



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:15 AM UTC

PDB ID : 8DPU / pdb_00008dpu
Title : The crystal structure of the IL-11 signalling complex
Authors : Metcalfe, R.D.; Aizel, K.; Griffin, M.D.W.
Deposited on : 2022-07-17
Resolution : 3.78 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
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

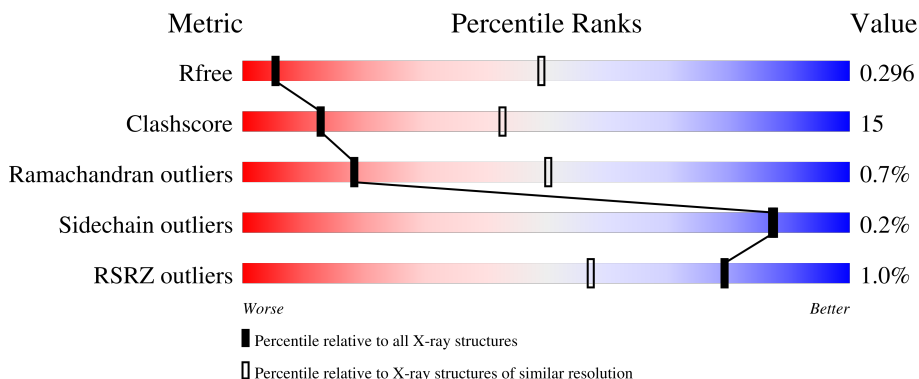
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.78 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.









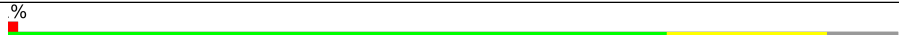
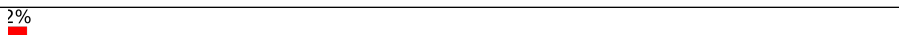
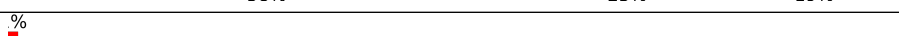
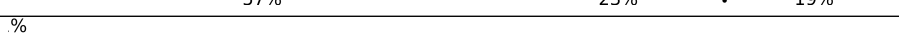
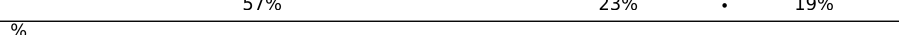
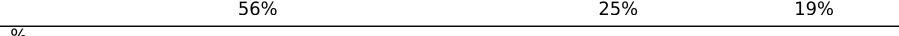


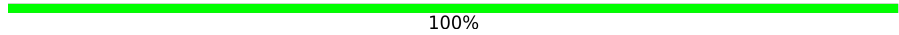
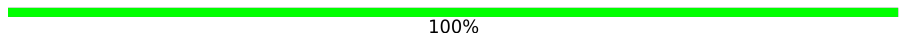
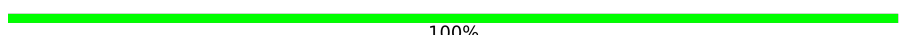
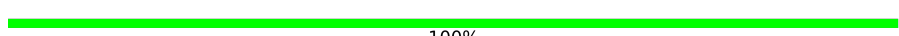


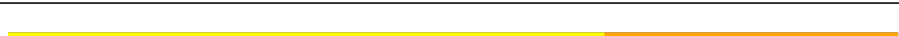




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1085 (3.94-3.62)
Clashscore	190562	1029 (3.92-3.64)
Ramachandran outliers	187476	1064 (3.94-3.62)
Sidechain outliers	187428	1059 (3.94-3.62)
RSRZ outliers	180081	1084 (3.94-3.62)

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	303	 62% 36% ..
1	D	303	 61% 36% ..
1	G	303	 61% 37% ..
1	J	303	 61% 36% ..
1	M	303	 61% 37% ..

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Mol	Chain	Length	Quality of chain
1	P	303	 60% 37% ..
2	B	179	 73% 19% 8%
2	E	179	 74% 17% 8% 2%
2	H	179	 74% 17% 8% 2%
2	K	179	 73% 18% 8% 2%
2	N	179	 73% 19% 8%
2	Q	179	 74% 18% 8%
3	C	348	 58% 23% 19% 2%
3	F	348	 57% 23% . 19%
3	I	348	 57% 23% . 19%
3	L	348	 56% 25% 19%
3	O	348	 58% 23% 19%
3	R	348	 57% 24% 19%
4	S	2	 100%
4	U	2	 100%
4	W	2	 100%
4	Y	2	 100%
4	a	2	 100%
4	c	2	 100%
5	T	3	 67% 33%
5	V	3	 67% 33%
5	X	3	 33% 67%
5	Z	3	 67% 33%
5	b	3	 67% 33%
5	d	3	 33% 67%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 35568 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 Interleukin-6 receptor subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	298	2394	1527	393	462	12	0	0	0
1	D	298	2394	1527	393	462	12	0	0	0
1	G	298	2394	1527	393	462	12	0	0	0
1	J	298	2394	1527	393	462	12	0	0	0
1	M	298	2394	1527	393	462	12	0	0	0
1	P	298	2394	1527	393	462	12	0	0	0

- Molecule 2 is a protein called Interleukin-11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	164	1255	797	237	219	2	0	0	0
2	E	164	1255	797	237	219	2	0	0	0
2	H	164	1255	797	237	219	2	0	0	0
2	K	164	1255	797	237	219	2	0	0	0
2	N	164	1255	797	237	219	2	0	0	0
2	Q	164	1255	797	237	219	2	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP P20809

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	GLY	-	expression tag	UNP P20809
H	0	GLY	-	expression tag	UNP P20809
K	0	GLY	-	expression tag	UNP P20809
N	0	GLY	-	expression tag	UNP P20809
Q	0	GLY	-	expression tag	UNP P20809

- Molecule 3 is a protein called Interleukin-11 receptor subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	283	Total	C	N	O	S	0	0	0
			2170	1380	379	403	8			
3	F	283	Total	C	N	O	S	0	0	0
			2170	1380	379	403	8			
3	I	283	Total	C	N	O	S	0	0	0
			2170	1380	379	403	8			
3	L	283	Total	C	N	O	S	0	0	0
			2170	1380	379	403	8			
3	O	283	Total	C	N	O	S	0	0	0
			2170	1380	379	403	8			
3	R	283	Total	C	N	O	S	0	0	0
			2170	1380	379	403	8			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	226	SER	CYS	engineered mutation	UNP Q14626
C	342	HIS	-	expression tag	UNP Q14626
C	343	HIS	-	expression tag	UNP Q14626
C	344	HIS	-	expression tag	UNP Q14626
C	345	HIS	-	expression tag	UNP Q14626
C	346	HIS	-	expression tag	UNP Q14626
C	347	HIS	-	expression tag	UNP Q14626
C	348	HIS	-	expression tag	UNP Q14626
F	226	SER	CYS	engineered mutation	UNP Q14626
F	342	HIS	-	expression tag	UNP Q14626
F	343	HIS	-	expression tag	UNP Q14626
F	344	HIS	-	expression tag	UNP Q14626
F	345	HIS	-	expression tag	UNP Q14626
F	346	HIS	-	expression tag	UNP Q14626
F	347	HIS	-	expression tag	UNP Q14626
F	348	HIS	-	expression tag	UNP Q14626
I	226	SER	CYS	engineered mutation	UNP Q14626

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Chain	Residue	Modelled	Actual	Comment	Reference
I	342	HIS	-	expression tag	UNP Q14626
I	343	HIS	-	expression tag	UNP Q14626
I	344	HIS	-	expression tag	UNP Q14626
I	345	HIS	-	expression tag	UNP Q14626
I	346	HIS	-	expression tag	UNP Q14626
I	347	HIS	-	expression tag	UNP Q14626
I	348	HIS	-	expression tag	UNP Q14626
L	226	SER	CYS	engineered mutation	UNP Q14626
L	342	HIS	-	expression tag	UNP Q14626
L	343	HIS	-	expression tag	UNP Q14626
L	344	HIS	-	expression tag	UNP Q14626
L	345	HIS	-	expression tag	UNP Q14626
L	346	HIS	-	expression tag	UNP Q14626
L	347	HIS	-	expression tag	UNP Q14626
L	348	HIS	-	expression tag	UNP Q14626
O	226	SER	CYS	engineered mutation	UNP Q14626
O	342	HIS	-	expression tag	UNP Q14626
O	343	HIS	-	expression tag	UNP Q14626
O	344	HIS	-	expression tag	UNP Q14626
O	345	HIS	-	expression tag	UNP Q14626
O	346	HIS	-	expression tag	UNP Q14626
O	347	HIS	-	expression tag	UNP Q14626
O	348	HIS	-	expression tag	UNP Q14626
R	226	SER	CYS	engineered mutation	UNP Q14626
R	342	HIS	-	expression tag	UNP Q14626
R	343	HIS	-	expression tag	UNP Q14626
R	344	HIS	-	expression tag	UNP Q14626
R	345	HIS	-	expression tag	UNP Q14626
R	346	HIS	-	expression tag	UNP Q14626
R	347	HIS	-	expression tag	UNP Q14626
R	348	HIS	-	expression tag	UNP Q14626

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



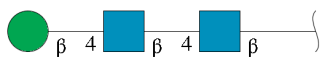
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	S	2	28	16	2	10	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	U	2	28	16	2	10	0	0	0
4	W	2	28	16	2	10	0	0	0
4	Y	2	28	16	2	10	0	0	0
4	a	2	28	16	2	10	0	0	0
4	c	2	28	16	2	10	0	0	0

- Molecule 5 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
			Total	C	N	O			
5	T	3	39	22	2	15	0	0	0
5	V	3	39	22	2	15	0	0	0
5	X	3	39	22	2	15	0	0	0
5	Z	3	39	22	2	15	0	0	0
5	b	3	39	22	2	15	0	0	0
5	d	3	39	22	2	15	0	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
6	A	1	Total 14	8	1	5	0	0
6	A	1	Total 14	8	1	5	0	0
6	C	1	Total 14	8	1	5	0	0
6	D	1	Total 14	8	1	5	0	0
6	D	1	Total 14	8	1	5	0	0
6	F	1	Total 14	8	1	5	0	0
6	G	1	Total 14	8	1	5	0	0
6	G	1	Total 14	8	1	5	0	0
6	I	1	Total 14	8	1	5	0	0
6	J	1	Total 14	8	1	5	0	0
6	J	1	Total 14	8	1	5	0	0
6	L	1	Total 14	8	1	5	0	0
6	M	1	Total 14	8	1	5	0	0
6	M	1	Total 14	8	1	5	0	0

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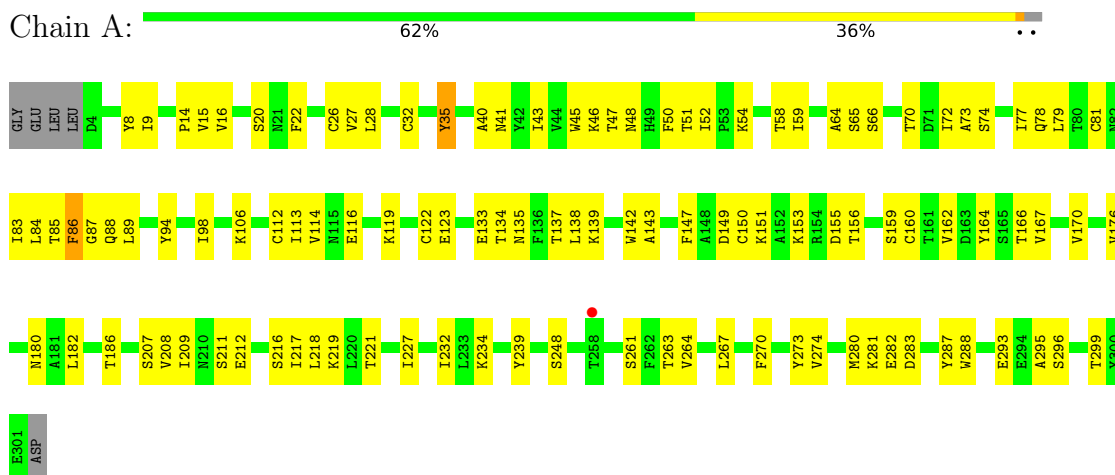
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	O	1	Total	C	N	O	0	0
			14	8	1	5		
6	P	1	Total	C	N	O	0	0
			14	8	1	5		
6	P	1	Total	C	N	O	0	0
			14	8	1	5		
6	R	1	Total	C	N	O	0	0
			14	8	1	5		

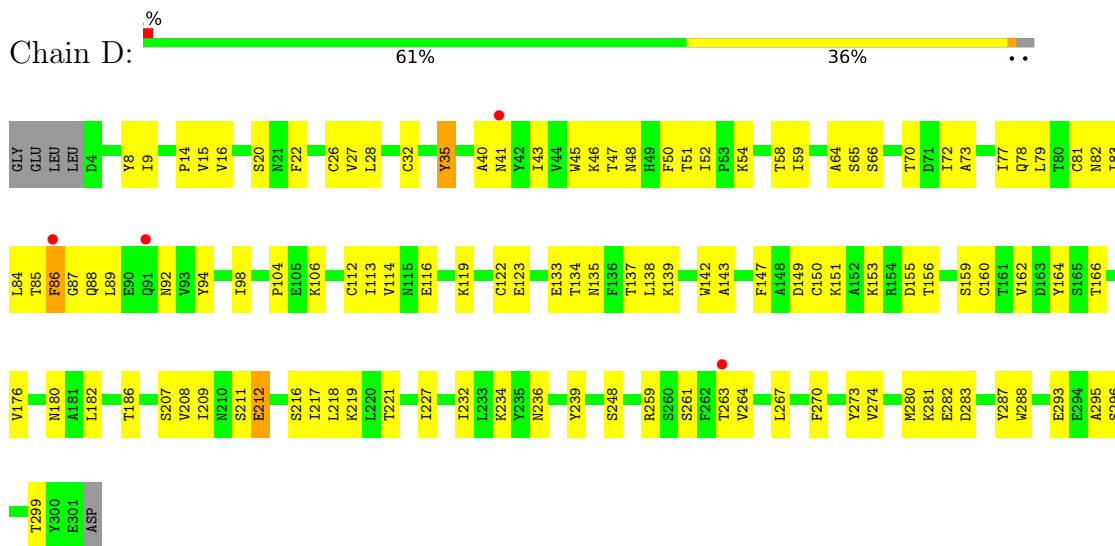
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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: Interleukin-6 receptor subunit beta



- Molecule 1: Interleukin-6 receptor subunit beta

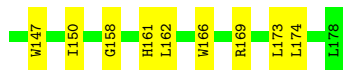
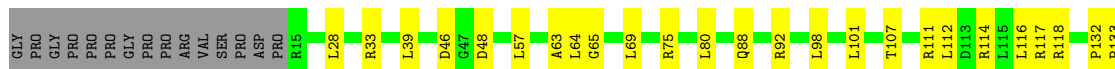


- Molecule 1: Interleukin-6 receptor subunit beta

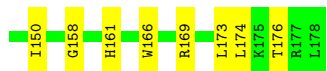
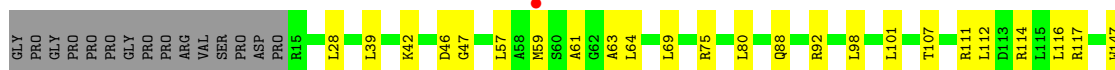
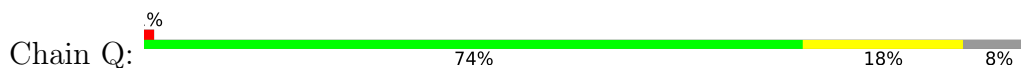




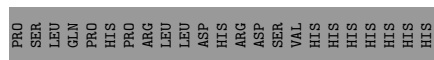
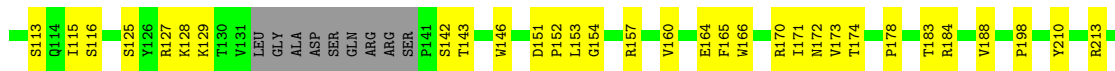
• Molecule 2: Interleukin-11



• Molecule 2: Interleukin-11

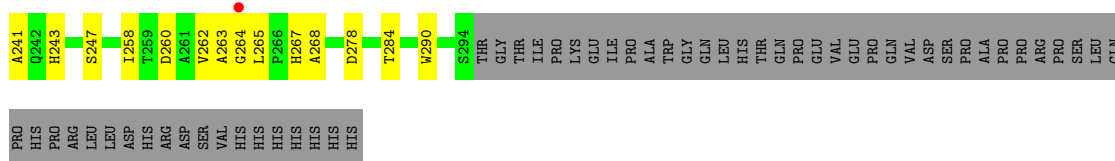


• Molecule 3: Interleukin-11 receptor subunit alpha

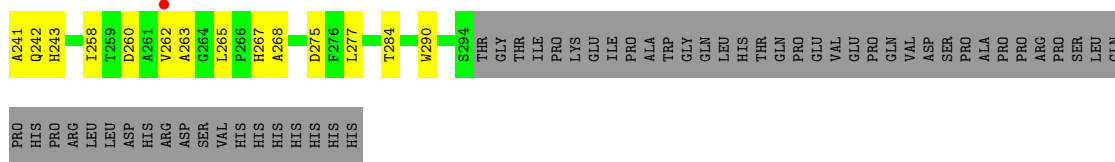
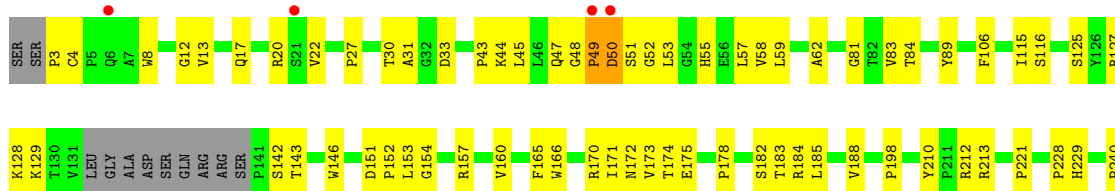


• Molecule 3: Interleukin-11 receptor subunit alpha

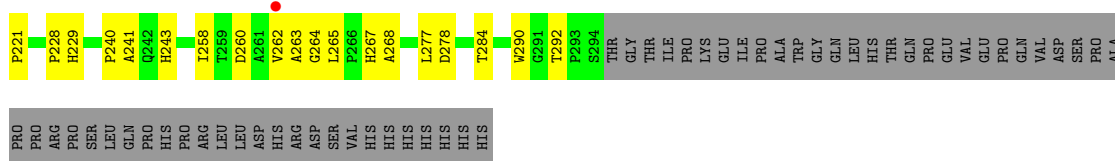
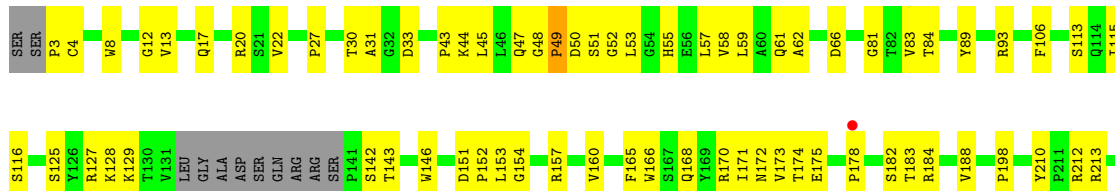




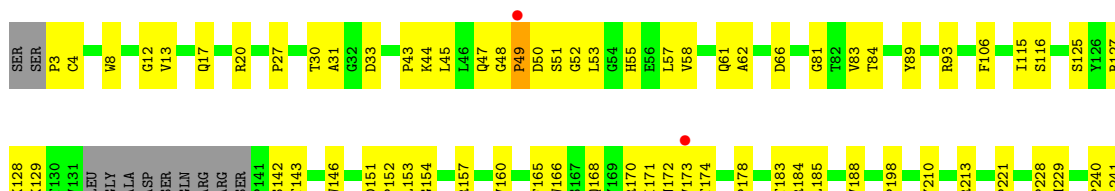
● Molecule 3: Interleukin-11 receptor subunit alpha

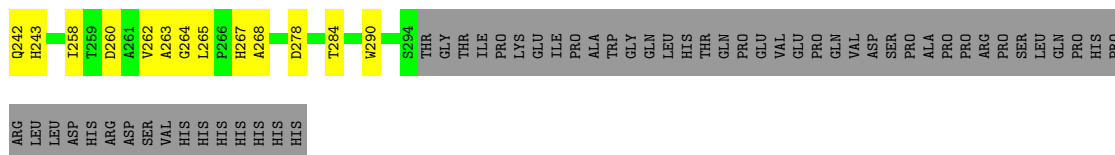


● Molecule 3: Interleukin-11 receptor subunit alpha

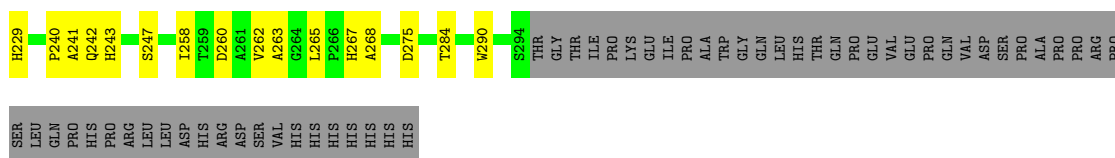
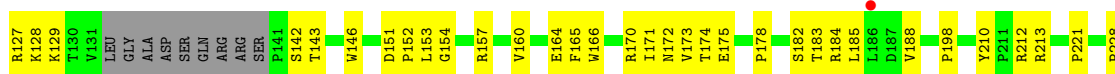
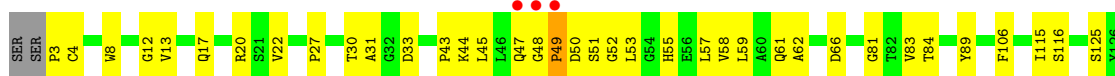


● Molecule 3: Interleukin-11 receptor subunit alpha





- Molecule 3: Interleukin-11 receptor subunit alpha



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



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



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



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



MAG1
MAG2


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

Chain a:  100%MAG1
MAG2

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

Chain c:  100%MAG1
MAG2


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

Chain T:  67% 33%MAG1
MAG2
BMA3

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

Chain V:  67% 33%MAG1
MAG2
BMA3

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

Chain X:  33% 67%MAG1
MAG2
BMA3

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


Chain Z:  67% 33%MAG1
MAG2
BMA3

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

Chain b:  67% 33%

MAG1
MAG2
BMA3

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

Chain d:  33% 67%

MAG1
MAG2
BMA3

4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α , β , γ	163.41Å 163.41Å 506.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.86 – 3.78 40.86 – 3.78	Depositor EDS
% Data completeness (in resolution range)	58.0 (40.86-3.78) 58.0 (40.86-3.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.29	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.77Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.276 , 0.295 0.277 , 0.296	Depositor DCC
R_{free} test set	2057 reflections (2.64%)	wwPDB-VP
Wilson B-factor (Å ²)	126.3	Xtrriage
Anisotropy	0.051	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 170.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.083 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	35568	wwPDB-VP
Average B, all atoms (Å ²)	175.0	wwPDB-VP

Xtrriage'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: BMA, NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.23	0/2457	0.71	3/3348 (0.1%)
1	D	0.23	0/2457	0.71	3/3348 (0.1%)
1	G	0.23	0/2457	0.71	3/3348 (0.1%)
1	J	0.23	0/2457	0.71	3/3348 (0.1%)
1	M	0.23	0/2457	0.71	3/3348 (0.1%)
1	P	0.23	0/2457	0.71	3/3348 (0.1%)
2	B	0.18	0/1280	0.58	0/1743
2	E	0.18	0/1280	0.58	0/1743
2	H	0.18	0/1280	0.58	0/1743
2	K	0.18	0/1280	0.58	0/1743
2	N	0.18	0/1280	0.58	0/1743
2	Q	0.18	0/1280	0.58	0/1743
3	C	0.31	1/2245 (0.0%)	0.68	7/3085 (0.2%)
3	F	0.31	1/2245 (0.0%)	0.68	7/3085 (0.2%)
3	I	0.31	1/2245 (0.0%)	0.68	7/3085 (0.2%)
3	L	0.31	1/2245 (0.0%)	0.68	7/3085 (0.2%)
3	O	0.31	1/2245 (0.0%)	0.68	7/3085 (0.2%)
3	R	0.31	1/2245 (0.0%)	0.68	7/3085 (0.2%)
All	All	0.25	6/35892 (0.0%)	0.67	60/49056 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	51	SER	N-CA	6.10	1.54	1.46
3	L	51	SER	N-CA	6.10	1.54	1.46
3	C	51	SER	N-CA	6.06	1.54	1.46
3	O	51	SER	N-CA	6.05	1.53	1.46
3	R	51	SER	N-CA	6.05	1.53	1.46

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	O	51	SER	N-CA-C	9.19	130.38	110.80
3	F	51	SER	N-CA-C	9.19	130.38	110.80
3	C	51	SER	N-CA-C	9.19	130.37	110.80
3	L	51	SER	N-CA-C	9.19	130.37	110.80
3	R	51	SER	N-CA-C	9.19	130.36	110.80

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	2394	0	2322	99	0
1	D	2394	0	2322	105	0
1	G	2394	0	2322	92	0
1	J	2394	0	2322	94	0
1	M	2394	0	2322	103	0
1	P	2394	0	2322	101	0
2	B	1255	0	1329	37	0
2	E	1255	0	1329	22	0
2	H	1255	0	1329	31	0
2	K	1255	0	1329	29	0
2	N	1255	0	1329	32	0
2	Q	1255	0	1329	31	0
3	C	2170	0	2082	65	0
3	F	2170	0	2082	70	9
3	I	2170	0	2082	67	1
3	L	2170	0	2082	70	0
3	O	2170	0	2082	70	0
3	R	2170	0	2082	72	0
4	S	28	0	25	0	0
4	U	28	0	25	0	0
4	W	28	0	25	0	0
4	Y	28	0	25	0	0
4	a	28	0	25	0	0
4	c	28	0	25	0	0
5	T	39	0	34	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	V	39	0	34	2	0
5	X	39	0	34	1	0
5	Z	39	0	34	2	0
5	b	39	0	34	2	0
5	d	39	0	34	1	0
6	A	28	0	26	4	0
6	C	14	0	13	1	0
6	D	28	0	26	4	0
6	F	14	0	13	0	0
6	G	28	0	26	4	0
6	I	14	0	13	0	0
6	J	28	0	26	4	0
6	L	14	0	13	0	0
6	M	28	0	26	4	0
6	O	14	0	13	0	0
6	P	28	0	26	4	0
6	R	14	0	13	0	0
All	All	35568	0	34986	1062	10

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 15.

The worst 5 of 1062 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:263:THR:HG22	3:C:260:ASP:HB2	1.39	1.04
3:C:93:ARG:HD2	1:D:88:GLN:HE21	1.23	1.02
3:C:93:ARG:HD2	1:D:88:GLN:NE2	1.78	0.98
2:B:46:ASP:HB3	1:D:92:ASN:HB2	1.51	0.91
1:A:170:VAL:HG12	2:B:118:ARG:HH21	1.34	0.90

The worst 5 of 10 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)
3:F:49:PRO:O	3:F:52:GLY:N[5_655]	1.26	0.94
3:F:50:ASP:N	3:F:50:ASP:O[5_655]	1.39	0.81
3:F:48:GLY:O	3:F:51:SER:N[5_655]	1.62	0.58
3:F:49:PRO:C	3:F:50:ASP:O[5_655]	1.64	0.56
3:F:48:GLY:O	3:F:50:ASP:C[5_655]	1.77	0.43

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	296/303 (98%)	278 (94%)	15 (5%)	3 (1%)	12	42
1	D	296/303 (98%)	279 (94%)	14 (5%)	3 (1%)	12	42
1	G	296/303 (98%)	278 (94%)	15 (5%)	3 (1%)	12	42
1	J	296/303 (98%)	278 (94%)	15 (5%)	3 (1%)	12	42
1	M	296/303 (98%)	279 (94%)	14 (5%)	3 (1%)	12	42
1	P	296/303 (98%)	278 (94%)	15 (5%)	3 (1%)	12	42
2	B	162/179 (90%)	157 (97%)	4 (2%)	1 (1%)	21	53
2	E	162/179 (90%)	157 (97%)	4 (2%)	1 (1%)	21	53
2	H	162/179 (90%)	157 (97%)	4 (2%)	1 (1%)	21	53
2	K	162/179 (90%)	157 (97%)	4 (2%)	1 (1%)	21	53
2	N	162/179 (90%)	157 (97%)	4 (2%)	1 (1%)	21	53
2	Q	162/179 (90%)	157 (97%)	4 (2%)	1 (1%)	21	53
3	C	279/348 (80%)	260 (93%)	18 (6%)	1 (0%)	30	61
3	F	279/348 (80%)	260 (93%)	18 (6%)	1 (0%)	30	61
3	I	279/348 (80%)	260 (93%)	18 (6%)	1 (0%)	30	61
3	L	279/348 (80%)	260 (93%)	18 (6%)	1 (0%)	30	61
3	O	279/348 (80%)	260 (93%)	18 (6%)	1 (0%)	30	61
3	R	279/348 (80%)	260 (93%)	18 (6%)	1 (0%)	30	61
All	All	4422/4980 (89%)	4172 (94%)	220 (5%)	30 (1%)	18	50

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	86	PHE
1	D	86	PHE
1	G	86	PHE
1	J	86	PHE

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Mol	Chain	Res	Type
1	M	86	PHE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	275/279 (99%)	274 (100%)	1 (0%)	84	83
1	D	275/279 (99%)	274 (100%)	1 (0%)	84	83
1	G	275/279 (99%)	274 (100%)	1 (0%)	84	83
1	J	275/279 (99%)	274 (100%)	1 (0%)	84	83
1	M	275/279 (99%)	274 (100%)	1 (0%)	84	83
1	P	275/279 (99%)	274 (100%)	1 (0%)	84	83
2	B	132/144 (92%)	132 (100%)	0	100	100
2	E	132/144 (92%)	132 (100%)	0	100	100
2	H	132/144 (92%)	132 (100%)	0	100	100
2	K	132/144 (92%)	132 (100%)	0	100	100
2	N	132/144 (92%)	132 (100%)	0	100	100
2	Q	132/144 (92%)	132 (100%)	0	100	100
3	C	234/293 (80%)	234 (100%)	0	100	100
3	F	234/293 (80%)	234 (100%)	0	100	100
3	I	234/293 (80%)	234 (100%)	0	100	100
3	L	234/293 (80%)	234 (100%)	0	100	100
3	O	234/293 (80%)	234 (100%)	0	100	100
3	R	234/293 (80%)	234 (100%)	0	100	100
All	All	3846/4296 (90%)	3840 (100%)	6 (0%)	87	87

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	160	CYS

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Mol	Chain	Res	Type
1	M	160	CYS
1	P	160	CYS
1	D	160	CYS
1	A	160	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	49	HIS
1	M	265	GLN
3	L	161	HIS
1	M	37	HIS
3	O	161	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

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	$\# Z > 2$
4	NAG	S	1	1,4	14,14,15	0.37	0	17,19,21	0.52	0
4	NAG	S	2	4	14,14,15	0.39	0	17,19,21	0.45	0
5	NAG	T	1	5,3	14,14,15	0.51	0	17,19,21	0.79	0
5	NAG	T	2	5	14,14,15	0.34	0	17,19,21	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BMA	T	3	5	11,11,12	1.61	3 (27%)	15,15,17	0.94	0
4	NAG	U	1	1,4	14,14,15	0.37	0	17,19,21	0.52	0
4	NAG	U	2	4	14,14,15	0.39	0	17,19,21	0.45	0
5	NAG	V	1	5,3	14,14,15	0.51	0	17,19,21	0.79	0
5	NAG	V	2	5	14,14,15	0.34	0	17,19,21	0.54	0
5	BMA	V	3	5	11,11,12	1.61	3 (27%)	15,15,17	0.94	0
4	NAG	W	1	1,4	14,14,15	0.37	0	17,19,21	0.52	0
4	NAG	W	2	4	14,14,15	0.39	0	17,19,21	0.45	0
5	NAG	X	1	5,3	14,14,15	0.51	0	17,19,21	0.79	0
5	NAG	X	2	5	14,14,15	0.34	0	17,19,21	0.54	0
5	BMA	X	3	5	11,11,12	1.61	3 (27%)	15,15,17	0.94	0
4	NAG	Y	1	1,4	14,14,15	0.37	0	17,19,21	0.52	0
4	NAG	Y	2	4	14,14,15	0.39	0	17,19,21	0.45	0
5	NAG	Z	1	5,3	14,14,15	0.51	0	17,19,21	0.79	0
5	NAG	Z	2	5	14,14,15	0.34	0	17,19,21	0.54	0
5	BMA	Z	3	5	11,11,12	1.61	3 (27%)	15,15,17	0.94	0
4	NAG	a	1	1,4	14,14,15	0.37	0	17,19,21	0.52	0
4	NAG	a	2	4	14,14,15	0.39	0	17,19,21	0.45	0
5	NAG	b	1	5,3	14,14,15	0.51	0	17,19,21	0.79	0
5	NAG	b	2	5	14,14,15	0.34	0	17,19,21	0.54	0
5	BMA	b	3	5	11,11,12	1.61	3 (27%)	15,15,17	0.94	0
4	NAG	c	1	1,4	14,14,15	0.37	0	17,19,21	0.52	0
4	NAG	c	2	4	14,14,15	0.39	0	17,19,21	0.45	0
5	NAG	d	1	5,3	14,14,15	0.51	0	17,19,21	0.79	0
5	NAG	d	2	5	14,14,15	0.34	0	17,19,21	0.54	0
5	BMA	d	3	5	11,11,12	1.61	3 (27%)	15,15,17	0.94	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
4	NAG	S	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	2/6/23/26	0/1/1/1
5	NAG	T	1	5,3	-	3/6/23/26	0/1/1/1
5	NAG	T	2	5	-	2/6/23/26	0/1/1/1
5	BMA	T	3	5	-	0/2/19/22	0/1/1/1
4	NAG	U	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	U	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	V	1	5,3	-	3/6/23/26	0/1/1/1
5	NAG	V	2	5	-	2/6/23/26	0/1/1/1
5	BMA	V	3	5	-	0/2/19/22	0/1/1/1
4	NAG	W	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	W	2	4	-	2/6/23/26	0/1/1/1
5	NAG	X	1	5,3	-	3/6/23/26	0/1/1/1
5	NAG	X	2	5	-	2/6/23/26	0/1/1/1
5	BMA	X	3	5	-	0/2/19/22	0/1/1/1
4	NAG	Y	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	Y	2	4	-	2/6/23/26	0/1/1/1
5	NAG	Z	1	5,3	-	3/6/23/26	0/1/1/1
5	NAG	Z	2	5	-	2/6/23/26	0/1/1/1
5	BMA	Z	3	5	-	0/2/19/22	0/1/1/1
4	NAG	a	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	a	2	4	-	2/6/23/26	0/1/1/1
5	NAG	b	1	5,3	-	3/6/23/26	0/1/1/1
5	NAG	b	2	5	-	2/6/23/26	0/1/1/1
5	BMA	b	3	5	-	0/2/19/22	0/1/1/1
4	NAG	c	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	c	2	4	-	2/6/23/26	0/1/1/1
5	NAG	d	1	5,3	-	3/6/23/26	0/1/1/1
5	NAG	d	2	5	-	2/6/23/26	0/1/1/1
5	BMA	d	3	5	-	0/2/19/22	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	d	3	BMA	C4-C5	3.24	1.59	1.53
5	X	3	BMA	C4-C5	3.24	1.59	1.53
5	Z	3	BMA	C4-C5	3.24	1.59	1.53
5	T	3	BMA	C4-C5	3.24	1.59	1.53
5	V	3	BMA	C4-C5	3.24	1.59	1.53

There are no bond angle outliers.

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

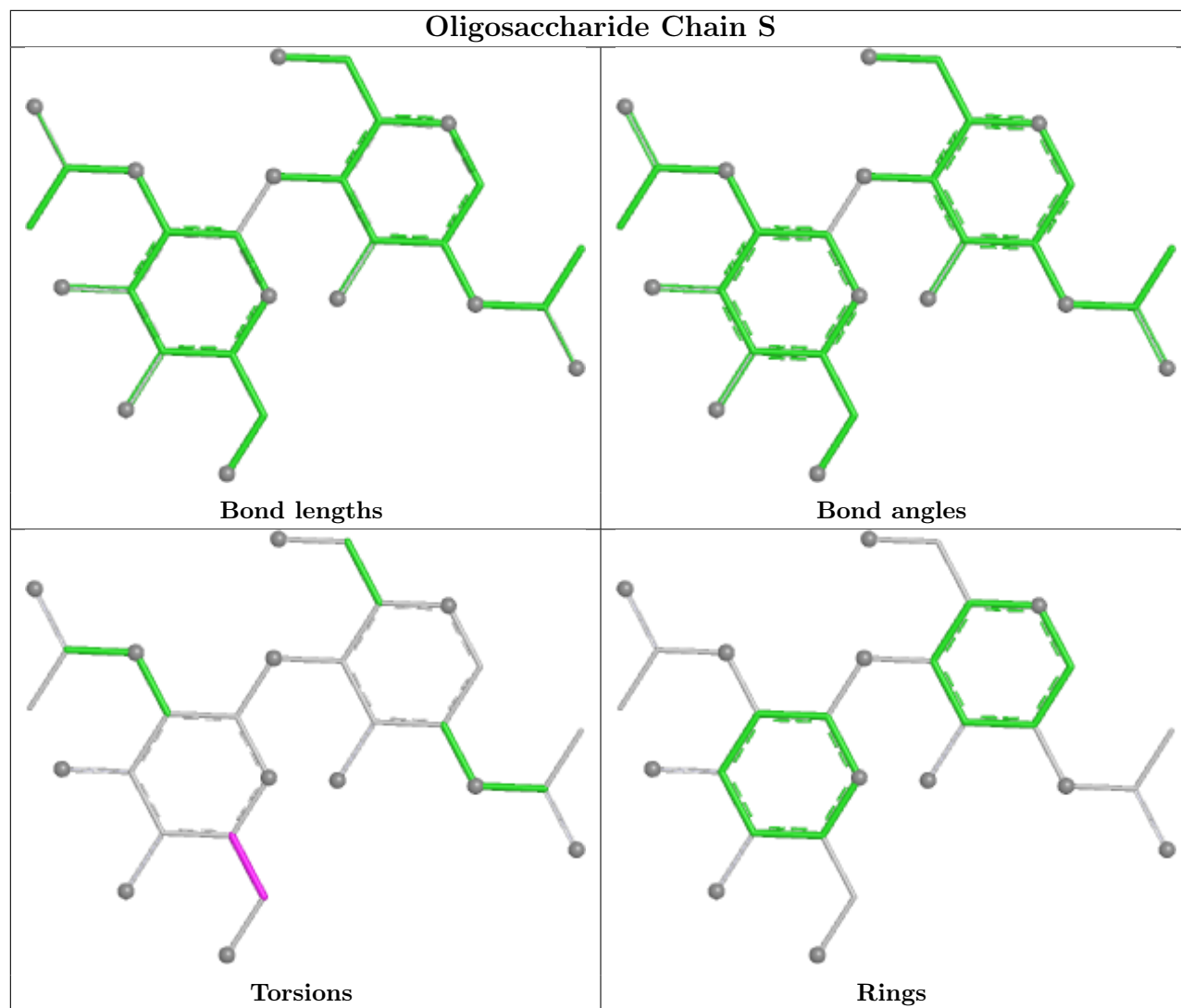
Mol	Chain	Res	Type	Atoms
4	S	2	NAG	O5-C5-C6-O6
4	U	2	NAG	O5-C5-C6-O6
4	W	2	NAG	O5-C5-C6-O6
4	Y	2	NAG	O5-C5-C6-O6
4	a	2	NAG	O5-C5-C6-O6

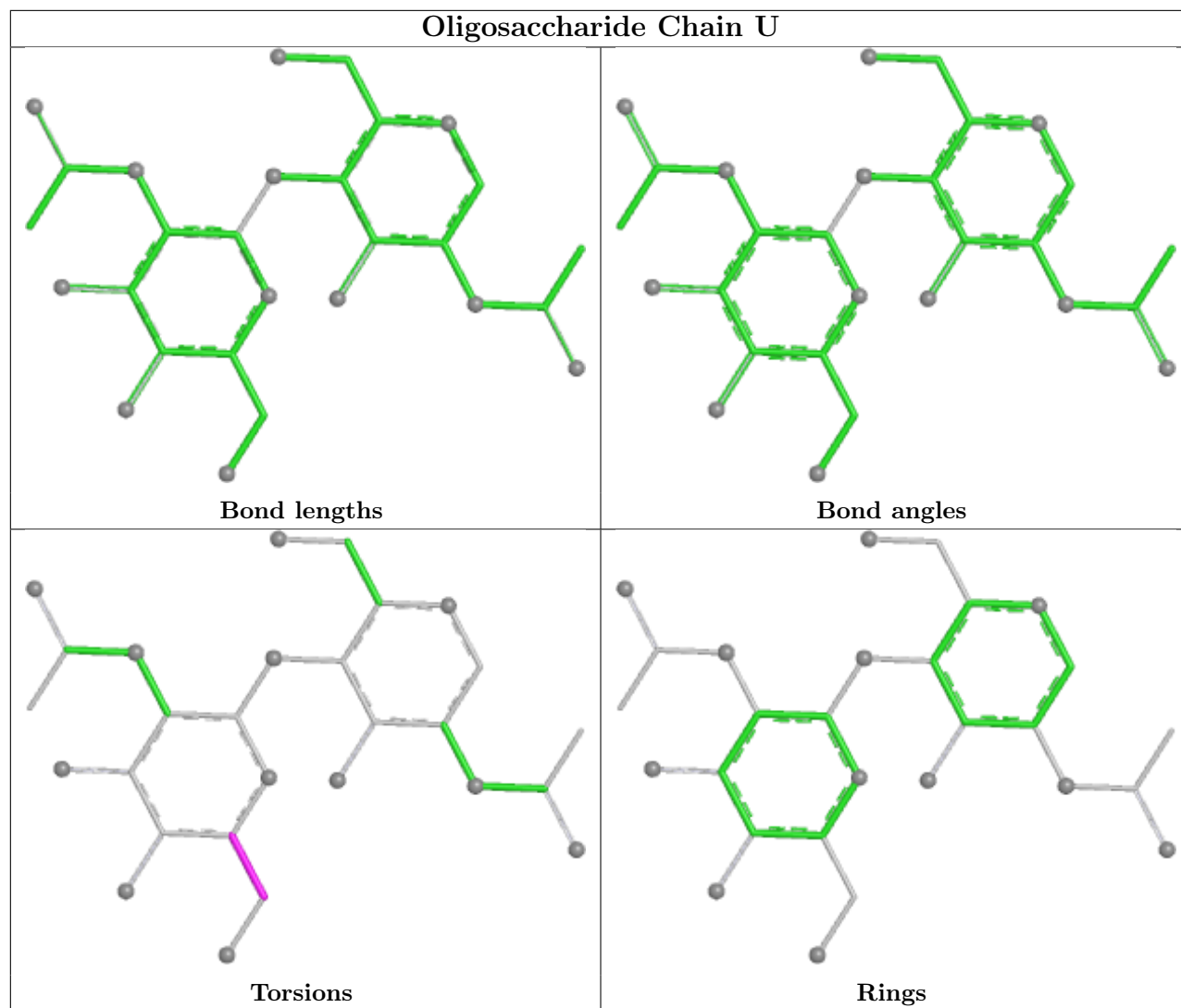
There are no ring outliers.

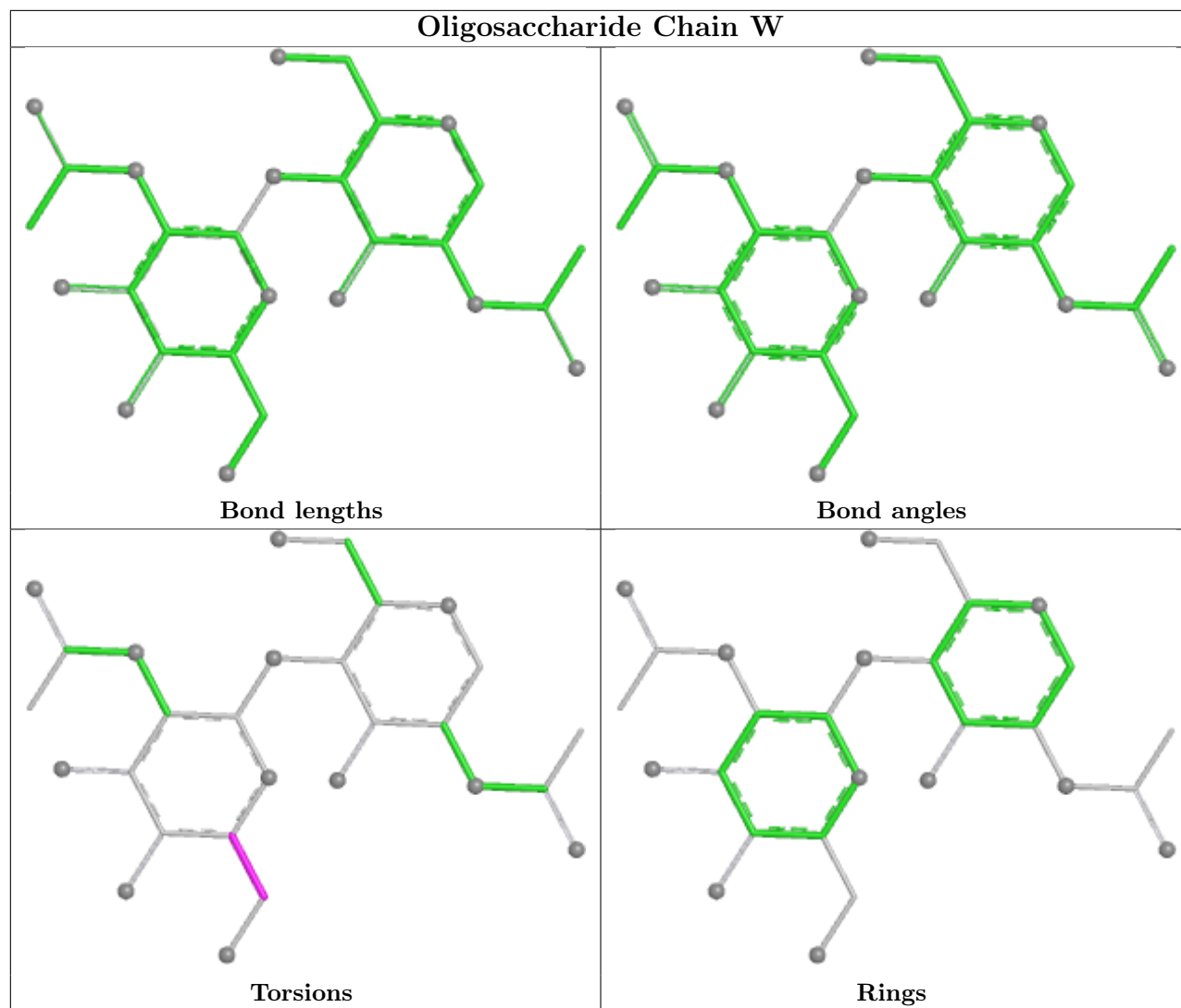
14 monomers are involved in 10 short contacts:

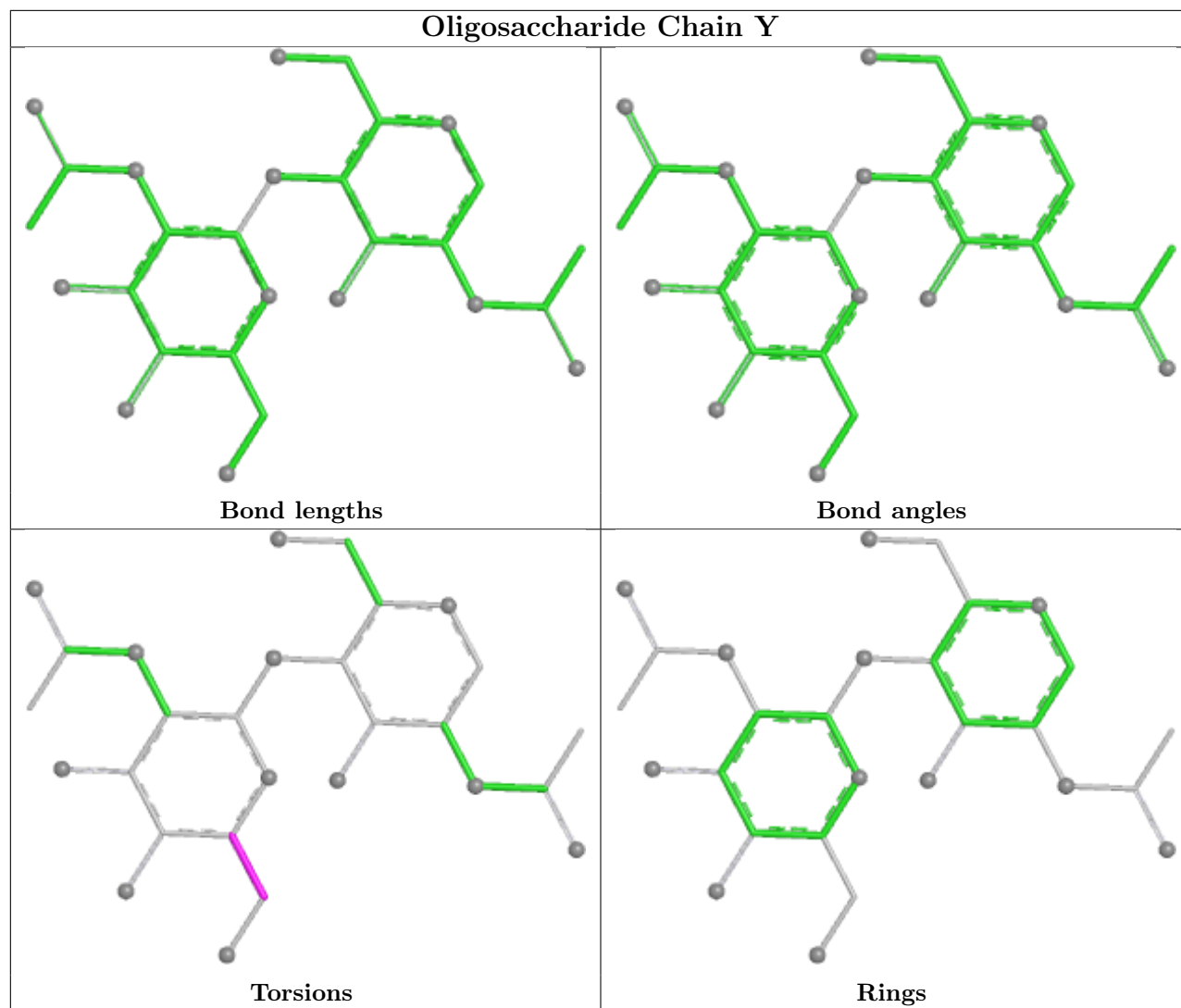
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	T	2	NAG	1	0
5	X	1	NAG	1	0
5	d	1	NAG	1	0
5	Z	3	BMA	1	0
5	T	3	BMA	1	0
5	b	1	NAG	1	0
5	Z	2	NAG	1	0
5	V	2	NAG	1	0
5	b	2	NAG	1	0
5	V	3	BMA	1	0
5	T	1	NAG	1	0
5	V	1	NAG	1	0
5	Z	1	NAG	1	0
5	b	3	BMA	1	0

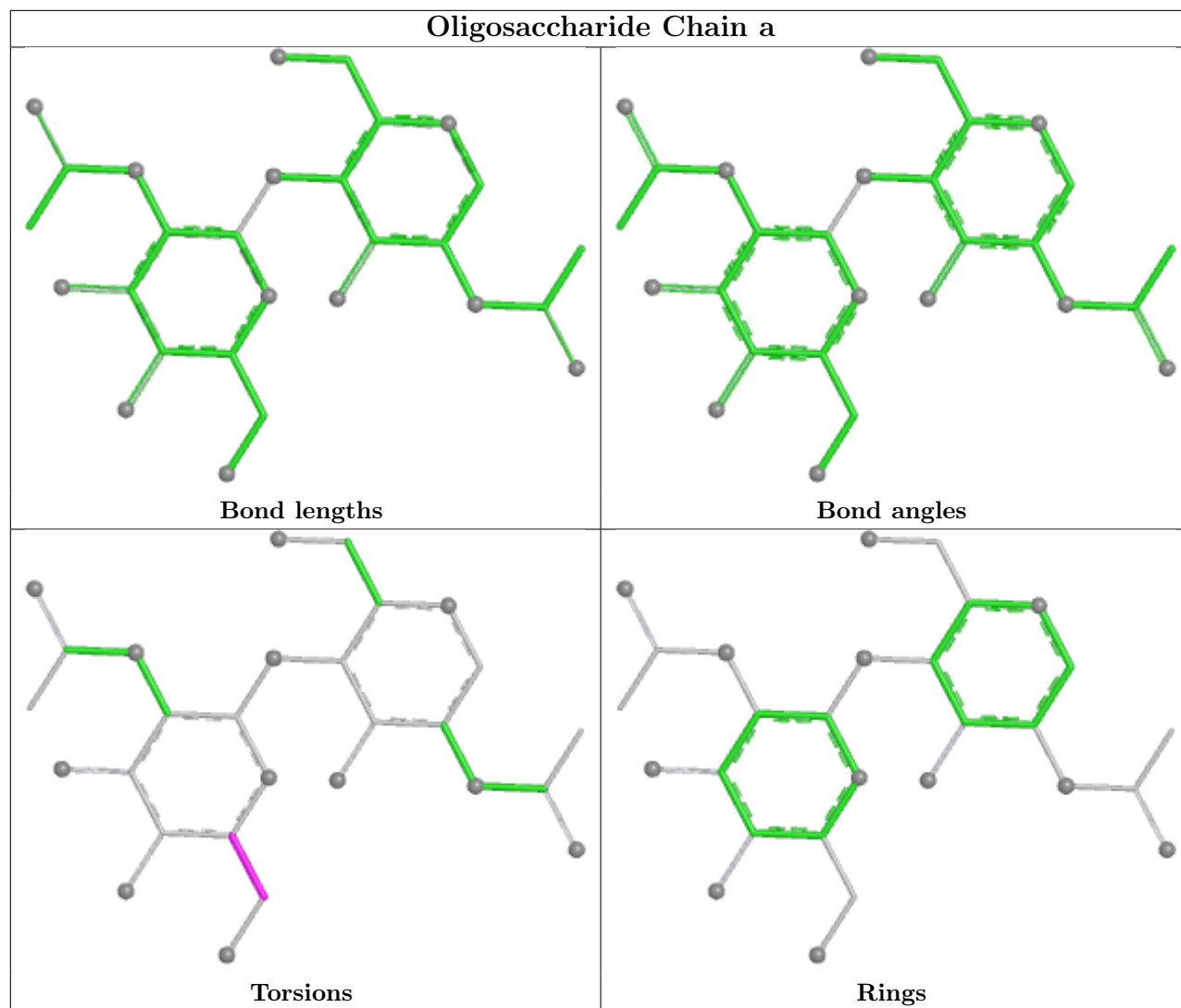
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

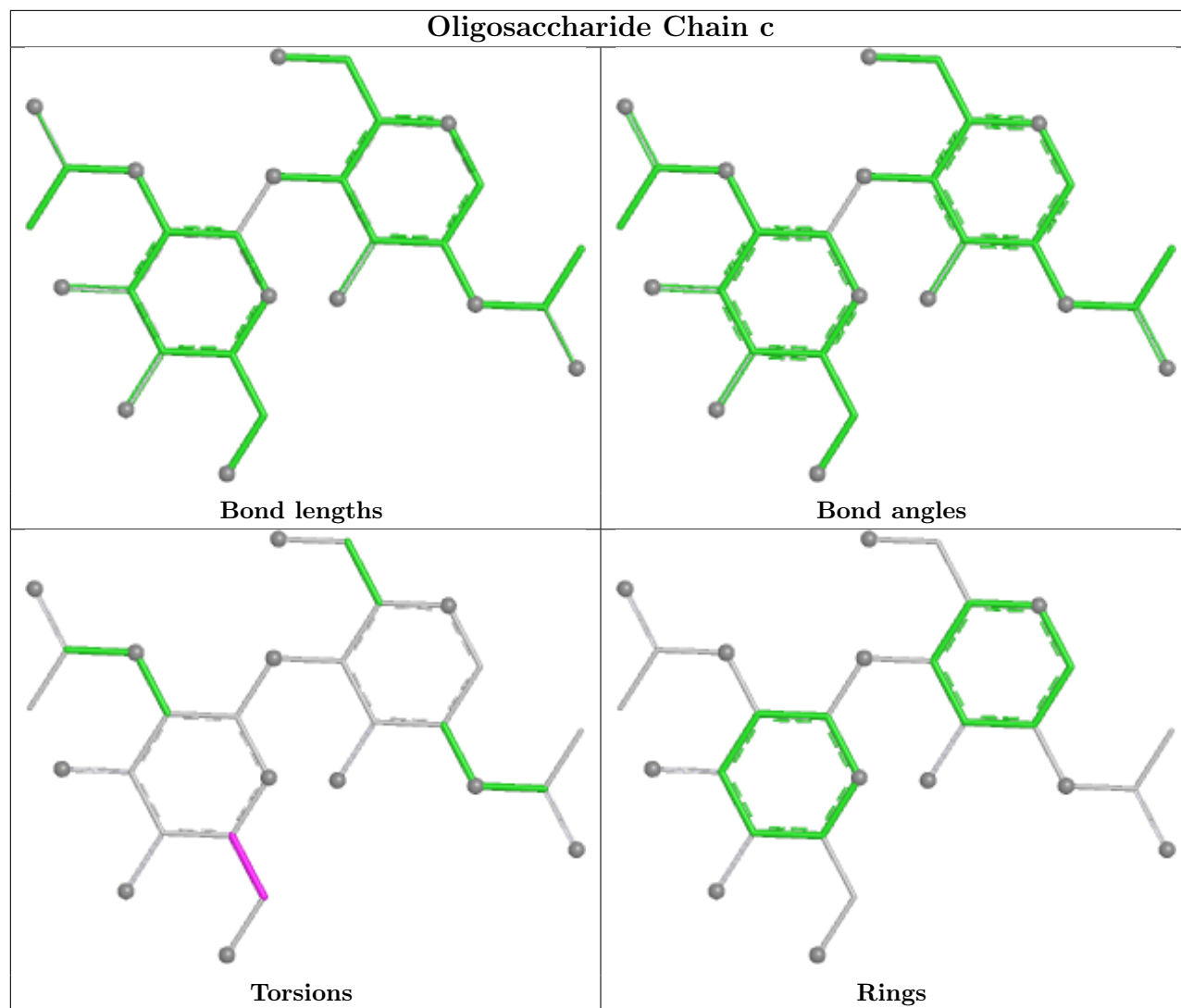


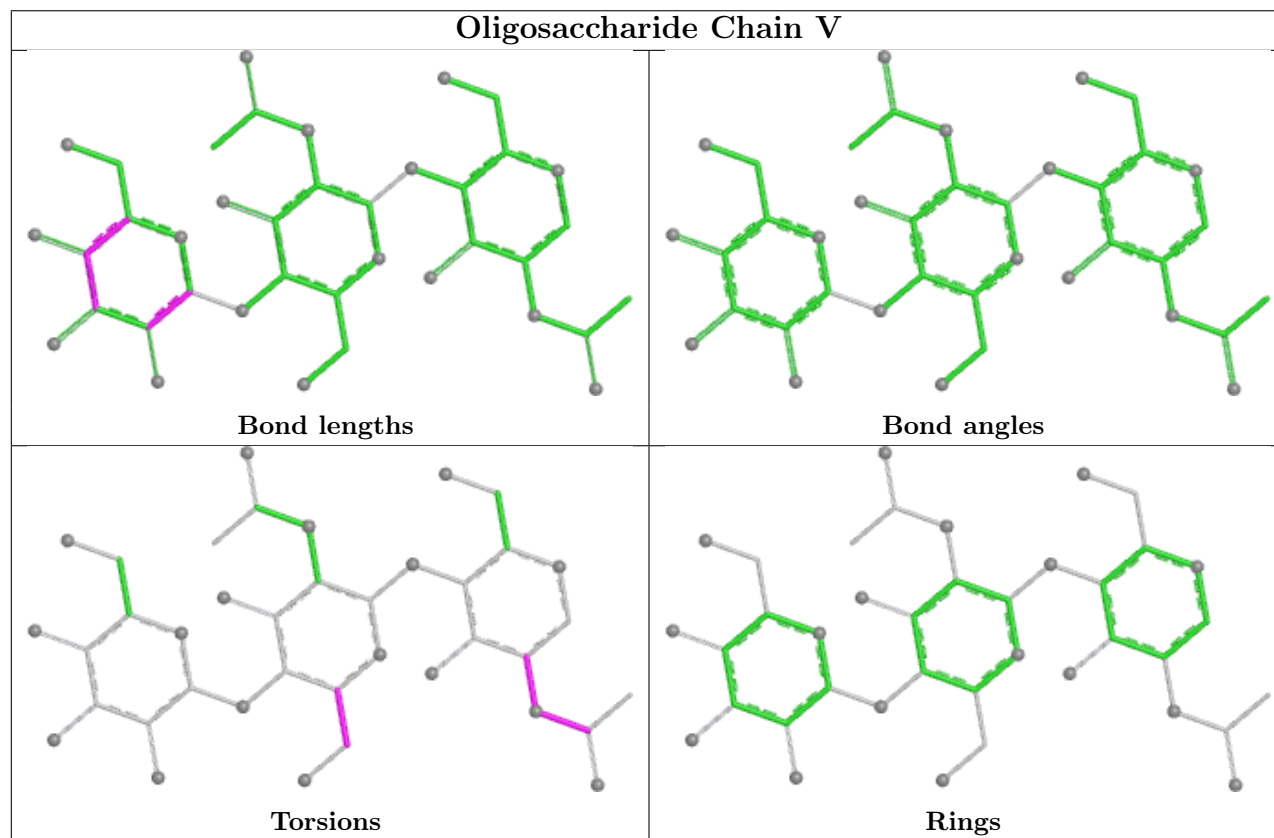
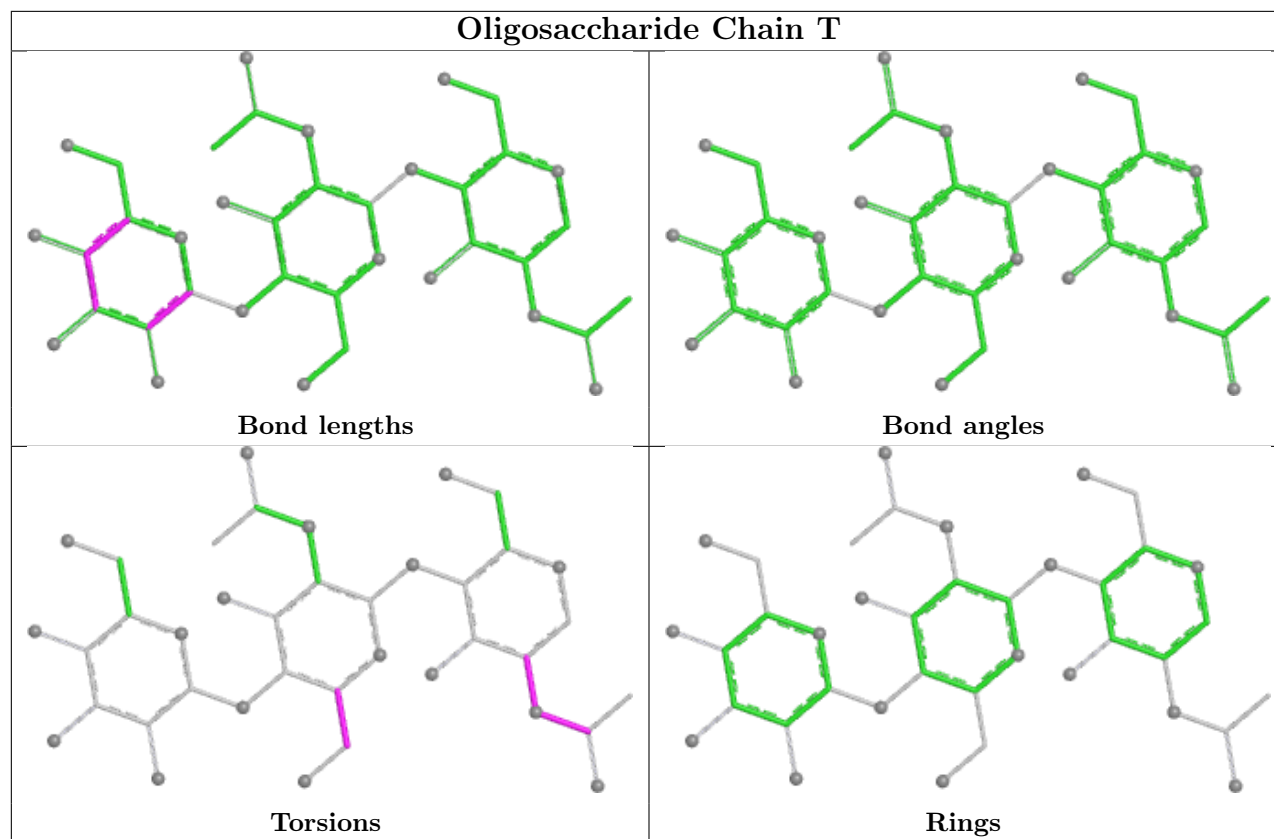


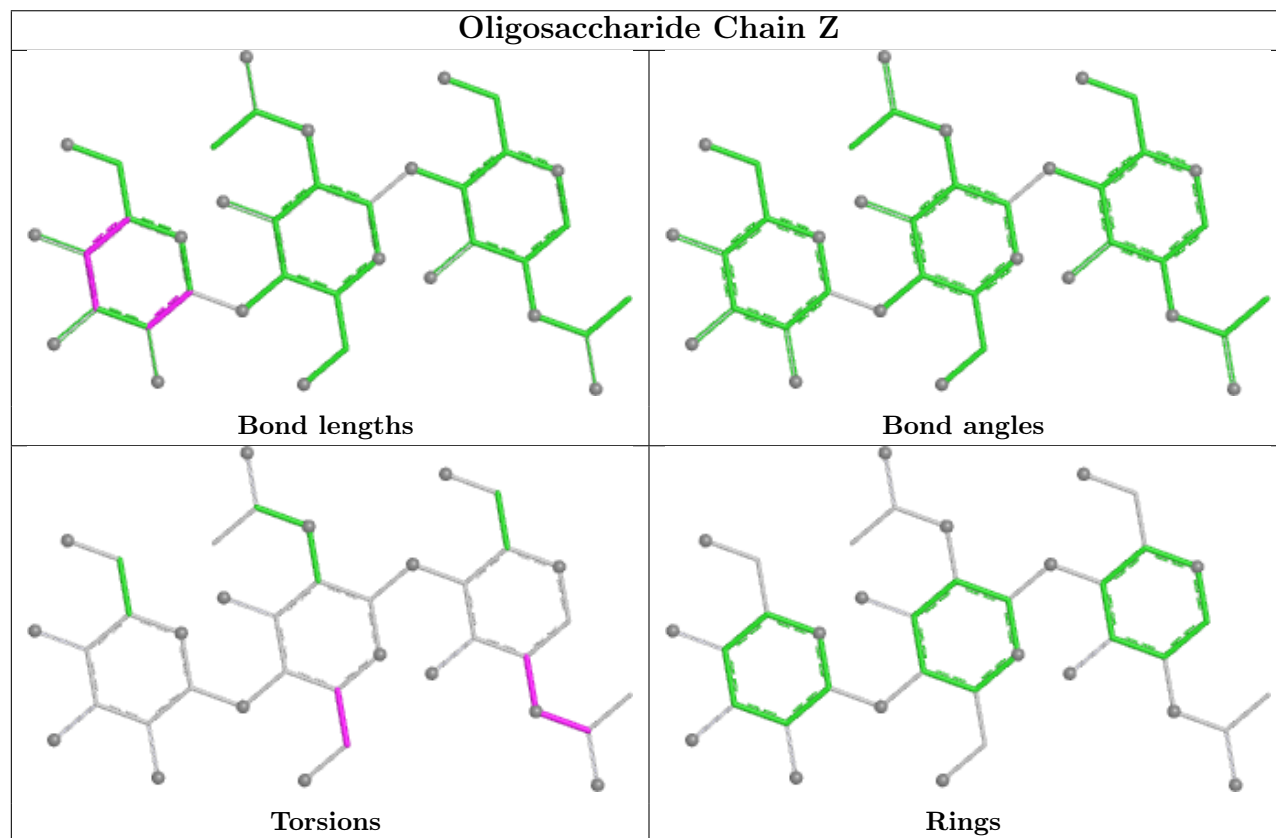
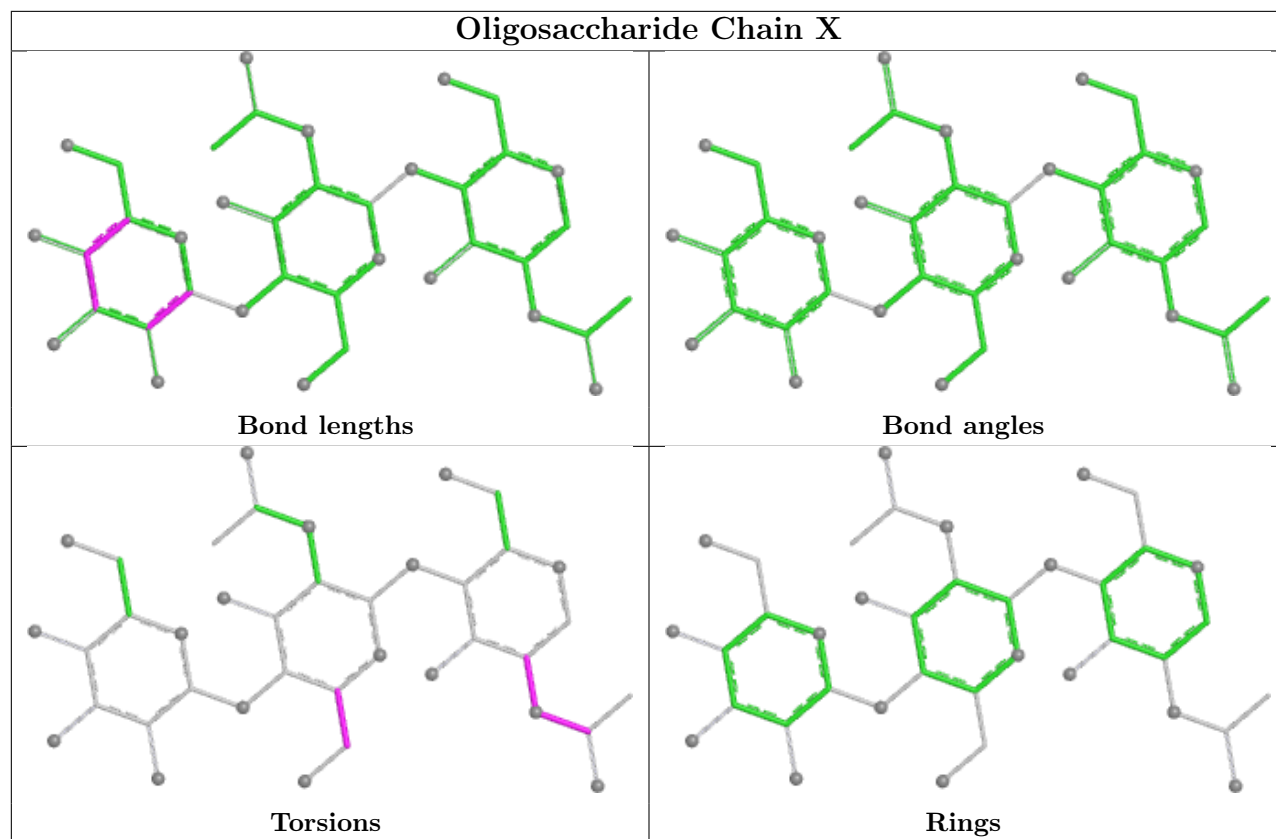


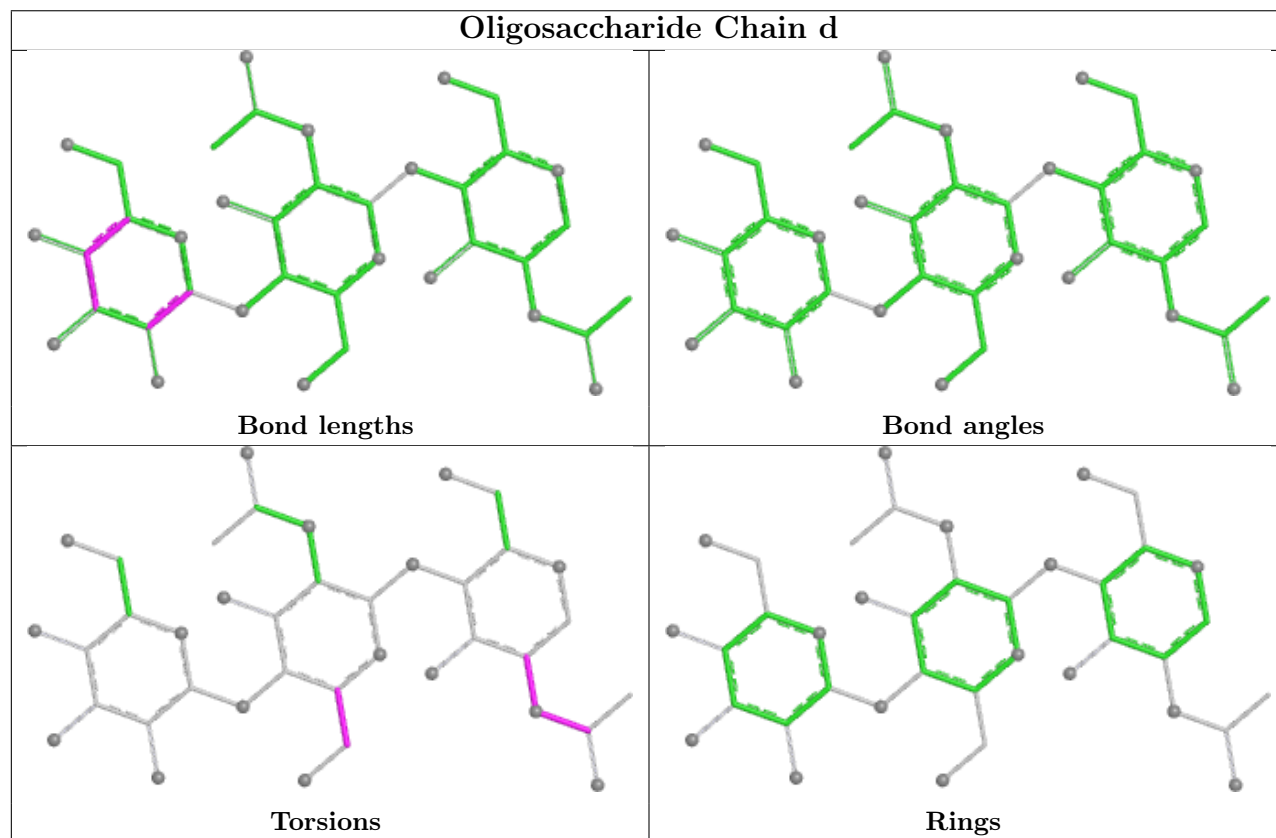
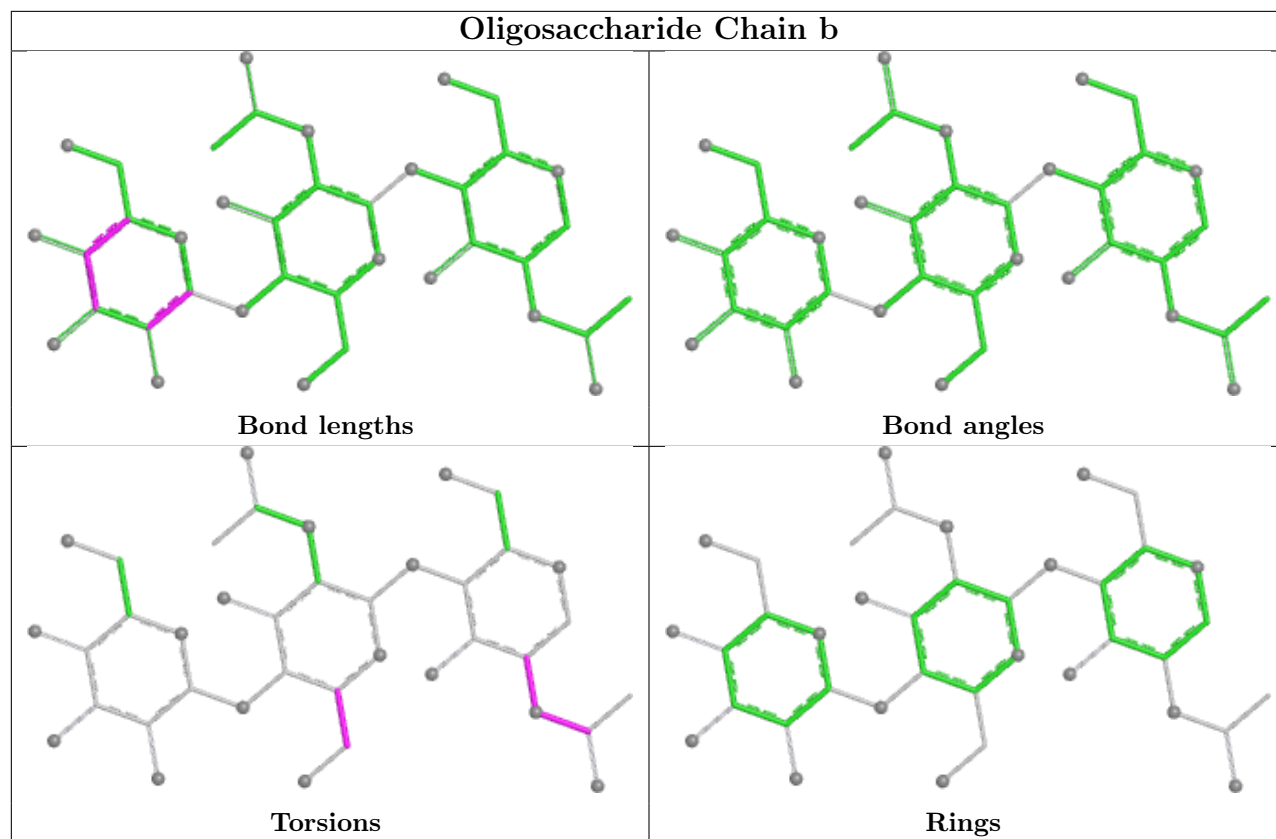












5.6 Ligand geometry

18 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	NAG	O	401	3	14,14,15	0.46	0	17,19,21	0.50	0
6	NAG	P	401	1	14,14,15	0.58	0	17,19,21	1.42	2 (11%)
6	NAG	G	401	1	14,14,15	0.58	0	17,19,21	1.42	2 (11%)
6	NAG	M	402	1	14,14,15	0.69	1 (7%)	17,19,21	0.61	0
6	NAG	D	402	1	14,14,15	0.69	1 (7%)	17,19,21	0.61	0
6	NAG	F	401	3	14,14,15	0.46	0	17,19,21	0.50	0
6	NAG	D	401	1	14,14,15	0.58	0	17,19,21	1.42	2 (11%)
6	NAG	M	401	1	14,14,15	0.58	0	17,19,21	1.42	2 (11%)
6	NAG	P	402	1	14,14,15	0.69	1 (7%)	17,19,21	0.61	0
6	NAG	L	401	3	14,14,15	0.46	0	17,19,21	0.50	0
6	NAG	A	402	1	14,14,15	0.69	1 (7%)	17,19,21	0.61	0
6	NAG	I	401	3	14,14,15	0.46	0	17,19,21	0.50	0
6	NAG	J	402	1	14,14,15	0.69	1 (7%)	17,19,21	0.61	0
6	NAG	A	401	1	14,14,15	0.58	0	17,19,21	1.42	2 (11%)
6	NAG	C	401	3	14,14,15	0.46	0	17,19,21	0.50	0
6	NAG	R	401	3	14,14,15	0.46	0	17,19,21	0.50	0
6	NAG	J	401	1	14,14,15	0.58	0	17,19,21	1.42	2 (11%)
6	NAG	G	402	1	14,14,15	0.68	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
6	NAG	O	401	3	-	2/6/23/26	0/1/1/1
6	NAG	P	401	1	-	6/6/23/26	0/1/1/1
6	NAG	G	401	1	-	6/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	M	402	1	-	4/6/23/26	0/1/1/1
6	NAG	D	402	1	-	4/6/23/26	0/1/1/1
6	NAG	F	401	3	-	2/6/23/26	0/1/1/1
6	NAG	D	401	1	-	6/6/23/26	0/1/1/1
6	NAG	M	401	1	-	6/6/23/26	0/1/1/1
6	NAG	P	402	1	-	4/6/23/26	0/1/1/1
6	NAG	L	401	3	-	2/6/23/26	0/1/1/1
6	NAG	A	402	1	-	4/6/23/26	0/1/1/1
6	NAG	I	401	3	-	2/6/23/26	0/1/1/1
6	NAG	J	402	1	-	4/6/23/26	0/1/1/1
6	NAG	A	401	1	-	6/6/23/26	0/1/1/1
6	NAG	C	401	3	-	2/6/23/26	0/1/1/1
6	NAG	R	401	3	-	2/6/23/26	0/1/1/1
6	NAG	J	401	1	-	6/6/23/26	0/1/1/1
6	NAG	G	402	1	-	4/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	402	NAG	C1-C2	2.16	1.55	1.52
6	A	402	NAG	C1-C2	2.15	1.55	1.52
6	P	402	NAG	C1-C2	2.15	1.55	1.52
6	M	402	NAG	C1-C2	2.15	1.55	1.52
6	D	402	NAG	C1-C2	2.15	1.55	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	401	NAG	C2-N2-C7	4.69	129.19	122.90
6	D	401	NAG	C2-N2-C7	4.69	129.18	122.90
6	J	401	NAG	C2-N2-C7	4.69	129.18	122.90
6	P	401	NAG	C2-N2-C7	4.69	129.18	122.90
6	G	401	NAG	C2-N2-C7	4.69	129.18	122.90

There are no chirality outliers.

5 of 72 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	401	NAG	C4-C5-C6-O6
6	F	401	NAG	C4-C5-C6-O6
6	I	401	NAG	C4-C5-C6-O6
6	L	401	NAG	C4-C5-C6-O6
6	O	401	NAG	C4-C5-C6-O6

There are no ring outliers.

13 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	P	401	NAG	2	0
6	G	401	NAG	2	0
6	M	402	NAG	2	0
6	D	402	NAG	2	0
6	D	401	NAG	2	0
6	M	401	NAG	2	0
6	P	402	NAG	2	0
6	A	402	NAG	2	0
6	J	402	NAG	2	0
6	A	401	NAG	2	0
6	C	401	NAG	1	0
6	J	401	NAG	2	0
6	G	402	NAG	2	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	298/303 (98%)	-0.31	1 (0%) 90 77	101, 159, 225, 294	0
1	D	298/303 (98%)	-0.11	4 (1%) 75 52	101, 159, 225, 294	0
1	G	298/303 (98%)	-0.27	2 (0%) 84 65	101, 159, 225, 294	0
1	J	298/303 (98%)	-0.20	1 (0%) 90 77	101, 159, 225, 294	0
1	M	298/303 (98%)	-0.27	0 100 100	101, 159, 225, 294	0
1	P	298/303 (98%)	-0.23	1 (0%) 90 77	101, 159, 225, 294	0
2	B	164/179 (91%)	-0.24	2 (1%) 76 54	85, 164, 253, 314	0
2	E	164/179 (91%)	-0.05	3 (1%) 67 46	85, 164, 253, 314	0
2	H	164/179 (91%)	-0.01	3 (1%) 67 46	85, 164, 253, 314	0
2	K	164/179 (91%)	-0.09	1 (0%) 85 67	85, 164, 253, 314	0
2	N	164/179 (91%)	-0.18	0 100 100	85, 164, 253, 314	0
2	Q	164/179 (91%)	-0.23	1 (0%) 85 67	85, 164, 253, 314	0
3	C	283/348 (81%)	0.23	8 (2%) 55 37	89, 171, 334, 433	0
3	F	283/348 (81%)	-0.08	4 (1%) 73 50	89, 171, 334, 433	0
3	I	283/348 (81%)	0.07	5 (1%) 67 46	89, 171, 334, 433	0
3	L	283/348 (81%)	-0.12	2 (0%) 84 65	89, 171, 334, 433	0
3	O	283/348 (81%)	-0.27	2 (0%) 84 65	89, 171, 334, 433	0
3	R	283/348 (81%)	-0.18	4 (1%) 73 50	89, 171, 334, 433	0
All	All	4470/4980 (89%)	-0.15	44 (0%) 79 57	85, 163, 281, 433	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	59	MET	3.7
3	F	48	GLY	3.1
3	O	49	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	86	PHE	3.1
2	B	59	MET	3.0

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.

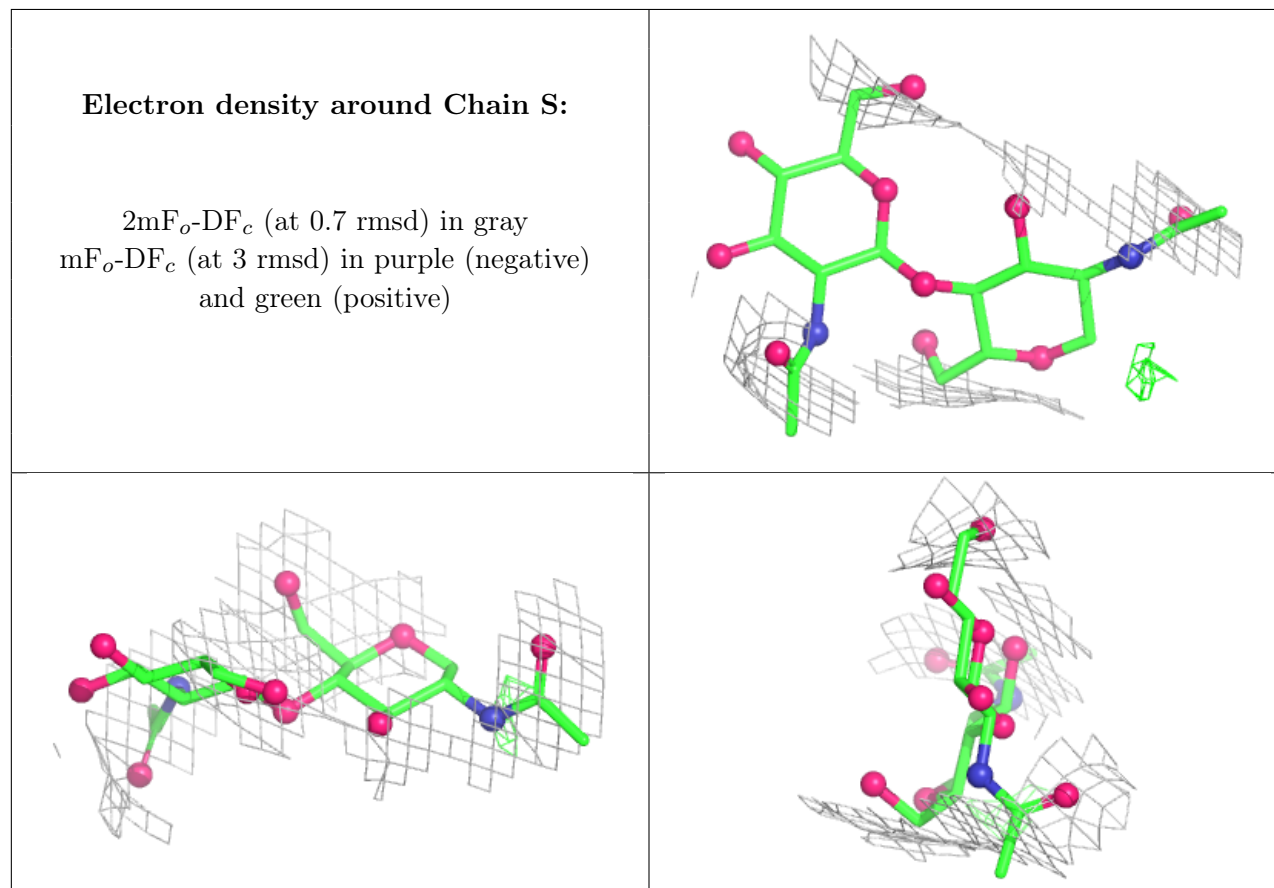
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	BMA	Z	3	11/12	0.33	0.15	93,93,93,93	0
5	BMA	V	3	11/12	0.42	0.12	93,93,93,93	0
5	BMA	X	3	11/12	0.48	0.11	93,93,93,93	0
5	BMA	T	3	11/12	0.48	0.12	93,93,93,93	0
4	NAG	W	2	14/15	0.58	0.12	155,211,229,230	0
4	NAG	U	2	14/15	0.60	0.10	155,211,229,230	0
4	NAG	Y	2	14/15	0.61	0.10	155,211,229,230	0
4	NAG	S	2	14/15	0.62	0.10	155,211,229,230	0
4	NAG	a	1	14/15	-	-	174,186,199,206	0
4	NAG	a	2	14/15	-	-	155,211,229,230	0
4	NAG	c	1	14/15	-	-	174,186,199,206	0
4	NAG	c	2	14/15	-	-	155,211,229,230	0
5	NAG	V	1	14/15	0.67	0.12	67,67,67,67	0
5	NAG	Z	1	14/15	0.68	0.12	67,67,67,67	0
5	NAG	Z	2	14/15	0.72	0.10	81,81,81,81	0
4	NAG	U	1	14/15	0.72	0.10	174,186,199,206	0
5	NAG	T	2	14/15	0.74	0.09	81,81,81,81	0
4	NAG	Y	1	14/15	0.74	0.09	174,186,199,206	0
5	NAG	T	1	14/15	0.75	0.11	67,67,67,67	0
5	NAG	V	2	14/15	0.76	0.09	81,81,81,81	0
4	NAG	W	1	14/15	0.76	0.12	174,186,199,206	0
4	NAG	S	1	14/15	0.79	0.10	174,186,199,206	0
5	NAG	X	1	14/15	0.82	0.08	67,67,67,67	0
5	NAG	X	2	14/15	0.83	0.08	81,81,81,81	0
5	NAG	b	1	14/15	-	-	67,67,67,67	0
5	NAG	b	2	14/15	-	-	81,81,81,81	0

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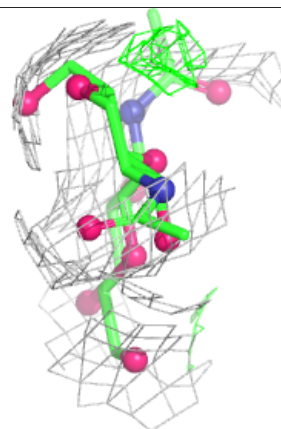
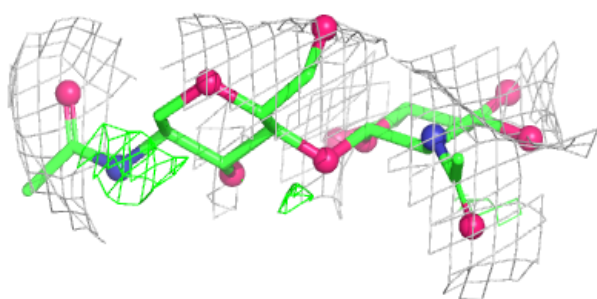
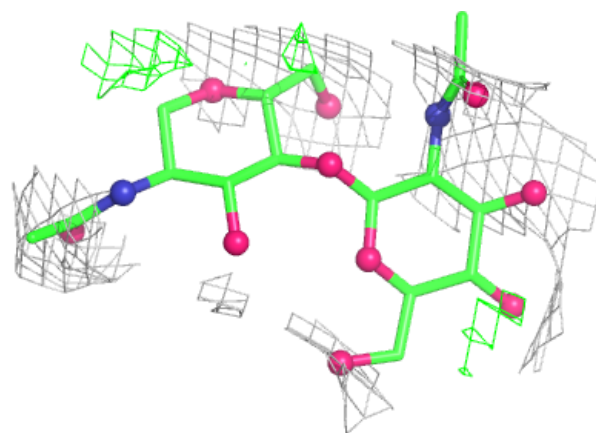
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	BMA	b	3	11/12	-	-	93,93,93,93	0
5	NAG	d	1	14/15	-	-	67,67,67,67	0
5	NAG	d	2	14/15	-	-	81,81,81,81	0
5	BMA	d	3	11/12	-	-	93,93,93,93	0

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.

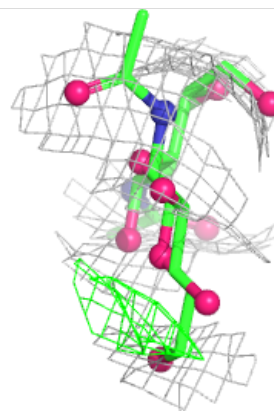
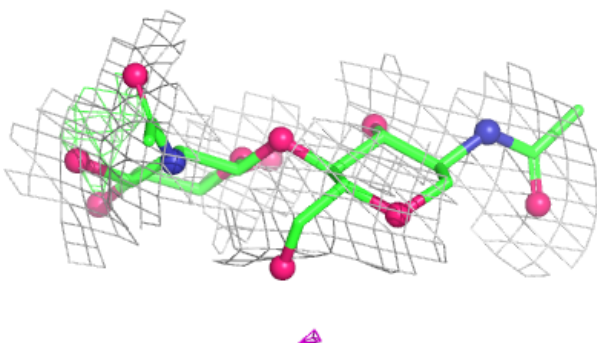
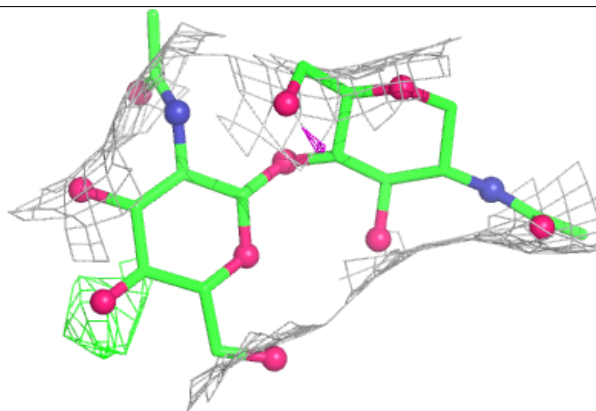


Electron density around Chain U:

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

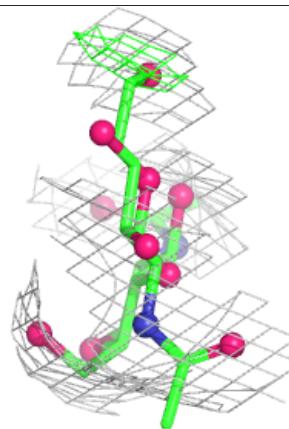
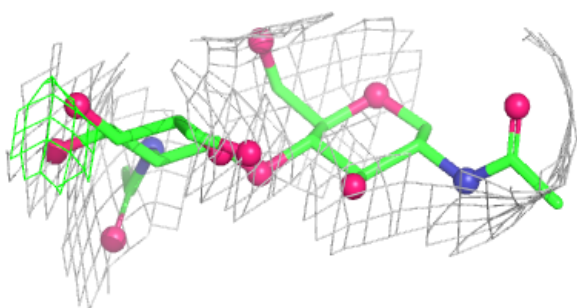
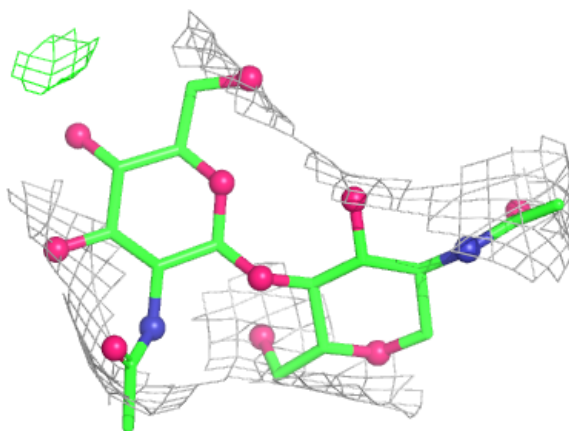
**Electron density around Chain W:**

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



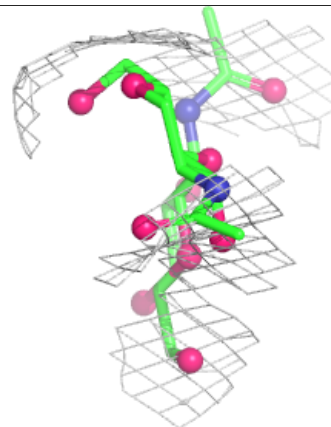
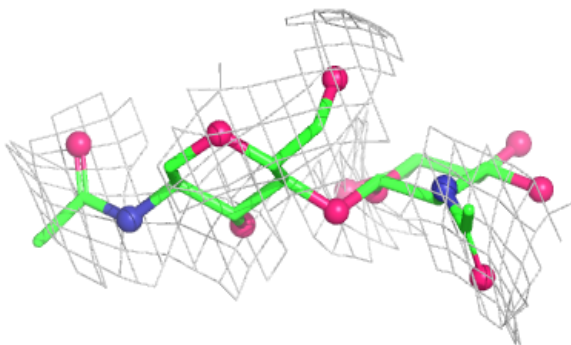
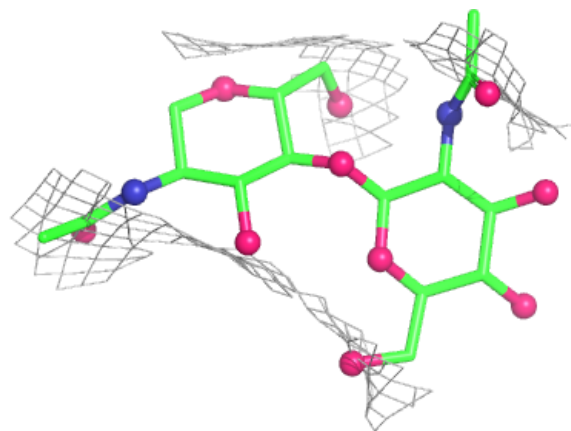
Electron density around Chain Y:

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



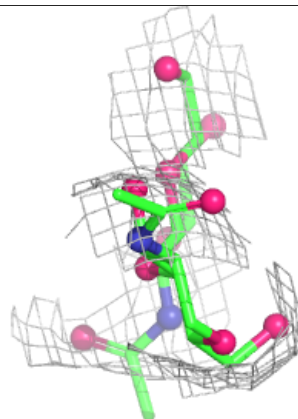
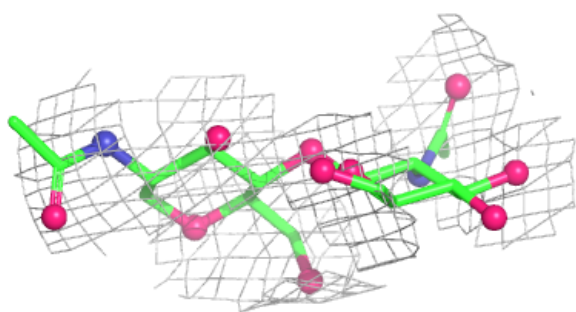
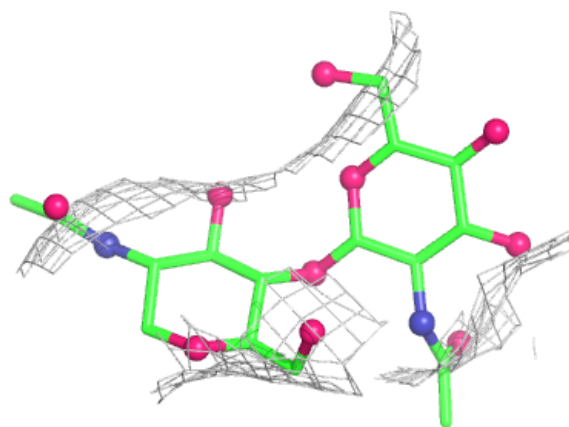
Electron density around Chain a:

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

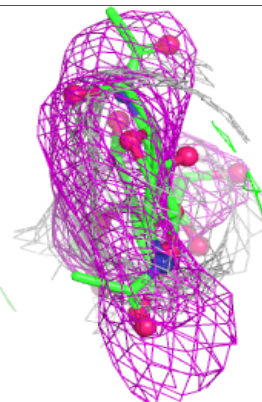
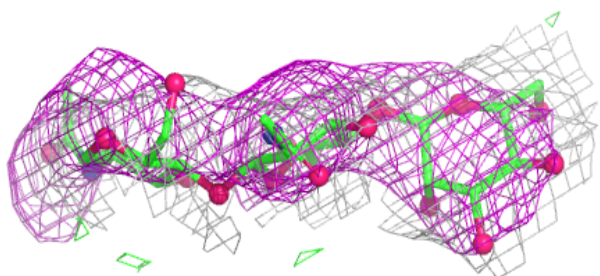
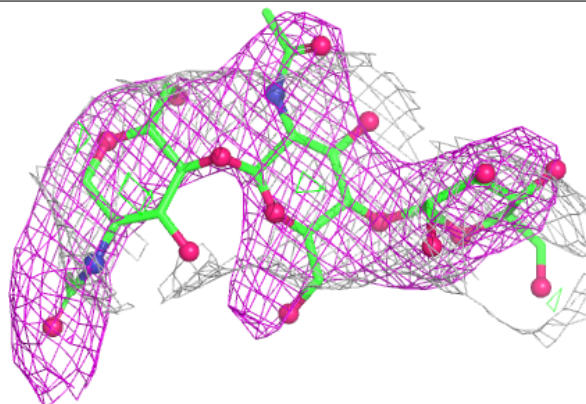


Electron density around Chain c:

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

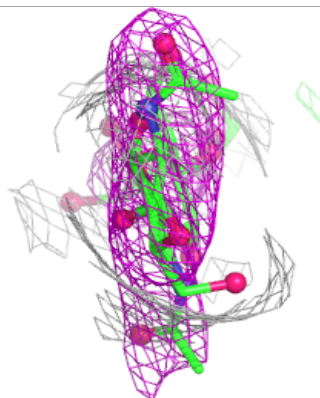
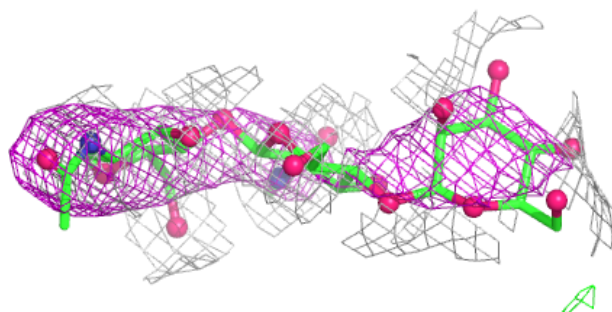
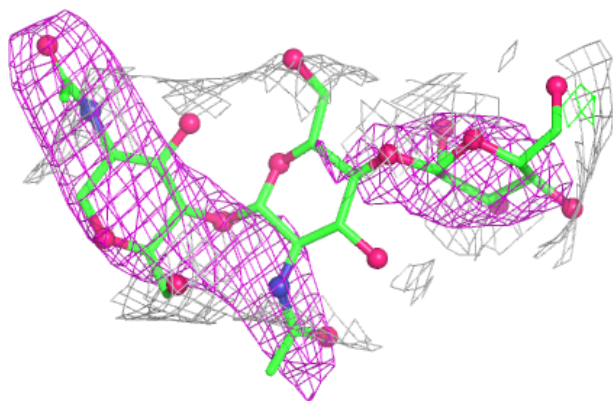
**Electron density around Chain T:**

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

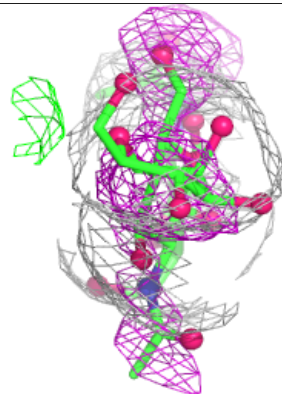
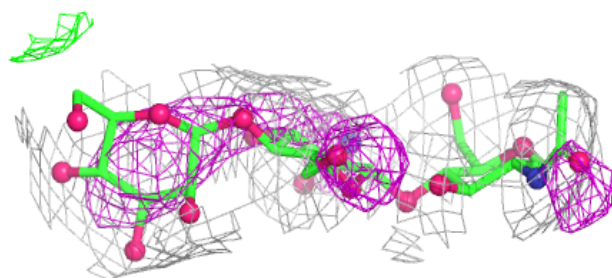
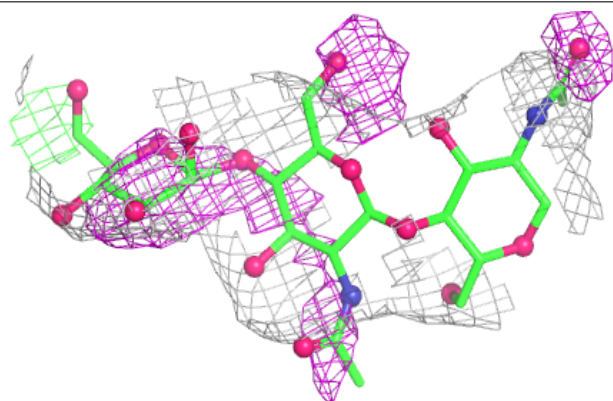


Electron density around Chain V:

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

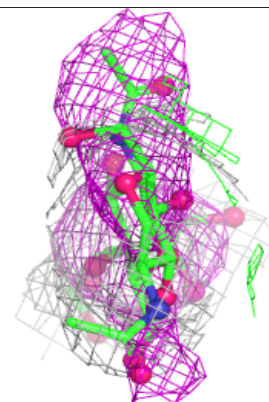
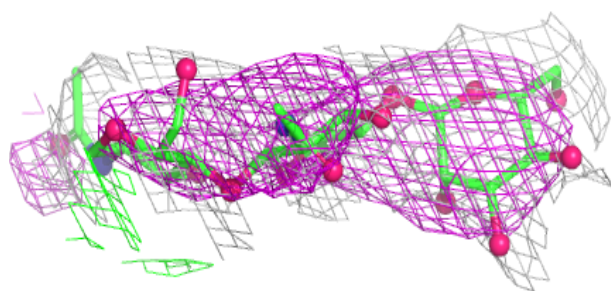
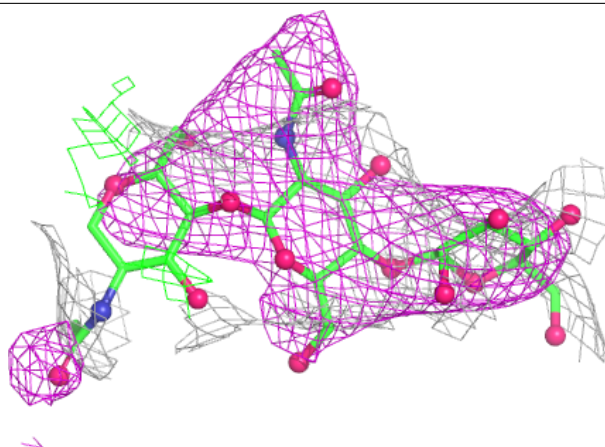
**Electron density around Chain X:**

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

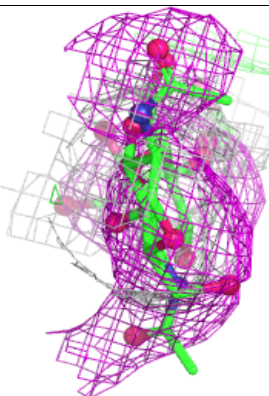
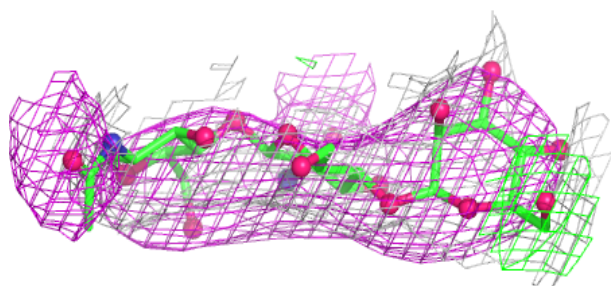
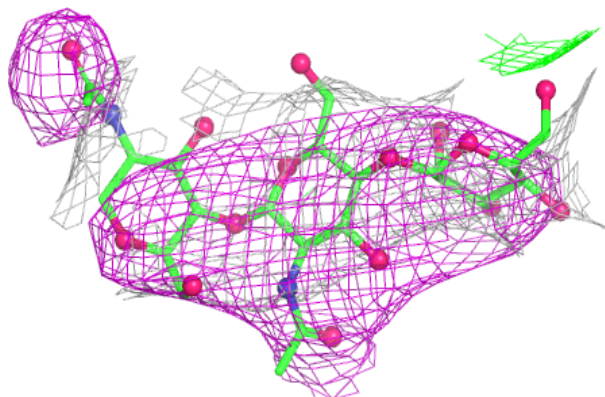


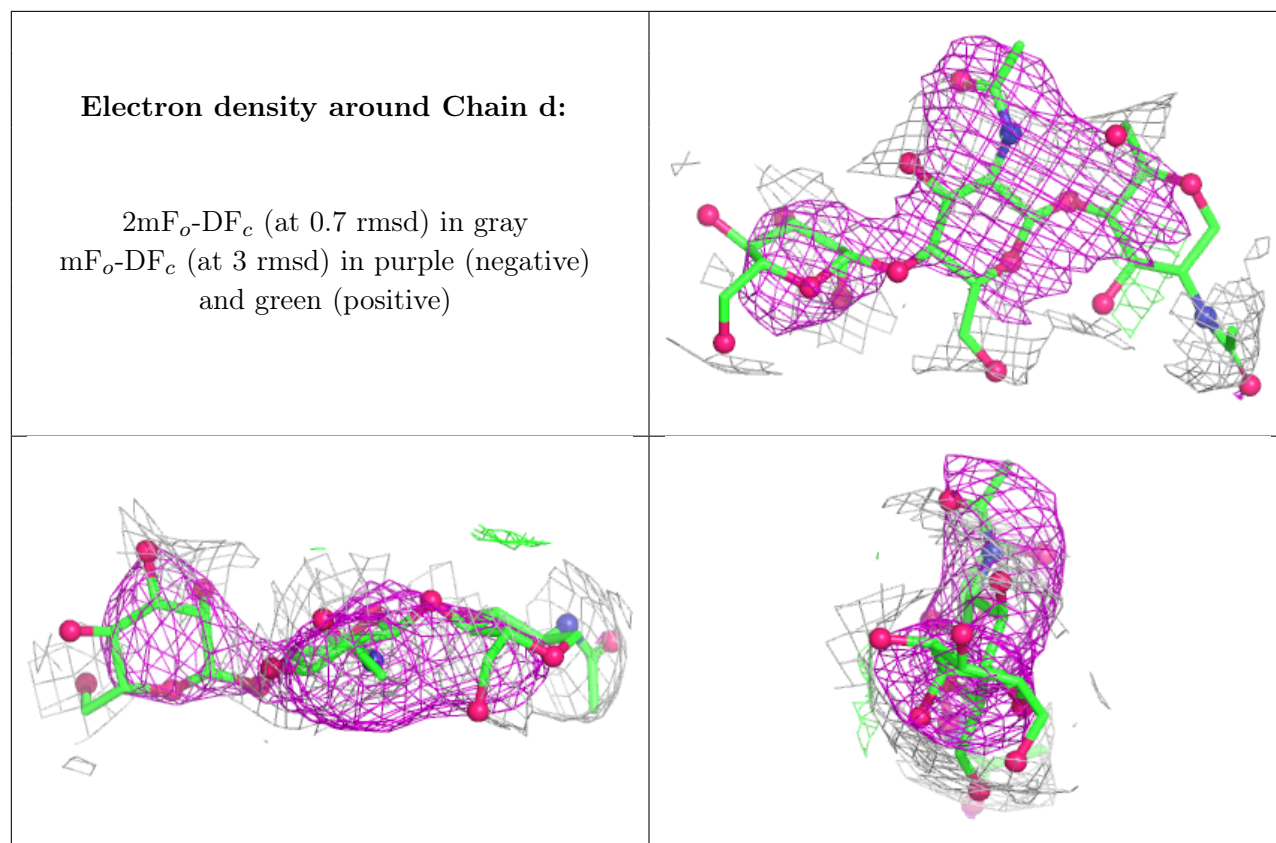
Electron density around Chain Z:

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

**Electron density around Chain b:**

$2mF_o-DF_c$ (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	J	402	14/15	0.40	0.12	149,179,207,213	0
6	NAG	D	401	14/15	0.42	0.16	78,78,78,78	0
6	NAG	G	402	14/15	0.52	0.09	149,179,207,213	0
6	NAG	A	401	14/15	0.52	0.12	78,78,78,78	0
6	NAG	P	402	14/15	0.53	0.11	149,179,207,213	0
6	NAG	D	402	14/15	0.60	0.09	149,179,207,213	0
6	NAG	O	401	14/15	0.63	0.10	77,183,262,267	0
6	NAG	G	401	14/15	0.63	0.20	78,78,78,78	0
6	NAG	R	401	14/15	0.63	0.08	77,183,262,267	0
6	NAG	P	401	14/15	0.65	0.13	78,78,78,78	0
6	NAG	J	401	14/15	0.67	0.14	78,78,78,78	0
6	NAG	M	402	14/15	0.67	0.08	149,179,207,213	0
6	NAG	A	402	14/15	0.69	0.07	149,179,207,213	0
6	NAG	C	401	14/15	0.70	0.10	77,183,262,267	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	NAG	F	401	14/15	0.71	0.07	77,183,262,267	0
6	NAG	M	401	14/15	0.75	0.10	78,78,78,78	0
6	NAG	L	401	14/15	0.77	0.09	77,183,262,267	0
6	NAG	I	401	14/15	0.79	0.09	77,183,262,267	0

6.5 Other polymers [i](#)

There are no such residues in this entry.