



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:06 PM UTC

PDB ID : 7OKS / pdb_00007oks
Title : X-ray structure of soluble EPCR in P212121 space group
Authors : Erausquin, E.; Dichiara, M.G.; Lopez-Sagaseta, J.
Deposited on : 2021-05-18
Resolution : 1.95 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

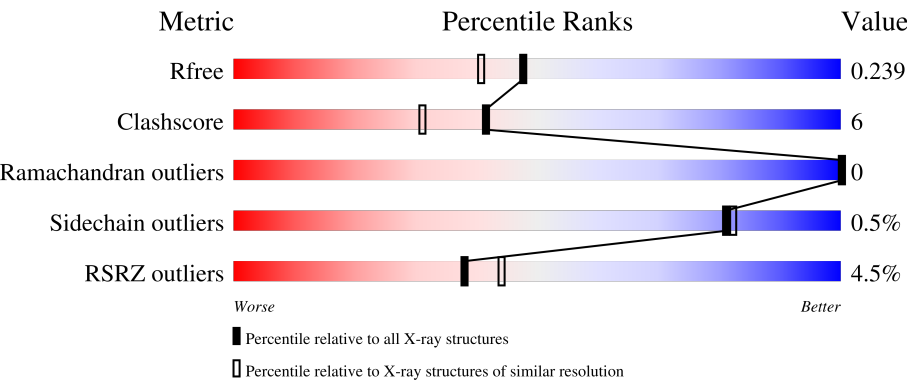
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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.



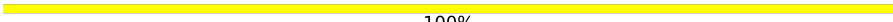
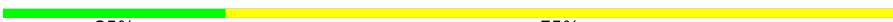
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	193	3% 78% 9% 13%
1	B	193	3% 75% 11% 13%
1	C	193	4% 75% 10% 14%
1	D	193	5% 79% 9% 12%
2	E	2	100%

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Mol	Chain	Length	Quality of chain
2	I	2	 100%
2	M	2	 50% 50%
2	O	2	 50% 50%
3	F	2	 50% 50%
3	H	2	 50% 50%
3	J	2	 50% 50%
3	L	2	 50% 50%
3	N	2	 100%
3	P	2	 50% 50%
4	G	2	 100%
5	K	4	 25% 75%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 6126 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 Endothelial protein C receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	S	3	1	0
			1335	860	232	237	6			
1	B	167	Total	C	N	O	S	0	2	0
			1313	847	225	236	5			
1	C	166	Total	C	N	O	S	0	1	0
			1353	866	242	241	4			
1	D	170	Total	C	N	O	S	0	1	0
			1345	865	238	238	4			

- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	I	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	M	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	O	2	Total	C	N	O	0	0	0
			24	14	1	9			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	N	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	P	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(5-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

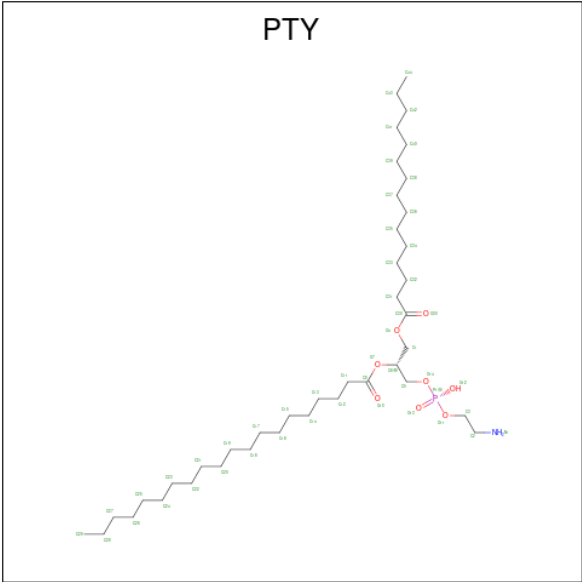
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	2	Total	C	N	O	0	0	0
			27	15	2	10			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



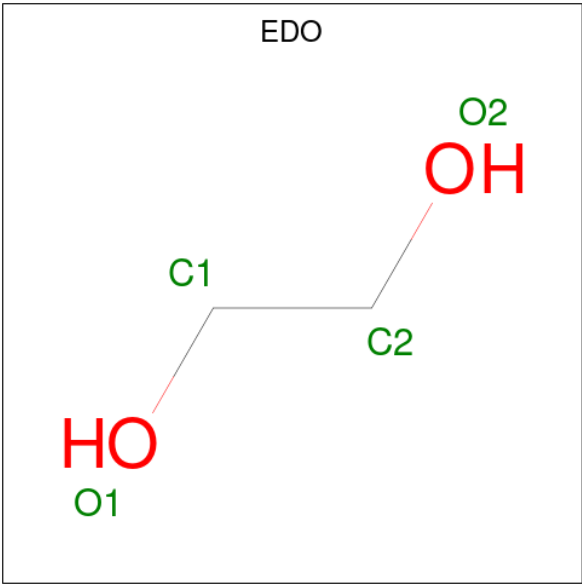
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	K	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 6 is PHOSPHATIDYLETHANOLAMINE (CCD ID: PTY) (formula: C₄₀H₈₀NO₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	O	P	0	0
			44	35	8	1		
6	B	1	Total	C	O	P	0	0
			44	35	8	1		
6	C	1	Total	C	O	P	0	0
			47	38	8	1		
6	D	1	Total	C	O	P	0	0
			45	36	8	1		

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

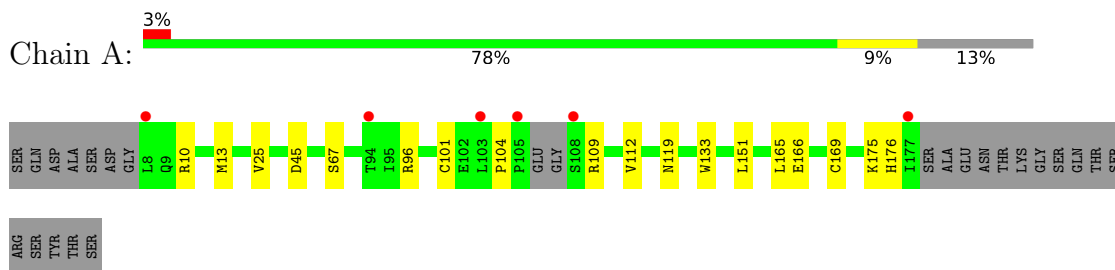
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	62	Total O 62 62	0	0
8	B	56	Total O 56 56	0	0
8	C	61	Total O 61 61	0	0
8	D	52	Total O 52 52	0	0

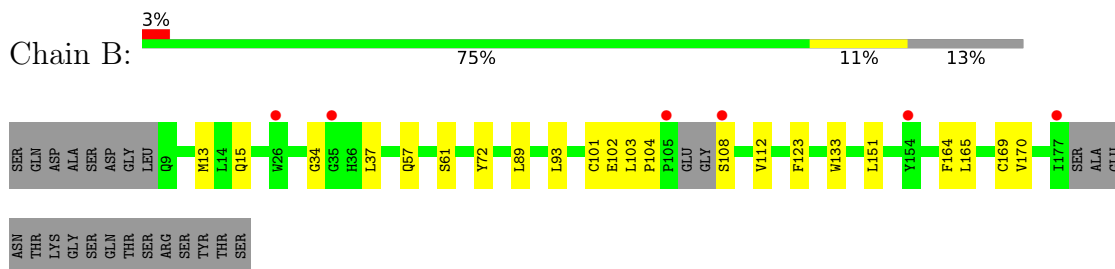
3 Residue-property plots [i](#)

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.

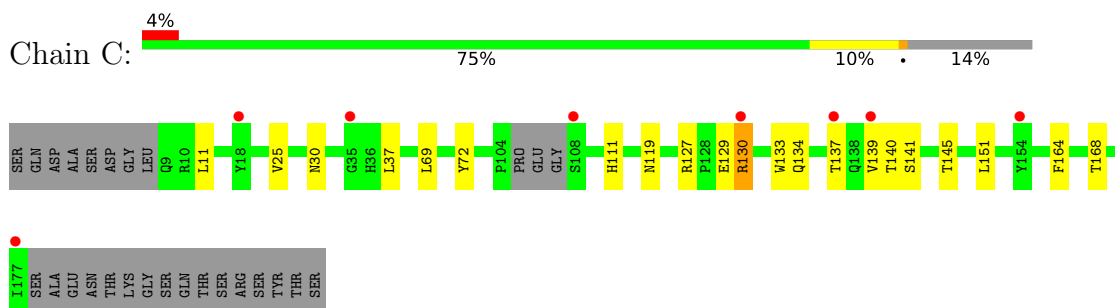
- Molecule 1: Endothelial protein C receptor



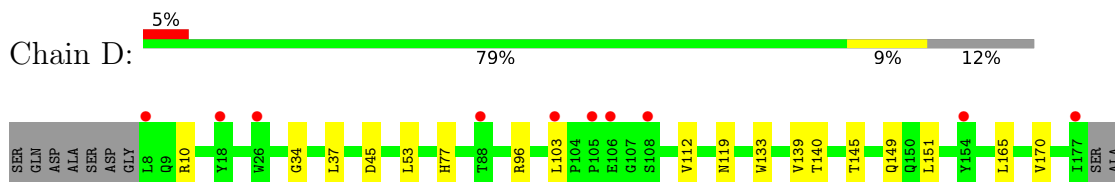
- Molecule 1: Endothelial protein C receptor



- Molecule 1: Endothelial protein C receptor

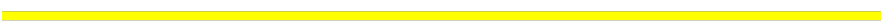


- Molecule 1: Endothelial protein C receptor



GLU
ASN
THR
LYS
GLY
SER
GLN
THR
SER
ARG
SER
TYR
THR
SER

- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

MAG1
FUC2

- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%

MAG1
FUC2

- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  50%  50%

MAG1
FUC2

- Molecule 2: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  50%  50%

MAG1
FUC2

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

Chain F:  50%  50%

MAG1
MAG2

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

Chain H:  50%  50%

MAG1
MAG2

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

Chain J:  50%  50%



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

Chain L:



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

Chain N:



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

Chain P:



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(5-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



- Molecule 5: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.44Å 94.02Å 124.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.32 – 1.95 40.32 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.32-1.95) 99.9 (40.32-1.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.199 , 0.239 0.199 , 0.239	Depositor DCC
R_{free} test set	3294 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.778	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6126	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.57% 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: PTY, FUC, NAG, BMA, EDO, 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	0.41	0/1375	0.59	0/1874
1	B	0.41	0/1350	0.59	0/1846
1	C	0.42	0/1392	0.61	0/1894
1	D	0.41	0/1386	0.58	0/1893
All	All	0.41	0/5503	0.59	0/7507

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	1335	0	1244	14	0
1	B	1313	0	1207	19	0
1	C	1353	0	1295	22	0
1	D	1345	0	1273	17	0
2	E	24	0	22	0	0
2	I	24	0	22	0	0
2	M	24	0	22	0	0
2	O	24	0	22	0	0
3	F	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	28	0	25	1	0
3	J	28	0	25	0	0
3	L	28	0	25	0	0
3	N	28	0	25	4	0
3	P	28	0	25	2	0
4	G	27	0	21	2	0
5	K	50	0	43	5	0
6	A	44	0	64	0	0
6	B	44	0	64	7	0
6	C	47	0	73	9	0
6	D	45	0	66	1	0
7	A	4	0	6	0	0
7	B	8	0	12	0	0
7	C	8	0	12	0	0
7	D	8	0	12	2	0
8	A	62	0	0	0	0
8	B	56	0	0	1	1
8	C	61	0	0	1	1
8	D	52	0	0	2	0
All	All	6126	0	5630	74	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (74) 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:96:ARG:HH22	3:N:2:NAG:H81	1.28	0.97
1:D:77:HIS:ND1	7:D:203:EDO:H11	1.92	0.84
1:D:45:ASP:HB2	7:D:203:EDO:H12	1.60	0.81
1:B:101:CYS:SG	1:B:169[B]:CYS:HB3	2.27	0.75
1:D:140:THR:H	5:K:1:NAG:C8	1.99	0.75
1:D:140:THR:H	5:K:1:NAG:H81	1.53	0.72
1:D:34:GLY:O	8:D:301:HOH:O	2.09	0.70
1:D:139:VAL:HA	5:K:1:NAG:H81	1.74	0.69
1:C:69:LEU:HD23	6:C:201:PTY:H121	1.75	0.69
1:D:145:THR:O	1:D:149:GLN:HG3	1.94	0.66
1:B:34:GLY:O	8:B:301:HOH:O	2.16	0.63
1:A:101:CYS:SG	1:A:169[C]:CYS:HB3	2.38	0.63
1:A:25:VAL:HG13	1:A:45:ASP:HB3	1.82	0.62
1:A:96:ARG:HH12	4:G:2:NAG:C7	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:LYS:HD3	1:A:176:HIS:CE1	2.38	0.58
6:C:201:PTY:H112	8:C:342:HOH:O	2.05	0.57
1:C:129:GLU:HG2	1:C:130[A]:ARG:HD2	1.89	0.53
1:C:168:THR:HG22	6:C:201:PTY:H291	1.90	0.53
1:C:140:THR:HG22	1:C:140:THR:O	2.09	0.52
1:B:72:TYR:CG	6:B:201:PTY:H121	2.44	0.52
1:D:103:LEU:HD11	1:D:170:VAL:HG13	1.92	0.51
1:B:102:GLU:O	1:B:104:PRO:HD3	2.11	0.51
1:D:96:ARG:NH2	3:N:2:NAG:H81	2.12	0.51
1:C:119:ASN:ND2	5:K:1:NAG:H83	2.26	0.51
1:A:112:VAL:HB	1:A:165:LEU:HB3	1.93	0.50
1:D:37:LEU:HD22	3:N:1:NAG:H82	1.94	0.49
1:B:37:LEU:HD13	3:H:1:NAG:H83	1.93	0.49
1:B:164:PHE:CE2	6:B:201:PTY:H111	2.48	0.48
1:D:133:TRP:CD1	1:D:151:LEU:HB3	2.48	0.48
1:C:72:TYR:CB	6:C:201:PTY:H132	2.45	0.47
1:A:96:ARG:HH22	4:G:2:NAG:C7	2.28	0.47
1:A:166:GLU:CD	1:C:111:HIS:HE2	2.22	0.47
1:C:129:GLU:CG	1:C:130[A]:ARG:HD2	2.44	0.47
1:B:123:PHE:CE2	6:B:201:PTY:H432	2.50	0.47
1:B:15:GLN:HB2	6:B:201:PTY:H161	1.96	0.46
1:C:72:TYR:CG	6:C:201:PTY:H132	2.50	0.46
1:B:133:TRP:CD1	1:B:151:LEU:HB3	2.50	0.46
1:C:133:TRP:CD1	1:C:151:LEU:HB3	2.50	0.46
1:D:10:ARG:HH11	1:D:10:ARG:HG2	1.80	0.46
1:D:112:VAL:HB	1:D:165:LEU:HB3	1.97	0.46
1:D:119:ASN:ND2	3:P:1:NAG:H83	2.31	0.46
1:A:133:TRP:CD1	1:A:151:LEU:HB3	2.52	0.45
1:B:112:VAL:HB	1:B:165:LEU:HB3	1.99	0.44
1:B:13:MET:HE1	1:B:169[B]:CYS:SG	2.58	0.44
1:C:127:ARG:HD3	1:C:134:GLN:CD	2.43	0.44
1:D:37:LEU:HD22	3:N:1:NAG:C8	2.48	0.44
1:B:57:GLN:NE2	1:B:61:SER:OG	2.48	0.43
1:C:140:THR:O	3:P:1:NAG:H82	2.18	0.43
1:C:127:ARG:HD3	1:C:134:GLN:NE2	2.33	0.43
1:B:103:LEU:HD21	1:B:170:VAL:HG13	2.00	0.43
1:A:10:ARG:HE	1:A:10:ARG:HB2	1.40	0.43
1:C:72:TYR:HB2	6:C:201:PTY:H132	2.01	0.43
1:A:104:PRO:HD3	1:A:109:ARG:O	2.19	0.43
1:C:129:GLU:HG2	1:C:130[B]:ARG:HG2	2.01	0.42
1:C:164:PHE:CZ	6:C:201:PTY:H122	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:LEU:C	1:B:93:LEU:HD12	2.44	0.42
1:B:164:PHE:CZ	6:B:201:PTY:H111	2.54	0.42
1:B:108:SER:HB3	8:D:331:HOH:O	2.19	0.42
1:C:137:THR:OG1	1:C:139:VAL:O	2.37	0.42
1:A:25:VAL:CG1	1:A:45:ASP:HB3	2.49	0.42
1:C:119:ASN:HD22	5:K:1:NAG:H83	1.85	0.42
1:A:13:MET:HE1	1:A:169[C]:CYS:SG	2.60	0.41
1:C:141:SER:O	1:C:145:THR:HG23	2.19	0.41
1:D:37:LEU:HG	1:D:53:LEU:HD12	2.00	0.41
1:A:175:LYS:HD3	1:A:176:HIS:NE2	2.34	0.41
1:C:11:LEU:HD21	6:C:201:PTY:H272	2.01	0.41
1:B:72:TYR:CE1	6:B:201:PTY:H332	2.55	0.41
1:A:119:ASN:ND2	3:F:1:NAG:H83	2.36	0.41
6:D:201:PTY:H191	6:D:201:PTY:H161	1.94	0.41
1:B:89:LEU:HD11	6:B:201:PTY:H443	2.03	0.40
1:B:89:LEU:HA	1:B:89:LEU:HD23	1.91	0.40
1:C:30:ASN:HB2	1:C:37:LEU:HD11	2.03	0.40
6:C:201:PTY:O10	6:C:201:PTY:H131	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:324:HOH:O	8:C:304:HOH:O[4_554]	2.08	0.12

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	166/193 (86%)	162 (98%)	4 (2%)	0	100	100
1	B	165/193 (86%)	160 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	163/193 (84%)	157 (96%)	6 (4%)	0	100	100
1	D	169/193 (88%)	163 (96%)	6 (4%)	0	100	100
All	All	663/772 (86%)	642 (97%)	21 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	139/171 (81%)	138 (99%)	1 (1%)	76	76
1	B	131/171 (77%)	131 (100%)	0	100	100
1	C	144/171 (84%)	141 (98%)	3 (2%)	47	41
1	D	140/171 (82%)	140 (100%)	0	100	100
All	All	554/684 (81%)	550 (99%)	4 (1%)	81	76

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	SER
1	C	25	VAL
1	C	130[A]	ARG
1	C	130[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	B	15	GLN
1	B	57	GLN
1	B	85	GLN
1	B	149	GLN

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Mol	Chain	Res	Type
1	C	9	GLN
1	C	28	GLN
1	C	57	GLN
1	C	176	HIS
1	D	57	GLN
1	D	155	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

26 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	1.05	1 (7%)	17,19,21	0.68	0
2	FUC	E	2	2	10,10,11	1.43	2 (20%)	14,14,16	1.02	0
3	NAG	F	1	1,3	14,14,15	0.46	0	17,19,21	0.67	1 (5%)
3	NAG	F	2	3	14,14,15	0.24	0	17,19,21	0.40	0
4	NAG	G	1	4,1	14,14,15	0.61	1 (7%)	17,19,21	0.87	0
4	NAG	G	2	4	13,13,15	0.37	0	14,17,21	0.78	0
3	NAG	H	1	1,3	14,14,15	0.64	1 (7%)	17,19,21	0.79	0
3	NAG	H	2	3	14,14,15	0.59	0	17,19,21	0.66	0
2	NAG	I	1	2,1	14,14,15	0.90	2 (14%)	17,19,21	0.74	0
2	FUC	I	2	2	10,10,11	1.49	1 (10%)	14,14,16	0.68	0
3	NAG	J	1	1,3	14,14,15	0.42	0	17,19,21	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	J	2	3	14,14,15	0.24	0	17,19,21	0.77	1 (5%)
5	NAG	K	1	1,5	14,14,15	0.60	0	17,19,21	0.83	0
5	NAG	K	2	5	14,14,15	0.18	0	17,19,21	0.50	0
5	BMA	K	3	5	11,11,12	1.59	3 (27%)	15,15,17	1.73	2 (13%)
5	MAN	K	4	5	11,11,12	1.21	1 (9%)	15,15,17	0.92	1 (6%)
3	NAG	L	1	1,3	14,14,15	0.27	0	17,19,21	0.54	0
3	NAG	L	2	3	14,14,15	0.32	0	17,19,21	0.69	1 (5%)
2	NAG	M	1	2,1	14,14,15	0.31	0	17,19,21	0.57	0
2	FUC	M	2	2	10,10,11	0.86	0	14,14,16	0.81	1 (7%)
3	NAG	N	1	1,3	14,14,15	0.66	1 (7%)	17,19,21	0.49	0
3	NAG	N	2	3	14,14,15	0.50	0	17,19,21	0.71	1 (5%)
2	NAG	O	1	2,1	14,14,15	0.49	0	17,19,21	0.74	1 (5%)
2	FUC	O	2	2	10,10,11	1.04	0	14,14,16	0.73	0
3	NAG	P	1	1,3	14,14,15	0.73	1 (7%)	17,19,21	0.68	1 (5%)
3	NAG	P	2	3	14,14,15	0.27	0	17,19,21	0.42	0

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

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	L	2	3	-	2/6/23/26	0/1/1/1
2	NAG	M	1	2,1	-	0/6/23/26	0/1/1/1
2	FUC	M	2	2	-	-	0/1/1/1
3	NAG	N	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	N	2	3	-	2/6/23/26	0/1/1/1
2	NAG	O	1	2,1	-	0/6/23/26	0/1/1/1
2	FUC	O	2	2	-	-	0/1/1/1
3	NAG	P	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	P	2	3	-	2/6/23/26	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	NAG	O5-C1	-3.79	1.37	1.43
5	K	3	BMA	O5-C1	2.92	1.48	1.43
2	E	2	FUC	C2-C3	2.72	1.56	1.52
2	I	2	FUC	C2-C3	2.63	1.56	1.52
2	E	2	FUC	C1-C2	2.62	1.58	1.52
3	P	1	NAG	C1-C2	2.61	1.55	1.52
2	I	1	NAG	O5-C1	2.48	1.47	1.43
5	K	3	BMA	C1-C2	2.45	1.58	1.52
5	K	4	MAN	O5-C5	2.41	1.48	1.43
5	K	3	BMA	C4-C5	2.38	1.58	1.53
3	N	1	NAG	O5-C1	-2.25	1.39	1.43
3	H	1	NAG	C1-C2	2.08	1.55	1.52
4	G	1	NAG	C1-C2	2.07	1.55	1.52
2	I	1	NAG	C1-C2	2.02	1.55	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	K	3	BMA	C1-O5-C5	5.12	119.04	112.19
3	J	2	NAG	C1-O5-C5	2.70	115.81	112.19
5	K	3	BMA	C3-C4-C5	2.37	114.53	110.23
3	L	2	NAG	C1-O5-C5	2.35	115.33	112.19
2	O	1	NAG	C1-O5-C5	2.28	115.24	112.19
3	N	2	NAG	C1-O5-C5	2.25	115.20	112.19
3	F	1	NAG	C1-O5-C5	2.15	115.06	112.19
2	M	2	FUC	O3-C3-C4	-2.11	105.39	110.38
5	K	4	MAN	O2-C2-C3	-2.06	105.89	110.15
3	P	1	NAG	C1-O5-C5	2.01	114.89	112.19

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	1	NAG	C1-C2-N2-C7
4	G	1	NAG	C1-C2-N2-C7
4	G	2	NAG	C3-C2-N2-C7
3	L	2	NAG	O5-C5-C6-O6
3	J	1	NAG	O5-C5-C6-O6
3	L	1	NAG	O5-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
3	P	2	NAG	O5-C5-C6-O6
3	L	1	NAG	C4-C5-C6-O6
3	J	2	NAG	O5-C5-C6-O6
3	L	2	NAG	C4-C5-C6-O6
3	F	1	NAG	C8-C7-N2-C2
3	F	1	NAG	O7-C7-N2-C2
3	L	1	NAG	C8-C7-N2-C2
3	L	1	NAG	O7-C7-N2-C2
3	N	2	NAG	C8-C7-N2-C2
3	N	2	NAG	O7-C7-N2-C2
3	P	1	NAG	C8-C7-N2-C2
3	P	1	NAG	O7-C7-N2-C2
5	K	1	NAG	C8-C7-N2-C2
5	K	1	NAG	O7-C7-N2-C2
3	J	2	NAG	C4-C5-C6-O6
3	P	2	NAG	C4-C5-C6-O6
4	G	2	NAG	C1-C2-N2-C7
5	K	3	BMA	O5-C5-C6-O6
5	K	1	NAG	C1-C2-N2-C7
4	G	1	NAG	C4-C5-C6-O6
3	H	1	NAG	C3-C2-N2-C7

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	K	3	BMA	C1-C2-C3-C4-C5-O5

7 monomers are involved in 15 short contacts:

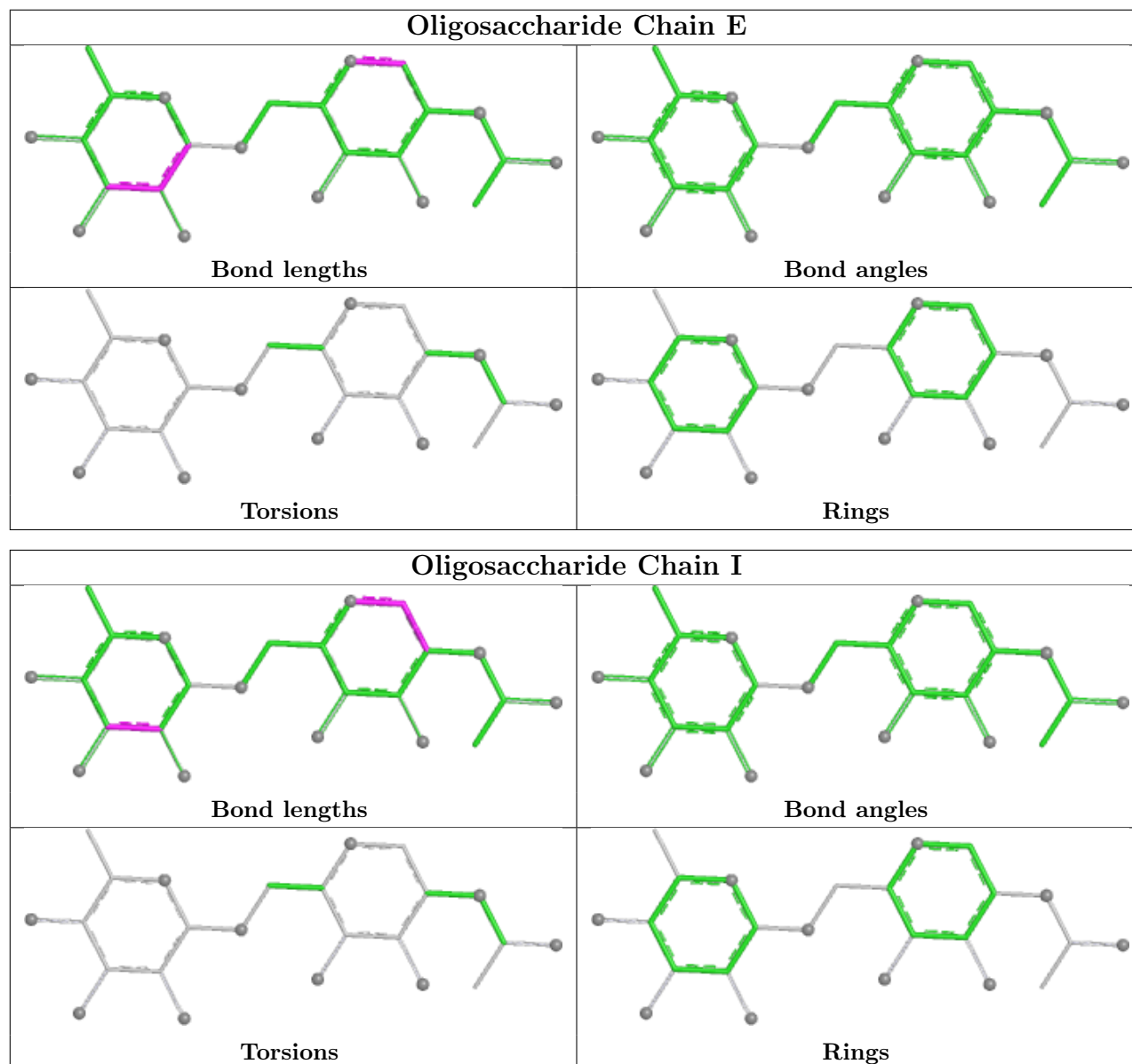
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	NAG	1	0
3	N	2	NAG	2	0
4	G	2	NAG	2	0

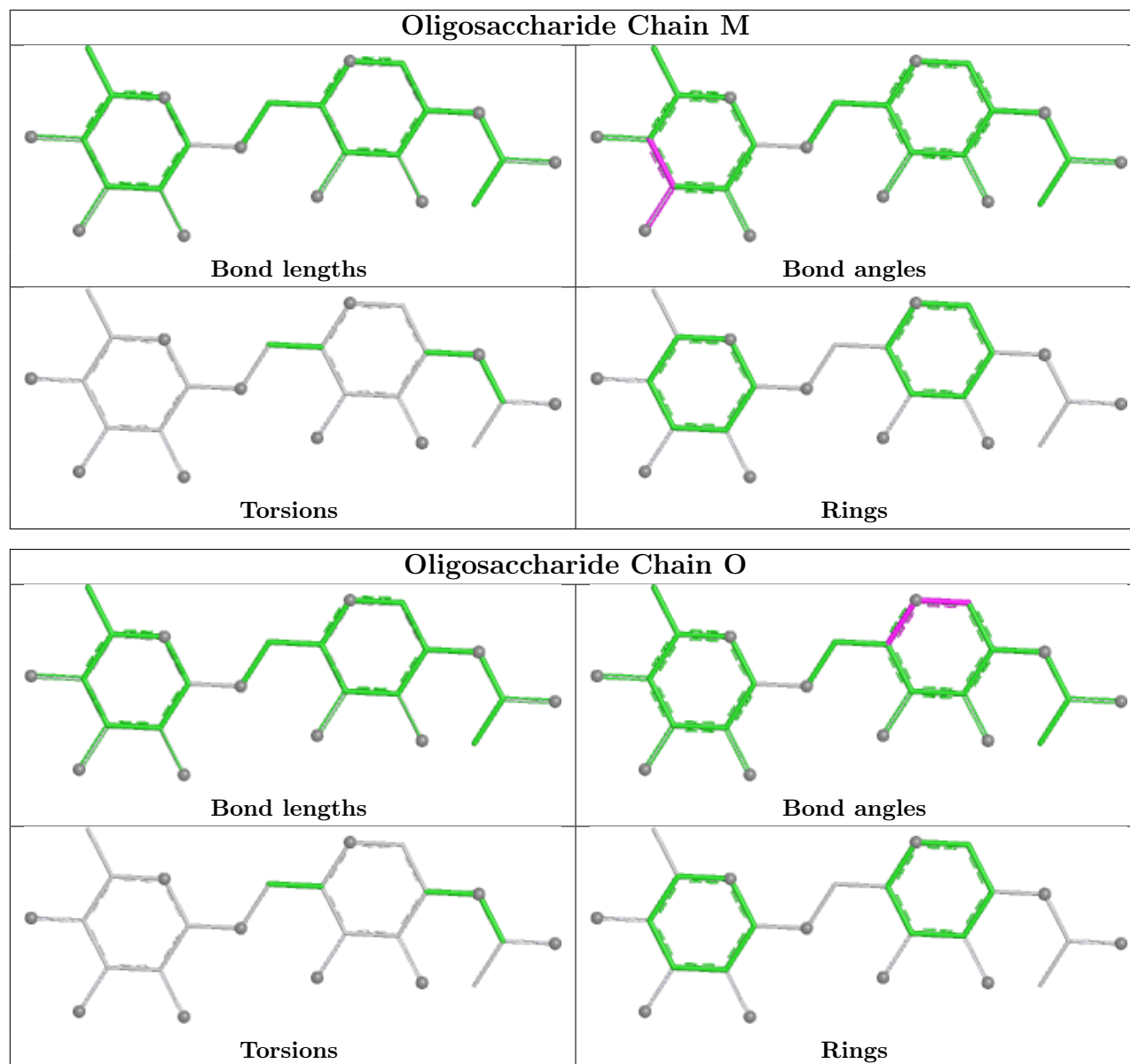
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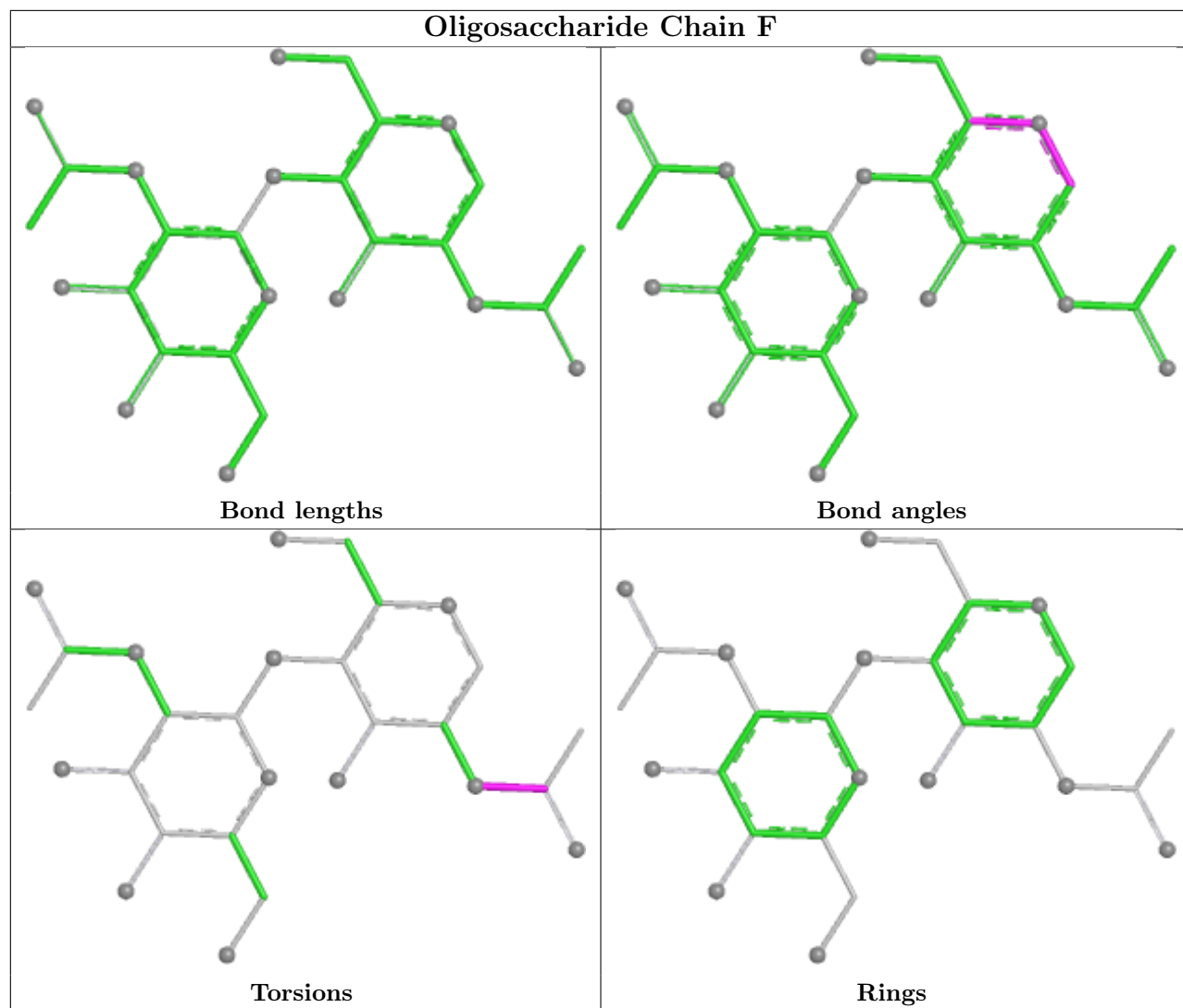
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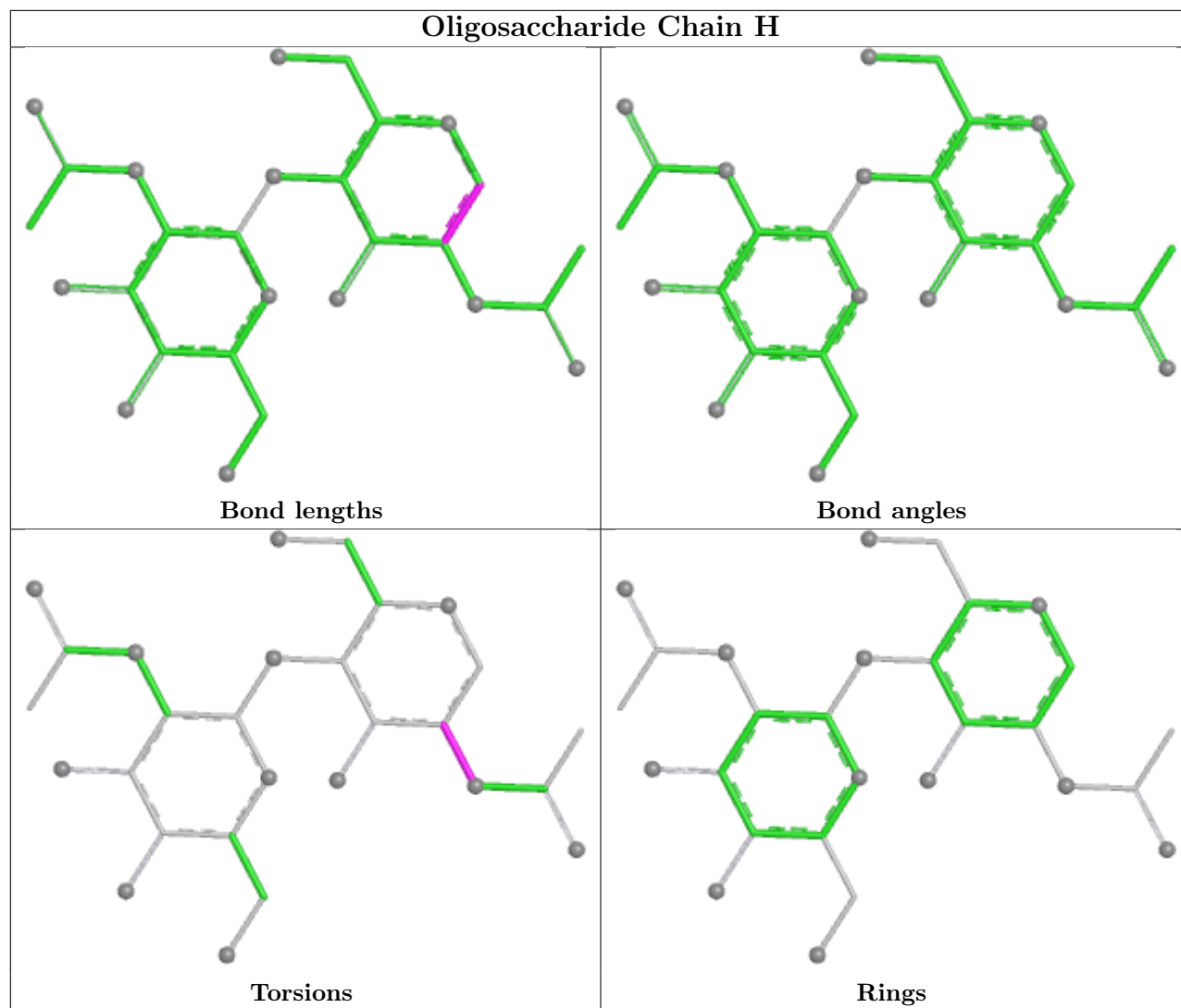
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	N	1	NAG	2	0
3	P	1	NAG	2	0
5	K	1	NAG	5	0
3	F	1	NAG	1	0

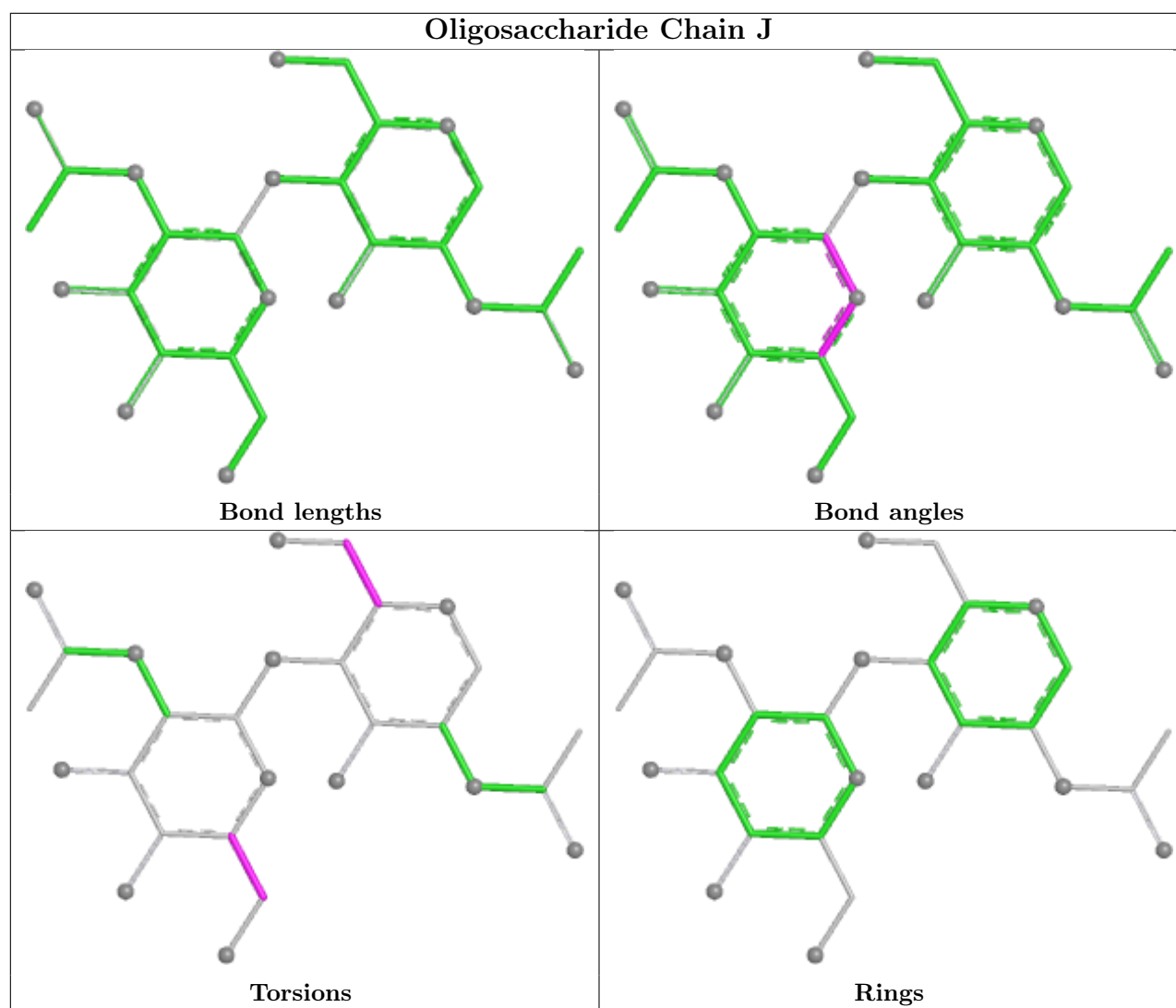
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

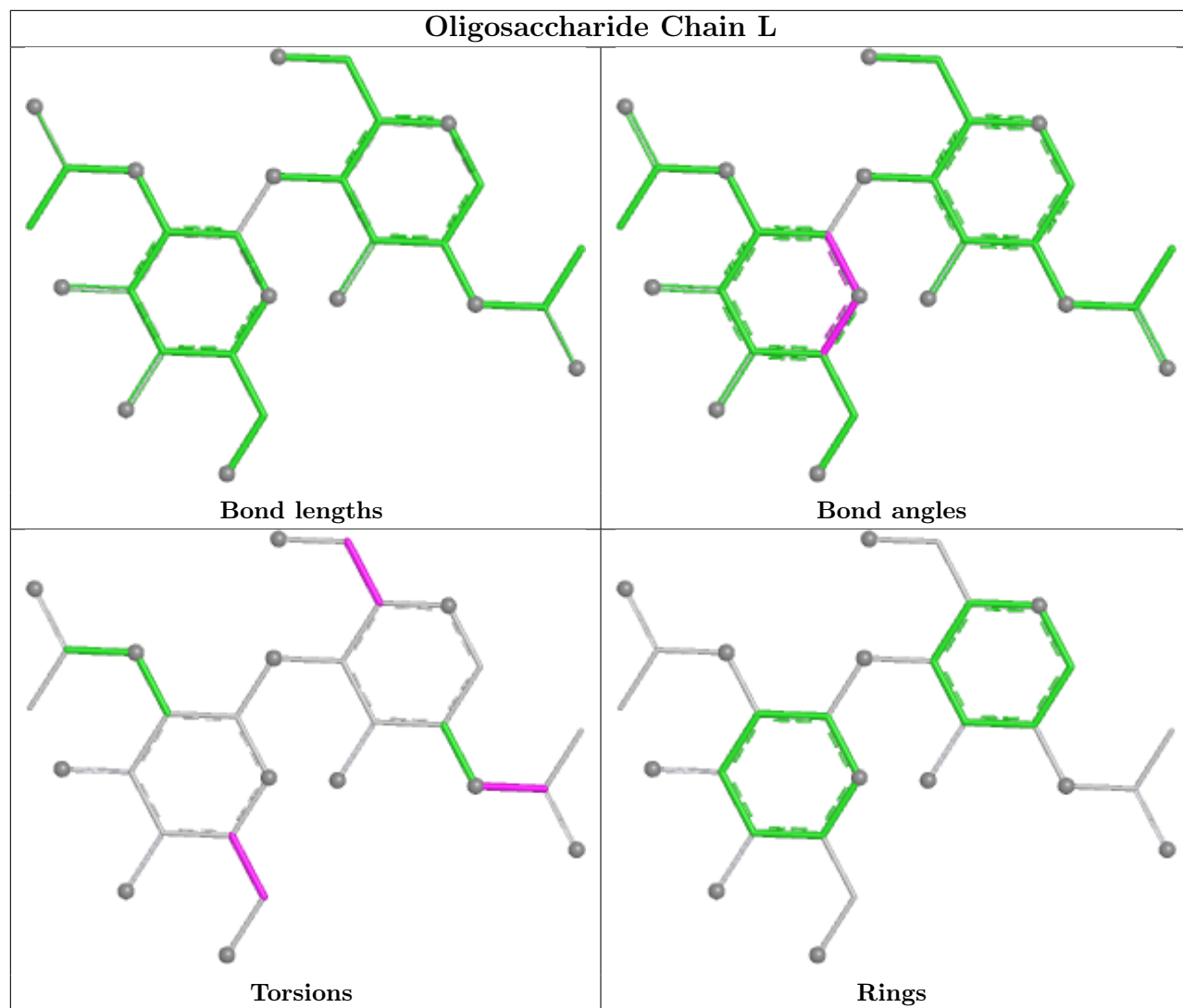


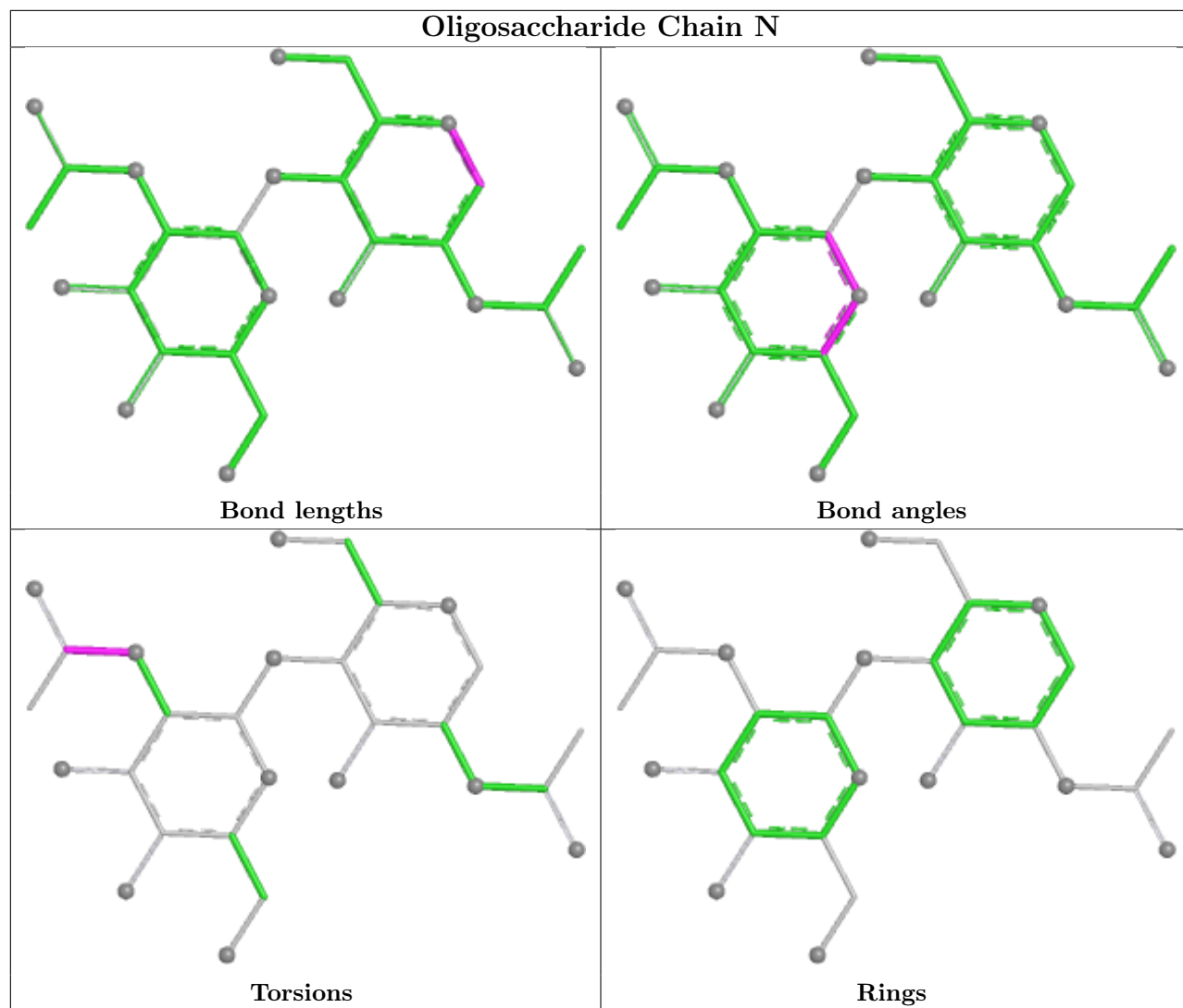


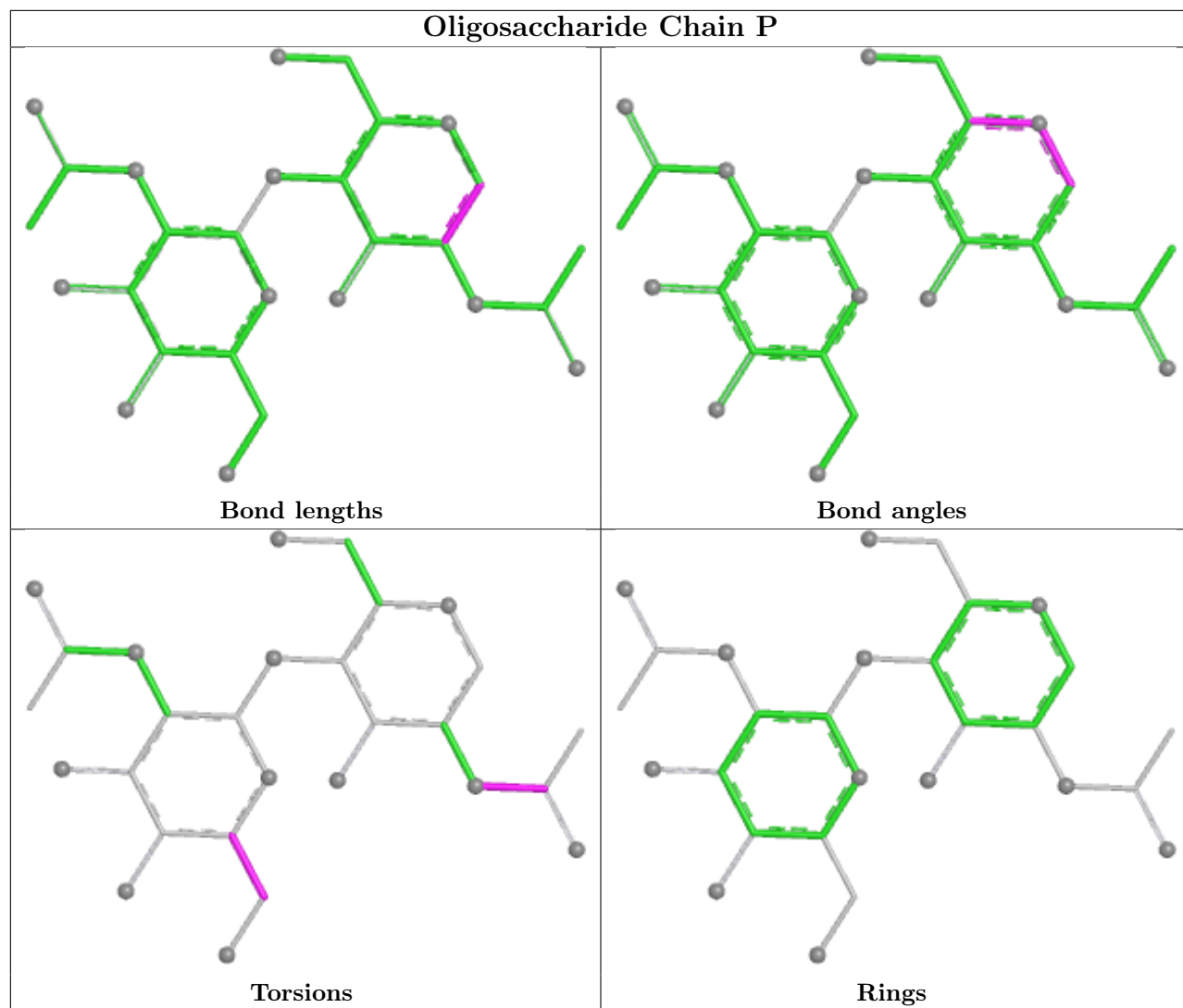


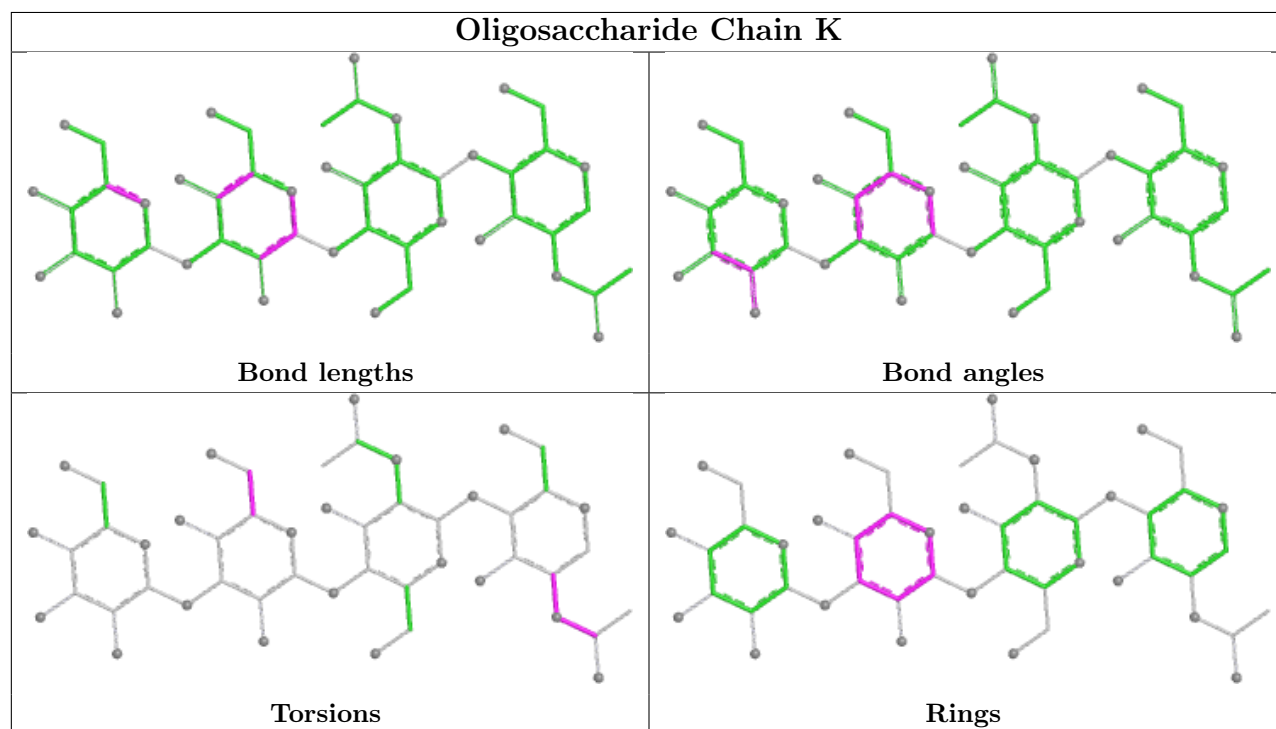
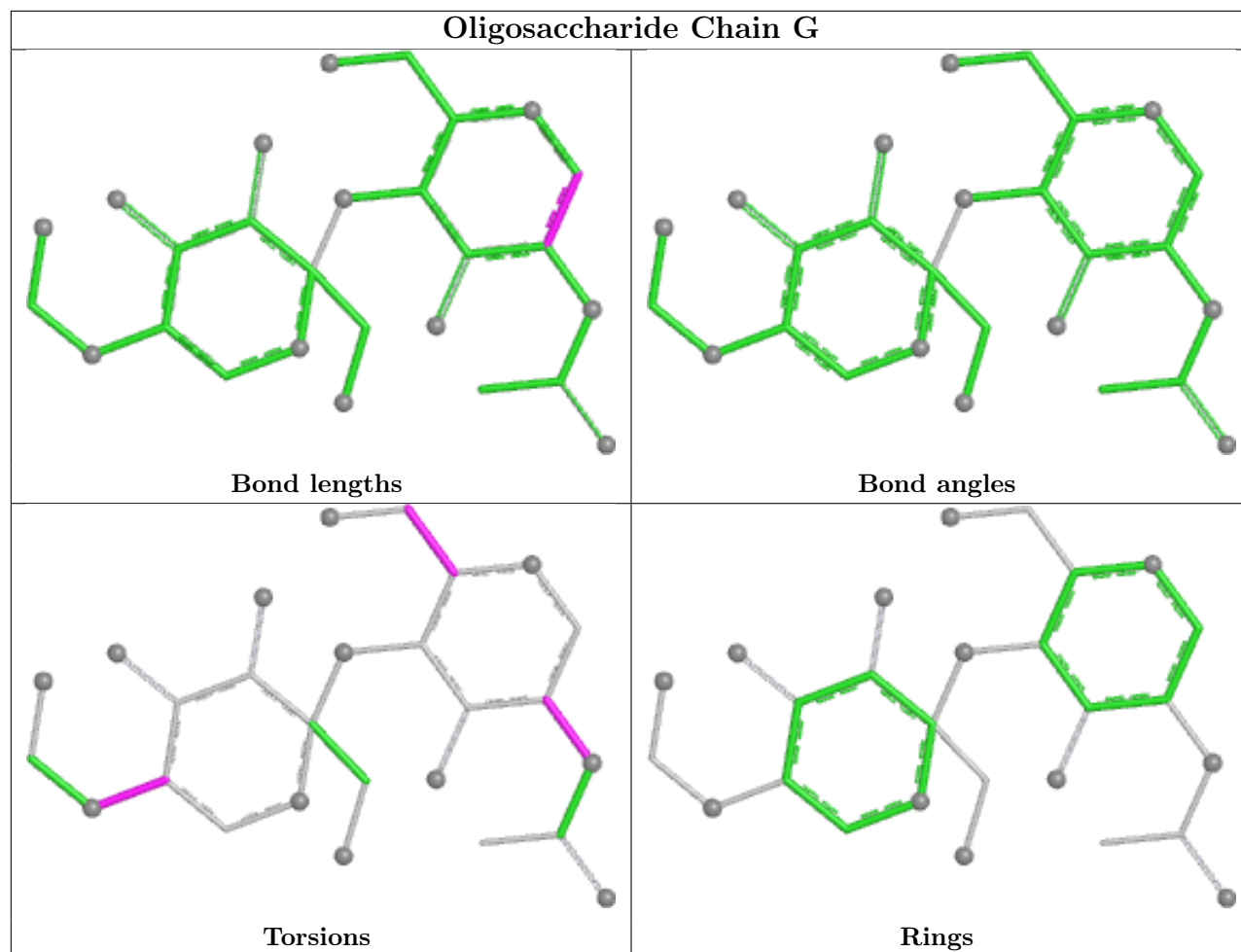












5.6 Ligand geometry

11 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	$\# Z > 2$
6	PTY	C	201	-	46,46,49	0.58	1 (2%)	49,51,54	1.32	3 (6%)
7	EDO	B	202	-	3,3,3	0.40	0	2,2,2	0.85	0
6	PTY	A	201	-	43,43,49	0.63	1 (2%)	46,48,54	0.99	2 (4%)
7	EDO	D	203	-	3,3,3	0.37	0	2,2,2	0.29	0
7	EDO	C	203	-	3,3,3	0.62	0	2,2,2	0.09	0
7	EDO	D	202	-	3,3,3	0.37	0	2,2,2	0.79	0
7	EDO	B	203	-	3,3,3	0.41	0	2,2,2	0.53	0
6	PTY	B	201	-	43,43,49	0.62	1 (2%)	46,48,54	1.18	4 (8%)
6	PTY	D	201	-	44,44,49	0.61	1 (2%)	47,49,54	1.00	1 (2%)
7	EDO	A	202	-	3,3,3	0.36	0	2,2,2	0.88	0
7	EDO	C	202	-	3,3,3	0.49	0	2,2,2	0.63	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	PTY	C	201	-	-	18/48/48/53	-
7	EDO	B	202	-	-	0/1/1/1	-
6	PTY	A	201	-	-	12/45/45/53	-
7	EDO	D	203	-	-	1/1/1/1	-
7	EDO	C	203	-	-	1/1/1/1	-
7	EDO	D	202	-	-	1/1/1/1	-
7	EDO	B	203	-	-	0/1/1/1	-
6	PTY	B	201	-	-	14/45/45/53	-
6	PTY	D	201	-	-	15/46/46/53	-
7	EDO	A	202	-	-	0/1/1/1	-
7	EDO	C	202	-	-	1/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	201	PTY	P1-O11	2.73	1.64	1.54
6	D	201	PTY	P1-O11	2.72	1.64	1.54
6	A	201	PTY	P1-O11	2.60	1.64	1.54
6	C	201	PTY	P1-O11	2.53	1.64	1.54

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	201	PTY	O11-P1-O14	-6.68	89.26	106.67
6	B	201	PTY	O11-P1-O14	-5.49	92.35	106.67
6	A	201	PTY	O11-P1-O14	-4.87	93.96	106.67
6	D	201	PTY	O11-P1-O14	-4.86	93.99	106.67
6	C	201	PTY	C6-O7-C8	3.75	126.77	117.80
6	A	201	PTY	O12-P1-O13	2.41	120.21	110.83
6	B	201	PTY	C6-O7-C8	2.23	123.14	117.80
6	C	201	PTY	O12-P1-O13	2.21	119.44	110.83
6	B	201	PTY	O4-C30-O30	-2.07	118.46	123.63
6	B	201	PTY	O12-P1-O13	2.05	118.81	110.83

There are no chirality outliers.

All (63) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	201	PTY	O4-C1-C6-O7
6	A	201	PTY	C5-O14-P1-O11
6	A	201	PTY	C5-O14-P1-O12
6	C	201	PTY	C8-C11-C12-C13
6	A	201	PTY	C14-C15-C16-C17
6	D	201	PTY	C12-C13-C14-C15
6	A	201	PTY	C34-C35-C36-C37
6	C	201	PTY	C19-C20-C21-C22
6	C	201	PTY	C25-C26-C27-C28
6	C	201	PTY	C15-C16-C17-C18
6	D	201	PTY	C39-C40-C41-C42
6	B	201	PTY	C33-C34-C35-C36
6	D	201	PTY	C22-C23-C24-C25
6	C	201	PTY	C18-C19-C20-C21
6	D	201	PTY	O4-C1-C6-O7
6	D	201	PTY	O4-C1-C6-C5
7	C	203	EDO	O1-C1-C2-O2
6	A	201	PTY	C5-O14-P1-O13

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Mol	Chain	Res	Type	Atoms
6	D	201	PTY	C23-C24-C25-C26
6	C	201	PTY	O14-C5-C6-O7
6	D	201	PTY	C31-C30-O4-C1
6	A	201	PTY	C37-C38-C39-C40
6	D	201	PTY	C41-C42-C43-C44
6	B	201	PTY	C30-C31-C32-C33
6	C	201	PTY	C38-C39-C40-C41
6	C	201	PTY	C6-C5-O14-P1
6	A	201	PTY	C38-C39-C40-C41
6	B	201	PTY	C8-C11-C12-C13
6	D	201	PTY	O30-C30-O4-C1
6	B	201	PTY	C17-C18-C19-C20
7	C	202	EDO	O1-C1-C2-O2
6	C	201	PTY	C36-C37-C38-C39
6	D	201	PTY	C36-C37-C38-C39
6	B	201	PTY	C5-O14-P1-O12
6	C	201	PTY	C24-C25-C26-C27
6	B	201	PTY	O14-C5-C6-O7
6	A	201	PTY	O4-C1-C6-C5
6	B	201	PTY	C23-C24-C25-C26
6	A	201	PTY	C22-C23-C24-C25
6	D	201	PTY	C5-O14-P1-O13
6	A	201	PTY	C19-C20-C21-C22
6	B	201	PTY	O14-C5-C6-C1
6	C	201	PTY	O14-C5-C6-C1
6	D	201	PTY	C19-C20-C21-C22
6	B	201	PTY	O4-C1-C6-O7
6	A	201	PTY	C16-C17-C18-C19
6	B	201	PTY	C14-C15-C16-C17
6	D	201	PTY	C32-C33-C34-C35
6	C	201	PTY	C12-C13-C14-C15
6	D	201	PTY	C21-C22-C23-C24
7	D	203	EDO	O1-C1-C2-O2
6	C	201	PTY	C17-C18-C19-C20
6	C	201	PTY	C40-C41-C42-C43
6	C	201	PTY	C41-C42-C43-C44
6	C	201	PTY	C5-C6-O7-C8
7	D	202	EDO	O1-C1-C2-O2
6	B	201	PTY	O4-C30-C31-C32
6	D	201	PTY	C16-C17-C18-C19
6	C	201	PTY	C39-C40-C41-C42
6	B	201	PTY	C12-C13-C14-C15

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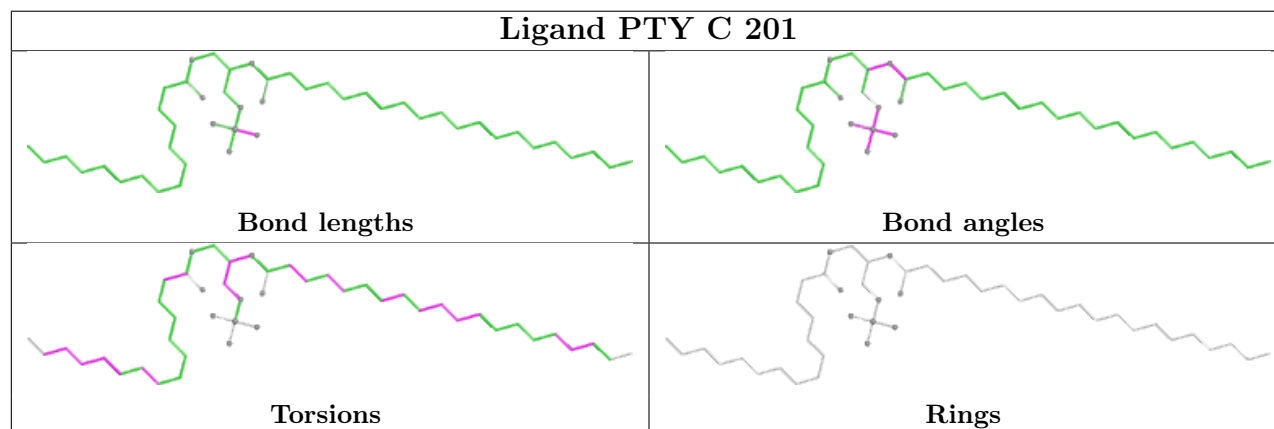
Mol	Chain	Res	Type	Atoms
6	B	201	PTY	O30-C30-C31-C32
6	B	201	PTY	C36-C37-C38-C39
6	C	201	PTY	O4-C30-C31-C32

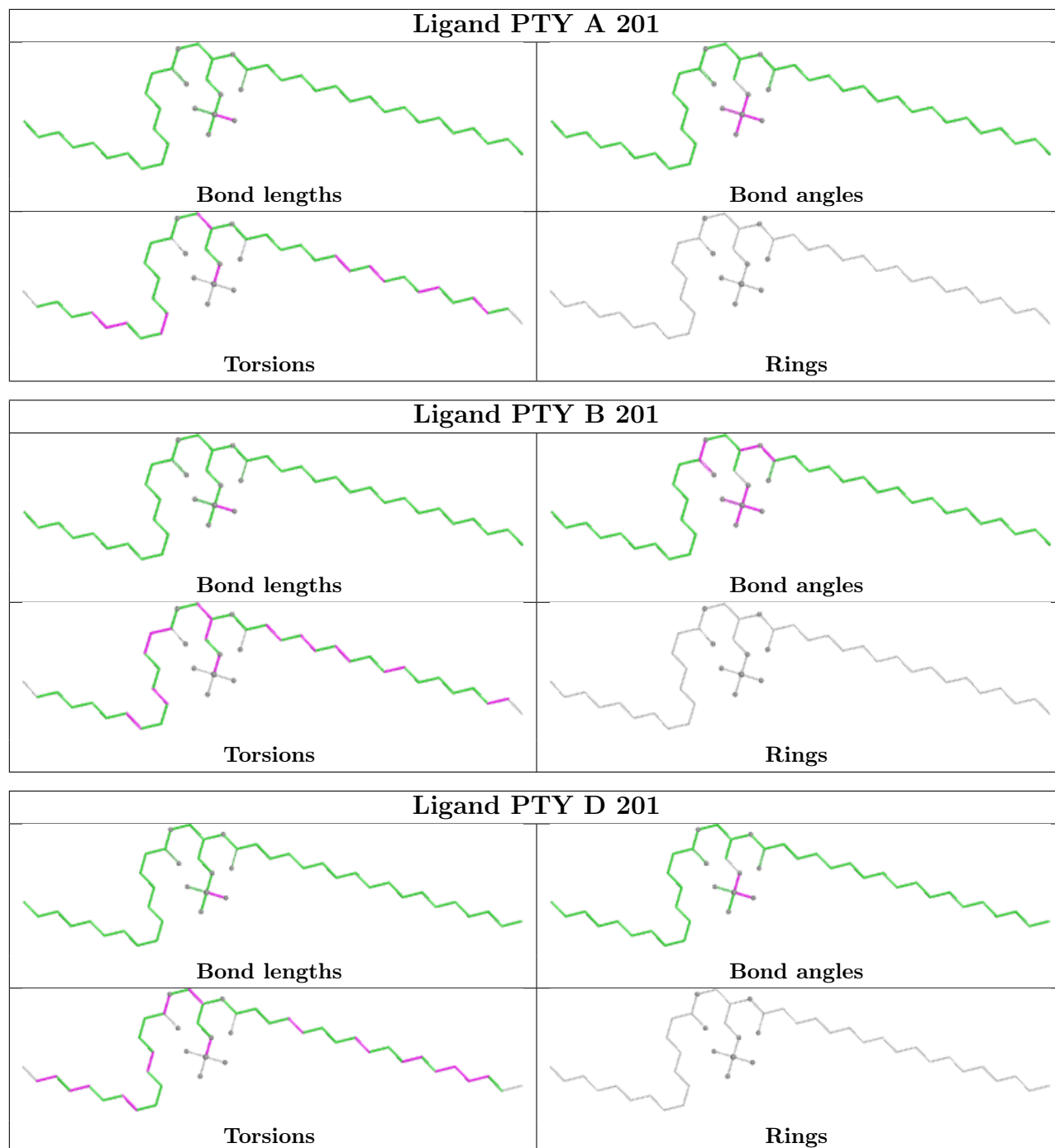
There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	201	PTY	9	0
7	D	203	EDO	2	0
6	B	201	PTY	7	0
6	D	201	PTY	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	168/193 (87%)	0.34	6 (3%)	46	53	16, 43, 60, 88	2 (1%)
1	B	167/193 (86%)	0.40	6 (3%)	46	53	18, 45, 62, 84	3 (1%)
1	C	166/193 (86%)	0.33	8 (4%)	35	41	30, 41, 57, 71	4 (2%)
1	D	170/193 (88%)	0.44	10 (5%)	28	32	30, 44, 67, 100	2 (1%)
All	All	671/772 (86%)	0.37	30 (4%)	38	44	16, 43, 63, 100	11 (1%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	88	THR	4.0
1	D	8	LEU	3.7
1	A	8	LEU	3.6
1	D	177	ILE	3.4
1	A	105	PRO	3.2
1	A	108	SER	3.1
1	C	130[A]	ARG	3.1
1	C	154	TYR	3.1
1	C	139	VAL	3.1
1	B	177	ILE	3.0
1	C	108	SER	3.0
1	B	105	PRO	2.8
1	D	154	TYR	2.7
1	B	26	TRP	2.7
1	D	106	GLU	2.6
1	D	18	TYR	2.6
1	D	108	SER	2.5
1	D	103	LEU	2.5
1	C	137	THR	2.4
1	A	94	THR	2.3
1	A	103	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	35	GLY	2.2
1	B	154	TYR	2.2
1	C	177	ILE	2.2
1	D	105	PRO	2.2
1	D	26	TRP	2.1
1	C	18	TYR	2.1
1	B	35	GLY	2.1
1	A	177	ILE	2.0
1	B	108	SER	2.0

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.

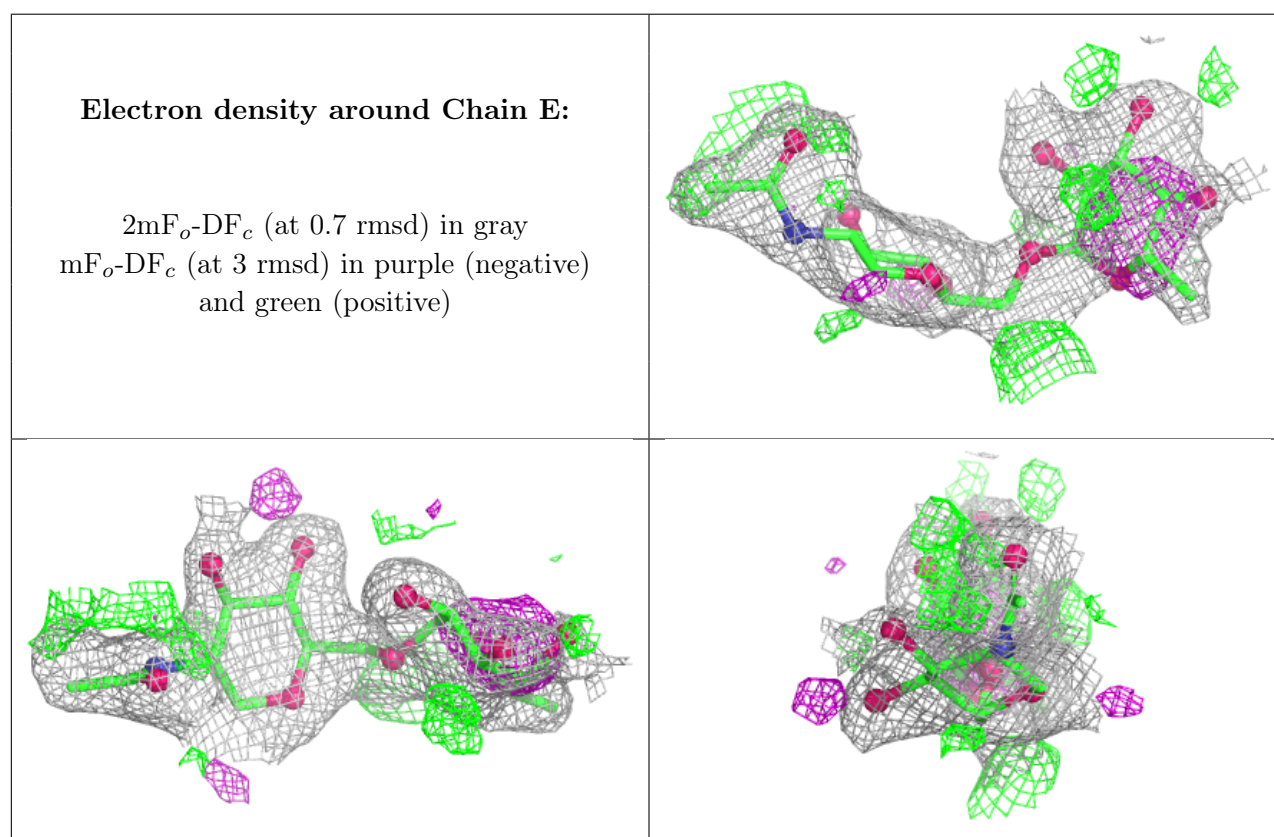
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	BMA	K	3	11/12	0.55	0.15	73,81,83,84	0
2	FUC	E	2	10/11	0.70	0.18	42,58,65,73	0
3	NAG	J	2	14/15	0.73	0.13	65,73,81,86	0
4	NAG	G	2	13/15	0.74	0.14	61,66,73,76	0
3	NAG	P	2	14/15	0.75	0.12	72,76,80,81	0
3	NAG	N	2	14/15	0.76	0.12	58,69,75,81	0
3	NAG	H	2	14/15	0.81	0.14	59,67,73,75	0
3	NAG	F	2	14/15	0.82	0.10	72,78,85,90	0
2	NAG	E	1	14/15	0.83	0.11	36,45,59,66	0
3	NAG	L	2	14/15	0.83	0.11	59,64,69,74	0
5	MAN	K	4	11/12	0.83	0.14	59,66,77,81	0
3	NAG	F	1	14/15	0.87	0.10	50,57,61,68	0
3	NAG	P	1	14/15	0.87	0.13	58,65,72,74	0
5	NAG	K	2	14/15	0.88	0.10	52,56,67,69	0
3	NAG	L	1	14/15	0.89	0.11	40,52,57,63	0
2	NAG	I	1	14/15	0.90	0.10	39,40,47,48	0
3	NAG	J	1	14/15	0.90	0.10	53,57,67,73	0
3	NAG	N	1	14/15	0.92	0.09	44,58,65,70	0
2	FUC	I	2	10/11	0.92	0.09	33,37,38,39	0

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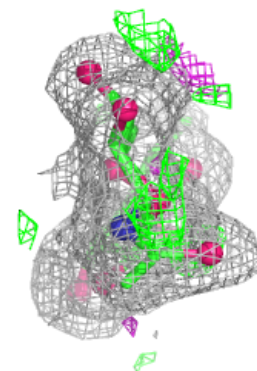
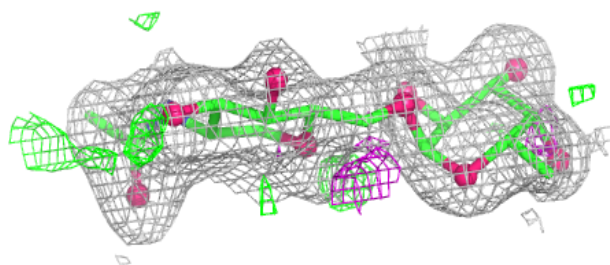
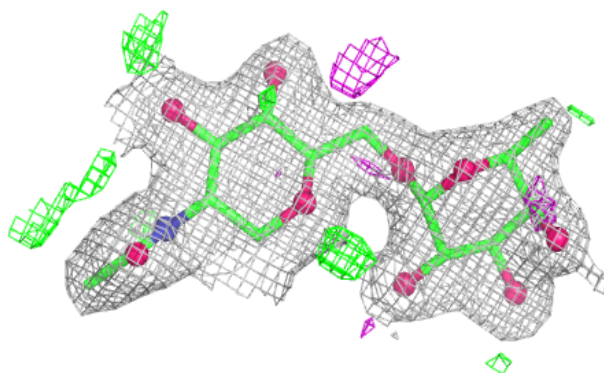
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FUC	O	2	10/11	0.93	0.08	43,46,52,54	0
4	NAG	G	1	14/15	0.93	0.10	39,47,56,57	0
2	NAG	M	1	14/15	0.94	0.08	37,42,50,55	0
2	FUC	M	2	10/11	0.94	0.07	44,47,49,54	0
5	NAG	K	1	14/15	0.94	0.09	33,45,50,59	0
3	NAG	H	1	14/15	0.95	0.07	36,42,51,53	0
2	NAG	O	1	14/15	0.96	0.07	37,42,54,57	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.

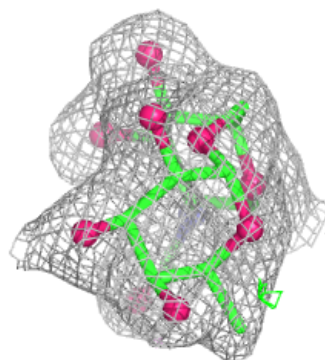
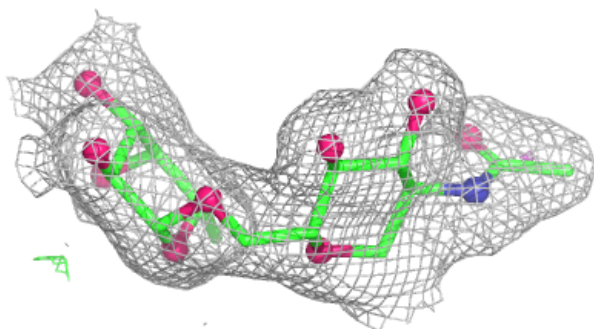
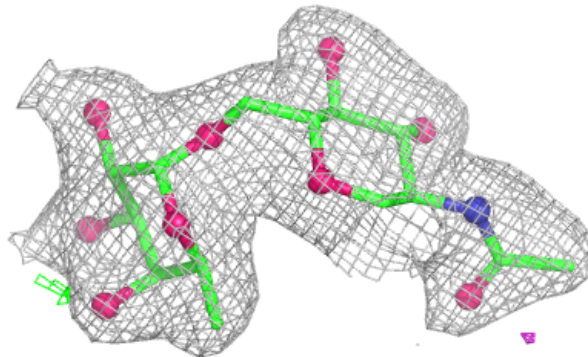


Electron density around Chain I:

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

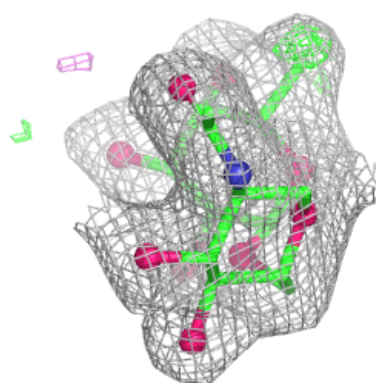
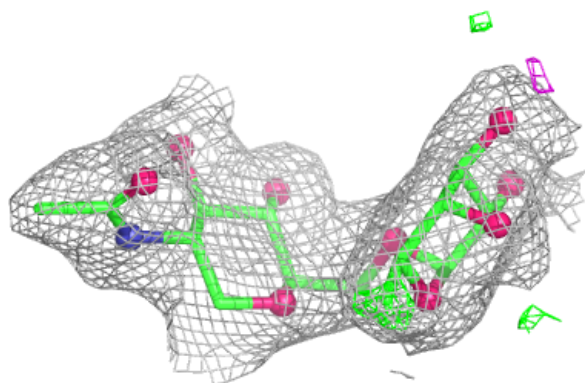
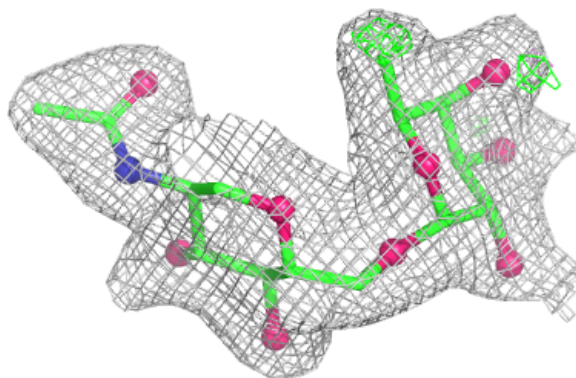
**Electron density around Chain M:**

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

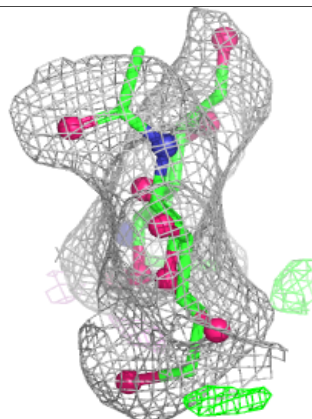
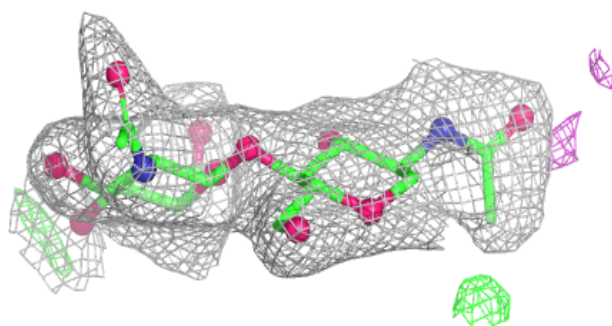
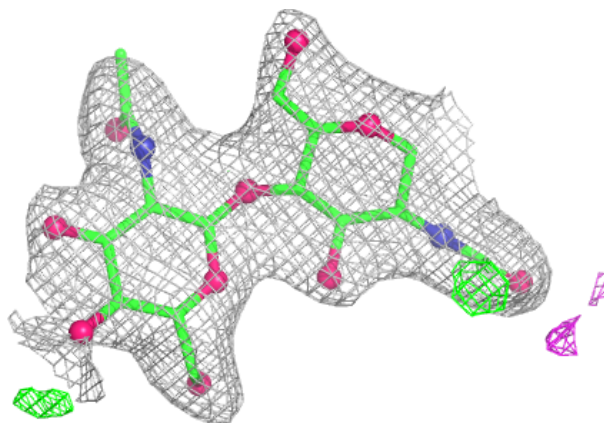


Electron density around Chain O:

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

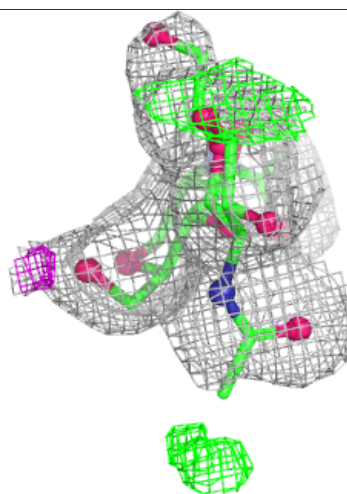
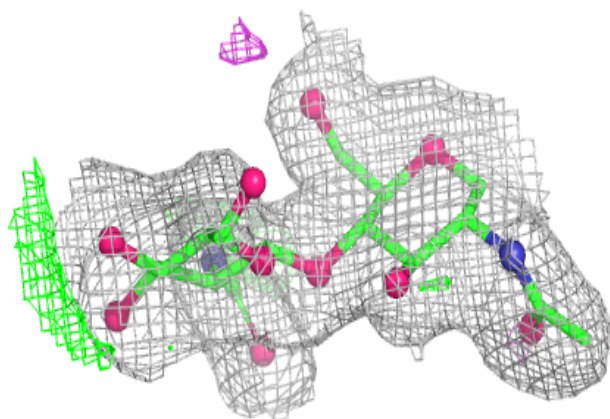
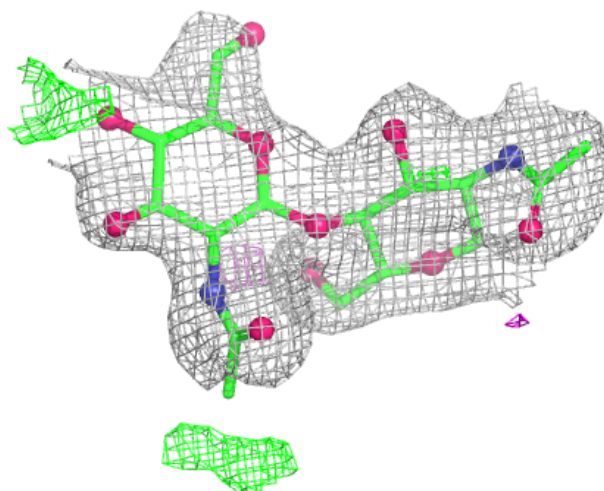
**Electron density around Chain F:**

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



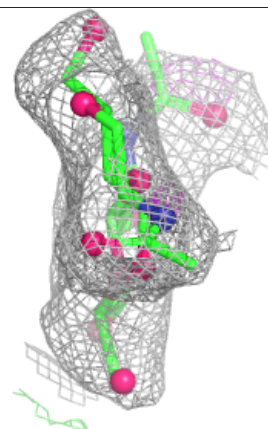
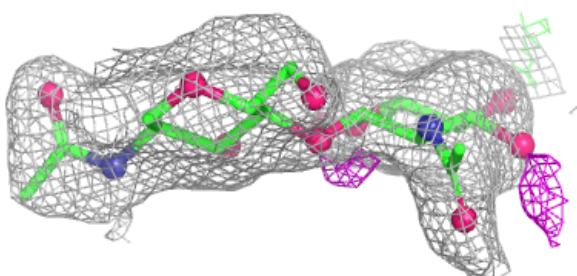
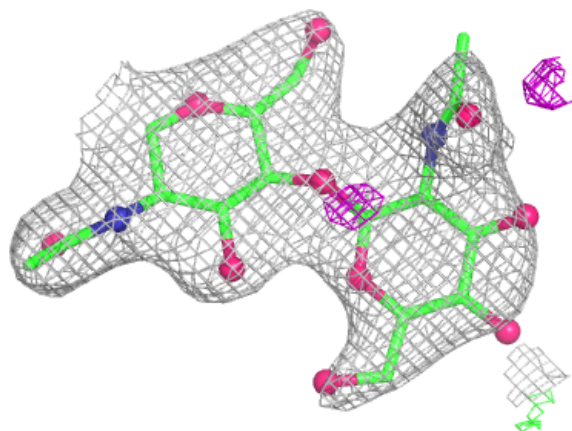
Electron density around Chain H:

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



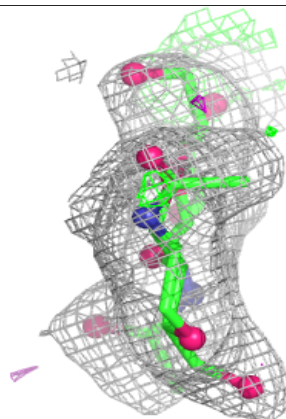
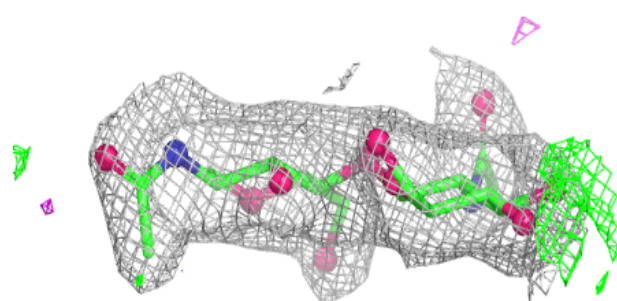
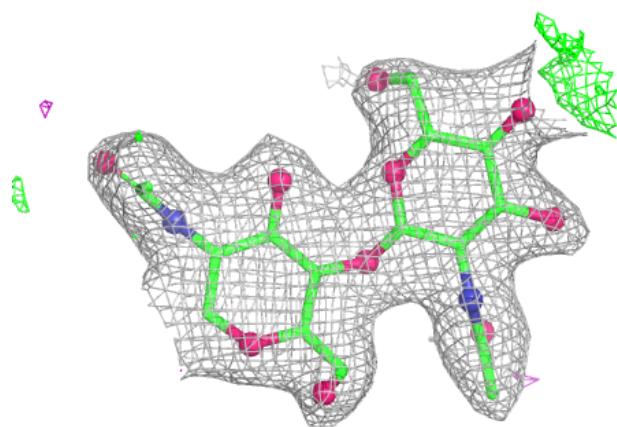
Electron density around Chain J:

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



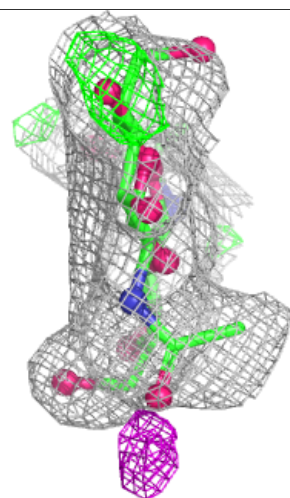
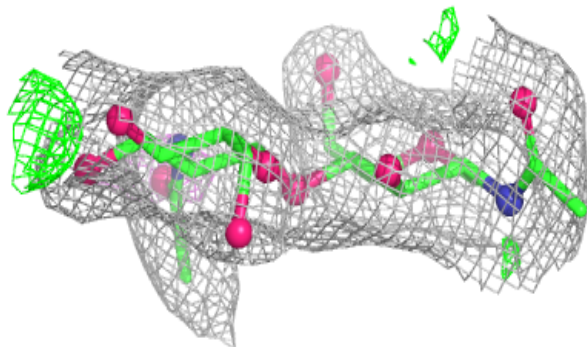
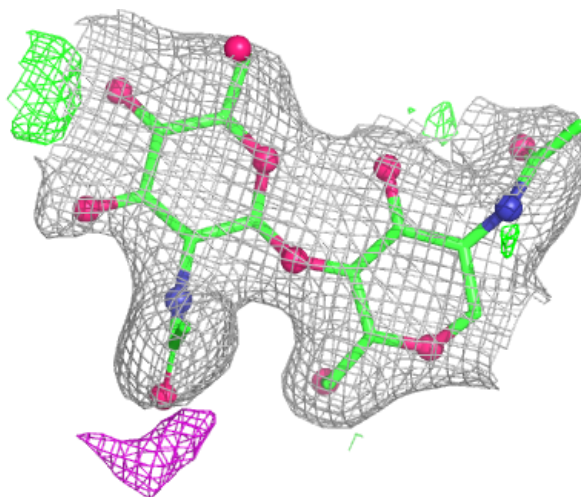
Electron density around Chain L:

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



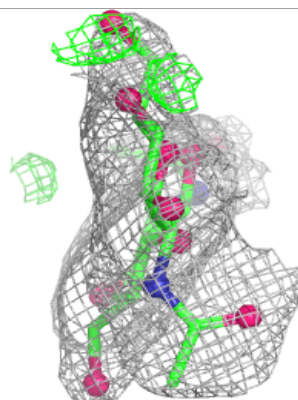
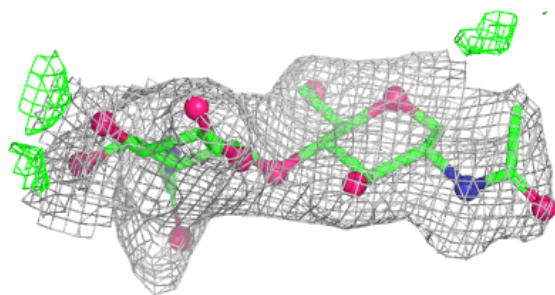
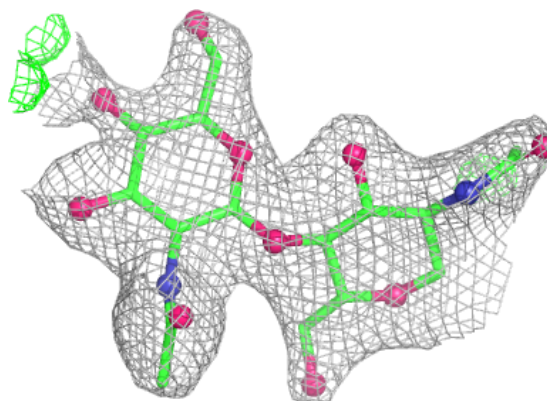
Electron density around Chain N:

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

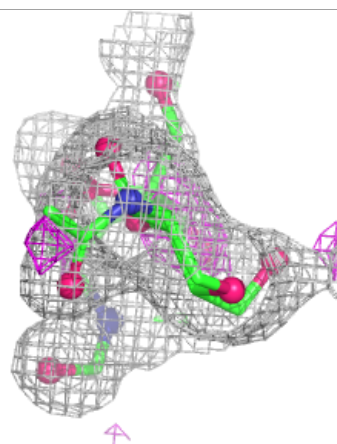
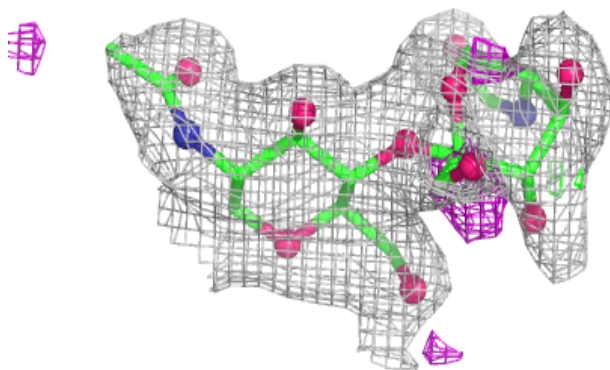
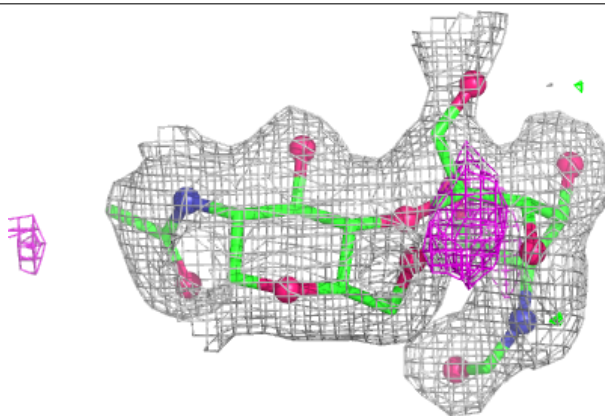


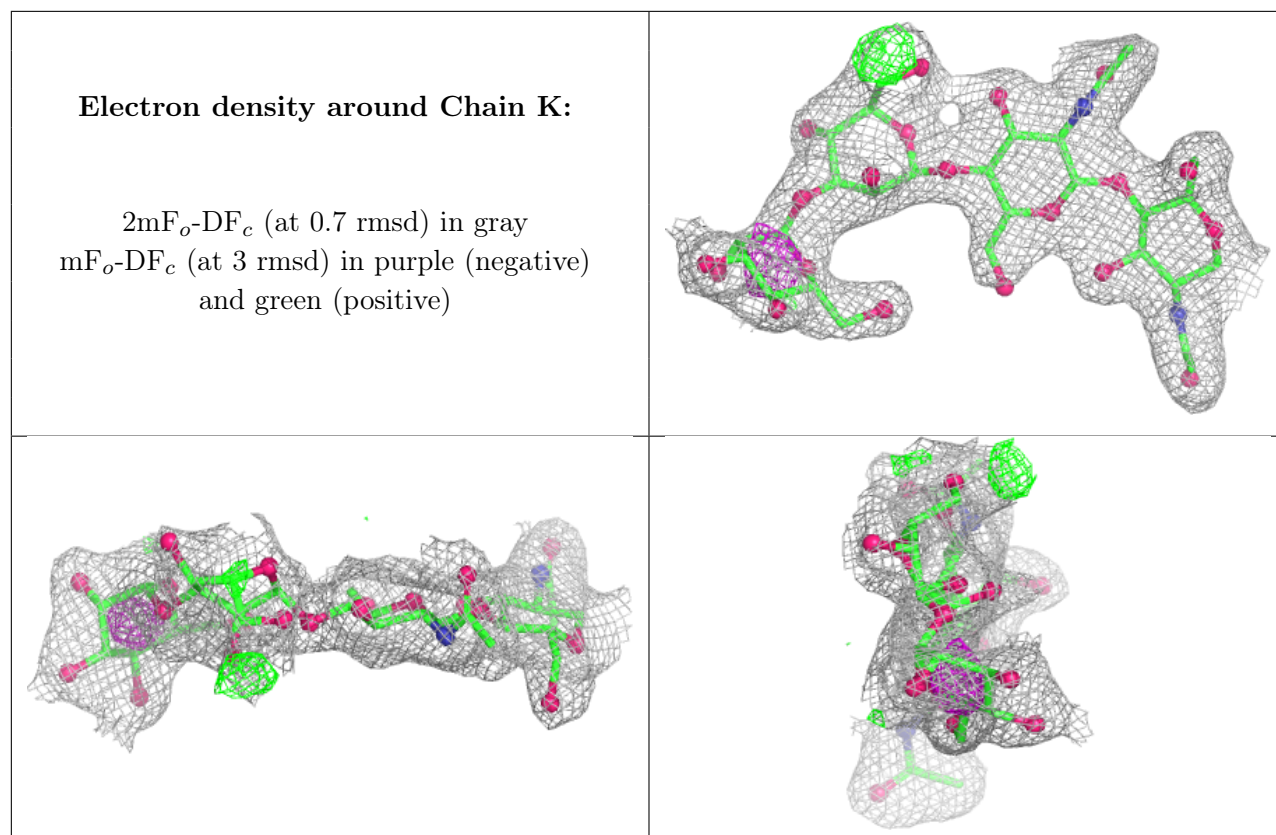
Electron density around Chain P:

$2mF_o-DF_c$ (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)





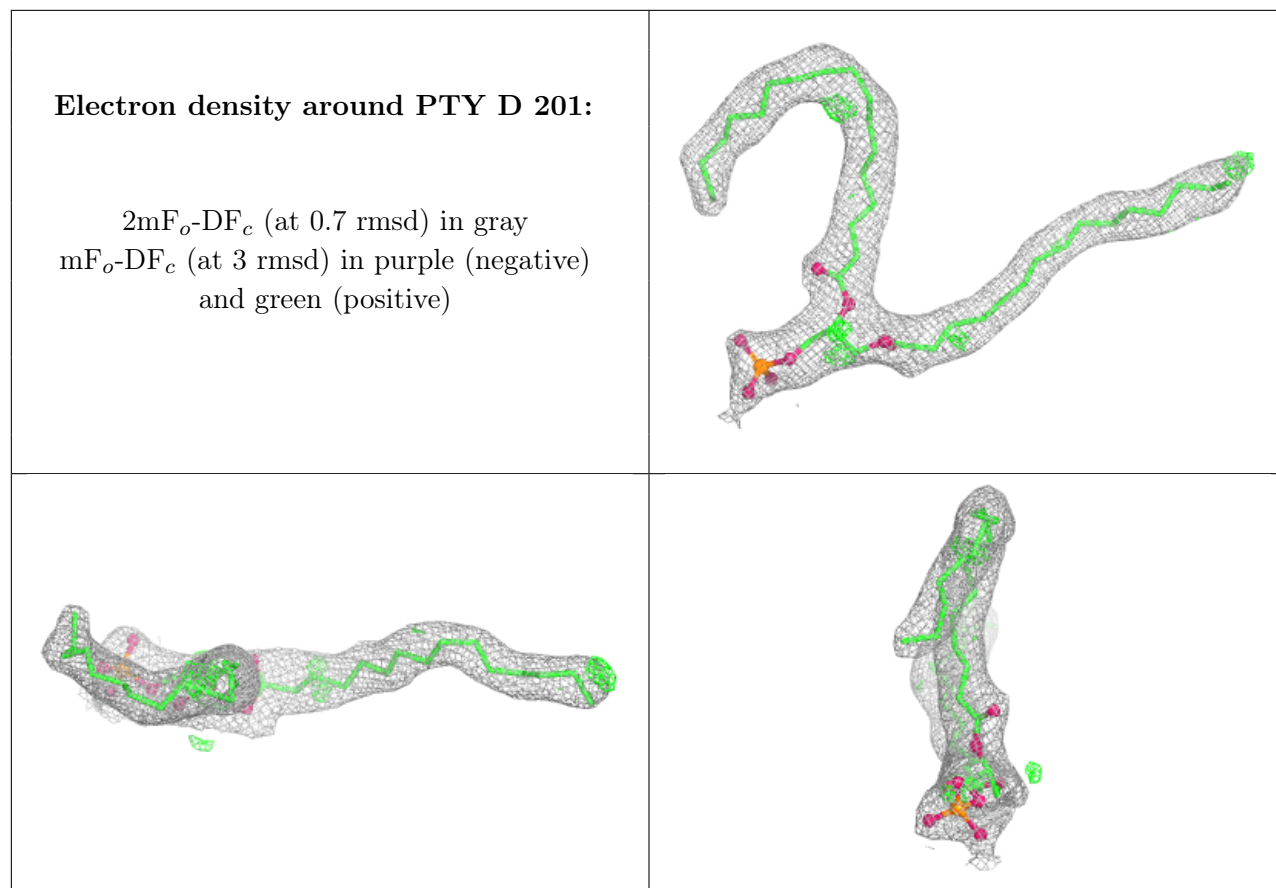
6.4 Ligands [i](#)

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	EDO	B	203	4/4	0.51	0.19	63,68,69,71	0
7	EDO	D	203	4/4	0.81	0.21	44,52,59,60	0
7	EDO	C	203	4/4	0.84	0.13	51,52,58,64	0
7	EDO	C	202	4/4	0.86	0.15	36,40,49,65	0
7	EDO	B	202	4/4	0.87	0.19	42,45,47,51	0
6	PTY	D	201	45/50	0.88	0.16	41,49,79,100	0
7	EDO	D	202	4/4	0.88	0.15	47,52,54,56	0
6	PTY	B	201	44/50	0.88	0.15	43,54,74,87	0
6	PTY	C	201	47/50	0.90	0.14	39,49,70,84	0
6	PTY	A	201	44/50	0.90	0.13	38,50,76,99	0
7	EDO	A	202	4/4	0.90	0.14	42,45,49,59	0

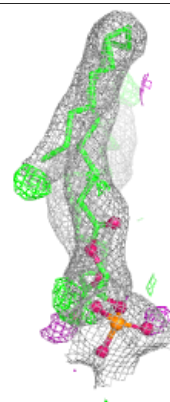
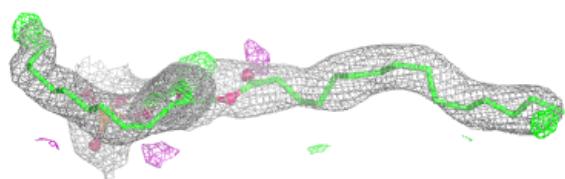
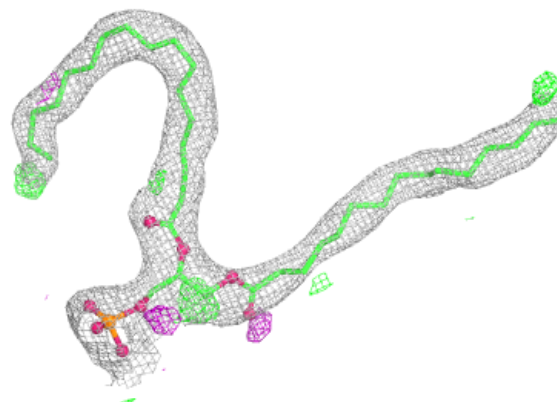
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different

orientation to approximate a three-dimensional view.

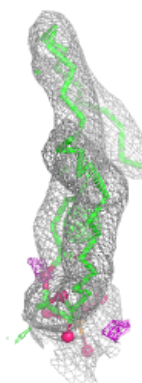
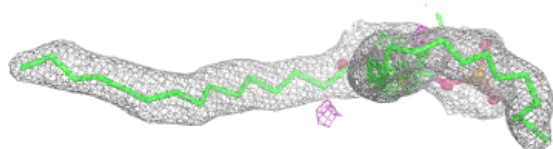


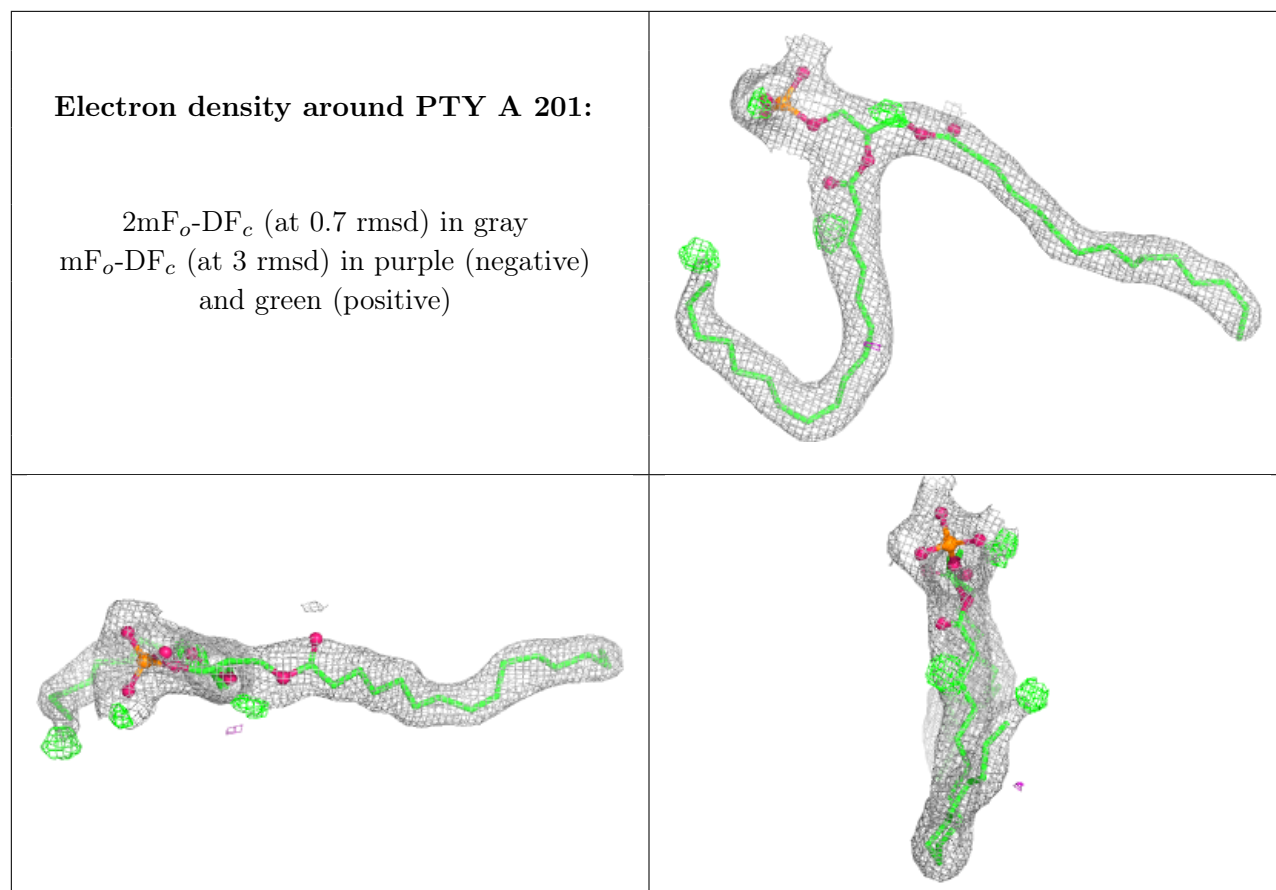
Electron density around PTY B 201:

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

**Electron density around PTY C 201:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.