



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2022 – 04:51 PM EST

PDB ID : 7LRF
Title : Netrin-1 in complex with SOS
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Deposited on : 2021-02-16
Resolution : 3.21 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.26
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

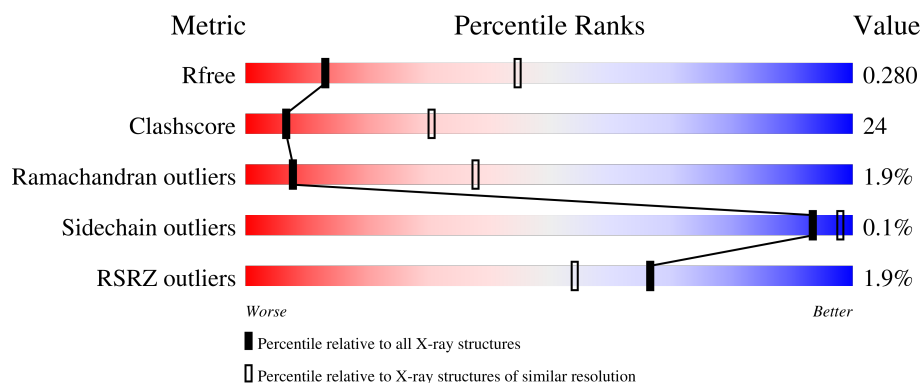
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.21 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	1335 (3.24-3.20)
Clashscore	141614	1460 (3.24-3.20)
Ramachandran outliers	138981	1437 (3.24-3.20)
Sidechain outliers	138945	1436 (3.24-3.20)
RSRZ outliers	127900	1291 (3.24-3.20)

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 $\leq 5\%$. 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	A	443	<div> <div> <div>0%</div> <div>58%</div> <div>34%</div> <div>6%</div> </div> </div>
1	B	443	<div> <div>2%</div> <div>58%</div> <div>33%</div> <div>7%</div> </div>
2	C	3	<div> <div>67%</div> <div>33%</div> </div>
3	D	2	<div> <div>100%</div> </div>
3	E	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	2	 100%
3	G	2	 50% 50%
3	H	2	 100%
3	I	2	 50% 50%
3	J	2	 100%
4	K	2	 100%
4	L	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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	F	2	-	-	-	X
3	NAG	H	2	-	-	-	X
5	EDO	A	502	-	-	-	X
5	EDO	B	501	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 6764 atoms, of which 38 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 Netrin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	418	Total	C	N	O	S	0	0	0
			3208	1964	590	617	37			
1	B	411	Total	C	N	O	S	0	0	0
			3092	1895	567	594	36			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	ALA	-	expression tag	UNP Q90922
A	23	PRO	-	expression tag	UNP Q90922
A	24	LEU	-	expression tag	UNP Q90922
A	25	ALA	-	expression tag	UNP Q90922
A	459	GLY	-	expression tag	UNP Q90922
A	460	SER	-	expression tag	UNP Q90922
A	461	LEU	-	expression tag	UNP Q90922
A	462	VAL	-	expression tag	UNP Q90922
A	463	PRO	-	expression tag	UNP Q90922
A	464	ARG	-	expression tag	UNP Q90922
B	22	ALA	-	expression tag	UNP Q90922
B	23	PRO	-	expression tag	UNP Q90922
B	24	LEU	-	expression tag	UNP Q90922
B	25	ALA	-	expression tag	UNP Q90922
B	459	GLY	-	expression tag	UNP Q90922
B	460	SER	-	expression tag	UNP Q90922
B	461	LEU	-	expression tag	UNP Q90922
B	462	VAL	-	expression tag	UNP Q90922
B	463	PRO	-	expression tag	UNP Q90922
B	464	ARG	-	expression tag	UNP Q90922

- Molecule 2 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.



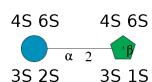
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- 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
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose.



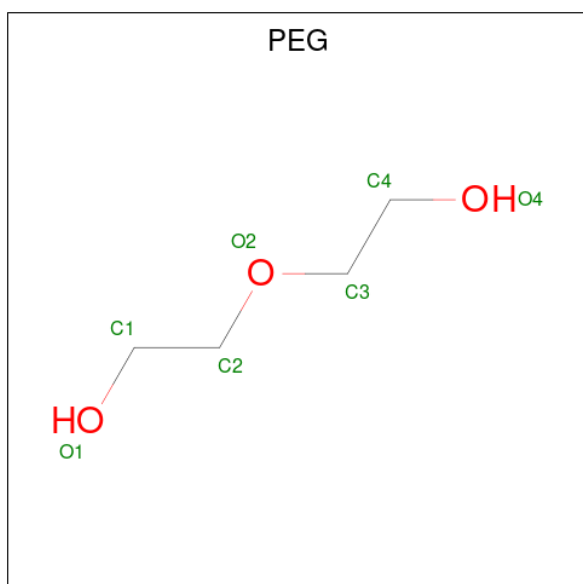
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	K	2	Total	C	O	S	0	0	0
			47	12	29	6			
4	L	2	Total	C	O	S	0	0	0
			55	12	35	8			

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O		0	0
			4	2	2			
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			17	4	10	3		
6	B	1	Total	C	H	O	0	0
			17	4	10	3		

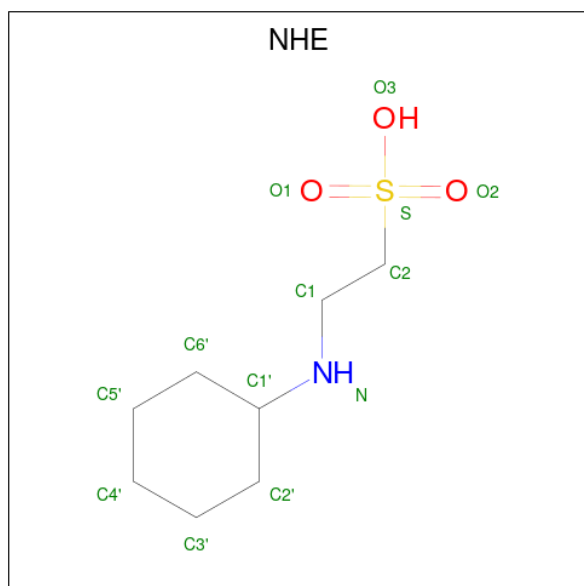
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	1	Total	Ca	0	0
			1	1		

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

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

- Molecule 9 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (three-letter code: NHE) (formula: C₈H₁₇NO₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	S	0	0
			13	8	1	3	1		

- Molecule 10 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	1	Total 1	Cl 1	0	0

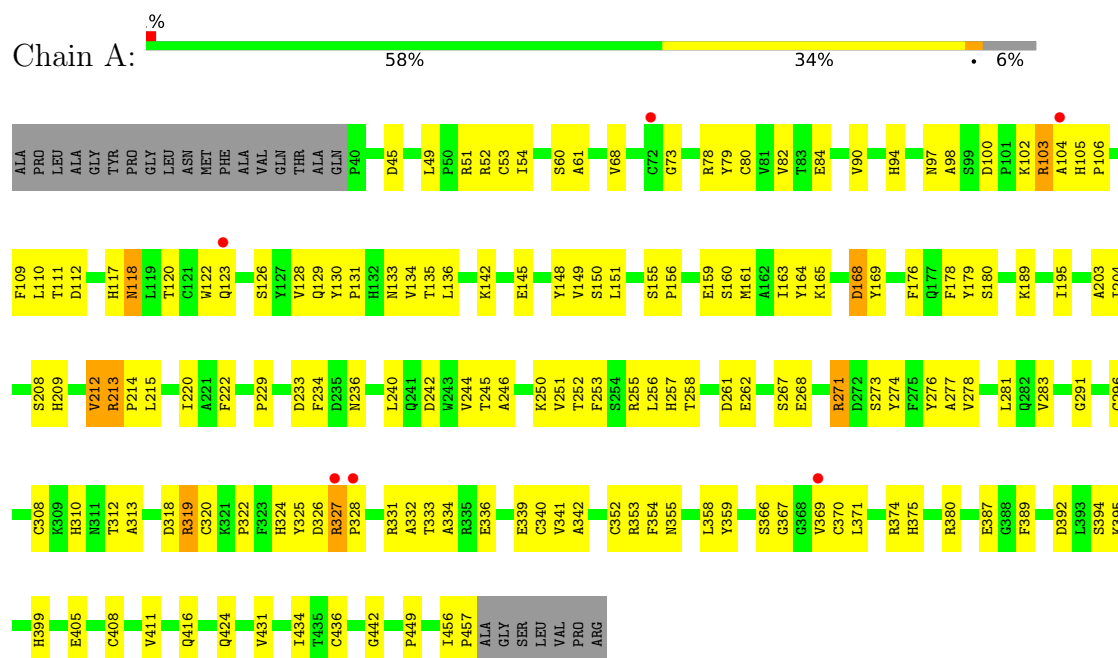
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	23	Total 23	O 23	0	0
11	B	19	Total 19	O 19	0	0

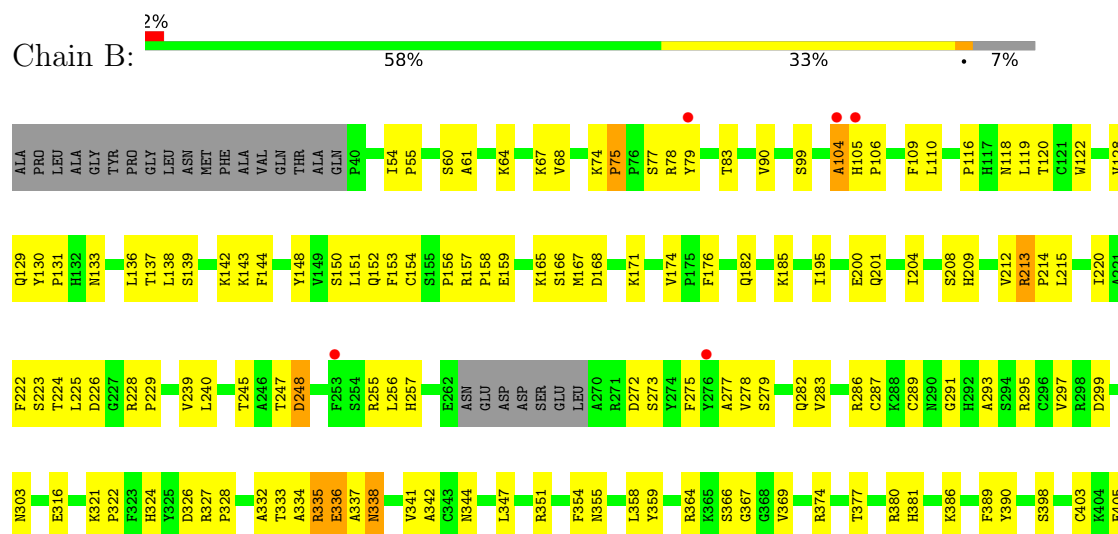
3 Residue-property plots

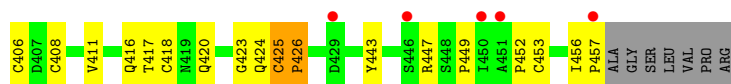
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Netrin-1



• Molecule 1: Netrin-1





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



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  50% 50%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  100%

MAG1
MAG2

- Molecule 4: 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose

Chain K:  100%

GU41
YTJ2

- Molecule 4: 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose

Chain L:  100%

GU41
YTJ2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.11Å 80.15Å 241.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.36 – 3.21 47.08 – 3.21	Depositor EDS
% Data completeness (in resolution range)	99.4 (35.36-3.21) 99.5 (47.08-3.21)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.18.2-3874_3874	Depositor
R, R_{free}	0.226 , 0.281 0.226 , 0.280	Depositor DCC
R_{free} test set	1196 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	81.5	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	6764	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, EDO, NAG, NA, GU4, PEG, NHE, YYJ, CA, BMA

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	0/3289	0.56	3/4469 (0.1%)
1	B	0.40	1/3171 (0.0%)	0.63	1/4316 (0.0%)
All	All	0.37	1/6460 (0.0%)	0.59	4/8785 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	425	CYS	CB-SG	-5.13	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	103	ARG	NE-CZ-NH1	-8.31	116.14	120.30
1	A	213	ARG	NE-CZ-NH2	-6.60	117.00	120.30
1	B	248	ASP	CB-CG-OD1	-6.40	112.54	118.30
1	A	213	ARG	NE-CZ-NH1	5.23	122.92	120.30

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	A	3208	0	2935	145	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3092	0	2777	141	2
2	C	39	0	34	1	0
3	D	28	0	25	3	0
3	E	28	0	25	0	0
3	F	28	0	25	4	0
3	G	28	0	25	3	0
3	H	28	0	25	1	0
3	I	28	0	25	1	0
3	J	28	0	25	2	0
4	K	47	0	6	5	0
4	L	55	0	6	3	2
5	A	12	12	18	2	0
5	B	4	6	6	2	0
6	A	7	10	10	0	0
6	B	7	10	10	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	1	0	0	0	0
9	B	13	0	17	1	0
10	B	1	0	0	0	0
11	A	23	0	0	6	0
11	B	19	0	0	2	0
All	All	6726	38	5994	298	3

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 24.

The worst 5 of 298 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)
4:K:2:YYJ:O5	4:K:2:YYJ:C2	1.65	1.29
4:L:2:YYJ:O5	4:L:2:YYJ:C2	1.66	1.25
1:B:60:SER:HB3	1:B:144:PHE:CE2	2.04	0.92
1:B:327:ARG:HG2	1:B:328:PRO:HD2	1.50	0.92
1:B:110:LEU:CD2	1:B:278:VAL:HG13	2.01	0.89

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:GLU:OE1	1:B:351:ARG:NH1[4_445]	1.83	0.37
1:A:213:ARG:NH1	4:L:1:GU4:O21[4_445]	2.06	0.14
1:B:364:ARG:NH1	4:L:2:YYJ:O1S4[3_655]	2.19	0.01

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	416/443 (94%)	357 (86%)	52 (12%)	7 (2%)	9	40
1	B	407/443 (92%)	346 (85%)	52 (13%)	9 (2%)	6	34
All	All	823/886 (93%)	703 (85%)	104 (13%)	16 (2%)	8	38

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	75	PRO
1	B	338	ASN
1	A	212	VAL
1	B	336	GLU
1	A	168	ASP

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	351/385 (91%)	351 (100%)	0	100	100
1	B	330/385 (86%)	329 (100%)	1 (0%)	92	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	681/770 (88%)	680 (100%)	1 (0%)	93	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	335	ARG

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

Mol	Chain	Res	Type
1	A	355	ASN
1	B	201	GLN
1	B	282	GLN
1	B	416	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 ⓘ

21 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	2,1	14,14,15	1.94	4 (28%)	17,19,21	1.11	1 (5%)
2	NAG	C	2	2	14,14,15	2.11	4 (28%)	17,19,21	1.38	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BMA	C	3	2	11,11,12	1.96	3 (27%)	15,15,17	1.21	1 (6%)
3	NAG	D	1	3,1	14,14,15	1.97	4 (28%)	17,19,21	1.31	3 (17%)
3	NAG	D	2	3	14,14,15	1.91	3 (21%)	17,19,21	1.15	1 (5%)
3	NAG	E	1	3,1	14,14,15	2.07	4 (28%)	17,19,21	1.27	2 (11%)
3	NAG	E	2	3	14,14,15	1.98	4 (28%)	17,19,21	1.10	1 (5%)
3	NAG	F	1	3,1	14,14,15	1.90	4 (28%)	17,19,21	1.41	2 (11%)
3	NAG	F	2	3	14,14,15	1.99	3 (21%)	17,19,21	1.08	1 (5%)
3	NAG	G	1	3,1	14,14,15	2.22	5 (35%)	17,19,21	2.72	7 (41%)
3	NAG	G	2	3	14,14,15	1.94	3 (21%)	17,19,21	1.72	3 (17%)
3	NAG	H	1	3,1	14,14,15	1.95	4 (28%)	17,19,21	2.13	4 (23%)
3	NAG	H	2	3	14,14,15	2.09	4 (28%)	17,19,21	1.89	6 (35%)
3	NAG	I	1	3,1	14,14,15	1.61	2 (14%)	17,19,21	3.16	3 (17%)
3	NAG	I	2	3	14,14,15	2.00	4 (28%)	17,19,21	1.02	1 (5%)
3	NAG	J	1	3,1	14,14,15	1.98	4 (28%)	17,19,21	1.28	1 (5%)
3	NAG	J	2	3	14,14,15	1.97	4 (28%)	17,19,21	1.12	2 (11%)
4	GU4	K	1	4	23,23,28	1.80	5 (21%)	25,36,45	1.56	5 (20%)
4	YYJ	K	2	4	24,24,28	4.02	8 (33%)	24,39,46	1.31	3 (12%)
4	GU4	L	1	4	27,27,28	1.88	6 (22%)	29,43,45	1.56	8 (27%)
4	YYJ	L	2	4	27,28,28	3.93	10 (37%)	28,46,46	1.22	4 (14%)

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	NAG	I	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	NAG	J	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
4	GU4	K	1	4	-	9/16/33/41	0/1/1/1
4	YYJ	K	2	4	-	11/19/38/42	0/1/1/1
4	GU4	L	1	4	-	6/21/38/41	0/1/1/1
4	YYJ	L	2	4	-	12/23/42/42	0/1/1/1

The worst 5 of 92 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	2	YYJ	O5-C2	14.67	1.66	1.43
4	K	2	YYJ	O5-C2	14.57	1.65	1.43
4	L	2	YYJ	C2-C3	-7.42	1.34	1.53
4	K	2	YYJ	C2-C3	-7.14	1.35	1.53
4	L	2	YYJ	O4-C4	-6.01	1.33	1.46

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1	NAG	C1-O5-C5	-11.16	97.07	112.19
3	G	1	NAG	C4-C3-C2	-6.82	101.03	111.02
3	H	1	NAG	C1-O5-C5	-6.31	103.64	112.19
3	G	1	NAG	C1-O5-C5	5.02	118.99	112.19
3	G	2	NAG	C4-C3-C2	4.71	117.93	111.02

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

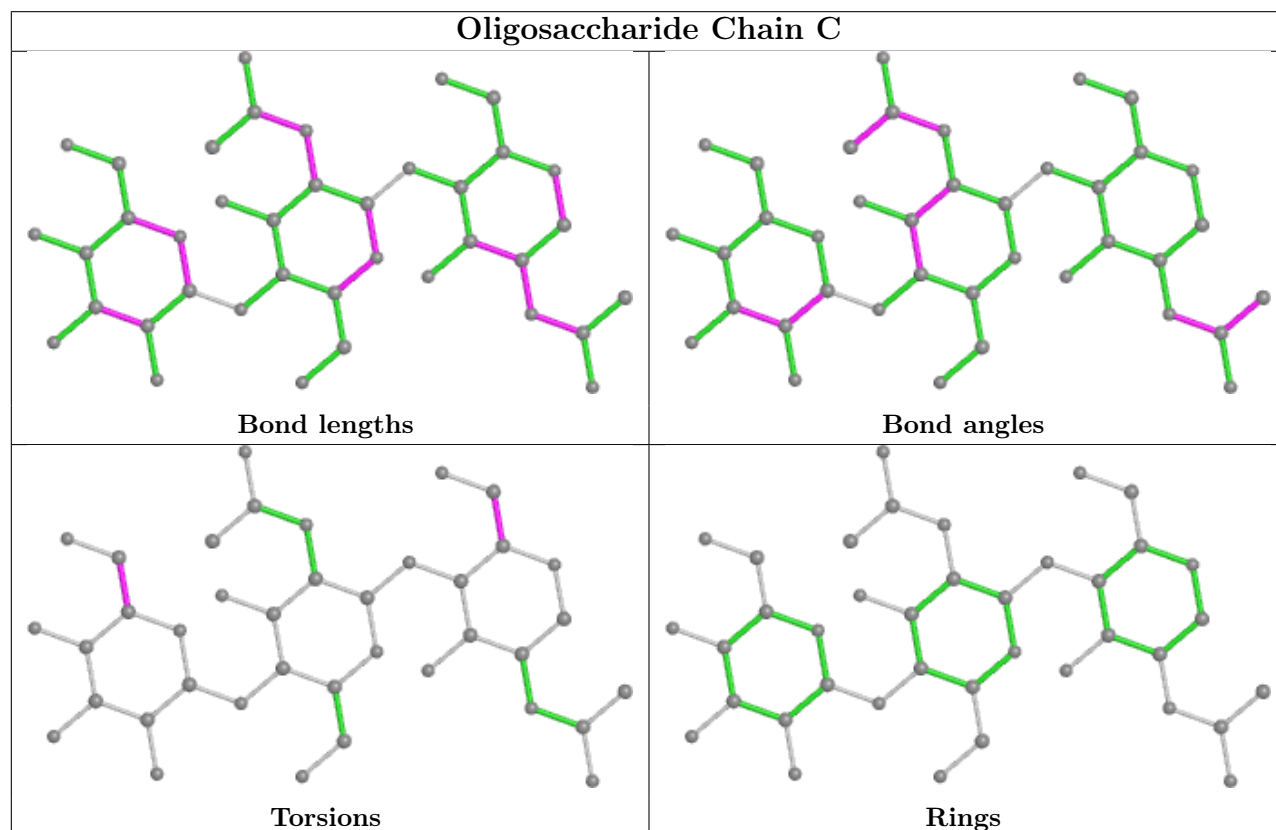
Mol	Chain	Res	Type	Atoms
4	K	1	GU4	O5-C5-C6-O6
4	K	1	GU4	C4-C5-C6-O6
4	K	1	GU4	C4-C3-O3-S3
4	K	1	GU4	C2-O2-S2-O11
4	K	1	GU4	C2-O2-S2-O10

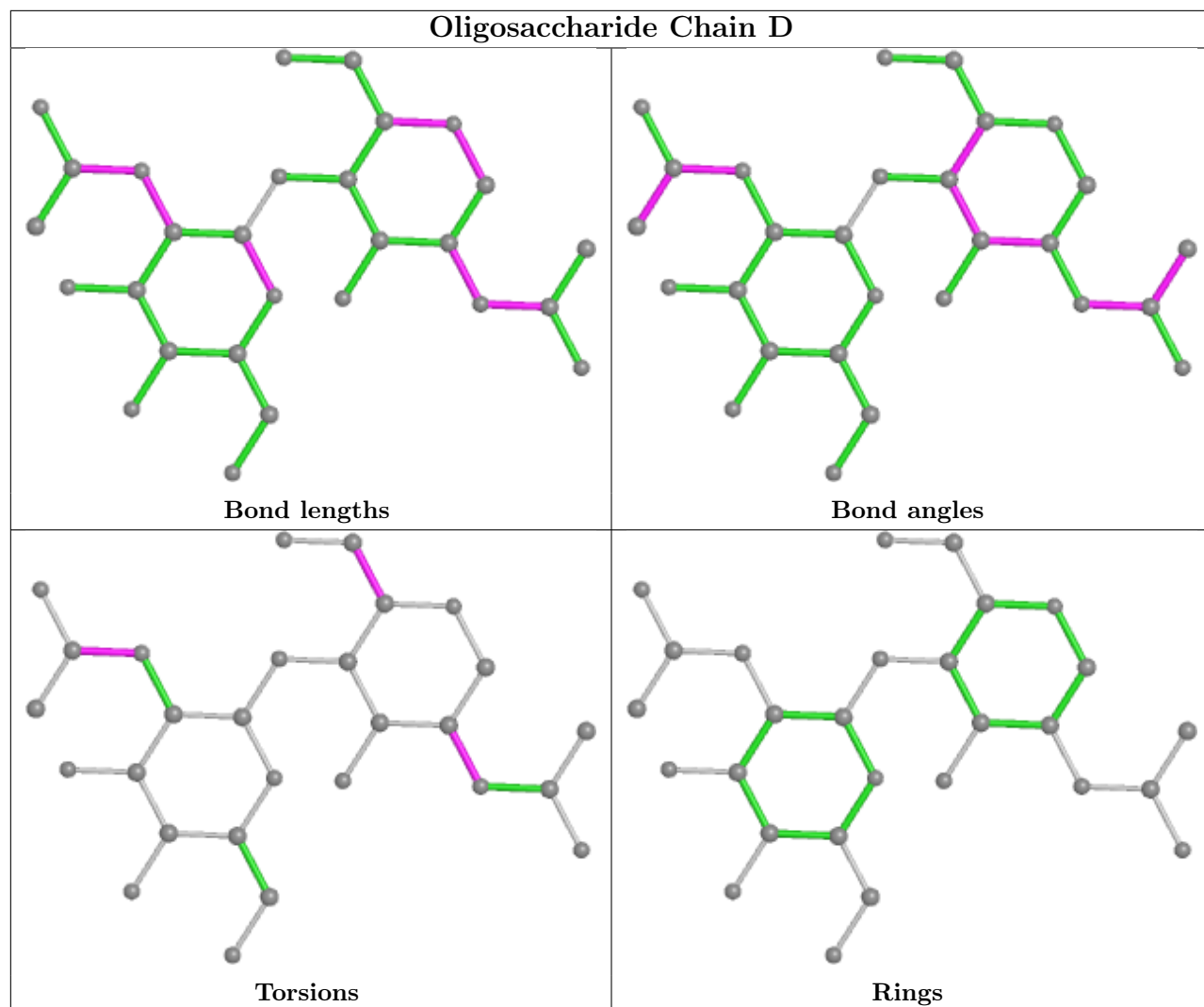
There are no ring outliers.

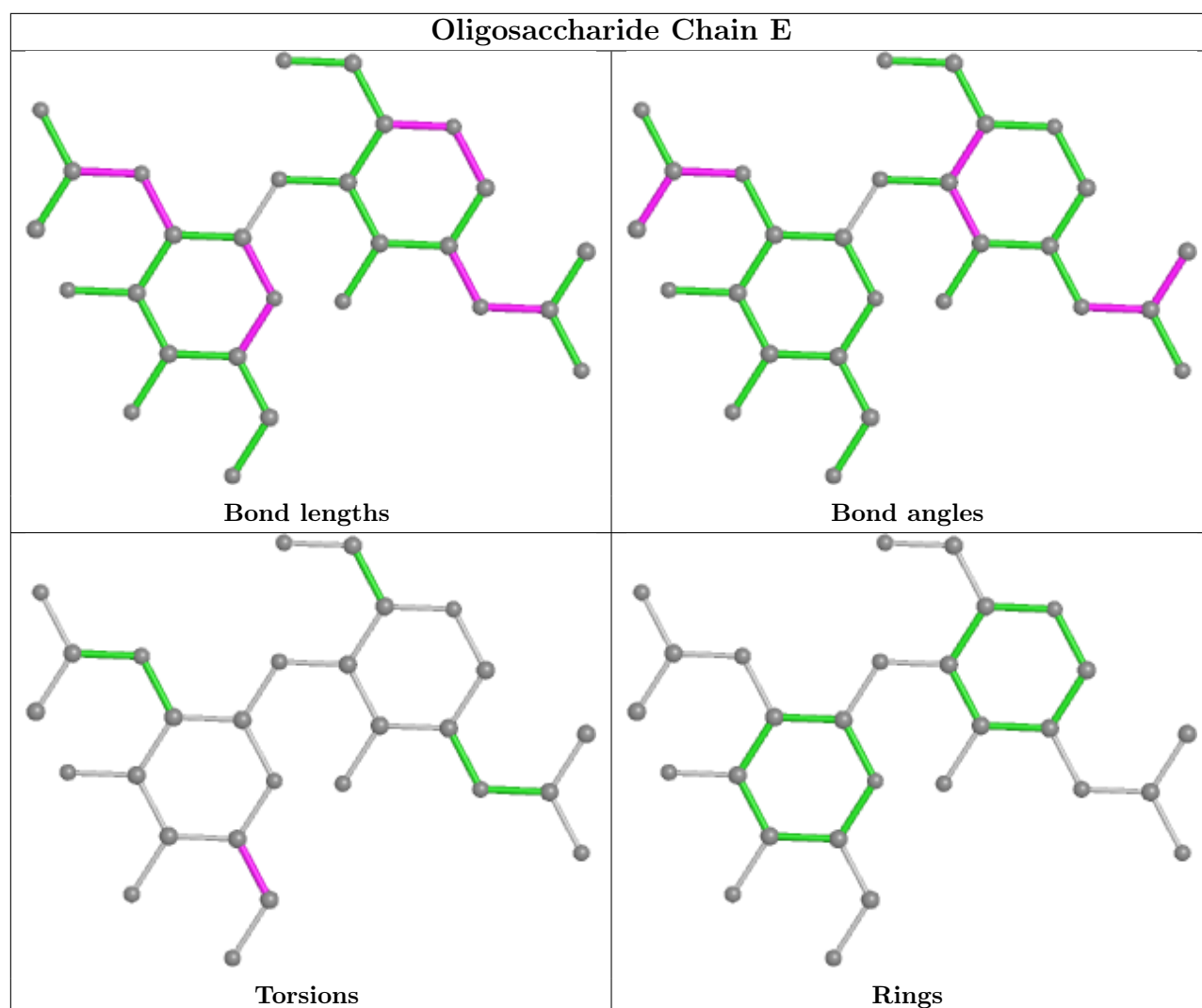
15 monomers are involved in 25 short contacts:

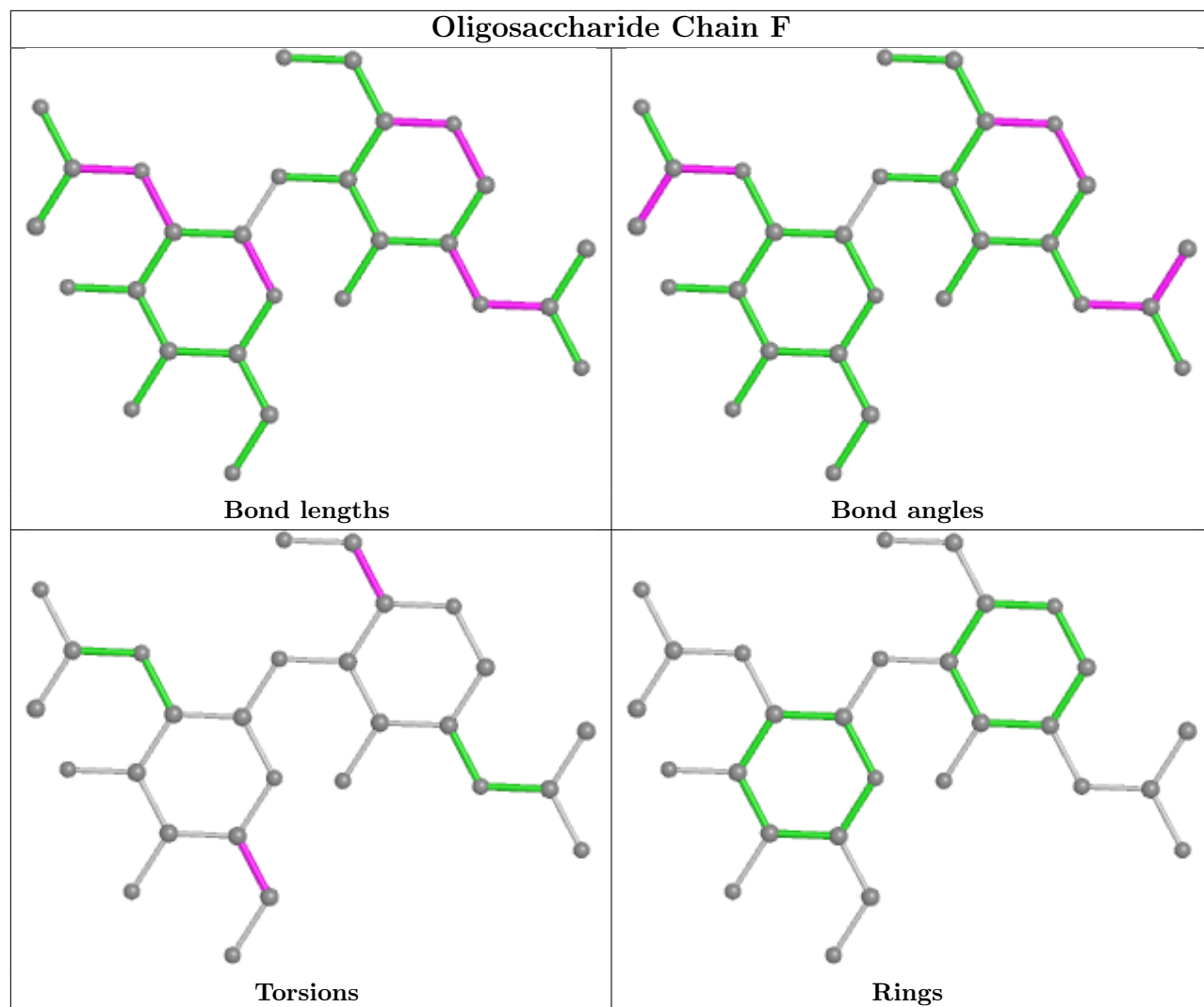
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	1	GU4	2	1
2	C	1	NAG	1	0
3	F	1	NAG	4	0
3	D	1	NAG	3	0
3	G	1	NAG	3	0
3	F	2	NAG	4	0
3	I	1	NAG	1	0
3	H	2	NAG	1	0
3	J	2	NAG	2	0
4	K	1	GU4	4	0
4	K	2	YYJ	2	0
4	L	2	YYJ	1	1
3	H	1	NAG	1	0
3	D	2	NAG	2	0
3	J	1	NAG	2	0

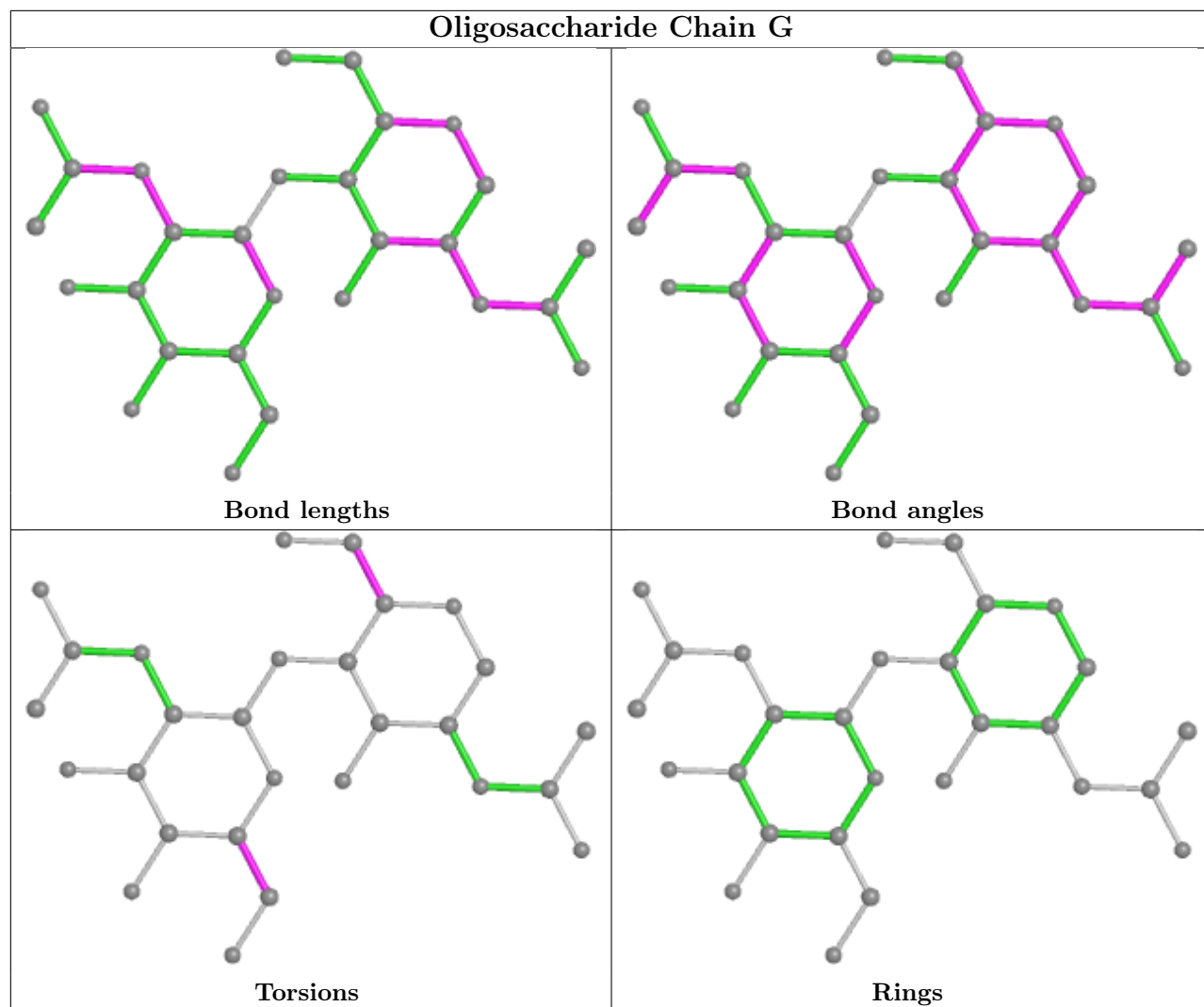
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

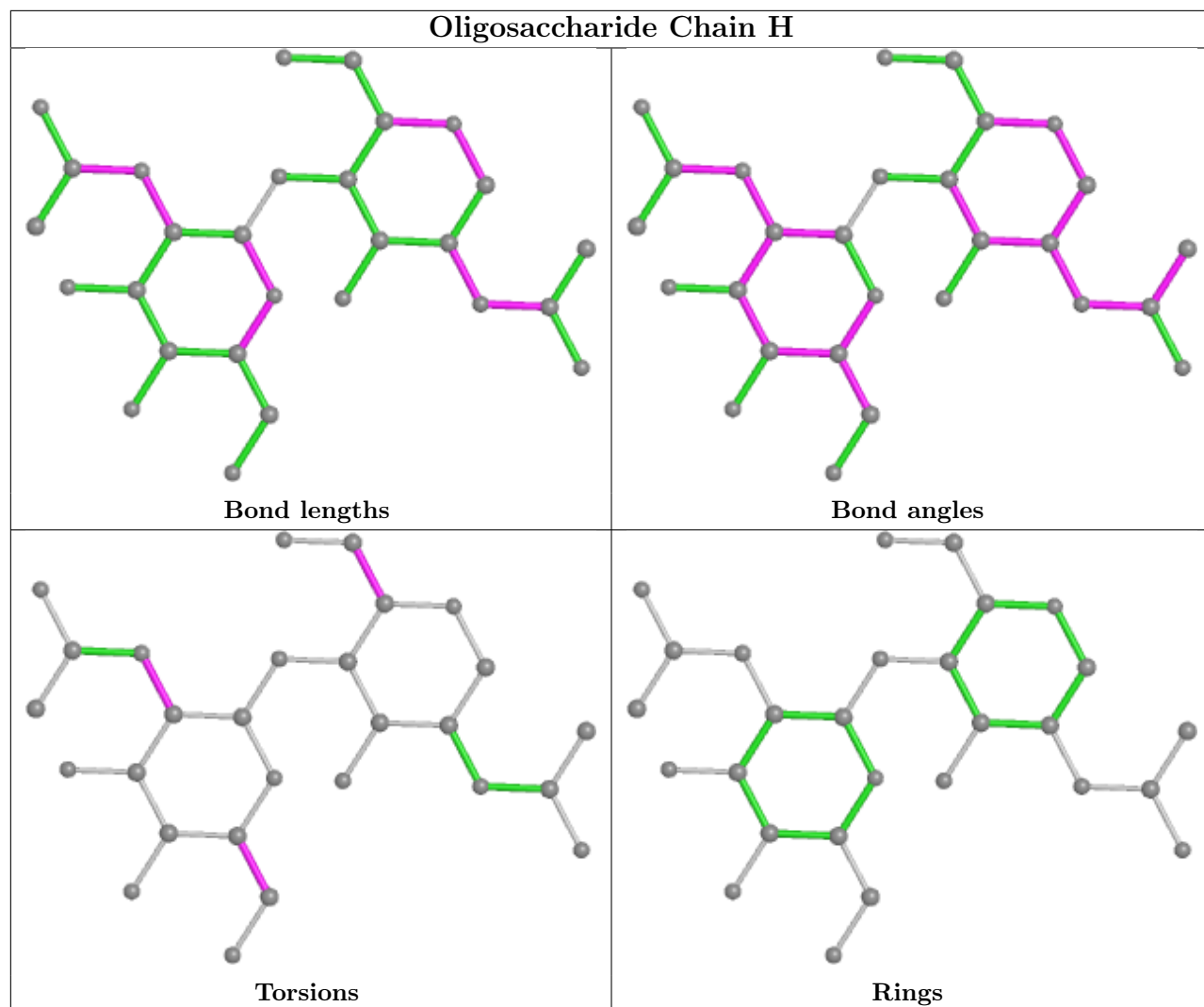


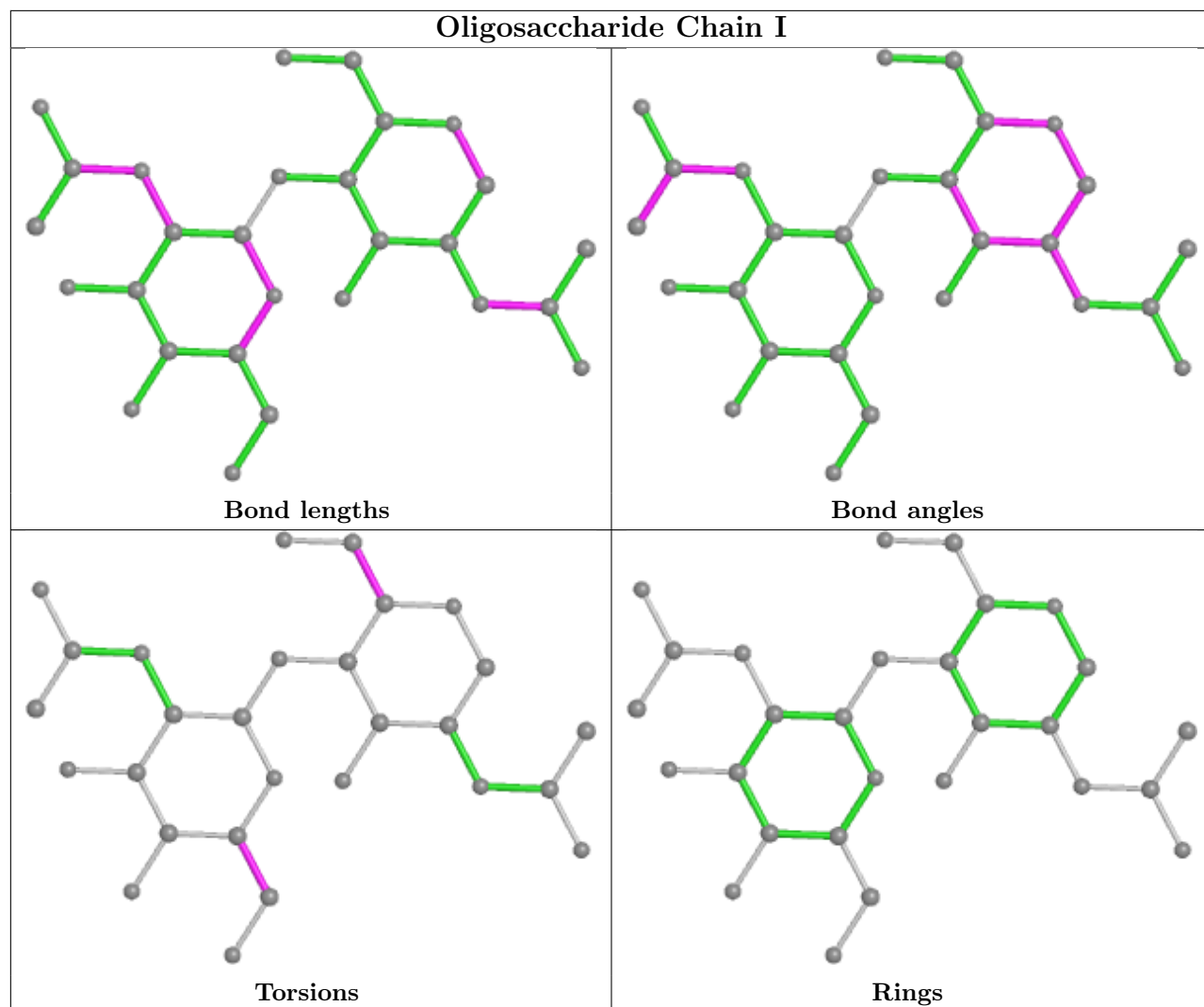


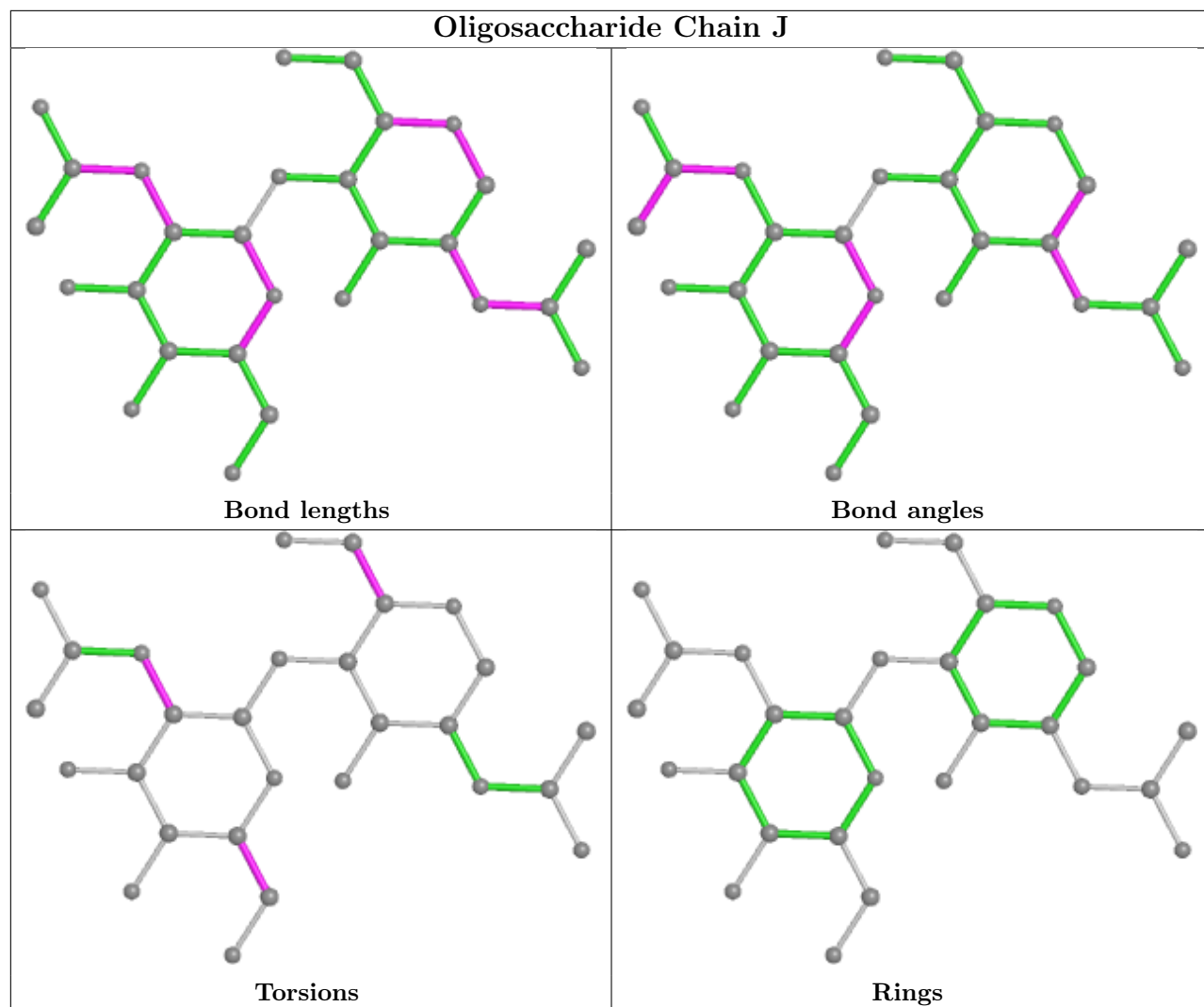




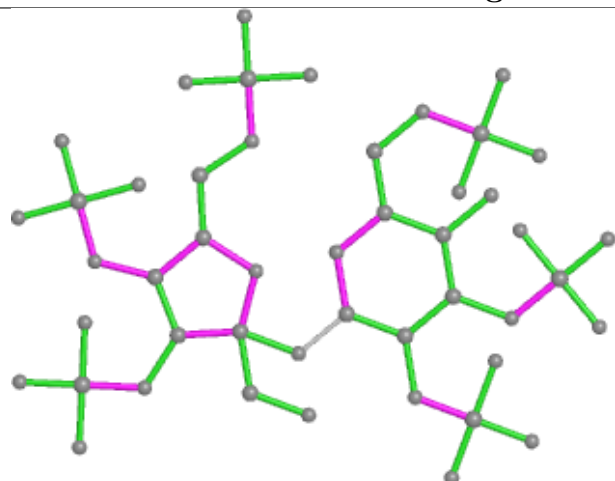




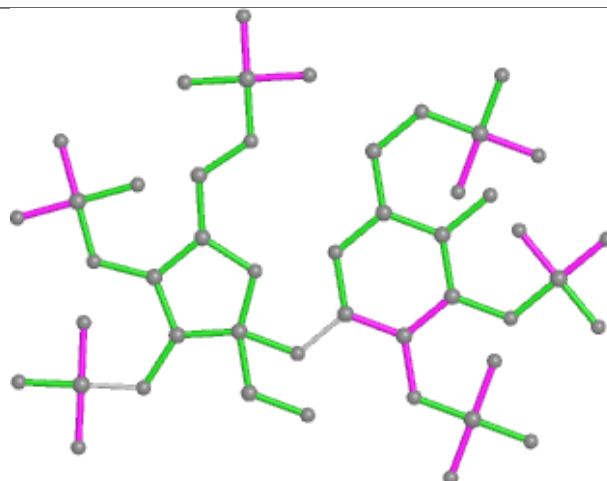




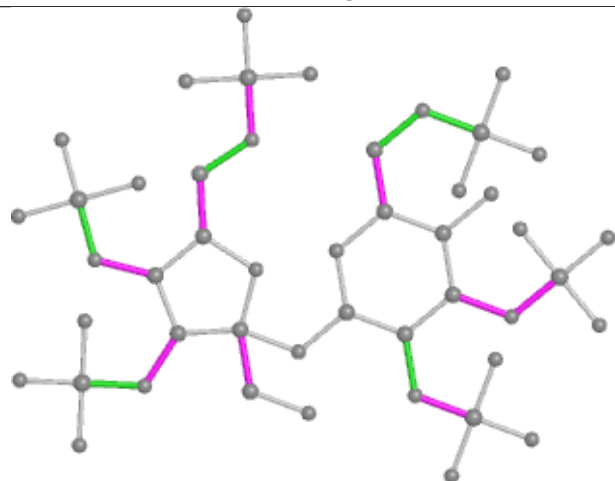
Oligosaccharide Chain K



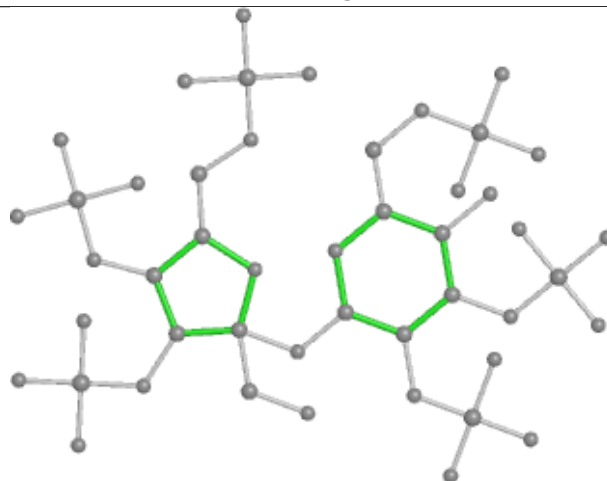
Bond lengths



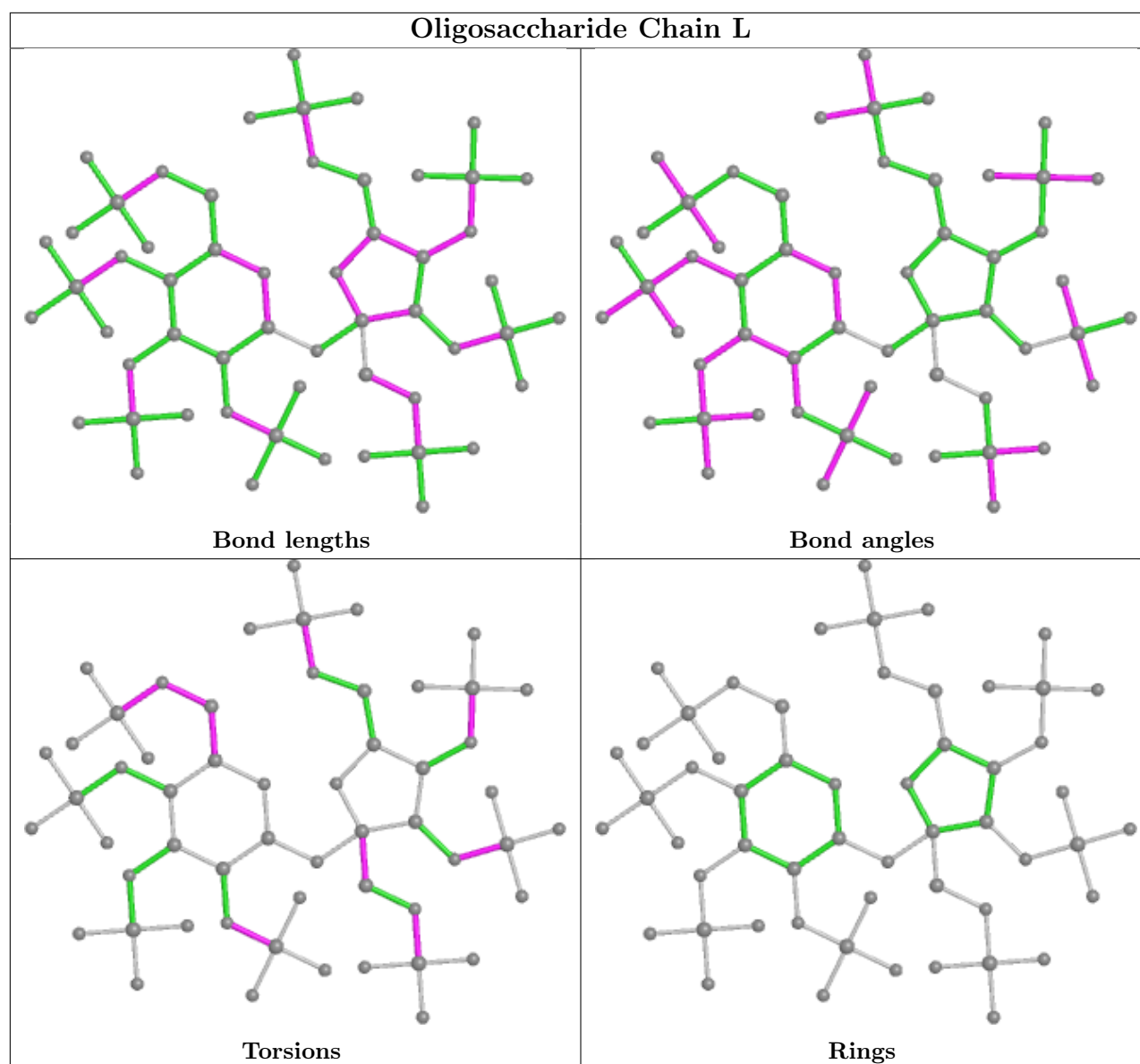
Bond angles



Torsions



Rings



5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	PEG	B	503	-	6,6,6	0.49	0	5,5,5	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NHE	B	502	-	13,13,13	1.29	3 (23%)	16,17,17	1.84	4 (25%)
5	EDO	A	503	-	3,3,3	0.49	0	2,2,2	0.03	0
5	EDO	A	501	-	3,3,3	0.48	0	2,2,2	0.27	0
5	EDO	B	501	-	3,3,3	0.47	0	2,2,2	0.33	0
5	EDO	A	502	-	3,3,3	0.50	0	2,2,2	0.26	0
6	PEG	A	504	-	6,6,6	0.47	0	5,5,5	0.36	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
6	PEG	B	503	-	-	0/4/4/4	-
9	NHE	B	502	-	-	1/7/15/15	0/1/1/1
5	EDO	A	503	-	-	0/1/1/1	-
5	EDO	A	501	-	-	1/1/1/1	-
5	EDO	B	501	-	-	0/1/1/1	-
5	EDO	A	502	-	-	0/1/1/1	-
6	PEG	A	504	-	-	0/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	502	NHE	C2-S	2.87	1.81	1.77
9	B	502	NHE	O1-S	2.26	1.51	1.45
9	B	502	NHE	O2-S	2.21	1.51	1.45

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	502	NHE	O3-S-O1	-3.80	101.99	111.27
9	B	502	NHE	O3-S-C2	3.56	111.52	105.77
9	B	502	NHE	C1-N-C1'	-3.35	107.56	114.14
9	B	502	NHE	O1-S-C2	3.28	110.86	106.92

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	502	NHE	C2-C1-N-C1'

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Mol	Chain	Res	Type	Atoms
5	A	501	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	502	NHE	1	0
5	A	503	EDO	2	0
5	B	501	EDO	2	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 [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, 95th 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 ²)	Q<0.9
1	A	418/443 (94%)	-0.03	6 (1%) 75 64	41, 86, 132, 188	0
1	B	411/443 (92%)	-0.01	10 (2%) 59 45	37, 82, 148, 203	0
All	All	829/886 (93%)	-0.02	16 (1%) 66 54	37, 85, 140, 203	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	104	ALA	4.0
1	A	369	VAL	3.8
1	A	327	ARG	3.0
1	B	105	HIS	3.0
1	A	72	CYS	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, 95th 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.

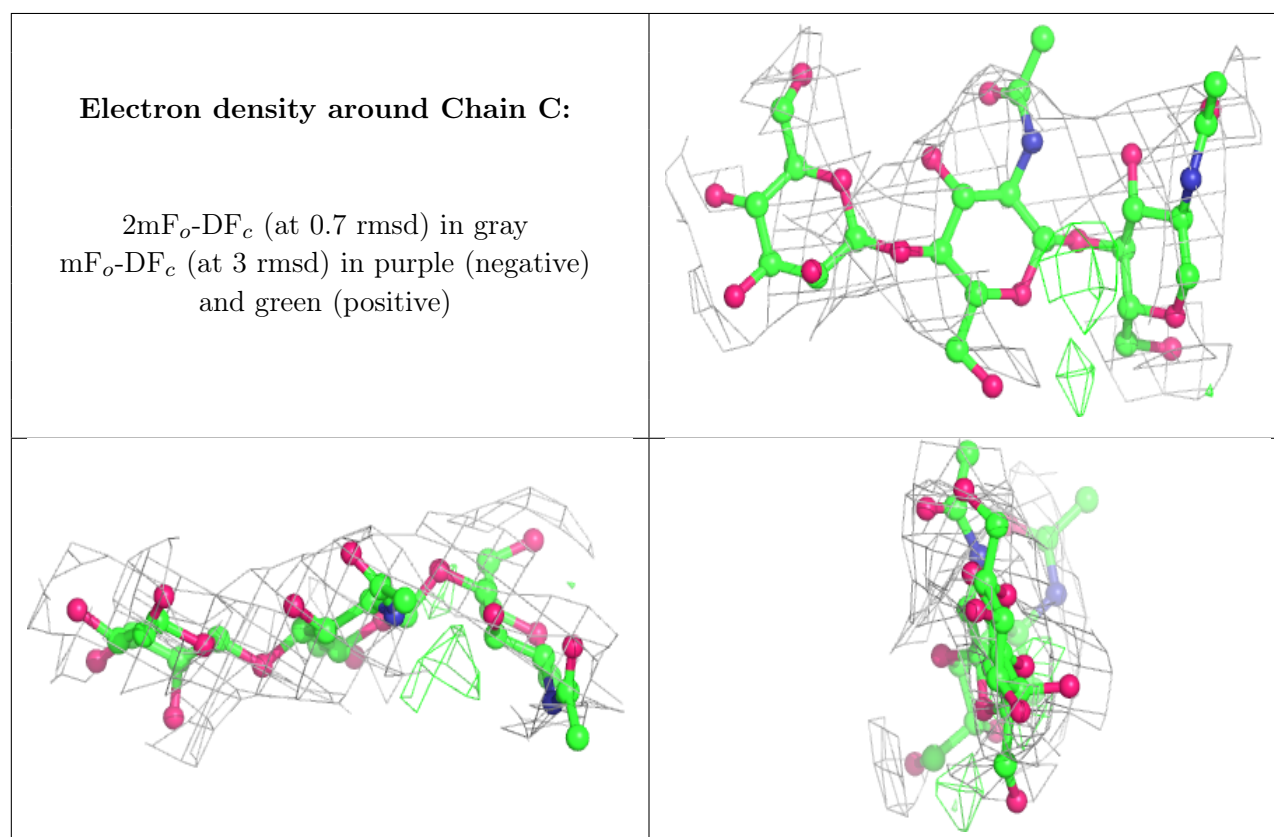
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	H	2	14/15	0.53	0.53	151,187,195,195	0
2	BMA	C	3	11/12	0.60	0.34	135,162,173,181	0
4	YYJ	L	2	28/28	0.65	0.27	201,222,251,262	0
3	NAG	F	2	14/15	0.68	0.46	153,190,193,197	0
3	NAG	H	1	14/15	0.68	0.26	134,154,180,181	0

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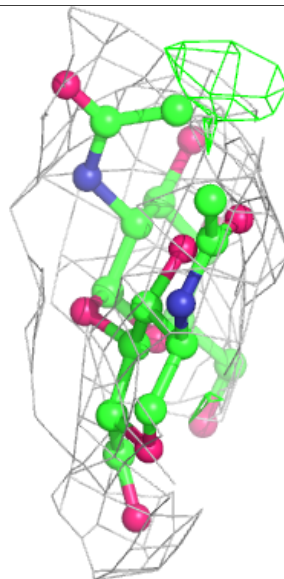
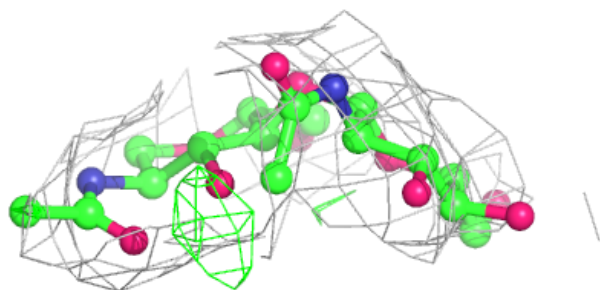
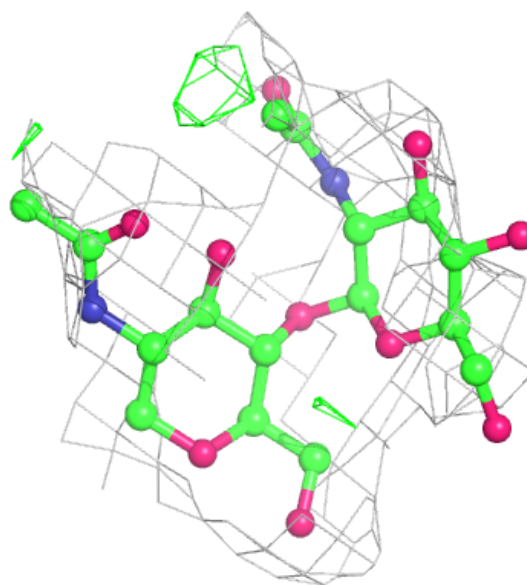
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	J	2	14/15	0.71	0.26	120,147,156,158	0
3	NAG	G	1	14/15	0.74	0.28	121,174,184,185	0
3	NAG	G	2	14/15	0.76	0.19	136,155,171,174	0
3	NAG	I	2	14/15	0.76	0.21	108,140,154,155	0
4	GU4	K	1	23/28	0.78	0.26	97,134,143,149	23
4	GU4	L	1	27/28	0.78	0.18	189,225,258,269	0
3	NAG	D	1	14/15	0.78	0.26	135,165,175,178	0
4	YYJ	K	2	24/28	0.80	0.17	136,154,169,174	24
3	NAG	D	2	14/15	0.81	0.35	145,166,176,176	0
2	NAG	C	2	14/15	0.81	0.27	130,150,164,166	0
3	NAG	F	1	14/15	0.83	0.28	166,176,185,191	0
3	NAG	E	2	14/15	0.84	0.39	138,149,160,161	0
3	NAG	I	1	14/15	0.86	0.15	112,122,131,136	0
3	NAG	J	1	14/15	0.87	0.24	79,108,131,133	0
3	NAG	E	1	14/15	0.87	0.23	86,100,119,127	0
2	NAG	C	1	14/15	0.87	0.17	87,121,136,145	0

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.



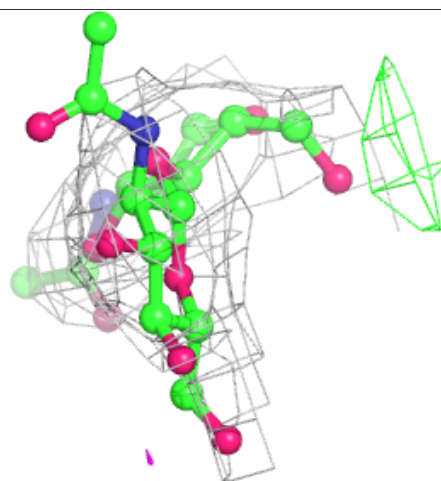
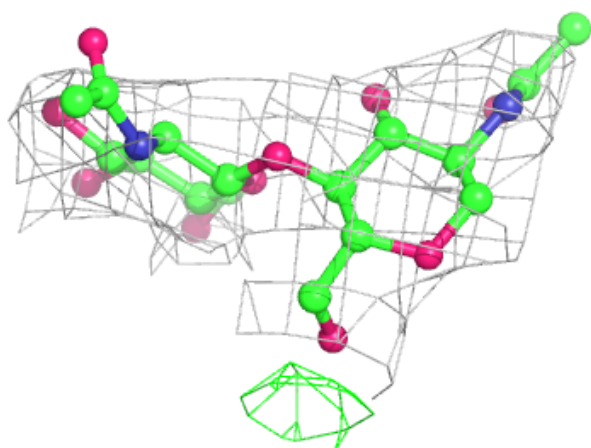
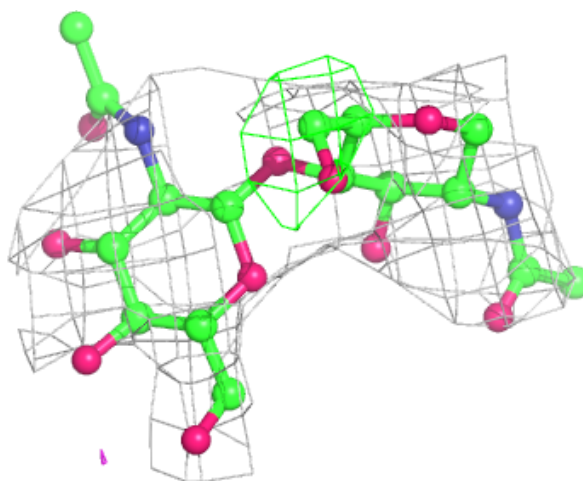
Electron density around Chain D:

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



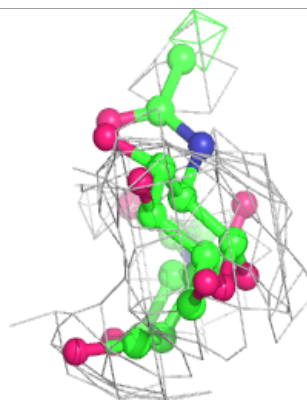
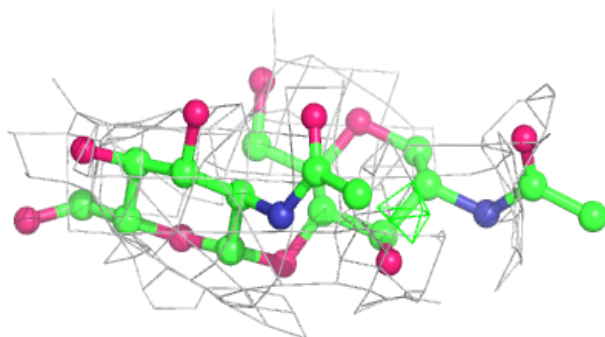
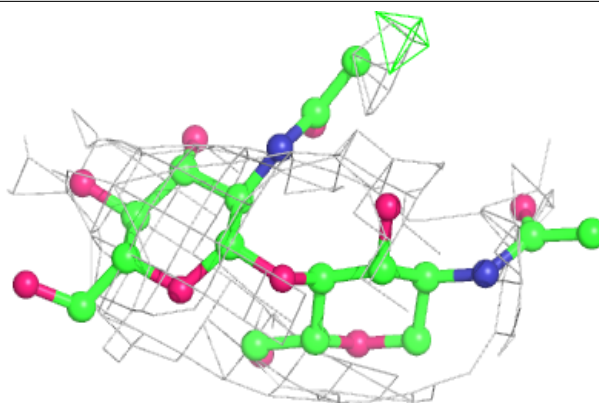
Electron density around Chain E:

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



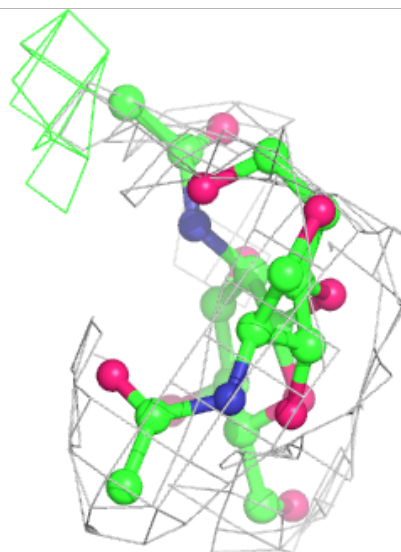
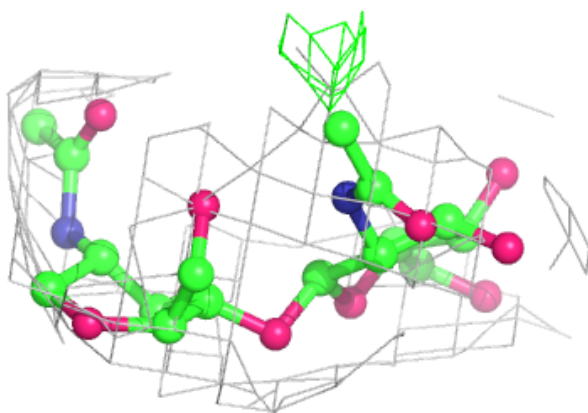
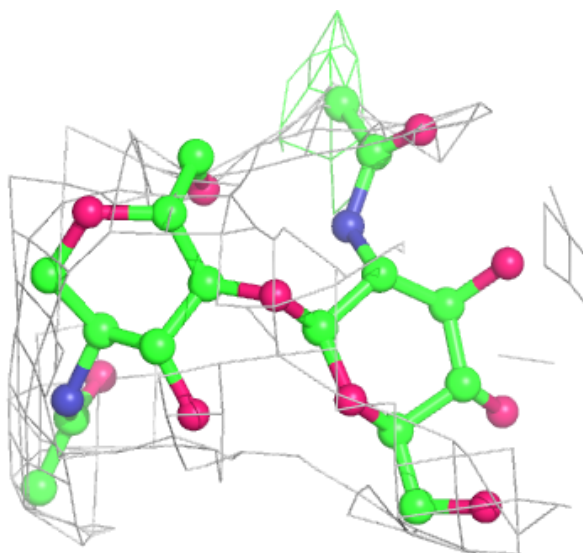
Electron density around Chain F:

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



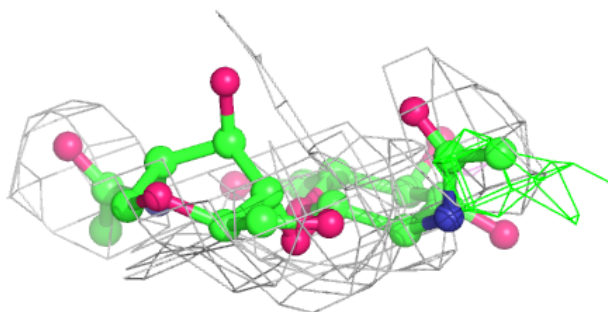
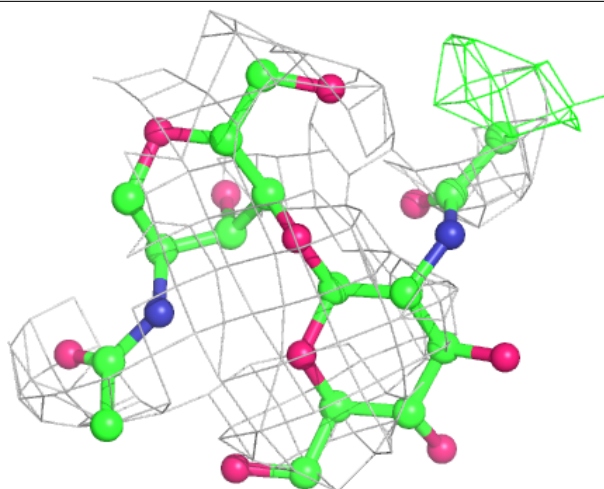
Electron density around Chain G:

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



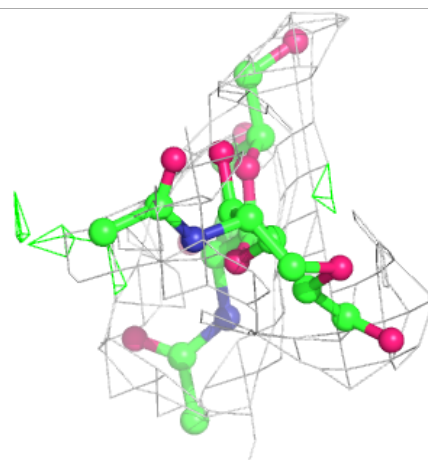
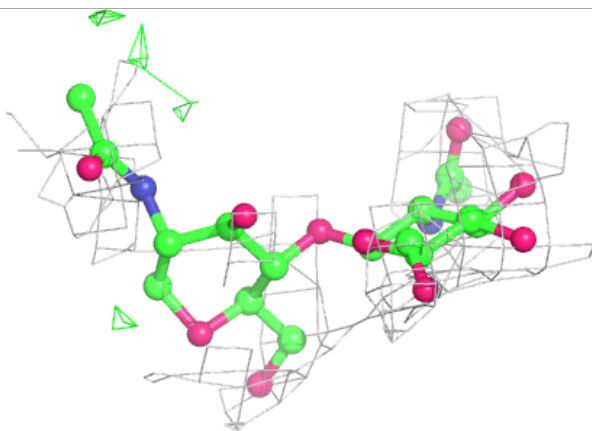
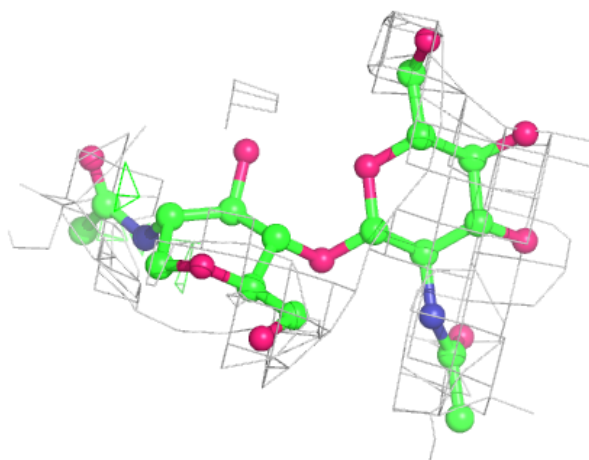
Electron density around Chain H:

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



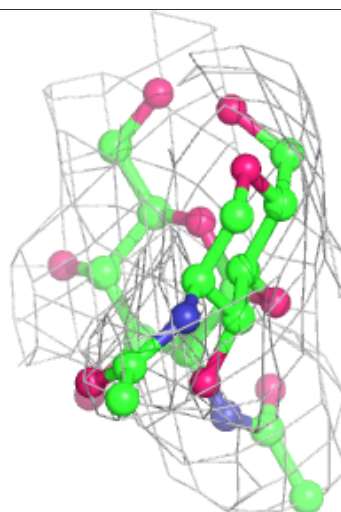
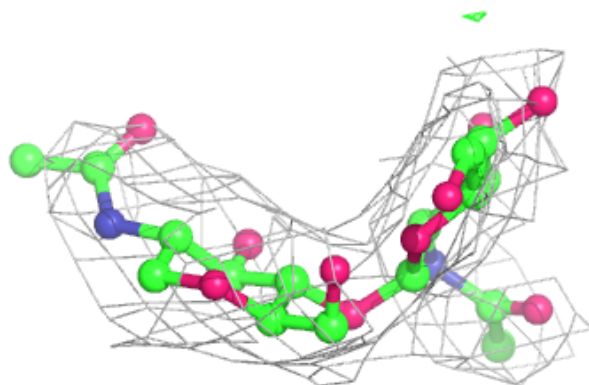
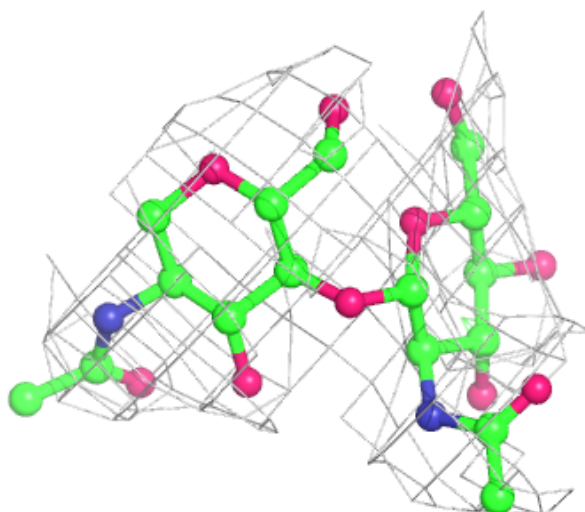
Electron density around Chain I:

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



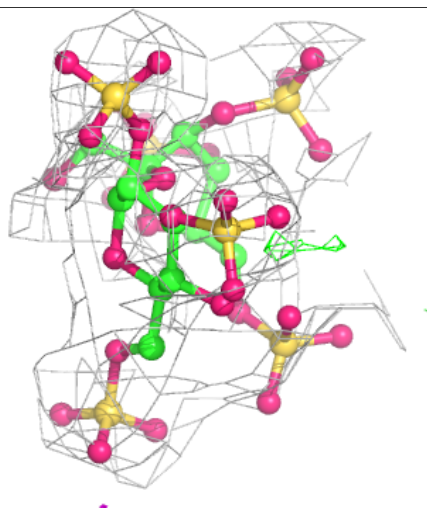
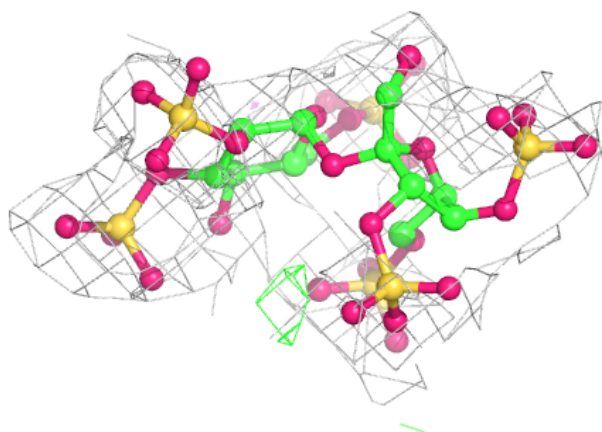
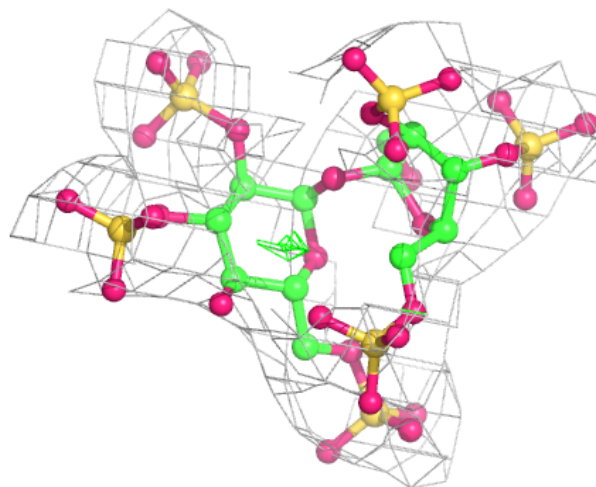
Electron density around Chain J:

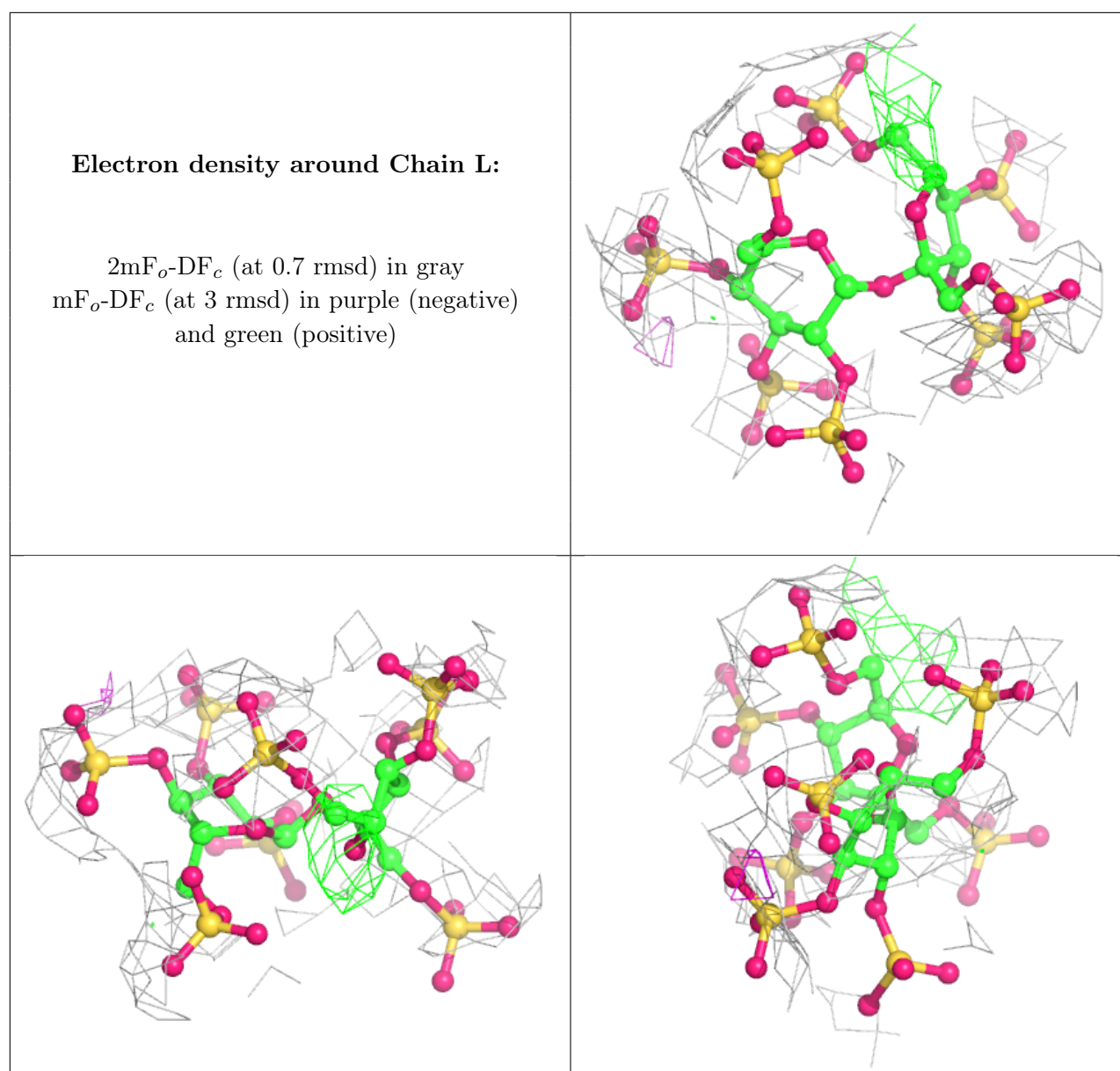
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain K:

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





6.4 Ligands ⓘ

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, 95th 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 ²)	Q<0.9
5	EDO	A	502	4/4	0.71	0.54	83,100,121,121	0
5	EDO	B	501	4/4	0.77	0.48	92,111,119,119	0
9	NHE	B	502	13/13	0.79	0.28	96,97,145,154	0
6	PEG	A	504	7/7	0.82	0.98	80,100,122,122	0
6	PEG	B	503	7/7	0.85	0.39	64,96,115,116	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	A	501	4/4	0.86	0.62	76,81,83,87	0
5	EDO	A	503	4/4	0.89	0.30	66,88,106,106	0
7	CA	A	505	1/1	0.93	0.33	305,305,305,305	0
10	CL	B	505	1/1	0.94	0.10	77,77,77,77	0
7	CA	B	504	1/1	0.95	0.22	137,137,137,137	0
8	NA	A	506	1/1	0.97	0.11	77,77,77,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.