



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 09:04 PM BST

PDB ID : 6SKE
Title : Teneurin 2 in complex with Latrophilin 2 Lec domain
Authors : Shahin, M.; Jackson, V.A.; Carrasquero, M.; Lowe, E.; Seiradake, E.
Deposited on : 2019-08-15
Resolution : 3.62 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
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

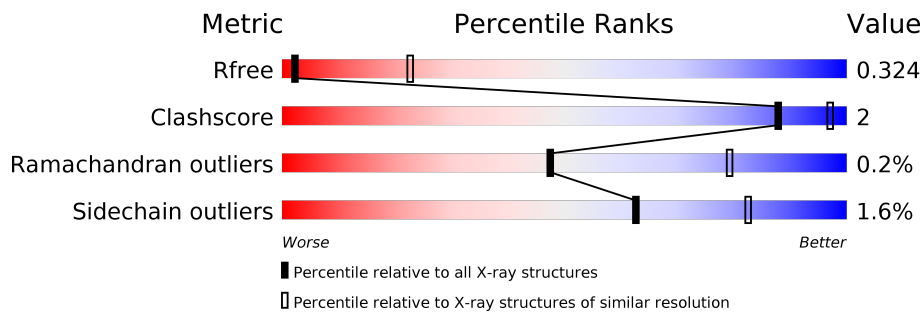
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.62 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.




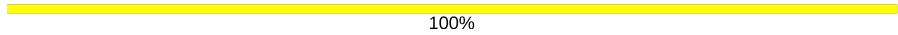




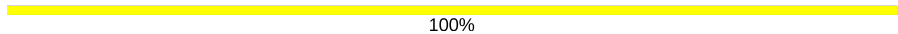
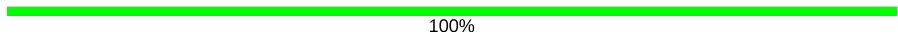

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1290 (3.74-3.50)
Clashscore	141614	1387 (3.74-3.50)
Ramachandran outliers	138981	1339 (3.74-3.50)
Sidechain outliers	138945	1339 (3.74-3.50)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1756	92% (green), 7% (yellow)
1	C	1756	92% (green), 7% (yellow)
2	B	108	86% (green), 11% (grey), 3% (yellow)
2	D	108	85% (green), 11% (grey), 4% (yellow)
3	E	8	13% (green), 88% (yellow)
3	K	8	13% (green), 88% (yellow)
4	F	2	50% (green), 50% (yellow)

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Mol	Chain	Length	Quality of chain
4	G	2	 50% 50%
4	H	2	 100%
4	I	2	 50% 50%
4	J	2	 50% 50%
4	L	2	 50% 50%
4	M	2	 50% 50%
4	N	2	 100%
4	O	2	 100%
4	P	2	 50% 50%

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 30006 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.

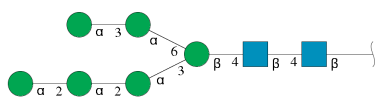
- Molecule 1 is a protein called Teneurin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1752	Total 13851	C 8739	N 2400	O 2653	S 59	0	1	0
1	C	1752	Total 13851	C 8739	N 2400	O 2653	S 59	0	1	0

- Molecule 2 is a protein called Adhesion G protein-coupled receptor L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	96	Total 757	C 468	N 125	O 153	S 11	0	0	0
2	D	96	Total 757	C 468	N 125	O 153	S 11	0	0	0

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



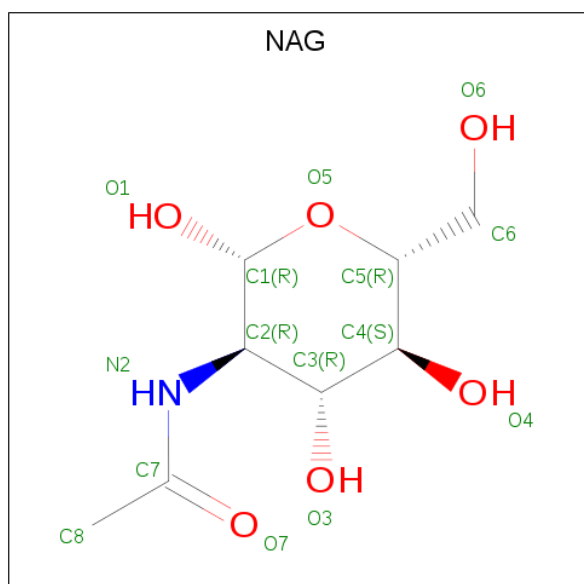
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	8	Total 94	C 52	N 2	O 40	0	0	0
3	K	8	Total 94	C 52	N 2	O 40	0	0	0

- Molecule 4 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
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	N	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	O	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

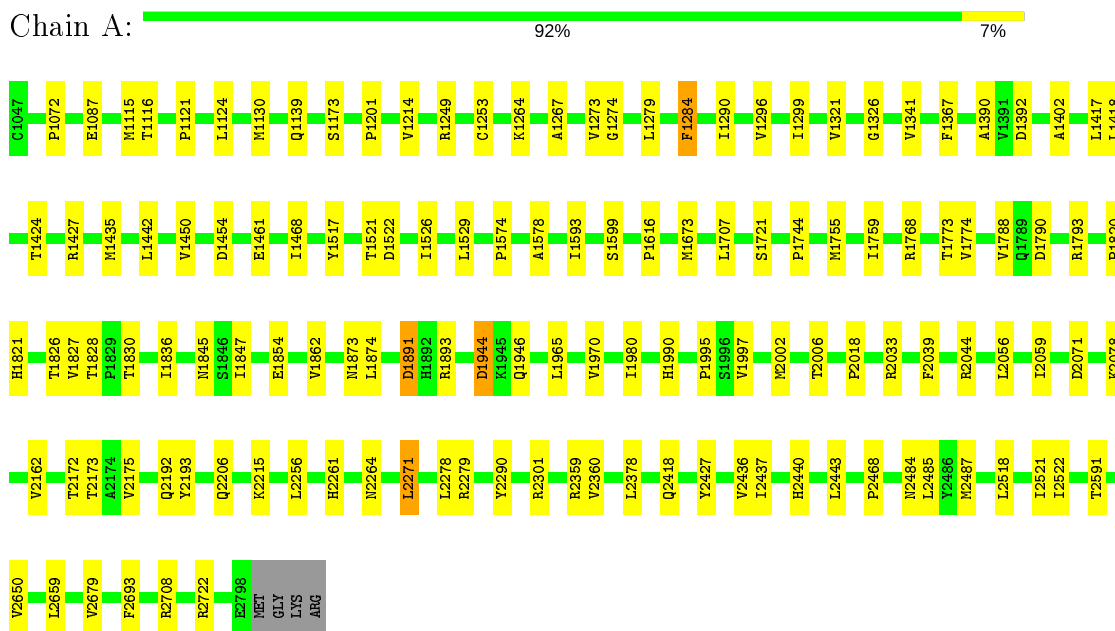
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	105	Total	O	0	0
			105	105		
6	C	105	Total	O	0	0
			105	105		

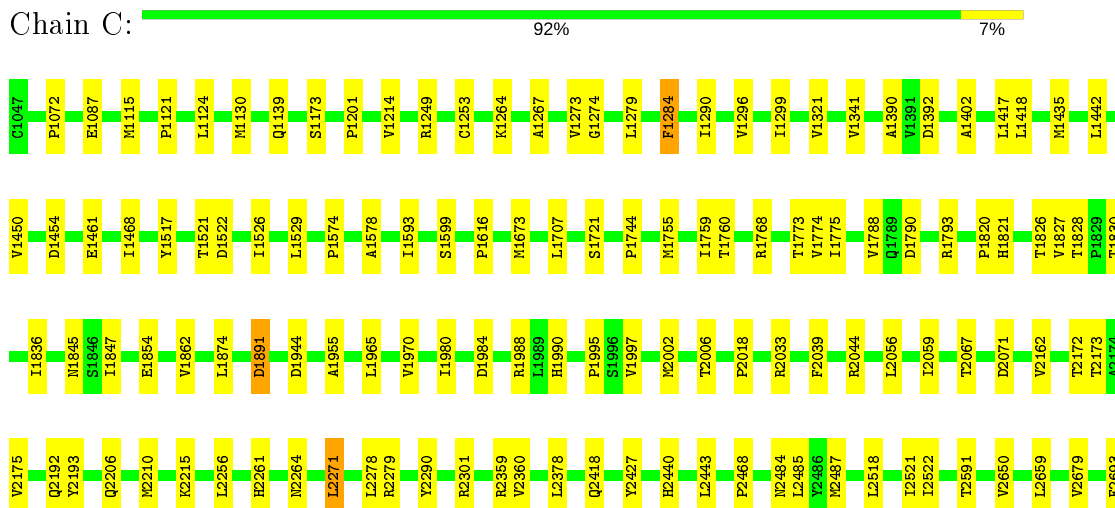
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: Teneurin-2



- Molecule 1: Teneurin-2

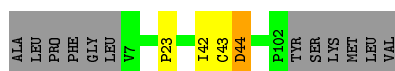
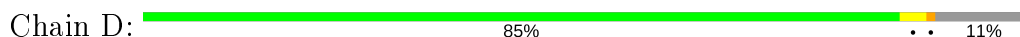




- Molecule 2: Adhesion G protein-coupled receptor L2



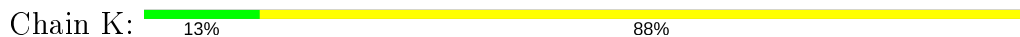
- Molecule 2: Adhesion G protein-coupled receptor L2



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



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




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



MAG1
MAG2

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

Chain H:  100%MAG1
MAG2

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

Chain I:  50% 50%MAG1
MAG2

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

Chain J:  50% 50%MAG1
MAG2

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

Chain L:  50% 50%MAG1
MAG2

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

Chain M:  50% 50%MAG1
MAG2

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

Chain N:  100%MAG1
MAG2

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

Chain O:  100%

MAC1
MAC2

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

Chain P:  50% 50%

MAC1
MAC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	90.87Å 109.92Å 152.21Å 90.19° 93.99° 111.93°	Depositor
Resolution (Å)	84.00 – 3.62 84.05 – 3.62	Depositor EDS
% Data completeness (in resolution range)	96.0 (84.00-3.62) 96.0 (84.05-3.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.58Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.270 , 0.269 0.319 , 0.324	Depositor DCC
R_{free} test set	2997 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	92.6	Xtrriage
Anisotropy	0.567	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 50.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	30006	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.01% 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: BMA, NAG, MAN

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	0.37	0/14147	0.61	0/19182
1	C	0.37	0/14147	0.60	0/19182
2	B	0.36	0/772	0.59	0/1048
2	D	0.36	0/772	0.59	0/1048
All	All	0.37	0/29838	0.60	0/40460

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	13851	0	13600	60	0
1	C	13851	0	13600	59	0
2	B	757	0	707	3	0
2	D	757	0	707	4	0
3	E	94	0	79	0	0
3	K	94	0	79	0	0
4	F	28	0	25	0	0
4	G	28	0	25	0	0
4	H	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	28	0	25	0	0
4	J	28	0	25	0	0
4	L	28	0	25	0	0
4	M	28	0	25	0	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
5	A	56	0	52	0	0
5	C	56	0	52	0	0
6	A	105	0	0	0	0
6	C	105	0	0	0	0
All	All	30006	0	29126	116	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 (116) 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)
2:B:23:PRO:HB3	1:C:2172:THR:HG21	1.61	0.82
1:C:1821:HIS:HD2	1:C:1830:THR:HG21	1.47	0.79
1:A:1821:HIS:HD2	1:A:1830:THR:HG21	1.47	0.78
1:A:2172:THR:HG21	2:D:23:PRO:HB3	1.73	0.69
1:C:2468:PRO:HB3	1:C:2485:LEU:HB3	1.75	0.69
1:A:2468:PRO:HB3	1:A:2485:LEU:HB3	1.75	0.68
1:A:1130:MET:HB2	1:A:1173:SER:HB2	1.78	0.65
1:A:1821:HIS:CD2	1:A:1830:THR:HG21	2.31	0.65
1:C:1821:HIS:CD2	1:C:1830:THR:HG21	2.31	0.65
1:C:1130:MET:HB2	1:C:1173:SER:HB2	1.79	0.65
1:A:1424:THR:HG21	1:C:2067:THR:HG22	1.79	0.64
1:C:1201:PRO:HB3	1:C:1214:VAL:HB	1.80	0.64
1:A:1201:PRO:HB3	1:A:1214:VAL:HB	1.80	0.62
1:A:2264:ASN:HD21	1:A:2271:LEU:HD22	1.65	0.62
1:C:2264:ASN:HD21	1:C:2271:LEU:HD22	1.65	0.62
1:A:1521:THR:HB	1:A:1574:PRO:HD2	1.84	0.60
1:C:1521:THR:HB	1:C:1574:PRO:HD2	1.84	0.59
1:A:1891:ASP:OD2	2:D:43:CYS:HA	2.03	0.58
1:C:2173:THR:HG22	1:C:2175:VAL:H	1.69	0.58
1:A:2173:THR:HG22	1:A:2175:VAL:H	1.69	0.57
1:A:1873:ASN:ND2	2:D:44:ASP:HB3	2.20	0.56
1:A:2290:TYR:CZ	1:A:2301:ARG:HG3	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1773:THR:HG23	1:A:1788:VAL:HB	1.88	0.55
1:C:2418:GLN:HB2	1:C:2427:TYR:HB3	1.89	0.55
1:C:2290:TYR:CZ	1:C:2301:ARG:HG3	2.41	0.55
1:C:1274:GLY:HA2	1:C:1321:VAL:HG11	1.89	0.54
1:A:1367:PHE:HB2	1:C:2071:ASP:HA	1.89	0.54
1:A:2418:GLN:HB2	1:A:2427:TYR:HB3	1.89	0.54
1:C:1854:GLU:HB2	1:C:1862:VAL:HB	1.91	0.53
1:A:1854:GLU:HB2	1:A:1862:VAL:HB	1.90	0.53
1:A:1390:ALA:HB1	1:A:1450:VAL:HG23	1.89	0.53
1:A:1970:VAL:HG22	1:A:1980:ILE:HG12	1.91	0.52
1:C:1773:THR:HG23	1:C:1788:VAL:HB	1.90	0.52
1:C:1390:ALA:HB1	1:C:1450:VAL:HG23	1.91	0.52
2:B:43:CYS:HA	1:C:1891:ASP:OD2	2.10	0.52
1:A:1274:GLY:HA2	1:A:1321:VAL:HG11	1.92	0.52
1:C:1970:VAL:HG22	1:C:1980:ILE:HG12	1.91	0.51
1:C:1299:ILE:HD12	1:C:1341:VAL:HG11	1.92	0.51
1:C:1827:VAL:HG13	1:C:1828:THR:HG23	1.94	0.50
1:A:1299:ILE:HD12	1:A:1341:VAL:HG11	1.94	0.50
1:A:2071:ASP:HB2	1:A:2078:LYS:HG3	1.94	0.50
1:C:1130:MET:HG2	1:C:1139:GLN:HG2	1.93	0.50
1:A:1130:MET:HG2	1:A:1139:GLN:HG2	1.93	0.50
1:A:1827:VAL:HG13	1:A:1828:THR:HG23	1.94	0.49
1:A:2039:PHE:HB2	1:A:2044:ARG:HB2	1.95	0.49
1:C:1744:PRO:HB2	1:C:2006:THR:HG21	1.94	0.49
1:A:1744:PRO:HB2	1:A:2006:THR:HG21	1.94	0.49
1:A:1820:PRO:HB3	1:A:1826:THR:HA	1.94	0.49
1:A:1442:LEU:HG	1:A:1461:GLU:HG3	1.95	0.49
1:C:2039:PHE:HB2	1:C:2044:ARG:HB2	1.94	0.48
1:C:1273:VAL:HG23	1:C:1578:ALA:HB1	1.95	0.48
1:C:1442:LEU:HG	1:C:1461:GLU:HG3	1.95	0.48
1:C:1820:PRO:HB3	1:C:1826:THR:HA	1.95	0.48
1:C:2659:LEU:HD21	1:C:2679:VAL:HG11	1.96	0.48
1:A:1273:VAL:HG23	1:A:1578:ALA:HB1	1.95	0.47
1:A:1788:VAL:HG22	1:A:1793:ARG:HG2	1.97	0.47
1:C:1995:PRO:HB2	1:C:2256:LEU:HB3	1.96	0.47
1:A:1995:PRO:HB2	1:A:2256:LEU:HB3	1.96	0.47
1:A:1290:ILE:HG12	1:A:1296:VAL:HG22	1.96	0.46
1:A:2056:LEU:HD21	1:A:2059:ILE:HD11	1.98	0.46
1:A:1517:TYR:HB3	1:A:1529:LEU:HD11	1.97	0.46
1:C:2056:LEU:HD21	1:C:2059:ILE:HD11	1.97	0.46
1:C:1290:ILE:HG12	1:C:1296:VAL:HG22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1517:TYR:HB3	1:C:1529:LEU:HD11	1.96	0.46
1:A:2659:LEU:HD21	1:A:2679:VAL:HG11	1.96	0.46
1:C:1755:MET:HG3	1:C:1759:ILE:HG12	1.98	0.46
1:C:1788:VAL:HG22	1:C:1793:ARG:HG2	1.98	0.46
1:A:1522:ASP:HB2	1:A:1526:ILE:HB	1.98	0.45
1:A:1755:MET:HG3	1:A:1759:ILE:HG12	1.98	0.45
1:A:2206:GLN:HB2	1:A:2215:LYS:HB3	1.99	0.45
1:C:2518:LEU:HB3	1:C:2522:ILE:HD12	1.99	0.45
1:C:2206:GLN:HB2	1:C:2215:LYS:HB3	1.99	0.44
1:C:1249:ARG:HB3	1:C:1264:LYS:HB3	1.99	0.44
1:C:1522:ASP:HB2	1:C:1526:ILE:HB	1.98	0.44
1:C:1121:PRO:HG2	1:C:1124:LEU:HB2	2.00	0.44
1:A:2518:LEU:HB3	1:A:2522:ILE:HD12	1.99	0.44
1:A:1121:PRO:HG2	1:A:1124:LEU:HB2	2.00	0.43
1:C:1417:LEU:HD21	1:C:1468:ILE:HG21	2.00	0.43
2:B:23:PRO:HB3	1:C:2172:THR:CG2	2.41	0.43
1:C:1267:ALA:HB3	1:C:1284:PHE:HB2	2.00	0.43
1:C:1955:ALA:HB3	1:C:2210:MET:HE3	2.00	0.43
1:C:1279:LEU:HD23	1:C:1290:ILE:HD12	2.01	0.43
1:A:1427:ARG:HB2	1:C:2780:GLN:OE1	2.19	0.43
1:C:2650:VAL:HG12	1:C:2708:ARG:HB3	2.01	0.43
1:A:1836:ILE:HB	1:A:1845:ASN:HB2	2.01	0.43
1:A:1267:ALA:HB3	1:A:1284:PHE:HB2	2.00	0.42
1:A:1249:ARG:HB3	1:A:1264:LYS:HB3	2.00	0.42
1:A:1279:LEU:HD23	1:A:1290:ILE:HD12	2.01	0.42
1:C:2484:ASN:HB3	1:C:2487:MET:HG2	2.01	0.42
1:A:1072:PRO:HB2	1:A:1087:GLU:HG2	2.02	0.42
1:A:1417:LEU:HD21	1:A:1468:ILE:HG21	2.01	0.42
1:A:2650:VAL:HG12	1:A:2708:ARG:HB3	2.01	0.42
1:C:1874:LEU:HD13	1:C:2521:ILE:HD12	2.01	0.42
1:C:1707:LEU:HB3	1:C:1721:SER:HB2	2.02	0.42
1:C:1836:ILE:HB	1:C:1845:ASN:HB2	2.01	0.42
1:C:2018:PRO:HD2	1:C:2279:ARG:HG2	2.02	0.42
1:A:2360:VAL:HG21	1:A:2443:LEU:HD21	2.01	0.42
1:A:2693:PHE:CD2	1:A:2708:ARG:HG3	2.55	0.42
1:A:1874:LEU:HD13	1:A:2521:ILE:HD12	2.01	0.42
1:C:1072:PRO:HB2	1:C:1087:GLU:HG2	2.02	0.42
1:A:1707:LEU:HB3	1:A:1721:SER:HB2	2.02	0.41
1:A:2484:ASN:HB3	1:A:2487:MET:HG2	2.01	0.41
1:C:1768:ARG:HH22	1:C:2033:ARG:HD2	1.85	0.41
1:C:1616:PRO:HG2	1:C:1830:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2162:VAL:HG11	1:C:2378:LEU:HD11	2.03	0.41
1:C:2693:PHE:CD2	1:C:2708:ARG:HG3	2.55	0.41
1:A:1616:PRO:HG2	1:A:1830:THR:HG22	2.02	0.41
1:A:2018:PRO:HD2	1:A:2279:ARG:HG2	2.02	0.41
1:A:1893:ARG:HG3	2:D:42:ILE:HD11	2.03	0.41
1:C:1760:THR:HG22	1:C:1775:ILE:HG23	2.03	0.41
1:C:2360:VAL:HG21	1:C:2443:LEU:HD21	2.02	0.41
1:A:2436:VAL:HG12	1:A:2437:ILE:HD12	2.03	0.40
1:A:1944:ASP:HB3	1:A:1946:GLN:H	1.87	0.40
1:A:1768:ARG:HH22	1:A:2033:ARG:HD2	1.85	0.40
1:A:2162:VAL:HG11	1:A:2378:LEU:HD11	2.03	0.40
1:C:1984:ASP:HB2	1:C:1988:ARG:O	2.22	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	1751/1756 (100%)	1688 (96%)	58 (3%)	5 (0%)	41	74
1	C	1751/1756 (100%)	1689 (96%)	58 (3%)	4 (0%)	47	79
2	B	94/108 (87%)	92 (98%)	2 (2%)	0	100	100
2	D	94/108 (87%)	92 (98%)	2 (2%)	0	100	100
All	All	3690/3728 (99%)	3561 (96%)	120 (3%)	9 (0%)	47	79

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1284	PHE
1	A	1997	VAL
1	C	1284	PHE

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Mol	Chain	Res	Type
1	C	1997	VAL
1	A	1402	ALA
1	A	1790	ASP
1	C	1402	ALA
1	C	1790	ASP
1	A	1326	GLY

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	1527/1529 (100%)	1500 (98%)	27 (2%)	59	81
1	C	1527/1529 (100%)	1501 (98%)	26 (2%)	60	82
2	B	88/98 (90%)	87 (99%)	1 (1%)	73	87
2	D	88/98 (90%)	87 (99%)	1 (1%)	73	87
All	All	3230/3254 (99%)	3175 (98%)	55 (2%)	62	82

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1115	MET
1	A	1116	THR
1	A	1253	CYS
1	A	1392	ASP
1	A	1418	LEU
1	A	1435	MET
1	A	1454	ASP
1	A	1593	ILE
1	A	1599	SER
1	A	1673	MET
1	A	1774	VAL
1	A	1847	ILE
1	A	1891	ASP
1	A	1944	ASP
1	A	1965	LEU

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Mol	Chain	Res	Type
1	A	1990[A]	HIS
1	A	1990[B]	HIS
1	A	2002	MET
1	A	2192	GLN
1	A	2193	TYR
1	A	2261	HIS
1	A	2271	LEU
1	A	2278	LEU
1	A	2359	ARG
1	A	2440	HIS
1	A	2591	THR
1	A	2722	ARG
2	B	44	ASP
1	C	1115	MET
1	C	1253	CYS
1	C	1392	ASP
1	C	1418	LEU
1	C	1435	MET
1	C	1454	ASP
1	C	1593	ILE
1	C	1599	SER
1	C	1673	MET
1	C	1774	VAL
1	C	1847	ILE
1	C	1891	ASP
1	C	1944	ASP
1	C	1965	LEU
1	C	1990[A]	HIS
1	C	1990[B]	HIS
1	C	2002	MET
1	C	2192	GLN
1	C	2193	TYR
1	C	2261	HIS
1	C	2271	LEU
1	C	2278	LEU
1	C	2359	ARG
1	C	2440	HIS
1	C	2591	THR
1	C	2722	ARG
2	D	44	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1311	ASN
1	A	1439	GLN
1	A	1483	HIS
1	A	1873	ASN
1	A	1892	HIS
1	A	2362	HIS
1	C	1311	ASN
1	C	1483	HIS
1	C	1892	HIS
1	C	2362	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](#)

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	$\# Z > 2$
3	NAG	E	1	1,3	14,14,15	0.39	0	17,19,21	0.78	1 (5%)
3	NAG	E	2	3	14,14,15	0.41	0	17,19,21	1.20	3 (17%)
3	BMA	E	3	3	11,11,12	0.64	0	15,15,17	0.73	0
3	MAN	E	4	3	11,11,12	0.74	0	15,15,17	1.04	2 (13%)
3	MAN	E	5	3	11,11,12	0.67	0	15,15,17	0.78	1 (6%)
3	MAN	E	6	3	11,11,12	0.64	0	15,15,17	0.75	1 (6%)
3	MAN	E	7	3	11,11,12	0.75	0	15,15,17	1.35	2 (13%)
3	MAN	E	8	3	11,11,12	0.59	0	15,15,17	0.98	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	F	1	1,4	14,14,15	0.44	0	17,19,21	0.79	0
4	NAG	F	2	4	14,14,15	0.43	0	17,19,21	0.81	1 (5%)
4	NAG	G	1	1,4	14,14,15	0.46	0	17,19,21	0.55	0
4	NAG	G	2	4	14,14,15	0.42	0	17,19,21	0.90	1 (5%)
4	NAG	H	1	1,4	14,14,15	0.42	0	17,19,21	0.84	1 (5%)
4	NAG	H	2	4	14,14,15	0.41	0	17,19,21	0.93	1 (5%)
4	NAG	I	1	1,4	14,14,15	0.45	0	17,19,21	0.77	0
4	NAG	I	2	4	14,14,15	0.43	0	17,19,21	0.69	1 (5%)
4	NAG	J	1	1,4	14,14,15	0.45	0	17,19,21	0.80	0
4	NAG	J	2	4	14,14,15	0.40	0	17,19,21	1.07	1 (5%)
3	NAG	K	1	1,3	14,14,15	0.40	0	17,19,21	0.79	1 (5%)
3	NAG	K	2	3	14,14,15	0.40	0	17,19,21	1.20	3 (17%)
3	BMA	K	3	3	11,11,12	0.64	0	15,15,17	0.73	0
3	MAN	K	4	3	11,11,12	0.74	0	15,15,17	1.04	2 (13%)
3	MAN	K	5	3	11,11,12	0.65	0	15,15,17	0.79	1 (6%)
3	MAN	K	6	3	11,11,12	0.65	0	15,15,17	0.75	1 (6%)
3	MAN	K	7	3	11,11,12	0.74	0	15,15,17	1.34	2 (13%)
3	MAN	K	8	3	11,11,12	0.58	0	15,15,17	0.97	2 (13%)
4	NAG	L	1	1,4	14,14,15	0.44	0	17,19,21	0.78	0
4	NAG	L	2	4	14,14,15	0.42	0	17,19,21	0.81	1 (5%)
4	NAG	M	1	1,4	14,14,15	0.45	0	17,19,21	0.55	0
4	NAG	M	2	4	14,14,15	0.39	0	17,19,21	0.90	1 (5%)
4	NAG	N	1	1,4	14,14,15	0.43	0	17,19,21	0.85	1 (5%)
4	NAG	N	2	4	14,14,15	0.43	0	17,19,21	0.92	1 (5%)
4	NAG	O	1	1,4	14,14,15	0.46	0	17,19,21	0.77	0
4	NAG	O	2	4	14,14,15	0.44	0	17,19,21	0.69	0
4	NAG	P	1	1,4	14,14,15	0.44	0	17,19,21	0.80	0
4	NAG	P	2	4	14,14,15	0.40	0	17,19,21	1.07	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
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
3	MAN	E	5	3	-	0/2/19/22	0/1/1/1
3	MAN	E	6	3	-	0/2/19/22	0/1/1/1
3	MAN	E	7	3	-	0/2/19/22	0/1/1/1
3	MAN	E	8	3	-	2/2/19/22	0/1/1/1
4	NAG	F	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	NAG	G	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	4/6/23/26	0/1/1/1
4	NAG	H	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	2/6/23/26	0/1/1/1
4	NAG	I	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
4	NAG	J	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	0/1/1/1
3	NAG	K	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	0/6/23/26	0/1/1/1
3	BMA	K	3	3	-	2/2/19/22	0/1/1/1
3	MAN	K	4	3	-	0/2/19/22	0/1/1/1
3	MAN	K	5	3	-	0/2/19/22	0/1/1/1
3	MAN	K	6	3	-	0/2/19/22	0/1/1/1
3	MAN	K	7	3	-	0/2/19/22	0/1/1/1
3	MAN	K	8	3	-	2/2/19/22	0/1/1/1
4	NAG	L	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	L	2	4	-	2/6/23/26	0/1/1/1
4	NAG	M	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	M	2	4	-	4/6/23/26	0/1/1/1
4	NAG	N	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	N	2	4	-	2/6/23/26	0/1/1/1
4	NAG	O	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
4	NAG	P	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	7	MAN	C1-O5-C5	4.28	117.99	112.19
3	K	7	MAN	C1-O5-C5	4.27	117.98	112.19
3	E	4	MAN	C1-O5-C5	2.80	115.99	112.19
3	K	2	NAG	C2-N2-C7	2.80	126.89	122.90
3	E	2	NAG	C2-N2-C7	2.79	126.88	122.90
3	K	4	MAN	C1-O5-C5	2.78	115.95	112.19
3	K	5	MAN	C1-O5-C5	2.67	115.80	112.19
4	P	2	NAG	C2-N2-C7	2.65	126.68	122.90
4	J	2	NAG	C2-N2-C7	2.63	126.64	122.90
3	E	5	MAN	C1-O5-C5	2.61	115.73	112.19
4	G	2	NAG	C2-N2-C7	2.49	126.45	122.90
3	K	2	NAG	O5-C1-C2	2.47	115.19	111.29
4	M	2	NAG	C2-N2-C7	2.47	126.42	122.90
3	E	2	NAG	O5-C1-C2	2.45	115.16	111.29
3	K	1	NAG	C1-O5-C5	2.33	115.35	112.19
3	K	6	MAN	C1-O5-C5	2.31	115.32	112.19
3	E	1	NAG	C1-O5-C5	2.31	115.32	112.19
3	E	6	MAN	C1-O5-C5	2.29	115.30	112.19
4	N	2	NAG	C1-C2-N2	-2.20	106.73	110.49
4	F	2	NAG	C2-N2-C7	2.18	126.01	122.90
4	H	2	NAG	C1-C2-N2	-2.17	106.77	110.49
4	L	2	NAG	C2-N2-C7	2.12	125.92	122.90
3	K	4	MAN	C1-C2-C3	2.10	112.25	109.67
3	E	4	MAN	C1-C2-C3	2.08	112.22	109.67
3	K	2	NAG	C1-C2-N2	-2.07	106.96	110.49
4	N	1	NAG	C2-N2-C7	2.05	125.83	122.90
3	E	2	NAG	C1-C2-N2	-2.05	106.98	110.49
3	E	8	MAN	C1-O5-C5	2.04	114.95	112.19
3	E	8	MAN	C1-C2-C3	2.03	112.16	109.67
3	K	8	MAN	C1-C2-C3	2.02	112.15	109.67
4	H	1	NAG	C2-N2-C7	2.01	125.77	122.90
3	K	7	MAN	C1-C2-C3	2.01	112.14	109.67
3	K	8	MAN	C1-O5-C5	2.01	114.91	112.19
3	E	7	MAN	C1-C2-C3	2.01	112.13	109.67
4	I	2	NAG	C1-O5-C5	2.00	114.91	112.19

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	2	NAG	C8-C7-N2-C2
4	H	2	NAG	O7-C7-N2-C2
4	M	1	NAG	C8-C7-N2-C2

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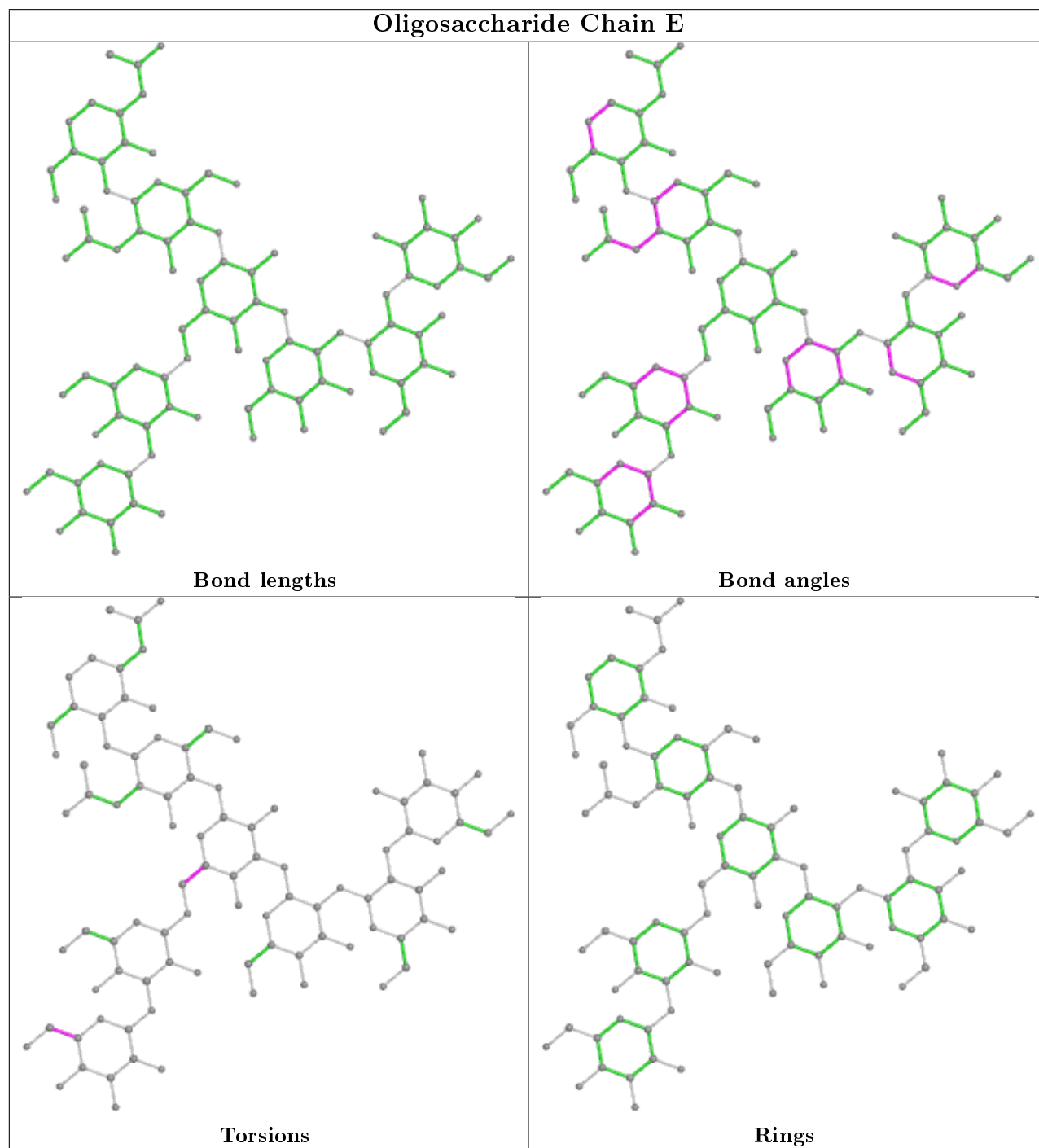
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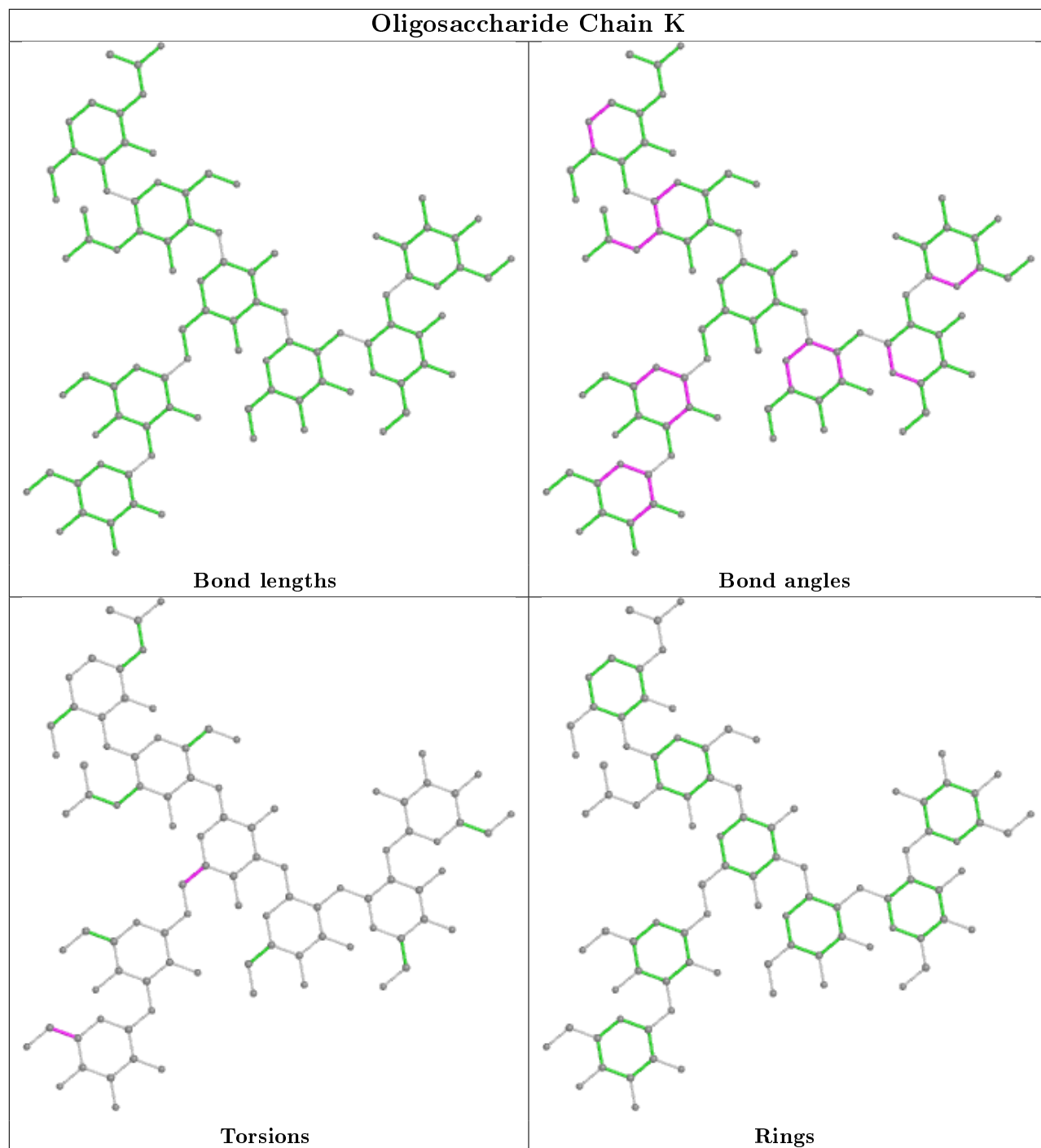
Mol	Chain	Res	Type	Atoms
4	M	1	NAG	O7-C7-N2-C2
4	O	2	NAG	C8-C7-N2-C2
4	O	2	NAG	O7-C7-N2-C2
4	I	2	NAG	C8-C7-N2-C2
4	I	2	NAG	O7-C7-N2-C2
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2
4	N	2	NAG	C8-C7-N2-C2
4	N	2	NAG	O7-C7-N2-C2
3	K	3	BMA	C4-C5-C6-O6
3	E	3	BMA	C4-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	L	2	NAG	O5-C5-C6-O6
3	K	3	BMA	O5-C5-C6-O6
3	E	3	BMA	O5-C5-C6-O6
3	K	8	MAN	C4-C5-C6-O6
3	E	8	MAN	C4-C5-C6-O6
4	G	2	NAG	C8-C7-N2-C2
4	M	2	NAG	C8-C7-N2-C2
4	F	2	NAG	C4-C5-C6-O6
4	L	2	NAG	C4-C5-C6-O6
3	K	8	MAN	O5-C5-C6-O6
3	E	8	MAN	O5-C5-C6-O6
4	G	2	NAG	O7-C7-N2-C2
4	M	2	NAG	O7-C7-N2-C2
4	L	1	NAG	C8-C7-N2-C2
4	F	1	NAG	C8-C7-N2-C2
4	N	1	NAG	C8-C7-N2-C2
4	H	1	NAG	C8-C7-N2-C2
4	I	1	NAG	C8-C7-N2-C2
4	O	1	NAG	C8-C7-N2-C2
4	L	1	NAG	O7-C7-N2-C2
4	M	2	NAG	C4-C5-C6-O6
4	G	2	NAG	C4-C5-C6-O6
4	F	1	NAG	O7-C7-N2-C2
4	N	1	NAG	O7-C7-N2-C2
4	H	1	NAG	O7-C7-N2-C2
4	I	1	NAG	O7-C7-N2-C2
4	O	1	NAG	O7-C7-N2-C2
4	G	2	NAG	O5-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6

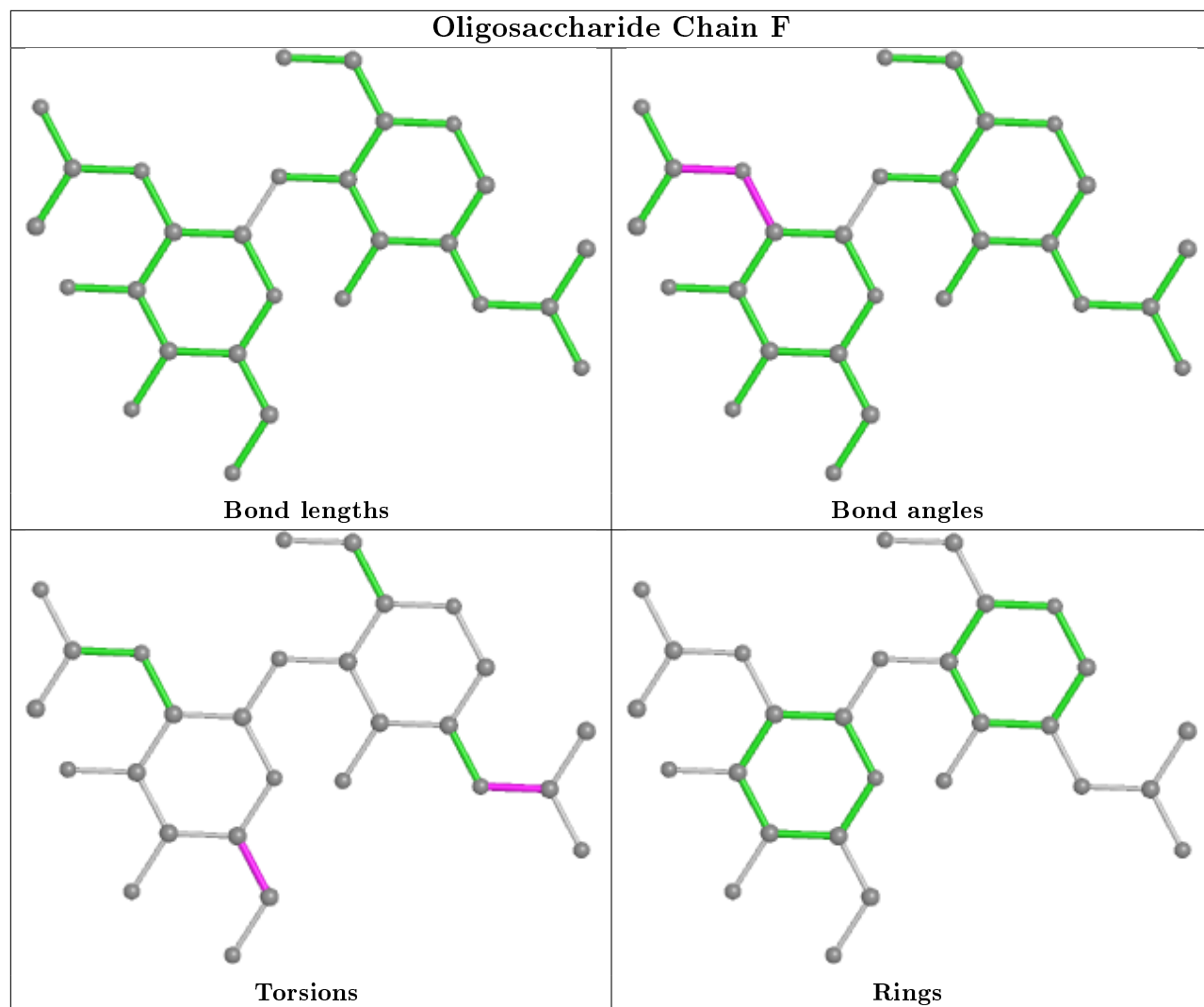
There are no ring outliers.

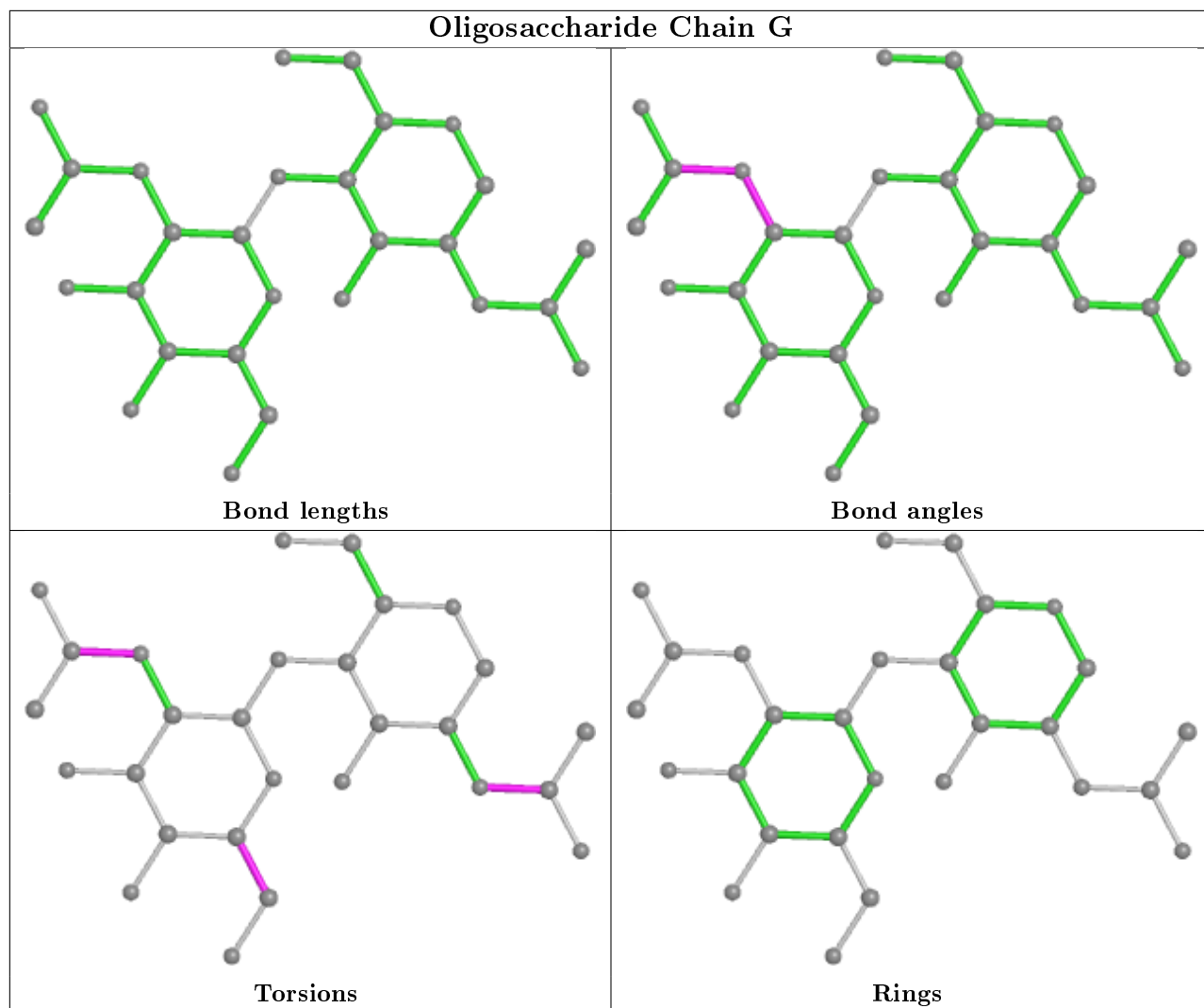
No monomer is involved in short contacts.

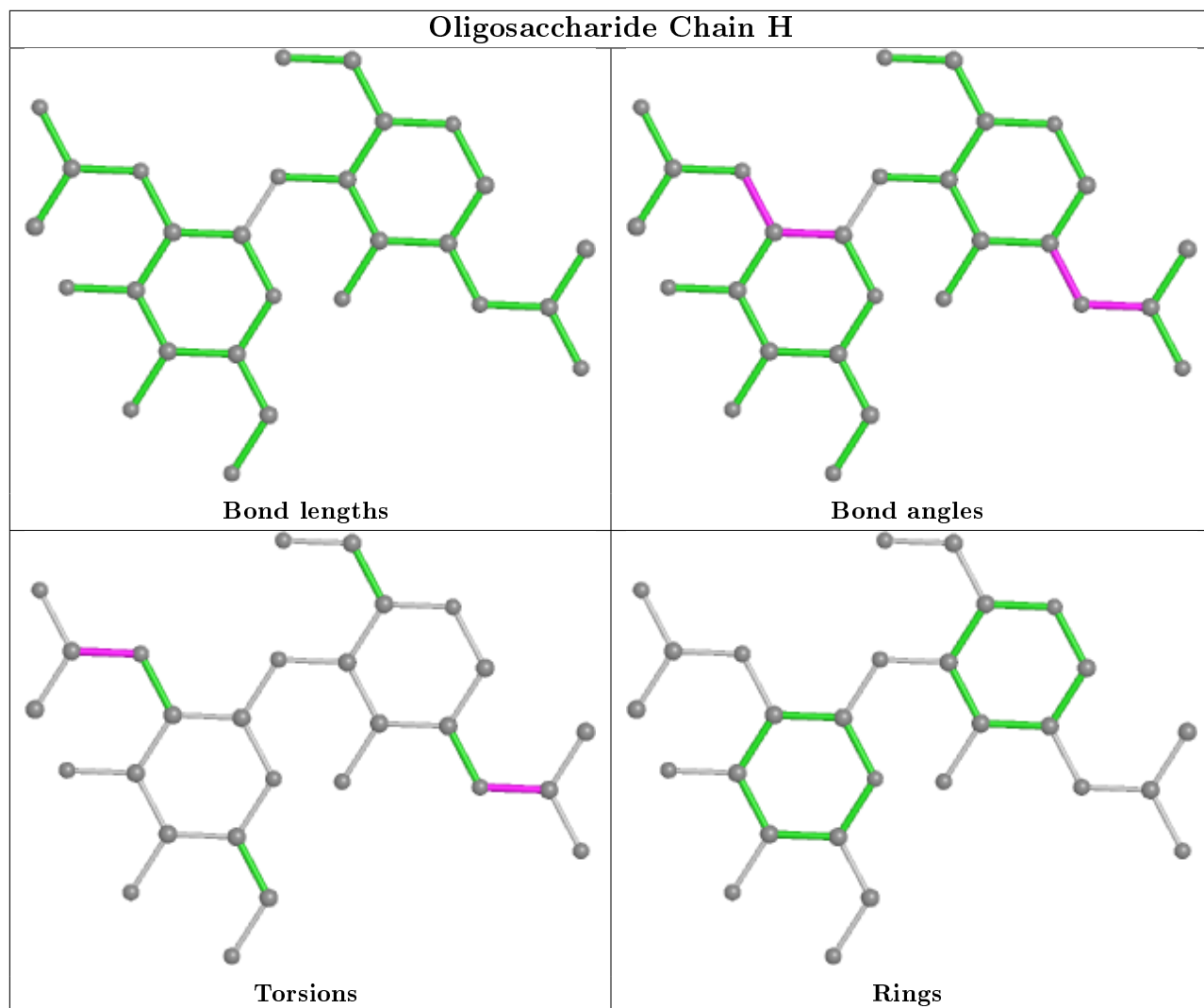
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

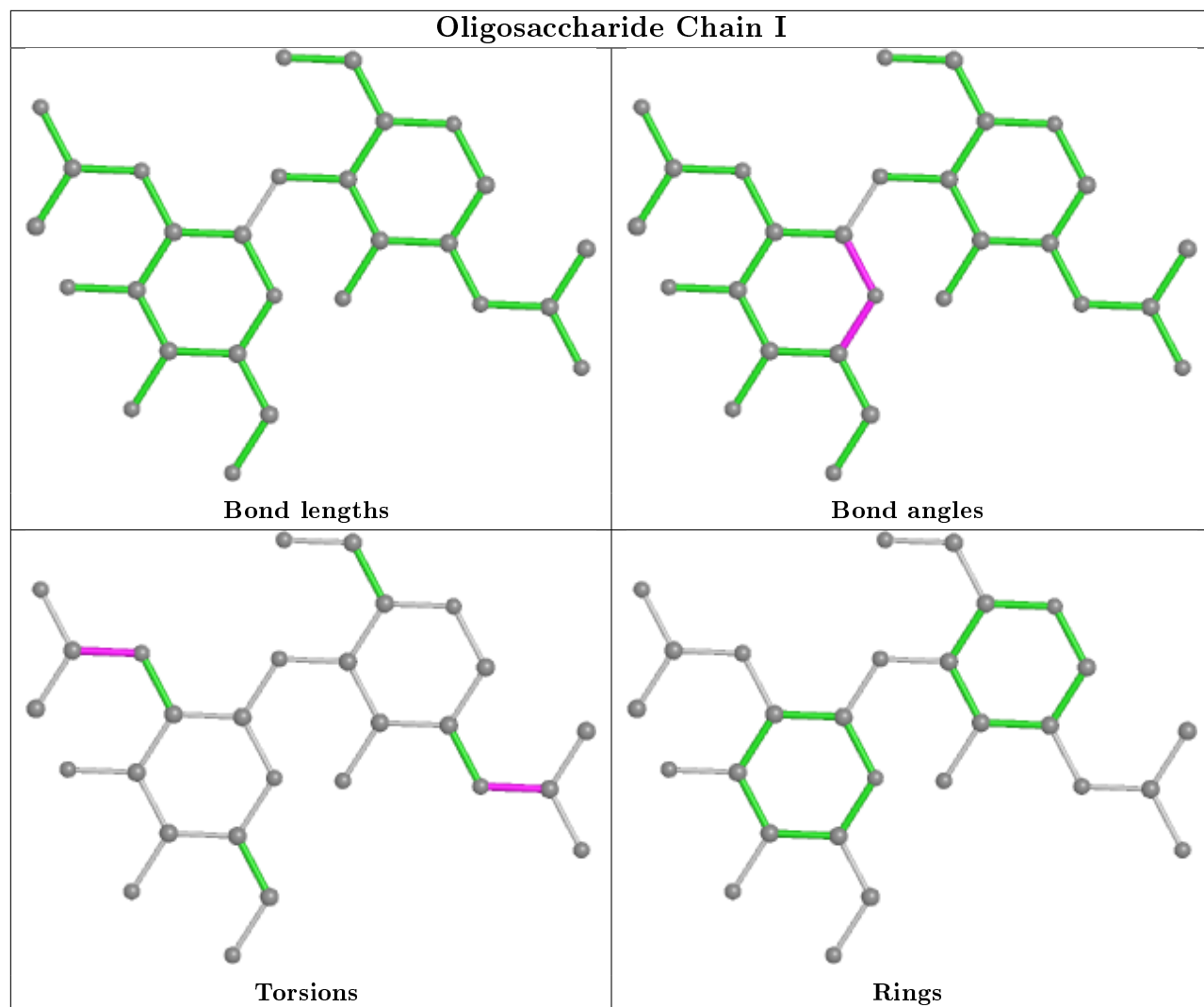


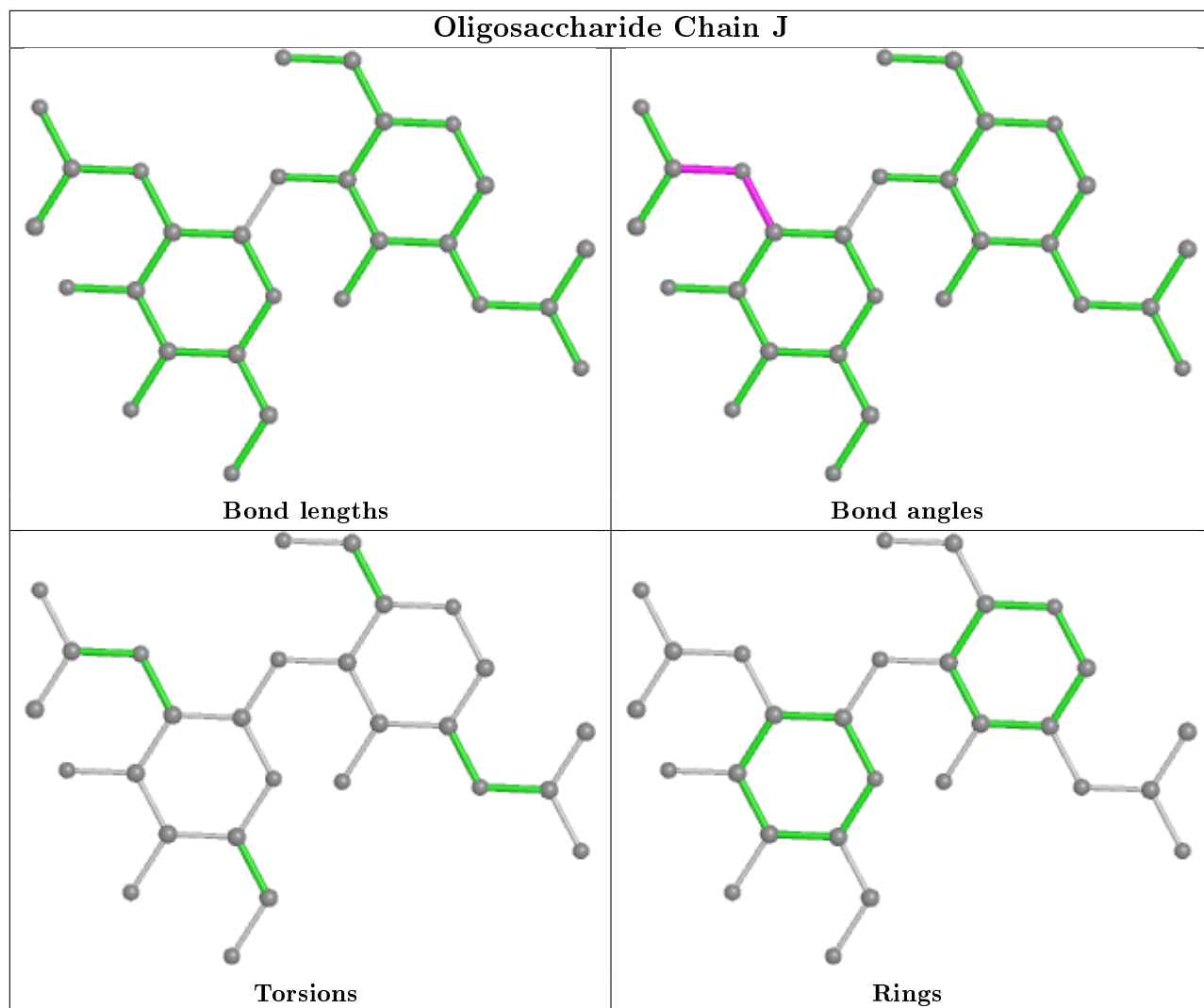


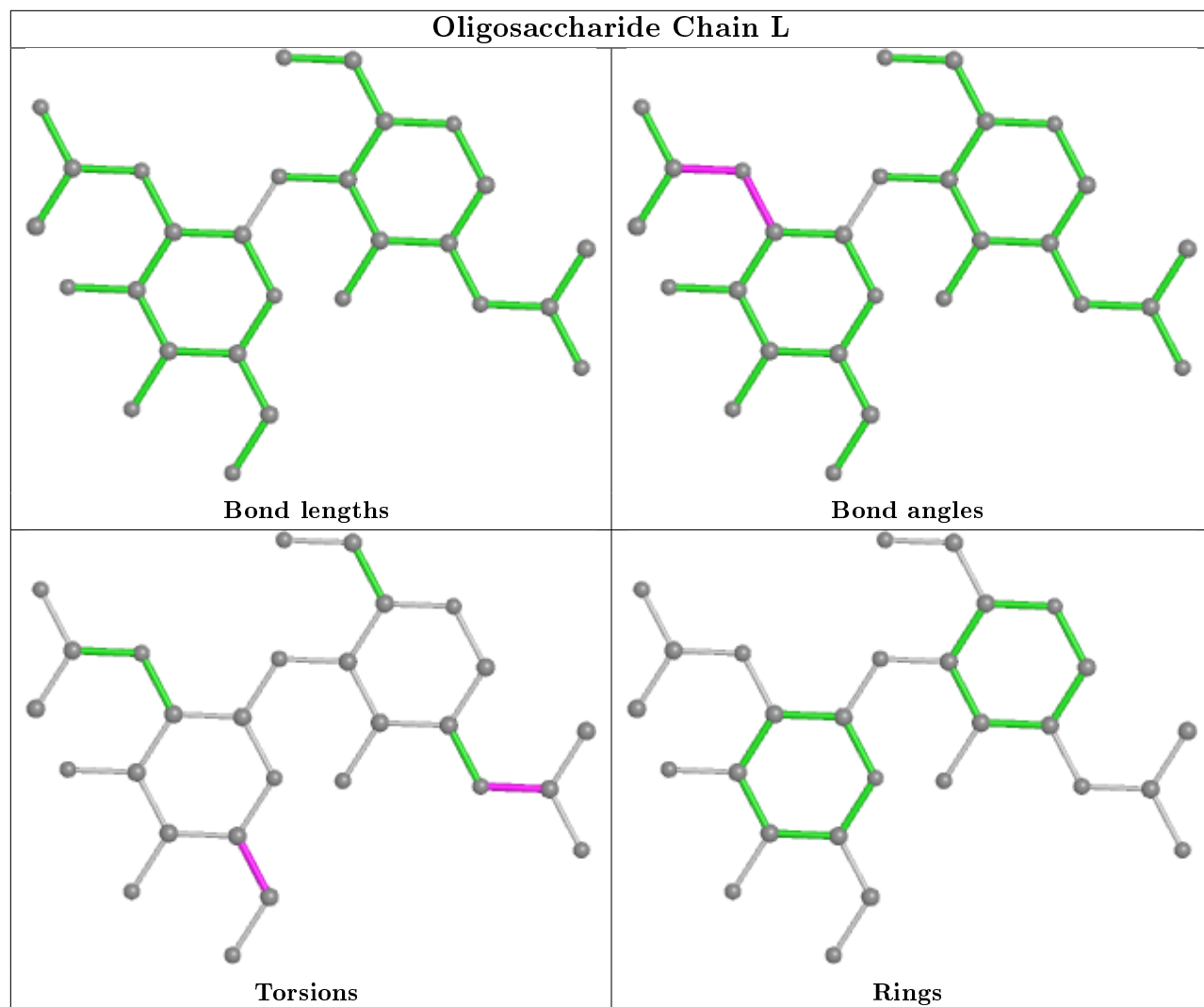


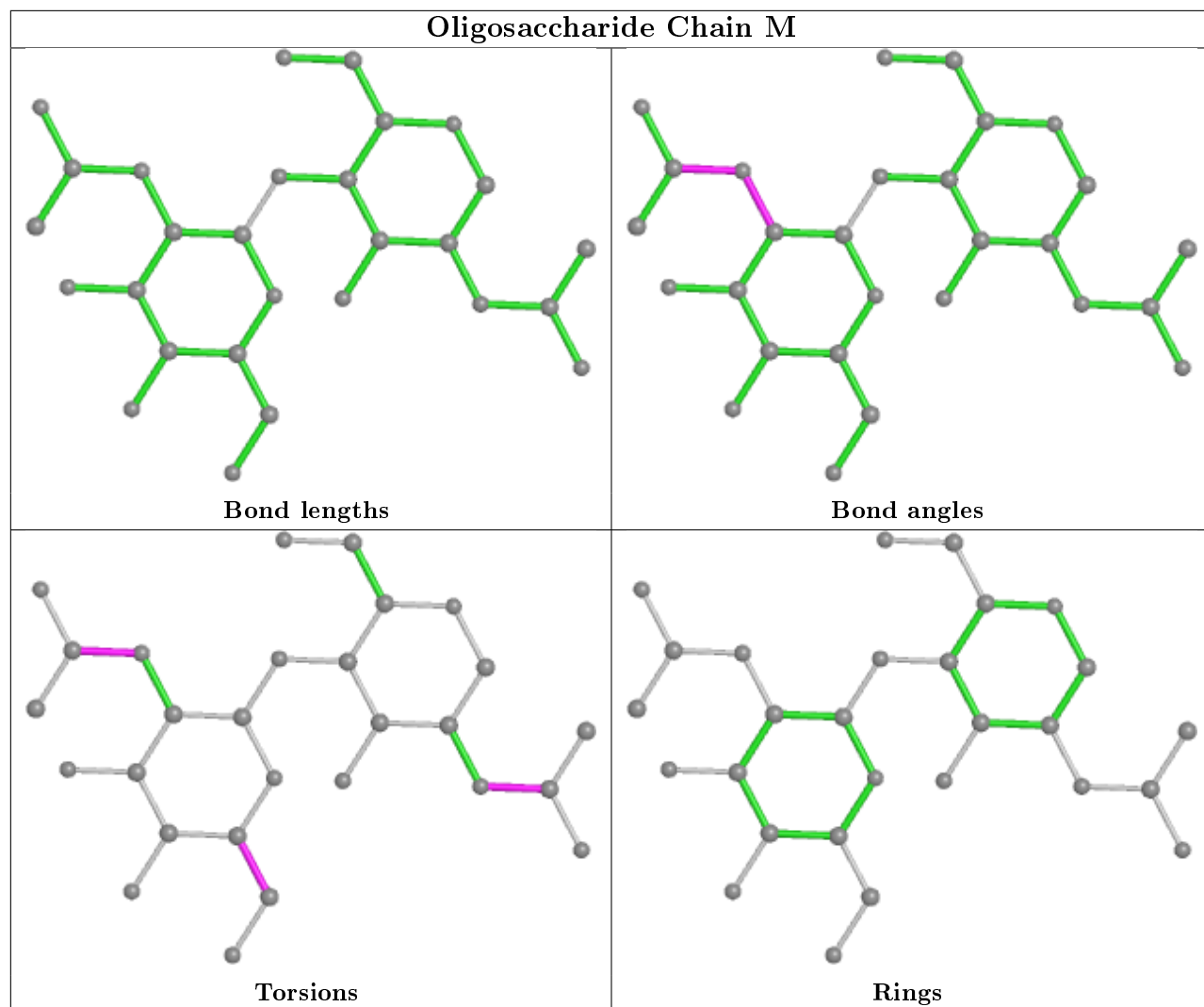


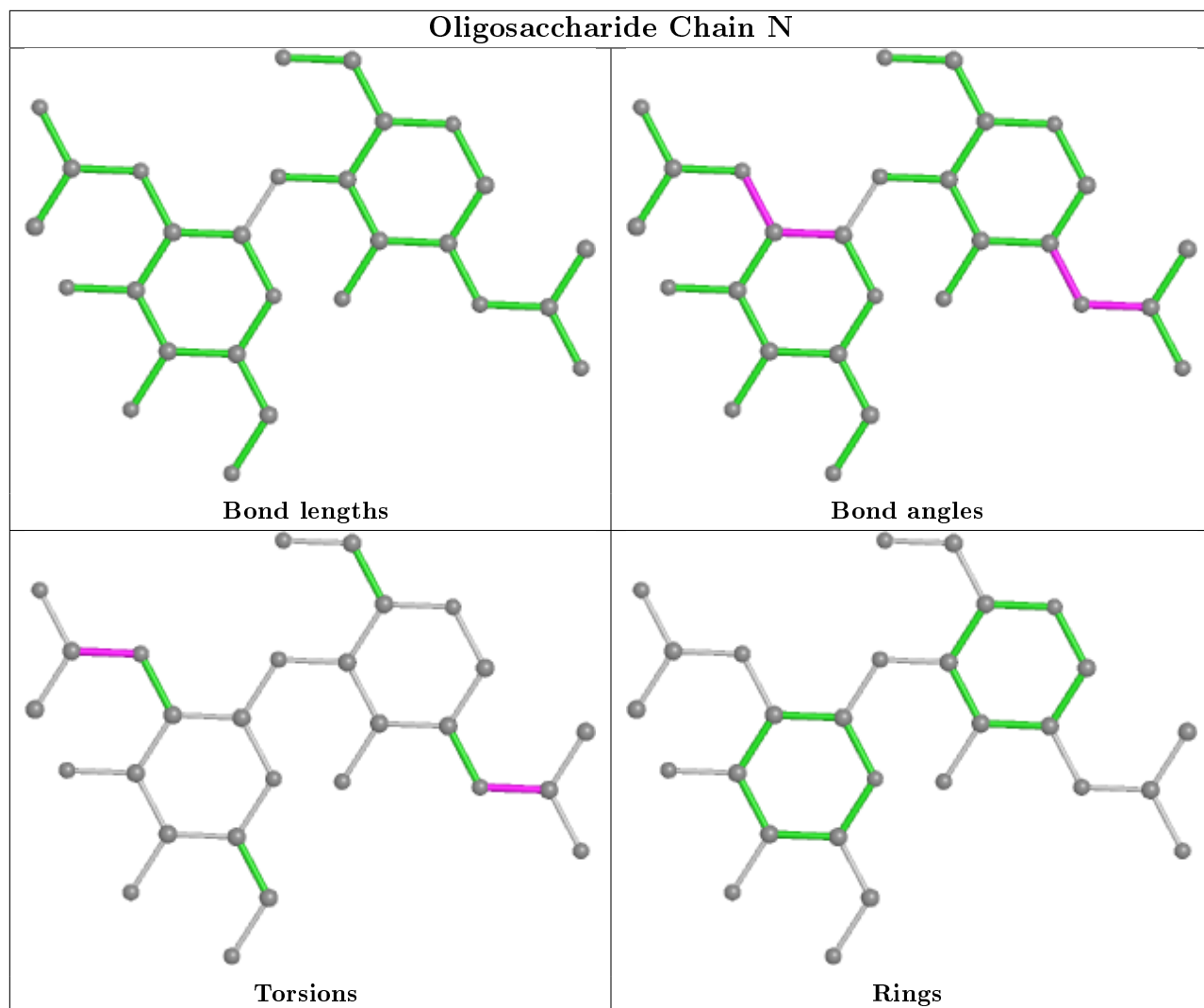


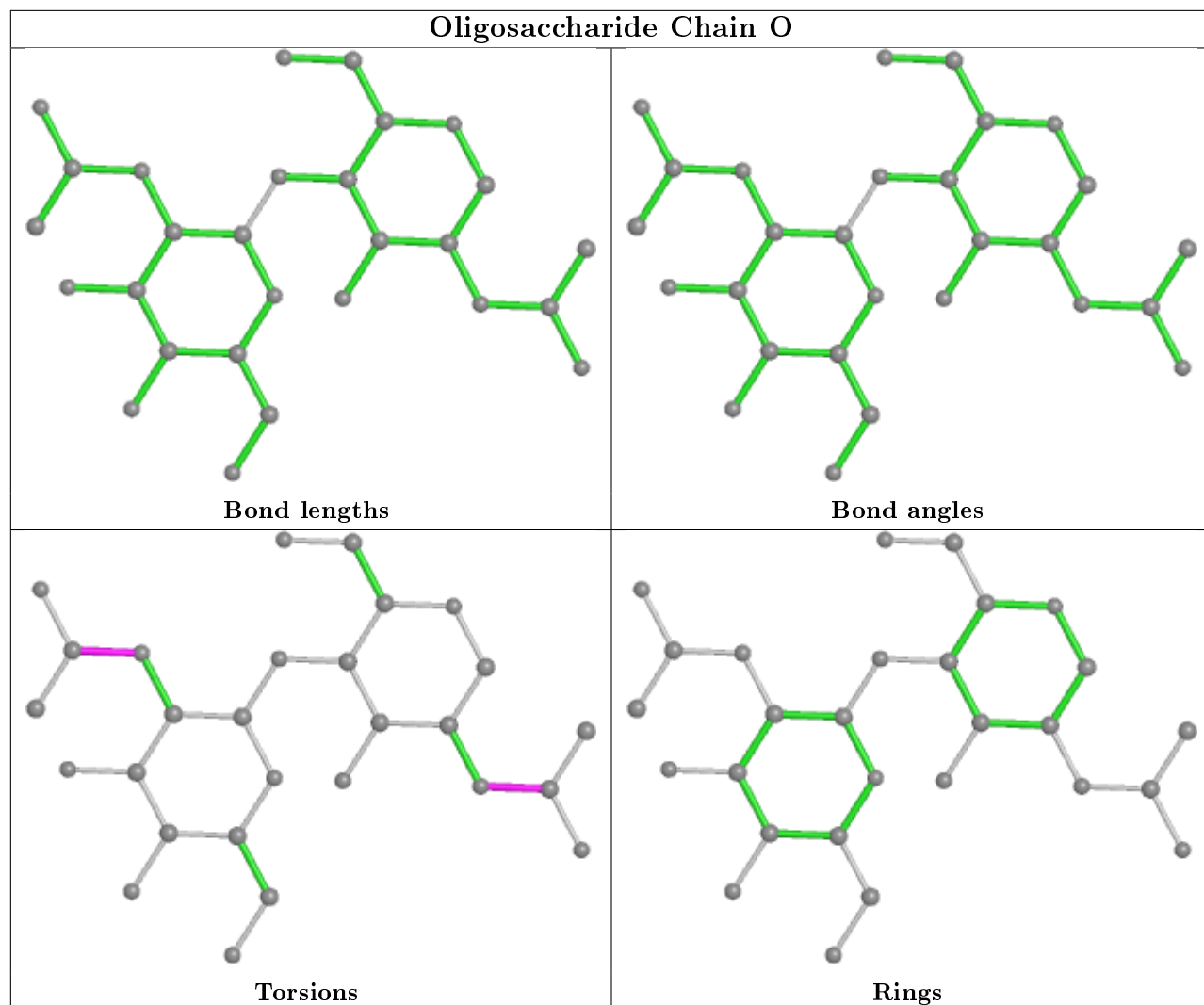


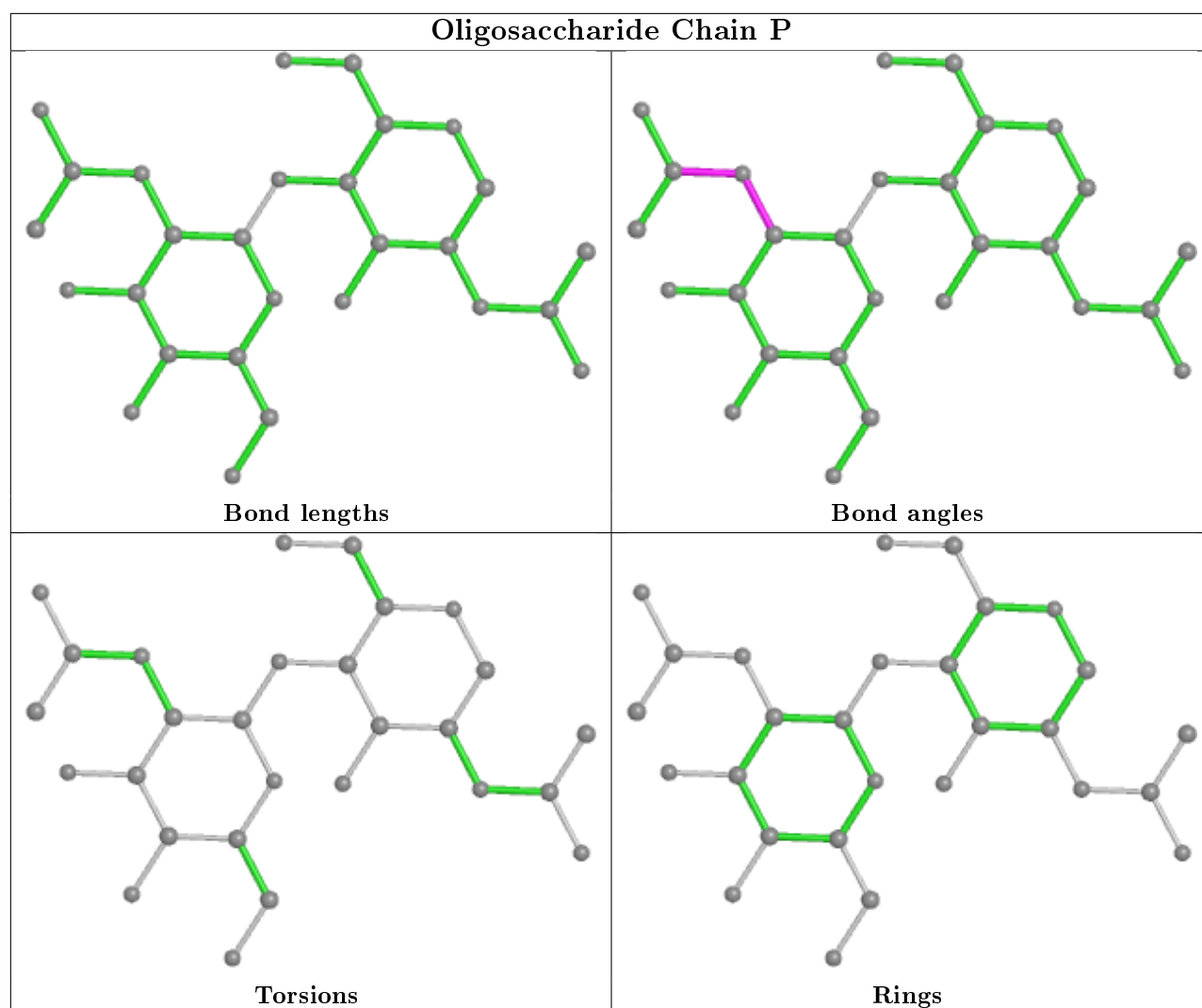












5.6 Ligand geometry [i](#)

8 ligands 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	$\# Z > 2$
5	NAG	C	3019	1	14,14,15	0.43	0	17,19,21	0.95	1 (5%)
5	NAG	A	3011	1	14,14,15	0.43	0	17,19,21	0.77	1 (5%)
5	NAG	C	3022	1	14,14,15	0.42	0	17,19,21	1.07	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	3019	1	14,14,15	0.43	0	17,19,21	0.95	1 (5%)
5	NAG	A	3022	1	14,14,15	0.42	0	17,19,21	0.88	0
5	NAG	C	3014	1	14,14,15	0.47	0	17,19,21	1.26	2 (11%)
5	NAG	A	3014	1	14,14,15	0.48	0	17,19,21	1.26	2 (11%)
5	NAG	C	3011	1	14,14,15	0.43	0	17,19,21	0.77	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
5	NAG	C	3019	1	-	2/6/23/26	0/1/1/1
5	NAG	A	3011	1	-	4/6/23/26	0/1/1/1
5	NAG	C	3022	1	-	2/6/23/26	0/1/1/1
5	NAG	A	3019	1	-	2/6/23/26	0/1/1/1
5	NAG	A	3022	1	-	2/6/23/26	0/1/1/1
5	NAG	C	3014	1	-	5/6/23/26	0/1/1/1
5	NAG	A	3014	1	-	5/6/23/26	0/1/1/1
5	NAG	C	3011	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	3014	NAG	C1-C2-N2	3.65	116.72	110.49
5	A	3014	NAG	C1-C2-N2	3.63	116.69	110.49
5	A	3014	NAG	C2-N2-C7	2.93	127.07	122.90
5	C	3014	NAG	C2-N2-C7	2.90	127.04	122.90
5	C	3022	NAG	O5-C1-C2	2.67	115.50	111.29
5	A	3019	NAG	O5-C1-C2	2.35	115.00	111.29
5	C	3019	NAG	O5-C1-C2	2.34	114.98	111.29
5	A	3011	NAG	C1-O5-C5	2.17	115.14	112.19
5	C	3011	NAG	C1-O5-C5	2.13	115.08	112.19
5	C	3022	NAG	C2-N2-C7	2.04	125.81	122.90

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	3019	NAG	C8-C7-N2-C2
5	C	3019	NAG	O7-C7-N2-C2
5	A	3011	NAG	O7-C7-N2-C2
5	C	3022	NAG	O7-C7-N2-C2
5	A	3019	NAG	C8-C7-N2-C2
5	A	3019	NAG	O7-C7-N2-C2
5	A	3022	NAG	C8-C7-N2-C2
5	A	3022	NAG	O7-C7-N2-C2
5	C	3011	NAG	O7-C7-N2-C2
5	A	3011	NAG	C8-C7-N2-C2
5	C	3022	NAG	C8-C7-N2-C2
5	C	3011	NAG	C8-C7-N2-C2
5	C	3014	NAG	C8-C7-N2-C2
5	C	3014	NAG	O7-C7-N2-C2
5	A	3014	NAG	C8-C7-N2-C2
5	A	3014	NAG	O7-C7-N2-C2
5	A	3011	NAG	O5-C5-C6-O6
5	C	3014	NAG	O5-C5-C6-O6
5	A	3014	NAG	O5-C5-C6-O6
5	C	3011	NAG	O5-C5-C6-O6
5	C	3014	NAG	C1-C2-N2-C7
5	A	3014	NAG	C1-C2-N2-C7
5	C	3011	NAG	C4-C5-C6-O6
5	A	3011	NAG	C4-C5-C6-O6
5	C	3014	NAG	C4-C5-C6-O6
5	A	3014	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.

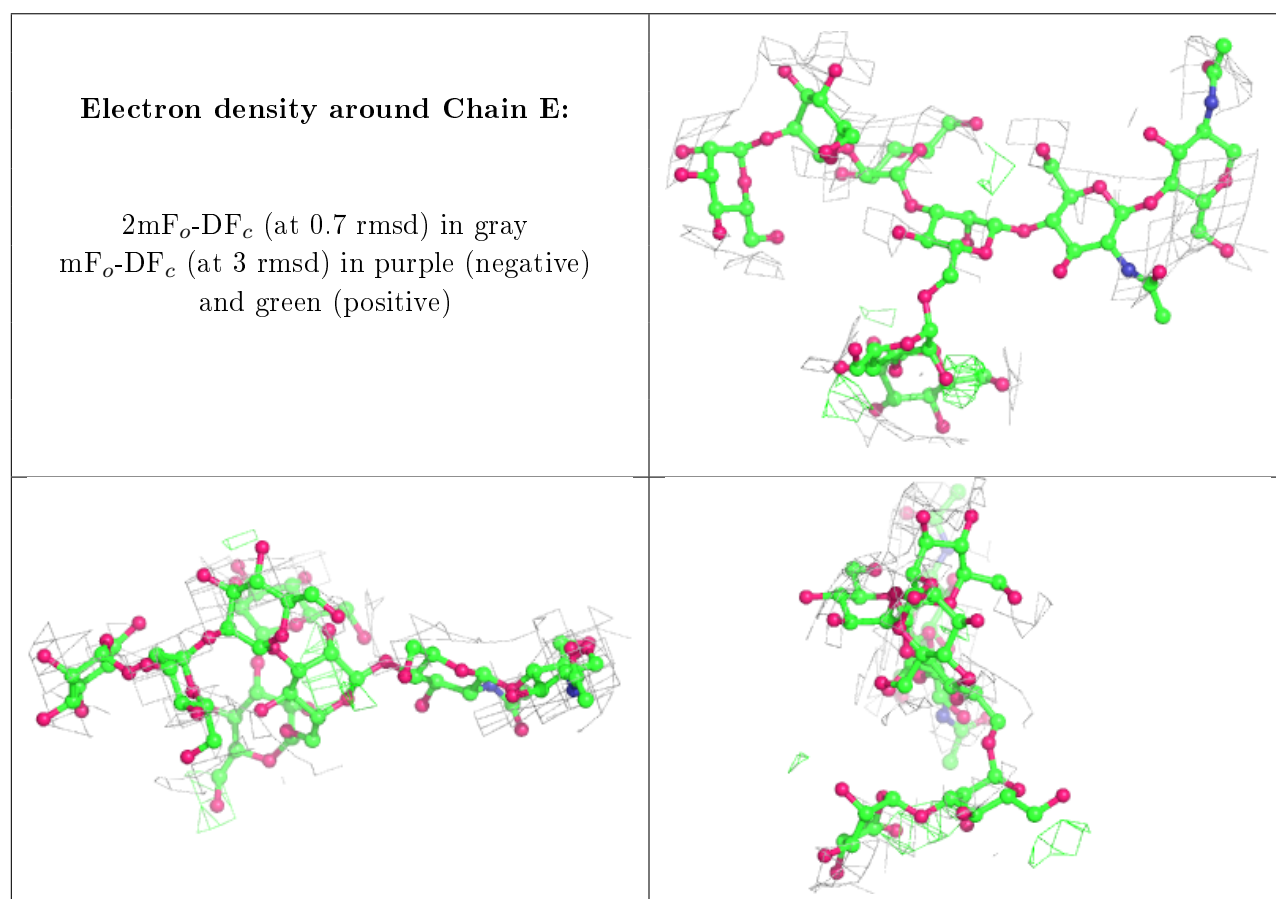
6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

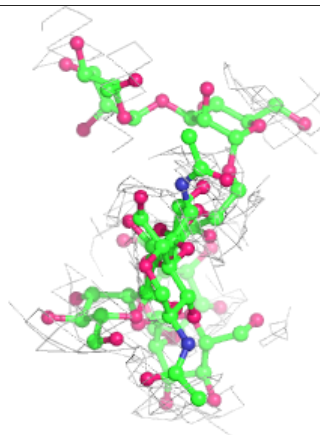
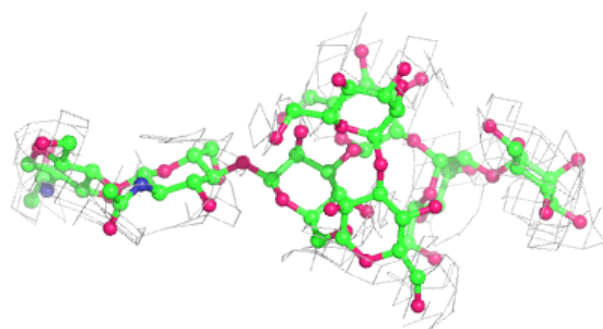
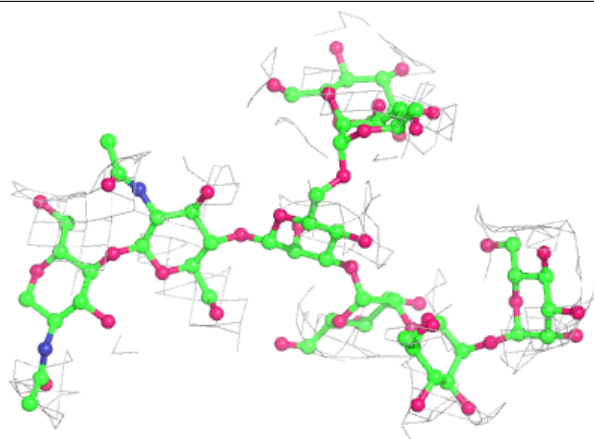
Unable to reproduce the depositor's R factor - this section is therefore empty.

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.



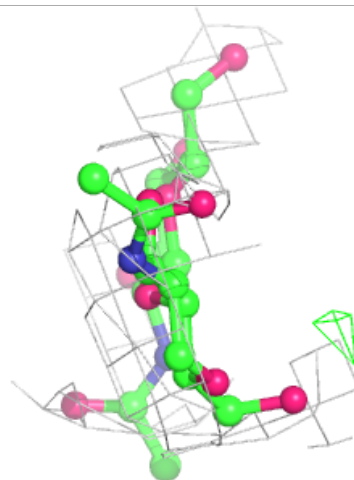
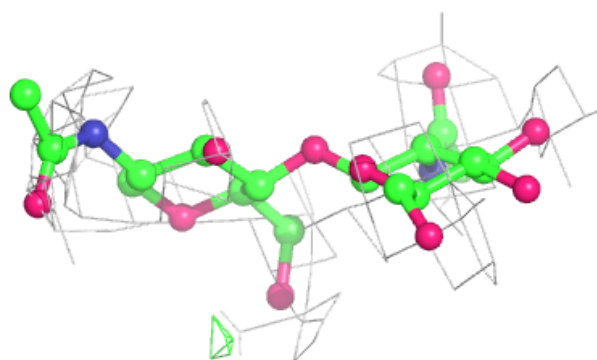
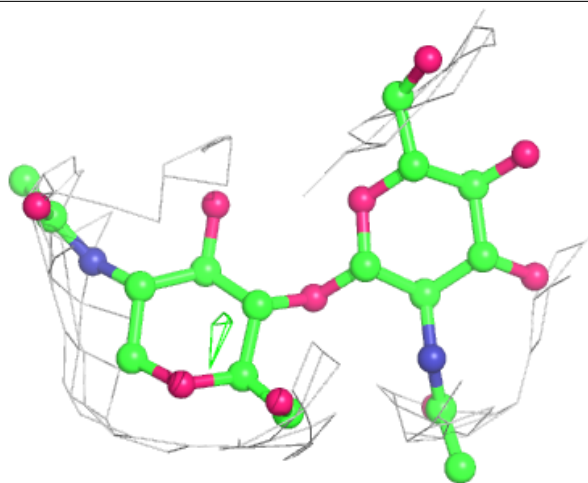
Electron density around Chain K:

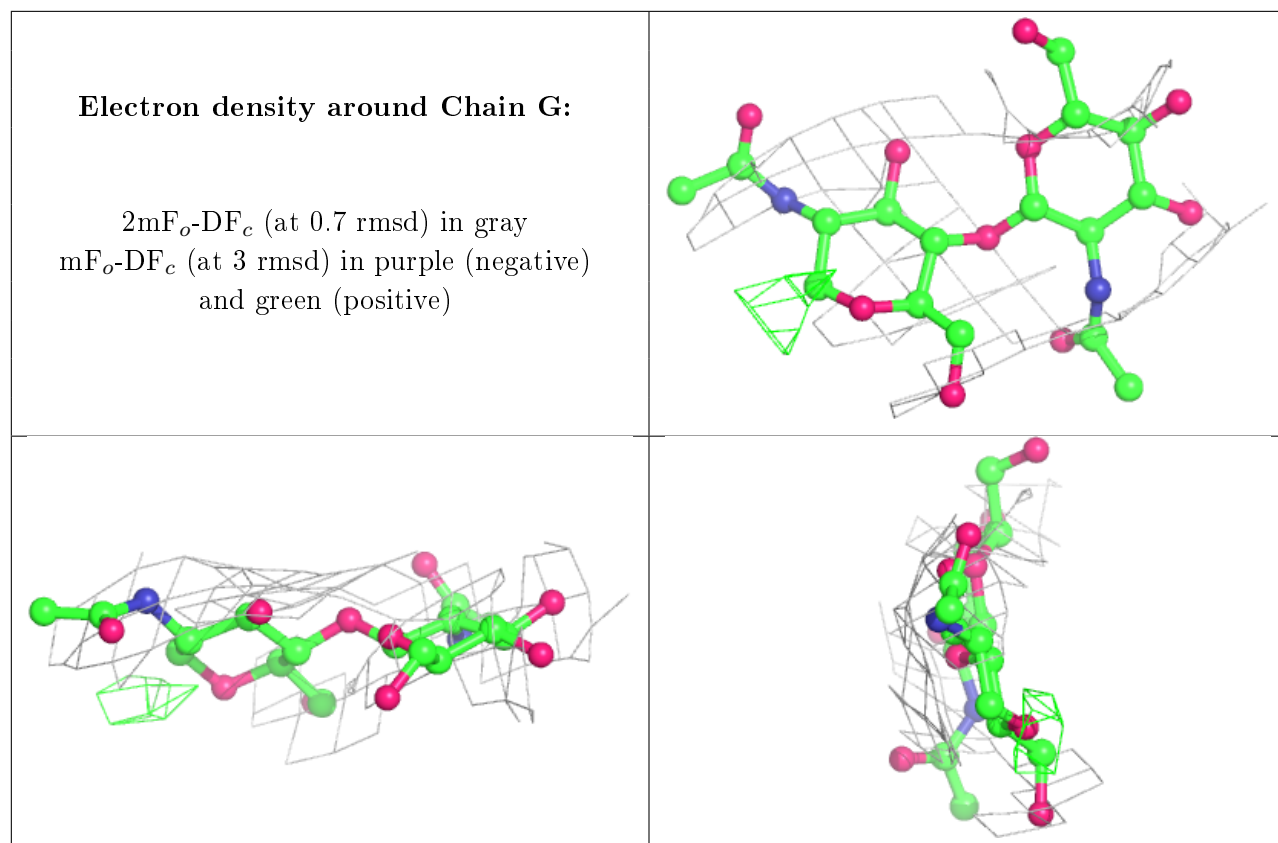
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain F:

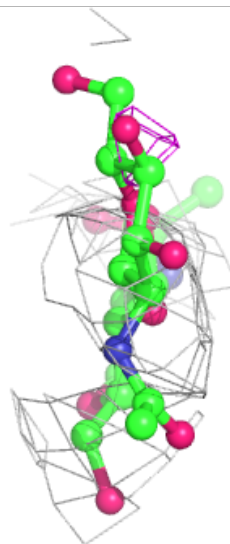
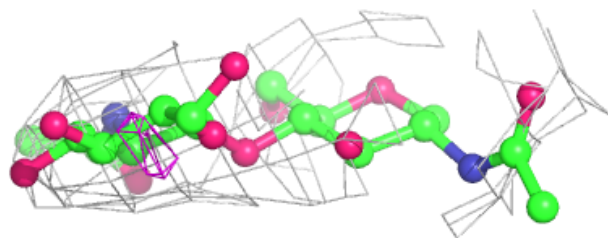
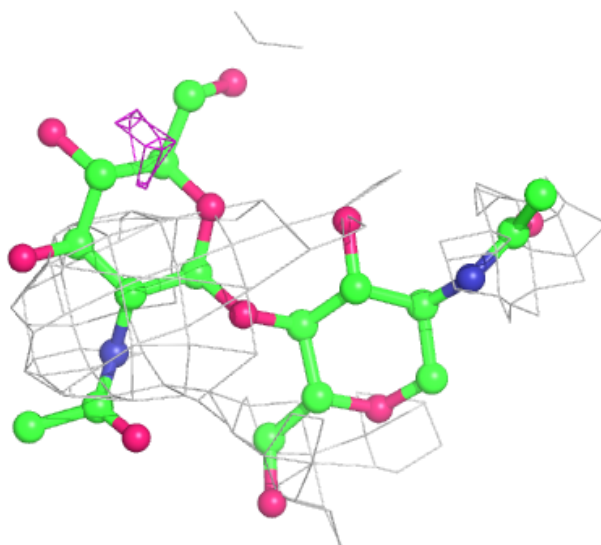
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

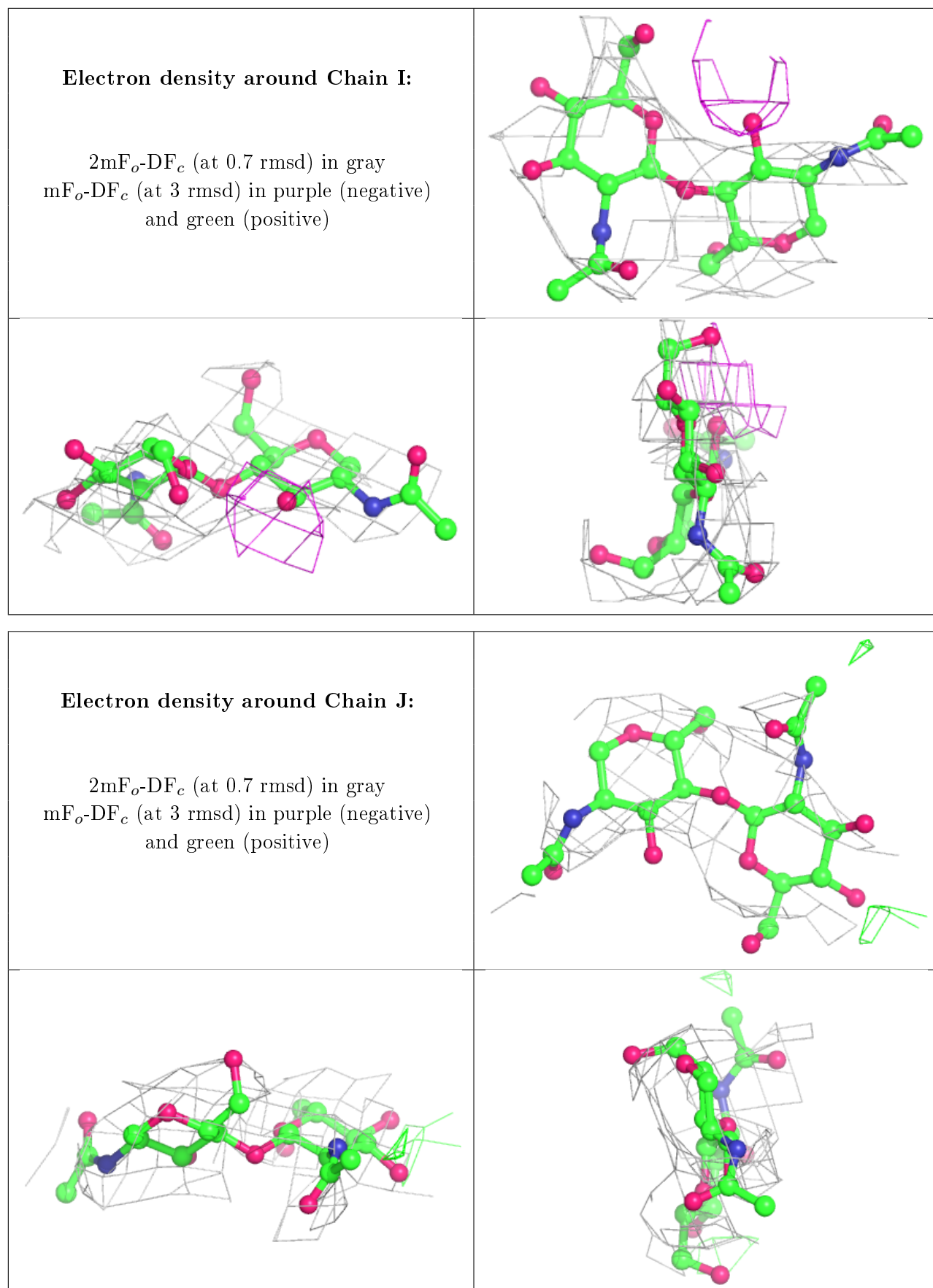




Electron density around Chain H:

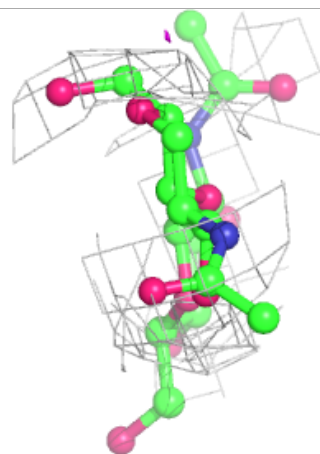
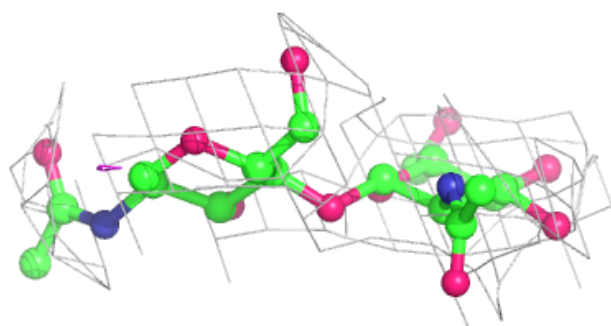
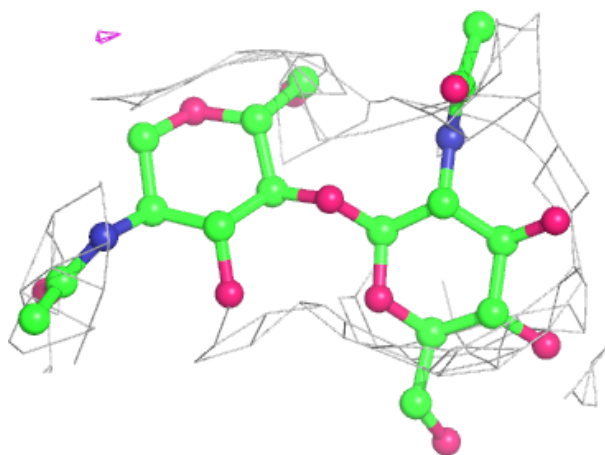
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

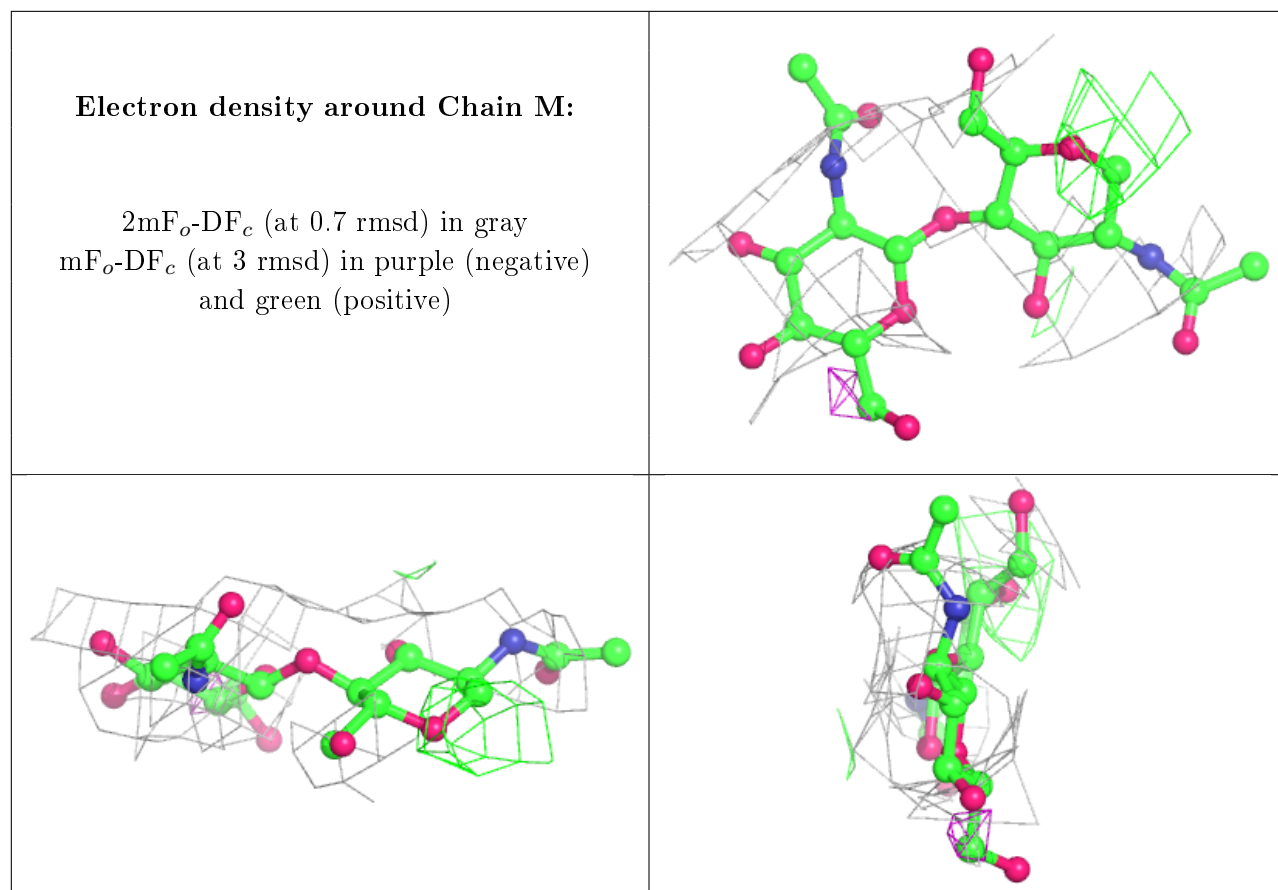




Electron density around Chain L:

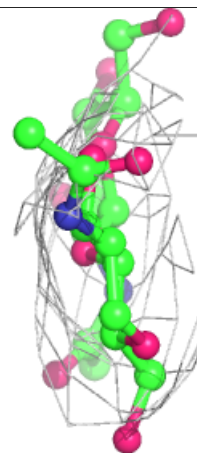
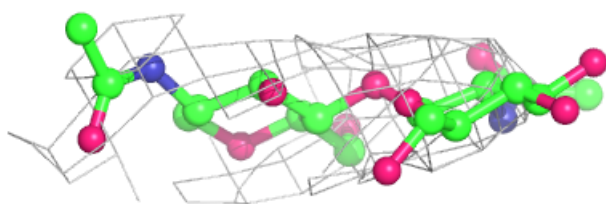
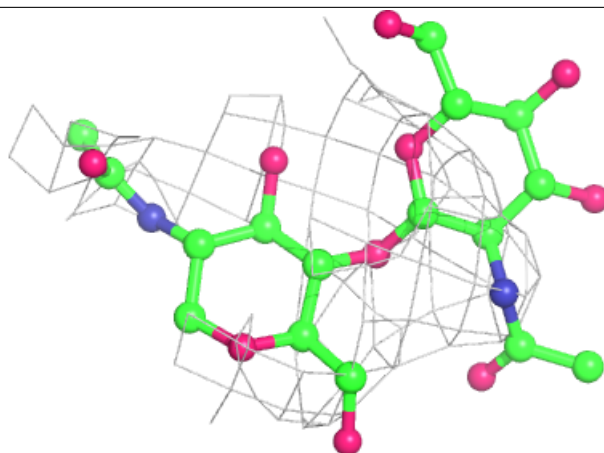
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



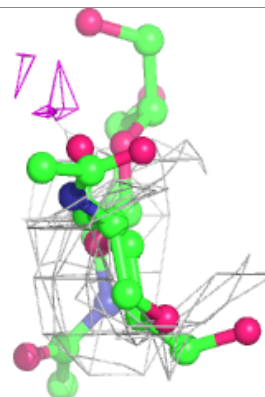
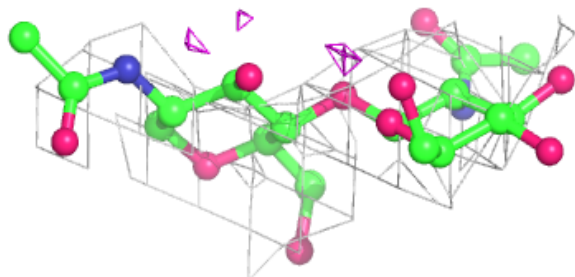
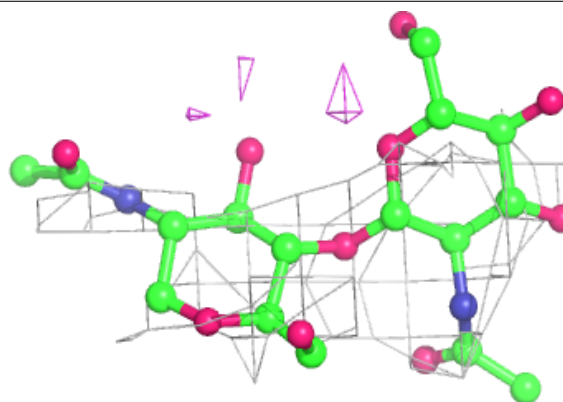


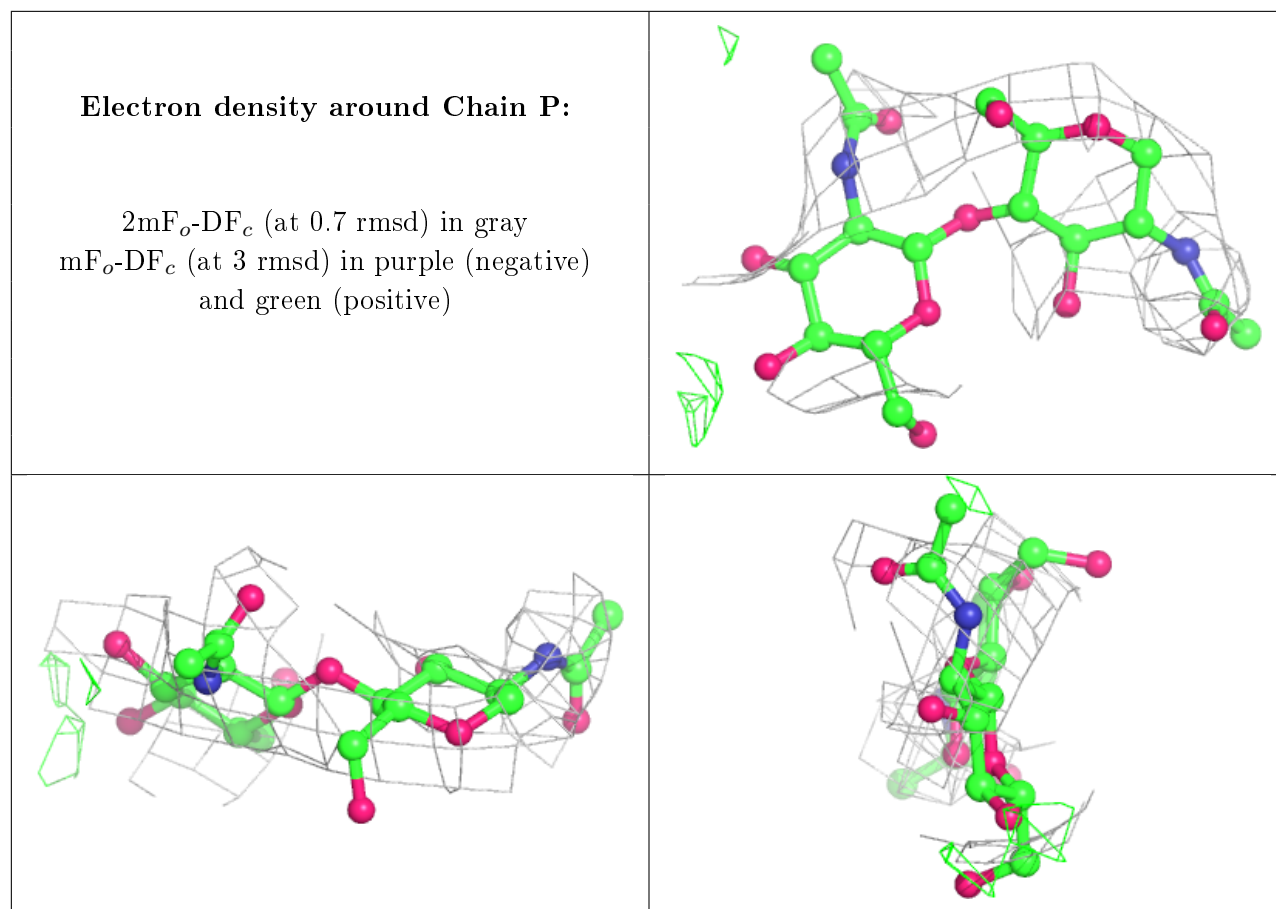
Electron density around Chain N:

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

**Electron density around Chain O:**

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





6.4 Ligands [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.