



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 26, 2024 – 08:24 AM EDT

PDB ID : 5VEN
Title : Murine ectonucleotide pyrophosphatase / phosphodiesterase 5 (ENPP5, NPP5)
Authors : Gorelik, A.; Randriamihaja, A.; Illes, K.; Nagar, B.
Deposited on : 2017-04-05
Resolution : 1.69 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

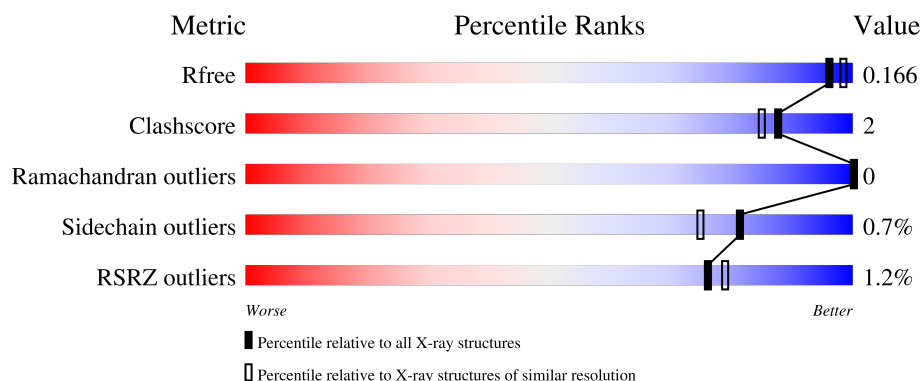
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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.



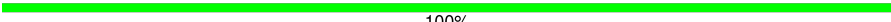
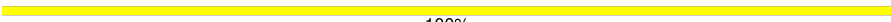

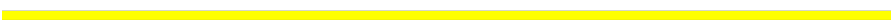

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	5161 (1.70-1.70)
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (1.70-1.70)

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	416	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>5%</div> <div>8%</div> </div> </div>
1	B	416	<div> <div>86%</div> <div>10%</div> </div>
2	C	5	<div> <div>20%</div> <div>80%</div> </div>
2	G	5	<div> <div>60%</div> <div>40%</div> </div>
3	D	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	E	2	 100%
3	H	2	 100%
3	I	2	 100%
4	F	2	 100%
4	J	2	 100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13636 atoms, of which 6335 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 Ectonucleotide pyrophosphatase/phosphodiesterase family member 5.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	382	Total	C	H	N	O	S	0	9	0
			6200	2048	3037	531	572	12			
1	B	373	Total	C	H	N	O	S	0	6	0
			6008	1988	2936	509	562	13			

There are 20 discrepancies between the modelled and reference sequences:

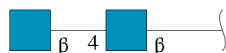
Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ASP	-	expression tag	UNP Q9EQG7
A	16	ARG	-	expression tag	UNP Q9EQG7
A	17	HIS	-	expression tag	UNP Q9EQG7
A	18	HIS	-	expression tag	UNP Q9EQG7
A	19	HIS	-	expression tag	UNP Q9EQG7
A	20	HIS	-	expression tag	UNP Q9EQG7
A	21	HIS	-	expression tag	UNP Q9EQG7
A	22	HIS	-	expression tag	UNP Q9EQG7
A	23	LYS	-	expression tag	UNP Q9EQG7
A	24	LEU	-	expression tag	UNP Q9EQG7
B	15	ASP	-	expression tag	UNP Q9EQG7
B	16	ARG	-	expression tag	UNP Q9EQG7
B	17	HIS	-	expression tag	UNP Q9EQG7
B	18	HIS	-	expression tag	UNP Q9EQG7
B	19	HIS	-	expression tag	UNP Q9EQG7
B	20	HIS	-	expression tag	UNP Q9EQG7
B	21	HIS	-	expression tag	UNP Q9EQG7
B	22	HIS	-	expression tag	UNP Q9EQG7
B	23	LYS	-	expression tag	UNP Q9EQG7
B	24	LEU	-	expression tag	UNP Q9EQG7

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	5	Total	C	H	N	O	0	0	0
			118	34	57	2	25			
2	G	5	Total	C	H	N	O	0	0	0
			118	34	57	2	25			

- 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	D	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			
3	E	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			
3	H	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			
3	I	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	2	Total	C	H	N	O	0	0	0
			48	14	24	1	9			
4	J	2	Total	C	H	N	O	0	0	0
			48	14	24	1	9			

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

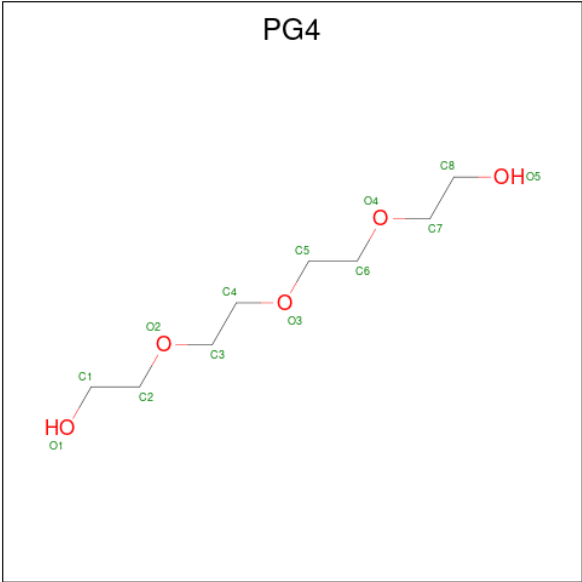
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	Zn	0	0
			4	4		
5	B	4	Total	Zn	0	0
			4	4		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
6	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
6	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
6	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

- Molecule 7 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).

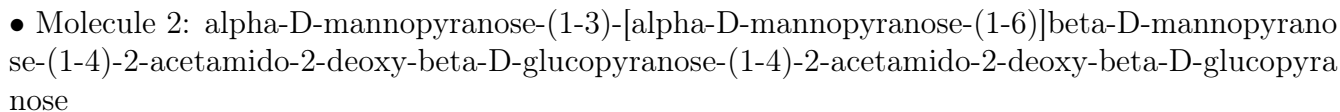
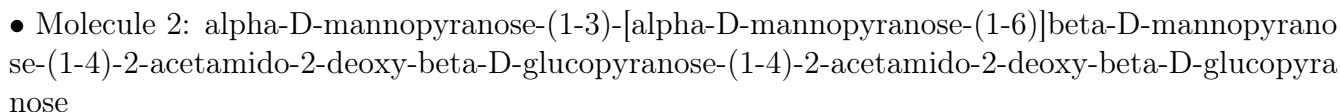


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			31	8	18	5		
7	B	1	Total	C	H	O	0	0
			31	8	18	5		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	349	Total	O	0	0
			349	349		
8	B	345	Total	O	0	0
			345	345		

- Molecule 1: Ectonucleotide pyrophosphatase/phosphodiesterase family member 5



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

Chain D:  100%

MAG1
MAG2

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

Chain E:  100%

MAG1
MAG2

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

Chain H:  100%

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

Chain F:  100%

MAG1
FUC2

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

Chain J:  100%

MAG1
FUC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	82.40Å 82.40Å 301.01Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.20 – 1.69 41.20 – 1.69	Depositor EDS
% Data completeness (in resolution range)	73.8 (41.20-1.69) 60.2 (41.20-1.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 1.69Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.129 , 0.164 0.130 , 0.166	Depositor DCC
R_{free} test set	5835 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	11.0	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13636	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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: NAG, PG4, MAN, ZN, FUC, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.56	0/3293	0.65	0/4484
1	B	0.55	0/3191	0.66	0/4347
All	All	0.56	0/6484	0.66	0/8831

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	3163	3037	3054	14	1
1	B	3072	2936	2950	9	0
2	C	61	57	52	0	0
2	G	61	57	52	0	0
3	D	28	27	25	0	0
3	E	28	27	25	0	0
3	H	28	27	25	1	0
3	I	28	27	25	0	0
4	F	24	24	22	0	0
4	J	24	24	22	0	0
5	A	4	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	4	0	0	0	0
6	A	28	28	26	0	0
6	B	28	28	26	0	0
7	A	13	18	18	1	0
7	B	13	18	18	0	0
8	A	349	0	0	5	0
8	B	345	0	0	4	0
All	All	7301	6335	6340	24	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 2.

The worst 5 of 24 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:A:372:ASP:OD2	8:A:601:HOH:O	1.95	0.85
1:B:278:LYS:NZ	8:B:601:HOH:O	2.09	0.84
1:B:365:LYS:NZ	1:B:394:ASN:O	2.17	0.78
1:A:26:GLU:OE1	1:A:29:LYS:NZ	2.18	0.76
1:A:242[B]:THR:HG23	1:A:348:MET:CE	2.18	0.74

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)
1:A:21:HIS:HE2	5:A:504:ZN:ZN[6_664]	1.31	0.29

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	389/416 (94%)	379 (97%)	10 (3%)	0	100	100
1	B	378/416 (91%)	370 (98%)	8 (2%)	0	100	100
All	All	767/832 (92%)	749 (98%)	18 (2%)	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	347/369 (94%)	344 (99%)	3 (1%)	75	67
1	B	336/369 (91%)	334 (99%)	2 (1%)	84	78
All	All	683/738 (92%)	678 (99%)	5 (1%)	81	75

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	HIS
1	A	77	TYR
1	A	325	TYR
1	B	77	TYR
1	B	325	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	HIS
1	A	394	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 ⓘ

22 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	C	1	2,1	14,14,15	0.48	0	17,19,21	0.72	0
2	NAG	C	2	2	14,14,15	0.88	1 (7%)	17,19,21	0.49	0
2	BMA	C	3	2	11,11,12	0.93	1 (9%)	15,15,17	1.03	1 (6%)
2	MAN	C	4	2	11,11,12	0.83	0	15,15,17	1.02	1 (6%)
2	MAN	C	5	2	11,11,12	1.10	1 (9%)	15,15,17	1.37	2 (13%)
3	NAG	D	1	3,1	14,14,15	0.47	0	17,19,21	0.49	0
3	NAG	D	2	3	14,14,15	0.47	0	17,19,21	0.48	0
3	NAG	E	1	3,1	14,14,15	0.24	0	17,19,21	0.69	0
3	NAG	E	2	3	14,14,15	0.38	0	17,19,21	0.45	0
4	NAG	F	1	4,1	14,14,15	1.11	1 (7%)	17,19,21	0.97	1 (5%)
4	FUC	F	2	4	10,10,11	1.17	1 (10%)	14,14,16	0.73	0
2	NAG	G	1	2,1	14,14,15	0.35	0	17,19,21	0.92	2 (11%)
2	NAG	G	2	2	14,14,15	0.62	0	17,19,21	0.77	0
2	BMA	G	3	2	11,11,12	1.59	3 (27%)	15,15,17	1.11	1 (6%)
2	MAN	G	4	2	11,11,12	0.75	0	15,15,17	0.94	0
2	MAN	G	5	2	11,11,12	1.08	0	15,15,17	1.00	0
3	NAG	H	1	3,1	14,14,15	0.61	0	17,19,21	0.56	0
3	NAG	H	2	3	14,14,15	0.45	0	17,19,21	0.96	1 (5%)
3	NAG	I	1	3,1	14,14,15	0.17	0	17,19,21	0.69	0
3	NAG	I	2	3	14,14,15	0.51	0	17,19,21	0.68	0
4	NAG	J	1	4,1	14,14,15	0.64	1 (7%)	17,19,21	0.53	0
4	FUC	J	2	4	10,10,11	1.28	2 (20%)	14,14,16	0.75	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	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	MAN	C	5	2	-	2/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
4	NAG	F	1	4,1	-	0/6/23/26	0/1/1/1
4	FUC	F	2	4	-	-	0/1/1/1
2	NAG	G	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	0/2/19/22	0/1/1/1
2	MAN	G	4	2	-	0/2/19/22	0/1/1/1
2	MAN	G	5	2	-	0/2/19/22	0/1/1/1
3	NAG	H	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	1/6/23/26	0/1/1/1
4	FUC	J	2	4	-	-	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1	NAG	O5-C1	3.47	1.49	1.43
2	C	2	NAG	C1-C2	3.05	1.56	1.52
4	F	2	FUC	O3-C3	2.84	1.50	1.43
2	G	3	BMA	C2-C3	-2.80	1.48	1.52
4	J	2	FUC	C1-C2	2.34	1.57	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	5	MAN	C1-O5-C5	3.76	117.23	112.19
4	F	1	NAG	C1-O5-C5	3.56	116.96	112.19
2	C	5	MAN	O2-C2-C3	-3.12	103.69	110.15
2	G	3	BMA	C1-C2-C3	-2.60	105.86	109.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	2	NAG	C1-O5-C5	2.59	115.66	112.19

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

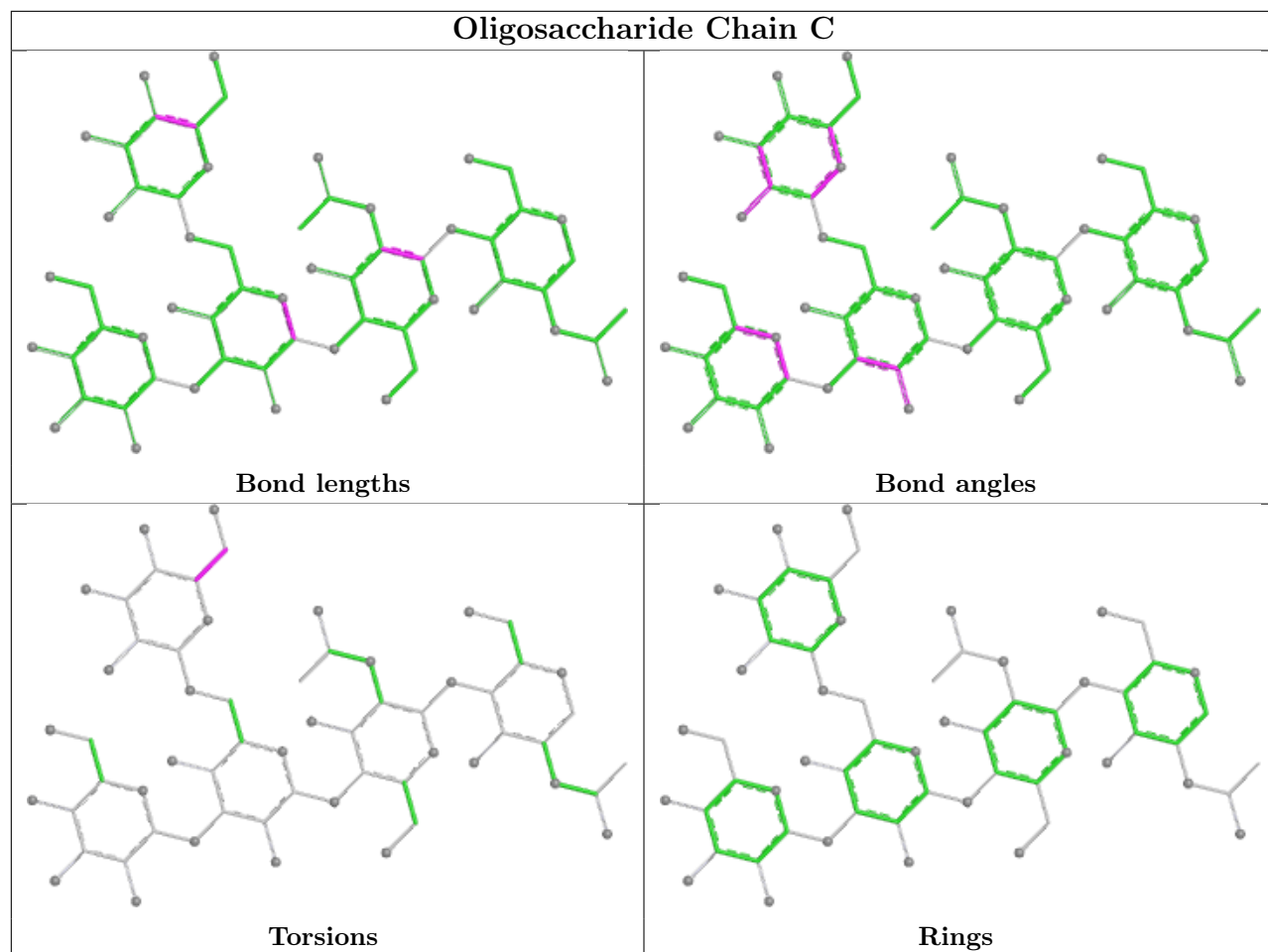
Mol	Chain	Res	Type	Atoms
3	H	2	NAG	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6

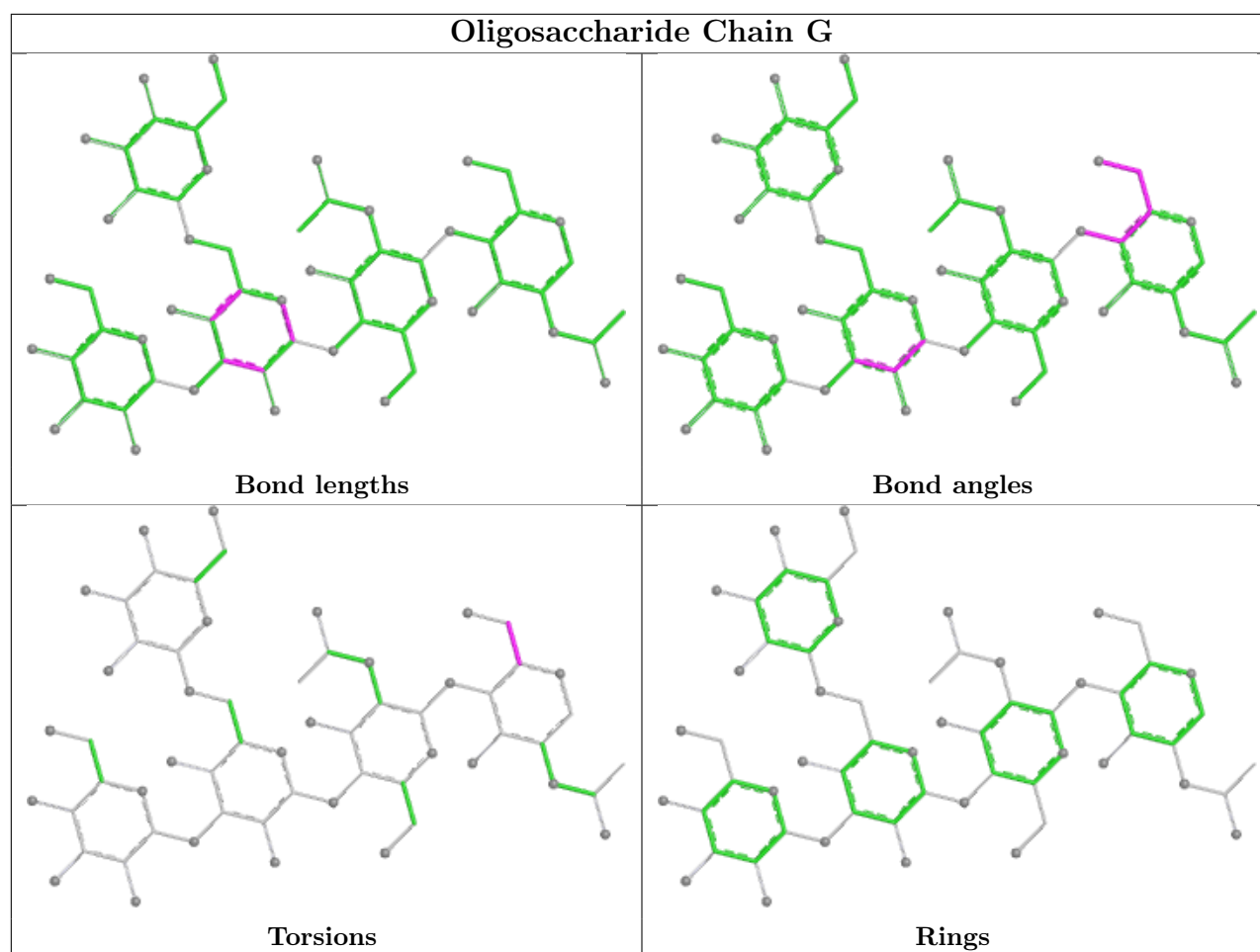
There are no ring outliers.

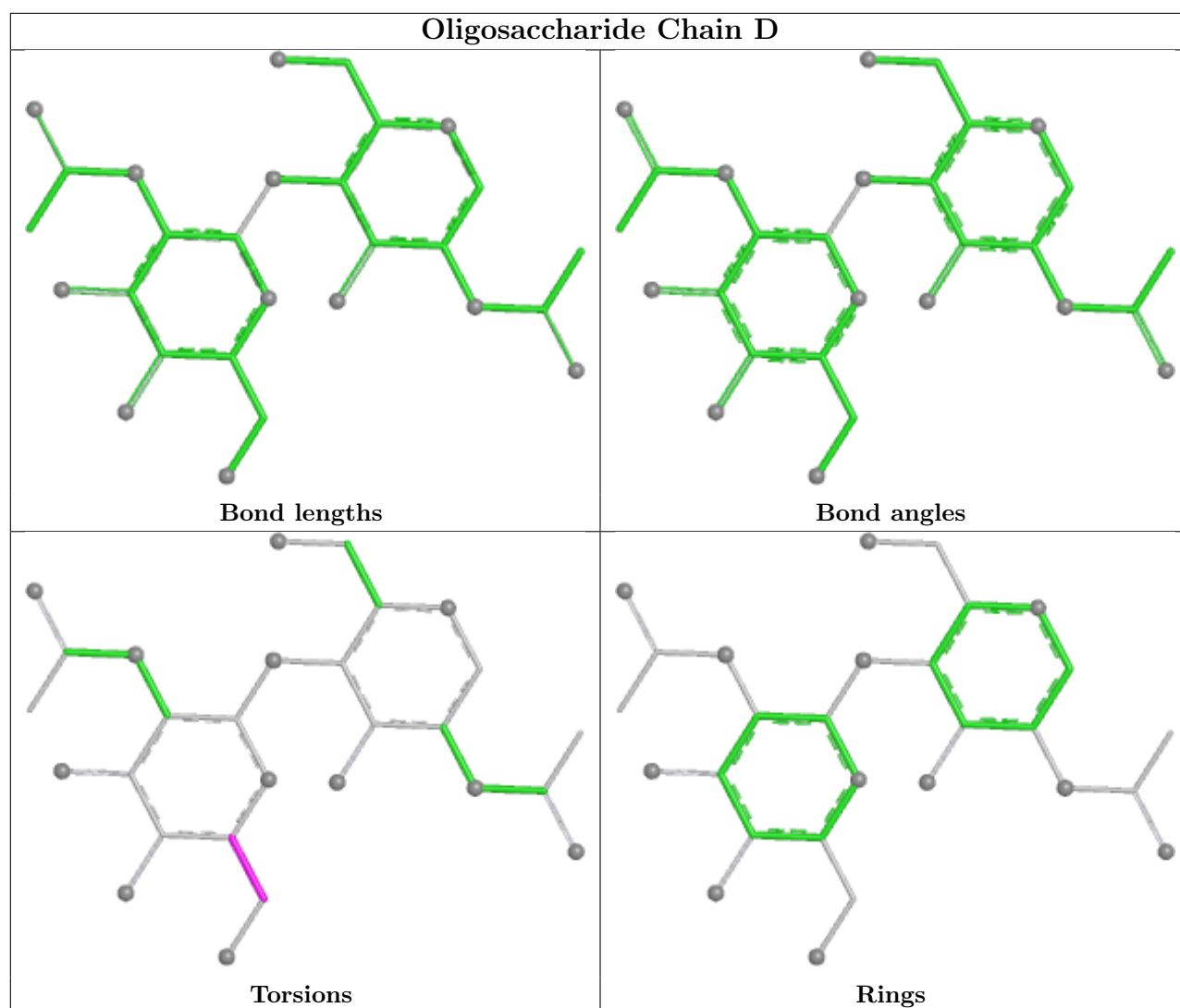
1 monomer is involved in 1 short contact:

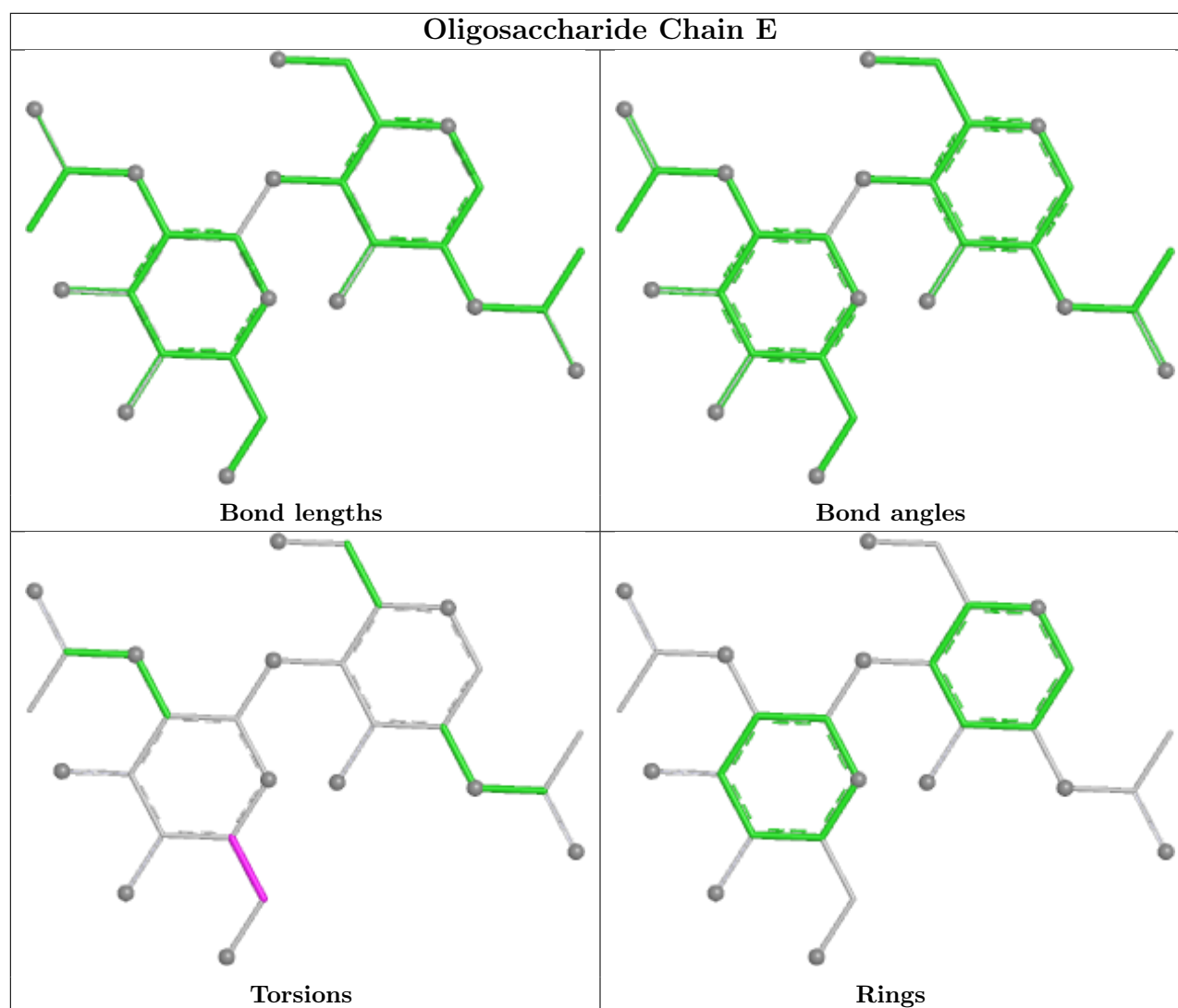
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	NAG	1	0

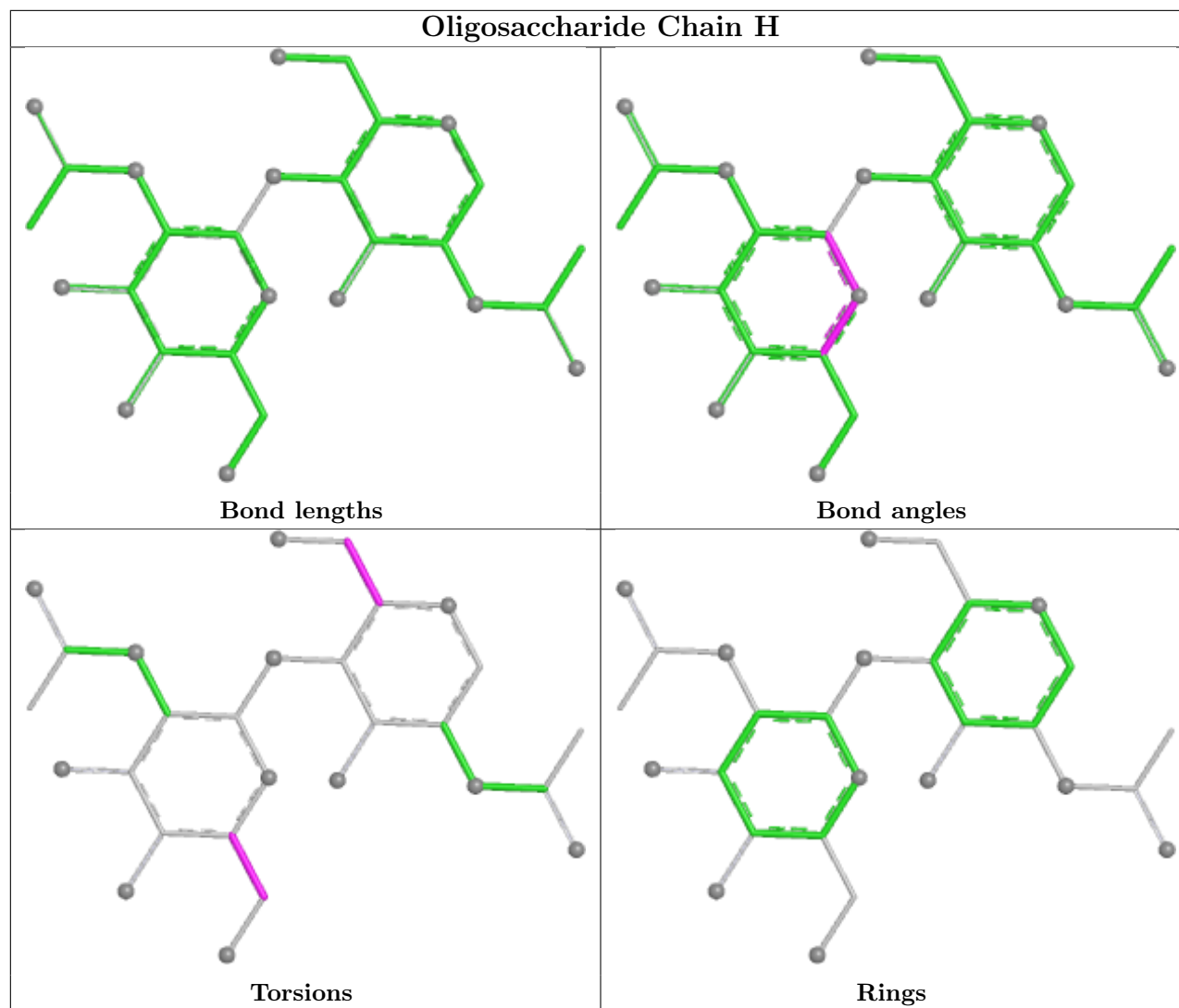
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

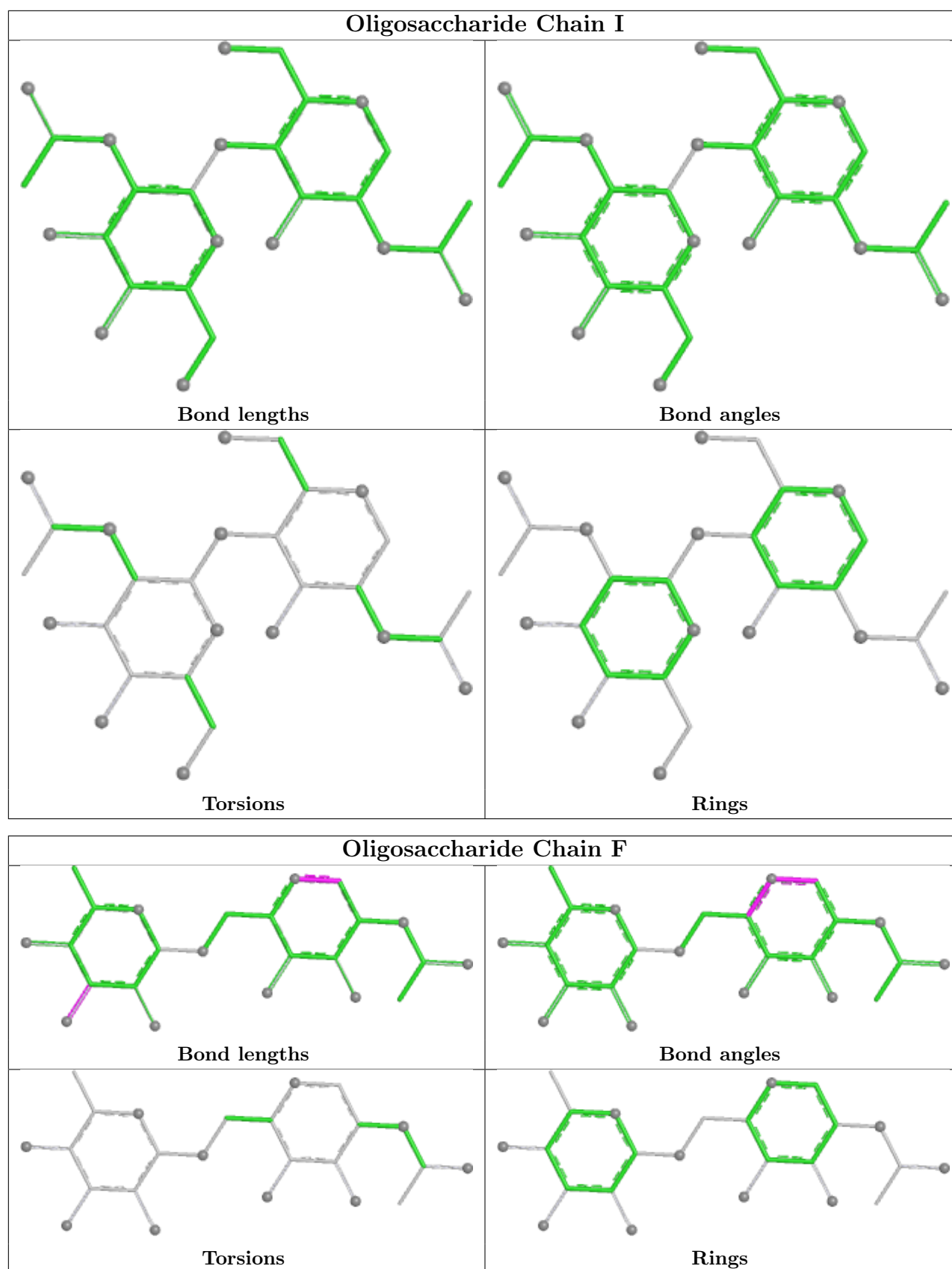


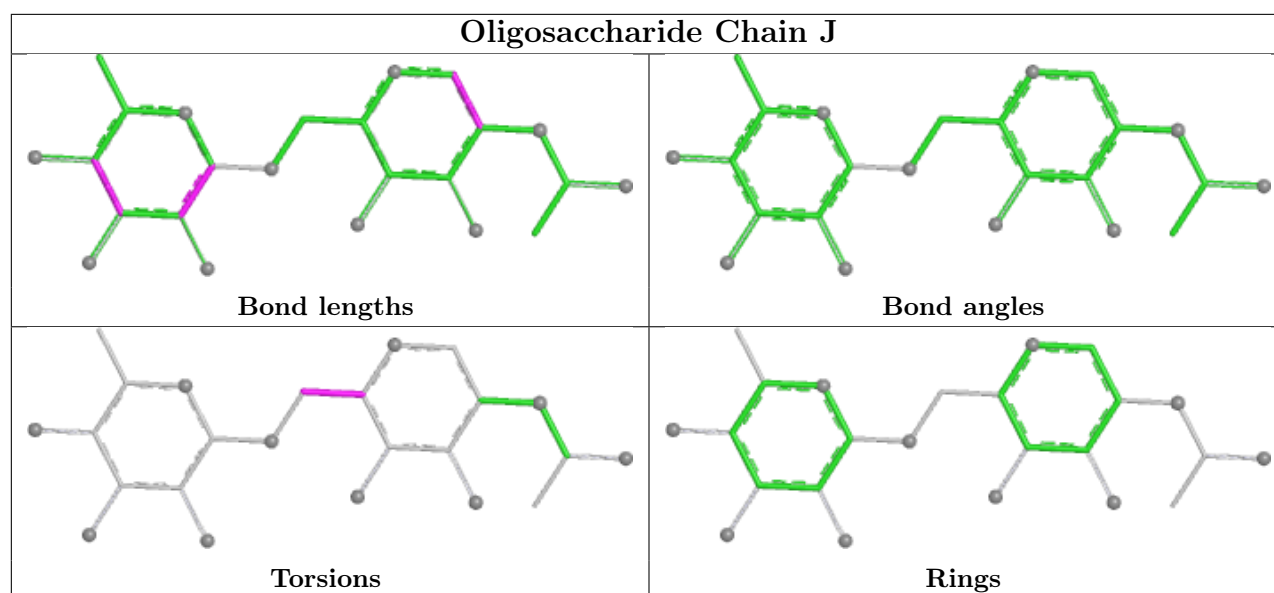












5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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	PG4	A	518	-	12,12,12	0.56	0	11,11,11	0.60	0
6	NAG	B	517	1	14,14,15	0.43	0	17,19,21	1.25	1 (5%)
7	PG4	B	518	-	12,12,12	0.56	0	11,11,11	0.36	0
6	NAG	A	514	1	14,14,15	0.57	0	17,19,21	0.74	0
6	NAG	B	514	1	14,14,15	0.24	0	17,19,21	0.70	0
6	NAG	A	517	1	14,14,15	0.70	1 (7%)	17,19,21	0.61	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
7	PG4	A	518	-	-	6/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	B	517	1	-	0/6/23/26	0/1/1/1
7	PG4	B	518	-	-	1/10/10/10	-
6	NAG	A	514	1	-	1/6/23/26	0/1/1/1
6	NAG	B	514	1	-	0/6/23/26	0/1/1/1
6	NAG	A	517	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	517	NAG	C1-C2	2.34	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	517	NAG	C1-O5-C5	3.51	116.88	112.19

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	514	NAG	C1-C2-N2-C7
7	A	518	PG4	O4-C7-C8-O5
6	A	517	NAG	C4-C5-C6-O6
7	A	518	PG4	C4-C3-O2-C2
7	A	518	PG4	O2-C3-C4-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	518	PG4	1	0

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	382/416 (91%)	-0.79	7 (1%) 67 70	5, 18, 41, 64	9 (2%)
1	B	373/416 (89%)	-0.73	2 (0%) 87 89	8, 23, 41, 50	6 (1%)
All	All	755/832 (90%)	-0.76	9 (1%) 76 79	5, 20, 41, 64	15 (1%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	PRO	3.8
1	A	24	LEU	3.8
1	A	20	HIS	3.6
1	A	23	LYS	2.9
1	A	393	TRP	2.7

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
3	NAG	H	2	14/15	0.63	0.15	53,60,72,72	0
3	NAG	E	2	14/15	0.71	0.15	48,57,67,70	0
3	NAG	I	2	14/15	0.73	0.15	52,61,71,73	0
3	NAG	D	2	14/15	0.74	0.14	52,57,67,68	0
3	NAG	H	1	14/15	0.80	0.13	41,49,57,60	0

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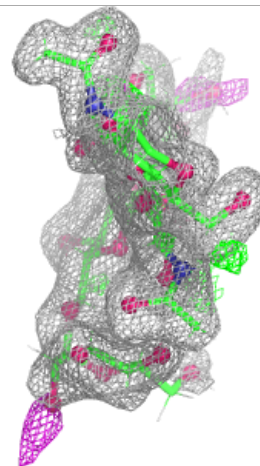
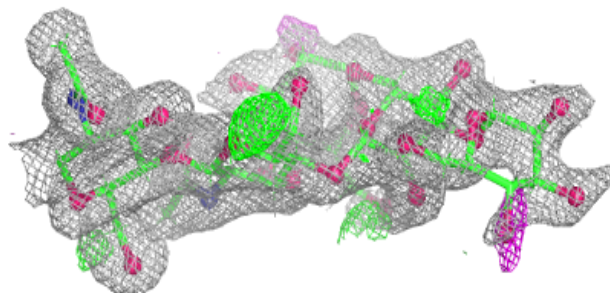
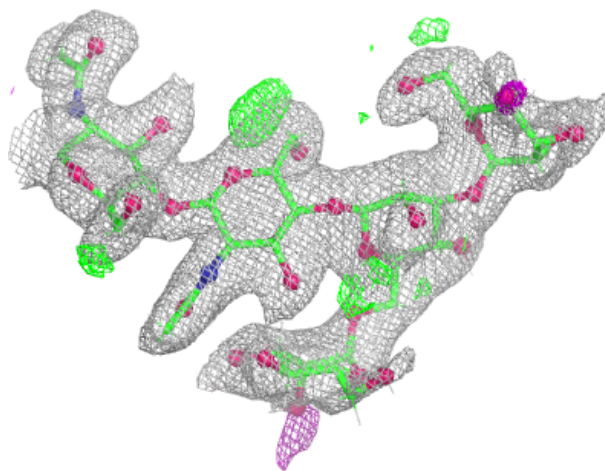
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	F	1	14/15	0.81	0.13	38,50,62,62	0
2	MAN	C	5	11/12	0.85	0.12	51,55,64,66	0
3	NAG	D	1	14/15	0.85	0.11	33,43,52,54	0
2	MAN	G	4	11/12	0.89	0.12	33,40,48,52	0
2	MAN	C	4	11/12	0.89	0.12	41,47,54,56	0
4	FUC	F	2	10/11	0.89	0.09	34,44,52,54	0
4	NAG	J	1	14/15	0.90	0.10	41,48,56,60	0
4	FUC	J	2	10/11	0.90	0.11	46,54,60,65	0
2	BMA	C	3	11/12	0.94	0.08	32,40,49,52	0
2	BMA	G	3	11/12	0.95	0.07	21,29,37,38	0
3	NAG	E	1	14/15	0.95	0.07	27,35,40,44	0
2	MAN	G	5	11/12	0.96	0.06	26,32,36,38	0
2	NAG	C	2	14/15	0.96	0.06	23,30,37,38	0
3	NAG	I	1	14/15	0.97	0.07	33,40,47,48	0
2	NAG	C	1	14/15	0.98	0.04	14,19,27,29	0
2	NAG	G	1	14/15	0.98	0.03	8,11,16,21	0
2	NAG	G	2	14/15	0.98	0.05	13,21,35,41	0

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

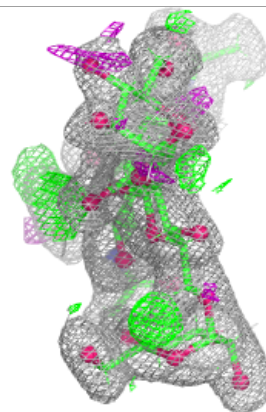
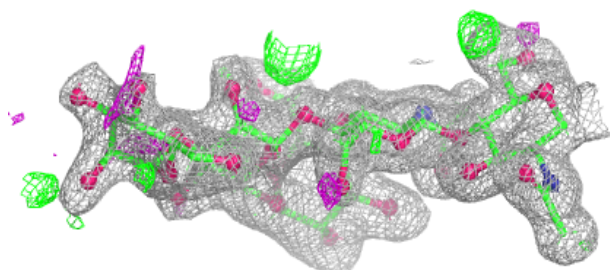
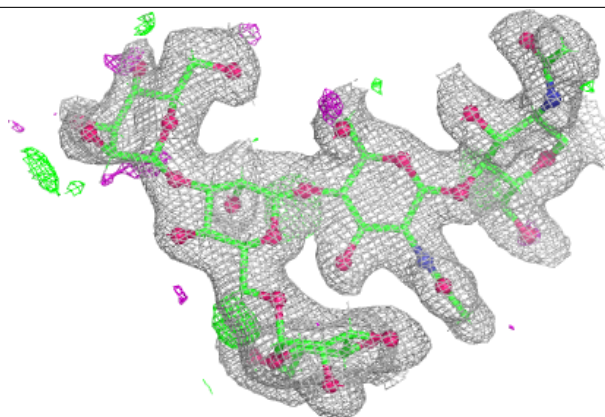
Electron density around Chain C:

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

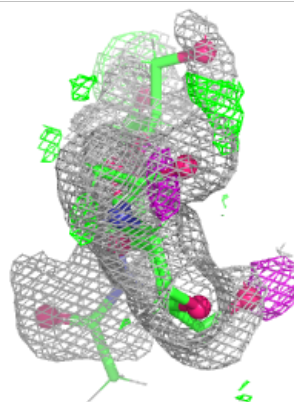
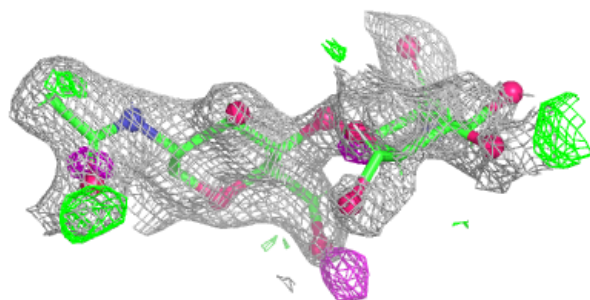
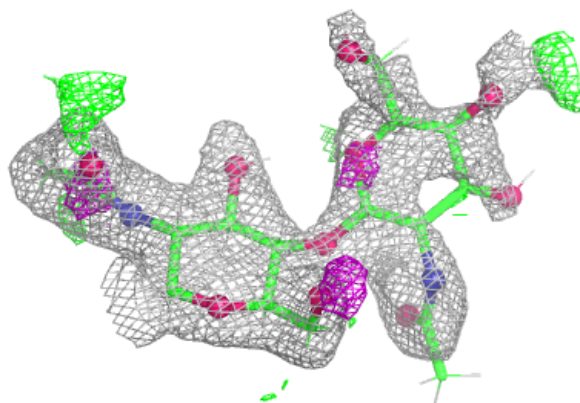


Electron density around Chain G:

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

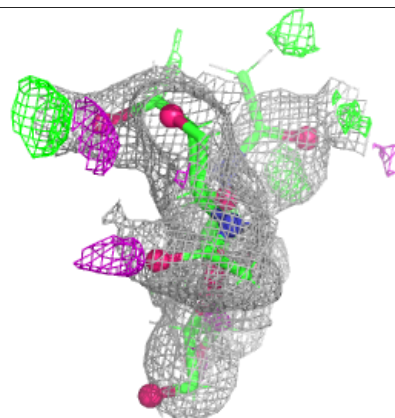
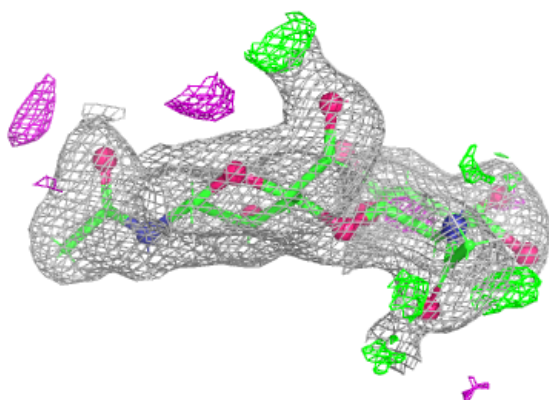
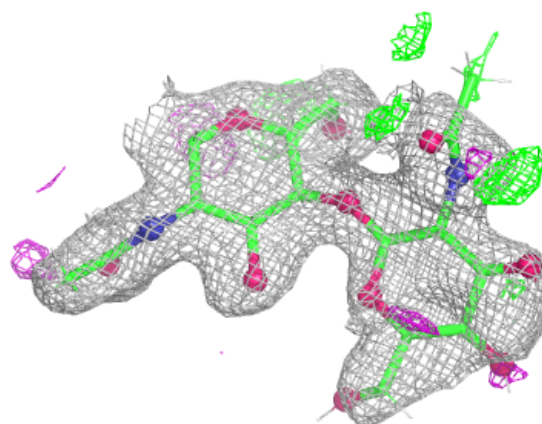
**Electron density around Chain D:**

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



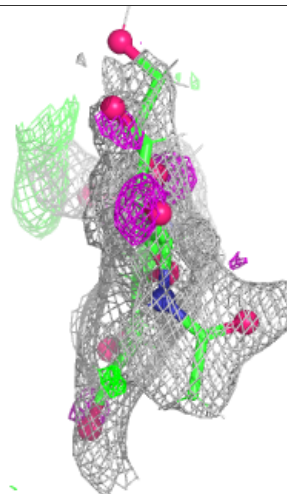
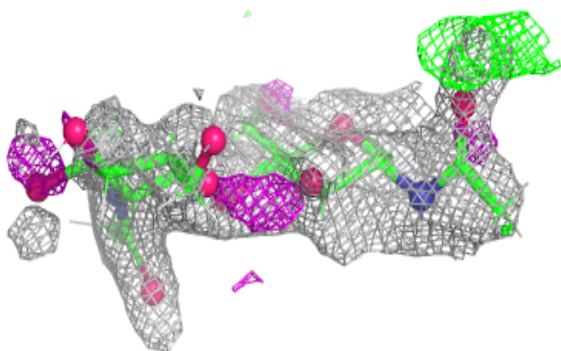
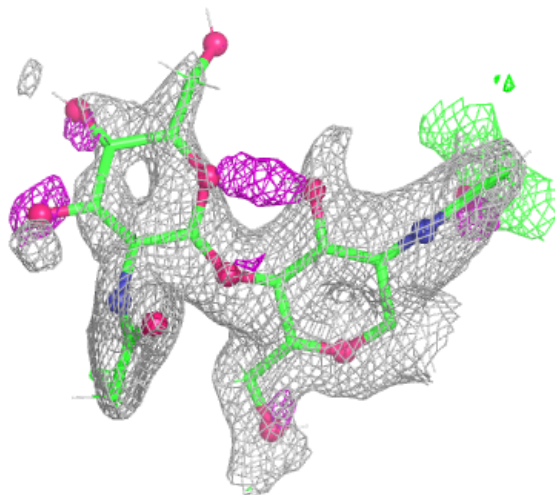
Electron density around Chain E:

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



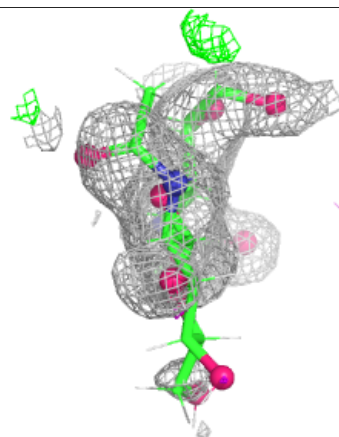
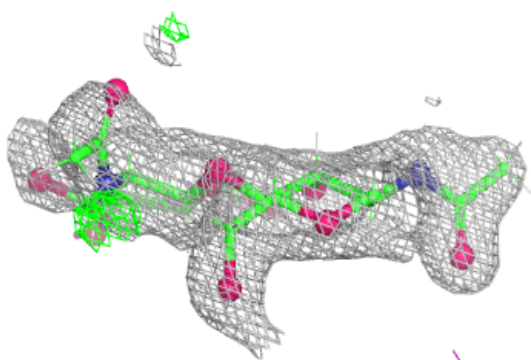
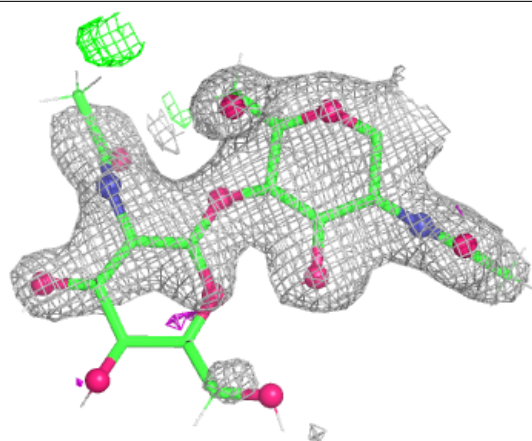
Electron density around Chain H:

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



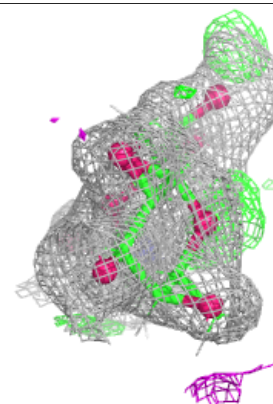
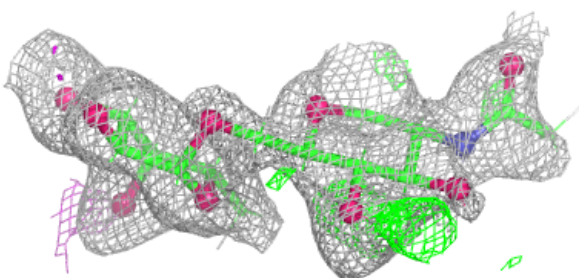
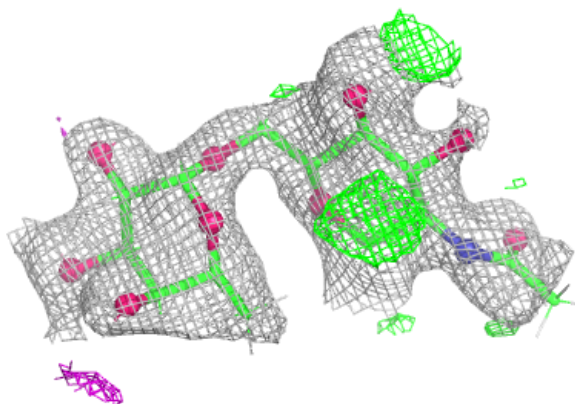
Electron density around Chain I:

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

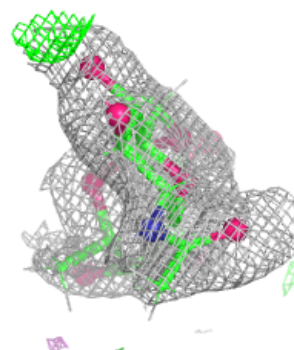
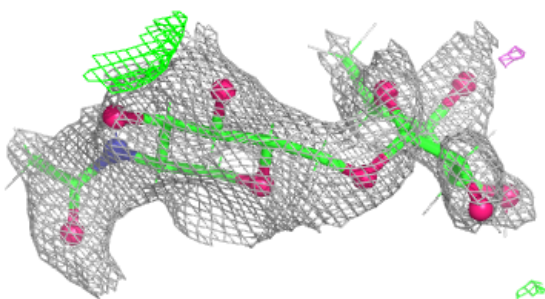
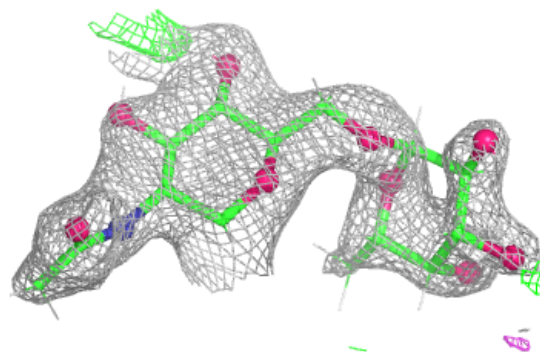


Electron density around Chain F:

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

**Electron density around Chain J:**

$2mF_o-DF_c$ (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
6	NAG	B	517	14/15	0.63	0.18	51,58,67,69	0
6	NAG	A	517	14/15	0.65	0.15	56,63,74,76	0
6	NAG	A	514	14/15	0.80	0.13	35,48,55,61	0
6	NAG	B	514	14/15	0.84	0.13	39,47,56,59	0
5	ZN	B	504	1/1	0.90	0.12	68,68,68,68	1
7	PG4	A	518	13/13	0.90	0.12	41,51,62,63	0
5	ZN	A	504	1/1	0.96	0.05	22,22,22,22	1
7	PG4	B	518	13/13	0.96	0.07	31,38,48,50	0
5	ZN	A	503	1/1	1.00	0.02	11,11,11,11	1
5	ZN	A	501	1/1	1.00	0.01	8,8,8,8	0
5	ZN	B	501	1/1	1.00	0.02	13,13,13,13	0
5	ZN	B	502	1/1	1.00	0.02	13,13,13,13	0
5	ZN	B	503	1/1	1.00	0.02	26,26,26,26	1
5	ZN	A	502	1/1	1.00	0.02	7,7,7,7	0

6.5 Other polymers [i](#)

There are no such residues in this entry.