



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 07:40 PM UTC

PDB ID : 2P37 / pdb_00002p37
Title : Crystal structure of a lectin from Canavalia maritima seeds (CML) in complex with man1-3man-OMe
Authors : Moreno, F.B.M.B.; Bezerra, G.A.; Oliveira, T.M.; Souza, E.P.; Rocha, B.A.M.; Benevides, R.G.; Delatorre, P.; Cavada, B.S.; de Azevedo Jr., W.
Deposited on : 2007-03-08
Resolution : 2.10 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

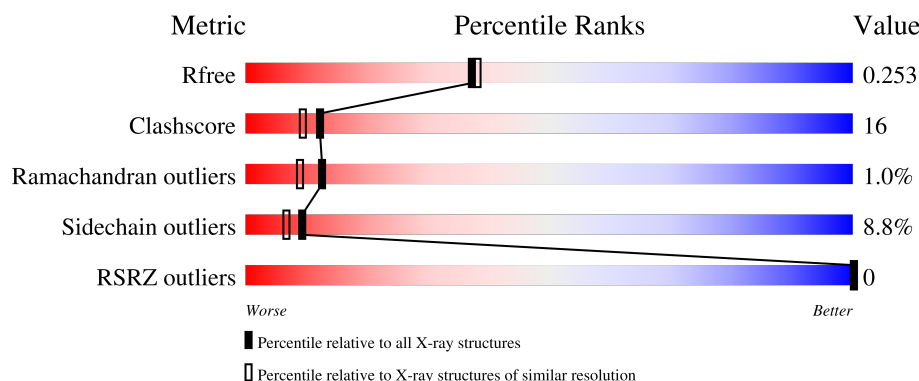
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

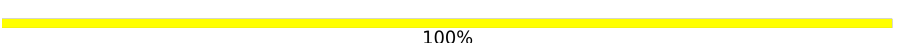
The reported resolution of this entry is 2.10 Å.

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.



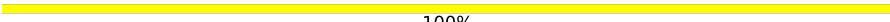
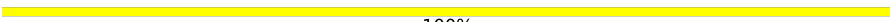
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	237	 71% 22% 5% 2% 2%
1	B	237	 74% 17% 5% 2% 2%
1	C	237	 63% 28% 5% 2% 2%
1	D	237	 63% 27% 6% 2% 2%
2	E	2	 100%

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	G	2	 100%
2	H	2	 50% 50%

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
2	ZEL	E	1	X	-	-	-
2	ZEL	F	1	X	-	-	-
2	ZEL	G	1	X	-	-	-

2 Entry composition [i](#)

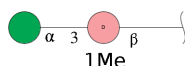
There are 5 unique types of molecules in this entry. The entry contains 7544 atoms, of which 6 are hydrogens and 0 are deuteriums.

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 Concanavalin A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	234	Total	C	N	O	S	0	0	0
			1775	1120	297	357	1			
1	B	234	Total	C	N	O	S	0	0	0
			1778	1122	297	358	1			
1	C	232	Total	C	H	N	O	S	0	0
			1767	1113	6	294	353	1		
1	D	233	Total	C	N	O	S	0	0	0
			1770	1118	295	356	1			

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-methyl beta-D-altropyranoside.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			24	13	11			
2	F	2	Total	C	O	0	0	0
			24	13	11			
2	G	2	Total	C	O	0	0	0
			24	13	11			
2	H	2	Total	C	O	0	0	0
			24	13	11			

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mn 1	0	0
3	C	1	Total 1	Mn 1	0	0
3	D	1	Total 1	Mn 1	0	0

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Ca 1	0	0
4	B	1	Total 1	Ca 1	0	0
4	C	1	Total 1	Ca 1	0	0
4	D	1	Total 1	Ca 1	0	0

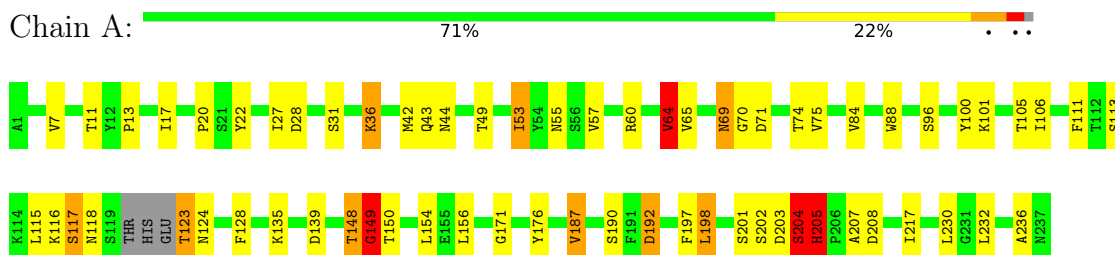
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	105	Total 105	O 105	0	0
5	B	114	Total 114	O 114	0	0
5	C	64	Total 64	O 64	0	0
5	D	67	Total 67	O 67	0	0

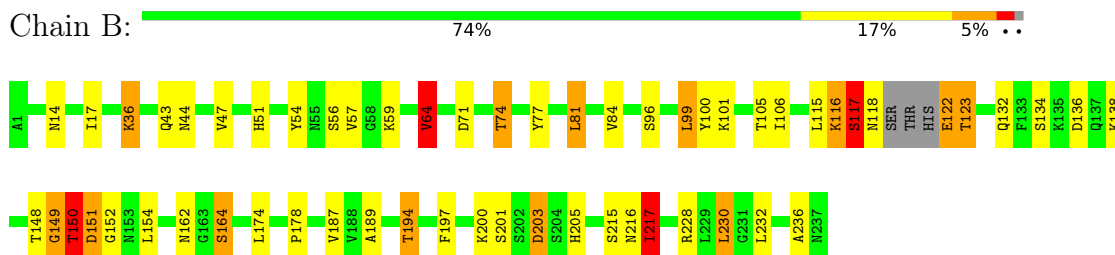
3 Residue-property plots

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.

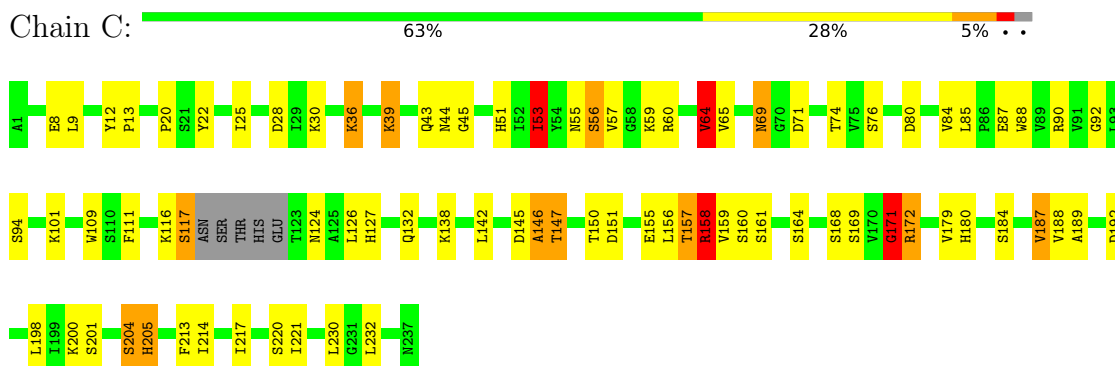
• Molecule 1: Concanavalin A



• Molecule 1: Concanavalin A

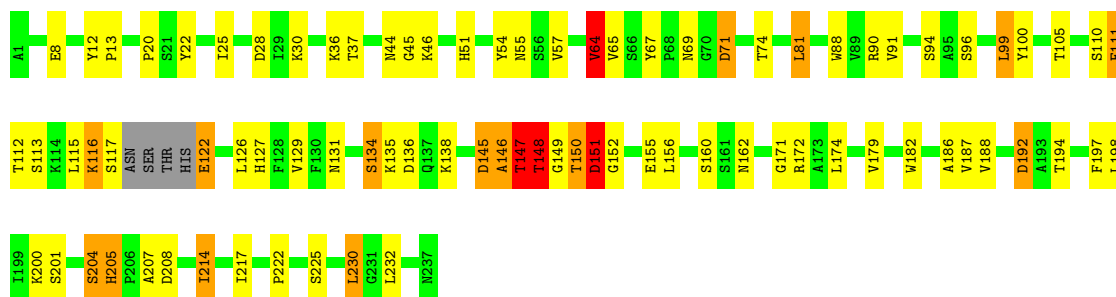


• Molecule 1: Concanavalin A



• Molecule 1: Concanavalin A





- Molecule 2: alpha-D-mannopyranose-(1-3)-methyl beta-D-altropyranoside

Chain E:  100%

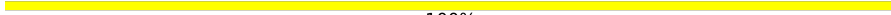
ZEL1
MAN2

- Molecule 2: alpha-D-mannopyranose-(1-3)-methyl beta-D-altropyranoside

Chain F:  100%

ZEL1
MAN2

- Molecule 2: alpha-D-mannopyranose-(1-3)-methyl beta-D-altropyranoside

Chain G:  100%

ZEL1
MAN2

- Molecule 2: alpha-D-mannopyranose-(1-3)-methyl beta-D-altropyranoside

Chain H:  50%  50%

ZEL1
MAN2

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	69.39Å 69.39Å 161.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.92 – 2.10 33.92 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.9 (33.92-2.10) 98.9 (33.92-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.187 , 0.255 0.186 , 0.253	Depositor DCC
R_{free} test set	2524 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.009	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 19.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l 0.477 for h,-h-k,-l 0.022 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7544	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.07% 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: MN, ZEL, MAN, 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	A	1.27	3/1814 (0.2%)	1.25	9/2469 (0.4%)
1	B	1.23	2/1817 (0.1%)	1.24	6/2473 (0.2%)
1	C	1.12	2/1800 (0.1%)	1.39	18/2450 (0.7%)
1	D	1.15	2/1809 (0.1%)	1.27	16/2462 (0.6%)
All	All	1.20	9/7240 (0.1%)	1.29	49/9854 (0.5%)

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	3
1	B	0	3
1	C	0	4
1	D	0	2
All	All	0	12

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	53	ILE	CA-CB	6.64	1.64	1.54
1	C	53	ILE	CA-CB	6.40	1.62	1.54
1	D	214	ILE	N-CA	-5.87	1.39	1.46
1	A	149	GLY	N-CA	5.69	1.53	1.45
1	B	84	VAL	CA-CB	5.67	1.61	1.55

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	205	HIS	N-CA-C	16.86	133.55	110.29
1	C	158	ARG	N-CA-C	-14.32	86.01	109.07
1	C	172	ARG	CA-C-N	13.28	141.72	123.00
1	C	172	ARG	C-N-CA	13.28	141.72	123.00
1	C	172	ARG	O-C-N	-12.78	105.20	122.97

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	148	THR	Peptide
1	A	149	GLY	Peptide
1	A	204	SER	Peptide
1	B	116	LYS	Peptide
1	B	117	SER	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	1775	0	1727	59	0
1	B	1778	0	1728	51	0
1	C	1761	6	1716	65	0
1	D	1770	0	1722	60	0
2	E	24	0	10	0	0
2	F	24	0	10	0	0
2	G	24	0	10	0	0
2	H	24	0	10	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	105	0	0	2	0
5	B	114	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	64	0	0	5	0
5	D	67	0	0	6	0
All	All	7538	6	6933	219	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 16.

The worst 5 of 219 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:215:SER:HB2	5:B:310:HOH:O	1.43	1.18
1:C:232:LEU:HG	5:C:275:HOH:O	1.45	1.16
1:B:59:LYS:HE2	5:B:285:HOH:O	1.48	1.13
1:B:117:SER:HB2	1:B:118:ASN:HB2	1.26	1.12
1:D:150:THR:HA	1:D:152:GLY:N	1.67	1.08

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	230/237 (97%)	217 (94%)	11 (5%)	2 (1%)	14	10
1	B	230/237 (97%)	219 (95%)	8 (4%)	3 (1%)	9	6
1	C	228/237 (96%)	216 (95%)	11 (5%)	1 (0%)	30	28
1	D	229/237 (97%)	218 (95%)	8 (4%)	3 (1%)	9	6
All	All	917/948 (97%)	870 (95%)	38 (4%)	9 (1%)	12	9

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	150	THR
1	B	151	ASP
1	C	147	THR
1	A	149	GLY
1	A	205	HIS

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	199/202 (98%)	185 (93%)	14 (7%)	14	11
1	B	199/202 (98%)	181 (91%)	18 (9%)	9	6
1	C	197/202 (98%)	176 (89%)	21 (11%)	6	4
1	D	198/202 (98%)	181 (91%)	17 (9%)	10	7
All	All	793/808 (98%)	723 (91%)	70 (9%)	9	7

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	99	LEU
1	D	122	GLU
1	D	192	ASP
1	B	164	SER
1	B	134	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	205	HIS
1	C	104	ASN
1	C	69	ASN
1	C	124	ASN
1	A	166	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 ⓘ

8 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	ZEL	E	1	2	13,13,13	0.60	0	18,18,18	2.15	5 (27%)
2	MAN	E	2	2	11,11,12	0.61	0	15,15,17	1.01	1 (6%)
2	ZEL	F	1	2	13,13,13	0.85	0	18,18,18	3.25	7 (38%)
2	MAN	F	2	2	11,11,12	1.00	1 (9%)	15,15,17	1.63	3 (20%)
2	ZEL	G	1	2	13,13,13	0.62	0	18,18,18	3.21	7 (38%)
2	MAN	G	2	2	11,11,12	0.77	0	15,15,17	1.34	1 (6%)
2	ZEL	H	1	2	13,13,13	0.71	0	18,18,18	2.92	9 (50%)
2	MAN	H	2	2	11,11,12	1.05	1 (9%)	15,15,17	1.29	3 (20%)

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	ZEL	E	1	2	1/1/5/5	2/4/24/24	0/1/1/1
2	MAN	E	2	2	-	0/2/19/22	0/1/1/1
2	ZEL	F	1	2	1/1/5/5	2/4/24/24	0/1/1/1
2	MAN	F	2	2	-	0/2/19/22	0/1/1/1
2	ZEL	G	1	2	1/1/5/5	0/4/24/24	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	G	2	2	-	0/2/19/22	0/1/1/1
2	ZEL	H	1	2	-	4/4/24/24	0/1/1/1
2	MAN	H	2	2	-	1/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	MAN	C2-C3	2.30	1.56	1.52
2	H	2	MAN	C2-C3	2.07	1.55	1.52

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	ZEL	O1-C1-C2	9.85	119.51	108.14
2	F	1	ZEL	C1-C2-C3	-7.75	93.72	110.01
2	F	1	ZEL	O1-C1-C2	7.06	116.28	108.14
2	H	1	ZEL	O1-C1-C2	6.91	116.11	108.14
2	G	1	ZEL	C1-C2-C3	-6.01	97.36	110.01

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	1	ZEL	C3
2	F	1	ZEL	C3
2	G	1	ZEL	C3

5 of 9 torsion outliers are listed below:

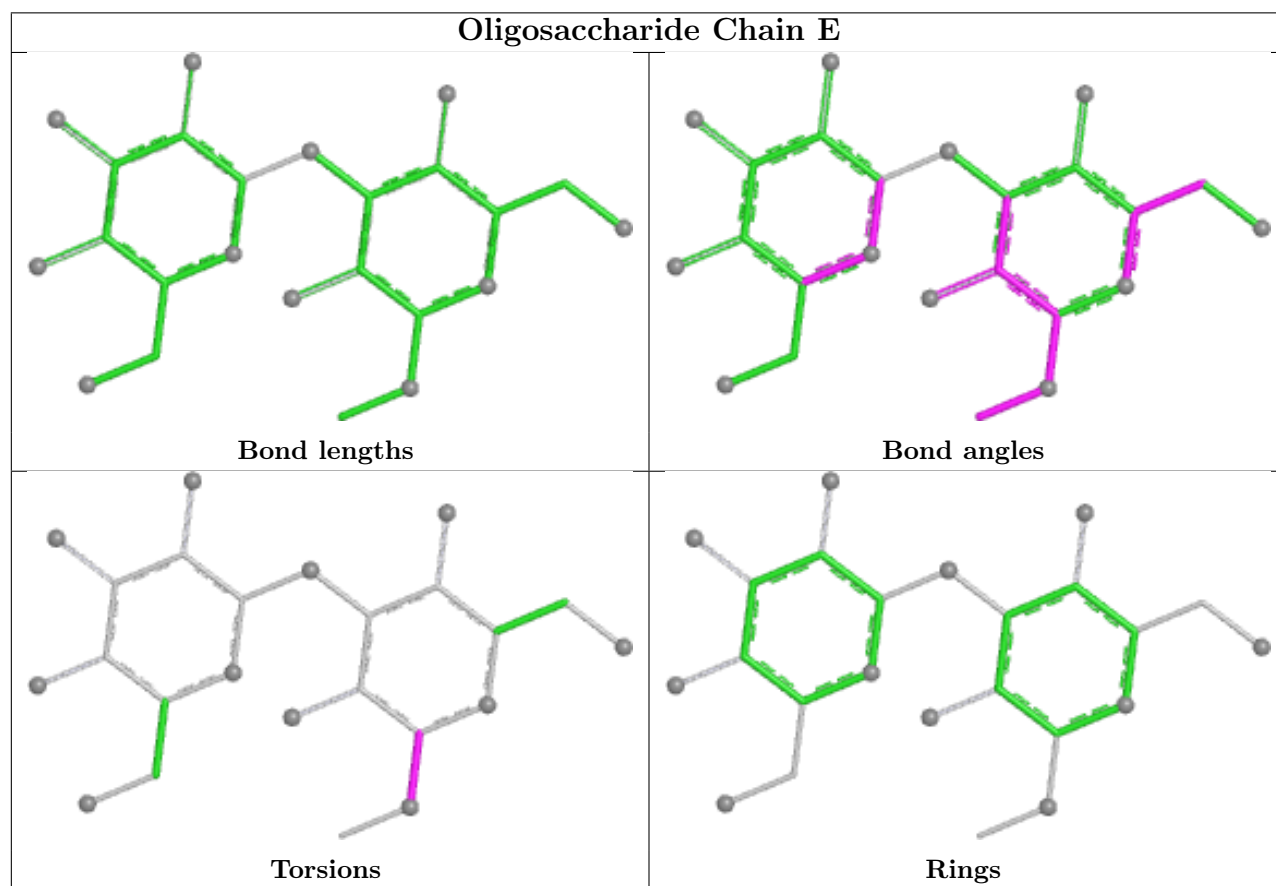
Mol	Chain	Res	Type	Atoms
2	H	1	ZEL	O5-C1-O1-C1M
2	H	1	ZEL	C2-C1-O1-C1M
2	H	1	ZEL	O5-C5-C6-O6
2	E	1	ZEL	C2-C1-O1-C1M
2	H	1	ZEL	C4-C5-C6-O6

There are no ring outliers.

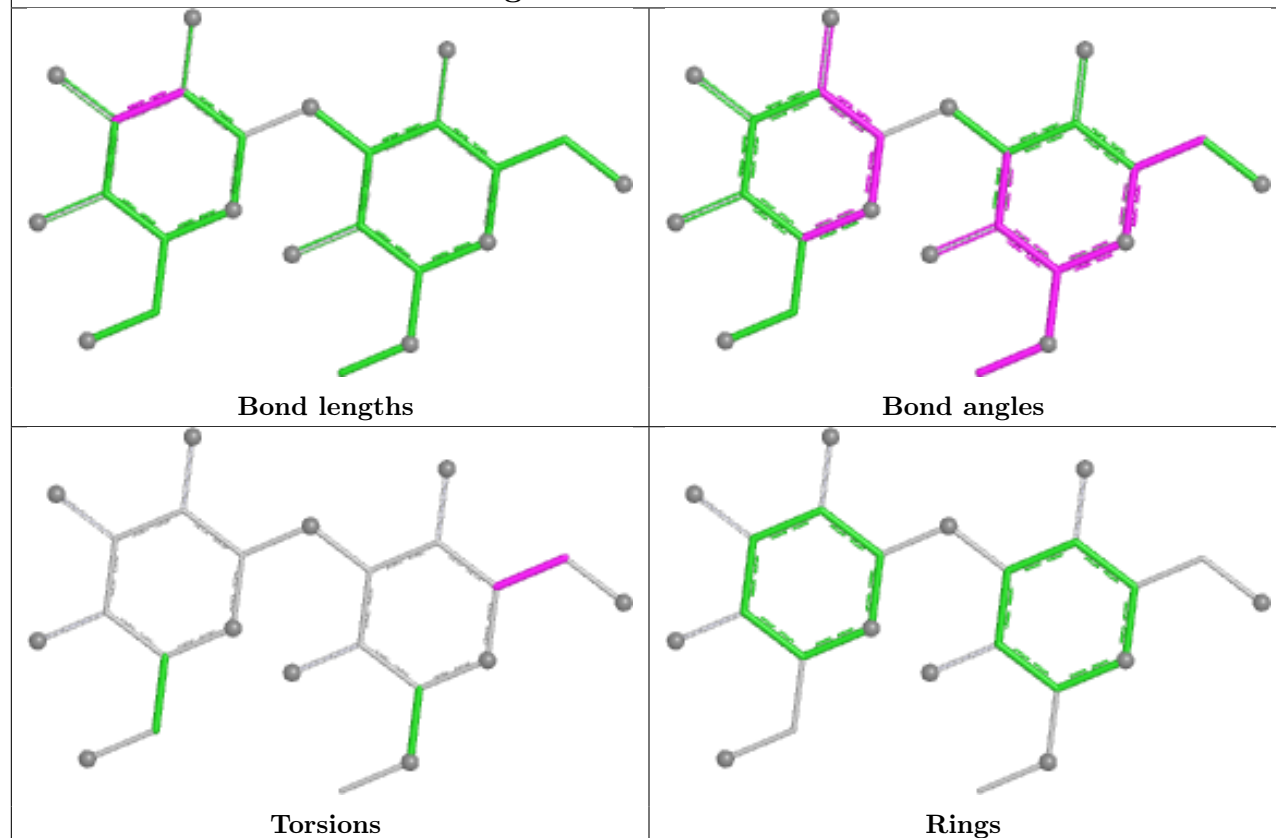
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	2	MAN	1	0

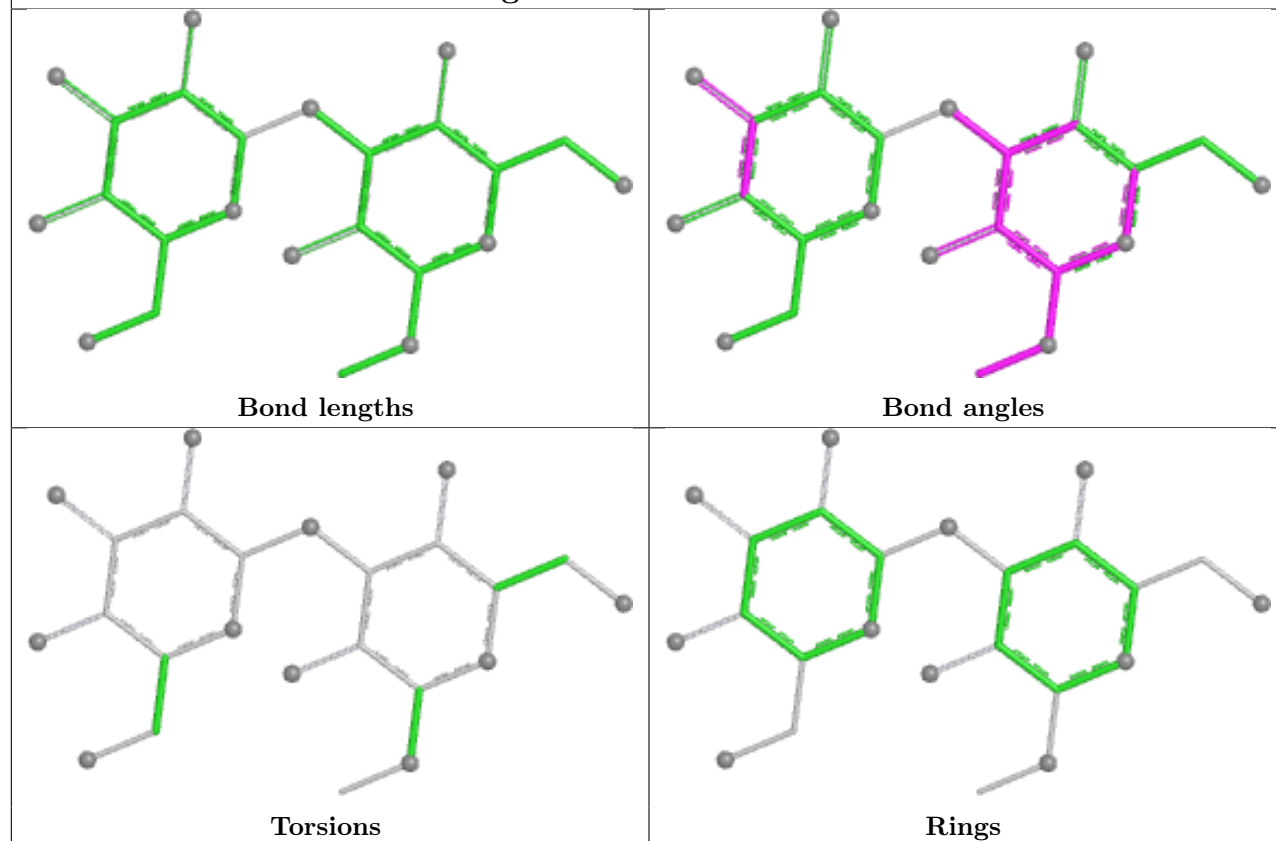
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

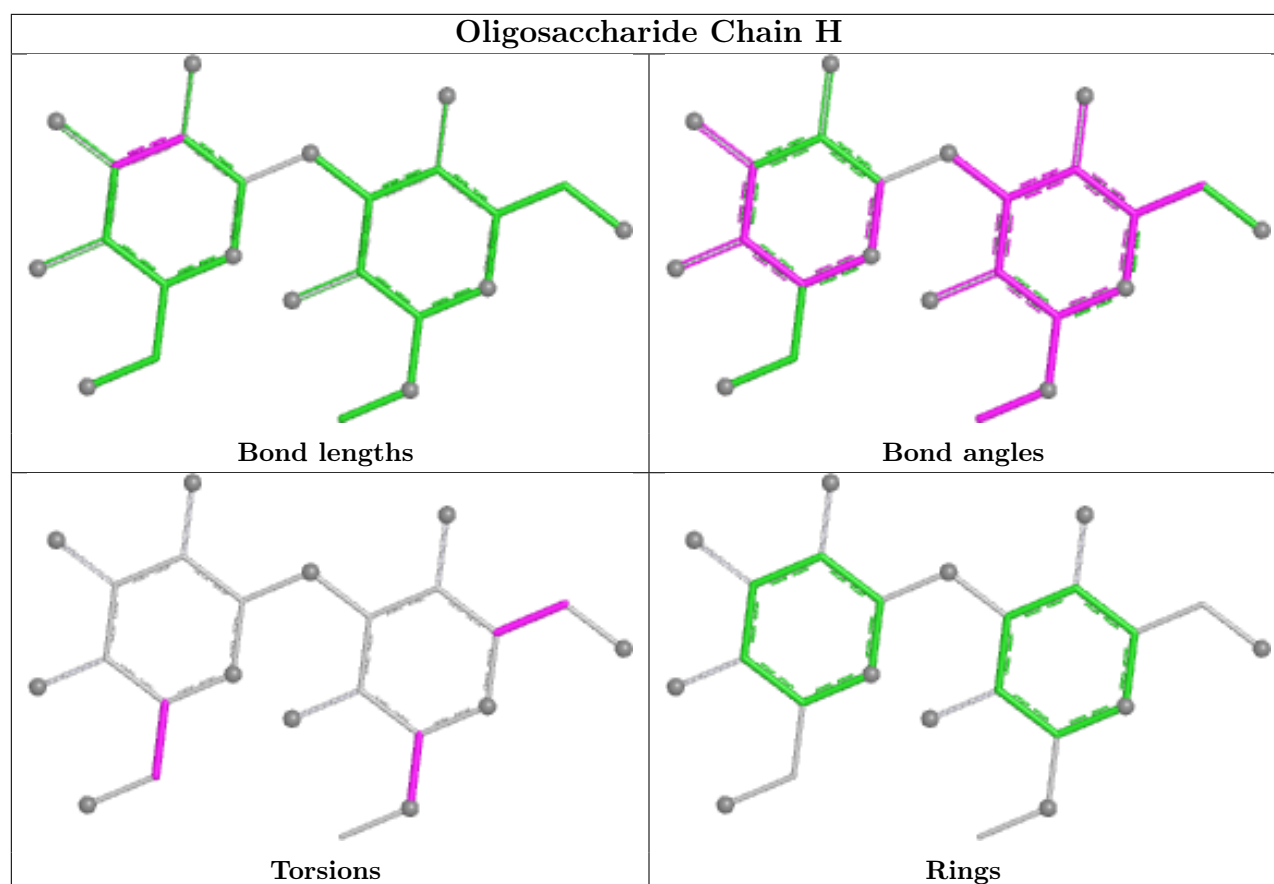


Oligosaccharide Chain F



Oligosaccharide Chain G





5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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	A	234/237 (98%)	-1.40	0 100 100	10, 18, 31, 47	6 (2%)
1	B	234/237 (98%)	-1.39	0 100 100	10, 18, 31, 43	4 (1%)
1	C	232/237 (97%)	-1.32	0 100 100	12, 24, 38, 47	6 (2%)
1	D	233/237 (98%)	-1.30	0 100 100	12, 24, 37, 47	6 (2%)
All	All	933/948 (98%)	-1.35	0 100 100	10, 21, 36, 47	22 (2%)

There are no RSRZ outliers to report.

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

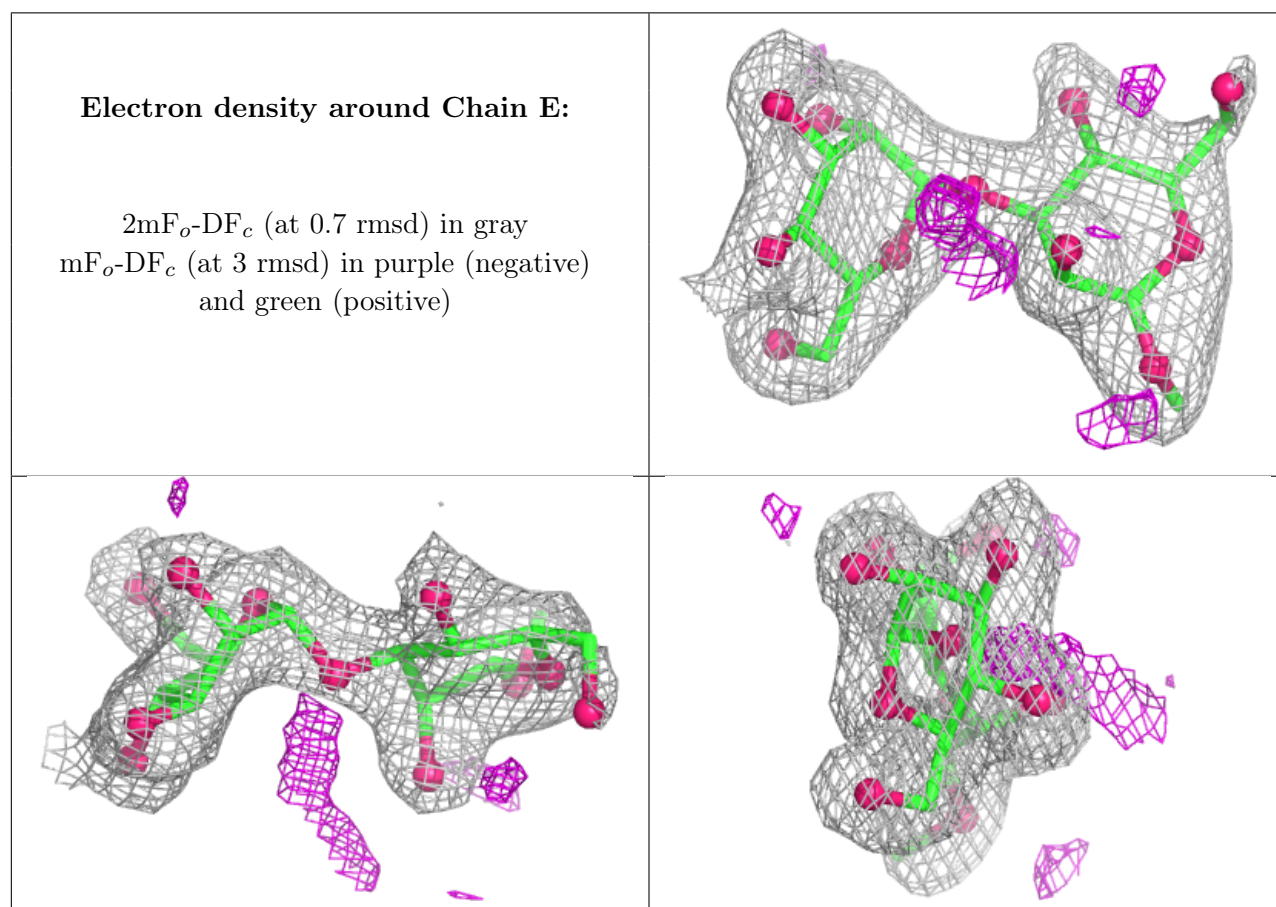
There are no non-standard protein/DNA/RNA residues in this entry.

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.

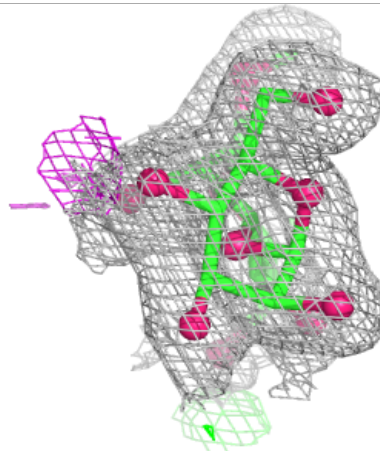
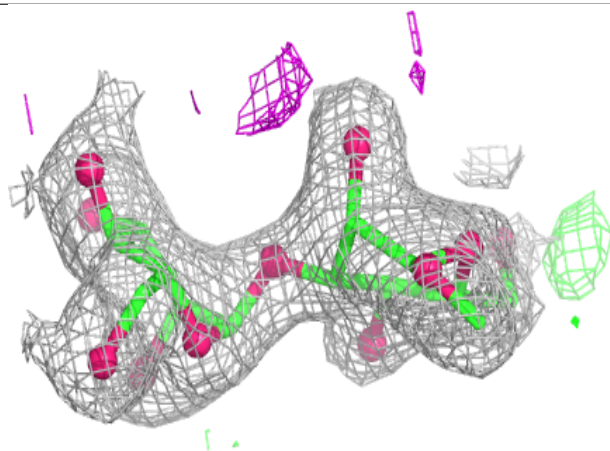
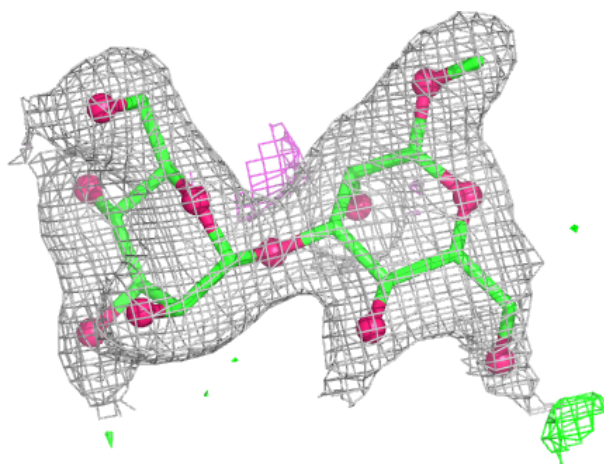
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZEL	E	1	13/13	0.98	0.04	25,33,37,40	0
2	ZEL	F	1	13/13	0.98	0.04	25,32,39,42	0
2	ZEL	H	1	13/13	0.98	0.05	32,40,43,46	0
2	MAN	F	2	11/12	0.99	0.03	14,20,22,23	0
2	ZEL	G	1	13/13	0.99	0.03	27,33,36,37	0
2	MAN	G	2	11/12	0.99	0.04	21,27,28,29	0
2	MAN	E	2	11/12	0.99	0.03	13,18,22,22	0
2	MAN	H	2	11/12	0.99	0.04	22,27,29,31	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.



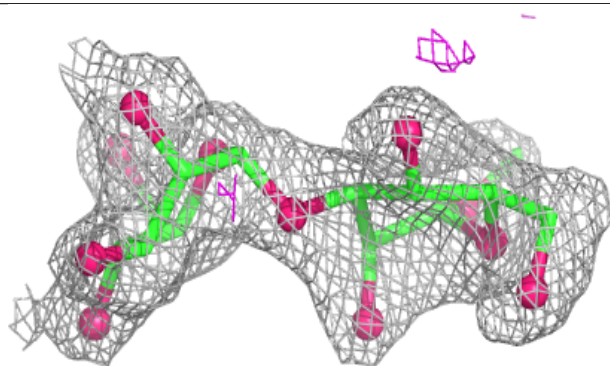
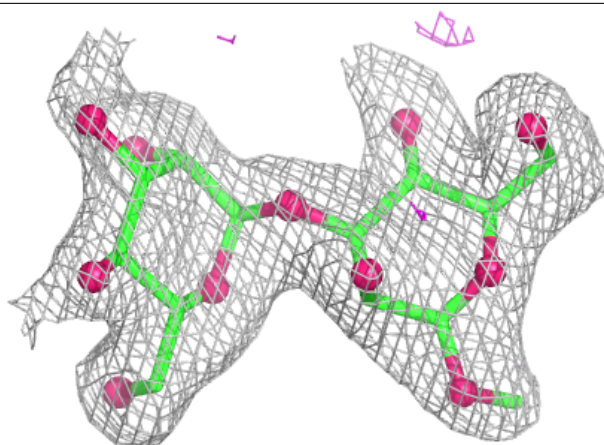
Electron density around Chain F:

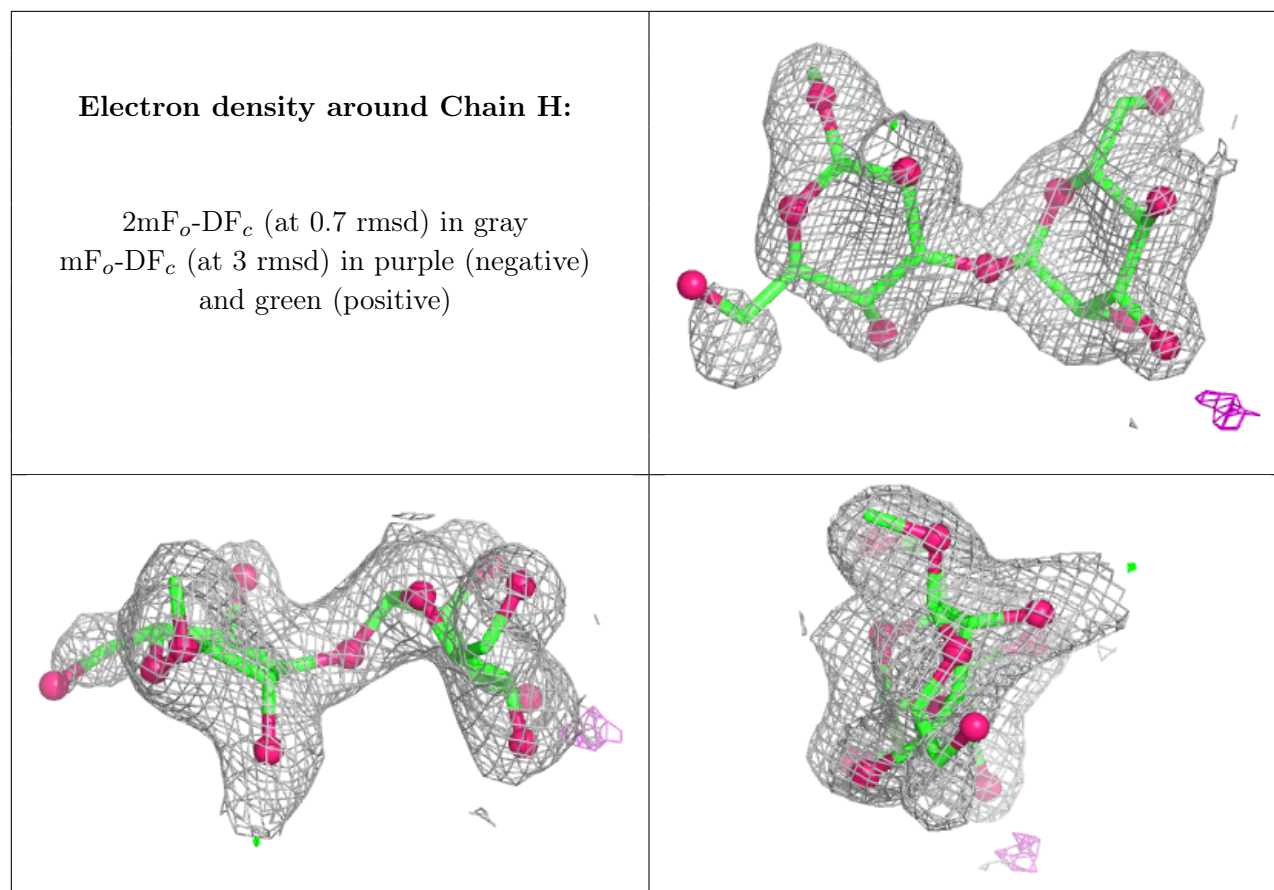
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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	MN	A	238	1/1	1.00	0.01	18,18,18,18	0
3	MN	B	238	1/1	1.00	0.01	18,18,18,18	0
3	MN	C	238	1/1	1.00	0.01	23,23,23,23	0
3	MN	D	238	1/1	1.00	0.01	23,23,23,23	0
4	CA	A	239	1/1	1.00	0.02	18,18,18,18	0
4	CA	B	239	1/1	1.00	0.01	17,17,17,17	0
4	CA	C	239	1/1	1.00	0.01	20,20,20,20	0
4	CA	D	239	1/1	1.00	0.03	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.