



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 28, 2025 – 03:17 pm GMT

PDB ID : 9H7Z / pdb_00009h7z
Title : Aspergillus niger Glucose Oxidase bound to Ba²⁺ ions
Authors : Bauer, J.A.; Baueroova, V.
Deposited on : 2024-10-28
Resolution : 1.71 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

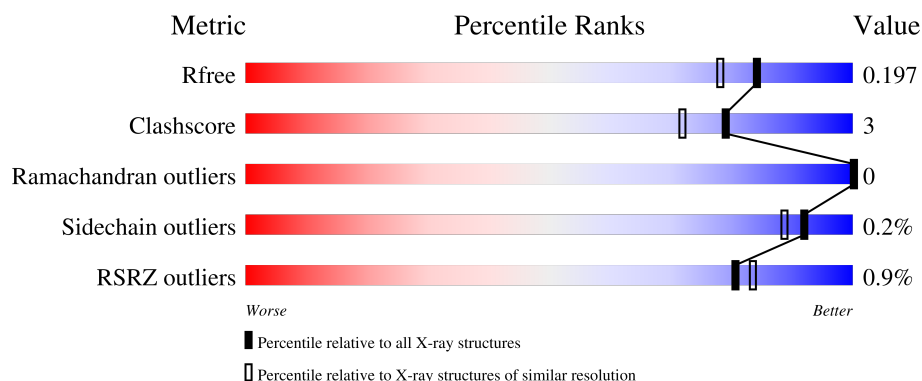
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.71 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.



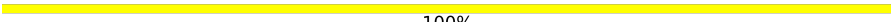
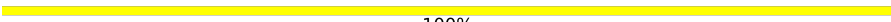


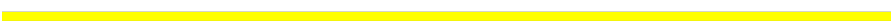
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	7106 (1.74-1.70)
Clashscore	180529	7746 (1.74-1.70)
Ramachandran outliers	177936	7654 (1.74-1.70)
Sidechain outliers	177891	7654 (1.74-1.70)
RSRZ outliers	164620	7104 (1.74-1.70)

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	605	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % 5% . </div> </div>
1	M	605	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % . . </div> </div>
2	B	6	<div style="display: flex; justify-content: space-between; align-items: center;"> 17% </div>
3	C	2	<div style="display: flex; justify-content: space-between; align-items: center;"> </div>
3	D	2	<div style="display: flex; justify-content: space-between; align-items: center;"> </div>

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Mol	Chain	Length	Quality of chain
3	E	2	 100%
3	I	2	 100%
3	U	2	 50%  50%
4	F	8	 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
5	EDO	A	602	-	-	X	-

2 Entry composition [i](#)

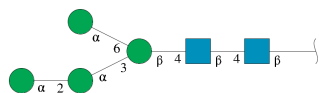
There are 13 unique types of molecules in this entry. The entry contains 19052 atoms, of which 8908 are hydrogens and 0 are deuteriums.

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 Glucose oxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	581	Total	C	H	N	O	S	0	5	0
			8748	2819	4270	767	877	15			
1	M	582	Total	C	H	N	O	S	0	4	0
			8757	2818	4276	771	878	14			

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	6	Total	C	H	N	O	0	0	0
			114	40	42	2	30			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



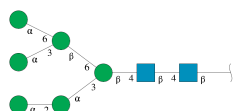
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			
3	D	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			
3	E	2	Total	C	N	O		0	0	0
			28	16	2	10				

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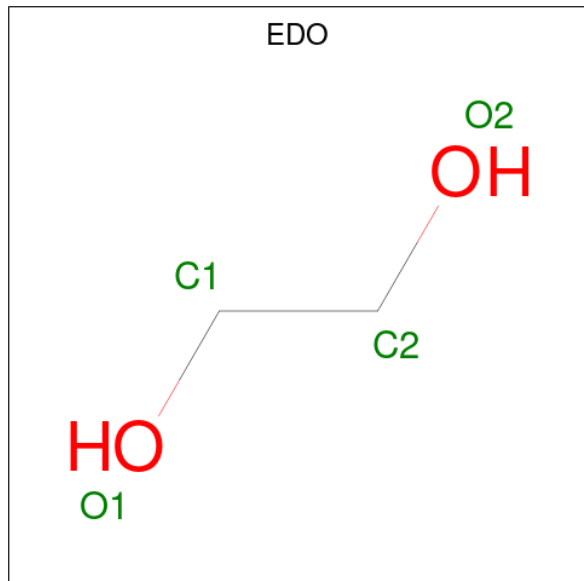
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			
3	U	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	8	Total	C	H	N	O	0	0	0
			165	52	71	2	40			

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



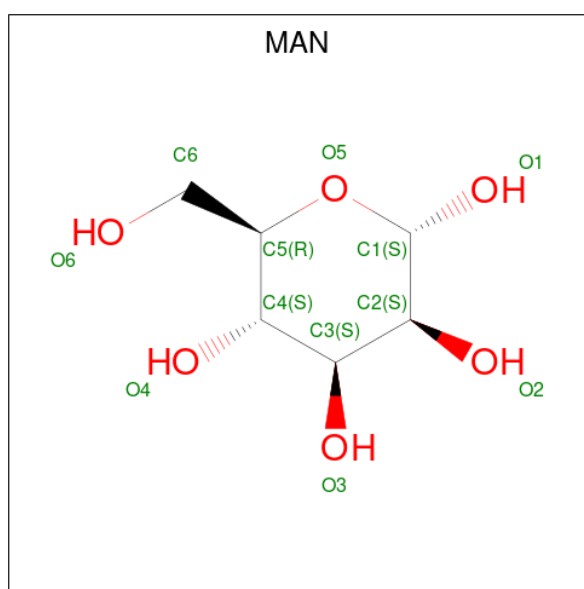
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	M	1	Total	C	H	O	0	0
			10	2	6	2		
5	M	1	Total	C	H	O	0	0
			10	2	6	2		
5	M	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 6 is alpha-D-mannopyranose (CCD ID: MAN) (formula: $C_6H_{12}O_6$).



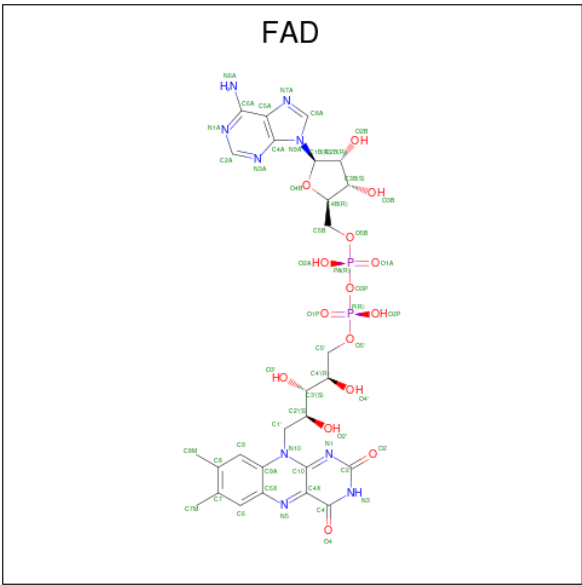
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			24	6	12	6		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
7	M	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
7	M	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 8 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	P	0	0
			84	27	31	9	15	2		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	M	1	Total	C	H	N	O	P	0	0
			84	27	31	9	15	2		

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	7	Total	Cl	0	0
			7	7		
9	M	3	Total	Cl	0	0
			3	3		

- Molecule 10 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	4	Total	Na	0	0
			4	4		
10	M	2	Total	Na	0	0
			2	2		

- Molecule 11 is BARIUM ION (CCD ID: BA) (formula: Ba).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	6	Total	Ba	0	0
			6	6		
11	M	6	Total	Ba	0	0
			6	6		

- Molecule 12 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	2	Total	Br	0	0
			2	2		
12	M	1	Total	Br	0	0
			1	1		

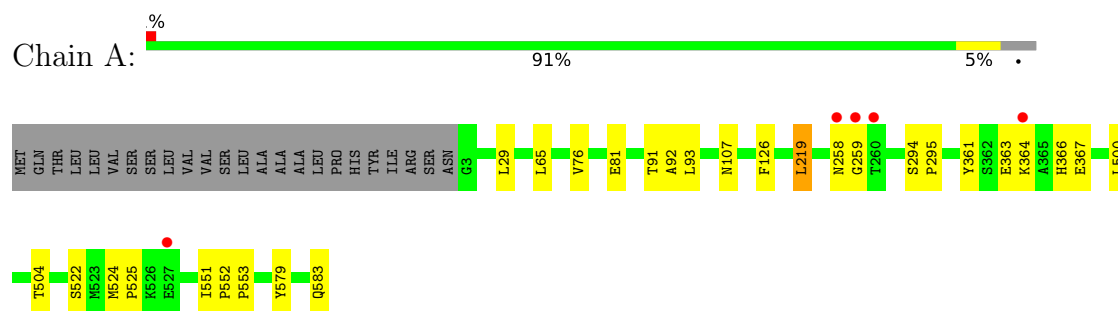
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	334	Total	O	0	0
			334	334		
13	M	330	Total	O	0	0
			330	330		

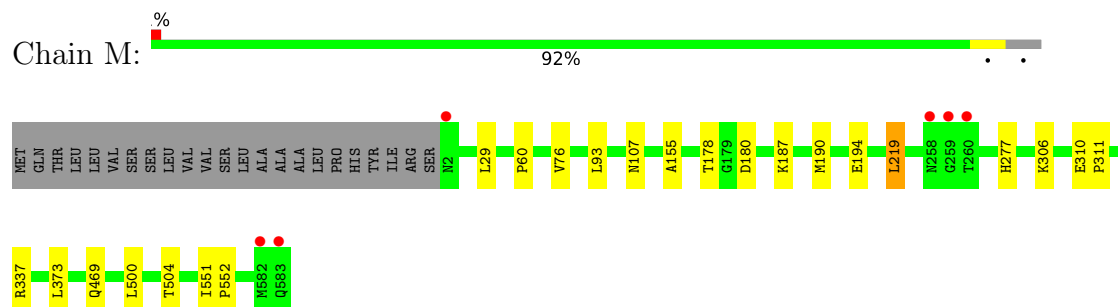
3 Residue-property plots

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.

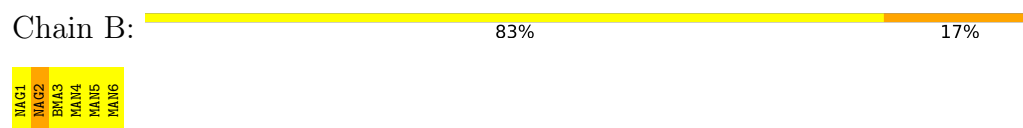
- Molecule 1: Glucose oxidase



- Molecule 1: Glucose oxidase



- Molecule 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  50% 50%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:  50% 50%

MAG1
MAG2

- Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  100%

MAG1
MAG2
BMA3
MAN4
MAN5
BMA6
MAN7
MAN8

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.22Å 82.25Å 103.30Å 90.00° 106.27° 90.00°	Depositor
Resolution (Å)	37.95 – 1.71 37.95 – 1.71	Depositor EDS
% Data completeness (in resolution range)	99.0 (37.95-1.71) 99.0 (37.95-1.71)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 1.71Å)	Xtriage
Refinement program	PHENIX 1.21rc1_5127	Depositor
R, R_{free}	0.177 , 0.199 0.175 , 0.197	Depositor DCC
R_{free} test set	7398 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	19052	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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, FAD, BA, MAN, BMA, CL, EDO, NA, BR

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.33	0/4602	0.47	0/6276
1	M	0.34	0/4601	0.46	0/6274
All	All	0.33	0/9203	0.46	0/12550

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	M	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	337[A]	ARG	Sidechain
1	M	337[B]	ARG	Sidechain

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	4478	4270	4271	27	0
1	M	4481	4276	4275	18	0
2	B	72	42	61	1	0
3	C	28	25	25	0	0
3	D	28	25	25	0	0
3	E	28	0	25	0	0
3	I	28	25	25	0	0
3	U	28	25	25	0	0
4	F	94	71	79	0	0
5	A	12	18	18	5	0
5	M	12	18	18	3	0
6	A	12	12	12	0	0
7	A	14	13	13	0	0
7	M	28	26	26	1	0
8	A	53	31	31	2	0
8	M	53	31	31	2	0
9	A	7	0	0	0	0
9	M	3	0	0	1	0
10	A	4	0	0	0	0
10	M	2	0	0	0	0
11	A	6	0	0	0	0
11	M	6	0	0	0	0
12	A	2	0	0	0	0
12	M	1	0	0	0	0
13	A	334	0	0	1	0
13	M	330	0	0	5	0
All	All	10144	8908	8960	48	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 3.

The worst 5 of 48 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:M:277:HIS:ND1	13:M:703:HOH:O	2.15	0.80
1:M:373:LEU:HB2	5:M:601:EDO:H21	1.67	0.75
1:M:469:GLN:OE1	13:M:701:HOH:O	2.10	0.70
1:A:107:ASN:HB2	8:A:606:FAD:C5X	2.24	0.68
1:M:107:ASN:HB2	8:M:606:FAD:C5X	2.24	0.67

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	584/605 (96%)	567 (97%)	17 (3%)	0	100	100
1	M	584/605 (96%)	566 (97%)	18 (3%)	0	100	100
All	All	1168/1210 (96%)	1133 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	471/487 (97%)	470 (100%)	1 (0%)	92	89
1	M	471/487 (97%)	470 (100%)	1 (0%)	92	89
All	All	942/974 (97%)	940 (100%)	2 (0%)	92	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	219	LEU
1	M	219	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	375	GLN

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Mol	Chain	Res	Type
1	M	398	ASN
1	M	493	ASN
1	M	469	GLN
1	M	236	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

24 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	B	1	1,2	14,14,15	0.69	0	17,19,21	0.96	1 (5%)
2	NAG	B	2	2	14,14,15	0.94	2 (14%)	17,19,21	1.19	2 (11%)
2	BMA	B	3	2	11,11,12	0.76	0	15,15,17	1.99	3 (20%)
2	MAN	B	4	2	11,11,12	0.95	0	15,15,17	1.78	4 (26%)
2	MAN	B	5	2	11,11,12	0.89	1 (9%)	15,15,17	3.17	5 (33%)
2	MAN	B	6	2	11,11,12	0.84	1 (9%)	15,15,17	1.13	1 (6%)
3	NAG	C	1	1,3	14,14,15	0.81	1 (7%)	17,19,21	1.02	0
3	NAG	C	2	3	14,14,15	0.65	0	17,19,21	1.14	1 (5%)
3	NAG	D	1	1,3	14,14,15	0.75	0	17,19,21	1.22	2 (11%)
3	NAG	D	2	3	14,14,15	0.69	0	17,19,21	1.18	0
3	NAG	E	1	1,3	14,14,15	0.58	0	17,19,21	1.06	3 (17%)
3	NAG	E	2	3	14,14,15	0.69	0	17,19,21	1.28	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	F	1	1,4	14,14,15	0.62	0	17,19,21	0.92	1 (5%)
4	NAG	F	2	4	14,14,15	0.98	1 (7%)	17,19,21	1.33	3 (17%)
4	BMA	F	3	4	11,11,12	0.97	1 (9%)	15,15,17	1.15	1 (6%)
4	MAN	F	4	4	11,11,12	0.90	1 (9%)	15,15,17	0.91	1 (6%)
4	MAN	F	5	4	11,11,12	0.89	1 (9%)	15,15,17	0.80	0
4	BMA	F	6	4	11,11,12	0.83	0	15,15,17	2.73	6 (40%)
4	MAN	F	7	4	11,11,12	0.55	0	15,15,17	1.82	3 (20%)
4	MAN	F	8	4	11,11,12	0.81	0	15,15,17	1.09	1 (6%)
3	NAG	I	1	1,3	14,14,15	1.02	1 (7%)	17,19,21	1.52	3 (17%)
3	NAG	I	2	3	14,14,15	0.85	0	17,19,21	1.43	2 (11%)
3	NAG	U	1	1,3	14,14,15	0.62	0	17,19,21	1.42	2 (11%)
3	NAG	U	2	3	14,14,15	0.68	0	17,19,21	0.96	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
2	MAN	B	4	2	-	0/2/19/22	0/1/1/1
2	MAN	B	5	2	-	2/2/19/22	0/1/1/1
2	MAN	B	6	2	-	0/2/19/22	0/1/1/1
3	NAG	C	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	NAG	E	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1
4	MAN	F	5	4	-	2/2/19/22	0/1/1/1
4	BMA	F	6	4	-	0/2/19/22	0/1/1/1
4	MAN	F	7	4	-	2/2/19/22	0/1/1/1
4	MAN	F	8	4	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	I	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	NAG	U	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	U	2	3	-	0/6/23/26	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	1	NAG	C2-N2	-2.44	1.42	1.46
4	F	5	MAN	O5-C1	-2.41	1.39	1.43
2	B	5	MAN	O5-C1	-2.29	1.40	1.43
4	F	3	BMA	C2-C3	2.28	1.55	1.52
3	C	1	NAG	O5-C1	-2.23	1.40	1.43

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	5	MAN	C1-C2-C3	-8.42	99.32	109.67
4	F	6	BMA	C1-C2-C3	-8.08	99.73	109.67
2	B	3	BMA	C1-O5-C5	5.87	120.15	112.19
2	B	5	MAN	O5-C1-C2	-5.45	102.36	110.77
2	B	5	MAN	C1-O5-C5	-5.29	105.03	112.19

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

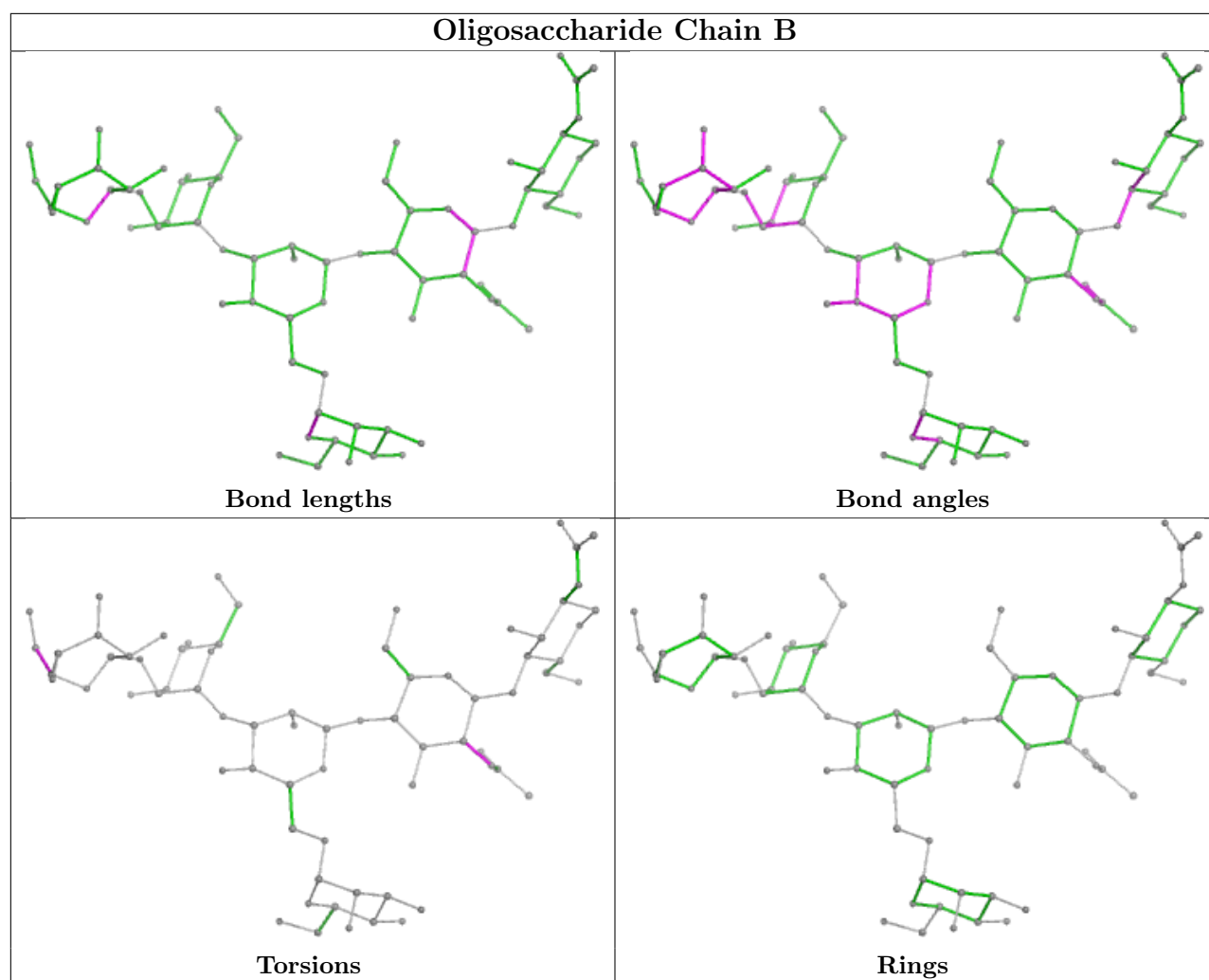
Mol	Chain	Res	Type	Atoms
2	B	5	MAN	C4-C5-C6-O6
2	B	5	MAN	O5-C5-C6-O6
4	F	7	MAN	O5-C5-C6-O6
4	F	7	MAN	C4-C5-C6-O6
4	F	3	BMA	C4-C5-C6-O6

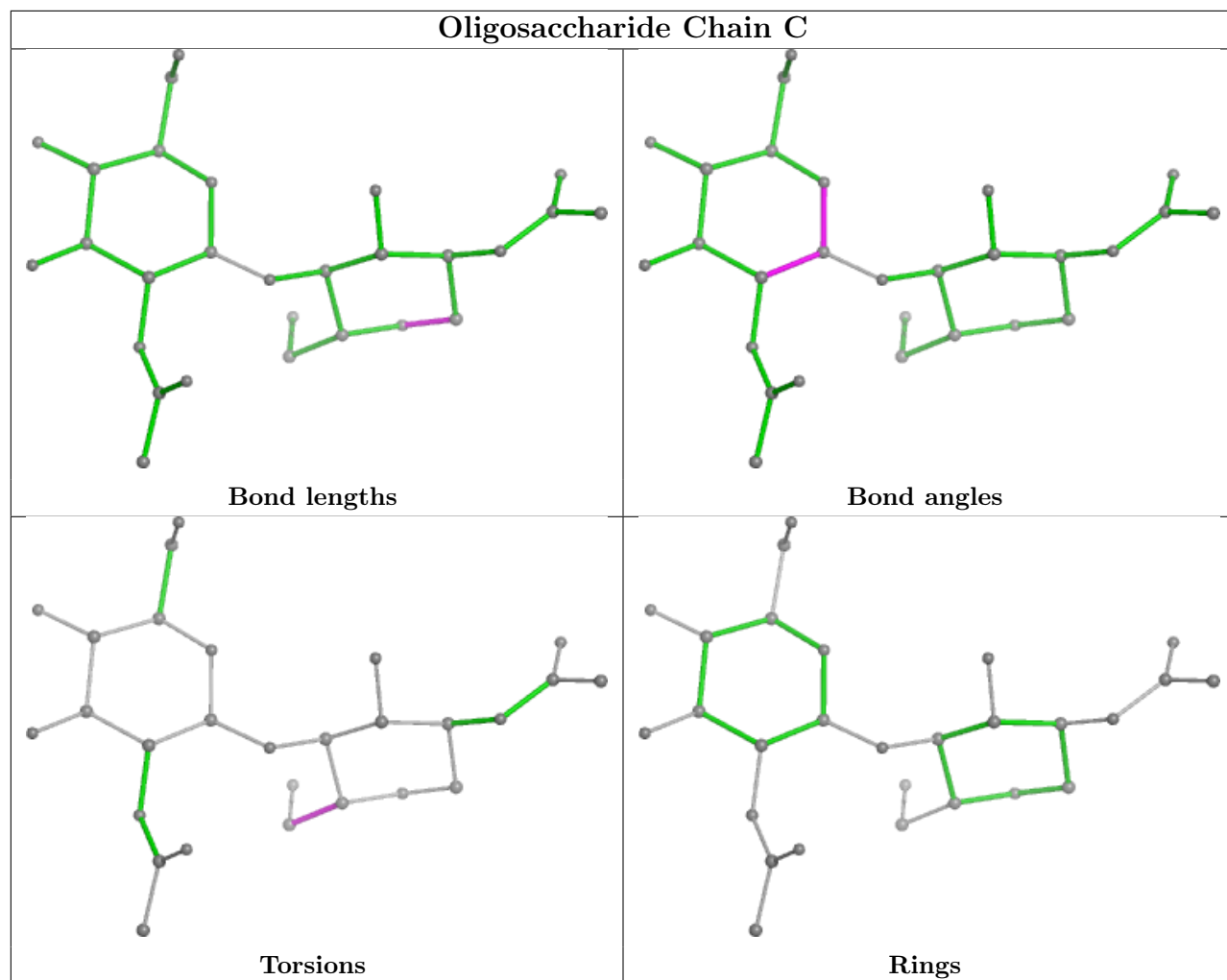
There are no ring outliers.

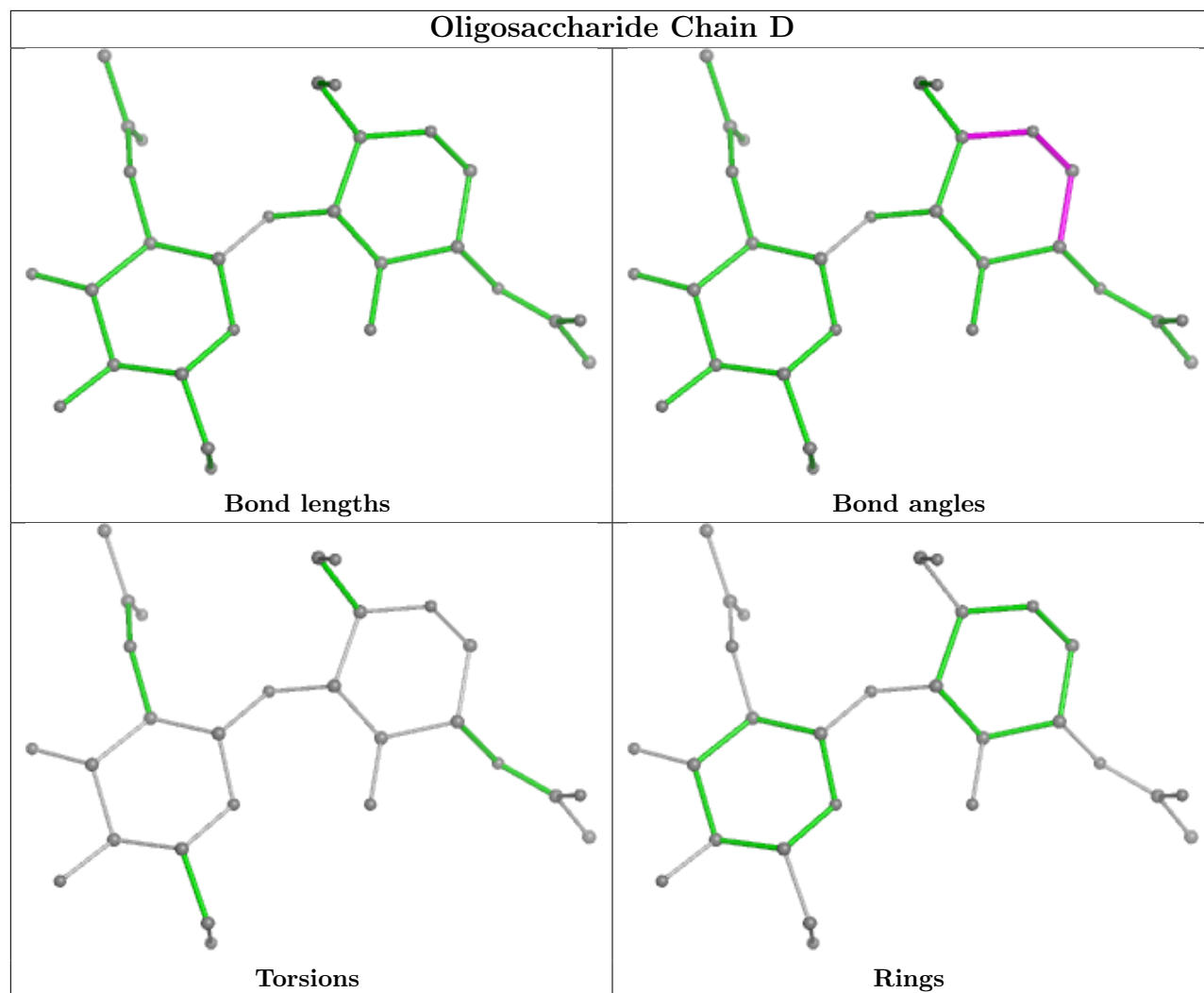
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	NAG	1	0

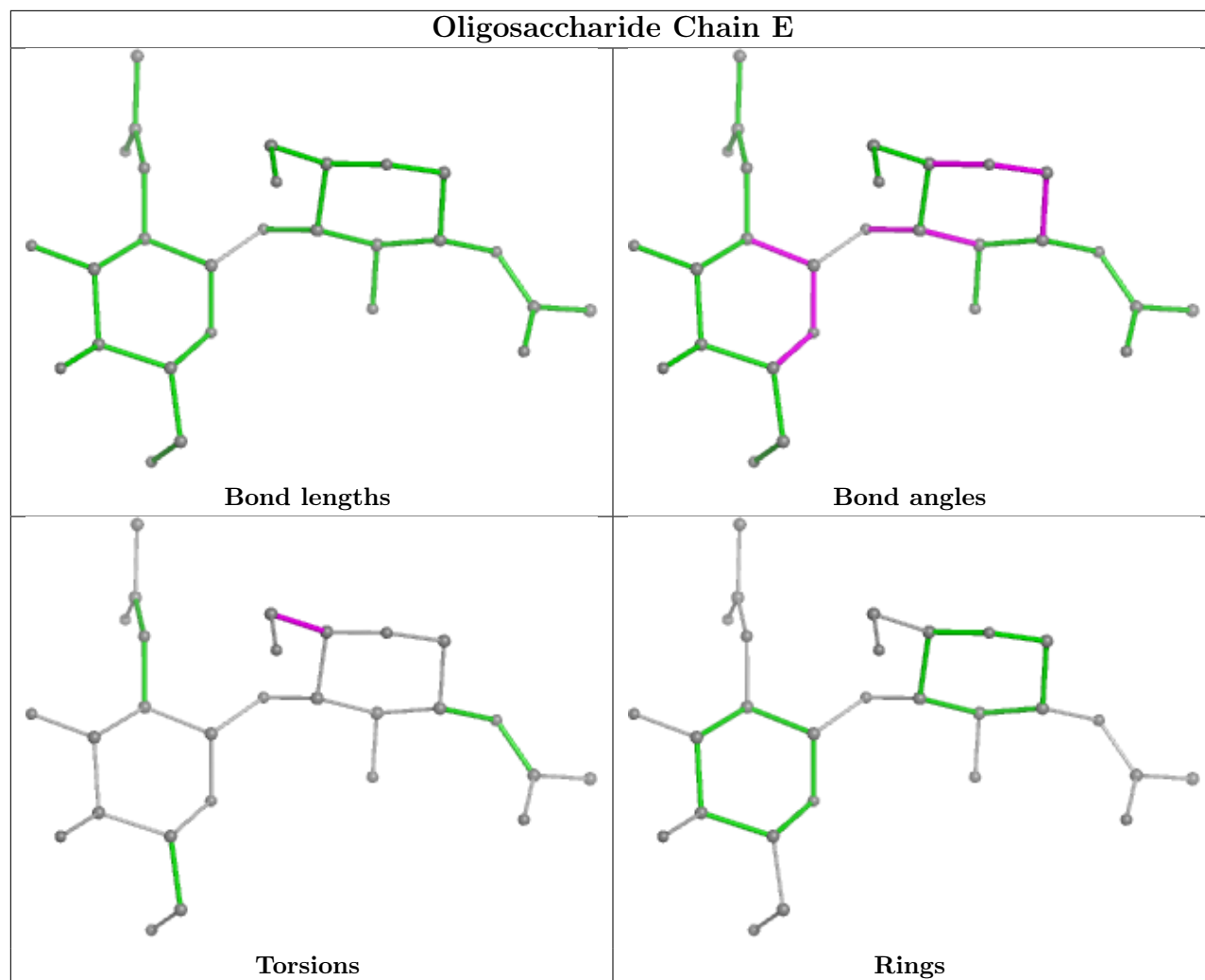
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

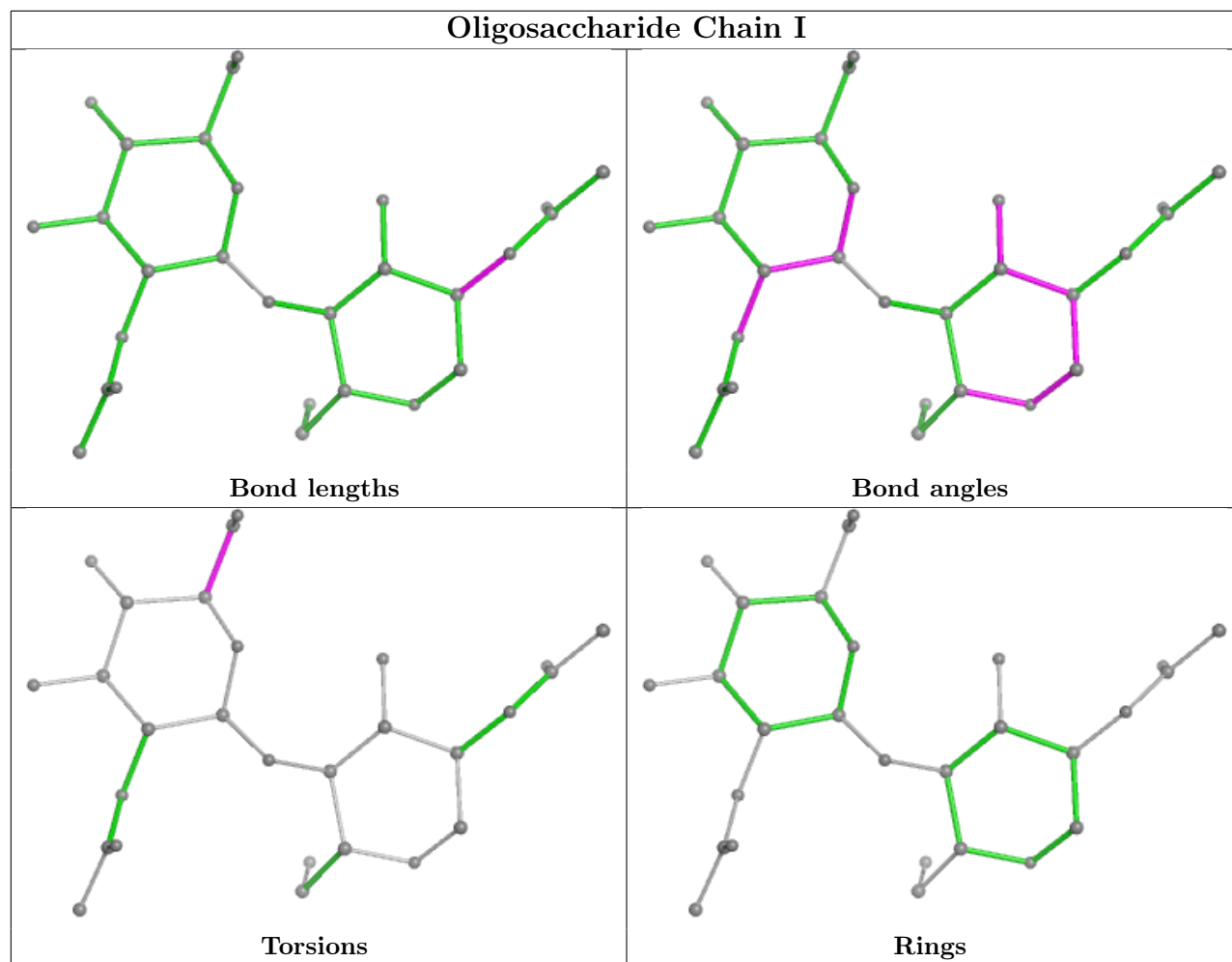


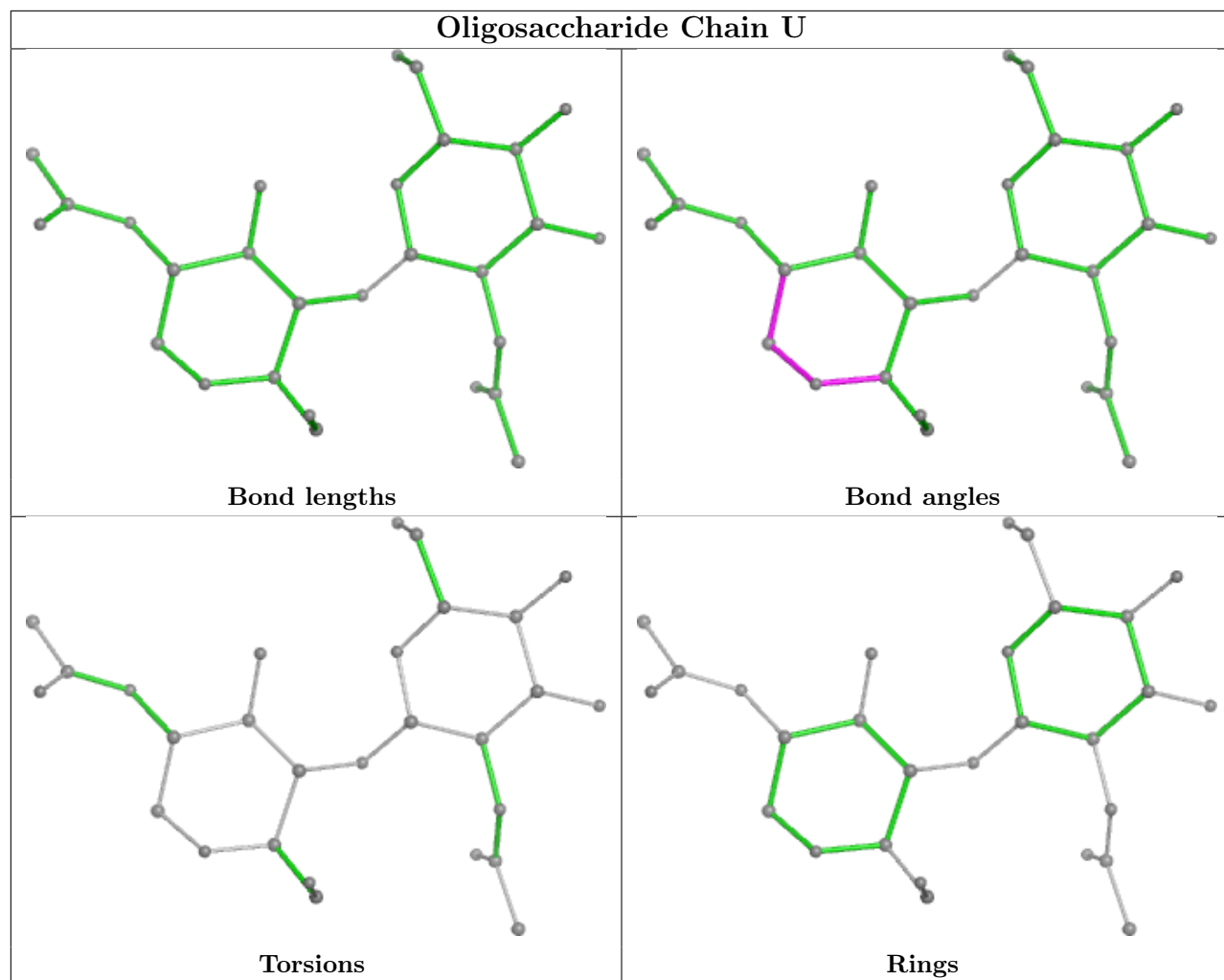


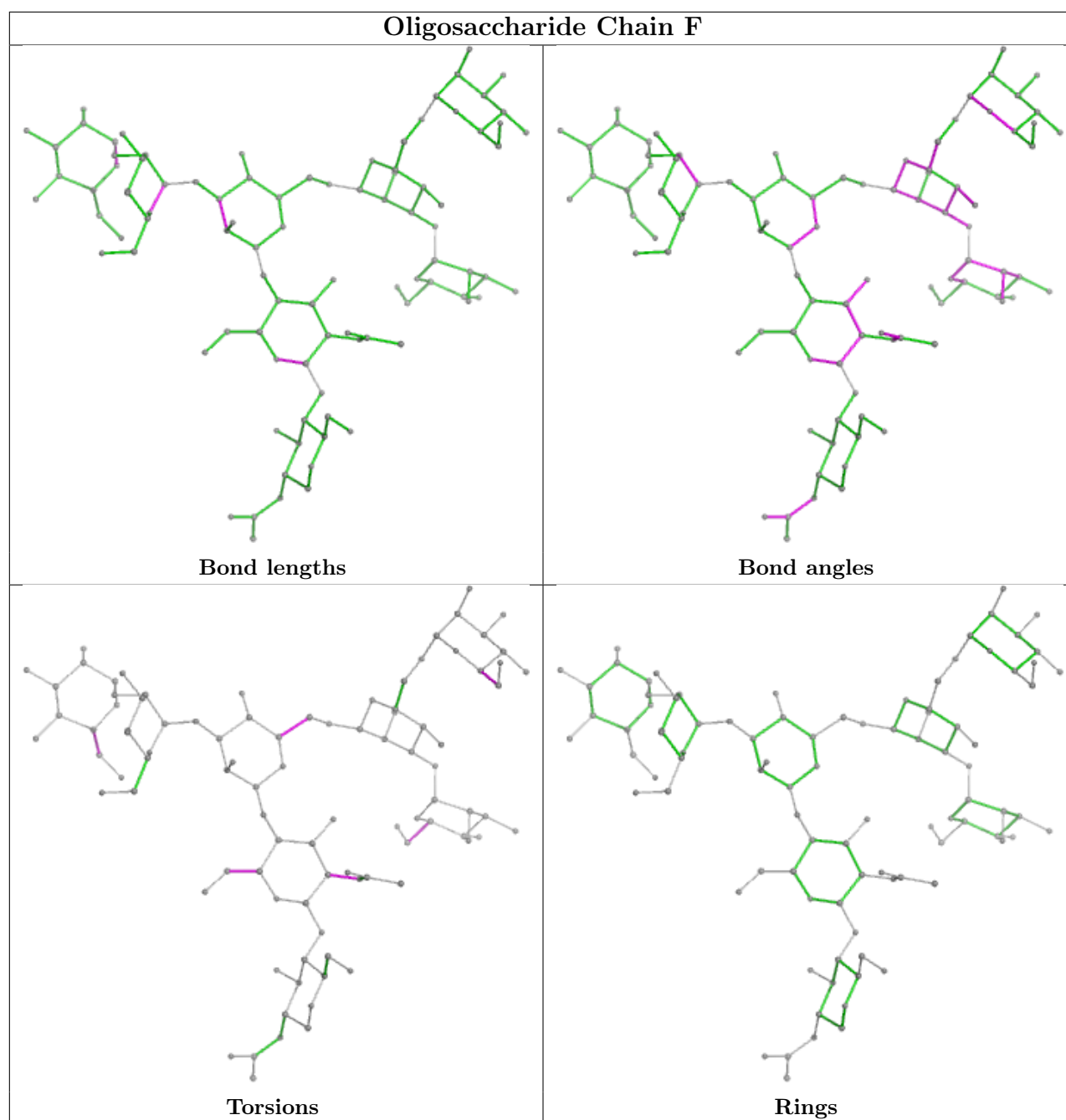


Oligosaccharide Chain E









5.6 Ligand geometry [i](#)

Of 43 ligands modelled in this entry, 31 are monoatomic - leaving 12 for Mogul analysis.

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
5	EDO	M	602	-	3,3,3	0.29	0	2,2,2	0.13	0
7	NAG	A	605	1	14,14,15	0.55	0	17,19,21	0.97	0
5	EDO	A	601	-	3,3,3	0.33	0	2,2,2	0.12	0
7	NAG	M	605	1	14,14,15	0.77	0	17,19,21	1.27	1 (5%)
6	MAN	A	604	-	12,12,12	0.60	0	17,17,17	1.00	1 (5%)
7	NAG	M	603	1,10	14,14,15	0.58	0	17,19,21	1.31	1 (5%)
5	EDO	M	601	-	3,3,3	0.31	0	2,2,2	0.22	0
5	EDO	A	603	-	3,3,3	0.29	0	2,2,2	0.26	0
8	FAD	A	606	-	53,58,58	1.04	3 (5%)	68,89,89	1.17	6 (8%)
5	EDO	A	602	-	3,3,3	0.41	0	2,2,2	0.34	0
8	FAD	M	606	-	53,58,58	1.05	4 (7%)	68,89,89	1.03	4 (5%)
5	EDO	M	604	-	3,3,3	0.30	0	2,2,2	0.15	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
5	EDO	M	602	-	-	1/1/1/1	-
7	NAG	A	605	1	-	0/6/23/26	0/1/1/1
5	EDO	A	601	-	-	1/1/1/1	-
7	NAG	M	605	1	-	0/6/23/26	0/1/1/1
6	MAN	A	604	-	-	1/2/22/22	0/1/1/1
7	NAG	M	603	1,10	-	0/6/23/26	0/1/1/1
5	EDO	M	601	-	-	1/1/1/1	-
5	EDO	A	603	-	-	0/1/1/1	-
8	FAD	A	606	-	-	3/30/50/50	0/6/6/6
5	EDO	A	602	-	-	0/1/1/1	-
8	FAD	M	606	-	-	4/30/50/50	0/6/6/6
5	EDO	M	604	-	-	0/1/1/1	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	606	FAD	C8A-N7A	-2.87	1.29	1.34
8	M	606	FAD	O2'-C2'	-2.58	1.37	1.43
8	A	606	FAD	C4'-C3'	2.56	1.58	1.53
8	A	606	FAD	O2'-C2'	-2.52	1.38	1.43
8	M	606	FAD	O4B-C1B	2.35	1.44	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	606	FAD	O4'-C4'-C5'	3.90	118.67	109.92
7	M	605	NAG	C1-O5-C5	3.63	117.11	112.19
8	A	606	FAD	O4B-C1B-C2B	-2.99	102.56	106.93
7	M	603	NAG	C1-O5-C5	2.82	116.01	112.19
8	A	606	FAD	O4'-C4'-C3'	-2.46	103.11	109.10

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

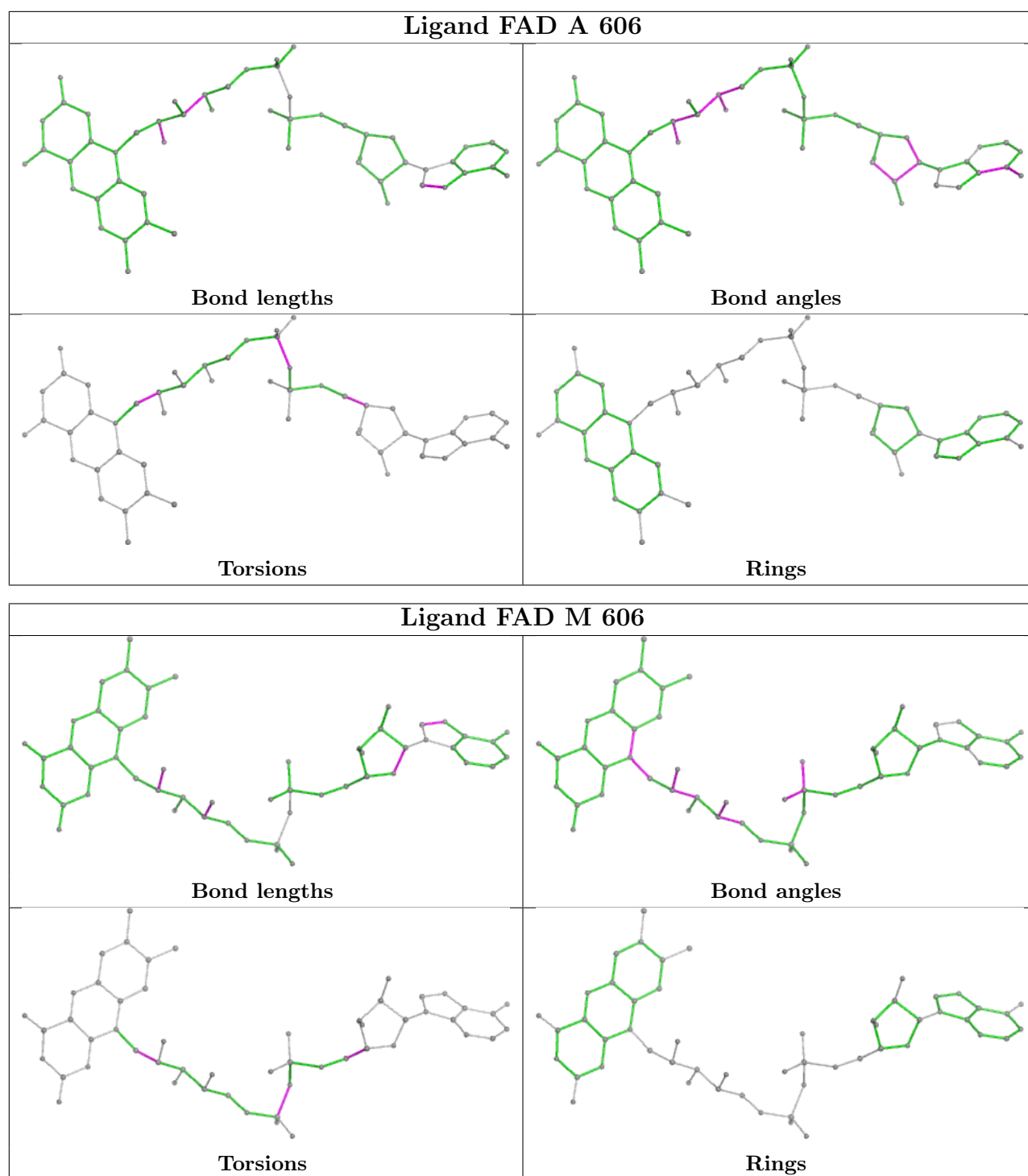
Mol	Chain	Res	Type	Atoms
8	A	606	FAD	N10-C1'-C2'-O2'
8	A	606	FAD	PA-O3P-P-O5'
8	M	606	FAD	N10-C1'-C2'-O2'
8	M	606	FAD	PA-O3P-P-O5'
5	A	601	EDO	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	602	EDO	2	0
5	A	601	EDO	1	0
7	M	603	NAG	1	0
5	M	601	EDO	1	0
8	A	606	FAD	2	0
5	A	602	EDO	4	0
8	M	606	FAD	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

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	581/605 (96%)	-0.19	5 (0%) 81 83	16, 36, 53, 127	5 (0%)
1	M	582/605 (96%)	-0.14	6 (1%) 79 82	18, 37, 56, 127	4 (0%)
All	All	1163/1210 (96%)	-0.16	11 (0%) 81 83	16, 36, 54, 127	9 (0%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	582	MET	3.6
1	A	259	GLY	3.0
1	M	260	THR	2.9
1	M	259	GLY	2.8
1	A	258	ASN	2.6

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	B	1	14/15	-	-	30,33,40,44	0
2	NAG	B	2	14/15	-	-	32,38,47,47	0
2	BMA	B	3	11/12	-	-	33,44,53,53	0
2	MAN	B	4	11/12	-	-	40,43,47,52	0
2	MAN	B	5	11/12	-	-	56,59,63,70	0

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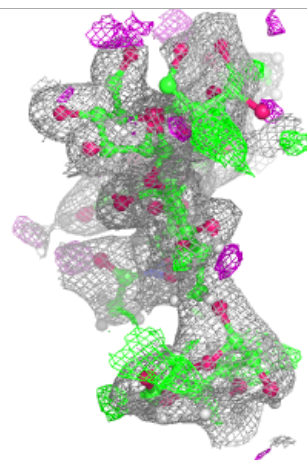
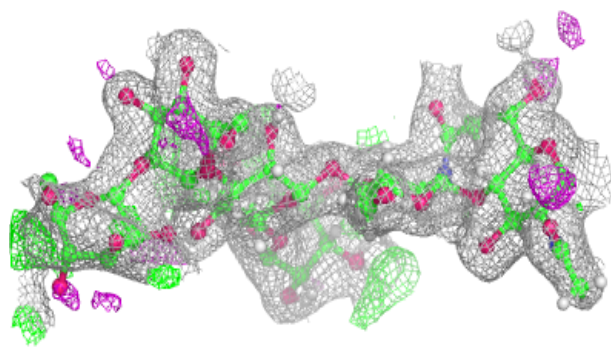
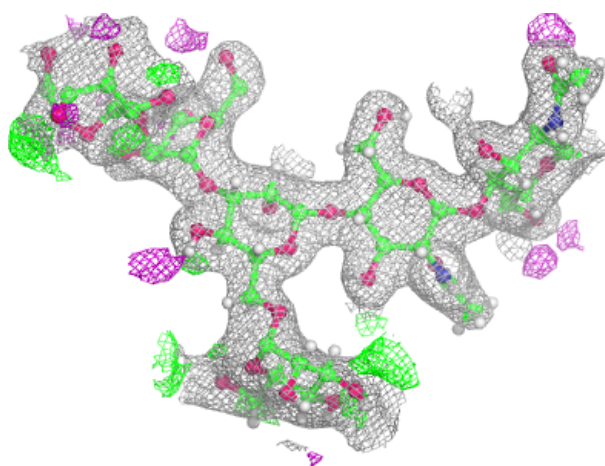
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MAN	B	6	11/12	-	-	49,54,64,67	0
4	NAG	F	2	14/15	0.53	0.18	31,35,43,43	0
3	NAG	E	2	14/15	0.64	0.14	56,65,68,73	0
3	NAG	D	2	14/15	0.70	0.14	57,69,85,86	0
4	NAG	F	1	14/15	0.83	0.13	29,31,36,41	0
3	NAG	I	2	14/15	0.83	0.11	53,63,76,81	0
3	NAG	D	1	14/15	0.84	0.11	41,52,62,64	0
3	NAG	E	1	14/15	0.87	0.10	50,54,58,61	0
3	NAG	I	1	14/15	0.93	0.08	49,58,65,71	0
3	NAG	U	1	14/15	-	-	36,44,51,53	0
3	NAG	U	2	14/15	-	-	50,63,75,82	0
3	NAG	C	1	14/15	0.94	0.07	44,54,65,68	0
3	NAG	C	2	14/15	0.95	0.06	62,72,83,90	0
4	BMA	F	3	11/12	-	-	36,41,49,52	0
4	MAN	F	4	11/12	-	-	40,46,55,55	0
4	MAN	F	5	11/12	-	-	49,57,66,72	0
4	BMA	F	6	11/12	-	-	43,45,51,51	0
4	MAN	F	7	11/12	-	-	56,69,78,85	0
4	MAN	F	8	11/12	-	-	44,55,64,73	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.

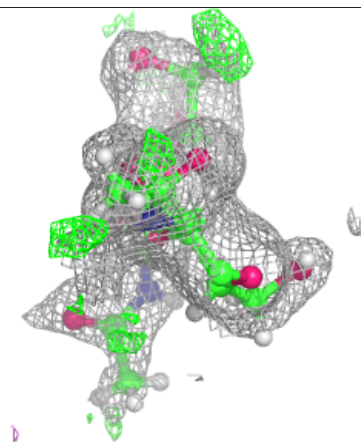
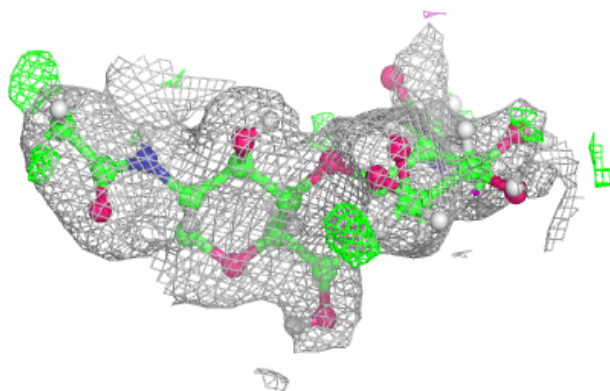
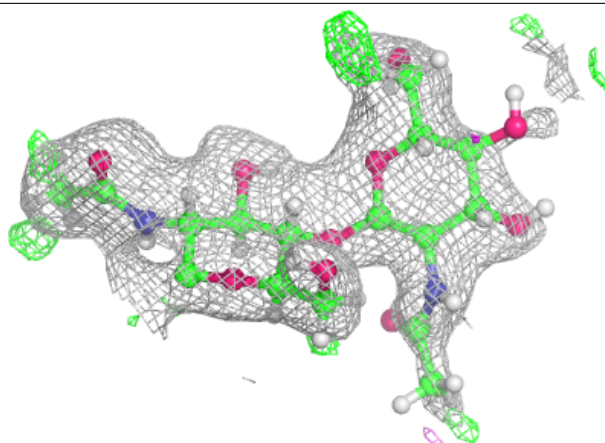
Electron density around Chain B:

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



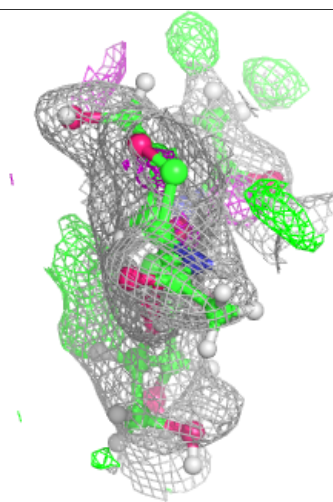
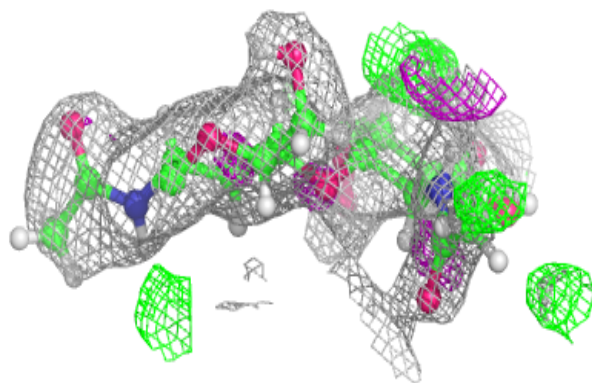
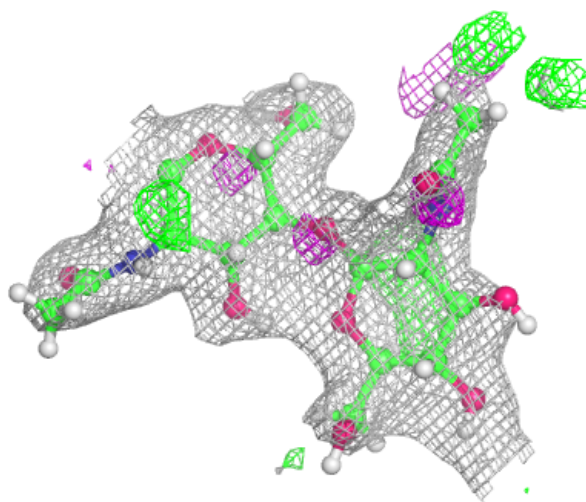
Electron density around Chain C:

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



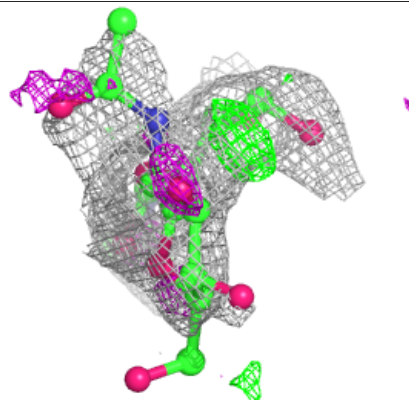
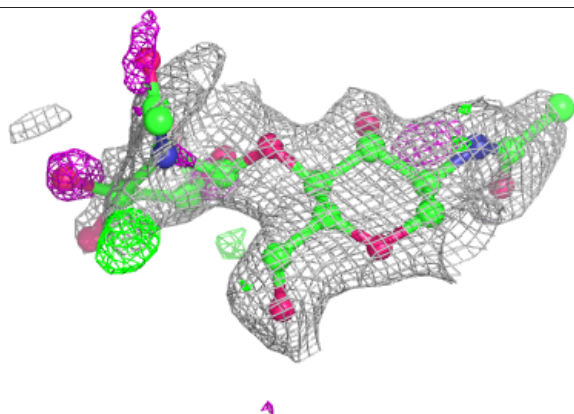
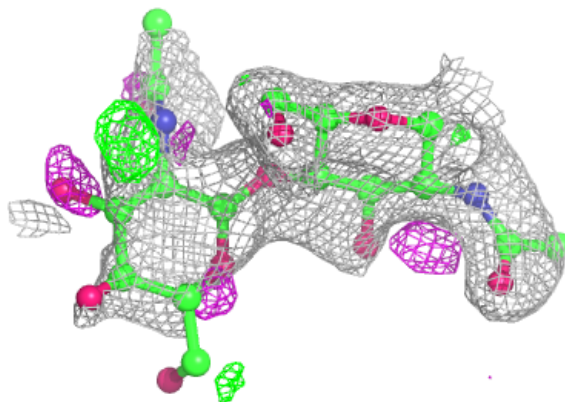
Electron density around Chain D:

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



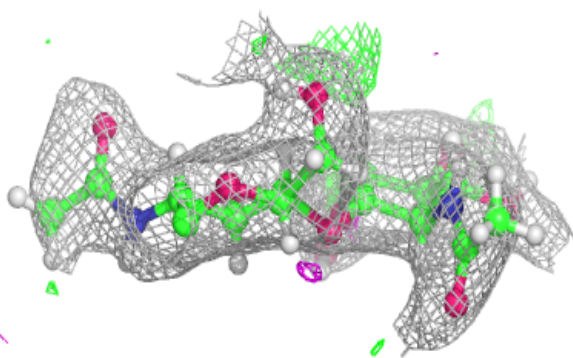
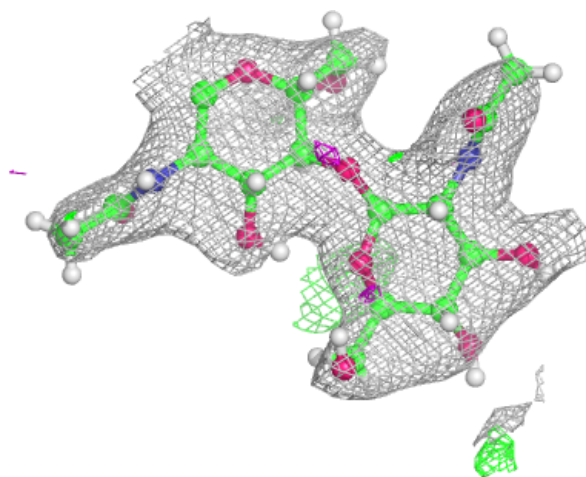
Electron density around Chain E:

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



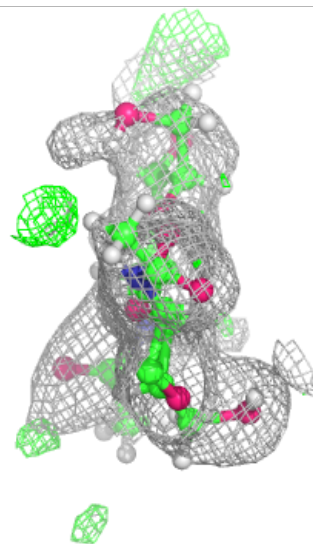
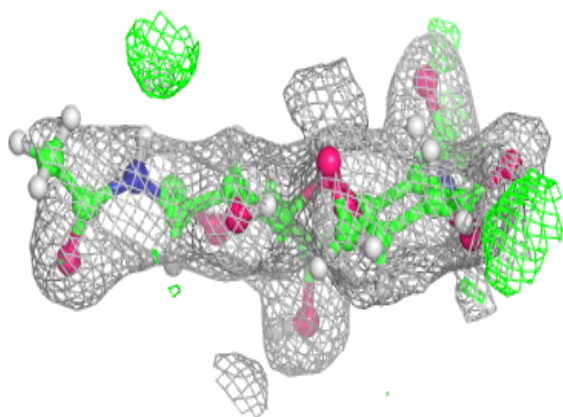
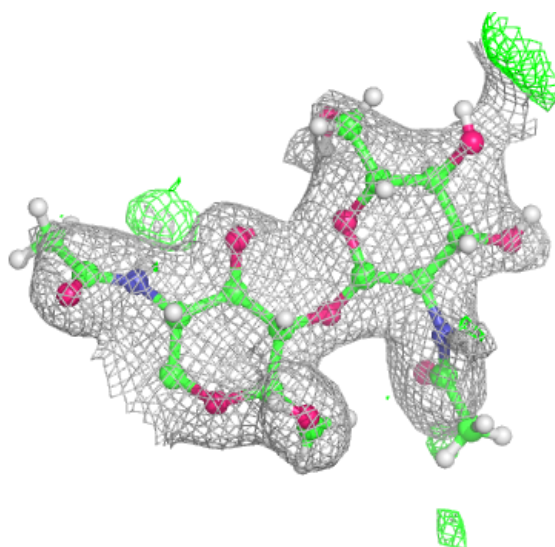
Electron density around Chain I:

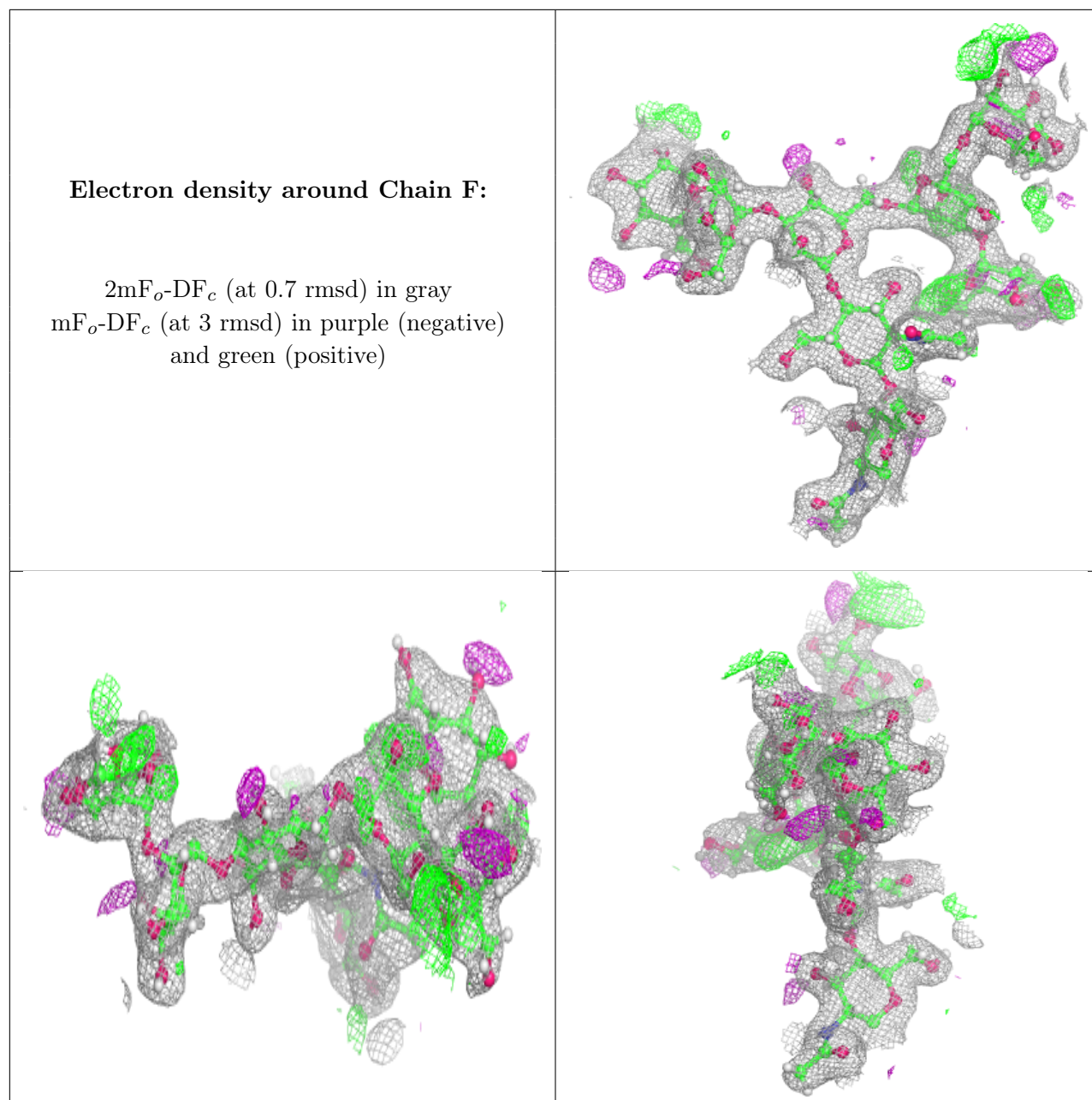
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain U:

$2mF_o-DF_c$ (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(\AA^2)	Q<0.9
6	MAN	A	604	12/12	0.44	0.17	64,74,80,90	0
7	NAG	M	605	14/15	0.65	0.15	55,67,82,87	0
7	NAG	A	605	14/15	0.69	0.15	49,64,81,84	0

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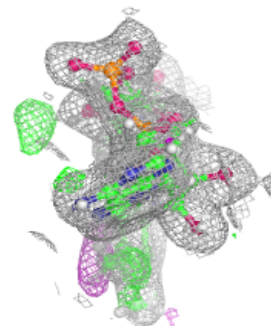
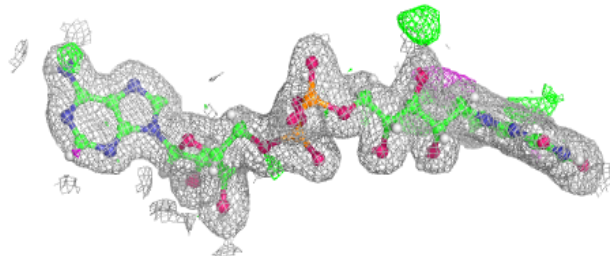
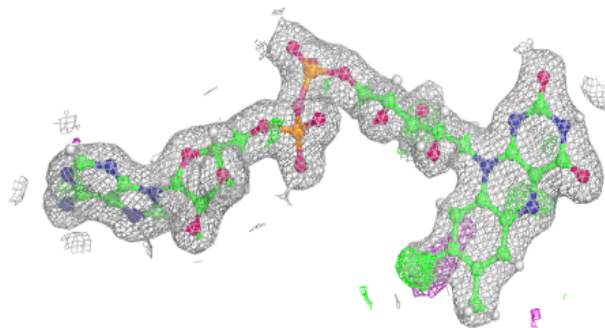
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	NAG	M	603	14/15	0.74	0.14	43,54,69,72	0
5	EDO	A	602	4/4	0.82	0.21	33,40,48,55	0
5	EDO	M	604	4/4	0.82	0.12	58,70,72,74	0
11	BA	A	623	1/1	0.82	0.18	71,71,71,71	1
10	NA	M	611	1/1	0.84	0.17	32,32,32,32	1
5	EDO	M	601	4/4	0.84	0.11	39,48,53,53	0
5	EDO	M	602	4/4	0.87	0.18	33,40,48,50	0
10	NA	A	616	1/1	0.87	0.39	38,38,38,38	1
9	CL	A	611	1/1	0.88	0.14	55,55,55,55	1
9	CL	A	612	1/1	0.89	0.15	53,53,53,53	1
10	NA	A	617	1/1	0.91	0.14	45,45,45,45	0
10	NA	M	610	1/1	0.91	0.12	42,42,42,42	1
9	CL	A	608	1/1	0.91	0.13	52,52,52,52	1
5	EDO	A	603	4/4	0.91	0.10	40,51,62,62	0
9	CL	A	613	1/1	0.92	0.10	50,50,50,50	1
5	EDO	A	601	4/4	0.92	0.12	46,55,61,61	0
11	BA	M	617	1/1	0.93	0.10	46,46,46,46	1
11	BA	A	622	1/1	0.94	0.09	45,45,45,45	1
10	NA	A	615	1/1	0.95	0.07	33,33,33,33	1
9	CL	A	610	1/1	0.95	0.09	44,44,44,44	1
9	CL	A	609	1/1	0.95	0.12	41,41,41,41	1
11	BA	M	615	1/1	0.95	0.08	50,50,50,50	1
9	CL	M	609	1/1	0.95	0.10	48,48,48,48	1
9	CL	M	607	1/1	0.96	0.08	36,36,36,36	1
11	BA	M	613	1/1	0.96	0.06	39,39,39,39	1
11	BA	A	621	1/1	0.96	0.09	47,47,47,47	1
11	BA	M	616	1/1	0.96	0.07	43,43,43,43	1
10	NA	A	614	1/1	0.96	0.07	31,31,31,31	1
12	BR	A	624	1/1	0.96	0.10	43,43,43,43	1
11	BA	A	618	1/1	0.97	0.05	31,31,31,31	1
11	BA	A	620	1/1	0.97	0.06	40,40,40,40	1
9	CL	A	607	1/1	0.97	0.07	41,41,41,41	1
8	FAD	A	606	53/53	0.97	0.06	22,26,32,35	0
8	FAD	M	606	53/53	0.97	0.06	24,27,34,36	0
11	BA	A	619	1/1	0.98	0.05	34,34,34,34	1
11	BA	M	612	1/1	0.98	0.05	32,32,32,32	1
9	CL	M	608	1/1	0.98	0.07	35,35,35,35	0
11	BA	M	614	1/1	0.98	0.06	38,38,38,38	1
12	BR	M	618	1/1	0.98	0.11	30,30,30,30	1
12	BR	A	625	1/1	0.99	0.04	38,38,38,38	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

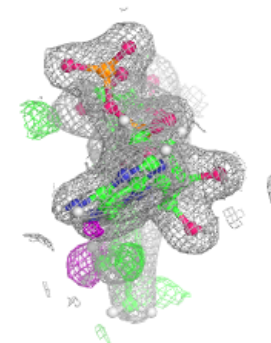
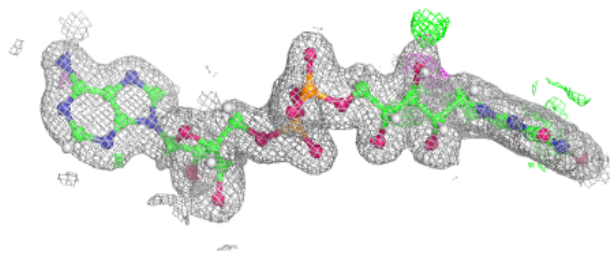
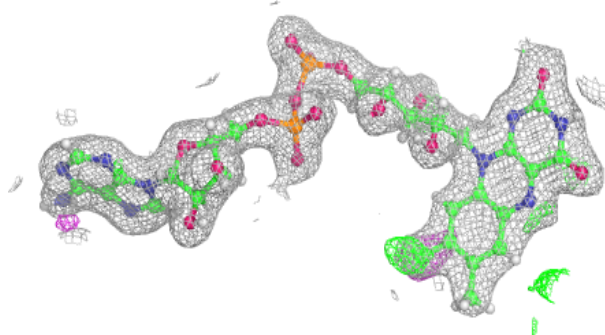
Electron density around FAD A 606:

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



Electron density around FAD M 606:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.