



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 19, 2021 – 08:13 PM EST

PDB ID : 6V6W  
Title : Crystal structure of antibody 438-B11 DSS mutant (Cys98A-100aA) in complex with an uncleaved prefusion optimized (UFO) soluble BG505 trimer and Fab 35O22  
Authors : Kumar, S.; Wilson, I.A.  
Deposited on : 2019-12-06  
Resolution : 6.50 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.

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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	:	2.16
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)	:	2.16

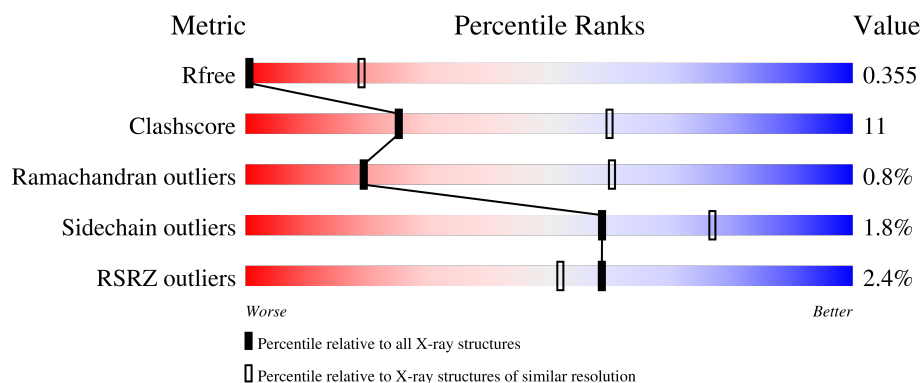
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 6.50 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.






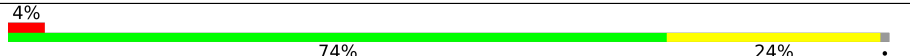
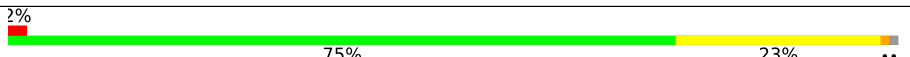
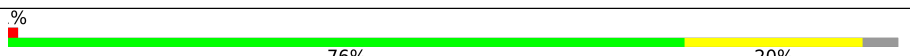
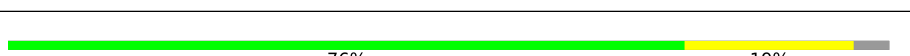
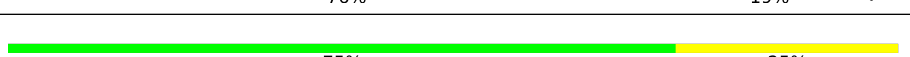

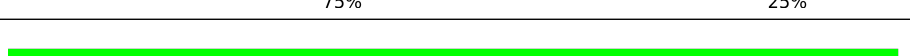
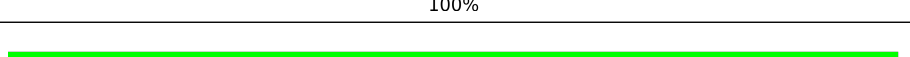
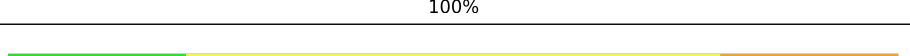
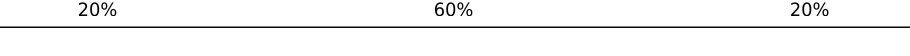
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1000 (9.00-3.90)
Clashscore	141614	1064 (9.00-3.90)
Ramachandran outliers	138981	1012 (9.00-3.88)
Sidechain outliers	138945	1010 (9.00-3.84)
RSRZ outliers	127900	1002 (9.00-3.80)

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	243	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>23%</div> <div>.</div> </div> </div>
1	D	243	<div> <div>4%</div> <div> <div></div> <div>75%</div> <div>23%</div> <div>.</div> </div> </div>
2	B	216	<div> <div>2%</div> <div> <div></div> <div>69%</div> <div>28%</div> <div>.</div> </div> </div>
2	E	216	<div> <div>0%</div> <div> <div></div> <div>73%</div> <div>25%</div> <div>..</div> </div> </div>
3	C	485	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>25%</div> <div>.</div> <div>7%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	G	485	
4	F	235	
4	I	235	
5	H	215	
5	J	215	
6	K	140	
6	T	140	
7	L	4	
7	O	4	
8	M	2	
8	P	2	
9	N	5	
9	Q	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
10	NAG	C	613	-	-	-	X
10	NAG	C	615	-	-	-	X
10	NAG	C	617	-	-	-	X
10	NAG	C	619	-	-	-	X
10	NAG	C	620	-	-	-	X
10	NAG	G	613	-	-	-	X
10	NAG	G	615	-	-	-	X
10	NAG	G	617	-	-	-	X
10	NAG	G	618	-	-	-	X
10	NAG	G	620	-	-	-	X
10	NAG	K	703	-	-	-	X
10	NAG	T	702	-	-	-	X
10	NAG	T	703	-	-	-	X
7	MAN	L	4	-	-	-	X
8	NAG	M	1	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	NAG	P	1	-	-	-	X
9	MAN	Q	4	-	-	-	X
9	MAN	Q	5	-	-	-	X

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 23434 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 35O22 Fab Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	240	Total	C	N	O	S	0	0	0
			1813	1150	303	352	8			
1	A	240	Total	C	N	O	S	0	0	0
			1813	1150	303	352	8			

- Molecule 2 is a protein called 35O22 Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	213	Total	C	N	O	S	0	0	0
			1615	1012	267	328	8			
2	B	213	Total	C	N	O	S	0	0	0
			1615	1012	267	328	8			

- Molecule 3 is a protein called Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	453	Total	C	N	O	S	0	0	0
			3563	2234	630	671	28			
3	C	453	Total	C	N	O	S	0	0	0
			3563	2234	630	671	28			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	62	ASP	GLU	conflict	UNP Q2N0S6
G	332	ASN	THR	conflict	UNP Q2N0S6
G	501	CYS	ALA	conflict	UNP Q2N0S6
G	507	GLY	-	expression tag	UNP Q2N0S6
G	508	GLY	-	expression tag	UNP Q2N0S6
G	509	GLY	-	expression tag	UNP Q2N0S6
G	510	GLY	-	expression tag	UNP Q2N0S6
G	511	GLY	-	expression tag	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
G	512	SER	-	expression tag	UNP Q2N0S6
G	513	GLY	-	expression tag	UNP Q2N0S6
G	514	GLY	-	expression tag	UNP Q2N0S6
G	515	GLY	-	expression tag	UNP Q2N0S6
G	516	GLY	-	expression tag	UNP Q2N0S6
G	517	SER	-	expression tag	UNP Q2N0S6
C	62	ASP	GLU	conflict	UNP Q2N0S6
C	332	ASN	THR	conflict	UNP Q2N0S6
C	501	CYS	ALA	conflict	UNP Q2N0S6
C	507	GLY	-	expression tag	UNP Q2N0S6
C	508	GLY	-	expression tag	UNP Q2N0S6
C	509	GLY	-	expression tag	UNP Q2N0S6
C	510	GLY	-	expression tag	UNP Q2N0S6
C	511	GLY	-	expression tag	UNP Q2N0S6
C	512	SER	-	expression tag	UNP Q2N0S6
C	513	GLY	-	expression tag	UNP Q2N0S6
C	514	GLY	-	expression tag	UNP Q2N0S6
C	515	GLY	-	expression tag	UNP Q2N0S6
C	516	GLY	-	expression tag	UNP Q2N0S6
C	517	SER	-	expression tag	UNP Q2N0S6

- Molecule 4 is a protein called B11 DSS Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	I	226	Total	C	N	O	S	0	0	0
			1716	1091	291	328	6			
4	F	226	Total	C	N	O	S	0	0	0
			1716	1091	291	328	6			

- Molecule 5 is a protein called B11 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	J	213	Total	C	N	O	S	0	0	0
			1634	1022	281	327	4			
5	H	213	Total	C	N	O	S	0	0	0
			1634	1022	281	327	4			

- Molecule 6 is a protein called Envelope glycoprotein gp41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	T	134	Total	C	N	O	S	0	0	0
			1069	677	182	203	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	K	134	Total	C	N	O	S	0	0	0
			1069	677	182	203	7			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	?	-	ILE	deletion	UNP Q2N0S9
T	?	-	VAL	deletion	UNP Q2N0S9
T	?	-	GLN	deletion	UNP Q2N0S9
T	?	-	GLN	deletion	UNP Q2N0S9
T	?	-	GLN	deletion	UNP Q2N0S9
T	?	-	SER	deletion	UNP Q2N0S9
T	?	-	ASN	deletion	UNP Q2N0S9
T	?	-	LEU	deletion	UNP Q2N0S9
T	?	-	LEU	deletion	UNP Q2N0S9
T	?	-	ARG	deletion	UNP Q2N0S9
T	?	-	ALA	deletion	UNP Q2N0S9
T	?	-	ILE	deletion	UNP Q2N0S9
T	?	-	GLU	deletion	UNP Q2N0S9
T	547A	ASN	ALA	conflict	UNP Q2N0S9
T	547B	PRO	GLN	conflict	UNP Q2N0S9
T	547C	ASP	GLN	conflict	UNP Q2N0S9
T	547D	TRP	HIS	conflict	UNP Q2N0S9
T	547F	PRO	LEU	conflict	UNP Q2N0S9
T	547G	ASP	LYS	conflict	UNP Q2N0S9
T	547H	MET	LEU	conflict	UNP Q2N0S9
T	605	CYS	THR	conflict	UNP Q2N0S9
K	?	-	ILE	deletion	UNP Q2N0S9
K	?	-	VAL	deletion	UNP Q2N0S9
K	?	-	GLN	deletion	UNP Q2N0S9
K	?	-	GLN	deletion	UNP Q2N0S9
K	?	-	GLN	deletion	UNP Q2N0S9
K	?	-	SER	deletion	UNP Q2N0S9
K	?	-	ASN	deletion	UNP Q2N0S9
K	?	-	LEU	deletion	UNP Q2N0S9
K	?	-	LEU	deletion	UNP Q2N0S9
K	?	-	ARG	deletion	UNP Q2N0S9
K	?	-	ALA	deletion	UNP Q2N0S9
K	?	-	ILE	deletion	UNP Q2N0S9
K	?	-	GLU	deletion	UNP Q2N0S9
K	547A	ASN	ALA	conflict	UNP Q2N0S9
K	547B	PRO	GLN	conflict	UNP Q2N0S9

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Chain	Residue	Modelled	Actual	Comment	Reference
K	547C	ASP	GLN	conflict	UNP Q2N0S9
K	547D	TRP	HIS	conflict	UNP Q2N0S9
K	547F	PRO	LEU	conflict	UNP Q2N0S9
K	547G	ASP	LYS	conflict	UNP Q2N0S9
K	547H	MET	LEU	conflict	UNP Q2N0S9
K	605	CYS	THR	conflict	UNP Q2N0S9

- Molecule 7 is an oligosaccharide called 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.



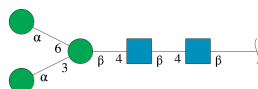
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	L	4	Total	C	N	O	0	0	0
			50	28	2	20			
7	O	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 8 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
8	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
8	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

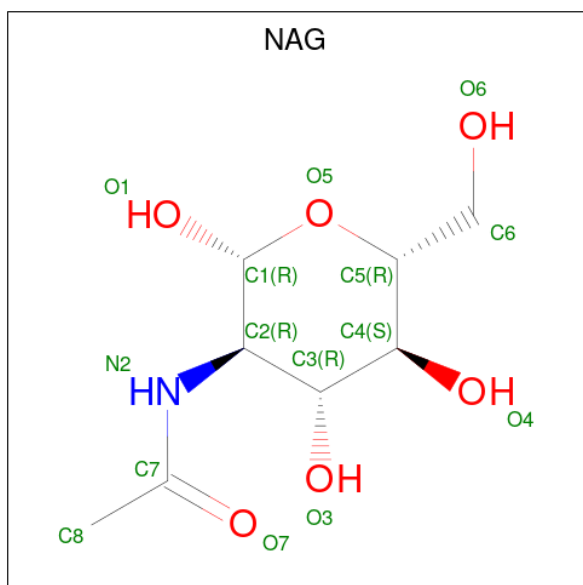
- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	N	5	Total	C	N	O	0	0	0
			61	34	2	25			
9	Q	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	G	1	Total	C	N	O	0	0
			14	8	1	5		
10	G	1	Total	C	N	O	0	0
			14	8	1	5		
10	G	1	Total	C	N	O	0	0
			14	8	1	5		
10	G	1	Total	C	N	O	0	0
			14	8	1	5		
10	G	1	Total	C	N	O	0	0
			14	8	1	5		
10	G	1	Total	C	N	O	0	0
			14	8	1	5		
10	G	1	Total	C	N	O	0	0
			14	8	1	5		
10	G	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	T	1	Total	C	N	O	0	0
			14	8	1	5		
10	T	1	Total	C	N	O	0	0
			14	8	1	5		
10	T	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	K	1	Total	C	N	O	0	0
			14	8	1	5		
10	K	1	Total	C	N	O	0	0
			14	8	1	5		
10	K	1	Total	C	N	O	0	0
			14	8	1	5		

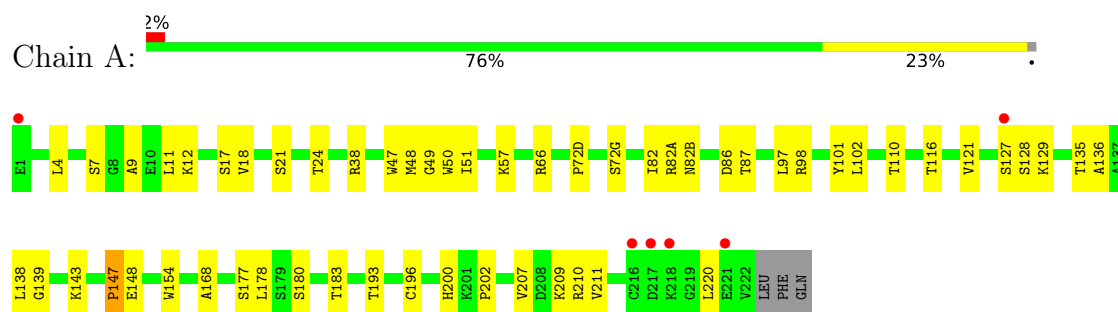
### 3 Residue-property plots

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.

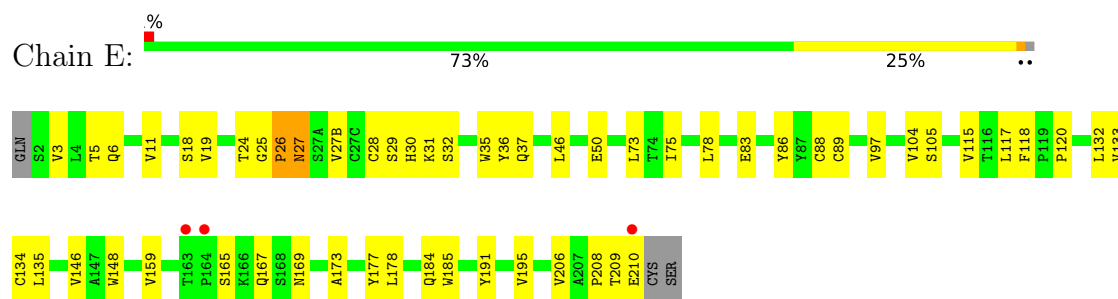
- Molecule 1: 35O22 Fab Heavy chain



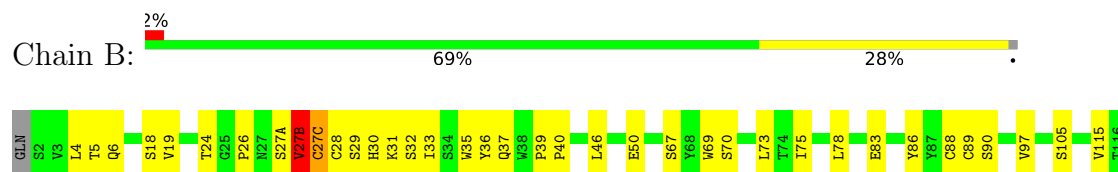
- Molecule 1: 35O22 Fab Heavy chain

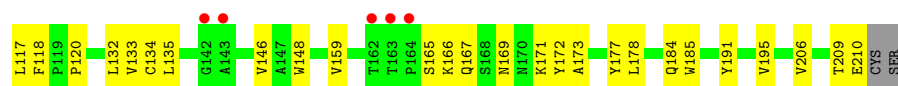


- Molecule 2: 35O22 Fab Light chain

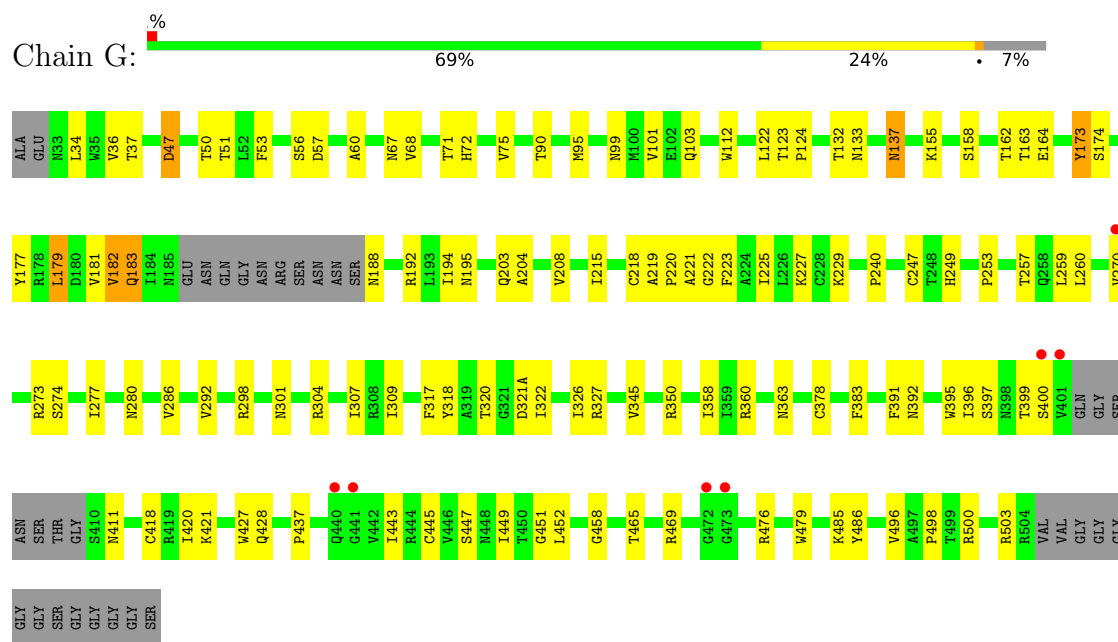


- Molecule 2: 35O22 Fab Light chain

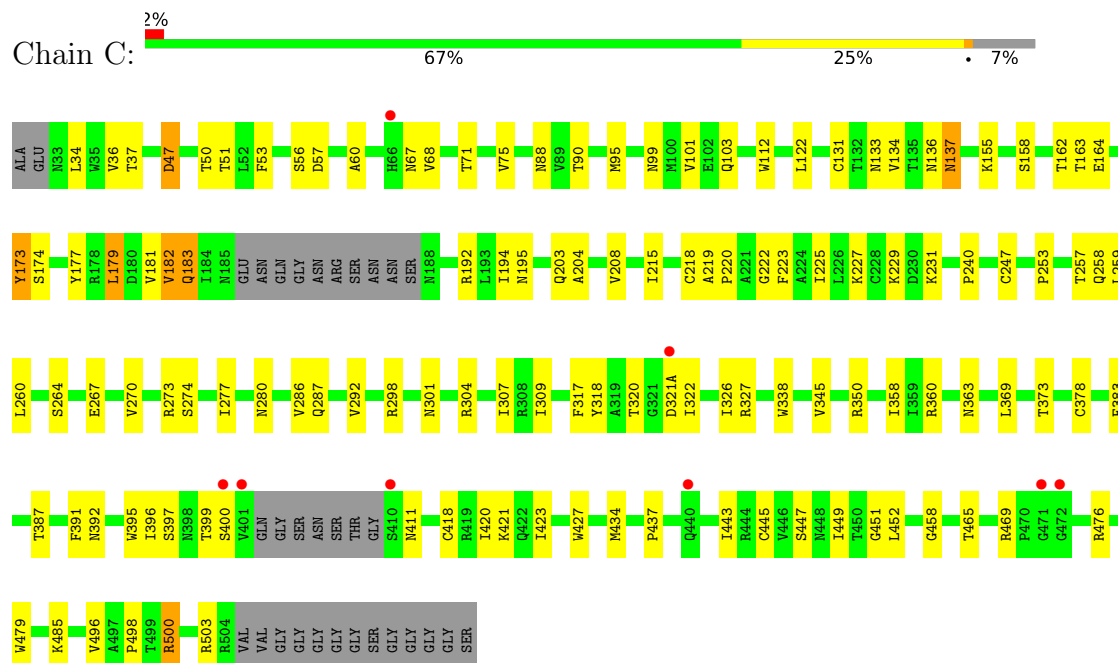


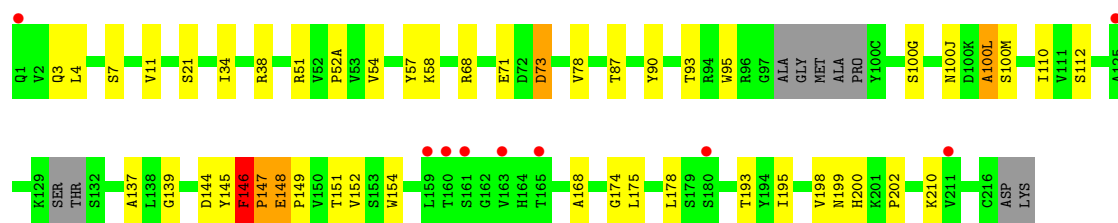


• Molecule 3: Envelope glycoprotein gp120

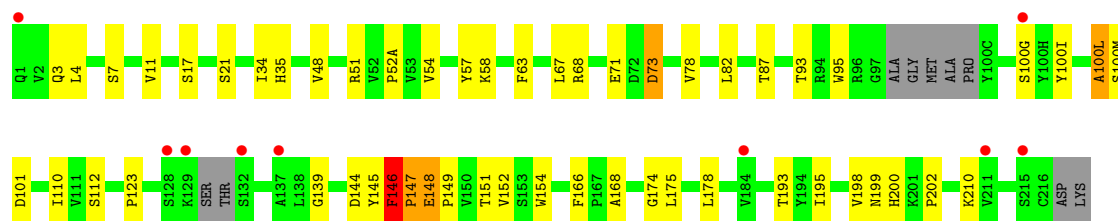


• Molecule 3: Envelope glycoprotein gp120

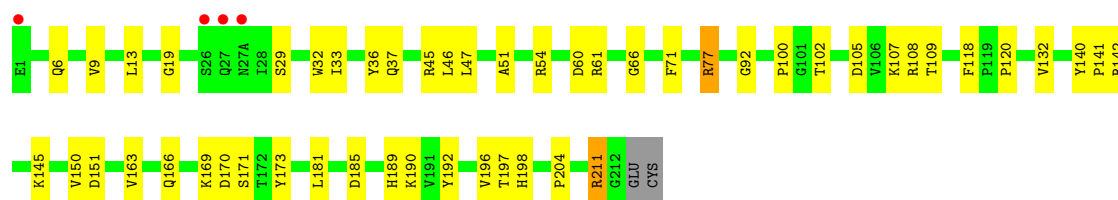
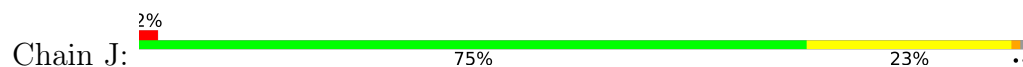




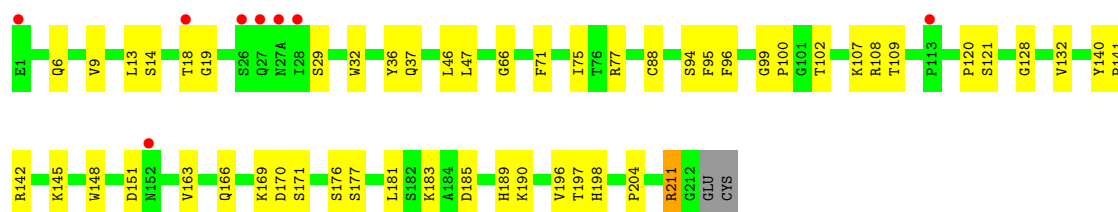
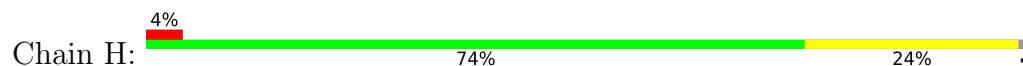
• Molecule 4: B11 DSS Fab heavy chain



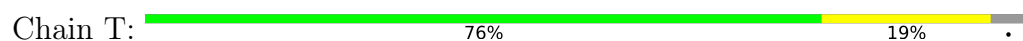
• Molecule 5: B11 Fab light chain



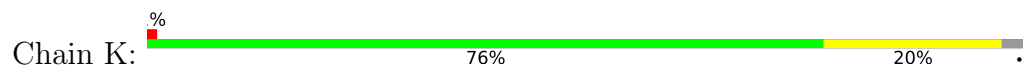
• Molecule 5: B11 Fab light chain

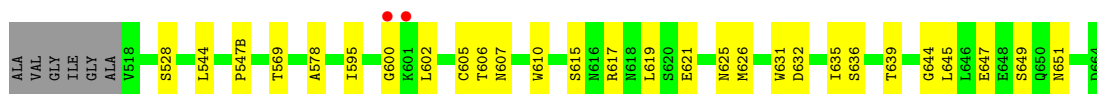


• Molecule 6: Envelope glycoprotein gp41



• Molecule 6: Envelope glycoprotein gp41





- Molecule 7: 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 L: 75% 25%



- Molecule 7: 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 O: 75% 25%



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M: 100%



- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P: 100%



- Molecule 9: 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 N: 20% 60% 20%



- Molecule 9: 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 Q: 20% 60% 20%

MAG1
MAG2
BM/A3
MAN4
MAN5

## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	148.53Å 148.53Å 843.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.72 – 6.50 46.72 – 6.50	Depositor EDS
% Data completeness (in resolution range)	97.2 (46.72-6.50) 97.2 (46.72-6.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.82 (at 6.67Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.309 , 0.355 0.309 , 0.355	Depositor DCC
$R_{free}$ test set	666 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	233.9	Xtriage
Anisotropy	0.538	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.19 , 108.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.359 for -h-k,k,-l	Xtriage
$F_o, F_c$ correlation	0.77	EDS
Total number of atoms	23434	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	279.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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, NAG, MAN

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	0.27	0/1860	0.49	0/2533
1	D	0.26	0/1860	0.49	0/2533
2	B	0.31	0/1659	0.55	2/2269 (0.1%)
2	E	0.48	2/1659 (0.1%)	0.56	1/2269 (0.0%)
3	C	0.26	0/3637	0.46	0/4939
3	G	0.26	0/3637	0.46	0/4939
4	F	0.26	0/1760	0.48	0/2396
4	I	0.26	0/1760	0.48	0/2396
5	H	0.26	0/1669	0.47	0/2267
5	J	0.26	0/1669	0.47	0/2267
6	K	0.26	0/1092	0.43	0/1486
6	T	0.24	0/1092	0.42	0/1486
All	All	0.28	2/23354 (0.0%)	0.48	3/31780 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	I	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	26	PRO	N-CA	13.70	1.70	1.47
2	E	25	GLY	C-N	6.14	1.46	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	26	PRO	CA-N-CD	-8.64	99.40	111.50
2	B	27(B)	VAL	CA-CB-CG2	5.66	119.39	110.90
2	B	27(A)	SER	N-CA-C	-5.25	96.82	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	I	146	PHE	Peptide

## 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	1813	0	1784	38	0
1	D	1813	0	1784	37	0
2	B	1615	0	1544	68	0
2	E	1615	0	1544	59	0
3	C	3563	0	3500	81	0
3	G	3563	0	3500	76	0
4	F	1716	0	1692	40	0
4	I	1716	0	1692	31	0
5	H	1634	0	1588	32	0
5	J	1634	0	1588	29	0
6	K	1069	0	1034	22	0
6	T	1069	0	1034	20	0
7	L	50	0	43	0	0
7	O	50	0	43	0	0
8	M	28	0	25	0	0
8	P	28	0	25	0	0
9	N	61	0	52	2	0
9	Q	61	0	52	2	0
10	C	126	0	117	2	0
10	G	126	0	117	2	0
10	K	42	0	39	2	0
10	T	42	0	39	1	0
All	All	23434	0	22836	496	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 11.

The worst 5 of 496 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:E:26:PRO:N	2:E:26:PRO:CA	1.70	1.48
2:B:27(C):CYS:C	2:B:33:ILE:HD11	1.36	1.46
2:B:27(C):CYS:O	2:B:33:ILE:HD11	1.22	1.32
2:E:3:VAL:CG2	2:E:26:PRO:HG3	1.69	1.22
2:B:28:CYS:SG	2:B:67:SER:O	1.99	1.19

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	238/243 (98%)	223 (94%)	14 (6%)	1 (0%)	34	72
1	D	238/243 (98%)	223 (94%)	14 (6%)	1 (0%)	34	72
2	B	211/216 (98%)	186 (88%)	23 (11%)	2 (1%)	17	57
2	E	211/216 (98%)	190 (90%)	20 (10%)	1 (0%)	29	69
3	C	447/485 (92%)	404 (90%)	40 (9%)	3 (1%)	22	63
3	G	447/485 (92%)	403 (90%)	41 (9%)	3 (1%)	22	63
4	F	220/235 (94%)	199 (90%)	17 (8%)	4 (2%)	8	40
4	I	220/235 (94%)	199 (90%)	17 (8%)	4 (2%)	8	40
5	H	211/215 (98%)	190 (90%)	20 (10%)	1 (0%)	29	69
5	J	211/215 (98%)	189 (90%)	21 (10%)	1 (0%)	29	69
6	K	132/140 (94%)	116 (88%)	15 (11%)	1 (1%)	19	60
6	T	132/140 (94%)	117 (89%)	13 (10%)	2 (2%)	10	46
All	All	2918/3068 (95%)	2639 (90%)	255 (9%)	24 (1%)	19	60

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	I	147	PRO
2	B	30	HIS
4	F	147	PRO
6	K	569	THR
3	G	301	ASN

### 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	203/206 (98%)	203 (100%)	0	100	100
1	D	203/206 (98%)	203 (100%)	0	100	100
2	B	186/189 (98%)	185 (100%)	1 (0%)	88	93
2	E	186/189 (98%)	185 (100%)	1 (0%)	88	93
3	C	405/424 (96%)	389 (96%)	16 (4%)	31	55
3	G	405/424 (96%)	389 (96%)	16 (4%)	31	55
4	F	193/199 (97%)	189 (98%)	4 (2%)	53	72
4	I	193/199 (97%)	189 (98%)	4 (2%)	53	72
5	H	183/185 (99%)	181 (99%)	2 (1%)	73	84
5	J	183/185 (99%)	181 (99%)	2 (1%)	73	84
6	K	116/118 (98%)	116 (100%)	0	100	100
6	T	116/118 (98%)	116 (100%)	0	100	100
All	All	2572/2642 (97%)	2526 (98%)	46 (2%)	59	77

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	I	148	GLU
3	C	57	ASP
4	F	146	PHE
5	J	77	ARG

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Mol	Chain	Res	Type
2	B	27(C)	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	E	6	GLN
2	E	27	ASN
2	B	6	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 ⓘ

22 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	$\# Z  > 2$
7	NAG	L	1	3,7	14,14,15	0.21	0	17,19,21	0.51	0
7	NAG	L	2	7	14,14,15	0.20	0	17,19,21	0.38	0
7	BMA	L	3	7	11,11,12	0.81	0	15,15,17	0.78	0
7	MAN	L	4	7	11,11,12	0.94	0	15,15,17	1.11	1 (6%)
8	NAG	M	1	8,3	14,14,15	0.27	0	17,19,21	0.50	0
8	NAG	M	2	8	14,14,15	0.24	0	17,19,21	0.45	0
9	NAG	N	1	9,3	14,14,15	0.21	0	17,19,21	0.49	0
9	NAG	N	2	9	14,14,15	0.40	0	17,19,21	1.29	2 (11%)
9	BMA	N	3	9	11,11,12	0.73	0	15,15,17	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	MAN	N	4	9	11,11,12	0.74	0	15,15,17	1.04	2 (13%)
9	MAN	N	5	9	11,11,12	0.71	0	15,15,17	1.08	2 (13%)
7	NAG	O	1	3,7	14,14,15	0.22	0	17,19,21	0.48	0
7	NAG	O	2	7	14,14,15	0.19	0	17,19,21	0.38	0
7	BMA	O	3	7	11,11,12	0.78	0	15,15,17	0.79	0
7	MAN	O	4	7	11,11,12	0.94	0	15,15,17	1.10	1 (6%)
8	NAG	P	1	8,3	14,14,15	0.26	0	17,19,21	0.49	0
8	NAG	P	2	8	14,14,15	0.24	0	17,19,21	0.42	0
9	NAG	Q	1	9,3	14,14,15	0.21	0	17,19,21	0.52	0
9	NAG	Q	2	9	14,14,15	0.40	0	17,19,21	1.29	2 (11%)
9	BMA	Q	3	9	11,11,12	0.76	0	15,15,17	0.78	0
9	MAN	Q	4	9	11,11,12	0.73	0	15,15,17	1.06	2 (13%)
9	MAN	Q	5	9	11,11,12	0.74	0	15,15,17	1.10	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	L	1	3,7	-	2/6/23/26	0/1/1/1
7	NAG	L	2	7	-	0/6/23/26	0/1/1/1
7	BMA	L	3	7	-	0/2/19/22	0/1/1/1
7	MAN	L	4	7	-	2/2/19/22	0/1/1/1
8	NAG	M	1	8,3	-	2/6/23/26	0/1/1/1
8	NAG	M	2	8	-	0/6/23/26	0/1/1/1
9	NAG	N	1	9,3	-	0/6/23/26	0/1/1/1
9	NAG	N	2	9	-	4/6/23/26	0/1/1/1
9	BMA	N	3	9	-	1/2/19/22	0/1/1/1
9	MAN	N	4	9	-	2/2/19/22	0/1/1/1
9	MAN	N	5	9	-	2/2/19/22	0/1/1/1
7	NAG	O	1	3,7	-	2/6/23/26	0/1/1/1
7	NAG	O	2	7	-	0/6/23/26	0/1/1/1
7	BMA	O	3	7	-	0/2/19/22	0/1/1/1
7	MAN	O	4	7	-	2/2/19/22	0/1/1/1
8	NAG	P	1	8,3	-	2/6/23/26	0/1/1/1
8	NAG	P	2	8	-	0/6/23/26	0/1/1/1
9	NAG	Q	1	9,3	-	1/6/23/26	0/1/1/1
9	NAG	Q	2	9	-	5/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	BMA	Q	3	9	-	1/2/19/22	0/1/1/1
9	MAN	Q	4	9	-	2/2/19/22	0/1/1/1
9	MAN	Q	5	9	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	Q	2	NAG	C2-N2-C7	4.42	129.20	122.90
9	N	2	NAG	C2-N2-C7	4.42	129.19	122.90
7	O	4	MAN	C1-O5-C5	2.70	115.86	112.19
7	L	4	MAN	C1-O5-C5	2.68	115.83	112.19
9	Q	4	MAN	O2-C2-C3	-2.39	105.35	110.14

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

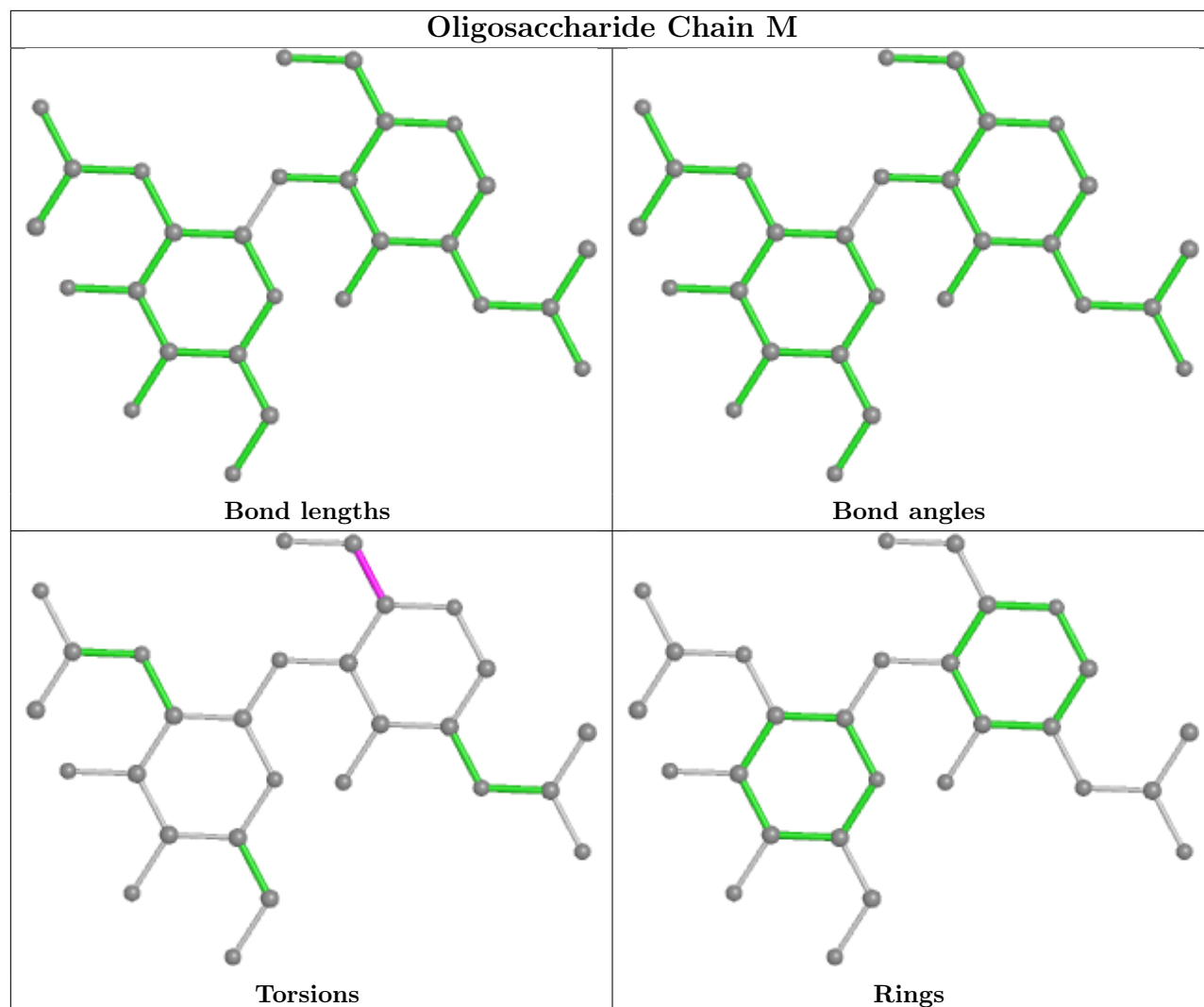
Mol	Chain	Res	Type	Atoms
7	L	4	MAN	C4-C5-C6-O6
7	O	4	MAN	C4-C5-C6-O6
9	N	2	NAG	C8-C7-N2-C2
9	N	2	NAG	O7-C7-N2-C2
9	Q	2	NAG	C8-C7-N2-C2

There are no ring outliers.

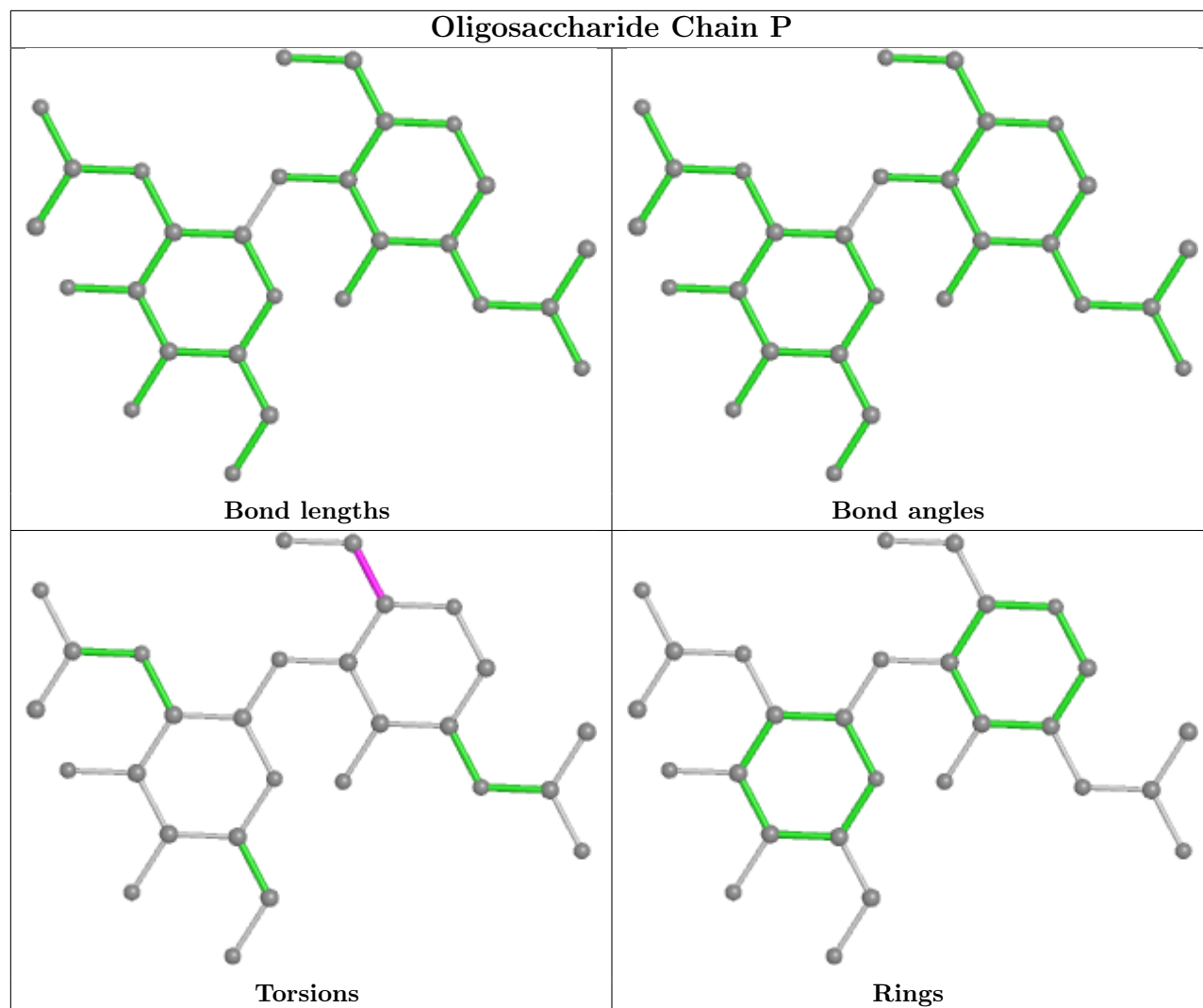
4 monomers are involved in 4 short contacts:

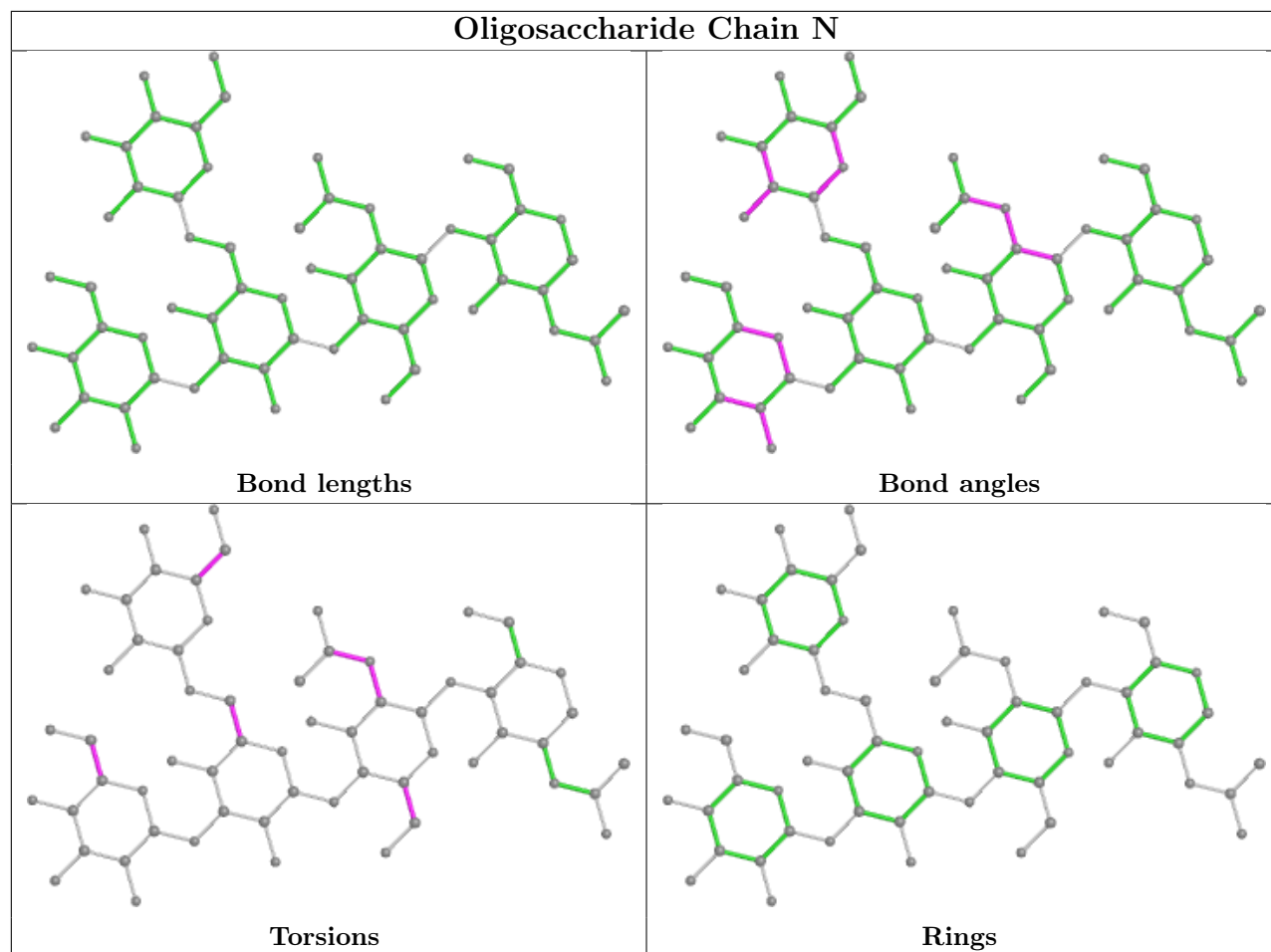
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	N	1	NAG	1	0
9	N	2	NAG	1	0
9	Q	2	NAG	1	0
9	Q	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

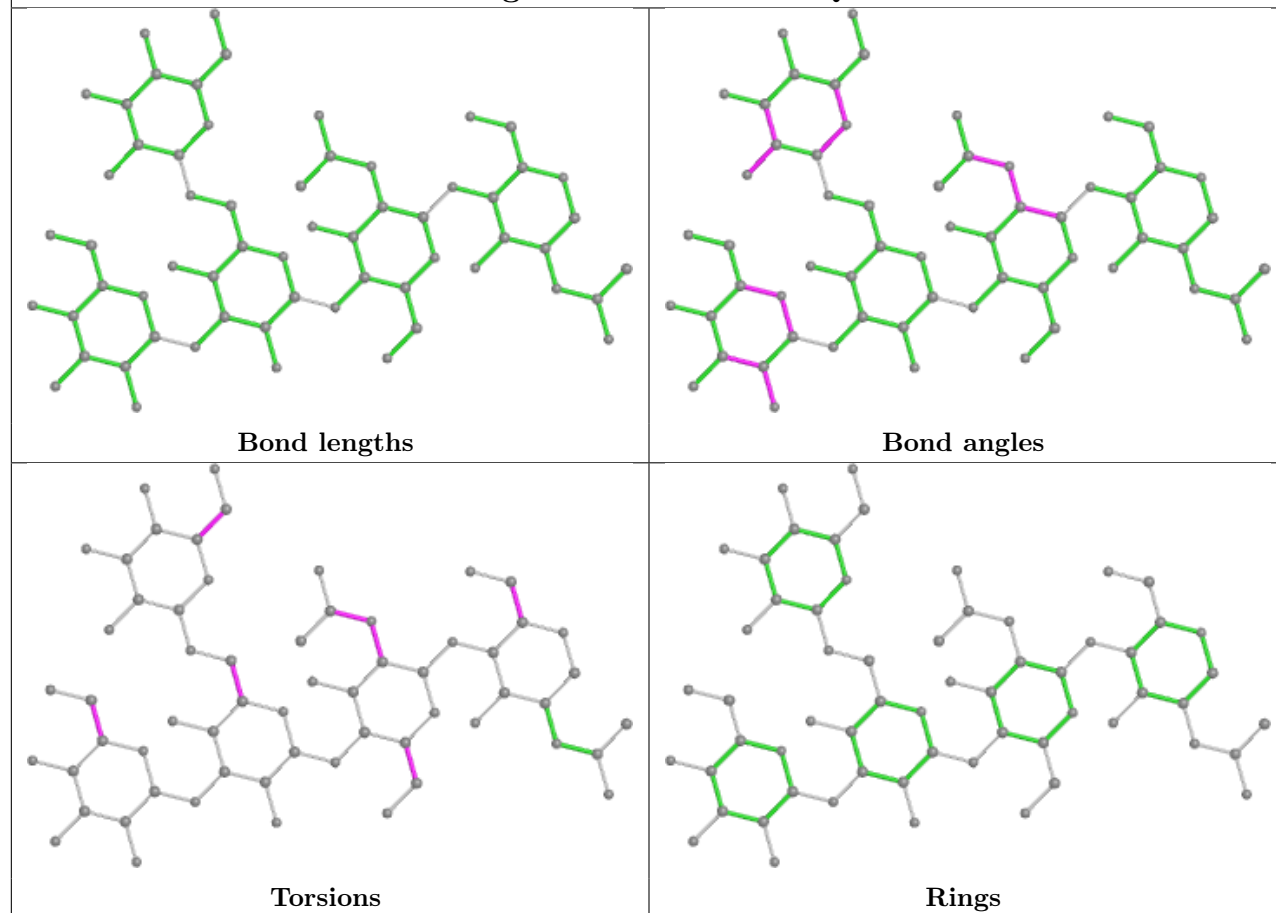




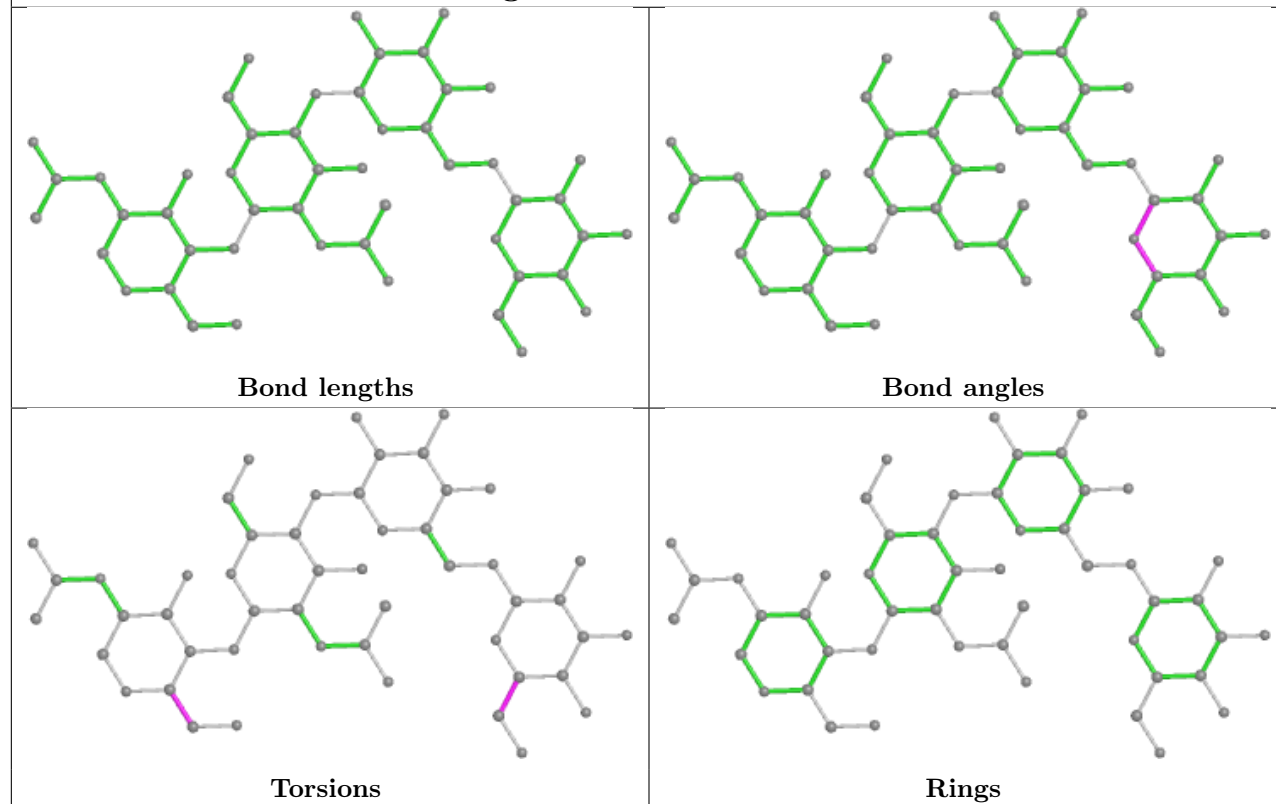




## Oligosaccharide Chain Q



## Oligosaccharide Chain O



## 5.6 Ligand geometry

24 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
10	NAG	T	701	6	14,14,15	0.25	0	17,19,21	0.45	0
10	NAG	K	701	6	14,14,15	0.26	0	17,19,21	0.45	0
10	NAG	G	612	3	14,14,15	0.36	0	17,19,21	0.41	0
10	NAG	G	616	3	14,14,15	0.30	0	17,19,21	0.57	0
10	NAG	G	618	3	14,14,15	0.52	0	17,19,21	0.54	0
10	NAG	G	617	3	14,14,15	0.33	0	17,19,21	0.51	0
10	NAG	C	618	3	14,14,15	0.48	0	17,19,21	0.55	0
10	NAG	C	620	3	14,14,15	0.25	0	17,19,21	0.43	0
10	NAG	C	615	3	14,14,15	0.32	0	17,19,21	0.58	0
10	NAG	K	703	6	14,14,15	0.40	0	17,19,21	0.56	0
10	NAG	G	620	3	14,14,15	0.25	0	17,19,21	0.42	0
10	NAG	C	614	3	14,14,15	0.22	0	17,19,21	0.48	0
10	NAG	C	617	3	14,14,15	0.32	0	17,19,21	0.48	0
10	NAG	C	619	3	14,14,15	0.33	0	17,19,21	0.57	0
10	NAG	G	615	3	14,14,15	0.35	0	17,19,21	0.57	0
10	NAG	C	616	3	14,14,15	0.28	0	17,19,21	0.56	0
10	NAG	C	612	3	14,14,15	0.34	0	17,19,21	0.42	0
10	NAG	C	613	3	14,14,15	0.27	0	17,19,21	0.39	0
10	NAG	T	703	6	14,14,15	0.44	0	17,19,21	0.56	0
10	NAG	T	702	6	14,14,15	0.31	0	17,19,21	0.36	0
10	NAG	G	619	3	14,14,15	0.30	0	17,19,21	0.55	0
10	NAG	G	614	3	14,14,15	0.24	0	17,19,21	0.47	0
10	NAG	G	613	3	14,14,15	0.25	0	17,19,21	0.41	0
10	NAG	K	702	6	14,14,15	0.31	0	17,19,21	0.37	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
10	NAG	T	701	6	-	2/6/23/26	0/1/1/1
10	NAG	K	701	6	-	2/6/23/26	0/1/1/1
10	NAG	G	612	3	-	3/6/23/26	0/1/1/1
10	NAG	G	616	3	-	1/6/23/26	0/1/1/1
10	NAG	G	618	3	-	1/6/23/26	0/1/1/1
10	NAG	G	617	3	-	1/6/23/26	0/1/1/1
10	NAG	C	618	3	-	1/6/23/26	0/1/1/1
10	NAG	C	620	3	-	2/6/23/26	0/1/1/1
10	NAG	C	615	3	-	3/6/23/26	0/1/1/1
10	NAG	K	703	6	-	2/6/23/26	0/1/1/1
10	NAG	G	620	3	-	2/6/23/26	0/1/1/1
10	NAG	C	614	3	-	2/6/23/26	0/1/1/1
10	NAG	C	617	3	-	1/6/23/26	0/1/1/1
10	NAG	C	619	3	-	2/6/23/26	0/1/1/1
10	NAG	G	615	3	-	3/6/23/26	0/1/1/1
10	NAG	C	616	3	-	1/6/23/26	0/1/1/1
10	NAG	C	612	3	-	3/6/23/26	0/1/1/1
10	NAG	C	613	3	-	1/6/23/26	0/1/1/1
10	NAG	T	703	6	-	2/6/23/26	0/1/1/1
10	NAG	T	702	6	-	2/6/23/26	0/1/1/1
10	NAG	G	619	3	-	2/6/23/26	0/1/1/1
10	NAG	G	614	3	-	2/6/23/26	0/1/1/1
10	NAG	G	613	3	-	1/6/23/26	0/1/1/1
10	NAG	K	702	6	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	T	701	NAG	O5-C5-C6-O6
10	K	701	NAG	O5-C5-C6-O6
10	C	615	NAG	O5-C5-C6-O6
10	G	615	NAG	O5-C5-C6-O6
10	C	614	NAG	C4-C5-C6-O6

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	G	618	NAG	1	0
10	C	618	NAG	1	0
10	C	615	NAG	1	0
10	K	703	NAG	1	0
10	G	615	NAG	1	0
10	T	703	NAG	1	0
10	K	702	NAG	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	240/243 (98%)	-0.23	6 (2%) 57 50	209, 293, 422, 436	0
1	D	240/243 (98%)	-0.17	9 (3%) 40 36	195, 301, 440, 465	0
2	B	213/216 (98%)	-0.15	5 (2%) 60 54	221, 295, 398, 412	0
2	E	213/216 (98%)	-0.15	3 (1%) 75 66	219, 290, 423, 441	0
3	C	453/485 (93%)	-0.14	8 (1%) 68 60	201, 255, 314, 383	0
3	G	453/485 (93%)	-0.16	7 (1%) 73 65	190, 254, 305, 355	0
4	F	226/235 (96%)	-0.08	9 (3%) 38 34	230, 272, 325, 360	0
4	I	226/235 (96%)	-0.03	9 (3%) 38 34	229, 267, 316, 366	0
5	H	213/215 (99%)	-0.17	8 (3%) 40 36	239, 287, 327, 371	0
5	J	213/215 (99%)	-0.23	4 (1%) 66 59	239, 279, 322, 361	0
6	K	134/140 (95%)	-0.41	2 (1%) 73 65	202, 239, 281, 313	0
6	T	134/140 (95%)	-0.42	0 100 100	191, 235, 283, 316	0
All	All	2958/3068 (96%)	-0.17	70 (2%) 59 52	190, 269, 398, 465	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	215	SER	5.4
5	H	27	GLN	5.4
4	I	1	GLN	5.1
5	H	27(A)	ASN	4.9
2	E	164	PRO	4.4

### 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 ⓘ

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.

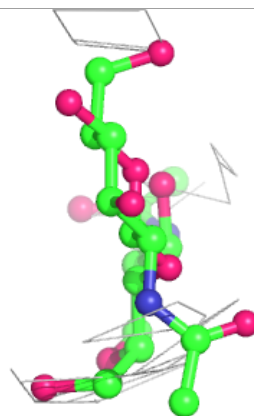
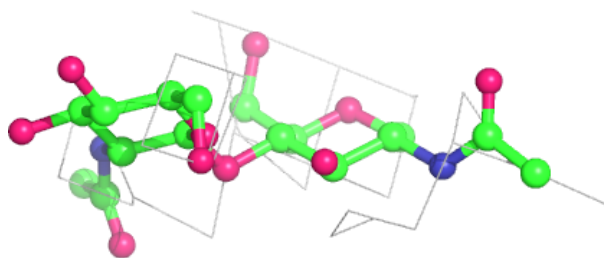
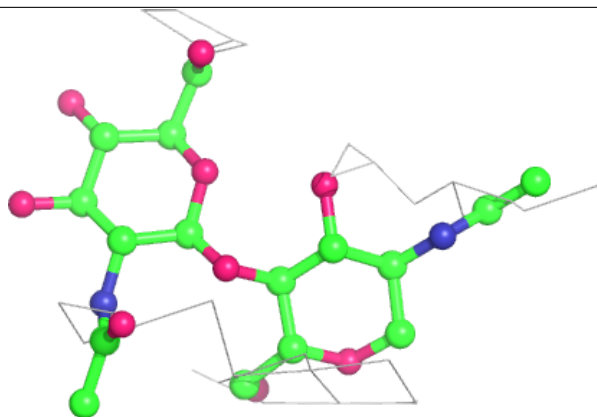
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
9	BMA	Q	3	11/12	0.64	0.39	294,296,299,300	0
9	MAN	Q	5	11/12	0.66	0.44	303,305,308,309	0
9	BMA	N	3	11/12	0.67	0.29	291,293,296,297	0
7	MAN	L	4	11/12	0.68	0.45	239,240,242,243	0
9	MAN	Q	4	11/12	0.72	0.47	295,297,300,301	0
9	NAG	N	1	14/15	0.72	0.33	275,277,279,280	0
8	NAG	M	2	14/15	0.73	0.37	245,248,248,250	0
9	MAN	N	5	11/12	0.74	0.37	300,302,305,306	0
9	NAG	N	2	14/15	0.74	0.32	283,284,286,287	0
8	NAG	M	1	14/15	0.76	0.43	238,239,241,241	0
7	MAN	O	4	11/12	0.78	0.37	241,243,245,246	0
8	NAG	P	1	14/15	0.80	0.42	241,242,244,244	0
9	NAG	Q	1	14/15	0.81	0.25	277,279,282,283	0
7	BMA	L	3	11/12	0.82	0.26	236,236,238,238	0
7	BMA	O	3	11/12	0.82	0.21	238,239,240,241	0
8	NAG	P	2	14/15	0.83	0.31	248,250,251,252	0
7	NAG	L	1	14/15	0.85	0.54	233,235,239,240	0
9	NAG	Q	2	14/15	0.85	0.26	285,287,289,290	0
9	MAN	N	4	11/12	0.86	0.34	293,294,297,298	0
7	NAG	O	1	14/15	0.88	0.29	236,238,242,242	0
7	NAG	L	2	14/15	0.93	0.24	234,236,239,242	0
7	NAG	O	2	14/15	0.94	0.19	237,239,242,244	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.



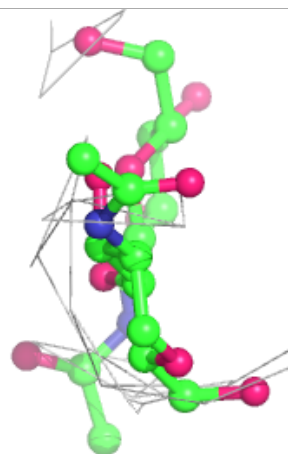
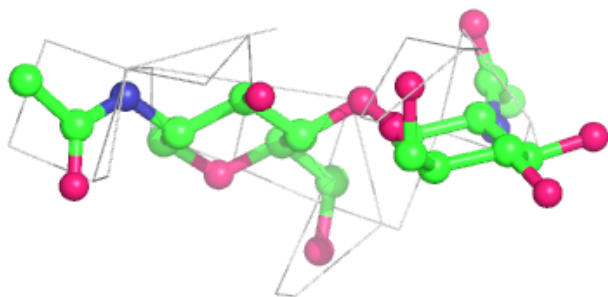
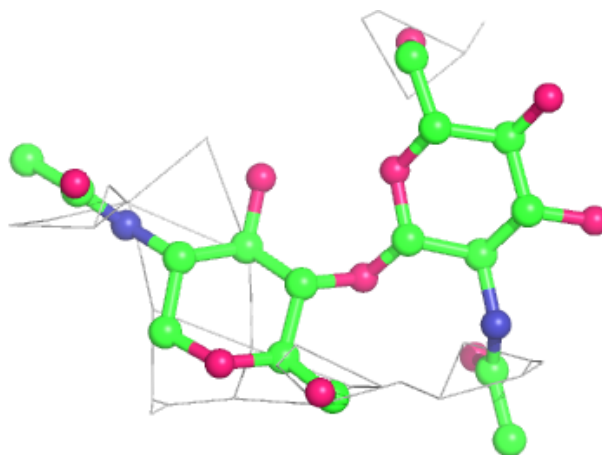
**Electron density around Chain M:**

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



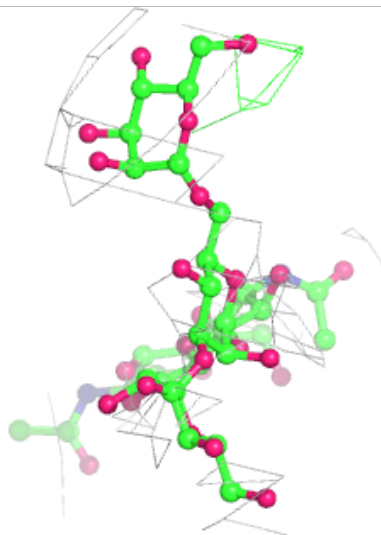
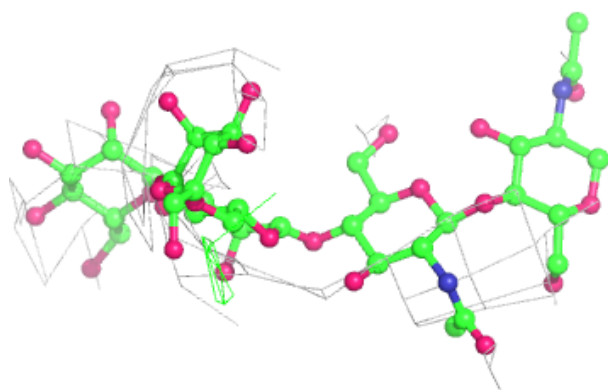
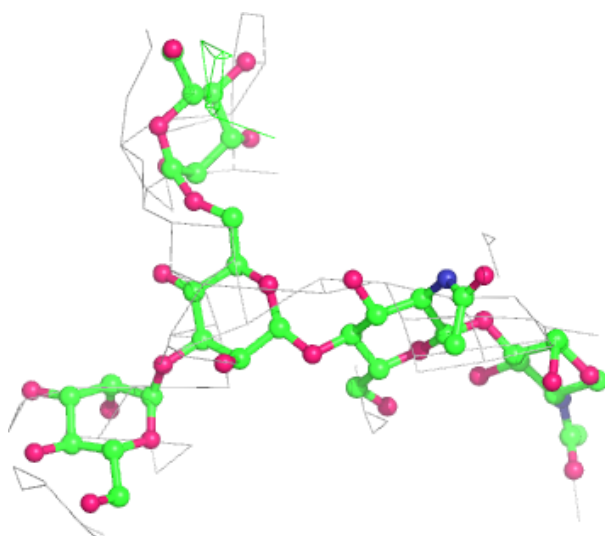
**Electron density around Chain P:**

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



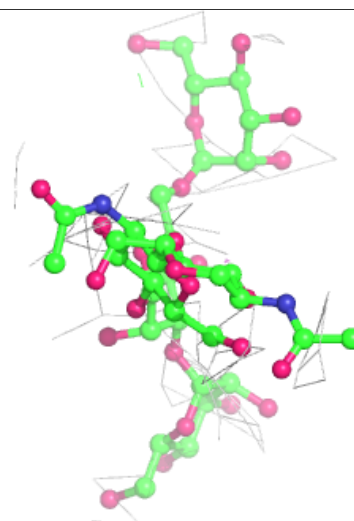
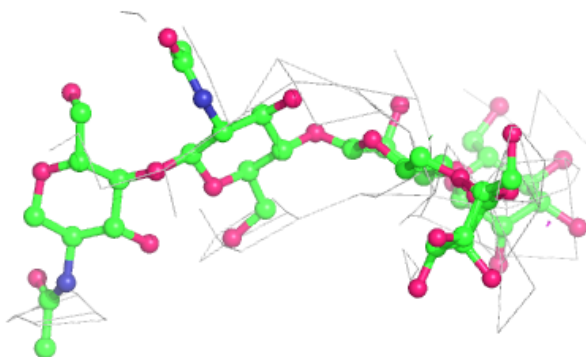
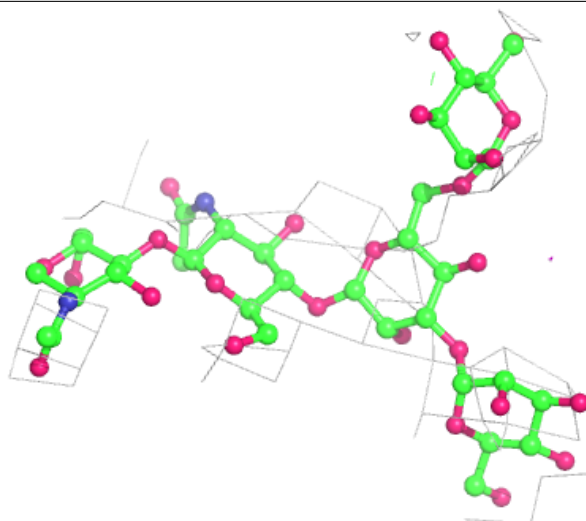
**Electron density around Chain N:**

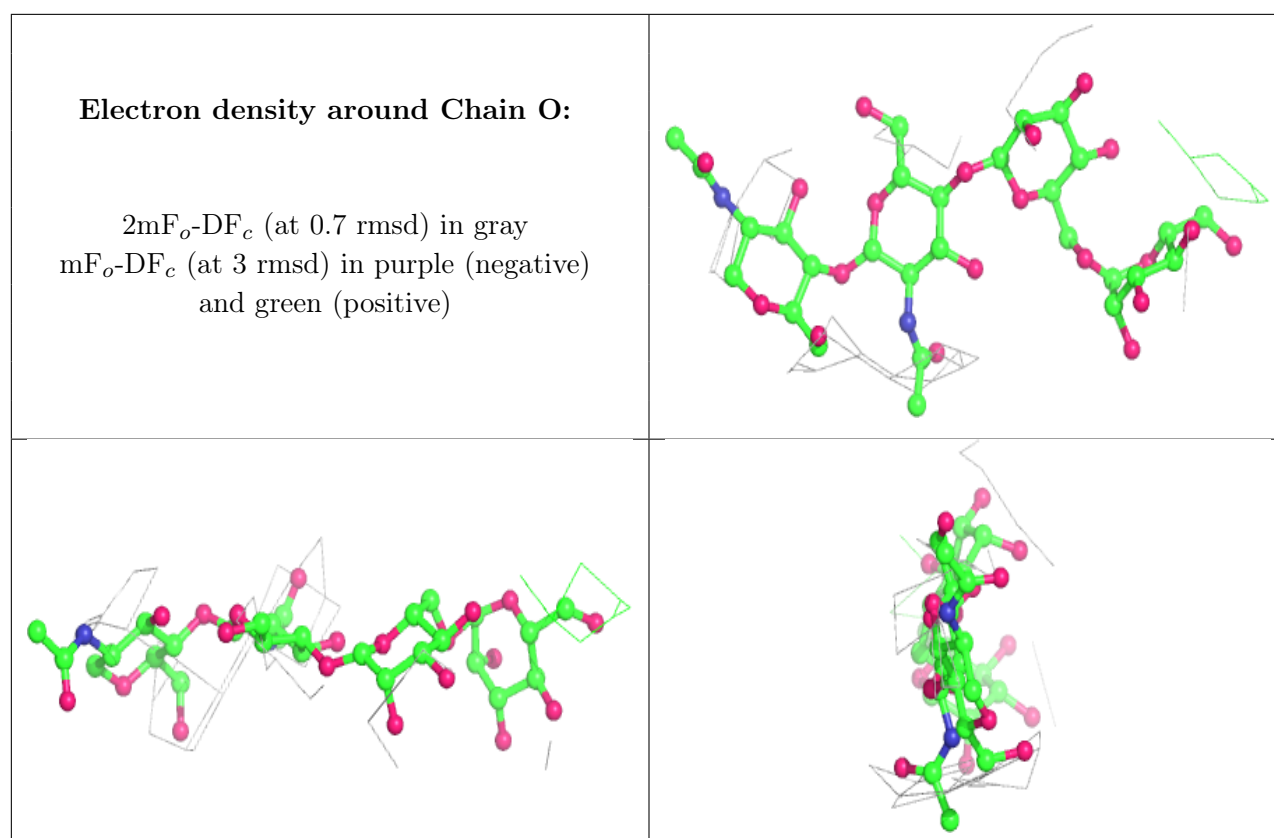
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain Q:**

$2mF_o-DF_c$  (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
10	NAG	G	620	14/15	0.35	0.55	267,273,277,278	0
10	NAG	T	703	14/15	0.49	0.63	278,282,285,286	0
10	NAG	G	612	14/15	0.51	0.39	253,256,260,260	0
10	NAG	K	703	14/15	0.51	0.57	281,285,288,289	0
10	NAG	C	620	14/15	0.52	0.52	269,276,280,281	0
10	NAG	G	618	14/15	0.52	0.55	248,257,262,262	0
10	NAG	C	615	14/15	0.62	0.43	236,238,240,240	0
10	NAG	G	617	14/15	0.68	0.54	231,233,236,237	0
10	NAG	G	615	14/15	0.69	0.44	234,235,237,237	0
10	NAG	C	619	14/15	0.69	0.41	279,281,284,285	0
10	NAG	T	702	14/15	0.69	0.47	283,286,288,289	0
10	NAG	C	612	14/15	0.71	0.28	256,259,263,263	0
10	NAG	C	613	14/15	0.71	0.69	233,235,238,239	0
10	NAG	C	616	14/15	0.72	0.34	280,283,286,286	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
10	NAG	G	613	14/15	0.75	0.66	231,232,235,236	0
10	NAG	G	619	14/15	0.76	0.38	277,278,281,282	0
10	NAG	T	701	14/15	0.77	0.30	281,283,285,287	0
10	NAG	G	614	14/15	0.78	0.28	239,244,247,248	0
10	NAG	G	616	14/15	0.78	0.24	277,280,283,283	0
10	NAG	C	617	14/15	0.79	0.49	233,236,239,240	0
10	NAG	K	702	14/15	0.80	0.31	286,289,291,291	0
10	NAG	C	614	14/15	0.83	0.23	242,247,250,251	0
10	NAG	C	618	14/15	0.86	0.40	251,260,264,265	0
10	NAG	K	701	14/15	0.86	0.32	284,286,288,289	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.