



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:32 PM UTC

PDB ID : 2P34 / pdb_00002p34
Title : Crystal structure of a lectin from Canavalia maritima seeds (CML) in complex with man1-4man-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

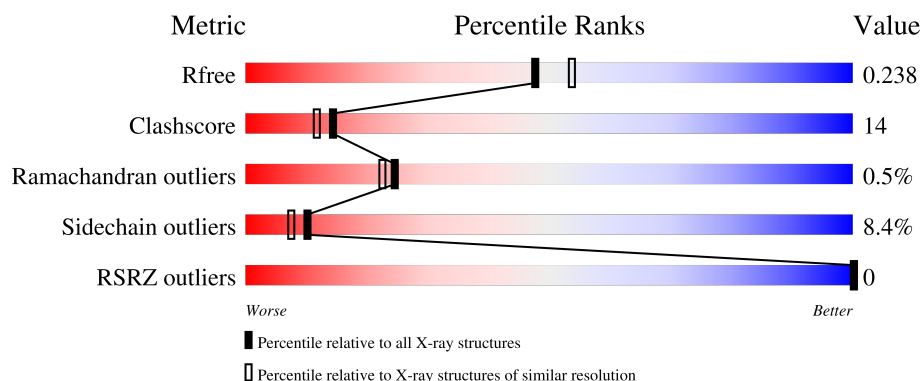
1 Overall quality at a glance ⓘ

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	76% 19% ...
1	B	237	70% 23% ...
1	C	237	62% 32% ...
1	D	237	68% 27% ...
2	E	2	100%

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	G	2	 50% 50%
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	MMA	E	1	X	-	-	-
2	MMA	F	1	X	-	-	-
2	MMA	G	1	X	-	-	-
2	MMA	H	1	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7655 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 Lectin.

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	234	Total	C	N	O	S	0	0	0
			1775	1120	297	357	1			
1	D	234	Total	C	N	O	S	0	0	0
			1778	1122	297	358	1			

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-methyl alpha-D-mannopyranoside.



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

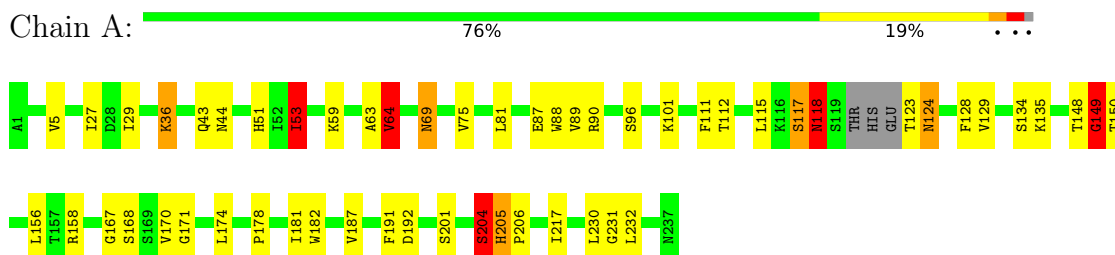
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	134	Total 134	O 134	0	0
5	B	137	Total 137	O 137	0	0
5	C	90	Total 90	O 90	0	0
5	D	84	Total 84	O 84	0	0

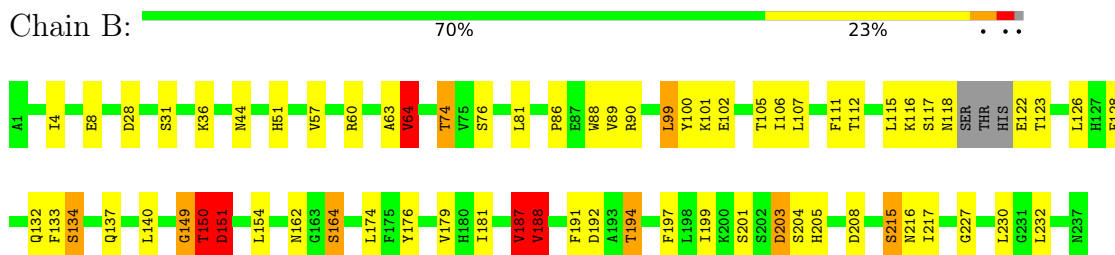
3 Residue-property plots

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.

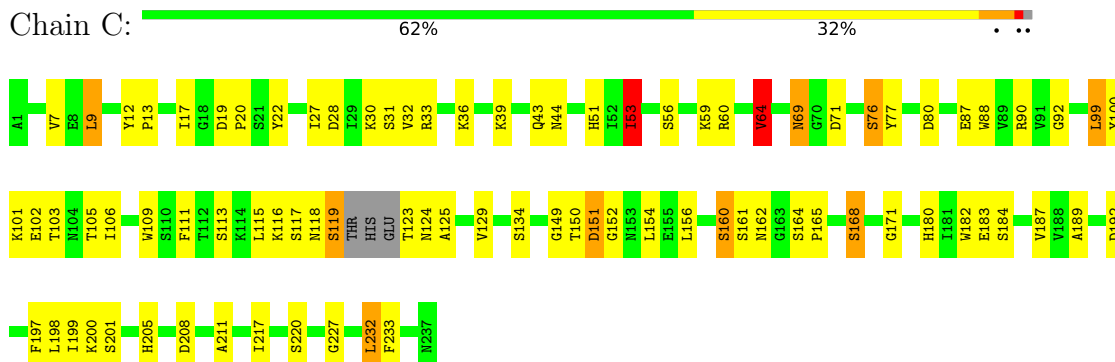
• Molecule 1: Lectin



• Molecule 1: Lectin

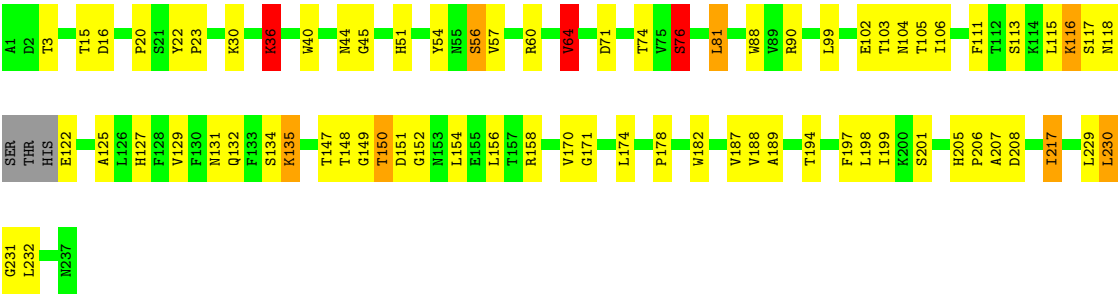


• Molecule 1: Lectin

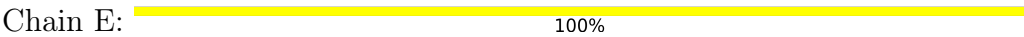


• Molecule 1: Lectin





• Molecule 2: alpha-D-mannopyranose-(1-4)-methyl alpha-D-mannopyranoside



• Molecule 2: alpha-D-mannopyranose-(1-4)-methyl alpha-D-mannopyranoside



• Molecule 2: alpha-D-mannopyranose-(1-4)-methyl alpha-D-mannopyranoside



• Molecule 2: alpha-D-mannopyranose-(1-4)-methyl alpha-D-mannopyranoside



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	69.45Å 69.45Å 161.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.52 – 2.10 33.52 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.6 (33.52-2.10) 96.5 (33.52-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.62 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.175 , 0.239 0.174 , 0.238	Depositor DCC
R_{free} test set	2489 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 21.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l 0.488 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7655	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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: MMA, MN, CA, MAN

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	1.23	5/1814 (0.3%)	1.24	9/2469 (0.4%)
1	B	1.21	4/1817 (0.2%)	1.24	10/2473 (0.4%)
1	C	1.29	2/1815 (0.1%)	1.40	8/2472 (0.3%)
1	D	1.08	2/1817 (0.1%)	1.23	10/2473 (0.4%)
All	All	1.21	13/7263 (0.2%)	1.28	37/9887 (0.4%)

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
1	B	0	3
1	D	0	2
All	All	0	6

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	119	SER	C-N	31.86	1.76	1.33
1	D	36	LYS	CE-NZ	7.29	1.71	1.49
1	A	204	SER	CA-C	7.05	1.61	1.53
1	C	53	ILE	CA-CB	6.97	1.63	1.54
1	B	188	VAL	CA-CB	6.15	1.62	1.54

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	119	SER	O-C-N	-32.15	87.06	123.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	119	SER	CA-C-N	17.59	147.79	122.99
1	C	119	SER	C-N-CA	17.59	147.79	122.99
1	D	229	LEU	CA-C-N	14.05	146.98	121.70
1	D	229	LEU	C-N-CA	14.05	146.98	121.70

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	204	SER	Peptide
1	B	149	GLY	Peptide
1	B	150	THR	Peptide
1	B	187	VAL	Peptide
1	D	116	LYS	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	38	0
1	B	1778	0	1728	53	0
1	C	1775	0	1727	59	0
1	D	1778	0	1728	59	0
2	E	24	0	23	0	0
2	F	24	0	23	0	0
2	G	24	0	23	2	0
2	H	24	0	23	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	134	0	0	4	0
5	B	137	0	0	7	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	90	0	0	5	0
5	D	84	0	0	5	1
All	All	7655	0	7002	201	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 201 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:D:36:LYS:CE	1:D:36:LYS:NZ	1.71	1.51
1:C:119:SER:C	1:C:123:THR:N	1.76	1.41
1:D:150:THR:HA	1:D:152:GLY:H	1.00	1.09
1:D:117:SER:HB3	1:D:118:ASN:CA	1.82	1.08
1:D:117:SER:CB	1:D:118:ASN:HA	1.78	1.06

All (1) 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)
5:B:527:HOH:O	5:D:415:HOH:O[1_665]	2.13	0.07

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%)	220 (96%)	9 (4%)	1 (0%)	30	28
1	B	230/237 (97%)	223 (97%)	6 (3%)	1 (0%)	30	28
1	C	232/237 (98%)	218 (94%)	11 (5%)	3 (1%)	9	6
1	D	230/237 (97%)	218 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	922/948 (97%)	879 (95%)	38 (4%)	5 (0%)	24	22

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	161	SER
1	B	204	SER
1	C	151	ASP
1	A	149	GLY
1	C	168	SER

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	199/202 (98%)	184 (92%)	15 (8%)	12	10
1	B	199/202 (98%)	180 (90%)	19 (10%)	8	5
1	C	199/202 (98%)	182 (92%)	17 (8%)	10	7
1	D	199/202 (98%)	183 (92%)	16 (8%)	11	8
All	All	796/808 (98%)	729 (92%)	67 (8%)	10	7

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	122	GLU
1	D	134	SER
1	D	230	LEU
1	B	164	SER
1	B	151	ASP

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	C	41	ASN
1	C	104	ASN
1	C	69	ASN
1	C	124	ASN
1	A	205	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 ⓘ

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	MMA	E	1	2	13,13,13	0.71	0	18,18,18	3.79	7 (38%)
2	MAN	E	2	2	11,11,12	1.37	2 (18%)	15,15,17	1.45	1 (6%)
2	MMA	F	1	2	13,13,13	0.96	1 (7%)	18,18,18	4.36	7 (38%)
2	MAN	F	2	2	11,11,12	1.50	2 (18%)	15,15,17	1.52	2 (13%)
2	MMA	G	1	2	13,13,13	0.68	0	18,18,18	2.16	8 (44%)
2	MAN	G	2	2	11,11,12	0.92	1 (9%)	15,15,17	1.32	2 (13%)
2	MMA	H	1	2	13,13,13	0.87	1 (7%)	18,18,18	2.15	4 (22%)
2	MAN	H	2	2	11,11,12	0.86	1 (9%)	15,15,17	1.07	1 (6%)

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	MMA	E	1	2	1/1/5/5	1/4/24/24	0/1/1/1
2	MAN	E	2	2	-	0/2/19/22	0/1/1/1
2	MMA	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	MMA	G	1	2	1/1/5/5	3/4/24/24	0/1/1/1
2	MAN	G	2	2	-	0/2/19/22	0/1/1/1
2	MMA	H	1	2	1/1/5/5	4/4/24/24	0/1/1/1
2	MAN	H	2	2	-	0/2/19/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	MAN	O5-C1	-3.46	1.37	1.43
2	E	2	MAN	O5-C1	-2.78	1.39	1.43
2	G	2	MAN	C2-C3	2.56	1.56	1.52
2	E	2	MAN	O2-C2	-2.46	1.38	1.43
2	F	2	MAN	C2-C3	2.32	1.56	1.52

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	MMA	O1-C1-C2	14.54	124.91	108.14
2	E	1	MMA	O1-C1-C2	9.33	118.91	108.14
2	E	1	MMA	C1-C2-C3	-8.24	92.68	110.01
2	F	1	MMA	C1-C2-C3	-7.49	94.25	110.01
2	H	1	MMA	C7-O1-C1	7.39	124.50	113.26

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	1	MMA	C1
2	F	1	MMA	C1
2	G	1	MMA	C1
2	H	1	MMA	C1

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	1	MMA	O5-C1-O1-C7
2	H	1	MMA	O5-C1-O1-C7
2	H	1	MMA	O5-C5-C6-O6
2	G	1	MMA	O5-C1-O1-C7

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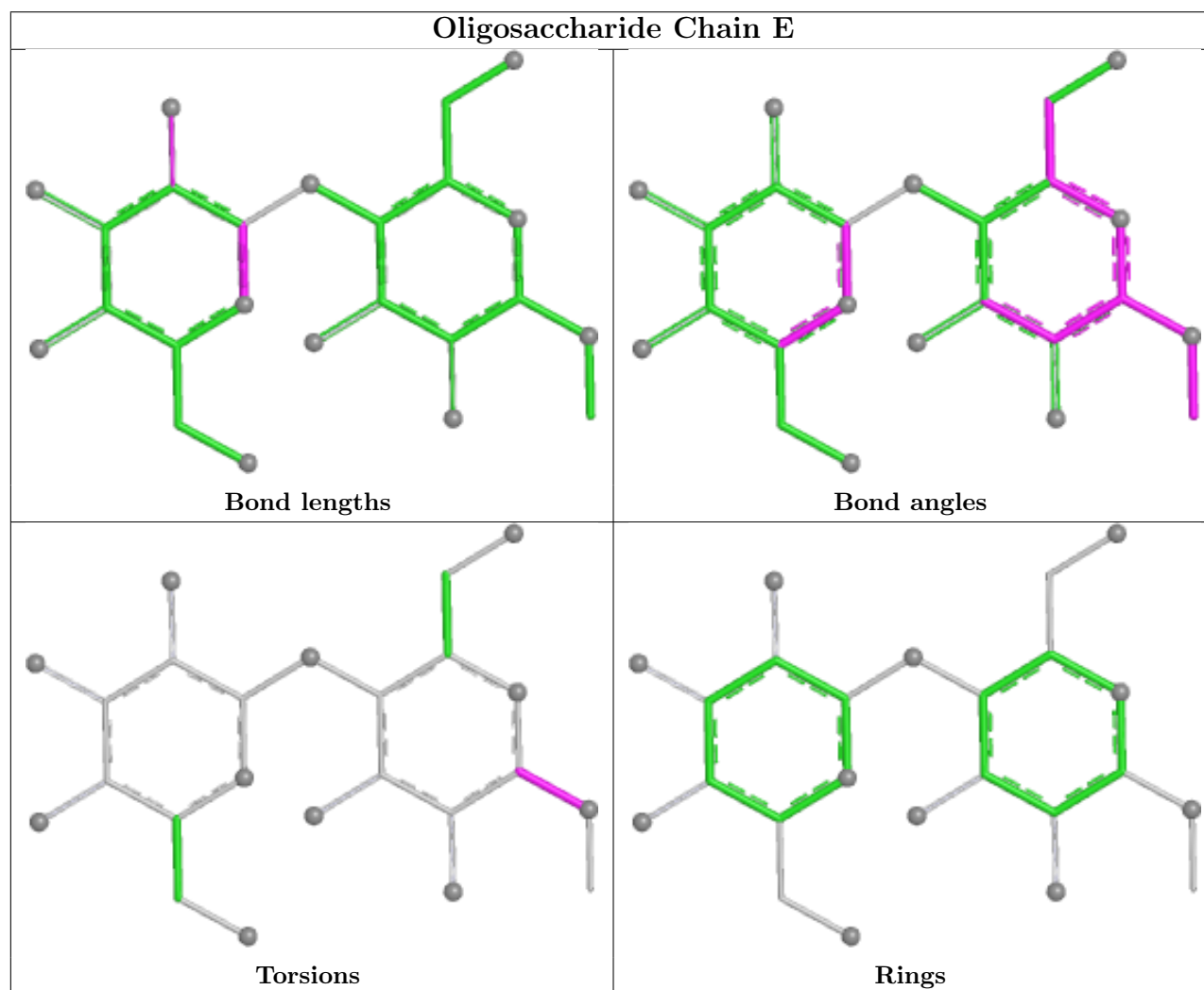
Mol	Chain	Res	Type	Atoms
2	G	1	MMA	C2-C1-O1-C7

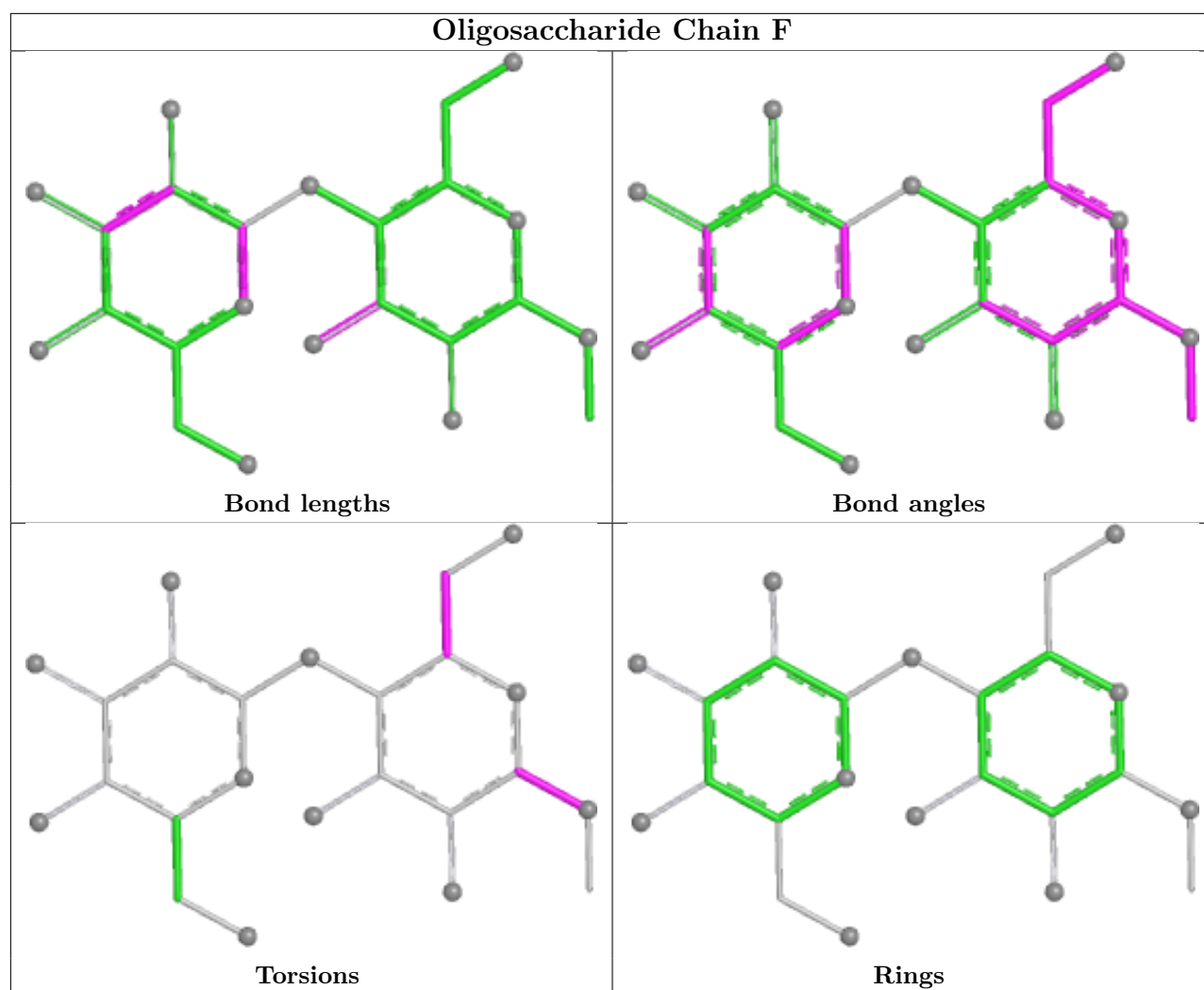
There are no ring outliers.

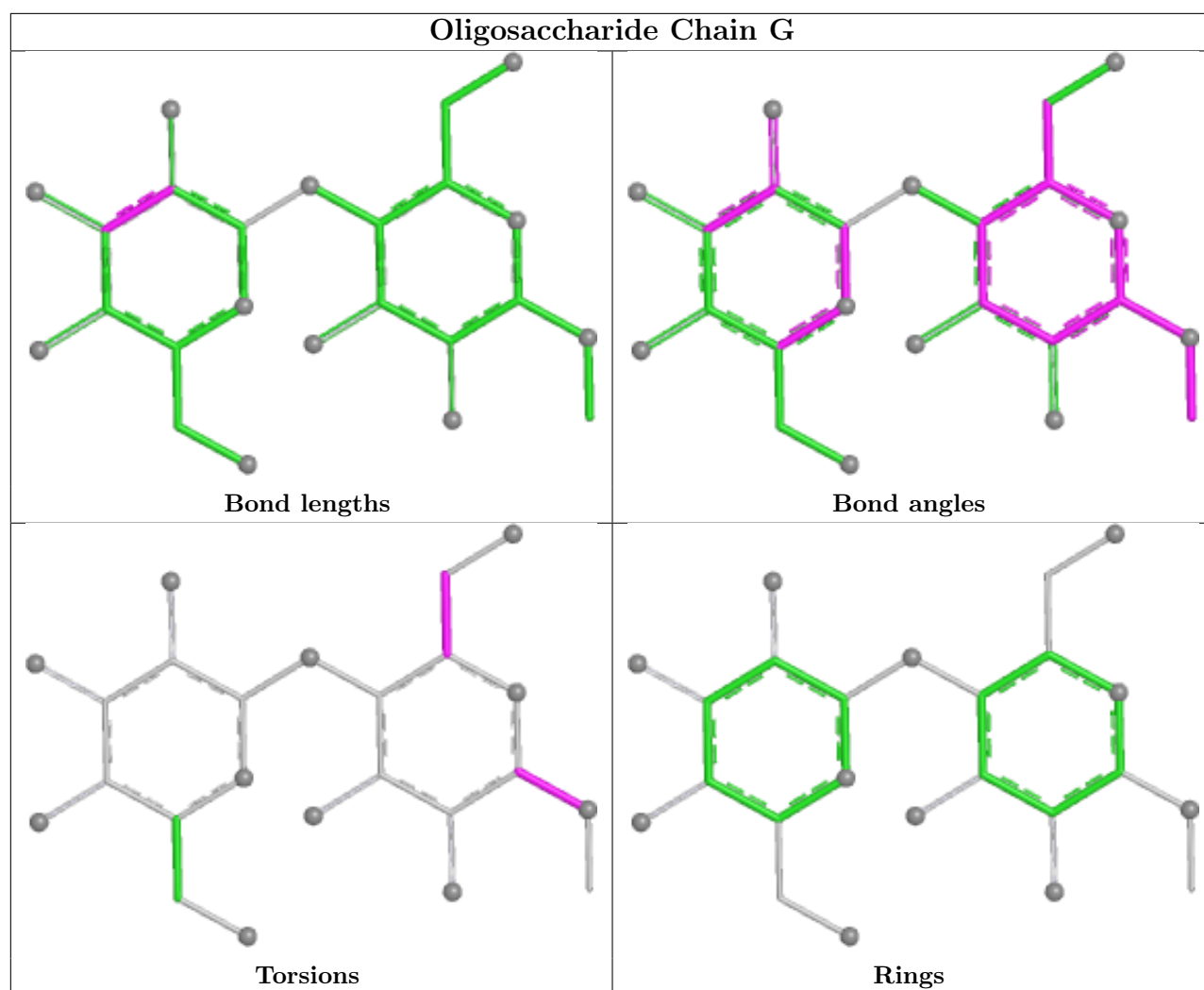
2 monomers are involved in 3 short contacts:

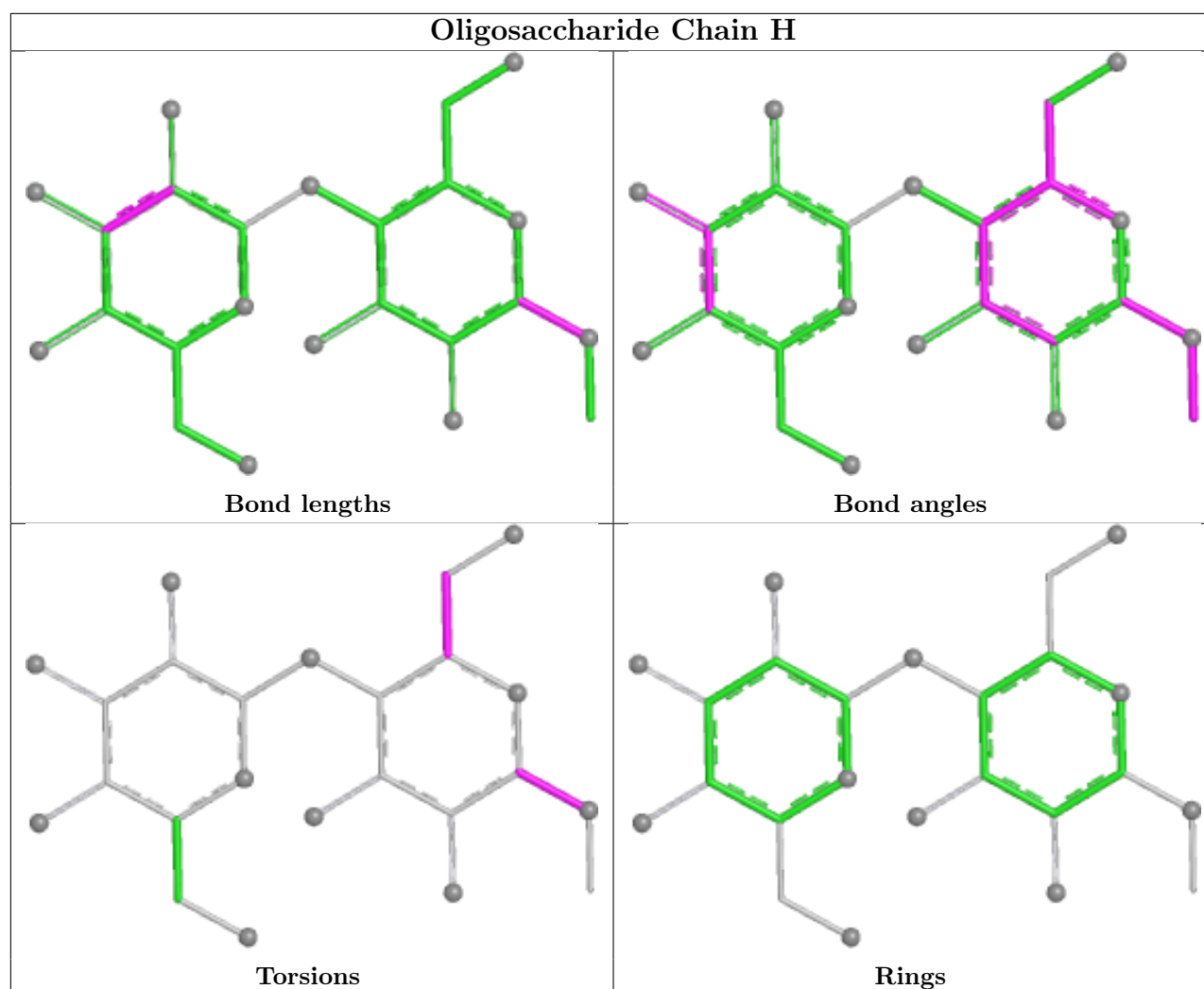
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	MMA	2	0
2	H	1	MMA	1	0

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](#)

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 ⓘ

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%)	-1.65	0 100 100	8, 15, 28, 46	6 (2%)
1	B	234/237 (98%)	-1.64	0 100 100	7, 16, 28, 43	4 (1%)
1	C	234/237 (98%)	-1.57	0 100 100	11, 21, 37, 51	6 (2%)
1	D	234/237 (98%)	-1.55	0 100 100	8, 21, 37, 49	6 (2%)
All	All	936/948 (98%)	-1.60	0 100 100	7, 18, 34, 51	22 (2%)

There are no RSRZ outliers to report.

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

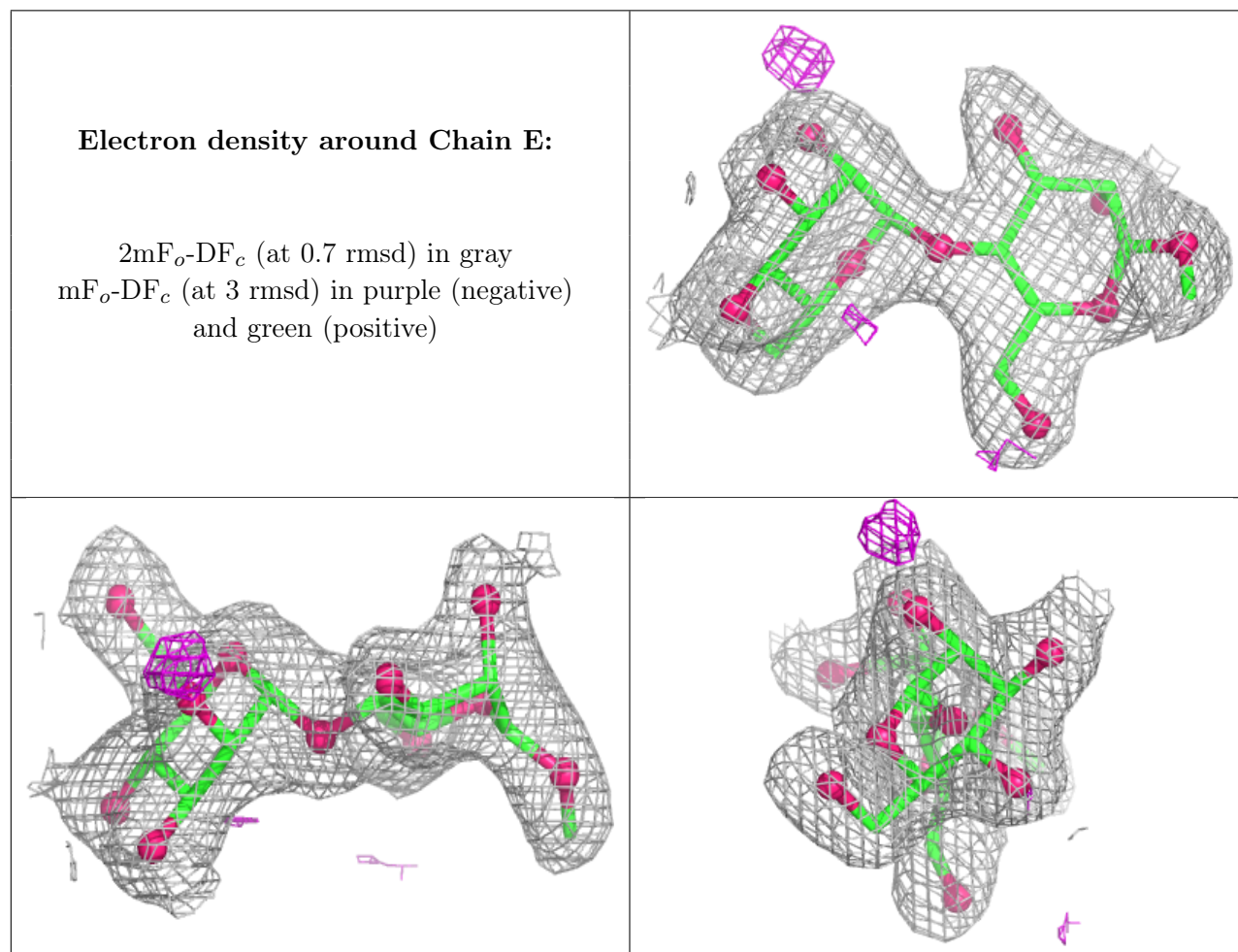
There are no non-standard protein/DNA/RNA residues in this entry.

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.

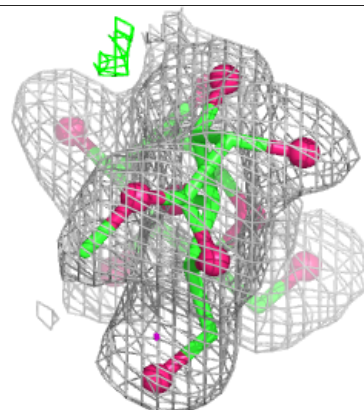
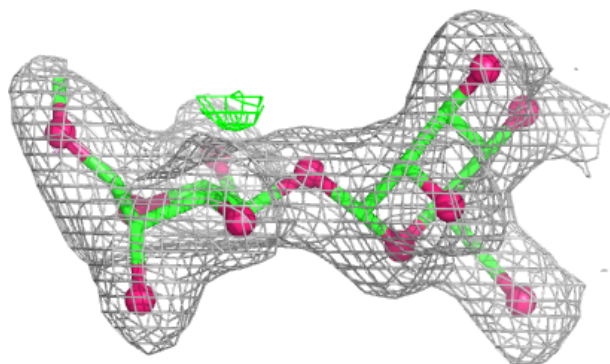
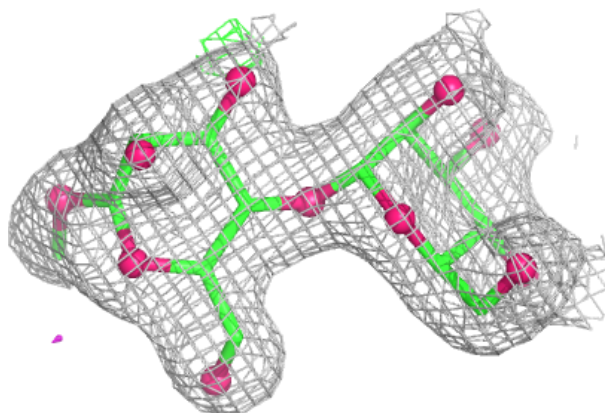
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MMA	H	1	13/13	0.97	0.06	47,56,64,64	0
2	MMA	G	1	13/13	0.99	0.04	46,56,62,63	0
2	MAN	G	2	11/12	0.99	0.03	27,34,40,41	0
2	MMA	F	1	13/13	0.99	0.03	19,26,29,31	0
2	MAN	H	2	11/12	0.99	0.03	21,34,40,41	0
2	MMA	E	1	13/13	1.00	0.02	20,24,28,30	0
2	MAN	F	2	11/12	1.00	0.01	11,13,16,17	0
2	MAN	E	2	11/12	1.00	0.02	9,16,18,19	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.

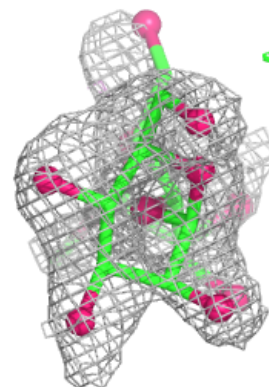
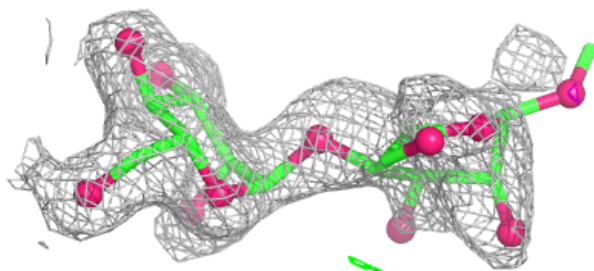
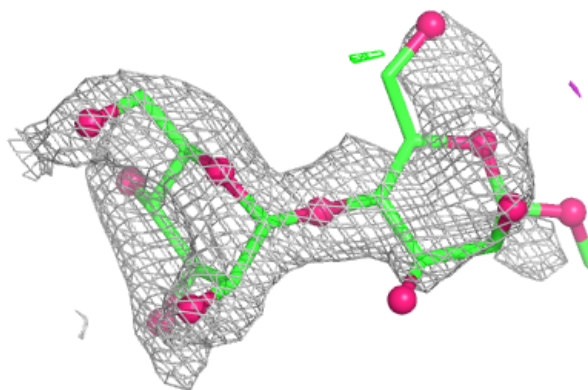


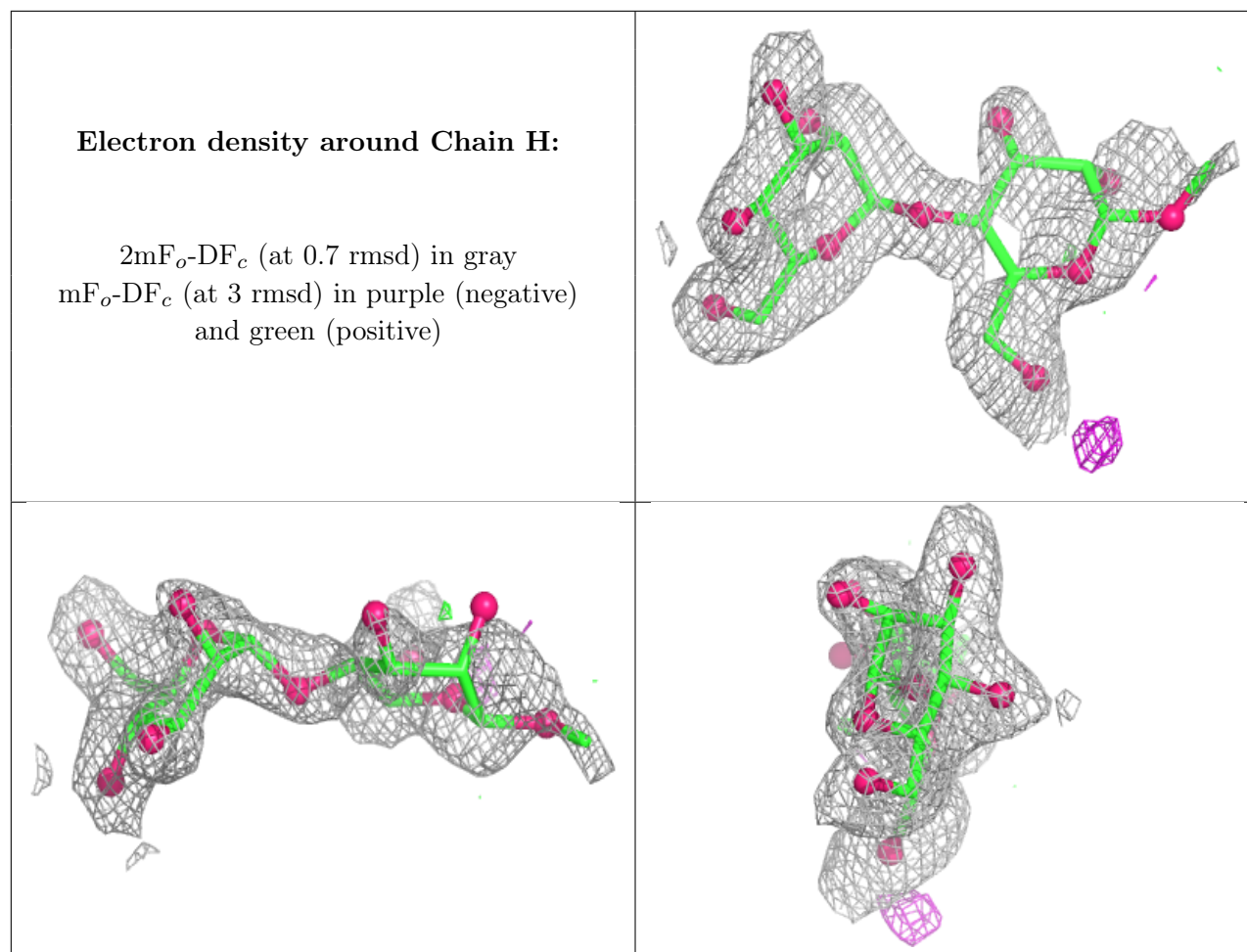
Electron density around Chain F:

$2mF_o-DF_c$ (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	301	1/1	1.00	0.01	14,14,14,14	0
3	MN	B	301	1/1	1.00	0.01	14,14,14,14	0
3	MN	C	301	1/1	1.00	0.01	18,18,18,18	0
3	MN	D	301	1/1	1.00	0.01	21,21,21,21	0
4	CA	A	302	1/1	1.00	0.02	13,13,13,13	0
4	CA	B	302	1/1	1.00	0.01	13,13,13,13	0
4	CA	C	302	1/1	1.00	0.01	16,16,16,16	0
4	CA	D	302	1/1	1.00	0.01	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.