



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:07 PM UTC

PDB ID : 6V44 / pdb_00006v44
Title : The crystal structure of hemagglutinin from swine influenza virus A/swine/Missouri/A01727926/2015
Authors : Yang, H.; Stevens, J.
Deposited on : 2019-11-27
Resolution : 2.20 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 ⓘ 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 Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

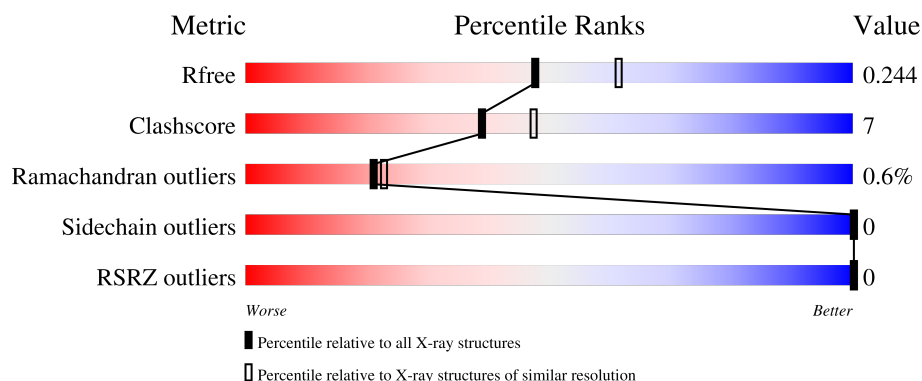
1 Overall quality at a glance ⓘ

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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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	332	
1	C	332	
1	E	332	
2	B	186	
2	D	186	

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Mol	Chain	Length	Quality of chain
2	F	186	84% 8% • 7%
3	G	6	17% 83%
3	H	6	17% 83%
3	I	6	83% 17%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12422 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 HA1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	0	0
			2487	1562	440	474	11			
1	C	320	Total	C	N	O	S	0	0	0
			2487	1562	440	474	11			
1	E	320	Total	C	N	O	S	0	0	0
			2487	1562	440	474	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	ALA	-	expression tag	UNP A0A140D8S6
A	-3	ASP	-	expression tag	UNP A0A140D8S6
A	-2	LEU	-	expression tag	UNP A0A140D8S6
A	-1	GLY	-	expression tag	UNP A0A140D8S6
C	-4	ALA	-	expression tag	UNP A0A140D8S6
C	-3	ASP	-	expression tag	UNP A0A140D8S6
C	-2	LEU	-	expression tag	UNP A0A140D8S6
C	-1	GLY	-	expression tag	UNP A0A140D8S6
E	-4	ALA	-	expression tag	UNP A0A140D8S6
E	-3	ASP	-	expression tag	UNP A0A140D8S6
E	-2	LEU	-	expression tag	UNP A0A140D8S6
E	-1	GLY	-	expression tag	UNP A0A140D8S6

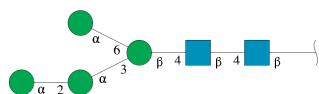
- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1415	878	251	282	4			
2	D	173	Total	C	N	O	S	0	0	0
			1415	878	251	282	4			
2	F	173	Total	C	N	O	S	0	0	0
			1415	878	251	282	4			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	175	SER	-	expression tag	UNP A0A140D8S6
B	176	GLY	-	expression tag	UNP A0A140D8S6
B	177	ARG	-	expression tag	UNP A0A140D8S6
B	178	SER	-	expression tag	UNP A0A140D8S6
B	179	GLY	-	expression tag	UNP A0A140D8S6
B	180	ARG	-	expression tag	UNP A0A140D8S6
B	181	LEU	-	expression tag	UNP A0A140D8S6
B	182	VAL	-	expression tag	UNP A0A140D8S6
B	183	PRO	-	expression tag	UNP A0A140D8S6
B	184	ARG	-	expression tag	UNP A0A140D8S6
B	185	GLY	-	expression tag	UNP A0A140D8S6
B	186	SER	-	expression tag	UNP A0A140D8S6
D	175	SER	-	expression tag	UNP A0A140D8S6
D	176	GLY	-	expression tag	UNP A0A140D8S6
D	177	ARG	-	expression tag	UNP A0A140D8S6
D	178	SER	-	expression tag	UNP A0A140D8S6
D	179	GLY	-	expression tag	UNP A0A140D8S6
D	180	ARG	-	expression tag	UNP A0A140D8S6
D	181	LEU	-	expression tag	UNP A0A140D8S6
D	182	VAL	-	expression tag	UNP A0A140D8S6
D	183	PRO	-	expression tag	UNP A0A140D8S6
D	184	ARG	-	expression tag	UNP A0A140D8S6
D	185	GLY	-	expression tag	UNP A0A140D8S6
D	186	SER	-	expression tag	UNP A0A140D8S6
F	175	SER	-	expression tag	UNP A0A140D8S6
F	176	GLY	-	expression tag	UNP A0A140D8S6
F	177	ARG	-	expression tag	UNP A0A140D8S6
F	178	SER	-	expression tag	UNP A0A140D8S6
F	179	GLY	-	expression tag	UNP A0A140D8S6
F	180	ARG	-	expression tag	UNP A0A140D8S6
F	181	LEU	-	expression tag	UNP A0A140D8S6
F	182	VAL	-	expression tag	UNP A0A140D8S6
F	183	PRO	-	expression tag	UNP A0A140D8S6
F	184	ARG	-	expression tag	UNP A0A140D8S6
F	185	GLY	-	expression tag	UNP A0A140D8S6
F	186	SER	-	expression tag	UNP A0A140D8S6

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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
3	G	6	Total	C	N	O	0	0	0
			72	40	2	30			
3	H	6	Total	C	N	O	0	0	0
			72	40	2	30			
3	I	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	83	Total	O	0	0
			83	83		

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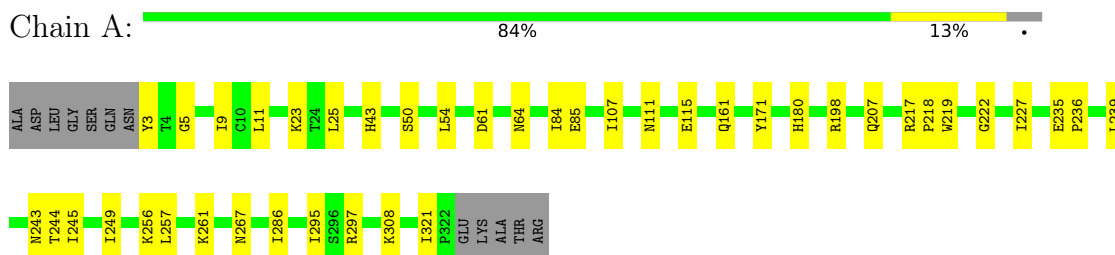
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	61	Total 61	O 61	0	0
5	C	99	Total 99	O 99	0	0
5	D	55	Total 55	O 55	0	0
5	E	94	Total 94	O 94	0	0
5	F	66	Total 66	O 66	0	0

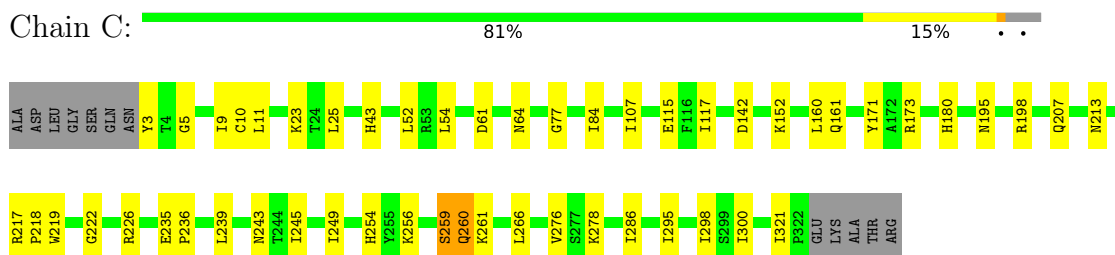
3 Residue-property plots

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.

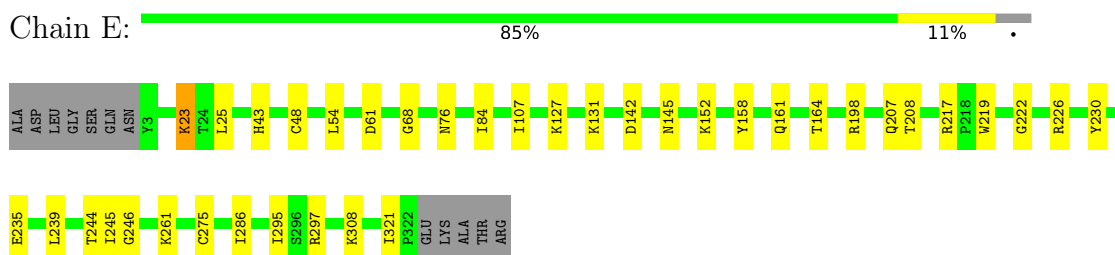
- Molecule 1: Hemagglutinin HA1 chain



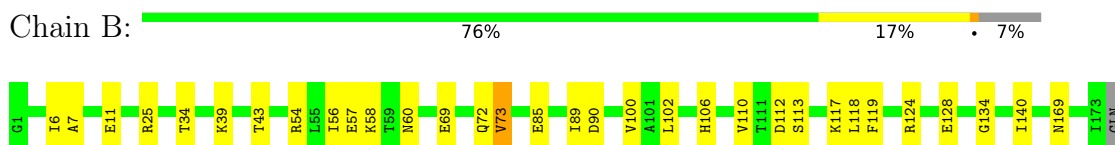
- Molecule 1: Hemagglutinin HA1 chain



- Molecule 1: Hemagglutinin HA1 chain



- Molecule 2: Hemagglutinin HA2 chain



SER
GLY
ARG
SER
GLY
ARG
LEU
VAL
PRO
ARG
GLY
SER

• Molecule 2: Hemagglutinin HA2 chain

Chain D:  81% 12% 7%

G1 A7 I18 D19 R25 H26 E30 T34 L52 I56 M60 E69 Q72 V73 L102 L118 F119 R124 R127 E128 N135 G136 C137 I140 R153 I173 GLN SER GLY ARG SER GLY ARG LEU VAL PRO ARG GLY SER

• Molecule 2: Hemagglutinin HA2 chain

Chain F:  84% 8% 7%

G1 A7 V14 R25 T34 K39 T43 R54 N60 E71 Q72 V73 I89 D90 L102 G134 M169 I173 GLN SER GLY ARG SER GLY ARG LEU VAL PRO ARG GLY SER

• Molecule 3: alpha-D-mannopyranose-(1-2)-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 G:  17% 83%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

• Molecule 3: alpha-D-mannopyranose-(1-2)-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 H:  17% 83%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

• Molecule 3: alpha-D-mannopyranose-(1-2)-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 I:  83% 17%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.97Å 240.00Å 68.95Å 90.00° 119.86° 90.00°	Depositor
Resolution (Å)	33.21 – 2.20 33.21 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (33.21-2.20) 96.4 (33.21-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.94 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.203 , 0.244 0.204 , 0.244	Depositor DCC
R_{free} test set	4806 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 25.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.357 for l,k,-h-l 0.357 for -h-l,k,h 0.028 for -h-l,-k,l 0.021 for h,-k,-h-l 0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12422	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 3.64% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.40	0/2546	0.68	1/3472 (0.0%)
1	C	0.42	0/2546	0.74	3/3472 (0.1%)
1	E	0.39	0/2546	0.67	1/3472 (0.0%)
2	B	0.45	0/1439	0.77	4/1938 (0.2%)
2	D	0.45	1/1439 (0.1%)	0.66	0/1938
2	F	0.41	0/1439	0.72	1/1938 (0.1%)
All	All	0.42	1/11955 (0.0%)	0.71	10/16230 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	30	GLU	CG-CD	5.43	1.65	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	260	GLN	CA-CB-CG	-11.07	91.96	114.10
2	F	71	GLU	CA-CB-CG	-7.13	99.83	114.10
2	B	57	GLU	CA-C-N	-6.77	113.77	122.77
2	B	57	GLU	C-N-CA	-6.77	113.77	122.77
2	B	58	LYS	CA-CB-CG	-5.93	102.23	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2487	0	2433	36	0
1	C	2487	0	2433	55	0
1	E	2487	0	2433	39	0
2	B	1415	0	1333	35	0
2	D	1415	0	1333	30	0
2	F	1415	0	1333	13	0
3	G	72	0	61	1	0
3	H	72	0	61	1	0
3	I	72	0	61	3	0
4	A	14	0	13	0	0
4	C	14	0	13	0	0
4	E	14	0	13	0	0
5	A	83	0	0	2	0
5	B	61	0	0	6	0
5	C	99	0	0	10	0
5	D	55	0	0	4	0
5	E	94	0	0	9	0
5	F	66	0	0	1	0
All	All	12422	0	11520	159	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 7.

The worst 5 of 159 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:F:25:ARG:HG3	2:F:34:THR:HG22	1.46	0.95
1:C:152:LYS:NZ	5:C:503:HOH:O	2.00	0.94
2:B:128:GLU:OE1	5:B:202:HOH:O	1.95	0.85
2:B:11:GLU:OE1	5:B:201:HOH:O	1.93	0.84
2:D:153:ARG:NH1	5:D:201:HOH:O	2.11	0.82

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	318/332 (96%)	301 (95%)	16 (5%)	1 (0%)	36	42
1	C	318/332 (96%)	302 (95%)	15 (5%)	1 (0%)	36	42
1	E	318/332 (96%)	303 (95%)	14 (4%)	1 (0%)	36	42
2	B	171/186 (92%)	159 (93%)	10 (6%)	2 (1%)	10	8
2	D	171/186 (92%)	160 (94%)	9 (5%)	2 (1%)	10	8
2	F	171/186 (92%)	159 (93%)	10 (6%)	2 (1%)	10	8
All	All	1467/1554 (94%)	1384 (94%)	74 (5%)	9 (1%)	21	23

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	61	ASP
1	C	61	ASP
1	E	61	ASP
2	B	60	ASN
2	D	60	ASN

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	281/290 (97%)	281 (100%)	0	100	100
1	C	281/290 (97%)	281 (100%)	0	100	100
1	E	281/290 (97%)	281 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	149/159 (94%)	149 (100%)	0	100	100
2	D	149/159 (94%)	149 (100%)	0	100	100
2	F	149/159 (94%)	149 (100%)	0	100	100
All	All	1290/1347 (96%)	1290 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	159	HIS
2	F	15	GLN
2	D	15	GLN
1	C	42	GLN
2	D	53	ASN

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 ⓘ

18 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	G	1	1,3	14,14,15	0.36	0	17,19,21	0.48	0
3	NAG	G	2	3	14,14,15	0.62	0	17,19,21	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BMA	G	3	3	11,11,12	1.01	2 (18%)	15,15,17	1.02	1 (6%)
3	MAN	G	4	3	11,11,12	1.17	1 (9%)	15,15,17	1.60	3 (20%)
3	MAN	G	5	3	11,11,12	1.66	3 (27%)	15,15,17	2.50	6 (40%)
3	MAN	G	6	3	11,11,12	1.92	2 (18%)	15,15,17	1.78	2 (13%)
3	NAG	H	1	1,3	14,14,15	0.35	0	17,19,21	0.51	0
3	NAG	H	2	3	14,14,15	0.56	0	17,19,21	0.59	0
3	BMA	H	3	3	11,11,12	0.95	1 (9%)	15,15,17	1.04	1 (6%)
3	MAN	H	4	3	11,11,12	1.09	1 (9%)	15,15,17	1.50	4 (26%)
3	MAN	H	5	3	11,11,12	1.72	3 (27%)	15,15,17	2.43	5 (33%)
3	MAN	H	6	3	11,11,12	1.82	2 (18%)	15,15,17	1.81	2 (13%)
3	NAG	I	1	1,3	14,14,15	0.29	0	17,19,21	0.77	0
3	NAG	I	2	3	14,14,15	0.52	0	17,19,21	0.64	0
3	BMA	I	3	3	11,11,12	1.48	2 (18%)	15,15,17	0.94	2 (13%)
3	MAN	I	4	3	11,11,12	0.92	0	15,15,17	1.98	3 (20%)
3	MAN	I	5	3	11,11,12	1.64	3 (27%)	15,15,17	2.58	5 (33%)
3	MAN	I	6	3	11,11,12	2.08	3 (27%)	15,15,17	1.52	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
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	BMA	G	3	3	-	2/2/19/22	0/1/1/1
3	MAN	G	4	3	-	0/2/19/22	0/1/1/1
3	MAN	G	5	3	-	2/2/19/22	0/1/1/1
3	MAN	G	6	3	-	0/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	BMA	H	3	3	-	2/2/19/22	0/1/1/1
3	MAN	H	4	3	-	0/2/19/22	0/1/1/1
3	MAN	H	5	3	-	2/2/19/22	0/1/1/1
3	MAN	H	6	3	-	0/2/19/22	0/1/1/1
3	NAG	I	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	BMA	I	3	3	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	I	4	3	-	0/2/19/22	0/1/1/1
3	MAN	I	5	3	-	2/2/19/22	0/1/1/1
3	MAN	I	6	3	-	0/2/19/22	0/1/1/1

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	6	MAN	C1-C2	4.40	1.62	1.52
3	H	6	MAN	C2-C3	4.34	1.59	1.52
3	G	6	MAN	C2-C3	4.17	1.58	1.52
3	G	6	MAN	C1-C2	3.99	1.61	1.52
3	I	5	MAN	C2-C3	3.83	1.58	1.52

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	5	MAN	C1-O5-C5	6.65	121.10	112.19
3	I	4	MAN	O2-C2-C3	-6.23	97.24	110.15
3	H	5	MAN	C1-O5-C5	5.37	119.39	112.19
3	G	5	MAN	C1-O5-C5	5.23	119.19	112.19
3	G	5	MAN	C1-C2-C3	5.18	117.19	109.64

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

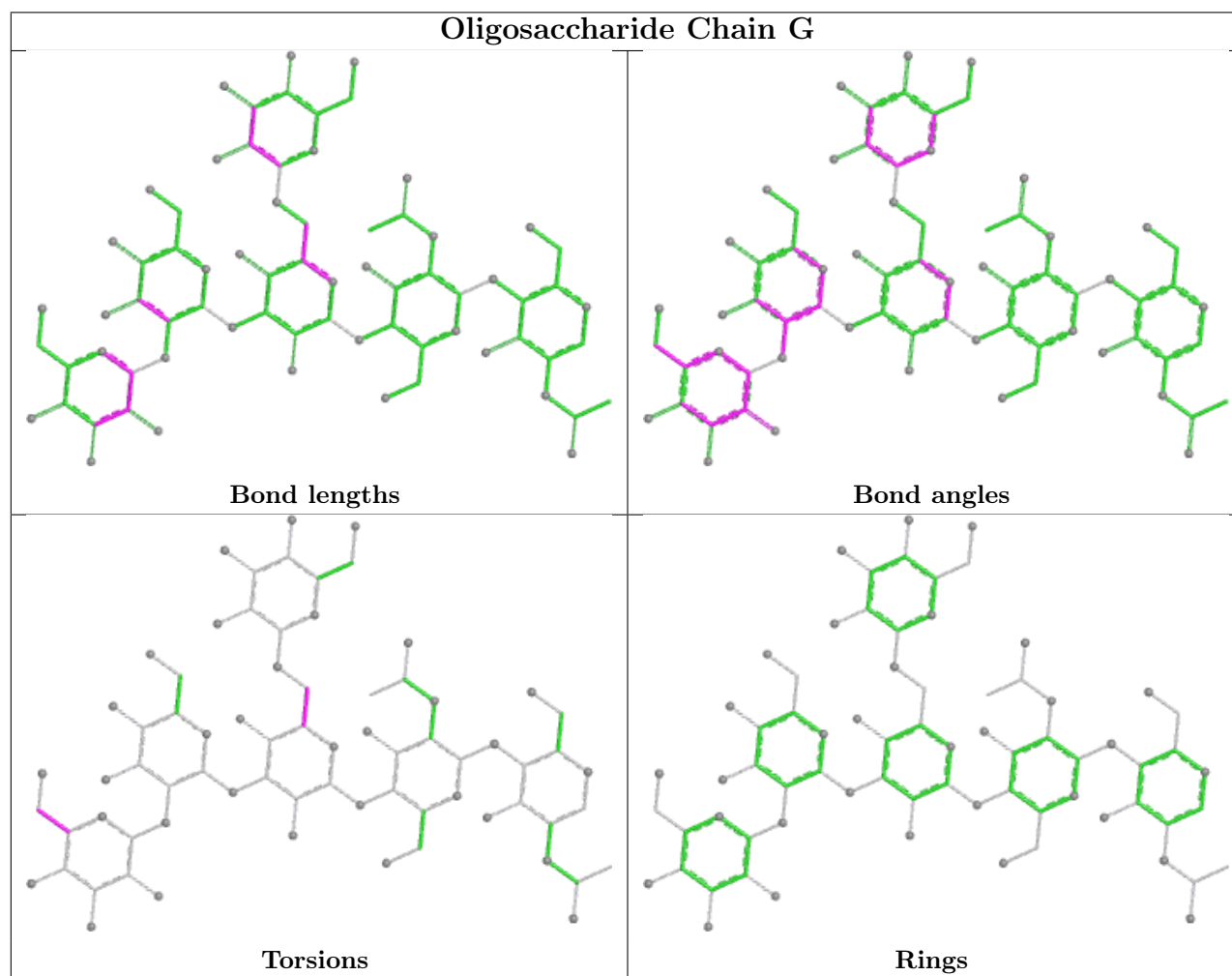
Mol	Chain	Res	Type	Atoms
3	H	5	MAN	O5-C5-C6-O6
3	I	5	MAN	O5-C5-C6-O6
3	G	5	MAN	O5-C5-C6-O6
3	H	5	MAN	C4-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6

There are no ring outliers.

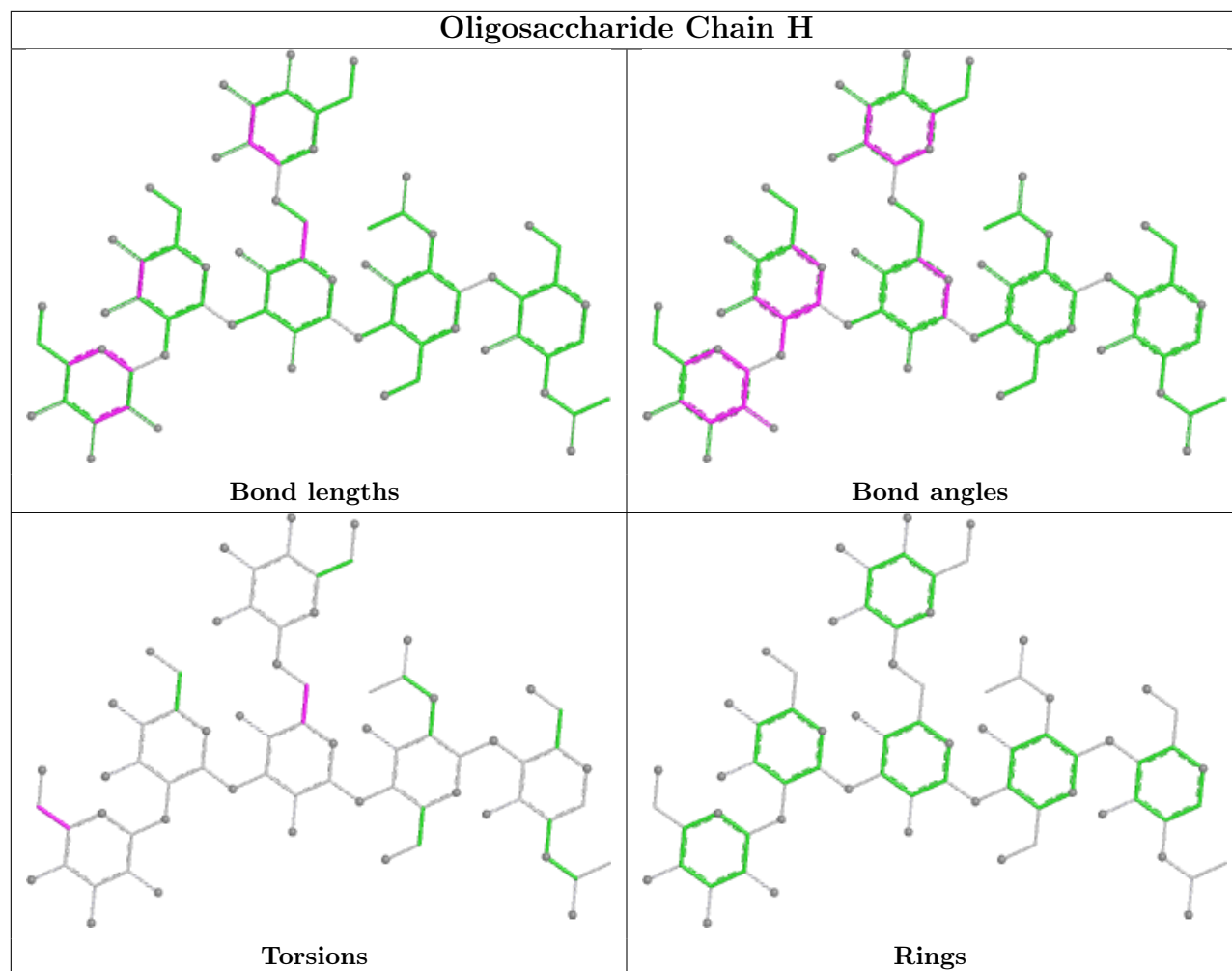
5 monomers are involved in 5 short contacts:

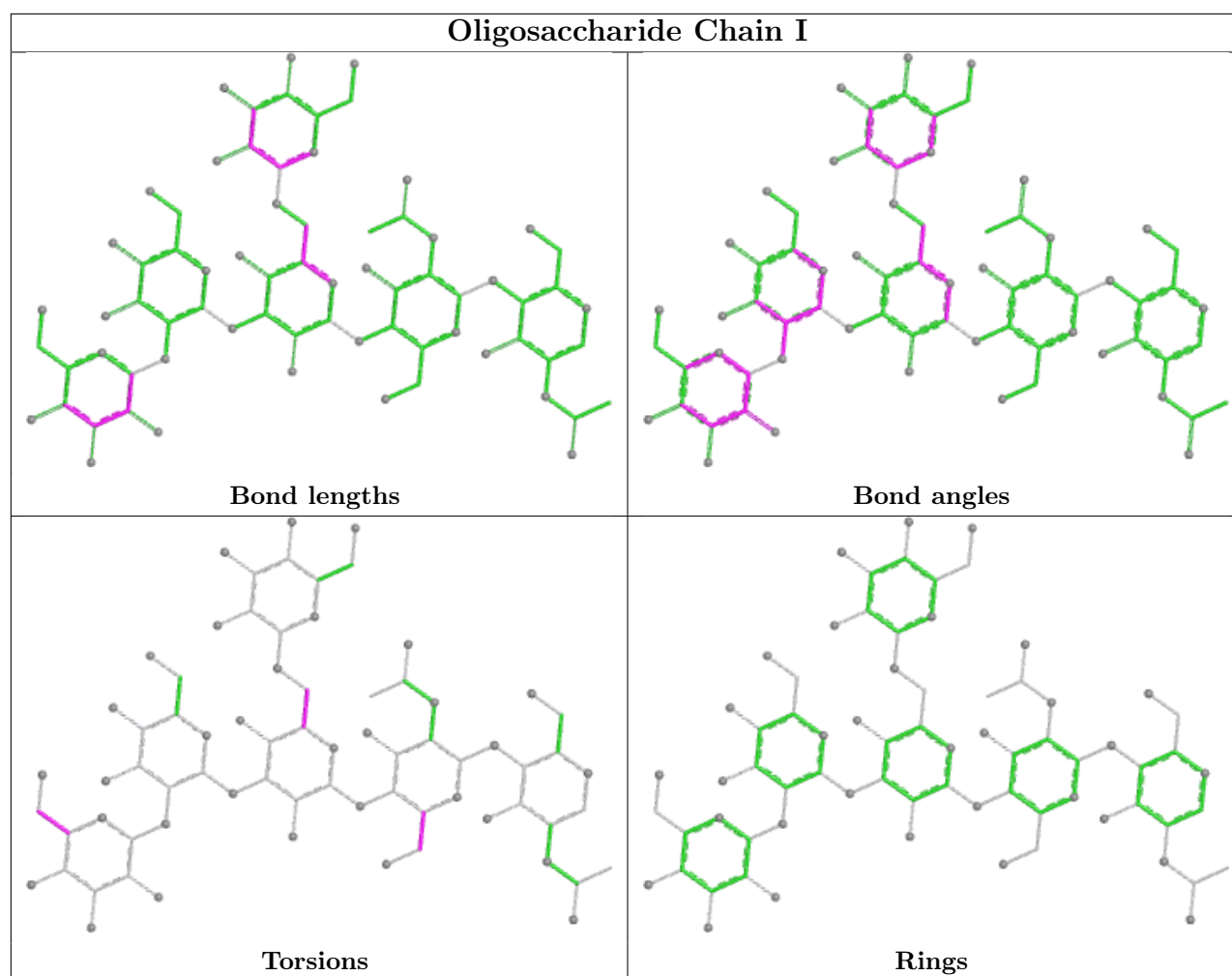
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	2	NAG	1	0
3	H	2	NAG	1	0
3	I	1	NAG	1	0
3	I	2	NAG	1	0
3	I	3	BMA	1	0

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 H





5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
4	NAG	E	407	1	14,14,15	0.21	0	17,19,21	0.68	1 (5%)
4	NAG	C	407	1	14,14,15	0.60	0	17,19,21	0.70	1 (5%)
4	NAG	A	407	1	14,14,15	0.38	0	17,19,21	0.68	1 (5%)

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	E	407	1	-	1/6/23/26	0/1/1/1
4	NAG	C	407	1	-	0/6/23/26	0/1/1/1
4	NAG	A	407	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	407	NAG	C1-O5-C5	2.51	115.56	112.19
4	A	407	NAG	C1-O5-C5	2.43	115.44	112.19
4	E	407	NAG	C1-O5-C5	2.35	115.33	112.19

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	407	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	320/332 (96%)	-0.93	0 100 100	31, 47, 66, 81	0
1	C	320/332 (96%)	-0.98	0 100 100	32, 47, 67, 82	0
1	E	320/332 (96%)	-0.98	0 100 100	33, 47, 65, 75	0
2	B	173/186 (93%)	-0.94	0 100 100	35, 49, 85, 141	0
2	D	173/186 (93%)	-0.87	0 100 100	34, 50, 83, 144	0
2	F	173/186 (93%)	-0.93	0 100 100	36, 50, 86, 155	0
All	All	1479/1554 (95%)	-0.95	0 100 100	31, 48, 70, 155	0

There are no RSRZ outliers to report.

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.

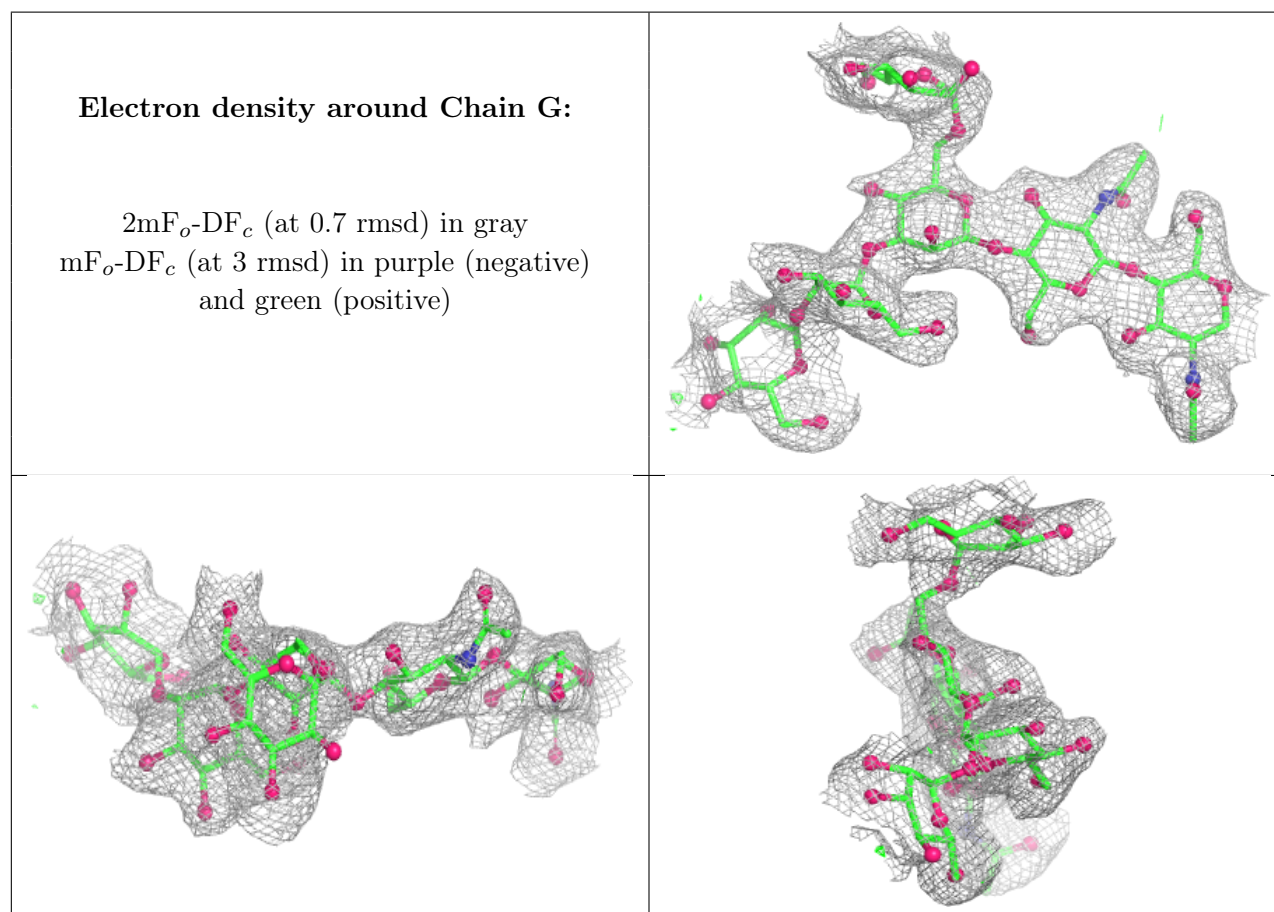
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	I	6	11/12	0.96	0.07	85,93,105,106	0
3	MAN	G	6	11/12	0.97	0.05	78,88,93,94	0
3	MAN	H	5	11/12	0.97	0.05	81,93,100,106	0
3	MAN	H	6	11/12	0.97	0.05	82,91,98,105	0
3	MAN	I	5	11/12	0.97	0.06	79,97,104,108	0
3	MAN	G	5	11/12	0.97	0.06	68,86,96,101	0

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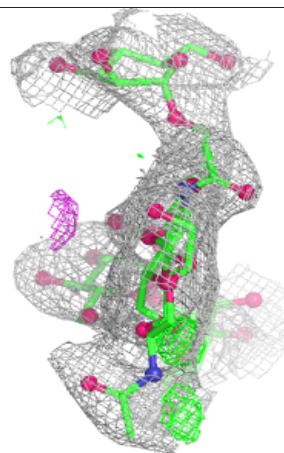
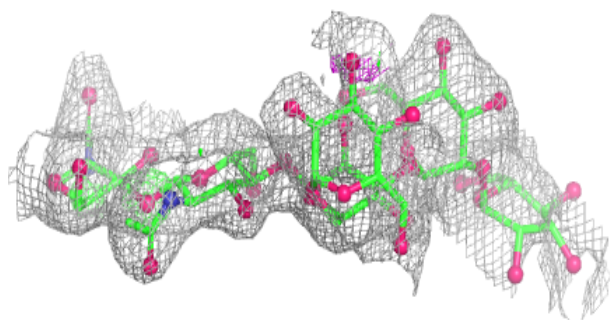
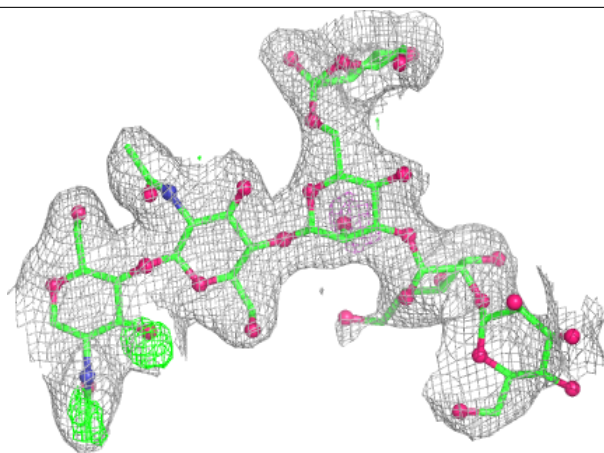
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	BMA	I	3	11/12	0.98	0.07	42,51,62,68	0
3	NAG	H	1	14/15	0.98	0.06	46,54,70,72	0
3	NAG	I	1	14/15	0.98	0.05	45,56,70,72	0
3	MAN	H	4	11/12	0.99	0.05	49,55,61,75	0
3	MAN	G	4	11/12	0.99	0.05	50,55,63,70	0
3	NAG	G	1	14/15	0.99	0.04	47,56,72,73	0
3	NAG	G	2	14/15	0.99	0.04	41,51,58,63	0
3	NAG	I	2	14/15	0.99	0.06	43,51,56,58	0
3	BMA	G	3	11/12	0.99	0.04	48,59,68,73	0
3	MAN	I	4	11/12	0.99	0.06	53,59,66,85	0
3	NAG	H	2	14/15	0.99	0.04	43,49,56,63	0
3	BMA	H	3	11/12	0.99	0.05	48,53,63,73	0

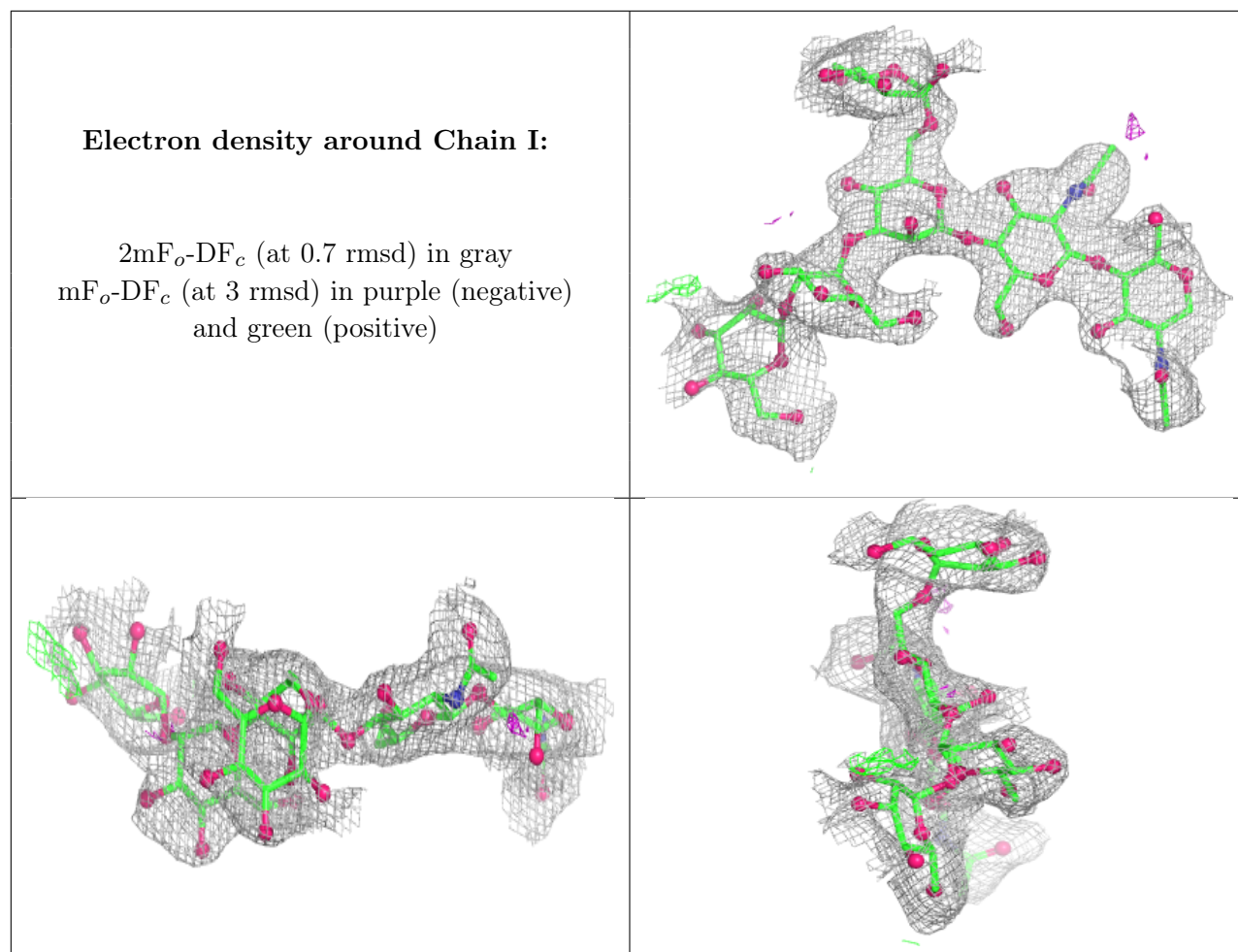
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain H:

$2mF_o-DF_c$ (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($\text{\AA}^2$)	Q<0.9
4	NAG	E	407	14/15	0.97	0.06	49,66,78,78	0
4	NAG	C	407	14/15	0.98	0.07	55,70,79,80	0
4	NAG	A	407	14/15	0.98	0.05	55,65,70,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.