



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 15, 2023 – 05:10 PM EDT

PDB ID : 1TFM
Title : CRYSTAL STRUCTURE OF A RIBOSOME INACTIVATING PROTEIN IN ITS NATURALLY INHIBITED FORM
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Deposited on : 2004-05-27
Resolution : 2.80 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
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) : 2.35

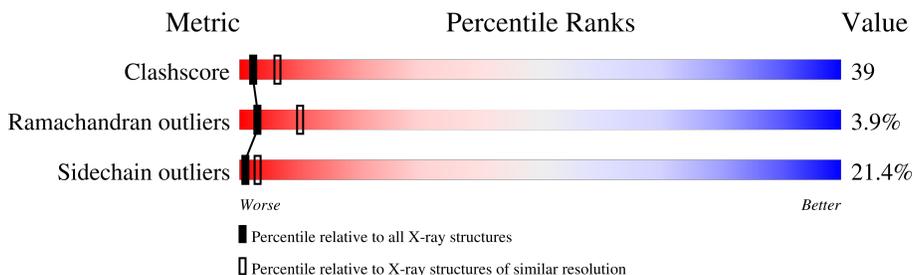
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	240	38% 41% 18% .
2	B	255	49% 39% 10% .
3	C	2	100%
4	D	4	100%
5	E	3	33% 67%
6	F	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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NAG	D	2	-	-	X	-
4	BMA	D	3	X	-	-	-
7	NAG	A	241	X	-	-	-
9	GAL	B	267	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 4101 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 Himalayan mistletoe ribosome-inactivating protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	240	1875	1191	319	361	4	0	0	0

- Molecule 2 is a protein called Himalayan mistletoe ribosome-inactivating protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	255	1938	1199	343	384	12	0	0	0

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



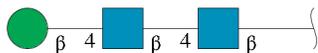
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	2	28	16	2	10	0	0	0

- Molecule 4 is an oligosaccharide called beta-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
			Total	C	N	O			
4	D	4	50	28	2	20	0	0	0

- Molecule 5 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.



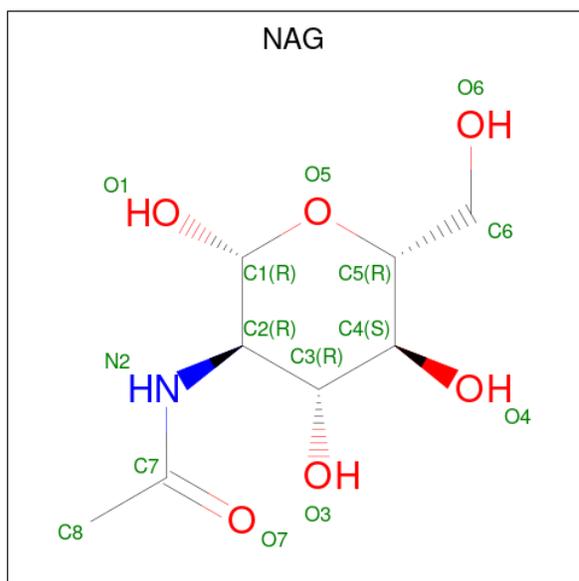
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	E	3	39	22	2	15	0	0	0

- Molecule 6 is an oligosaccharide called beta-D-galactopyranose-(1-4)-beta-D-glucopyranose.



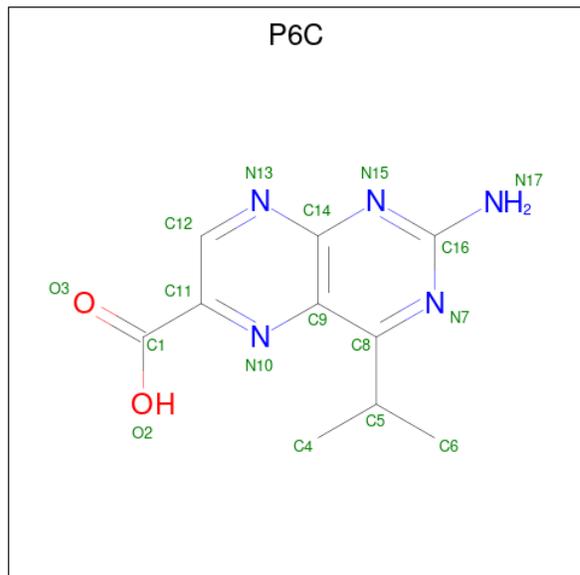
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
6	F	2	23	12	11	0	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



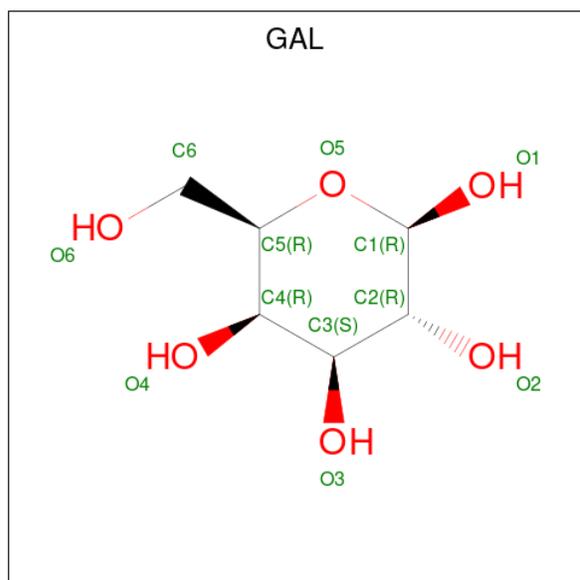
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
7	A	1	14	8	1	5	0	0

- Molecule 8 is 2-AMINO-4-ISOPROPYL-PTERIDINE-6-CARBOXYLIC ACID (three-letter code: P6C) (formula: C₁₀H₁₁N₅O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
8	A	1	17	10	5	2	0	0

- Molecule 9 is beta-D-galactopyranose (three-letter code: GAL) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
9	B	1	11	6	5	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	51	Total 51	O 51	0	0
10	B	55	Total 55	O 55	0	0

MAG1
MAG2

- Molecule 4: beta-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 D:  100%MAG1
MAG2
BMA3
BMA4

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

Chain E:  33% 67%MAG1
MAG2
BMA3

- Molecule 6: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain F:  100%BGC1
GAL2

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	109.42Å 109.42Å 309.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.80	Depositor
% Data completeness (in resolution range)	100.0 (20.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.234 , 0.289	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4101	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

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: BMA, NAG, P6C, BGC, GAL

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	0.70	5/1913 (0.3%)	1.01	14/2602 (0.5%)
2	B	0.50	0/1978	0.94	7/2697 (0.3%)
All	All	0.60	5/3891 (0.1%)	0.97	21/5299 (0.4%)

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	A	0	5
2	B	0	6
All	All	0	11

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	LEU	C-O	13.56	1.49	1.23
1	A	92	GLY	C-N	9.93	1.56	1.34
1	A	18	PHE	C-N	7.22	1.50	1.34
1	A	17	TYR	C-N	5.53	1.46	1.34
1	A	127	ILE	C-N	5.35	1.46	1.34

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	131	ILE	CB-CG1-CD1	19.49	168.48	113.90
1	A	142	ASN	CA-C-N	-8.08	99.43	117.20
1	A	17	TYR	O-C-N	-7.67	110.43	122.70
1	A	95	LEU	O-C-N	-6.59	112.15	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	ASN	O-C-N	6.45	133.02	122.70

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	142	ASN	Mainchain
1	A	18	PHE	Sidechain
1	A	217	PRO	Mainchain
1	A	90	GLY	Peptide
1	A	95	LEU	Mainchain

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	1875	0	1849	167	0
2	B	1938	0	1851	128	0
3	C	28	0	25	3	0
4	D	50	0	43	8	0
5	E	39	0	34	3	0
6	F	23	0	21	0	0
7	A	14	0	13	1	0
8	A	17	0	10	0	0
9	B	11	0	10	7	0
10	A	51	0	0	5	0
10	B	55	0	0	0	0
All	All	4101	0	3856	305	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 39.

The worst 5 of 305 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:A:18:PHE:HB3	1:A:167:LEU:HD21	1.26	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1:NAG:H62	3:C:2:NAG:H2	1.16	1.09
1:A:101:ARG:HG2	1:A:101:ARG:HH11	1.11	1.08
4:D:2:NAG:H3	4:D:2:NAG:H83	1.36	1.06
1:A:240:CYS:OXT	1:A:240:CYS:SG	2.14	1.04

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	238/240 (99%)	191 (80%)	37 (16%)	10 (4%)	3	9
2	B	253/255 (99%)	219 (87%)	25 (10%)	9 (4%)	3	11
All	All	491/495 (99%)	410 (84%)	62 (13%)	19 (4%)	3	10

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	91	PRO
1	A	110	TYR
1	A	143	THR
1	A	204	THR
1	A	217	PRO

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	205/205 (100%)	154 (75%)	51 (25%)	0	2
2	B	211/211 (100%)	173 (82%)	38 (18%)	1	5
All	All	416/416 (100%)	327 (79%)	89 (21%)	1	3

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	38	SER
2	B	163	SER
2	B	50	ARG
2	B	119	THR
2	B	182	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	221	ASN
2	B	198	ASN
2	B	30	GLN
2	B	166	ASN
2	B	17	ASN

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](#)

11 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	C	1	3,2	14,14,15	0.74	0	17,19,21	2.79	9 (52%)
3	NAG	C	2	3	14,14,15	0.70	0	17,19,21	1.53	3 (17%)
4	NAG	D	1	2,4	14,14,15	0.46	0	17,19,21	1.49	4 (23%)
4	NAG	D	2	4	14,14,15	0.51	0	17,19,21	1.84	7 (41%)
4	BMA	D	3	4	11,11,12	0.63	0	15,15,17	2.14	4 (26%)
4	BMA	D	4	4	11,11,12	0.54	0	15,15,17	1.37	3 (20%)
5	NAG	E	1	2,5	14,14,15	0.55	0	17,19,21	1.74	5 (29%)
5	NAG	E	2	5	14,14,15	0.67	0	17,19,21	1.63	3 (17%)
5	BMA	E	3	5	11,11,12	0.49	0	15,15,17	1.47	3 (20%)
6	BGC	F	1	6	12,12,12	0.52	0	17,17,17	1.60	5 (29%)
6	GAL	F	2	6	11,11,12	0.55	0	15,15,17	1.88	4 (26%)

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	C	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	C	2	3	-	5/6/23/26	0/1/1/1
4	NAG	D	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	5/6/23/26	0/1/1/1
4	BMA	D	3	4	1/1/4/5	2/2/19/22	0/1/1/1
4	BMA	D	4	4	-	2/2/19/22	0/1/1/1
5	NAG	E	1	2,5	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1
5	BMA	E	3	5	-	1/2/19/22	1/1/1/1
6	BGC	F	1	6	-	2/2/22/22	0/1/1/1
6	GAL	F	2	6	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C1-C2-N2	6.14	120.97	110.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	C1-O5-C5	6.07	120.42	112.19
5	E	2	NAG	C4-C3-C2	4.69	117.90	111.02
3	C	2	NAG	C4-C3-C2	4.60	117.76	111.02
4	D	3	BMA	C2-C3-C4	4.36	118.45	110.89

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	D	3	BMA	C3

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	C3-C2-N2-C7
3	C	2	NAG	O7-C7-N2-C2
3	C	2	NAG	C8-C7-N2-C2
4	D	4	BMA	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6

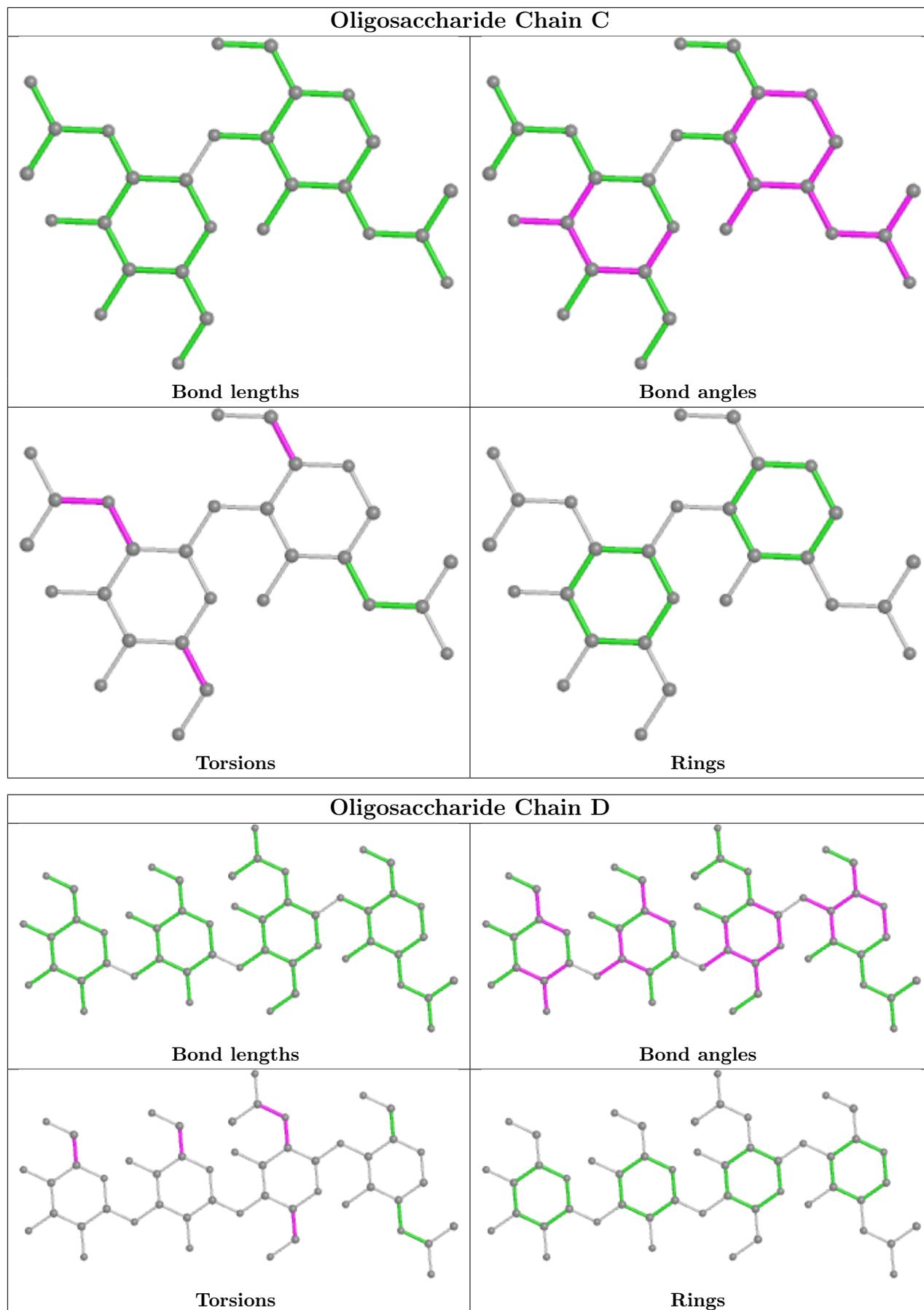
All (1) ring outliers are listed below:

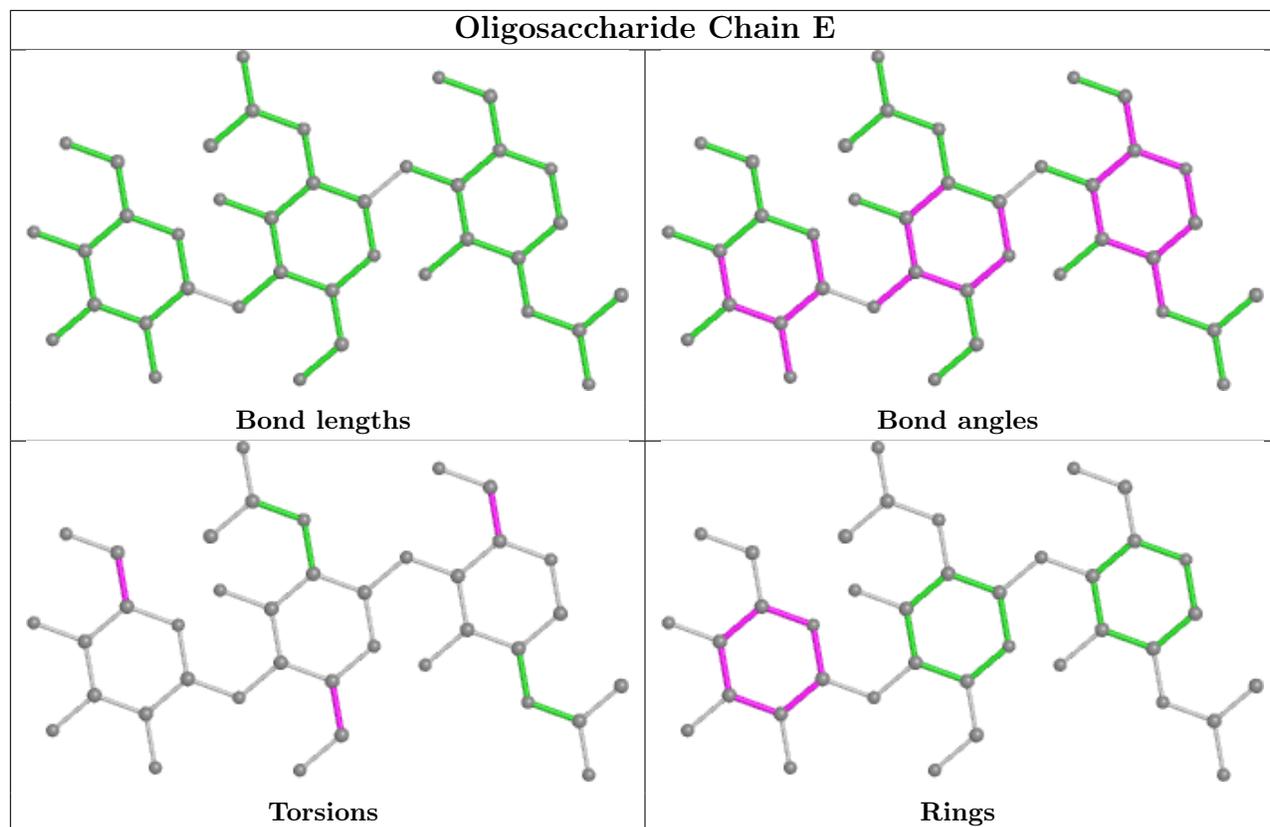
Mol	Chain	Res	Type	Atoms
5	E	3	BMA	C1-C2-C3-C4-C5-O5

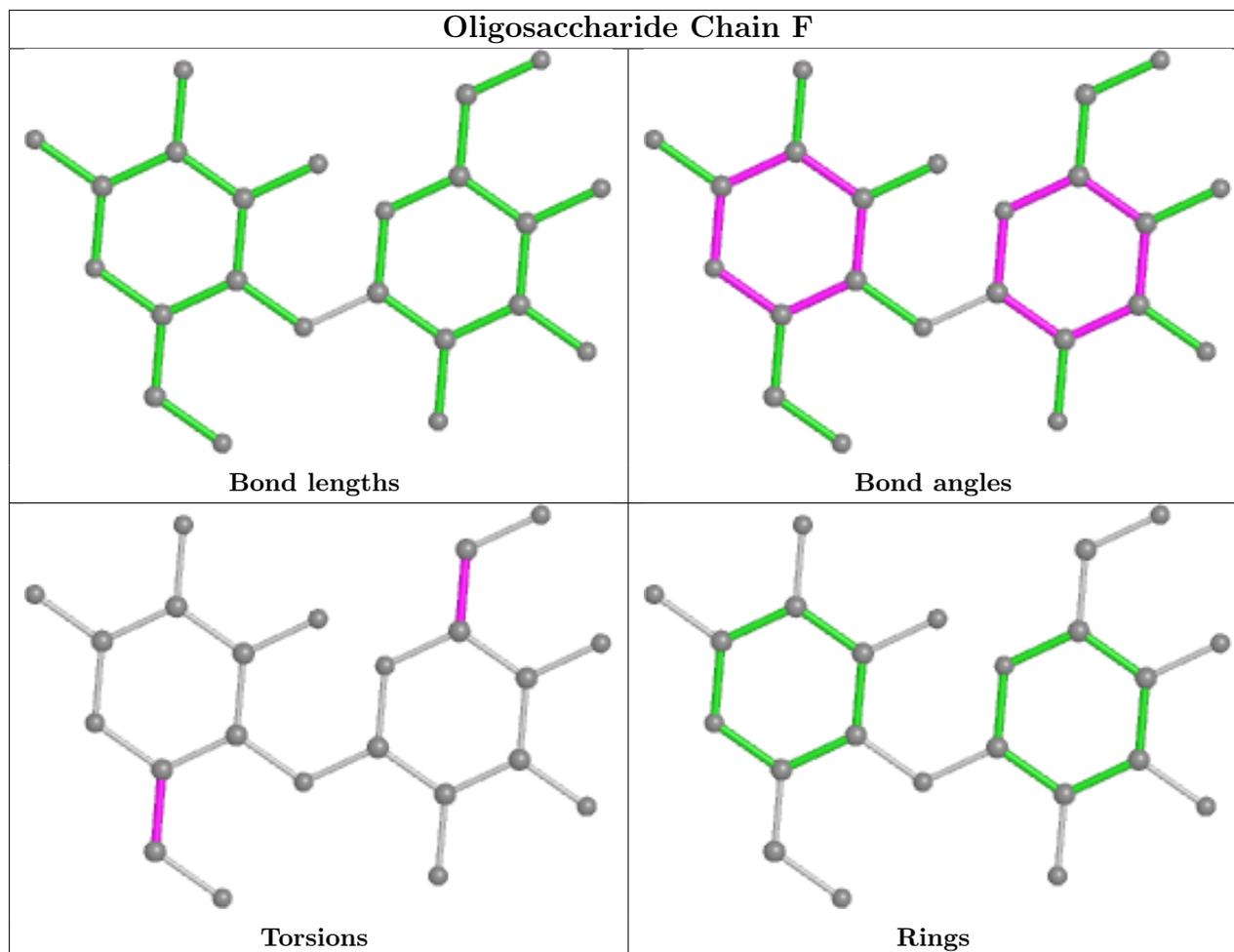
8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	NAG	7	0
4	D	1	NAG	3	0
5	E	3	BMA	3	0
4	D	3	BMA	1	0
3	C	1	NAG	3	0
5	E	2	NAG	3	0
4	D	4	BMA	1	0
3	C	2	NAG	3	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](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
9	GAL	B	267	-	11,11,12	1.17	1 (9%)	15,15,17	1.82	4 (26%)
7	NAG	A	241	1	14,14,15	0.49	0	17,19,21	1.48	2 (11%)
8	P6C	A	242	-	18,18,18	2.59	4 (22%)	23,26,26	3.71	12 (52%)

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
9	GAL	B	267	-	-	0/2/19/22	0/1/1/1
7	NAG	A	241	1	1/1/5/7	4/6/23/26	0/1/1/1
8	P6C	A	242	-	-	2/8/8/8	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	242	P6C	C8-C5	7.32	1.61	1.51
8	A	242	P6C	C9-C14	5.01	1.49	1.40
8	A	242	P6C	C8-N7	3.71	1.35	1.31
9	B	267	GAL	O5-C1	3.07	1.48	1.43
8	A	242	P6C	C14-N13	-2.31	1.33	1.37

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	242	P6C	C4-C5-C8	9.16	126.43	110.96
8	A	242	P6C	N13-C14-N15	7.48	124.36	115.82
8	A	242	P6C	C9-C8-N7	-5.93	116.92	122.81
8	A	242	P6C	C16-N7-C8	5.87	121.03	116.26
8	A	242	P6C	C12-N13-C14	5.79	122.51	116.69

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	A	241	NAG	C1

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	241	NAG	C8-C7-N2-C2
7	A	241	NAG	O7-C7-N2-C2
8	A	242	P6C	C4-C5-C8-C9
8	A	242	P6C	C4-C5-C8-N7
7	A	241	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	267	GAL	7	0
7	A	241	NAG	1	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

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.