



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 29, 2024 – 02:03 am BST

PDB ID : 2C7F
Title : The Structure of a family 51 arabinofuranosidase, Araf51, from Clostridium thermocellum in complex with 1,5-alpha-L-Arabinotriose.
Authors : Taylor, E.J.; Smith, N.L.; Turkenburg, J.P.; D'Souza, S.; Gilbert, H.J.; Davies, G.J.
Deposited on : 2005-11-23
Resolution : 2.70 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
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)	:	2.36.2

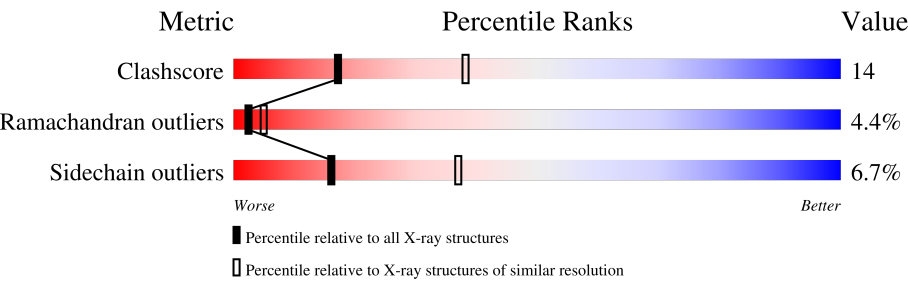
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)

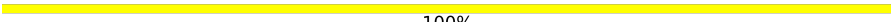
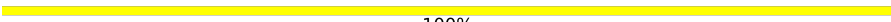

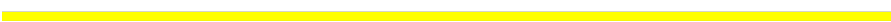
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	513	
1	B	513	
1	C	513	
1	D	513	
1	E	513	
1	F	513	
2	G	3	
2	I	3	

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Mol	Chain	Length	Quality of chain
2	J	3	 100%
2	K	3	 100%
3	H	2	 100%
3	L	2	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24046 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.

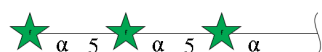
- Molecule 1 is a protein called ALPHA-L-ARABINOFURANOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total	C	N	O	S	0	0	0
			3971	2523	676	750	22			
1	B	497	Total	C	N	O	S	0	0	0
			3972	2518	680	753	21			
1	C	496	Total	C	N	O	S	0	1	0
			3977	2523	679	753	22			
1	D	499	Total	C	N	O	S	0	0	0
			3978	2522	680	754	22			
1	E	492	Total	C	N	O	S	0	0	1
			3886	2465	663	738	20			
1	F	496	Total	C	N	O	S	0	0	0
			3959	2513	674	751	21			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	173	ALA	GLU	engineered mutation	UNP Q4CJG5
B	173	ALA	GLU	engineered mutation	UNP Q4CJG5
C	173	ALA	GLU	engineered mutation	UNP Q4CJG5
D	173	ALA	GLU	engineered mutation	UNP Q4CJG5
E	173	ALA	GLU	engineered mutation	UNP Q4CJG5
F	173	ALA	GLU	engineered mutation	UNP Q4CJG5

- Molecule 2 is an oligosaccharide called alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose.



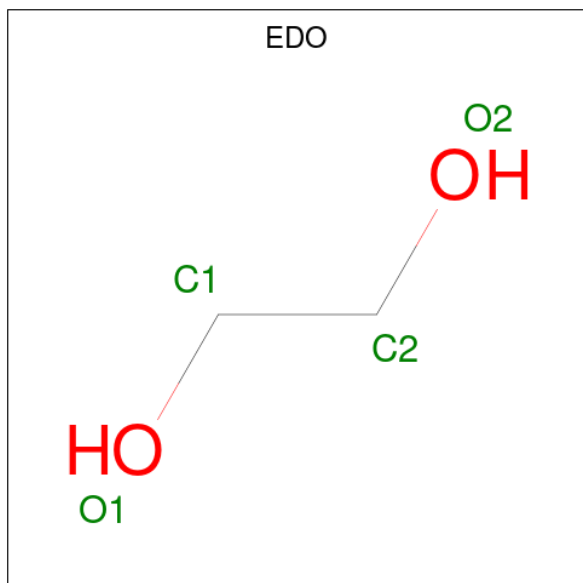
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	G	3	Total	C	O	0	0	0
			28	15	13			
2	I	3	Total	C	O	0	0	0
			28	15	13			
2	J	3	Total	C	O	0	0	0
			28	15	13			
2	K	3	Total	C	O	0	0	0
			28	15	13			

- Molecule 3 is an oligosaccharide called alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	H	2	Total	C	O	0	0	0
			19	10	9			
3	L	2	Total	C	O	0	0	0
			19	10	9			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0

- Molecule 5 is water.

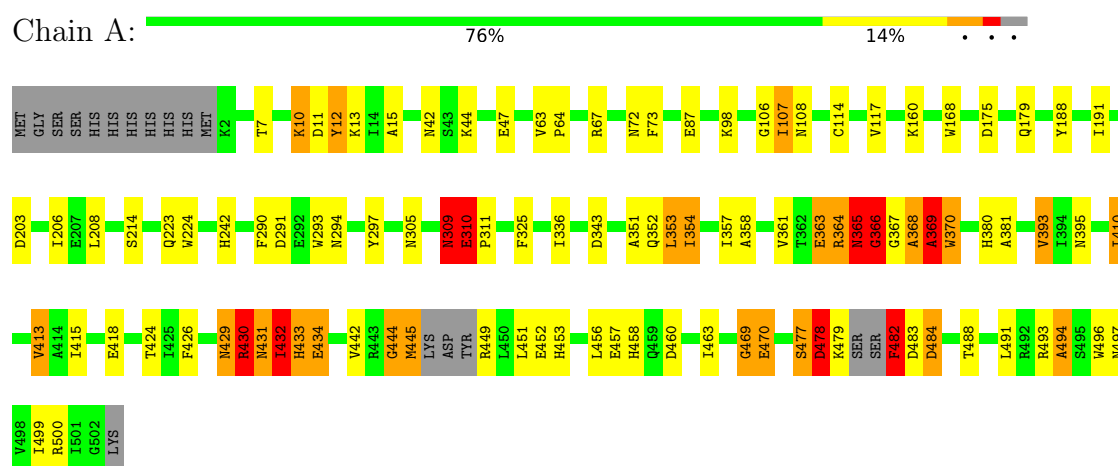
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	26	Total O 26 26	0	0
5	B	16	Total O 16 16	0	0
5	C	19	Total O 19 19	0	0
5	D	21	Total O 21 21	0	0
5	E	15	Total O 15 15	0	0
5	F	20	Total O 20 20	0	0

3 Residue-property plots

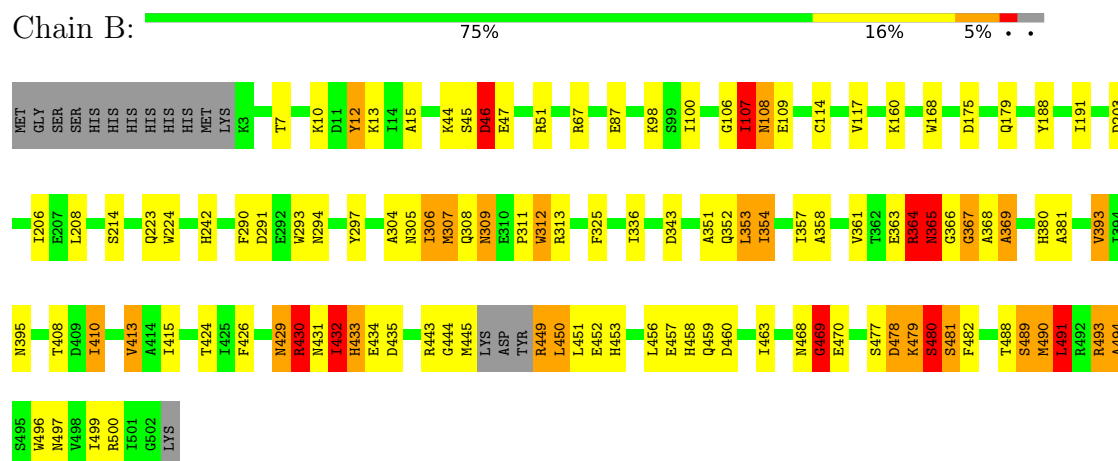
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS failed to run properly.

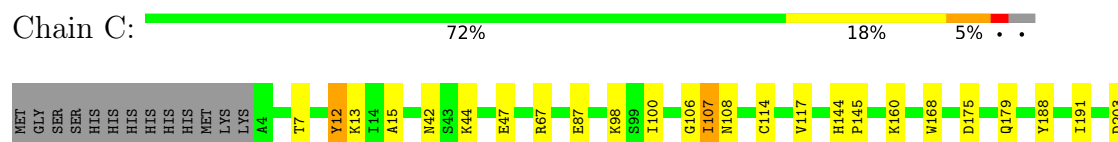
• Molecule 1: ALPHA-L-ARABINOFURANOSIDASE

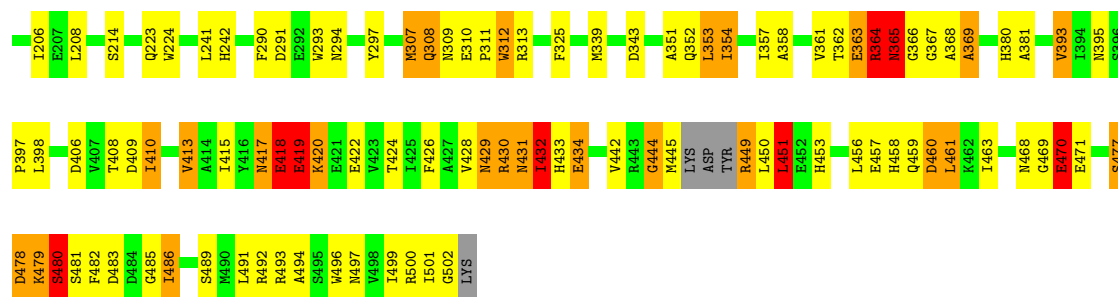


• Molecule 1: ALPHA-L-ARABINOFURANOSIDASE



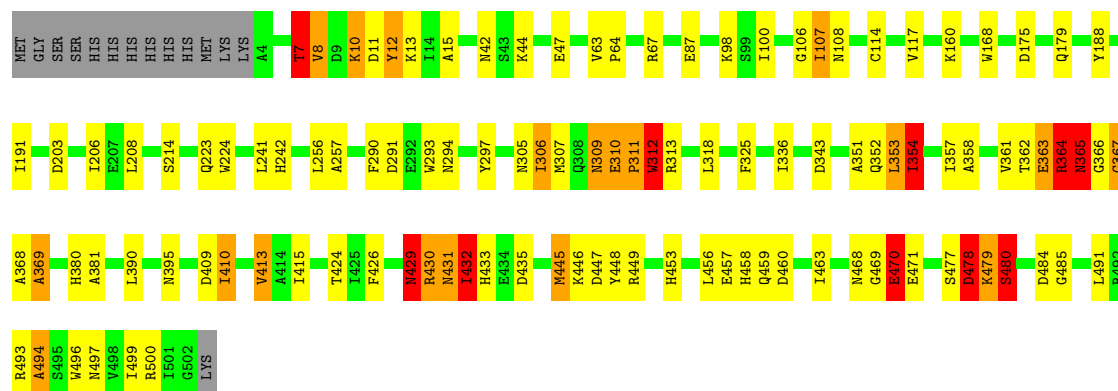
• Molecule 1: ALPHA-L-ARABINOFURANOSIDASE





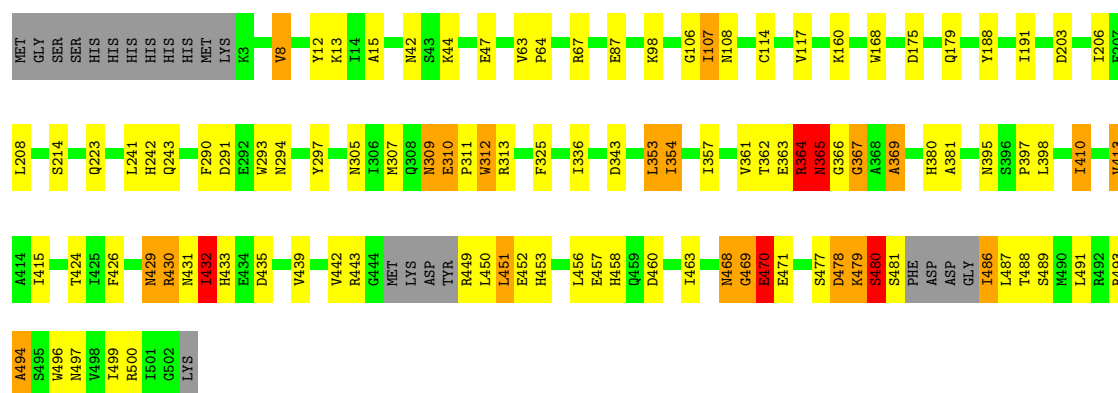
• Molecule 1: ALPHA-L-ARABINOFURANOSIDASE

Chain D: 75% 17%



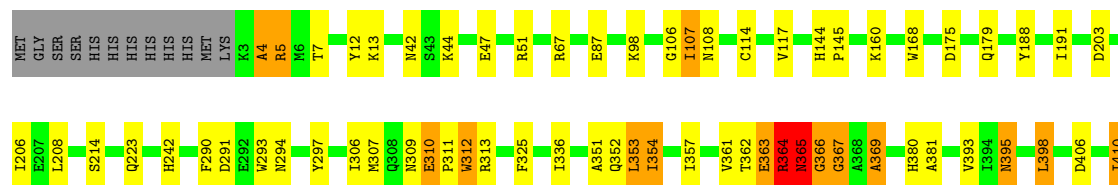
• Molecule 1: ALPHA-L-ARABINOFURANOSIDASE

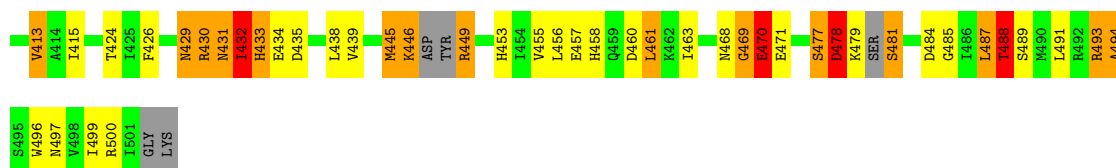
Chain E: 75% 16%




• Molecule 1: ALPHA-L-ARABINOFURANOSIDASE

Chain F: 75% 14% 6%





- Molecule 2: alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose

Chain G:  100%

AHR1
AHR2
AHR3

- Molecule 2: alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose

Chain I:  100%

AHR1
AHR2
AHR3

- Molecule 2: alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose

Chain J:  100%

AHR1
AHR2
AHR3

- Molecule 2: alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose

Chain K:  100%

AHR1
AHR2
AHR3

- Molecule 3: alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose

Chain H:  100%

AHR1
AHR2

- Molecule 3: alpha-L-arabinofuranose-(1-5)-alpha-L-arabinofuranose

Chain L:  100%

AHR1
AHR2

4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	173.34Å 173.34Å 272.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	145.86 – 2.70	Depositor
% Data completeness (in resolution range)	99.7 (145.86-2.70)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.242 , 0.255	Depositor
Wilson B-factor (Å ²)	53.2	Xtriage
Anisotropy	0.027	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	24046	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: EDO, AHR

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.35	0/4061	0.57	1/5499 (0.0%)
1	B	0.36	0/4063	0.59	2/5503 (0.0%)
1	C	0.36	0/4068	0.58	0/5514
1	D	0.34	0/4071	0.57	1/5516 (0.0%)
1	E	0.33	0/3973	0.55	0/5382
1	F	0.32	0/4049	0.55	1/5485 (0.0%)
All	All	0.34	0/24285	0.57	5/32899 (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	A	0	18
1	B	0	20
1	C	0	17
1	D	0	15
1	E	0	11
1	F	1	17
All	All	1	98

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	46	ASP	N-CA-C	6.22	127.80	111.00
1	F	461	LEU	CA-CB-CG	5.84	128.74	115.30
1	A	310	GLU	N-CA-C	5.37	125.50	111.00
1	B	491	LEU	CA-CB-CG	5.25	127.36	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	390	LEU	CB-CG-CD2	5.05	119.59	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	479	LYS	CA

5 of 98 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	223	GLN	Peptide
1	A	309	ASN	Peptide
1	A	353	LEU	Peptide
1	A	365	ASN	Peptide
1	A	72	ASN	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	3971	0	3869	112	0
1	B	3972	0	3852	113	0
1	C	3977	0	3857	123	0
1	D	3978	0	3854	111	0
1	E	3886	0	3756	98	0
1	F	3959	0	3834	106	0
2	G	28	0	0	0	0
2	I	28	0	0	0	0
2	J	28	0	0	0	0
2	K	28	0	0	0	0
3	H	19	0	0	0	0
3	L	19	0	0	0	0
4	A	12	0	18	0	0
4	B	4	0	6	0	0
4	C	4	0	6	0	0
4	D	4	0	6	0	0
4	E	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	4	0	6	0	0
5	A	26	0	0	0	0
5	B	16	0	0	0	0
5	C	19	0	0	0	0
5	D	21	0	0	0	0
5	E	15	0	0	1	0
5	F	20	0	0	0	0
All	All	24046	0	23076	653	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 14.

The worst 5 of 653 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:C:478:ASP:CB	1:C:479:LYS:HB2	1.30	1.62
1:A:431:ASN:HA	1:A:432:ILE:CG2	1.39	1.53
1:E:431:ASN:CB	1:E:432:ILE:HG22	1.35	1.52
1:C:478:ASP:HB3	1:C:479:LYS:CB	1.46	1.45
1:A:431:ASN:CA	1:A:432:ILE:HG22	1.43	1.43

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	490/513 (96%)	445 (91%)	26 (5%)	19 (4%)	3 6
1	B	493/513 (96%)	440 (89%)	28 (6%)	25 (5%)	2 3
1	C	493/513 (96%)	438 (89%)	30 (6%)	25 (5%)	2 3
1	D	497/513 (97%)	445 (90%)	31 (6%)	21 (4%)	3 5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	484/513 (94%)	438 (90%)	27 (6%)	19 (4%)	3	6
1	F	490/513 (96%)	442 (90%)	27 (6%)	21 (4%)	2	5
All	All	2947/3078 (96%)	2648 (90%)	169 (6%)	130 (4%)	2	5

5 of 130 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	TRP
1	A	309	ASN
1	A	310	GLU
1	A	354	ILE
1	A	365	ASN

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	428/450 (95%)	400 (94%)	28 (6%)	17	38
1	B	427/450 (95%)	397 (93%)	30 (7%)	15	35
1	C	428/450 (95%)	395 (92%)	33 (8%)	13	30
1	D	428/450 (95%)	400 (94%)	28 (6%)	17	38
1	E	415/450 (92%)	392 (94%)	23 (6%)	21	46
1	F	425/450 (94%)	396 (93%)	29 (7%)	16	36
All	All	2551/2700 (94%)	2380 (93%)	171 (7%)	16	37

5 of 171 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	463	ILE
1	F	13	LYS
1	E	8	VAL
1	E	365	ASN
1	F	179	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	468	ASN
1	F	453	HIS
1	F	72	ASN
1	F	380	HIS
1	F	497	ASN

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 ⓘ

16 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	AHR	G	1	2	10,10,10	0.58	0	13,14,14	1.33	3 (23%)
2	AHR	G	2	2	9,9,10	0.51	0	10,12,14	1.24	1 (10%)
2	AHR	G	3	2	9,9,10	1.64	1 (11%)	10,12,14	1.76	3 (30%)
3	AHR	H	1	3	10,10,10	0.53	0	13,14,14	1.30	2 (15%)
3	AHR	H	2	3	9,9,10	1.65	1 (11%)	10,12,14	1.73	3 (30%)
2	AHR	I	1	2	10,10,10	0.60	0	13,14,14	1.23	2 (15%)
2	AHR	I	2	2	9,9,10	0.54	0	10,12,14	1.27	1 (10%)
2	AHR	I	3	2	9,9,10	1.65	1 (11%)	10,12,14	1.69	3 (30%)
2	AHR	J	1	2	10,10,10	0.60	0	13,14,14	1.32	2 (15%)
2	AHR	J	2	2	9,9,10	0.57	0	10,12,14	1.31	1 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	AHR	J	3	2	9,9,10	1.64	1 (11%)	10,12,14	1.70	3 (30%)
2	AHR	K	1	2	10,10,10	0.57	0	13,14,14	1.37	2 (15%)
2	AHR	K	2	2	9,9,10	0.66	0	10,12,14	1.37	1 (10%)
2	AHR	K	3	2	9,9,10	1.64	1 (11%)	10,12,14	1.68	2 (20%)
3	AHR	L	1	3	10,10,10	0.56	0	13,14,14	1.29	2 (15%)
3	AHR	L	2	3	9,9,10	1.62	1 (11%)	10,12,14	1.71	3 (30%)

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	AHR	G	1	2	-	0/2/18/18	0/1/1/1
2	AHR	G	2	2	-	2/2/15/18	0/1/1/1
2	AHR	G	3	2	-	0/2/15/18	0/1/1/1
3	AHR	H	1	3	-	2/2/18/18	0/1/1/1
3	AHR	H	2	3	-	0/2/15/18	0/1/1/1
2	AHR	I	1	2	-	1/2/18/18	0/1/1/1
2	AHR	I	2	2	-	2/2/15/18	0/1/1/1
2	AHR	I	3	2	-	0/2/15/18	0/1/1/1
2	AHR	J	1	2	-	2/2/18/18	0/1/1/1
2	AHR	J	2	2	-	2/2/15/18	0/1/1/1
2	AHR	J	3	2	-	0/2/15/18	0/1/1/1
2	AHR	K	1	2	-	2/2/18/18	0/1/1/1
2	AHR	K	2	2	-	2/2/15/18	0/1/1/1
2	AHR	K	3	2	-	0/2/15/18	0/1/1/1
3	AHR	L	1	3	-	2/2/18/18	0/1/1/1
3	AHR	L	2	3	-	0/2/15/18	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)
2	G	3	AHR	O5-C5	-4.72	1.22	1.42
2	I	3	AHR	O5-C5	-4.70	1.22	1.42
3	H	2	AHR	O5-C5	-4.70	1.22	1.42
2	J	3	AHR	O5-C5	-4.70	1.22	1.42
2	K	3	AHR	O5-C5	-4.67	1.22	1.42

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	2	AHR	O5-C5-C4	3.18	122.20	111.29
2	G	3	AHR	O4-C4-C3	3.17	107.51	104.70
2	K	3	AHR	O5-C5-C4	3.17	122.16	111.29
2	I	3	AHR	O4-C4-C3	3.16	107.50	104.70
2	K	3	AHR	O4-C4-C3	3.15	107.50	104.70

There are no chirality outliers.

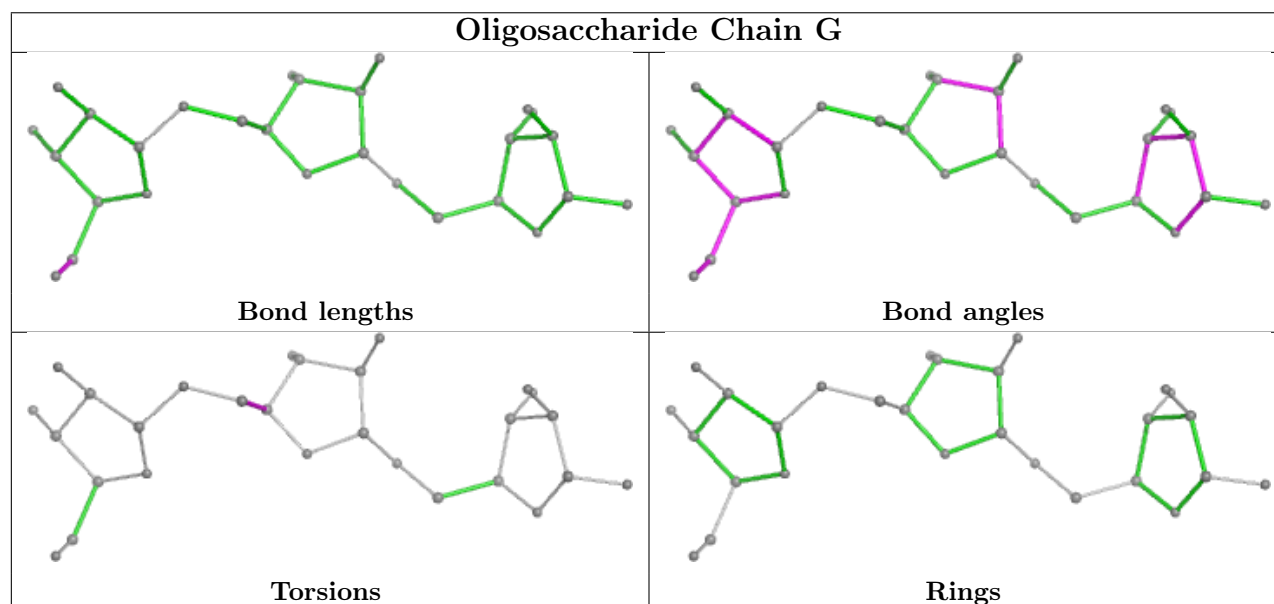
5 of 17 torsion outliers are listed below:

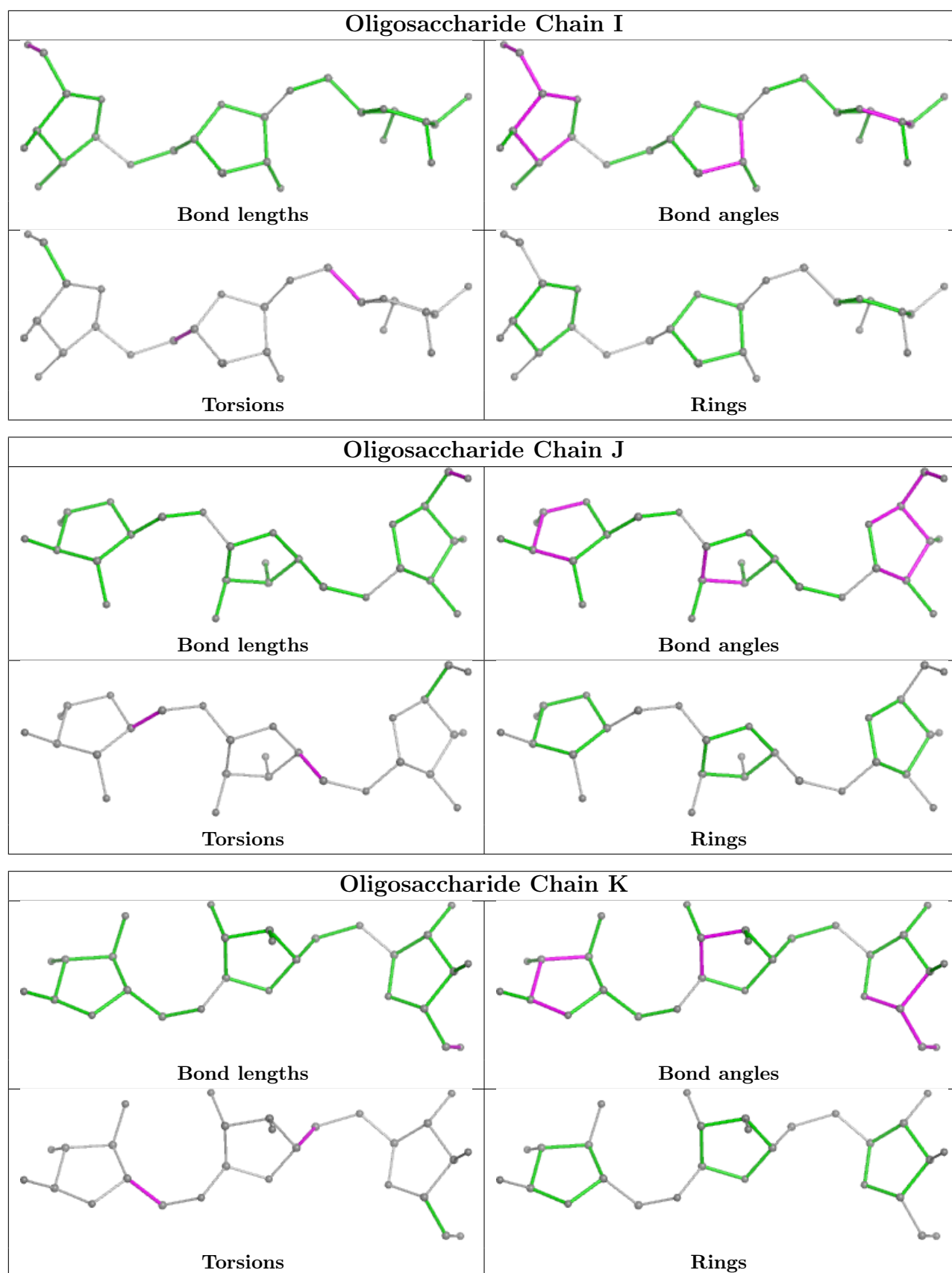
Mol	Chain	Res	Type	Atoms
2	K	1	AHR	O4-C4-C5-O5
2	G	2	AHR	O4-C4-C5-O5
2	I	2	AHR	O4-C4-C5-O5
2	J	2	AHR	O4-C4-C5-O5
2	K	2	AHR	O4-C4-C5-O5

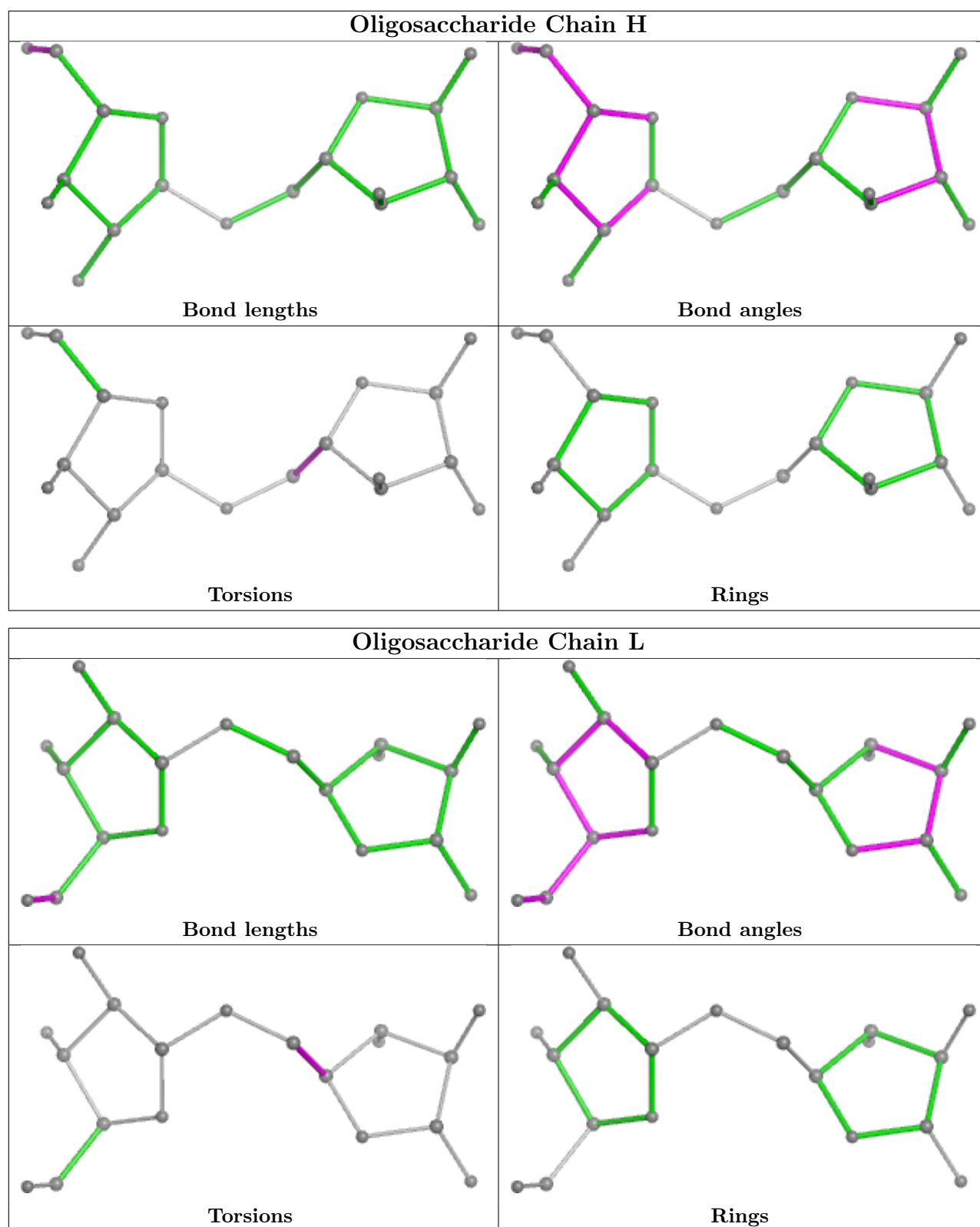
There are no ring outliers.

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](#)

9 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	$\# Z > 2$
4	EDO	A	604	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	E	604	-	3,3,3	0.50	0	2,2,2	0.25	0
4	EDO	E	605	-	3,3,3	0.57	0	2,2,2	0.41	0
4	EDO	C	604	-	3,3,3	0.45	0	2,2,2	0.36	0
4	EDO	A	606	-	3,3,3	0.49	0	2,2,2	0.27	0
4	EDO	F	603	-	3,3,3	0.81	0	2,2,2	0.68	0
4	EDO	B	603	-	3,3,3	0.51	0	2,2,2	0.21	0
4	EDO	A	605	-	3,3,3	0.49	0	2,2,2	0.23	0
4	EDO	D	604	-	3,3,3	0.46	0	2,2,2	0.35	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
4	EDO	A	604	-	-	0/1/1/1	-
4	EDO	E	604	-	-	0/1/1/1	-
4	EDO	E	605	-	-	1/1/1/1	-
4	EDO	C	604	-	-	1/1/1/1	-
4	EDO	A	606	-	-	1/1/1/1	-
4	EDO	F	603	-	-	1/1/1/1	-
4	EDO	B	603	-	-	1/1/1/1	-
4	EDO	A	605	-	-	1/1/1/1	-
4	EDO	D	604	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	606	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	B	603	EDO	O1-C1-C2-O2
4	C	604	EDO	O1-C1-C2-O2
4	D	604	EDO	O1-C1-C2-O2
4	E	605	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.