



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 14, 2025 – 12:16 PM EDT

PDB ID : 9MQV / pdb_00009mqv
Title : Crystal structure of human 1122A11 Fab in complex with influenza virus neuraminidase from A/Singapore/INFIMH-16-0019/2016 (H3N2)
Authors : Zhu, X.; Wilson, I.A.
Deposited on : 2025-01-06
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

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>.

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

MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

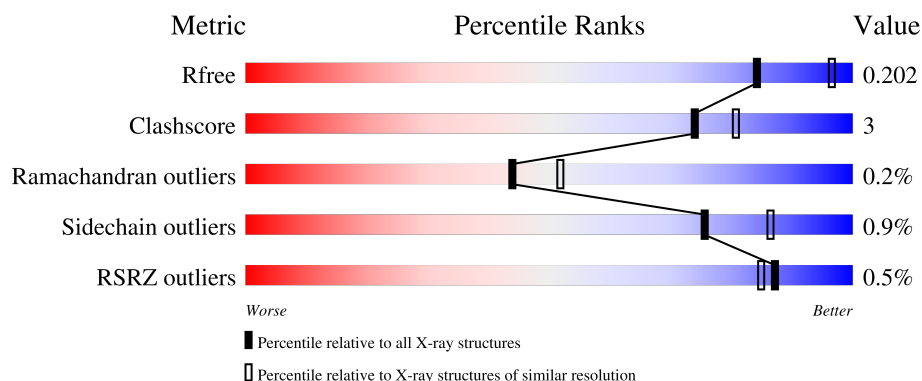
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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.




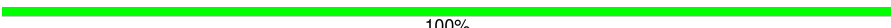
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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 $\leq 5\%$. 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	395	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 91% 6% . </div> </div>
2	H	238	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green, yellow, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 82% 13% 5% </div> </div>
3	L	212	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 92% 7% . </div> </div>
4	B	3	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green, yellow, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 100% </div> </div>
4	D	3	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green, yellow, grey);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 100% </div> </div>

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Mol	Chain	Length	Quality of chain
5	C	8	 38% 62%
6	E	2	 100%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6820 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 Neuraminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	0	0	0
			2966	1838	528	578	22			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	GLY	-	expression tag	UNP A0A5B8WQ58
A	76	SER	-	expression tag	UNP A0A5B8WQ58
A	77	PRO	-	expression tag	UNP A0A5B8WQ58
A	78	SER	-	expression tag	UNP A0A5B8WQ58
A	79	ARG	-	expression tag	UNP A0A5B8WQ58
A	80	SER	-	expression tag	UNP A0A5B8WQ58
A	81	GLY	-	expression tag	UNP A0A5B8WQ58
A	212	ILE	VAL	conflict	UNP A0A5B8WQ58
A	329	ASN	SER	conflict	UNP A0A5B8WQ58

- Molecule 2 is a protein called 1122A11 FAB IGG1 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	227	Total	C	N	O	S	0	0	0
			1708	1071	291	337	9			

- Molecule 3 is a protein called 1122A11 FAB LAMBDA LIGHT CHAIN.

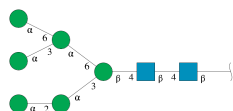
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	209	Total	C	N	O	S	0	0	0
			1566	982	259	319	6			

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



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

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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
5	C	8	Total	C	N	O	0	0	0
			94	52	2	40			

- 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
6	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	236	Total	O	0	0
			236	236		
9	H	76	Total	O	0	0
			76	76		
9	L	53	Total	O	0	0
			53	53		

MAG1
MAG2
BMA3

- Molecule 5: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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 C:



MAG1
MAG2
BMA3
MAM4
MAM5
MAM6
MAM7
MAM8

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

Chain E:



MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	115.90Å 115.90Å 76.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.63 – 2.20 38.63 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (38.63-2.20) 99.5 (38.63-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.169 , 0.204 0.168 , 0.202	Depositor DCC
R_{free} test set	2652 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.038 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6820	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NAG, BMA, CA, 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	0.11	0/3032	0.34	0/4110
2	H	0.15	0/1749	0.36	0/2382
3	L	0.10	0/1605	0.31	0/2192
All	All	0.12	0/6386	0.34	0/8684

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	2966	0	2816	13	0
2	H	1708	0	1659	21	0
3	L	1566	0	1524	8	0
4	B	39	0	34	0	0
4	D	39	0	34	0	0
5	C	94	0	79	0	0
6	E	28	0	25	0	0
7	A	1	0	0	0	0
8	A	14	0	13	0	0
9	A	236	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	H	76	0	0	1	0
9	L	53	0	0	1	0
All	All	6820	0	6184	38	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 3.

All (38) 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:L:61:ARG:HG3	9:L:347:HOH:O	1.81	0.80
2:H:6:GLN:H	2:H:105:GLN:HE22	1.28	0.79
2:H:119:PRO:HB3	2:H:147:TYR:HB3	1.72	0.72
1:A:221:ASP:HB3	1:A:244:GLY:HA2	1.81	0.63
2:H:166:LEU:HD21	2:H:191:VAL:HG21	1.80	0.62
1:A:245:ASN:ND2	9:A:603:HOH:O	2.36	0.58
2:H:152:VAL:HG23	2:H:187:LEU:HD21	1.86	0.57
2:H:171:VAL:HG22	2:H:191:VAL:HB	1.86	0.57
3:L:110:LYS:HG2	3:L:141:PRO:HD3	1.87	0.57
1:A:279:SER:HB3	1:A:409:ILE:HG22	1.86	0.56
1:A:251:ASP:N	9:A:606:HOH:O	2.41	0.53
2:H:177:VAL:HG21	3:L:160:GLU:HB3	1.92	0.51
1:A:225:THR:OG1	1:A:226:GLN:N	2.46	0.49
2:H:146:ASP:HB3	2:H:184:LEU:HD13	1.93	0.49
2:H:36:TRP:CE2	2:H:80:MET:HB2	2.48	0.48
1:A:177:ALA:HB2	1:A:193:CYS:HB3	1.95	0.48
2:H:47:TRP:CG	3:L:96:VAL:HB	2.49	0.47
1:A:318:CYS:O	1:A:386:PRO:HA	2.14	0.47
2:H:126:PRO:HD2	2:H:227:PRO:HA	1.95	0.46
2:H:154:VAL:HG22	2:H:210:VAL:HG23	1.97	0.46
1:A:347:HIS:CG	1:A:348:GLY:H	2.35	0.45
2:H:47:TRP:CD2	3:L:96:VAL:HB	2.52	0.45
2:H:13:LYS:HD2	2:H:113:SER:HA	1.97	0.45
2:H:145:LYS:HE2	2:H:146:ASP:OD2	2.17	0.45
1:A:121:TYR:CG	1:A:228:SER:HA	2.53	0.44
3:L:61:ARG:NH1	3:L:82:ASP:OD2	2.42	0.43
1:A:284:TYR:CG	1:A:285:PRO:HA	2.54	0.43
2:H:136:GLY:N	9:H:304:HOH:O	2.51	0.42
2:H:149:PRO:O	2:H:212:HIS:HE1	2.02	0.42
1:A:296:LYS:HB3	1:A:296:LYS:HE2	1.73	0.42
2:H:150:GLU:CD	2:H:151:PRO:HA	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:54:ARG:HD3	3:L:62:PHE:O	2.21	0.41
1:A:151:ASP:OD2	1:A:152:ARG:HG3	2.20	0.41
3:L:136:ILE:HG12	3:L:196:VAL:HG21	2.03	0.41
2:H:222:ARG:NH1	2:H:226:GLU:OE2	2.54	0.41
1:A:431:LYS:HE2	2:H:100(A):GLU:O	2.21	0.40
2:H:83:ARG:HG3	2:H:85:GLU:HG2	2.03	0.40
2:H:222:ARG:HG2	2:H:226:GLU:OE1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	378/395 (96%)	367 (97%)	10 (3%)	1 (0%)	37	42
2	H	223/238 (94%)	217 (97%)	6 (3%)	0	100	100
3	L	207/212 (98%)	203 (98%)	3 (1%)	1 (0%)	25	28
All	All	808/845 (96%)	787 (97%)	19 (2%)	2 (0%)	44	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	151	ASP
1	A	222	ILE

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	334/342 (98%)	333 (100%)	1 (0%)	91	96
2	H	193/203 (95%)	192 (100%)	1 (0%)	86	93
3	L	177/180 (98%)	173 (98%)	4 (2%)	45	59
All	All	704/725 (97%)	698 (99%)	6 (1%)	75	86

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	296	LYS
2	H	191	VAL
3	L	9	SER
3	L	20	SER
3	L	42	GLN
3	L	152	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	173	GLN
1	A	274	HIS
2	H	179	GLN
2	H	203	GLN
2	H	212	HIS
3	L	37	GLN
3	L	42	GLN
3	L	69	ASN
3	L	195	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 ⓘ

16 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	B	1	1,4	14,14,15	0.29	0	17,19,21	0.56	0
4	NAG	B	2	4	14,14,15	0.56	0	17,19,21	0.60	0
4	BMA	B	3	4	11,11,12	0.75	0	15,15,17	0.73	0
5	NAG	C	1	1,5	14,14,15	0.26	0	17,19,21	0.55	0
5	NAG	C	2	5	14,14,15	0.39	0	17,19,21	0.50	0
5	BMA	C	3	5	11,11,12	0.53	0	15,15,17	0.58	0
5	MAN	C	4	5	11,11,12	0.70	0	15,15,17	1.08	1 (6%)
5	MAN	C	5	5	11,11,12	1.02	1 (9%)	15,15,17	0.78	1 (6%)
5	MAN	C	6	5	11,11,12	0.66	0	15,15,17	0.93	2 (13%)
5	MAN	C	7	5	11,11,12	0.88	0	15,15,17	1.19	2 (13%)
5	MAN	C	8	5	11,11,12	0.67	0	15,15,17	0.95	2 (13%)
4	NAG	D	1	1,4	14,14,15	0.36	0	17,19,21	0.49	0
4	NAG	D	2	4	14,14,15	0.20	0	17,19,21	0.52	0
4	BMA	D	3	4	11,11,12	0.59	0	15,15,17	0.71	0
6	NAG	E	1	1,6	14,14,15	0.33	0	17,19,21	0.58	0
6	NAG	E	2	6	14,14,15	0.27	0	17,19,21	0.44	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	B	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	0/6/23/26	0/1/1/1
4	BMA	B	3	4	-	1/2/19/22	0/1/1/1
5	NAG	C	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	C	2	5	-	0/6/23/26	0/1/1/1
5	BMA	C	3	5	-	0/2/19/22	0/1/1/1
5	MAN	C	4	5	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MAN	C	5	5	-	2/2/19/22	0/1/1/1
5	MAN	C	6	5	-	0/2/19/22	0/1/1/1
5	MAN	C	7	5	-	2/2/19/22	0/1/1/1
5	MAN	C	8	5	-	2/2/19/22	0/1/1/1
4	NAG	D	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
6	NAG	E	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	E	2	6	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	5	MAN	O5-C1	-2.58	1.39	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	4	MAN	C1-O5-C5	2.74	115.86	112.19
5	C	7	MAN	C1-O5-C5	2.45	115.48	112.19
5	C	8	MAN	C1-O5-C5	2.45	115.47	112.19
5	C	6	MAN	C1-O5-C5	2.32	115.30	112.19
5	C	5	MAN	O2-C2-C3	-2.21	105.57	110.15
5	C	8	MAN	O2-C2-C3	-2.05	105.90	110.15
5	C	7	MAN	C3-C4-C5	2.03	113.92	110.23
5	C	6	MAN	O2-C2-C3	-2.02	105.97	110.15

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	5	MAN	O5-C5-C6-O6
6	E	2	NAG	O5-C5-C6-O6
6	E	2	NAG	C4-C5-C6-O6
5	C	8	MAN	O5-C5-C6-O6
5	C	5	MAN	C4-C5-C6-O6
5	C	7	MAN	C4-C5-C6-O6
5	C	7	MAN	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
5	C	8	MAN	C4-C5-C6-O6

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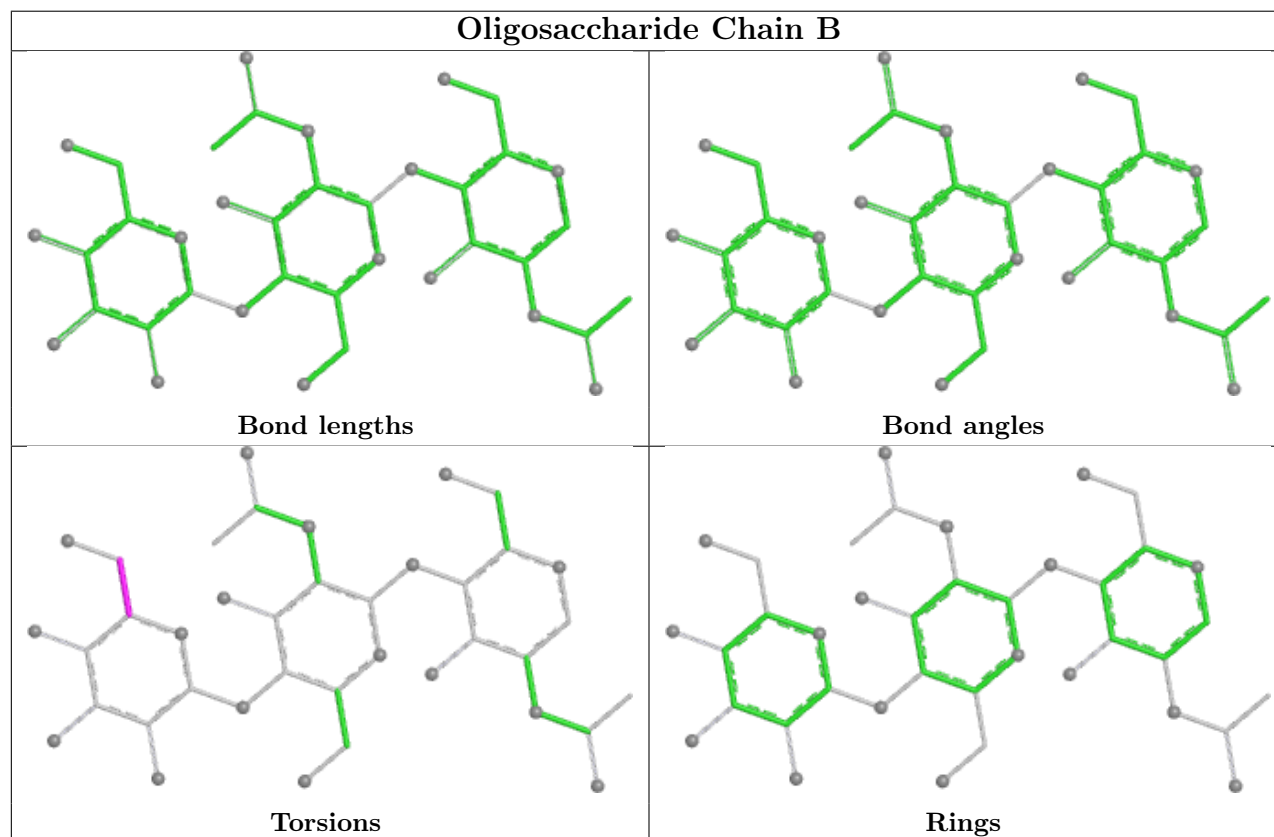
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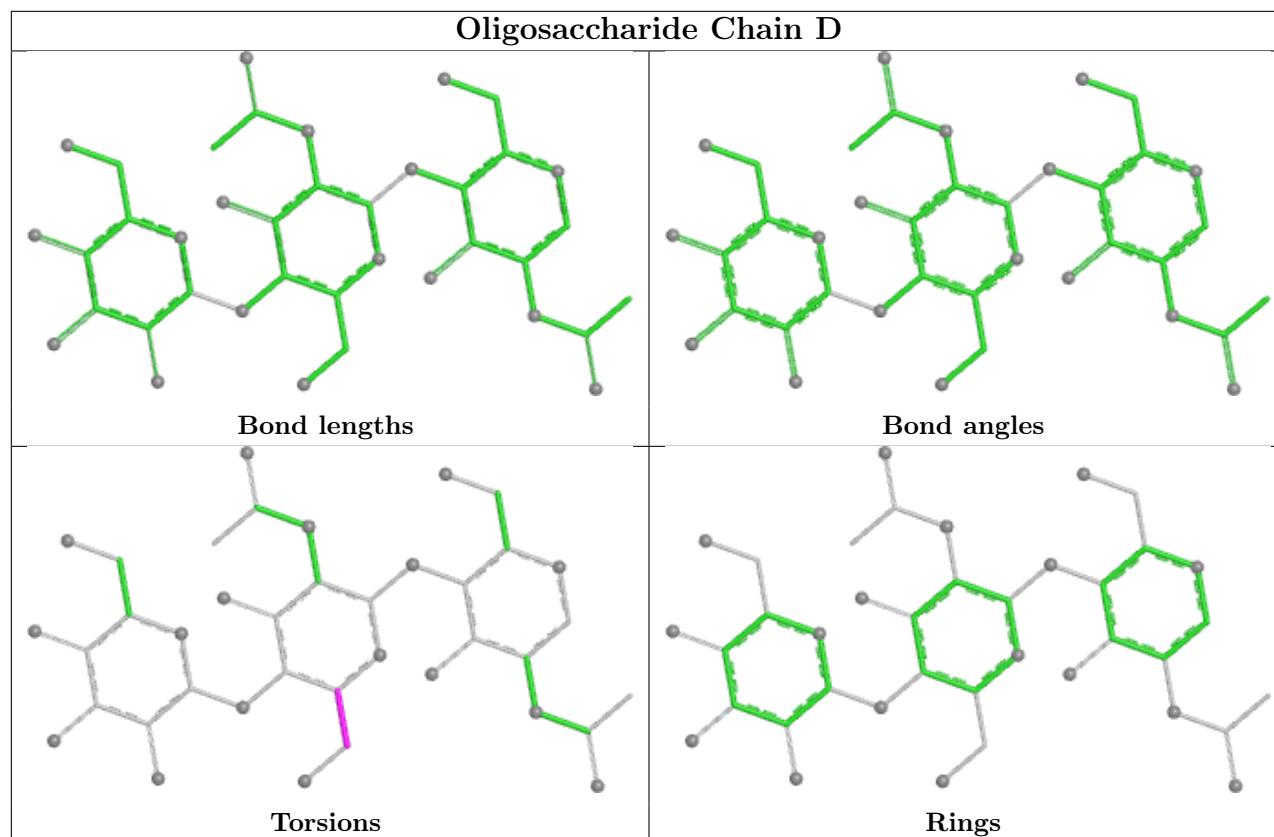
Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O5-C5-C6-O6
4	B	3	BMA	O5-C5-C6-O6
5	C	1	NAG	C1-C2-N2-C7

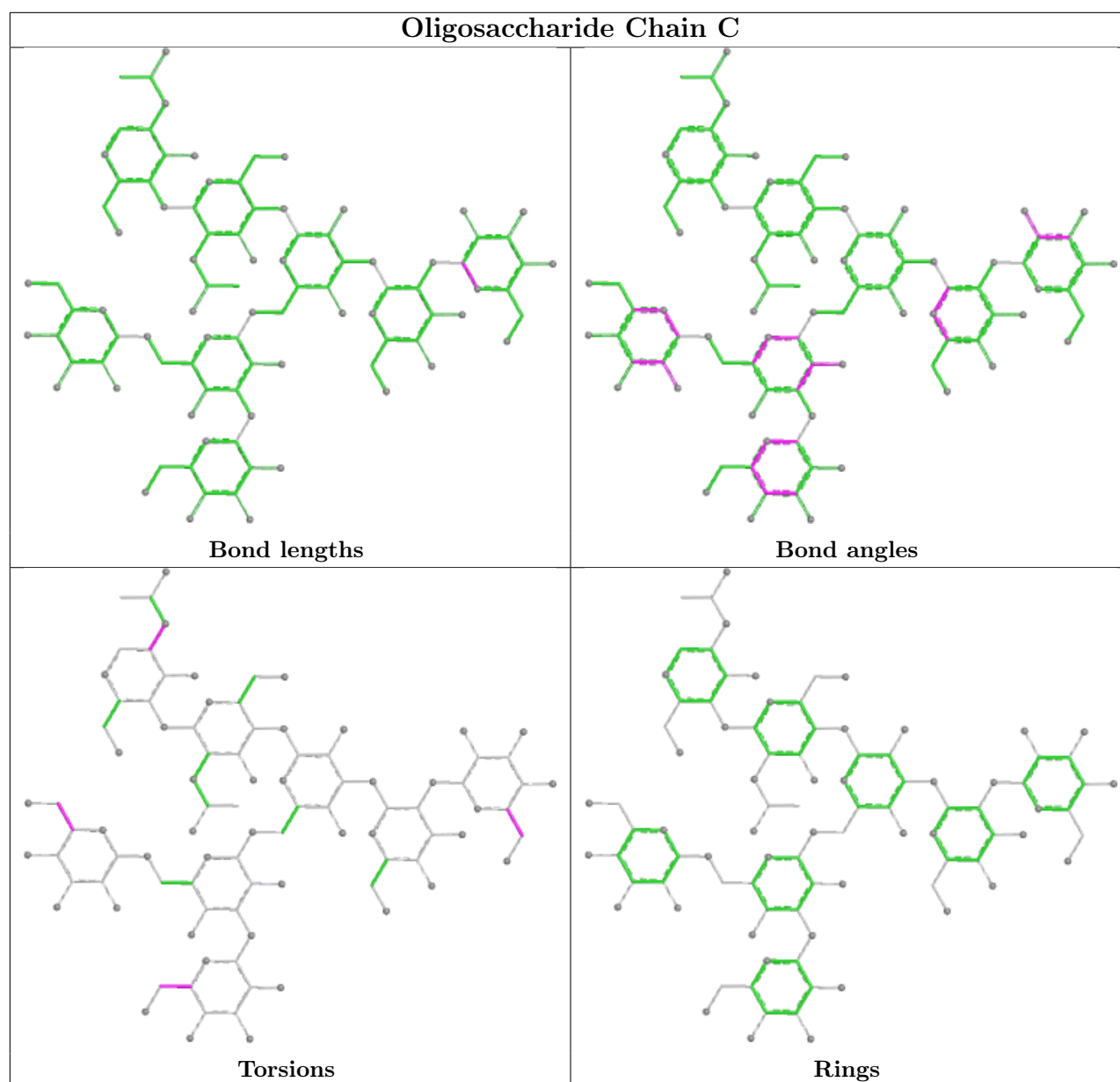
There are no ring outliers.

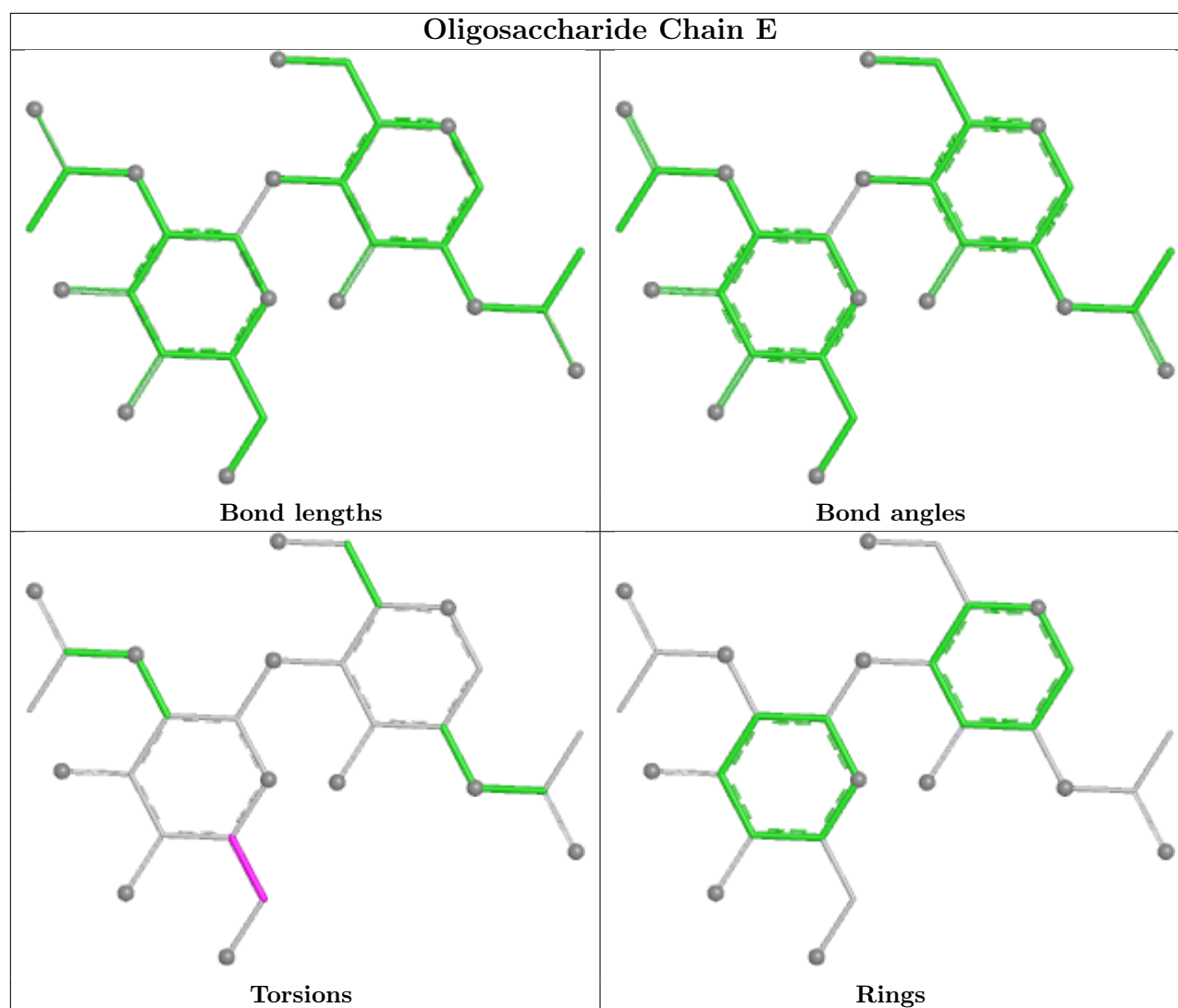
No monomer is involved in short contacts.

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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
8	NAG	A	502	1	14,14,15	0.31	0	17,19,21	0.46	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	A	502	1	-	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.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	502	NAG	O5-C5-C6-O6
8	A	502	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [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	382/395 (96%)	-0.53	2 (0%) 87 85	25, 35, 53, 102	0
2	H	227/238 (95%)	0.03	0 100 100	29, 55, 89, 126	0
3	L	209/212 (98%)	0.12	2 (0%) 79 76	32, 59, 103, 137	0
All	All	818/845 (96%)	-0.21	4 (0%) 87 85	25, 44, 89, 137	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	212	THR	3.8
1	A	468	HIS	3.5
1	A	245	ASN	2.4
3	L	190	ARG	2.3

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.

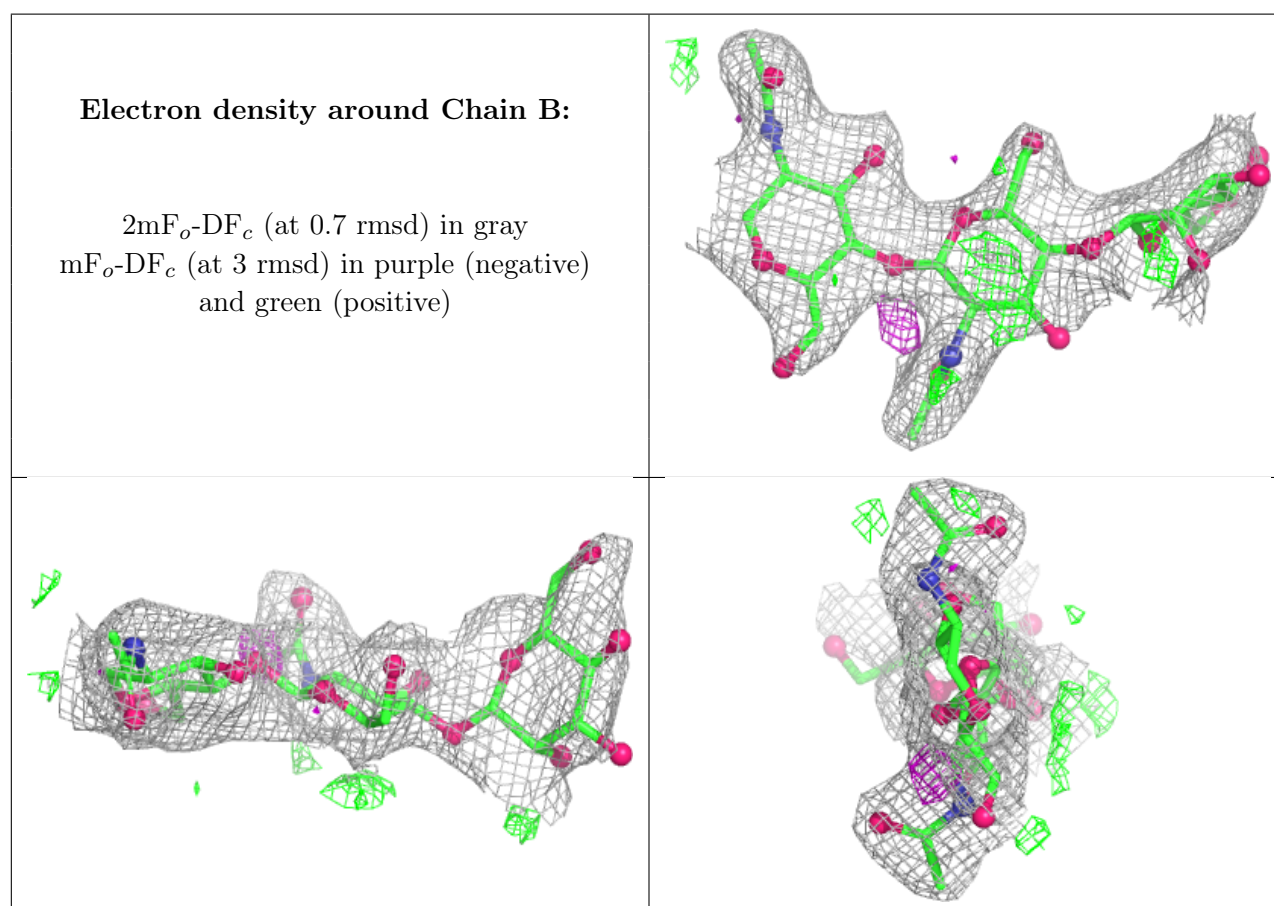
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	B	1	14/15	-	-	45,59,64,70	0
4	NAG	B	2	14/15	-	-	60,81,102,109	0
4	BMA	B	3	11/12	-	-	100,108,117,118	0
4	BMA	D	3	11/12	0.48	0.13	74,93,104,105	0

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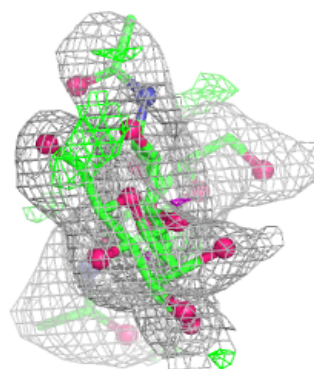
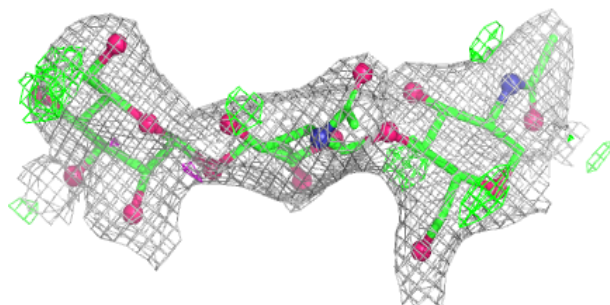
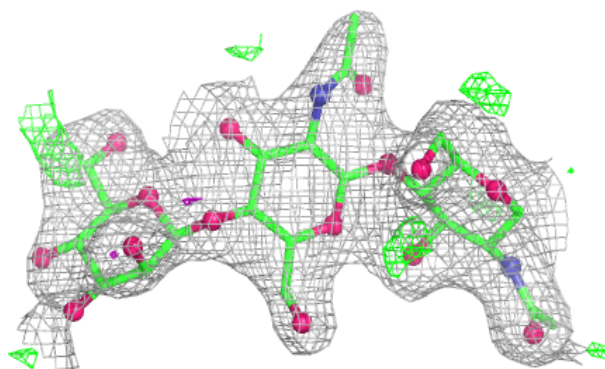
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	D	2	14/15	0.74	0.13	70,83,90,95	0
4	NAG	D	1	14/15	0.88	0.10	43,59,68,83	0
5	NAG	C	1	14/15	-	-	31,39,48,52	0
5	NAG	C	2	14/15	-	-	33,37,45,50	0
5	BMA	C	3	11/12	-	-	36,42,48,54	0
5	MAN	C	4	11/12	-	-	38,48,53,54	0
5	MAN	C	5	11/12	-	-	65,75,86,96	0
5	MAN	C	6	11/12	-	-	54,59,76,87	0
5	MAN	C	7	11/12	-	-	69,77,88,89	0
5	MAN	C	8	11/12	-	-	84,88,92,92	0
6	NAG	E	1	14/15	0.96	0.07	64,87,98,103	0
6	NAG	E	2	14/15	0.97	0.06	92,107,110,110	0

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



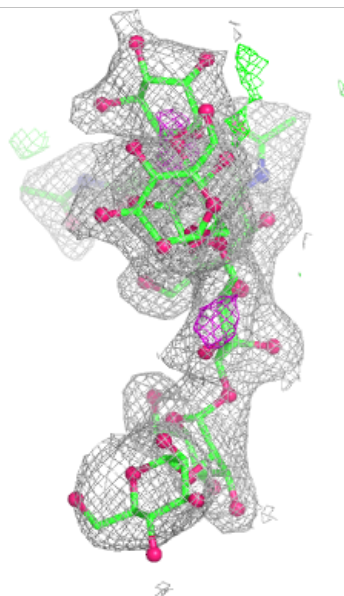
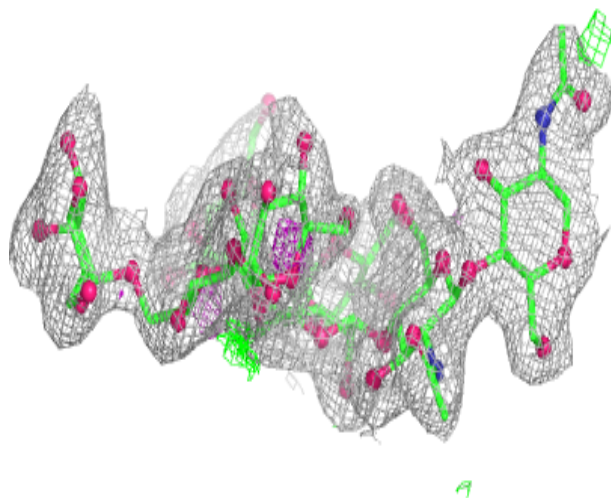
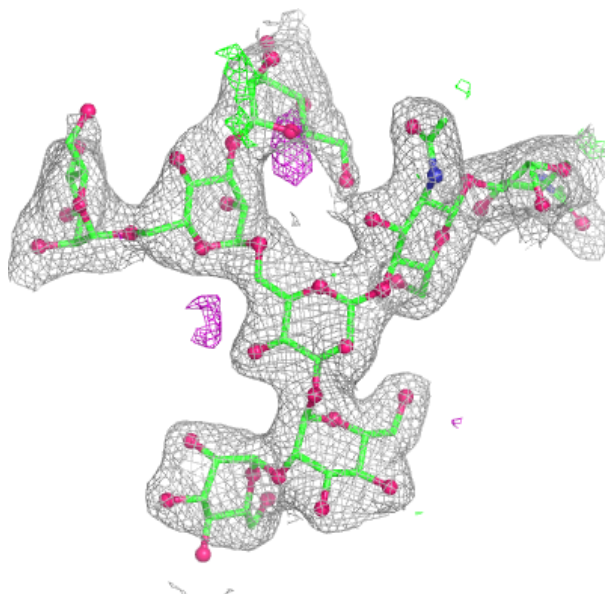
Electron density around Chain D:

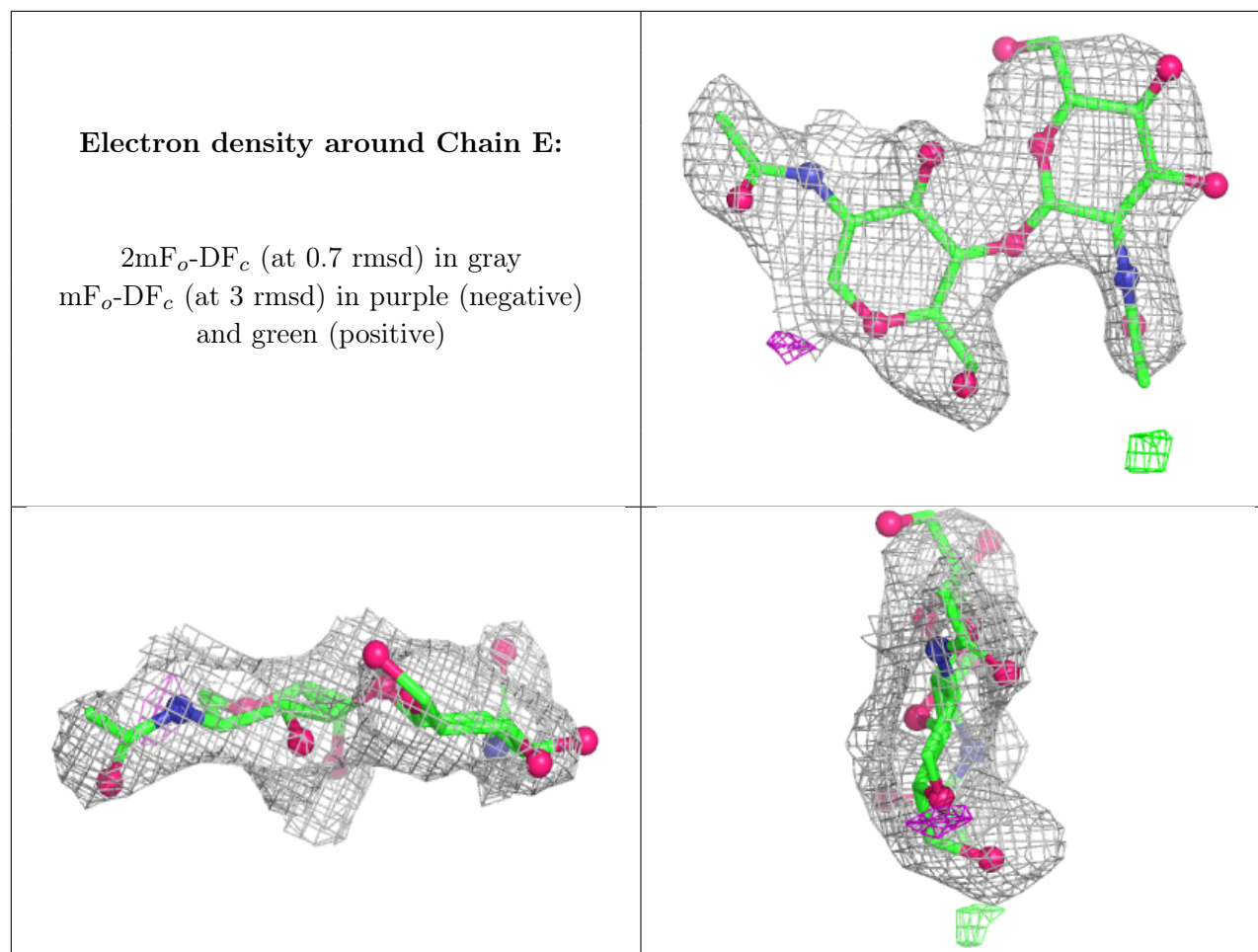
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain C:

$2mF_o-DF_c$ (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, 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(\AA^2)	Q<0.9
8	NAG	A	502	14/15	0.78	0.13	63,76,83,93	0
7	CA	A	501	1/1	0.99	0.10	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.