



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 01:27 AM BST

PDB ID : 4JM0
Title : Structure of Human Cytomegalovirus Immune Modulator UL141
Authors : Nemcovicova, I.; Zajonc, D.M.
Deposited on : 2013-03-13
Resolution : 3.25 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

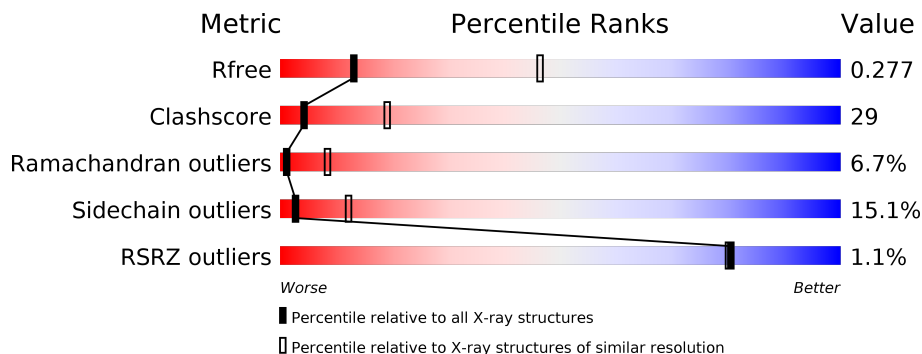
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



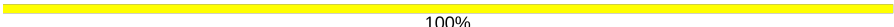
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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 on 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	256	<div style="display: flex; align-items: center;"> <div style="width: 10px; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="flex-grow: 1; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; text-align: center;">%</div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, orange 40%, yellow 61%, green 82%, grey 100%);"></div> <div style="position: absolute; top: 5px; left: 40%; width: 20%; text-align: center;">40%</div> <div style="position: absolute; top: 5px; left: 61%; width: 20%; text-align: center;">21%</div> <div style="position: absolute; top: 5px; left: 82%; width: 15%; text-align: center;">7%</div> <div style="position: absolute; top: 5px; left: 95%; width: 5%; text-align: center;">32%</div> </div> </div>
1	B	256	<div style="display: flex; align-items: center;"> <div style="flex-grow: 1; position: relative;"> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, green 0%, yellow 38%, orange 64%, red 69%, grey 100%);"></div> <div style="position: absolute; top: 5px; left: 38%; width: 20%; text-align: center;">38%</div> <div style="position: absolute; top: 5px; left: 64%; width: 20%; text-align: center;">26%</div> <div style="position: absolute; top: 5px; left: 83%; width: 10%; text-align: center;">5%</div> <div style="position: absolute; top: 5px; left: 95%; width: 5%; text-align: center;">29%</div> </div> </div>
2	C	2	<div style="display: flex; align-items: center;"> <div style="flex-grow: 1; position: relative;"> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, yellow 0%, orange 50%, grey 100%);"></div> <div style="position: absolute; top: 5px; left: 50%; width: 40%; text-align: center;">50%</div> <div style="position: absolute; top: 5px; left: 90%; width: 10%; text-align: center;">50%</div> </div> </div>
2	D	2	<div style="display: flex; align-items: center;"> <div style="flex-grow: 1; position: relative;"> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background-color: yellow;"></div> <div style="position: absolute; top: 5px; left: 50%; width: 100%; text-align: center;">100%</div> </div> </div>
2	E	2	<div style="display: flex; align-items: center;"> <div style="flex-grow: 1; position: relative;"> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background-color: orange;"></div> <div style="position: absolute; top: 5px; left: 50%; width: 100%; text-align: center;">100%</div> </div> </div>
2	F	2	<div style="display: flex; align-items: center;"> <div style="flex-grow: 1; position: relative;"> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background-color: yellow;"></div> <div style="position: absolute; top: 5px; left: 50%; width: 100%; text-align: center;">100%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	G	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	D	2	-	-	-	X
2	NAG	E	1	-	-	X	-
2	NAG	F	2	-	-	-	X

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2863 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 Protein UL141.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	175	1331	855	227	240	9	0	0	0
1	B	183	1392	893	230	257	12	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	280	HIS	-	expression tag	UNP Q6RJQ3
A	281	HIS	-	expression tag	UNP Q6RJQ3
A	282	HIS	-	expression tag	UNP Q6RJQ3
A	283	HIS	-	expression tag	UNP Q6RJQ3
A	284	HIS	-	expression tag	UNP Q6RJQ3
A	285	HIS	-	expression tag	UNP Q6RJQ3
B	280	HIS	-	expression tag	UNP Q6RJQ3
B	281	HIS	-	expression tag	UNP Q6RJQ3
B	282	HIS	-	expression tag	UNP Q6RJQ3
B	283	HIS	-	expression tag	UNP Q6RJQ3
B	284	HIS	-	expression tag	UNP Q6RJQ3
B	285	HIS	-	expression tag	UNP Q6RJQ3

- 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
			Total	C	N	O			
2	C	2	28	16	2	10	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	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	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

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

Chain D:  100%

MAG1
MAG2

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

Chain E:  100%

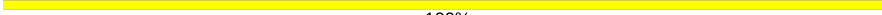
MAG1
MAG2

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

Chain F:  100%

MAG1
MAG2

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

Chain G:  100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	96.06 Å 96.06 Å 136.07 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	11.98 – 3.25 11.98 – 3.25	Depositor EDS
% Data completeness (in resolution range)	97.5 (11.98-3.25) 99.7 (11.98-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 3.28 Å)	Xtrriage
Refinement program	REFMAC 5.6.0104	Depositor
R, R_{free}	0.201 , 0.279 0.210 , 0.277	Depositor DCC
R_{free} test set	930 reflections (8.02%)	wwPDB-VP
Wilson B-factor (Å ²)	76.9	Xtrriage
Anisotropy	0.053	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 61.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.053 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	2863	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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: 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	1.07	5/1366 (0.4%)	1.10	7/1868 (0.4%)
1	B	1.09	4/1427 (0.3%)	1.04	4/1949 (0.2%)
All	All	1.08	9/2793 (0.3%)	1.07	11/3817 (0.3%)

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	B	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	188	TRP	CD2-CE2	6.91	1.49	1.41
1	A	116	TRP	CD2-CE2	6.26	1.48	1.41
1	A	188	TRP	CD2-CE2	5.98	1.48	1.41
1	B	116	TRP	CD2-CE2	5.73	1.48	1.41
1	A	193	TRP	CD2-CE2	5.61	1.48	1.41

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	183	LEU	CA-CB-CG	7.85	133.36	115.30
1	B	123	LEU	CA-CB-CG	6.35	129.91	115.30
1	B	236	THR	N-CA-CB	5.80	121.32	110.30
1	B	93	LEU	CB-CG-CD2	-5.47	101.71	111.00
1	A	67	CYS	O-C-N	5.21	131.04	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	230	GLU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1331	0	1220	69	0
1	B	1392	0	1277	84	0
2	C	28	0	25	1	0
2	D	28	0	26	2	0
2	E	28	0	26	12	0
2	F	28	0	25	4	0
2	G	28	0	25	0	0
All	All	2863	0	2624	155	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 29.

The worst 5 of 155 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:A:84:CYS:SG	1:A:234:CYS:CB	2.15	1.34
1:A:147:ASN:HD21	2:E:1:NAG:C1	1.55	1.19
1:B:68:THR:O	1:B:68:THR:HG22	1.56	1.05
1:A:180:ARG:HH21	1:B:73:SER:HA	1.16	1.04
1:B:67:CYS:SG	1:B:143:CYS:CB	2.48	1.00

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	167/256 (65%)	139 (83%)	19 (11%)	9 (5%)	2	12
1	B	175/256 (68%)	145 (83%)	16 (9%)	14 (8%)	1	6
All	All	342/512 (67%)	284 (83%)	35 (10%)	23 (7%)	1	8

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	236	THR
1	B	36	ALA
1	B	67	CYS
1	B	108	GLN

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	132/224 (59%)	113 (86%)	19 (14%)	3	14
1	B	140/224 (62%)	118 (84%)	22 (16%)	2	11
All	All	272/448 (61%)	231 (85%)	41 (15%)	3	12

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	236	THR

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Mol	Chain	Res	Type
1	B	62	GLN
1	B	166	LEU
1	B	33	PHE
1	B	35	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	155	GLN
1	B	155	GLN
1	B	117	ASN
1	A	120	GLN
1	B	62	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1	2	14,14,15	0.89	0	17,19,21	2.03	6 (35%)
2	NAG	C	2	2	14,14,15	0.81	0	17,19,21	2.66	5 (29%)
2	NAG	D	1	1,2	14,14,15	0.57	0	17,19,21	0.67	0
2	NAG	D	2	2	14,14,15	0.57	0	17,19,21	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	E	1	1,2	14,14,15	1.05	2 (14%)	17,19,21	1.94	5 (29%)
2	NAG	E	2	2	14,14,15	0.68	0	17,19,21	1.78	3 (17%)
2	NAG	F	1	1,2	14,14,15	0.56	0	17,19,21	0.67	0
2	NAG	F	2	2	14,14,15	0.57	0	17,19,21	0.66	0
2	NAG	G	1	1,2	14,14,15	0.79	0	17,19,21	2.12	5 (29%)
2	NAG	G	2	2	14,14,15	0.78	0	17,19,21	1.30	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2	-	4/6/23/26	0/1/1/1
2	NAG	C	2	2	-	3/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	NAG	C4-C3	2.30	1.58	1.52
2	E	1	NAG	O5-C5	-2.08	1.39	1.43

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C2-N2-C7	6.53	132.21	122.90
2	G	1	NAG	C2-N2-C7	5.71	131.03	122.90
2	C	2	NAG	C1-O5-C5	5.62	119.81	112.19
2	C	1	NAG	C4-C3-C2	4.83	118.09	111.02
2	C	2	NAG	C1-C2-N2	4.79	118.67	110.49

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

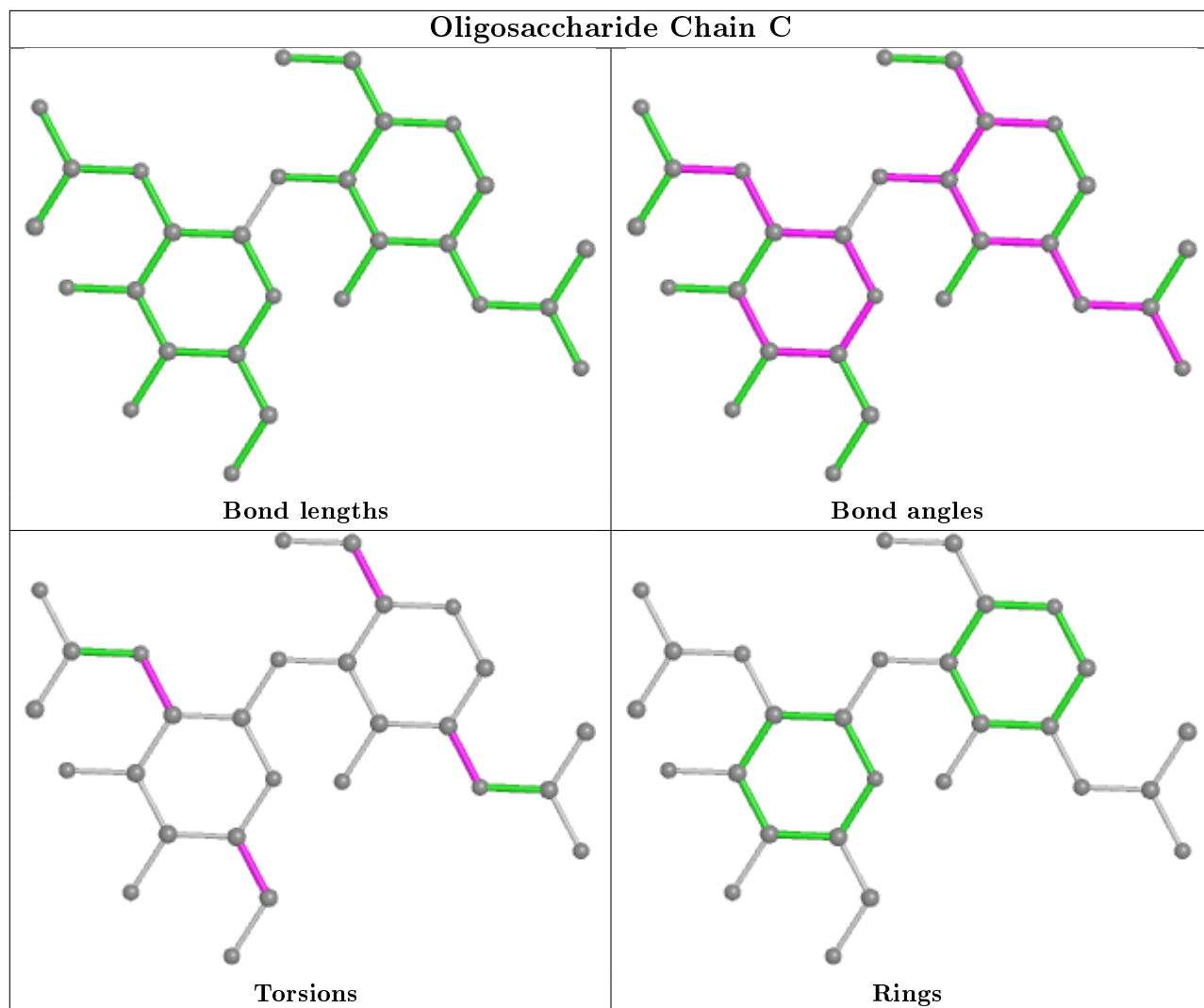
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C3-C2-N2-C7
2	C	1	NAG	O5-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6

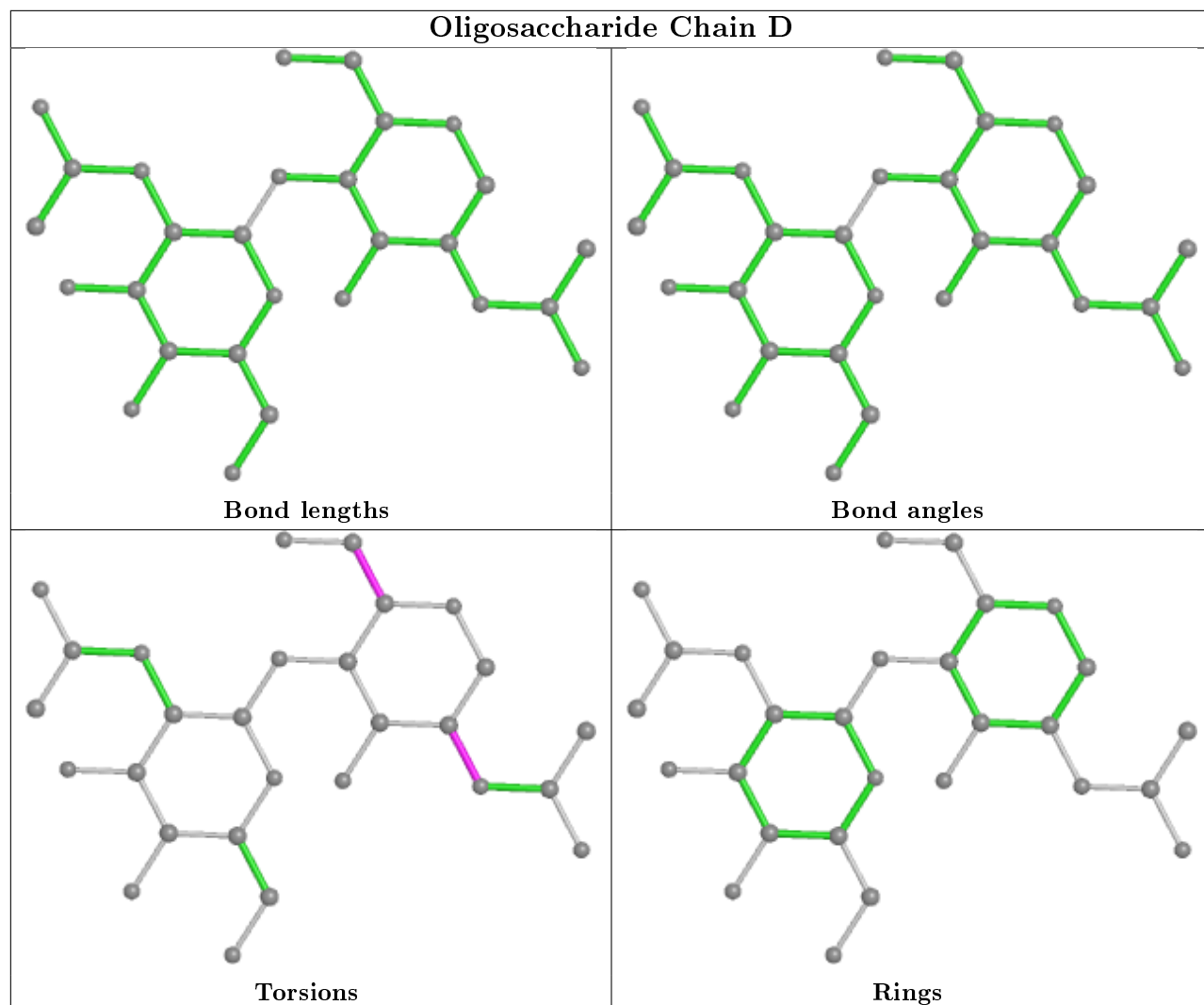
There are no ring outliers.

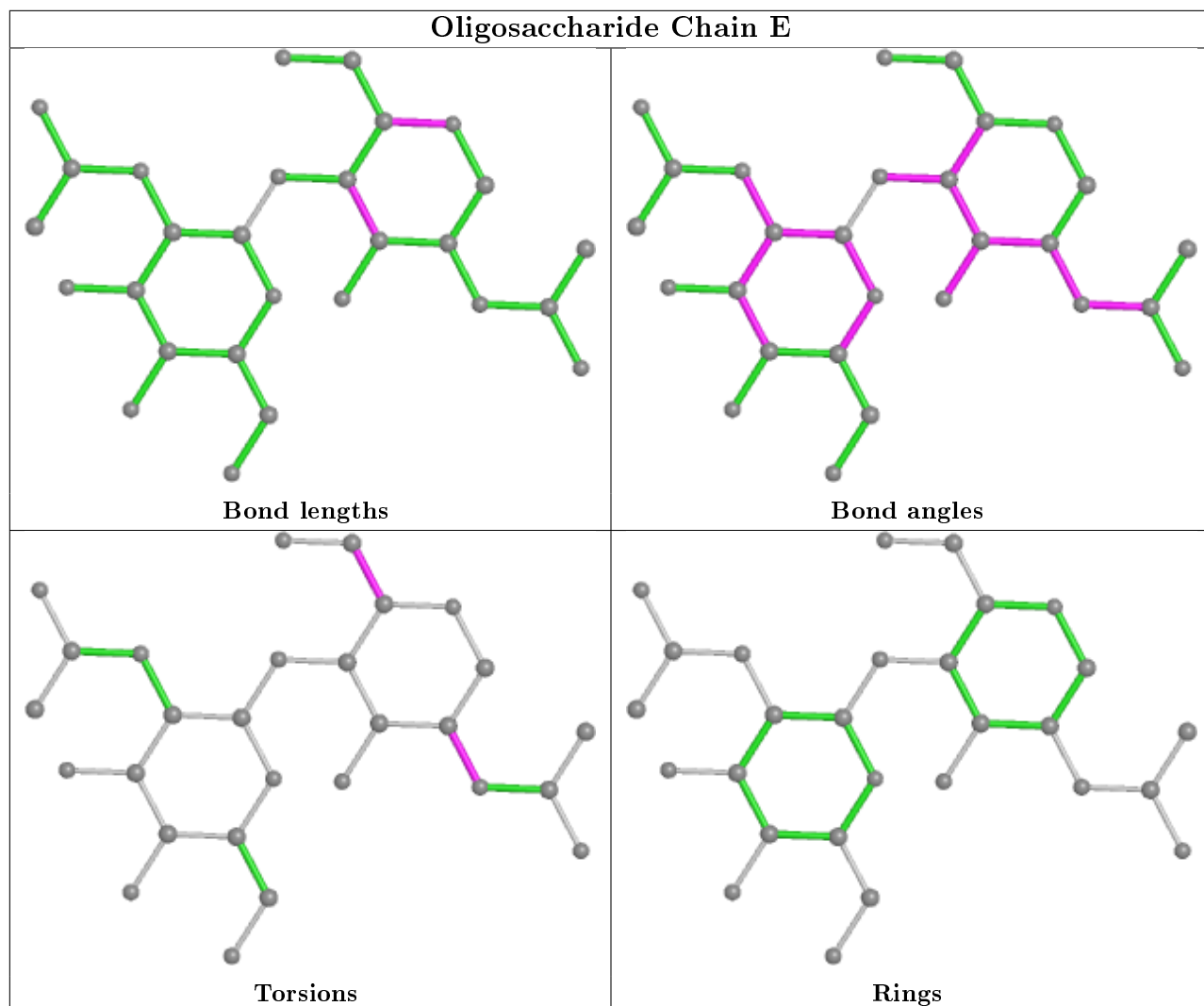
7 monomers are involved in 19 short contacts:

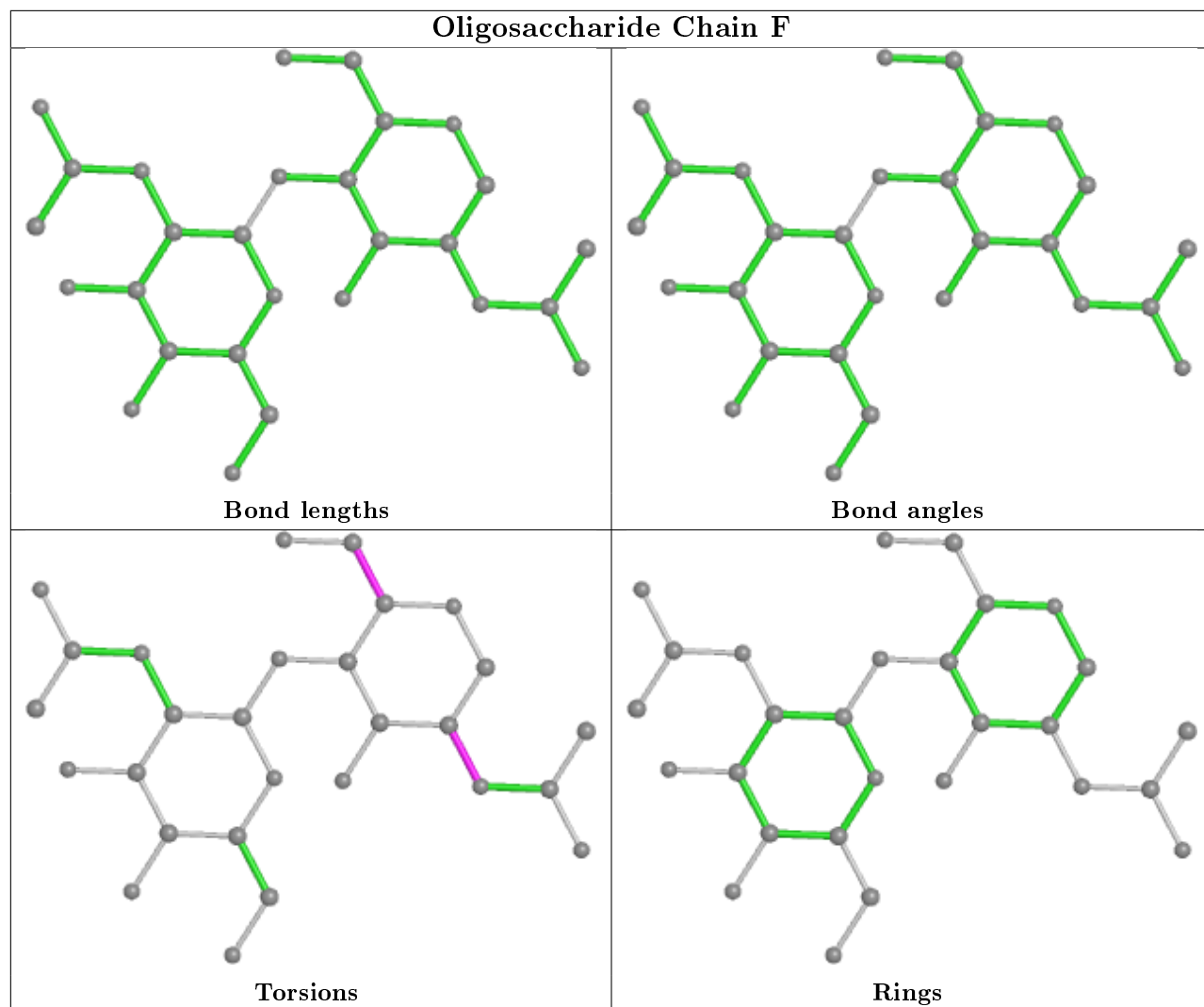
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	NAG	4	0
2	C	1	NAG	1	0
2	E	1	NAG	12	0
2	D	1	NAG	2	0
2	F	2	NAG	2	0
2	D	2	NAG	2	0
2	E	2	NAG	6	0

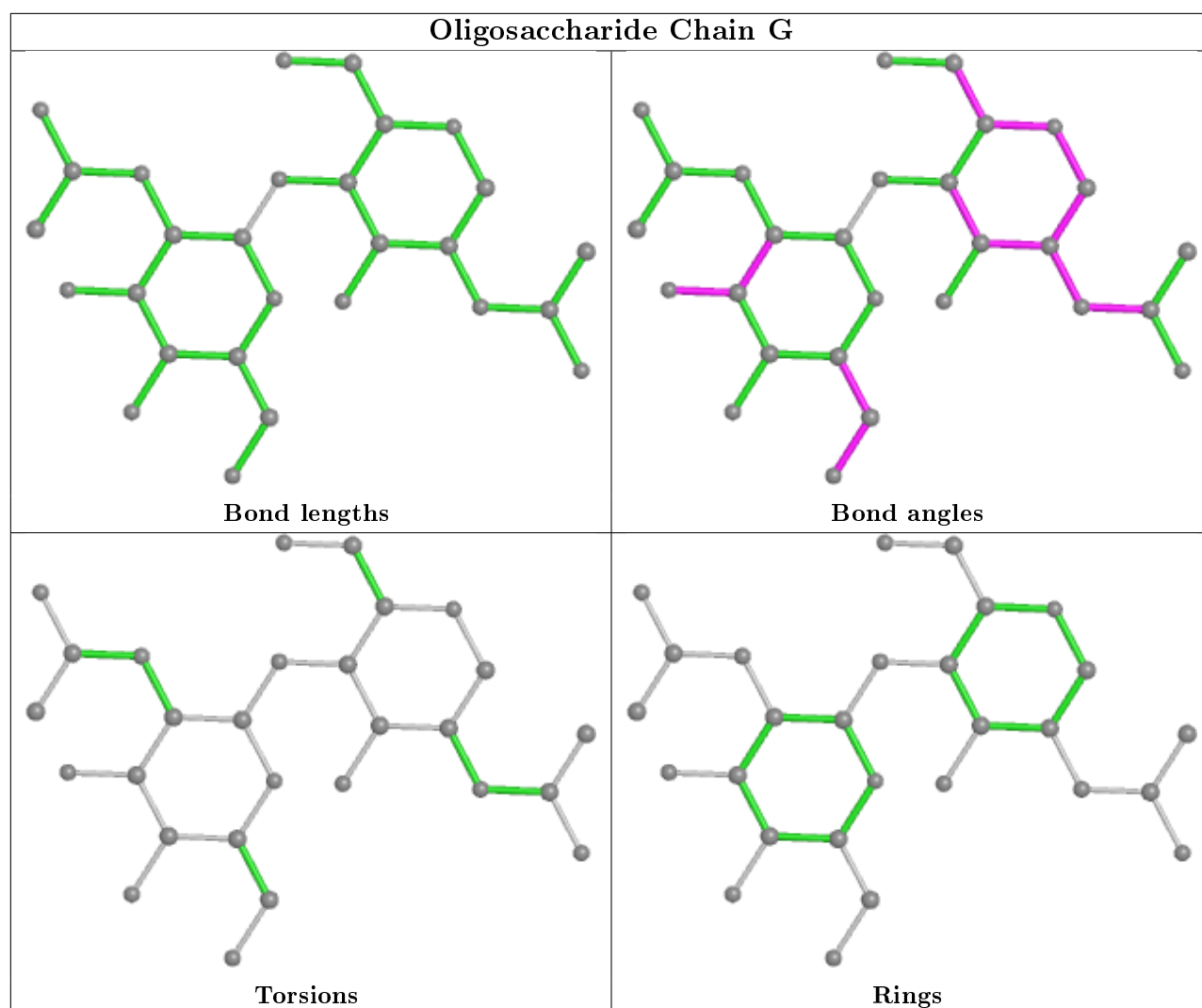
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











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	175/256 (68%)	-0.39	3 (1%) 70 67	44, 70, 130, 153	0
1	B	183/256 (71%)	-0.51	1 (0%) 91 90	42, 66, 125, 155	0
All	All	358/512 (69%)	-0.45	4 (1%) 80 80	42, 68, 129, 155	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	200	CYS	4.2
1	B	200	CYS	3.3
1	A	231	PRO	3.2
1	A	216	ALA	3.0

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.

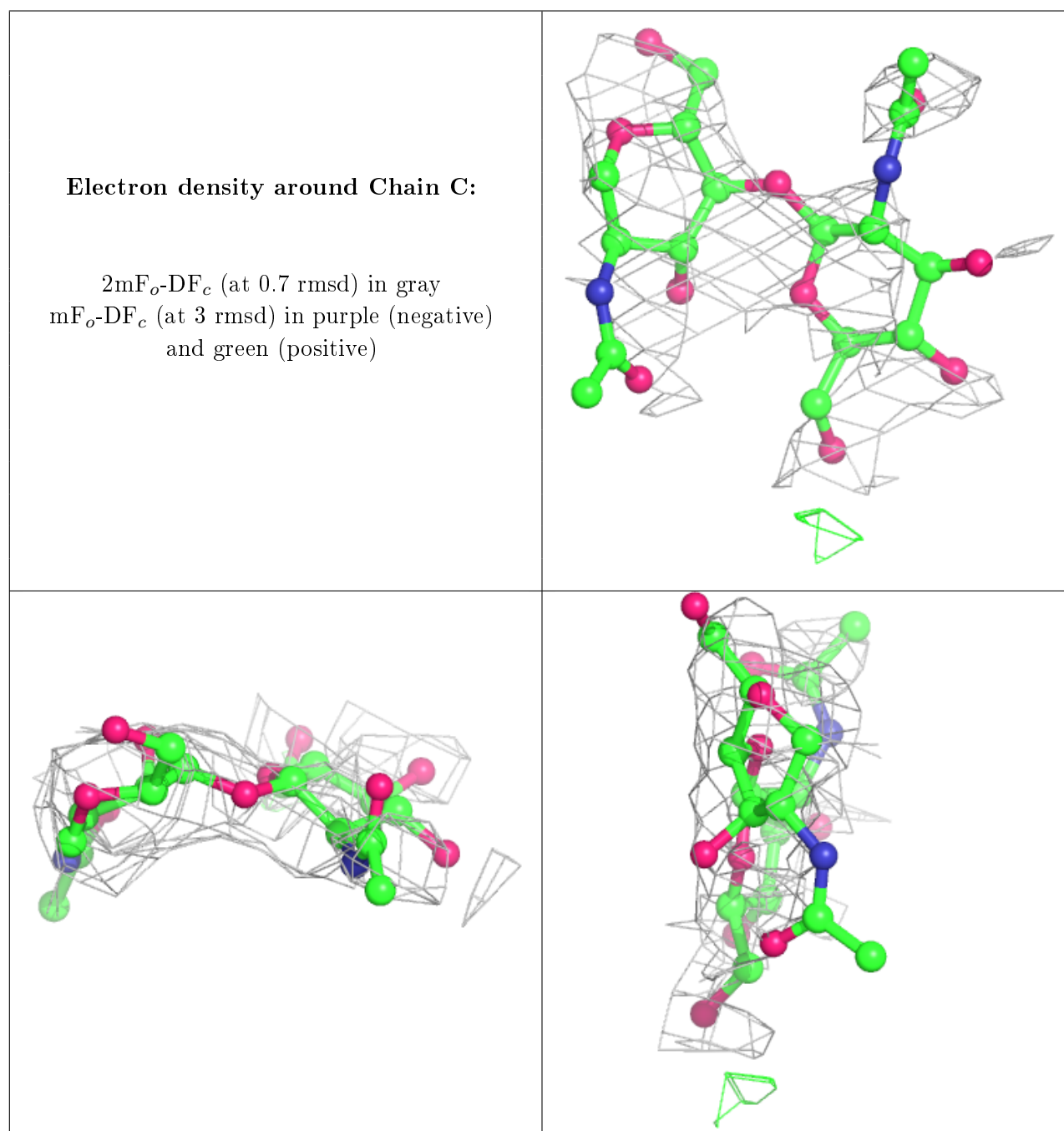
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	C	2	14/15	0.49	0.40	111,179,192,192	0
2	NAG	F	2	14/15	0.61	0.57	109,128,140,149	0
2	NAG	D	2	14/15	0.66	0.56	109,128,140,149	0
2	NAG	F	1	14/15	0.74	0.34	81,102,112,113	0
2	NAG	D	1	14/15	0.74	0.36	81,102,112,113	0

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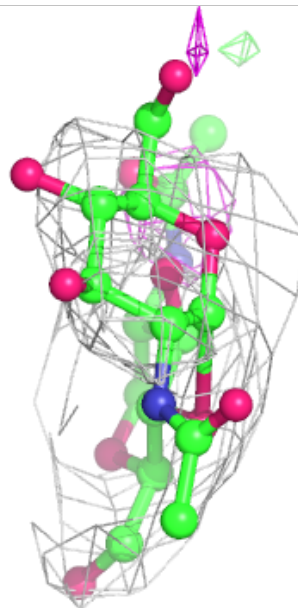
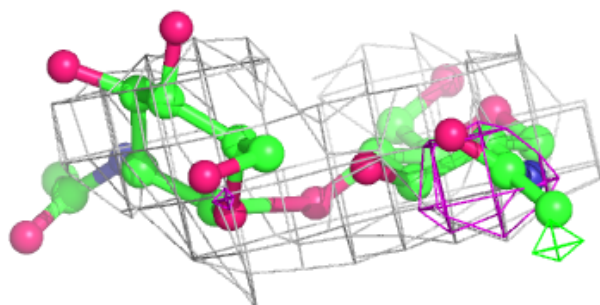
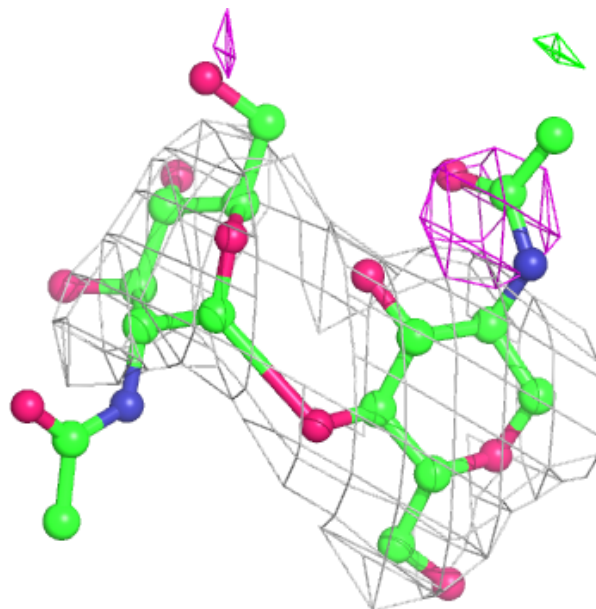
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	E	2	14/15	0.77	0.36	109,128,140,149	0
2	NAG	C	1	14/15	0.81	0.39	103,125,133,163	0
2	NAG	E	1	14/15	0.83	0.29	81,102,112,113	0
2	NAG	G	2	14/15	0.90	0.26	76,83,103,110	0
2	NAG	G	1	14/15	0.94	0.18	62,75,91,111	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



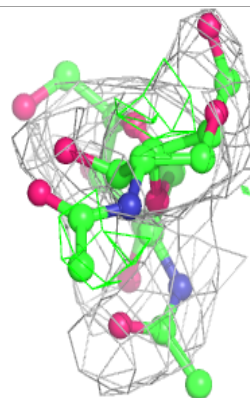
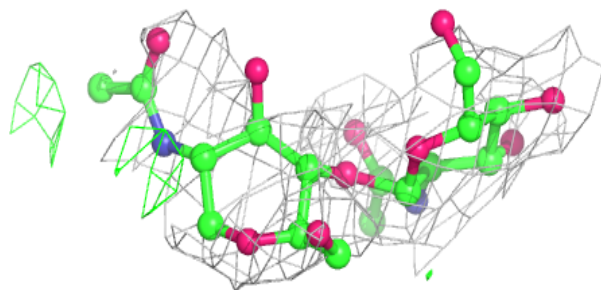
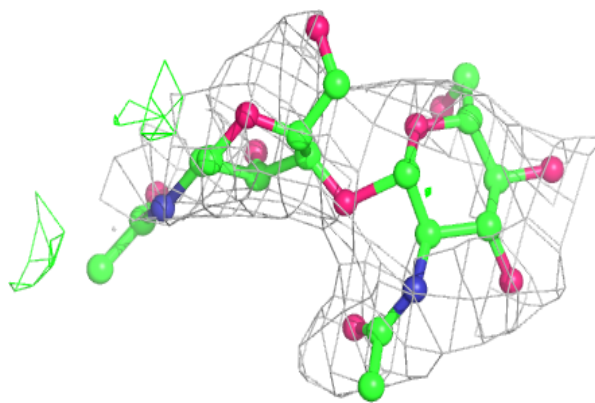
Electron density around Chain D:

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

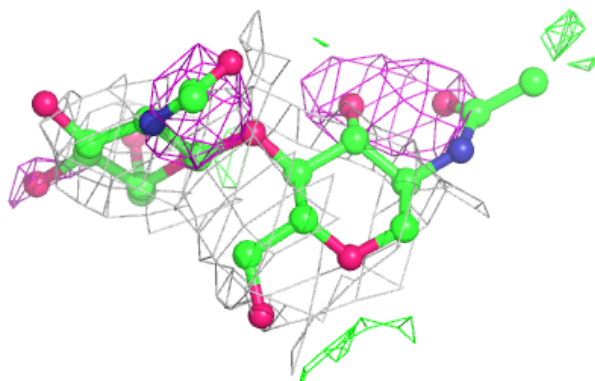
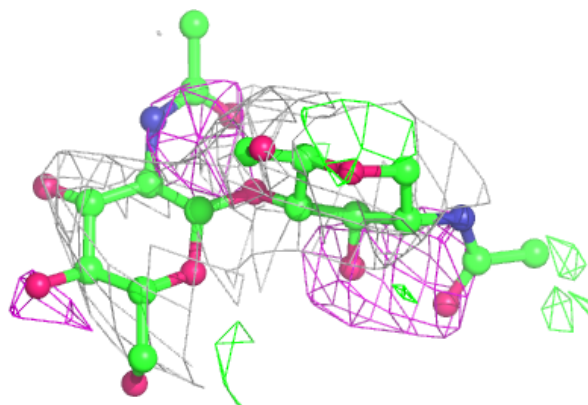


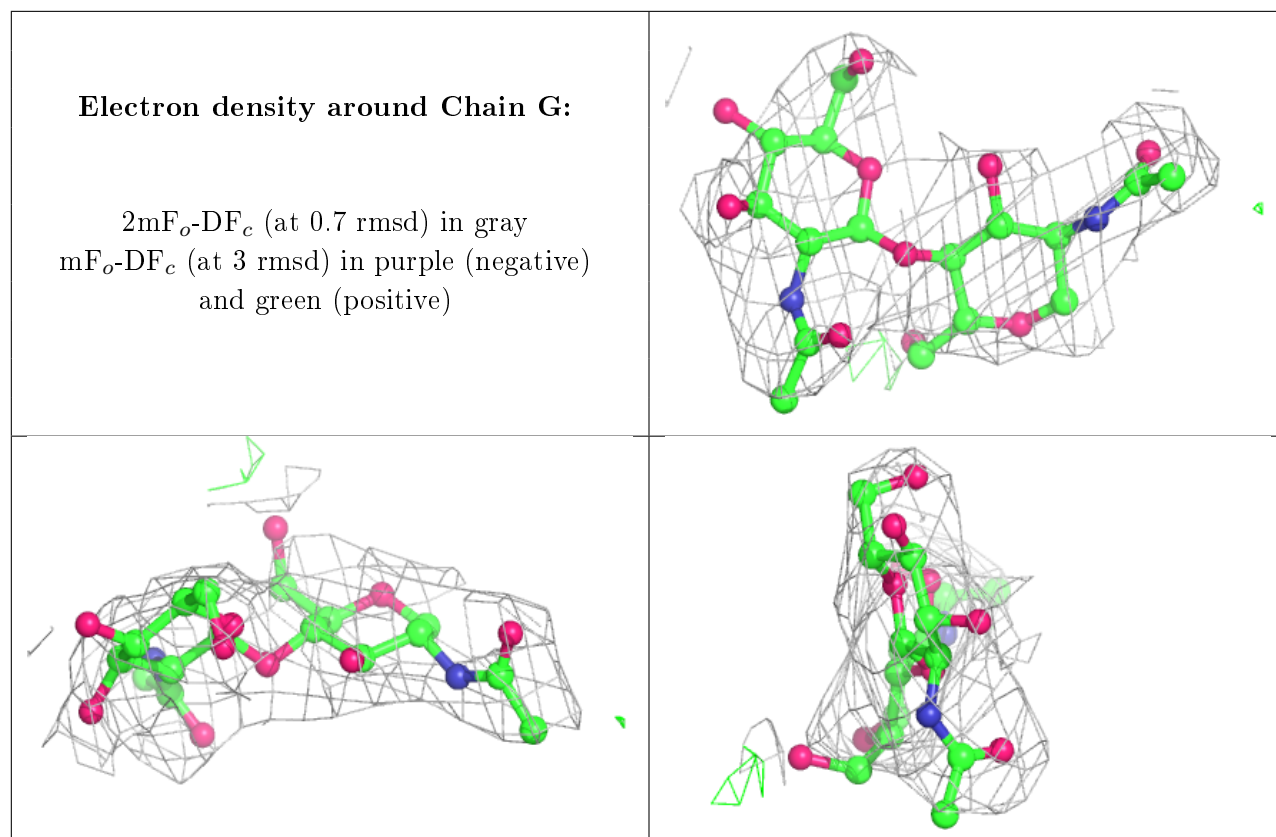
Electron density around Chain E:

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

**Electron density around Chain F:**

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.