



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 15, 2023 – 02:57 AM EDT

PDB ID : 7UDH  
Title : Integrin alaphIIBbeta3 complex with BMS4-3  
Authors : Lin, F.-Y.; Zhu, J.; Zhu, J.; Springer, T.A.  
Deposited on : 2022-03-19  
Resolution : 2.00 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 : 2.36  
buster-report : 1.1.7 (2018)  
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) : 2.36

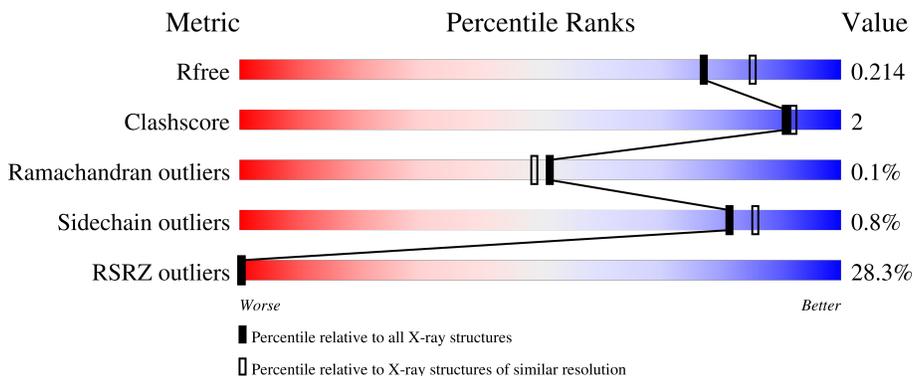
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	457	 28% (poor fit), 95% (0 outliers), 6% (1 outlier), 1% (2+ outliers)
1	C	457	 14% (poor fit), 96% (0 outliers), 6% (1 outlier), 1% (2+ outliers)
2	B	472	 26% (poor fit), 93% (0 outliers), 6% (1 outlier), 1% (2+ outliers)
2	D	472	 20% (poor fit), 94% (0 outliers), 5% (1 outlier), 1% (2+ outliers)
3	E	221	 62% (poor fit), 94% (0 outliers), 6% (1 outlier), 1% (2+ outliers)

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Mol	Chain	Length	Quality of chain
3	H	221	
4	F	214	
4	L	214	
5	G	4	
6	I	2	
6	K	2	
7	J	5	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	NAG	I	1	-	-	X	-
7	NAG	J	1	-	-	X	-

## 2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 22567 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 Integrin alpha-IIb heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	454	Total	C	N	O	S	0	4	0
			3499	2226	601	664	8			
1	C	453	Total	C	N	O	S	0	4	0
			3502	2224	604	666	8			

- Molecule 2 is a protein called Isoform Beta-3C of Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	466	Total	C	N	O	S	4	3	0
			3610	2248	616	712	34			
2	D	471	Total	C	N	O	S	3	0	0
			3623	2255	619	715	34			

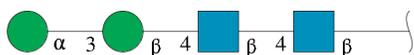
- Molecule 3 is a protein called 10E5 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	214	Total	C	N	O	S	0	0	0
			1631	1035	264	326	6			
3	H	216	Total	C	N	O	S	0	0	0
			1642	1041	266	329	6			

- Molecule 4 is a protein called 10E5 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	F	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			
4	L	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



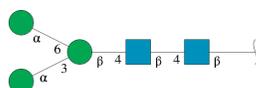
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	G	4	50	28	2	20	0	0	0

- Molecule 6 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
			Total	C	N	O			
6	I	2	28	16	2	10	0	0	0
6	K	2	28	16	2	10	0	0	0

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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
			Total	C	N	O			
7	J	5	61	34	2	25	0	0	0

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	L	1	Total	O	S	0	0
			5	4	1		

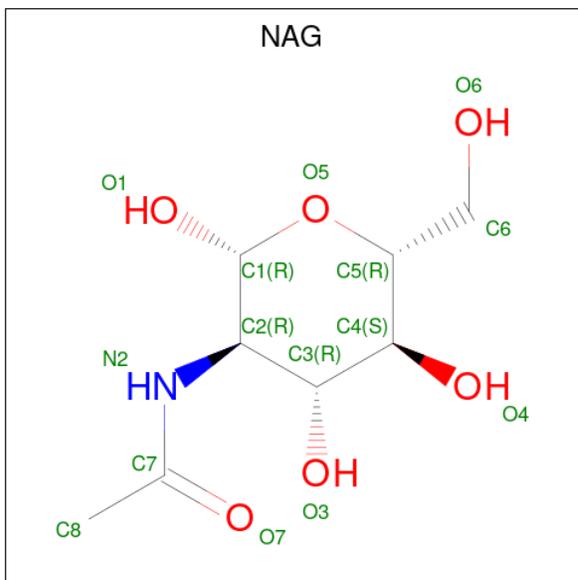
- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	4	Total	Ca	0	0
			4	4		
9	C	4	Total	Ca	0	0
			4	4		

- Molecule 10 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

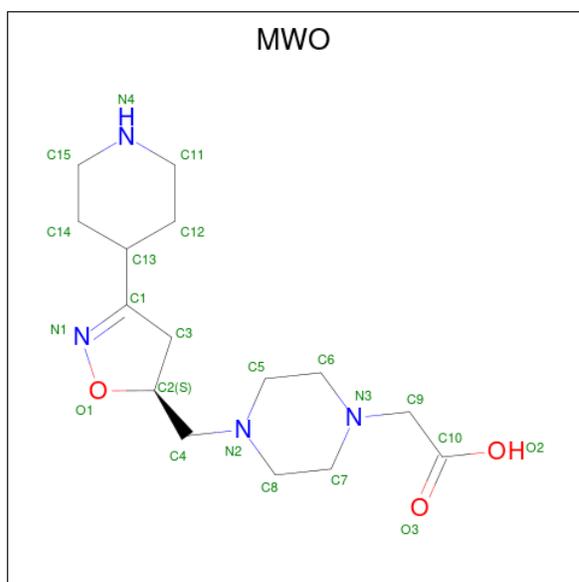
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	3	Total	Mn	0	0
			3	3		
10	D	3	Total	Mn	0	0
			3	3		

- Molecule 11 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>).



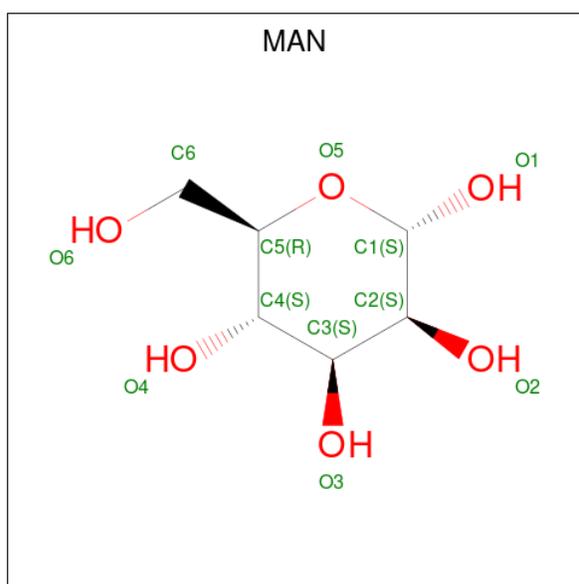
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	1	Total	C	N	O	0	0
			14	8	1	5		
11	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 12 is (4-{{(5S)-3-(piperidin-4-yl)-4,5-dihydro-1,2-oxazol-5-yl}methyl}piperazin-1-yl)acetic acid (three-letter code: MWO) (formula: C<sub>15</sub>H<sub>26</sub>N<sub>4</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	B	1	Total	C	N	O	0	0
			22	15	4	3		
12	D	1	Total	C	N	O	0	0
			22	15	4	3		

- Molecule 13 is alpha-D-mannopyranose (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	C	1	Total	C	O	0	0
			11	6	5		

- Molecule 14 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	C	2	Total Cl 2 2	0	0
14	D	1	Total Cl 1 1	0	0

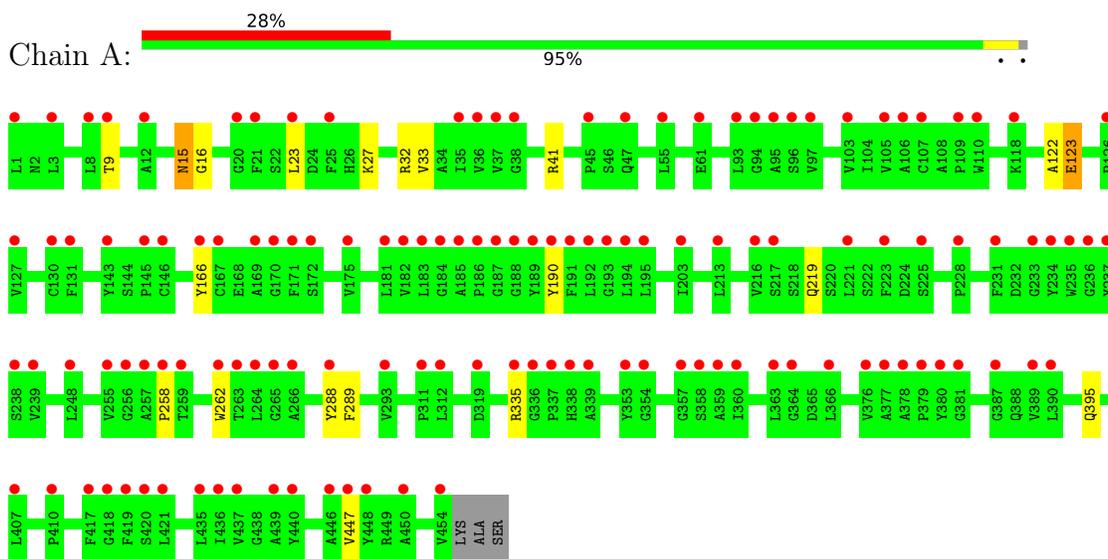
- Molecule 15 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	A	542	Total O 542 542	0	0
15	B	319	Total O 319 319	0	0
15	C	232	Total O 232 232	0	0
15	D	200	Total O 200 200	0	0
15	E	29	Total O 29 29	0	0
15	F	20	Total O 20 20	0	0
15	H	45	Total O 45 45	0	0
15	L	87	Total O 87 87	0	0

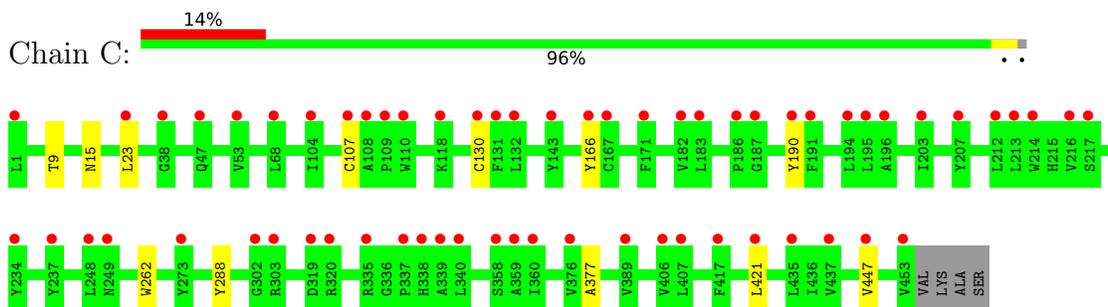
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

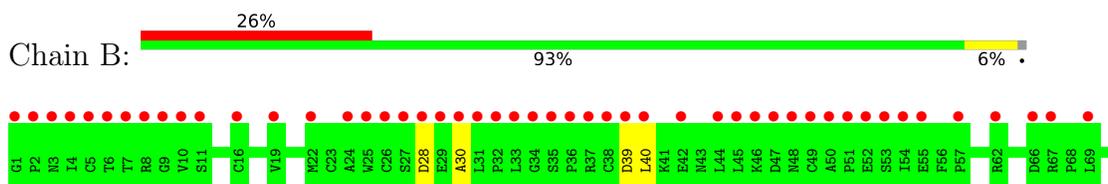
- Molecule 1: Integrin alpha-IIb heavy chain

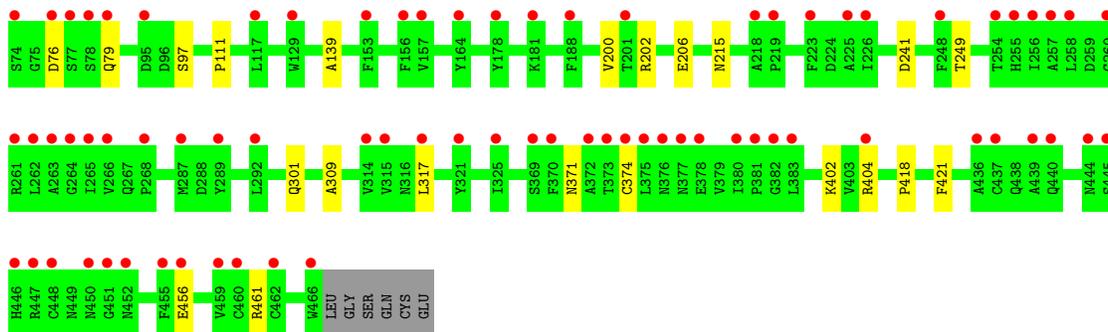


- Molecule 1: Integrin alpha-IIb heavy chain



- Molecule 2: Isoform Beta-3C of Integrin beta-3

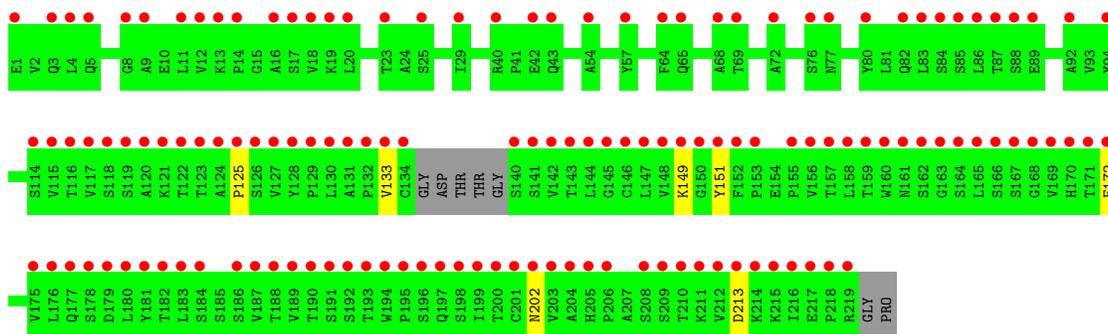




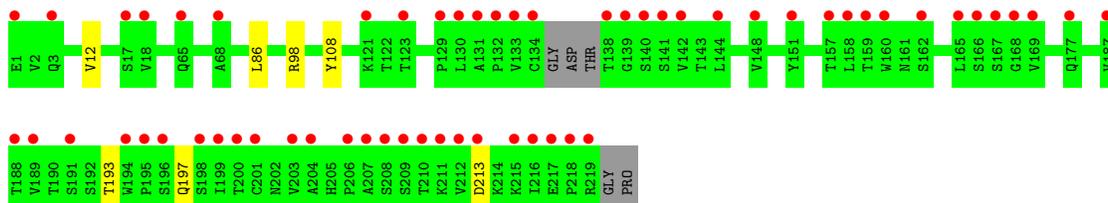
- Molecule 2: Isoform Beta-3C of Integrin beta-3



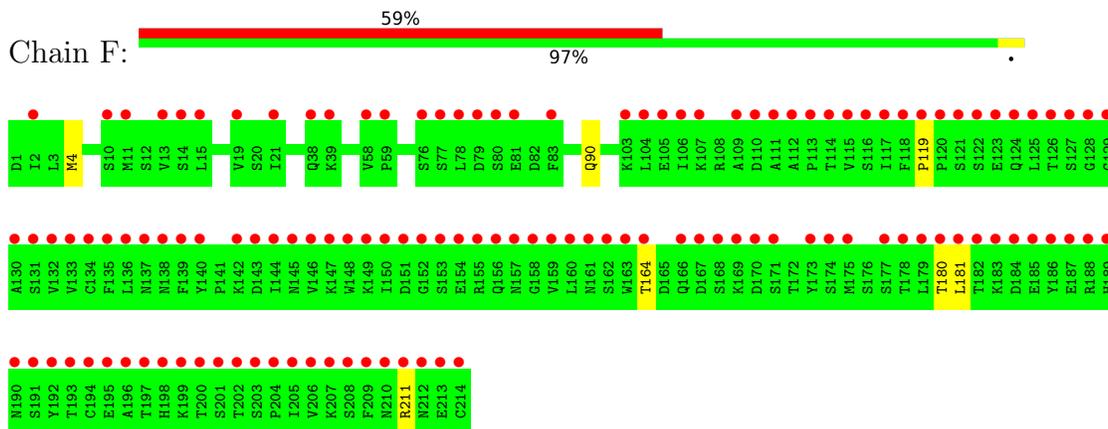
- Molecule 3: 10E5 Fab heavy chain



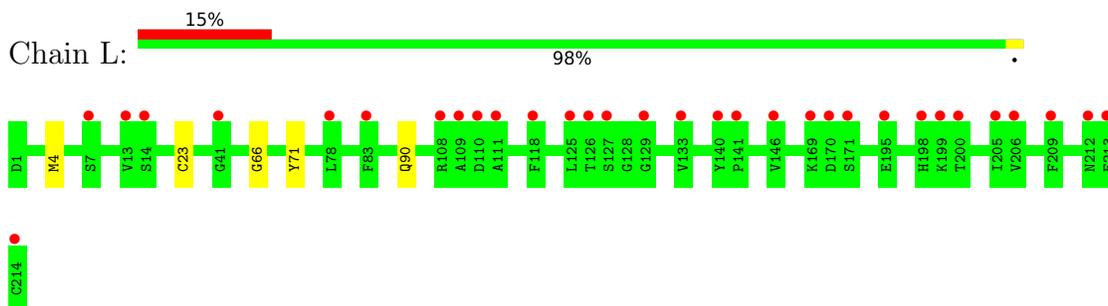
- Molecule 3: 10E5 Fab heavy chain



- Molecule 4: 10E5 Fab light chain



- Molecule 4: 10E5 Fab light chain



- Molecule 5: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  40% 60%

MAG1
MAG2
EMG3
MAN4
MAN5

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	258.33Å 144.67Å 105.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.99 – 2.00 48.99 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.4 (48.99-2.00) 97.4 (48.99-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.01 (at 2.00Å)	Xtrriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, $R_{free}$	0.185 , 0.214 0.185 , 0.214	Depositor DCC
$R_{free}$ test set	2000 reflections (0.78%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.2	Xtrriage
Anisotropy	0.243	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 61.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	22567	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.13% 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: CL, BMA, SO4, MN, MAN, CA, NAG, MWO

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	0.30	0/3608	0.53	0/4918
1	C	0.27	0/3605	0.50	0/4912
2	B	0.28	0/3680	0.48	0/4989
2	D	0.26	0/3690	0.47	0/5003
3	E	0.24	0/1673	0.45	0/2290
3	H	0.25	0/1684	0.48	0/2305
4	F	0.24	0/1673	0.44	0/2269
4	L	0.25	0/1673	0.47	0/2269
All	All	0.27	0/21286	0.48	0/28955

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3499	0	3345	9	0
1	C	3502	0	3334	4	0
2	B	3610	0	3531	19	0
2	D	3623	0	3541	28	0
3	E	1631	0	1590	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1642	0	1600	4	0
4	F	1637	0	1553	5	0
4	L	1637	0	1553	3	0
5	G	50	0	42	0	0
6	I	28	0	25	7	0
6	K	28	0	25	1	0
7	J	61	0	52	8	0
8	A	20	0	0	0	0
8	C	20	0	0	0	0
8	L	5	0	0	0	0
9	A	4	0	0	0	0
9	C	4	0	0	0	0
10	B	3	0	0	0	0
10	D	3	0	0	0	0
11	B	14	0	13	0	0
11	D	14	0	13	5	0
12	B	22	0	0	0	0
12	D	22	0	0	0	0
13	C	11	0	10	0	0
14	C	2	0	0	0	0
14	D	1	0	0	0	0
15	A	542	0	0	3	1
15	B	319	0	0	2	0
15	C	232	0	0	0	1
15	D	200	0	0	2	0
15	E	29	0	0	0	0
15	F	20	0	0	1	0
15	H	45	0	0	0	0
15	L	87	0	0	1	0
All	All	22567	0	20227	72	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 2.

The worst 5 of 72 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)
2:D:320:ASN:HD21	7:J:1:NAG:C1	0.99	1.59
2:D:99:ASN:ND2	11:D:2004:NAG:C1	1.68	1.56
2:B:371:ASN:HD21	6:I:1:NAG:C1	0.97	1.53
2:B:371:ASN:ND2	6:I:1:NAG:C1	1.73	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:320:ASN:ND2	7:J:1:NAG:C1	1.76	1.45

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)
15:A:1035:HOH:O	15:C:786:HOH:O[1_554]	2.11	0.09

## 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	456/457 (100%)	440 (96%)	15 (3%)	1 (0%)	47	44
1	C	455/457 (100%)	441 (97%)	14 (3%)	0	100	100
2	B	467/472 (99%)	452 (97%)	14 (3%)	1 (0%)	47	44
2	D	469/472 (99%)	451 (96%)	18 (4%)	0	100	100
3	E	210/221 (95%)	196 (93%)	14 (7%)	0	100	100
3	H	212/221 (96%)	203 (96%)	9 (4%)	0	100	100
4	F	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
4	L	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
All	All	2693/2728 (99%)	2587 (96%)	104 (4%)	2 (0%)	51	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
2	B	76	ASP

### 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	366/364 (100%)	359 (98%)	7 (2%)	57	61
1	C	365/364 (100%)	360 (99%)	5 (1%)	67	72
2	B	415/417 (100%)	412 (99%)	3 (1%)	84	88
2	D	416/417 (100%)	413 (99%)	3 (1%)	84	88
3	E	186/190 (98%)	186 (100%)	0	100	100
3	H	187/190 (98%)	187 (100%)	0	100	100
4	F	188/188 (100%)	187 (100%)	1 (0%)	88	92
4	L	188/188 (100%)	188 (100%)	0	100	100
All	All	2311/2318 (100%)	2292 (99%)	19 (1%)	81	86

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

Mol	Chain	Res	Type
1	C	288	TYR
2	D	215	ASN
4	F	181	LEU
2	D	143	ARG
2	B	215	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	371	ASN
2	D	82	GLN
2	D	320	ASN
2	D	301	GLN
2	B	301	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

13 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
5	NAG	G	1	5,2	14,14,15	0.24	0	17,19,21	0.40	0
5	NAG	G	2	5	14,14,15	0.34	0	17,19,21	0.35	0
5	BMA	G	3	5	11,11,12	1.05	1 (9%)	15,15,17	0.96	1 (6%)
5	MAN	G	4	5	11,11,12	0.66	0	15,15,17	1.09	2 (13%)
6	NAG	I	1	6	14,14,15	0.24	0	17,19,21	0.46	0
6	NAG	I	2	6	14,14,15	0.27	0	17,19,21	0.38	0
7	NAG	J	1	7	14,14,15	0.32	0	17,19,21	0.45	0
7	NAG	J	2	7	14,14,15	0.33	0	17,19,21	0.40	0
7	BMA	J	3	7	11,11,12	0.99	0	15,15,17	0.73	0
7	MAN	J	4	7	11,11,12	0.78	0	15,15,17	0.95	2 (13%)
7	MAN	J	5	7	11,11,12	0.78	1 (9%)	15,15,17	1.16	2 (13%)
6	NAG	K	1	6	14,14,15	0.24	0	17,19,21	0.38	0
6	NAG	K	2	6	14,14,15	0.21	0	17,19,21	0.39	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
5	NAG	G	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	0/1/1/1
6	NAG	I	1	6	-	1/6/23/26	0/1/1/1
6	NAG	I	2	6	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	J	1	7	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	0/6/23/26	0/1/1/1
7	BMA	J	3	7	-	1/2/19/22	0/1/1/1
7	MAN	J	4	7	-	2/2/19/22	0/1/1/1
7	MAN	J	5	7	-	1/2/19/22	0/1/1/1
6	NAG	K	1	6	-	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	4/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	3	BMA	O5-C1	-2.48	1.39	1.43
7	J	5	MAN	C1-C2	2.12	1.57	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	J	5	MAN	C1-O5-C5	3.41	116.81	112.19
5	G	4	MAN	C1-O5-C5	2.46	115.52	112.19
7	J	4	MAN	C1-O5-C5	2.30	115.31	112.19
5	G	4	MAN	O2-C2-C3	-2.29	105.55	110.14
7	J	4	MAN	O2-C2-C3	-2.26	105.61	110.14

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

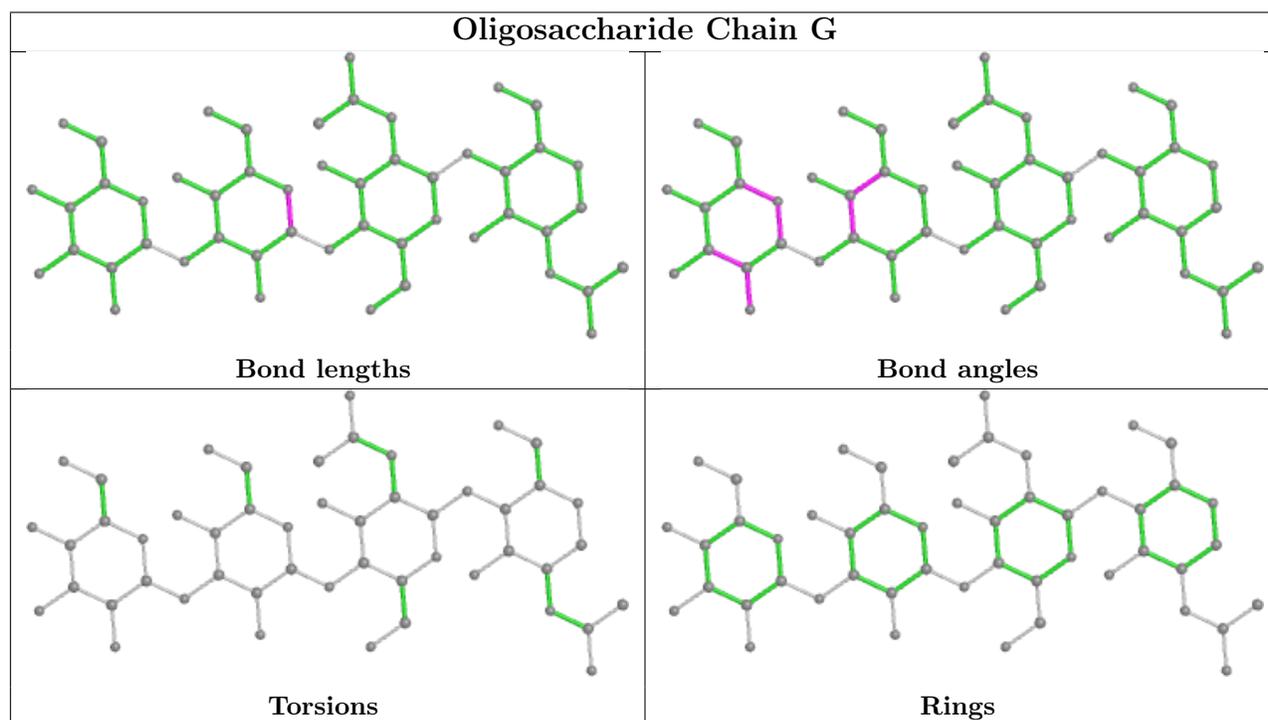
Mol	Chain	Res	Type	Atoms
7	J	4	MAN	O5-C5-C6-O6
6	I	2	NAG	O5-C5-C6-O6
7	J	4	MAN	C4-C5-C6-O6
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2

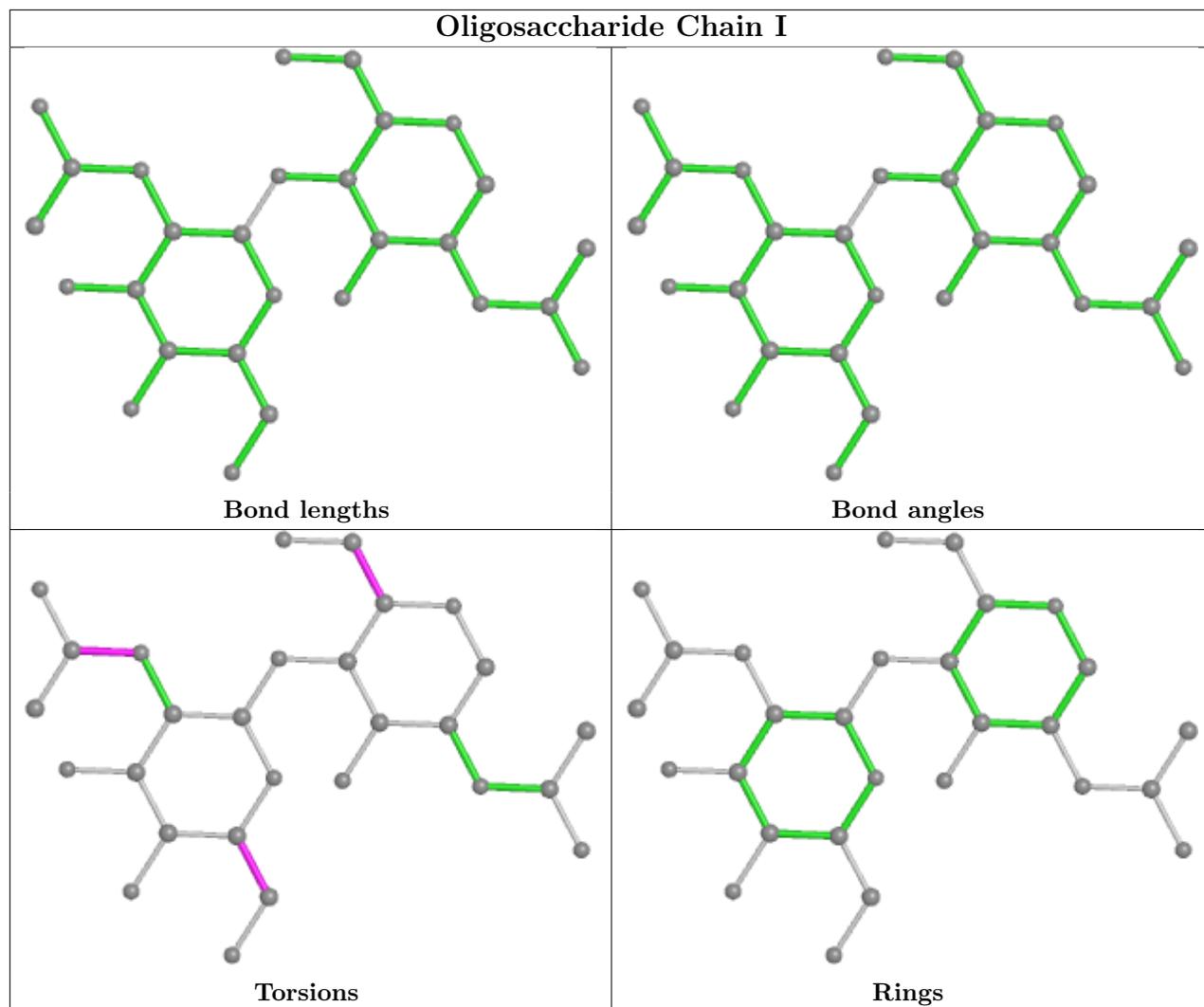
There are no ring outliers.

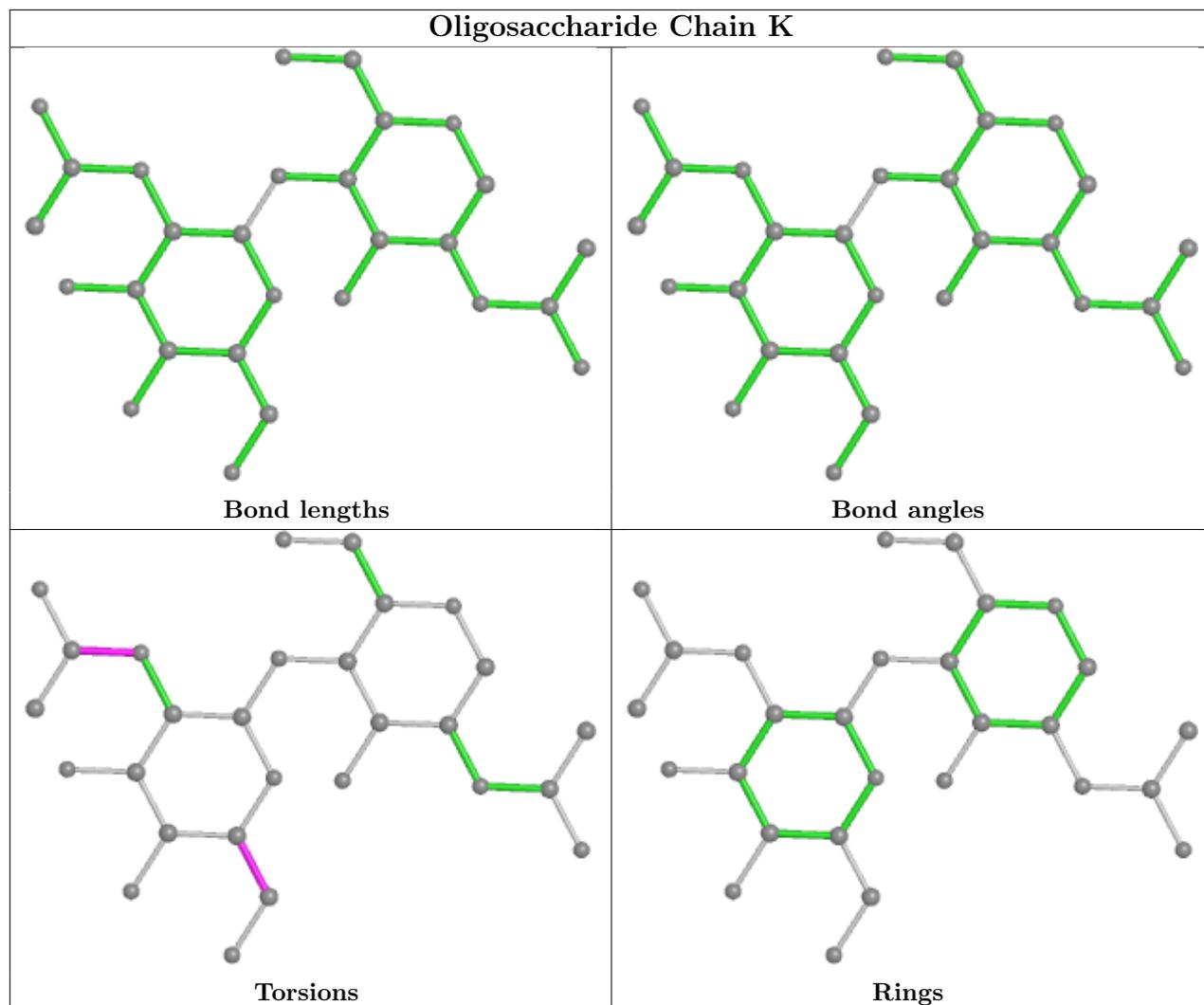
3 monomers are involved in 16 short contacts:

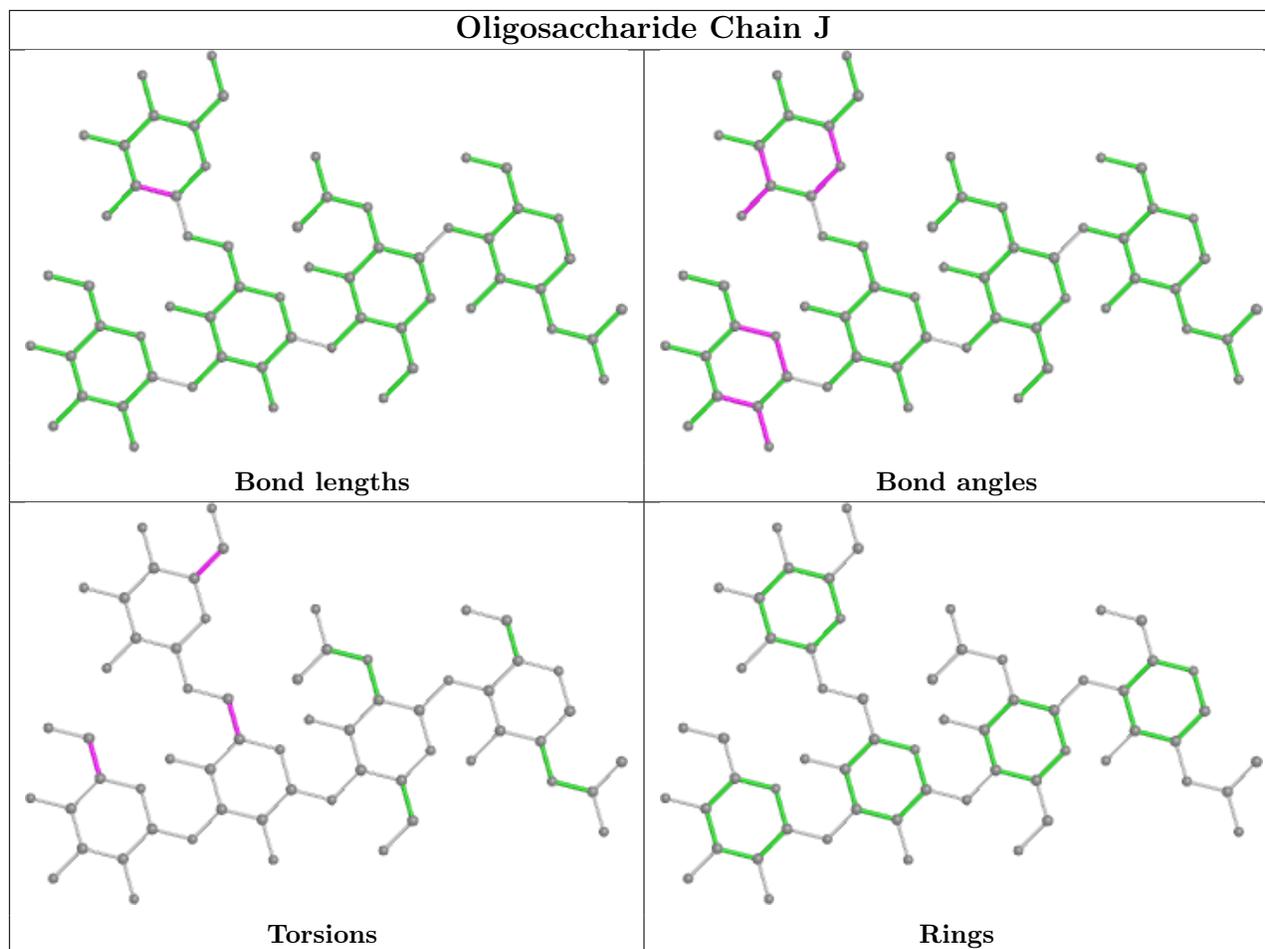
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	J	1	NAG	8	0
6	I	1	NAG	7	0
6	K	1	NAG	1	0

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 31 ligands modelled in this entry, 17 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	$\# Z  > 2$
13	MAN	C	501	-	11,11,12	0.80	0	15,15,17	1.09	2 (13%)
8	SO4	A	502	-	4,4,4	0.15	0	6,6,6	0.07	0
8	SO4	C	504	-	4,4,4	0.14	0	6,6,6	0.05	0
8	SO4	A	508	-	4,4,4	0.14	0	6,6,6	0.05	0
11	NAG	D	2004	-	14,14,15	0.21	0	17,19,21	0.40	0
8	SO4	C	502	-	4,4,4	0.14	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
11	NAG	B	2004	2	14,14,15	0.16	0	17,19,21	0.44	0
12	MWO	D	2006	10	23,24,24	3.15	9 (39%)	27,32,32	2.19	8 (29%)
8	SO4	C	511	-	4,4,4	0.14	0	6,6,6	0.06	0
8	SO4	A	507	-	4,4,4	0.15	0	6,6,6	0.08	0
8	SO4	A	501	-	4,4,4	0.15	0	6,6,6	0.06	0
8	SO4	L	301	-	4,4,4	0.14	0	6,6,6	0.05	0
12	MWO	B	2005	10	23,24,24	3.16	9 (39%)	27,32,32	2.12	6 (22%)
8	SO4	C	503	-	4,4,4	0.15	0	6,6,6	0.04	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
13	MAN	C	501	-	-	2/2/19/22	0/1/1/1
11	NAG	D	2004	-	-	0/6/23/26	0/1/1/1
11	NAG	B	2004	2	-	2/6/23/26	0/1/1/1
12	MWO	D	2006	10	-	3/12/39/39	0/3/3/3
12	MWO	B	2005	10	-	3/12/39/39	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	D	2006	MWO	C4-N2	-8.43	1.31	1.47
12	B	2005	MWO	C4-N2	-8.38	1.31	1.47
12	B	2005	MWO	O1-C2	-7.45	1.36	1.46
12	D	2006	MWO	O1-C2	-7.34	1.36	1.46
12	D	2006	MWO	C5-N2	-5.11	1.32	1.46

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	2005	MWO	C3-C1-N1	-7.25	109.89	114.37
12	D	2006	MWO	C3-C1-N1	-6.27	110.50	114.37
12	D	2006	MWO	O1-C2-C3	5.47	109.41	104.33
12	B	2005	MWO	O1-C2-C3	4.21	108.24	104.33
12	B	2005	MWO	C12-C13-C14	-3.24	103.14	109.97

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

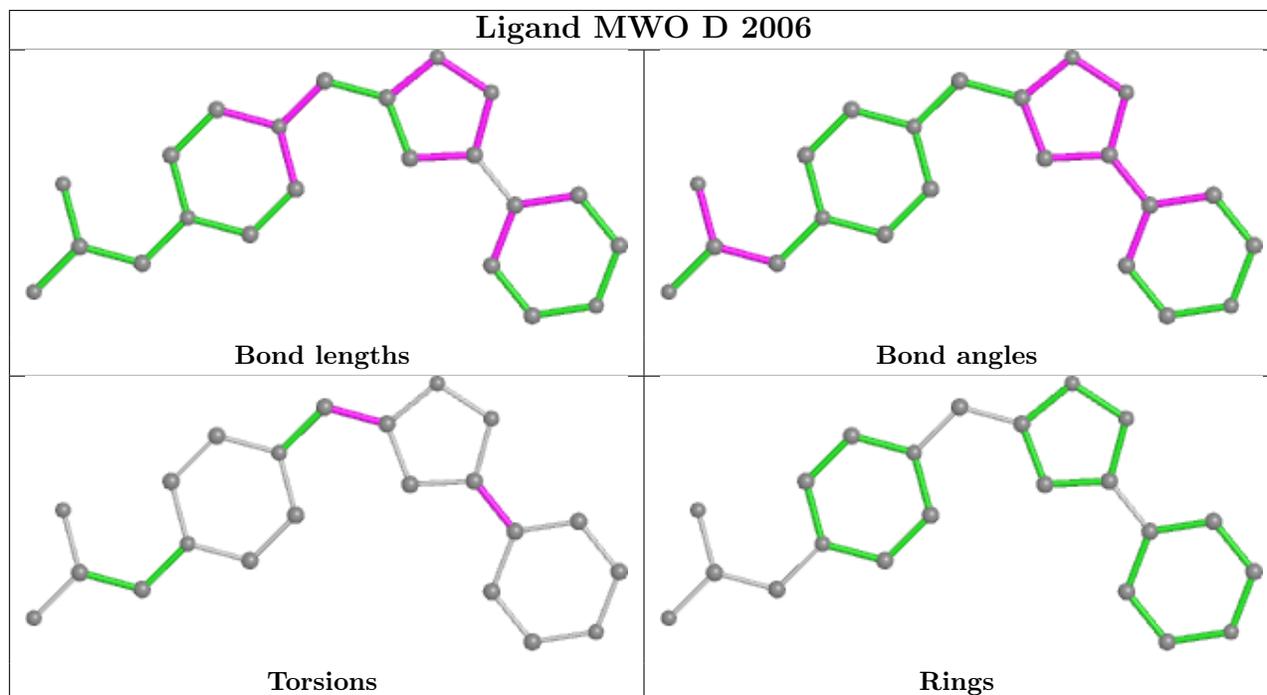
Mol	Chain	Res	Type	Atoms
12	B	2005	MWO	N1-C1-C13-C12
12	B	2005	MWO	C3-C2-C4-N2
12	B	2005	MWO	O1-C2-C4-N2
12	D	2006	MWO	C3-C2-C4-N2
12	D	2006	MWO	O1-C2-C4-N2

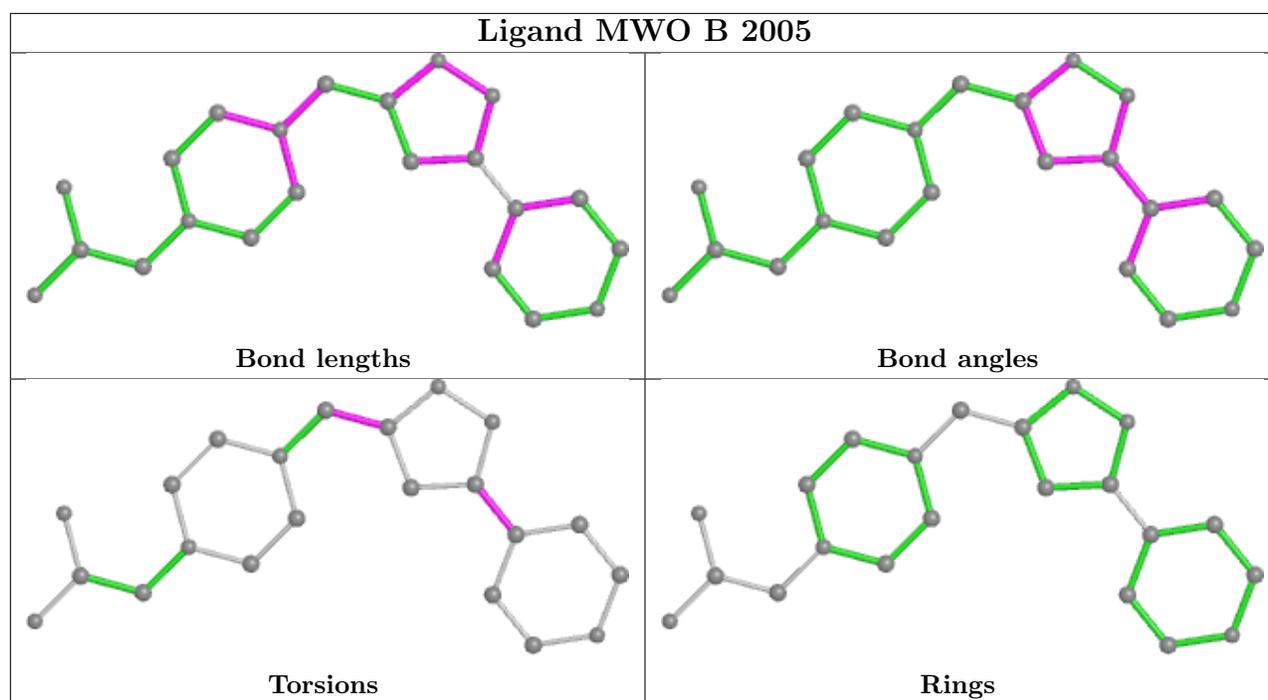
There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	D	2004	NAG	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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	454/457 (99%)	1.43	130 (28%) 0 0	30, 43, 74, 136	0
1	C	453/457 (99%)	1.00	62 (13%) 3 2	38, 57, 90, 138	0
2	B	466/472 (98%)	1.64	124 (26%) 0 0	32, 65, 152, 196	1 (0%)
2	D	471/472 (99%)	1.39	96 (20%) 1 0	40, 74, 147, 199	1 (0%)
3	E	214/221 (96%)	3.56	137 (64%) 0 0	71, 135, 197, 233	0
3	H	216/221 (97%)	1.43	59 (27%) 0 0	49, 102, 162, 187	0
4	F	214/214 (100%)	3.47	126 (58%) 0 0	69, 125, 193, 226	0
4	L	214/214 (100%)	1.14	32 (14%) 2 2	53, 85, 117, 210	0
All	All	2702/2728 (99%)	1.69	766 (28%) 0 0	30, 72, 164, 233	2 (0%)

The worst 5 of 766 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	125	LEU	18.5
3	E	212	VAL	18.4
2	B	77	SER	17.0
4	F	126	THR	15.0
3	E	201	CYS	15.0

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

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

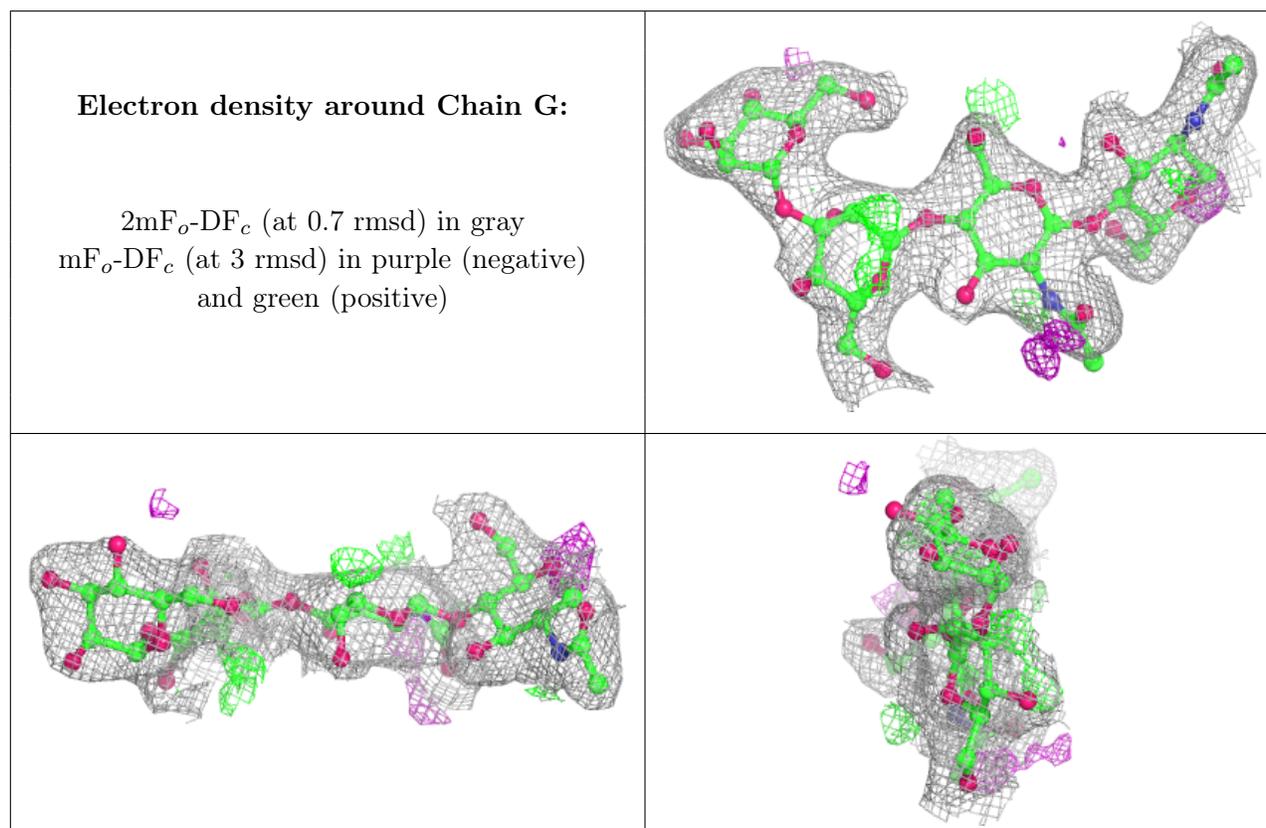
### 6.3 Carbohydrates [i](#)

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.

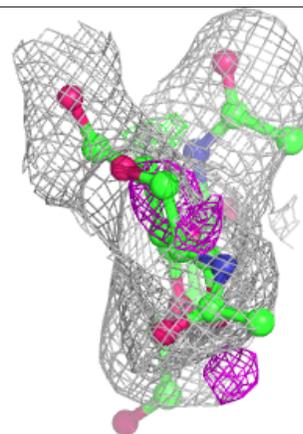
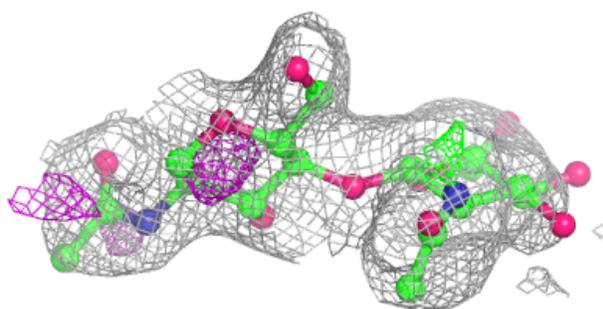
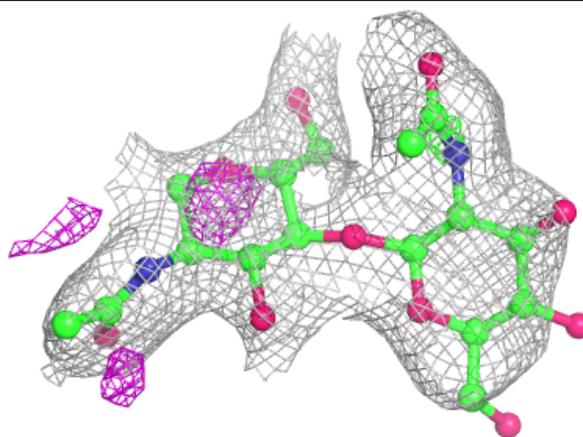
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
7	BMA	J	3	11/12	0.62	0.40	141,145,154,155	0
5	BMA	G	3	11/12	0.64	0.17	130,136,140,142	0
7	MAN	J	4	11/12	0.67	0.25	131,135,139,141	0
6	NAG	I	1	14/15	0.71	0.30	98,106,112,119	0
6	NAG	K	2	14/15	0.72	0.34	127,152,160,161	0
7	NAG	J	2	14/15	0.73	0.24	98,110,127,139	0
7	MAN	J	5	11/12	0.78	0.33	144,148,151,154	0
6	NAG	I	2	14/15	0.80	0.26	128,134,138,140	0
5	MAN	G	4	11/12	0.80	0.17	113,126,130,131	0
6	NAG	K	1	14/15	0.84	0.24	103,109,127,139	0
7	NAG	J	1	14/15	0.85	0.14	55,64,81,95	0
5	NAG	G	2	14/15	0.91	0.15	71,88,104,119	0
5	NAG	G	1	14/15	0.93	0.12	37,48,65,69	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.



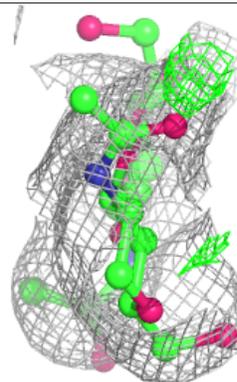
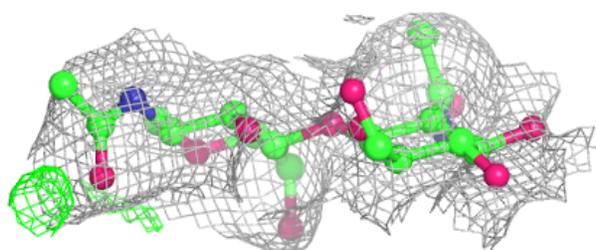
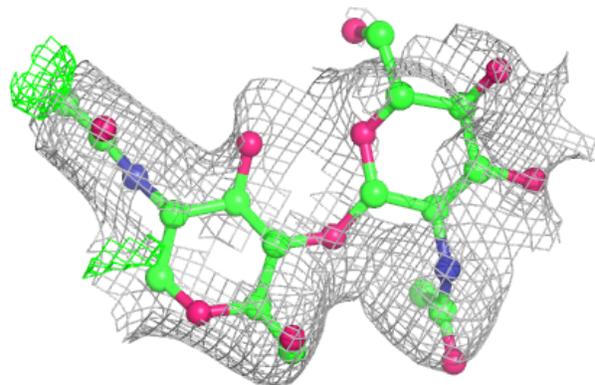
**Electron density around Chain I:**

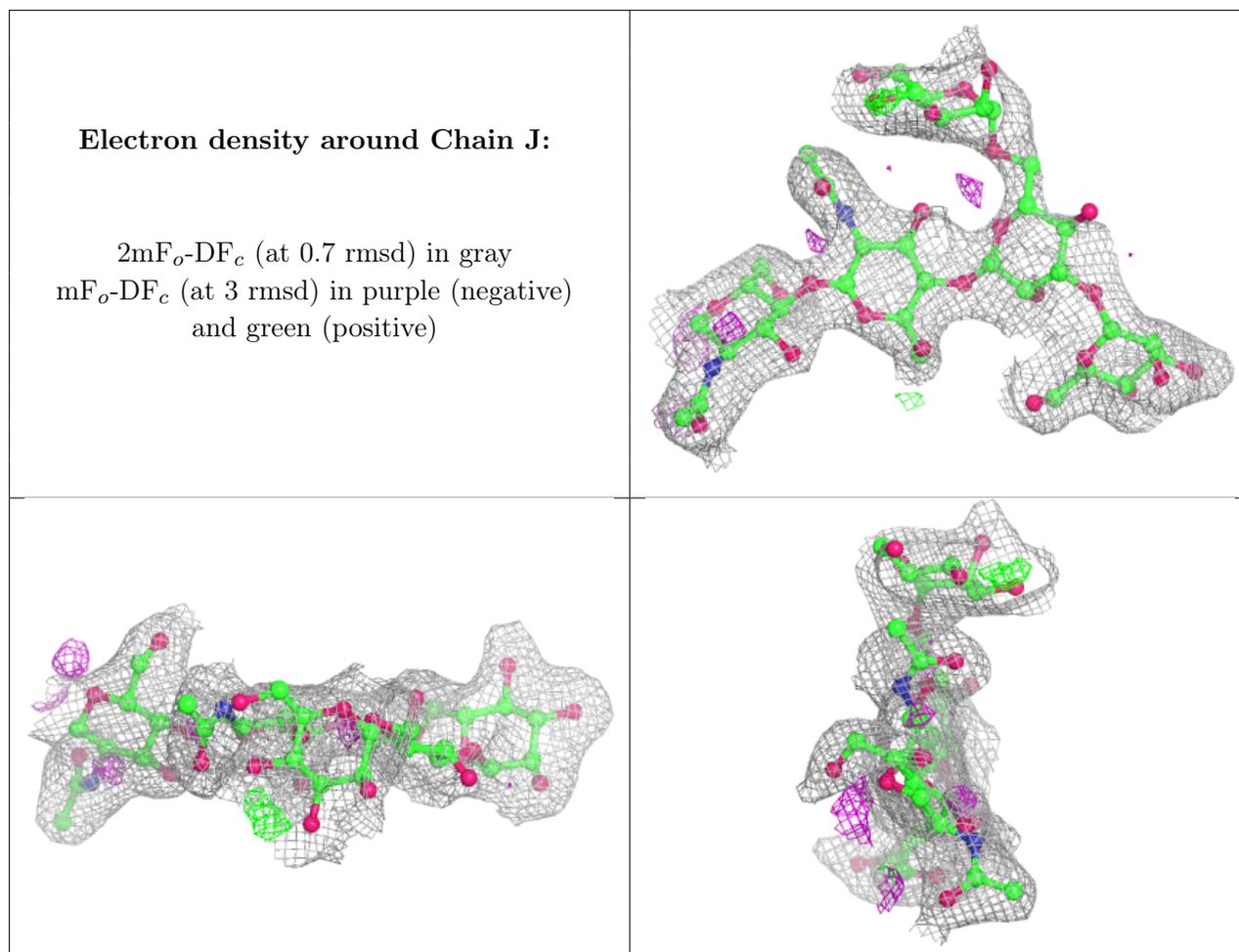
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain K:**

$2mF_o-DF_c$  (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(Å <sup>2</sup> )	Q<0.9
14	CL	C	506	1/1	0.46	0.25	129,129,129,129	0
8	SO4	C	503	5/5	0.60	0.34	177,178,178,180	0
11	NAG	D	2004	14/15	0.62	0.29	99,110,119,120	0
8	SO4	A	507	5/5	0.63	0.30	167,169,171,171	0
13	MAN	C	501	11/12	0.67	0.32	134,136,140,140	0
11	NAG	B	2004	14/15	0.75	0.29	114,130,138,139	0
8	SO4	C	502	5/5	0.78	0.28	156,157,159,160	0
8	SO4	A	508	5/5	0.84	0.26	137,140,144,144	0
8	SO4	C	511	5/5	0.87	0.30	170,170,171,171	0
14	CL	C	505	1/1	0.87	0.56	108,108,108,108	0
12	MWO	D	2006	22/22	0.87	0.20	52,77,103,106	0

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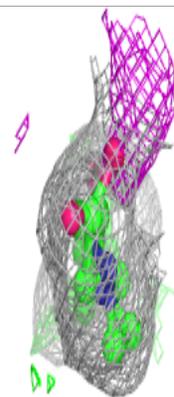
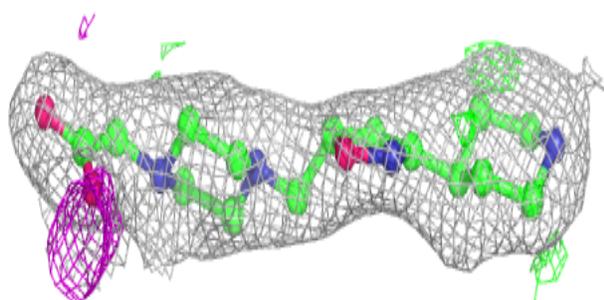
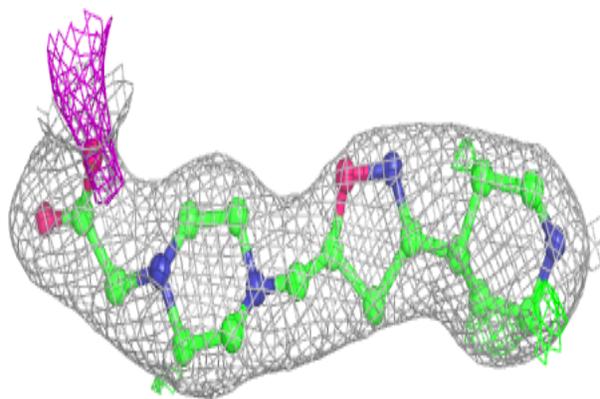
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
12	MWO	B	2005	22/22	0.88	0.23	36,66,85,88	0
8	SO4	L	301	5/5	0.89	0.19	144,145,145,146	0
8	SO4	A	501	5/5	0.90	0.22	117,118,120,123	0
14	CL	D	2005	1/1	0.90	0.27	110,110,110,110	0
9	CA	C	507	1/1	0.92	0.05	73,73,73,73	0
8	SO4	C	504	5/5	0.93	0.15	132,133,133,141	0
9	CA	C	510	1/1	0.94	0.11	51,51,51,51	0
10	MN	D	2002	1/1	0.95	0.06	61,61,61,61	0
8	SO4	A	502	5/5	0.97	0.13	72,73,75,77	0
9	CA	A	503	1/1	0.97	0.06	47,47,47,47	0
10	MN	B	2002	1/1	0.97	0.06	74,74,74,74	0
9	CA	C	509	1/1	0.98	0.10	57,57,57,57	0
10	MN	D	2003	1/1	0.98	0.10	50,50,50,50	0
10	MN	B	2003	1/1	0.99	0.13	37,37,37,37	0
10	MN	D	2001	1/1	0.99	0.12	48,48,48,48	0
9	CA	C	508	1/1	0.99	0.08	60,60,60,60	0
9	CA	A	505	1/1	0.99	0.17	37,37,37,37	0
9	CA	A	506	1/1	0.99	0.19	39,39,39,39	0
9	CA	A	504	1/1	0.99	0.15	39,39,39,39	0
10	MN	B	2001	1/1	1.00	0.19	36,36,36,36	0

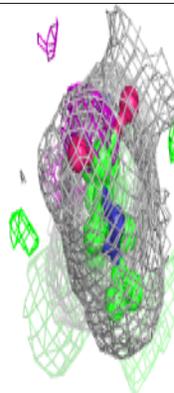
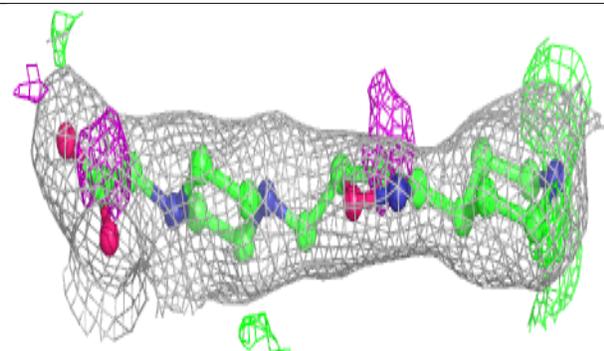
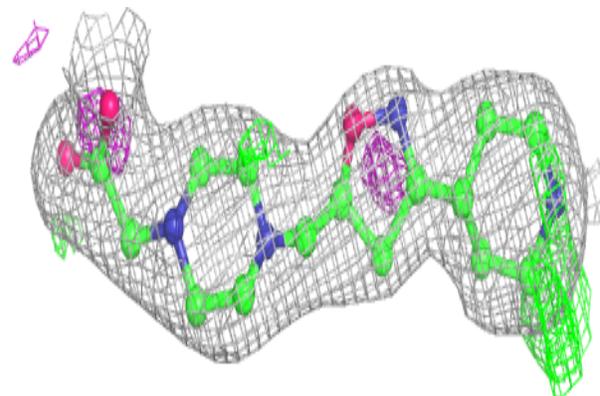
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around MWO D 2006:**

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

**Electron density around MWO B 2005:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.