



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:35 PM UTC

PDB ID : 4UFB / pdb_00004ufb
Title : Crystal structure of the Angiotensin-1 converting enzyme N-domain in complex with Lys-Pro
Authors : Masuyer, G.; Douglas, R.G.; Sturrock, E.D.; Acharya, K.R.
Deposited on : 2015-03-16
Resolution : 1.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

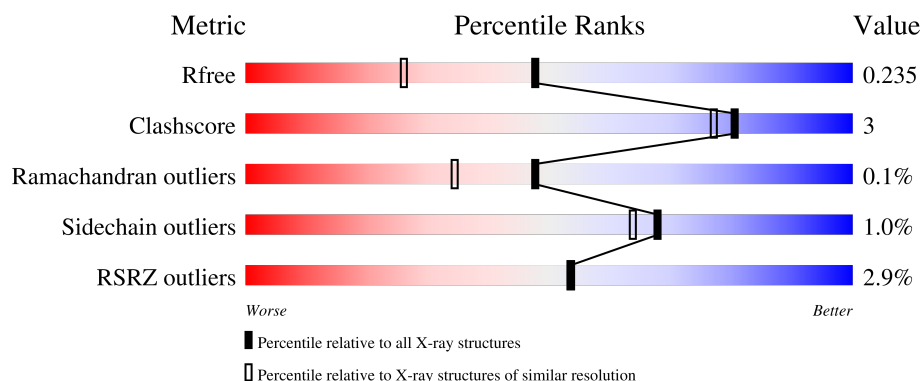
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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.



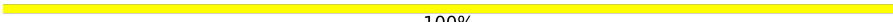
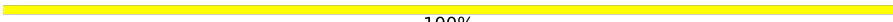
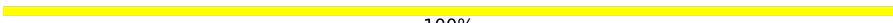
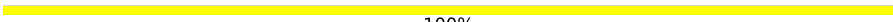
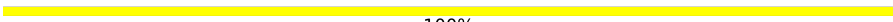
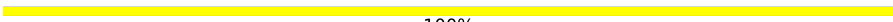
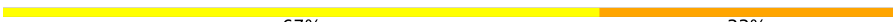
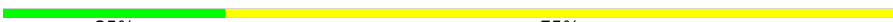
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	629	2% 89% 6% .
1	B	629	6% 89% 7% .
1	C	629	2% 93% . .
1	D	629	2% 90% 7% .
2	E	2	100%

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Mol	Chain	Length	Quality of chain
2	H	2	 100%
2	K	2	 100%
2	N	2	 100%
3	F	2	 50% 50%
3	I	2	 100%
3	L	2	 100%
3	O	2	 100%
4	G	3	 100%
4	J	3	 67% 33%
5	M	4	 25% 75%
5	P	4	 50% 50%

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 22065 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 ANGIOTENSIN-CONVERTING ENZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	603	Total	C	N	O	S	0	0	0
			4917	3159	842	897	19			
1	B	605	Total	C	N	O	S	0	2	0
			4938	3174	847	898	19			
1	C	607	Total	C	N	O	S	0	1	0
			4953	3181	852	901	19			
1	D	609	Total	C	N	O	S	0	5	0
			5002	3212	861	910	19			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	629	LEU	-	expression tag	UNP P12821
A	9	GLN	ASN	engineered mutation	UNP P12821
A	25	GLN	ASN	engineered mutation	UNP P12821
A	82	GLN	ASN	engineered mutation	UNP P12821
A	117	GLN	ASN	engineered mutation	UNP P12821
A	131	GLN	ASN	engineered mutation	UNP P12821
A	289	GLN	ASN	engineered mutation	UNP P12821
A	545	ARG	GLN	engineered mutation	UNP P12821
A	576	LEU	PRO	engineered mutation	UNP P12821
B	629	LEU	-	expression tag	UNP P12821
B	9	GLN	ASN	engineered mutation	UNP P12821
B	25	GLN	ASN	engineered mutation	UNP P12821
B	82	GLN	ASN	engineered mutation	UNP P12821
B	117	GLN	ASN	engineered mutation	UNP P12821
B	131	GLN	ASN	engineered mutation	UNP P12821
B	289	GLN	ASN	engineered mutation	UNP P12821
B	545	ARG	GLN	engineered mutation	UNP P12821
B	576	LEU	PRO	engineered mutation	UNP P12821
C	629	LEU	-	expression tag	UNP P12821
C	9	GLN	ASN	engineered mutation	UNP P12821
C	25	GLN	ASN	engineered mutation	UNP P12821

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Chain	Residue	Modelled	Actual	Comment	Reference
C	82	GLN	ASN	engineered mutation	UNP P12821
C	117	GLN	ASN	engineered mutation	UNP P12821
C	131	GLN	ASN	engineered mutation	UNP P12821
C	289	GLN	ASN	engineered mutation	UNP P12821
C	545	ARG	GLN	engineered mutation	UNP P12821
C	576	LEU	PRO	engineered mutation	UNP P12821
D	629	LEU	-	expression tag	UNP P12821
D	9	GLN	ASN	engineered mutation	UNP P12821
D	25	GLN	ASN	engineered mutation	UNP P12821
D	82	GLN	ASN	engineered mutation	UNP P12821
D	117	GLN	ASN	engineered mutation	UNP P12821
D	131	GLN	ASN	engineered mutation	UNP P12821
D	289	GLN	ASN	engineered mutation	UNP P12821
D	545	ARG	GLN	engineered mutation	UNP P12821
D	576	LEU	PRO	engineered mutation	UNP P12821

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



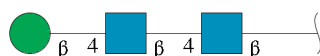
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	H	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	K	2	Total	C	N	O	0	0	0
			24	14	1	9			
2	N	2	Total	C	N	O	0	0	0
			24	14	1	9			

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



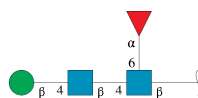
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



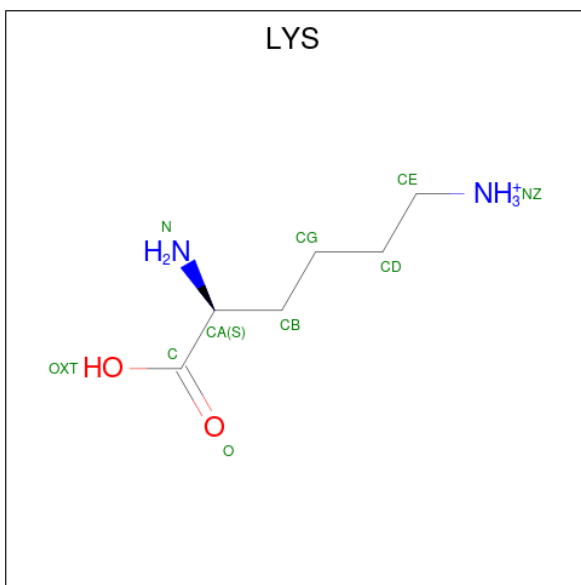
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



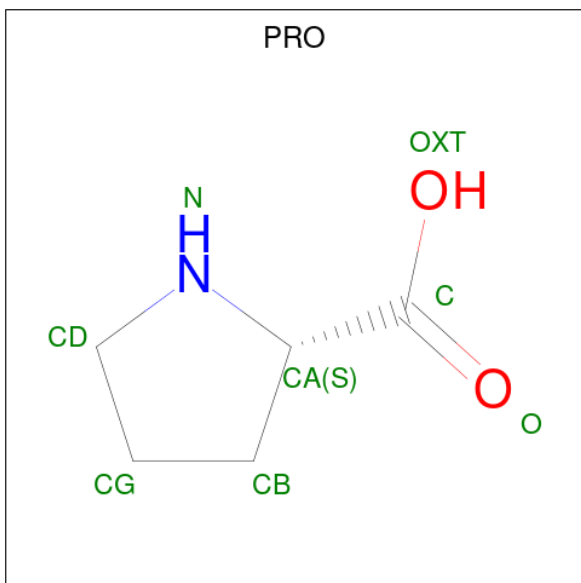
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	M	4	Total	C	N	O	0	0	0
			49	28	2	19			
5	P	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 6 is LYSINE (CCD ID: LYS) (formula: C₆H₁₅N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			9	6	2	1		
6	B	1	Total	C	N	O	0	0
			9	6	2	1		
6	C	1	Total	C	N	O	0	0
			9	6	2	1		
6	D	1	Total	C	N	O	0	0
			9	6	2	1		

- Molecule 7 is PROLINE (CCD ID: PRO) (formula: C₅H₉NO₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N O 8 5 1 2	0	0
7	B	1	Total C N O 8 5 1 2	0	0
7	C	1	Total C N O 8 5 1 2	0	0
7	D	1	Total C N O 8 5 1 2	0	0

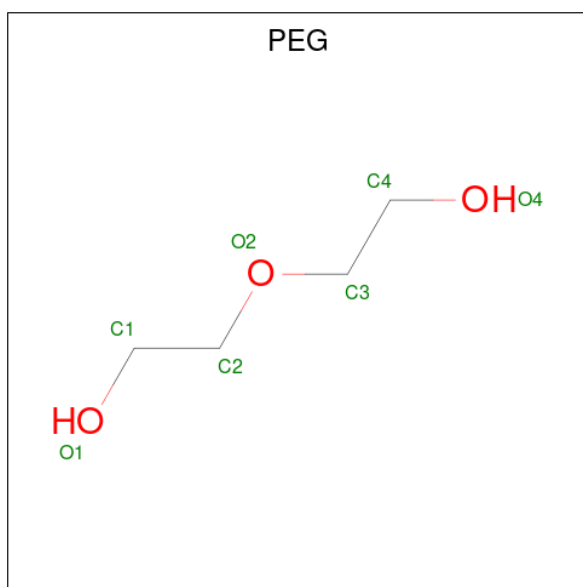
- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Zn 1 1	0	0
8	B	1	Total Zn 1 1	0	0
8	C	1	Total Zn 1 1	0	0
8	D	1	Total Zn 1 1	0	0

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

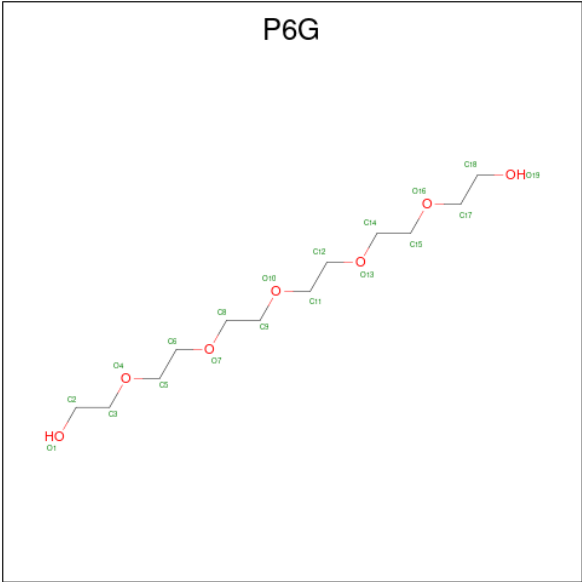
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total Cl 1 1	0	0
9	B	1	Total Cl 1 1	0	0
9	C	1	Total Cl 1 1	0	0
9	D	1	Total Cl 1 1	0	0

- Molecule 10 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 11 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			19	12	7		
11	A	1	Total	C	O	0	0
			19	12	7		
11	B	1	Total	C	O	0	0
			19	12	7		
11	C	1	Total	C	O	0	0
			19	12	7		
11	D	1	Total	C	O	0	0
			19	12	7		
11	D	1	Total	C	O	0	0
			19	12	7		

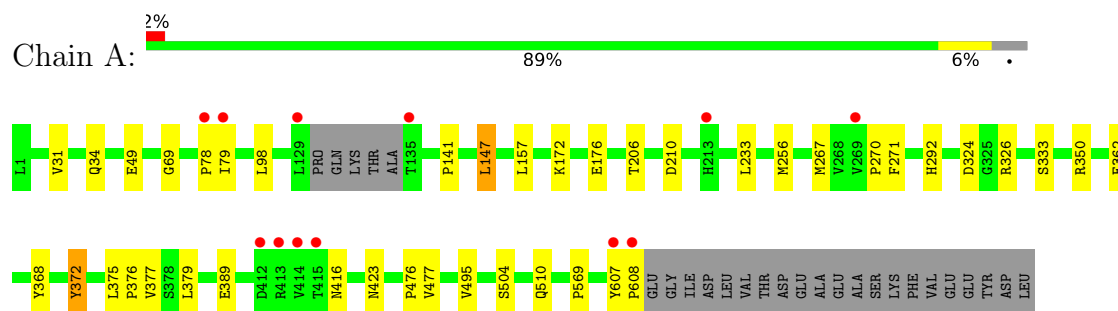
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	360	Total	O	0	0
			360	360		
12	B	387	Total	O	0	0
			387	387		
12	C	434	Total	O	0	0
			434	434		
12	D	430	Total	O	0	0
			430	430		

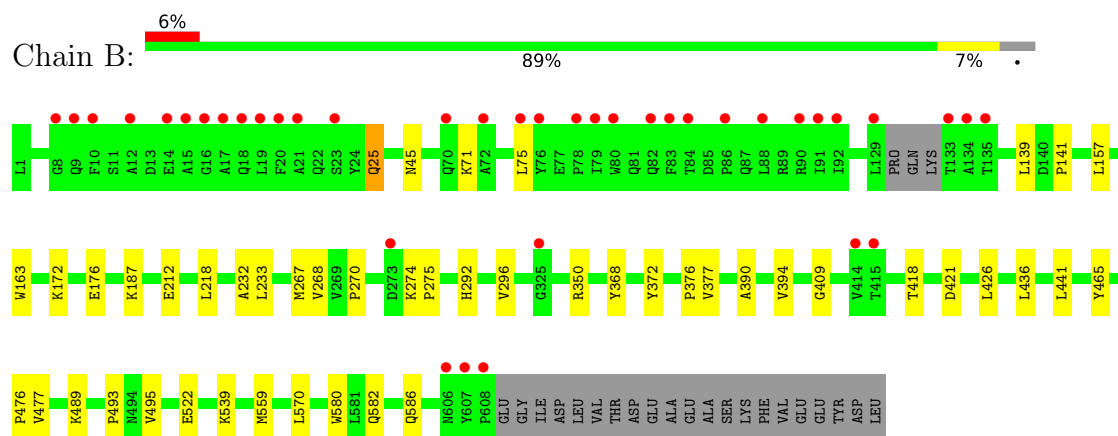
3 Residue-property plots [i](#)

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.

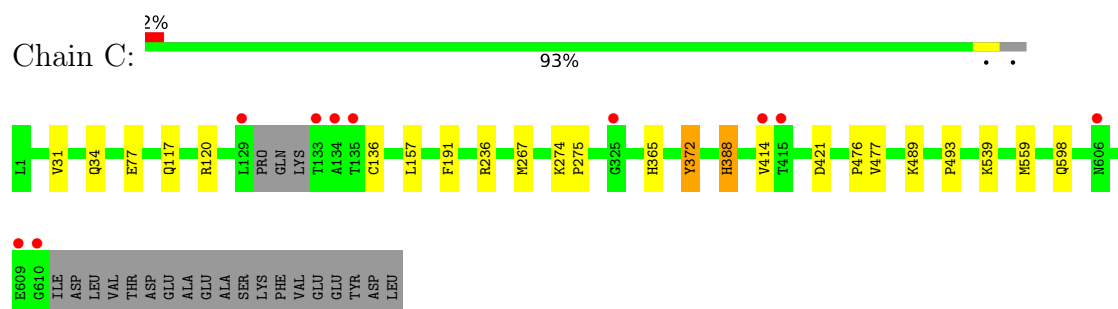
• Molecule 1: ANGIOTENSIN-CONVERTING ENZYME



• Molecule 1: ANGIOTENSIN-CONVERTING ENZYME

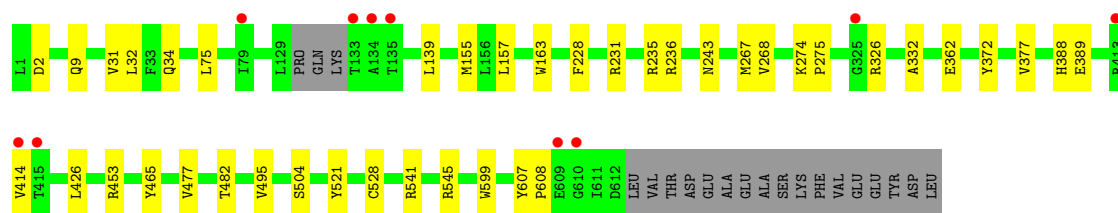


• Molecule 1: ANGIOTENSIN-CONVERTING ENZYME



• Molecule 1: ANGIOTENSIN-CONVERTING ENZYME





- 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 H: 100%

MAG1
FUC2

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

Chain K: 100%

MAG1
FUC2

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

Chain N: 100%

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 I: 100%

MAG1
MAG2

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

Chain L:  100%

NAG1
NAG2

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

Chain O:  100%

NAG1
NAG2

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

Chain G:  100%

NAG1
NAG2
BMA3

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

Chain J:  67% 33%

NAG1
NAG2
BMA3

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  25% 75%

NAG1
NAG2
BMA3
FUC4

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  50% 50%

NAG1
NAG2
BMA3
FUC4

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.48Å 101.59Å 114.51Å 85.46° 85.90° 81.62°	Depositor
Resolution (Å)	113.94 – 1.80 113.94 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.2 (113.94-1.80) 97.2 (113.94-1.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.207 , 0.235 0.207 , 0.235	Depositor DCC
R_{free} test set	14577 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	22065	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.35 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.7728e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: P6G, ZN, PEG, BMA, FUC, NAG, CL

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	0/5072	0.80	3/6911 (0.0%)
1	B	0.52	0/5097	0.78	1/6944 (0.0%)
1	C	0.53	0/5112	0.78	1/6963 (0.0%)
1	D	0.53	0/5170	0.76	0/7041
All	All	0.53	0/20451	0.78	5/27859 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	271	PHE	CA-C-N	5.44	125.26	119.28
1	A	271	PHE	C-N-CA	5.44	125.26	119.28
1	B	441	LEU	N-CA-C	5.38	117.22	111.36
1	A	79	ILE	N-CA-C	5.32	117.74	111.09
1	C	136	CYS	N-CA-C	5.15	117.63	109.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	4917	0	4681	22	0
1	B	4938	0	4698	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4953	0	4722	19	0
1	D	5002	0	4785	30	0
2	E	24	0	22	0	0
2	H	24	0	22	0	0
2	K	24	0	22	0	0
2	N	24	0	22	4	0
3	F	28	0	25	1	0
3	I	28	0	25	0	0
3	L	28	0	25	0	0
3	O	28	0	25	0	0
4	G	39	0	34	0	0
4	J	39	0	34	1	0
5	M	49	0	43	0	0
5	P	49	0	43	0	0
6	A	9	0	12	1	0
6	B	9	0	12	0	0
6	C	9	0	12	0	0
6	D	9	0	12	2	0
7	A	8	0	7	0	0
7	B	8	0	7	0	0
7	C	8	0	7	0	0
7	D	8	0	7	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	C	1	0	0	0	0
9	D	1	0	0	0	0
10	A	21	0	30	0	0
10	B	28	0	40	3	0
10	C	14	0	20	1	0
10	D	7	0	10	0	0
11	A	38	0	52	2	0
11	B	19	0	26	6	0
11	C	19	0	26	1	0
11	D	38	0	52	5	0
12	A	360	0	0	0	0
12	B	387	0	0	2	0
12	C	434	0	0	2	0
12	D	430	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	22065	0	19560	105	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 3.

The worst 5 of 105 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:235:ARG:HH11	11:D:1201:P6G:H172	1.32	0.92
1:C:365:HIS:HD1	1:C:388:HIS:HD2	1.16	0.88
1:B:292:HIS:HE2	11:B:1203:P6G:H31	1.42	0.83
1:C:236:ARG:HD2	1:C:267:MET:HE3	1.62	0.79
1:C:365:HIS:HD1	1:C:388:HIS:CD2	2.02	0.77

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	599/629 (95%)	588 (98%)	9 (2%)	2 (0%)	36	25
1	B	603/629 (96%)	590 (98%)	12 (2%)	1 (0%)	43	31
1	C	604/629 (96%)	595 (98%)	9 (2%)	0	100	100
1	D	610/629 (97%)	598 (98%)	12 (2%)	0	100	100
All	All	2416/2516 (96%)	2371 (98%)	42 (2%)	3 (0%)	48	34

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	416	ASN

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Mol	Chain	Res	Type
1	B	45	ASN
1	A	78	PRO

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	516/541 (95%)	512 (99%)	4 (1%)	73	70
1	B	516/541 (95%)	509 (99%)	7 (1%)	59	52
1	C	519/541 (96%)	515 (99%)	4 (1%)	73	70
1	D	527/541 (97%)	522 (99%)	5 (1%)	70	67
All	All	2078/2164 (96%)	2058 (99%)	20 (1%)	68	64

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	421	ASP
1	D	372	TYR
1	D	388	HIS
1	D	377	VAL
1	B	368	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	224	ASN
1	C	388	HIS
1	C	371	GLN
1	C	585	ASN
1	A	598	GLN

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 ⓘ

30 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	0.71	0	17,19,21	1.18	1 (5%)
2	FUC	E	2	2	10,10,11	0.92	0	14,14,16	1.09	1 (7%)
3	NAG	F	1	3,1	14,14,15	0.55	0	17,19,21	1.12	1 (5%)
3	NAG	F	2	3	14,14,15	0.70	0	17,19,21	1.27	3 (17%)
4	NAG	G	1	4,1	14,14,15	0.47	0	17,19,21	1.43	3 (17%)
4	NAG	G	2	4	14,14,15	0.51	0	17,19,21	0.93	1 (5%)
4	BMA	G	3	4	11,11,12	0.76	0	15,15,17	1.43	3 (20%)
2	NAG	H	1	2,1	14,14,15	0.71	0	17,19,21	2.38	6 (35%)
2	FUC	H	2	2	10,10,11	0.80	0	14,14,16	1.46	2 (14%)
3	NAG	I	1	3,1	14,14,15	0.59	0	17,19,21	1.34	2 (11%)
3	NAG	I	2	3	14,14,15	0.65	0	17,19,21	1.22	1 (5%)
4	NAG	J	1	4,1	14,14,15	0.44	0	17,19,21	0.94	1 (5%)
4	NAG	J	2	4	14,14,15	0.51	0	17,19,21	1.01	1 (5%)
4	BMA	J	3	4	11,11,12	0.67	0	15,15,17	1.20	3 (20%)
2	NAG	K	1	2,1	14,14,15	0.56	0	17,19,21	1.53	3 (17%)
2	FUC	K	2	2	10,10,11	0.83	0	14,14,16	1.78	3 (21%)
3	NAG	L	1	3,1	14,14,15	0.51	0	17,19,21	1.15	1 (5%)
3	NAG	L	2	3	14,14,15	0.57	0	17,19,21	1.15	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	M	1	1,5	14,14,15	0.63	0	17,19,21	0.87	1 (5%)
5	NAG	M	2	5	14,14,15	0.61	0	17,19,21	0.90	1 (5%)
5	BMA	M	3	5	11,11,12	0.63	0	15,15,17	1.50	2 (13%)
5	FUC	M	4	5	10,10,11	0.61	0	14,14,16	0.64	0
2	NAG	N	1	2,1	14,14,15	0.49	0	17,19,21	1.77	5 (29%)
2	FUC	N	2	2	10,10,11	0.77	0	14,14,16	1.40	2 (14%)
3	NAG	O	1	3,1	14,14,15	0.52	0	17,19,21	1.15	1 (5%)
3	NAG	O	2	3	14,14,15	0.64	0	17,19,21	1.23	1 (5%)
5	NAG	P	1	1,5	14,14,15	0.67	0	17,19,21	0.78	1 (5%)
5	NAG	P	2	5	14,14,15	0.56	0	17,19,21	0.83	0
5	BMA	P	3	5	11,11,12	0.56	0	15,15,17	1.16	2 (13%)
5	FUC	P	4	5	10,10,11	0.57	0	14,14,16	0.69	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	-	2/6/23/26	0/1/1/1
2	FUC	E	2	2	-	-	0/1/1/1
3	NAG	F	1	3,1	-	0/6/23/26	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	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
2	NAG	H	1	2,1	-	2/6/23/26	0/1/1/1
2	FUC	H	2	2	-	-	0/1/1/1
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	0/1/1/1
4	BMA	J	3	4	-	0/2/19/22	0/1/1/1
2	NAG	K	1	2,1	-	2/6/23/26	0/1/1/1
2	FUC	K	2	2	-	-	0/1/1/1
3	NAG	L	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
5	NAG	M	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	M	2	5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BMA	M	3	5	-	0/2/19/22	0/1/1/1
5	FUC	M	4	5	-	-	0/1/1/1
2	NAG	N	1	2,1	-	6/6/23/26	0/1/1/1
2	FUC	N	2	2	-	-	0/1/1/1
3	NAG	O	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	O	2	3	-	0/6/23/26	0/1/1/1
5	NAG	P	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	P	2	5	-	0/6/23/26	0/1/1/1
5	BMA	P	3	5	-	0/2/19/22	0/1/1/1
5	FUC	P	4	5	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	NAG	C2-N2-C7	-7.33	113.08	122.90
2	K	1	NAG	C4-C3-C2	4.20	117.17	111.02
2	K	2	FUC	C1-C2-C3	4.17	115.72	109.64
3	I	1	NAG	C1-O5-C5	4.13	117.72	112.19
2	N	2	FUC	C1-C2-C3	4.00	115.46	109.64

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	K	1	NAG	O5-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6
2	N	1	NAG	O5-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6

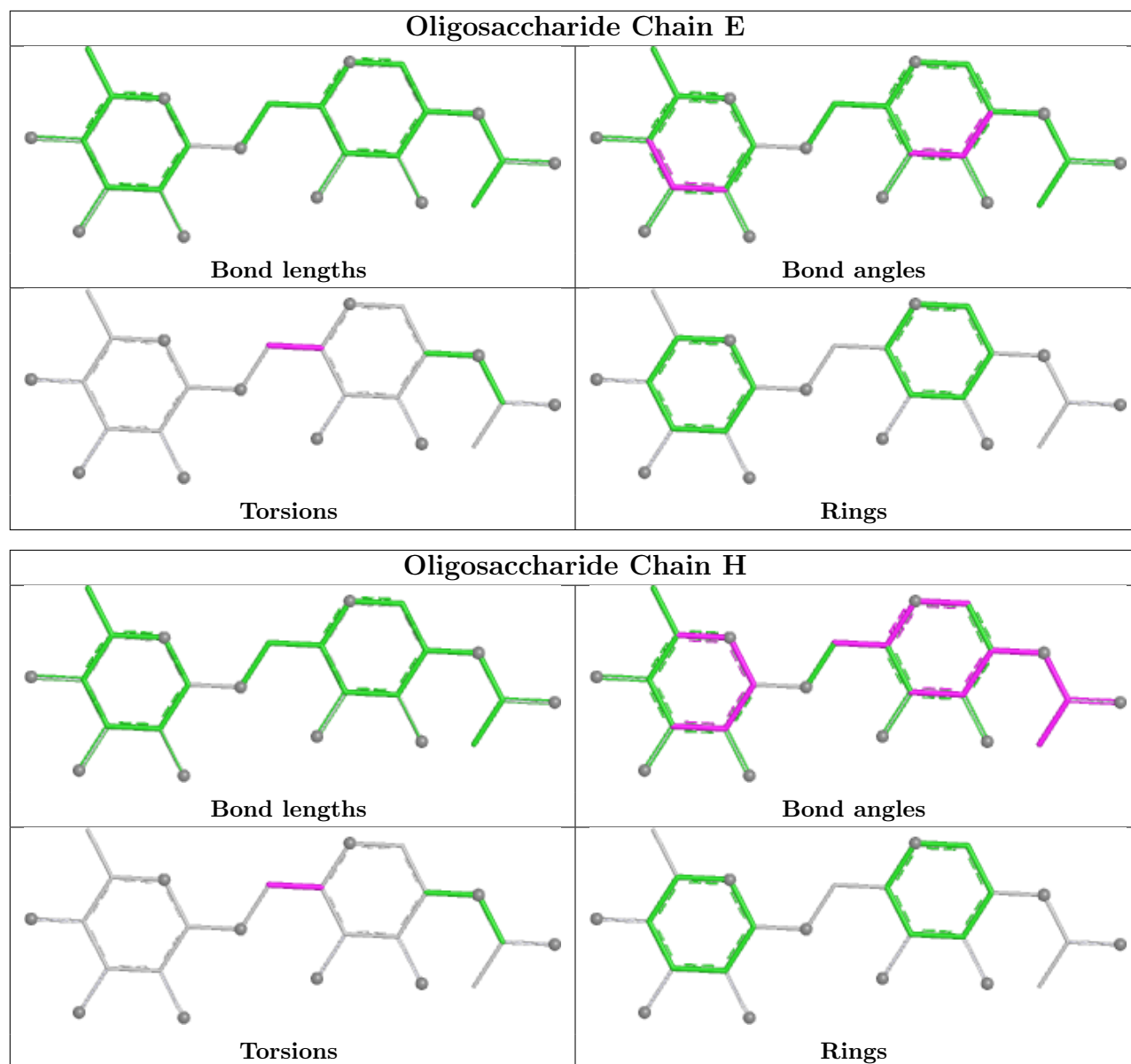
There are no ring outliers.

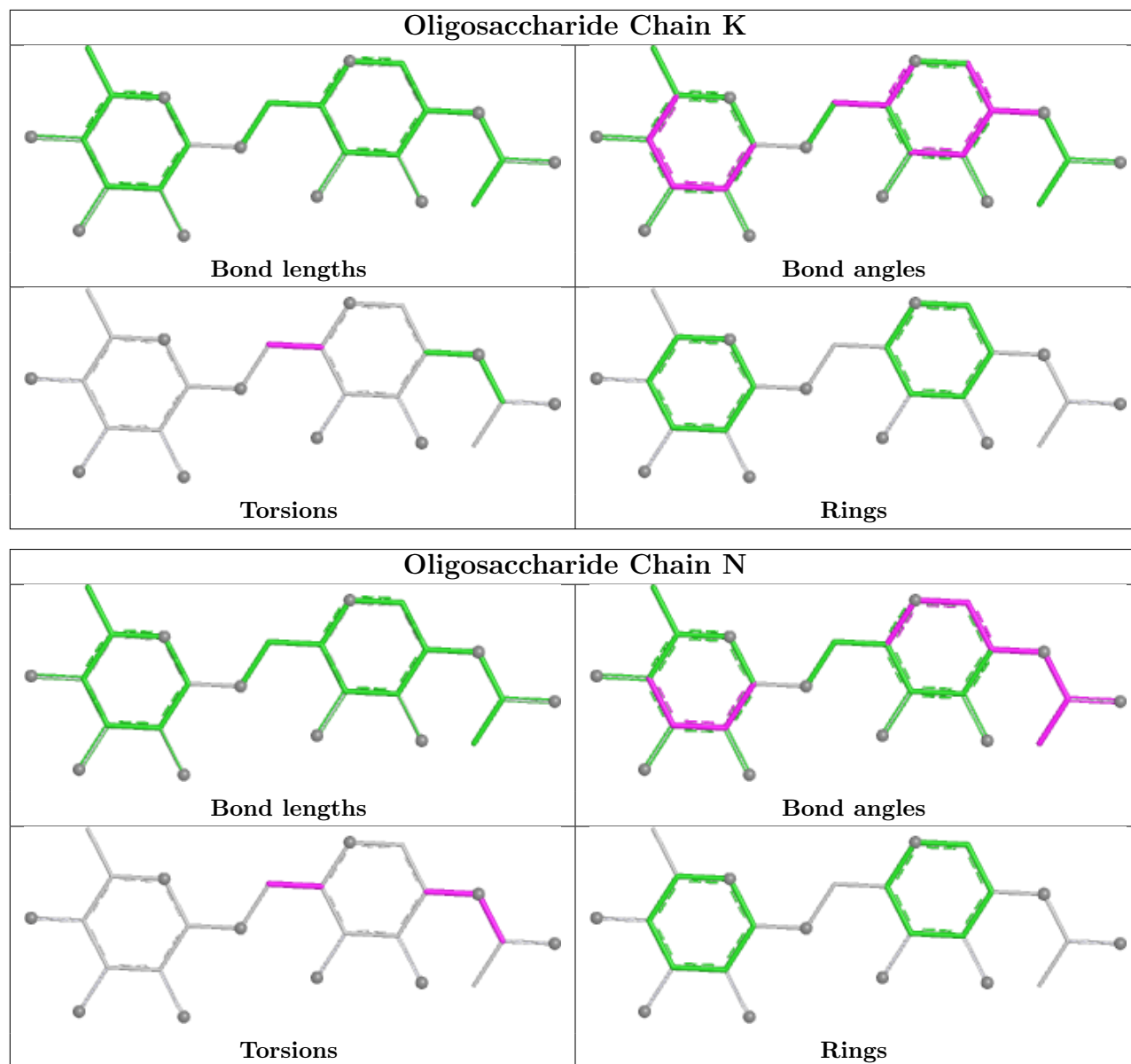
4 monomers are involved in 6 short contacts:

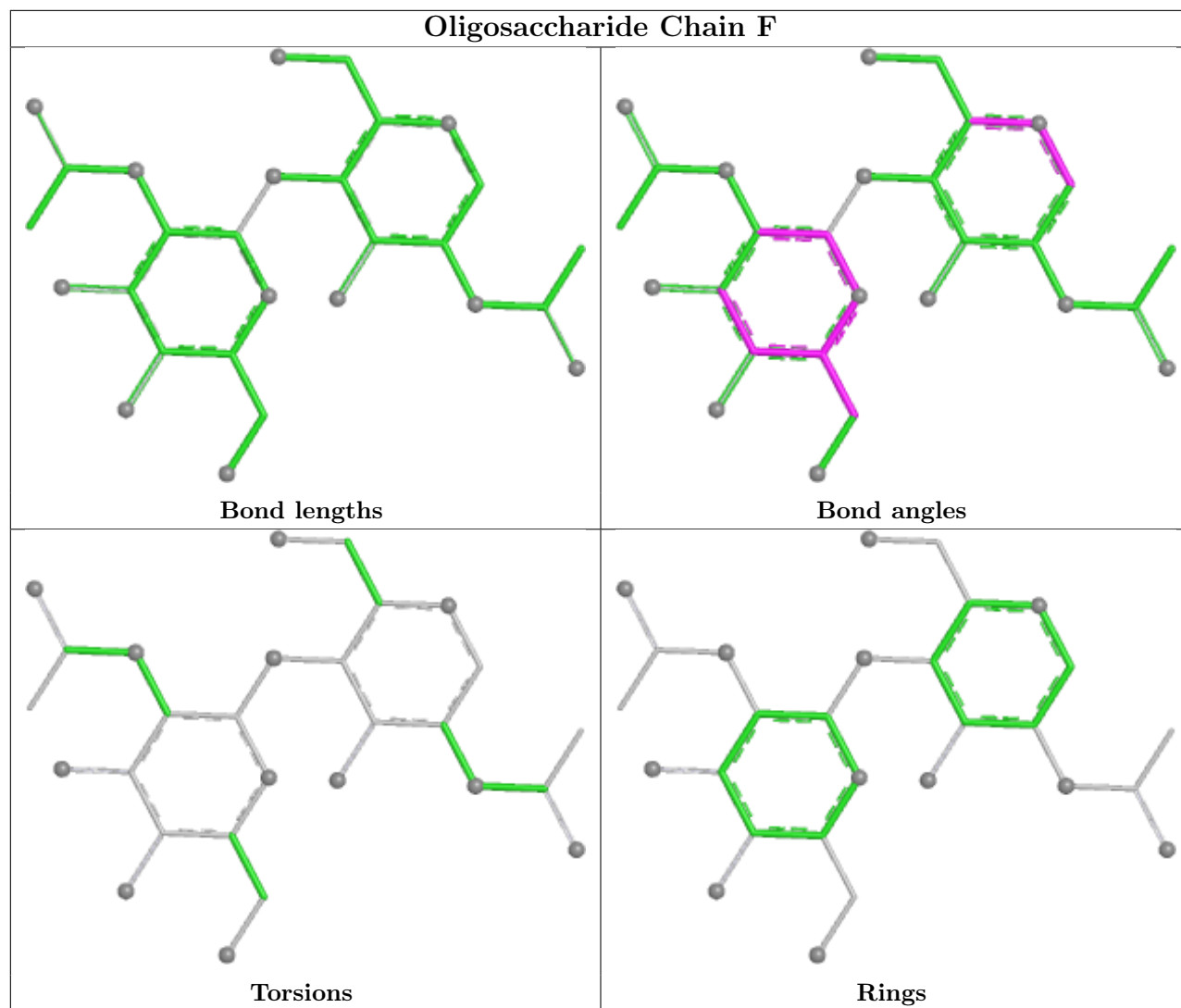
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	2	NAG	1	0
2	N	1	NAG	3	0
4	J	3	BMA	1	0
2	N	2	FUC	1	0

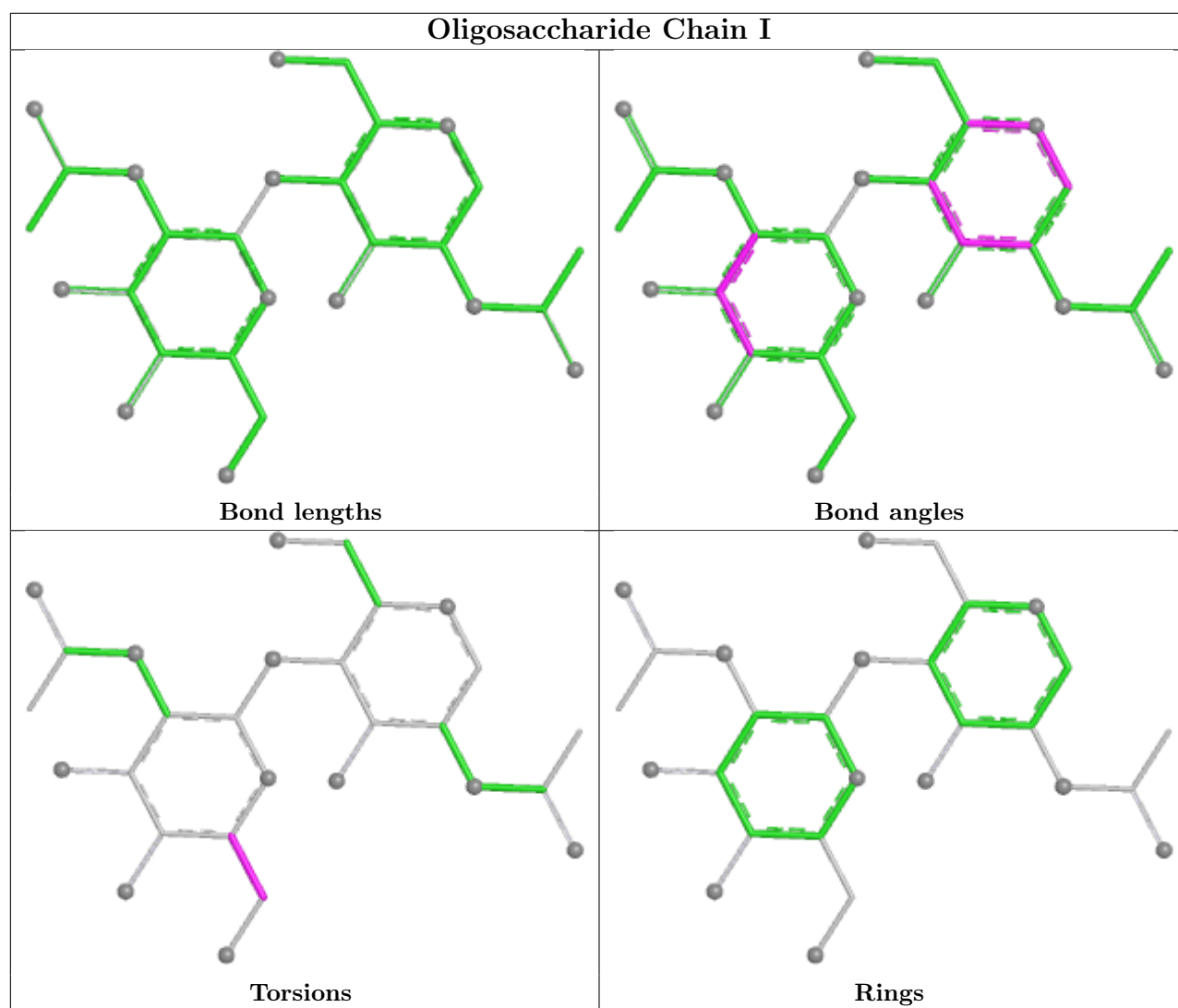
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

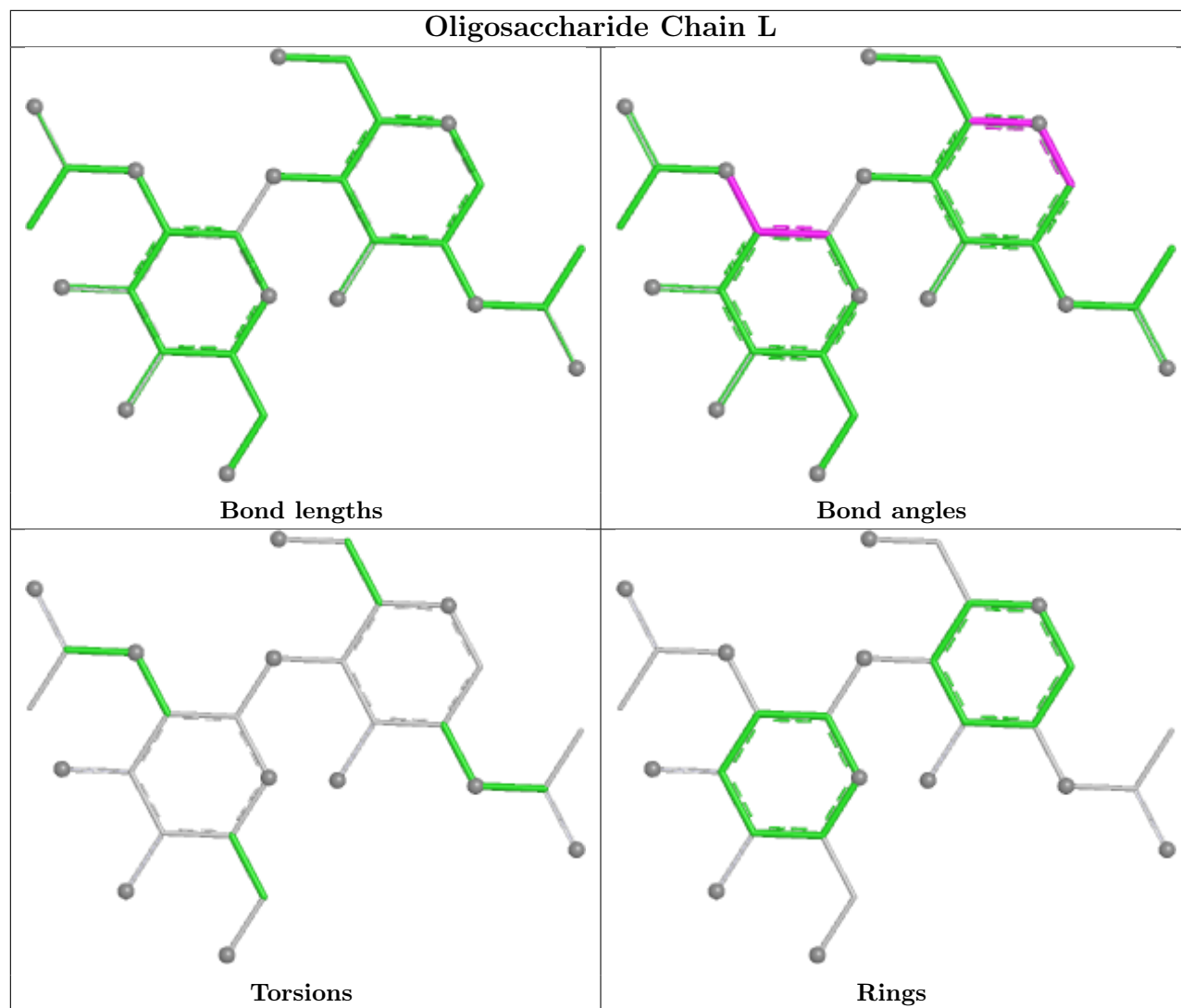
bond angles, torsion angles, and ring geometry for oligosaccharide.

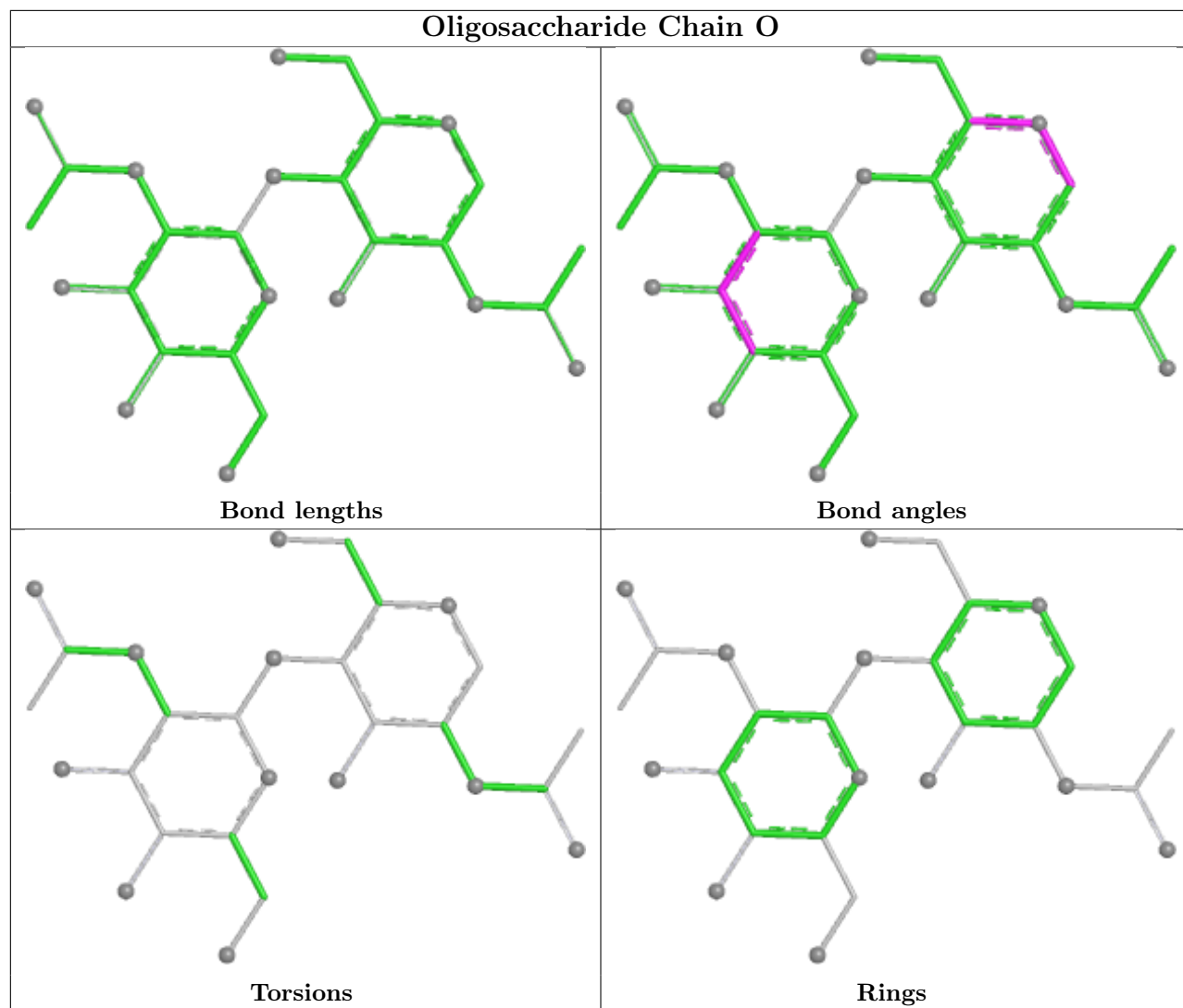


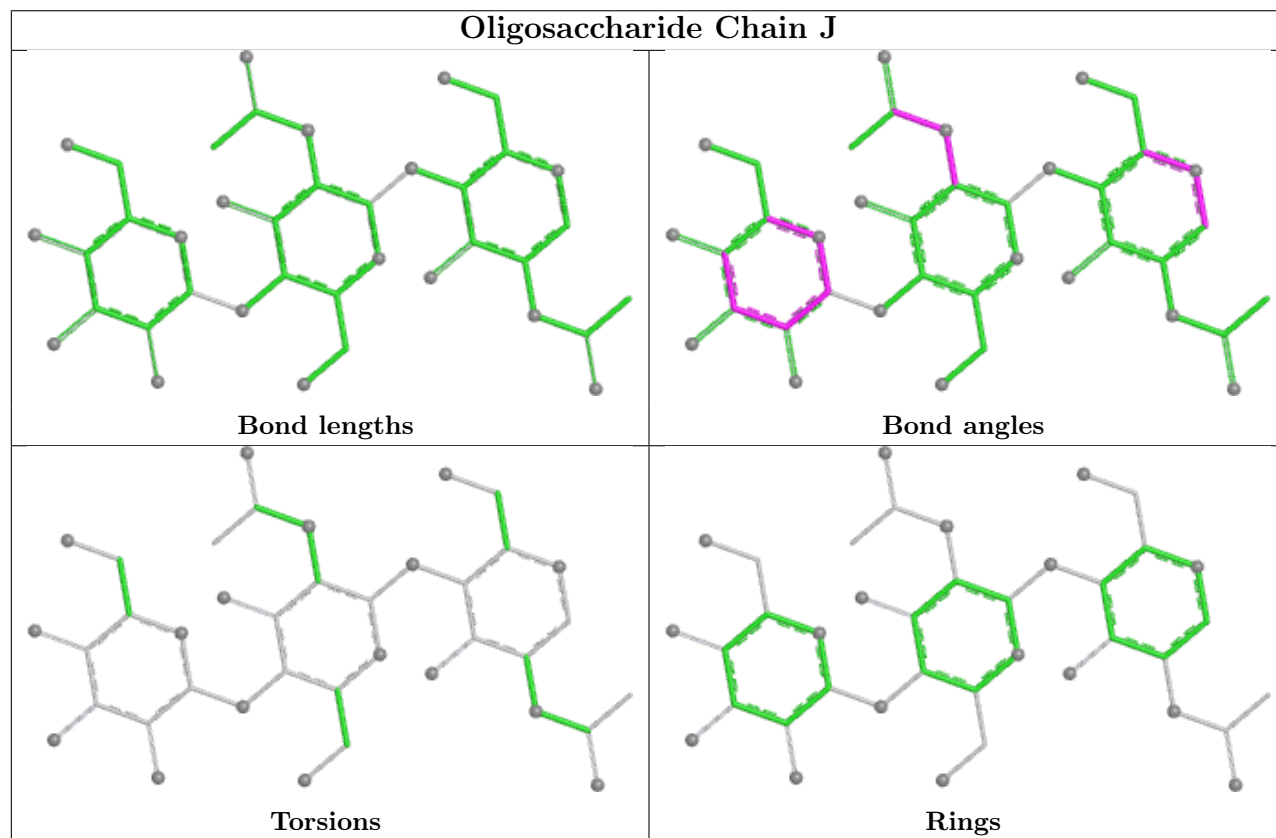
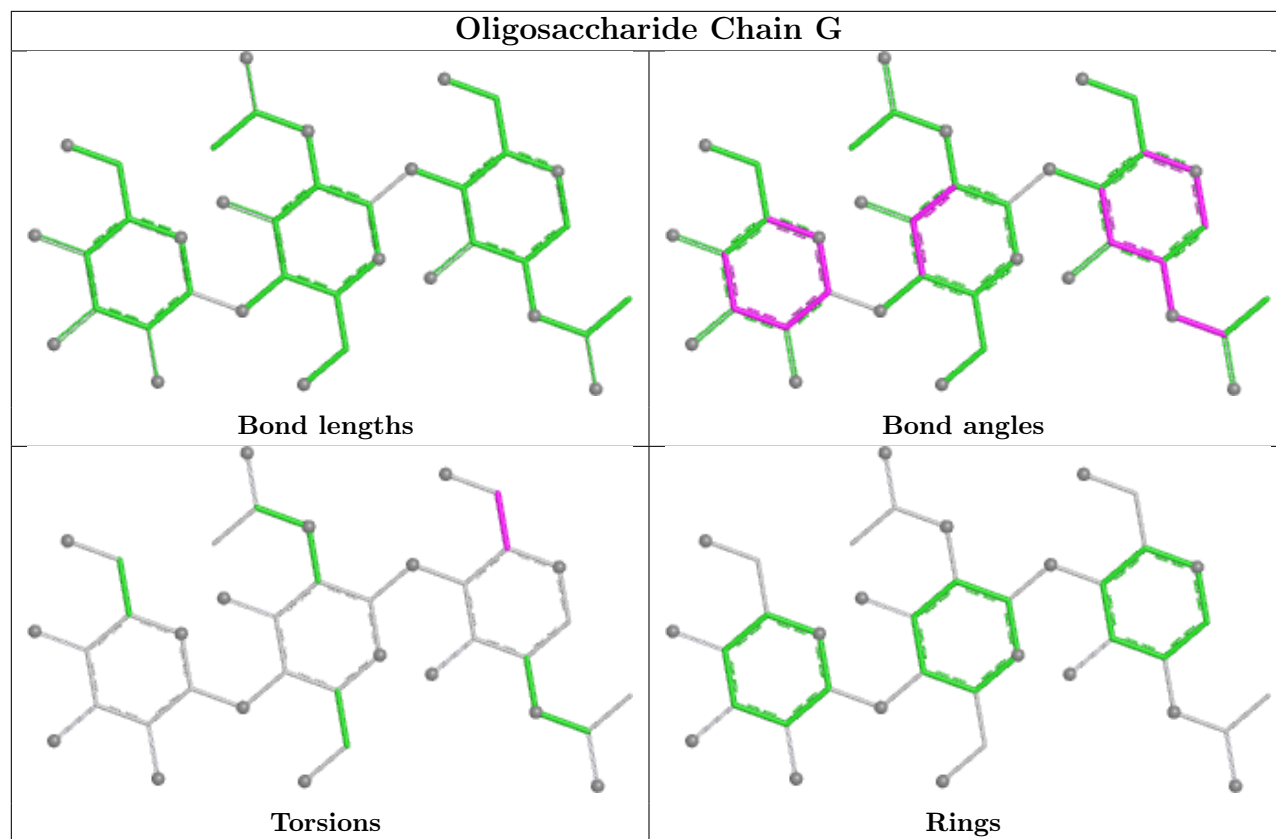


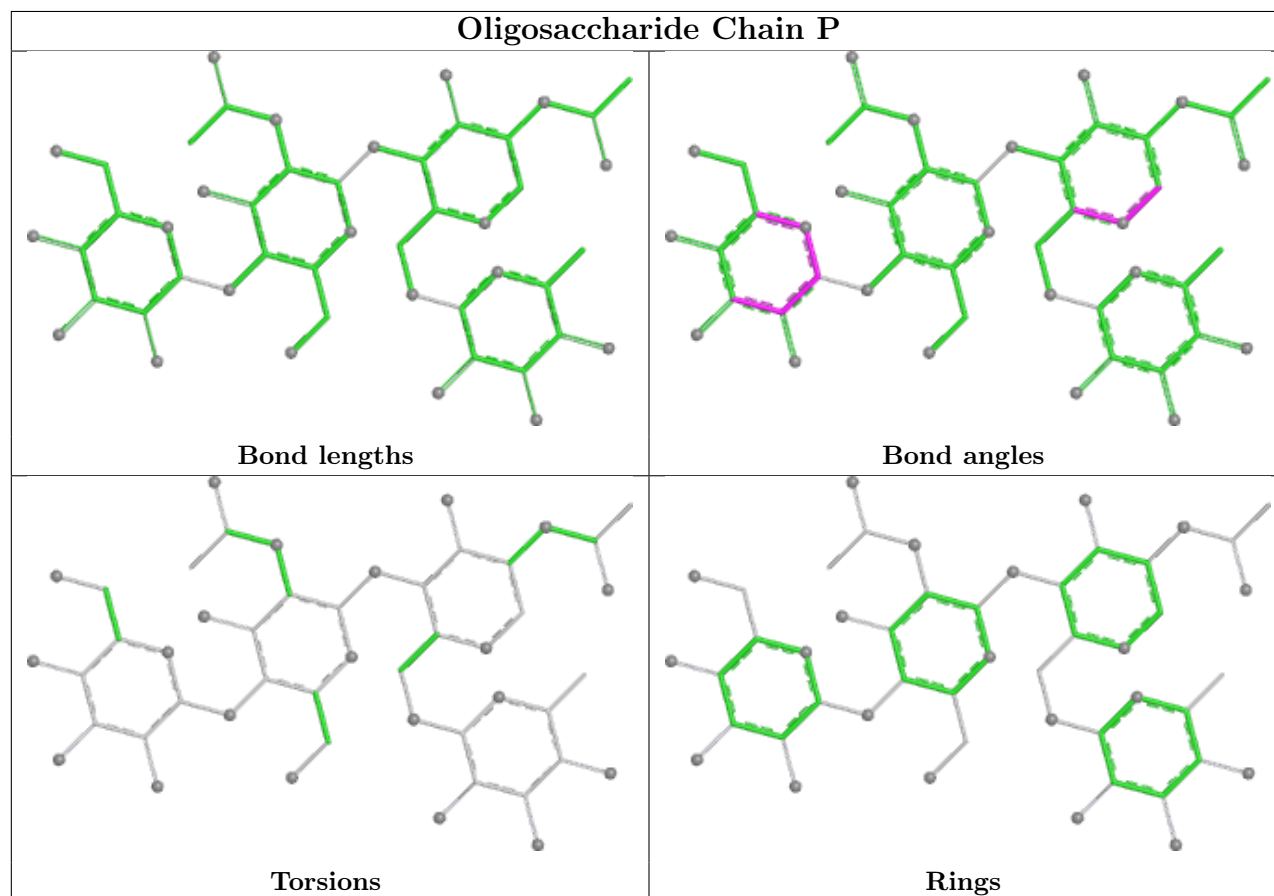
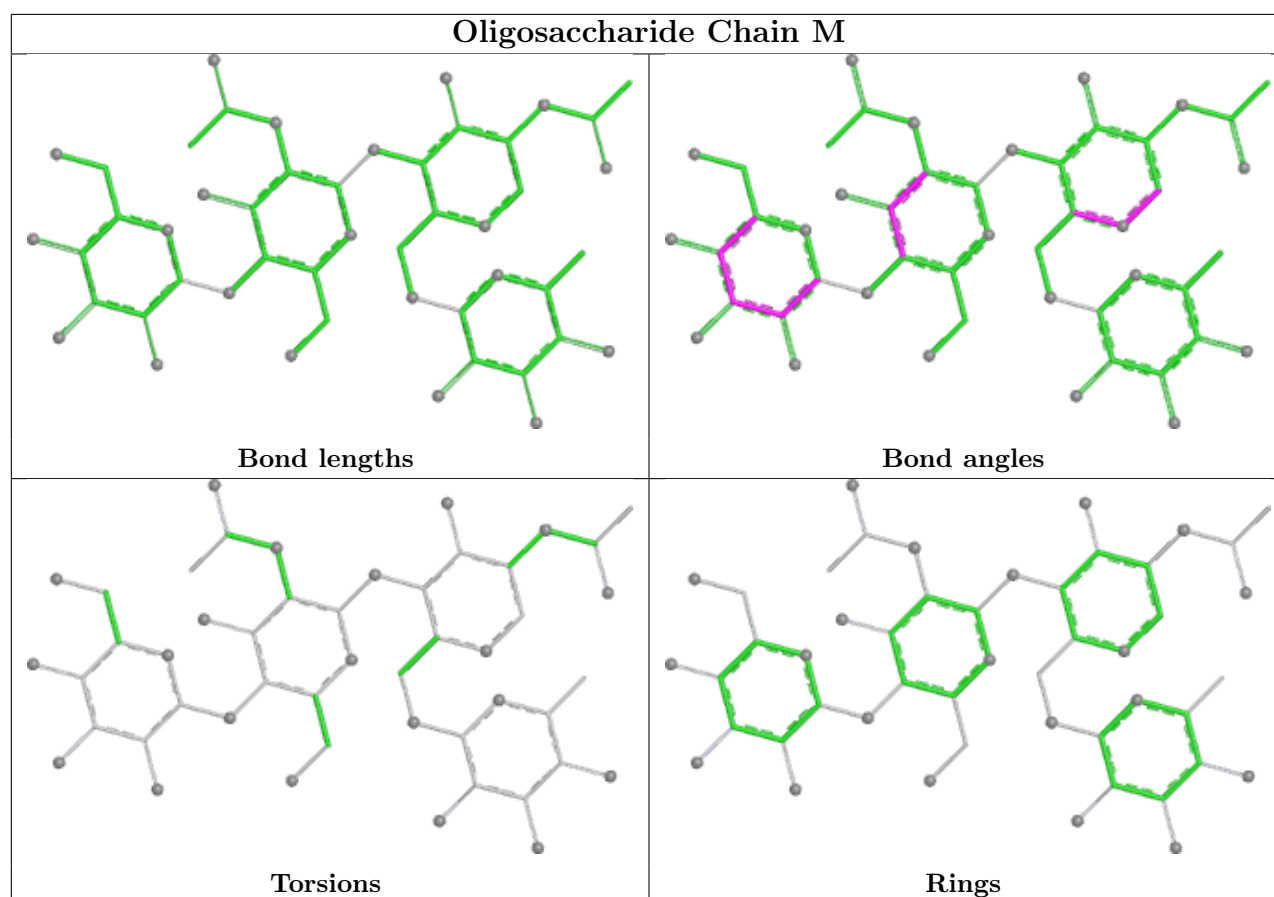












5.6 Ligand geometry

Of 32 ligands modelled in this entry, 8 are monoatomic - leaving 24 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	PRO	C	1304	-	8,8,8	0.84	1 (12%)	10,10,10	1.53	2 (20%)
7	PRO	A	1304	-	8,8,8	0.91	1 (12%)	10,10,10	1.27	1 (10%)
11	P6G	C	1202	-	18,18,18	0.52	0	17,17,17	0.22	0
6	LYS	D	1303	-	7,8,9	0.60	0	3,8,10	0.31	0
6	LYS	B	1303	-	7,8,9	0.46	0	3,8,10	0.50	0
10	PEG	A	1200	-	6,6,6	0.44	0	5,5,5	0.34	0
10	PEG	C	1200	-	6,6,6	0.41	0	5,5,5	0.42	0
10	PEG	A	1203	-	6,6,6	0.47	0	5,5,5	0.21	0
10	PEG	C	1201	-	6,6,6	0.46	0	5,5,5	0.35	0
10	PEG	A	1201	-	6,6,6	0.40	0	5,5,5	0.46	0
10	PEG	B	1204	-	6,6,6	0.41	0	5,5,5	0.37	0
6	LYS	C	1303	-	7,8,9	0.56	0	3,8,10	0.61	0
7	PRO	B	1304	-	8,8,8	0.93	1 (12%)	10,10,10	1.36	1 (10%)
11	P6G	D	1202	-	18,18,18	0.52	0	17,17,17	0.21	0
11	P6G	A	1202	-	18,18,18	0.48	0	17,17,17	0.29	0
6	LYS	A	1303	-	7,8,9	0.50	0	3,8,10	0.29	0
11	P6G	A	1204	-	18,18,18	0.52	0	17,17,17	0.20	0
10	PEG	D	1200	-	6,6,6	0.44	0	5,5,5	0.34	0
10	PEG	B	1202	-	6,6,6	0.52	0	5,5,5	0.28	0
10	PEG	B	1205	-	6,6,6	0.45	0	5,5,5	0.29	0
11	P6G	B	1203	-	18,18,18	0.62	0	17,17,17	0.48	0
11	P6G	D	1201	-	18,18,18	0.56	0	17,17,17	0.49	0
10	PEG	B	1201	-	6,6,6	0.51	0	5,5,5	0.18	0
7	PRO	D	1304	-	8,8,8	0.81	1 (12%)	10,10,10	1.27	2 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	PRO	C	1304	-	-	0/4/11/11	0/1/1/1
7	PRO	A	1304	-	-	0/4/11/11	0/1/1/1
11	P6G	C	1202	-	-	11/16/16/16	-
6	LYS	D	1303	-	-	1/6/7/9	-
6	LYS	B	1303	-	-	0/6/7/9	-
10	PEG	A	1200	-	-	3/4/4/4	-
10	PEG	C	1200	-	-	3/4/4/4	-
10	PEG	A	1203	-	-	0/4/4/4	-
10	PEG	C	1201	-	-	2/4/4/4	-
10	PEG	A	1201	-	-	3/4/4/4	-
10	PEG	B	1204	-	-	1/4/4/4	-
6	LYS	C	1303	-	-	2/6/7/9	-
7	PRO	B	1304	-	-	0/4/11/11	0/1/1/1
11	P6G	D	1202	-	-	10/16/16/16	-
11	P6G	A	1202	-	-	5/16/16/16	-
6	LYS	A	1303	-	-	1/6/7/9	-
11	P6G	A	1204	-	-	11/16/16/16	-
10	PEG	D	1200	-	-	3/4/4/4	-
10	PEG	B	1202	-	-	3/4/4/4	-
10	PEG	B	1205	-	-	2/4/4/4	-
11	P6G	B	1203	-	-	13/16/16/16	-
11	P6G	D	1201	-	-	8/16/16/16	-
10	PEG	B	1201	-	-	3/4/4/4	-
7	PRO	D	1304	-	-	0/4/11/11	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1304	PRO	OXT-C	-2.37	1.23	1.30
7	A	1304	PRO	OXT-C	-2.29	1.23	1.30
7	C	1304	PRO	OXT-C	-2.17	1.23	1.30
7	D	1304	PRO	OXT-C	-2.10	1.24	1.30

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	1304	PRO	OXT-C-O	-3.16	116.91	124.08
7	B	1304	PRO	OXT-C-O	-2.75	117.84	124.08
7	C	1304	PRO	OXT-C-CA	2.45	121.79	113.51
7	D	1304	PRO	OXT-C-O	-2.45	118.53	124.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1304	PRO	OXT-C-O	-2.41	118.62	124.08

There are no chirality outliers.

5 of 85 torsion outliers are listed below:

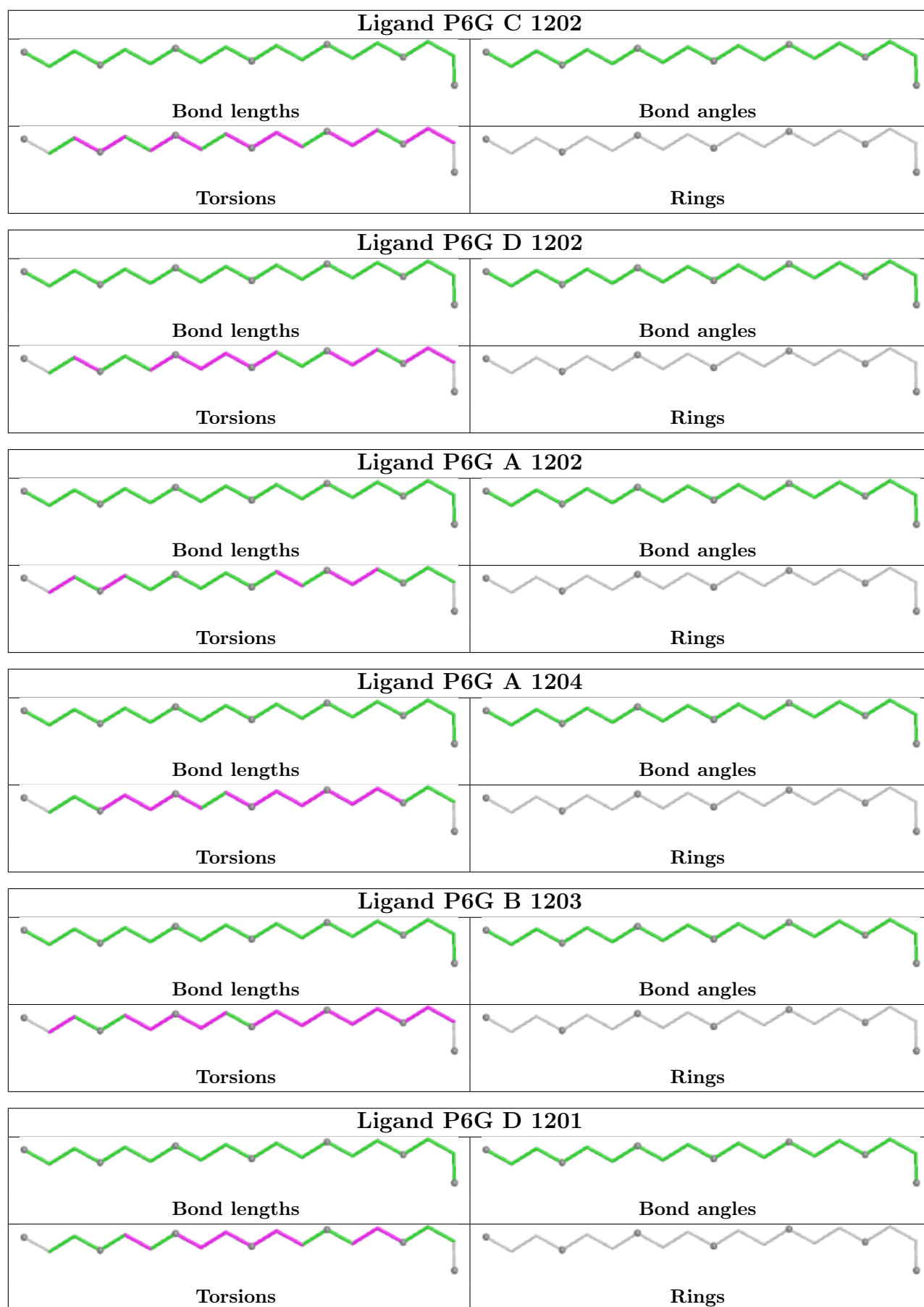
Mol	Chain	Res	Type	Atoms
11	A	1202	P6G	O4-C5-C6-O7
11	A	1202	P6G	O7-C8-C9-O10
11	D	1201	P6G	O10-C11-C12-O13
11	B	1203	P6G	O7-C8-C9-O10
11	B	1203	P6G	O10-C11-C12-O13

There are no ring outliers.

9 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	C	1202	P6G	1	0
6	D	1303	LYS	2	0
10	C	1200	PEG	1	0
11	A	1202	P6G	1	0
6	A	1303	LYS	1	0
11	A	1204	P6G	1	0
11	B	1203	P6G	6	0
11	D	1201	P6G	5	0
10	B	1201	PEG	3	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	603/629 (95%)	-0.06	12 (1%) 65 65	18, 28, 47, 76	0
1	B	605/629 (96%)	0.09	39 (6%) 25 24	11, 28, 53, 80	2 (0%)
1	C	607/629 (96%)	-0.28	10 (1%) 70 71	16, 24, 39, 85	1 (0%)
1	D	609/629 (96%)	-0.24	10 (1%) 70 71	14, 24, 39, 72	5 (0%)
All	All	2424/2516 (96%)	-0.12	71 (2%) 53 53	11, 26, 47, 85	8 (0%)

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	79	ILE	7.3
1	B	83	PHE	6.3
1	C	414	VAL	5.9
1	B	80	TRP	5.7
1	C	133	THR	5.7

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FUC	E	2	10/11	0.47	0.23	71,73,74,74	0
2	FUC	N	2	10/11	0.60	0.20	56,59,60,61	0

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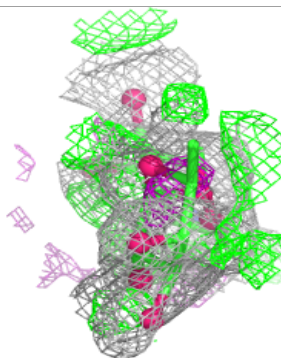
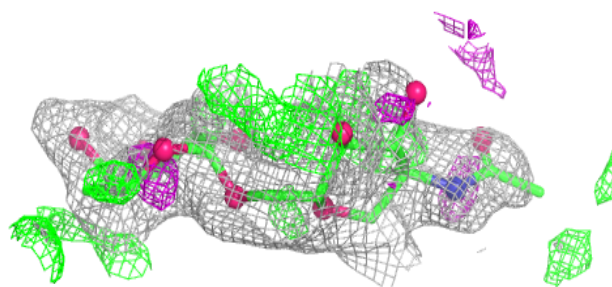
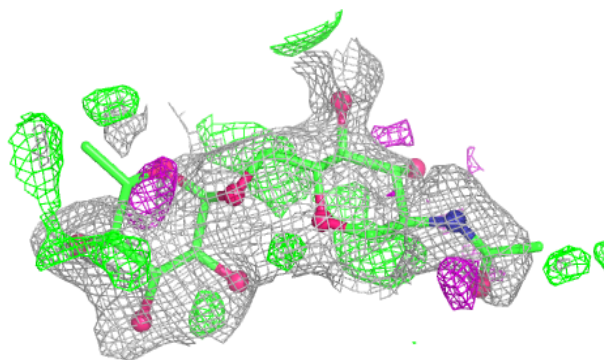
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	F	2	14/15	0.60	0.15	61,68,71,74	0
2	FUC	H	2	10/11	0.63	0.23	59,65,68,70	0
2	FUC	K	2	10/11	0.65	0.22	59,65,68,70	0
4	BMA	J	3	11/12	0.65	0.13	74,76,77,77	0
2	NAG	E	1	14/15	0.67	0.19	51,58,62,66	0
3	NAG	O	2	14/15	0.68	0.14	62,67,69,71	0
5	BMA	M	3	11/12	0.68	0.16	57,59,62,62	0
5	BMA	P	3	11/12	0.71	0.14	61,63,66,67	0
4	BMA	G	3	11/12	0.73	0.12	81,82,82,84	0
3	NAG	I	2	14/15	0.74	0.12	66,71,74,74	0
4	NAG	G	2	14/15	0.80	0.13	74,75,77,79	0
3	NAG	L	2	14/15	0.81	0.12	45,49,57,60	0
2	NAG	K	1	14/15	0.81	0.13	42,49,51,56	0
4	NAG	J	2	14/15	0.81	0.14	61,65,67,70	0
2	NAG	H	1	14/15	0.82	0.13	39,44,47,53	0
4	NAG	G	1	14/15	0.82	0.14	68,71,72,73	0
3	NAG	O	1	14/15	0.84	0.12	39,43,49,56	0
5	NAG	P	2	14/15	0.85	0.12	46,50,54,59	0
3	NAG	I	1	14/15	0.86	0.10	41,46,51,57	0
2	NAG	N	1	14/15	0.87	0.11	35,40,47,52	0
5	FUC	M	4	10/11	0.88	0.11	41,43,45,46	0
4	NAG	J	1	14/15	0.89	0.10	52,55,58,58	0
5	NAG	M	2	14/15	0.89	0.12	44,49,54,54	0
3	NAG	F	1	14/15	0.89	0.09	39,42,46,54	0
5	FUC	P	4	10/11	0.90	0.10	40,41,44,44	0
3	NAG	L	1	14/15	0.92	0.08	31,34,37,41	0
5	NAG	P	1	14/15	0.94	0.09	34,37,38,41	0
5	NAG	M	1	14/15	0.94	0.07	33,36,40,40	0

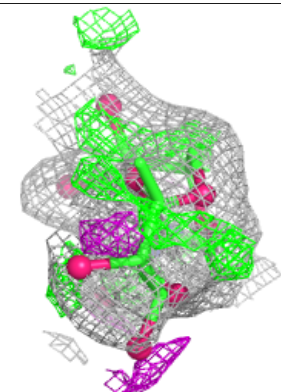
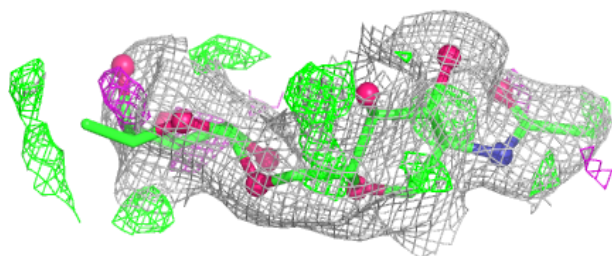
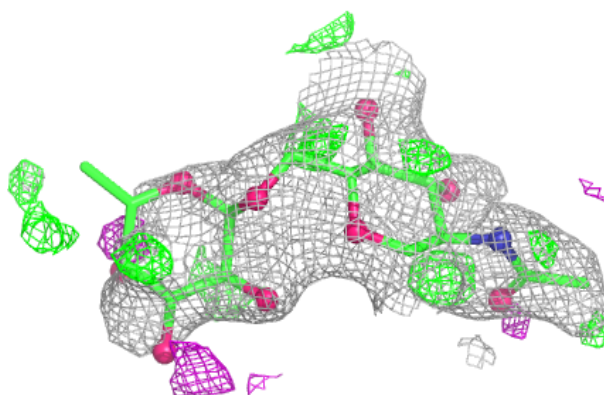
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

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

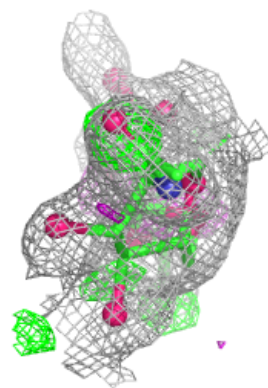
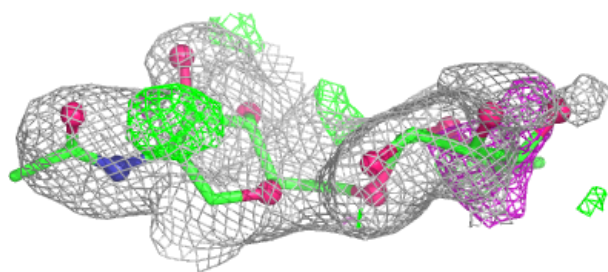
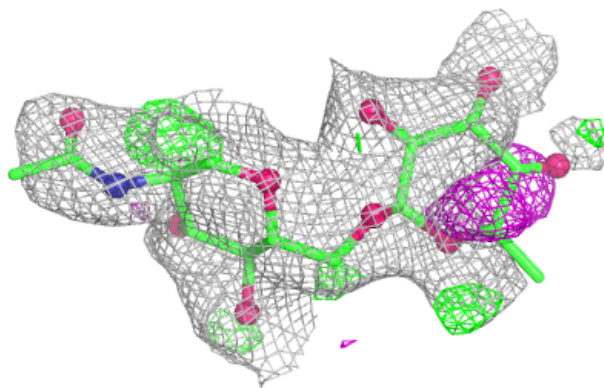
**Electron density around Chain H:**

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and green (positive)

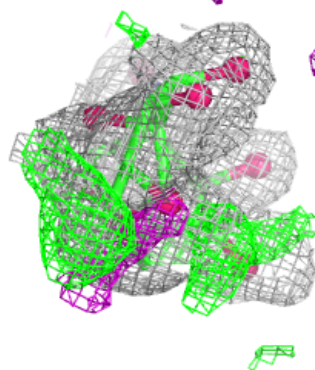
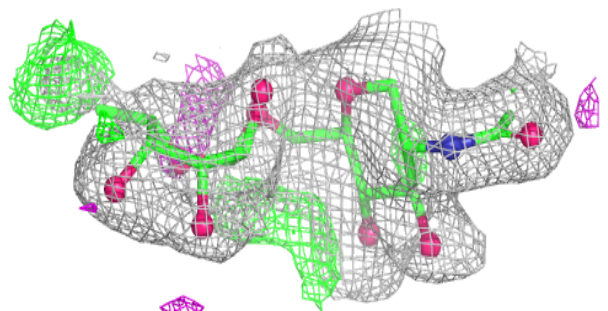
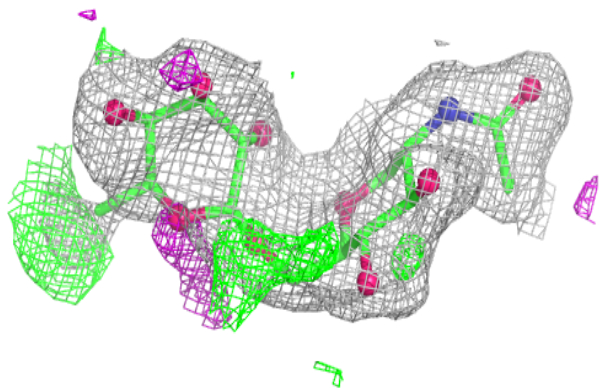


Electron density around Chain K:

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

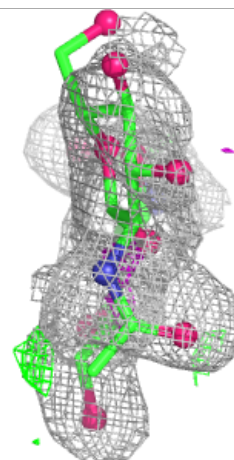
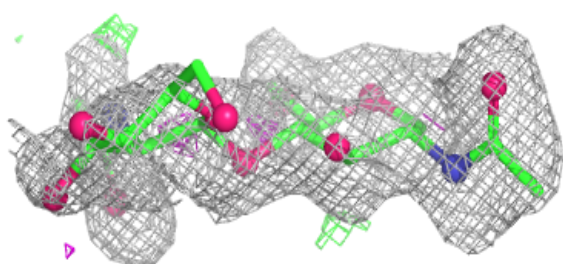
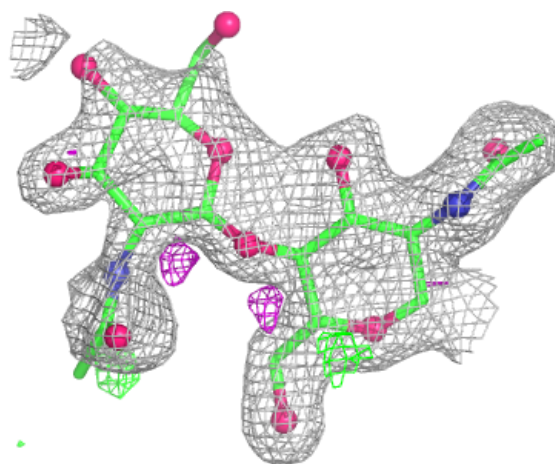
**Electron density around Chain N:**

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



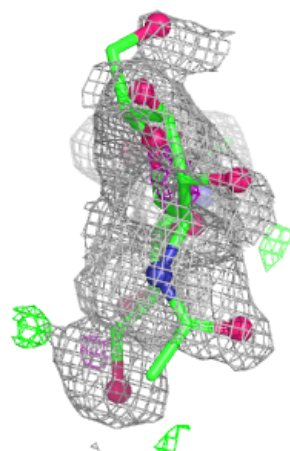
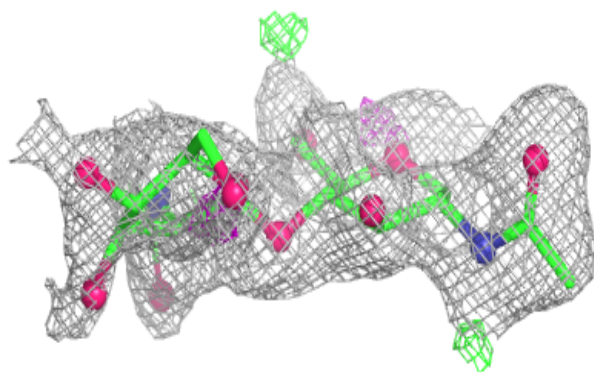
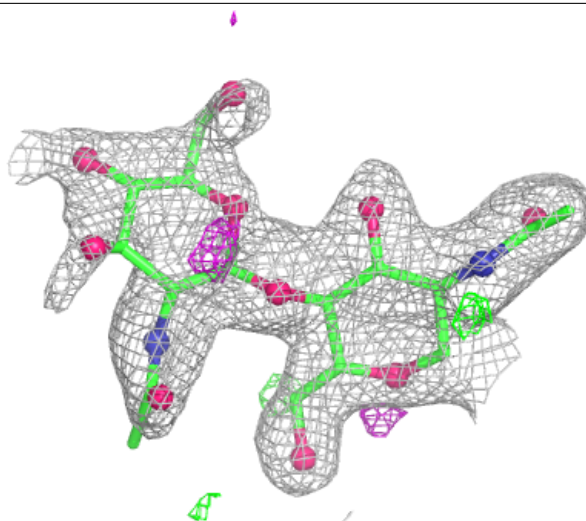
Electron density around Chain F:

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and green (positive)



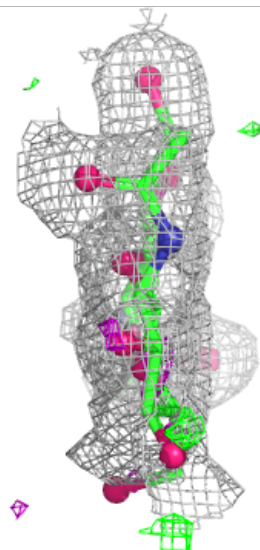
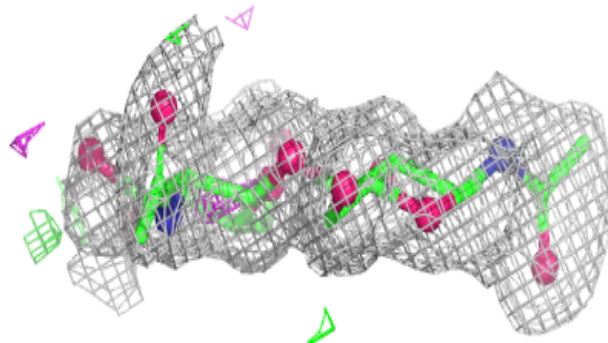
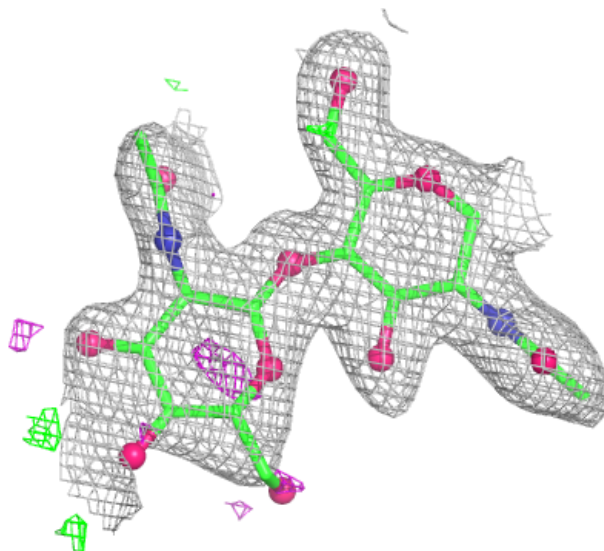
Electron density around Chain I:

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and green (positive)



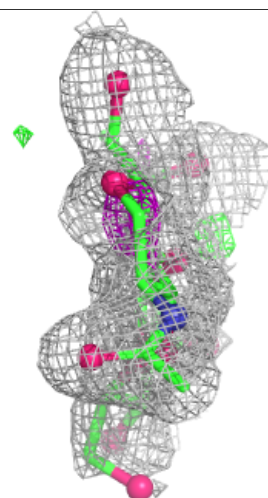
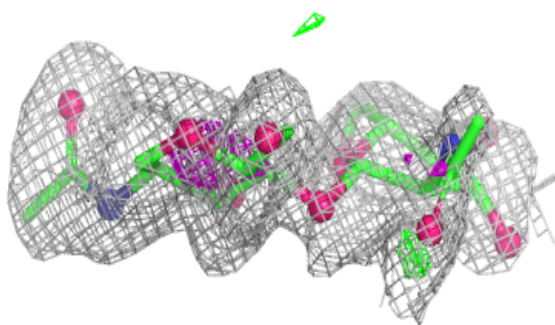
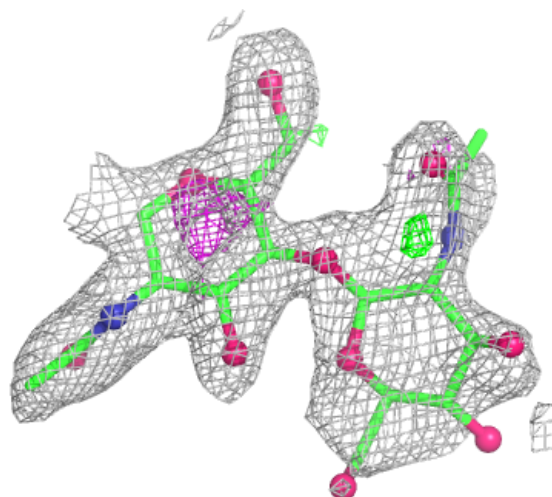
Electron density around Chain L:

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and green (positive)



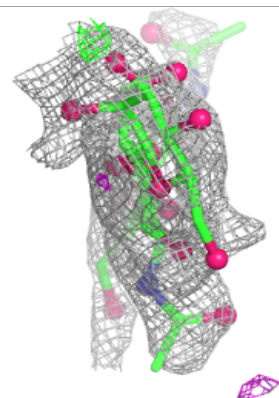
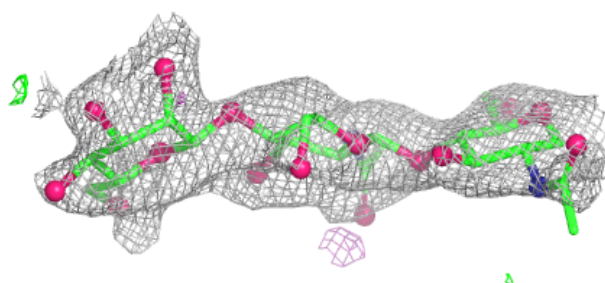
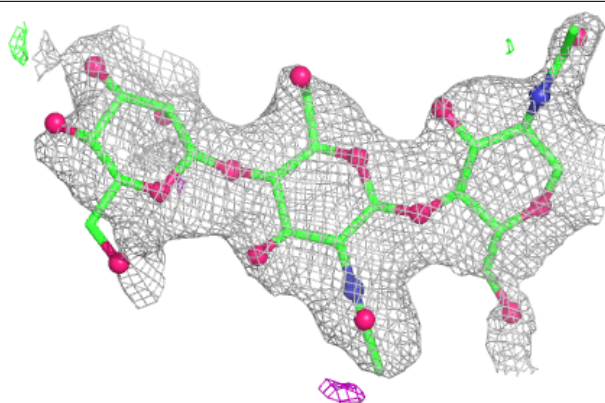
Electron density around Chain O:

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

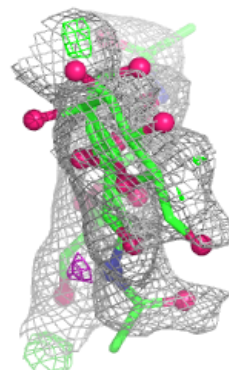
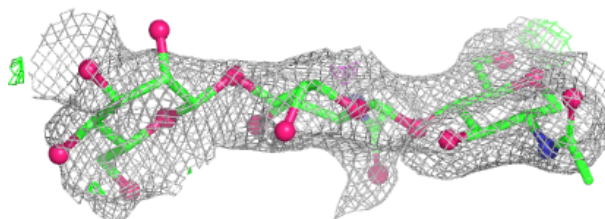
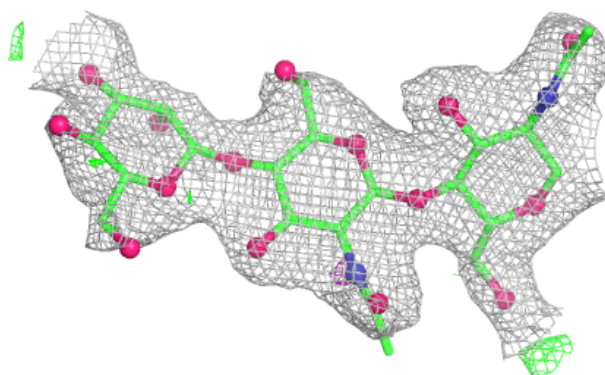


Electron density around Chain G:

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and green (positive)

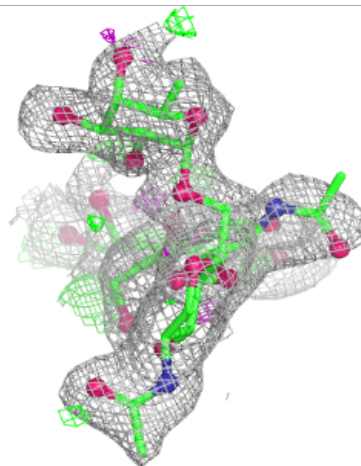
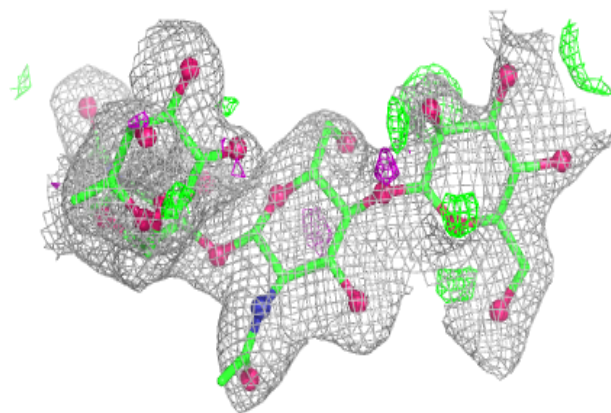
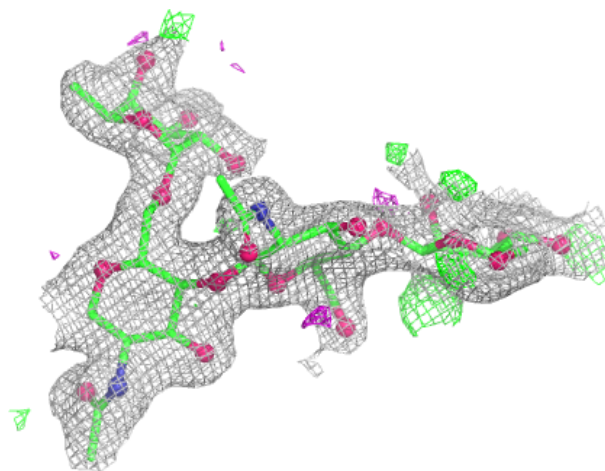
**Electron density around Chain J:**

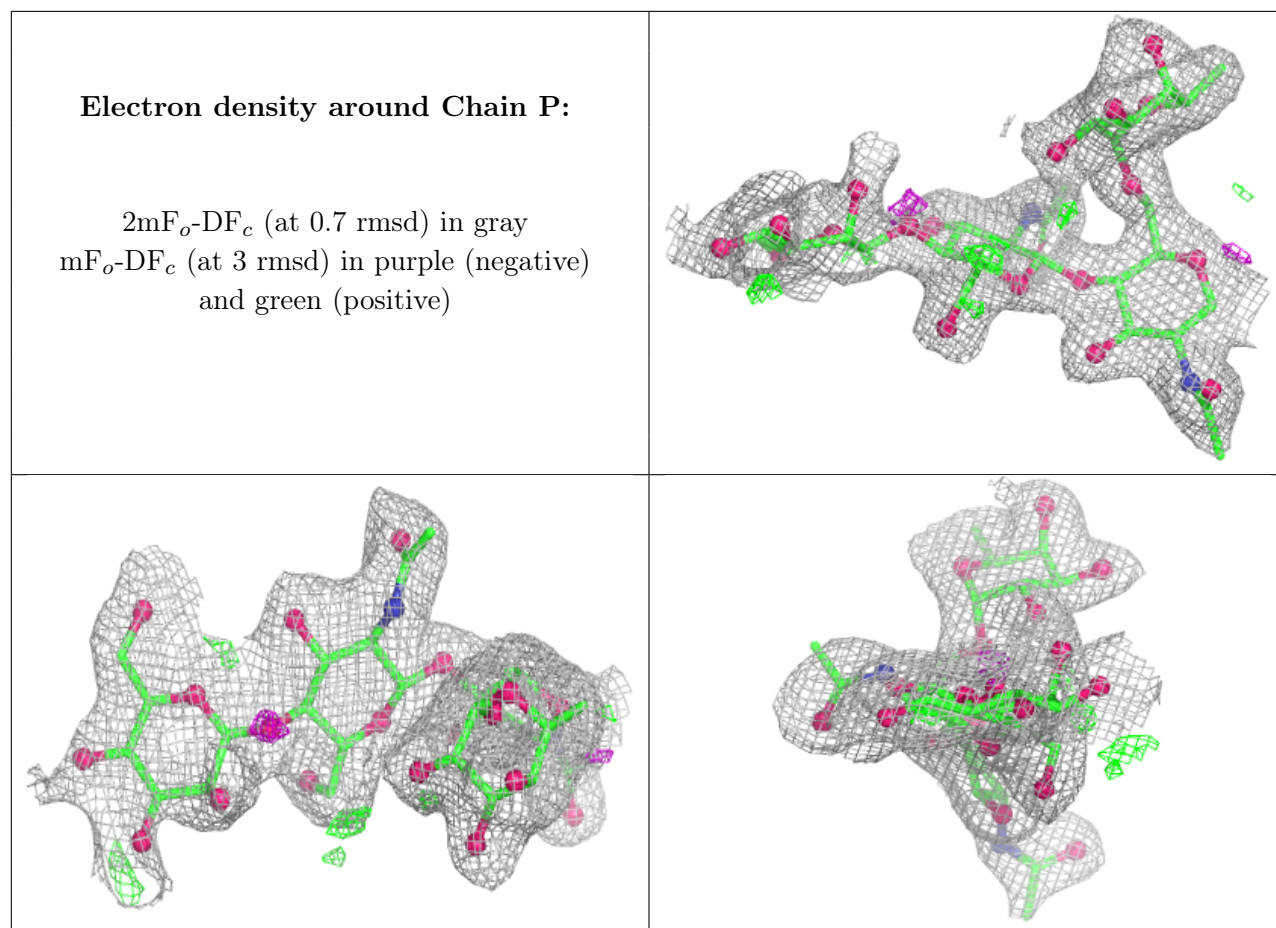
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain M:

$2mF_o-DF_c$ (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
11	P6G	A	1204	19/19	0.79	0.23	61,70,77,77	0
10	PEG	B	1204	7/7	0.81	0.21	54,54,58,61	0
10	PEG	A	1200	7/7	0.85	0.15	56,58,63,64	0
10	PEG	B	1201	7/7	0.85	0.16	46,47,49,50	0
11	P6G	D	1202	19/19	0.85	0.18	50,55,61,61	0
11	P6G	B	1203	19/19	0.86	0.16	42,46,55,56	0
10	PEG	B	1205	7/7	0.87	0.18	61,62,64,65	0
10	PEG	D	1200	7/7	0.88	0.11	54,55,58,59	0
11	P6G	C	1202	19/19	0.88	0.15	43,50,56,56	0
11	P6G	D	1201	19/19	0.88	0.13	32,41,49,51	0
10	PEG	A	1203	7/7	0.88	0.15	50,50,52,54	0
10	PEG	A	1201	7/7	0.90	0.13	41,44,48,50	0

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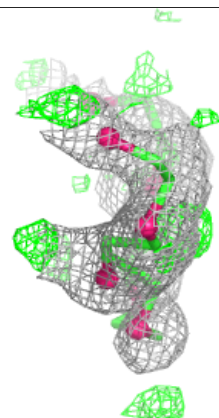
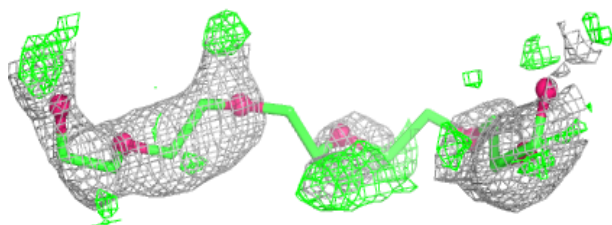
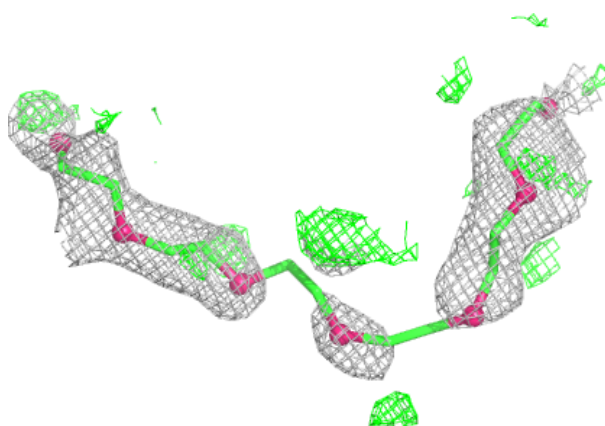
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
10	PEG	B	1202	7/7	0.90	0.13	39,41,42,43	0
10	PEG	C	1201	7/7	0.90	0.13	39,40,42,43	0
10	PEG	C	1200	7/7	0.91	0.11	47,47,48,49	0
11	P6G	A	1202	19/19	0.92	0.12	40,43,45,46	0
6	LYS	A	1303	9/10	0.92	0.12	21,24,35,35	0
6	LYS	C	1303	9/10	0.93	0.10	21,24,33,35	0
6	LYS	D	1303	9/10	0.94	0.10	20,22,33,39	0
7	PRO	D	1304	8/8	0.94	0.07	18,20,21,22	0
6	LYS	B	1303	9/10	0.94	0.10	22,24,35,40	0
7	PRO	A	1304	8/8	0.95	0.07	21,23,24,24	0
7	PRO	C	1304	8/8	0.96	0.07	21,22,24,25	0
7	PRO	B	1304	8/8	0.96	0.06	19,23,24,24	0
8	ZN	A	1001	1/1	1.00	0.01	21,21,21,21	0
8	ZN	B	1001	1/1	1.00	0.01	21,21,21,21	0
8	ZN	C	1001	1/1	1.00	0.01	19,19,19,19	0
8	ZN	D	1001	1/1	1.00	0.01	19,19,19,19	0
9	CL	A	1002	1/1	1.00	0.01	21,21,21,21	0
9	CL	B	1002	1/1	1.00	0.02	22,22,22,22	0
9	CL	C	1002	1/1	1.00	0.01	18,18,18,18	0
9	CL	D	1002	1/1	1.00	0.02	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.

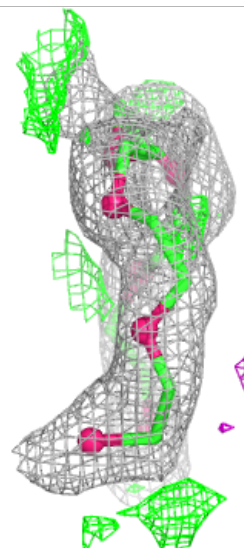
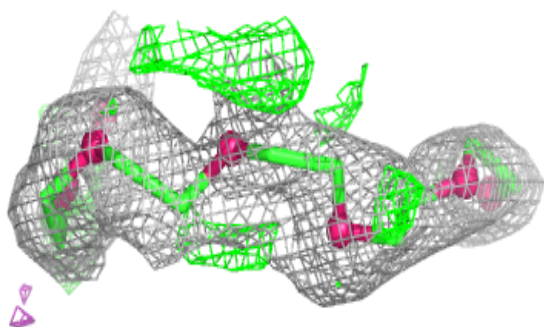
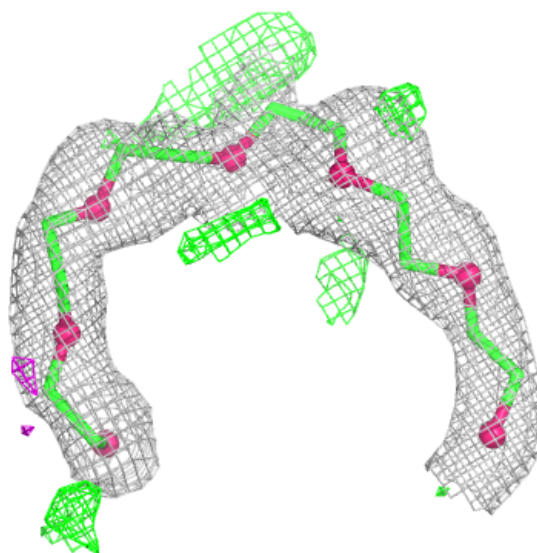
Electron density around P6G A 1204:

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and green (positive)



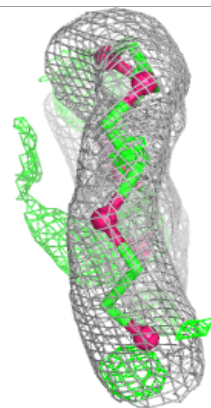
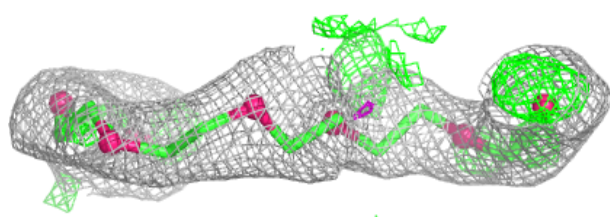
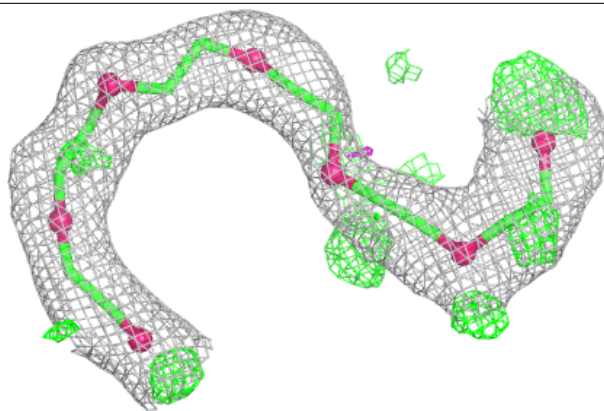
Electron density around P6G D 1202:

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and green (positive)



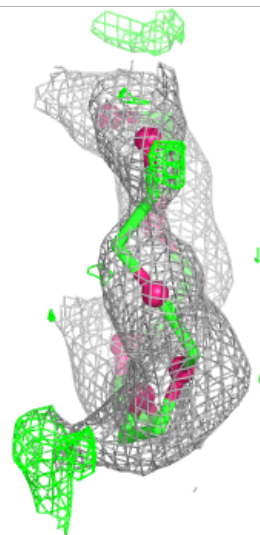
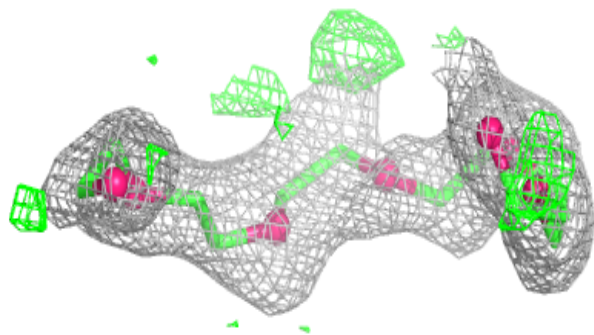
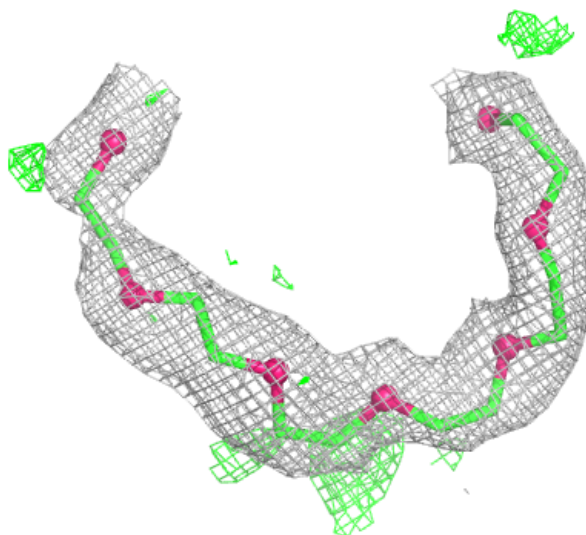
Electron density around P6G B 1203:

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and green (positive)



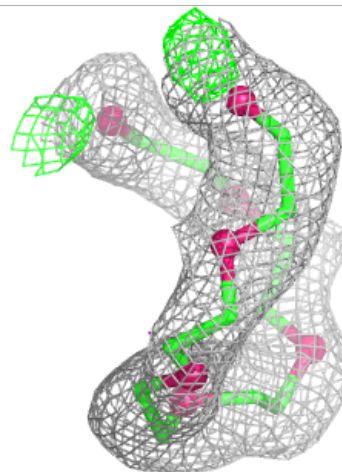
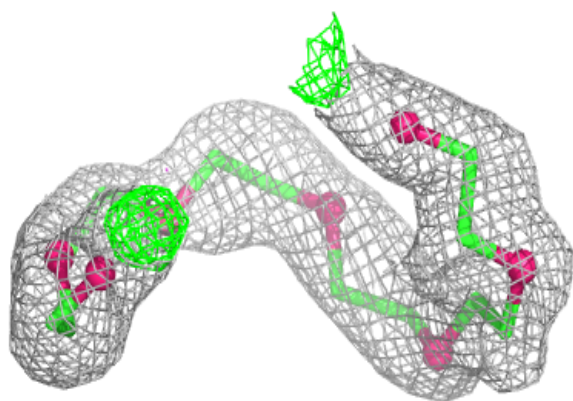
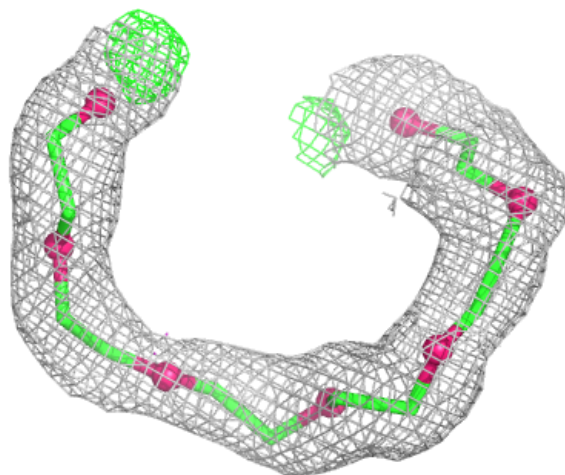
Electron density around P6G C 1202:

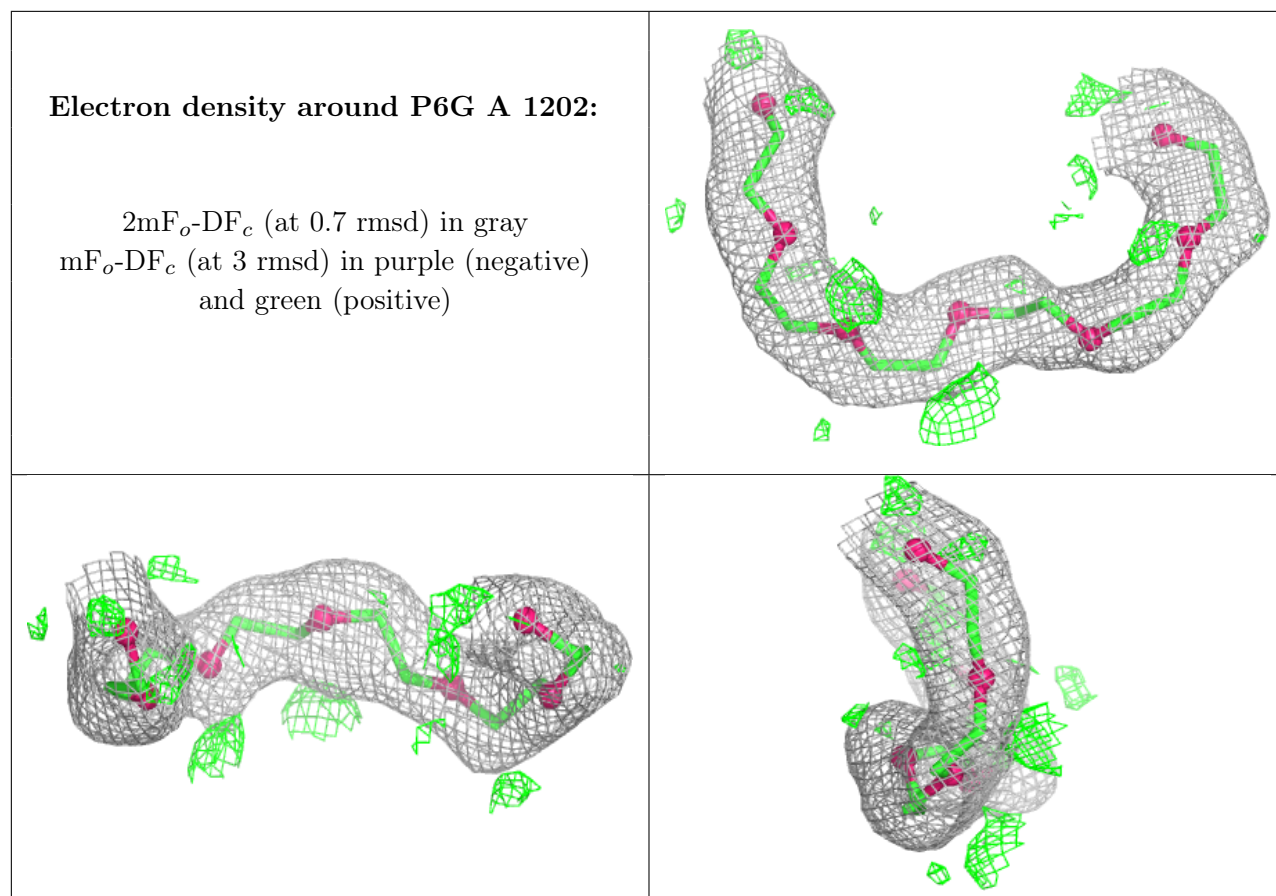
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around P6G D 1201:

$2mF_o-DF_c$ (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.