wwPDB X-ray Structure Validation Summary Report (i)

Jun 11, 2024 – 08:51 PM EDT

PDB ID	:	6N5E
Title	:	Broadly protective antibodies directed to a subdominant influenza hemagglutinin epitope
Authors	:	Bajic, G.; Schmidt, A.G.
Deposited on	:	2018-11-21
Resolution	:	3.00 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

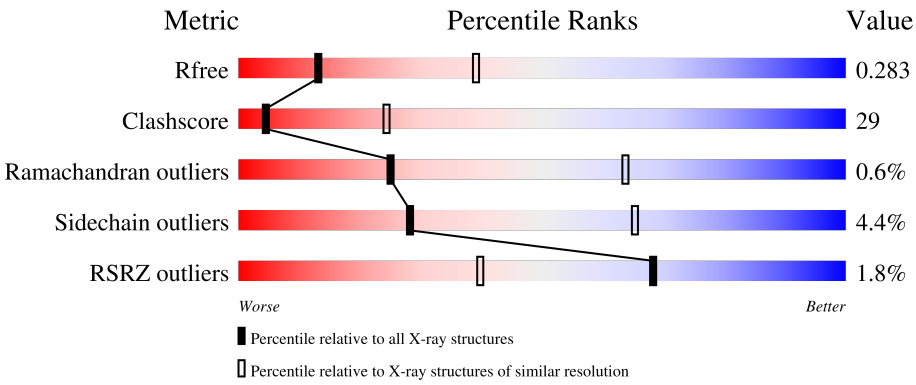
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 >=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 <=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	282	.% 56% 40% •
1	B	282	.% 55% 43% •
1	C	282	.% 57% 38% • •
2	E	238	51% 40% • • 5%
2	G	238	2% 42% 47% • 7%

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Mol	Chain	Length	Quality of chain
2	H	238	%, 47%, 45%, 5%
3	D	217	%, 52%, 43%
3	F	217	7%, 47%, 40%, 9%
3	I	217	2%, 53%, 40%
4	J	2	50%, 50%
4	K	2	100%
4	L	2	100%
4	M	2	100%
4	N	2	50%, 50%

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
4	NAG	M	2	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 16381 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	2188	1374	382	421	11	0	0	0
1	B	282	2188	1374	382	421	11	0	0	0
1	C	277	2153	1353	376	413	11	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	188	ASP	ASN	conflict	UNP P03437
B	188	ASP	ASN	conflict	UNP P03437
C	188	ASP	ASN	conflict	UNP P03437

- Molecule 2 is a protein called FL-1066 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	225	1707	1080	282	337	8	0	0	0
2	E	226	1715	1084	283	340	8	0	0	0
2	G	222	1687	1067	279	333	8	0	0	0

- Molecule 3 is a protein called FL-1066 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	I	211	1573	990	264	315	4	0	0	0
3	F	197	1457	915	245	293	4	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	211	1573	990	264	315	4	0	0	0

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

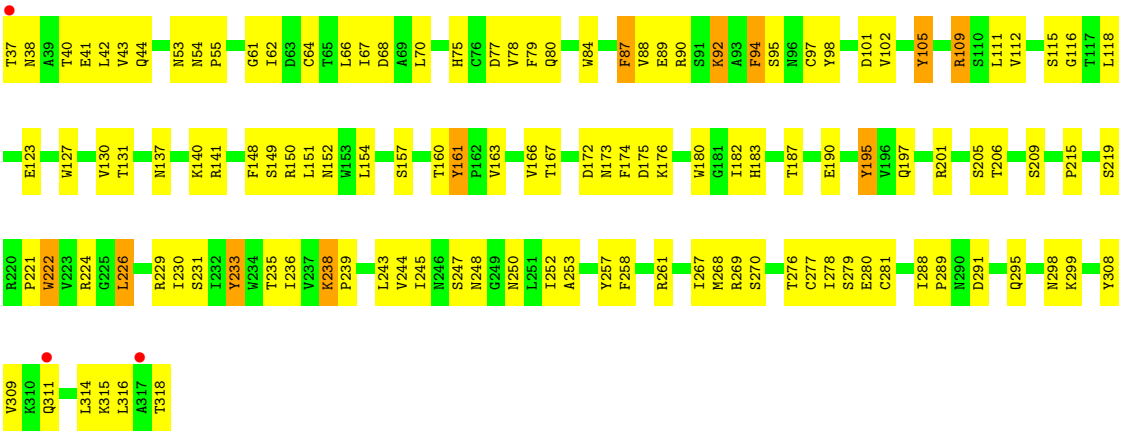
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	J	2	28	16	2	10	0	0	0
4	K	2	28	16	2	10	0	0	0
4	L	2	28	16	2	10	0	0	0
4	M	2	28	16	2	10	0	0	0
4	N	2	28	16	2	10	0	0	0

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: Hemagglutinin

Chain A:

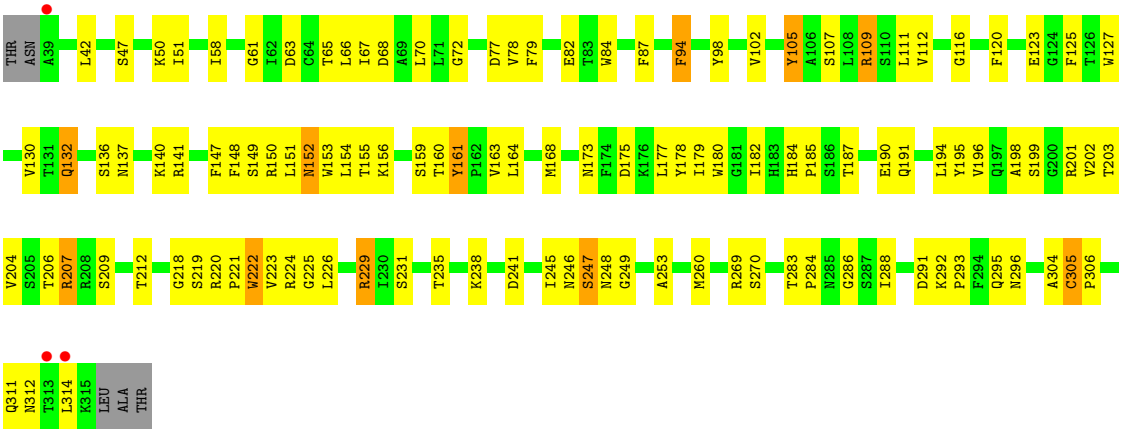


• Molecule 1: Hemagglutinin

Chain B:

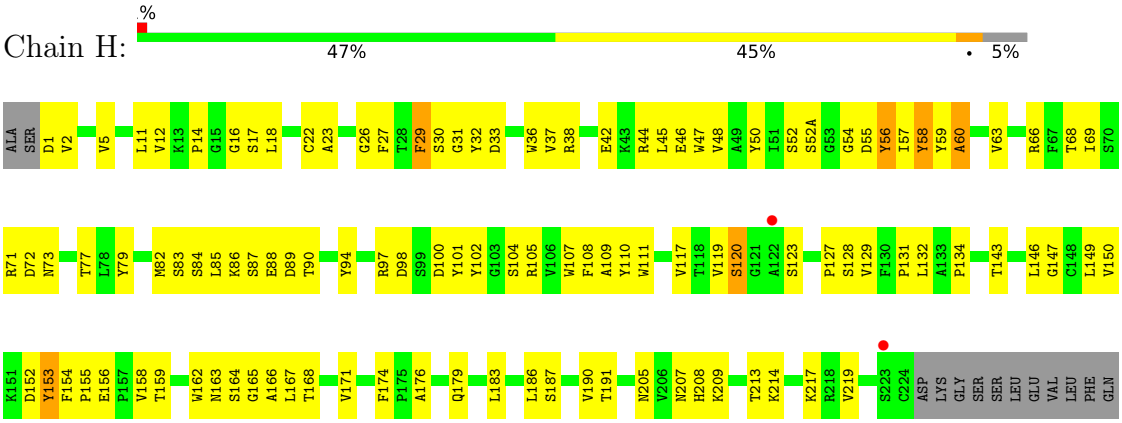
• Molecule 1: Hemagglutinin

Chain C:



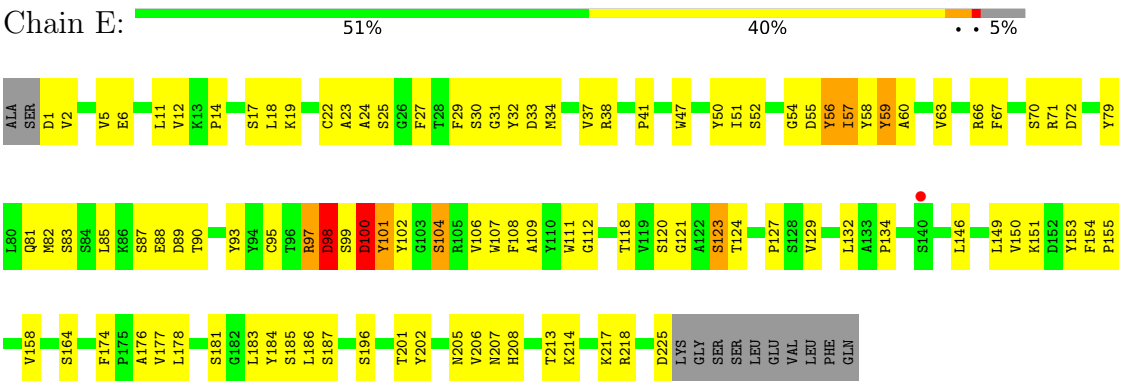
• Molecule 2: FL-1066 heavy chain

Chain H:



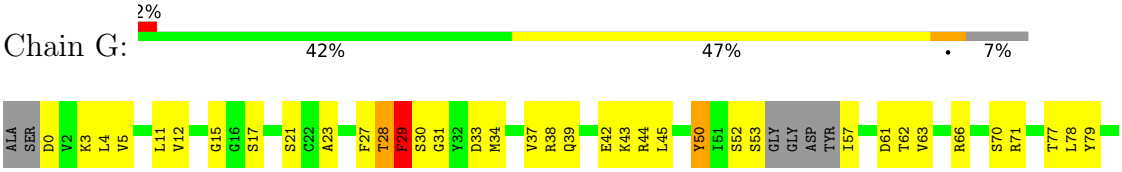
• Molecule 2: FL-1066 heavy chain

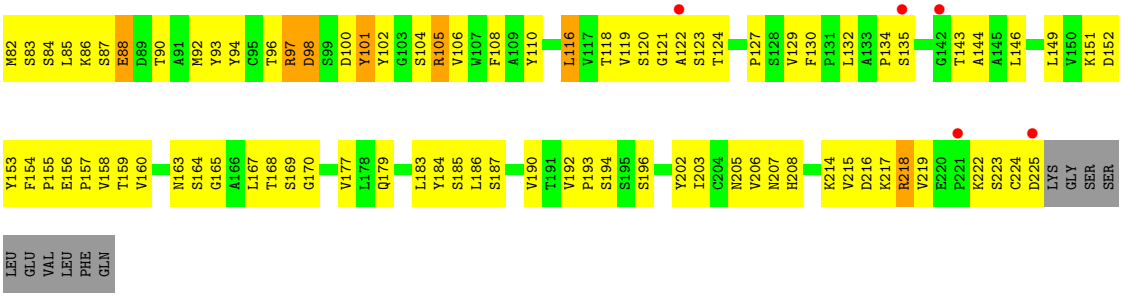
Chain E:



• Molecule 2: FL-1066 heavy chain

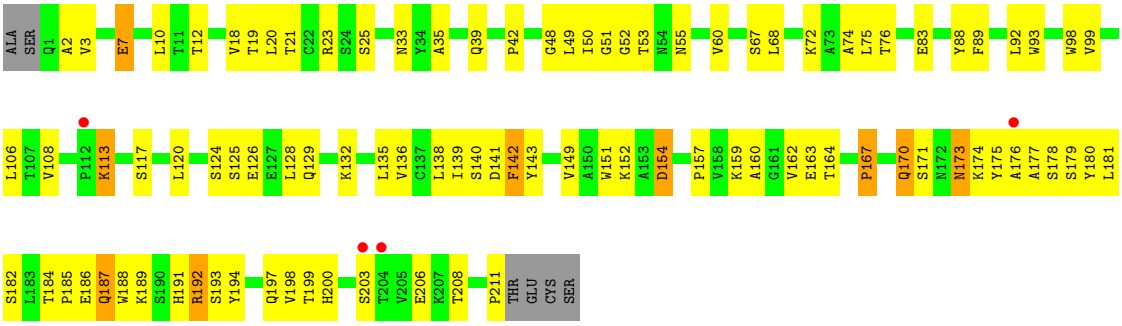
Chain G:





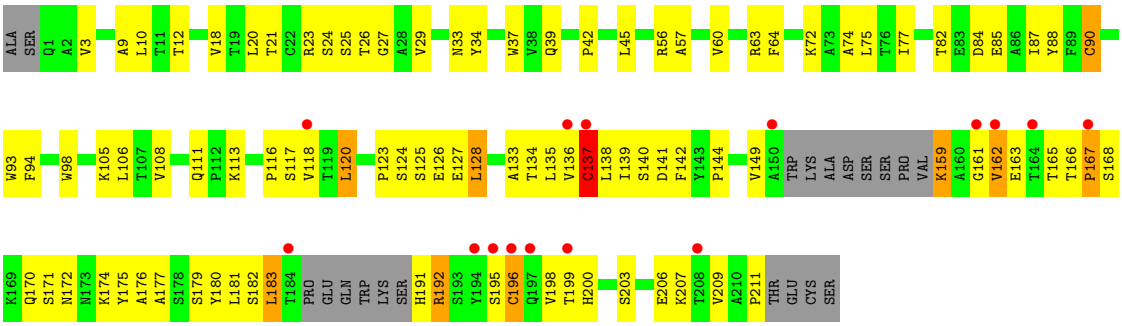
- Molecule 3: FL-1066 light chain

Chain I:



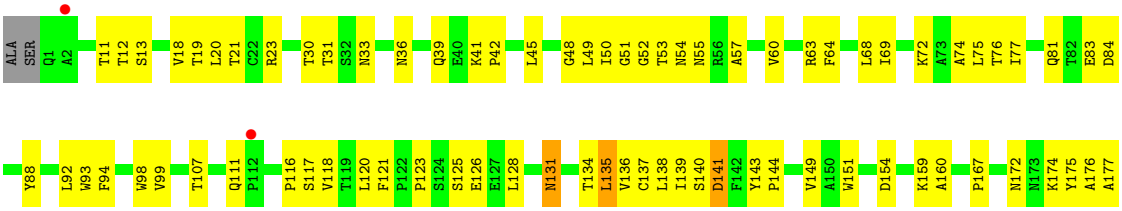
- Molecule 3: FL-1066 light chain

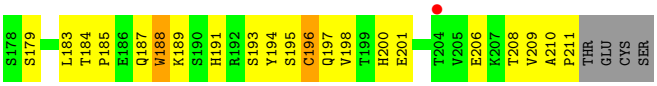
Chain F:



- Molecule 3: FL-1066 light chain

Chain D:





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

Chain J: 50% 50%

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

Chain K: 100%

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

Chain L: 100%

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

Chain M: 100%

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

Chain N: 50% 50%

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	153.56Å 153.56Å 91.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.33 – 3.00 44.33 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.33-3.00) 99.8 (44.33-3.00)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.249 , 0.287 0.247 , 0.283	Depositor DCC
R_{free} test set	2303 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å^2)	60.7	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 9.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	0.088 for -h,-k,l 0.094 for h,-h-k,-l 0.398 for -k,-h,-l	Xtriage
Reported twinning fraction	0.490 for -k,-h,-l	Depositor
Outliers	0 of 48395 reflections	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	16381	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.30% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG

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	0.36	0/2240	0.64	1/3051 (0.0%)
1	B	0.40	0/2240	0.69	1/3051 (0.0%)
1	C	0.39	0/2205	0.67	2/3002 (0.1%)
2	E	0.44	0/1758	0.74	1/2391 (0.0%)
2	G	0.49	0/1728	0.89	5/2349 (0.2%)
2	H	0.39	0/1750	0.69	0/2380
3	D	0.44	0/1612	0.79	2/2206 (0.1%)
3	F	0.45	1/1488 (0.1%)	0.84	3/2032 (0.1%)
3	I	0.37	0/1612	0.68	1/2206 (0.0%)
All	All	0.41	1/16633 (0.0%)	0.73	16/22668 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	162	VAL	CB-CG2	-5.47	1.41	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	116	LEU	CB-CG-CD1	-10.46	93.21	111.00
3	F	137	CYS	CA-CB-SG	7.11	126.79	114.00
3	D	135	LEU	CA-CB-CG	6.80	130.94	115.30
3	I	7	GLU	CA-CB-CG	6.57	127.86	113.40
3	D	68	LEU	CA-CB-CG	6.50	130.24	115.30

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	2188	0	2139	105	1
1	B	2188	0	2137	111	0
1	C	2153	0	2100	95	1
2	E	1715	0	1662	110	0
2	G	1687	0	1642	109	1
2	H	1707	0	1658	110	0
3	D	1573	0	1531	87	0
3	F	1457	0	1424	136	0
3	I	1573	0	1531	96	1
4	J	28	0	25	1	0
4	K	28	0	25	1	0
4	L	28	0	25	3	0
4	M	28	0	25	2	0
4	N	28	0	25	0	0
All	All	16381	0	15949	922	2

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 29.

The worst 5 of 922 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)
3:F:118:VAL:CB	3:F:139:ILE:HD13	1.37	1.50
3:F:118:VAL:HB	3:F:139:ILE:CD1	1.48	1.44
2:E:99:SER:HB2	2:E:106:VAL:O	1.04	1.18
2:E:178:LEU:HD23	2:E:184:TYR:CE1	1.79	1.17
3:F:117:SER:O	3:F:140:SER:OG	1.60	1.17

All (2) 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)
1:A:160:THR:OG1	2:G:194:SER:OG[2_655]	2.06	0.14
1:C:50:LYS:NZ	3:I:83:GLU:OE2[3_654]	2.13	0.07

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	280/282 (99%)	261 (93%)	18 (6%)	1 (0%)	34	72
1	B	280/282 (99%)	262 (94%)	18 (6%)	0	100	100
1	C	275/282 (98%)	261 (95%)	13 (5%)	1 (0%)	34	72
2	E	224/238 (94%)	203 (91%)	16 (7%)	5 (2%)	6	31
2	G	218/238 (92%)	200 (92%)	17 (8%)	1 (0%)	29	68
2	H	223/238 (94%)	200 (90%)	21 (9%)	2 (1%)	17	55
3	D	209/217 (96%)	189 (90%)	20 (10%)	0	100	100
3	F	191/217 (88%)	175 (92%)	15 (8%)	1 (0%)	29	68
3	I	209/217 (96%)	199 (95%)	9 (4%)	1 (0%)	29	68
All	All	2109/2211 (95%)	1950 (92%)	147 (7%)	12 (1%)	25	64

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	57	ILE
2	E	181	SER
2	G	105	ARG
1	A	226	LEU
1	C	132	GLN

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	249/249 (100%)	237 (95%)	12 (5%)	25	62
1	B	249/249 (100%)	240 (96%)	9 (4%)	35	70
1	C	245/249 (98%)	230 (94%)	15 (6%)	18	53
2	E	192/202 (95%)	183 (95%)	9 (5%)	26	63
2	G	190/202 (94%)	180 (95%)	10 (5%)	22	58
2	H	191/202 (95%)	185 (97%)	6 (3%)	40	75
3	D	173/178 (97%)	169 (98%)	4 (2%)	50	80
3	F	160/178 (90%)	154 (96%)	6 (4%)	33	69
3	I	173/178 (97%)	164 (95%)	9 (5%)	23	59
All	All	1822/1887 (97%)	1742 (96%)	80 (4%)	28	65

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	100	ASP
3	F	137	CYS
2	G	135	SER
3	I	170	GLN
3	F	196	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	172	ASN
3	D	39	GLN
3	D	54	ASN
1	C	152	ASN
1	C	298	ASN

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)

10 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	$\#\|Z\| > 2$
4	NAG	J	1	4,1	14,14,15	0.27	0	17,19,21	1.46	2 (11%)
4	NAG	J	2	4	14,14,15	0.29	0	17,19,21	0.66	0
4	NAG	K	1	4,1	14,14,15	0.50	0	17,19,21	0.80	0
4	NAG	K	2	4	14,14,15	0.30	0	17,19,21	0.45	0
4	NAG	L	1	4,1	14,14,15	0.63	0	17,19,21	1.05	2 (11%)
4	NAG	L	2	4	14,14,15	0.79	1 (7%)	17,19,21	0.71	1 (5%)
4	NAG	M	1	4,1	14,14,15	0.27	0	17,19,21	0.74	0
4	NAG	M	2	4	14,14,15	0.73	0	17,19,21	0.59	0
4	NAG	N	1	4,1	14,14,15	0.43	0	17,19,21	2.47	2 (11%)
4	NAG	N	2	4	14,14,15	0.25	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
4	NAG	J	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	J	2	4	-	4/6/23/26	0/1/1/1
4	NAG	K	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	K	2	4	-	2/6/23/26	0/1/1/1
4	NAG	L	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	L	2	4	-	1/6/23/26	0/1/1/1
4	NAG	M	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	M	2	4	-	3/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	2	NAG	O5-C1	-2.38	1.39	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	N	1	NAG	C1-O5-C5	9.41	124.94	112.19
4	J	1	NAG	C2-N2-C7	4.50	129.31	122.90
4	L	1	NAG	C1-O5-C5	2.74	115.90	112.19
4	N	1	NAG	O5-C5-C6	-2.52	103.25	107.20
4	J	1	NAG	O4-C4-C5	-2.46	103.18	109.30

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

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

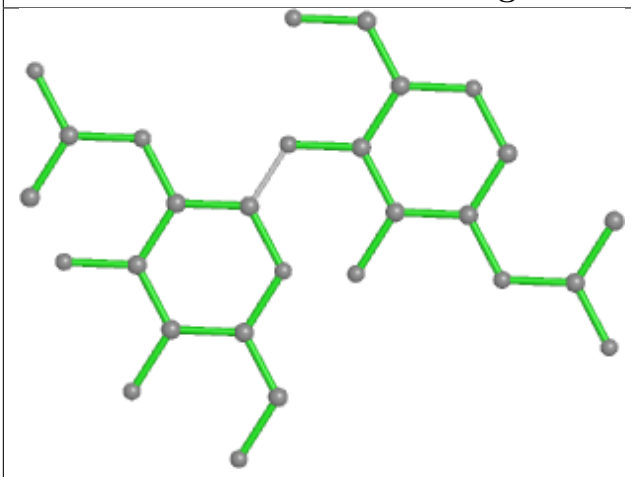
There are no ring outliers.

7 monomers are involved in 7 short contacts:

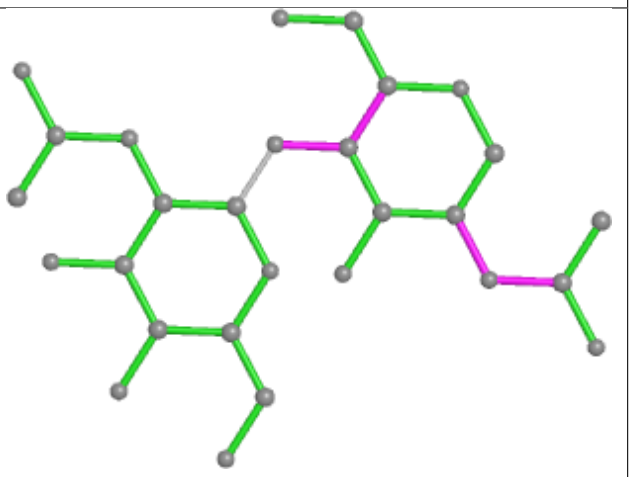
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	K	1	NAG	1	0
4	M	2	NAG	2	0
4	L	2	NAG	2	0
4	K	2	NAG	1	0
4	L	1	NAG	3	0
4	J	1	NAG	1	0
4	M	1	NAG	2	0

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

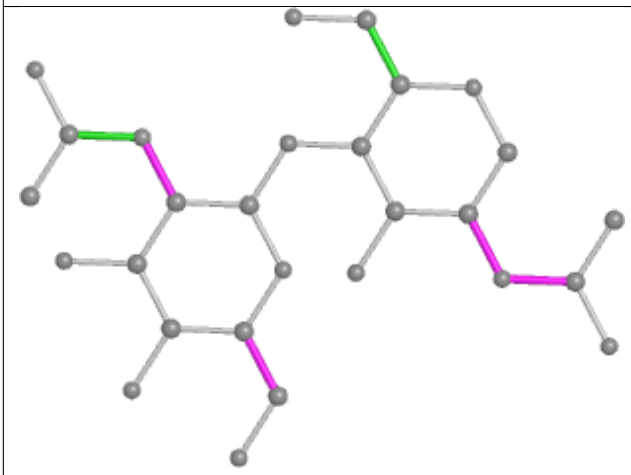
Oligosaccharide Chain J



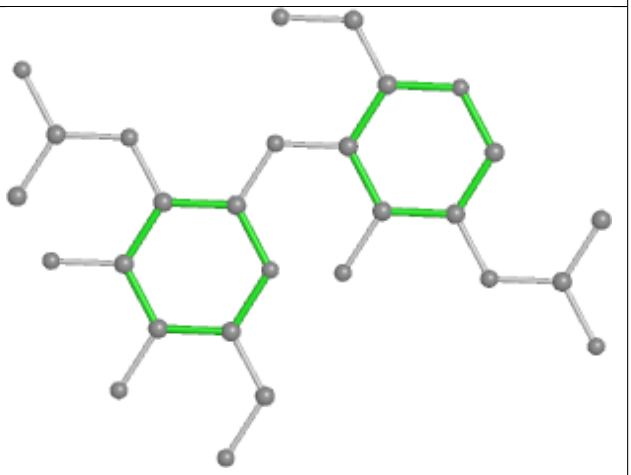
Bond lengths



Bond angles

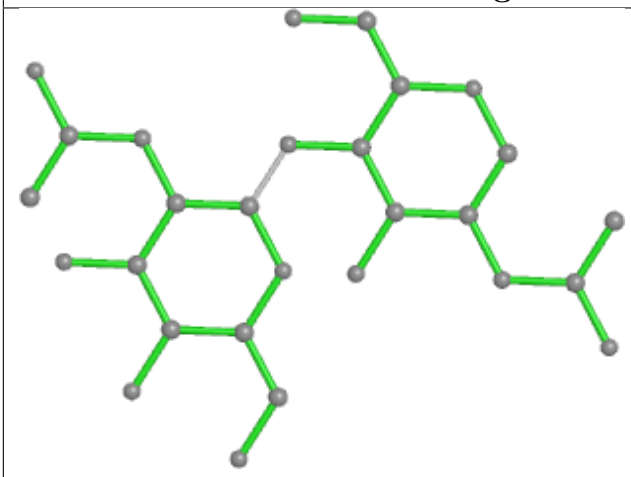


Torsions

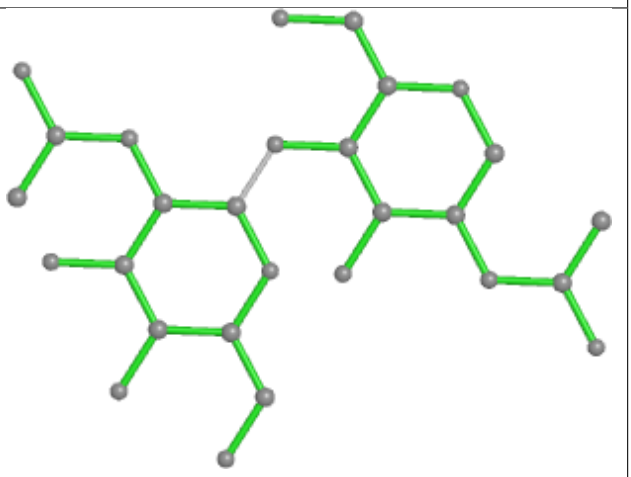


Rings

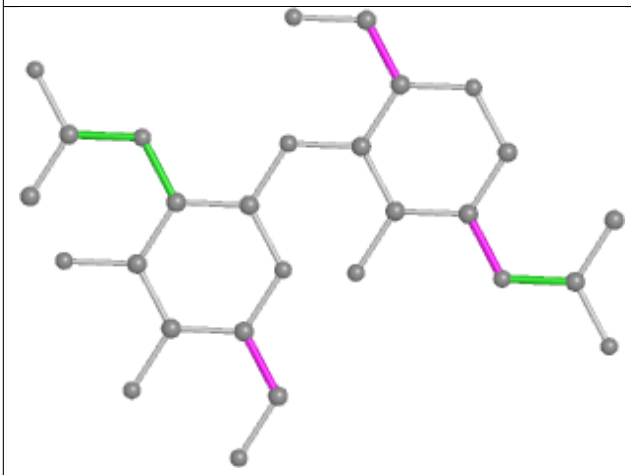
Oligosaccharide Chain K



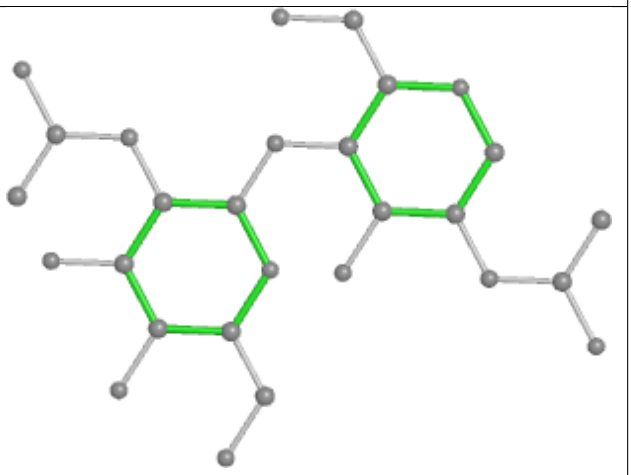
Bond lengths



Bond angles

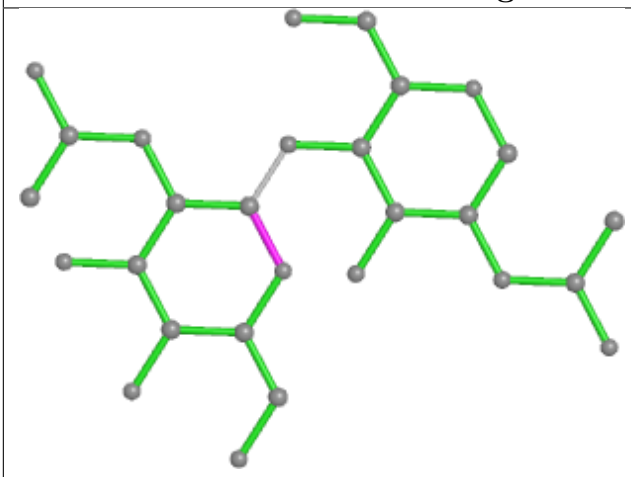


Torsions

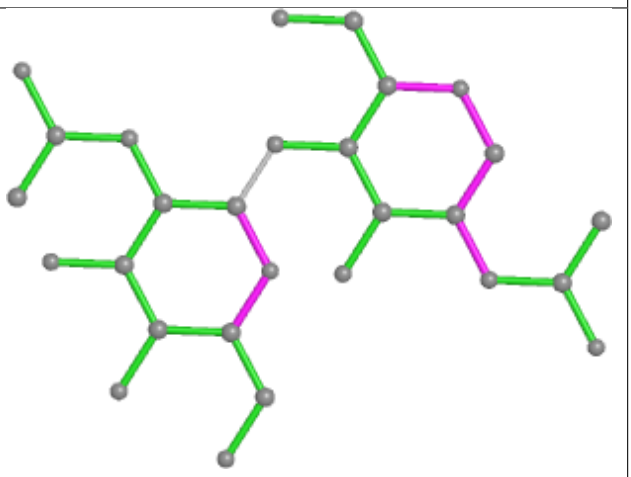


Rings

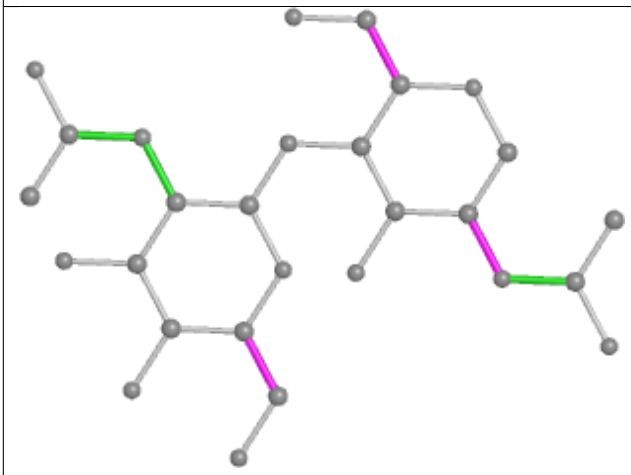
Oligosaccharide Chain L



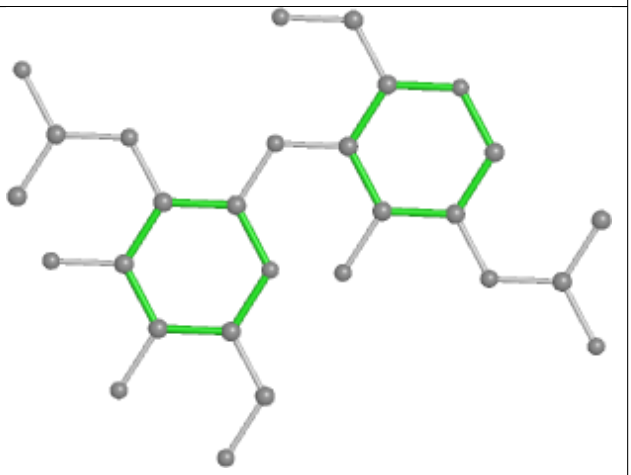
Bond lengths



Bond angles

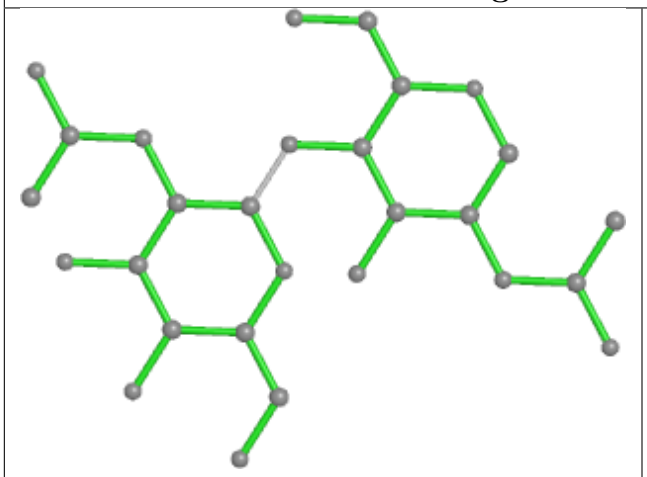


Torsions

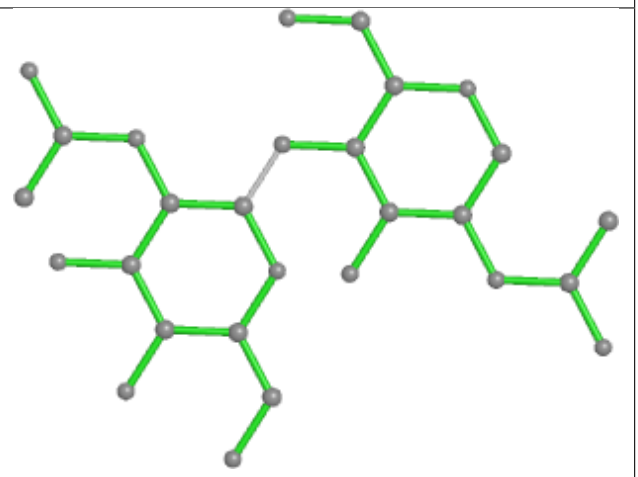


Rings

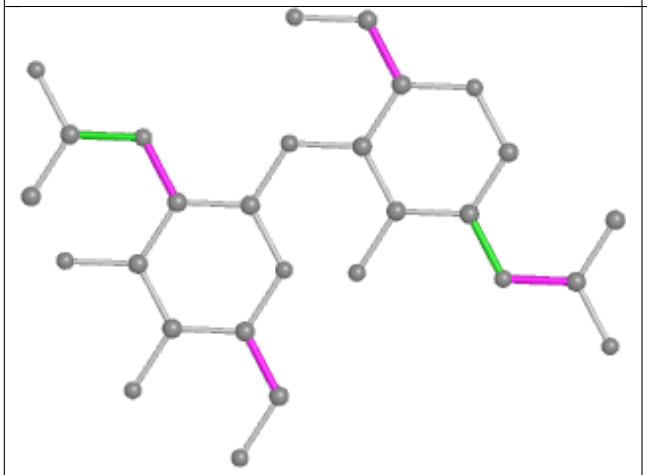
Oligosaccharide Chain M



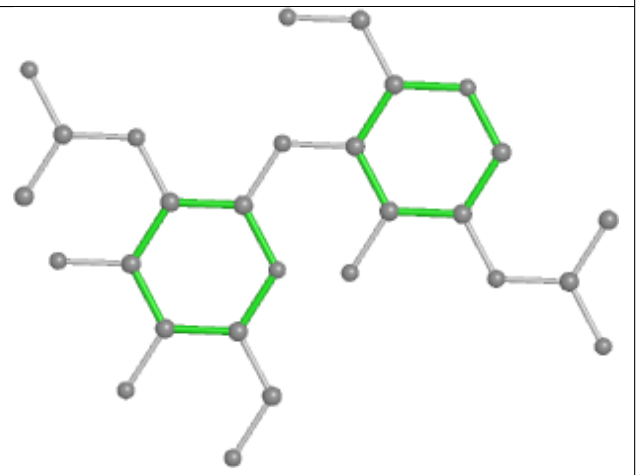
Bond lengths



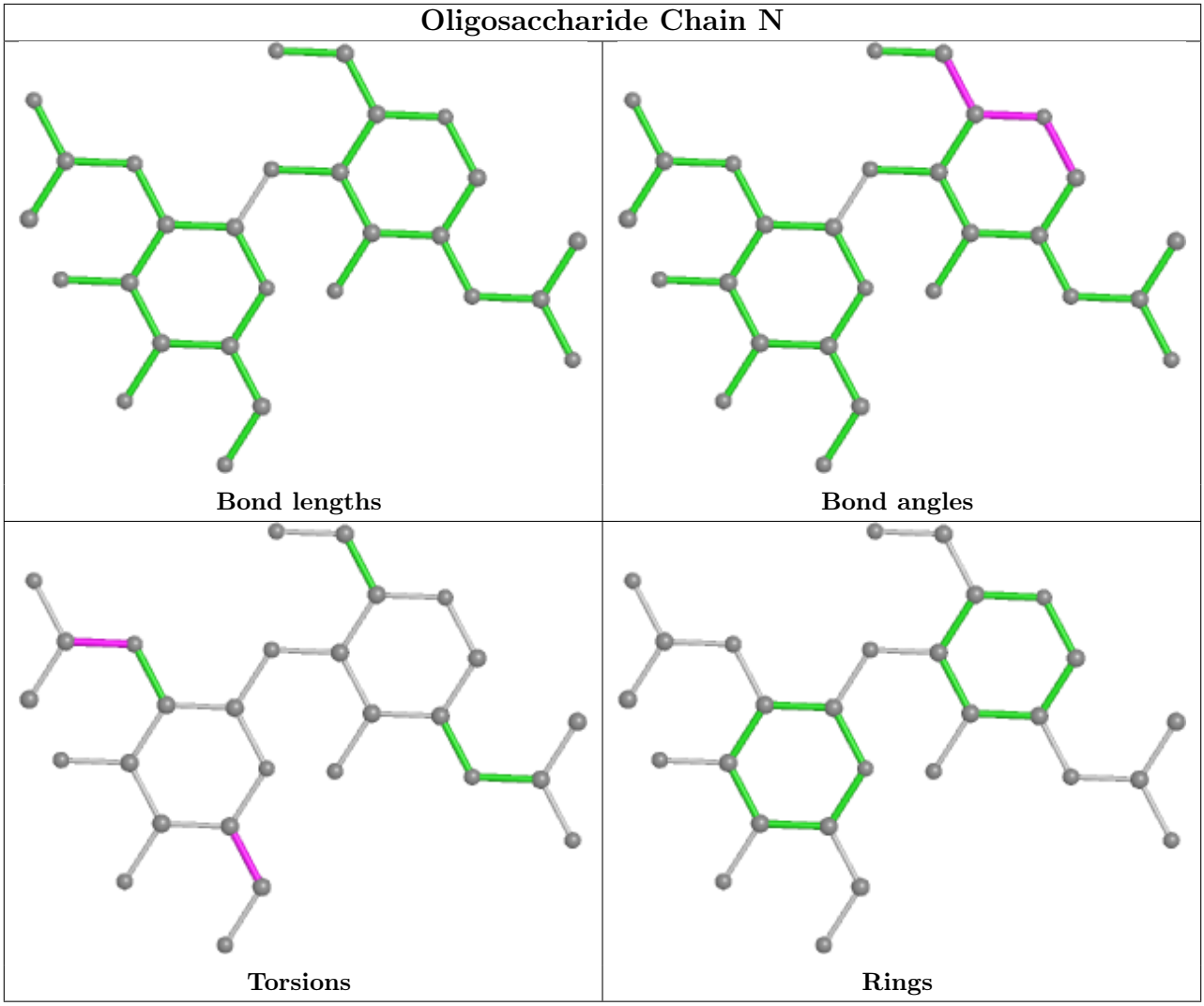
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

There are no ligands in this entry.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	282/282 (100%)	-0.36	3 (1%)	80	56	37, 49, 68, 87	0
1	B	282/282 (100%)	-0.38	3 (1%)	80	56	32, 47, 71, 82	0
1	C	277/282 (98%)	-0.29	3 (1%)	80	56	38, 49, 64, 98	0
2	E	226/238 (94%)	-0.35	1 (0%)	92	79	35, 50, 70, 88	0
2	G	222/238 (93%)	-0.15	5 (2%)	60	31	41, 57, 93, 114	0
2	H	225/238 (94%)	-0.38	2 (0%)	84	63	35, 44, 70, 97	0
3	D	211/217 (97%)	-0.23	3 (1%)	75	49	43, 59, 85, 104	0
3	F	197/217 (90%)	0.28	15 (7%)	13	4	42, 64, 118, 129	0
3	I	211/217 (97%)	-0.28	4 (1%)	66	37	37, 53, 77, 101	0
All	All	2133/2211 (96%)	-0.25	39 (1%)	68	40	32, 51, 89, 129	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	150	ALA	5.4
3	F	118	VAL	5.1
1	C	313	THR	4.3
3	F	199	THR	4.1
2	G	122	ALA	3.9

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

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

6.3 Carbohydrates (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

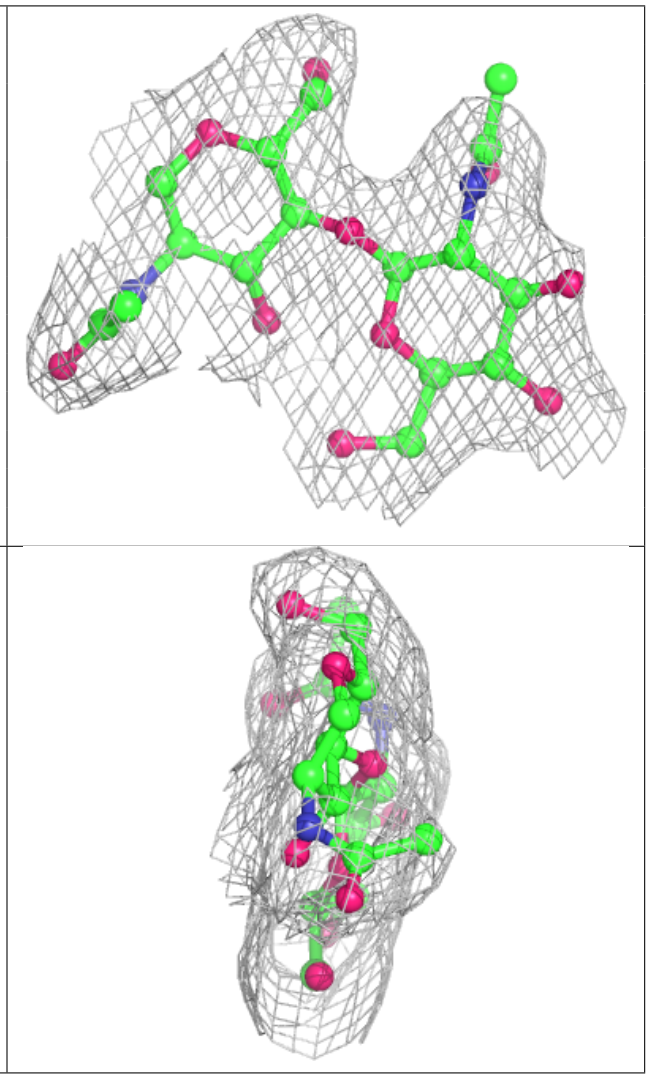
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	M	2	14/15	0.73	0.40	81,86,89,89	0
4	NAG	L	1	14/15	0.82	0.18	65,68,74,79	0
4	NAG	J	2	14/15	0.84	0.19	55,57,59,60	0
4	NAG	M	1	14/15	0.85	0.24	63,72,81,83	0
4	NAG	K	2	14/15	0.85	0.16	62,66,69,80	0
4	NAG	L	2	14/15	0.87	0.22	72,74,77,78	0
4	NAG	K	1	14/15	0.89	0.16	63,65,70,70	0
4	NAG	J	1	14/15	0.92	0.11	52,53,55,55	0
4	NAG	N	1	14/15	0.92	0.13	48,52,57,58	0
4	NAG	N	2	14/15	0.93	0.12	50,52,54,55	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.

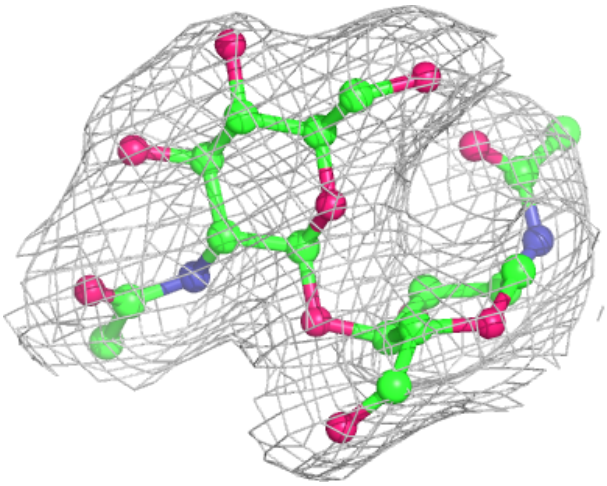
Electron density around Chain J:

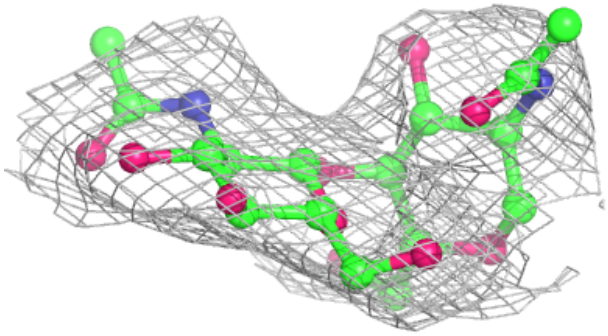
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

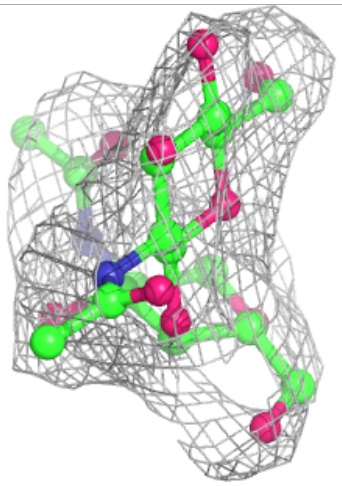


Electron density around Chain K:

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

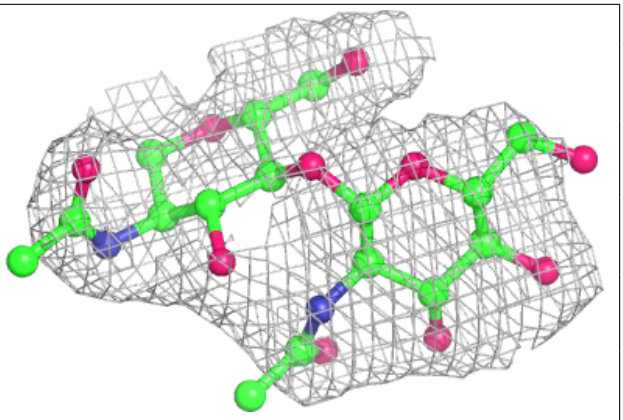


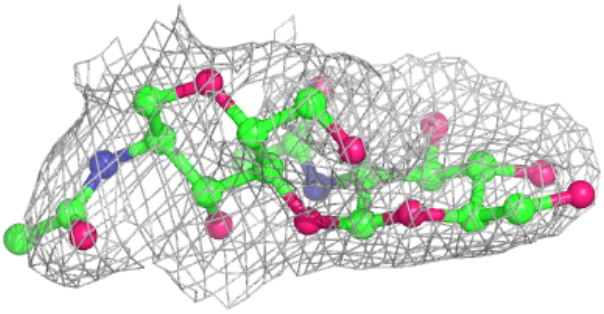


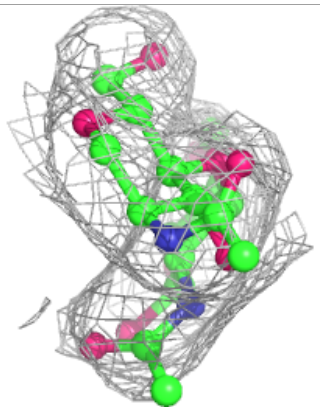


Electron density around Chain L:

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

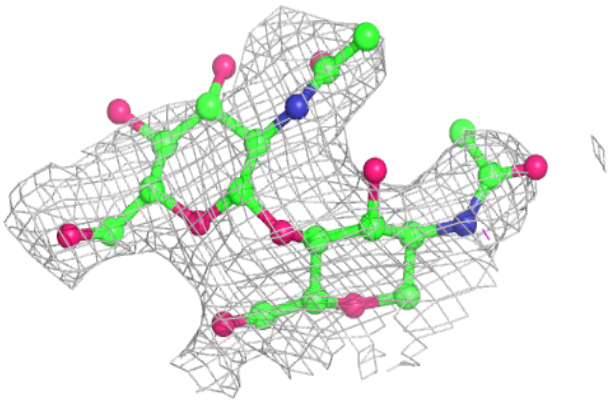


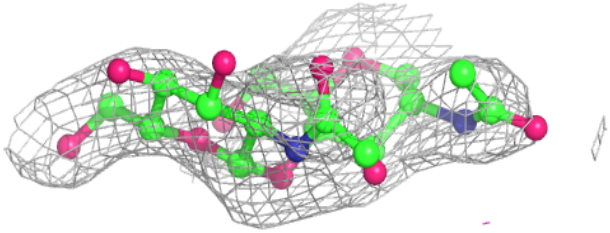


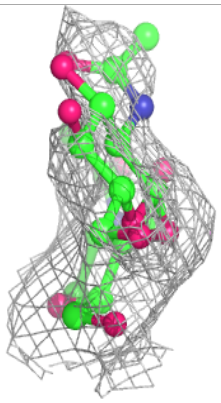


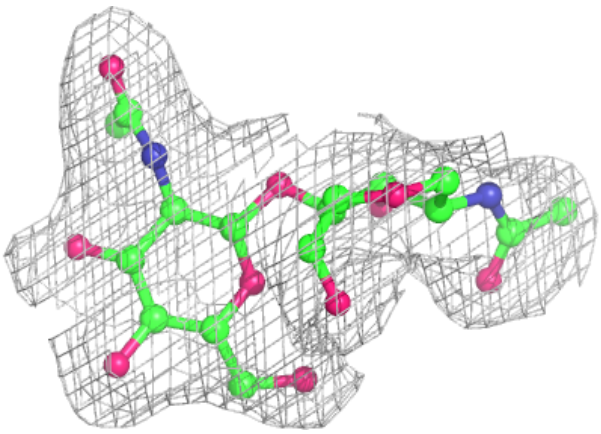
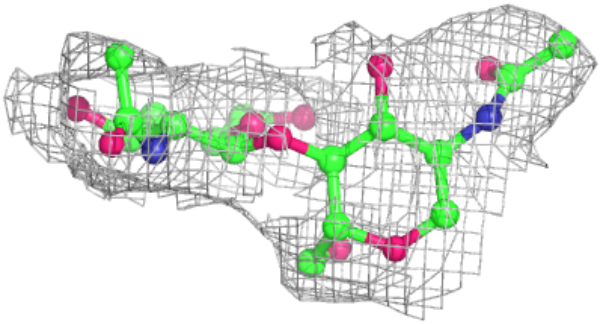
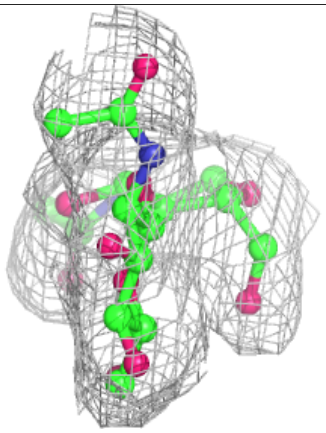
Electron density around Chain M:

$2mF_o$-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 N: $2mF_o$-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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.