



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 12:44 PM UTC

PDB ID : 6IAA / pdb_00006iaa
Title : hRobo2 ectodomain
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Deposited on : 2018-11-26
Resolution : 3.60 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

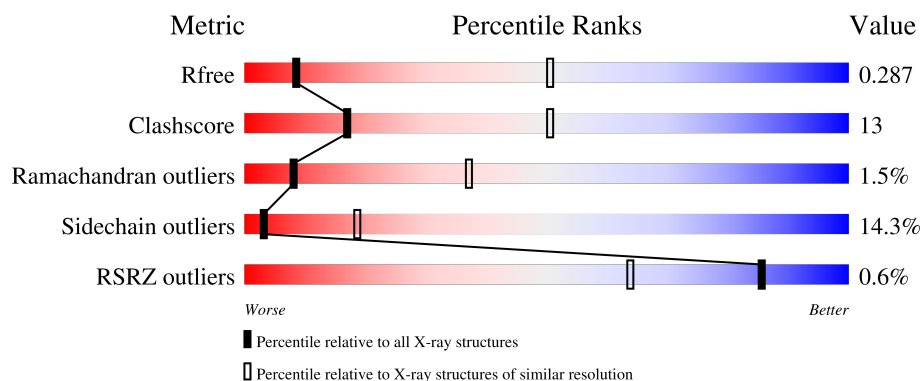
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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.



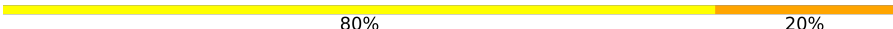
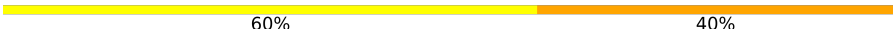
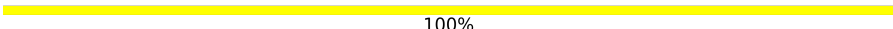
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	859	 60% 29% 6% 5%
1	B	859	 62% 27% 6% 5%
1	C	859	 61% 29% 5% 5%
2	D	2	 100%
2	F	2	 100%

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Mol	Chain	Length	Quality of chain
2	H	2	 50% 50%
3	E	5	 80% 20%
3	G	5	 60% 40%
3	I	5	 100%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19296 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 Roundabout homolog 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	815	Total	C	N	O	S	Se	0	0	0
			6343	3969	1125	1226	12	11			
1	B	815	Total	C	N	O	S	Se	0	0	0
			6343	3969	1125	1226	12	11			
1	C	815	Total	C	N	O	S	Se	0	0	0
			6343	3969	1125	1226	12	11			

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	ASP	-	expression tag	UNP Q9HCK4
A	12	TYR	-	expression tag	UNP Q9HCK4
A	13	LYS	-	expression tag	UNP Q9HCK4
A	14	ASP	-	expression tag	UNP Q9HCK4
A	15	ASP	-	expression tag	UNP Q9HCK4
A	16	ASP	-	expression tag	UNP Q9HCK4
A	17	ASP	-	expression tag	UNP Q9HCK4
A	18	LYS	-	expression tag	UNP Q9HCK4
A	19	ARG	-	expression tag	UNP Q9HCK4
A	20	PRO	-	expression tag	UNP Q9HCK4
A	21	HIS	-	expression tag	UNP Q9HCK4
A	860	LYS	-	expression tag	UNP Q9HCK4
A	861	LEU	-	expression tag	UNP Q9HCK4
A	862	GLY	-	expression tag	UNP Q9HCK4
A	863	SER	-	expression tag	UNP Q9HCK4
A	864	HIS	-	expression tag	UNP Q9HCK4
A	865	HIS	-	expression tag	UNP Q9HCK4
A	866	HIS	-	expression tag	UNP Q9HCK4
A	867	HIS	-	expression tag	UNP Q9HCK4
A	868	HIS	-	expression tag	UNP Q9HCK4
A	869	HIS	-	expression tag	UNP Q9HCK4
B	11	ASP	-	expression tag	UNP Q9HCK4
B	12	TYR	-	expression tag	UNP Q9HCK4

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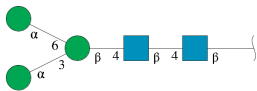
Chain	Residue	Modelled	Actual	Comment	Reference
B	13	LYS	-	expression tag	UNP Q9HCK4
B	14	ASP	-	expression tag	UNP Q9HCK4
B	15	ASP	-	expression tag	UNP Q9HCK4
B	16	ASP	-	expression tag	UNP Q9HCK4
B	17	ASP	-	expression tag	UNP Q9HCK4
B	18	LYS	-	expression tag	UNP Q9HCK4
B	19	ARG	-	expression tag	UNP Q9HCK4
B	20	PRO	-	expression tag	UNP Q9HCK4
B	21	HIS	-	expression tag	UNP Q9HCK4
B	860	LYS	-	expression tag	UNP Q9HCK4
B	861	LEU	-	expression tag	UNP Q9HCK4
B	862	GLY	-	expression tag	UNP Q9HCK4
B	863	SER	-	expression tag	UNP Q9HCK4
B	864	HIS	-	expression tag	UNP Q9HCK4
B	865	HIS	-	expression tag	UNP Q9HCK4
B	866	HIS	-	expression tag	UNP Q9HCK4
B	867	HIS	-	expression tag	UNP Q9HCK4
B	868	HIS	-	expression tag	UNP Q9HCK4
B	869	HIS	-	expression tag	UNP Q9HCK4
C	11	ASP	-	expression tag	UNP Q9HCK4
C	12	TYR	-	expression tag	UNP Q9HCK4
C	13	LYS	-	expression tag	UNP Q9HCK4
C	14	ASP	-	expression tag	UNP Q9HCK4
C	15	ASP	-	expression tag	UNP Q9HCK4
C	16	ASP	-	expression tag	UNP Q9HCK4
C	17	ASP	-	expression tag	UNP Q9HCK4
C	18	LYS	-	expression tag	UNP Q9HCK4
C	19	ARG	-	expression tag	UNP Q9HCK4
C	20	PRO	-	expression tag	UNP Q9HCK4
C	21	HIS	-	expression tag	UNP Q9HCK4
C	860	LYS	-	expression tag	UNP Q9HCK4
C	861	LEU	-	expression tag	UNP Q9HCK4
C	862	GLY	-	expression tag	UNP Q9HCK4
C	863	SER	-	expression tag	UNP Q9HCK4
C	864	HIS	-	expression tag	UNP Q9HCK4
C	865	HIS	-	expression tag	UNP Q9HCK4
C	866	HIS	-	expression tag	UNP Q9HCK4
C	867	HIS	-	expression tag	UNP Q9HCK4
C	868	HIS	-	expression tag	UNP Q9HCK4
C	869	HIS	-	expression tag	UNP Q9HCK4

- 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	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is an oligosaccharide called 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.

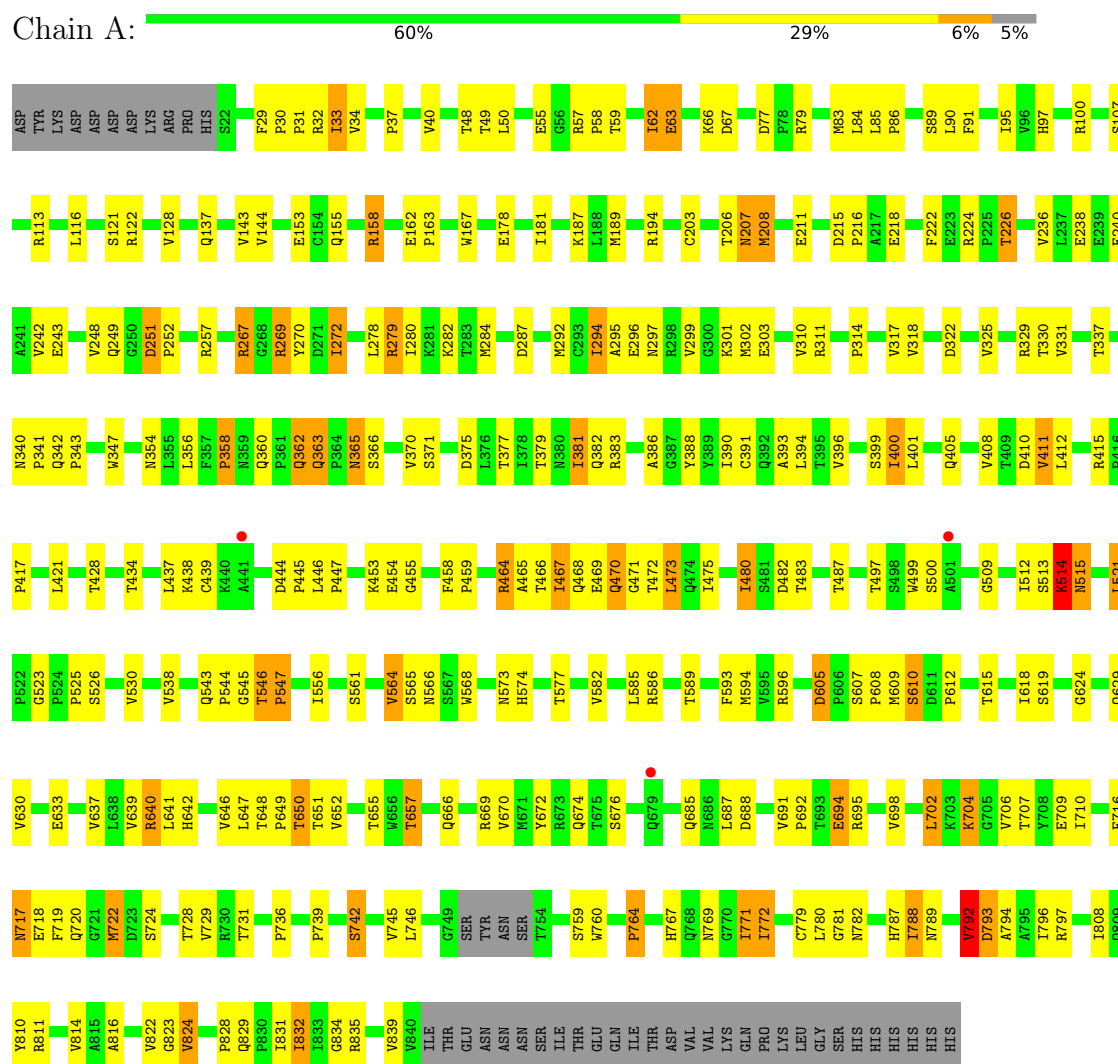


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	5	Total	C	N	O	0	0	0
			61	34	2	25			
3	G	5	Total	C	N	O	0	0	0
			61	34	2	25			
3	I	5	Total	C	N	O	0	0	0
			61	34	2	25			

3 Residue-property plots

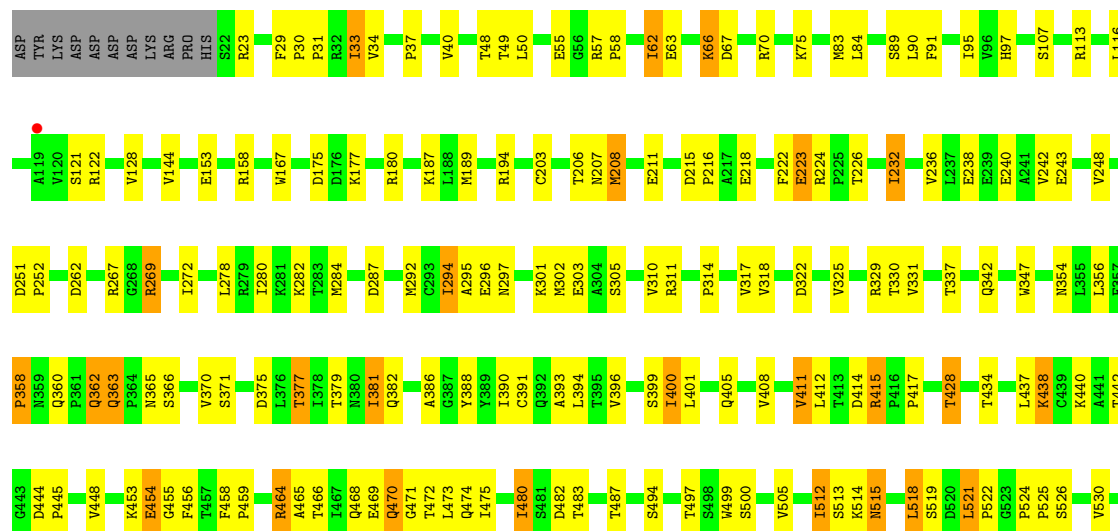
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

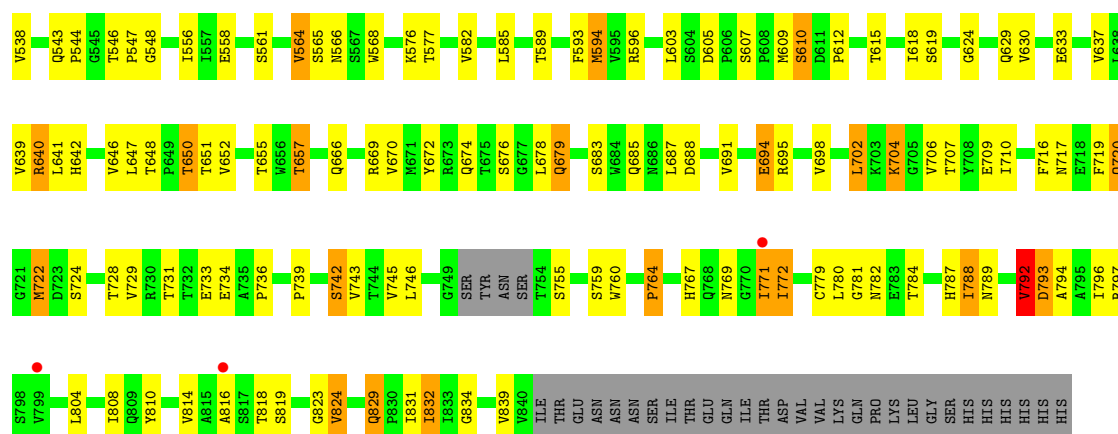
• Molecule 1: Roundabout homolog 2



• Molecule 1: Roundabout homolog 2







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

Chain D: 100%



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

Chain F: 100%



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

Chain H: 50%



- Molecule 3: 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 E: 80%



- Molecule 3: 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 G: 60%



- Molecule 3: 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:

100%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	290.77Å 81.57Å 158.66Å 90.00° 94.00° 90.00°	Depositor
Resolution (Å)	78.65 – 3.60 78.65 – 3.60	Depositor EDS
% Data completeness (in resolution range)	85.1 (78.65-3.60) 85.1 (78.65-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 3.58Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.222 , 0.287 0.223 , 0.287	Depositor DCC
R_{free} test set	1909 reflections (4.39%)	wwPDB-VP
Wilson B-factor (Å ²)	95.0	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 66.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	19296	wwPDB-VP
Average B, all atoms (Å ²)	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.90 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6991e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MAN, BMA, NAG

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	0.65	4/6472 (0.1%)	1.08	15/8806 (0.2%)
1	B	0.61	2/6472 (0.0%)	1.04	13/8806 (0.1%)
1	C	0.66	2/6472 (0.0%)	1.07	12/8806 (0.1%)
All	All	0.64	8/19416 (0.0%)	1.06	40/26418 (0.2%)

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	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	113	ARG	CZ-NH2	10.57	1.47	1.33
1	A	63	GLU	CD-OE2	-10.42	1.05	1.25
1	C	63	GLU	CD-OE2	8.83	1.42	1.25
1	A	113	ARG	CZ-NH2	8.77	1.44	1.33
1	C	113	ARG	CZ-NH2	8.68	1.44	1.33

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	63	GLU	OE1-CD-OE2	14.38	157.41	122.90
1	A	63	GLU	CG-CD-OE2	-12.65	89.30	118.40
1	C	722	MSE	CG-SE-CE	9.23	119.23	98.92
1	B	302	MSE	CG-SE-CE	8.95	118.61	98.92
1	A	722	MSE	CG-SE-CE	8.51	117.64	98.92

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	63	GLU	Sidechain

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	6343	0	6309	174	0
1	B	6343	0	6309	152	0
1	C	6343	0	6309	157	0
2	D	28	0	25	1	0
2	F	28	0	25	0	0
2	H	28	0	25	2	0
3	E	61	0	52	1	0
3	G	61	0	52	1	0
3	I	61	0	52	1	0
All	All	19296	0	19158	488	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 13.

The worst 5 of 488 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:526:SER:OG	1:B:543:GLN:HG2	1.54	1.06
1:C:438:LYS:HA	1:C:472:THR:HG22	1.39	1.04
1:C:232:ILE:HD12	1:C:232:ILE:H	1.33	0.91
1:B:394:LEU:HD13	1:B:399:SER:HB3	1.53	0.91
1:B:232:ILE:H	1:B:232:ILE:HD12	1.36	0.88

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	811/859 (94%)	721 (89%)	75 (9%)	15 (2%)	6	34
1	B	811/859 (94%)	724 (89%)	77 (10%)	10 (1%)	10	41
1	C	811/859 (94%)	722 (89%)	78 (10%)	11 (1%)	9	38
All	All	2433/2577 (94%)	2167 (89%)	230 (10%)	36 (2%)	8	37

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	515	ASN
1	A	546	THR
1	B	512	ILE
1	A	358	PRO
1	A	454	GLU

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	715/747 (96%)	620 (87%)	95 (13%)	4	21
1	B	715/747 (96%)	609 (85%)	106 (15%)	3	17
1	C	715/747 (96%)	610 (85%)	105 (15%)	3	17
All	All	2145/2241 (96%)	1839 (86%)	306 (14%)	3	19

5 of 306 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	356	LEU
1	C	704	LYS
1	C	382	GLN
1	C	538	VAL
1	C	792	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	631	GLN
1	C	663	GLN
1	C	773	GLN
1	A	829	GLN
1	A	789	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 ⓘ

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	D	1	2,1	14,14,15	0.54	0	17,19,21	2.06	5 (29%)
2	NAG	D	2	2	14,14,15	0.69	0	17,19,21	1.41	2 (11%)
3	NAG	E	1	1,3	14,14,15	0.65	0	17,19,21	1.66	2 (11%)
3	NAG	E	2	3	14,14,15	1.03	1 (7%)	17,19,21	2.36	9 (52%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BMA	E	3	3	11,11,12	1.00	0	15,15,17	1.61	4 (26%)
3	MAN	E	4	3	11,11,12	0.37	0	15,15,17	1.23	2 (13%)
3	MAN	E	5	3	11,11,12	0.75	0	15,15,17	2.06	3 (20%)
2	NAG	F	1	2,1	14,14,15	0.63	0	17,19,21	2.48	5 (29%)
2	NAG	F	2	2	14,14,15	0.63	0	17,19,21	1.44	2 (11%)
3	NAG	G	1	1,3	14,14,15	0.52	0	17,19,21	2.38	5 (29%)
3	NAG	G	2	3	14,14,15	0.53	0	17,19,21	1.22	3 (17%)
3	BMA	G	3	3	11,11,12	1.25	1 (9%)	15,15,17	2.70	6 (40%)
3	MAN	G	4	3	11,11,12	0.71	0	15,15,17	1.74	4 (26%)
3	MAN	G	5	3	11,11,12	0.41	0	15,15,17	1.02	1 (6%)
2	NAG	H	1	2,1	14,14,15	0.76	0	17,19,21	1.56	3 (17%)
2	NAG	H	2	2	14,14,15	0.95	1 (7%)	17,19,21	1.58	3 (17%)
3	NAG	I	1	1,3	14,14,15	0.62	0	17,19,21	2.09	4 (23%)
3	NAG	I	2	3	14,14,15	0.82	0	17,19,21	2.94	9 (52%)
3	BMA	I	3	3	11,11,12	0.68	0	15,15,17	1.40	2 (13%)
3	MAN	I	4	3	11,11,12	0.68	0	15,15,17	1.65	4 (26%)
3	MAN	I	5	3	11,11,12	0.64	0	15,15,17	0.79	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
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
3	NAG	E	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1
3	MAN	E	4	3	-	1/2/19/22	0/1/1/1
3	MAN	E	5	3	-	0/2/19/22	0/1/1/1
2	NAG	F	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
3	NAG	G	1	1,3	-	5/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	BMA	G	3	3	-	2/2/19/22	0/1/1/1
3	MAN	G	4	3	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	G	5	3	-	2/2/19/22	1/1/1/1
2	NAG	H	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	H	2	2	-	3/6/23/26	0/1/1/1
3	NAG	I	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	BMA	I	3	3	-	2/2/19/22	1/1/1/1
3	MAN	I	4	3	-	2/2/19/22	0/1/1/1
3	MAN	I	5	3	-	1/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	3	BMA	C2-C3	3.35	1.57	1.52
2	H	2	NAG	C1-C2	2.52	1.55	1.52
3	E	2	NAG	C1-C2	2.25	1.55	1.52

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	2	NAG	C4-C3-C2	-7.15	100.54	111.02
2	F	1	NAG	C1-O5-C5	6.13	120.40	112.19
3	G	3	BMA	C1-C2-C3	5.34	117.42	109.64
3	E	5	MAN	C1-O5-C5	5.26	119.24	112.19
3	G	1	NAG	C1-O5-C5	5.17	119.11	112.19

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	F	1	NAG	C8-C7-N2-C2

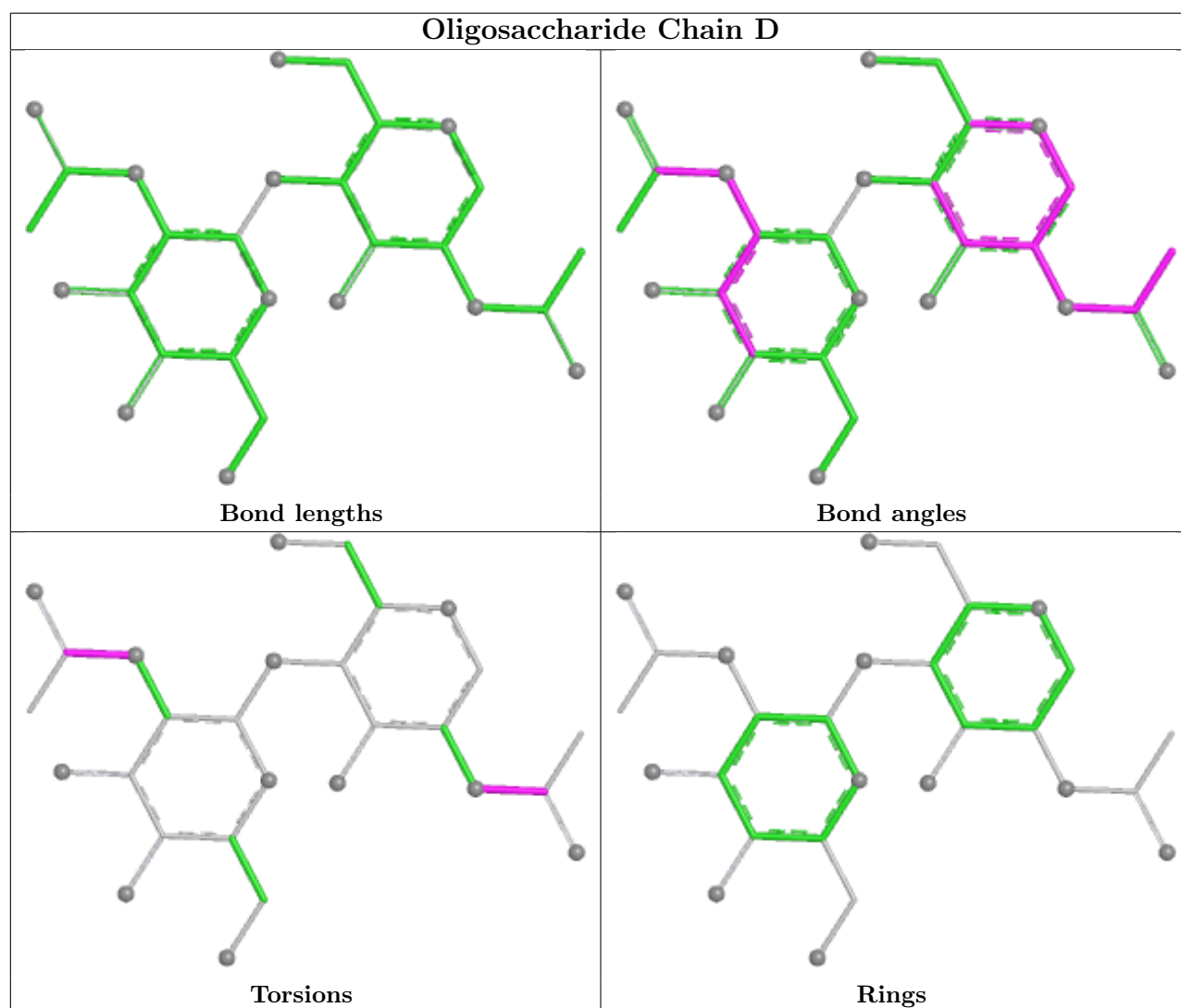
All (2) ring outliers are listed below:

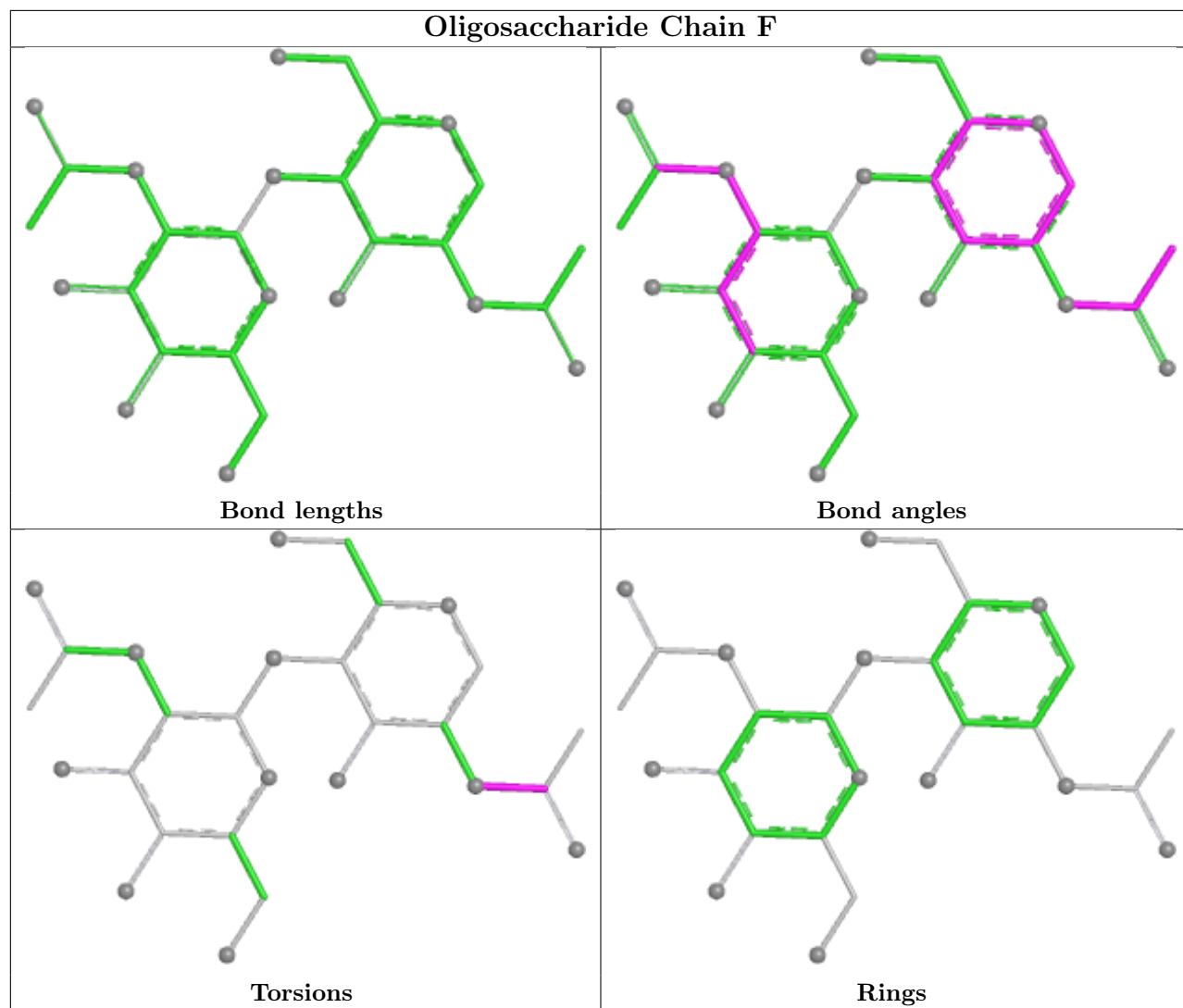
Mol	Chain	Res	Type	Atoms
3	G	5	MAN	C1-C2-C3-C4-C5-O5
3	I	3	BMA	C1-C2-C3-C4-C5-O5

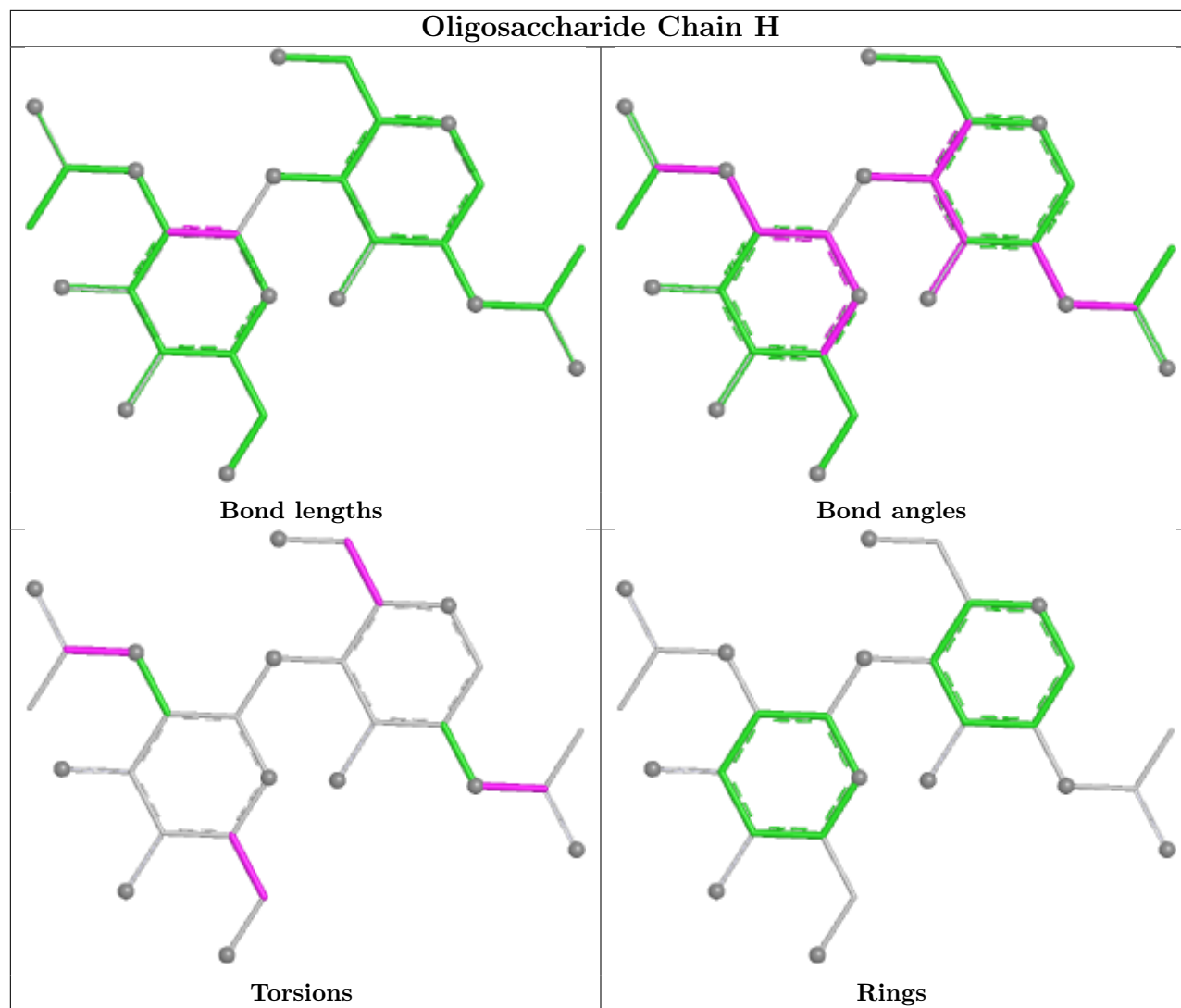
7 monomers are involved in 6 short contacts:

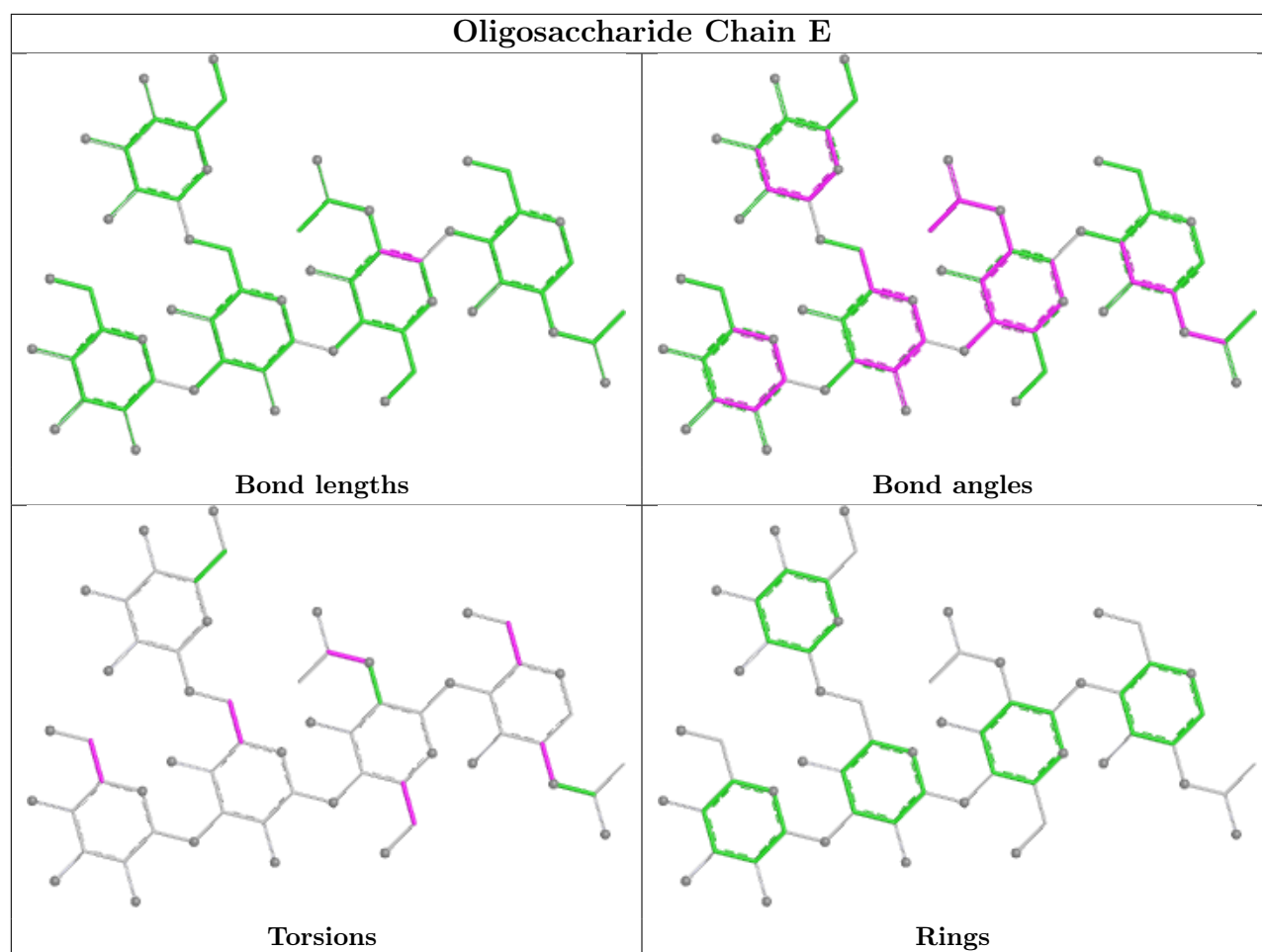
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1	NAG	2	0
3	G	2	NAG	1	0
2	D	1	NAG	1	0
3	I	5	MAN	1	0
2	D	2	NAG	1	0
3	E	1	NAG	1	0
3	G	3	BMA	1	0

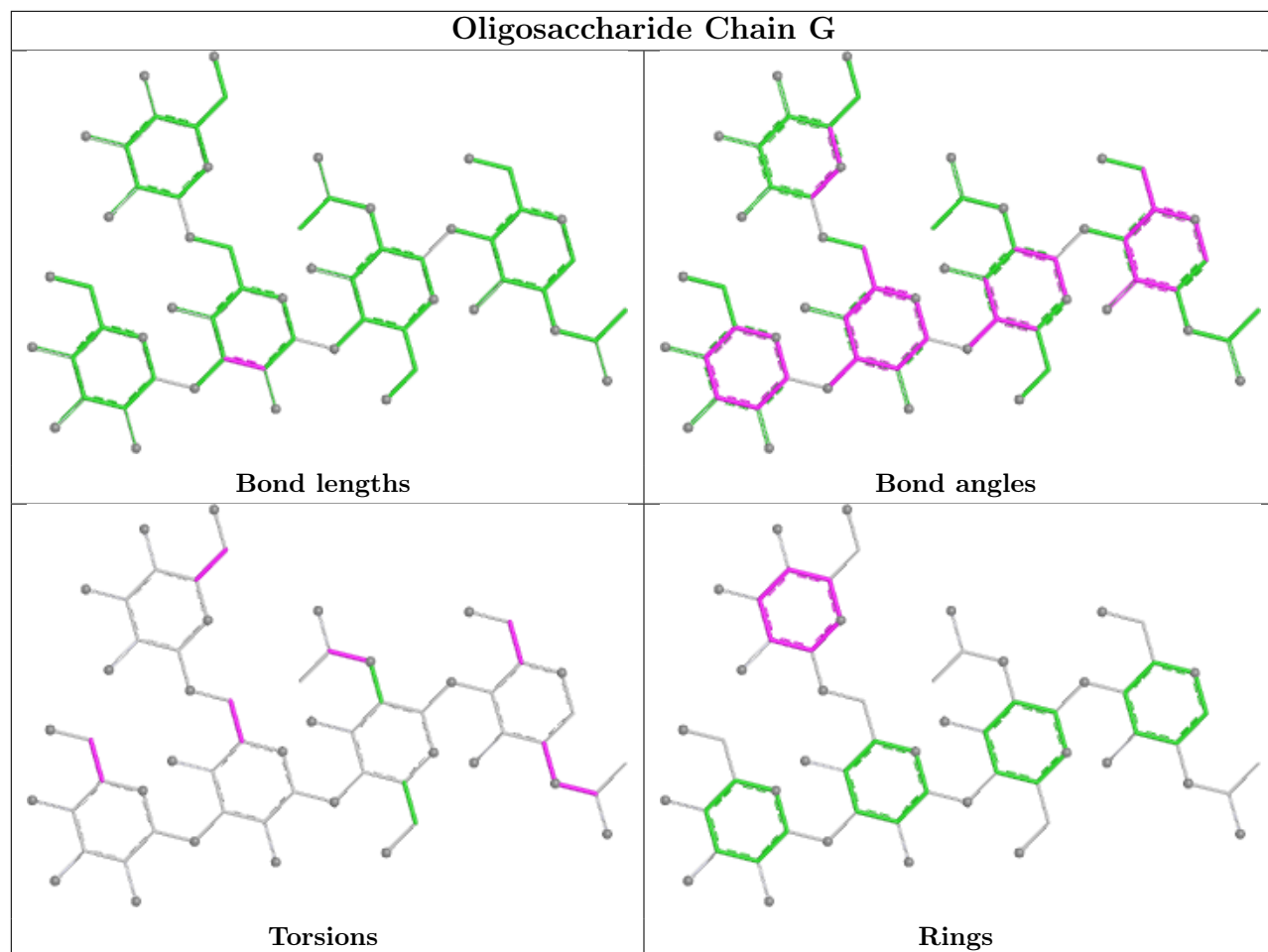
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

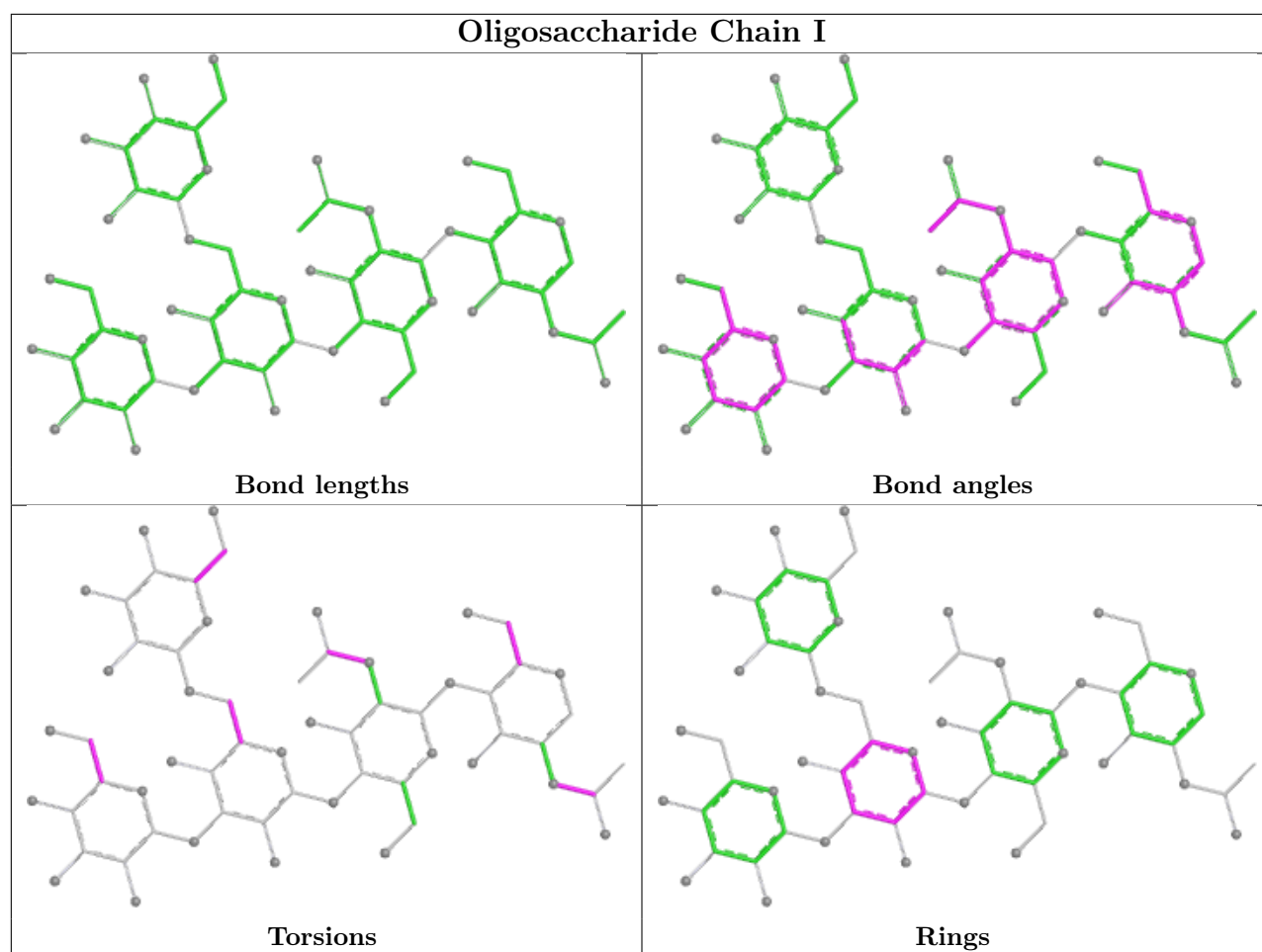












5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	804/859 (93%)	-0.08	3 (0%) 88 70	38, 104, 211, 282	0
1	B	804/859 (93%)	-0.06	7 (0%) 81 56	53, 114, 248, 348	0
1	C	804/859 (93%)	-0.23	4 (0%) 87 66	40, 84, 234, 308	0
All	All	2412/2577 (93%)	-0.12	14 (0%) 85 64	38, 101, 234, 348	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	216	PRO	3.4
1	C	799	VAL	3.3
1	A	441	ALA	3.1
1	B	816	ALA	2.4
1	B	762	PRO	2.4

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
2	NAG	F	1	14/15	0.59	0.13	113,155,162,179	0
3	BMA	E	3	11/12	0.65	0.10	173,178,185,200	0
2	NAG	D	2	14/15	0.67	0.09	158,189,205,208	0

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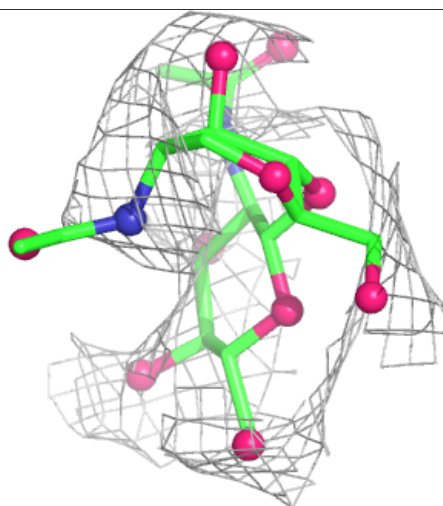
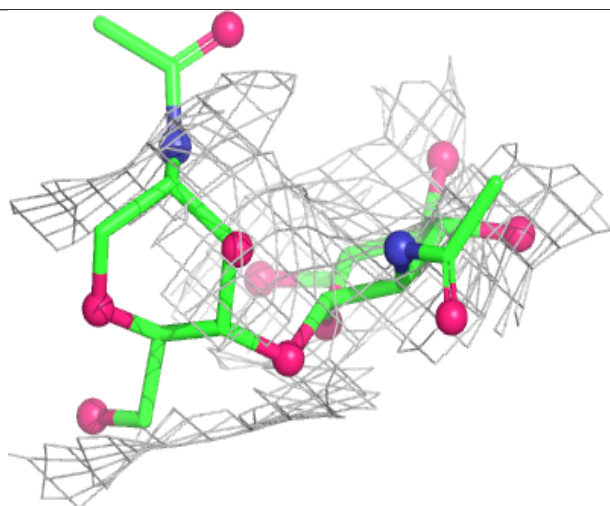
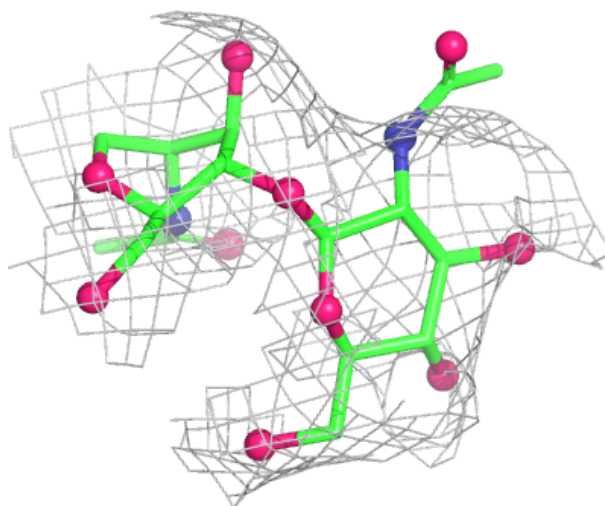
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	F	2	14/15	0.69	0.10	169,178,184,187	0
3	NAG	E	2	14/15	0.72	0.12	110,156,174,174	0
3	NAG	G	2	14/15	0.74	0.10	110,129,156,158	0
3	MAN	I	4	11/12	0.75	0.12	166,198,220,224	0
2	NAG	H	2	14/15	0.76	0.09	147,174,181,187	0
3	MAN	E	4	11/12	0.76	0.11	192,207,212,216	0
3	BMA	I	3	11/12	0.78	0.10	153,159,171,189	0
3	NAG	G	1	14/15	0.78	0.13	106,129,142,146	0
2	NAG	H	1	14/15	0.79	0.10	107,124,131,143	0
3	BMA	G	3	11/12	0.81	0.08	133,147,164,171	0
3	MAN	E	5	11/12	0.82	0.09	145,162,169,174	0
2	NAG	D	1	14/15	0.82	0.09	133,144,150,160	0
3	NAG	E	1	14/15	0.85	0.11	124,128,165,174	0
3	MAN	I	5	11/12	0.86	0.10	152,165,184,185	0
3	NAG	I	2	14/15	0.87	0.10	99,118,136,156	0
3	MAN	G	5	11/12	0.88	0.09	151,165,174,176	0
3	NAG	I	1	14/15	0.88	0.10	92,104,115,132	0
3	MAN	G	4	11/12	0.92	0.07	152,168,175,183	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.

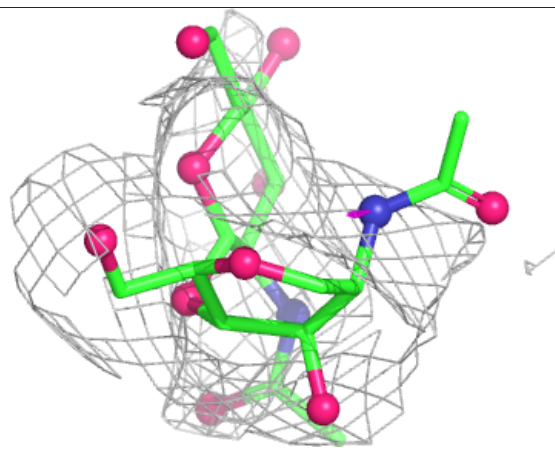
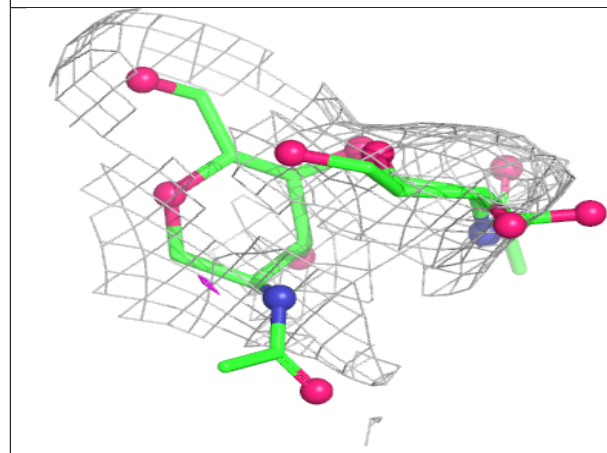
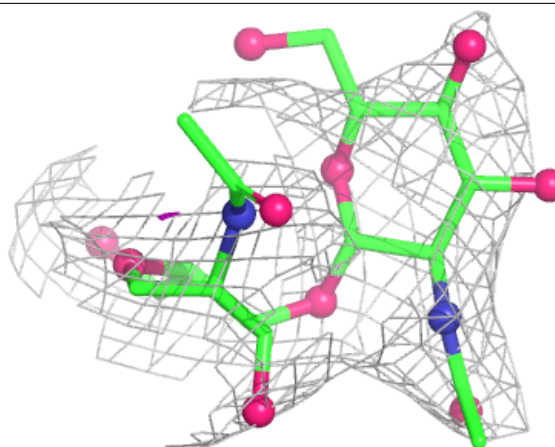
Electron density around Chain D:

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



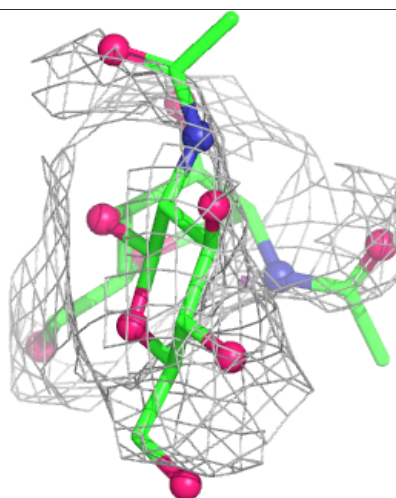
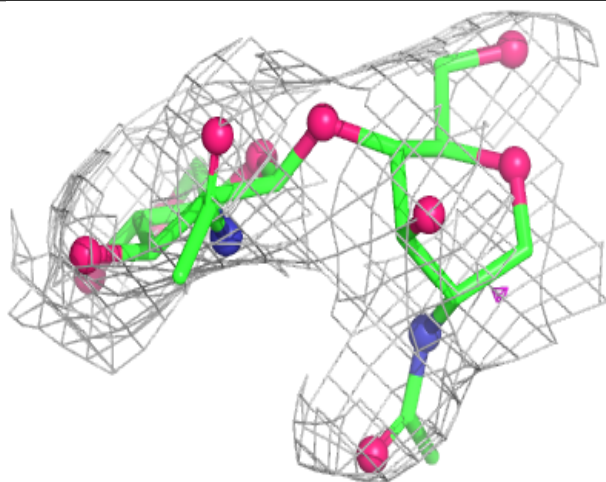
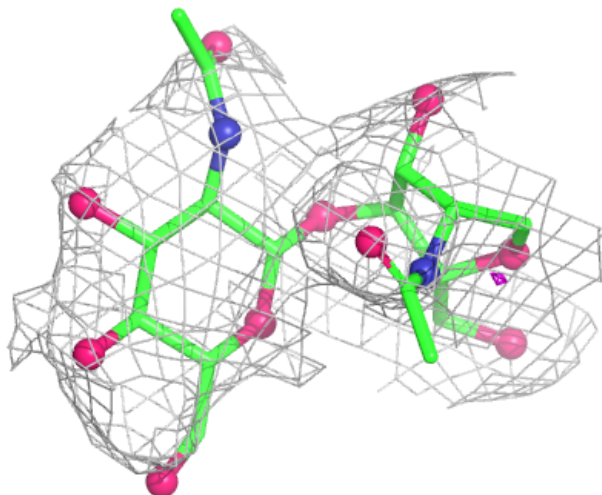
Electron density around Chain F:

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



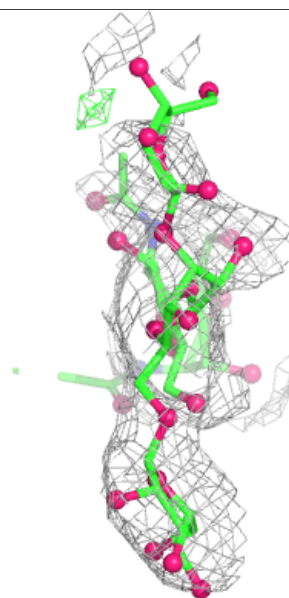
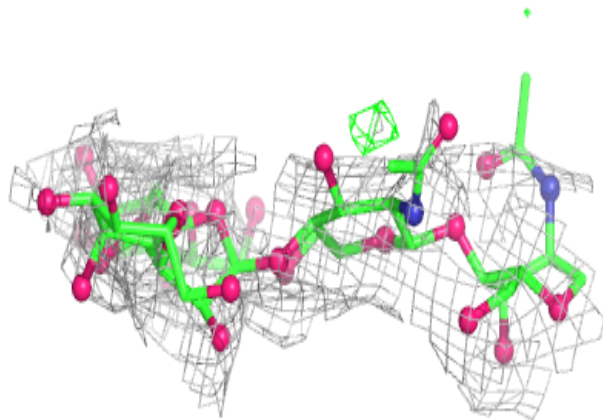
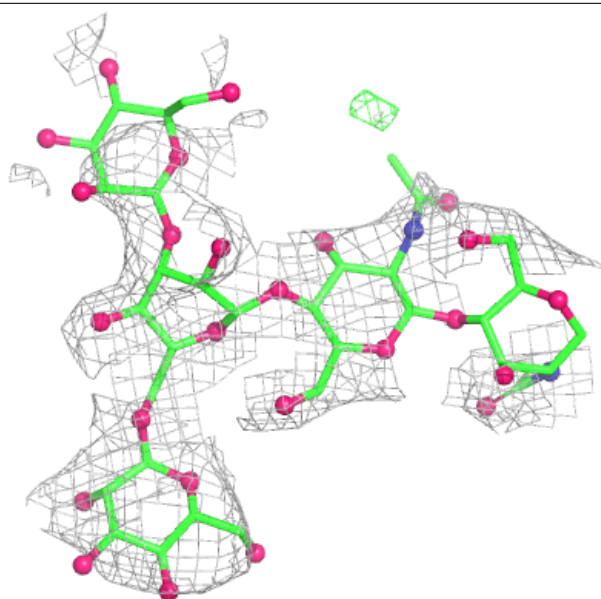
Electron density around Chain H:

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



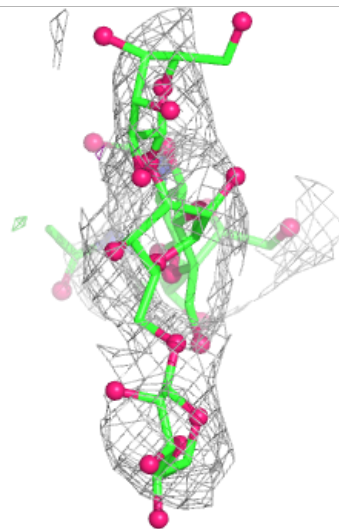
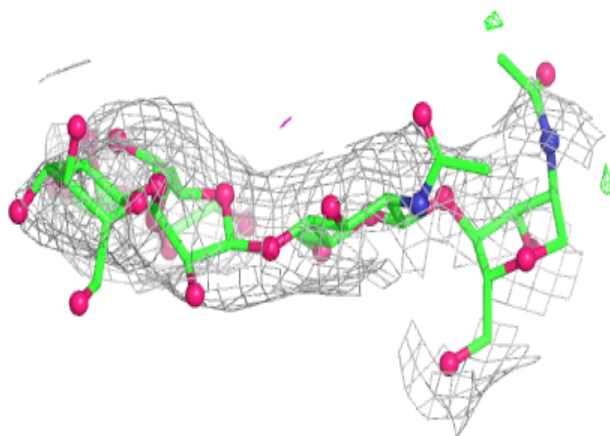
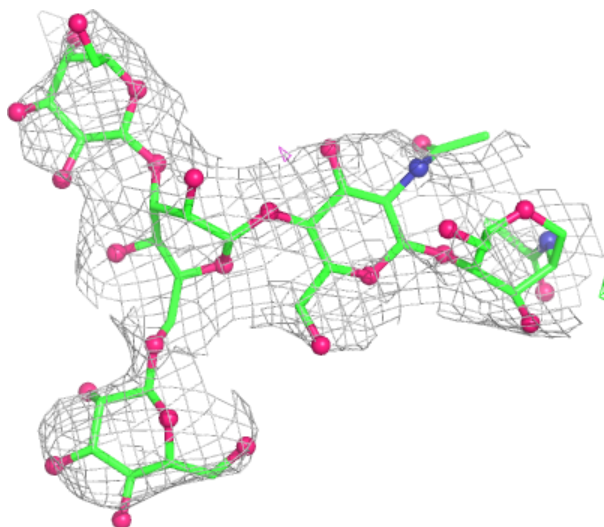
Electron density around Chain E:

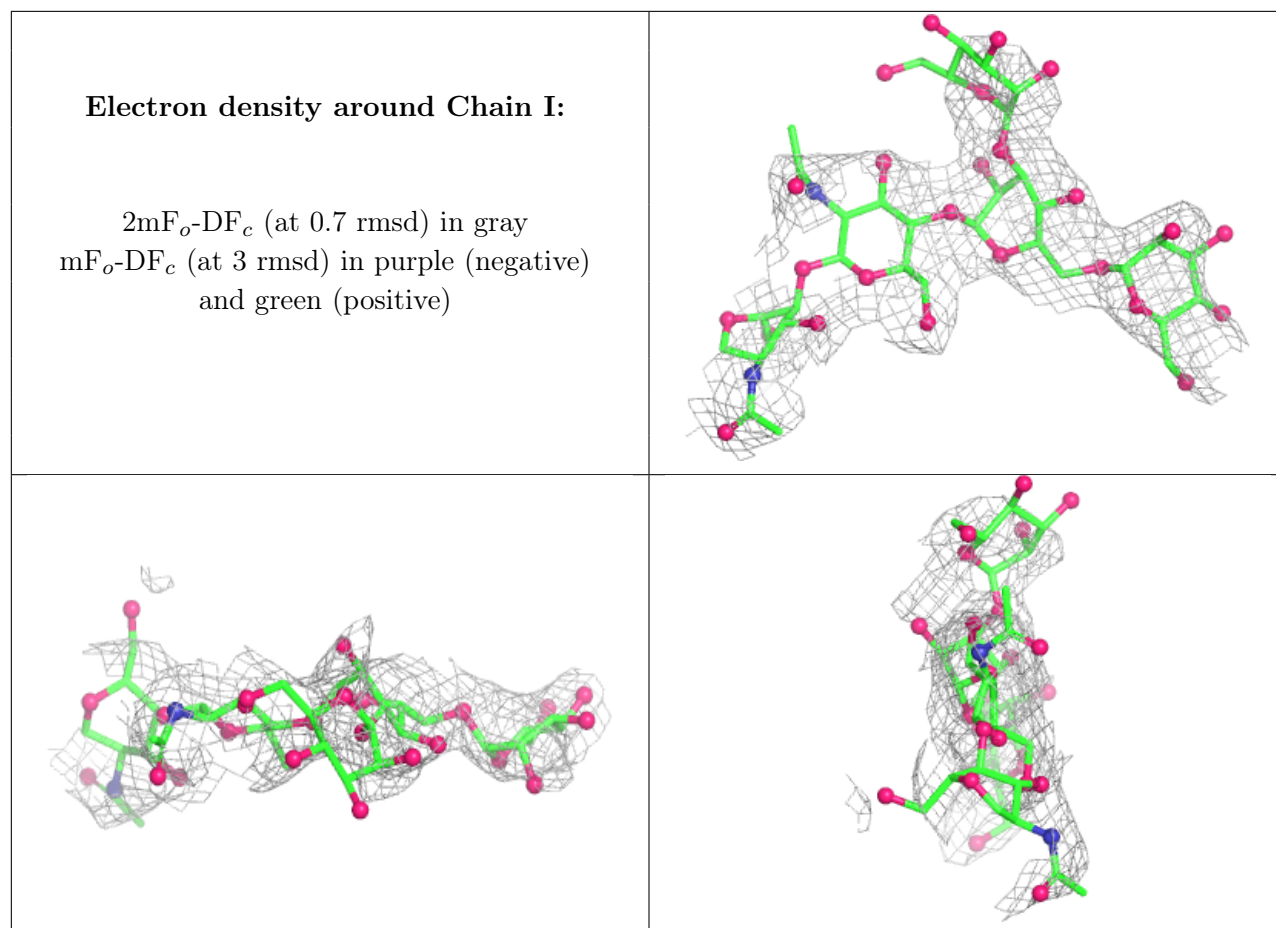
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.