



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:56 AM UTC

PDB ID : 2CML / pdb_00002cml
Title : Structure of Neuraminidase from English Duck Subtype N6 Complexed with 30 MM ZANAMIVIR, Crystal Soaked for 3 Hours at 291 K.
Authors : Rudino-Pinera, E.; Tunnah, P.; Lukacik, P.; Crennell, S.J.; Webster, R.G.; Laver, W.G.; Garman, E.F.
Deposited on : 2006-05-10
Resolution : 2.15 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)
Xtrriage (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

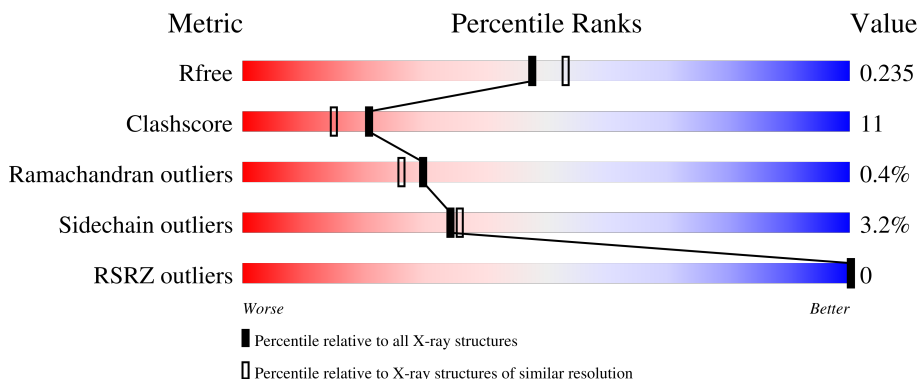
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	389	80% 18% ..
1	B	389	81% 15% ..
1	C	389	82% 16% .
1	D	389	83% 14% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	2	 50% 50%
2	H	2	 100%
2	I	2	 100%
3	F	3	 100%
4	G	5	 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	E	1	X	-	-	-
2	NAG	E	2	X	-	-	-
2	NAG	H	1	X	-	-	-
2	NAG	H	2	X	-	-	-
2	NAG	I	1	X	-	-	-
2	NAG	I	2	X	-	-	-
4	NAG	G	1	X	-	-	-
4	NAG	G	2	X	-	-	-
5	ZMR	A	1477	X	-	-	-
5	ZMR	A	1478	X	-	-	-
5	ZMR	B	2477	X	-	-	-
5	ZMR	B	2478	X	-	-	-
5	ZMR	C	3477	X	-	-	-
5	ZMR	C	3478	X	-	-	-
5	ZMR	D	4477	X	-	-	-
5	ZMR	D	4478	X	-	-	-
7	NAG	A	1482	X	-	-	-
7	NAG	A	1483	X	-	-	-
7	NAG	B	2480	X	-	-	-
7	NAG	B	2481	X	-	-	-
7	NAG	B	2482	X	-	-	-
7	NAG	B	2483	X	-	-	-
7	NAG	C	3486	X	-	-	-
7	NAG	C	3487	X	-	-	-
7	NAG	C	3488	X	-	-	-
7	NAG	D	4482	X	-	X	-
7	NAG	D	4483	X	-	-	-
9	MAN	B	2484	-	-	X	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	MAN	C	3490	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 13060 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 NEURAMINIDASE.

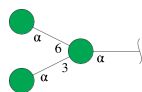
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	389	Total 3008	C 1875	N 535	O 571	S 27	0	0	0
1	B	389	Total 3008	C 1875	N 535	O 571	S 27	0	0	0
1	C	389	Total 3008	C 1875	N 535	O 571	S 27	0	0	0
1	D	389	Total 3009	C 1875	N 535	O 572	S 27	0	0	0

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



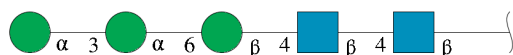
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	2	Total 28	C 16	N 2	O 10	0	0	0
2	H	2	Total 28	C 16	N 2	O 10	0	0	0
2	I	2	Total 28	C 16	N 2	O 10	0	0	0

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



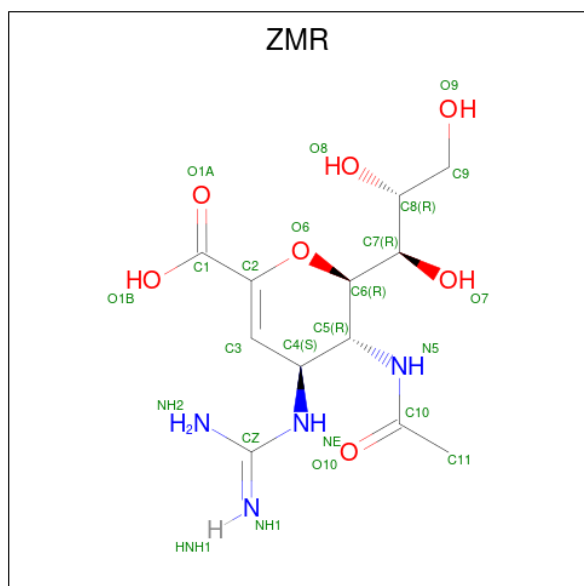
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	F	3	Total	C	O	0	0	0
			33	18	15			

- Molecule 4 is an oligosaccharide called 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
4	G	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 5 is ZANAMIVIR (CCD ID: ZMR) (formula: $C_{12}H_{20}N_4O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			23	12	4	7		
5	A	1	Total	C	N	O	0	0
			23	12	4	7		
5	B	1	Total	C	N	O	0	0
			23	12	4	7		
5	B	1	Total	C	N	O	0	0
			23	12	4	7		

Continued on next page...

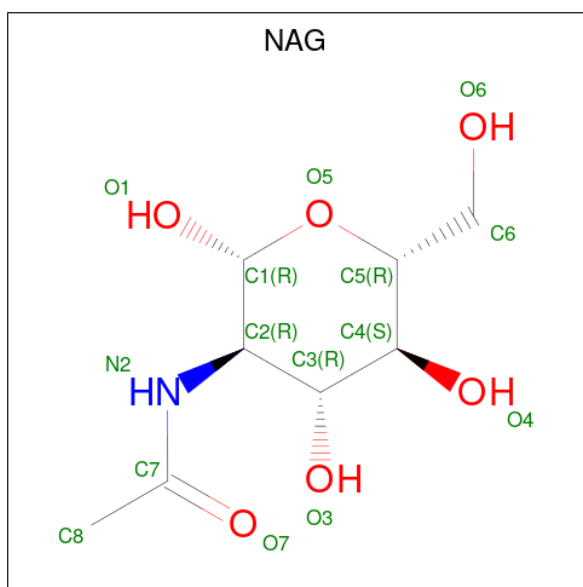
Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			23	12	4	7		
5	C	1	Total	C	N	O	0	0
			23	12	4	7		
5	D	1	Total	C	N	O	0	0
			23	12	4	7		
5	D	1	Total	C	N	O	0	0
			23	12	4	7		

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



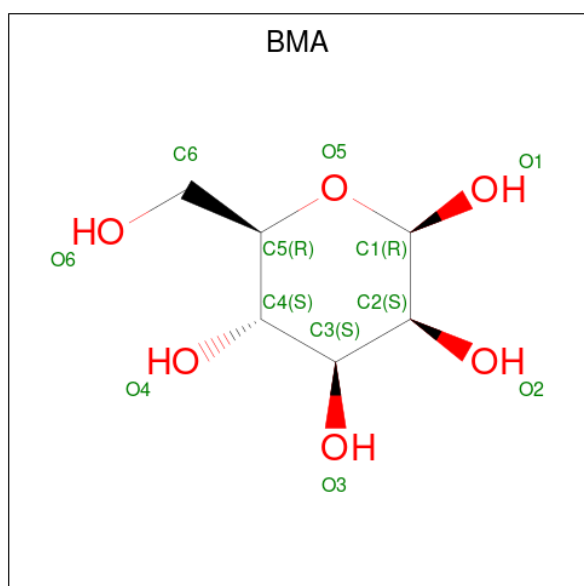
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

Continued from previous page...

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

- Molecule 8 is beta-D-mannopyranose (CCD ID: BMA) (formula: C₆H₁₂O₆).



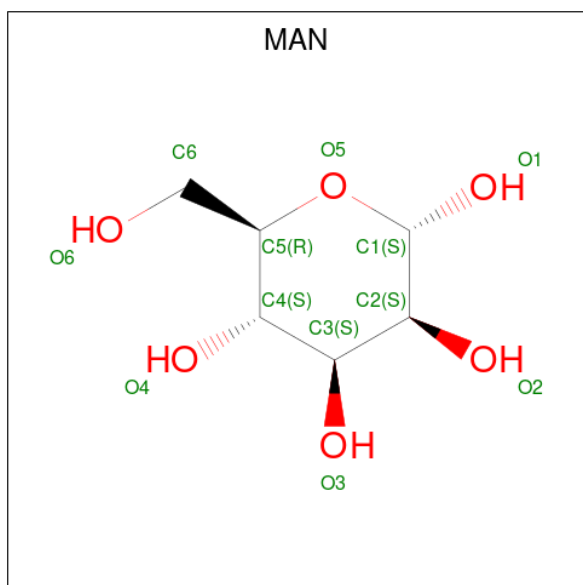
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	A	1	Total 11	C 6	O 5	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	1	Total C O 11 6 5	0	0
8	D	1	Total C O 11 6 5	0	0

- Molecule 9 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C O 11 6 5	0	0
9	B	1	Total C O 11 6 5	0	0
9	B	1	Total C O 11 6 5	0	0
9	C	1	Total C O 11 6 5	0	0
9	C	1	Total C O 11 6 5	0	0
9	C	1	Total C O 11 6 5	0	0
9	D	1	Total C O 11 6 5	0	0
9	D	1	Total C O 11 6 5	0	0


- Molecule 10 is water.

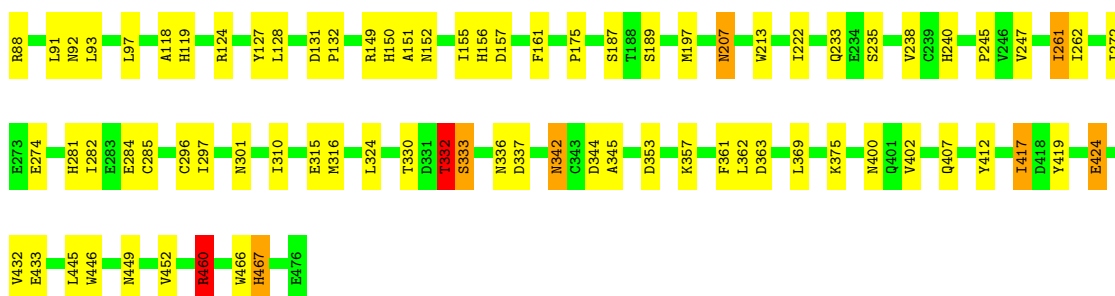
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	103	Total 103	O 103	0	0
10	B	109	Total 109	O 109	0	0
10	C	96	Total 96	O 96	0	0
10	D	78	Total 78	O 78	0	0

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.

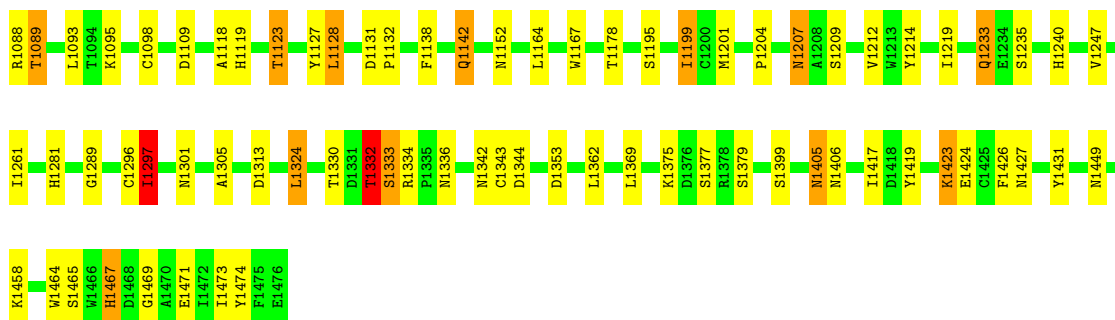
• Molecule 1: NEURAMINIDASE

Chain A: 




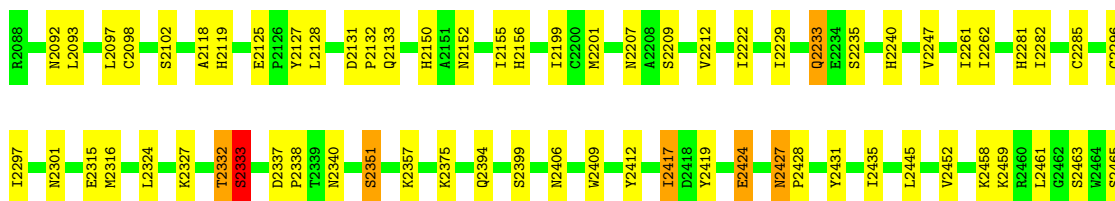
• Molecule 1: NEURAMINIDASE

Chain B: 



• Molecule 1: NEURAMINIDASE

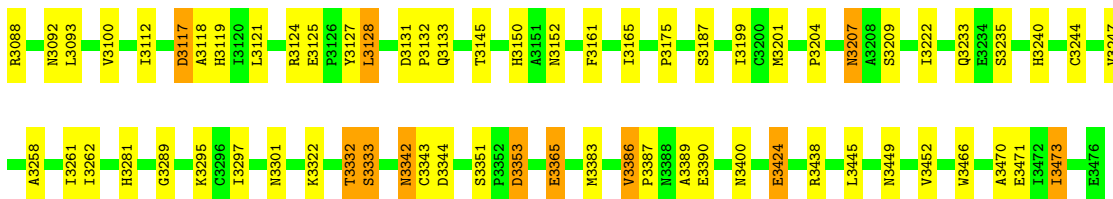
Chain C: 





- Molecule 1: NEURAMINIDASE

Chain D: 83% 14%



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

Chain E: 50% 50%



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

Chain H: 100%



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

Chain I: 100%



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

Chain F: 100%



- Molecule 4: 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%

MAC1
MAC2
BMA3
MAN4
MAN5

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	106.24Å 73.69Å 106.68Å 90.00° 90.29° 90.00°	Depositor
Resolution (Å)	30.70 – 2.15 30.70 – 2.15	Depositor EDS
% Data completeness (in resolution range)	90.3 (30.70-2.15) 90.2 (30.70-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.16Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.180 , 0.232 0.186 , 0.235	Depositor DCC
R_{free} test set	4038 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	15.1	Xtrriage
Anisotropy	0.217	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 34.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.017 for l,k,-h 0.025 for h,-k,-l 0.021 for l,-k,h	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13060	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% 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: ZMR, NAG, MAN, CA, BMA

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	1.24	5/3083 (0.2%)	1.17	12/4185 (0.3%)
1	B	1.24	3/3083 (0.1%)	1.16	12/4185 (0.3%)
1	C	1.27	5/3083 (0.2%)	1.14	8/4185 (0.2%)
1	D	1.29	8/3084 (0.3%)	1.20	9/4185 (0.2%)
All	All	1.26	21/12333 (0.2%)	1.17	41/16740 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	3222	ILE	CA-CB	9.25	1.61	1.54
1	C	2222	ILE	CA-CB	8.78	1.60	1.54
1	D	3125	GLU	CA-C	8.19	1.58	1.53
1	D	3258	ALA	CA-CB	7.02	1.62	1.53
1	B	1123	THR	CA-CB	6.70	1.64	1.53

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2118	ALA	N-CA-C	-8.13	98.49	110.52
1	C	2233	GLN	N-CA-C	7.73	120.79	111.82
1	D	3118	ALA	CA-C-N	-7.38	112.01	122.41
1	D	3118	ALA	C-N-CA	-7.38	112.01	122.41
1	A	118	ALA	CA-C-N	-7.19	111.94	123.23

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	332	THR	Peptide
1	B	1332	THR	Peptide
1	C	2332	THR	Peptide
1	D	3332	THR	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	3008	0	2888	58	0
1	B	3008	0	2888	63	0
1	C	3008	0	2888	66	0
1	D	3009	0	2888	55	0
2	E	28	0	22	6	0
2	H	28	0	22	7	0
2	I	28	0	22	8	0
3	F	33	0	30	8	0
4	G	61	0	51	14	0
5	A	46	0	30	1	0
5	B	46	0	30	0	0
5	C	46	0	30	3	0
5	D	46	0	30	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	28	0	22	5	0
7	B	56	0	44	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	42	0	33	11	0
7	D	28	0	22	9	0
8	A	11	0	10	3	0
8	C	11	0	10	2	0
8	D	11	0	10	4	0
9	B	33	0	30	7	0
9	C	33	0	30	8	0
9	D	22	0	20	1	0
10	A	103	0	0	0	0
10	B	109	0	0	1	0
10	C	96	0	0	2	0
10	D	78	0	0	1	0
All	All	13060	0	12050	259	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 11.

The worst 5 of 259 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3152:ASN:HD21	7:D:4483:NAG:C1	1.01	1.60
1:A:152:ASN:HD21	7:A:1482:NAG:C1	0.98	1.59
1:C:2152:ASN:HD21	7:C:3487:NAG:C1	1.15	1.59
1:A:207:ASN:HD21	4:G:1:NAG:C1	0.97	1.57
1:A:92:ASN:HD21	2:E:1:NAG:C1	1.10	1.56

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	387/389 (100%)	365 (94%)	20 (5%)	2 (0%)	24	20
1	B	387/389 (100%)	368 (95%)	18 (5%)	1 (0%)	36	34
1	C	387/389 (100%)	370 (96%)	16 (4%)	1 (0%)	36	34
1	D	387/389 (100%)	373 (96%)	12 (3%)	2 (0%)	24	20
All	All	1548/1556 (100%)	1476 (95%)	66 (4%)	6 (0%)	30	26

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	333	SER
1	C	2333	SER
1	D	3333	SER
1	A	207	ASN
1	D	3207	ASN

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	331/331 (100%)	321 (97%)	10 (3%)	36	38
1	B	331/331 (100%)	319 (96%)	12 (4%)	31	31
1	C	331/331 (100%)	321 (97%)	10 (3%)	36	38
1	D	331/331 (100%)	321 (97%)	10 (3%)	36	38
All	All	1324/1324 (100%)	1282 (97%)	42 (3%)	34	36

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2351	SER
1	D	3342	ASN
1	C	2424	GLU
1	D	3128	LEU
1	D	3365	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1406	ASN
1	D	3427	ASN
1	C	2152	ASN
1	D	3422	ASN
1	D	3207	ASN

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](#)

14 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	E	1	2,1	14,14,15	2.32	1 (7%)	17,19,21	2.64	7 (41%)
2	NAG	E	2	2	14,14,15	2.12	1 (7%)	17,19,21	2.35	6 (35%)
3	MAN	F	1	3	11,11,12	0.77	0	15,15,17	1.83	6 (40%)
3	MAN	F	2	3	11,11,12	0.66	0	15,15,17	1.75	2 (13%)
3	MAN	F	3	3	11,11,12	0.78	0	15,15,17	1.59	4 (26%)
4	NAG	G	1	4,1	14,14,15	2.38	1 (7%)	17,19,21	3.26	9 (52%)
4	NAG	G	2	4	14,14,15	2.57	1 (7%)	17,19,21	2.87	9 (52%)
4	BMA	G	3	4	11,11,12	0.57	0	15,15,17	1.43	2 (13%)
4	MAN	G	4	4	11,11,12	0.49	0	15,15,17	1.74	2 (13%)
4	MAN	G	5	4	11,11,12	1.08	1 (9%)	15,15,17	2.09	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	H	1	2,1	14,14,15	2.58	2 (14%)	17,19,21	3.12	4 (23%)
2	NAG	H	2	2	14,14,15	2.22	1 (7%)	17,19,21	2.46	6 (35%)
2	NAG	I	1	2	14,14,15	2.28	1 (7%)	17,19,21	3.77	9 (52%)
2	NAG	I	2	2	14,14,15	2.09	1 (7%)	17,19,21	2.68	7 (41%)

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	E	1	2,1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	E	2	2	1/1/5/7	0/6/23/26	0/1/1/1
3	MAN	F	1	3	-	0/2/19/22	0/1/1/1
3	MAN	F	2	3	-	0/2/19/22	0/1/1/1
3	MAN	F	3	3	-	2/2/19/22	0/1/1/1
4	NAG	G	1	4,1	1/1/5/7	2/6/23/26	0/1/1/1
4	NAG	G	2	4	1/1/5/7	1/6/23/26	0/1/1/1
4	BMA	G	3	4	-	2/2/19/22	0/1/1/1
4	MAN	G	4	4	-	0/2/19/22	0/1/1/1
4	MAN	G	5	4	-	1/2/19/22	0/1/1/1
2	NAG	H	1	2,1	1/1/5/7	1/6/23/26	0/1/1/1
2	NAG	H	2	2	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	I	1	2	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	I	2	2	1/1/5/7	4/6/23/26	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)
4	G	2	NAG	O4-C4	-9.33	1.19	1.43
2	H	1	NAG	O4-C4	-9.17	1.20	1.43
4	G	1	NAG	O4-C4	-8.75	1.21	1.43
2	E	1	NAG	O4-C4	-8.42	1.22	1.43
2	H	2	NAG	O4-C4	-8.13	1.22	1.43

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	1	NAG	C1-O5-C5	-9.27	99.76	112.19
4	G	1	NAG	C1-O5-C5	-8.11	101.31	112.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	NAG	C3-C4-C5	8.00	124.74	110.23
2	H	1	NAG	C2-N2-C7	-7.56	112.76	122.90
4	G	2	NAG	C3-C4-C5	7.48	123.79	110.23

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	1	NAG	C4
2	E	2	NAG	C4
2	H	1	NAG	C4
2	H	2	NAG	C4
2	I	1	NAG	C4

5 of 17 torsion outliers are listed below:

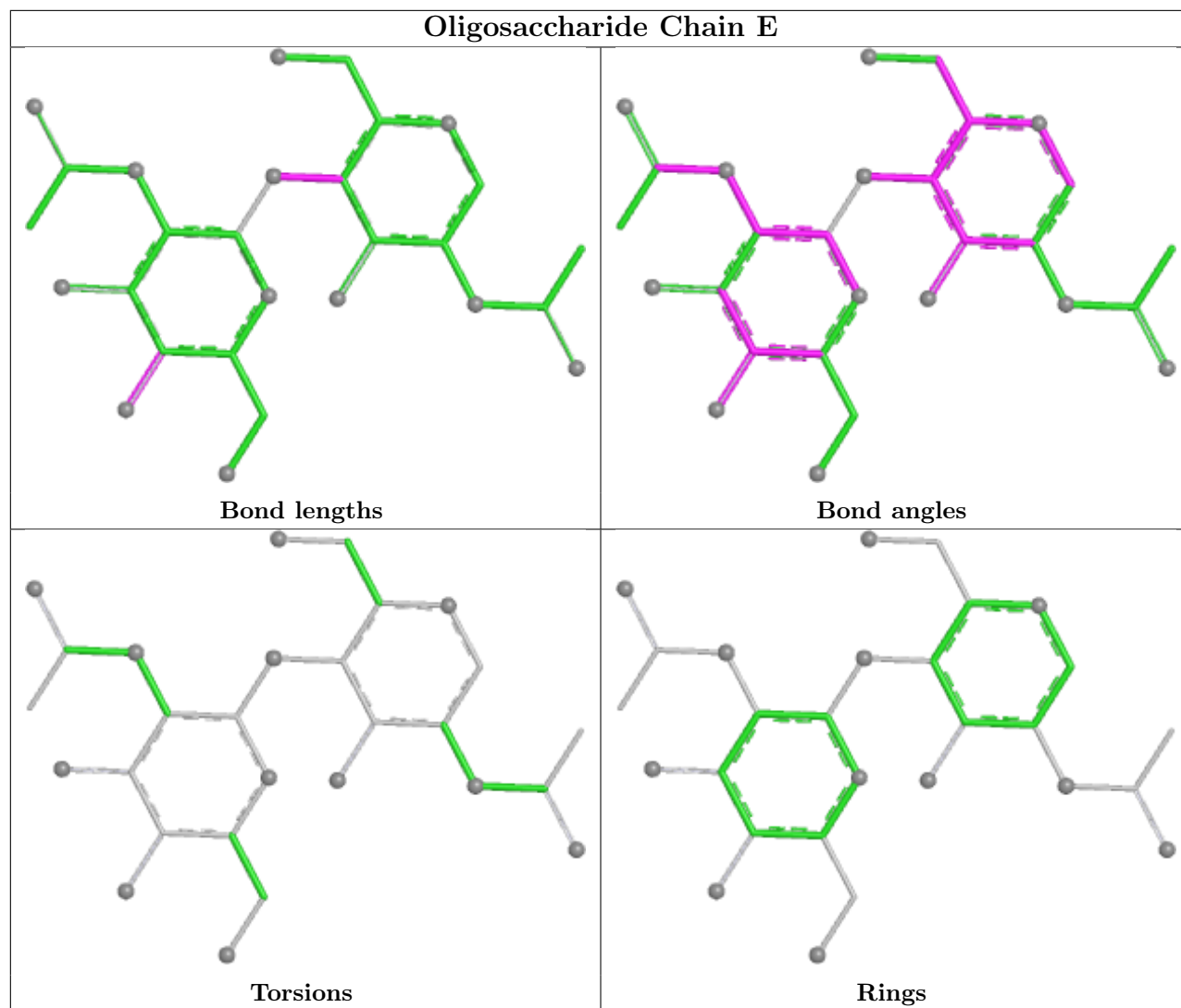
Mol	Chain	Res	Type	Atoms
4	G	1	NAG	O5-C5-C6-O6
3	F	3	MAN	O5-C5-C6-O6
2	I	2	NAG	C4-C5-C6-O6
4	G	3	BMA	O5-C5-C6-O6
4	G	1	NAG	C4-C5-C6-O6

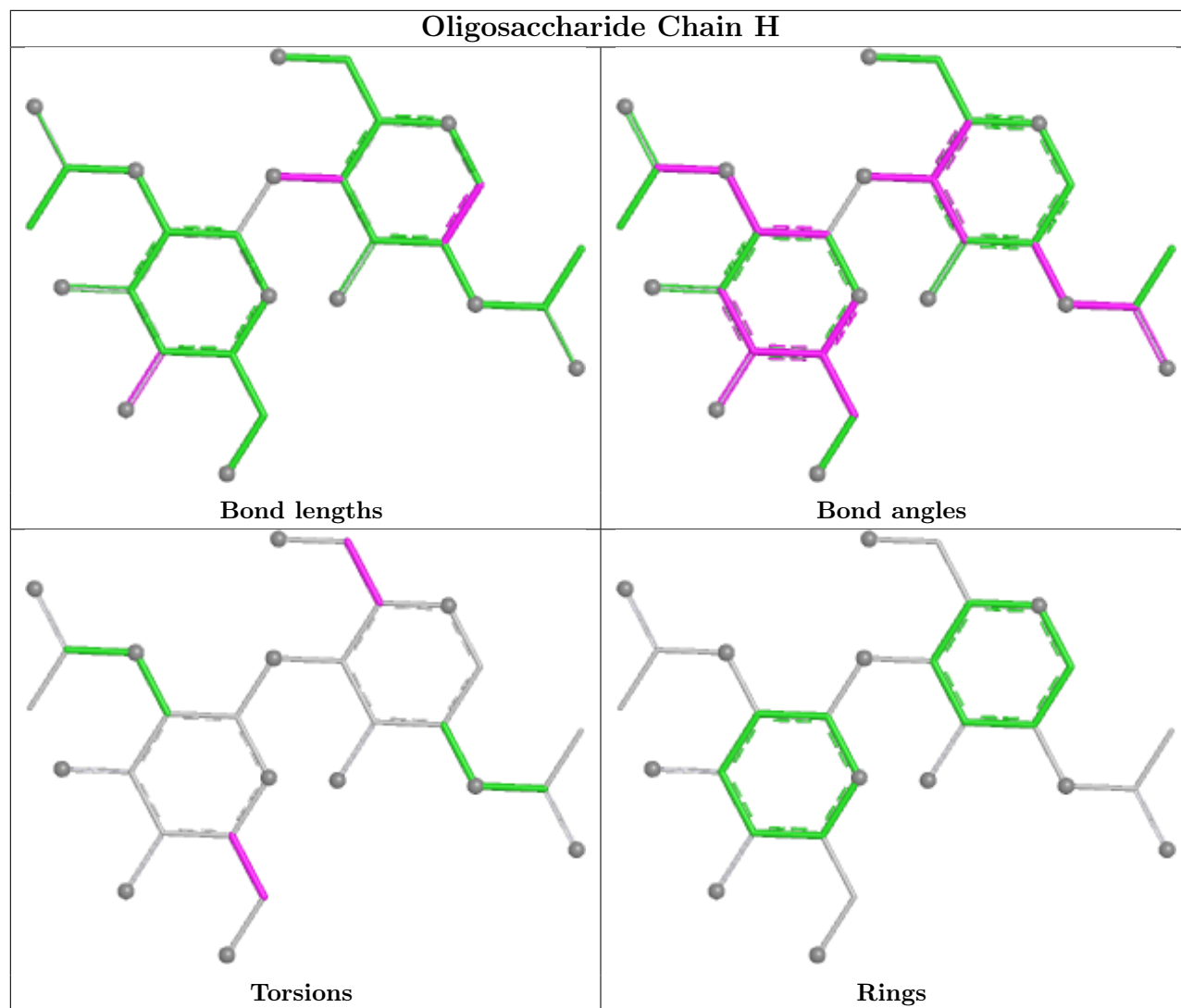
There are no ring outliers.

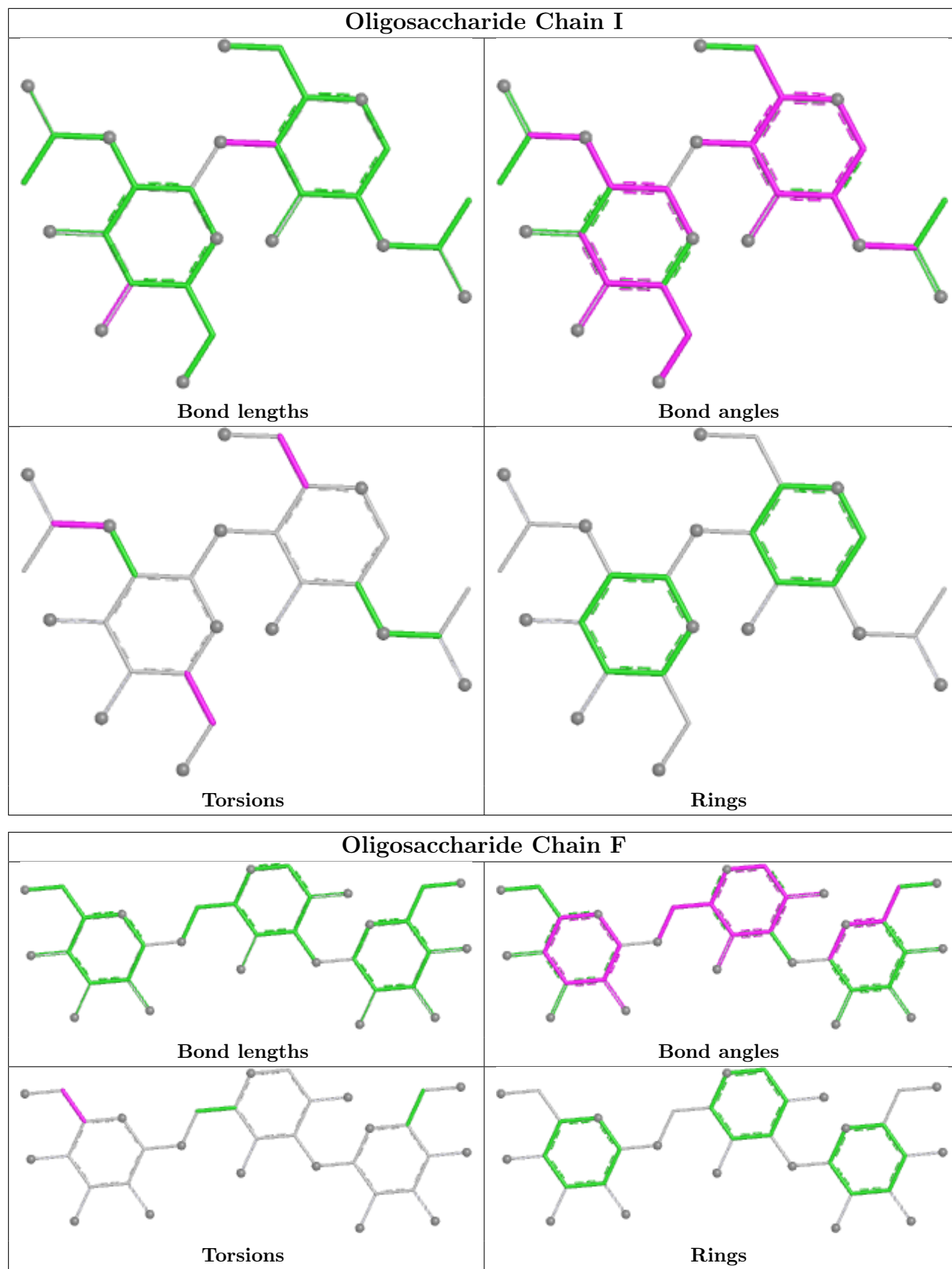
13 monomers are involved in 43 short contacts:

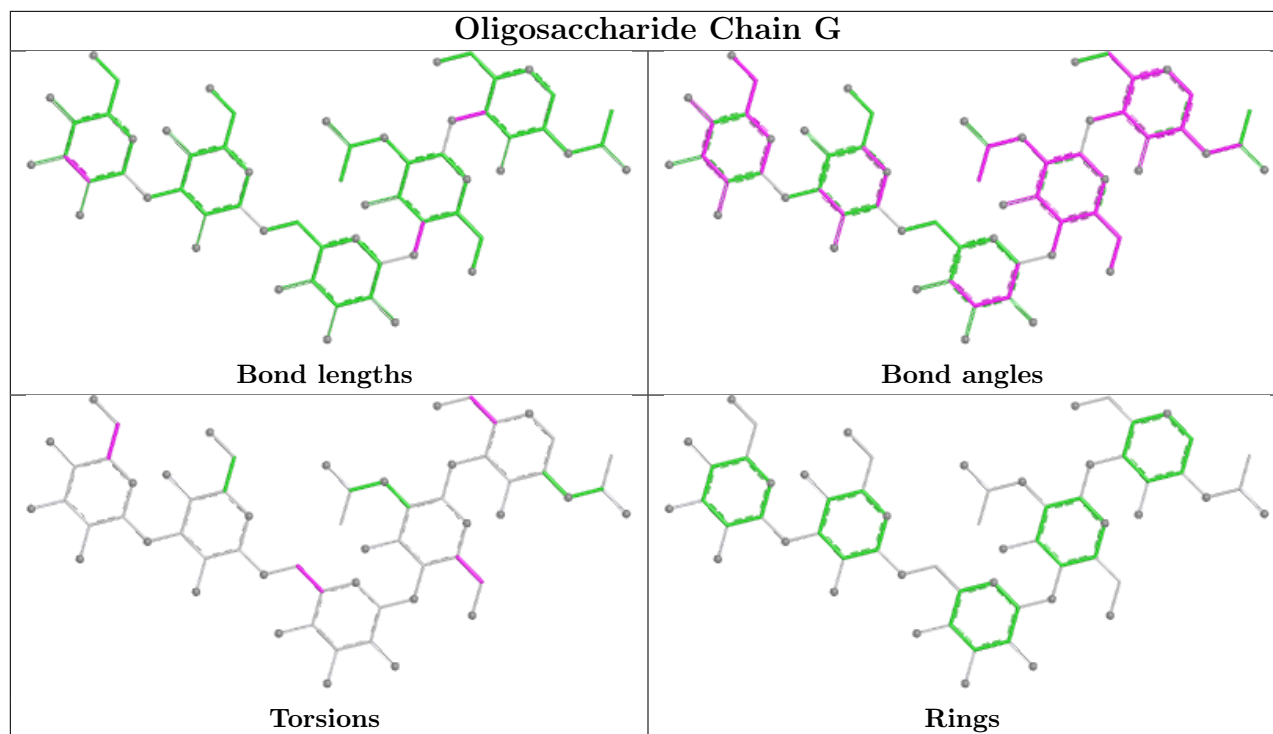
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	6	0
4	G	1	NAG	4	0
2	H	1	NAG	6	0
2	I	1	NAG	6	0
4	G	3	BMA	4	0
4	G	2	NAG	3	0
4	G	5	MAN	3	0
2	I	2	NAG	4	0
2	H	2	NAG	2	0
4	G	4	MAN	5	0
3	F	3	MAN	3	0
3	F	2	MAN	3	0
3	F	1	MAN	5	0

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









5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 4 are monoatomic - leaving 30 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
7	NAG	B	2481	-	14,14,15	2.23	1 (7%)	17,19,21	2.25	4 (23%)
7	NAG	D	4483	1	14,14,15	1.69	1 (7%)	17,19,21	2.36	4 (23%)
5	ZMR	B	2477	-	22,23,23	2.90	7 (31%)	24,32,32	2.89	8 (33%)
8	BMA	D	4486	-	11,11,12	0.48	0	15,15,17	1.88	4 (26%)
7	NAG	C	3488	-	14,14,15	2.15	1 (7%)	17,19,21	2.39	7 (41%)
7	NAG	B	2480	1	14,14,15	2.20	1 (7%)	17,19,21	2.47	6 (35%)
9	MAN	B	2486	-	11,11,12	0.96	0	15,15,17	1.84	4 (26%)
5	ZMR	A	1478	-	22,23,23	3.13	4 (18%)	24,32,32	3.28	10 (41%)
9	MAN	D	4480	-	11,11,12	1.07	1 (9%)	15,15,17	2.69	9 (60%)
5	ZMR	C	3477	-	22,23,23	3.09	7 (31%)	24,32,32	2.89	11 (45%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	A	1482	1	14,14,15	2.33	1 (7%)	17,19,21	2.22	3 (17%)
9	MAN	B	2484	-	11,11,12	0.78	0	15,15,17	2.13	3 (20%)
7	NAG	B	2482	-	14,14,15	2.36	1 (7%)	17,19,21	2.81	6 (35%)
5	ZMR	B	2478	-	22,23,23	3.16	4 (18%)	24,32,32	3.29	13 (54%)
7	NAG	A	1483	-	14,14,15	2.08	1 (7%)	17,19,21	2.55	7 (41%)
5	ZMR	C	3478	-	22,23,23	3.08	4 (18%)	24,32,32	2.76	10 (41%)
5	ZMR	D	4477	-	22,23,23	3.25	4 (18%)	24,32,32	2.62	8 (33%)
8	BMA	A	1709	-	11,11,12	0.89	0	15,15,17	2.02	5 (33%)
7	NAG	B	2483	-	14,14,15	2.35	1 (7%)	17,19,21	2.55	5 (29%)
9	MAN	C	3492	-	11,11,12	0.76	0	15,15,17	1.58	1 (6%)
7	NAG	C	3486	-	14,14,15	2.05	1 (7%)	17,19,21	2.55	4 (23%)
7	NAG	C	3487	1	14,14,15	2.20	1 (7%)	17,19,21	2.32	6 (35%)
9	MAN	C	3490	-	11,11,12	0.71	0	15,15,17	2.04	3 (20%)
8	BMA	C	3493	-	11,11,12	0.94	0	15,15,17	1.59	3 (20%)
7	NAG	D	4482	-	14,14,15	2.31	2 (14%)	17,19,21	2.60	5 (29%)
9	MAN	B	2485	-	11,11,12	0.90	0	15,15,17	1.82	5 (33%)
9	MAN	C	3484	-	11,11,12	0.64	0	15,15,17	1.82	4 (26%)
5	ZMR	A	1477	-	22,23,23	3.10	4 (18%)	24,32,32	2.72	10 (41%)
5	ZMR	D	4478	-	22,23,23	3.02	4 (18%)	24,32,32	3.04	11 (45%)
9	MAN	D	4481	-	11,11,12	0.84	0	15,15,17	1.42	2 (13%)

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
7	NAG	B	2481	-	1/1/5/7	2/6/23/26	0/1/1/1
7	NAG	D	4483	1	1/1/5/7	2/6/23/26	0/1/1/1
5	ZMR	B	2477	-	2/2/9/12	6/22/38/38	0/1/1/1
8	BMA	D	4486	-	-	2/2/19/22	0/1/1/1
7	NAG	C	3488	-	1/1/5/7	4/6/23/26	0/1/1/1
7	NAG	B	2480	1	1/1/5/7	2/6/23/26	0/1/1/1
9	MAN	B	2486	-	-	0/2/19/22	0/1/1/1
5	ZMR	A	1478	-	2/2/9/12	11/22/38/38	0/1/1/1
9	MAN	D	4480	-	-	1/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ZMR	C	3477	-	2/2/9/12	5/22/38/38	0/1/1/1
7	NAG	A	1482	1	1/1/5/7	2/6/23/26	0/1/1/1
9	MAN	B	2484	-	-	0/2/19/22	0/1/1/1
7	NAG	B	2482	-	1/1/5/7	2/6/23/26	0/1/1/1
5	ZMR	B	2478	-	2/2/9/12	7/22/38/38	0/1/1/1
7	NAG	A	1483	-	1/1/5/7	1/6/23/26	0/1/1/1
5	ZMR	C	3478	-	2/2/9/12	6/22/38/38	0/1/1/1
5	ZMR	D	4477	-	2/2/9/12	5/22/38/38	0/1/1/1
8	BMA	A	1709	-	-	2/2/19/22	0/1/1/1
7	NAG	B	2483	-	1/1/5/7	0/6/23/26	0/1/1/1
9	MAN	C	3492	-	-	2/2/19/22	0/1/1/1
7	NAG	C	3486	-	1/1/5/7	2/6/23/26	0/1/1/1
7	NAG	C	3487	1	1/1/5/7	0/6/23/26	0/1/1/1
9	MAN	C	3490	-	-	2/2/19/22	0/1/1/1
8	BMA	C	3493	-	-	2/2/19/22	0/1/1/1
7	NAG	D	4482	-	1/1/5/7	3/6/23/26	0/1/1/1
9	MAN	B	2485	-	-	2/2/19/22	0/1/1/1
9	MAN	C	3484	-	-	2/2/19/22	0/1/1/1
5	ZMR	A	1477	-	2/2/9/12	5/22/38/38	0/1/1/1
5	ZMR	D	4478	-	2/2/9/12	11/22/38/38	0/1/1/1
9	MAN	D	4481	-	-	2/2/19/22	0/1/1/1

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	4477	ZMR	C8-C7	-11.38	1.33	1.53
5	A	1478	ZMR	C8-C7	-10.63	1.34	1.53
5	B	2478	ZMR	C8-C7	-10.46	1.35	1.53
5	A	1477	ZMR	C8-C7	-10.35	1.35	1.53
5	C	3478	ZMR	C8-C7	-10.21	1.35	1.53

The worst 5 of 181 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	2483	NAG	C3-C4-C5	8.10	124.92	110.23
5	B	2478	ZMR	C8-C7-C6	7.14	126.48	113.05
5	B	2477	ZMR	O6-C6-C7	-7.04	93.60	105.98
7	B	2482	NAG	C1-C2-N2	-6.54	100.12	110.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1478	ZMR	O6-C2-C3	-6.48	117.36	124.62

5 of 27 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1477	ZMR	C7
5	A	1477	ZMR	C8
5	A	1478	ZMR	C7
5	A	1478	ZMR	C8
5	B	2477	ZMR	C7

5 of 93 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1477	ZMR	C6-C7-C8-O8
5	A	1477	ZMR	O7-C7-C8-C9
5	A	1477	ZMR	C7-C8-C9-O9
5	A	1478	ZMR	O1A-C1-C2-C3
5	A	1478	ZMR	O1A-C1-C2-O6

There are no ring outliers.

24 monomers are involved in 63 short contacts:

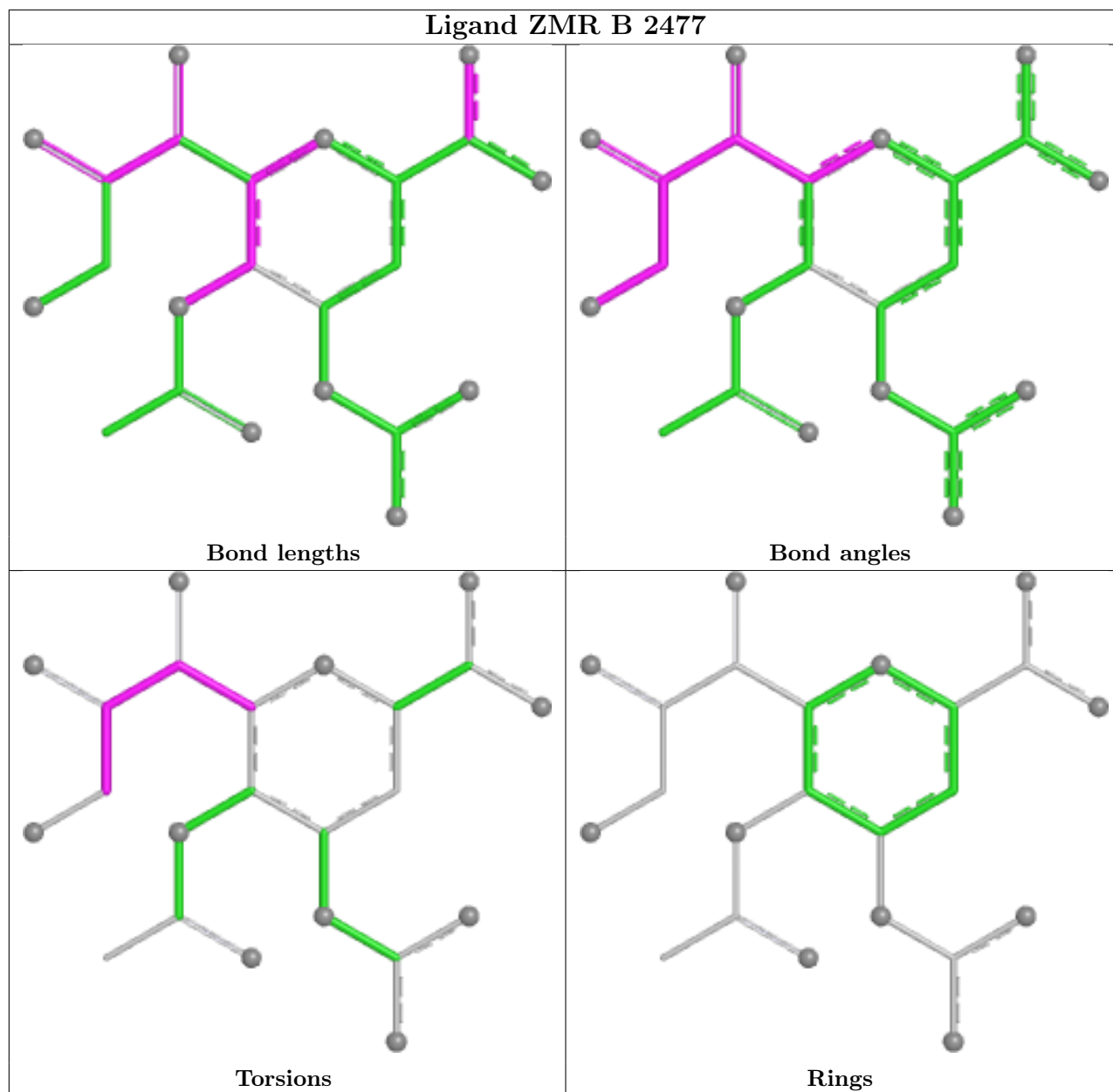
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	2481	NAG	2	0
7	D	4483	NAG	2	0
8	D	4486	BMA	4	0
7	C	3488	NAG	1	0
7	B	2480	NAG	5	0
9	B	2486	MAN	2	0
5	A	1478	ZMR	1	0
9	D	4480	MAN	1	0
5	C	3477	ZMR	1	0
7	A	1482	NAG	5	0
9	B	2484	MAN	7	0
7	B	2482	NAG	6	0
7	A	1483	NAG	1	0
5	C	3478	ZMR	2	0
8	A	1709	BMA	3	0
7	B	2483	NAG	2	0
9	C	3492	MAN	3	0
7	C	3486	NAG	5	0

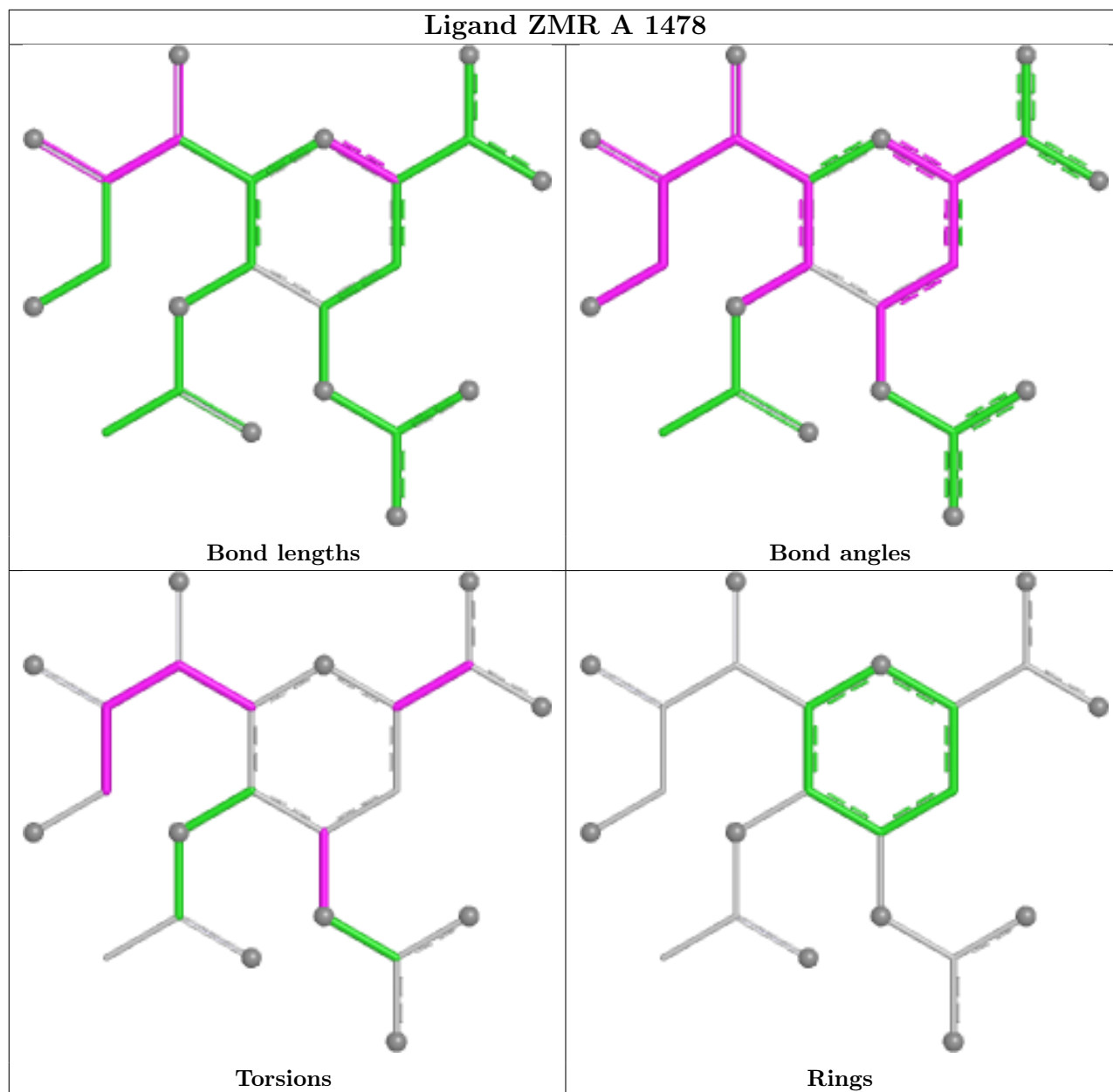
Continued on next page...

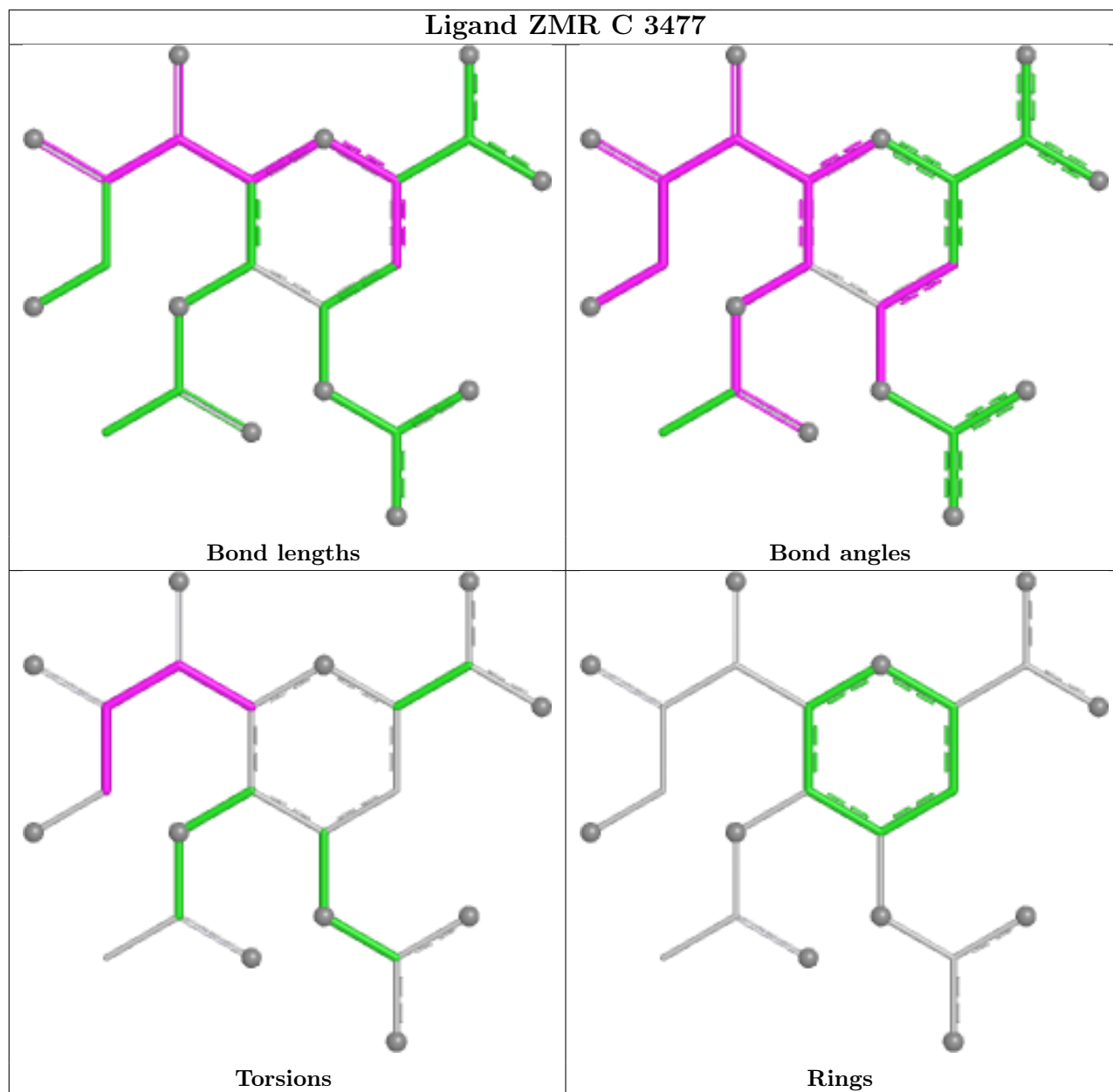
Continued from previous page...

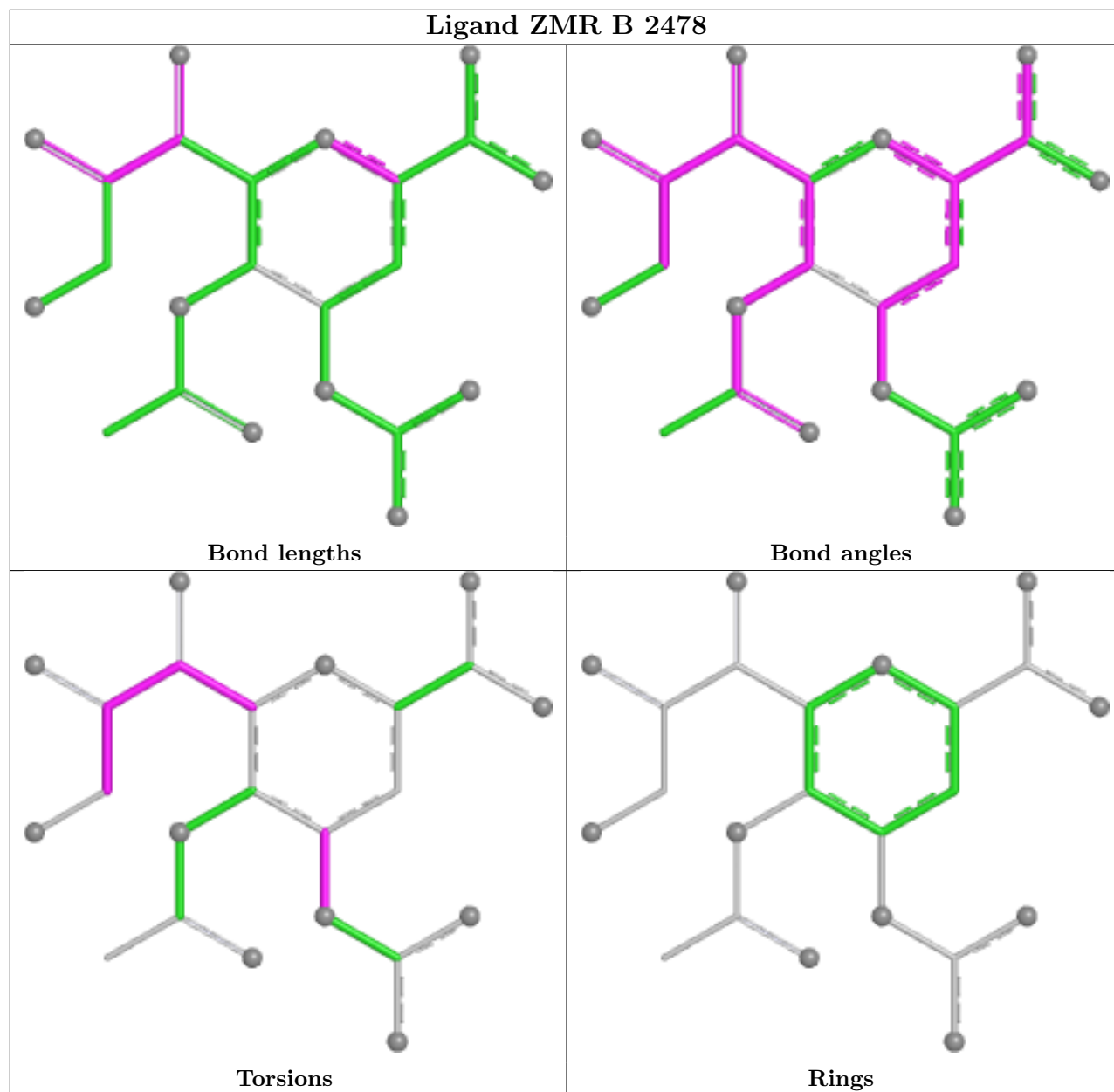
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	3487	NAG	6	0
9	C	3490	MAN	6	0
8	C	3493	BMA	2	0
7	D	4482	NAG	7	0
9	B	2485	MAN	4	0
9	C	3484	MAN	2	0

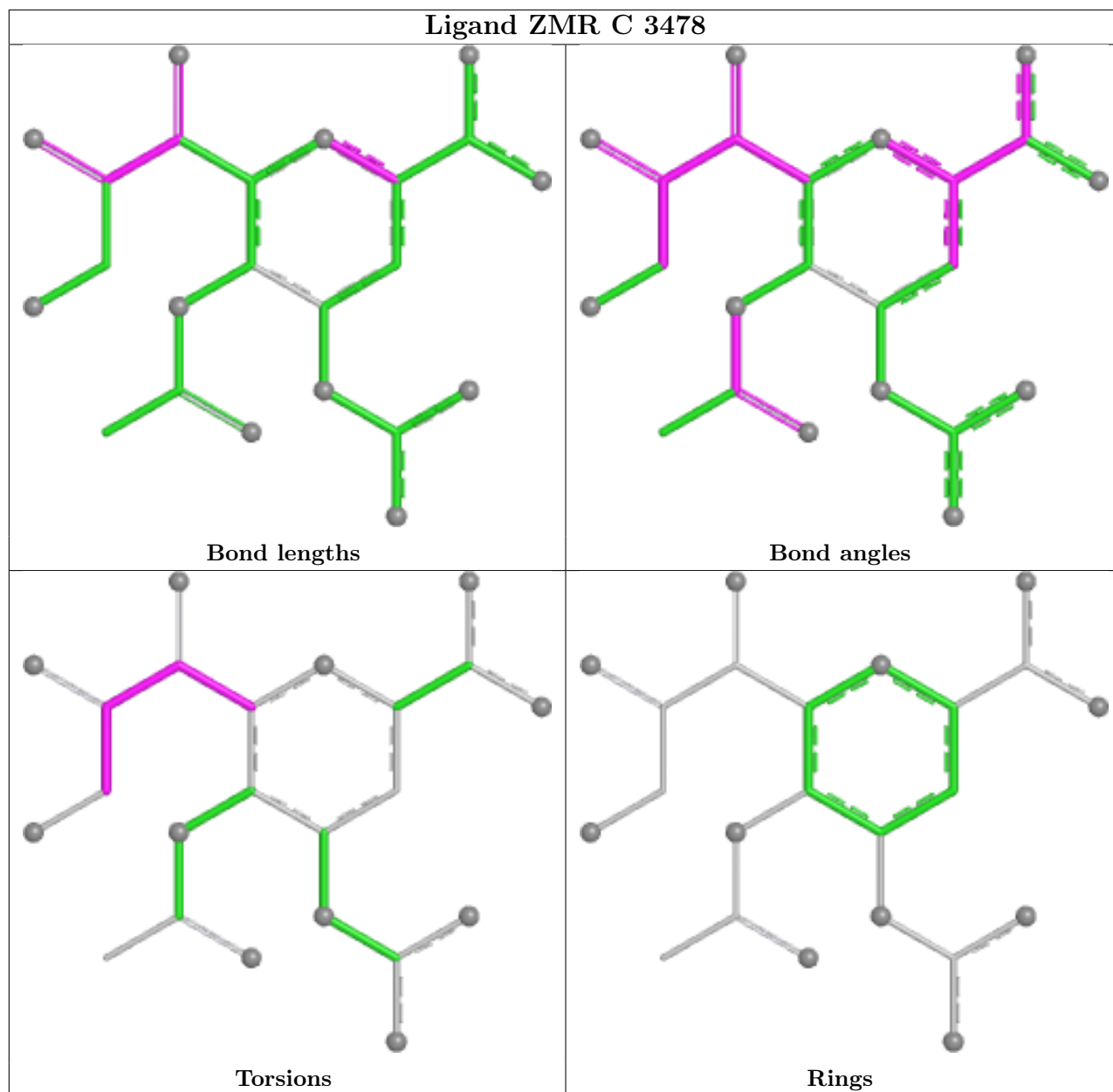
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

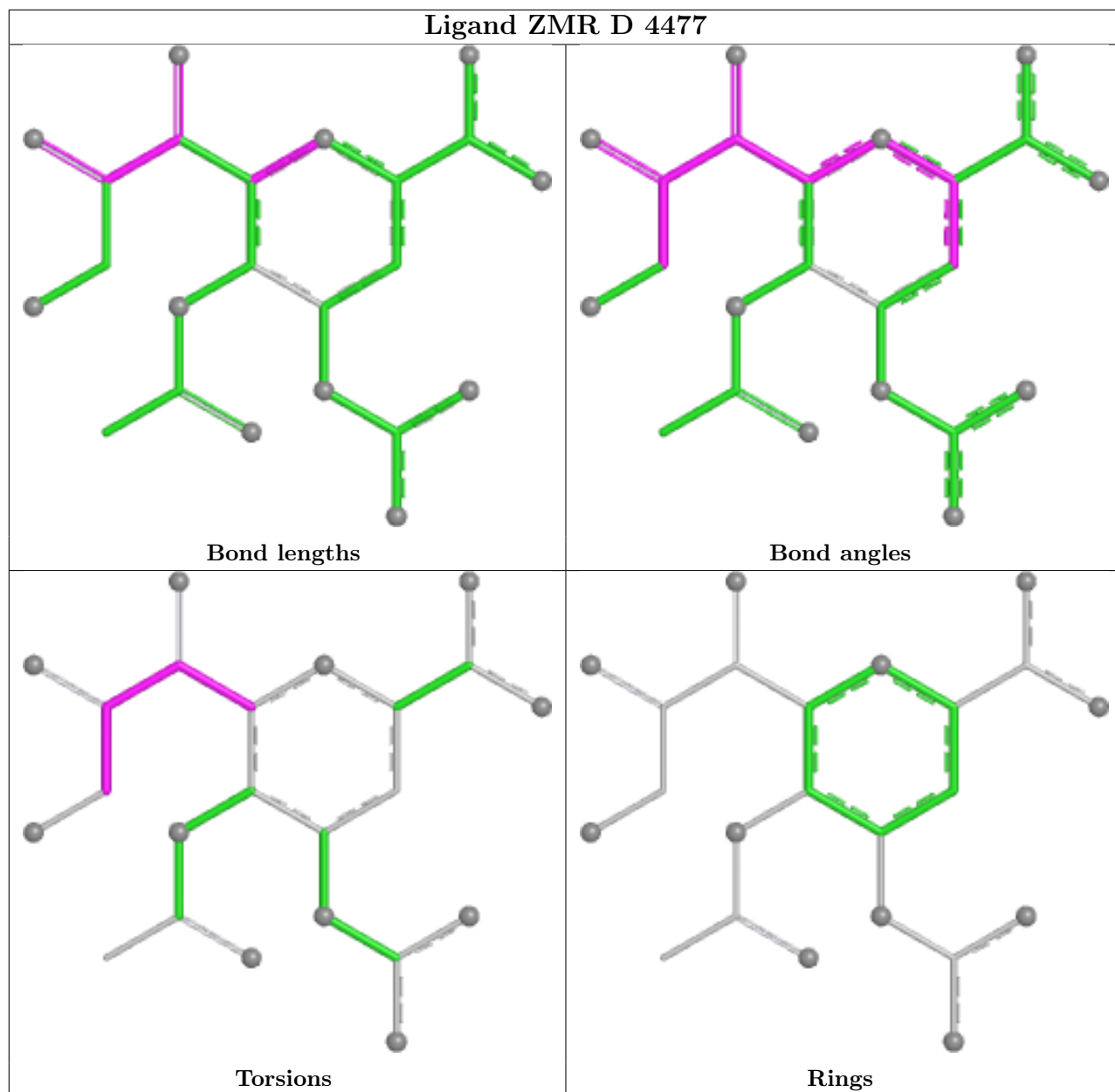


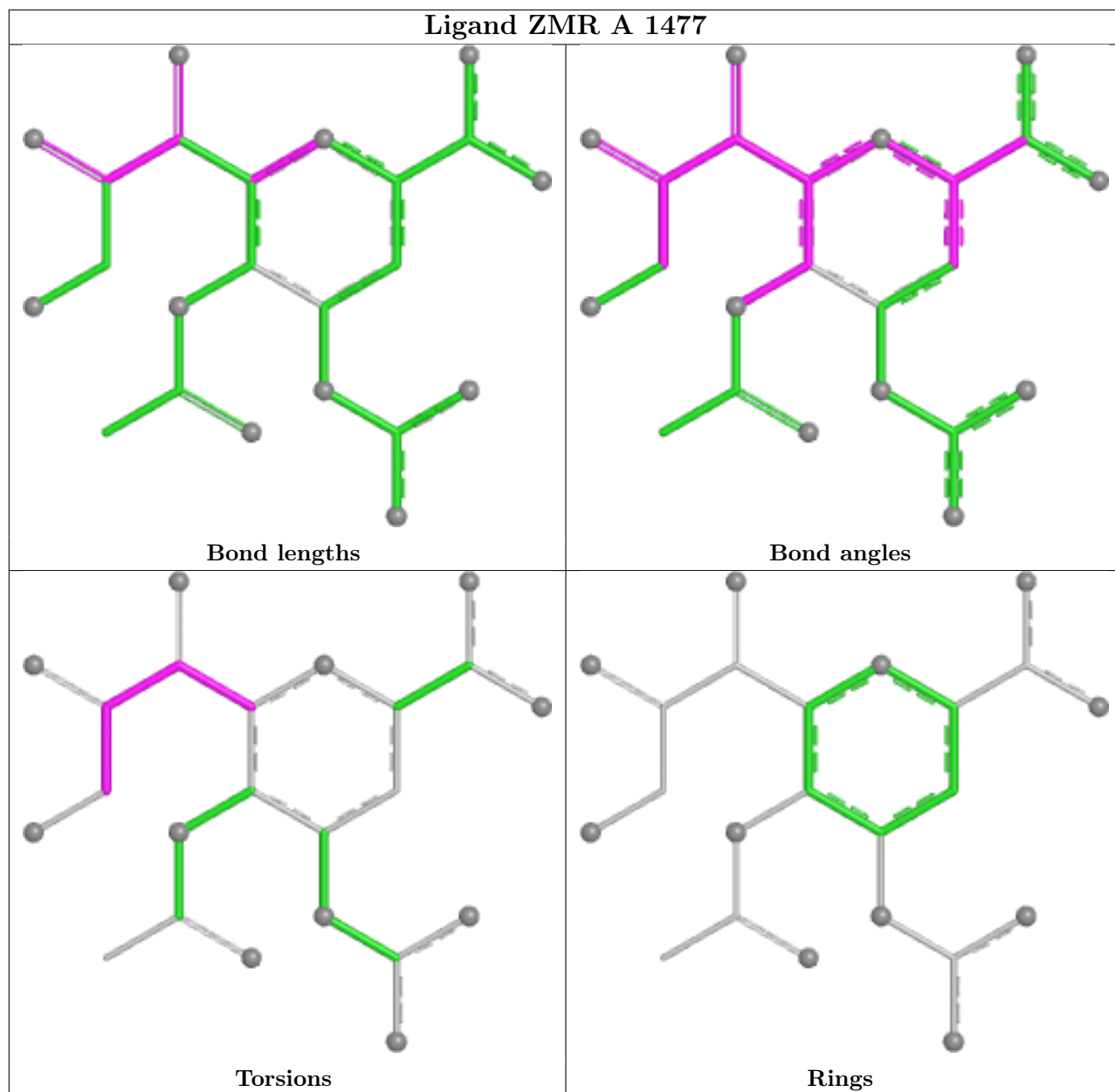


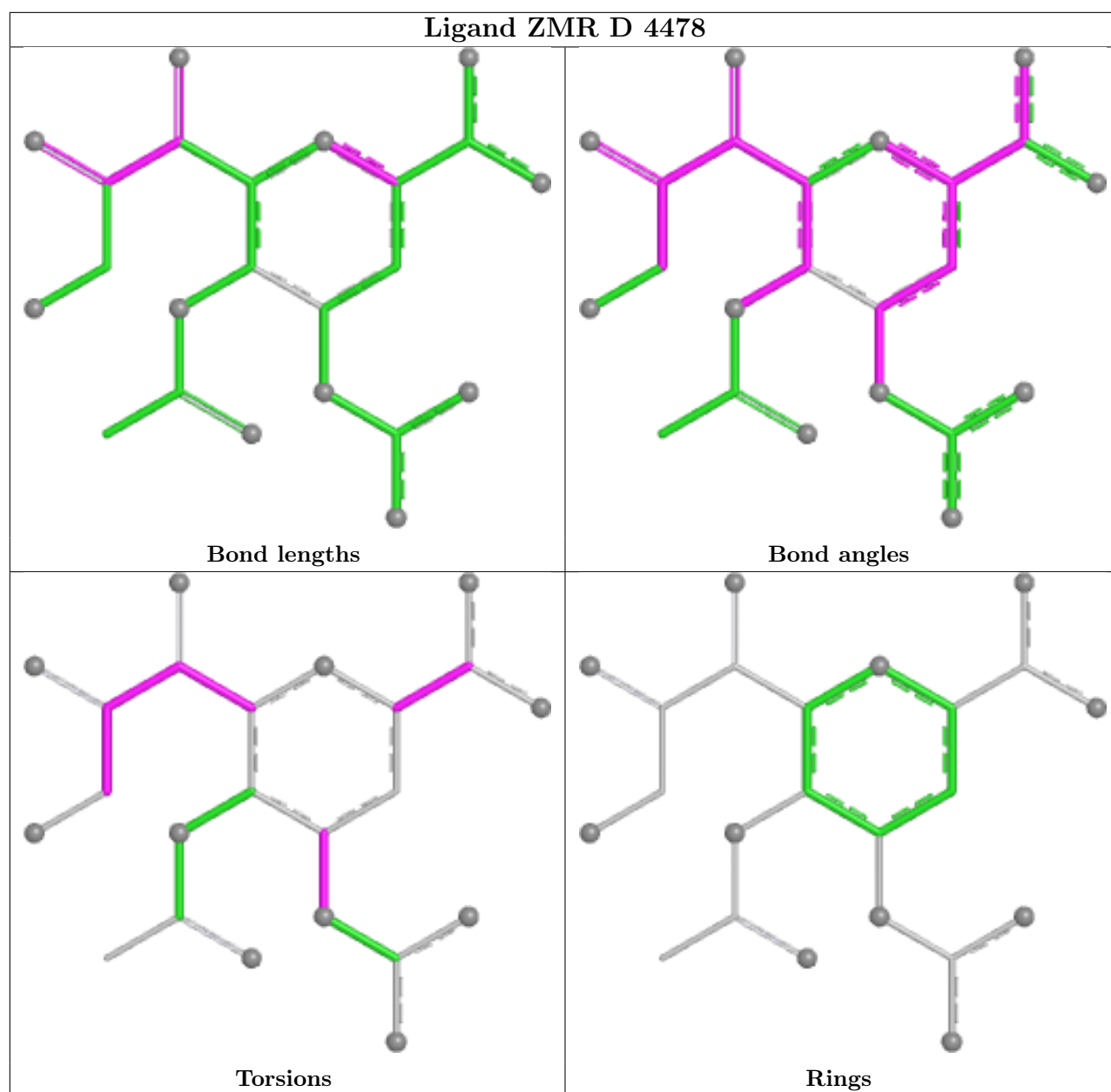












5.7 Other polymers [i](#)

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	389/389 (100%)	-0.59	0 100 100	5, 11, 18, 30	0
1	B	389/389 (100%)	-0.56	0 100 100	5, 12, 20, 36	0
1	C	389/389 (100%)	-0.56	0 100 100	5, 12, 20, 37	0
1	D	389/389 (100%)	-0.55	0 100 100	5, 12, 19, 31	0
All	All	1556/1556 (100%)	-0.56	0 100 100	5, 12, 20, 37	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

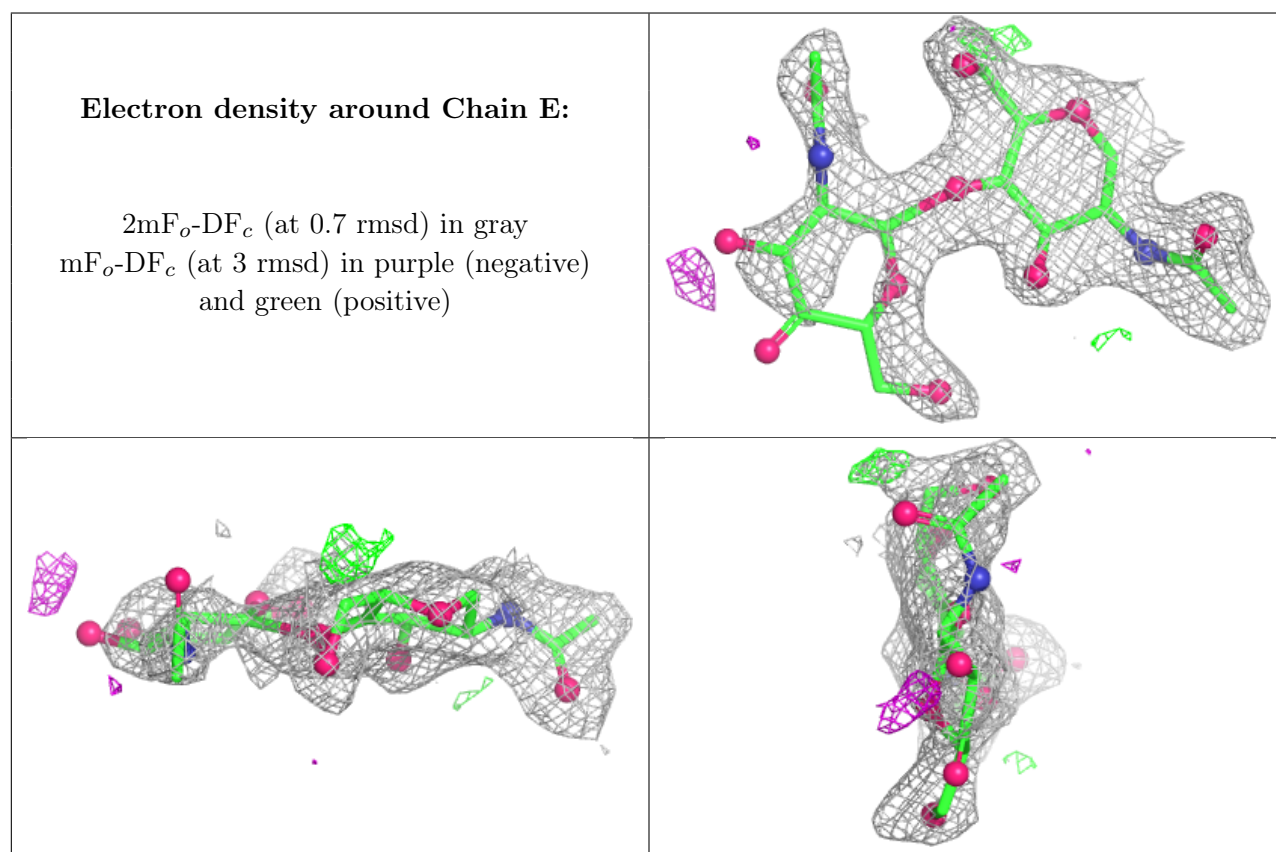
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	E	2	14/15	0.65	0.22	71,74,75,75	0
4	NAG	G	1	14/15	0.78	0.15	33,41,46,47	0
2	NAG	H	1	14/15	0.80	0.13	34,41,44,44	0
2	NAG	I	2	14/15	0.82	0.12	21,30,36,36	0
3	MAN	F	3	11/12	0.83	0.13	32,36,41,46	0
2	NAG	I	1	14/15	0.87	0.10	24,30,31,32	0
4	NAG	G	2	14/15	0.87	0.10	21,25,27,29	0
3	MAN	F	2	11/12	0.89	0.10	21,31,32,33	0
2	NAG	H	2	14/15	0.91	0.08	21,28,31,31	0

Continued on next page...

Continued from previous page...

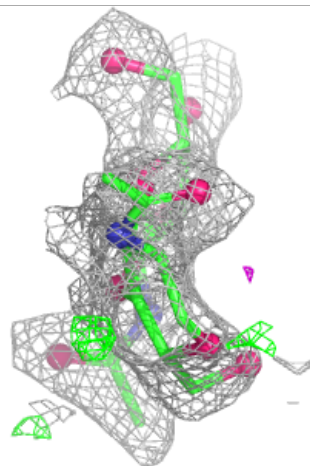
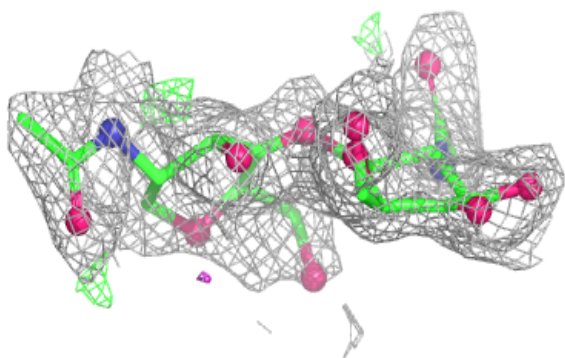
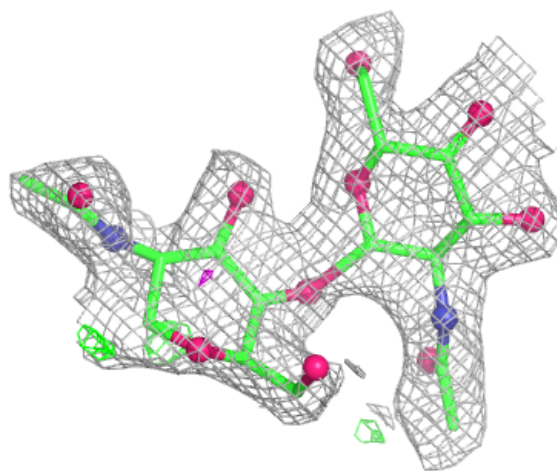
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MAN	F	1	11/12	0.91	0.12	31,35,40,40	0
4	MAN	G	4	11/12	0.91	0.09	24,27,30,30	0
4	MAN	G	5	11/12	0.91	0.08	19,25,28,30	0
2	NAG	E	1	14/15	0.92	0.07	16,25,27,27	0
4	BMA	G	3	11/12	0.92	0.08	26,31,32,33	0

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.



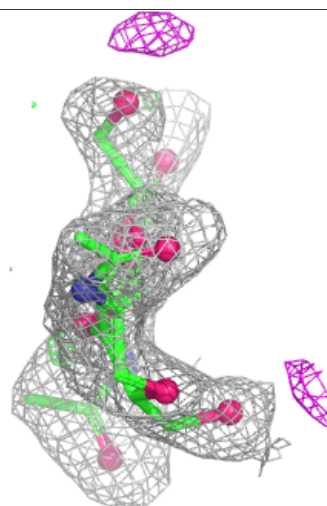
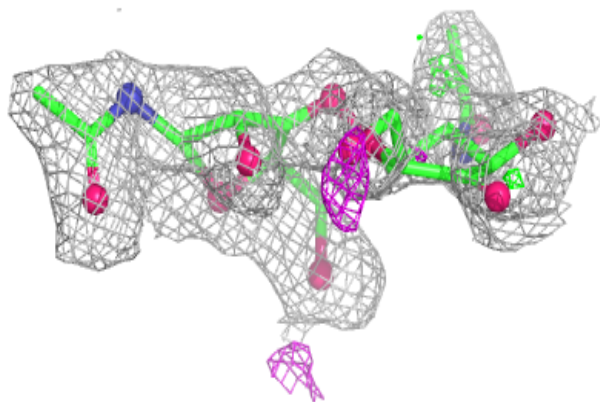
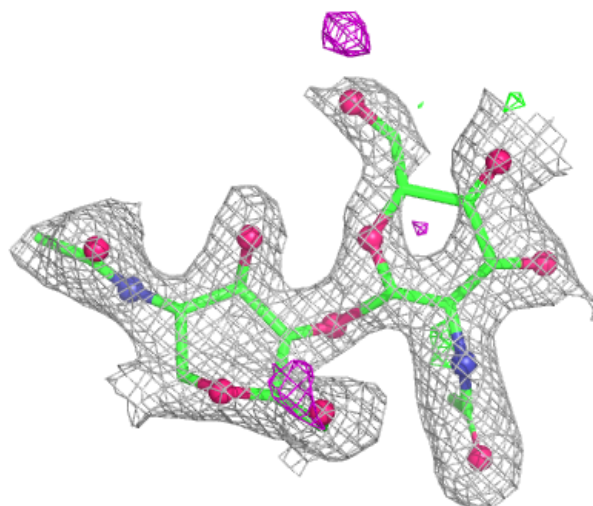
Electron density around Chain H:

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



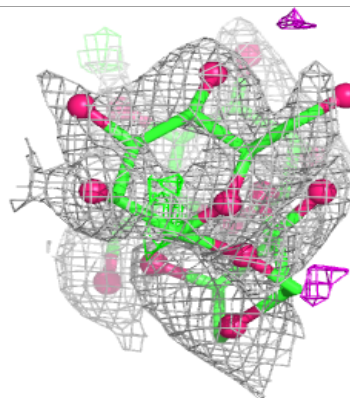
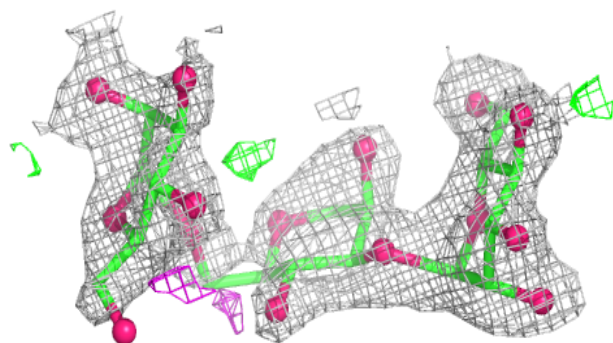
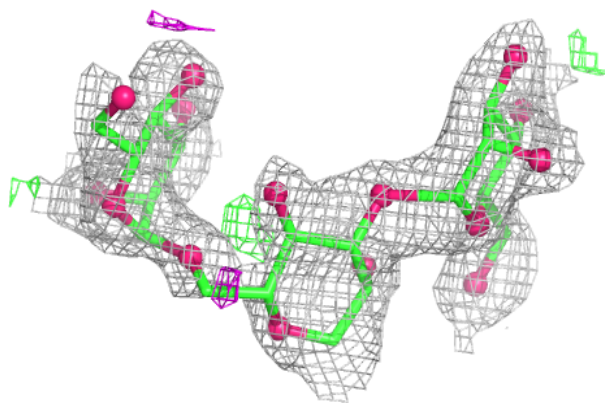
Electron density around Chain I:

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

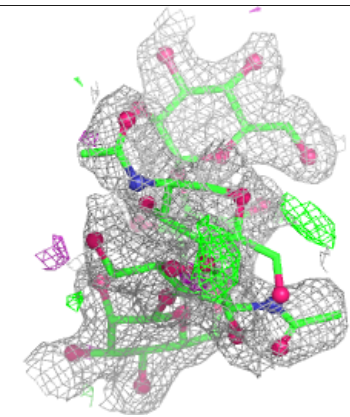
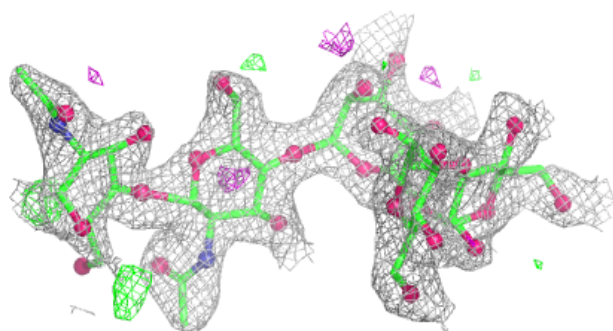
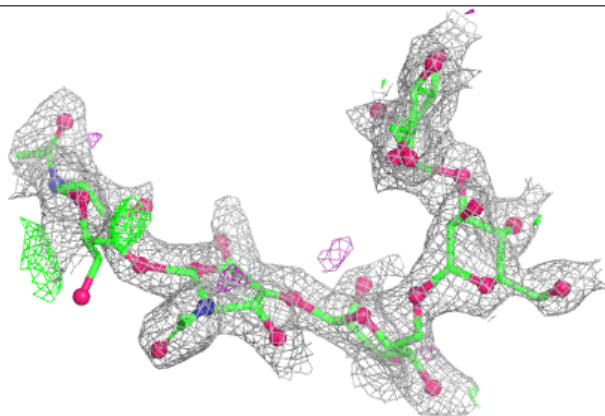


Electron density around Chain F:

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

**Electron density around Chain G:**

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



6.4 Ligands i

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

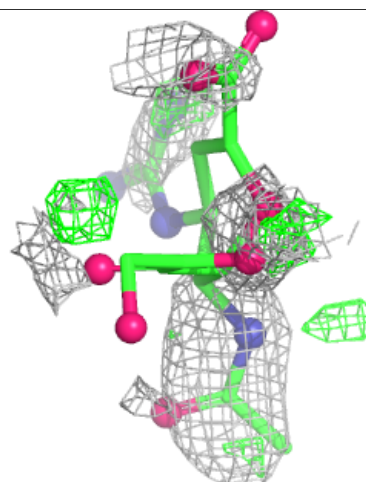
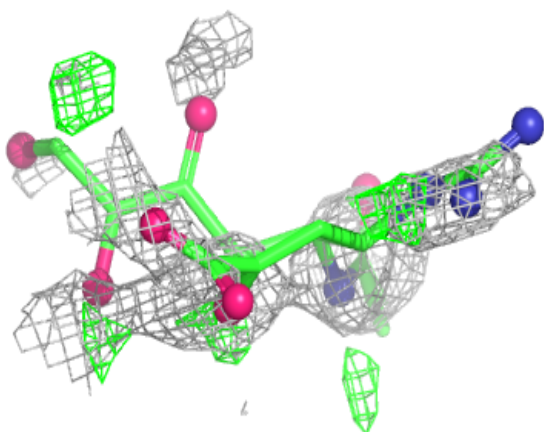
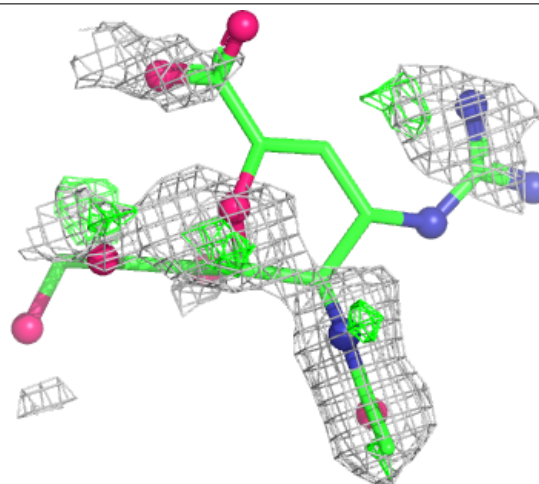
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	D	4482	14/15	0.57	0.29	73,78,79,80	0
7	NAG	B	2481	14/15	0.61	0.22	66,72,74,74	0
5	ZMR	A	1478	23/23	0.64	0.34	36,41,45,47	23
9	MAN	D	4481	11/12	0.64	0.22	65,69,70,70	0
7	NAG	C	3488	14/15	0.67	0.20	63,68,70,70	0
9	MAN	C	3492	11/12	0.70	0.19	60,65,67,67	0
7	NAG	A	1483	14/15	0.71	0.21	71,77,79,80	0
5	ZMR	C	3478	23/23	0.71	0.28	28,35,37,39	23
9	MAN	D	4480	11/12	0.74	0.18	44,49,52,52	0
5	ZMR	D	4478	23/23	0.74	0.31	38,44,48,49	23
7	NAG	B	2483	14/15	0.75	0.13	30,36,37,38	0
7	NAG	B	2482	14/15	0.77	0.17	44,52,53,53	0
5	ZMR	B	2478	23/23	0.80	0.25	35,42,44,45	23
8	BMA	D	4486	11/12	0.82	0.15	41,43,45,46	0
9	MAN	C	3490	11/12	0.83	0.11	29,33,35,36	0
9	MAN	B	2485	11/12	0.83	0.13	42,47,49,49	0
9	MAN	B	2484	11/12	0.84	0.14	41,44,45,46	0
7	NAG	C	3486	14/15	0.85	0.13	42,47,49,49	0
8	BMA	C	3493	11/12	0.86	0.11	33,34,36,37	0
9	MAN	B	2486	11/12	0.86	0.13	48,49,50,50	0
7	NAG	A	1482	14/15	0.87	0.11	23,28,32,34	0
7	NAG	C	3487	14/15	0.90	0.09	19,22,30,31	0
9	MAN	C	3484	11/12	0.90	0.08	29,30,34,37	0
8	BMA	A	1709	11/12	0.90	0.10	31,36,37,37	0
7	NAG	B	2480	14/15	0.91	0.08	14,26,30,30	0
7	NAG	D	4483	14/15	0.92	0.09	16,25,26,27	0
5	ZMR	C	3477	23/23	0.96	0.05	5,11,16,16	0
5	ZMR	B	2477	23/23	0.97	0.04	2,10,13,16	0
6	CA	A	1479	1/1	0.97	0.05	20,20,20,20	0
5	ZMR	A	1477	23/23	0.97	0.05	6,10,13,15	0
5	ZMR	D	4477	23/23	0.97	0.04	5,10,13,16	0
6	CA	C	3479	1/1	0.98	0.05	21,21,21,21	0
6	CA	D	4479	1/1	0.98	0.03	19,19,19,19	0
6	CA	B	2479	1/1	0.98	0.04	25,25,25,25	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.

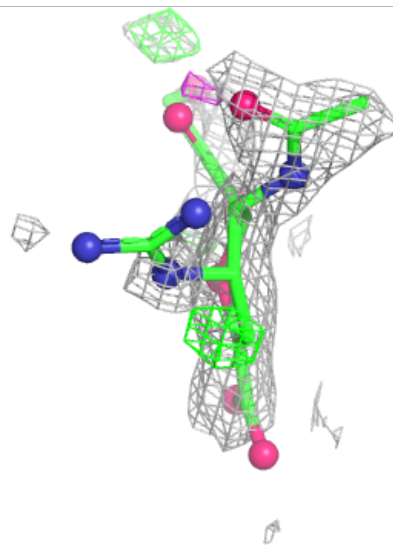
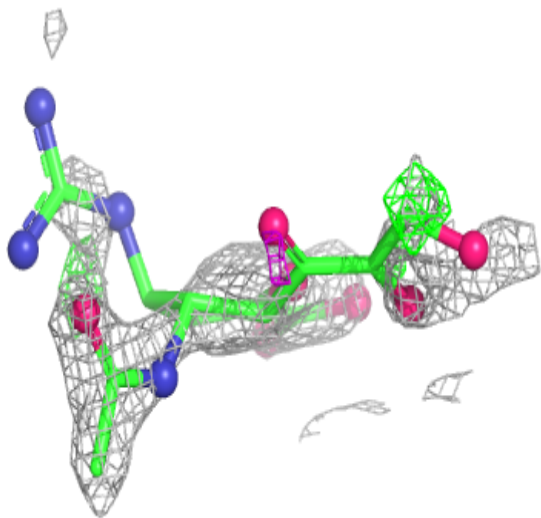
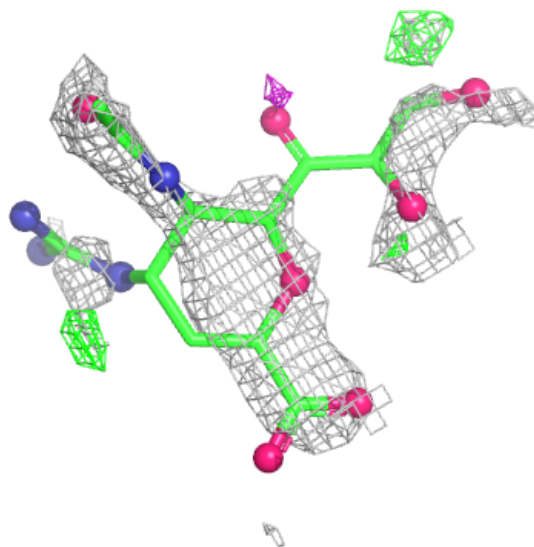
Electron density around ZMR A 1478:

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



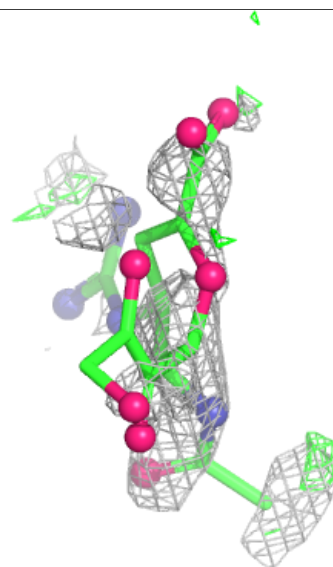
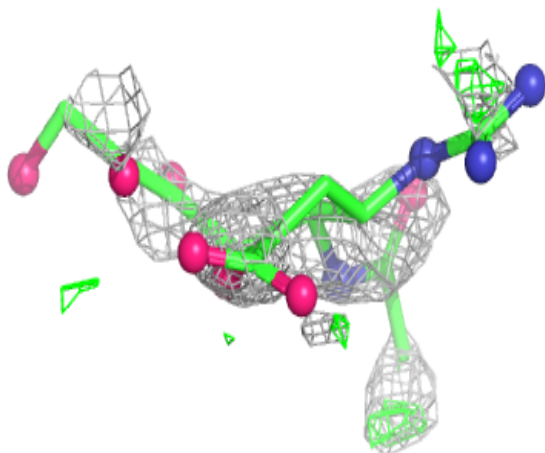
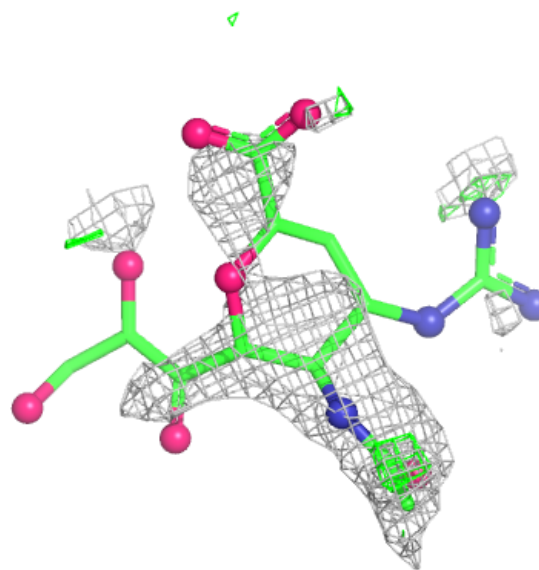
Electron density around ZMR C 3478:

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



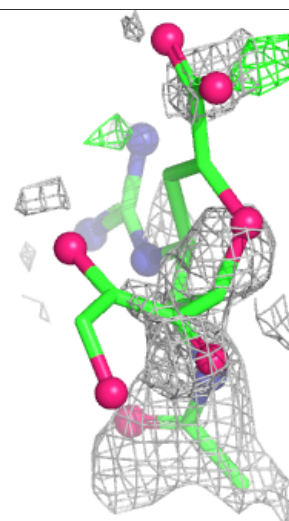
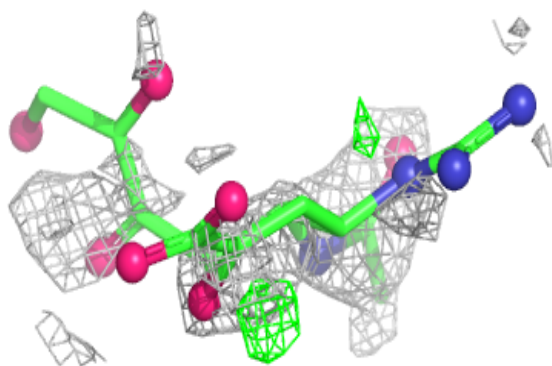
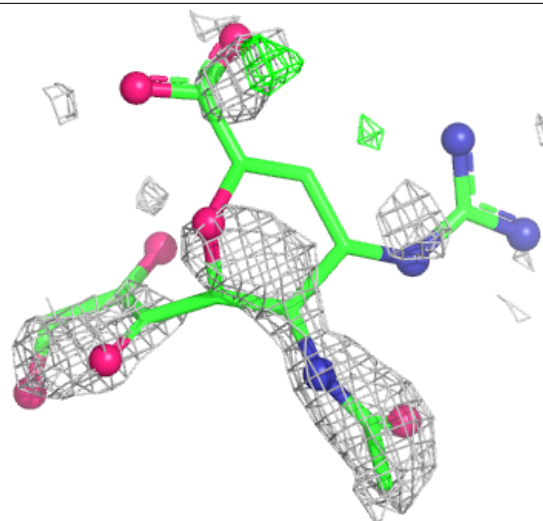
Electron density around ZMR D 4478:

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



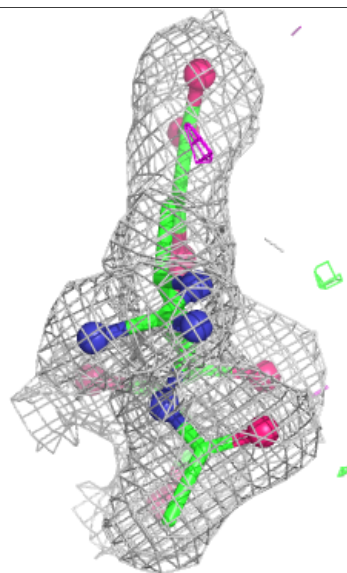
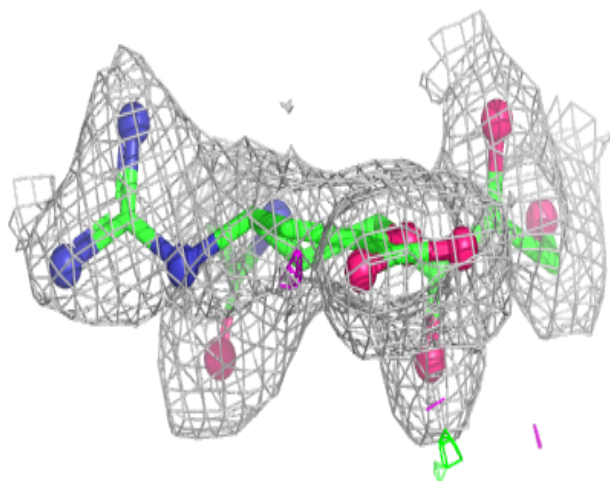
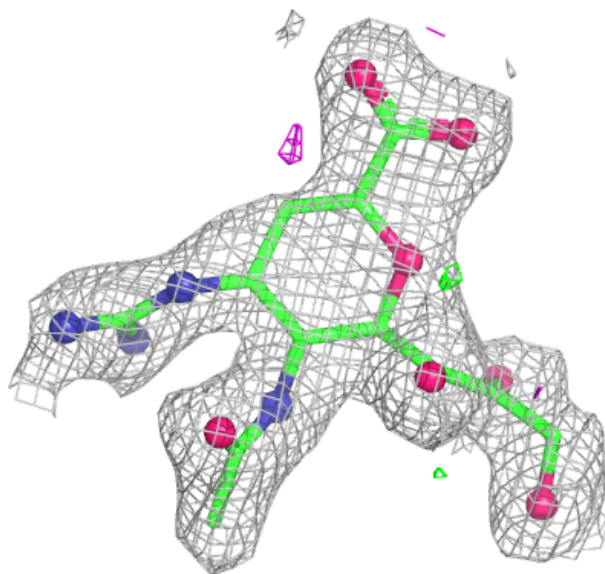
Electron density around ZMR B 2478:

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



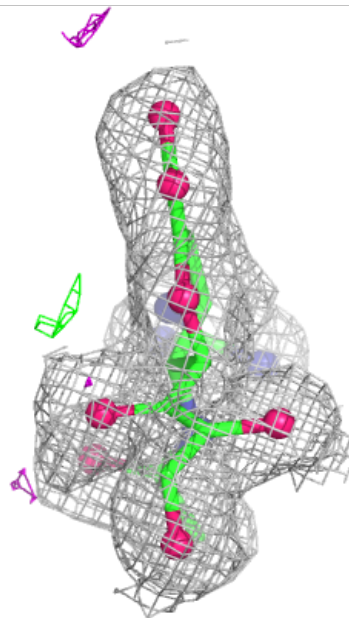
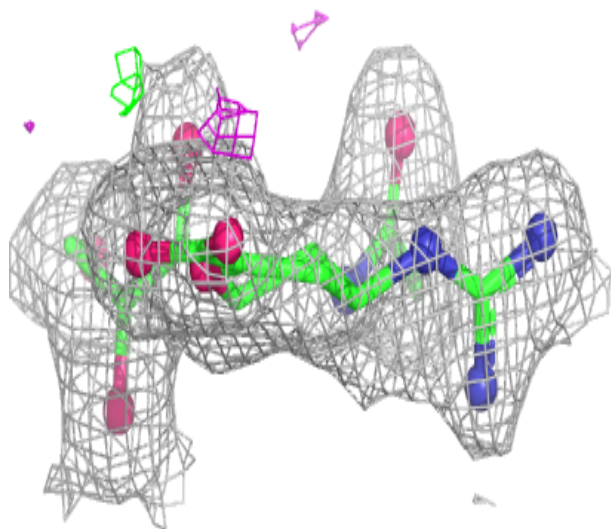
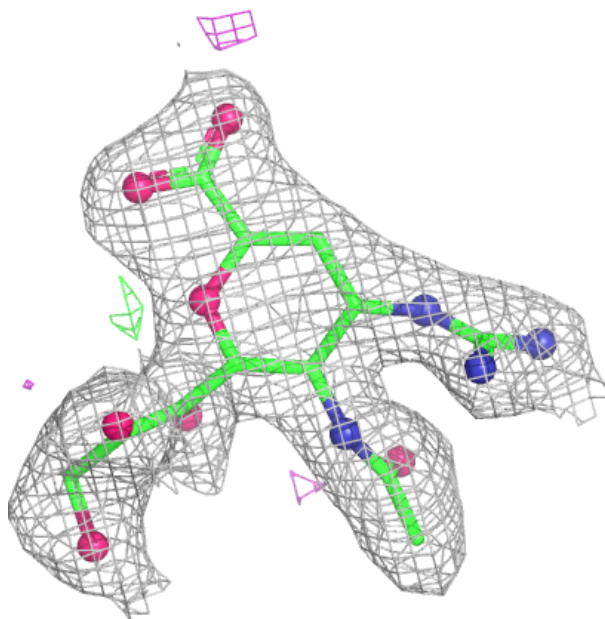
Electron density around ZMR C 3477:

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



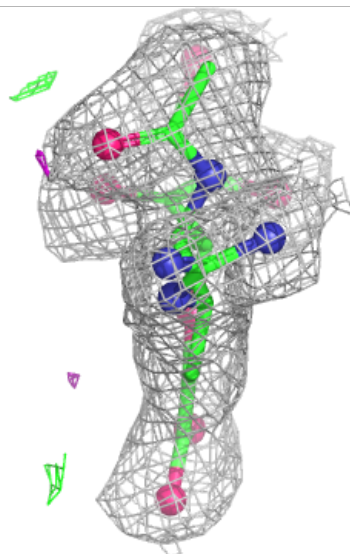
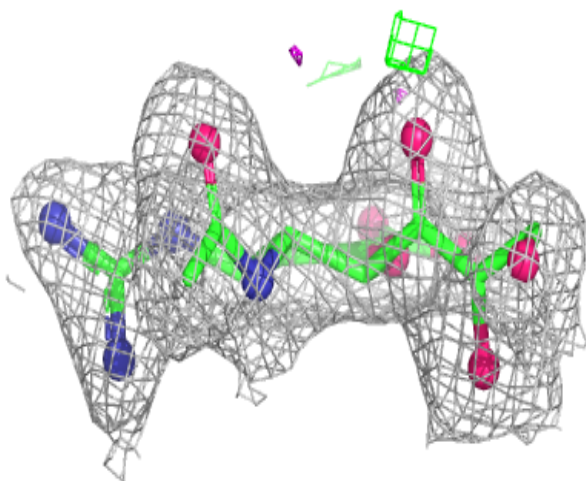
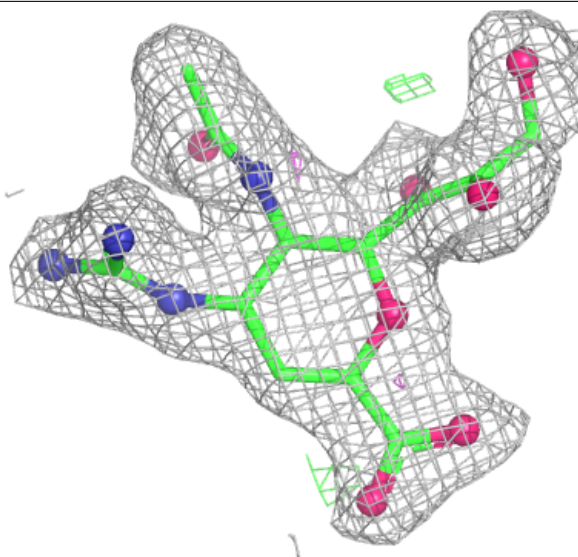
Electron density around ZMR B 2477:

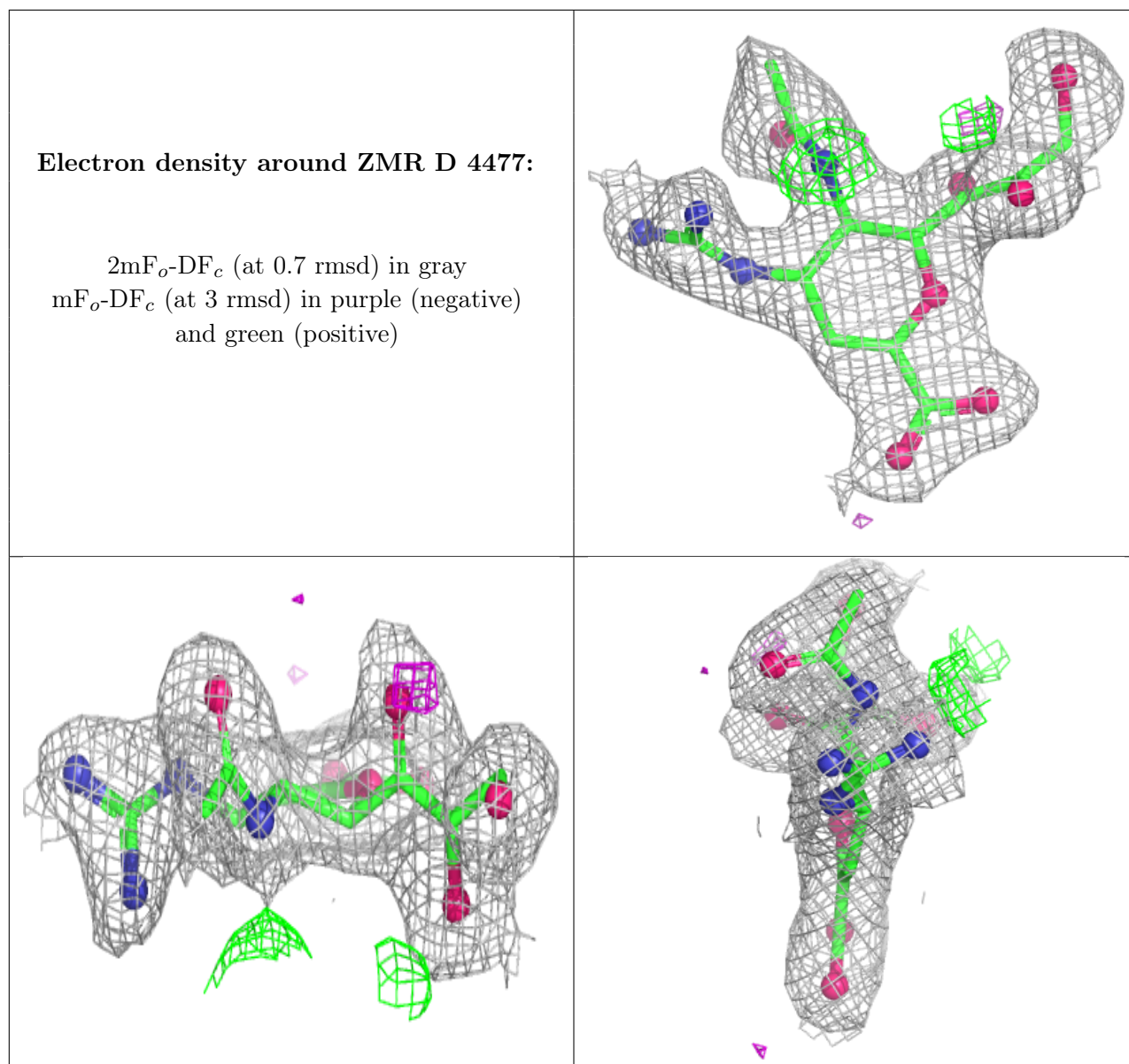
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZMR A 1477:

$2mF_o-DF_c$ (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.