



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 11:48 AM BST

PDB ID : 2QKI  
Title : Human C3c in complex with the inhibitor compstatin  
Authors : Janssen, B.J.C.; Halff, E.F.; Lambris, J.D.; Gros, P.  
Deposited on : 2007-07-11  
Resolution : 2.40 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 : 2.13.1  
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) : 2.13.1

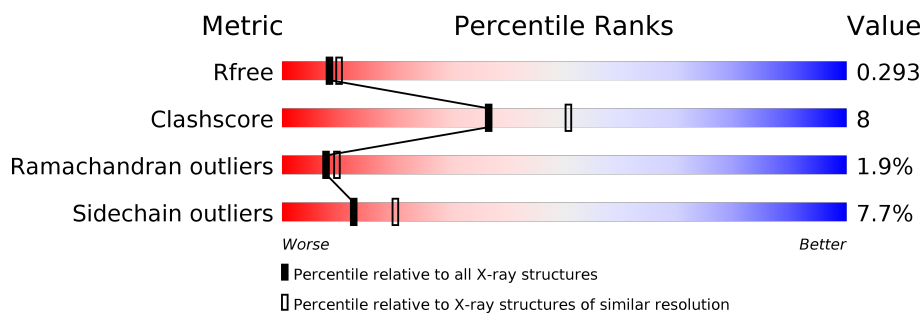
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	643	
1	D	643	
2	B	188	
2	E	188	
3	C	343	
3	F	343	
4	G	15	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
4	H	15	
5	I	2	
5	J	2	

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
5	NAG	J	1	X	-	-	-
8	GOL	A	809	-	-	X	-
8	GOL	E	916	-	-	X	-
8	GOL	F	840	-	-	X	-

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 18480 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 Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	631	Total	C	N	O	S	0	0	0
			4912	3131	831	935	15			
1	D	632	Total	C	N	O	S	0	0	0
			4919	3137	829	938	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	292	LEU	PRO	SEE REMARK 999	UNP P01024
D	292	LEU	PRO	SEE REMARK 999	UNP P01024

- Molecule 2 is a protein called Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	184	Total	C	N	O	S	0	0	0
			1484	954	250	275	5			
2	E	186	Total	C	N	O	S	0	0	0
			1500	964	252	279	5			

- Molecule 3 is a protein called Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	292	Total	C	N	O	S	0	0	0
			2372	1497	388	467	20			
3	F	295	Total	C	N	O	S	0	0	0
			2395	1510	392	473	20			

- Molecule 4 is a protein called compstatin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	15	Total	C	N	O	S	0	0	1
			113	71	22	18	2			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	15	Total	C	N	O	S	0	0	1
			113	71	22	18	2			

- Molecule 5 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
5	I	2	Total	C	N	O		0	0	0
			28	16	2	10				
5	J	2	Total	C	N	O		0	0	0
			28	16	2	10				

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	K	0	0
			1	1		
6	D	2	Total	K	0	0
			2	2		
6	C	1	Total	K	0	0
			1	1		
6	F	1	Total	K	0	0
			1	1		

- Molecule 7 is BROMIDE ION (three-letter code: BR) (formula: Br).

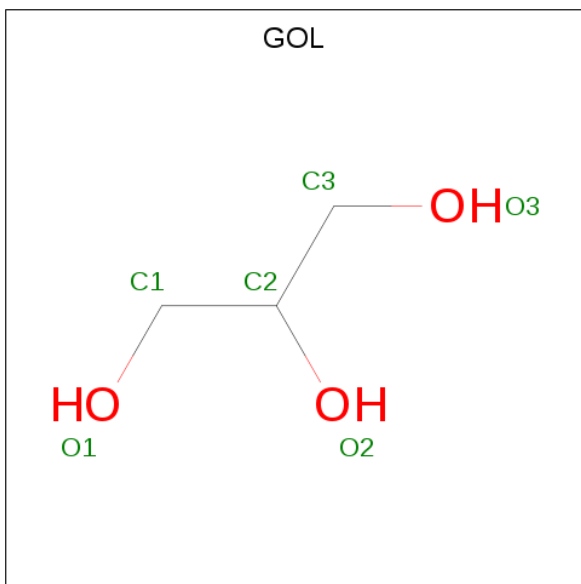
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	15	Total	Br	0	0
			15	15		
7	E	3	Total	Br	0	0
			3	3		
7	B	3	Total	Br	0	0
			3	3		
7	C	1	Total	Br	0	0
			1	1		
7	A	8	Total	Br	0	0
			8	8		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	F	2	Total	Br	0	0
			2	2		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	C	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total 6	C 3	O 3	0	0
8	D	1	Total 6	C 3	O 3	0	0
8	D	1	Total 6	C 3	O 3	0	0
8	D	1	Total 6	C 3	O 3	0	0
8	E	1	Total 6	C 3	O 3	0	0
8	E	1	Total 6	C 3	O 3	0	0
8	F	1	Total 6	C 3	O 3	0	0
8	H	1	Total 6	C 3	O 3	0	0

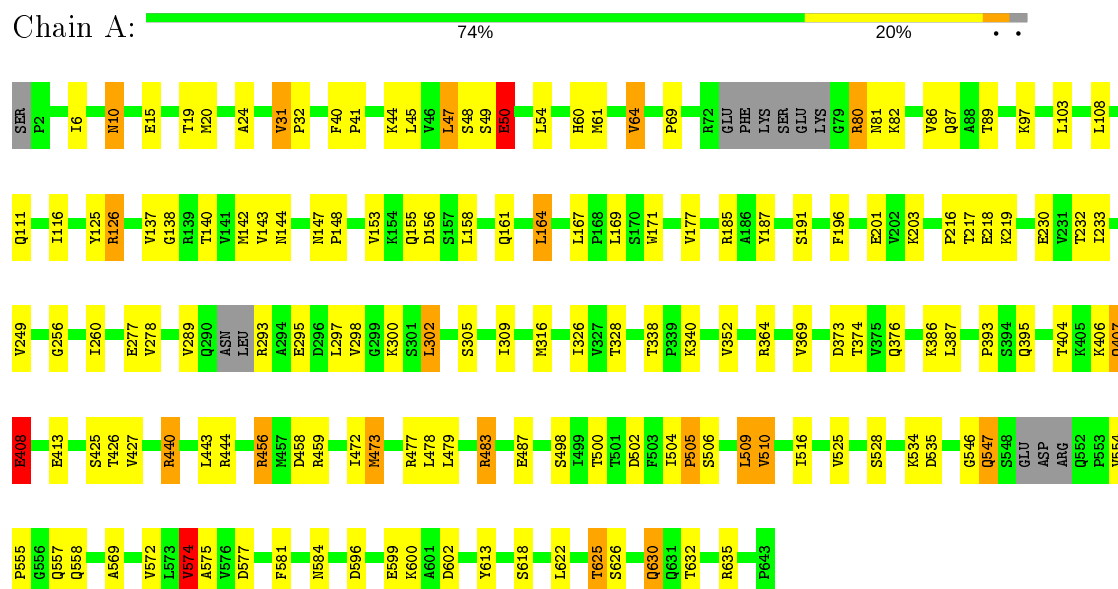
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	111	Total 111	O 111	0	0
9	B	47	Total 47	O 47	0	0
9	C	23	Total 23	O 23	0	0
9	D	188	Total 188	O 188	0	0
9	E	62	Total 62	O 62	0	0
9	F	35	Total 35	O 35	0	0
9	H	5	Total 5	O 5	0	0

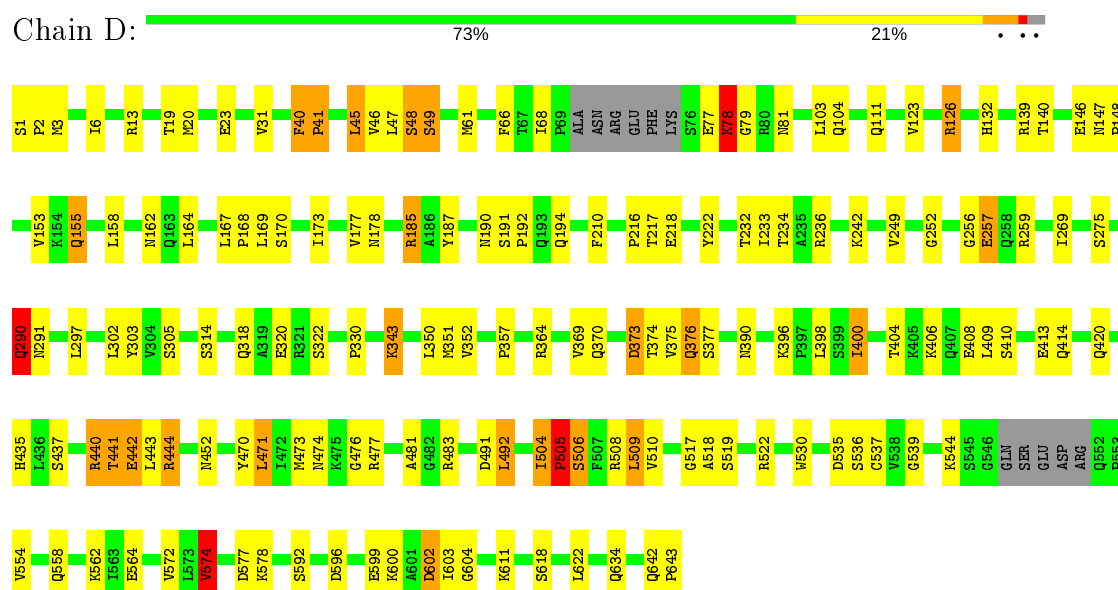
### 3 Residue-property plots

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. 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. 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: Complement C3

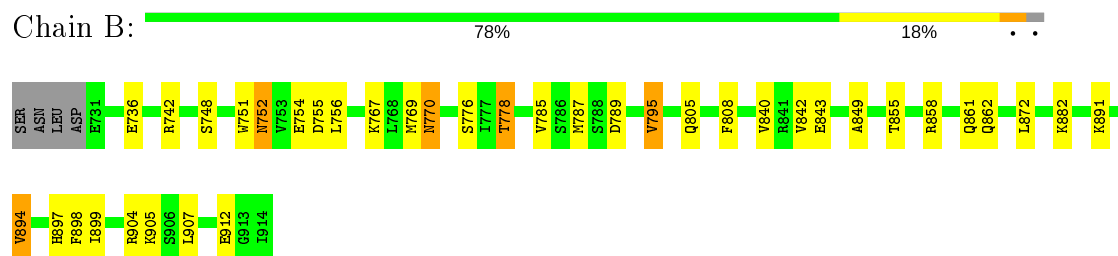


#### • Molecule 1: Complement C3

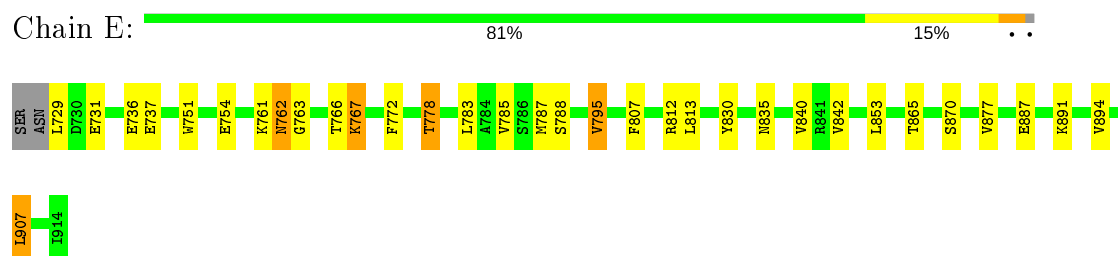




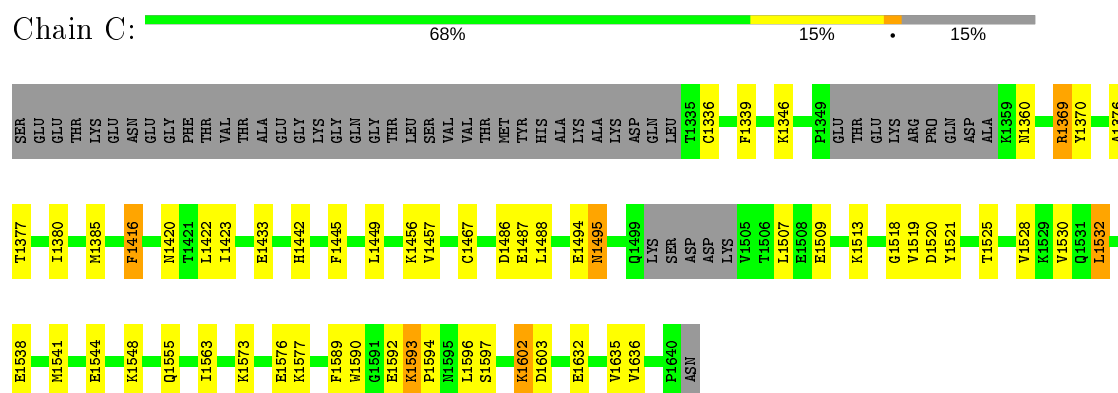
- Molecule 2: Complement C3



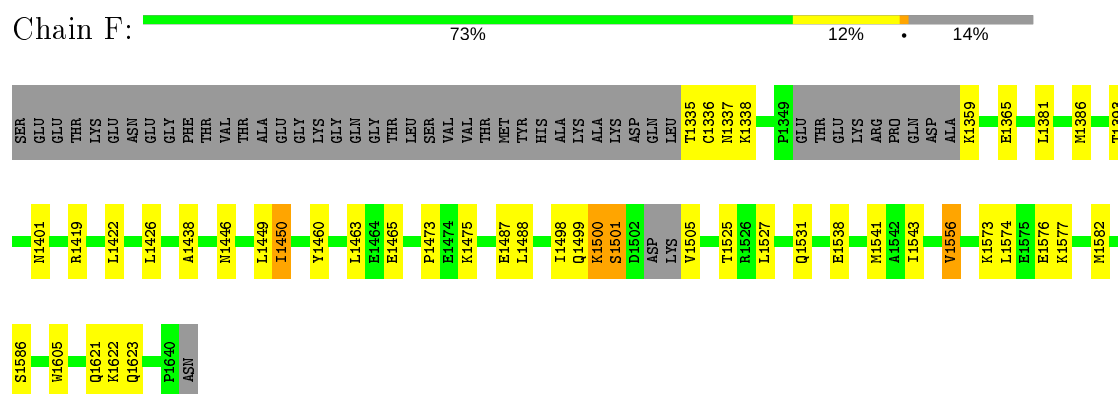
- Molecule 2: Complement C3



- Molecule 3: Complement C3



- Molecule 3: Complement C3



- Molecule 4: compstatin

Chain G:  93% 7%



- Molecule 4: compstatin

Chain H:  47% 40% 13%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  50% 50%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.81Å 124.75Å 127.37Å 90.00° 95.08° 90.00°	Depositor
Resolution (Å)	33.00 – 2.40 32.77 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.3 (33.00-2.40) 96.2 (32.77-2.40)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.22 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.3.0008	Depositor
R, $R_{free}$	0.213 , 0.281 0.268 , 0.293	Depositor DCC
$R_{free}$ test set	5005 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.0	Xtriage
Anisotropy	0.515	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 22.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	18480	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, ACE, K, BR, NH2

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	0.48	1/5009 (0.0%)	0.71	3/6804 (0.0%)
1	D	0.52	0/5017	0.70	3/6817 (0.0%)
2	B	0.47	0/1516	0.63	0/2060
2	E	0.52	0/1532	0.67	0/2082
3	C	0.85	10/2418 (0.4%)	0.63	3/3261 (0.1%)
3	F	0.45	0/2441	0.57	0/3291
4	G	0.39	0/114	0.56	0/156
4	H	0.56	0/114	0.82	0/156
All	All	0.55	11/18161 (0.1%)	0.67	9/24627 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	4
3	C	0	1
All	All	0	5

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1495	ASN	CG-OD1	23.53	1.75	1.24
3	C	1520	ASP	CG-OD2	11.48	1.51	1.25
3	C	1495	ASN	CB-CG	10.92	1.76	1.51
3	C	1602	LYS	CE-NZ	8.22	1.69	1.49
3	C	1518	GLY	C-O	7.93	1.36	1.23

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	504	ILE	C-N-CD	-21.38	73.56	120.60
1	A	504	ILE	C-N-CA	13.21	177.47	122.00
3	C	1495	ASN	CB-CG-ND2	7.48	134.66	116.70
3	C	1520	ASP	CB-CG-OD2	-7.36	111.68	118.30
1	A	574	VAL	CB-CA-C	-6.86	98.38	111.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	1635	VAL	Mainchain
1	D	290	GLN	Peptide
1	D	40	PHE	Peptide
1	D	504	ILE	Peptide
1	D	505	PRO	Peptide

## 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	4912	0	4976	88	0
1	D	4919	0	4986	112	0
2	B	1484	0	1511	22	0
2	E	1500	0	1526	22	0
3	C	2372	0	2280	30	0
3	F	2395	0	2302	23	0
4	G	113	0	98	0	0
4	H	113	0	98	6	0
5	I	28	0	25	1	0
5	J	28	0	25	1	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
6	D	2	0	0	0	0
6	F	1	0	0	0	0
7	A	8	0	0	3	0
7	B	3	0	0	0	0
7	C	1	0	0	0	0
7	D	15	0	0	5	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	3	0	0	0	0
7	F	2	0	0	0	0
8	A	30	0	40	7	0
8	B	6	0	8	1	0
8	C	6	0	8	1	0
8	D	42	0	56	16	0
8	E	12	0	16	5	0
8	F	6	0	8	5	0
8	H	6	0	8	0	0
9	A	111	0	0	1	0
9	B	47	0	0	1	0
9	C	23	0	0	0	0
9	D	188	0	0	4	0
9	E	62	0	0	1	0
9	F	35	0	0	1	0
9	H	5	0	0	0	0
All	All	18480	0	17971	285	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 8.

The worst 5 of 285 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:C:1602:LYS:NZ	3:C:1602:LYS:CE	1.69	1.53
3:C:1495:ASN:CG	3:C:1495:ASN:CB	1.76	1.49
3:C:1495:ASN:CG	3:C:1495:ASN:OD1	1.75	1.24
1:D:139:ARG:HD2	8:D:807:GOL:H31	1.47	0.95
1:D:574:VAL:HG13	2:E:751:TRP:HE3	1.33	0.93

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	623/643 (97%)	583 (94%)	32 (5%)	8 (1%)	12	17
1	D	626/643 (97%)	587 (94%)	24 (4%)	15 (2%)	6	6
2	B	182/188 (97%)	172 (94%)	10 (6%)	0	100	100
2	E	184/188 (98%)	175 (95%)	7 (4%)	2 (1%)	14	20
3	C	286/343 (83%)	262 (92%)	16 (6%)	8 (3%)	5	4
3	F	289/343 (84%)	266 (92%)	17 (6%)	6 (2%)	7	8
4	G	13/15 (87%)	10 (77%)	2 (15%)	1 (8%)	1	0
4	H	13/15 (87%)	10 (77%)	2 (15%)	1 (8%)	1	0
All	All	2216/2378 (93%)	2065 (93%)	110 (5%)	41 (2%)	8	10

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	505	PRO
3	C	1593	LYS
1	D	41	PRO
1	D	78	LYS
1	D	290	GLN

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	555/567 (98%)	504 (91%)	51 (9%)	9	13
1	D	557/567 (98%)	512 (92%)	45 (8%)	11	18
2	B	171/175 (98%)	155 (91%)	16 (9%)	8	13
2	E	173/175 (99%)	159 (92%)	14 (8%)	11	18
3	C	266/309 (86%)	252 (95%)	14 (5%)	22	37
3	F	269/309 (87%)	256 (95%)	13 (5%)	25	41

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	G	11/11 (100%)	11 (100%)	0	100	100
4	H	11/11 (100%)	9 (82%)	2 (18%)	1	2
All	All	2013/2124 (95%)	1858 (92%)	155 (8%)	13	20

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	1420	ASN
1	D	140	THR
3	F	1401	ASN
3	C	1433	GLU
3	C	1532	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	1555	GLN
1	D	318	GLN
3	F	1620	ASN
1	D	155	GLN
1	D	332	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 ⓘ

4 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	$\# Z  > 2$
5	NAG	I	1	1,5	14,14,15	0.54	0	17,19,21	0.94	0
5	NAG	I	2	5	14,14,15	0.60	0	17,19,21	1.65	3 (17%)
5	NAG	J	1	1,5	14,14,15	0.60	0	17,19,21	1.11	2 (11%)
5	NAG	J	2	5	14,14,15	0.70	0	17,19,21	1.51	2 (11%)

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
5	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	2/6/23/26	0/1/1/1
5	NAG	J	1	1,5	1/1/5/7	2/6/23/26	0/1/1/1
5	NAG	J	2	5	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	2	NAG	C1-O5-C5	4.77	118.66	112.19
5	J	2	NAG	C4-C3-C2	4.33	117.36	111.02
5	I	2	NAG	O5-C1-C2	3.62	117.01	111.29
5	J	2	NAG	C3-C4-C5	3.29	116.11	110.24
5	J	1	NAG	O5-C1-C2	-2.76	106.93	111.29

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	J	1	NAG	C1

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	J	2	NAG	O7-C7-N2-C2
5	I	2	NAG	C8-C7-N2-C2
5	I	2	NAG	O7-C7-N2-C2

*Continued on next page...*

*Continued from previous page...*

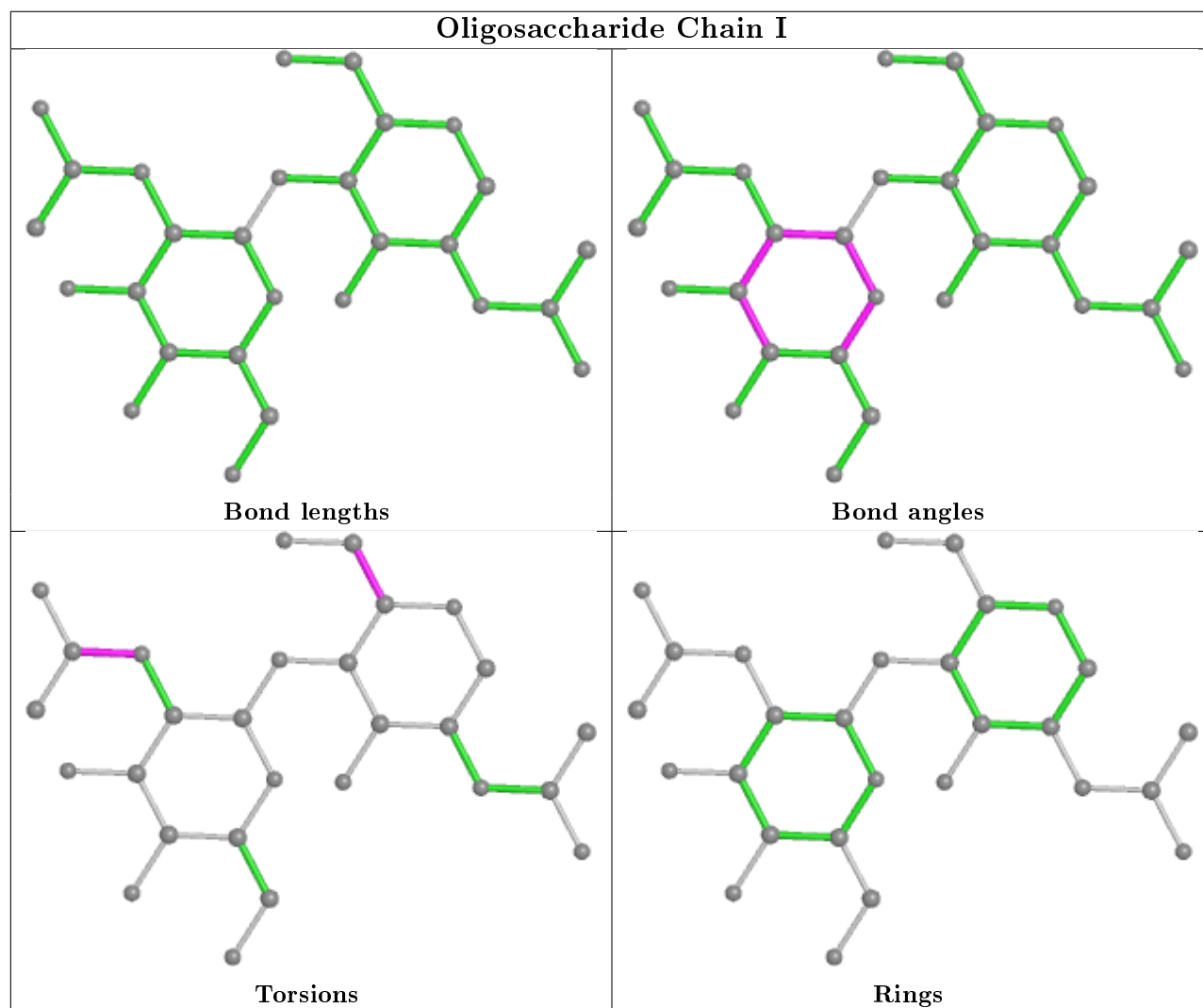
Mol	Chain	Res	Type	Atoms
5	J	2	NAG	C8-C7-N2-C2
5	I	1	NAG	O5-C5-C6-O6

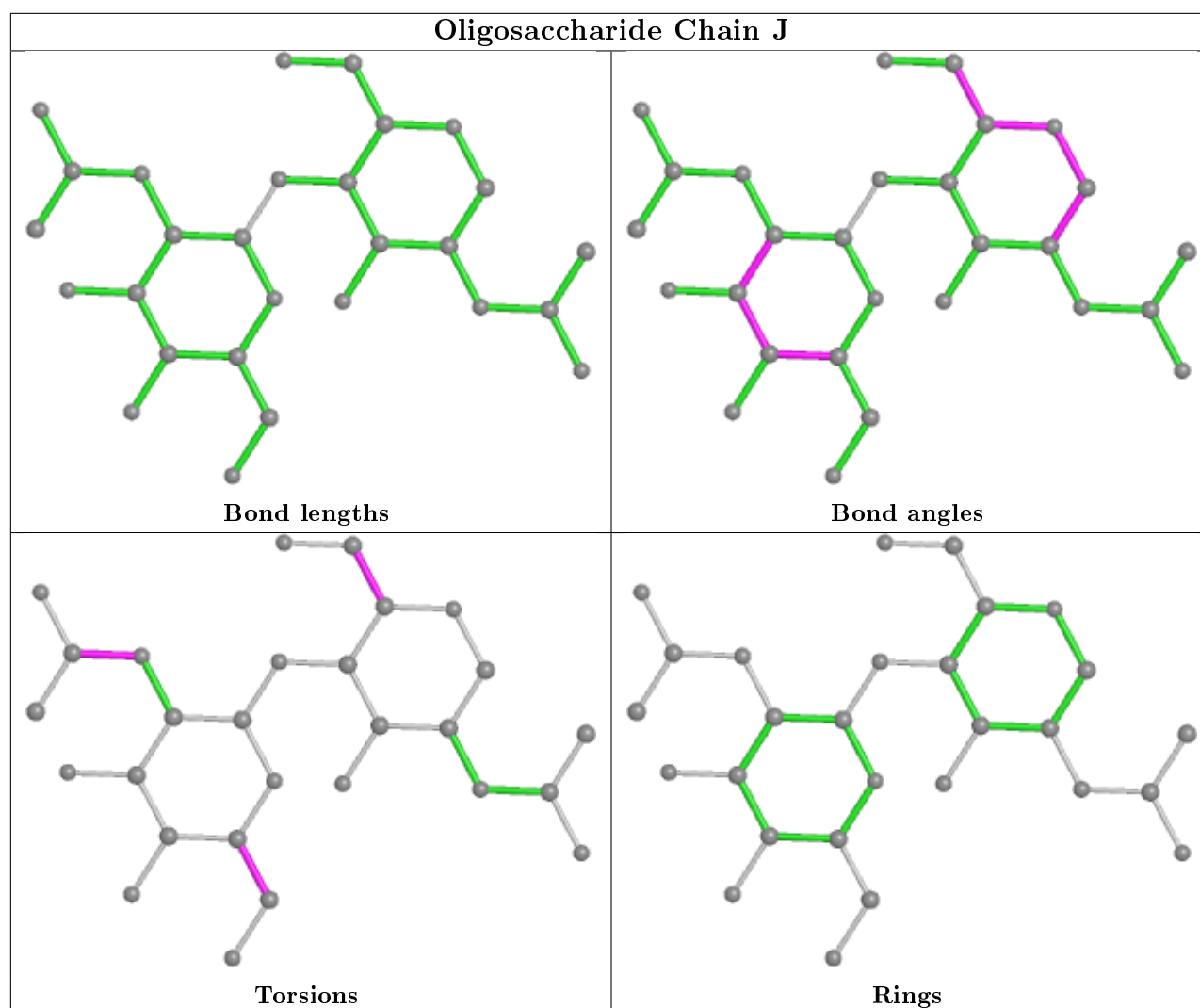
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	1	NAG	1	0
5	J	1	NAG	1	0

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





## 5.6 Ligand geometry [i](#)

Of 55 ligands modelled in this entry, 37 are monoatomic - leaving 18 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	GOL	A	821	-	5,5,5	0.37	0	5,5,5	0.32	0
8	GOL	A	802	-	5,5,5	0.52	0	5,5,5	0.67	0
8	GOL	D	811	-	5,5,5	0.32	0	5,5,5	0.37	0
8	GOL	F	840	-	5,5,5	0.42	0	5,5,5	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	GOL	B	915	-	5,5,5	0.35	0	5,5,5	0.55	0
8	GOL	A	816	-	5,5,5	0.46	0	5,5,5	0.56	0
8	GOL	D	807	-	5,5,5	0.47	0	5,5,5	0.34	0
8	GOL	H	820	-	5,5,5	0.29	0	5,5,5	0.45	0
8	GOL	D	824	-	5,5,5	0.38	0	5,5,5	0.41	0
8	GOL	A	845	-	5,5,5	0.45	0	5,5,5	0.27	0
8	GOL	D	825	-	5,5,5	0.42	0	5,5,5	0.29	0
8	GOL	D	822	-	5,5,5	0.33	0	5,5,5	0.63	0
8	GOL	D	818	-	5,5,5	0.41	0	5,5,5	0.33	0
8	GOL	C	819	-	5,5,5	0.36	0	5,5,5	0.19	0
8	GOL	D	823	-	5,5,5	0.44	0	5,5,5	0.32	0
8	GOL	E	915	-	5,5,5	0.34	0	5,5,5	0.15	0
8	GOL	A	809	-	5,5,5	0.55	0	5,5,5	0.41	0
8	GOL	E	916	-	5,5,5	0.32	0	5,5,5	0.56	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	GOL	A	821	-	-	2/4/4/4	-
8	GOL	A	802	-	-	2/4/4/4	-
8	GOL	D	811	-	-	2/4/4/4	-
8	GOL	F	840	-	-	4/4/4/4	-
8	GOL	B	915	-	-	4/4/4/4	-
8	GOL	A	816	-	-	4/4/4/4	-
8	GOL	D	807	-	-	4/4/4/4	-
8	GOL	H	820	-	-	4/4/4/4	-
8	GOL	D	824	-	-	4/4/4/4	-
8	GOL	A	845	-	-	2/4/4/4	-
8	GOL	D	825	-	-	4/4/4/4	-
8	GOL	D	822	-	-	4/4/4/4	-
8	GOL	D	818	-	-	2/4/4/4	-
8	GOL	C	819	-	-	2/4/4/4	-
8	GOL	D	823	-	-	4/4/4/4	-
8	GOL	E	915	-	-	2/4/4/4	-
8	GOL	A	809	-	-	4/4/4/4	-
8	GOL	E	916	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 56 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	F	840	GOL	O1-C1-C2-C3
8	F	840	GOL	C1-C2-C3-O3
8	D	807	GOL	C1-C2-C3-O3
8	A	845	GOL	O1-C1-C2-C3
8	D	825	GOL	O1-C1-C2-C3

There are no ring outliers.

13 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	802	GOL	1	0
8	D	811	GOL	3	0
8	F	840	GOL	5	0
8	B	915	GOL	1	0
8	D	807	GOL	3	0
8	D	824	GOL	2	0
8	D	825	GOL	2	0
8	D	822	GOL	2	0
8	D	818	GOL	2	0
8	C	819	GOL	1	0
8	D	823	GOL	2	0
8	A	809	GOL	6	0
8	E	916	GOL	5	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

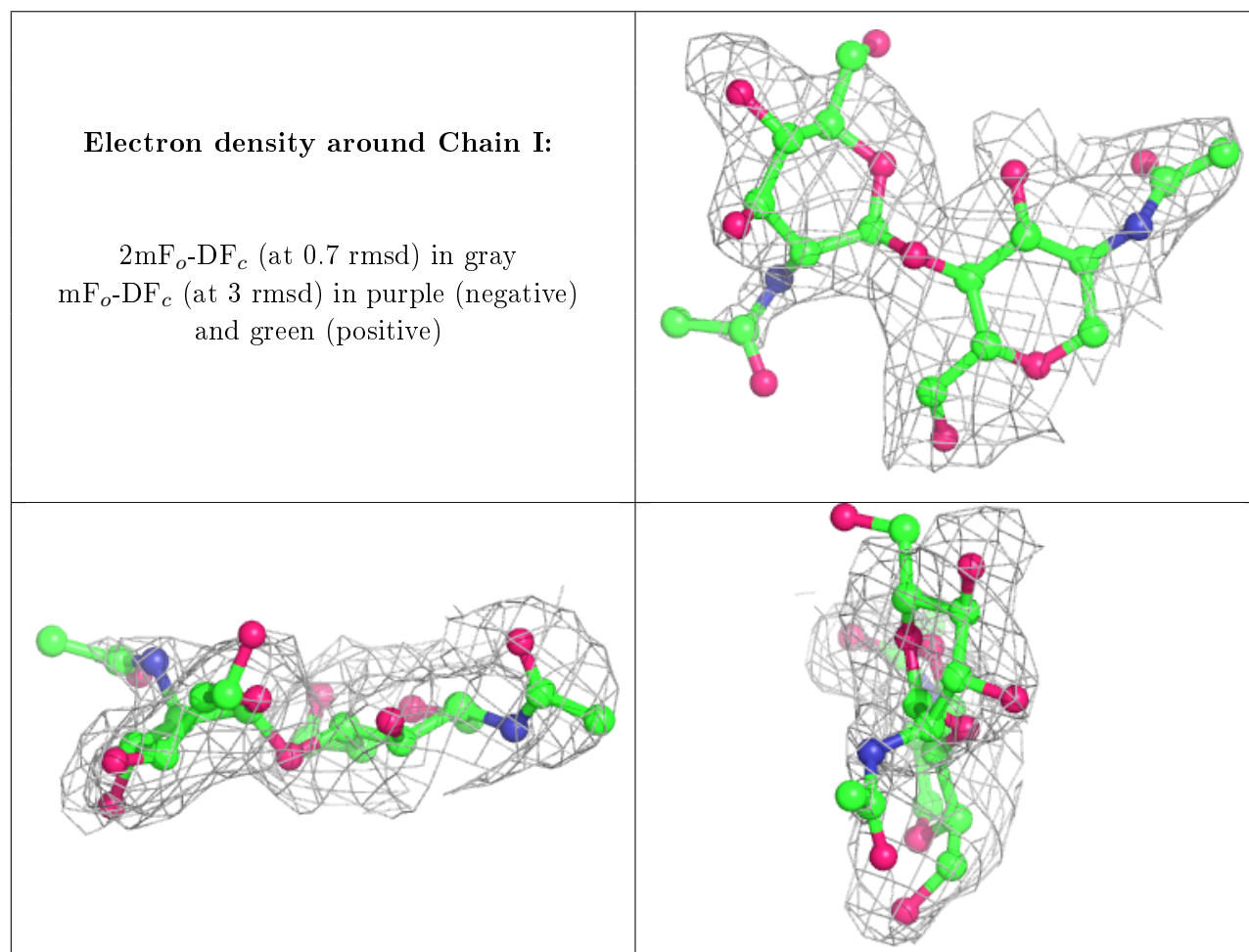
### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

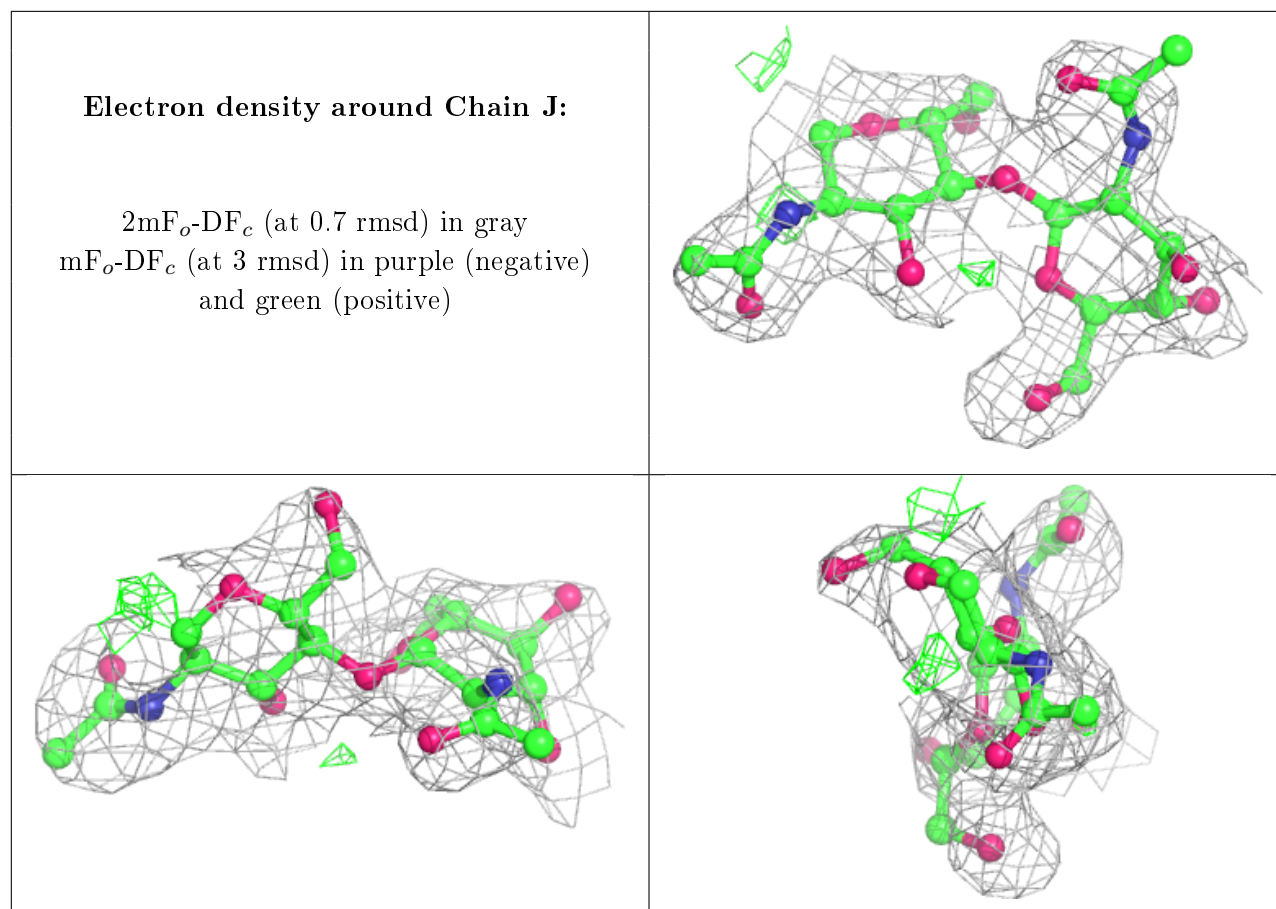
Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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.





## 6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

## 6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.