



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 05:13 PM UTC

PDB ID : 1A0T / pdb_00001a0t
Title : SUCROSE-SPECIFIC PORIN, WITH BOUND SUCROSE MOLECULES
Authors : Diederichs, K.; Welte, W.
Deposited on : 1997-12-08
Resolution : 2.40 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

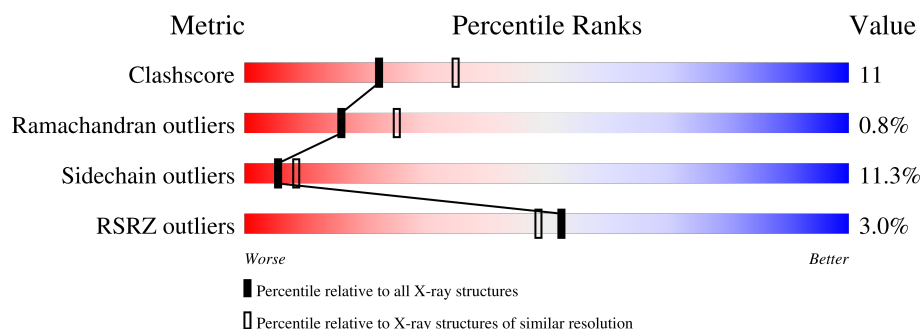
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	P	413	3% 71% 23% 5%
1	Q	413	3% 73% 22% 5%
1	R	413	3% 72% 22% 6%
2	A	2	50% 50%
2	B	2	100%
2	C	2	100%
2	D	2	100%

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Mol	Chain	Length	Quality of chain
2	E	2	 50%50%
2	F	2	 100%

2 Entry composition

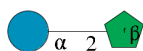
There are 4 unique types of molecules in this entry. The entry contains 10077 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SUCROSE-SPECIFIC PORIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	413	Total	C	N	O	S	0	0	0
			3202	2011	553	628	10			
1	Q	413	Total	C	N	O	S	0	0	0
			3202	2011	553	628	10			
1	R	413	Total	C	N	O	S	0	0	0
			3202	2011	553	628	10			

- Molecule 2 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	A	2	Total	C	O	0	0	0
			23	12	11			
2	B	2	Total	C	O	0	0	0
			23	12	11			
2	C	2	Total	C	O	0	0	0
			23	12	11			
2	D	2	Total	C	O	0	0	0
			23	12	11			
2	E	2	Total	C	O	0	0	0
			23	12	11			
2	F	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	P	1	Total	Ca	0	0
			1	1		

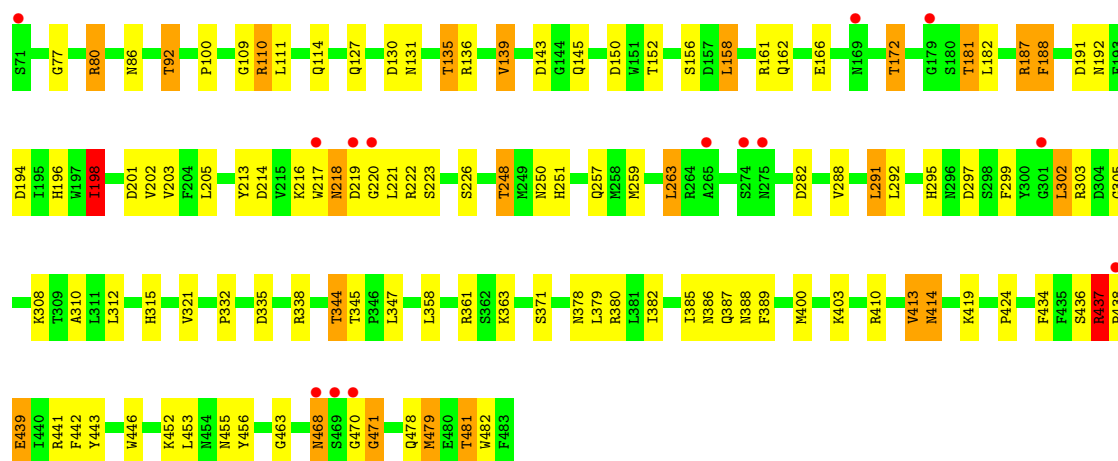
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	Q	1	Total 1	Ca 1	0	0
3	R	1	Total 1	Ca 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	109	Total 109	O 109	0	0
4	Q	111	Total 111	O 111	0	0
4	R	110	Total 110	O 110	0	0



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain A: 50% 50%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain B: 100%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain C: 100%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain D: 100%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain E: 50% 50%



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain F:

100%

SLE1
FR02

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	111.80Å 111.80Å 147.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	100.00 – 2.40 96.82 – 2.40	Depositor EDS
% Data completeness (in resolution range)	67.4 (100.00-2.40) 68.8 (96.82-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.19 (at 2.29Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.207 , 0.246 0.214 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	22.0	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l 0.050 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10077	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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 56.29 % 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 2.7954e-05. 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: GLC, FRU, CA

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	P	0.65	0/3283	1.07	25/4443 (0.6%)
1	Q	0.64	0/3283	1.08	22/4443 (0.5%)
1	R	0.65	0/3283	1.07	24/4443 (0.5%)
All	All	0.65	0/9849	1.07	71/13329 (0.5%)

There are no bond length outliers.

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	437	ARG	N-CA-C	10.63	133.31	109.81
1	Q	437	ARG	N-CA-C	10.63	133.29	109.81
1	R	202	VAL	N-CA-C	-10.60	100.53	110.82
1	P	437	ARG	N-CA-C	10.59	133.22	109.81
1	P	202	VAL	N-CA-C	-9.26	101.84	110.82

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	3202	0	2985	69	0
1	Q	3202	0	2985	67	0
1	R	3202	0	2985	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	23	0	21	3	0
2	B	23	0	21	0	0
2	C	23	0	21	3	0
2	D	23	0	21	0	0
2	E	23	0	21	4	0
2	F	23	0	21	0	0
3	P	1	0	0	0	0
3	Q	1	0	0	0	0
3	R	1	0	0	0	0
4	P	109	0	0	3	0
4	Q	111	0	0	4	0
4	R	110	0	0	5	0
All	All	10077	0	9081	200	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 11.

The worst 5 of 200 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:P:110:ARG:HH11	1:P:114:GLN:HE22	1.15	0.93
1:Q:250:ASN:HD21	1:Q:257:GLN:HE21	1.21	0.88
1:R:110:ARG:HH11	1:R:114:GLN:HE22	1.21	0.88
1:P:150:ASP:O	1:Q:161:ARG:HD2	1.76	0.86
1:Q:110:ARG:HH11	1:Q:114:GLN:HE22	1.24	0.85

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	P	411/413 (100%)	387 (94%)	21 (5%)	3 (1%)	18	28
1	Q	411/413 (100%)	389 (95%)	18 (4%)	4 (1%)	12	20
1	R	411/413 (100%)	390 (95%)	18 (4%)	3 (1%)	18	28
All	All	1233/1239 (100%)	1166 (95%)	57 (5%)	10 (1%)	16	25

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	218	ASN
1	Q	218	ASN
1	R	218	ASN
1	Q	220	GLY
1	R	220	GLY

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	P	327/327 (100%)	291 (89%)	36 (11%)	6	9
1	Q	327/327 (100%)	289 (88%)	38 (12%)	5	8
1	R	327/327 (100%)	290 (89%)	37 (11%)	5	8
All	All	981/981 (100%)	870 (89%)	111 (11%)	5	8

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Q	292	LEU
1	R	481	THR
1	Q	468	ASN
1	R	479	MET
1	R	380	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	R	114	GLN
1	R	251	HIS
1	R	125	HIS
1	R	218	ASN
1	R	315	HIS

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 ⓘ

12 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	GLC	A	1	2	11,11,12	0.92	0	15,15,17	0.82	0
2	FRU	A	2	2	11,12,12	1.23	1 (9%)	10,18,18	0.77	0
2	GLC	B	1	2	11,11,12	0.69	0	15,15,17	0.74	0
2	FRU	B	2	2	11,12,12	0.63	0	10,18,18	0.54	0
2	GLC	C	1	2	11,11,12	1.05	1 (9%)	15,15,17	0.85	0
2	FRU	C	2	2	11,12,12	1.37	1 (9%)	10,18,18	0.91	0
2	GLC	D	1	2	11,11,12	0.56	0	15,15,17	0.99	1 (6%)
2	FRU	D	2	2	11,12,12	0.84	1 (9%)	10,18,18	0.57	0
2	GLC	E	1	2	11,11,12	0.97	0	15,15,17	0.86	0
2	FRU	E	2	2	11,12,12	1.28	1 (9%)	10,18,18	0.92	1 (10%)
2	GLC	F	1	2	11,11,12	0.69	0	15,15,17	0.71	0
2	FRU	F	2	2	11,12,12	0.59	0	10,18,18	0.55	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	GLC	A	1	2	-	2/2/19/22	0/1/1/1
2	FRU	A	2	2	-	3/5/24/24	0/1/1/1
2	GLC	B	1	2	-	2/2/19/22	0/1/1/1
2	FRU	B	2	2	-	0/5/24/24	0/1/1/1
2	GLC	C	1	2	-	2/2/19/22	0/1/1/1
2	FRU	C	2	2	-	5/5/24/24	0/1/1/1
2	GLC	D	1	2	-	0/2/19/22	0/1/1/1
2	FRU	D	2	2	-	0/5/24/24	0/1/1/1
2	GLC	E	1	2	-	2/2/19/22	0/1/1/1
2	FRU	E	2	2	-	2/5/24/24	0/1/1/1
2	GLC	F	1	2	-	2/2/19/22	0/1/1/1
2	FRU	F	2	2	-	2/5/24/24	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	FRU	O2-C2	4.21	1.48	1.40
2	E	2	FRU	O2-C2	3.75	1.47	1.40
2	A	2	FRU	O2-C2	3.64	1.47	1.40
2	D	2	FRU	O2-C2	2.29	1.44	1.40
2	C	1	GLC	O5-C5	2.10	1.47	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	GLC	C1-O5-C5	2.18	115.11	112.19
2	E	2	FRU	O1-C1-C2	-2.11	107.02	111.67

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	FRU	O1-C1-C2-C3
2	C	2	FRU	O1-C1-C2-O2
2	E	2	FRU	C4-C5-C6-O6
2	A	2	FRU	C4-C5-C6-O6

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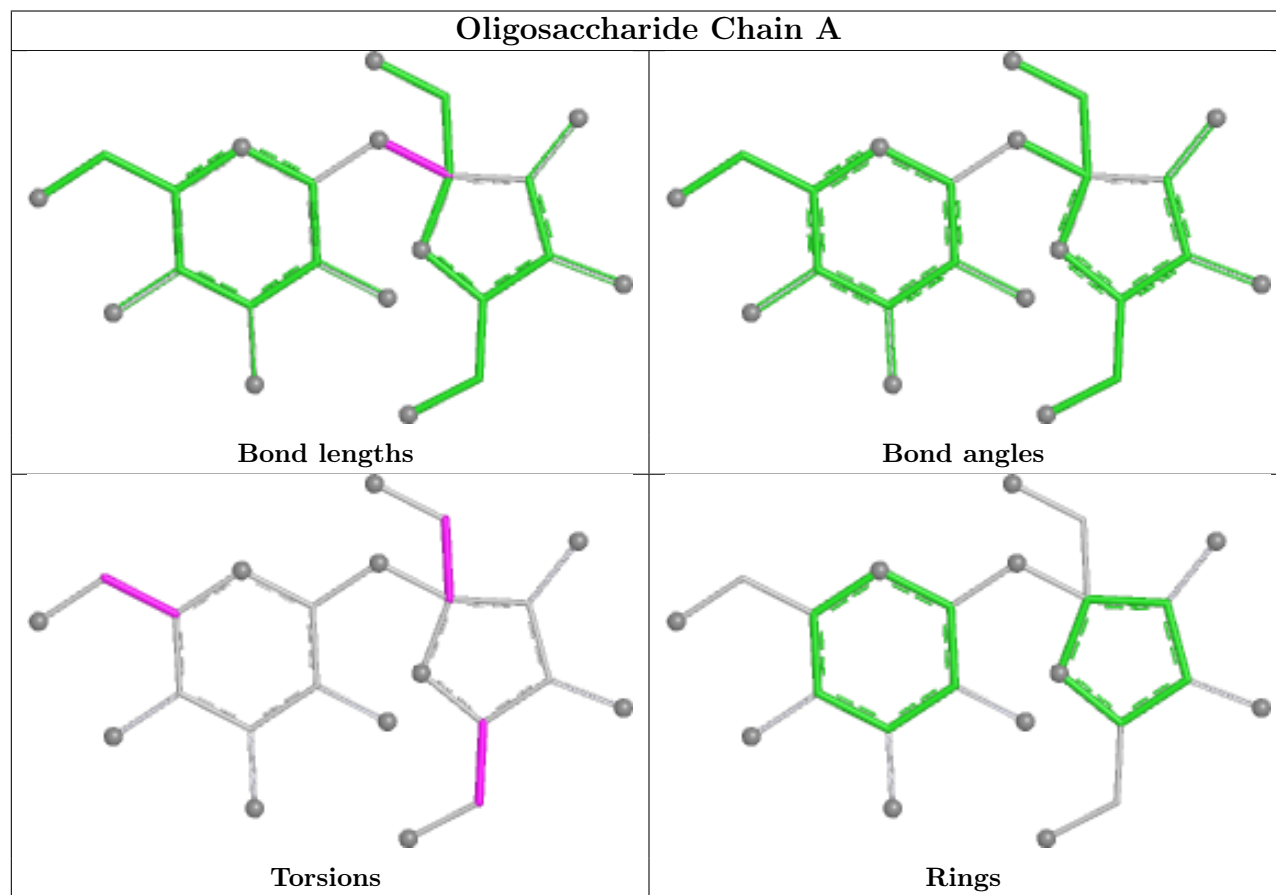
Mol	Chain	Res	Type	Atoms
2	A	2	FRU	O5-C5-C6-O6

There are no ring outliers.

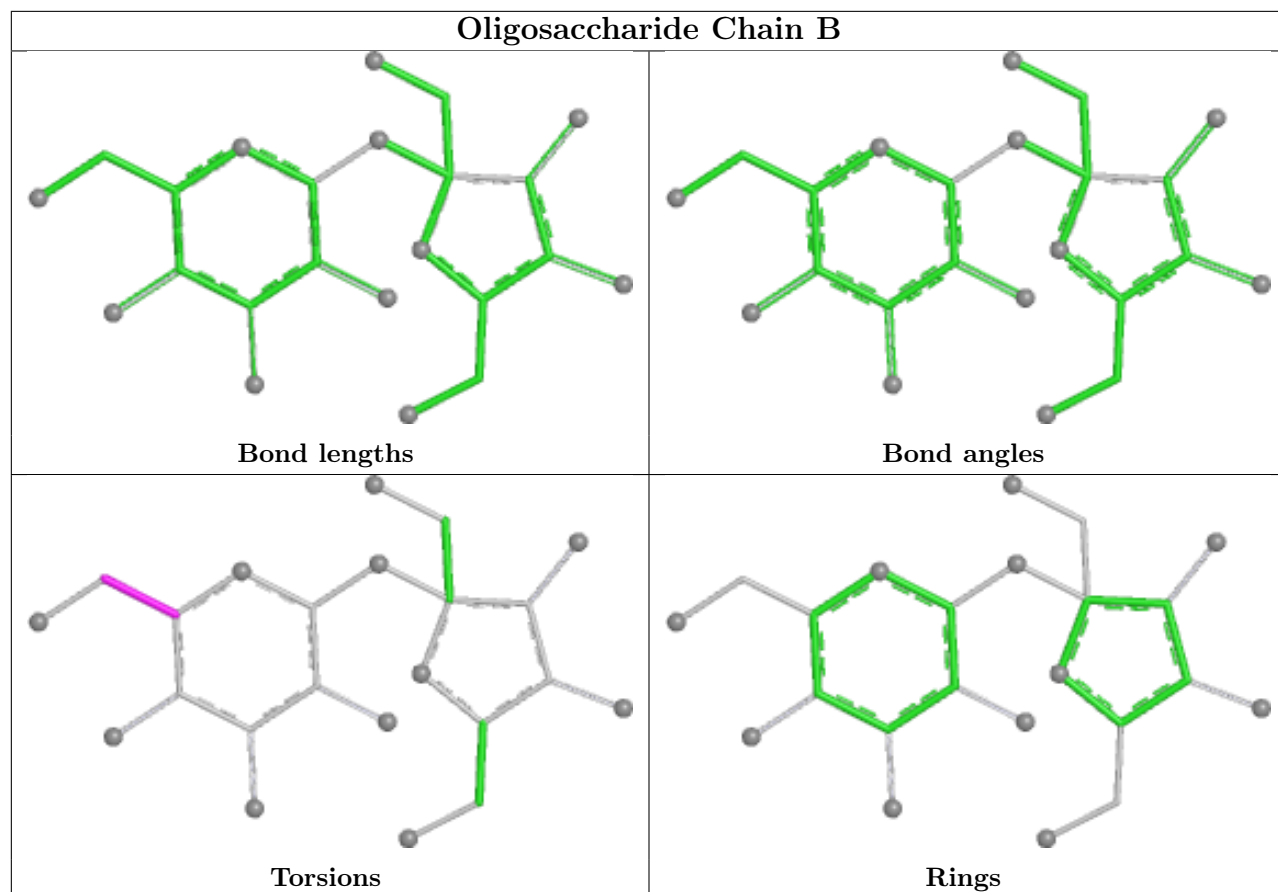
6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	FRU	2	0
2	A	2	FRU	2	0
2	A	1	GLC	1	0
2	E	2	FRU	2	0
2	E	1	GLC	2	0
2	C	1	GLC	1	0

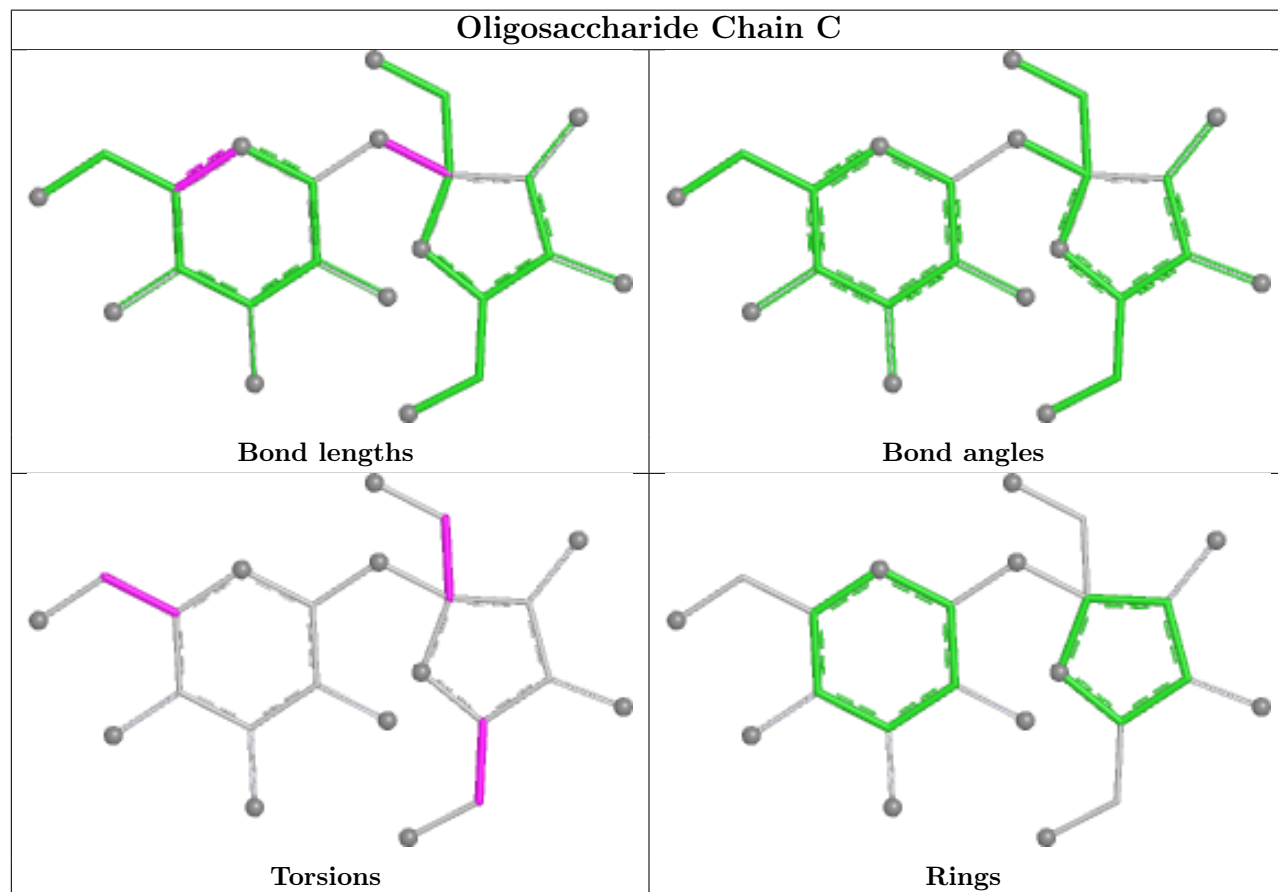
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



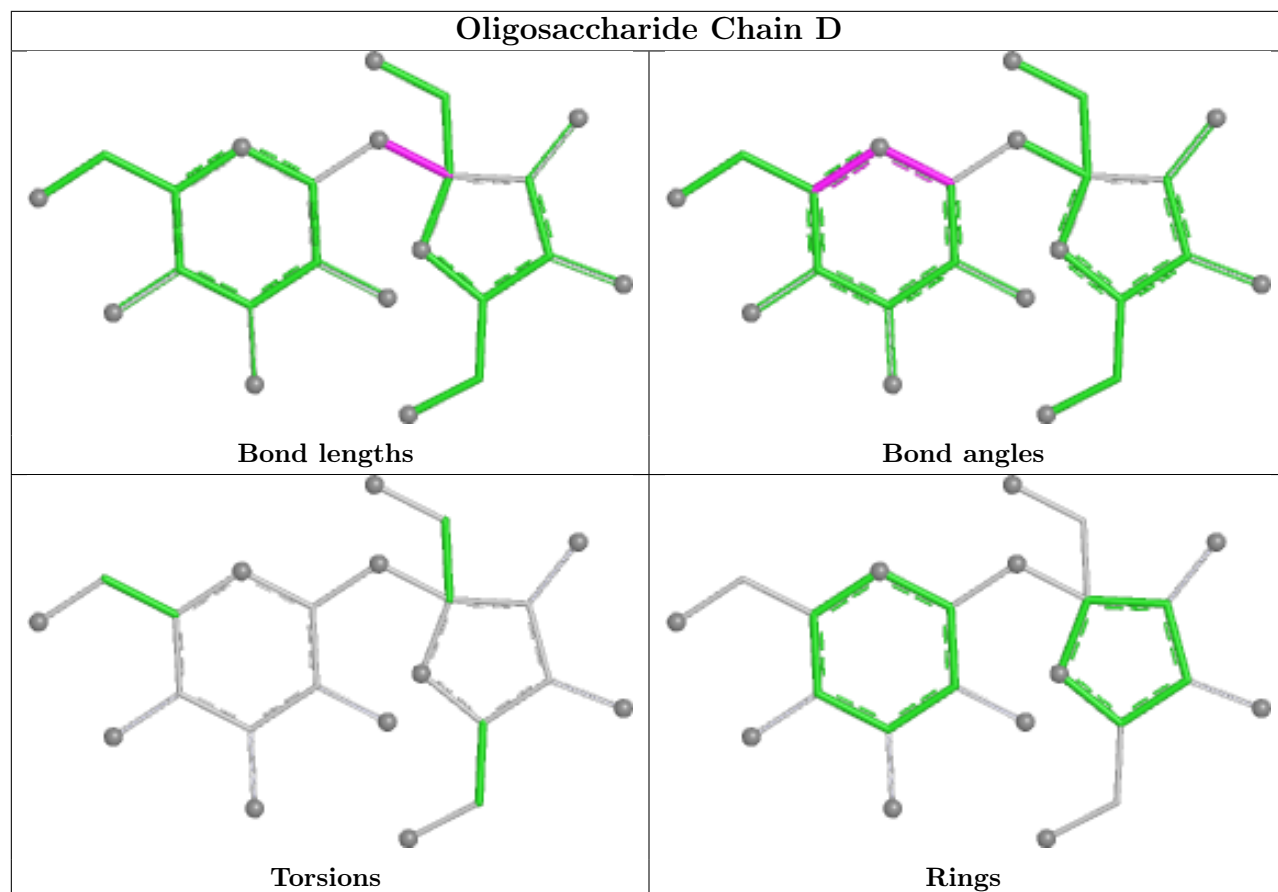
Oligosaccharide Chain B



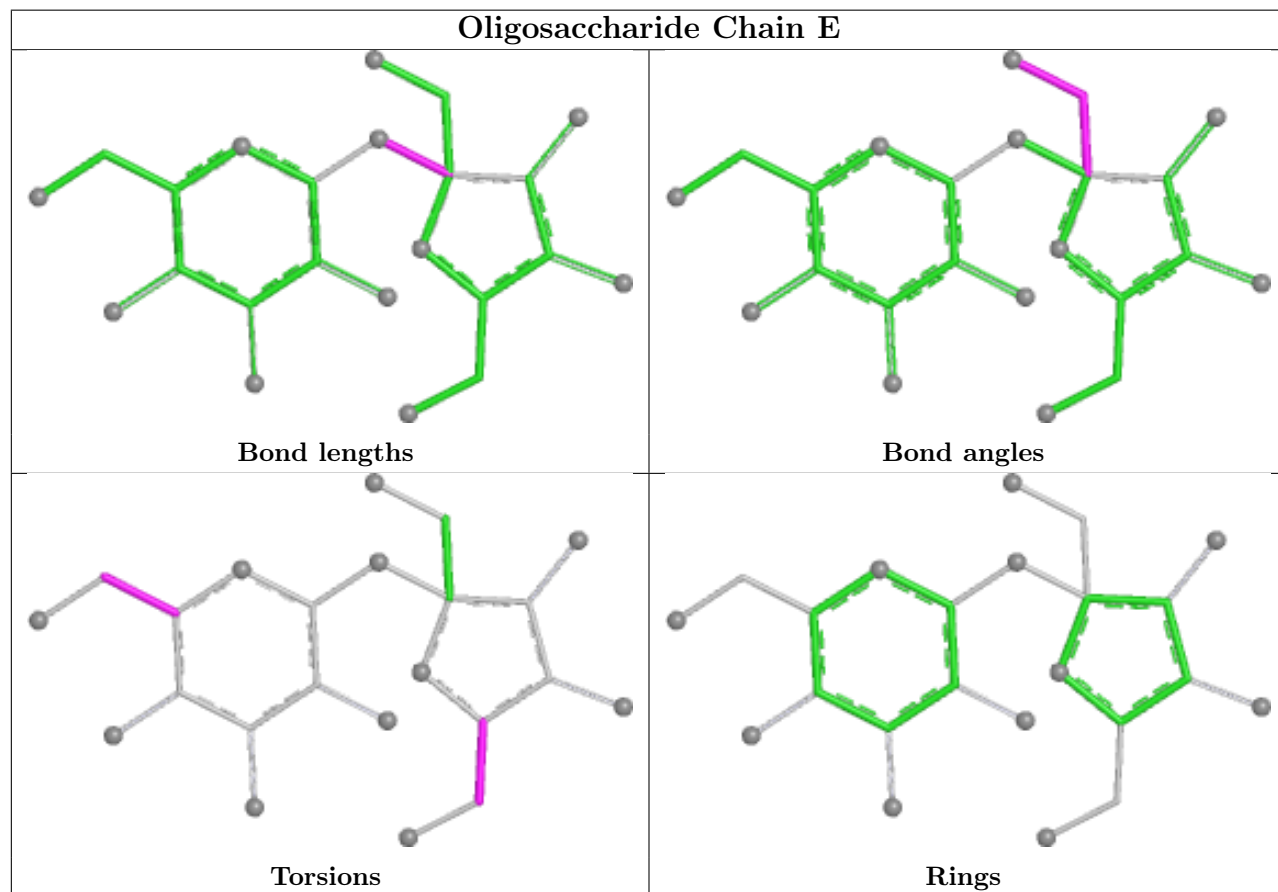
Oligosaccharide Chain C

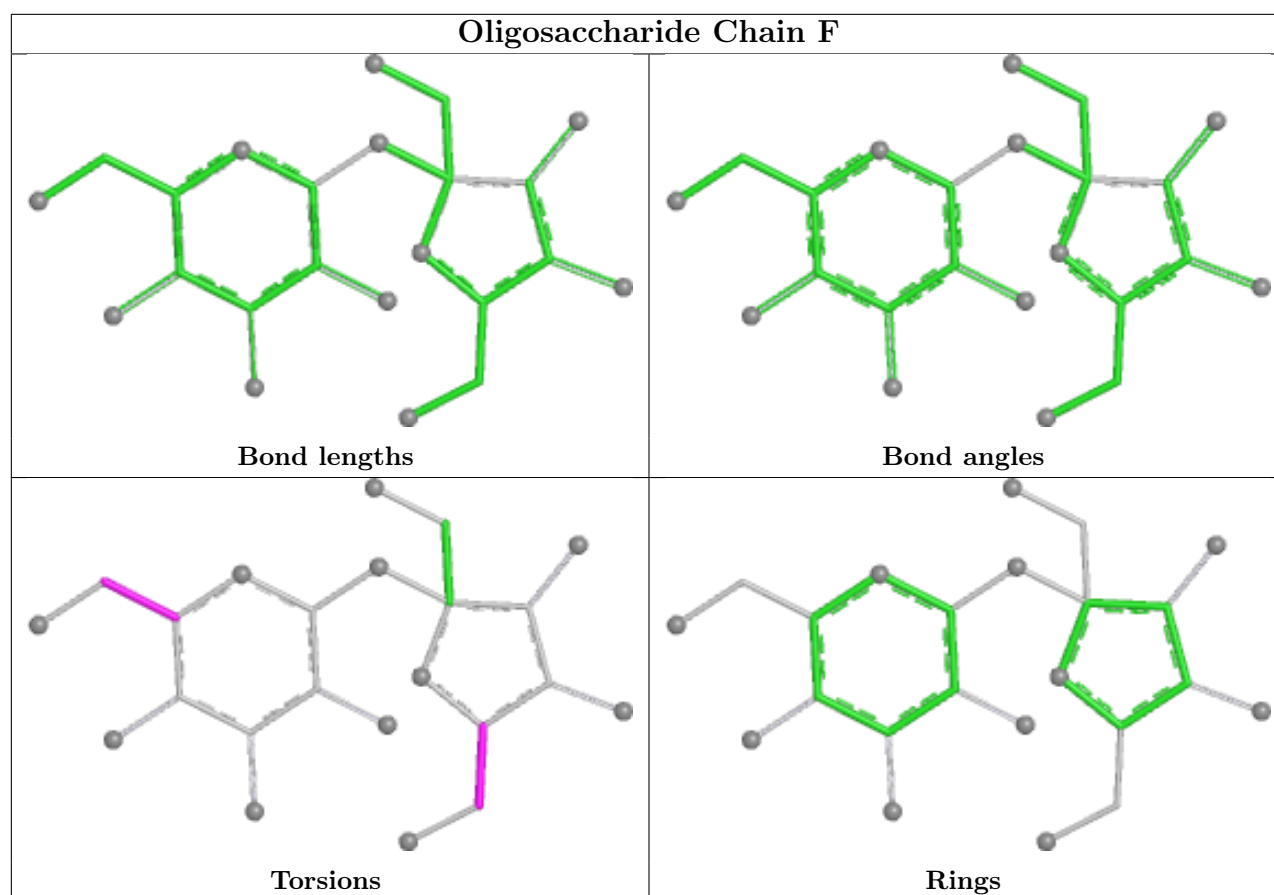


Oligosaccharide Chain D



Oligosaccharide Chain E





5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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](#)

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	P	413/413 (100%)	0.05	11 (2%) 56 52	11, 25, 52, 84	0
1	Q	413/413 (100%)	0.08	12 (2%) 53 50	11, 24, 51, 84	0
1	R	413/413 (100%)	0.05	14 (3%) 48 44	10, 24, 51, 83	0
All	All	1239/1239 (100%)	0.06	37 (2%) 52 48	10, 25, 52, 84	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	470	GLY	6.9
1	Q	71	SER	6.0
1	R	469	SER	5.6
1	Q	274	SER	5.5
1	Q	469	SER	5.4

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.

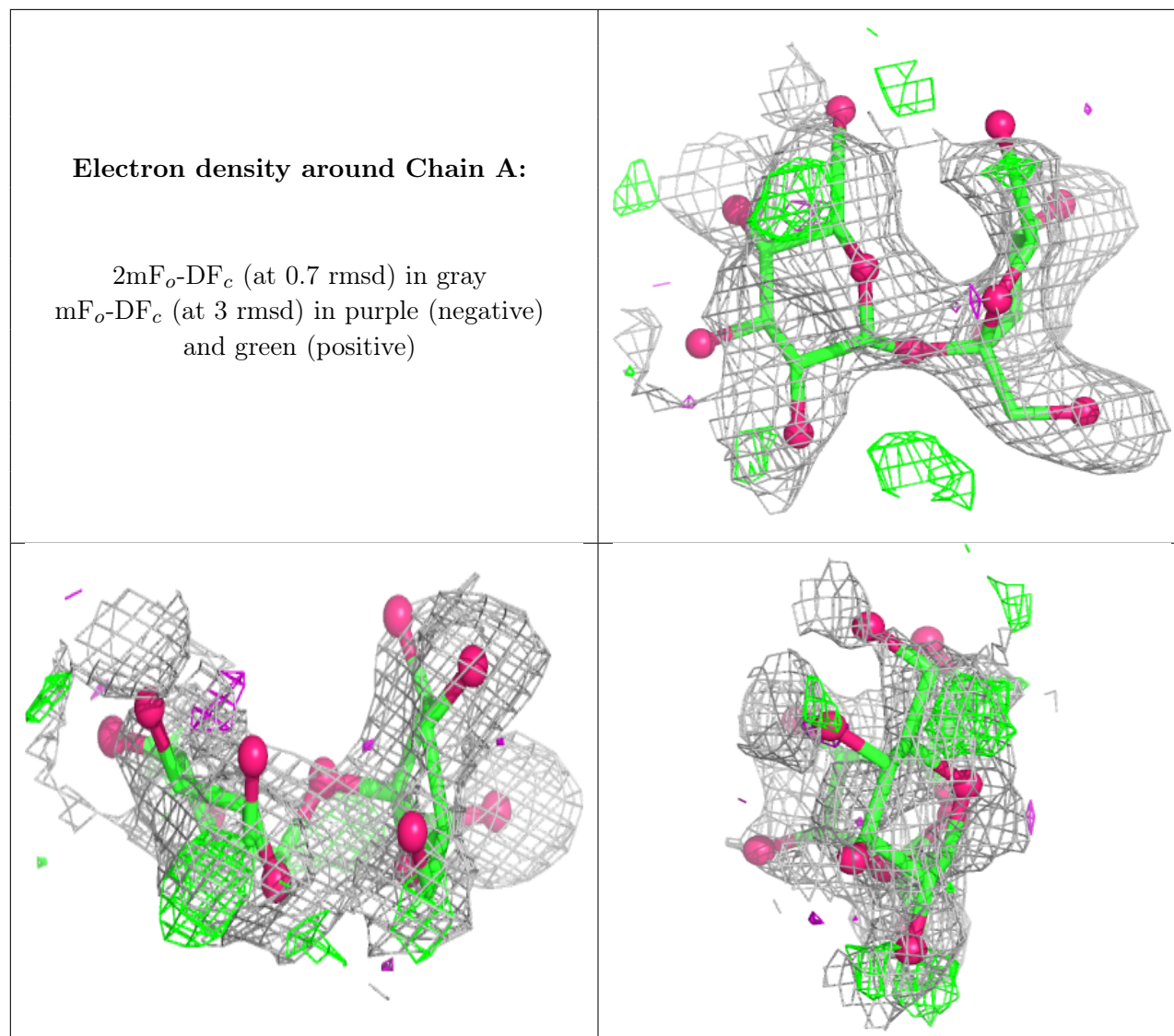
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLC	A	1	11/12	-	-	26,30,32,33	11
2	FRU	A	2	12/12	-	-	20,27,29,30	12
2	GLC	B	1	11/12	-	-	29,31,33,33	11

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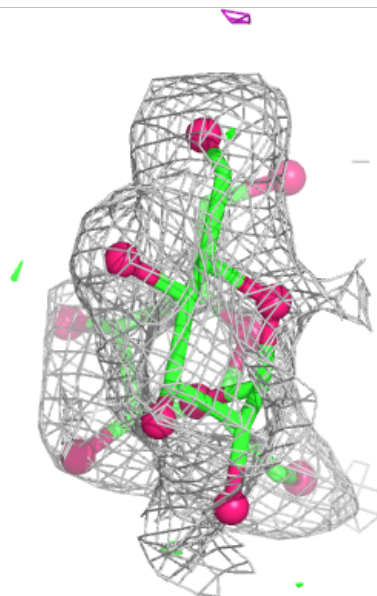
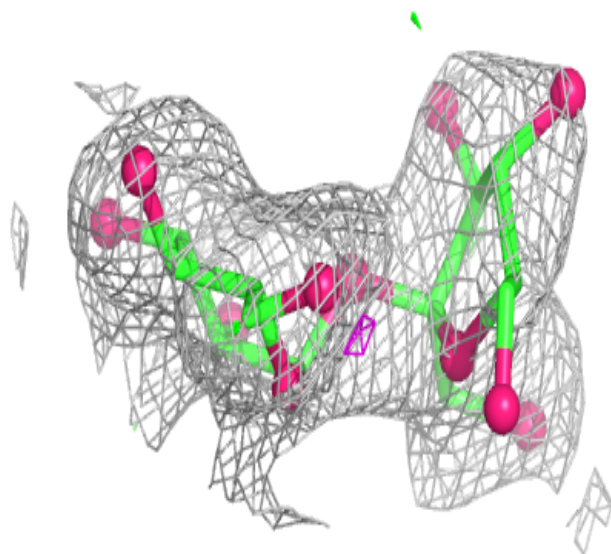
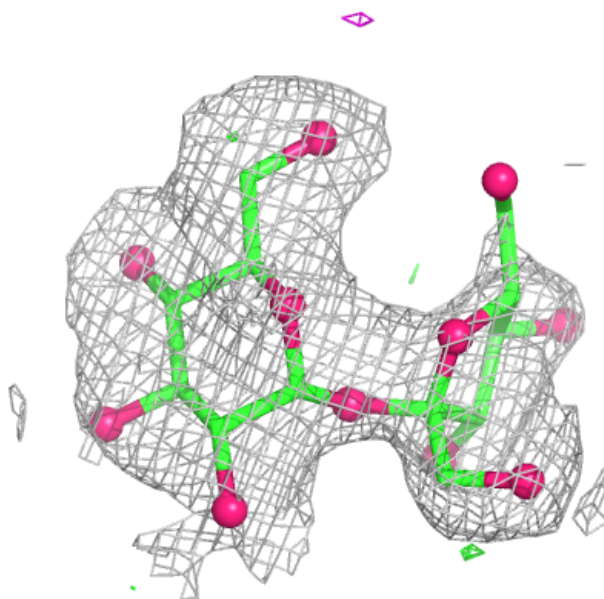
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FRU	B	2	12/12	-	-	32,35,36,37	12
2	GLC	C	1	11/12	-	-	25,30,32,33	11
2	FRU	C	2	12/12	-	-	21,28,29,31	12
2	FRU	F	2	12/12	0.74	0.22	32,34,35,36	12
2	GLC	F	1	11/12	0.79	0.18	29,31,33,33	11
2	GLC	D	1	11/12	0.79	0.20	29,31,33,33	11
2	FRU	D	2	12/12	0.82	0.19	32,35,35,36	12
2	GLC	E	1	11/12	0.86	0.13	24,30,32,33	11
2	FRU	E	2	12/12	0.91	0.12	20,28,30,30	12

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.



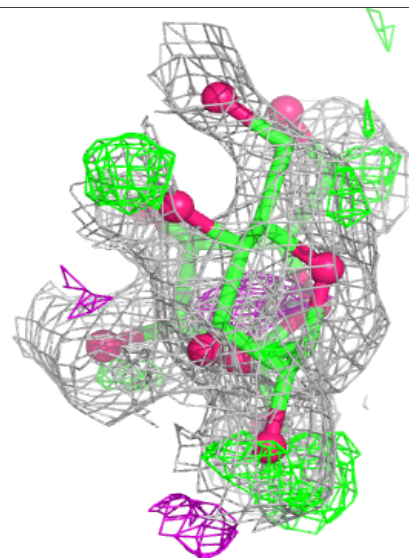
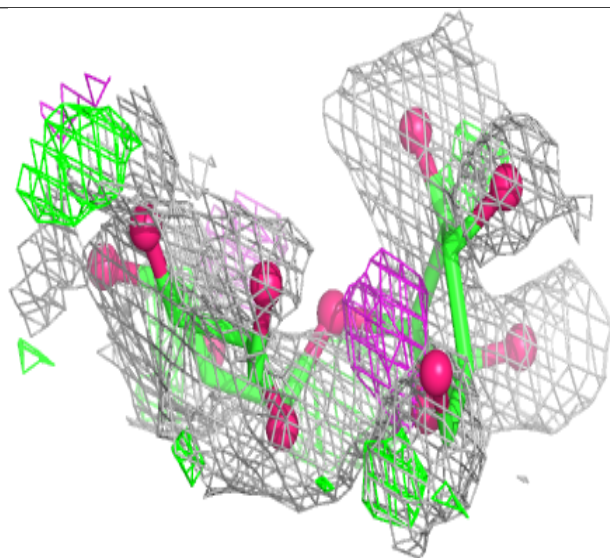
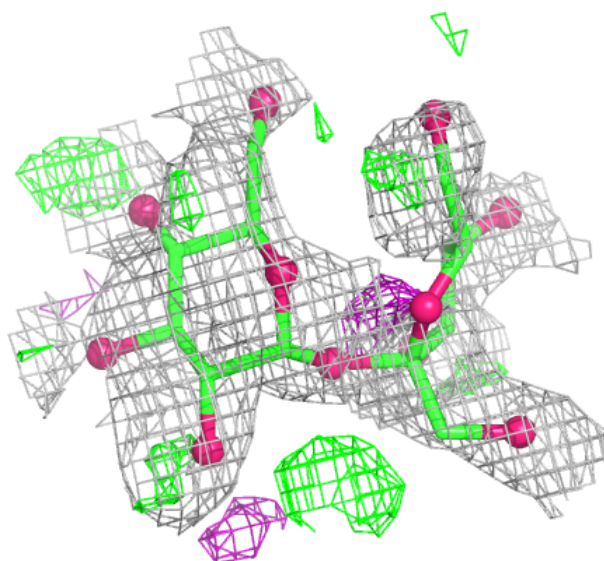
Electron density around Chain B:

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



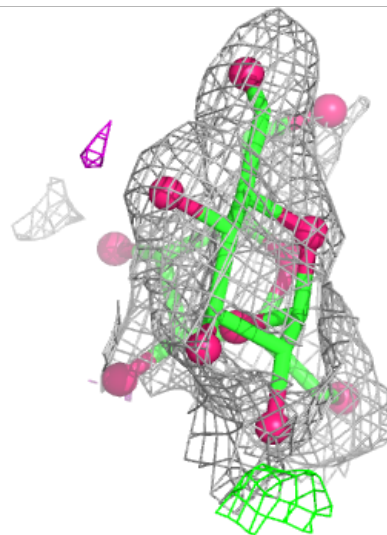
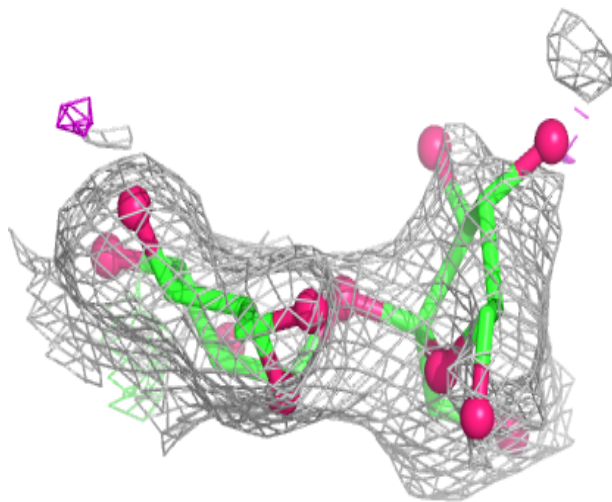
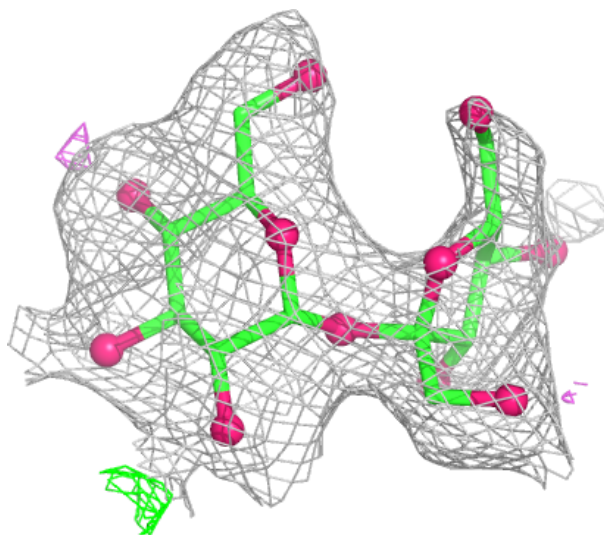
Electron density around Chain C:

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



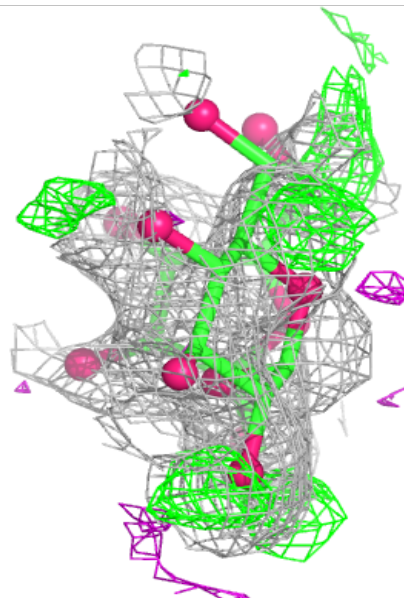
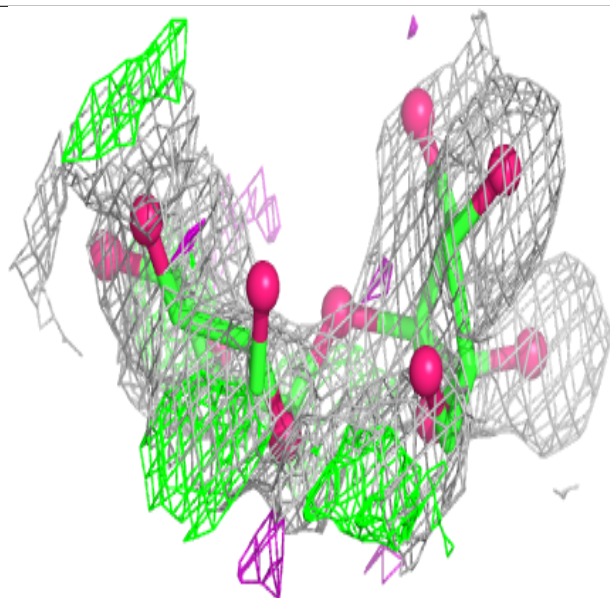
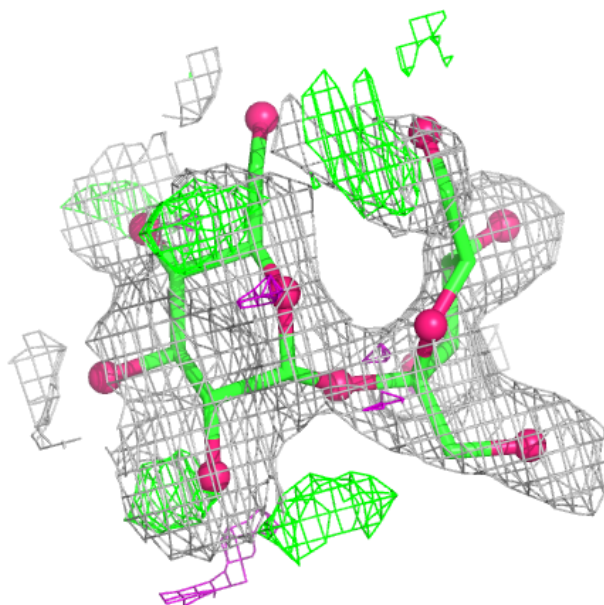
Electron density around Chain D:

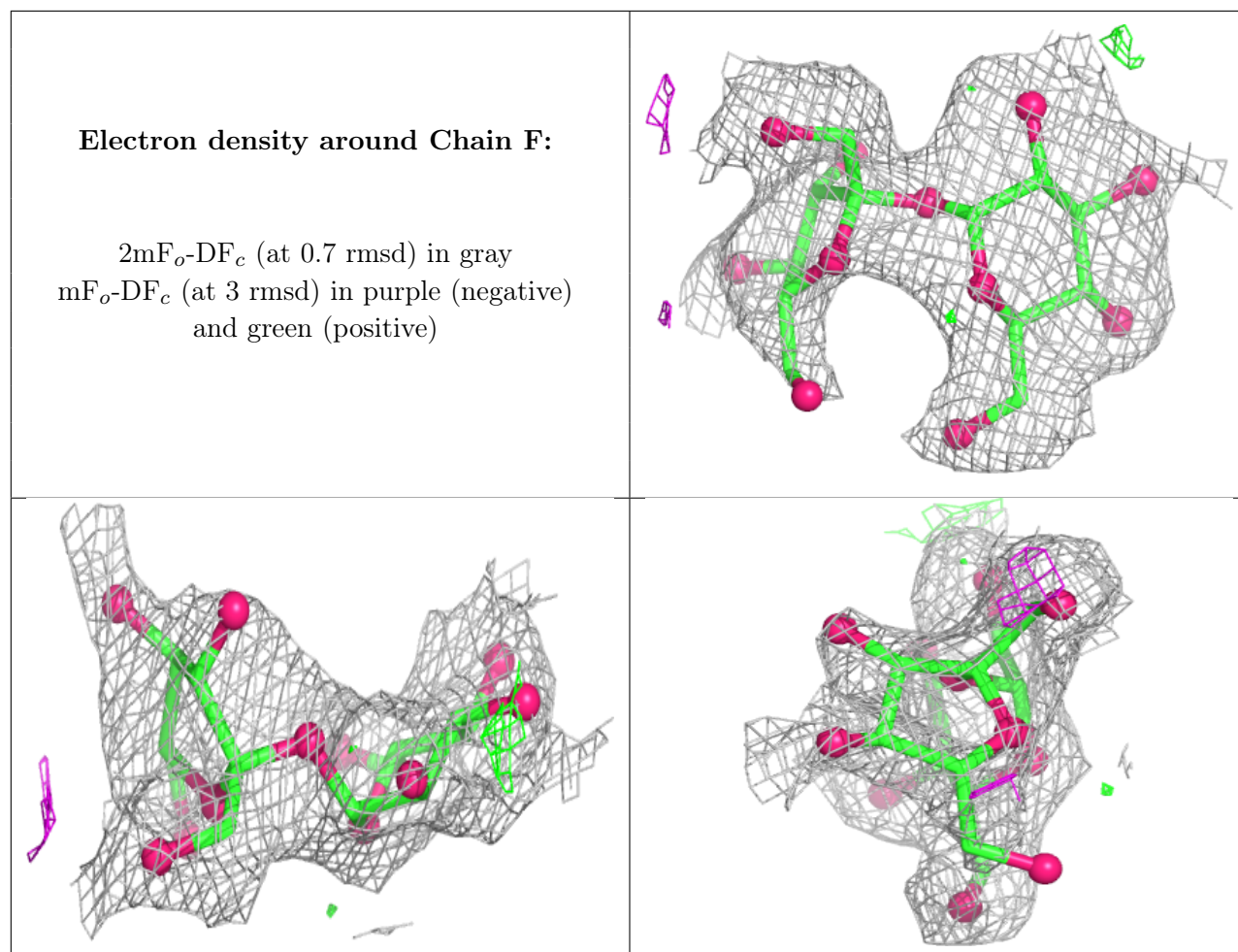
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.4 Ligands [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($\text{\AA}^2$)	Q<0.9
3	CA	Q	10	1/1	0.96	0.04	29,29,29,29	0
3	CA	P	10	1/1	0.97	0.04	30,30,30,30	0
3	CA	R	10	1/1	0.98	0.03	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.