



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 10:36 AM UTC

PDB ID : 8BHH / pdb_00008bhh
Title : The crystal structure of a feruloyl esterase C from *Fusarium oxysporum* in complex with p-coumaric acid
Authors : Dimarogona, M.; Topakas, E.; Kosinas, C.; Ferousi, C.; Nikolaivits, E.
Deposited on : 2022-10-31
Resolution : 1.69 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

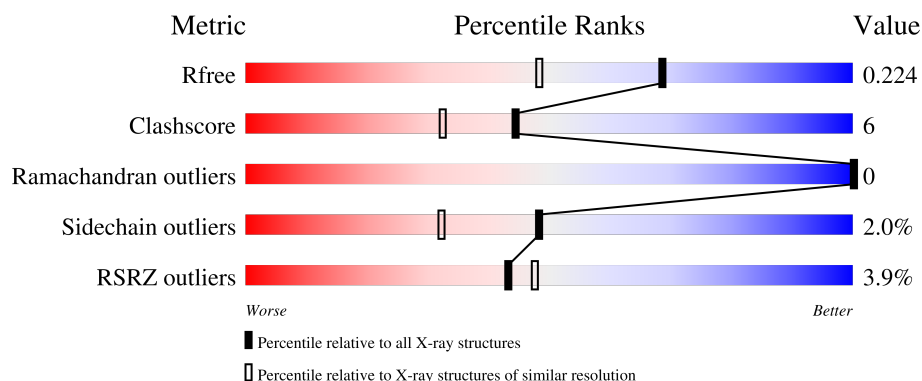
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	508	6% 87% 11% ..
1	B	508	% 88% 11% .
2	C	10	90% 10%
2	G	10	100%
2	I	10	90% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	E	6	 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
6	EDO	A	605	-	-	X	-
8	PG4	B	601	-	-	X	-
9	P6G	B	602	-	-	X	-

2 Entry composition [i](#)

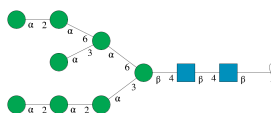
There are 11 unique types of molecules in this entry. The entry contains 9410 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Carboxylic ester hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	503	Total	C	N	O	S	0	6	0
			3968	2506	690	751	21			
1	B	504	Total	C	N	O	S	0	7	0
			3970	2511	685	752	22			

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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.



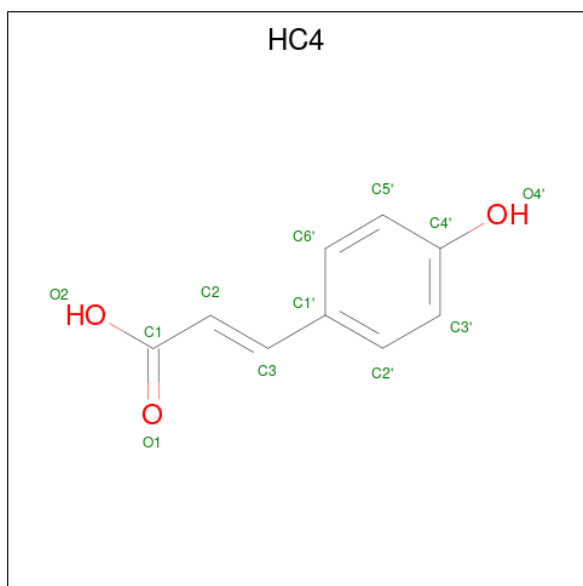
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	0	0
			116	64	2	50			
2	G	10	Total	C	N	O	0	0	0
			116	64	2	50			
2	I	10	Total	C	N	O	0	0	0
			116	64	2	50			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-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
3	E	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 4 is 4'-HYDROXYCINNAMIC ACID (CCD ID: HC4) (formula: C₉H₈O₃) (labeled as "Ligand of Interest" by depositor).



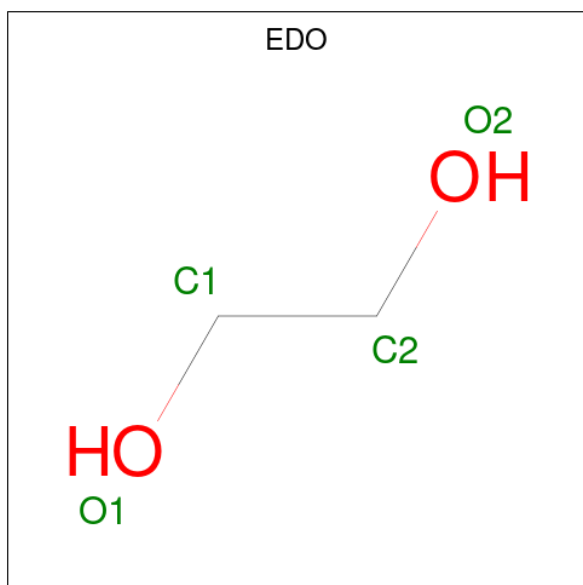
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	9	3		
4	B	1	Total	C	O	0	0
			12	9	3		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

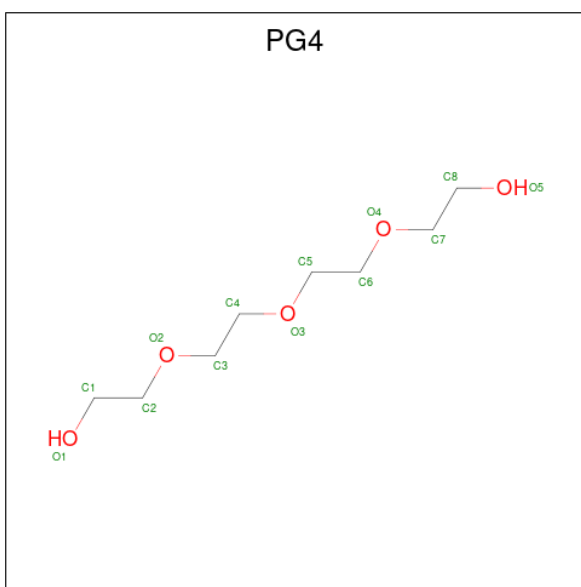


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

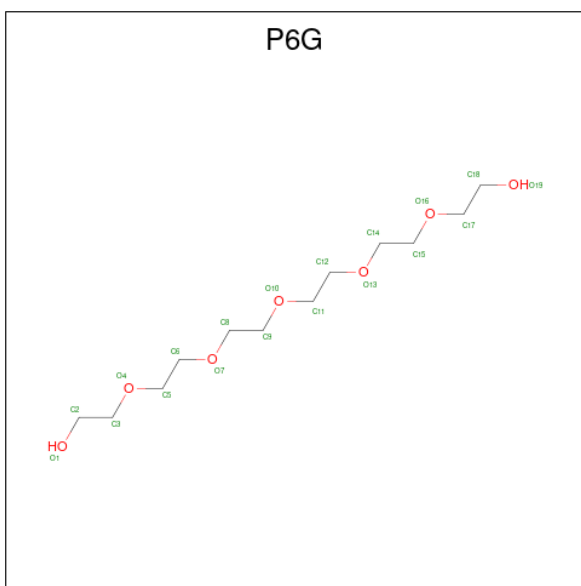
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0
7	B	1	Total Ca 1 1	0	0

- Molecule 8 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 9 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			19	12	7		

- Molecule 10 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	O	0	0
			7	4	3		

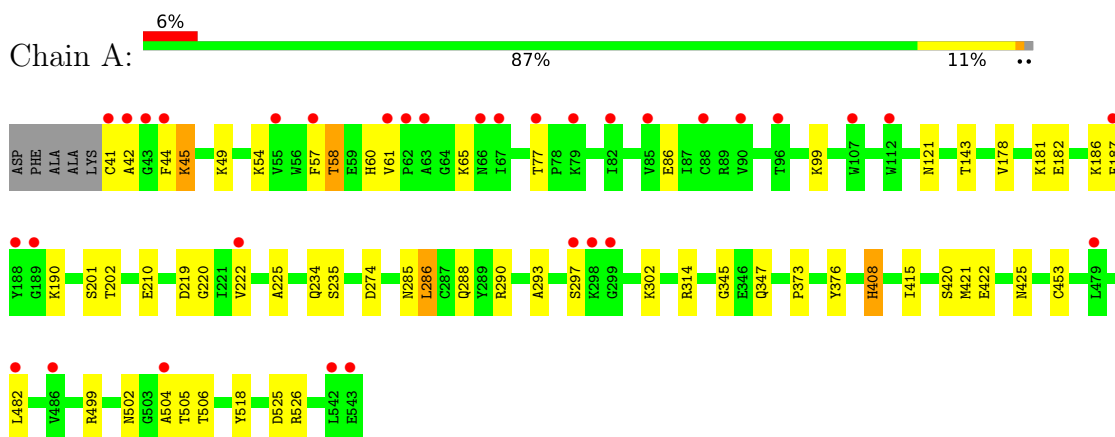
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	378	Total	O	0	0
			378	378		
11	B	513	Total	O	0	0
			513	513		

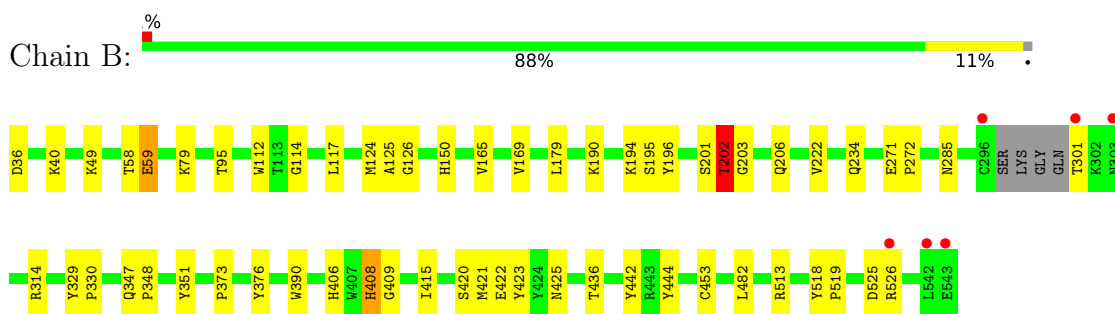
3 Residue-property plots [i](#)

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.

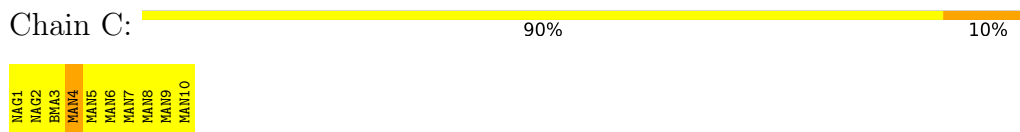
- Molecule 1: Carboxylic ester hydrolase



- Molecule 1: Carboxylic ester hydrolase



- Molecule 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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

Chain G:

100%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10

● Molecule 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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

Chain I:

90%

10%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10

● Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-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

Chain E:

100%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.70Å 89.64Å 116.98Å 90.00° 103.99° 90.00°	Depositor
Resolution (Å)	113.51 – 1.69 113.51 – 1.69	Depositor EDS
% Data completeness (in resolution range)	69.5 (113.51-1.69) 69.5 (113.51-1.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 1.69Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.171 , 0.217 0.180 , 0.224	Depositor DCC
R_{free} test set	5158 reflections (3.41%)	wwPDB-VP
Wilson B-factor (Å ²)	25.2	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9410	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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, EDO, BMA, PEG, CA, P6G, HC4, MAN, PG4

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	1.13	4/4080 (0.1%)	1.38	17/5543 (0.3%)
1	B	1.16	3/4088 (0.1%)	1.29	10/5554 (0.2%)
All	All	1.15	7/8168 (0.1%)	1.34	27/11097 (0.2%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	408	HIS	CE1-NE2	6.56	1.39	1.32
1	A	210	GLU	C-O	5.72	1.30	1.24
1	B	409	GLY	C-O	5.70	1.29	1.24
1	A	345	GLY	C-O	5.49	1.27	1.23
1	A	61	VAL	N-CA	5.47	1.50	1.45

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	219	ASP	CA-C-N	8.51	127.44	121.65
1	A	219	ASP	C-N-CA	8.51	127.44	121.65
1	B	36	ASP	CA-CB-CG	7.08	119.68	112.60
1	B	59	GLU	CB-CG-CD	6.50	123.64	112.60
1	B	408	HIS	CA-CB-CG	6.22	120.02	113.80

There are no chirality outliers.

There are no planarity outliers.

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	3968	0	3774	43	0
1	B	3970	0	3772	49	0
2	C	116	0	97	1	0
2	G	116	0	97	0	0
2	I	116	0	97	0	1
3	E	72	0	61	0	0
4	A	12	0	6	1	0
4	B	12	0	6	3	0
5	A	14	0	13	0	0
5	B	42	0	39	0	0
6	A	16	0	24	9	0
6	B	24	0	36	1	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	B	13	0	18	13	0
9	B	19	0	26	9	0
10	B	7	0	10	0	0
11	A	378	0	0	8	0
11	B	513	0	0	8	1
All	All	9410	0	8076	99	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 6.

The worst 5 of 99 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)
11:A:736:HOH:O	9:B:602:P6G:H141	1.48	1.12
1:B:285:ASN:HD21	1:B:421[B]:MET:HE1	1.31	0.96
1:A:41:CYS:O	1:A:58:THR:HG21	1.74	0.87
8:B:601:PG4:H62	11:B:931:HOH:O	1.74	0.87
1:B:422:GLU:HG2	8:B:601:PG4:H71	1.60	0.84

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)
2:I:10:MAN:O6	11:B:1078:HOH:O[2_544]	2.11	0.09

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	507/508 (100%)	491 (97%)	16 (3%)	0	100	100
1	B	507/508 (100%)	497 (98%)	10 (2%)	0	100	100
All	All	1014/1016 (100%)	988 (97%)	26 (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	422/419 (101%)	409 (97%)	13 (3%)	35	18
1	B	423/419 (101%)	419 (99%)	4 (1%)	70	62
All	All	845/838 (101%)	828 (98%)	17 (2%)	48	32

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	202	THR
1	B	513	ARG
1	A	202	THR
1	A	286	LEU
1	A	302	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	52	ASN
1	B	285	ASN
1	B	408	HIS
1	B	347	GLN
1	A	425	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 ⓘ

36 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	2,1	14,14,15	0.99	1 (7%)	17,19,21	2.10	5 (29%)
2	MAN	C	10	2	11,11,12	0.81	0	15,15,17	1.36	2 (13%)
2	NAG	C	2	2	14,14,15	0.85	1 (7%)	17,19,21	1.56	3 (17%)
2	BMA	C	3	2	11,11,12	0.73	0	15,15,17	1.55	3 (20%)
2	MAN	C	4	2	11,11,12	1.07	2 (18%)	15,15,17	1.37	2 (13%)
2	MAN	C	5	2	11,11,12	0.91	1 (9%)	15,15,17	1.77	5 (33%)
2	MAN	C	6	2	11,11,12	0.81	0	15,15,17	2.05	4 (26%)
2	MAN	C	7	2	11,11,12	0.92	0	15,15,17	2.09	4 (26%)
2	MAN	C	8	2	11,11,12	0.88	0	15,15,17	2.09	5 (33%)
2	MAN	C	9	2	11,11,12	1.25	0	15,15,17	2.34	4 (26%)
3	NAG	E	1	3,1	14,14,15	0.55	0	17,19,21	1.31	3 (17%)
3	NAG	E	2	3	14,14,15	0.61	0	17,19,21	1.52	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BMA	E	3	3	11,11,12	0.41	0	15,15,17	1.57	2 (13%)
3	MAN	E	4	3	11,11,12	0.79	0	15,15,17	1.50	4 (26%)
3	MAN	E	5	3	11,11,12	0.73	0	15,15,17	1.10	1 (6%)
3	MAN	E	6	3	11,11,12	1.29	1 (9%)	15,15,17	1.21	0
2	NAG	G	1	2,1	14,14,15	1.04	2 (14%)	17,19,21	1.63	4 (23%)
2	MAN	G	10	2	11,11,12	1.40	2 (18%)	15,15,17	1.89	2 (13%)
2	NAG	G	2	2	14,14,15	0.79	0	17,19,21	1.77	4 (23%)
2	BMA	G	3	2	11,11,12	0.93	1 (9%)	15,15,17	1.72	4 (26%)
2	MAN	G	4	2	11,11,12	1.07	1 (9%)	15,15,17	2.09	5 (33%)
2	MAN	G	5	2	11,11,12	1.04	0	15,15,17	1.59	2 (13%)
2	MAN	G	6	2	11,11,12	1.22	1 (9%)	15,15,17	1.86	5 (33%)
2	MAN	G	7	2	11,11,12	0.93	1 (9%)	15,15,17	1.93	4 (26%)
2	MAN	G	8	2	11,11,12	0.78	0	15,15,17	1.77	4 (26%)
2	MAN	G	9	2	11,11,12	0.63	0	15,15,17	1.52	3 (20%)
2	NAG	I	1	2,1	14,14,15	0.97	1 (7%)	17,19,21	1.23	2 (11%)
2	MAN	I	10	2	11,11,12	0.63	0	15,15,17	2.18	7 (46%)
2	NAG	I	2	2	14,14,15	1.02	1 (7%)	17,19,21	2.23	4 (23%)
2	BMA	I	3	2	11,11,12	0.63	0	15,15,17	1.44	1 (6%)
2	MAN	I	4	2	11,11,12	0.81	0	15,15,17	1.44	3 (20%)
2	MAN	I	5	2	11,11,12	1.09	1 (9%)	15,15,17	1.83	3 (20%)
2	MAN	I	6	2	11,11,12	0.86	0	15,15,17	1.53	2 (13%)
2	MAN	I	7	2	11,11,12	0.55	0	15,15,17	1.75	4 (26%)
2	MAN	I	8	2	11,11,12	1.05	1 (9%)	15,15,17	2.15	5 (33%)
2	MAN	I	9	2	11,11,12	1.02	1 (9%)	15,15,17	1.54	4 (26%)

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	2,1	-	2/6/23/26	0/1/1/1
2	MAN	C	10	2	-	0/2/19/22	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	MAN	C	5	2	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	C	6	2	-	0/2/19/22	0/1/1/1
2	MAN	C	7	2	-	0/2/19/22	0/1/1/1
2	MAN	C	8	2	-	0/2/19/22	0/1/1/1
2	MAN	C	9	2	-	2/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
3	MAN	E	5	3	-	1/2/19/22	0/1/1/1
3	MAN	E	6	3	-	0/2/19/22	0/1/1/1
2	NAG	G	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	G	10	2	-	0/2/19/22	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	0/2/19/22	0/1/1/1
2	MAN	G	4	2	-	0/2/19/22	0/1/1/1
2	MAN	G	5	2	-	0/2/19/22	0/1/1/1
2	MAN	G	6	2	-	0/2/19/22	0/1/1/1
2	MAN	G	7	2	-	0/2/19/22	0/1/1/1
2	MAN	G	8	2	-	0/2/19/22	0/1/1/1
2	MAN	G	9	2	-	0/2/19/22	0/1/1/1
2	NAG	I	1	2,1	-	0/6/23/26	0/1/1/1
2	MAN	I	10	2	-	2/2/19/22	0/1/1/1
2	NAG	I	2	2	-	1/6/23/26	0/1/1/1
2	BMA	I	3	2	-	0/2/19/22	0/1/1/1
2	MAN	I	4	2	-	0/2/19/22	0/1/1/1
2	MAN	I	5	2	-	2/2/19/22	0/1/1/1
2	MAN	I	6	2	-	0/2/19/22	0/1/1/1
2	MAN	I	7	2	-	0/2/19/22	0/1/1/1
2	MAN	I	8	2	-	0/2/19/22	0/1/1/1
2	MAN	I	9	2	-	0/2/19/22	0/1/1/1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	5	MAN	O5-C1	2.98	1.48	1.43
2	I	1	NAG	C1-C2	2.64	1.55	1.52
2	C	2	NAG	O5-C1	2.39	1.47	1.43
2	I	2	NAG	O5-C5	2.33	1.48	1.43
2	G	10	MAN	C2-C3	2.28	1.56	1.52

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	2	NAG	C1-O5-C5	-6.65	103.28	112.19
2	G	10	MAN	C1-O5-C5	6.25	120.56	112.19
2	C	7	MAN	C1-O5-C5	6.24	120.55	112.19
2	C	9	MAN	C1-C2-C3	5.96	118.31	109.64
2	G	7	MAN	C1-C2-C3	-5.12	102.18	109.64

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

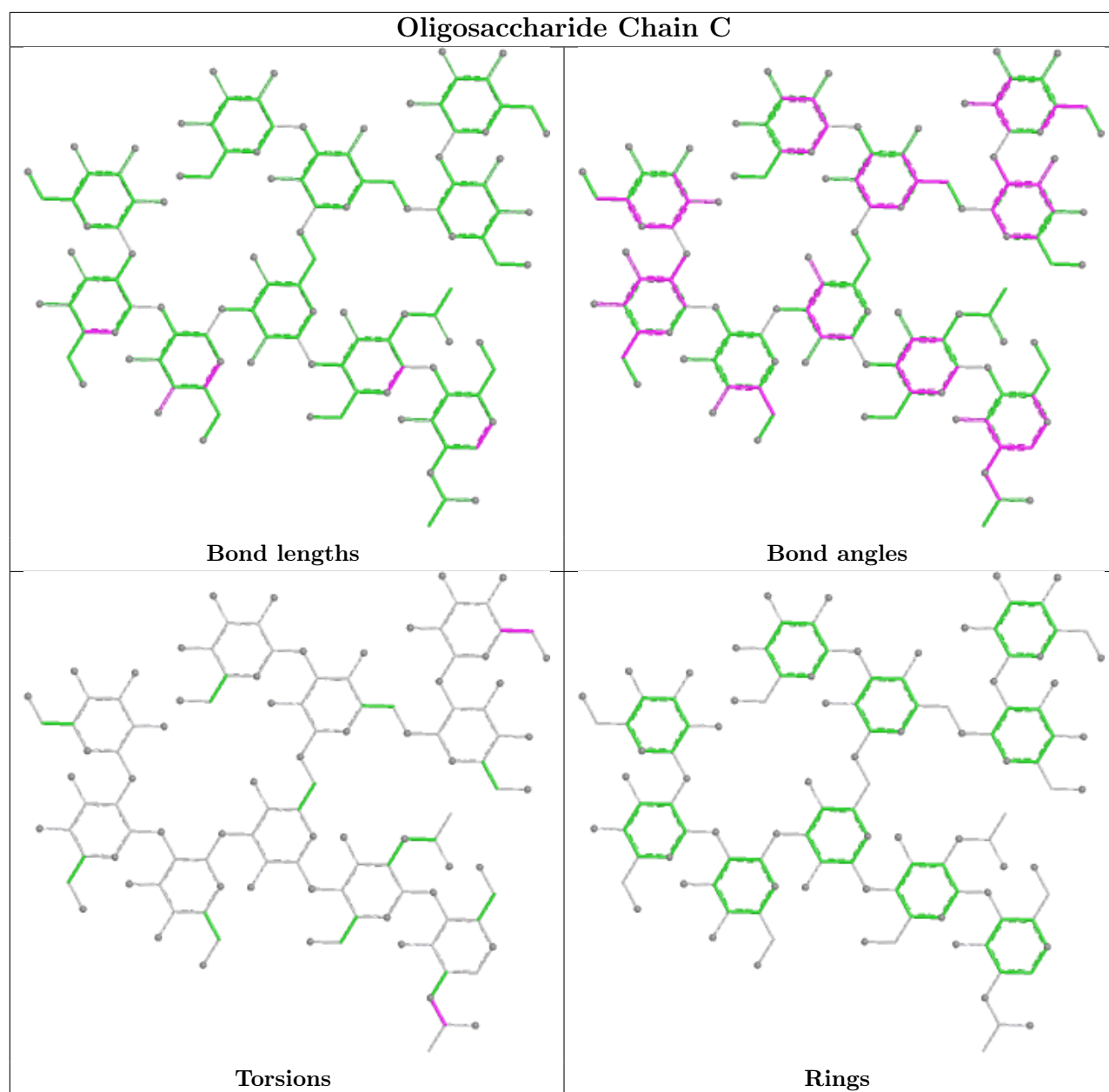
Mol	Chain	Res	Type	Atoms
2	I	10	MAN	O5-C5-C6-O6
2	I	10	MAN	C4-C5-C6-O6
2	C	9	MAN	C4-C5-C6-O6
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2

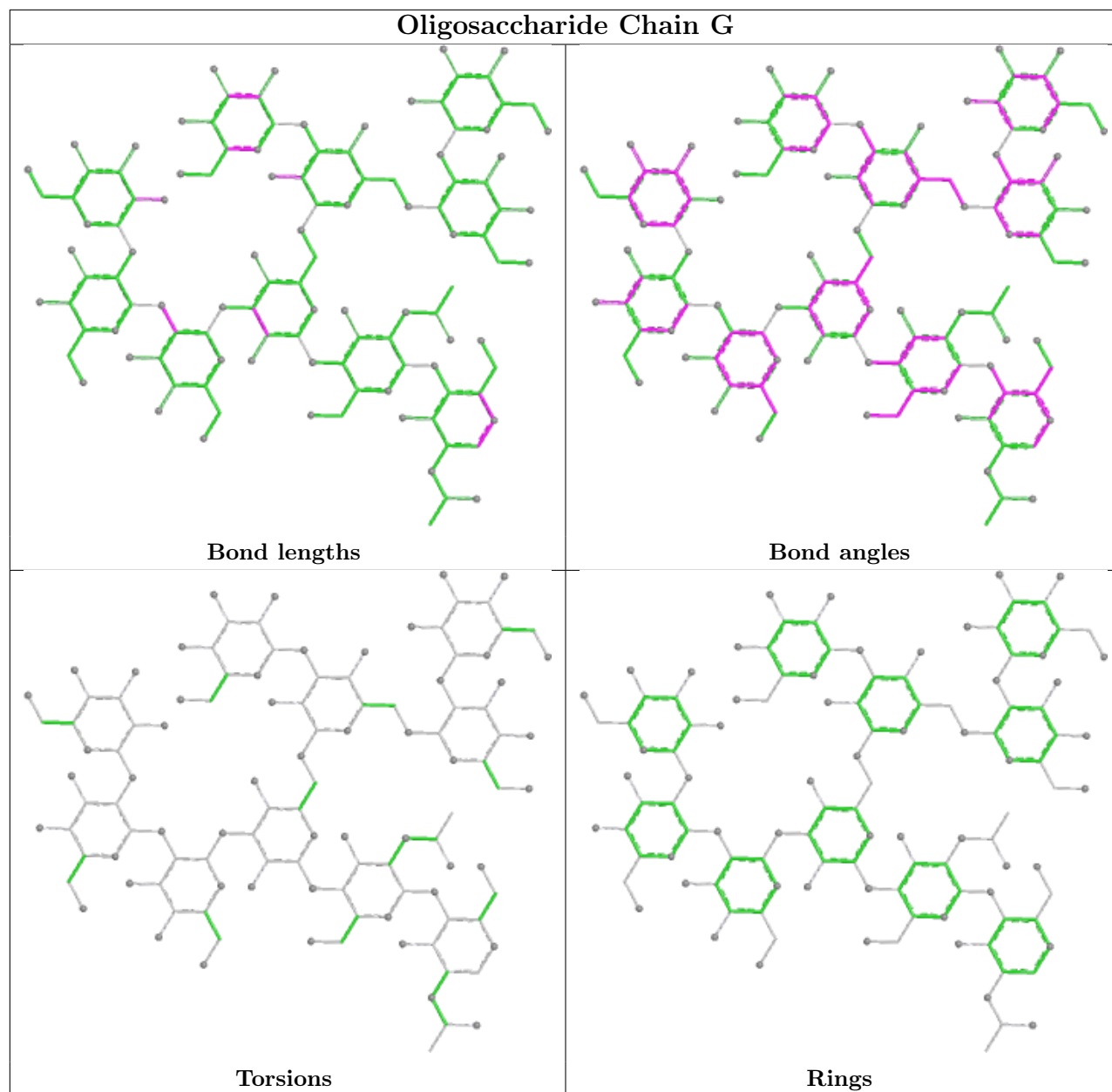
There are no ring outliers.

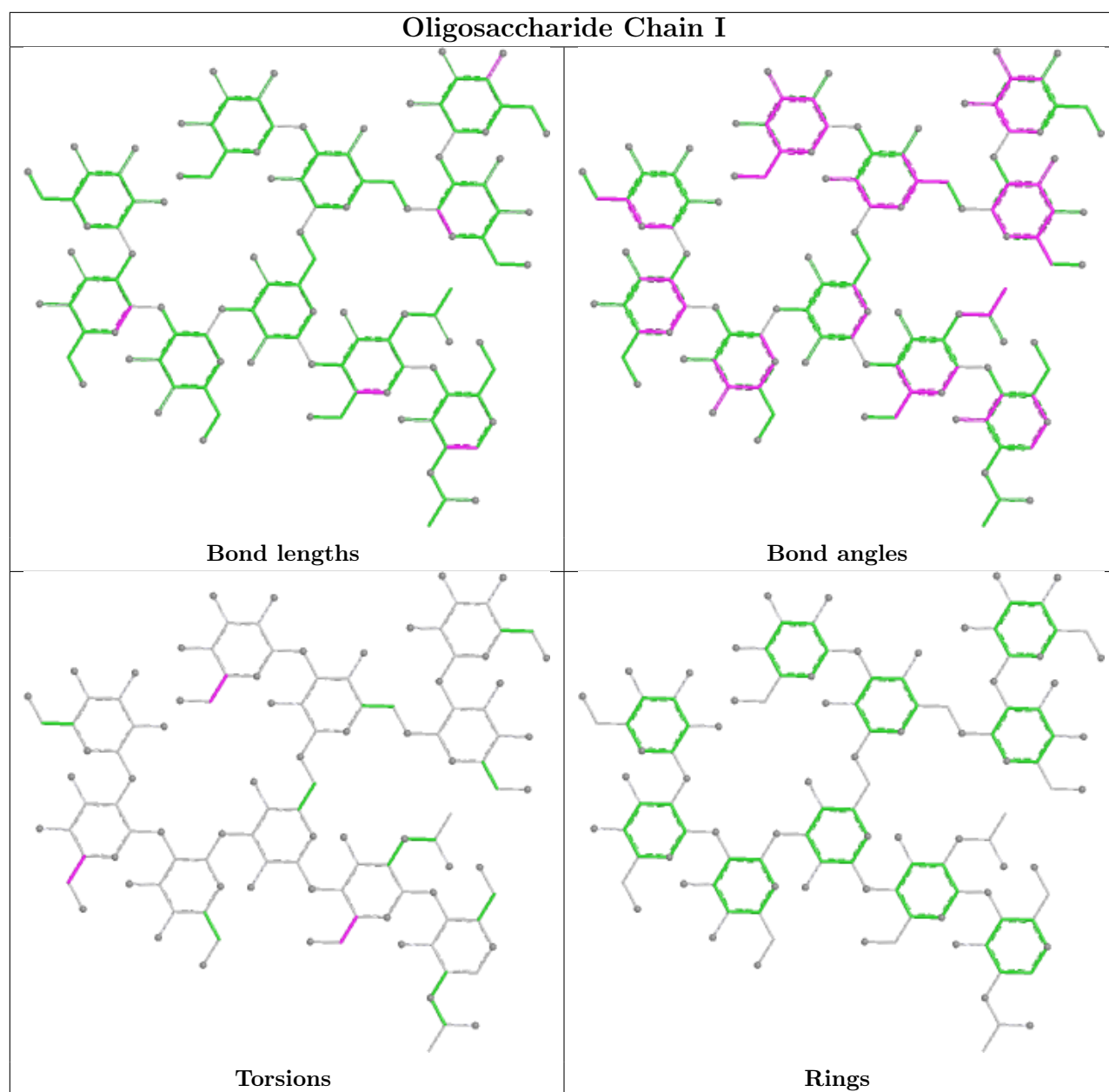
2 monomers are involved in 2 short contacts:

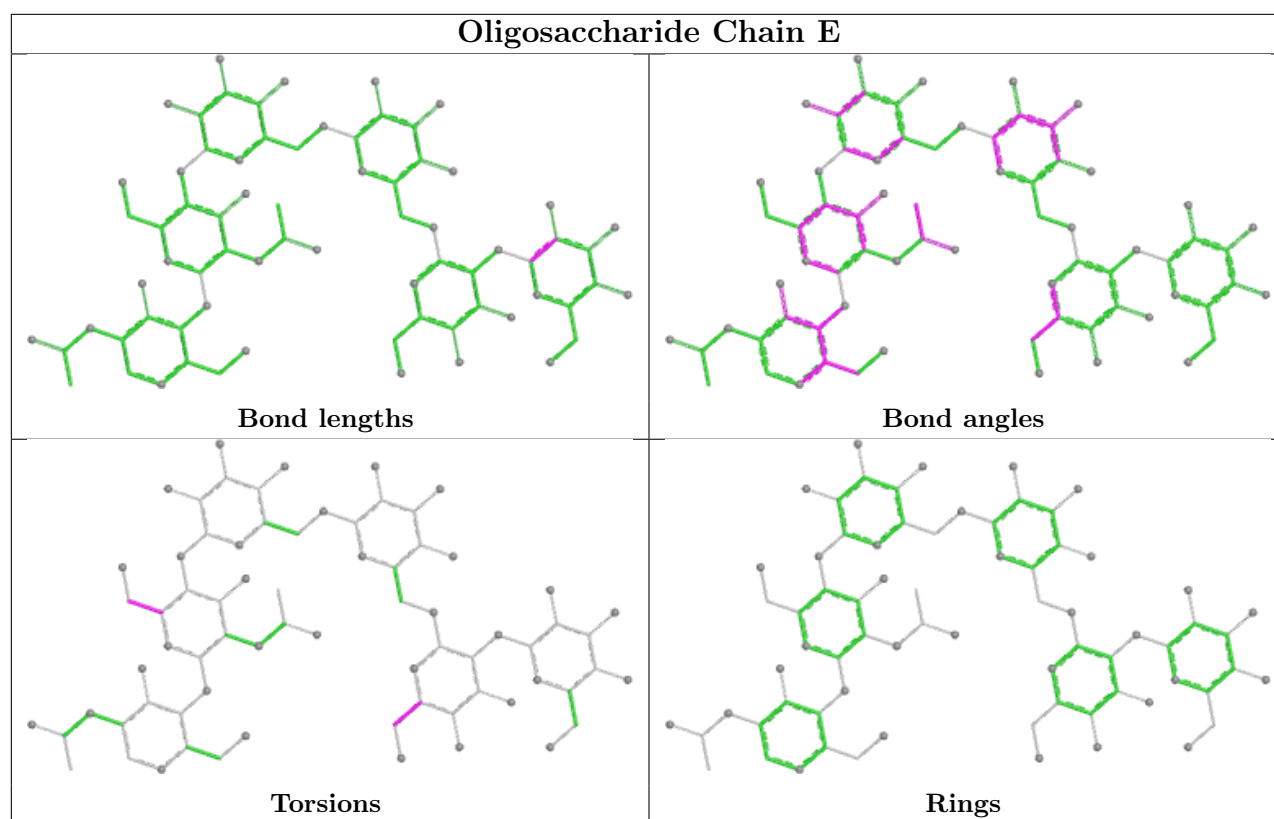
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	4	MAN	1	0
2	I	10	MAN	0	1

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 21 ligands modelled in this entry, 2 are monoatomic - leaving 19 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	$\# Z > 2$
6	EDO	B	608	-	3,3,3	0.52	0	2,2,2	0.53	0
8	PG4	B	601	-	12,12,12	0.57	0	11,11,11	0.59	0
6	EDO	B	606	-	3,3,3	0.37	0	2,2,2	0.62	0
10	PEG	B	609	-	6,6,6	0.28	0	5,5,5	0.19	0
5	NAG	B	603	1	14,14,15	0.85	1 (7%)	17,19,21	1.34	4 (23%)
6	EDO	A	606	-	3,3,3	0.27	0	2,2,2	0.10	0
6	EDO	B	610	-	3,3,3	0.18	0	2,2,2	0.17	0
6	EDO	B	613	-	3,3,3	0.11	0	2,2,2	0.27	0
6	EDO	A	604	-	3,3,3	0.25	0	2,2,2	0.36	0
5	NAG	A	602	1	14,14,15	0.88	0	17,19,21	1.08	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	B	607	-	3,3,3	0.35	0	2,2,2	0.44	0
6	EDO	A	605	-	3,3,3	0.61	0	2,2,2	0.52	0
4	HC4	B	604	-	12,12,12	0.88	1 (8%)	15,15,15	0.60	0
9	P6G	B	602	-	18,18,18	0.25	0	17,17,17	0.34	0
6	EDO	B	605	-	3,3,3	0.19	0	2,2,2	0.32	0
6	EDO	A	603	-	3,3,3	0.31	0	2,2,2	0.36	0
5	NAG	B	611	1	14,14,15	0.77	0	17,19,21	1.34	1 (5%)
5	NAG	B	612	1	14,14,15	0.76	0	17,19,21	1.69	2 (11%)
4	HC4	A	601	-	12,12,12	0.94	0	15,15,15	0.44	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
6	EDO	B	608	-	-	1/1/1/1	-
8	PG4	B	601	-	-	6/10/10/10	-
6	EDO	B	606	-	-	0/1/1/1	-
10	PEG	B	609	-	-	1/4/4/4	-
5	NAG	B	603	1	-	0/6/23/26	0/1/1/1
6	EDO	A	606	-	-	1/1/1/1	-
6	EDO	B	610	-	-	1/1/1/1	-
6	EDO	B	613	-	-	1/1/1/1	-
6	EDO	A	604	-	-	1/1/1/1	-
5	NAG	A	602	1	-	0/6/23/26	0/1/1/1
6	EDO	B	607	-	-	1/1/1/1	-
6	EDO	A	605	-	-	1/1/1/1	-
4	HC4	B	604	-	-	0/5/5/5	0/1/1/1
9	P6G	B	602	-	-	8/16/16/16	-
6	EDO	B	605	-	-	1/1/1/1	-
6	EDO	A	603	-	-	1/1/1/1	-
5	NAG	B	611	1	-	2/6/23/26	0/1/1/1
5	NAG	B	612	1	-	1/6/23/26	0/1/1/1
4	HC4	A	601	-	-	2/5/5/5	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	604	HC4	O1-C1	2.29	1.28	1.23
5	B	603	NAG	C3-C2	2.14	1.57	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	612	NAG	C1-O5-C5	5.36	119.36	112.19
5	B	612	NAG	C1-C2-N2	-3.38	105.11	110.43
5	B	603	NAG	O3-C3-C2	-2.89	103.39	109.40
5	B	611	NAG	C1-C2-N2	2.74	114.74	110.43
5	B	603	NAG	C8-C7-N2	-2.40	112.14	116.12

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

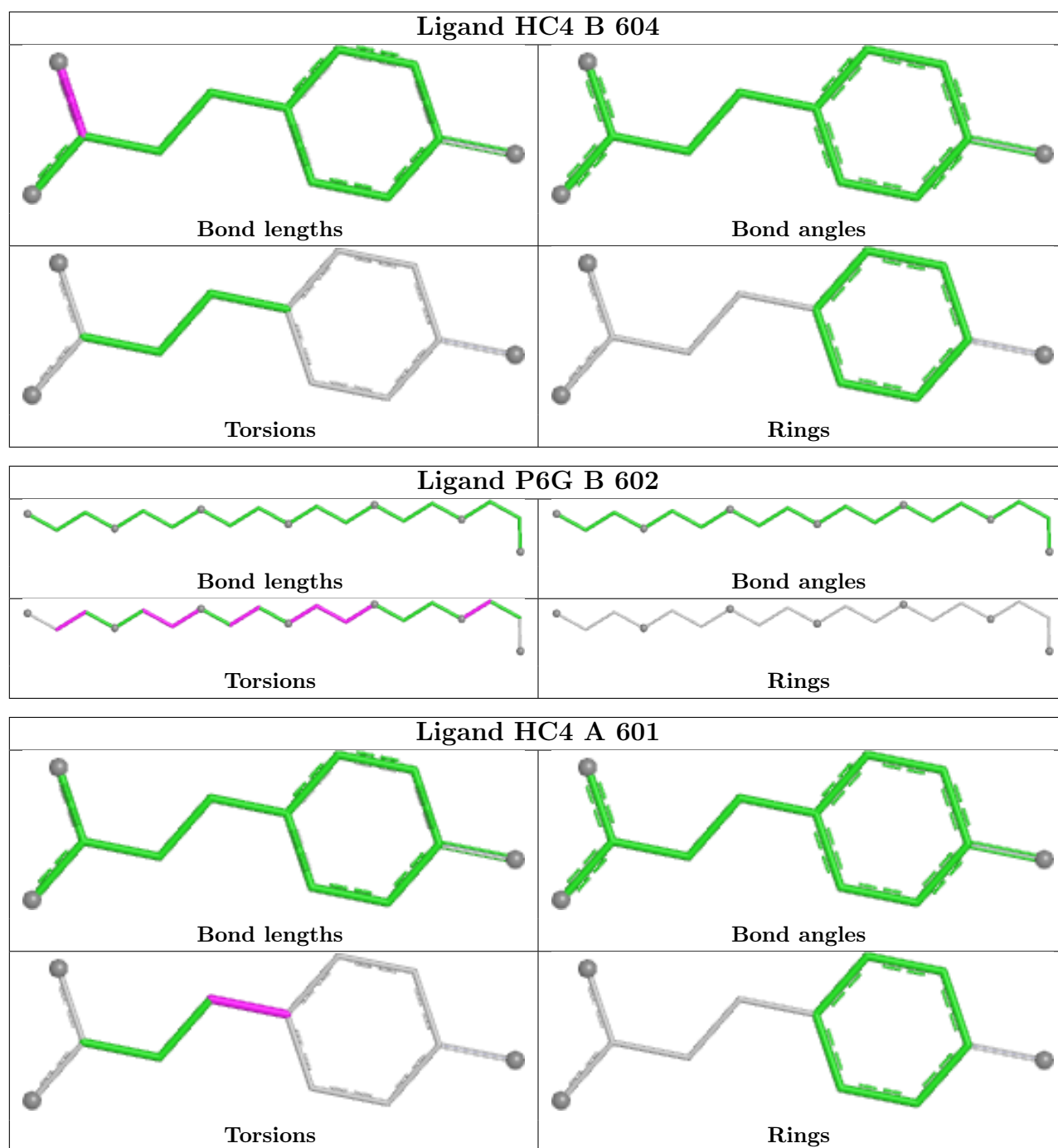
Mol	Chain	Res	Type	Atoms
8	B	601	PG4	C3-C4-O3-C5
9	B	602	P6G	O7-C8-C9-O10
9	B	602	P6G	O10-C11-C12-O13
10	B	609	PEG	O1-C1-C2-O2
9	B	602	P6G	O16-C17-C18-O19

There are no ring outliers.

7 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	601	PG4	13	0
6	A	606	EDO	1	0
6	B	607	EDO	1	0
6	A	605	EDO	8	0
4	B	604	HC4	3	0
9	B	602	P6G	9	0
4	A	601	HC4	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 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 [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	503/508 (99%)	0.52	33 (6%) 24 26	10, 30, 57, 77	6 (1%)
1	B	504/508 (99%)	-0.04	6 (1%) 76 80	9, 24, 38, 74	7 (1%)
All	All	1007/1016 (99%)	0.24	39 (3%) 43 47	9, 26, 52, 77	13 (1%)

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	41	CYS	4.8
1	A	542	LEU	4.4
1	A	67	ILE	4.2
1	B	301	THR	3.9
1	A	187	PHE	3.6

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	MAN	C	9	11/12	0.82	0.13	39,45,60,61	0
2	MAN	C	4	11/12	0.87	0.12	28,31,37,46	0
3	MAN	E	4	11/12	0.91	0.08	43,54,57,57	0
2	MAN	C	5	11/12	0.92	0.08	29,33,37,42	0
2	MAN	C	6	11/12	0.93	0.08	38,40,44,44	0

Continued on next page...

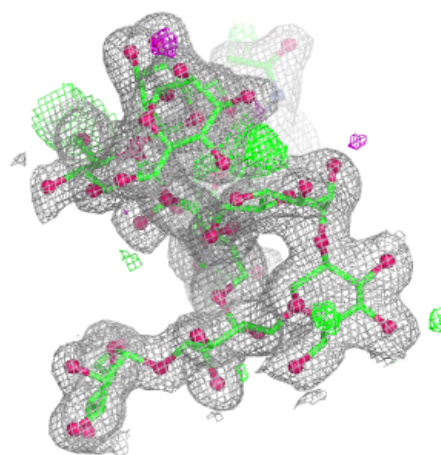
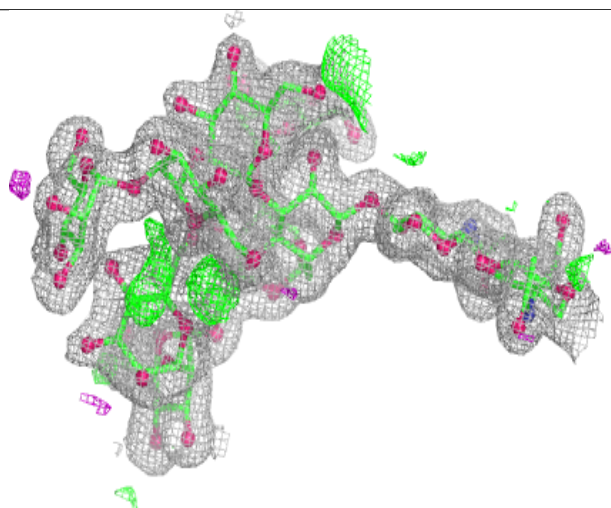
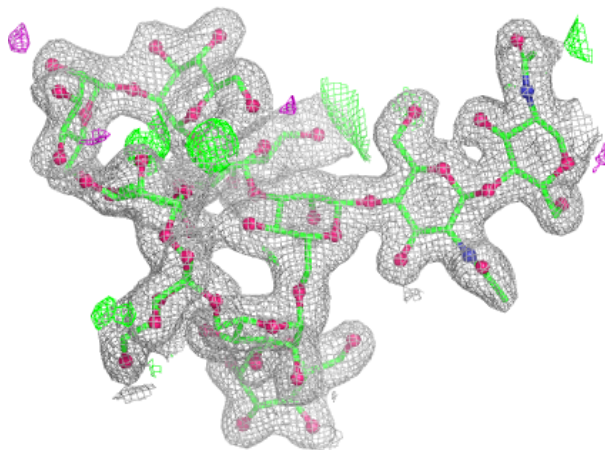
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MAN	C	8	11/12	0.93	0.08	23,26,31,31	0
3	NAG	E	2	14/15	0.94	0.07	40,46,53,58	0
3	MAN	E	5	11/12	0.94	0.09	40,44,49,49	0
3	MAN	E	6	11/12	0.94	0.08	36,40,42,57	0
2	BMA	C	3	11/12	0.95	0.06	21,23,24,25	0
2	NAG	G	1	14/15	-	-	25,27,34,37	0
2	NAG	G	2	14/15	-	-	22,23,26,28	0
2	BMA	G	3	11/12	-	-	22,23,26,27	0
2	MAN	G	4	11/12	-	-	20,21,27,35	0
2	MAN	G	5	11/12	-	-	21,22,24,24	0
2	MAN	G	6	11/12	-	-	18,21,22,23	0
2	MAN	G	7	11/12	-	-	31,34,37,38	0
2	MAN	G	8	11/12	-	-	30,32,38,43	0
2	MAN	G	9	11/12	-	-	48,56,60,69	0
2	MAN	G	10	11/12	-	-	34,37,41,42	0
2	NAG	I	1	14/15	-	-	23,26,31,32	0
2	NAG	I	2	14/15	-	-	25,27,30,31	0
2	BMA	I	3	11/12	-	-	19,21,23,23	0
2	MAN	I	4	11/12	-	-	20,22,29,38	0
2	MAN	I	5	11/12	-	-	24,25,36,41	0
2	MAN	I	6	11/12	-	-	26,33,39,40	0
2	MAN	I	7	11/12	-	-	20,22,25,27	0
2	MAN	I	8	11/12	-	-	21,23,28,32	0
2	MAN	I	9	11/12	-	-	23,25,26,26	0
2	MAN	I	10	11/12	-	-	29,32,40,56	0
2	NAG	C	1	14/15	0.95	0.08	24,27,33,43	0
2	NAG	C	2	14/15	0.96	0.06	25,28,35,35	0
3	NAG	E	1	14/15	0.96	0.07	37,41,50,54	0
2	MAN	C	7	11/12	0.97	0.05	21,23,25,25	0
2	MAN	C	10	11/12	0.97	0.06	22,27,29,30	0
3	BMA	E	3	11/12	0.97	0.05	41,58,69,77	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.

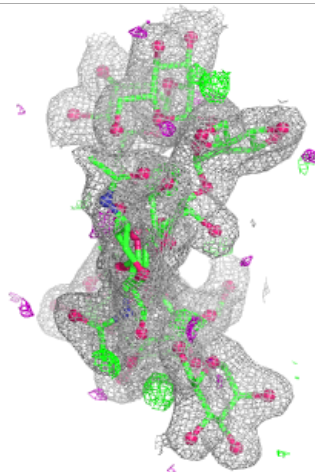
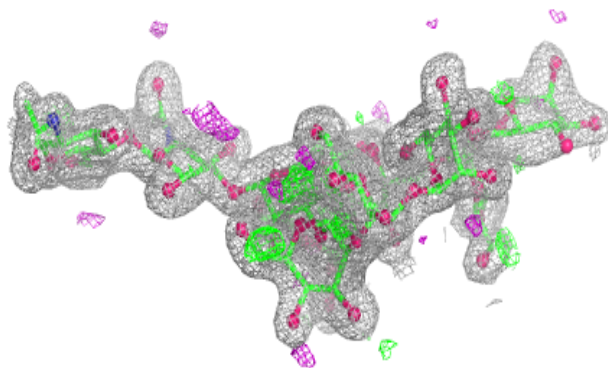
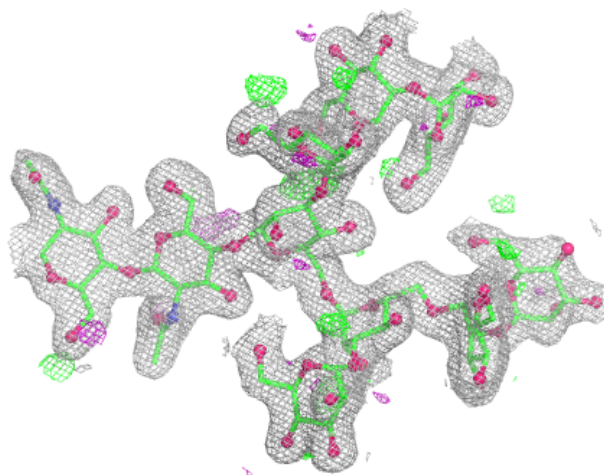
Electron density around Chain C:

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



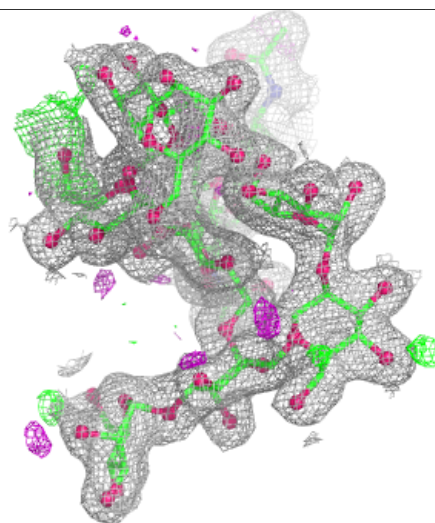
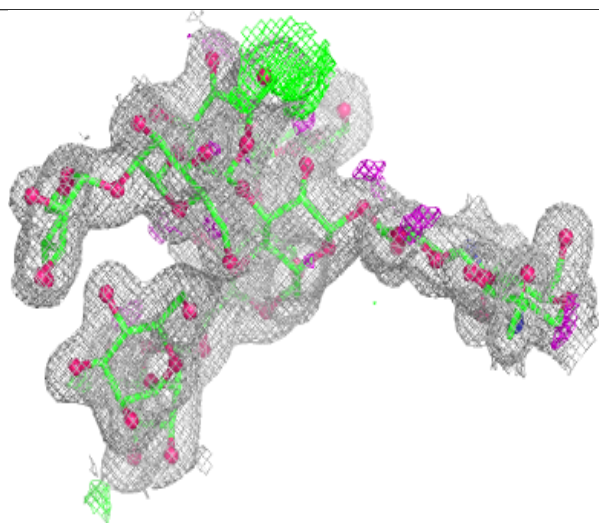
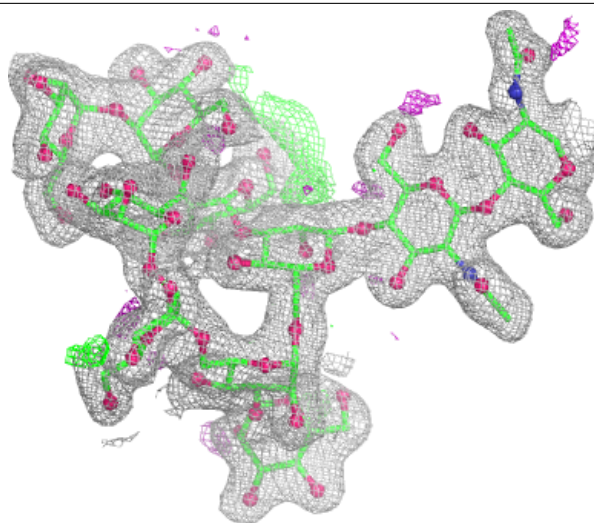
Electron density around Chain G:

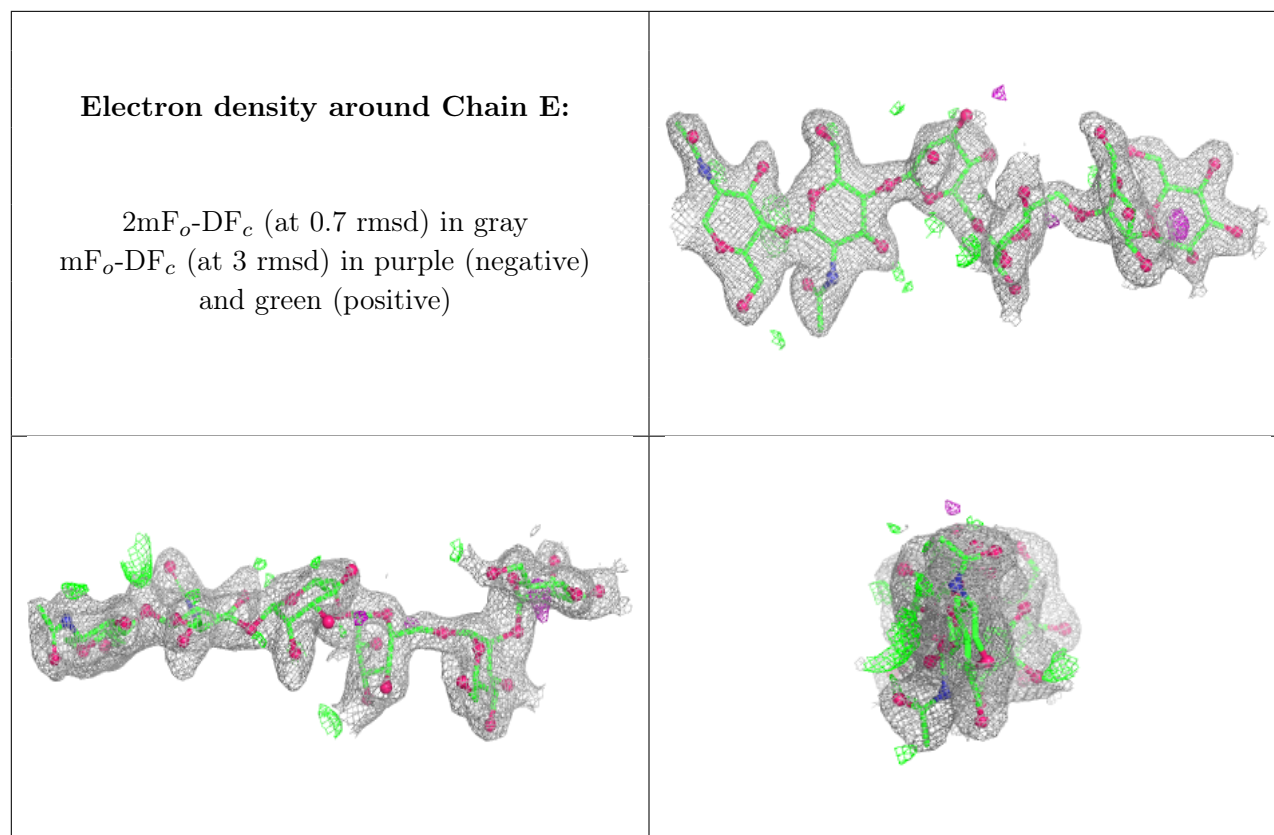
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.4 Ligands ⓘ

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
5	NAG	B	612	14/15	0.81	0.14	51,63,77,85	0
9	P6G	B	602	19/19	0.81	0.23	36,55,80,82	0
5	NAG	B	611	14/15	0.82	0.13	43,50,57,57	0
6	EDO	B	613	4/4	0.83	0.16	53,54,57,62	0
8	PG4	B	601	13/13	0.83	0.19	32,48,53,59	0
5	NAG	A	602	14/15	0.83	0.12	40,49,55,58	0
6	EDO	B	608	4/4	0.85	0.15	52,53,57,58	0
6	EDO	B	610	4/4	0.86	0.14	58,60,61,62	0
6	EDO	A	606	4/4	0.87	0.16	39,51,54,59	0
6	EDO	A	603	4/4	0.87	0.14	49,54,55,55	0
6	EDO	A	604	4/4	0.87	0.16	58,62,65,68	0
6	EDO	B	605	4/4	0.89	0.15	43,61,62,63	0
10	PEG	B	609	7/7	0.89	0.14	51,53,55,61	0
6	EDO	B	606	4/4	0.90	0.14	40,43,53,61	0

Continued on next page...

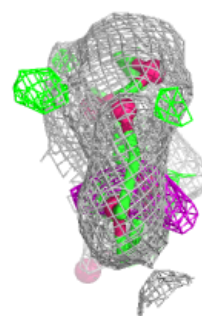
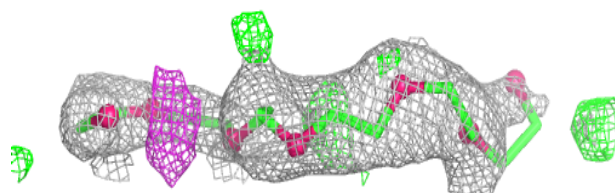
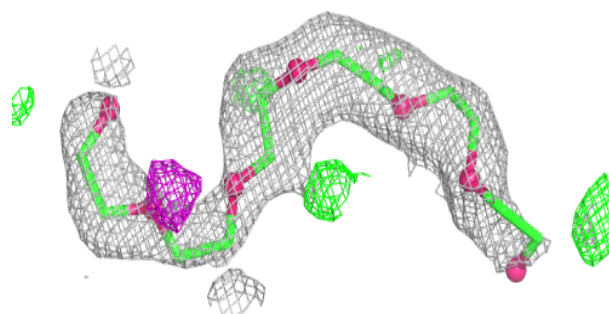
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	B	607	4/4	0.90	0.14	44,45,47,47	0
5	NAG	B	603	14/15	0.91	0.10	26,34,39,42	0
6	EDO	A	605	4/4	0.92	0.12	41,42,45,46	0
4	HC4	B	604	12/12	0.95	0.06	20,21,26,27	0
4	HC4	A	601	12/12	0.96	0.07	22,24,29,33	0
7	CA	B	614	1/1	0.99	0.02	26,26,26,26	0
7	CA	A	607	1/1	0.99	0.03	26,26,26,26	0

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.

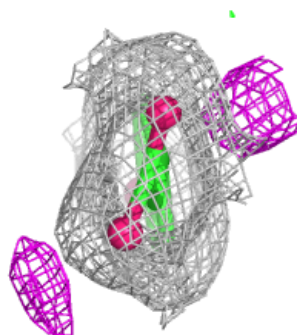
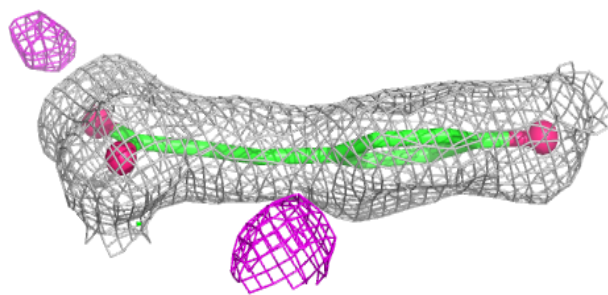
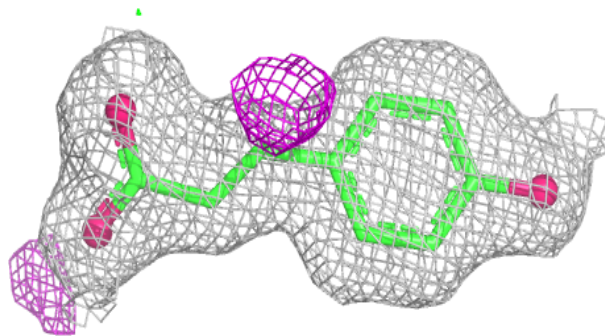
Electron density around P6G B 602:

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

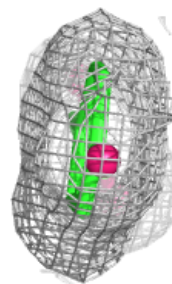
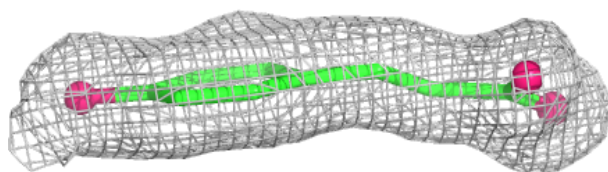
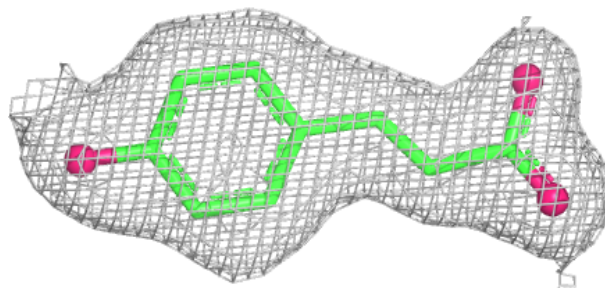


Electron density around HC4 B 604:

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

**Electron density around HC4 A 601:**

$2mF_o-DF_c$ (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.