



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 2, 2021 – 03:16 pm GMT

PDB ID : 6YV3  
Title : Structure of recombinant human beta-glucocerebrosidase in complex with galacto-configured cyclophellitol aziridine inhibitor  
Authors : Rowland, R.J.; Davies, G.J.  
Deposited on : 2020-04-27  
Resolution : 1.80 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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.4 (270009), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

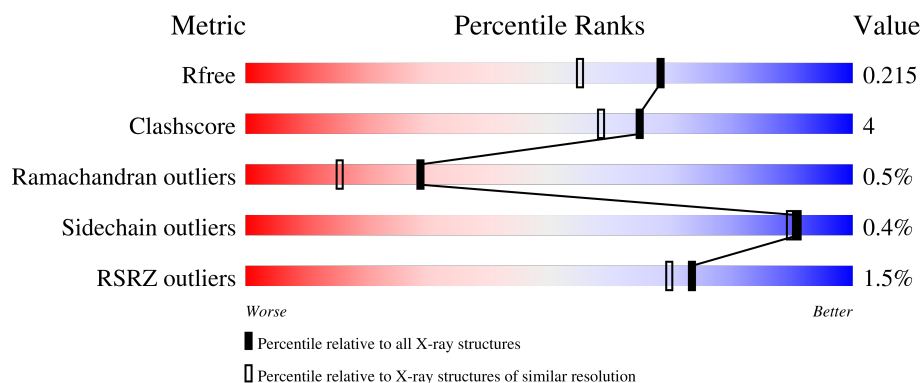
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 of 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	AAA	497	<div> <div>2%</div> <div>93%</div> <div>7%</div> </div>
1	BBB	497	<div> <div>%</div> <div>92%</div> <div>8%</div> </div>
2	A	2	<div> <div>100%</div> </div>
2	B	2	<div> <div>100%</div> </div>

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	NAG	BBB	503	-	-	-	X
3	NAG	BBB	504	-	-	-	X
5	EDO	BBB	523	-	-	X	-
7	GOL	BBB	505	-	-	X	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 17017 atoms, of which 7987 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 Glucosylceramidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	495	Total	C	H	N	O	S	212	9	0
			7830	2539	3877	680	718	16			
1	BBB	496	Total	C	H	N	O	S	206	5	0
			7833	2547	3880	672	717	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	495	HIS	ARG	conflict	UNP P04062
BBB	495	HIS	ARG	conflict	UNP P04062

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



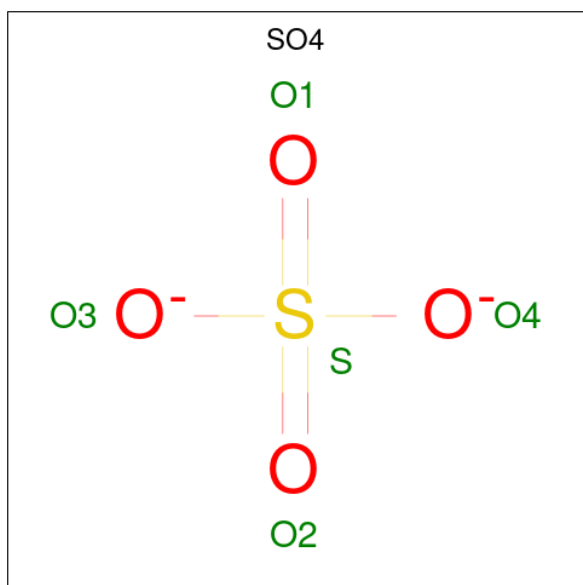
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	2	Total	C	H	N	O	5	0	0
			55	16	27	2	10			
2	B	2	Total	C	H	N	O	5	0	0
			55	16	27	2	10			

- Molecule 3 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
3	AAA	1	Total	C	H	N	O	3	0
			28	8	14	1	5		
3	AAA	1	Total	C	H	N	O	3	0
			28	8	14	1	5		
3	BBB	1	Total	C	H	N	O	3	0
			28	8	14	1	5		
3	BBB	1	Total	C	H	N	O	3	0
			28	8	14	1	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



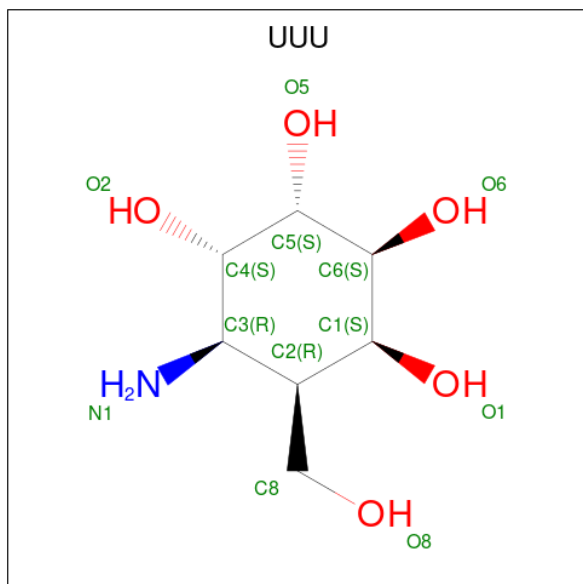
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	AAA	1	Total	O	S	0	0
			5	4	1		
4	AAA	1	Total	O	S	0	0
			5	4	1		
4	AAA	1	Total	O	S	0	0
			5	4	1		
4	AAA	1	Total	O	S	0	0
			5	4	1		
4	AAA	1	Total	O	S	0	0
			5	4	1		
4	AAA	1	Total	O	S	0	0
			5	4	1		
4	BBB	1	Total	O	S	0	0
			5	4	1		
4	BBB	1	Total	O	S	0	0
			5	4	1		
4	BBB	1	Total	O	S	0	0
			5	4	1		
4	BBB	1	Total	O	S	0	0
			5	4	1		
4	BBB	1	Total	O	S	0	0
			5	4	1		
4	BBB	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



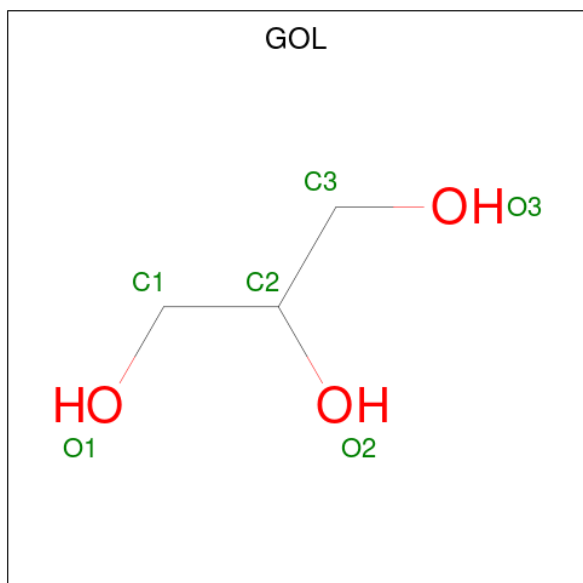
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	AAA	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		
5	BBB	1	Total	C	H	O	1	0
			10	2	6	2		

- Molecule 6 is (1S,2S,3S,4S,5R,6R)-5-amino-6-(hydroxymethyl)cyclohexane-1,2,3,4-tetrol (three-letter code: UUU) (formula:  $C_7H_{15}NO_5$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	AAA	1	Total	C	H	N	O	3	0
			26	7	14	1	4		
6	BBB	1	Total	C	H	N	O	3	0
			26	7	14	1	4		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	BBB	1	Total	C	H	O	2	0
			14	3	8	3		

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	BBB	1	Total	Na	0	0
			1	1		

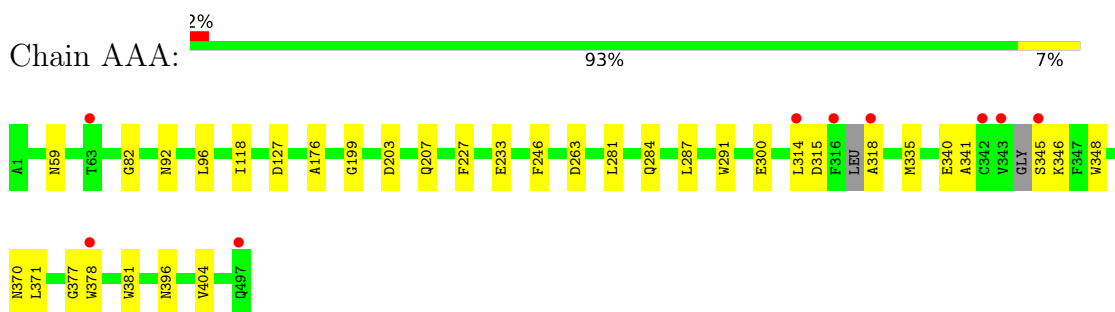
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	AAA	412	Total	O	0	0
			412	412		
9	BBB	443	Total	O	0	0
			443	443		

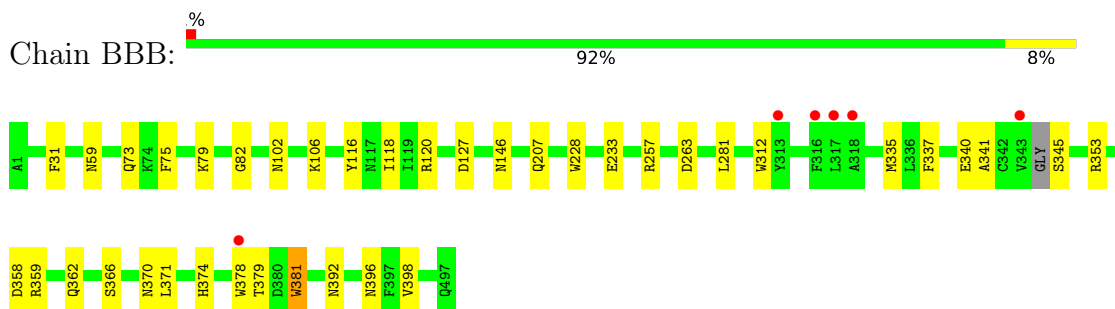
### 3 Residue-property plots [i](#)

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: Glucosylceramidase



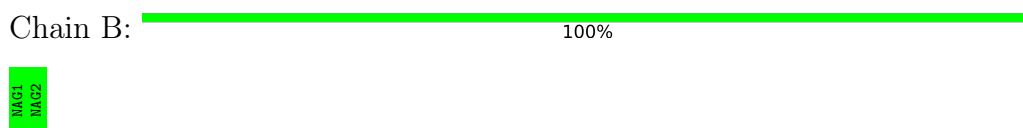
- Molecule 1: Glucosylceramidase



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



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.56Å 285.27Å 91.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.20 – 1.80 72.09 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (72.20-1.80) 99.9 (72.09-1.80)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.95 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.175 , 0.203 0.190 , 0.215	Depositor DCC
$R_{free}$ test set	6677 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	17017	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL, NAG, UUU, NA, EDO

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	AAA	0.69	1/4070 (0.0%)	0.76	0/5549
1	BBB	0.69	1/4073 (0.0%)	0.79	0/5553
All	All	0.69	2/8143 (0.0%)	0.77	0/11102

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	340	GLU	CD-OE2	16.07	1.43	1.25
1	AAA	340	GLU	CD-OE2	14.55	1.41	1.25

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	AAA	3953	3877	3832	27	0
1	BBB	3953	3880	3850	38	0
2	A	28	27	25	0	0
2	B	28	27	25	0	0
3	AAA	28	28	26	0	0
3	BBB	28	28	26	1	0
4	AAA	35	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	BBB	35	0	0	1	0
5	AAA	12	18	18	0	0
5	BBB	44	66	66	7	0
6	AAA	12	14	0	0	0
6	BBB	12	14	0	1	0
7	BBB	6	8	8	4	0
8	BBB	1	0	0	0	0
9	AAA	412	0	0	4	0
9	BBB	443	0	0	2	0
All	All	9030	7987	7876	66	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 4.

The worst 5 of 66 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:BBB:398:VAL:HG11	6:BBB:524:UUU:O8	1.66	0.94
1:BBB:102[A]:ASN:OD1	9:BBB:601:HOH:O	2.00	0.80
1:BBB:312:TRP:CE2	1:BBB:366[B]:SER:OG	2.36	0.78
1:AAA:345:SER:HB3	9:AAA:689:HOH:O	1.87	0.75
1:AAA:207:GLN:NE2	1:AAA:263:ASP:OD1	2.18	0.73

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	AAA	498/497 (100%)	481 (97%)	15 (3%)	2 (0%)	34	21
1	BBB	497/497 (100%)	478 (96%)	16 (3%)	3 (1%)	25	12
All	All	995/994 (100%)	959 (96%)	31 (3%)	5 (0%)	29	15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	233	GLU
1	BBB	281	LEU
1	AAA	233	GLU
1	AAA	281	LEU
1	BBB	381	TRP

### 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	AAA	423/424 (100%)	422 (100%)	1 (0%)	93	92
1	BBB	426/424 (100%)	424 (100%)	2 (0%)	88	87
All	All	849/848 (100%)	846 (100%)	3 (0%)	91	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	335	MET
1	BBB	59	ASN
1	BBB	335	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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.

There are no bond length outliers.

There are no bond angle outliers.

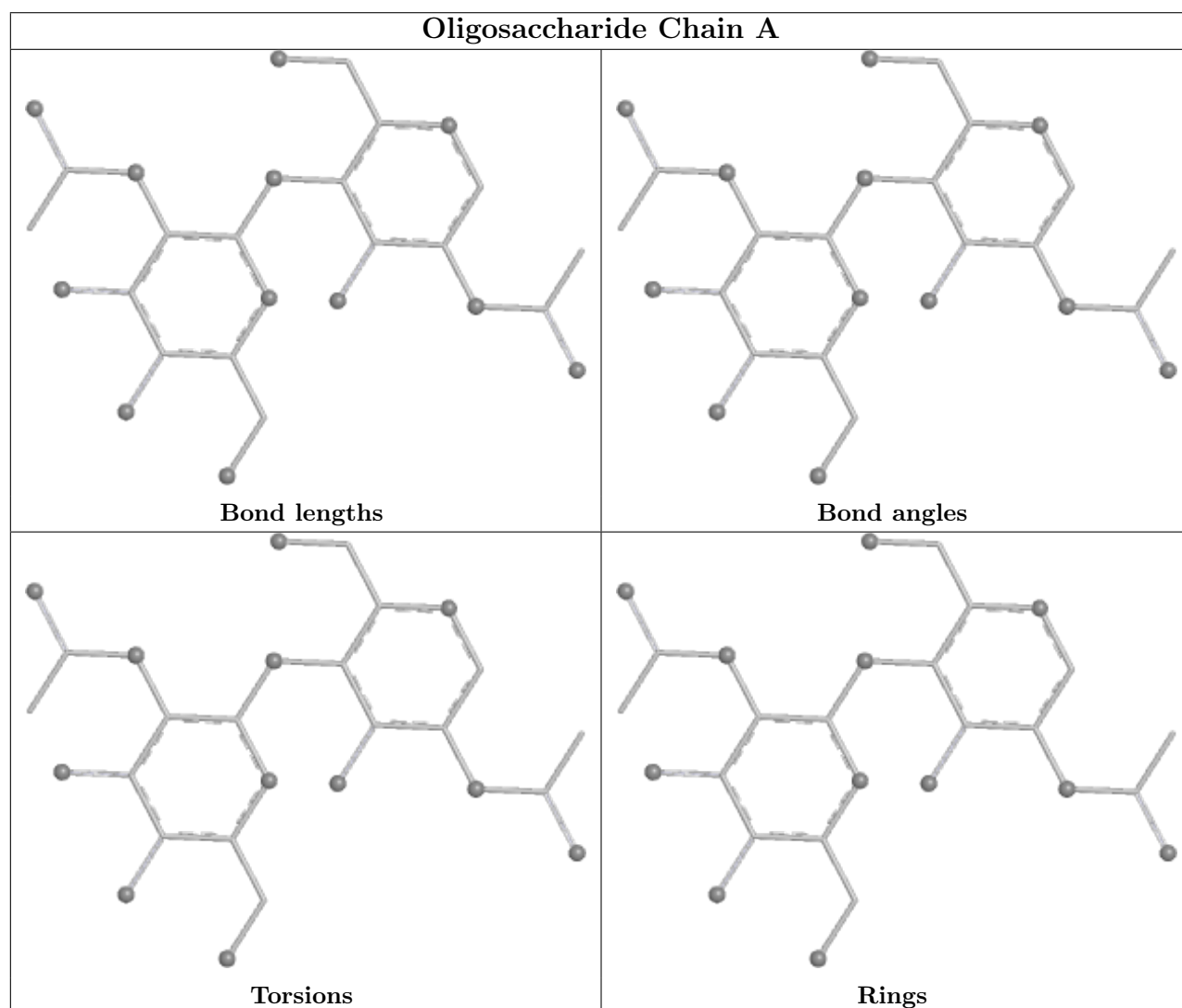
There are no chirality outliers.

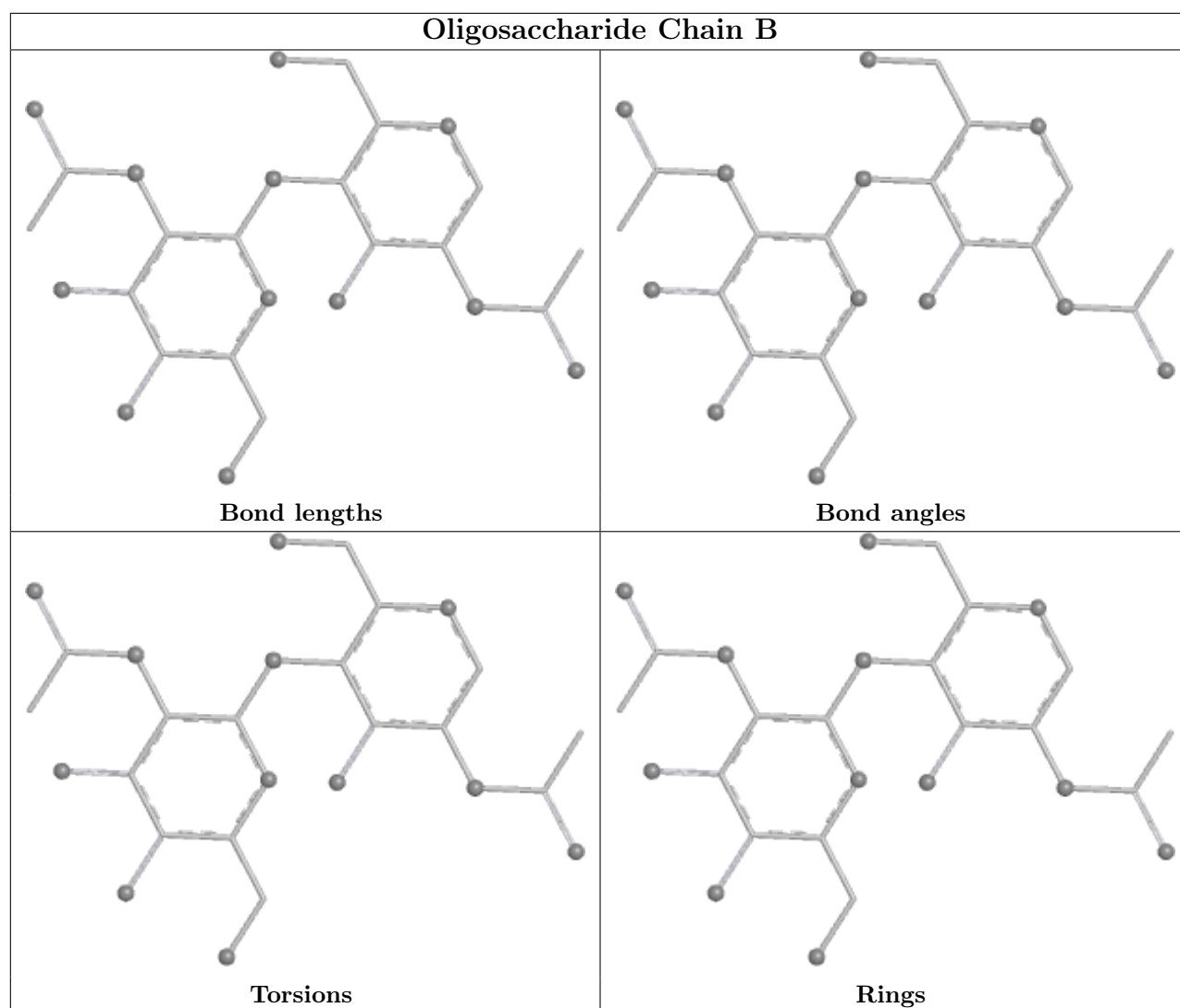
There are no torsion outliers.

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 36 ligands modelled in this entry, 1 is monoatomic - leaving 35 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

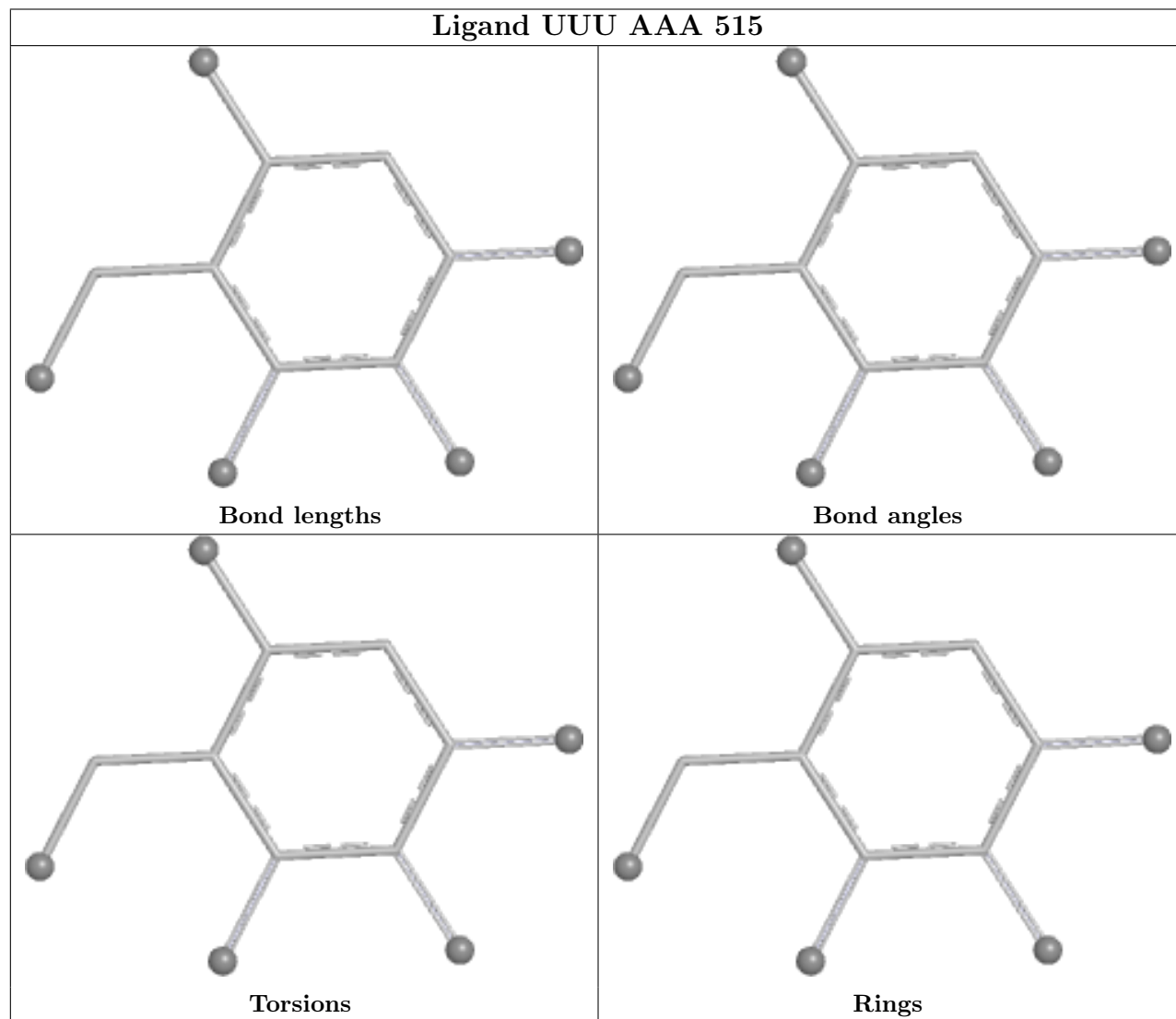
There are no torsion outliers.

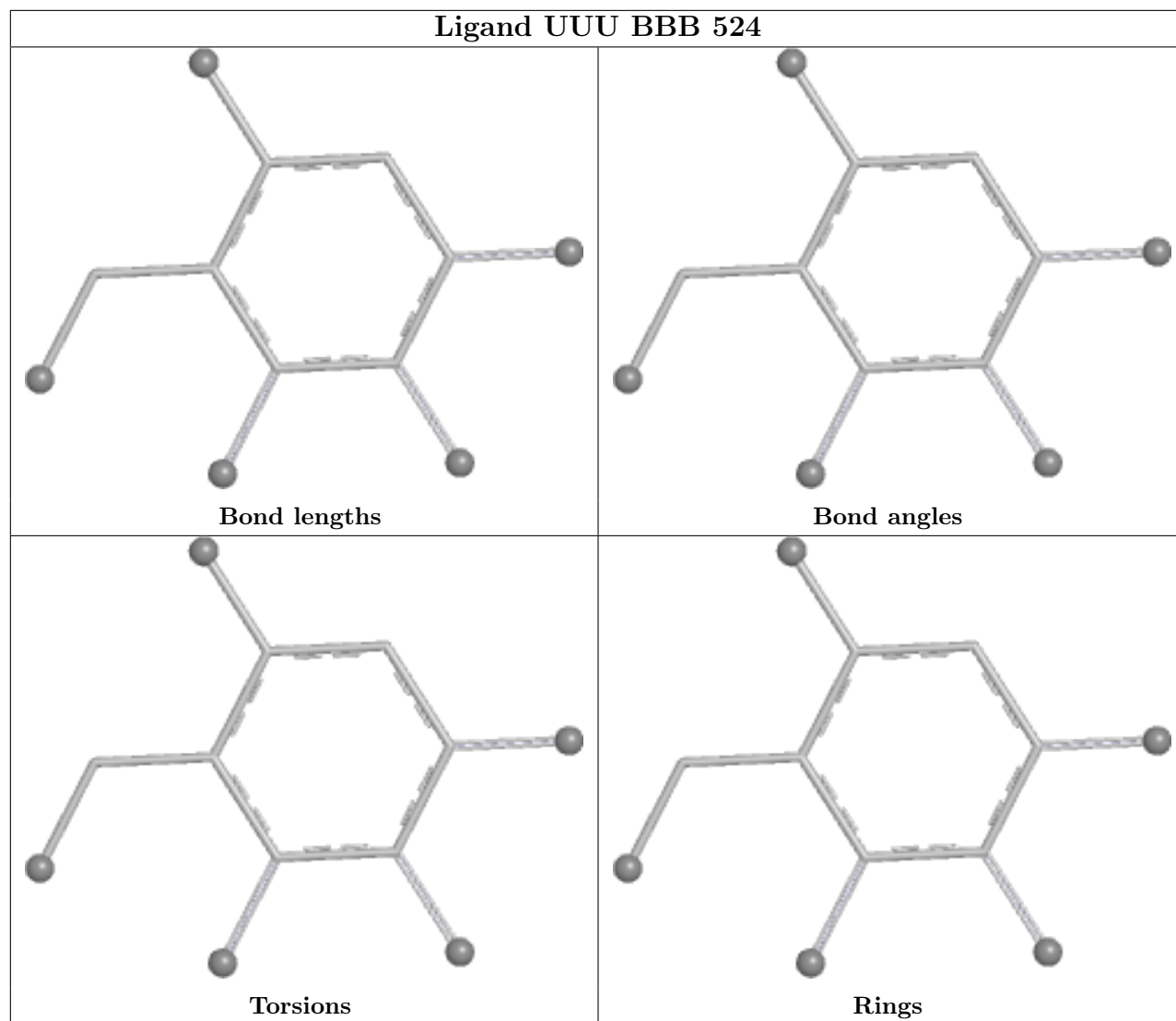
There are no ring outliers.

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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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, 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	AAA	495/497 (99%)	-0.21	9 (1%) 68 64	19, 27, 50, 100	3 (0%)
1	BBB	496/497 (99%)	-0.33	6 (1%) 79 76	17, 25, 46, 85	7 (1%)
All	All	991/994 (99%)	-0.27	15 (1%) 73 70	17, 26, 49, 100	10 (1%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	318	ALA	8.0
1	AAA	342	CYS	3.7
1	BBB	316	PHE	3.7
1	BBB	317	LEU	3.4
1	BBB	343	VAL	2.9

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

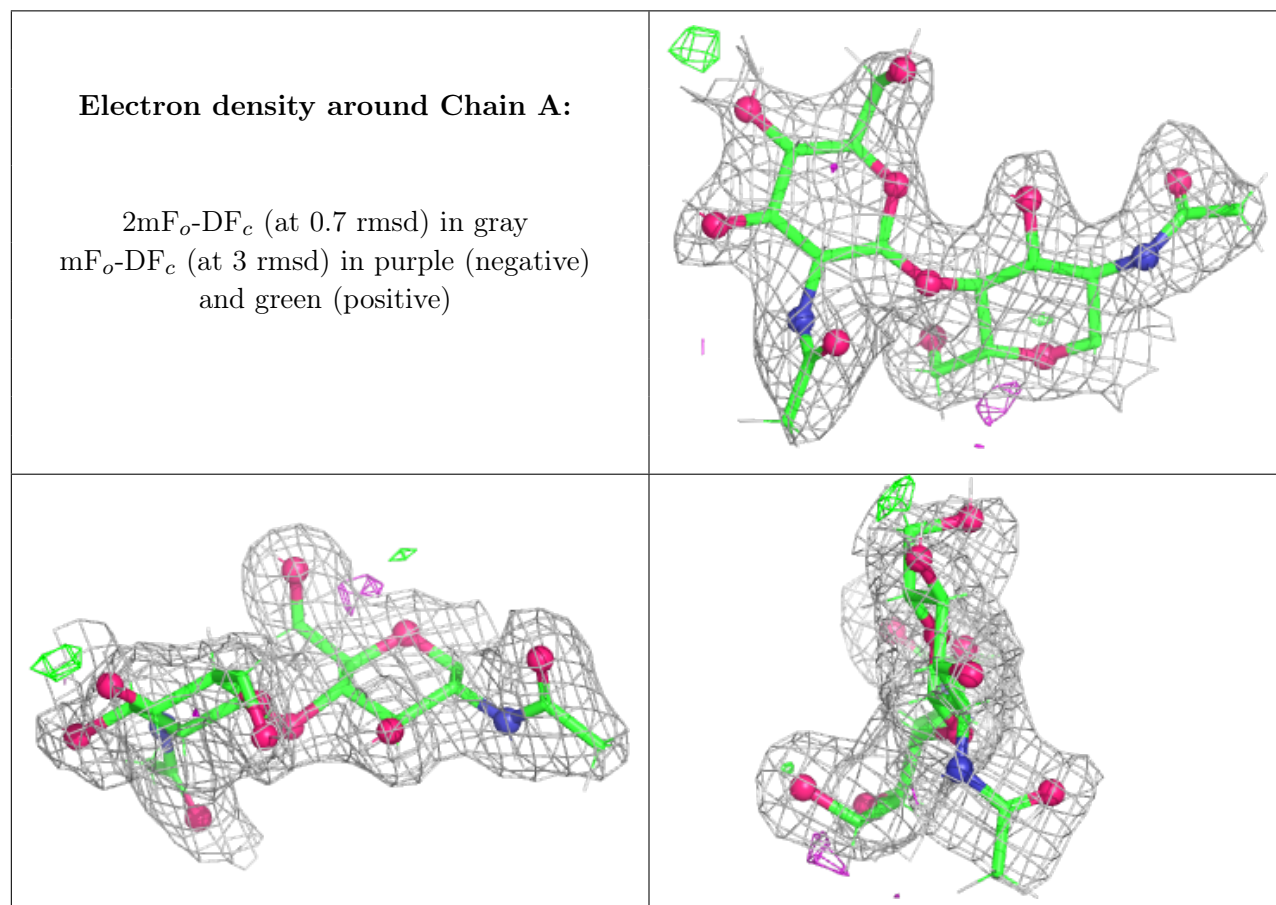
There are no non-standard protein/DNA/RNA residues in this entry.

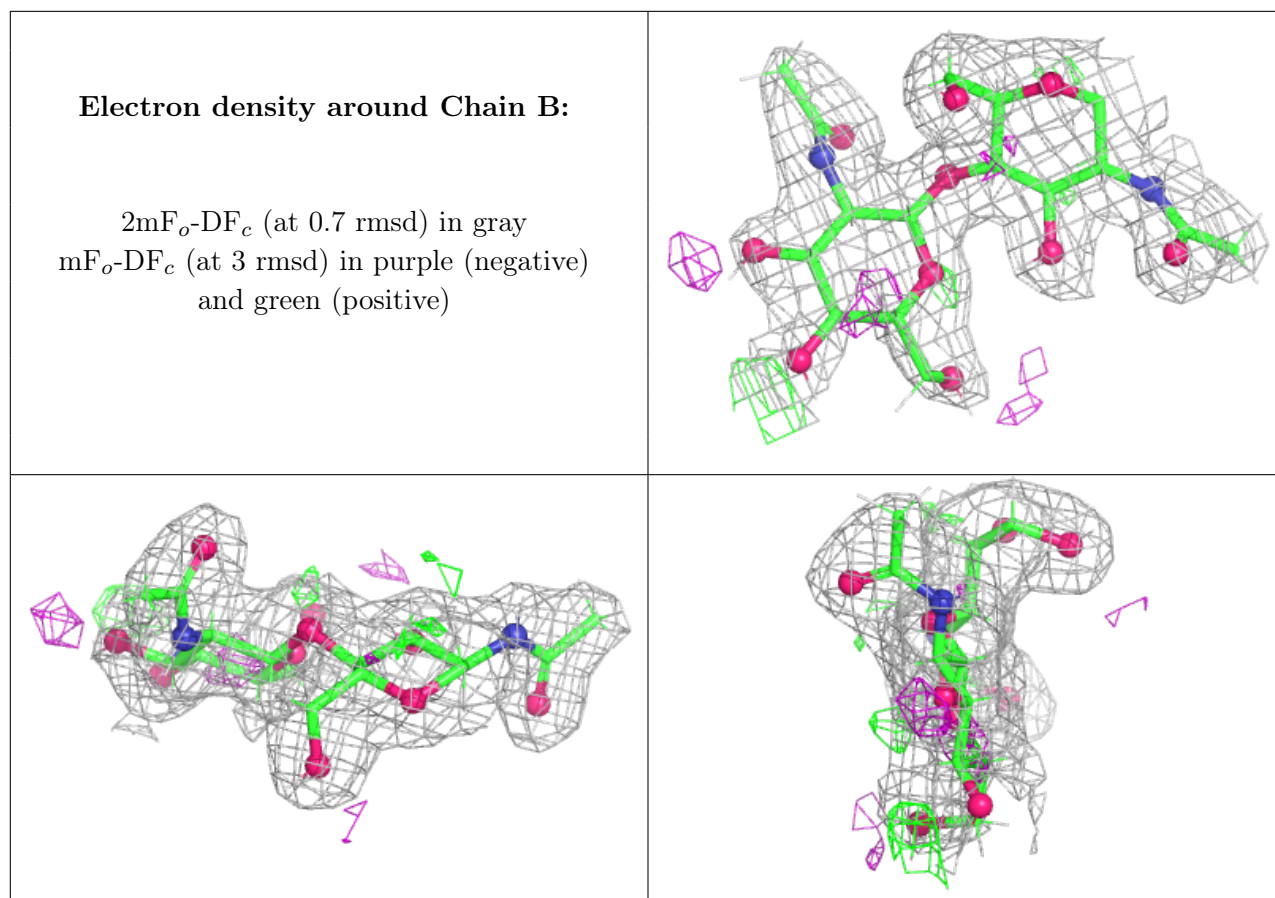
### 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
2	NAG	A	2	14/15	0.84	0.15	47,56,62,63	3
2	NAG	B	2	14/15	0.86	0.14	44,59,71,75	3
2	NAG	B	1	14/15	0.90	0.10	32,37,40,44	2
2	NAG	A	1	14/15	0.93	0.07	31,36,38,43	2

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](#)

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	NAG	BBB	503	14/15	0.58	0.41	93,103,108,112	3
5	EDO	AAA	513	4/4	0.70	0.17	59,60,61,61	1
5	EDO	BBB	518	4/4	0.72	0.22	43,49,50,51	1
3	NAG	BBB	504	14/15	0.73	0.43	80,94,99,101	3
3	NAG	AAA	504	14/15	0.74	0.17	50,55,63,67	3
5	EDO	BBB	514	4/4	0.75	0.17	50,52,53,53	1
5	EDO	AAA	512	4/4	0.76	0.20	37,45,47,48	1
5	EDO	BBB	515	4/4	0.77	0.14	44,47,48,50	1
4	SO4	AAA	511	5/5	0.78	0.35	85,89,97,103	0
5	EDO	BBB	516	4/4	0.79	0.34	53,54,57,57	1
5	EDO	BBB	513	4/4	0.79	0.14	51,52,53,54	1
7	GOL	BBB	505	6/6	0.79	0.22	42,50,52,52	2
5	EDO	BBB	519	4/4	0.84	0.13	65,68,71,72	1

*Continued on next page...*

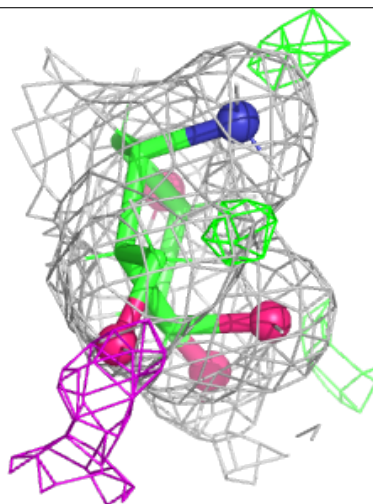
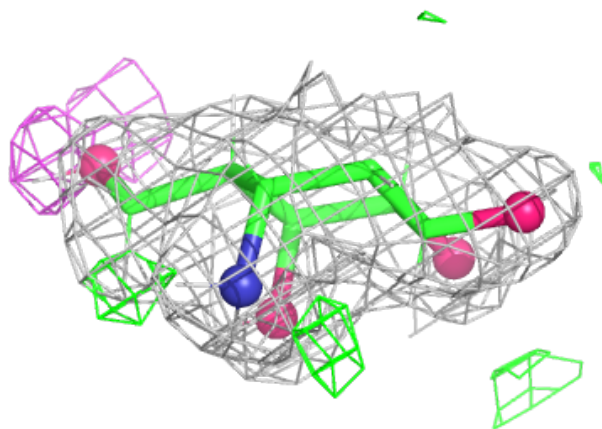
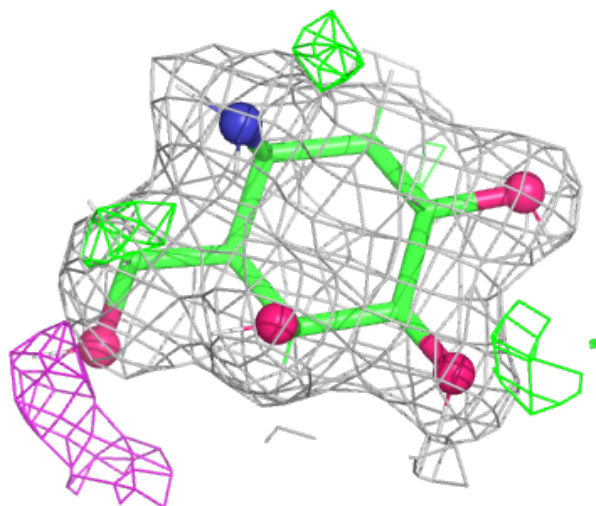
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	AAA	503	14/15	0.85	0.21	72,85,90,93	3
4	SO4	AAA	510	5/5	0.85	0.14	85,85,92,101	0
5	EDO	BBB	521	4/4	0.87	0.12	42,50,56,59	1
5	EDO	BBB	520	4/4	0.87	0.14	62,62,63,63	1
4	SO4	BBB	510	5/5	0.88	0.19	80,81,86,88	0
4	SO4	BBB	512	5/5	0.88	0.15	79,83,86,87	0
5	EDO	AAA	514	4/4	0.88	0.10	36,44,50,52	1
5	EDO	BBB	523	4/4	0.90	0.27	46,49,57,59	1
6	UUU	AAA	515	12/13	0.92	0.11	32,34,39,48	3
5	EDO	BBB	517	4/4	0.92	0.12	48,48,51,51	1
4	SO4	BBB	511	5/5	0.93	0.12	63,63,71,74	0
4	SO4	AAA	507	5/5	0.93	0.14	68,73,78,81	0
5	EDO	BBB	522	4/4	0.93	0.15	46,48,58,58	1
6	UUU	BBB	524	12/13	0.94	0.10	26,29,35,43	3
4	SO4	AAA	506	5/5	0.95	0.15	52,54,58,62	0
4	SO4	AAA	509	5/5	0.95	0.12	48,57,64,66	0
4	SO4	BBB	508	5/5	0.95	0.12	52,56,60,61	0
4	SO4	BBB	509	5/5	0.95	0.15	53,55,67,70	0
4	SO4	AAA	508	5/5	0.96	0.07	53,54,56,60	0
4	SO4	BBB	506	5/5	0.98	0.13	52,53,57,60	0
4	SO4	AAA	505	5/5	0.99	0.11	33,36,37,39	0
4	SO4	BBB	507	5/5	0.99	0.07	30,31,35,36	0
8	NA	BBB	525	1/1	0.99	0.19	23,23,23,23	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

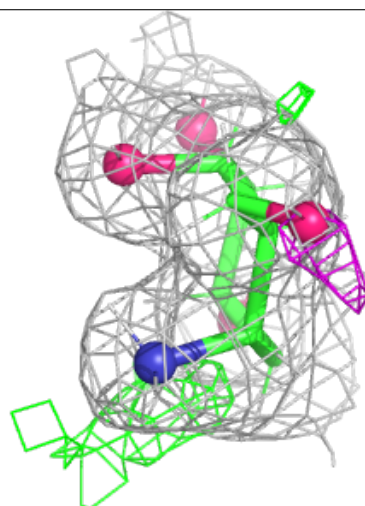
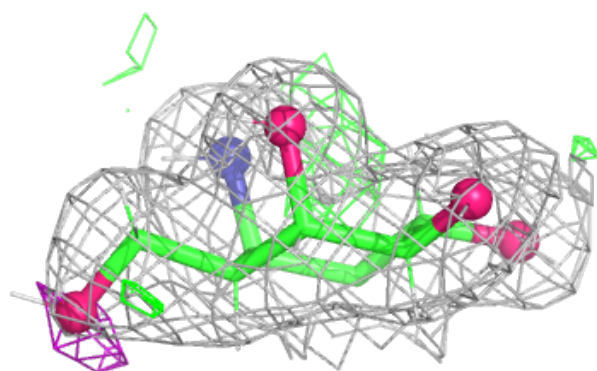
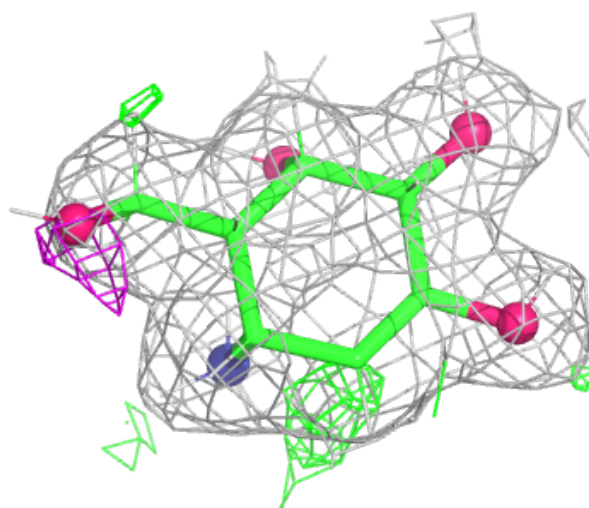
**Electron density around UUU AAA 515:**

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



**Electron density around UUU BBB 524:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.