



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 09:51 AM BST

PDB ID : 2HR7  
Title : Insulin receptor (domains 1-3)  
Authors : Garrett, T.P.J.; Ward, C.W.  
Deposited on : 2006-07-19  
Resolution : 2.32 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

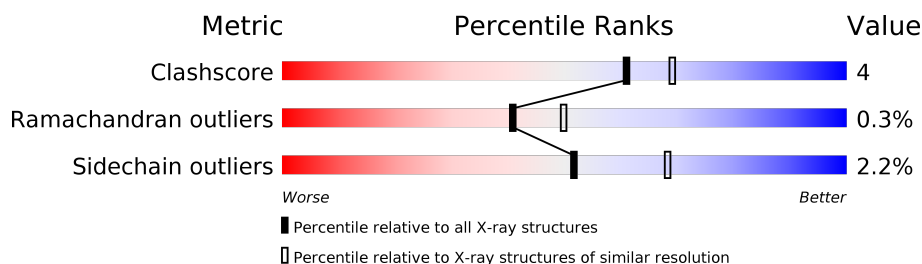
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.32 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))
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)



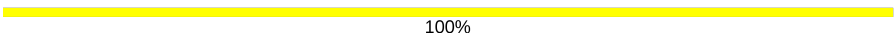


The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	486	85% 10% .
1	B	486	82% 12% . .
2	C	2	100%
3	D	6	17% 83%
3	I	6	17% 83%
4	E	3	100%
5	F	4	50% 50%
5	K	4	50% 50%

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Mol	Chain	Length	Quality of chain
6	G	3	 67%33%
6	H	3	 67%33%
6	L	3	 100%
6	M	3	 67%33%
7	J	7	 29%57%14%

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
11	GOL	B	588	-	X	-	-
8	NAG	A	501	X	-	-	-

## 2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 8665 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 Insulin receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	466	Total	C	N	O	S	3	12	1
			3747	2348	670	687	42			
1	B	465	Total	C	N	O	S	0	22	1
			3770	2365	669	693	43			

There are 6 discrepancies between the modelled and reference sequences:

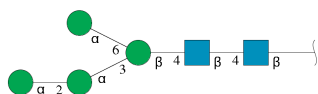
Chain	Residue	Modelled	Actual	Comment	Reference
A	144	HIS	TYR	variant	UNP P06213
A	421	ILE	THR	variant	UNP P06213
A	486	SER	-	cloning artifact	UNP P06213
B	144	HIS	TYR	variant	UNP P06213
B	421	ILE	THR	variant	UNP P06213
B	486	SER	-	cloning artifact	UNP P06213

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

- 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.



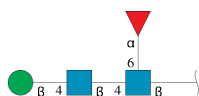
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	6	Total	C	N	O	0	0	0
			72	40	2	30			
3	I	6	Total	C	N	O	0	0	0
			72	40	2	30			

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



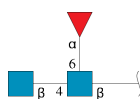
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



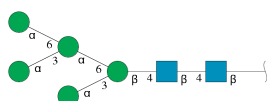
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	F	4	Total	C	N	O	0	0	0
			49	28	2	19			
5	K	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



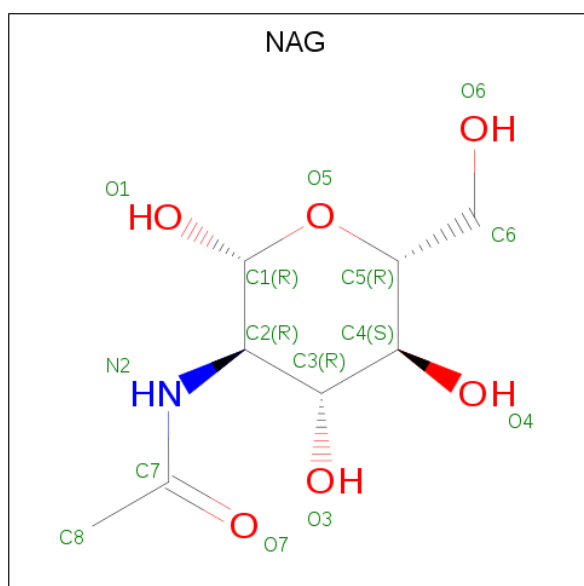
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	G	3	Total	C	N	O	0	0	0
			38	22	2	14			
6	H	3	Total	C	N	O	0	0	0
			38	22	2	14			
6	L	3	Total	C	N	O	0	0	0
			38	22	2	14			
6	M	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



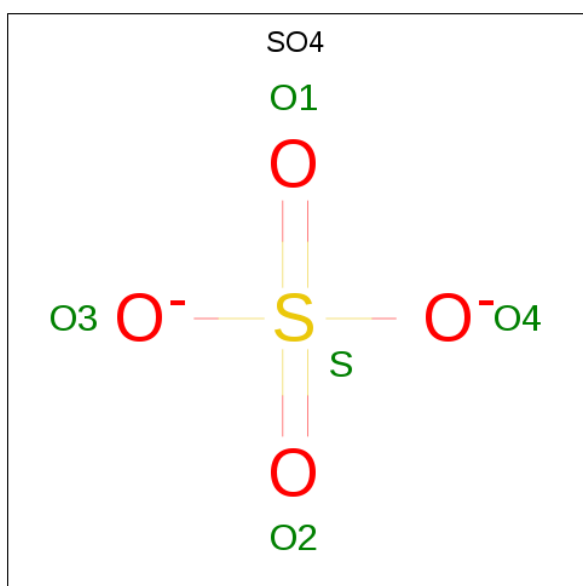
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	J	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



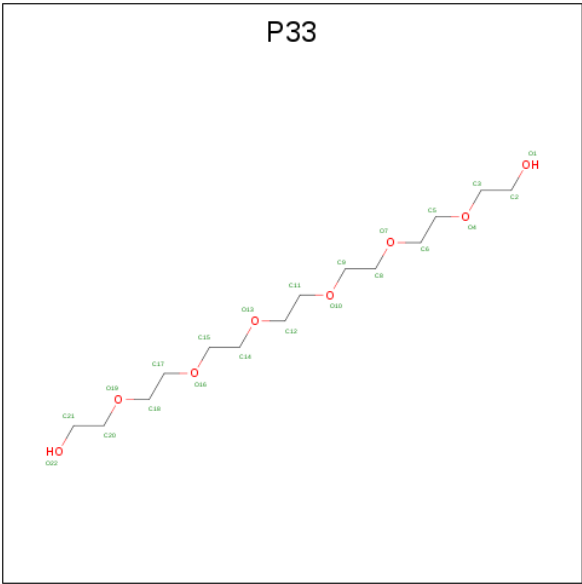
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



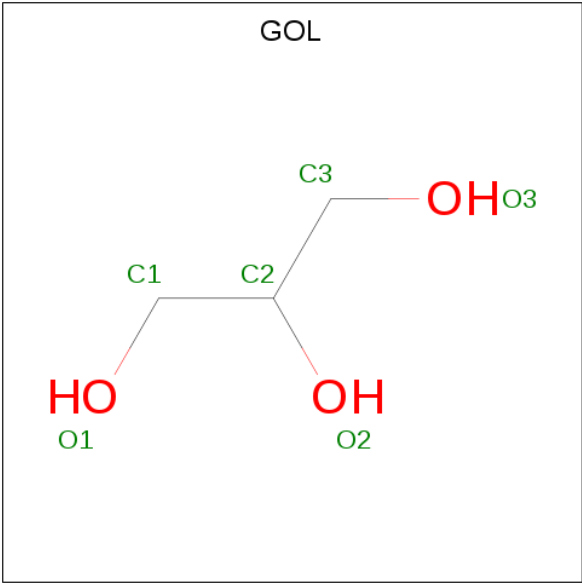
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	A	1	Total	O	S	0	0
			5	4	1		
9	B	1	Total	O	S	0	0
			5	4	1		
9	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 10 is 3,6,9,12,15,18-HEXAOSAICOSANE-1,20-DIOL (three-letter code: P33) (formula: C<sub>14</sub>H<sub>30</sub>O<sub>8</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			22	14	8		

- Molecule 11 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	192	Total	O	0	0
			192	192		

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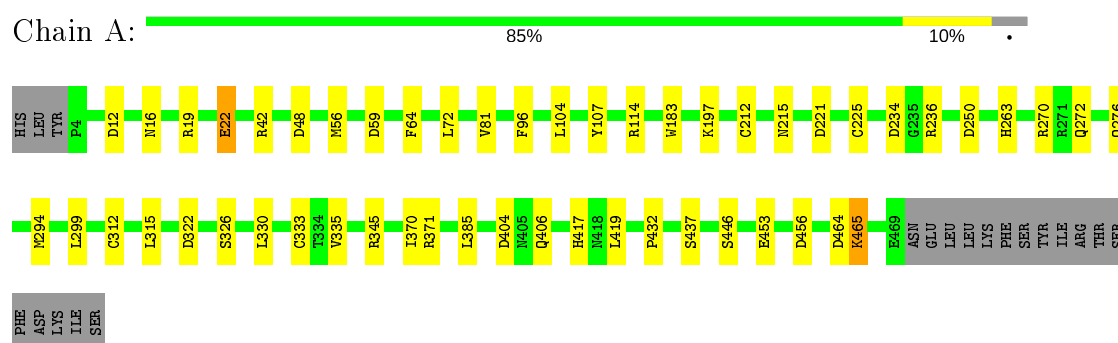
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	B	179	Total 180	O 180	0	1

### 3 Residue-property plots

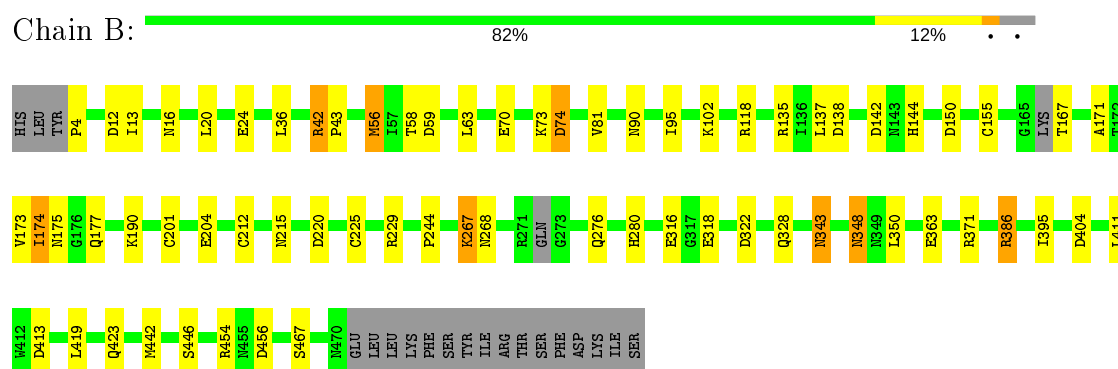
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

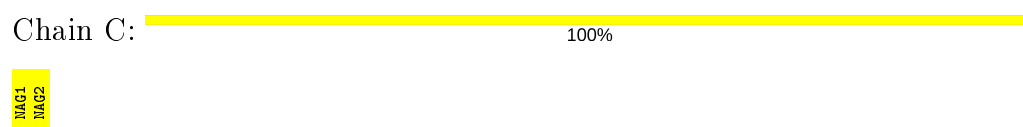
- Molecule 1: Insulin receptor



- Molecule 1: Insulin receptor



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



- 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 D:  17% 83%



- 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:  17% 83%



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

Chain E:  100%



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  50% 50%



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  50% 50%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  67% 33%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  67% 33%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:

100%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

67%

33%



- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:

29%

57%

14%



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.86Å 130.24Å 160.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.32	Depositor
% Data completeness (in resolution range)	100.0 (40.00-2.32)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC 5.2.0003	Depositor
R, $R_{free}$	0.195 , 0.231	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8665	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, BMA, NAG, FUC, P33, MAN, SO4

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	0.92	1/3875 (0.0%)	0.89	14/5236 (0.3%)
1	B	0.88	2/3913 (0.1%)	0.94	17/5288 (0.3%)
All	All	0.90	3/7788 (0.0%)	0.92	31/10524 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	270	ARG	CD-NE	-28.27	0.98	1.46
1	B	42	ARG	NE-CZ	16.32	1.54	1.33
1	B	42	ARG	CD-NE	6.33	1.57	1.46

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	42	ARG	CD-NE-CZ	-7.82	112.65	123.60
1	B	142	ASP	CB-CG-OD2	7.78	125.30	118.30
1	B	150	ASP	CB-CG-OD2	7.62	125.16	118.30
1	B	322	ASP	CB-CG-OD2	7.48	125.03	118.30
1	B	12	ASP	CB-CG-OD2	7.34	124.91	118.30

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	3747	0	3655	24	0
1	B	3770	0	3640	46	0
2	C	28	0	25	0	0
3	D	72	0	61	0	0
3	I	72	0	61	0	0
4	E	39	0	34	0	0
5	F	49	0	43	2	0
5	K	49	0	43	0	0
6	G	38	0	34	0	0
6	H	38	0	34	0	0
6	L	38	0	34	0	0
6	M	38	0	34	3	0
7	J	83	0	70	2	0
8	A	28	0	26	0	0
8	B	28	0	26	0	0
9	A	30	0	0	1	0
9	B	10	0	0	0	0
10	A	22	0	29	0	0
11	A	78	0	104	3	0
11	B	36	0	48	4	0
12	A	192	0	0	3	0
12	B	180	0	0	8	0
All	All	8665	0	8001	72	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 72 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:B:411:LEU:HD13	1:B:442:MET:CE	1.73	1.17
1:B:348[B]:ASN:HD21	1:B:350[B]:LEU:HD23	1.07	1.16
1:B:411:LEU:HD13	1:B:442:MET:HE3	1.35	1.05
1:B:348[B]:ASN:ND2	1:B:350[B]:LEU:HD23	1.76	0.99
5:F:2:NAG:O3	5:F:3:BMA:H2	1.71	0.89

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	A	476/486 (98%)	455 (96%)	20 (4%)	1 (0%)	47	58
1	B	481/486 (99%)	458 (95%)	21 (4%)	2 (0%)	34	41
All	All	957/972 (98%)	913 (95%)	41 (4%)	3 (0%)	41	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	268	ASN
1	A	272	GLN
1	B	174	ILE

### 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	431/441 (98%)	426 (99%)	5 (1%)	71	83
1	B	431/441 (98%)	414 (96%)	17 (4%)	32	45
All	All	862/882 (98%)	840 (97%)	22 (3%)	52	62

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	177	GLN
1	B	229	ARG
1	B	386[B]	ARG

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Mol	Chain	Res	Type
1	B	204[A]	GLU
1	B	204[B]	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	HIS
1	A	281	ASN
1	A	328	GLN
1	B	34	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 ⓘ

44 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	$\# Z  > 2$
2	NAG	C	1	1,2	14,14,15	0.57	0	17,19,21	1.38	2 (11%)
2	NAG	C	2	2	14,14,15	0.47	0	17,19,21	0.99	1 (5%)
3	NAG	D	1	1,3	14,14,15	0.78	0	17,19,21	1.67	3 (17%)
3	NAG	D	2	3	14,14,15	0.75	0	17,19,21	1.31	4 (23%)
3	BMA	D	3	3	11,11,12	0.77	0	15,15,17	1.00	0
3	MAN	D	4	3	11,11,12	0.68	0	15,15,17	1.42	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	MAN	D	5	3	11,11,12	0.59	0	15,15,17	1.19	1 (6%)
3	MAN	D	6	3	11,11,12	0.78	0	15,15,17	1.53	3 (20%)
4	NAG	E	1	1,4	14,14,15	0.93	1 (7%)	17,19,21	2.27	5 (29%)
4	NAG	E	2	4	14,14,15	0.77	0	17,19,21	1.36	3 (17%)
4	BMA	E	3	4	11,11,12	0.77	0	15,15,17	1.51	2 (13%)
5	NAG	F	1	1,5	14,14,15	0.86	1 (7%)	17,19,21	1.41	1 (5%)
5	NAG	F	2	5	14,14,15	0.97	1 (7%)	17,19,21	2.41	7 (41%)
5	BMA	F	3	5	11,11,12	0.68	0	15,15,17	2.15	4 (26%)
5	FUC	F	4	5	10,10,11	0.88	0	14,14,16	1.16	1 (7%)
6	NAG	G	1	1,6	14,14,15	0.54	0	17,19,21	1.52	4 (23%)
6	NAG	G	2	6	14,14,15	0.64	0	17,19,21	0.86	0
6	FUC	G	3	6	10,10,11	0.61	0	14,14,16	0.86	0
6	NAG	H	1	1,6	14,14,15	0.57	0	17,19,21	1.31	2 (11%)
6	NAG	H	2	6	14,14,15	0.57	0	17,19,21	0.88	0
6	FUC	H	3	6	10,10,11	0.72	0	14,14,16	0.90	0
3	NAG	I	1	1,3	14,14,15	0.83	0	17,19,21	1.91	5 (29%)
3	NAG	I	2	3	14,14,15	0.68	0	17,19,21	1.76	5 (29%)
3	BMA	I	3	3	11,11,12	0.69	0	15,15,17	1.30	1 (6%)
3	MAN	I	4	3	11,11,12	0.66	0	15,15,17	1.35	2 (13%)
3	MAN	I	5	3	11,11,12	0.45	0	15,15,17	1.37	1 (6%)
3	MAN	I	6	3	11,11,12	0.56	0	15,15,17	0.82	0
7	NAG	J	1	1,7	14,14,15	1.08	1 (7%)	17,19,21	1.43	2 (11%)
7	NAG	J	2	7	14,14,15	0.81	1 (7%)	17,19,21	1.36	3 (17%)
7	BMA	J	3	7	11,11,12	0.74	0	15,15,17	1.01	0
7	MAN	J	4	7	11,11,12	0.80	0	15,15,17	1.55	4 (26%)
7	MAN	J	5	7	11,11,12	0.65	0	15,15,17	0.81	0
7	MAN	J	6	7	11,11,12	0.67	0	15,15,17	1.28	1 (6%)
7	MAN	J	7	7	11,11,12	0.63	0	15,15,17	1.33	1 (6%)
5	NAG	K	1	1,5	14,14,15	0.72	0	17,19,21	0.94	0
5	NAG	K	2	5	14,14,15	0.52	0	17,19,21	1.08	0
5	BMA	K	3	5	11,11,12	0.81	0	15,15,17	1.40	2 (13%)
5	FUC	K	4	5	10,10,11	0.54	0	14,14,16	1.00	1 (7%)
6	NAG	L	1	1,6	14,14,15	0.79	1 (7%)	17,19,21	1.16	1 (5%)
6	NAG	L	2	6	14,14,15	0.59	0	17,19,21	1.60	4 (23%)
6	FUC	L	3	6	10,10,11	1.08	0	14,14,16	2.06	6 (42%)
6	NAG	M	1	1,6	14,14,15	0.56	0	17,19,21	1.14	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	NAG	M	2	6	14,14,15	0.69	0	17,19,21	1.55	3 (17%)
6	FUC	M	3	6	10,10,11	0.90	0	14,14,16	1.42	4 (28%)

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
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	MAN	D	4	3	-	0/2/19/22	0/1/1/1
3	MAN	D	5	3	-	1/2/19/22	0/1/1/1
3	MAN	D	6	3	-	0/2/19/22	0/1/1/1
4	NAG	E	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	BMA	E	3	4	-	2/2/19/22	0/1/1/1
5	NAG	F	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	F	2	5	-	0/6/23/26	0/1/1/1
5	BMA	F	3	5	-	2/2/19/22	0/1/1/1
5	FUC	F	4	5	-	-	0/1/1/1
6	NAG	G	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	G	2	6	-	2/6/23/26	0/1/1/1
6	FUC	G	3	6	-	-	0/1/1/1
6	NAG	H	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	H	2	6	-	2/6/23/26	0/1/1/1
6	FUC	H	3	6	-	-	0/1/1/1
3	NAG	I	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
3	BMA	I	3	3	-	2/2/19/22	0/1/1/1
3	MAN	I	4	3	-	0/2/19/22	0/1/1/1
3	MAN	I	5	3	-	1/2/19/22	0/1/1/1
3	MAN	I	6	3	-	0/2/19/22	0/1/1/1
7	NAG	J	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	2/6/23/26	0/1/1/1
7	BMA	J	3	7	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	J	4	7	-	2/2/19/22	0/1/1/1
7	MAN	J	5	7	-	2/2/19/22	0/1/1/1
7	MAN	J	6	7	-	0/2/19/22	0/1/1/1
7	MAN	J	7	7	-	2/2/19/22	0/1/1/1
5	NAG	K	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	K	2	5	-	0/6/23/26	0/1/1/1
5	BMA	K	3	5	-	2/2/19/22	0/1/1/1
5	FUC	K	4	5	-	-	0/1/1/1
6	NAG	L	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	L	2	6	-	5/6/23/26	0/1/1/1
6	FUC	L	3	6	-	-	0/1/1/1
6	NAG	M	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	M	2	6	-	2/6/23/26	0/1/1/1
6	FUC	M	3	6	-	-	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	1	NAG	O5-C5	-2.62	1.38	1.43
7	J	1	NAG	O5-C1	-2.56	1.39	1.43
5	F	2	NAG	O5-C1	-2.36	1.40	1.43
7	J	2	NAG	O5-C1	-2.35	1.40	1.43
6	L	1	NAG	C1-C2	2.32	1.55	1.52

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	2	NAG	O4-C4-C3	6.78	126.02	110.35
5	F	3	BMA	C1-O5-C5	5.82	120.08	112.19
4	E	1	NAG	O5-C1-C2	-5.12	103.20	111.29
7	J	1	NAG	C1-C2-N2	-4.58	102.66	110.49
3	I	5	MAN	C1-O5-C5	4.44	118.21	112.19

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	G	1	NAG	C8-C7-N2-C2
6	G	1	NAG	O7-C7-N2-C2
6	H	1	NAG	C8-C7-N2-C2

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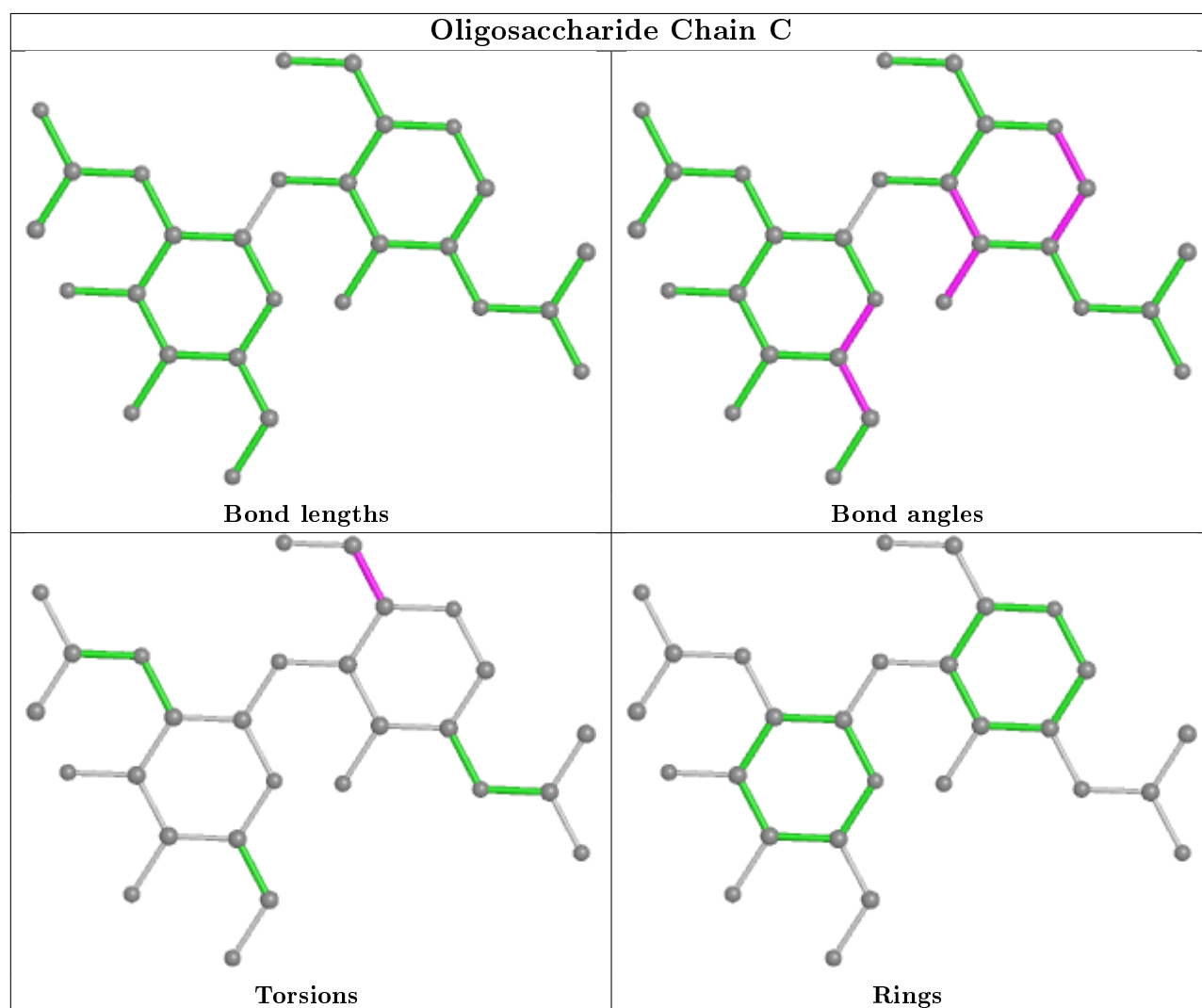
Mol	Chain	Res	Type	Atoms
6	H	1	NAG	O7-C7-N2-C2
5	F	3	BMA	O5-C5-C6-O6

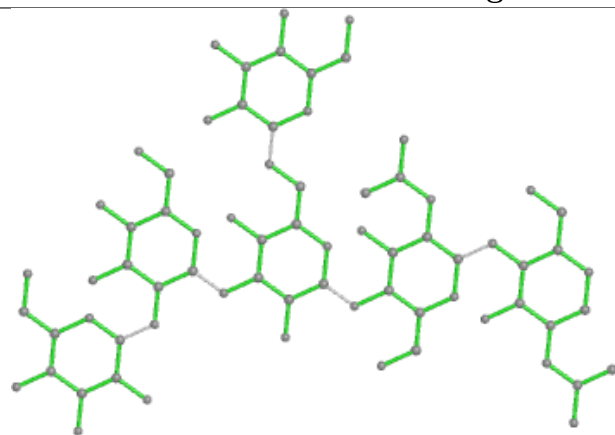
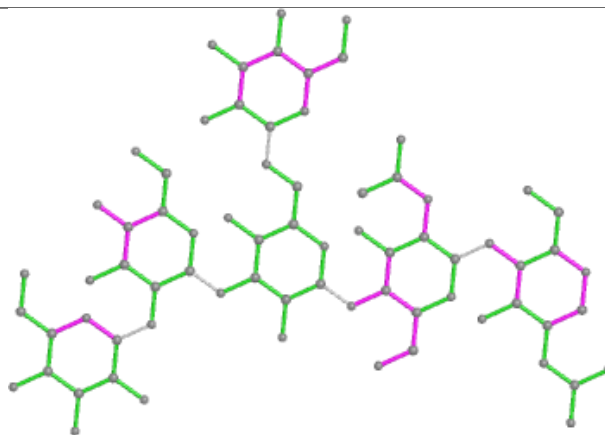
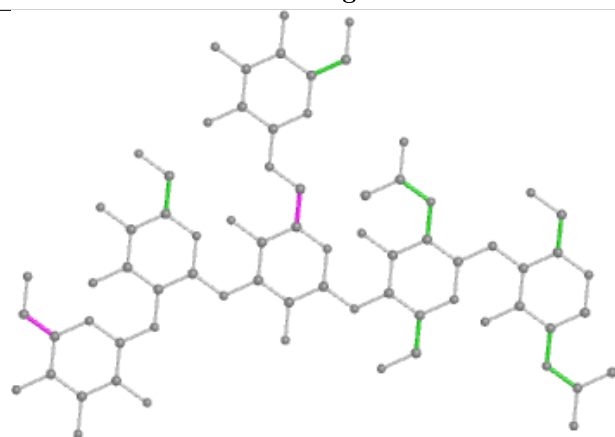
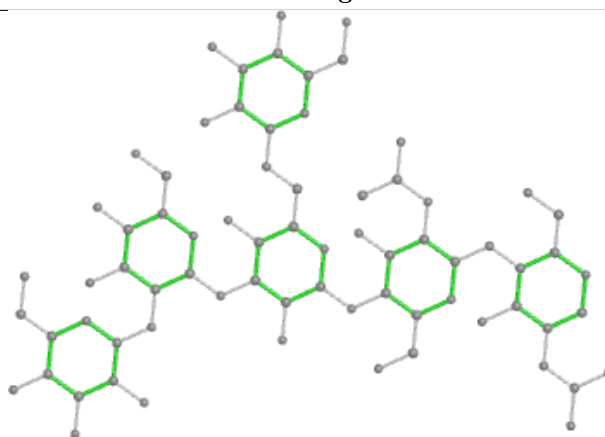
There are no ring outliers.

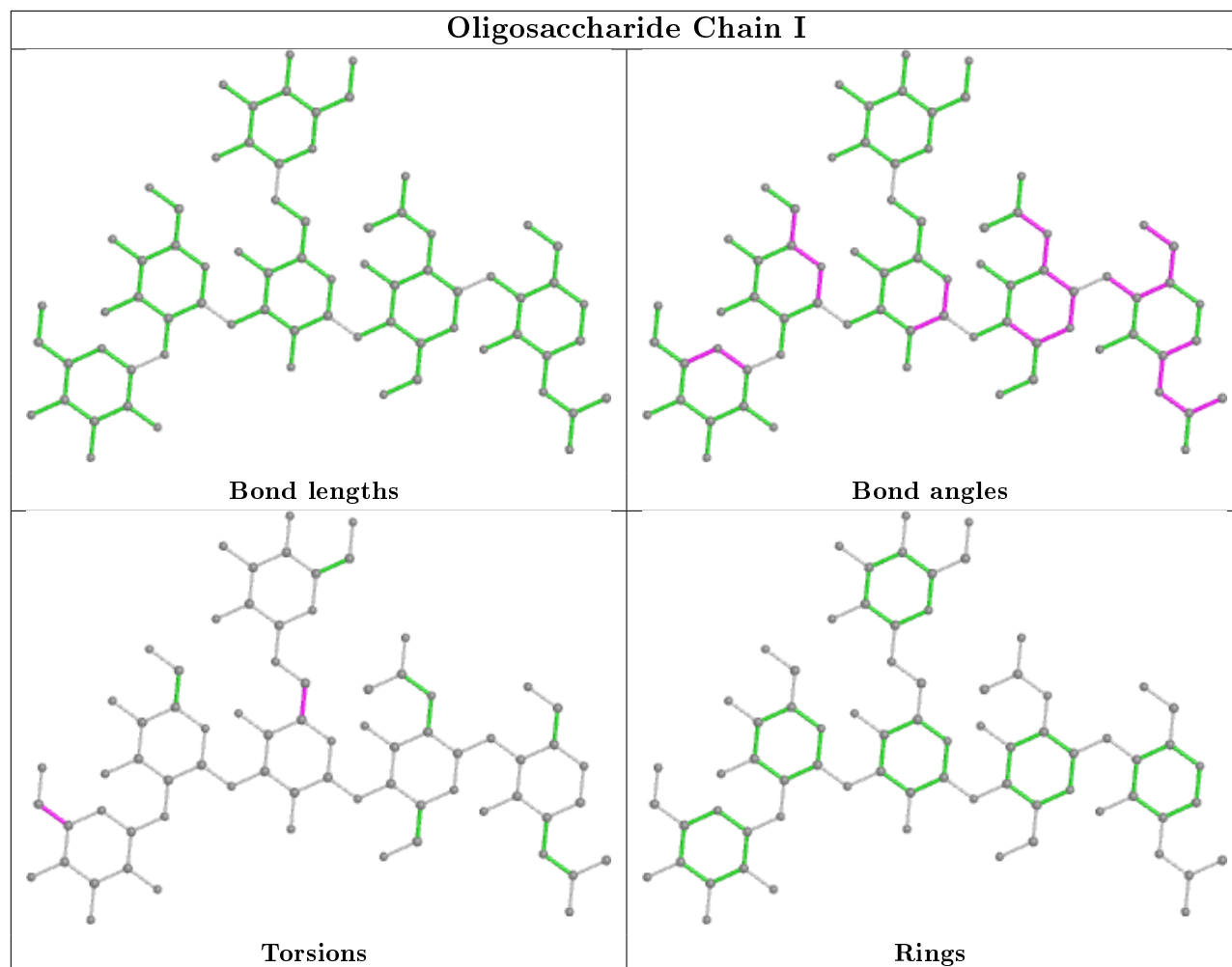
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	2	NAG	2	0
7	J	1	NAG	2	0
6	M	3	FUC	3	0
5	F	3	BMA	2	0

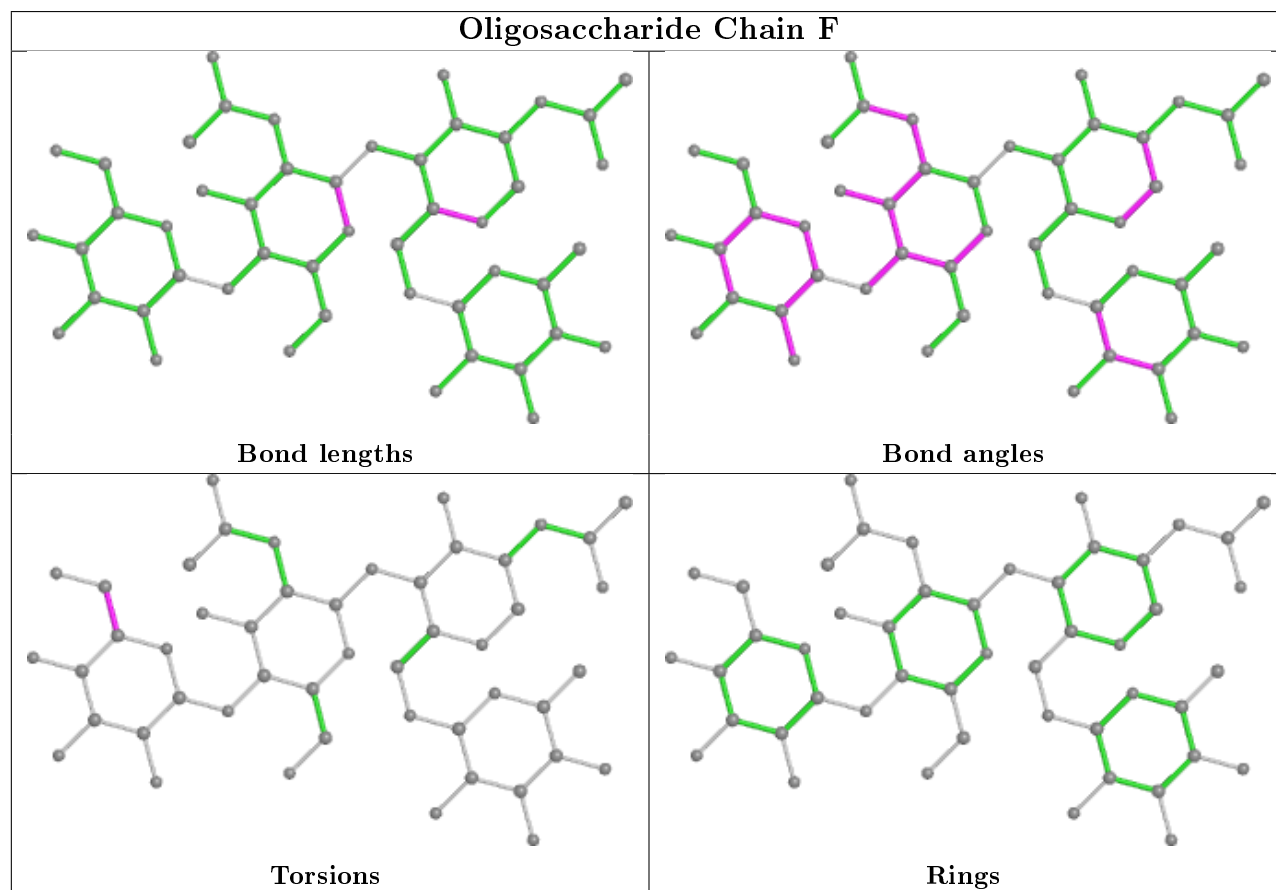
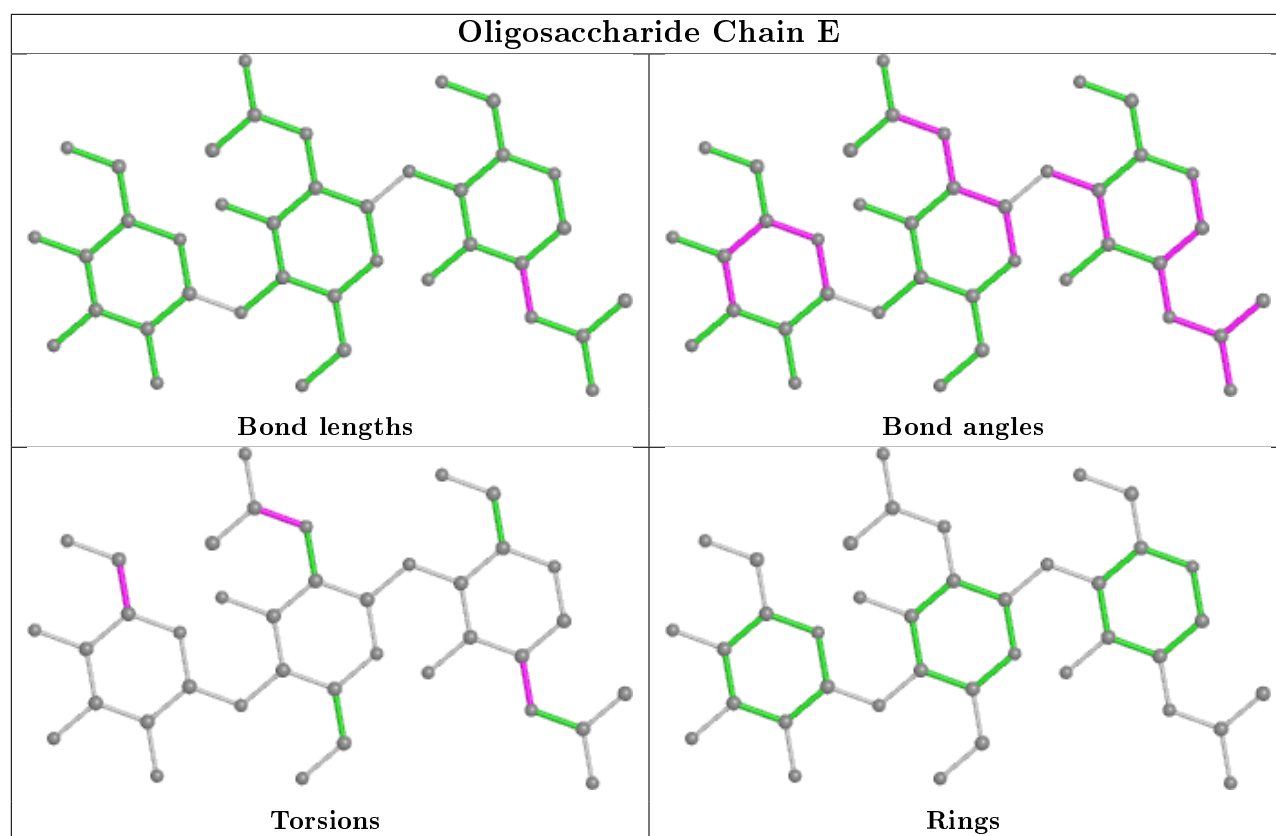
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

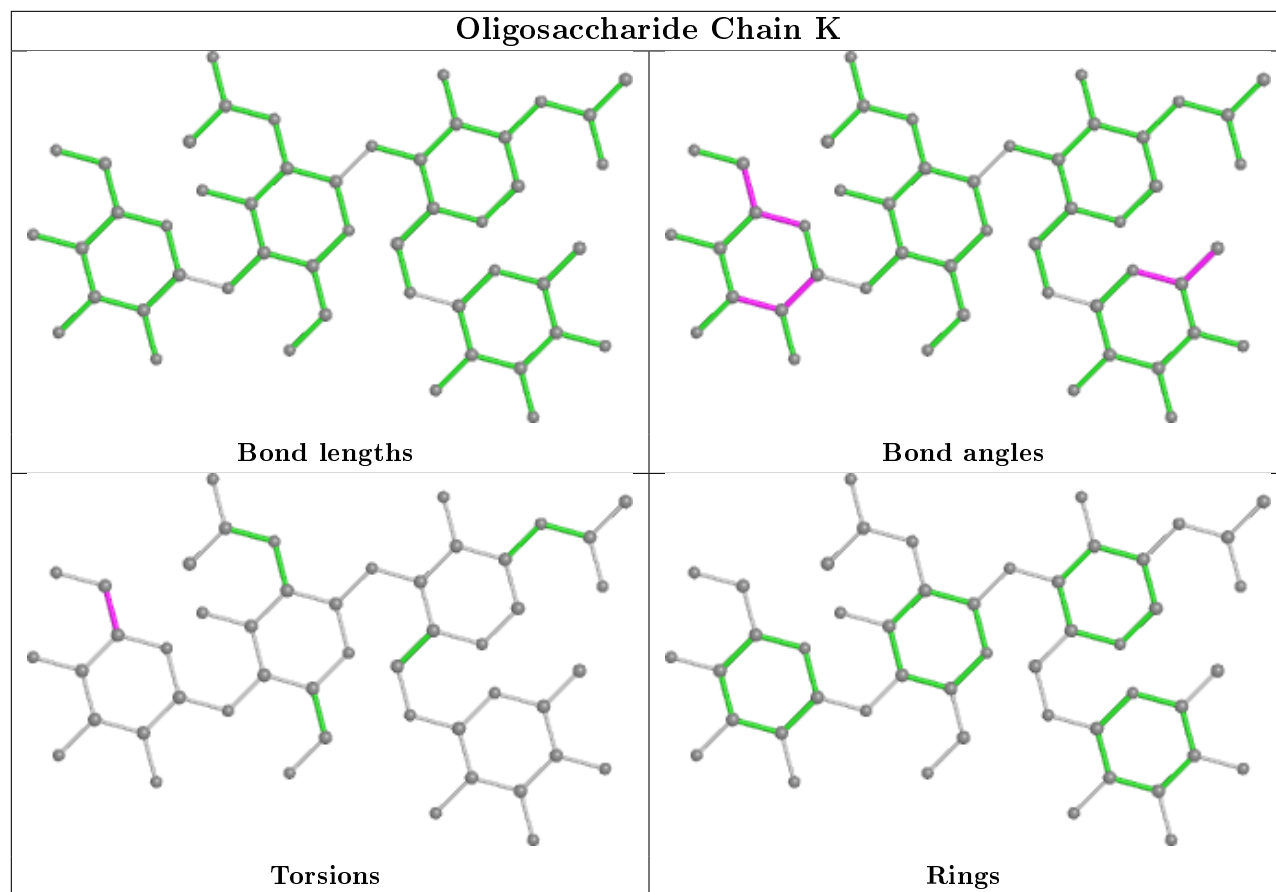


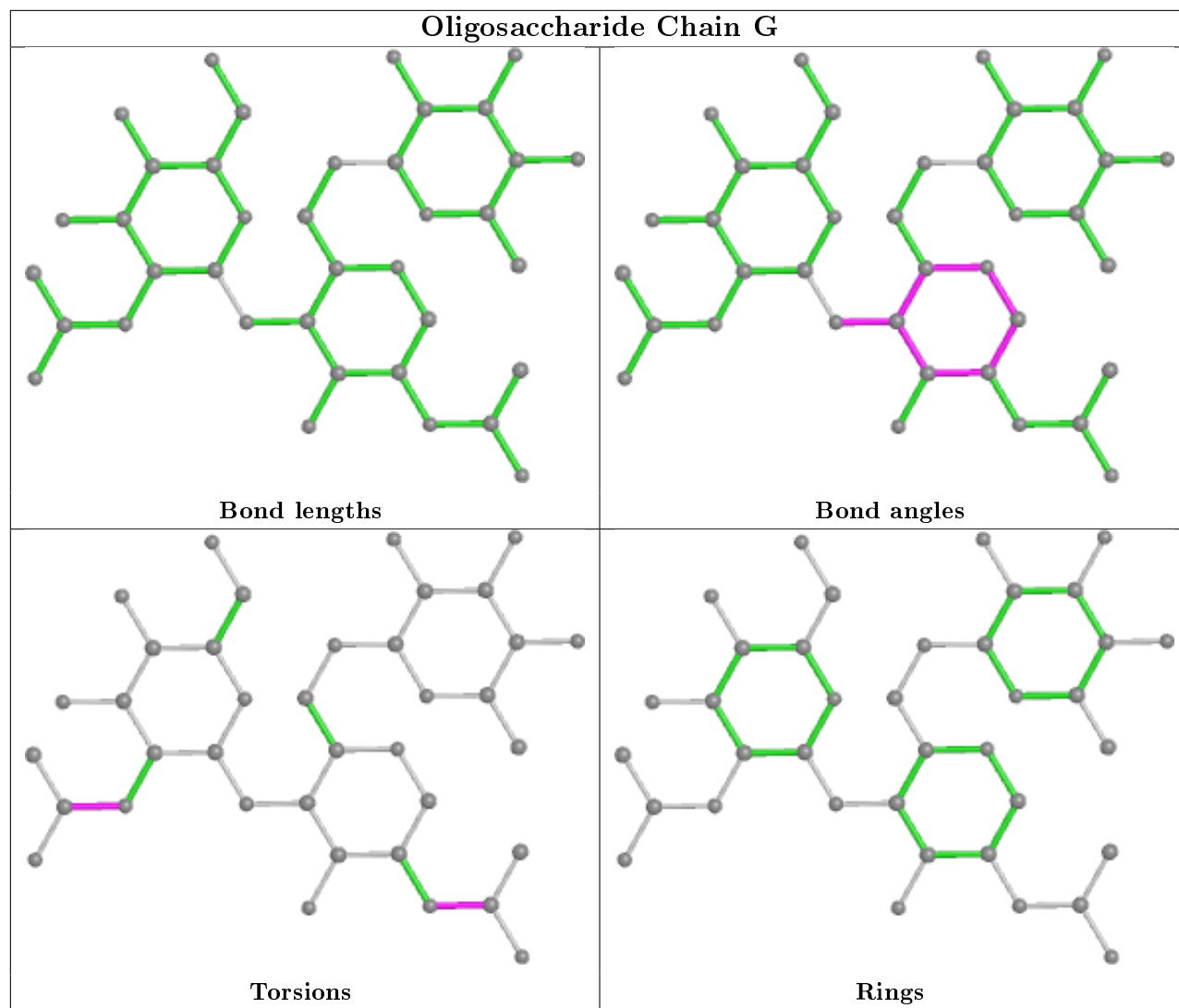
**Oligosaccharide Chain D****Bond lengths****Bond angles****Torsions****Rings**

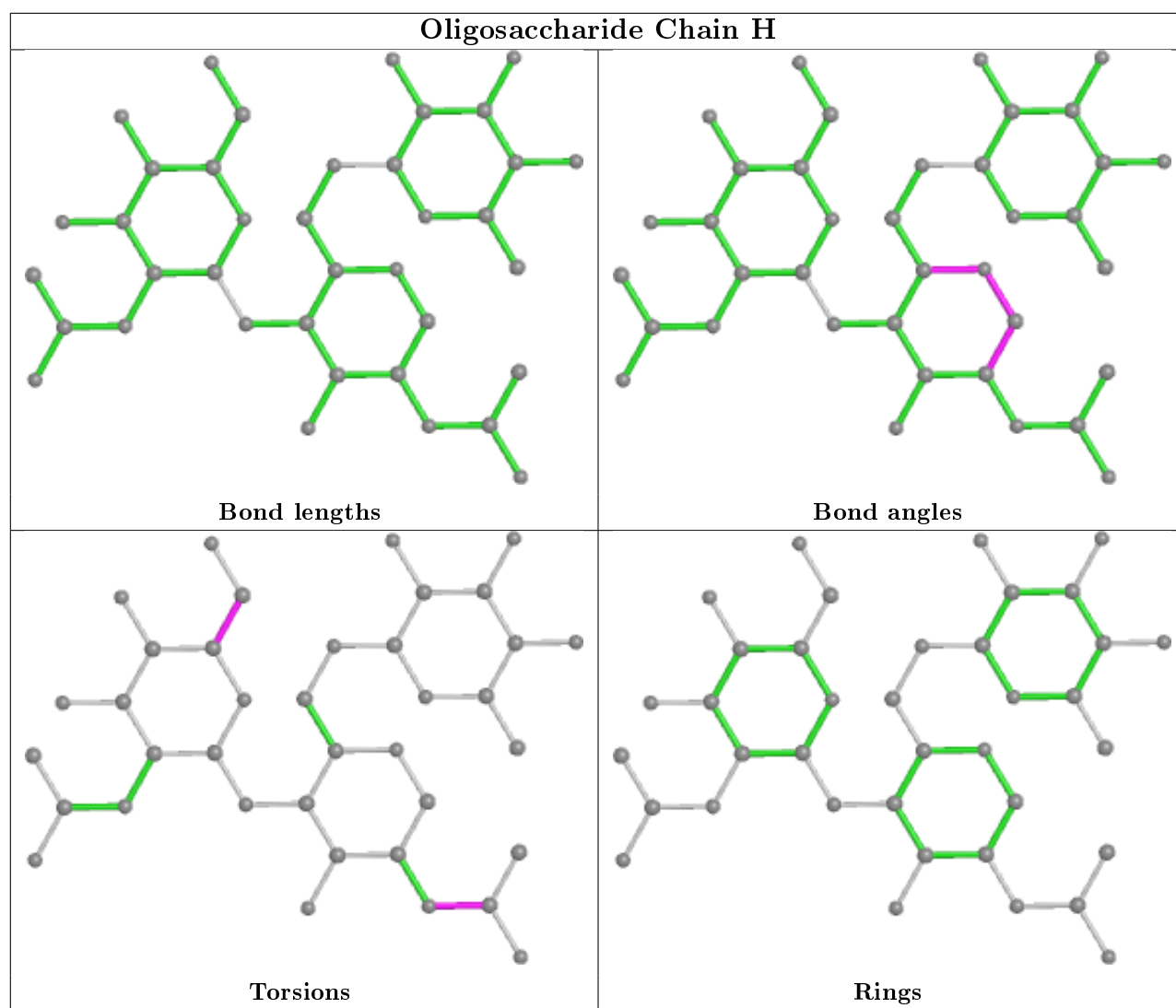


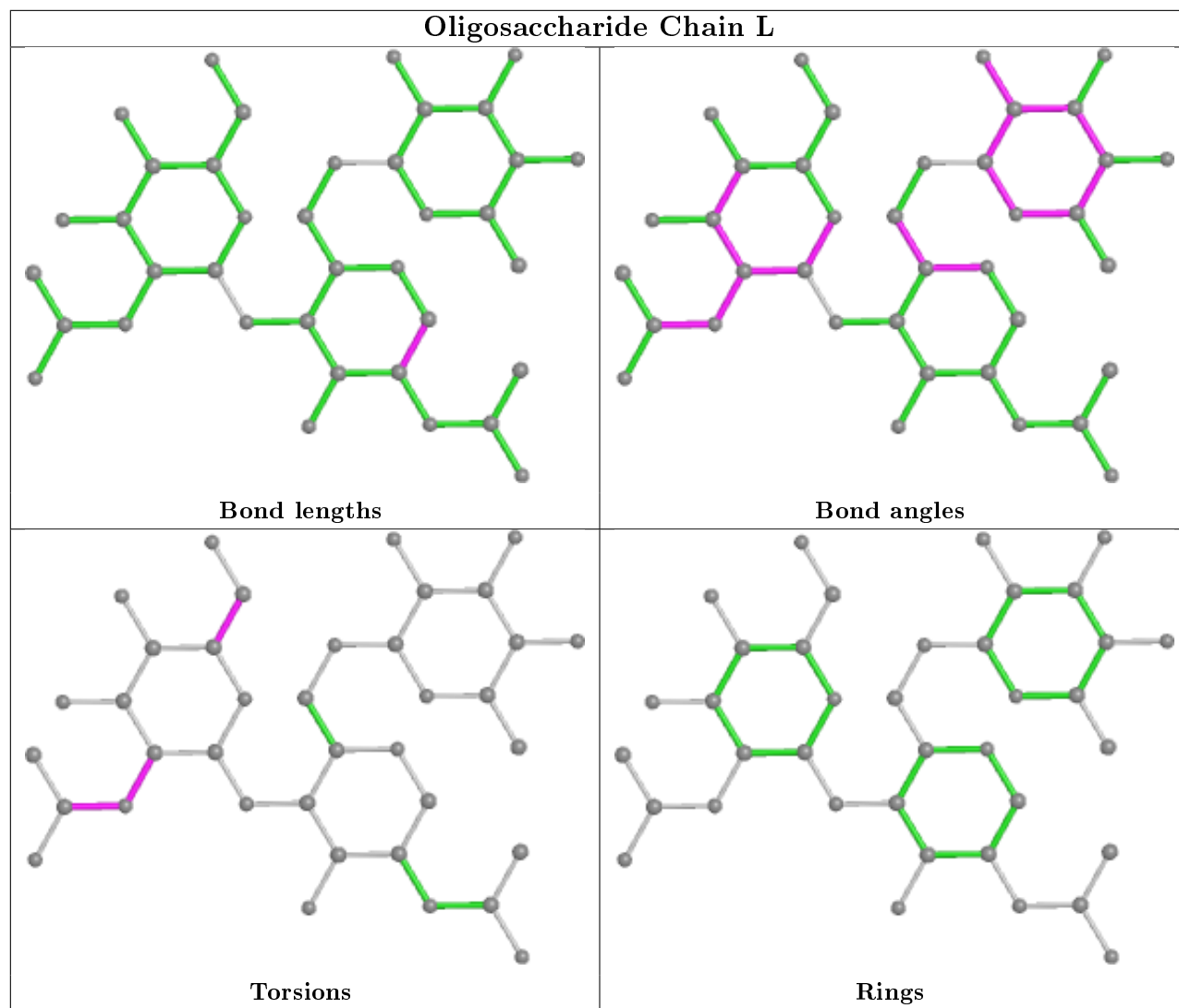


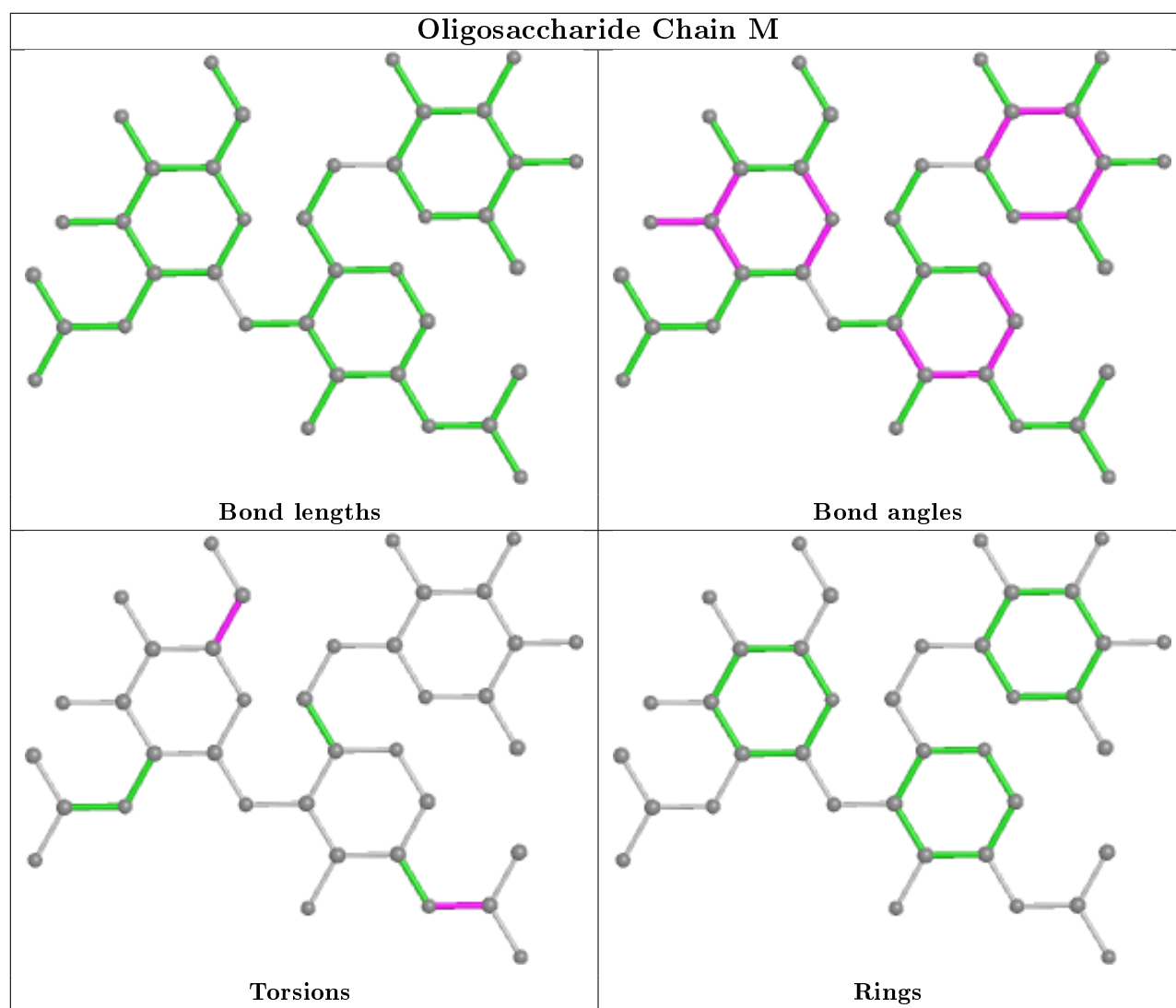


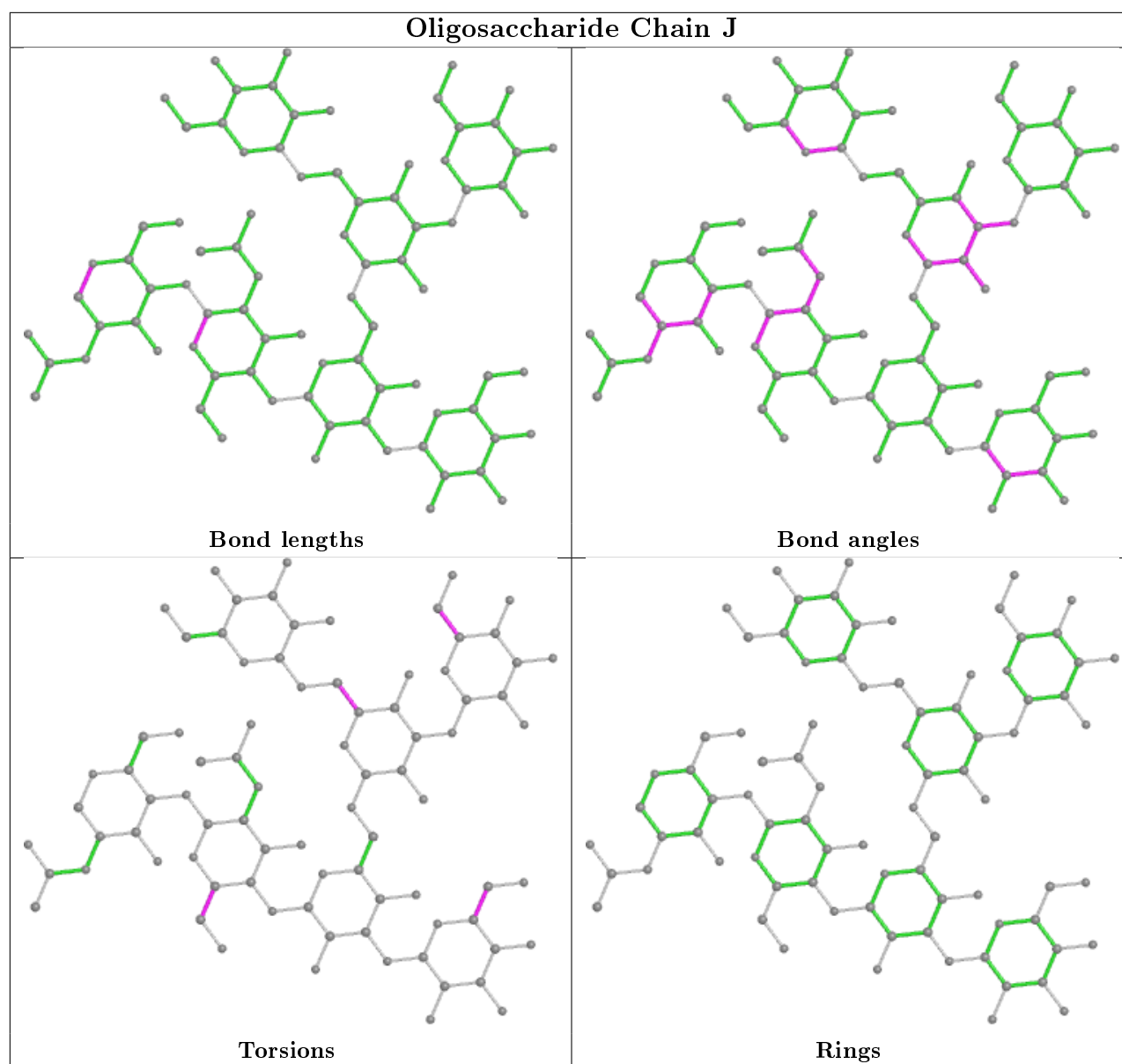












## 5.6 Ligand geometry [i](#)

32 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
9	SO4	A	607	-	4,4,4	0.15	0	6,6,6	0.61	0
11	GOL	A	582	-	5,5,5	0.45	0	5,5,5	0.84	0
11	GOL	A	611	-	5,5,5	0.31	0	5,5,5	0.66	0
11	GOL	B	588	-	5,5,5	0.72	0	5,5,5	1.75	2 (40%)
8	NAG	B	581	1	14,14,15	0.46	0	17,19,21	1.59	2 (11%)
9	SO4	A	602	-	4,4,4	0.37	0	6,6,6	0.99	0
9	SO4	A	605	-	4,4,4	0.35	0	6,6,6	0.59	0
11	GOL	A	584	-	5,5,5	0.30	0	5,5,5	0.33	0
8	NAG	A	581	1	14,14,15	0.80	0	17,19,21	1.40	4 (23%)
9	SO4	A	608	-	4,4,4	0.15	0	6,6,6	0.14	0
9	SO4	A	603	-	4,4,4	0.25	0	6,6,6	0.50	0
8	NAG	B	511	1	14,14,15	0.63	0	17,19,21	1.52	2 (11%)
11	GOL	A	583	-	5,5,5	0.41	0	5,5,5	0.51	0
11	GOL	A	599	-	5,5,5	0.47	0	5,5,5	0.38	0
11	GOL	A	597	-	5,5,5	0.91	0	5,5,5	1.00	0
10	P33	A	609	-	21,21,21	1.04	1 (4%)	20,20,20	0.85	0
11	GOL	B	598	-	5,5,5	0.65	0	5,5,5	0.78	0
8	NAG	A	501	1	14,14,15	0.73	0	17,19,21	1.29	2 (11%)
11	GOL	A	595	-	5,5,5	0.50	0	5,5,5	0.52	0
9	SO4	B	604	-	4,4,4	0.29	0	6,6,6	0.52	0
11	GOL	B	580	-	5,5,5	0.51	0	5,5,5	0.31	0
9	SO4	A	601	-	4,4,4	0.29	0	6,6,6	0.66	0
11	GOL	B	607	-	5,5,5	0.48	0	5,5,5	0.40	0
9	SO4	B	606	-	4,4,4	0.26	0	6,6,6	0.40	0
11	GOL	A	596	-	5,5,5	0.40	0	5,5,5	0.33	0
11	GOL	A	610	-	5,5,5	0.40	0	5,5,5	0.84	0
11	GOL	A	585	-	5,5,5	0.38	0	5,5,5	0.60	0
11	GOL	B	589	-	5,5,5	0.33	0	5,5,5	0.62	0
11	GOL	B	586	-	5,5,5	0.52	0	5,5,5	1.23	0
11	GOL	A	594	-	5,5,5	0.39	0	5,5,5	0.67	0
11	GOL	A	612	-	5,5,5	0.43	0	5,5,5	0.77	0
11	GOL	A	587	-	5,5,5	0.36	0	5,5,5	0.74	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
11	GOL	A	582	-	-	4/4/4/4	-
11	GOL	A	611	-	-	3/4/4/4	-
11	GOL	B	588	-	-	4/4/4/4	-
8	NAG	B	581	1	-	4/6/23/26	0/1/1/1
11	GOL	A	584	-	-	4/4/4/4	-
8	NAG	A	581	1	-	3/6/23/26	0/1/1/1
8	NAG	B	511	1	-	2/6/23/26	0/1/1/1
11	GOL	A	583	-	-	2/4/4/4	-
11	GOL	A	599	-	-	0/4/4/4	-
11	GOL	A	597	-	-	4/4/4/4	-
10	P33	A	609	-	-	6/19/19/19	-
11	GOL	B	598	-	-	0/4/4/4	-
8	NAG	A	501	1	1/1/5/7	2/6/23/26	0/1/1/1
11	GOL	A	595	-	-	4/4/4/4	-
11	GOL	B	580	-	-	2/4/4/4	-
11	GOL	B	607	-	-	2/4/4/4	-
11	GOL	A	596	-	-	2/4/4/4	-
11	GOL	A	610	-	-	2/4/4/4	-
11	GOL	A	585	-	-	1/4/4/4	-
11	GOL	B	589	-	-	4/4/4/4	-
11	GOL	B	586	-	-	2/4/4/4	-
11	GOL	A	594	-	-	1/4/4/4	-
11	GOL	A	612	-	-	0/4/4/4	-
11	GOL	A	587	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	609	P33	O22-C21	-3.52	1.23	1.42

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	581	NAG	O5-C5-C6	4.34	114.00	107.20
8	B	511	NAG	C1-O5-C5	3.88	117.44	112.19
8	A	501	NAG	C4-C3-C2	3.65	116.37	111.02
8	A	581	NAG	C1-C2-N2	3.04	115.68	110.49
8	B	511	NAG	C4-C3-C2	-3.00	106.62	111.02

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	A	501	NAG	C1

5 of 62 torsion outliers are listed below:

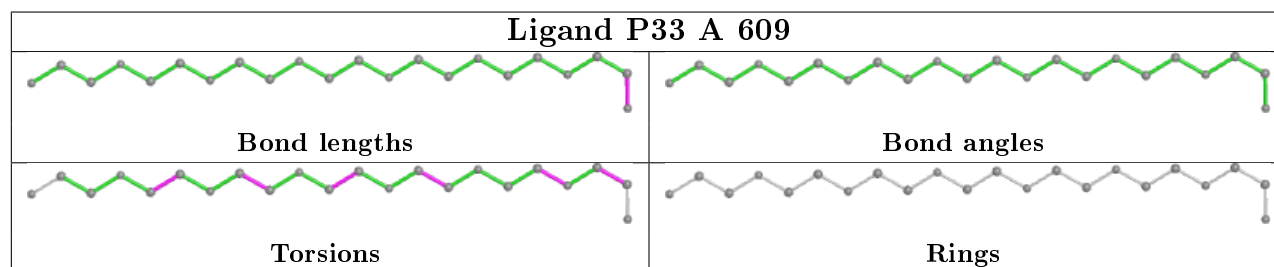
Mol	Chain	Res	Type	Atoms
11	A	582	GOL	O1-C1-C2-O2
11	A	582	GOL	O1-C1-C2-C3
11	A	611	GOL	O1-C1-C2-C3
11	B	588	GOL	O1-C1-C2-C3
11	B	588	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	B	588	GOL	2	0
9	A	602	SO4	1	0
11	A	584	GOL	1	0
11	B	586	GOL	2	0
11	A	612	GOL	2	0

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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.