



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 13, 2020 – 10:21 AM BST

PDB ID : 6TJY  
Title : Crystal structure of haemagglutinin from (A/seal/Germany/1/2014) seal H10N7 influenza virus  
Authors : Zhang, J.; Xiong, X.; Purkiss, A.; Walker, P.; Gamblin, S.; Skehel, J.J.  
Deposited on : 2019-11-27  
Resolution : 2.82 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

The 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 : 2.14.6  
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) : 2.14.6

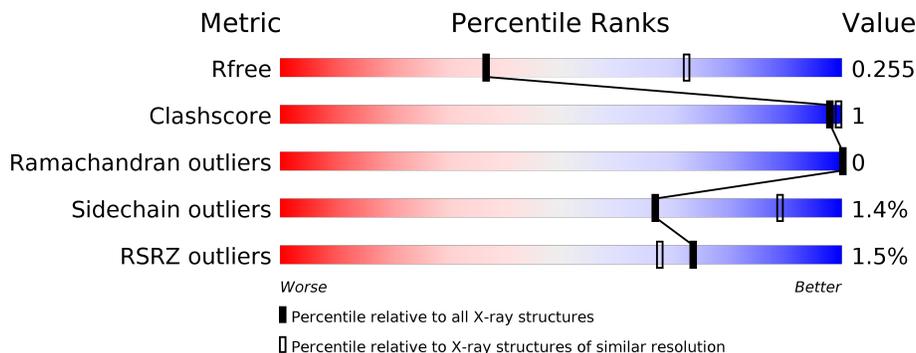
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.82 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.



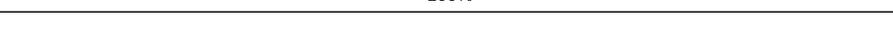
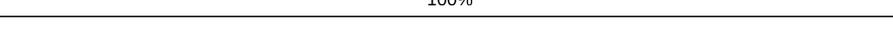
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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 on 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	325	97%
1	C	325	2% 96%
1	E	325	% 96%
1	G	325	8% 93%
1	I	325	2% 97%
1	K	325	94% 5%

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	B	177	 92% 5% .
2	D	177	 94% . .
2	F	177	 95% . .
2	H	177	 92% 5% .
2	J	177	 94% . .
2	L	177	 96% . .
3	M	3	 33% 67%
4	N	2	 100%
4	O	2	 100%
4	P	2	 100%

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
3	BMA	M	3	-	-	-	X
4	NAG	P	2	-	-	-	X
6	NAG	B	202	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 23432 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	320	2446	1516	444	470	16	0	1	0
1	C	320	2417	1501	437	463	16	0	0	0
1	E	320	2423	1507	439	461	16	0	1	0
1	G	317	2289	1411	420	442	16	0	0	0
1	I	320	2411	1498	432	465	16	0	1	0
1	K	320	2448	1518	444	470	16	0	1	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ASP	-	expression tag	UNP A0A0A7HR51
A	0	PRO	-	expression tag	UNP A0A0A7HR51
A	219	GLN	LEU	conflict	UNP A0A0A7HR51
C	-1	ASP	-	expression tag	UNP A0A0A7HR51
C	0	PRO	-	expression tag	UNP A0A0A7HR51
C	219	GLN	LEU	conflict	UNP A0A0A7HR51
E	-1	ASP	-	expression tag	UNP A0A0A7HR51
E	0	PRO	-	expression tag	UNP A0A0A7HR51
E	219	GLN	LEU	conflict	UNP A0A0A7HR51
G	-1	ASP	-	expression tag	UNP A0A0A7HR51
G	0	PRO	-	expression tag	UNP A0A0A7HR51
G	219	GLN	LEU	conflict	UNP A0A0A7HR51
I	-1	ASP	-	expression tag	UNP A0A0A7HR51
I	0	PRO	-	expression tag	UNP A0A0A7HR51
I	219	GLN	LEU	conflict	UNP A0A0A7HR51
K	-1	ASP	-	expression tag	UNP A0A0A7HR51
K	0	PRO	-	expression tag	UNP A0A0A7HR51

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
K	219	GLN	LEU	conflict	UNP A0A0A7HR51

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	172	1386	857	241	280	8	0	0	0
2	D	172	1386	857	241	280	8	0	0	0
2	F	172	1386	857	241	280	8	0	0	0
2	H	172	1379	854	240	277	8	0	0	0
2	J	172	1386	857	241	280	8	0	0	0
2	L	172	1386	857	241	280	8	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	LYS	-	expression tag	UNP A0A0A7HNL0
D	177	LYS	-	expression tag	UNP A0A0A7HNL0
F	177	LYS	-	expression tag	UNP A0A0A7HNL0
H	177	LYS	-	expression tag	UNP A0A0A7HNL0
J	177	LYS	-	expression tag	UNP A0A0A7HNL0
L	177	LYS	-	expression tag	UNP A0A0A7HNL0

- Molecule 3 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
			Total	C	N	O			
3	M	3	39	22	2	15	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.

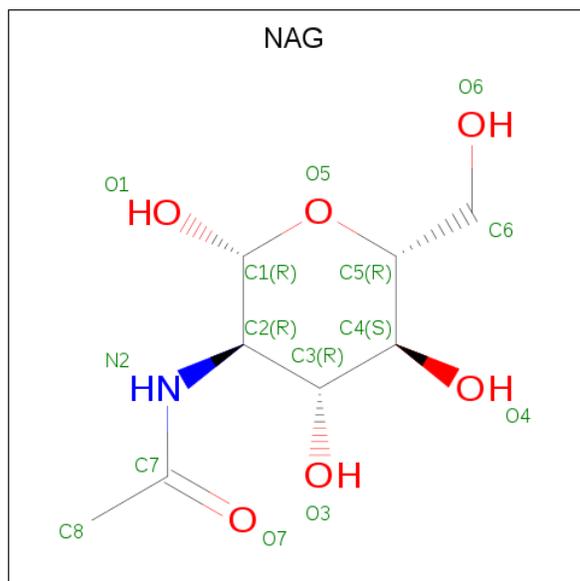


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	N	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	O	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	D	1	Total	Ca	0	0
			1	1		
5	E	1	Total	Ca	0	0
			1	1		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

Continued on next page...

*Continued from previous page...*

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	54	Total	O	0	0
			54	54		
7	B	31	Total	O	0	0
			31	31		
7	C	52	Total	O	0	0
			52	52		
7	D	59	Total	O	0	0
			59	59		
7	E	22	Total	O	0	0
			22	22		
7	F	38	Total	O	0	0
			38	38		
7	G	17	Total	O	0	0
			17	17		
7	H	40	Total	O	0	0
			40	40		
7	I	11	Total	O	0	0
			11	11		
7	J	30	Total	O	0	0
			30	30		
7	K	98	Total	O	0	0
			98	98		
7	L	41	Total	O	0	0
			41	41		

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

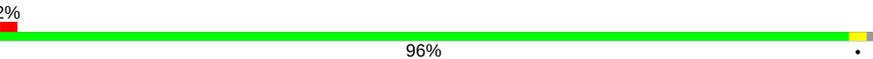
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 HA1

Chain A:  97%



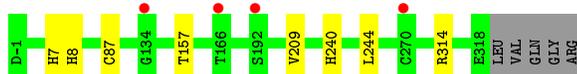
- Molecule 1: Hemagglutinin HA1

Chain C:  96%

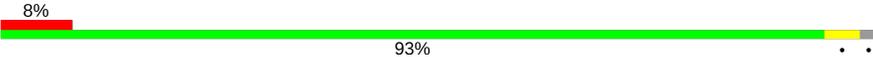


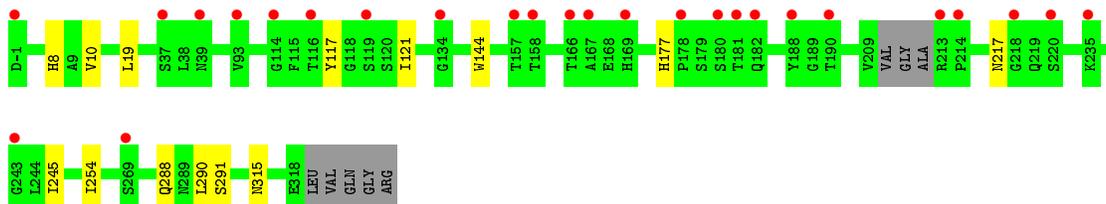
- Molecule 1: Hemagglutinin HA1

Chain E:  96%



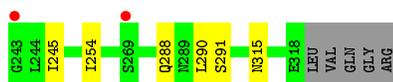
- Molecule 1: Hemagglutinin HA1

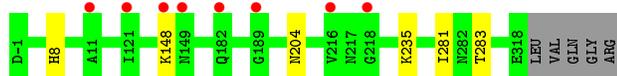
Chain G:  93%



- Molecule 1: Hemagglutinin HA1

Chain I:  97%





- Molecule 1: Hemagglutinin HA1



- Molecule 2: Hemagglutinin HA2



- Molecule 2: Hemagglutinin HA2



- Molecule 2: Hemagglutinin HA2



- Molecule 2: Hemagglutinin HA2



- Molecule 2: Hemagglutinin HA2



- Molecule 2: Hemagglutinin HA2





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

Chain M:  33% 67%



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

Chain N:  100%

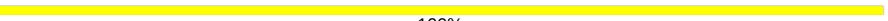


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  100%



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

Chain P:  100%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.42Å 212.93Å 156.90Å 90.00° 101.51° 90.00°	Depositor
Resolution (Å)	35.04 – 2.82 35.04 – 2.82	Depositor EDS
% Data completeness (in resolution range)	98.1 (35.04-2.82) 98.2 (35.04-2.82)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.35 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.216 , 0.257 0.217 , 0.255	Depositor DCC
$R_{free}$ test set	5254 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.7	Xtrriage
Anisotropy	0.871	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 34.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	23432	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.38 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5657e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, BMA, 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	0.35	0/2499	0.57	0/3385
1	C	0.35	0/2467	0.57	0/3346
1	E	0.36	0/2476	0.57	0/3356
1	G	0.37	0/2335	0.56	0/3174
1	I	0.36	0/2464	0.54	0/3342
1	K	0.36	0/2501	0.57	0/3388
2	B	0.36	0/1411	0.53	0/1903
2	D	0.37	0/1411	0.55	0/1903
2	F	0.36	0/1411	0.54	0/1903
2	H	0.37	0/1404	0.54	0/1894
2	J	0.36	0/1411	0.54	0/1903
2	L	0.36	0/1411	0.53	0/1903
All	All	0.36	0/23201	0.56	0/31400

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	2446	0	2400	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2417	0	2346	2	0
1	E	2423	0	2357	4	0
1	G	2289	0	2091	6	0
1	I	2411	0	2341	1	0
1	K	2448	0	2407	8	0
2	B	1386	0	1290	5	0
2	D	1386	0	1291	3	0
2	F	1386	0	1291	3	0
2	H	1379	0	1283	6	0
2	J	1386	0	1292	3	0
2	L	1386	0	1291	2	0
3	M	39	0	34	0	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	B	28	0	26	0	0
6	C	14	0	13	0	0
6	G	14	0	13	0	0
6	J	14	0	13	0	0
7	A	54	0	0	0	0
7	B	31	0	0	0	0
7	C	52	0	0	0	0
7	D	59	0	0	0	0
7	E	22	0	0	0	0
7	F	38	0	0	0	0
7	G	17	0	0	0	0
7	H	40	0	0	0	0
7	I	11	0	0	0	0
7	J	30	0	0	0	0
7	K	98	0	0	0	0
7	L	41	0	0	0	0
All	All	23432	0	21854	33	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 1.

The worst 5 of 33 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)
1:G:144:TRP:HA	1:G:245:ILE:HG22	1.74	0.69
1:G:10:VAL:H	1:G:315:ASN:HD21	1.47	0.61
2:B:55:ILE:HG23	2:B:99:LEU:HD21	1.83	0.60
2:B:99:LEU:HD22	2:H:94:TYR:OH	2.02	0.60
2:J:54:ARG:NH2	2:J:103:GLU:OE2	2.37	0.57

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	319/325 (98%)	311 (98%)	8 (2%)	0	100	100
1	C	318/325 (98%)	306 (96%)	12 (4%)	0	100	100
1	E	319/325 (98%)	307 (96%)	12 (4%)	0	100	100
1	G	313/325 (96%)	299 (96%)	14 (4%)	0	100	100
1	I	319/325 (98%)	306 (96%)	13 (4%)	0	100	100
1	K	319/325 (98%)	309 (97%)	10 (3%)	0	100	100
2	B	170/177 (96%)	164 (96%)	6 (4%)	0	100	100
2	D	170/177 (96%)	164 (96%)	6 (4%)	0	100	100
2	F	170/177 (96%)	164 (96%)	6 (4%)	0	100	100
2	H	170/177 (96%)	162 (95%)	8 (5%)	0	100	100
2	J	170/177 (96%)	165 (97%)	5 (3%)	0	100	100
2	L	170/177 (96%)	165 (97%)	5 (3%)	0	100	100
All	All	2927/3012 (97%)	2822 (96%)	105 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	270/275 (98%)	267 (99%)	3 (1%)	73	91
1	C	262/275 (95%)	256 (98%)	6 (2%)	50	80
1	E	260/275 (94%)	257 (99%)	3 (1%)	71	91
1	G	226/275 (82%)	222 (98%)	4 (2%)	59	85
1	I	262/275 (95%)	258 (98%)	4 (2%)	65	88
1	K	271/275 (98%)	268 (99%)	3 (1%)	73	91
2	B	146/151 (97%)	142 (97%)	4 (3%)	44	77
2	D	146/151 (97%)	144 (99%)	2 (1%)	67	89
2	F	146/151 (97%)	146 (100%)	0	100	100
2	H	144/151 (95%)	142 (99%)	2 (1%)	67	89
2	J	146/151 (97%)	144 (99%)	2 (1%)	67	89
2	L	146/151 (97%)	146 (100%)	0	100	100
All	All	2425/2556 (95%)	2392 (99%)	33 (1%)	67	89

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	113	SER
1	G	8	HIS
1	K	8	HIS
1	E	8	HIS
1	E	87	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	205	ASN
2	F	106	HIS
2	L	30	GLN
1	E	282	ASN

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type
2	F	30	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

9 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	M	1	3,2,5	14,14,15	0.29	0	17,19,21	1.06	1 (5%)
3	NAG	M	2	3	14,14,15	0.65	0	17,19,21	1.42	1 (5%)
3	BMA	M	3	3	11,11,12	0.41	0	15,15,17	0.96	0
4	NAG	N	1	2,4	14,14,15	0.45	0	17,19,21	0.89	1 (5%)
4	NAG	N	2	4	14,14,15	0.32	0	17,19,21	0.75	1 (5%)
4	NAG	O	1	2,5,4	14,14,15	0.46	0	17,19,21	1.05	1 (5%)
4	NAG	O	2	4	14,14,15	0.40	0	17,19,21	1.58	3 (17%)
4	NAG	P	1	2,5,4	14,14,15	0.36	0	17,19,21	1.07	1 (5%)
4	NAG	P	2	4	14,14,15	0.38	0	17,19,21	0.84	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
3	NAG	M	1	3,2,5	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	2/6/23/26	0/1/1/1
3	BMA	M	3	3	-	0/2/19/22	0/1/1/1
4	NAG	N	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	2/6/23/26	0/1/1/1
4	NAG	O	1	2,5,4	-	0/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	NAG	P	1	2,5,4	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	O	2	NAG	C1-O5-C5	5.08	119.07	112.19
3	M	2	NAG	C4-C3-C2	4.32	117.35	111.02
3	M	1	NAG	C1-O5-C5	3.79	117.33	112.19
4	O	1	NAG	C1-O5-C5	2.92	116.15	112.19
4	N	1	NAG	C4-C3-C2	2.40	114.54	111.02

There are no chirality outliers.

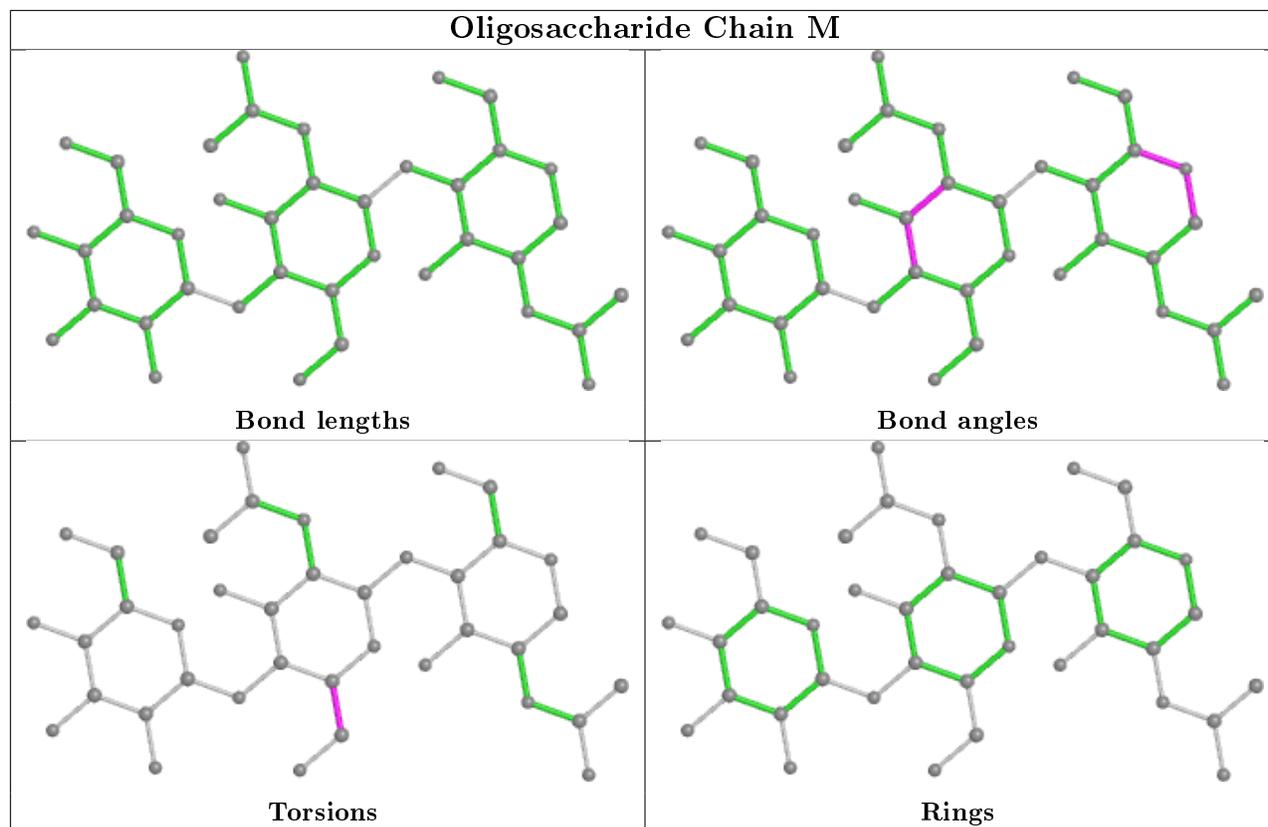
All (4) torsion outliers are listed below:

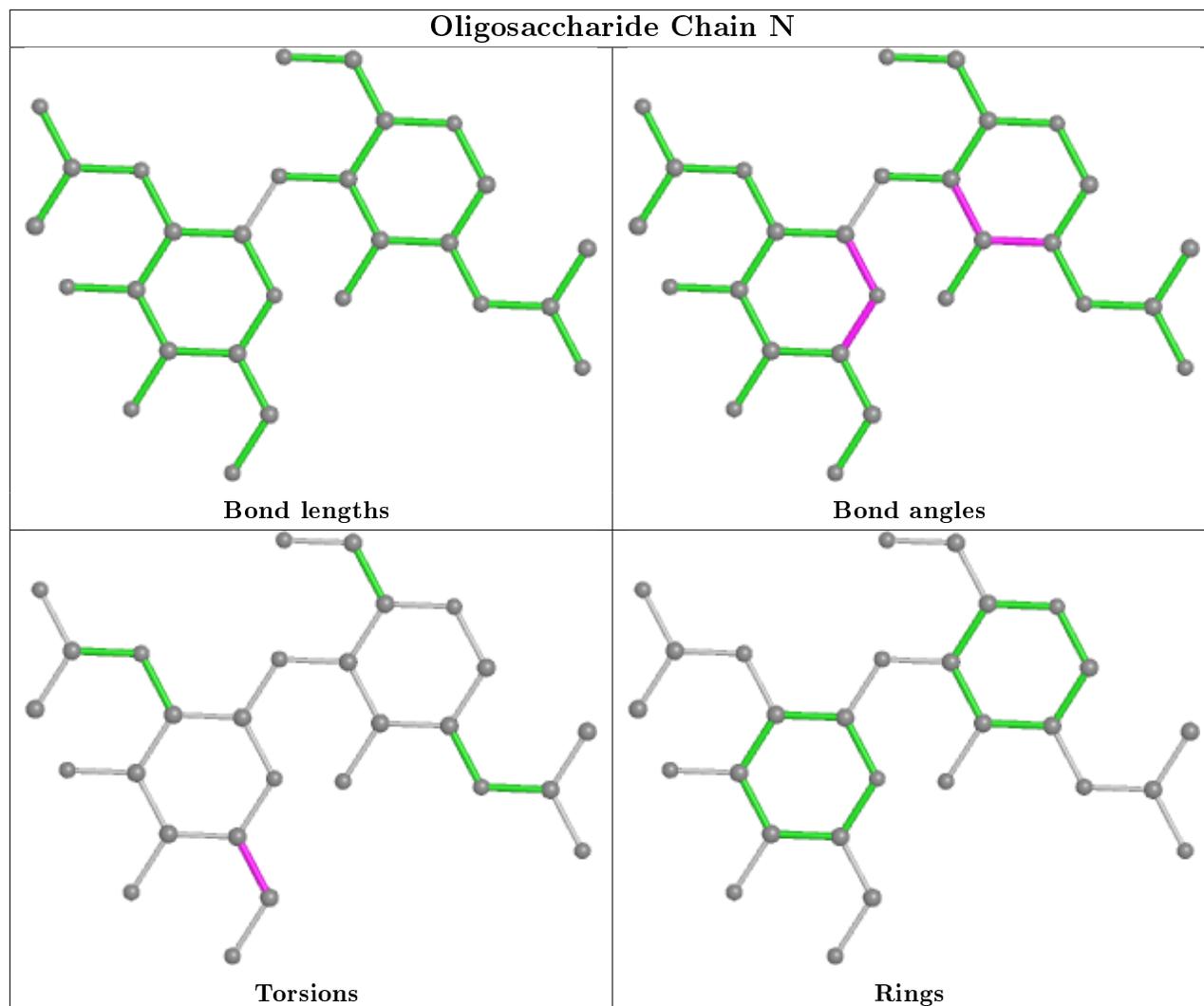
Mol	Chain	Res	Type	Atoms
4	N	2	NAG	O5-C5-C6-O6
4	N	2	NAG	C4-C5-C6-O6
3	M	2	NAG	C4-C5-C6-O6
3	M	2	NAG	O5-C5-C6-O6

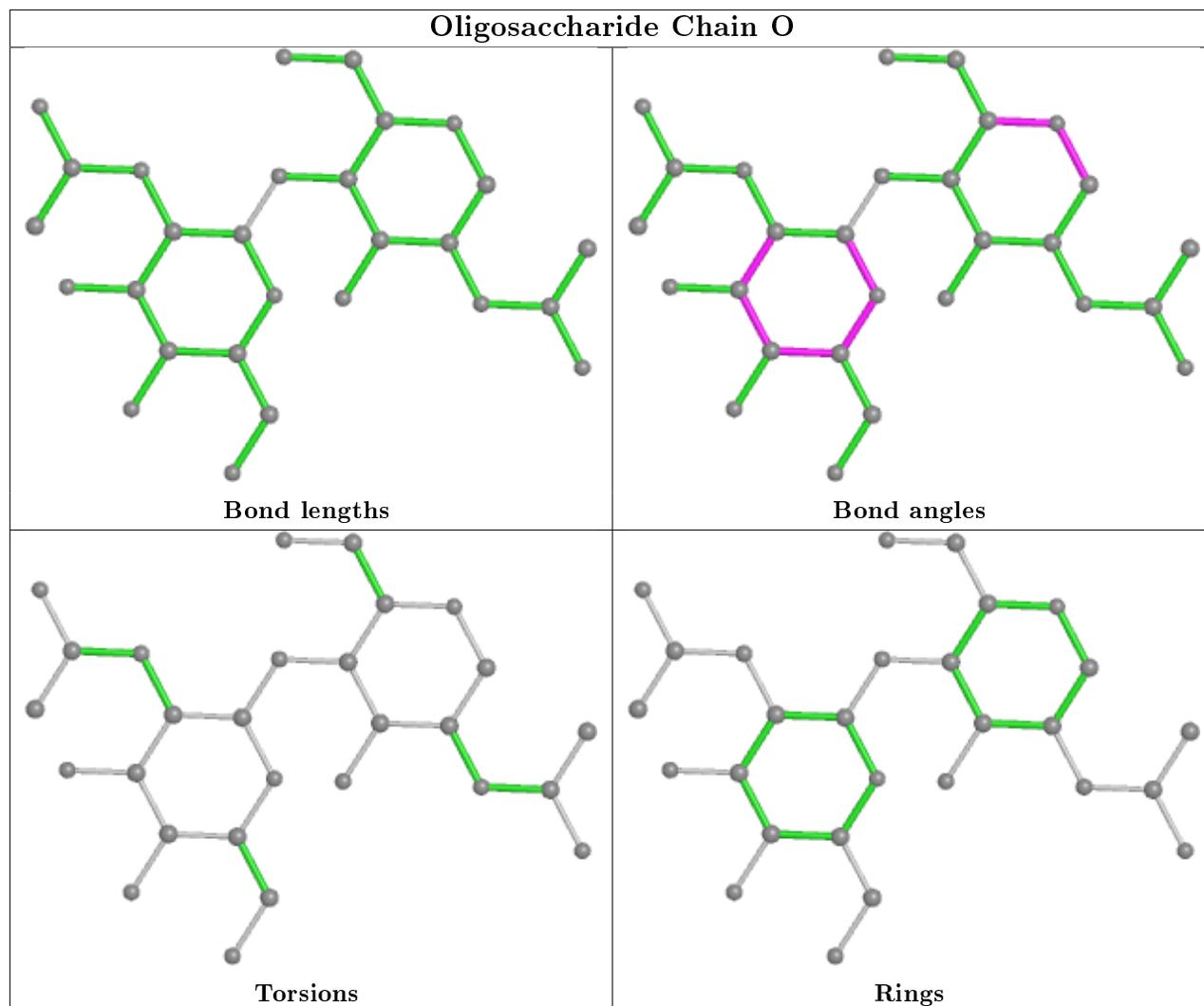
There are no ring outliers.

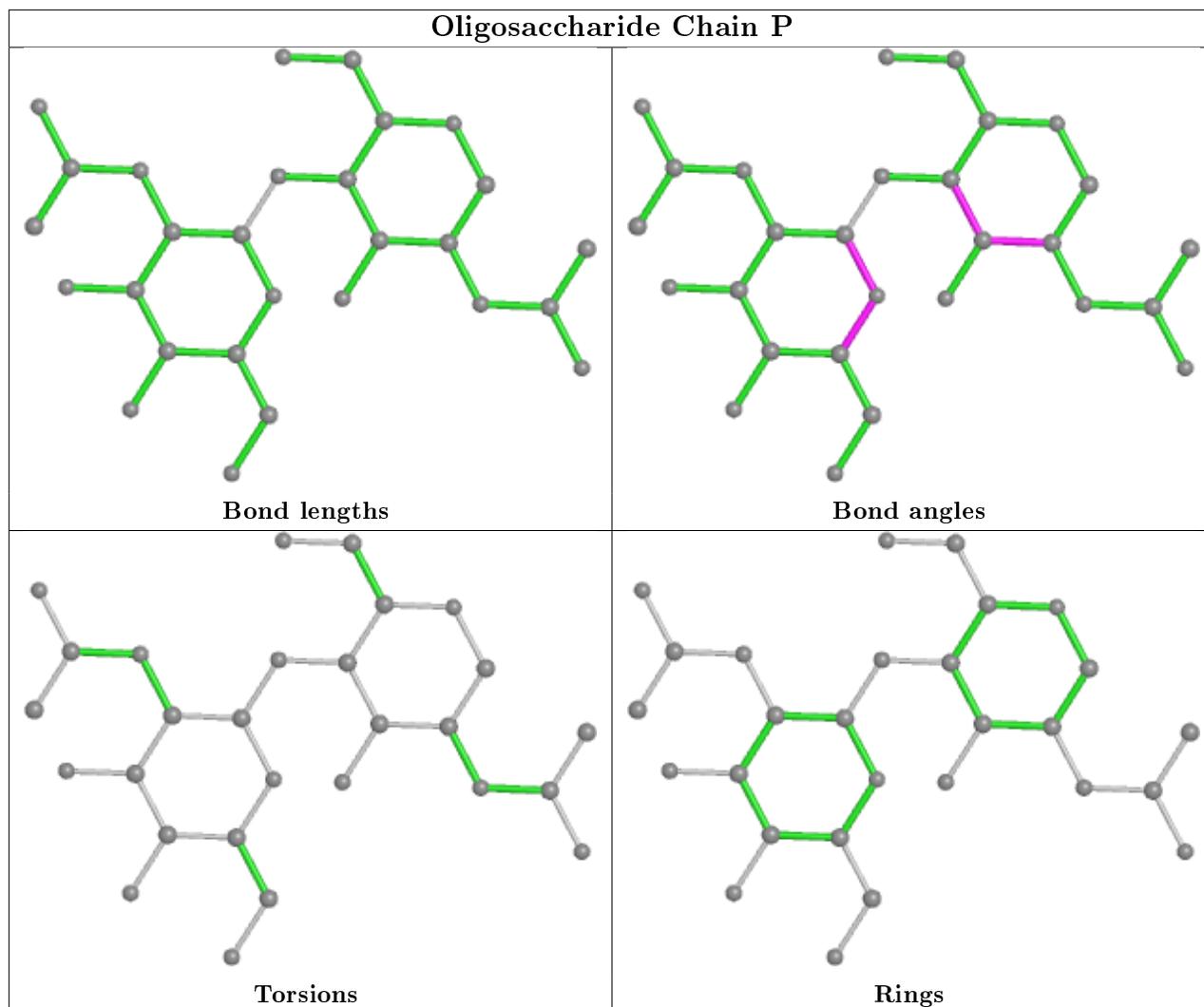
No monomer is involved in short contacts.

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 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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
6	NAG	G	401	1	14,14,15	0.45	0	17,19,21	1.02	1 (5%)
6	NAG	B	201	2	14,14,15	0.39	0	17,19,21	1.10	0
6	NAG	B	202	2	14,14,15	0.53	0	17,19,21	0.81	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	NAG	C	401	1	14,14,15	0.38	0	17,19,21	1.24	1 (5%)
6	NAG	J	201	2	14,14,15	0.39	0	17,19,21	1.01	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
6	NAG	G	401	1	-	0/6/23/26	0/1/1/1
6	NAG	B	201	2	-	2/6/23/26	0/1/1/1
6	NAG	B	202	2	-	0/6/23/26	0/1/1/1
6	NAG	C	401	1	-	1/6/23/26	0/1/1/1
6	NAG	J	201	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	401	NAG	C1-O5-C5	4.01	117.63	112.19
6	J	201	NAG	C1-O5-C5	3.19	116.52	112.19
6	G	401	NAG	C1-O5-C5	2.86	116.06	112.19
6	B	202	NAG	O5-C5-C6	2.24	110.72	107.20

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	401	NAG	C3-C2-N2-C7
6	B	201	NAG	C4-C5-C6-O6
6	B	201	NAG	O5-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

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	320/325 (98%)	-0.23	1 (0%) 94 93	40, 58, 87, 94	0
1	C	320/325 (98%)	-0.10	5 (1%) 72 65	38, 64, 107, 118	0
1	E	320/325 (98%)	-0.13	4 (1%) 77 72	46, 77, 110, 123	0
1	G	317/325 (97%)	0.45	26 (8%) 11 6	42, 89, 138, 173	0
1	I	320/325 (98%)	0.06	8 (2%) 57 47	50, 82, 127, 151	0
1	K	320/325 (98%)	-0.35	0 100 100	40, 54, 74, 85	0
2	B	172/177 (97%)	-0.12	0 100 100	42, 59, 85, 92	0
2	D	172/177 (97%)	-0.29	1 (0%) 89 86	35, 53, 68, 84	0
2	F	172/177 (97%)	-0.13	0 100 100	40, 62, 86, 106	0
2	H	172/177 (97%)	-0.24	0 100 100	38, 56, 76, 99	0
2	J	172/177 (97%)	-0.18	0 100 100	45, 62, 80, 99	0
2	L	172/177 (97%)	-0.15	0 100 100	40, 55, 80, 88	0
All	All	2949/3012 (97%)	-0.10	45 (1%) 73 67	35, 64, 112, 173	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	181	THR	6.7
1	G	180	SER	5.5
1	G	218	GLY	4.6
1	G	214	PRO	4.4
1	G	167	ALA	4.3

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

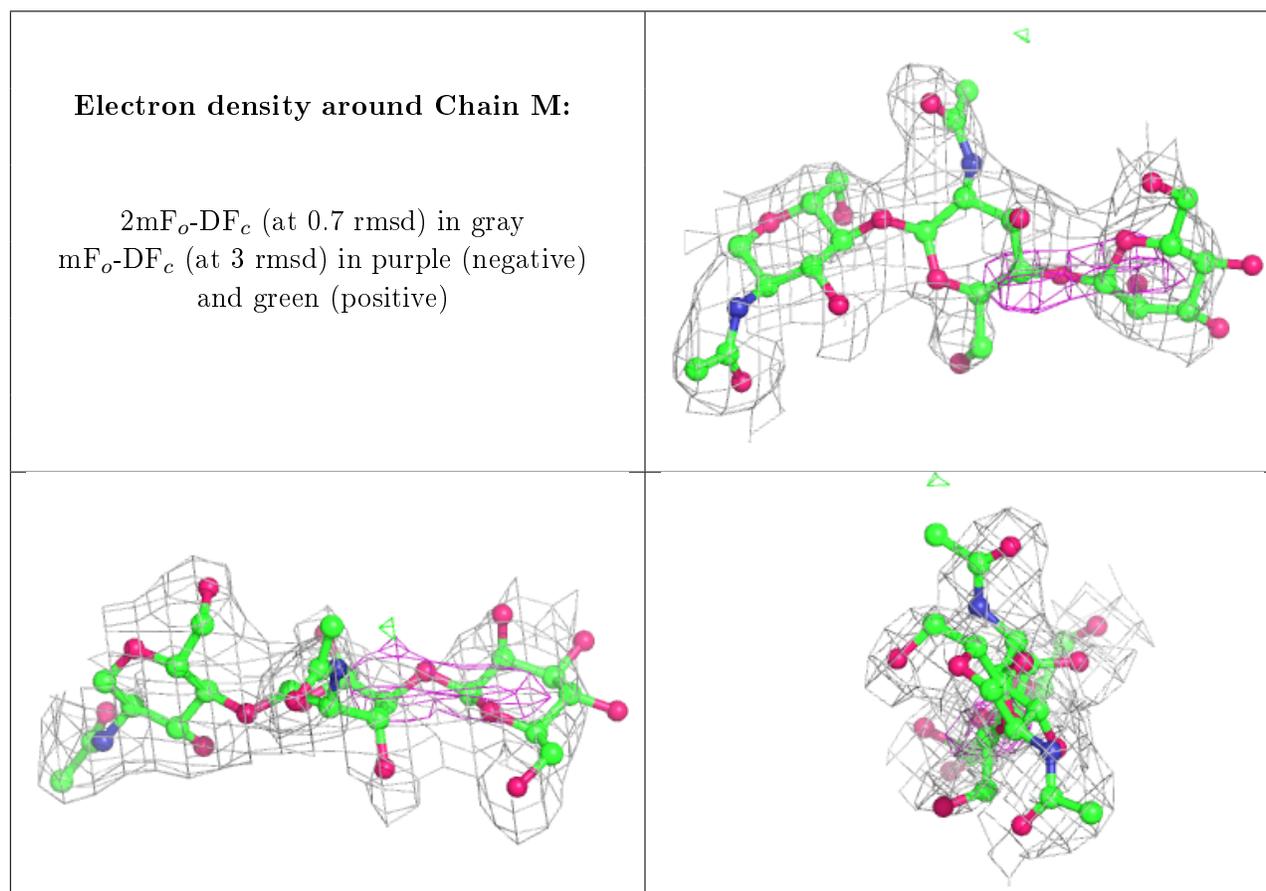
There are no non-standard protein/DNA/RNA residues in this entry.

### 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, 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.

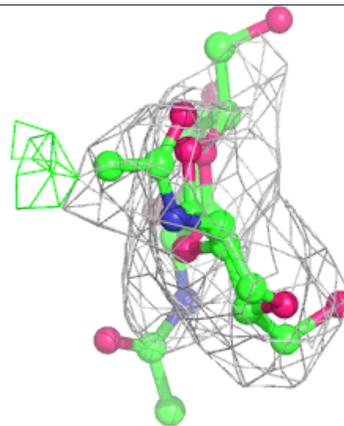
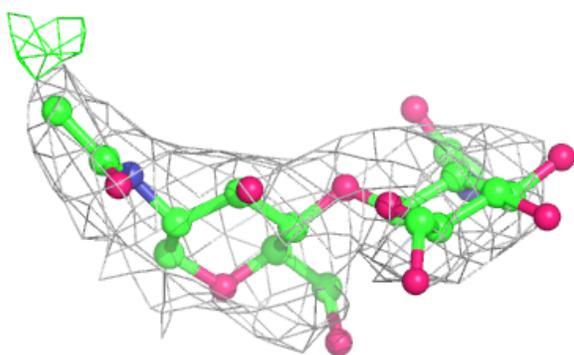
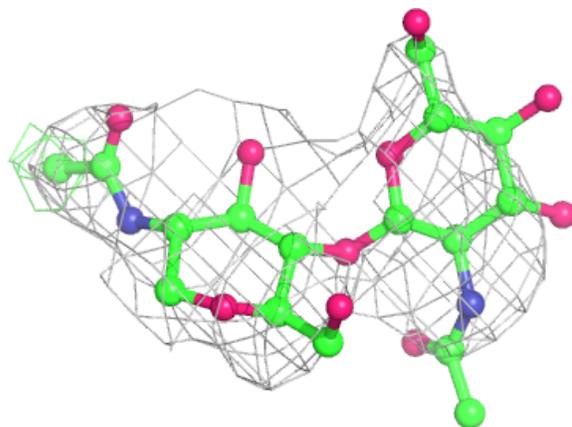
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	BMA	M	3	11/12	0.66	0.42	112,120,124,126	0
3	NAG	M	2	14/15	0.77	0.31	79,93,103,113	0
4	NAG	P	2	14/15	0.79	0.54	113,119,122,122	0
4	NAG	N	1	14/15	0.83	0.21	101,107,112,120	0
4	NAG	N	2	14/15	0.87	0.43	117,126,130,133	0
4	NAG	P	1	14/15	0.88	0.31	86,94,98,108	0
4	NAG	O	2	14/15	0.92	0.25	85,92,97,98	0
3	NAG	M	1	14/15	0.94	0.13	61,63,68,76	0
4	NAG	O	1	14/15	0.95	0.11	57,63,69,77	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.



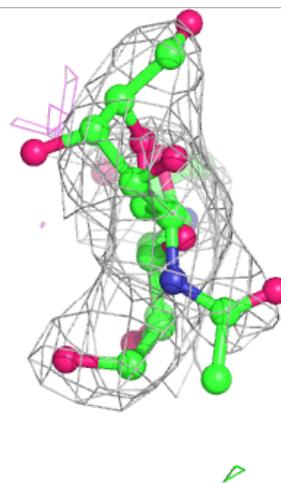
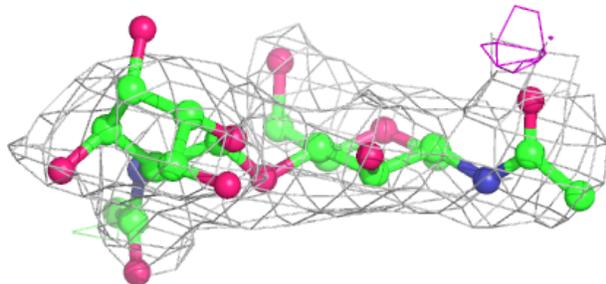
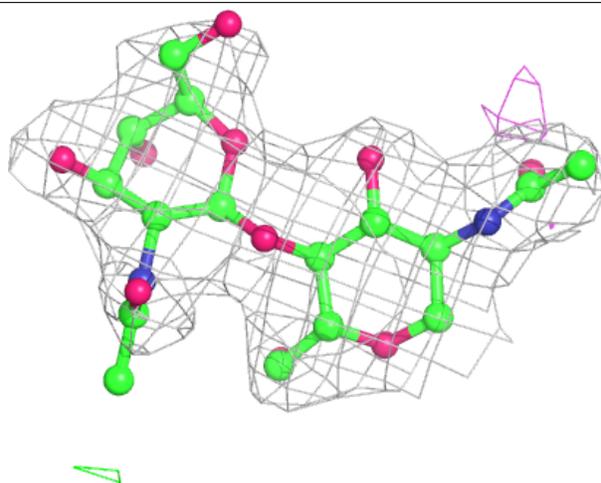
**Electron density around Chain N:**

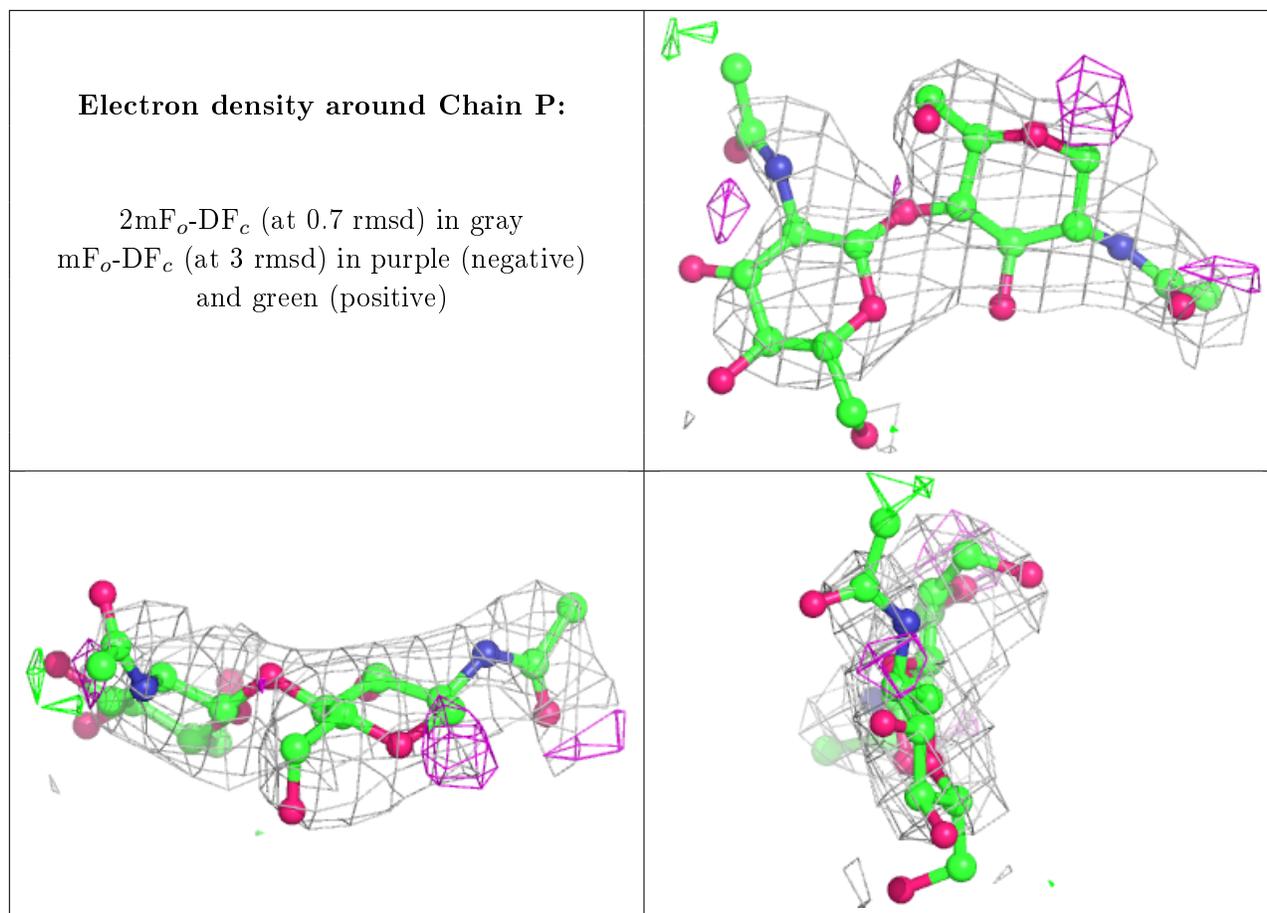
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain O:**

$2mF_o-DF_c$  (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
6	NAG	B	202	14/15	0.79	0.41	115,120,122,123	0
6	NAG	J	201	14/15	0.81	0.19	92,96,101,101	0
5	CA	E	401	1/1	0.85	0.22	103,103,103,103	0
6	NAG	C	401	14/15	0.86	0.22	79,85,87,90	0
6	NAG	G	401	14/15	0.88	0.27	89,94,98,99	0
6	NAG	B	201	14/15	0.88	0.28	79,84,88,90	0
5	CA	D	204	1/1	0.93	0.08	64,64,64,64	0
5	CA	A	401	1/1	0.94	0.08	57,57,57,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.