



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 12:18 AM BST

PDB ID : 6B1E
Title : The structure of DPP4 in complex with Vildagliptin
Authors : Scapin, G.
Deposited on : 2017-09-18
Resolution : 1.77 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

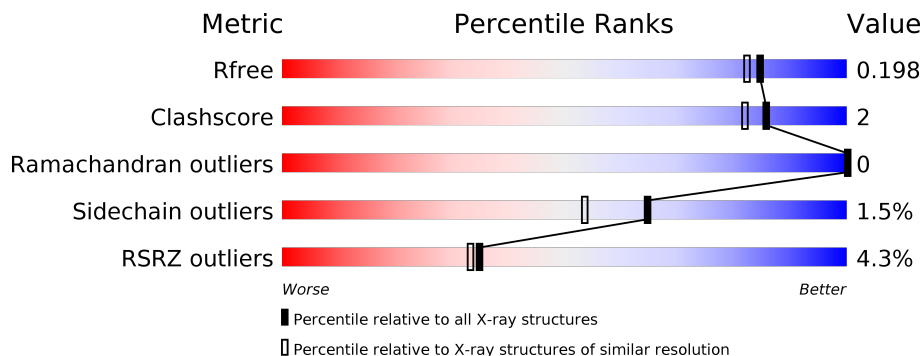
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 Å.

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




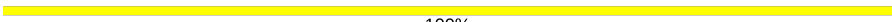

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	728	 4% 94% 5%
1	B	728	 4% 95%
2	C	2	 100%
2	D	2	 50% 50%
2	E	2	 100%
2	F	2	 100%

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Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	H	2	 100%
2	I	2	 100%

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

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

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 14219 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.

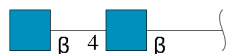
- Molecule 1 is a protein called Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	728	6028	3873	992	1136	27	0	13	0
1	B	728	6003	3856	984	1136	27	0	10	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	THR	SER	engineered mutation	UNP P27487
B	39	THR	SER	engineered mutation	UNP P27487

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



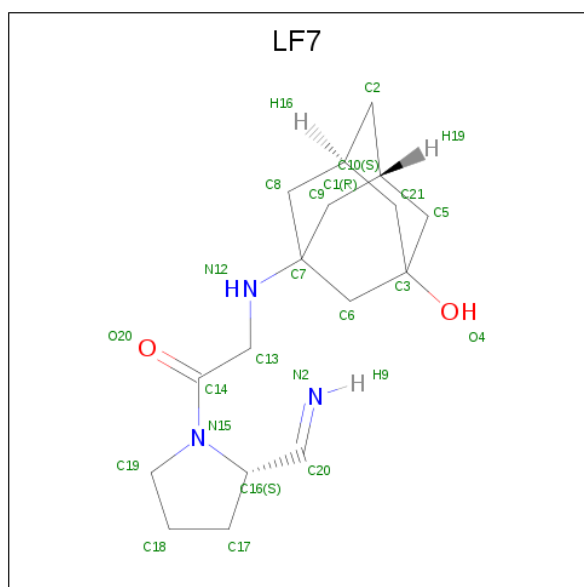
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	28	16	2	10	0	0	0
2	D	2	28	16	2	10	0	0	0
2	E	2	28	16	2	10	0	0	0
2	F	2	28	16	2	10	0	0	0
2	G	2	28	16	2	10	0	0	0
2	H	2	28	16	2	10	0	0	0

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

- Molecule 3 is 2-[[[(1r,3s,5R,7S)-3-hydroxytricyclo[3.3.1.1^{3,7}]decan-1-yl]amino]-1-[(2S)-2-[(E)-iminomethyl]pyrrolidin-1-yl]ethan-1-one (three-letter code: LF7) (formula: C₁₇H₂₇N₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	22	17	3	2	0	0
3	B	1	22	17	3	2	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Na 1 1	0	0

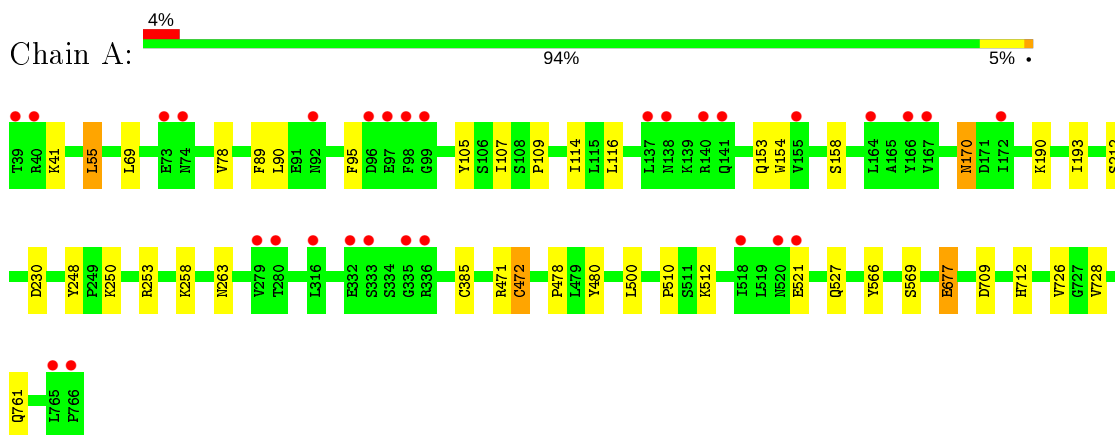
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	967	Total O 967 967	0	0
6	B	910	Total O 910 910	0	0

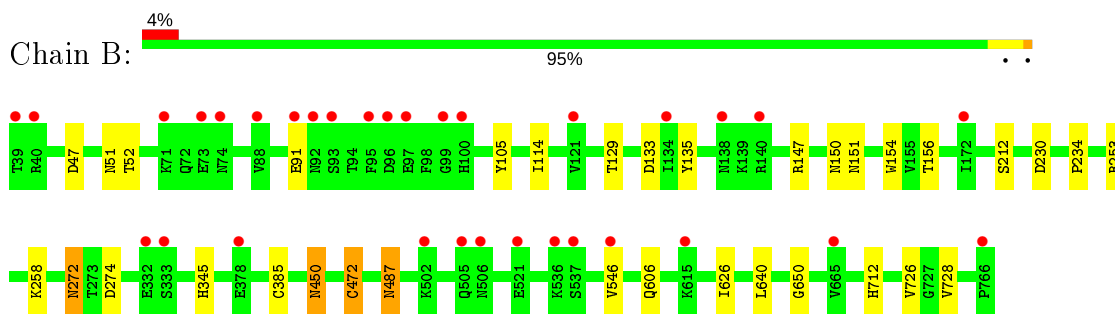
3 Residue-property plots [i](#)

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.

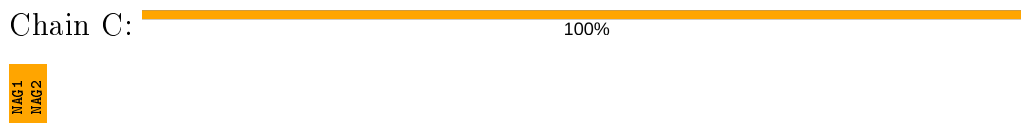
- Molecule 1: Dipeptidyl peptidase 4



- Molecule 1: Dipeptidyl peptidase 4



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




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



MAG1
MAG2

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

Chain E:  100%MAG1
MAG2

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

Chain F:  100%MAG1
MAG2

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

Chain G:  100%MAG1
MAG2

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

Chain H:  100%MAG1
MAG2

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

Chain I:  100%MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	118.31Å 125.75Å 136.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.77 29.87 – 1.77	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-1.77) 99.9 (29.87-1.77)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.38 (at 1.77Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.161 , 0.186 0.172 , 0.198	Depositor DCC
R_{free} test set	9938 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtrriage
Anisotropy	0.206	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14219	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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: NA, LF7, NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.52	0/6245	0.61	0/8491
1	B	0.50	0/6208	0.60	0/8445
All	All	0.51	0/12453	0.61	0/16936

There are no bond length outliers.

There are no bond angle outliers.

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	6028	0	5768	27	0
1	B	6003	0	5738	27	0
2	C	28	0	25	1	0
2	D	28	0	25	0	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
3	A	22	0	25	0	0
3	B	22	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	42	0	39	0	0
4	B	28	0	26	1	0
5	A	1	0	0	0	0
6	A	967	0	0	3	0
6	B	910	0	0	3	0
All	All	14219	0	11796	53	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 2.

All (53) 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:B:258:LYS:HZ1	1:B:712:HIS:HD2	1.08	0.93
1:B:472:CYS:SG	6:B:953:HOH:O	2.27	0.93
1:A:190:LYS:HE3	1:A:193[A]:ILE:HD12	1.62	0.81
1:A:78:VAL:HG23	1:A:89:PHE:HB2	1.63	0.79
1:A:253:ARG:HH21	1:B:253:ARG:HH21	1.31	0.75
1:A:69:LEU:CD2	1:A:78:VAL:HG22	2.21	0.71
1:B:258:LYS:HZ1	1:B:712:HIS:CD2	2.01	0.66
1:A:153:GLN:HE22	1:A:170:ASN:ND2	1.95	0.64
1:B:114:ILE:HG23	1:B:135:TYR:HB3	1.79	0.63
1:B:258:LYS:NZ	1:B:712:HIS:HD2	1.91	0.63
1:B:272:ASN:C	1:B:272:ASN:HD22	2.01	0.63
1:B:129:THR:HA	6:B:903:HOH:O	2.00	0.61
1:A:69:LEU:HD23	1:A:78:VAL:HG22	1.81	0.61
1:B:47:ASP:OD2	1:B:52[B]:THR:HG21	2.00	0.60
1:A:258:LYS:NZ	1:A:712:HIS:HD2	1.99	0.60
1:A:250:LYS:NZ	6:A:902:HOH:O	2.35	0.58
1:B:546[A]:VAL:HG21	1:B:626:ILE:HD11	1.85	0.57
1:B:47:ASP:HA	1:B:52[B]:THR:HG22	1.86	0.56
1:A:105:TYR:HB2	1:A:114:ILE:HD11	1.88	0.55
1:B:154:TRP:NE1	1:B:156[B]:THR:OG1	2.40	0.55
1:A:471[A]:ARG:HG3	1:A:480:TYR:CE2	2.42	0.54
1:B:726:VAL:HG23	1:B:728:VAL:HG23	1.90	0.54
1:A:258:LYS:HZ3	1:A:712:HIS:HD2	1.55	0.52
1:A:761:GLN:NE2	6:A:906:HOH:O	2.42	0.52
1:B:546[B]:VAL:HG12	1:B:606:GLN:OE1	2.10	0.52
1:B:105:TYR:HB2	1:B:114:ILE:HD11	1.92	0.51
1:B:272:ASN:HD21	1:B:274:ASP:HB2	1.77	0.50
1:B:640:LEU:HD11	1:B:650:GLY:HA3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:LEU:HD21	1:A:95:PHE:HE2	1.78	0.49
1:A:248:TYR:CZ	1:B:234:PRO:HB2	2.48	0.49
1:B:133:ASP:OD2	1:B:147:ARG:NH1	2.47	0.48
2:C:1:NAG:H4	2:C:2:NAG:H2	1.49	0.47
1:A:69:LEU:HD13	1:A:107:ILE:HD12	1.96	0.47
1:A:154:TRP:CE2	1:A:212[A]:SER:HB3	2.50	0.47
1:A:709:ASP:O	1:A:712:HIS:HE1	1.99	0.46
1:B:487:ASN:C	1:B:487:ASN:HD22	2.19	0.46
1:A:258:LYS:HZ3	1:A:712:HIS:CD2	2.34	0.45
1:B:114:ILE:CG2	1:B:135:TYR:HB3	2.46	0.45
1:A:472:CYS:O	1:A:478:PRO:HA	2.17	0.44
1:B:345:HIS:HD2	6:B:1028:HOH:O	2.00	0.44
1:A:677:GLU:CD	1:A:677:GLU:H	2.21	0.44
1:B:154:TRP:CE2	1:B:212[B]:SER:HB3	2.53	0.44
1:A:471[A]:ARG:HD2	6:A:1127:HOH:O	2.17	0.43
1:B:150:ASN:O	1:B:151:ASN:HB2	2.19	0.43
1:B:147:ARG:HE	4:B:804:NAG:H83	1.84	0.43
1:A:510:PRO:HD3	1:A:569:SER:HB2	2.02	0.42
1:A:726:VAL:HG23	1:A:728:VAL:HG23	2.01	0.42
1:B:154:TRP:CE2	1:B:212[A]:SER:HB2	2.56	0.41
1:A:109:PRO:HG2	1:A:158:SER:O	2.21	0.41
1:A:55:LEU:HD12	1:A:500:LEU:CD2	2.51	0.41
1:A:69:LEU:HD13	1:A:107:ILE:CD1	2.51	0.40
1:A:512:LYS:HE3	1:A:527:GLN:OE1	2.21	0.40

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	739/728 (102%)	718 (97%)	21 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	736/728 (101%)	714 (97%)	22 (3%)	0	100	100
All	All	1475/1456 (101%)	1432 (97%)	43 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	666/653 (102%)	655 (98%)	11 (2%)	60	48
1	B	663/653 (102%)	654 (99%)	9 (1%)	67	56
All	All	1329/1306 (102%)	1309 (98%)	20 (2%)	65	53

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LYS
1	A	55	LEU
1	A	116	LEU
1	A	170	ASN
1	A	230	ASP
1	A	263	ASN
1	A	385	CYS
1	A	472	CYS
1	A	521	GLU
1	A	566	TYR
1	A	677	GLU
1	B	51	ASN
1	B	91	GLU
1	B	230	ASP
1	B	272	ASN
1	B	385	CYS
1	B	450[A]	ASN
1	B	450[B]	ASN

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Mol	Chain	Res	Type
1	B	472	CYS
1	B	487	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	141	GLN
1	A	169	ASN
1	A	170	ASN
1	A	263	ASN
1	A	435	GLN
1	A	572	ASN
1	A	694	ASN
1	A	712	HIS
1	A	761	GLN
1	B	169	ASN
1	B	272	ASN
1	B	345	HIS
1	B	487	ASN
1	B	572	ASN
1	B	685	ASN
1	B	694	ASN
1	B	712	HIS

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	C	1	1,2	14,14,15	0.50	0	17,19,21	1.36	1 (5%)
2	NAG	C	2	2	14,14,15	0.68	1 (7%)	17,19,21	2.61	6 (35%)
2	NAG	D	1	1,2	14,14,15	0.54	0	17,19,21	0.85	0
2	NAG	D	2	2	14,14,15	0.40	0	17,19,21	1.29	1 (5%)
2	NAG	E	1	1,2	14,14,15	0.60	0	17,19,21	1.18	2 (11%)
2	NAG	E	2	2	14,14,15	0.43	0	17,19,21	1.93	4 (23%)
2	NAG	F	1	1,2	14,14,15	0.48	0	17,19,21	1.16	2 (11%)
2	NAG	F	2	2	14,14,15	0.85	1 (7%)	17,19,21	1.52	2 (11%)
2	NAG	G	1	1,2	14,14,15	0.62	0	17,19,21	0.84	0
2	NAG	G	2	2	14,14,15	0.50	0	17,19,21	0.99	0
2	NAG	H	1	1,2	14,14,15	0.47	0	17,19,21	0.99	1 (5%)
2	NAG	H	2	2	14,14,15	0.51	0	17,19,21	1.38	2 (11%)
2	NAG	I	1	1,2	14,14,15	0.48	0	17,19,21	0.98	1 (5%)
2	NAG	I	2	2	14,14,15	0.46	0	17,19,21	1.39	2 (11%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	NAG	C1-C2	2.16	1.55	1.52
2	C	2	NAG	C1-C2	2.11	1.55	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C1-O5-C5	6.96	121.62	112.19
2	E	2	NAG	C1-O5-C5	5.64	119.83	112.19
2	C	2	NAG	C2-N2-C7	5.51	130.75	122.90
2	C	1	NAG	C1-O5-C5	4.58	118.39	112.19
2	D	2	NAG	C1-O5-C5	4.52	118.32	112.19
2	H	2	NAG	C1-O5-C5	4.19	117.87	112.19
2	F	2	NAG	C4-C3-C2	4.14	117.08	111.02
2	I	2	NAG	O5-C5-C6	3.51	112.70	107.20
2	C	2	NAG	O5-C5-C6	3.26	112.32	107.20
2	C	2	NAG	C1-C2-N2	3.15	115.87	110.49
2	E	2	NAG	O5-C5-C6	2.99	111.89	107.20
2	I	1	NAG	C2-N2-C7	-2.85	118.85	122.90
2	F	1	NAG	C4-C3-C2	2.70	114.97	111.02
2	E	1	NAG	O5-C1-C2	-2.60	107.18	111.29
2	H	1	NAG	O5-C1-C2	-2.58	107.21	111.29
2	F	2	NAG	C2-N2-C7	2.54	126.53	122.90
2	E	2	NAG	C2-N2-C7	2.46	126.41	122.90
2	C	2	NAG	O7-C7-N2	2.36	126.29	121.95
2	F	1	NAG	O5-C5-C6	2.28	110.78	107.20
2	I	2	NAG	O7-C7-C8	-2.15	118.07	122.06
2	E	1	NAG	C1-O5-C5	2.11	115.05	112.19
2	E	2	NAG	C8-C7-N2	2.02	119.52	116.10
2	H	2	NAG	C6-C5-C4	-2.02	108.28	113.00
2	C	2	NAG	O5-C1-C2	2.01	114.47	111.29

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C1-C2-N2-C7
2	F	2	NAG	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	I	2	NAG	O5-C5-C6-O6
2	F	2	NAG	C4-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6

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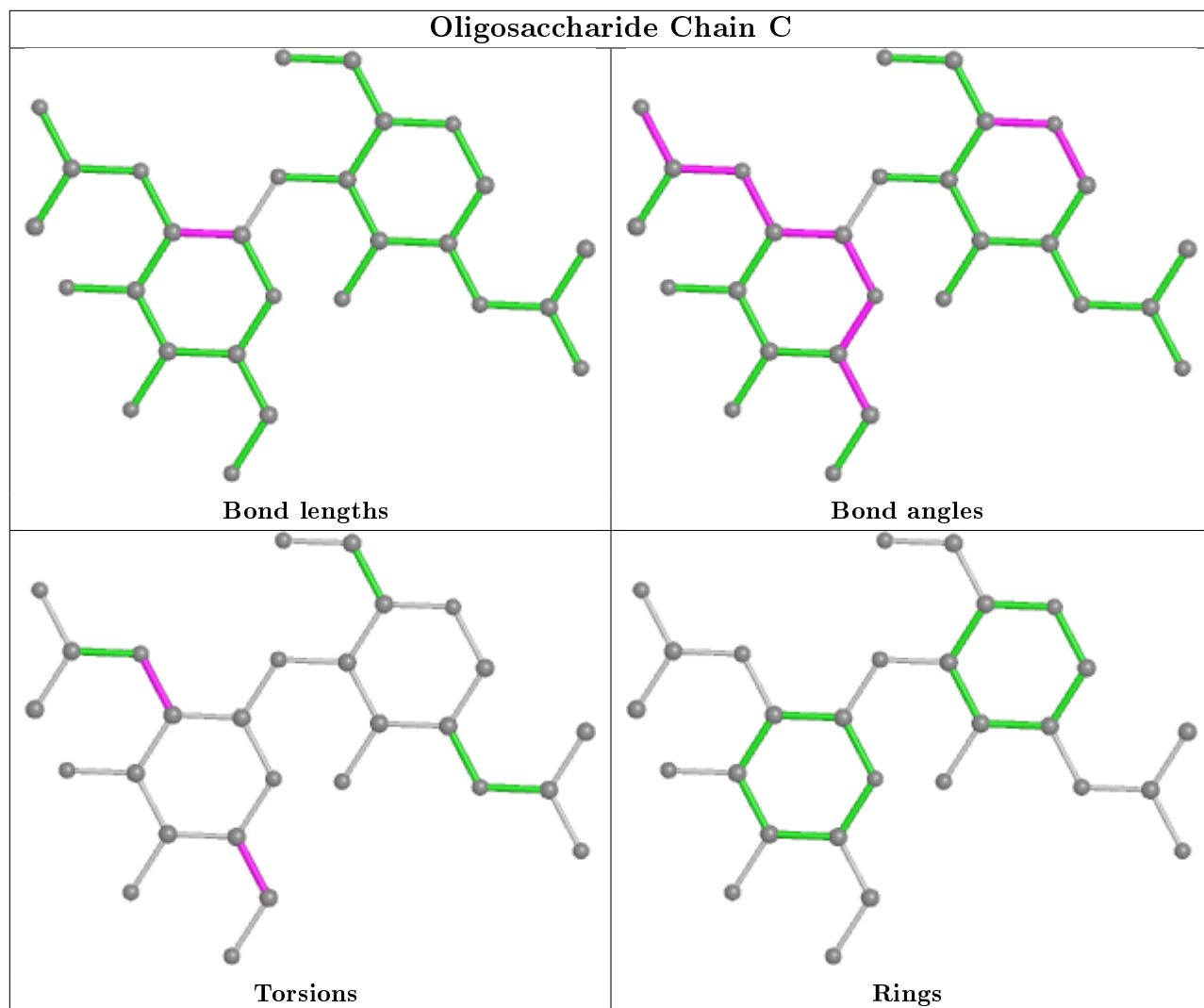
Mol	Chain	Res	Type	Atoms
2	I	2	NAG	C4-C5-C6-O6
2	E	2	NAG	C8-C7-N2-C2
2	E	2	NAG	O7-C7-N2-C2
2	C	2	NAG	C4-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	G	2	NAG	C4-C5-C6-O6
2	H	2	NAG	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6
2	H	2	NAG	O5-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6

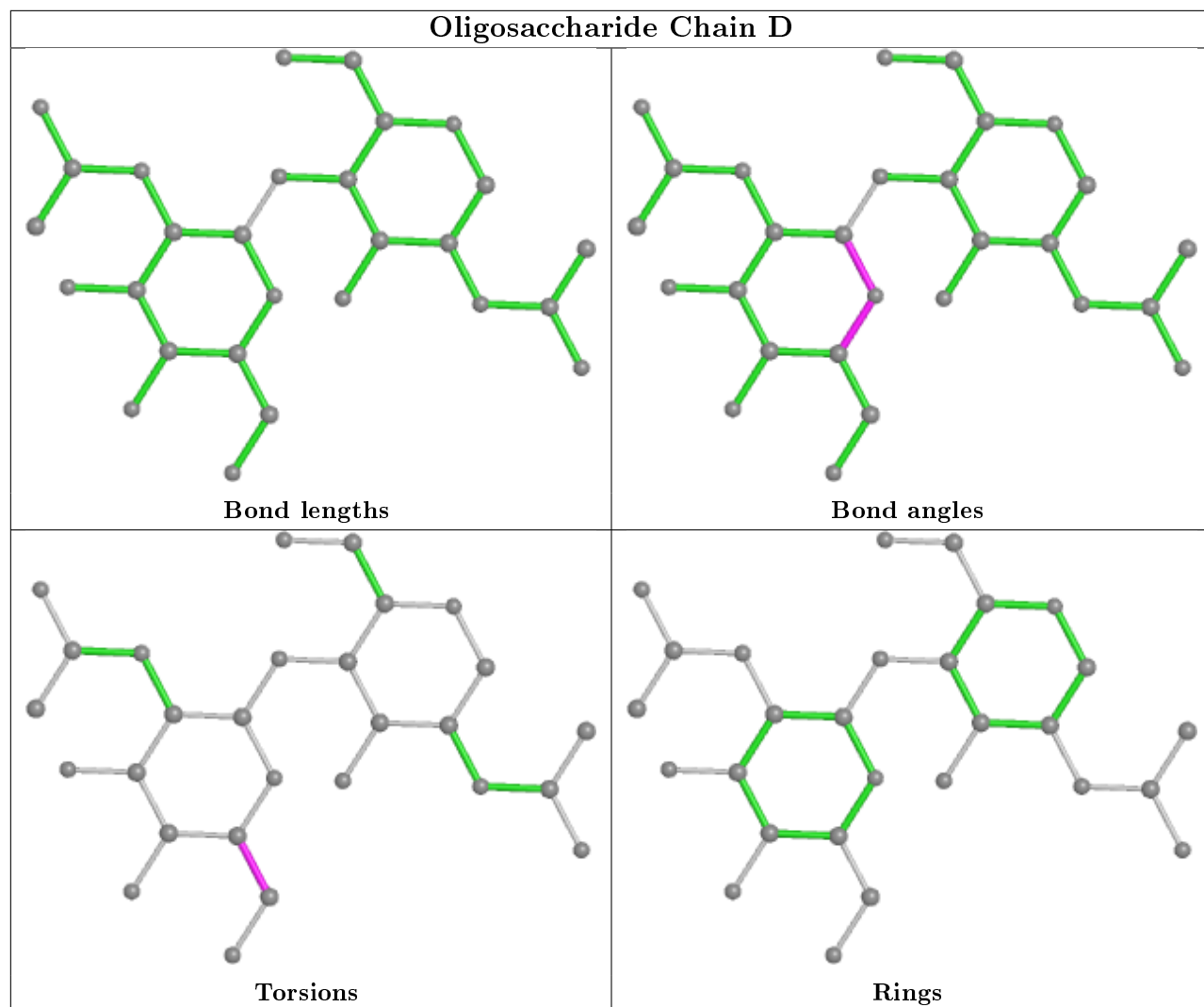
There are no ring outliers.

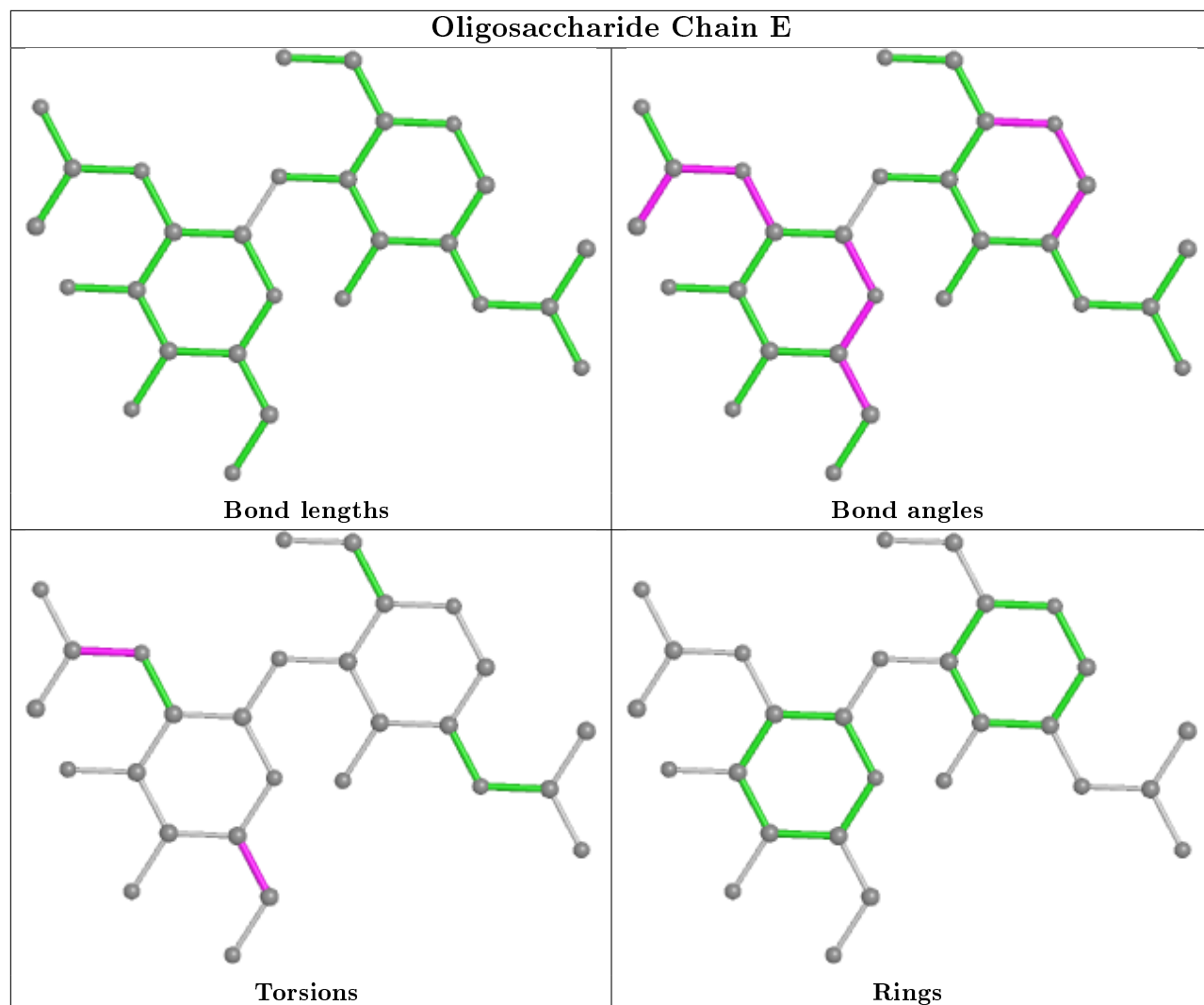
2 monomers are involved in 1 short contact:

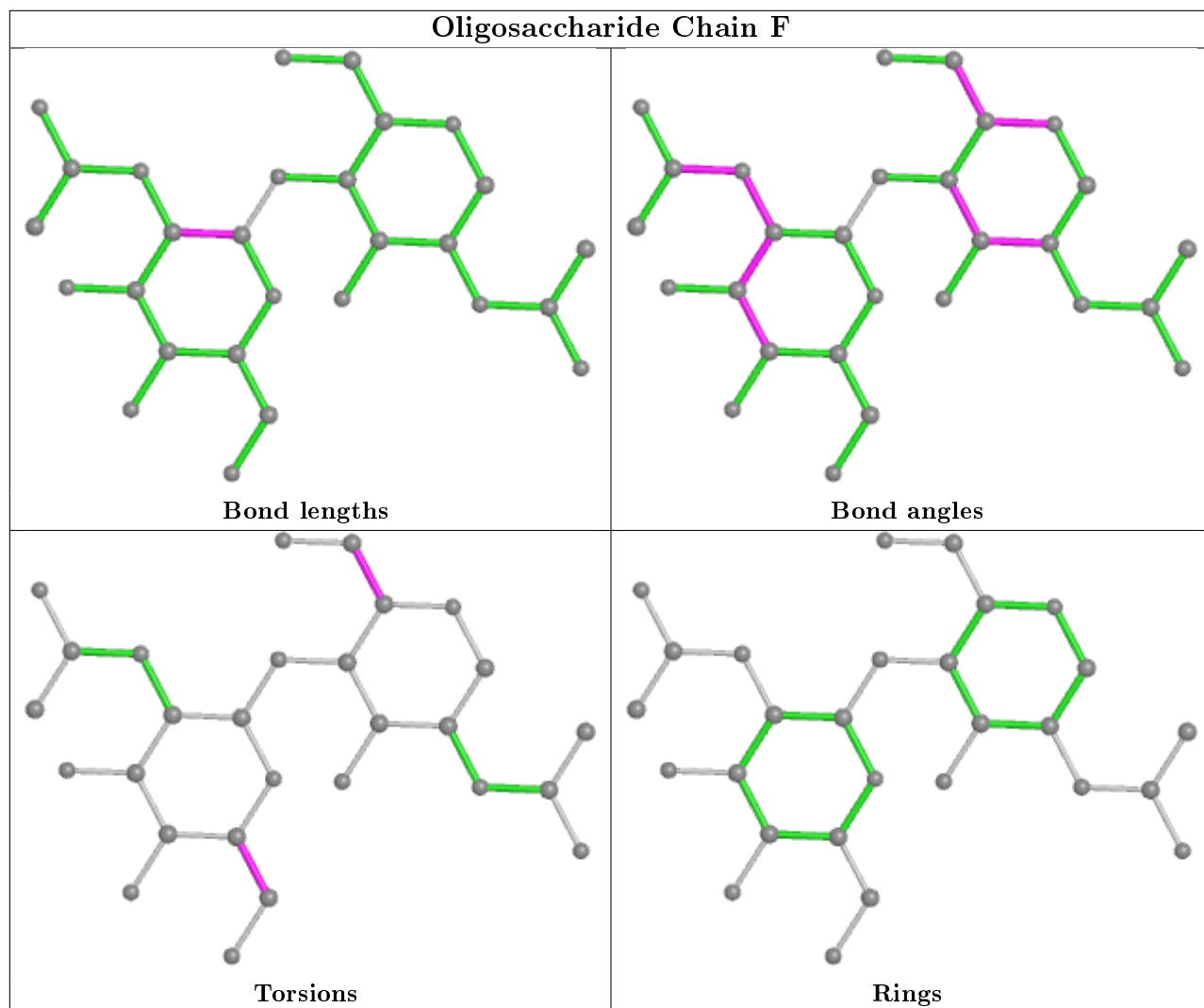
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	1	0
2	C	2	NAG	1	0

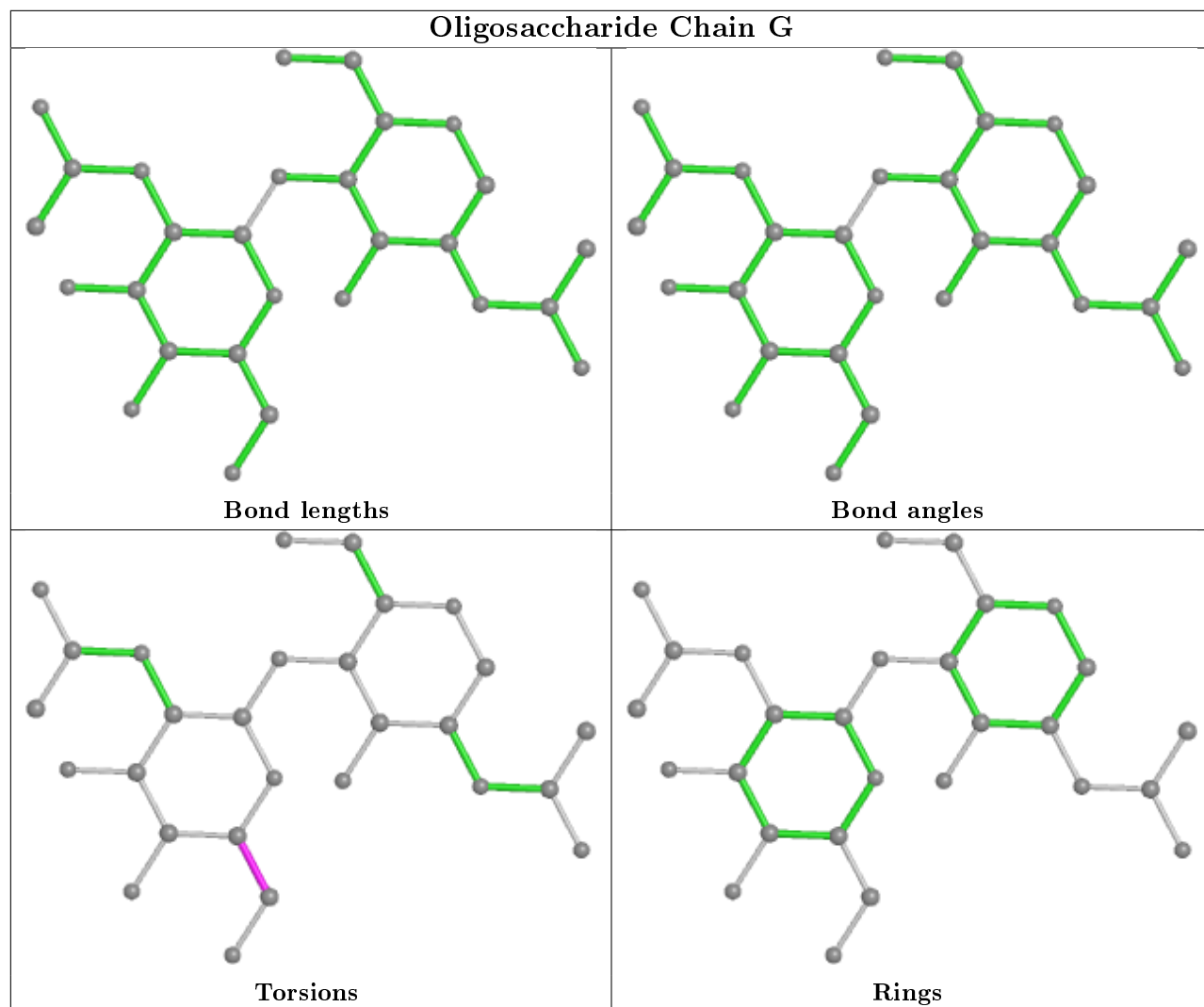
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

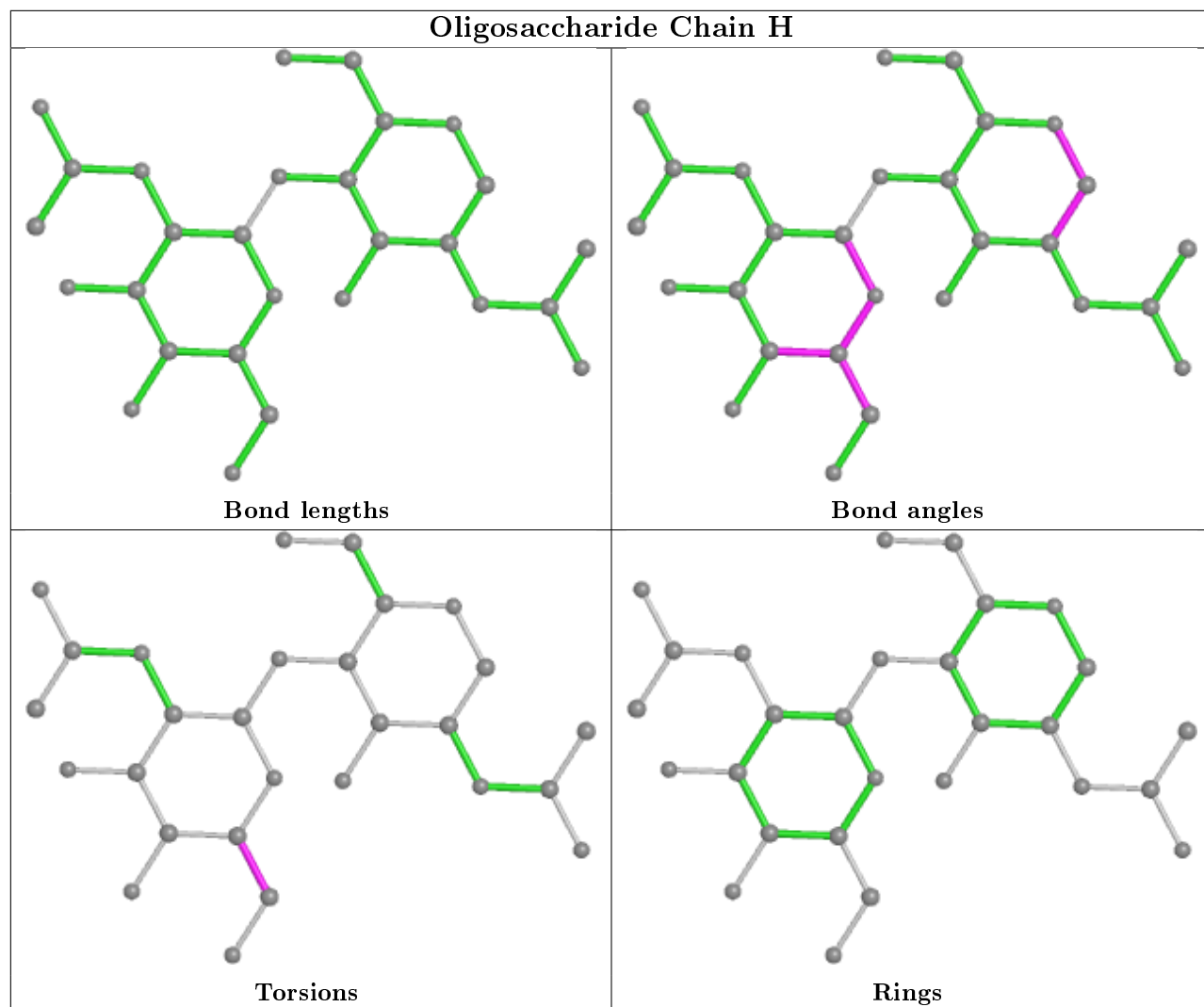


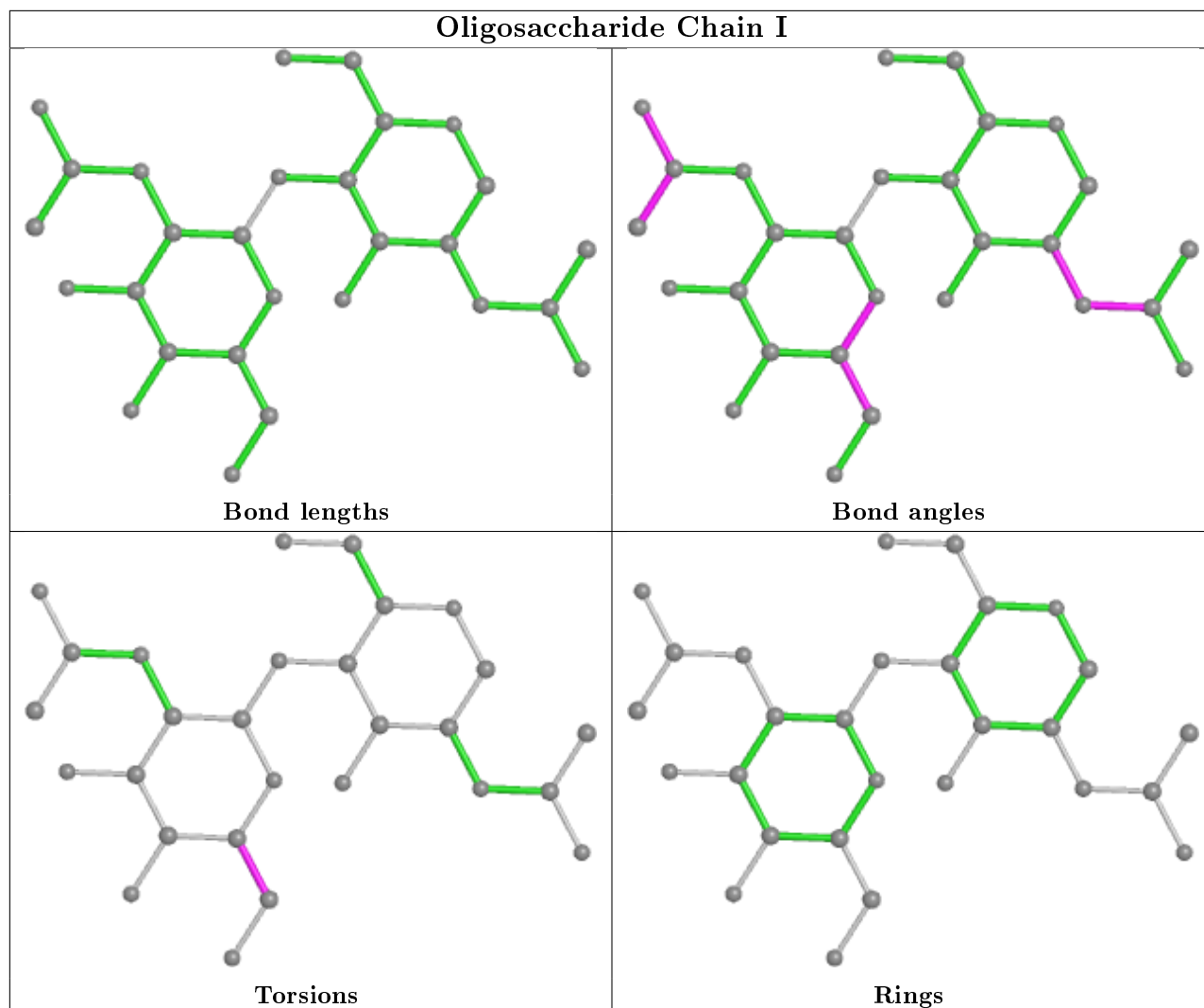












5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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$
4	NAG	B	804	1	14,14,15	0.49	0	17,19,21	1.12	1 (5%)
4	NAG	A	802	1	14,14,15	0.53	0	17,19,21	1.83	5 (29%)
4	NAG	B	811	1	14,14,15	0.53	0	17,19,21	1.26	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	808	1	14,14,15	0.53	0	17,19,21	1.15	2 (11%)
3	LF7	A	801	-	23,25,25	0.83	1 (4%)	33,39,39	1.23	2 (6%)
3	LF7	B	801	1	23,25,25	0.65	0	33,39,39	0.82	1 (3%)
4	NAG	A	807	1	14,14,15	0.48	0	17,19,21	1.00	1 (5%)

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
4	NAG	B	804	1	-	2/6/23/26	0/1/1/1
4	NAG	A	802	1	-	2/6/23/26	0/1/1/1
4	NAG	B	811	1	-	0/6/23/26	0/1/1/1
4	NAG	A	808	1	-	0/6/23/26	0/1/1/1
3	LF7	A	801	-	-	1/10/52/52	0/5/4/4
3	LF7	B	801	1	-	1/10/52/52	0/5/4/4
4	NAG	A	807	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	801	LF7	C16-N15	-2.53	1.46	1.48

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	802	NAG	C1-O5-C5	4.46	118.23	112.19
3	A	801	LF7	C6-C7-C9	4.45	112.07	108.99
4	B	804	NAG	C1-O5-C5	3.75	117.27	112.19
4	B	811	NAG	C1-O5-C5	3.71	117.22	112.19
4	A	802	NAG	O4-C4-C3	3.07	117.44	110.35
4	A	808	NAG	C1-O5-C5	2.90	116.12	112.19
4	A	808	NAG	O5-C5-C6	2.71	111.46	107.20
3	A	801	LF7	C6-C7-C8	-2.41	107.32	108.99
4	A	807	NAG	C1-O5-C5	2.36	115.39	112.19
4	A	802	NAG	O5-C5-C6	2.11	110.52	107.20
4	A	802	NAG	O5-C1-C2	2.08	114.58	111.29
3	B	801	LF7	C9-C7-C8	2.06	111.64	108.93
4	A	802	NAG	O4-C4-C5	2.03	114.34	109.30

There are no chirality outliers.

All (6) torsion outliers are listed below:

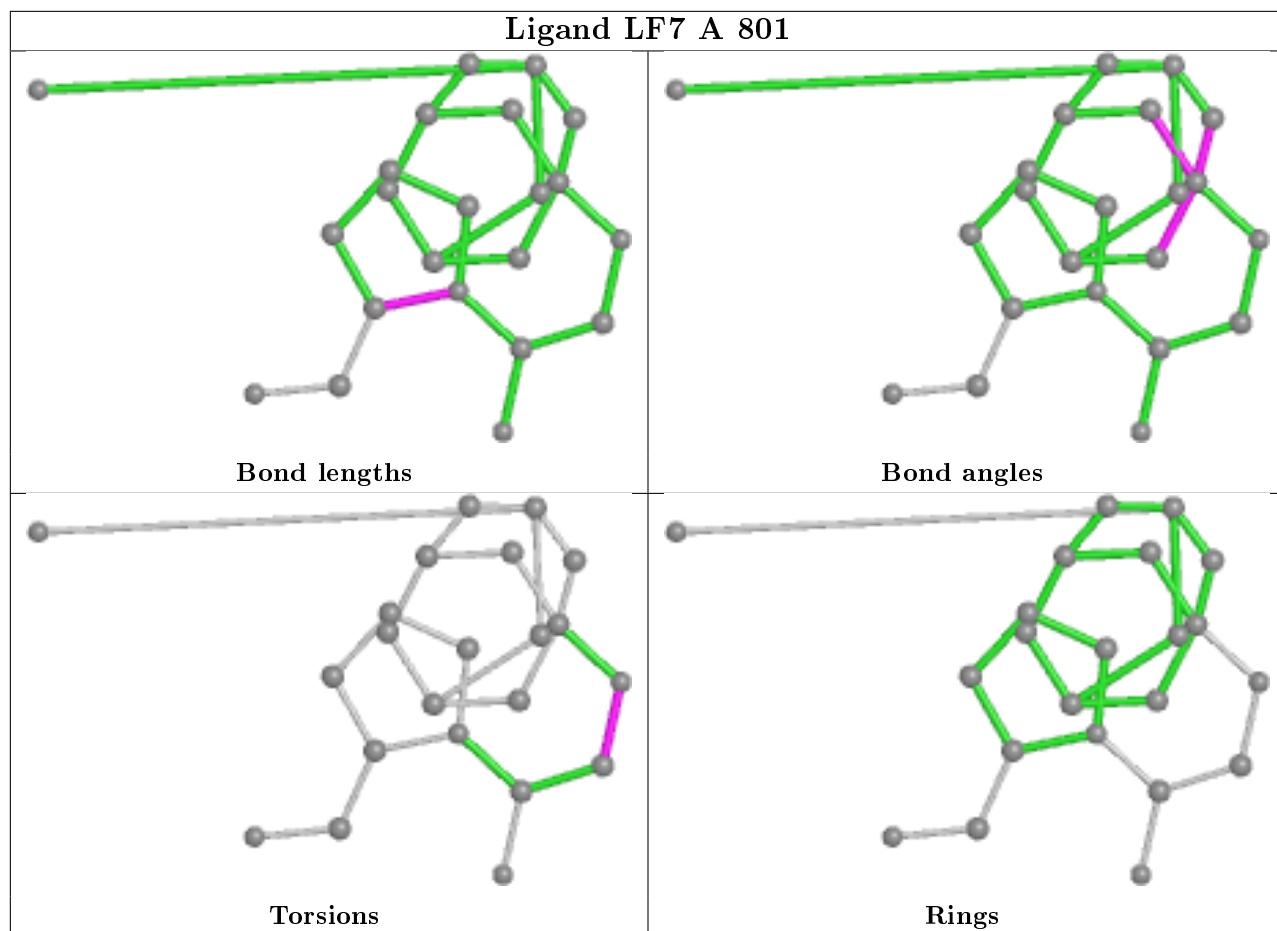
Mol	Chain	Res	Type	Atoms
4	A	802	NAG	O5-C5-C6-O6
4	A	802	NAG	C4-C5-C6-O6
3	A	801	LF7	C14-C13-N12-C7
3	B	801	LF7	C14-C13-N12-C7
4	B	804	NAG	C4-C5-C6-O6
4	B	804	NAG	O5-C5-C6-O6

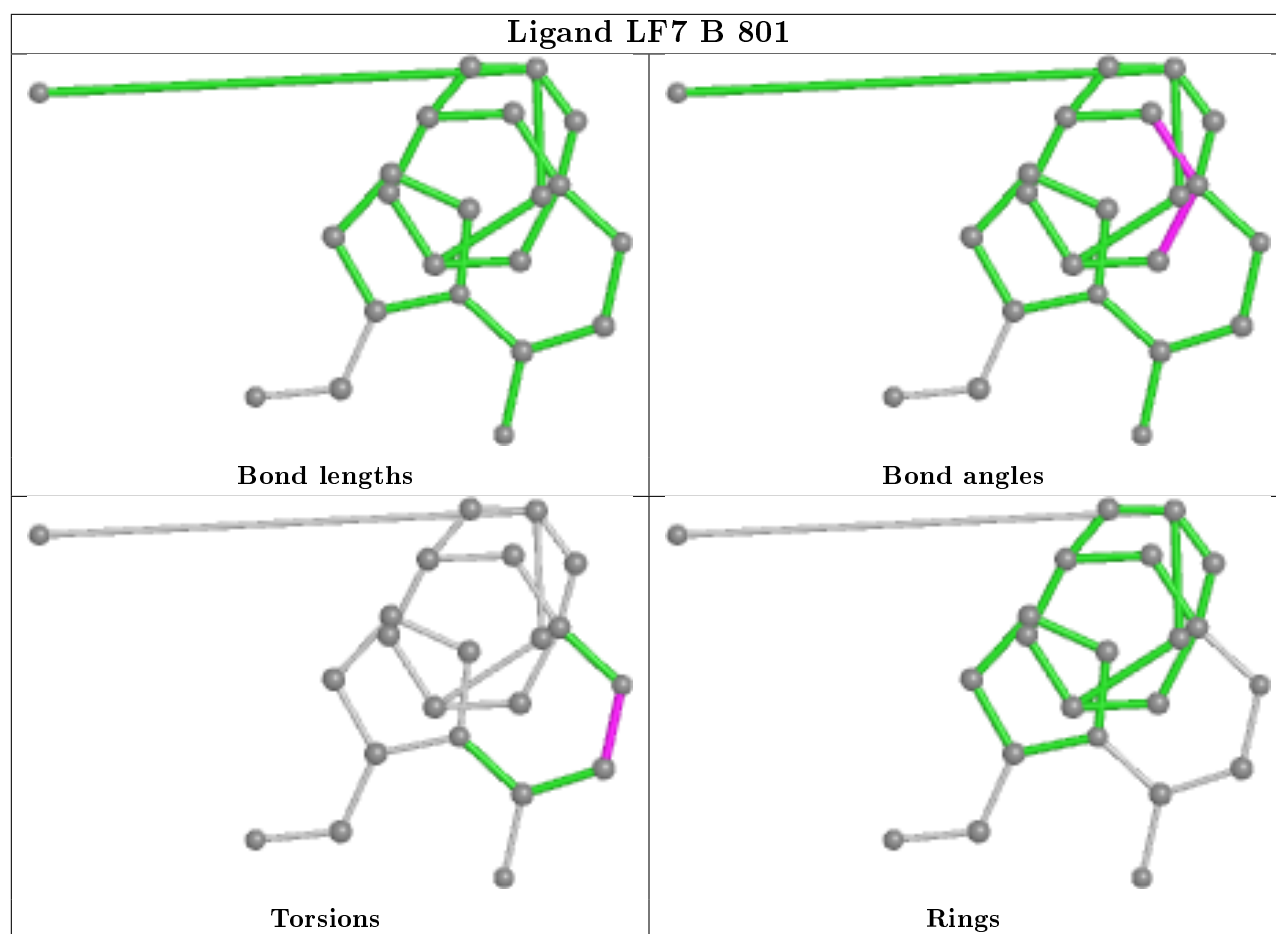
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	804	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 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

6.1 Protein, DNA and RNA chains

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	728/728 (100%)	0.17	30 (4%) 37 35	12, 20, 39, 55	0
1	B	728/728 (100%)	0.23	32 (4%) 34 32	12, 21, 41, 57	0
All	All	1456/1456 (100%)	0.20	62 (4%) 35 33	12, 20, 41, 57	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	39	THR	7.9
1	A	39	THR	7.2
1	B	766	PRO	6.8
1	A	766	PRO	6.4
1	A	279	VAL	5.4
1	A	138	ASN	5.3
1	A	73	GLU	4.6
1	A	74	ASN	4.5
1	A	97	GLU	3.9
1	A	99	GLY	3.7
1	A	96	ASP	3.6
1	B	140	ARG	3.5
1	B	138	ASN	3.4
1	B	73	GLU	3.4
1	B	333	SER	3.4
1	B	121	VAL	3.2
1	B	546[A]	VAL	3.2
1	B	40	ARG	3.1
1	B	96	ASP	3.0
1	B	97	GLU	3.0
1	A	92	ASN	3.0
1	A	140	ARG	3.0
1	B	100	HIS	2.9
1	B	506	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	98	PHE	2.8
1	B	505	GLN	2.8
1	A	333	SER	2.7
1	A	520	ASN	2.7
1	B	521	GLU	2.7
1	A	172	ILE	2.7
1	B	74	ASN	2.7
1	B	332	GLU	2.7
1	B	88	VAL	2.6
1	B	92	ASN	2.6
1	B	502	LYS	2.6
1	A	518	ILE	2.6
1	B	91	GLU	2.6
1	A	521	GLU	2.5
1	A	137	LEU	2.5
1	A	141	GLN	2.5
1	B	71	LYS	2.4
1	B	134	ILE	2.4
1	A	765	LEU	2.4
1	B	537	SER	2.4
1	B	93	SER	2.4
1	A	280	THR	2.4
1	A	336	ARG	2.3
1	B	615	LYS	2.3
1	B	172	ILE	2.3
1	A	166	TYR	2.3
1	B	665	VAL	2.3
1	B	536	LYS	2.3
1	A	335	GLY	2.3
1	B	99	GLY	2.3
1	A	155	VAL	2.2
1	B	378	GLU	2.2
1	A	40	ARG	2.2
1	A	167	VAL	2.2
1	A	164	LEU	2.1
1	A	316	LEU	2.1
1	B	95	PHE	2.1
1	A	332	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

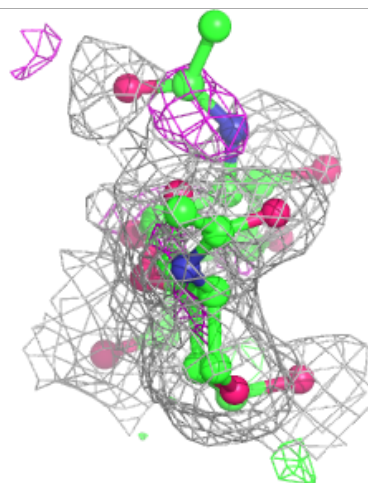
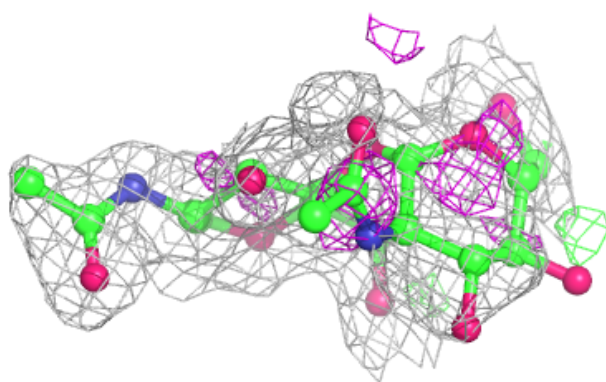
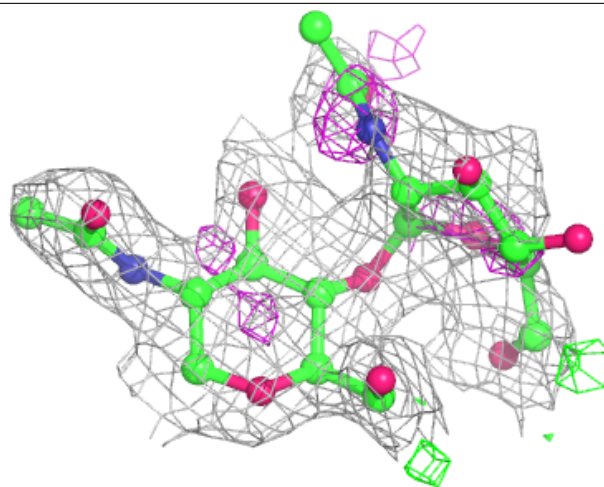
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	F	2	14/15	0.40	0.43	61,64,65,65	0
2	NAG	C	2	14/15	0.57	0.52	59,62,63,63	0
2	NAG	I	2	14/15	0.60	0.27	45,49,51,52	0
2	NAG	E	2	14/15	0.63	0.48	55,59,61,62	0
2	NAG	D	2	14/15	0.73	0.26	45,48,50,51	0
2	NAG	C	1	14/15	0.76	0.28	39,45,50,55	0
2	NAG	F	1	14/15	0.79	0.15	43,47,52,57	0
2	NAG	G	2	14/15	0.81	0.25	41,45,47,48	0
2	NAG	E	1	14/15	0.83	0.24	33,40,42,49	0
2	NAG	H	2	14/15	0.84	0.30	38,42,45,46	0
2	NAG	D	1	14/15	0.86	0.19	30,37,43,44	0
2	NAG	G	1	14/15	0.90	0.20	27,34,41,41	0
2	NAG	I	1	14/15	0.90	0.10	24,30,35,40	0
2	NAG	H	1	14/15	0.91	0.14	20,26,33,33	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.

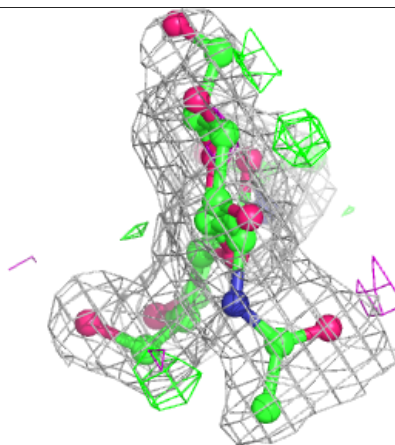
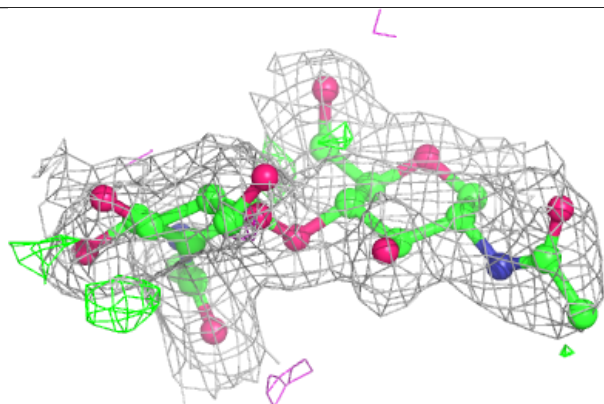
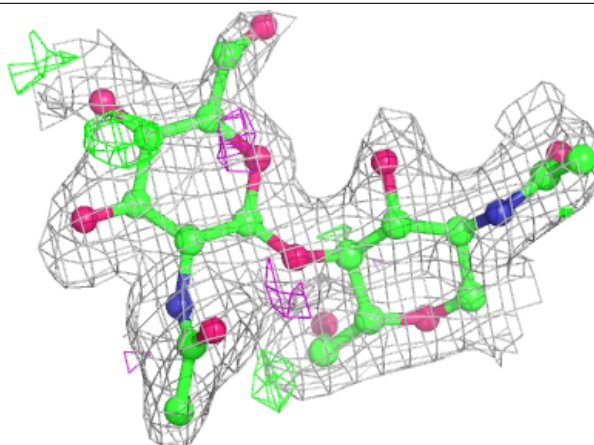
Electron density around Chain C:

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

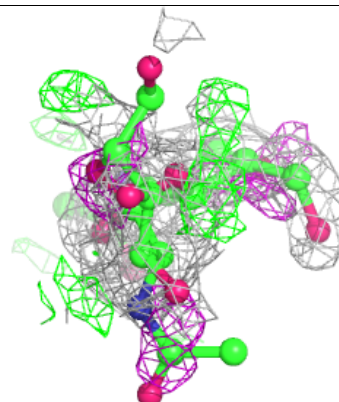
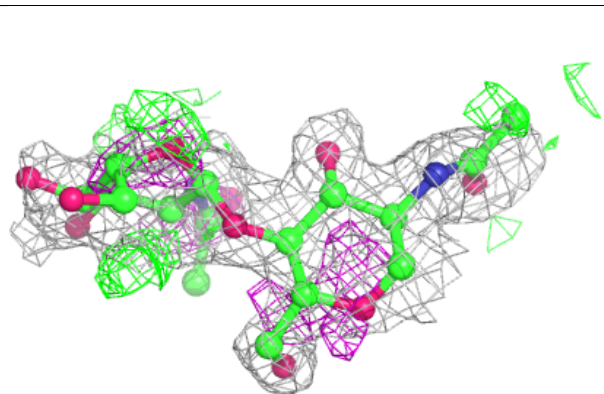
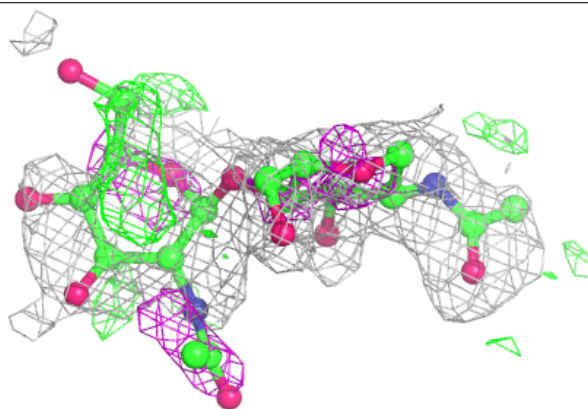


Electron density around Chain D:

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

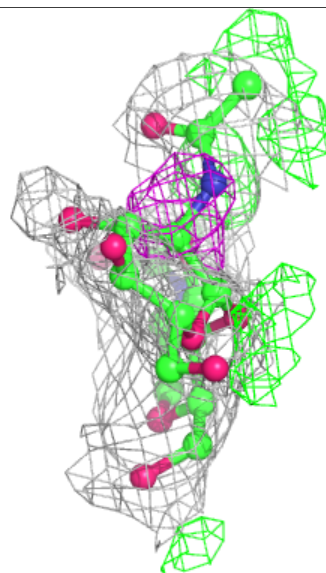
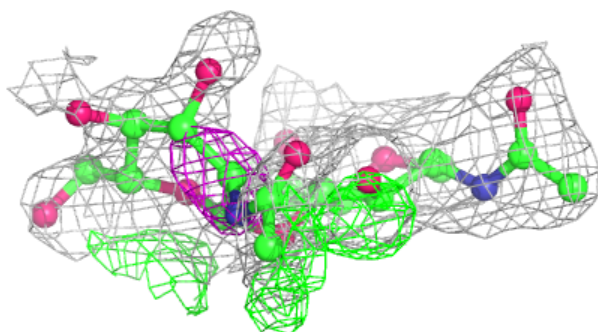
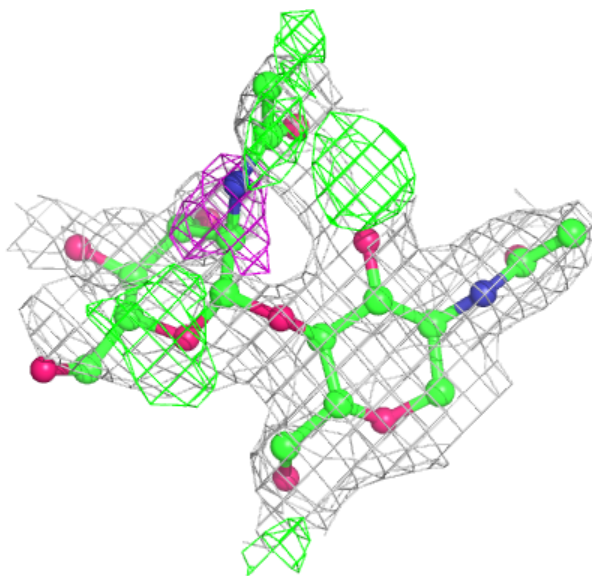
**Electron density around Chain E:**

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



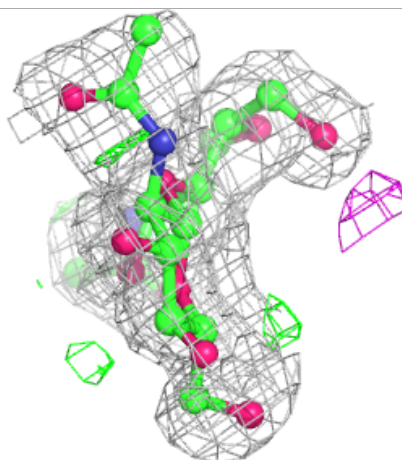
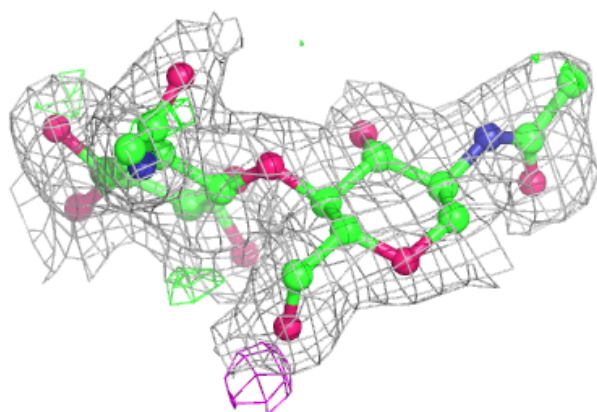
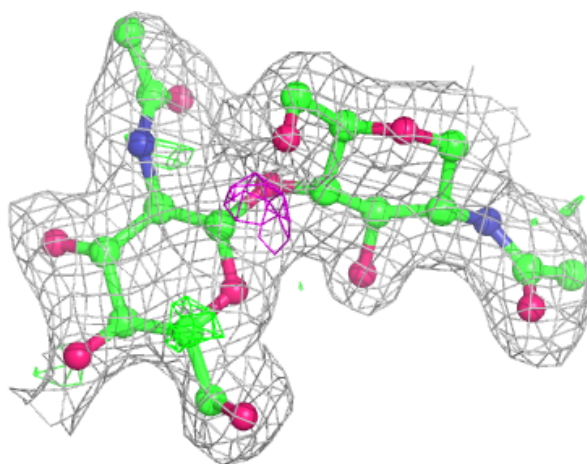
Electron density around Chain F:

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



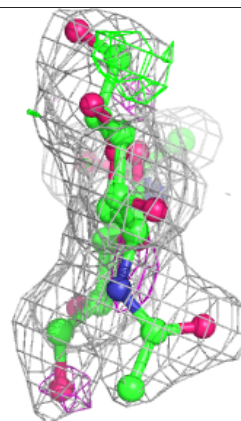
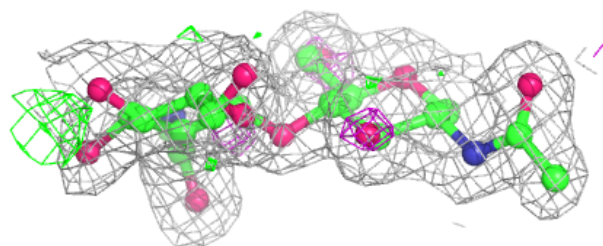
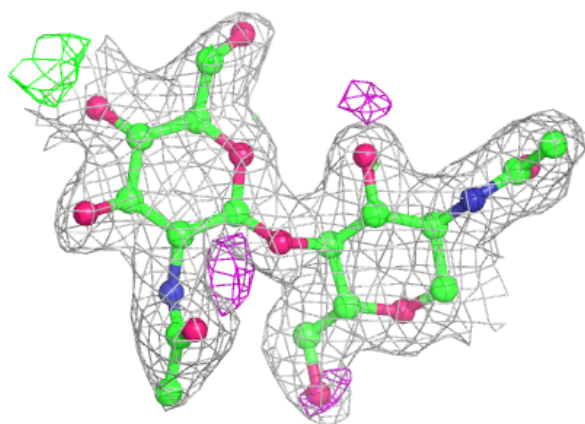
Electron density around Chain G:

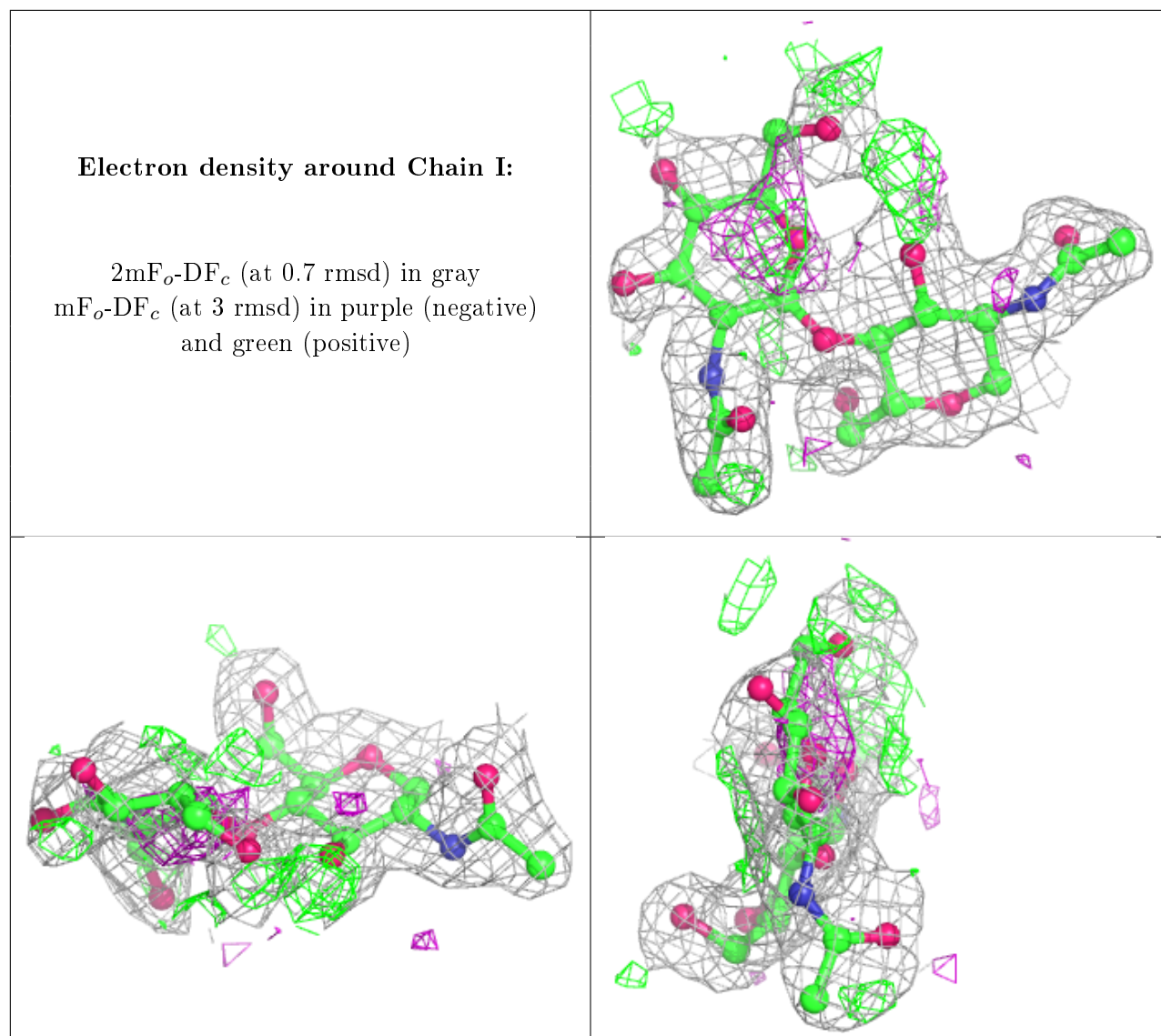
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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.

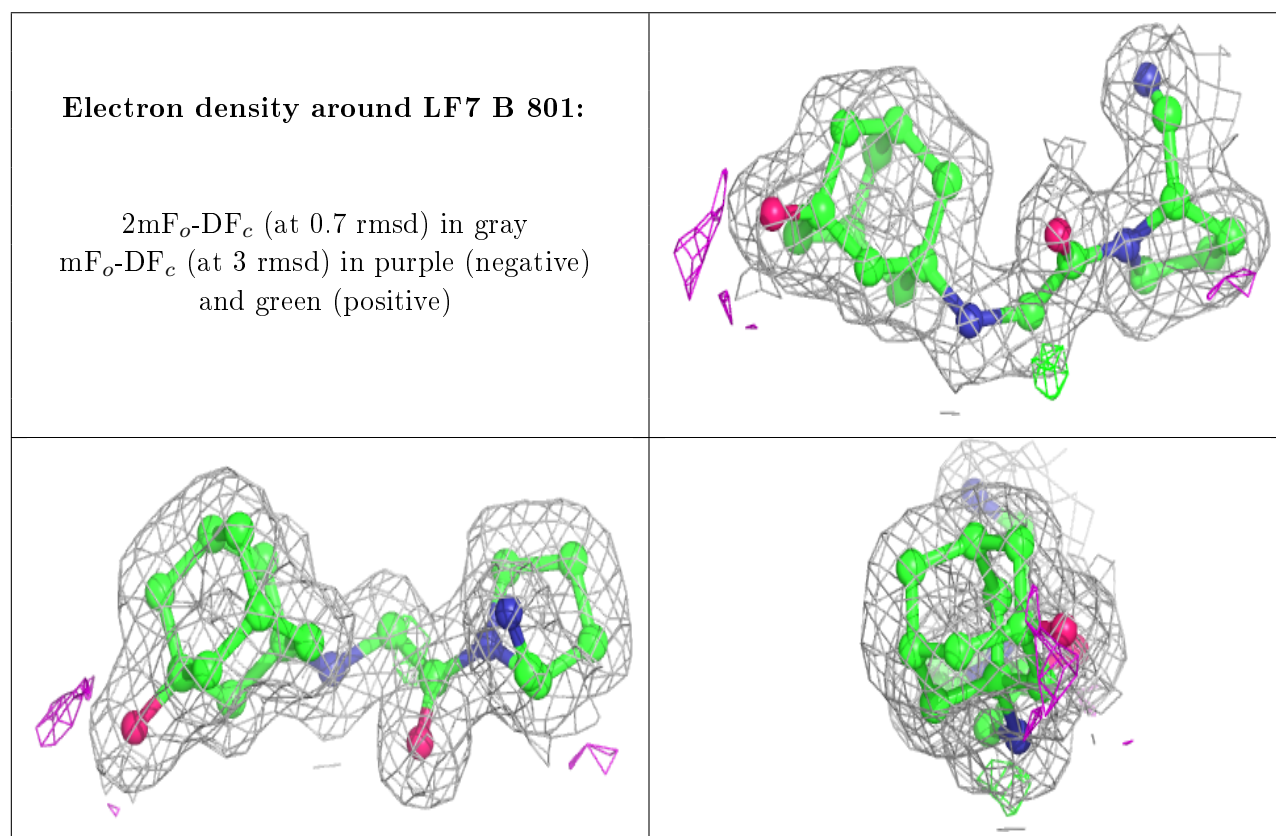
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	B	804	14/15	0.65	0.38	46,52,54,54	0
4	NAG	A	802	14/15	0.83	0.17	38,43,49,55	0
4	NAG	B	811	14/15	0.83	0.23	31,38,41,42	0
4	NAG	A	808	14/15	0.84	0.21	34,40,42,42	0
3	LF7	B	801	22/22	0.94	0.08	12,15,18,21	0
4	NAG	A	807	14/15	0.94	0.14	25,33,36,43	0
3	LF7	A	801	22/22	0.97	0.07	11,14,16,19	0

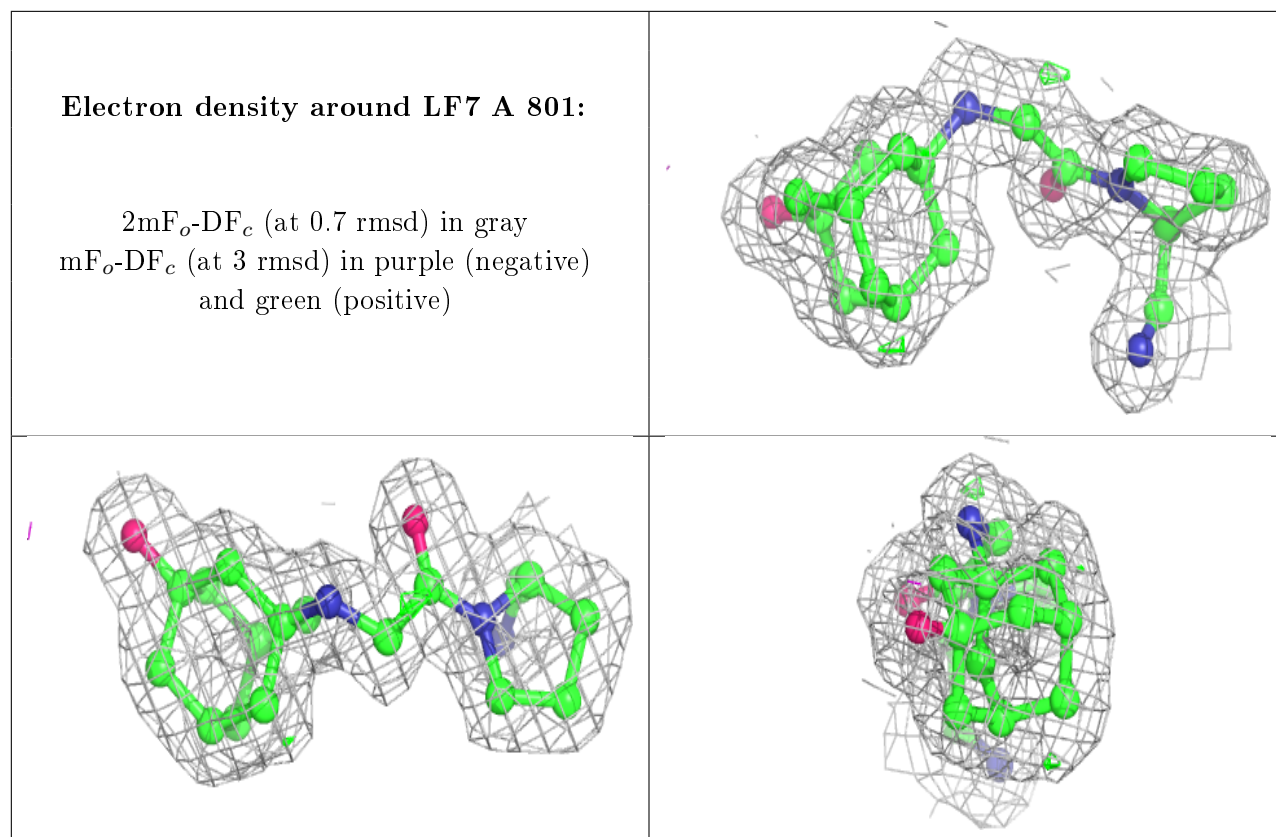
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NA	A	811	1/1	0.99	0.07	20,20,20,20	0

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.





6.5 Other polymers [i](#)

There are no such residues in this entry.