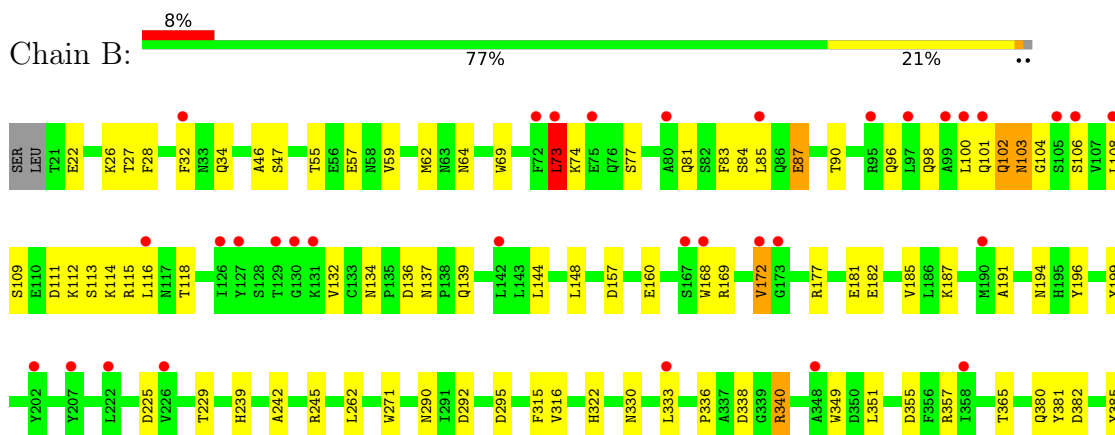
### 3 Residue-property plots

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.

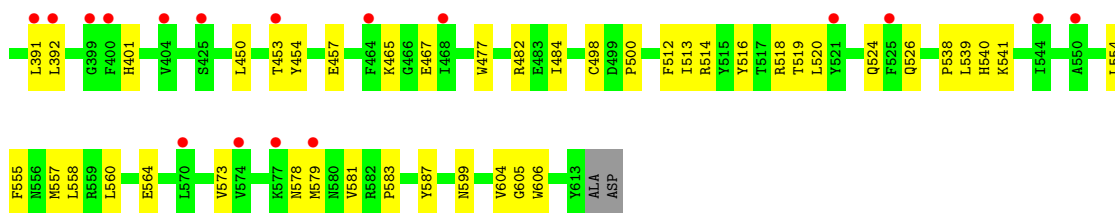
#### • Molecule 1: Angiotensin-converting enzyme 2



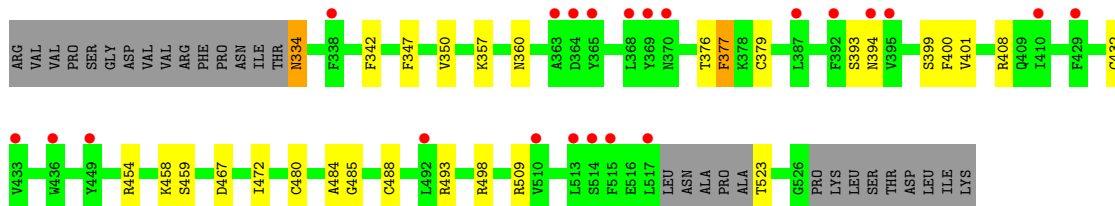
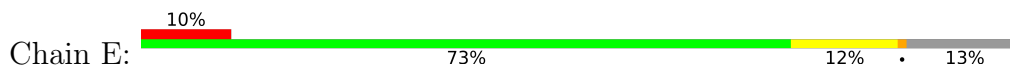
#### • Molecule 1: Angiotensin-converting enzyme 2



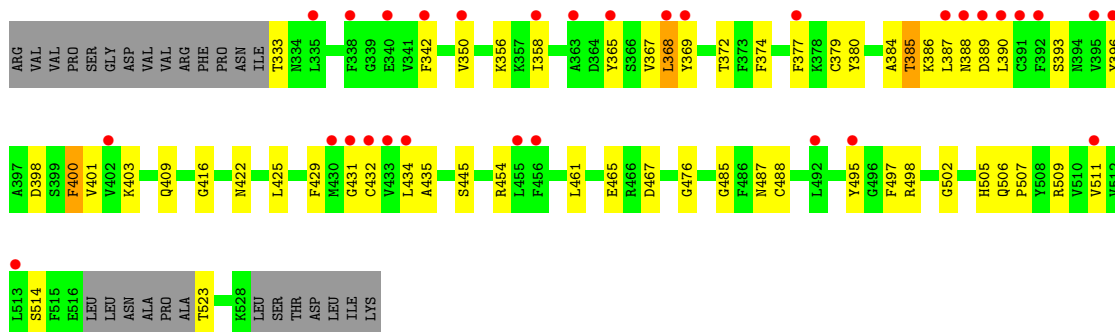




• Molecule 2: Spike protein S1



• Molecule 2: Spike protein S1



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



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

Chain J:

67%

33%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.05Å 118.47Å 110.84Å 90.00° 93.65° 90.00°	Depositor
Resolution (Å)	30.39 – 2.84 80.85 – 2.84	Depositor EDS
% Data completeness (in resolution range)	54.5 (30.39-2.84) 51.0 (80.85-2.84)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.46 (at 2.82Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.214 , 0.271 0.219 , 0.266	Depositor DCC
$R_{free}$ test set	1341 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	74.6	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 38.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	12955	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, EDO, NAG, CL, ZN

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	0.26	0/4997	0.48	1/6787 (0.0%)
1	B	0.24	0/4975	0.48	1/6757 (0.0%)
2	E	0.26	0/1546	0.53	0/2099
2	F	0.29	0/1560	0.54	1/2117 (0.0%)
All	All	0.26	0/13078	0.49	3/17760 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	73	LEU	CA-CB-CG	6.24	129.66	115.30
2	F	368	LEU	CB-CG-CD2	-6.18	100.50	111.00
1	A	299	ASP	CB-CG-OD2	-6.05	112.86	118.30

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	4860	0	4630	87	0
1	B	4838	0	4607	73	0
2	E	1504	0	1422	16	0
2	F	1517	0	1447	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	28	0	25	1	0
4	D	39	0	34	2	0
4	J	39	0	34	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	28	0	26	2	0
7	B	14	0	13	0	0
7	E	14	0	13	1	0
7	F	14	0	13	0	0
8	A	20	0	30	0	0
8	B	16	0	24	1	0
9	A	9	0	0	1	0
9	B	9	0	0	0	0
9	E	1	0	0	0	0
9	F	1	0	0	0	0
All	All	12955	0	12318	217	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 9.

The worst 5 of 217 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:419:LYS:HE3	1:A:426:PRO:HA	1.48	0.92
1:B:74:LYS:HE3	1:B:106:SER:HB3	1.51	0.88
1:B:340:ARG:HH21	3:C:1:NAG:H81	1.50	0.76
1:A:538:PRO:HD2	1:A:541:LYS:HD3	1.69	0.74
1:B:182:GLU:HA	1:B:185:VAL:HG12	1.70	0.73

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	594/597 (100%)	568 (96%)	24 (4%)	2 (0%)	41	61
1	B	591/597 (99%)	565 (96%)	26 (4%)	0	100	100
2	E	185/217 (85%)	168 (91%)	17 (9%)	0	100	100
2	F	186/217 (86%)	167 (90%)	18 (10%)	1 (0%)	29	51
All	All	1556/1628 (96%)	1468 (94%)	85 (6%)	3 (0%)	47	69

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	340	ARG
1	A	337	ALA
2	F	385	THR

### 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	525/526 (100%)	504 (96%)	21 (4%)	31	57
1	B	523/526 (99%)	502 (96%)	21 (4%)	31	57
2	E	163/189 (86%)	159 (98%)	4 (2%)	47	71
2	F	165/189 (87%)	160 (97%)	5 (3%)	41	65
All	All	1376/1430 (96%)	1325 (96%)	51 (4%)	34	59

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	103	ASN
1	B	381	TYR
2	F	400	PHE
1	B	111	ASP
1	B	333	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	121	ASN
2	E	334	ASN
1	B	175	GLN
2	F	487	ASN
1	B	417	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 ⓘ

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	$\# Z  > 2$
3	NAG	C	1	3,1	14,14,15	0.62	0	17,19,21	0.78	0
3	NAG	C	2	3	14,14,15	0.57	0	17,19,21	0.35	0
4	NAG	D	1	4,1	14,14,15	1.03	1 (7%)	17,19,21	0.98	2 (11%)
4	NAG	D	2	4	14,14,15	0.35	0	17,19,21	0.59	0
4	BMA	D	3	4	11,11,12	0.72	0	15,15,17	0.95	0
4	NAG	J	1	4,1	14,14,15	0.56	0	17,19,21	0.55	0
4	NAG	J	2	4	14,14,15	0.29	0	17,19,21	0.48	0
4	BMA	J	3	4	11,11,12	0.59	0	15,15,17	1.12	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
3	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	1/6/23/26	0/1/1/1
4	NAG	D	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	D	2	4	-	1/6/23/26	0/1/1/1
4	BMA	D	3	4	-	2/2/19/22	0/1/1/1
4	NAG	J	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
4	BMA	J	3	4	-	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)
4	D	1	NAG	O5-C1	-3.55	1.38	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	3	BMA	C1-O5-C5	2.65	115.78	112.19
4	D	1	NAG	C3-C4-C5	2.50	114.71	110.24
4	D	1	NAG	O4-C4-C5	-2.26	103.67	109.30

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	J	3	BMA	O5-C5-C6-O6
4	J	2	NAG	O5-C5-C6-O6
4	J	1	NAG	O5-C5-C6-O6
4	J	3	BMA	C4-C5-C6-O6
4	J	1	NAG	C4-C5-C6-O6

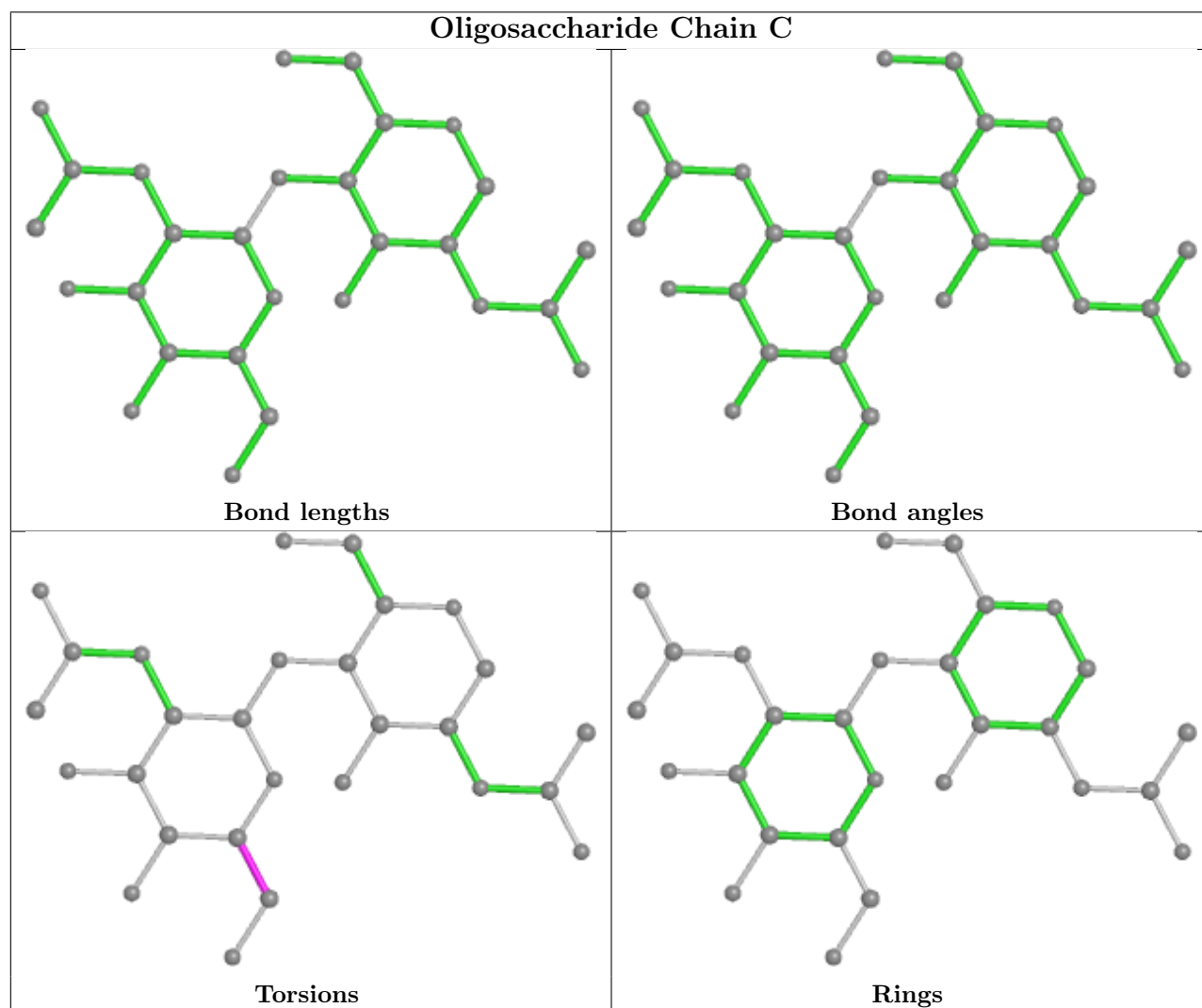
There are no ring outliers.

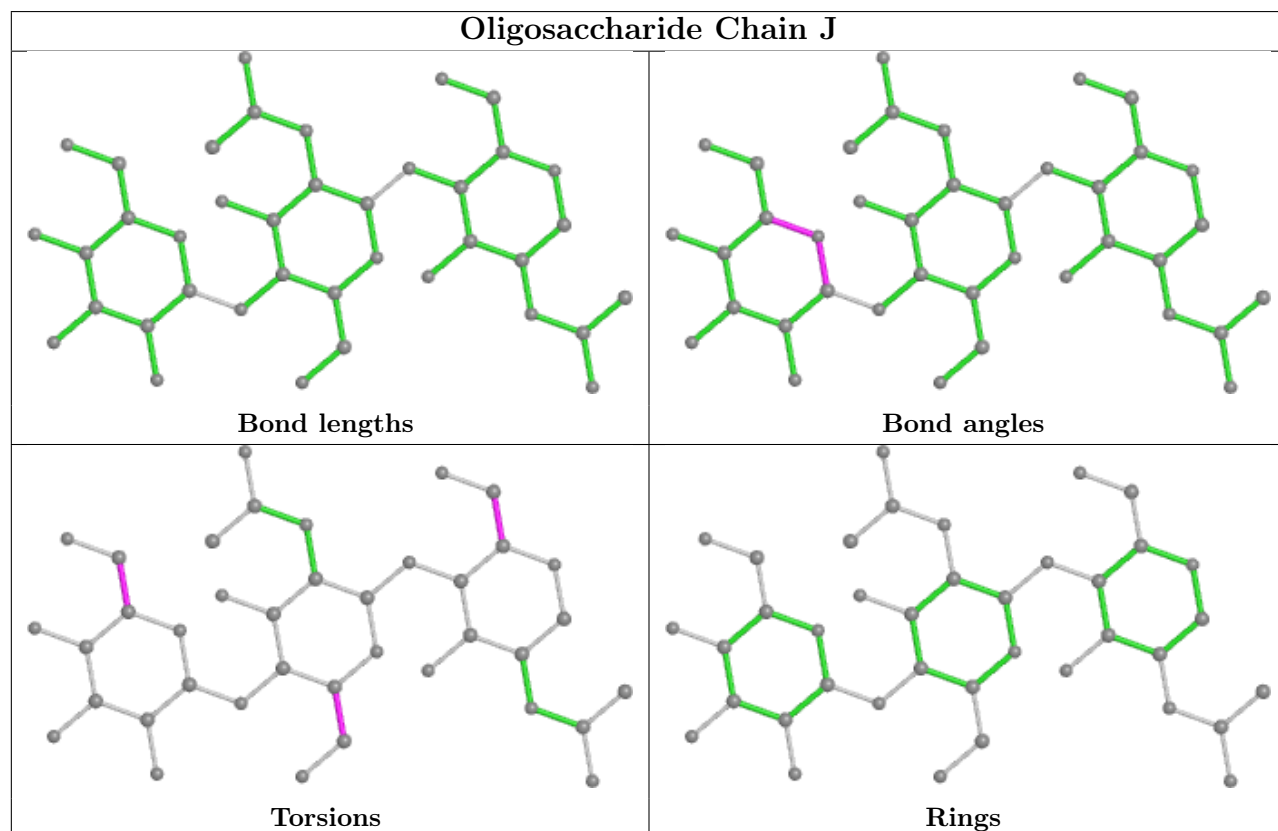
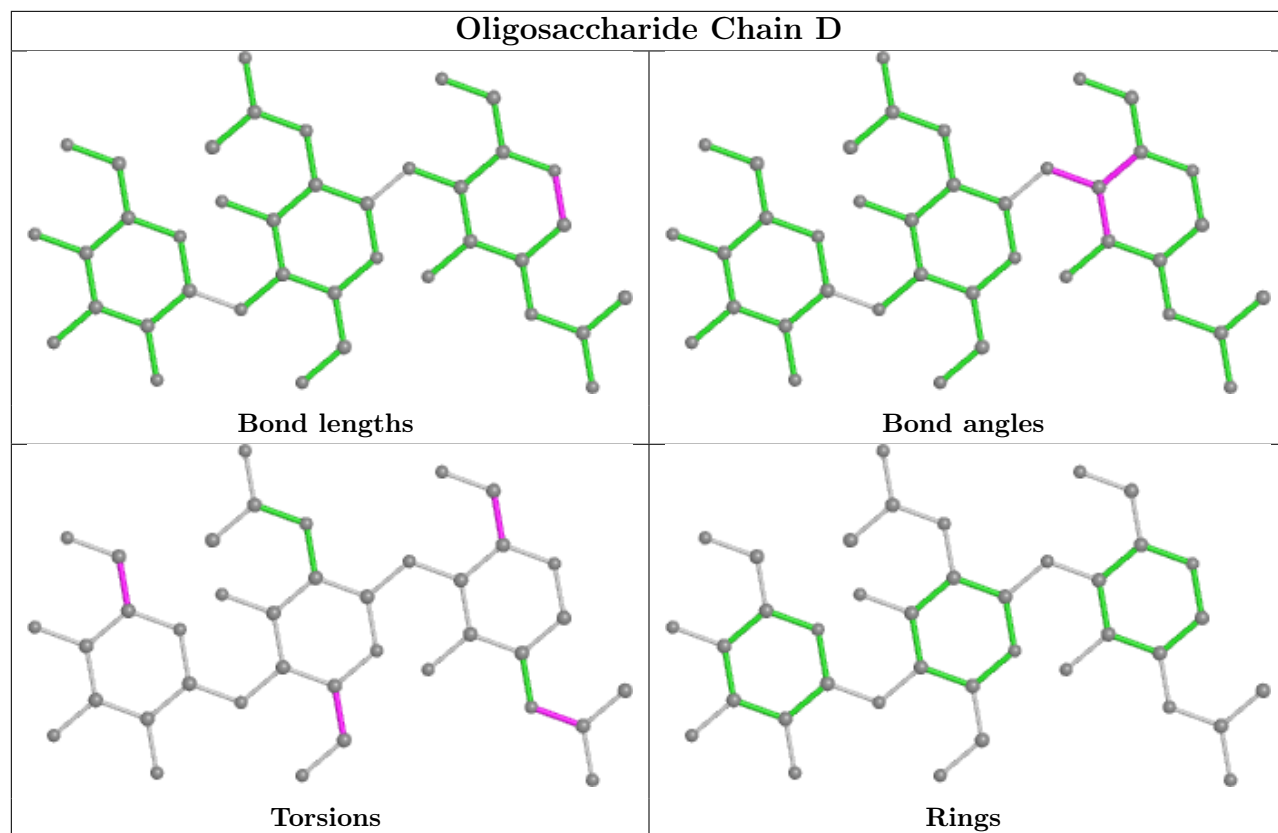
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	1	0
4	D	1	NAG	2	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

Of 18 ligands modelled in this entry, 4 are monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
8	EDO	B	703	-	3,3,3	0.46	0	2,2,2	0.34	0
7	NAG	E	601	2	14,14,15	0.30	0	17,19,21	0.42	0
7	NAG	F	601	2	14,14,15	0.42	0	17,19,21	0.49	0
8	EDO	A	706	-	3,3,3	0.46	0	2,2,2	0.32	0
8	EDO	A	704	-	3,3,3	0.46	0	2,2,2	0.26	0
8	EDO	A	708	-	3,3,3	0.46	0	2,2,2	0.31	0
8	EDO	B	706	-	3,3,3	0.47	0	2,2,2	0.33	0
7	NAG	A	709	1	14,14,15	0.29	0	17,19,21	0.45	0
8	EDO	A	707	-	3,3,3	0.45	0	2,2,2	0.35	0
8	EDO	B	704	-	3,3,3	0.47	0	2,2,2	0.27	0
8	EDO	B	707	-	3,3,3	0.47	0	2,2,2	0.29	0
7	NAG	A	703	1	14,14,15	0.49	0	17,19,21	0.56	0
7	NAG	B	705	1	14,14,15	0.43	0	17,19,21	0.57	0
8	EDO	A	705	-	3,3,3	0.47	0	2,2,2	0.27	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
8	EDO	B	703	-	-	1/1/1/1	-
7	NAG	E	601	2	-	1/6/23/26	0/1/1/1
7	NAG	F	601	2	-	1/6/23/26	0/1/1/1
8	EDO	A	706	-	-	0/1/1/1	-
8	EDO	A	704	-	-	0/1/1/1	-
8	EDO	A	708	-	-	0/1/1/1	-
8	EDO	B	706	-	-	1/1/1/1	-
7	NAG	A	709	1	-	2/6/23/26	0/1/1/1
8	EDO	A	707	-	-	0/1/1/1	-
8	EDO	B	704	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	EDO	B	707	-	-	0/1/1/1	-
7	NAG	A	703	1	-	2/6/23/26	0/1/1/1
7	NAG	B	705	1	-	0/6/23/26	0/1/1/1
8	EDO	A	705	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	703	NAG	O5-C5-C6-O6
7	A	703	NAG	C4-C5-C6-O6
7	A	709	NAG	C4-C5-C6-O6
7	E	601	NAG	O5-C5-C6-O6
7	F	601	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	601	NAG	1	0
8	B	706	EDO	1	0
7	A	709	NAG	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	595/597 (99%)	0.59	51 (8%)	10 5	47, 95, 144, 178	0
1	B	593/597 (99%)	0.59	50 (8%)	11 5	47, 83, 154, 195	0
2	E	188/217 (86%)	0.68	22 (11%)	4 2	56, 85, 148, 177	0
2	F	190/217 (87%)	0.82	31 (16%)	1 1	76, 111, 176, 212	0
All	All	1566/1628 (96%)	0.63	154 (9%)	7 4	47, 94, 156, 212	0

The worst 5 of 154 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	104	GLY	7.9
1	B	129	THR	7.8
1	B	130	GLY	7.5
2	F	363	ALA	6.9
2	E	387	LEU	6.7

### 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.

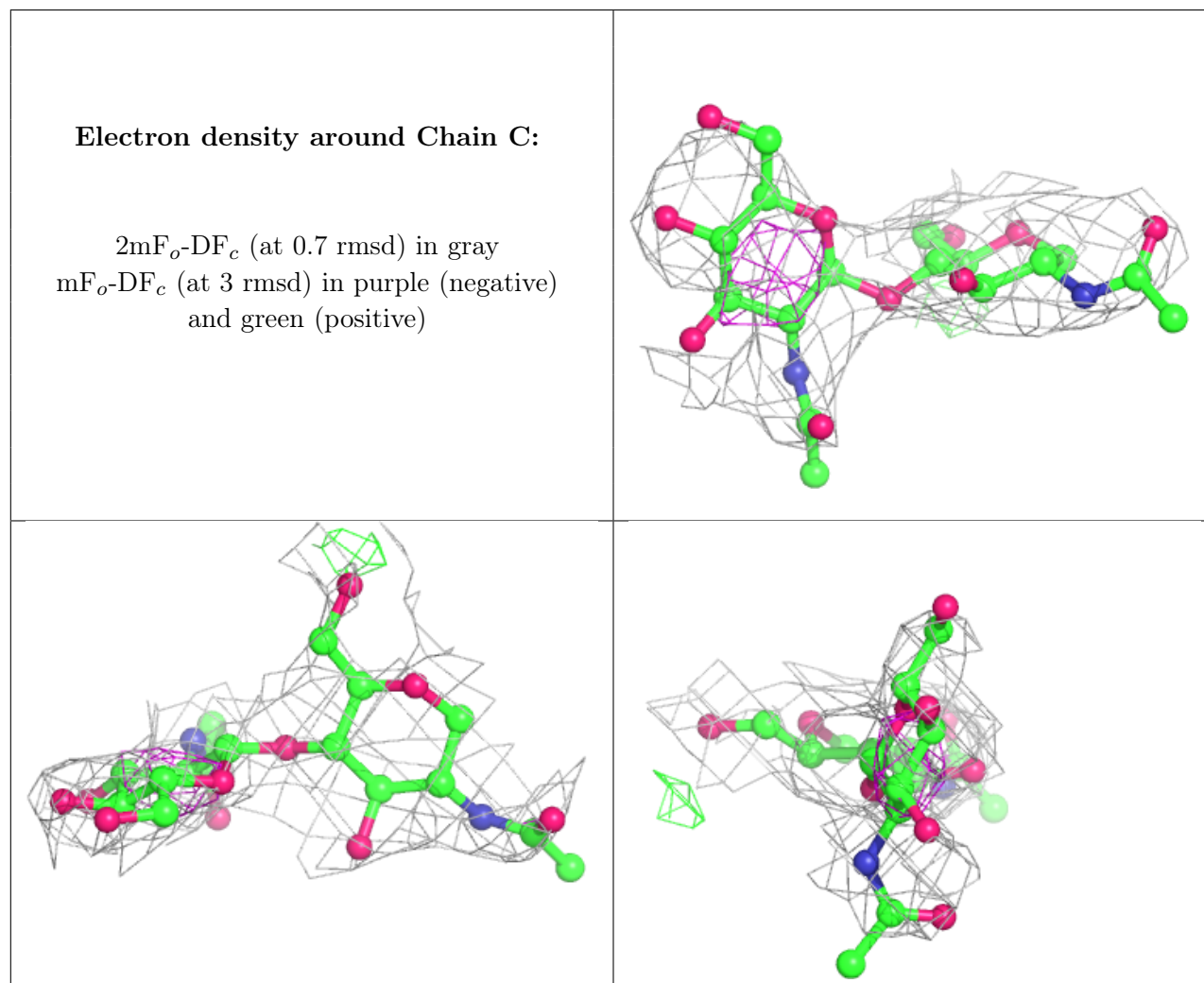
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	C	2	14/15	0.74	0.30	114,120,123,123	0
4	BMA	D	3	11/12	0.76	0.29	119,126,128,128	0

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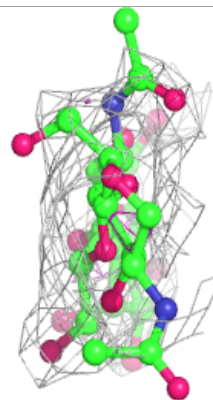
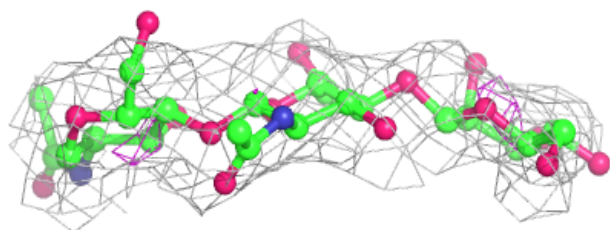
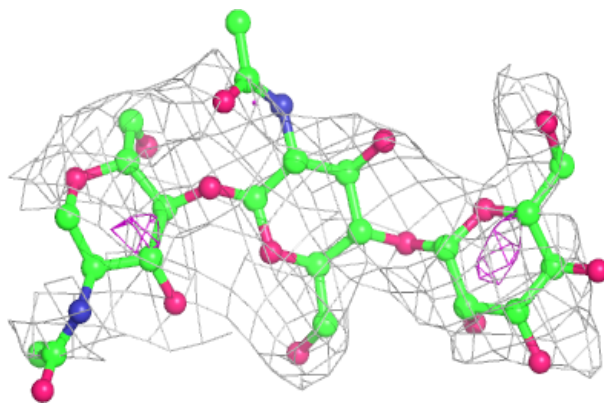
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	D	2	14/15	0.81	0.21	108,123,125,126	0
4	NAG	J	2	14/15	0.81	0.18	102,106,113,116	0
4	BMA	J	3	11/12	0.82	0.21	104,114,115,116	0
4	NAG	J	1	14/15	0.84	0.16	79,89,99,103	0
3	NAG	C	1	14/15	0.87	0.24	95,108,113,117	0
4	NAG	D	1	14/15	0.88	0.18	123,126,128,132	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.

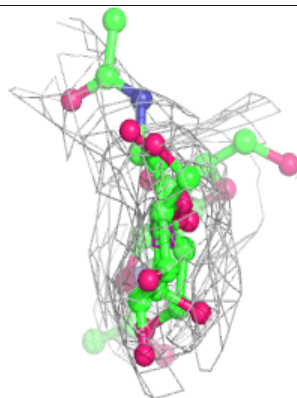
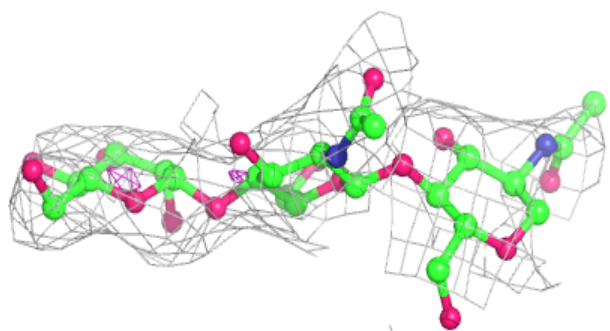
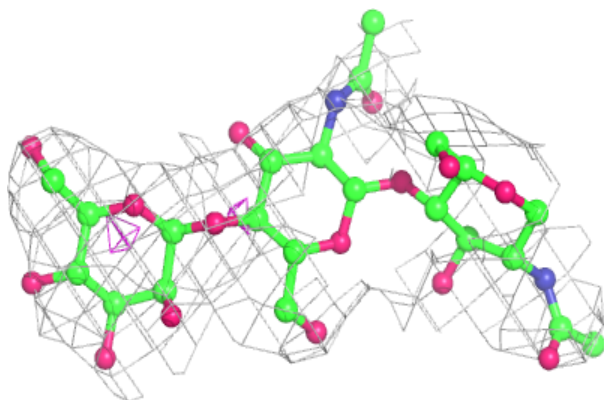


**Electron density around Chain D:**

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

**Electron density around Chain J:**

$2mF_o-DF_c$  (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, 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	NAG	F	601	14/15	0.67	0.28	122,126,127,127	0
7	NAG	A	703	14/15	0.71	0.20	110,122,124,125	0
7	NAG	E	601	14/15	0.76	0.22	92,98,104,105	0
7	NAG	B	705	14/15	0.76	0.24	80,105,116,116	0
8	EDO	B	703	4/4	0.77	0.25	63,65,68,69	0
8	EDO	B	707	4/4	0.82	0.31	60,63,63,63	0
8	EDO	A	706	4/4	0.83	0.31	65,69,71,73	0
6	CL	B	702	1/1	0.89	0.21	77,77,77,77	0
8	EDO	A	705	4/4	0.91	0.18	56,58,59,61	0
8	EDO	B	704	4/4	0.91	0.18	68,73,74,74	0
8	EDO	B	706	4/4	0.91	0.21	54,55,56,56	0
8	EDO	A	704	4/4	0.91	0.18	54,56,57,57	0
8	EDO	A	707	4/4	0.92	0.23	60,67,70,76	0
7	NAG	A	709	14/15	0.93	0.17	92,93,103,109	0
8	EDO	A	708	4/4	0.93	0.23	42,49,49,50	0
6	CL	A	702	1/1	0.97	0.10	51,51,51,51	0
5	ZN	A	701	1/1	0.97	0.13	89,89,89,89	0
5	ZN	B	701	1/1	0.99	0.21	59,59,59,59	0

## 6.5 Other polymers

There are no such residues in this entry.