



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 11:31 PM UTC

PDB ID : 5EWS / pdb_00005ews
Title : Sugar binding protein - human galectin-2
Authors : Su, J.Y.; Si, Y.L.
Deposited on : 2015-11-21
Resolution : 2.00 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

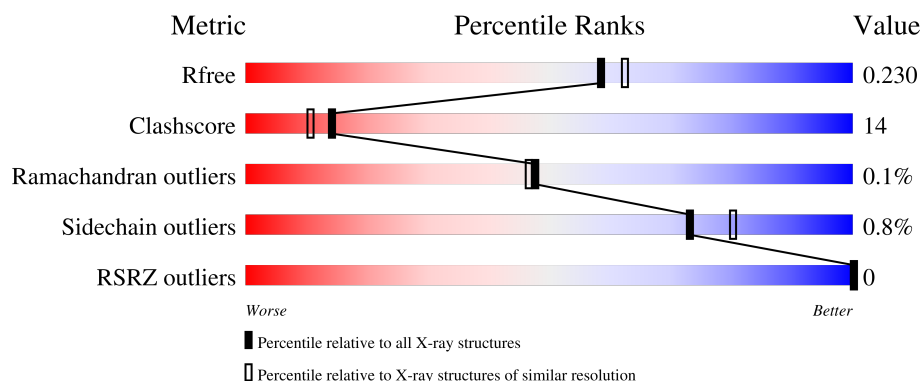
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.



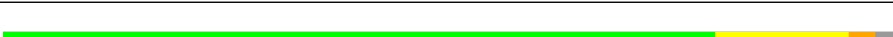
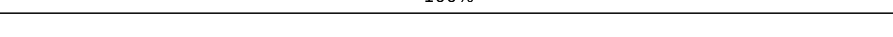
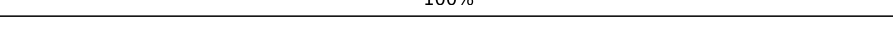
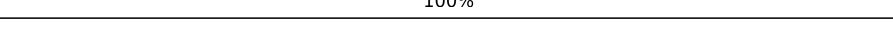
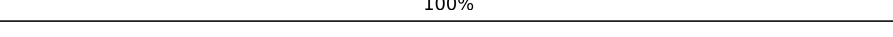
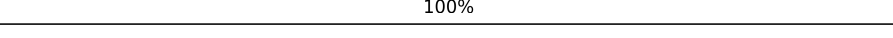
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	134	
1	B	134	
1	C	134	
1	D	134	
1	E	134	

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Mol	Chain	Length	Quality of chain
1	F	134	
1	G	134	
1	H	134	
1	I	134	
1	J	134	
1	K	134	
1	L	134	
1	M	134	
1	N	134	
1	O	134	
1	P	134	
2	Q	2	
2	R	2	
2	S	2	
2	T	2	
2	U	2	
2	V	2	
2	W	2	
2	X	2	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BGC	W	1	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16873 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 Galectin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	131	Total	C	N	O	S	0	0	0
			1012	637	173	196	6			
1	A	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	C	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	D	131	Total	C	N	O	S	0	0	0
			1014	639	175	194	6			
1	E	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	F	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	G	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	H	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	I	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	J	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	K	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	L	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	M	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	N	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	O	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			
1	P	131	Total	C	N	O	S	0	0	0
			1017	640	175	196	6			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLY	-	expression tag	UNP P05162
B	2	SER	-	expression tag	UNP P05162
B	3	HIS	-	expression tag	UNP P05162
A	1	GLY	-	expression tag	UNP P05162
A	2	SER	-	expression tag	UNP P05162
A	3	HIS	-	expression tag	UNP P05162
C	1	GLY	-	expression tag	UNP P05162
C	2	SER	-	expression tag	UNP P05162
C	3	HIS	-	expression tag	UNP P05162
D	1	GLY	-	expression tag	UNP P05162
D	2	SER	-	expression tag	UNP P05162
D	3	HIS	-	expression tag	UNP P05162
E	1	GLY	-	expression tag	UNP P05162
E	2	SER	-	expression tag	UNP P05162
E	3	HIS	-	expression tag	UNP P05162
F	1	GLY	-	expression tag	UNP P05162
F	2	SER	-	expression tag	UNP P05162
F	3	HIS	-	expression tag	UNP P05162
G	1	GLY	-	expression tag	UNP P05162
G	2	SER	-	expression tag	UNP P05162
G	3	HIS	-	expression tag	UNP P05162
H	1	GLY	-	expression tag	UNP P05162
H	2	SER	-	expression tag	UNP P05162
H	3	HIS	-	expression tag	UNP P05162
I	1	GLY	-	expression tag	UNP P05162
I	2	SER	-	expression tag	UNP P05162
I	3	HIS	-	expression tag	UNP P05162
J	1	GLY	-	expression tag	UNP P05162
J	2	SER	-	expression tag	UNP P05162
J	3	HIS	-	expression tag	UNP P05162
K	1	GLY	-	expression tag	UNP P05162
K	2	SER	-	expression tag	UNP P05162
K	3	HIS	-	expression tag	UNP P05162
L	1	GLY	-	expression tag	UNP P05162
L	2	SER	-	expression tag	UNP P05162
L	3	HIS	-	expression tag	UNP P05162
M	1	GLY	-	expression tag	UNP P05162
M	2	SER	-	expression tag	UNP P05162
M	3	HIS	-	expression tag	UNP P05162
N	1	GLY	-	expression tag	UNP P05162
N	2	SER	-	expression tag	UNP P05162
N	3	HIS	-	expression tag	UNP P05162

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Chain	Residue	Modelled	Actual	Comment	Reference
O	1	GLY	-	expression tag	UNP P05162
O	2	SER	-	expression tag	UNP P05162
O	3	HIS	-	expression tag	UNP P05162
P	1	GLY	-	expression tag	UNP P05162
P	2	SER	-	expression tag	UNP P05162
P	3	HIS	-	expression tag	UNP P05162

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	Q	2	Total	C	O	0	0	0
			23	12	11			
2	R	2	Total	C	O	0	0	0
			23	12	11			
2	S	2	Total	C	O	0	0	0
			23	12	11			
2	T	2	Total	C	O	0	0	0
			23	12	11			
2	U	2	Total	C	O	0	0	0
			23	12	11			
2	V	2	Total	C	O	0	0	0
			23	12	11			
2	W	2	Total	C	O	0	0	0
			23	12	11			
2	X	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	22	Total	O	0	0
			22	22		
3	A	29	Total	O	0	0
			29	29		
3	C	24	Total	O	0	0
			24	24		
3	D	28	Total	O	0	0
			28	28		

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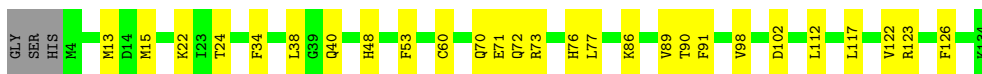
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	29	Total 29	O 29	0	0
3	F	16	Total 16	O 16	0	0
3	G	25	Total 25	O 25	0	0
3	H	27	Total 27	O 27	0	0
3	I	40	Total 40	O 40	0	0
3	J	32	Total 32	O 32	0	0
3	K	24	Total 24	O 24	0	0
3	L	21	Total 21	O 21	0	0
3	M	36	Total 36	O 36	0	0
3	N	34	Total 34	O 34	0	0
3	O	23	Total 23	O 23	0	0
3	P	15	Total 15	O 15	0	0

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.

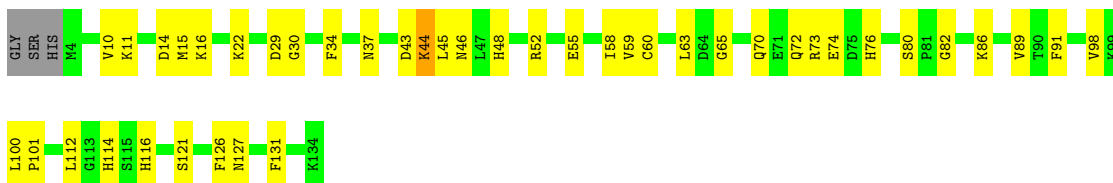
• Molecule 1: Galectin-2

Chain B:  78% 20% .



• Molecule 1: Galectin-2

Chain A:  66% 31% ..



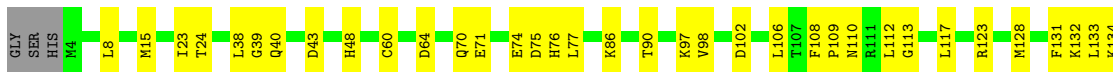
• Molecule 1: Galectin-2

Chain C:  66% 31% ..



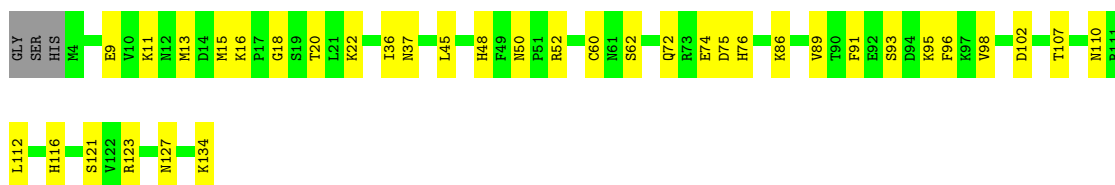
• Molecule 1: Galectin-2

Chain D:  72% 26% .



• Molecule 1: Galectin-2

Chain E:  71% 27% .



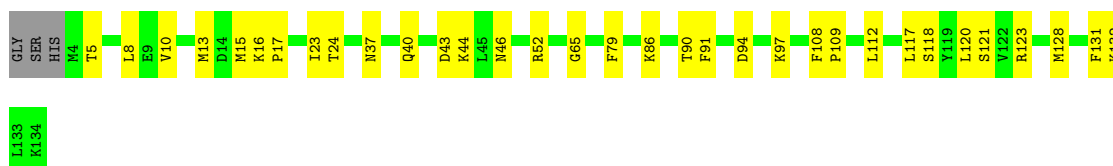
- Molecule 1: Galectin-2

Chain F: 73% 24% ..



- Molecule 1: Galectin-2

Chain G: 73% 25% .



- Molecule 1: Galectin-2

Chain H: 75% 22% .



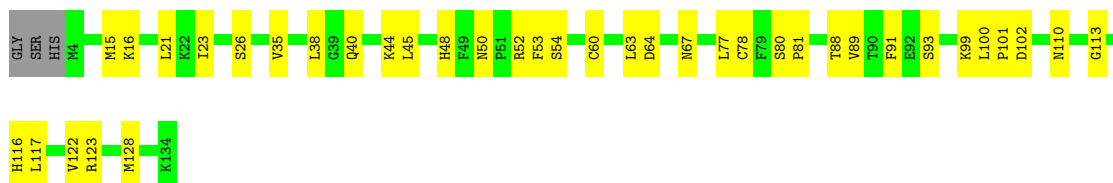
- Molecule 1: Galectin-2

Chain I: 75% 23% .



- Molecule 1: Galectin-2

Chain J: 69% 28% .



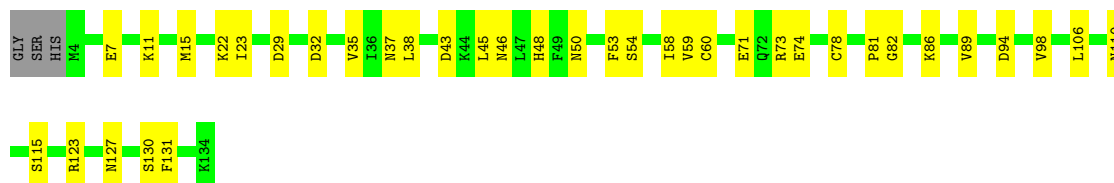
- Molecule 1: Galectin-2

Chain K: 75% 22% ...



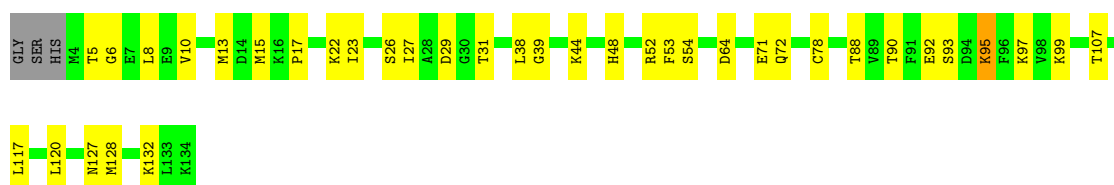
• Molecule 1: Galectin-2

Chain L: 70% 28% .



• Molecule 1: Galectin-2

Chain M: 70% 27% ..



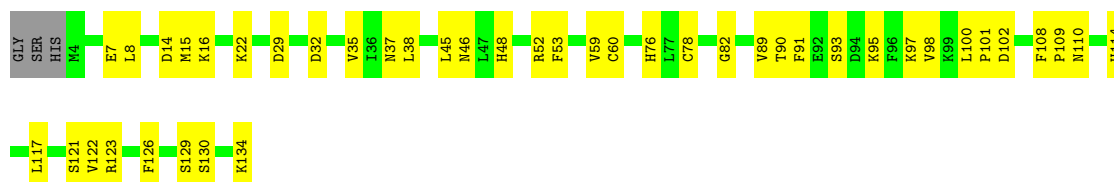
• Molecule 1: Galectin-2

Chain N: 63% 35% .



• Molecule 1: Galectin-2

Chain O: 66% 32% .



• Molecule 1: Galectin-2

Chain P: 80% 15% ..



- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain Q:  100%

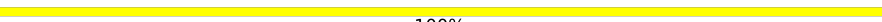
BGC1
GAL2

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain R:  100%

BGC1
GAL2

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain S:  100%

BGC1
GAL2

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain T:  100%

BGC1
GAL2

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain U:  100%

BGC1
GAL2

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain V:  100%

BGC1
GAL2

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain W:  100%

BGC1
GAL2

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-glucopyranose

Chain X:  100%

BGC1
GAL2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.40Å 106.94Å 121.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.95 – 2.00 48.95 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.6 (48.95-2.00) 92.7 (48.95-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.214 , 0.249 0.201 , 0.230	Depositor DCC
R_{free} test set	1993 reflections (1.54%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.514	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.469 for h,-k,-l 0.459 for -h,k,-l 0.458 for -h,-k,l	Xtriage
Reported twinning fraction	0.490 for -h,-k,l	Depositor
Outliers	0 of 127534 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	16873	wwPDB-VP
Average B, all atoms (Å ²)	31.0	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 33.95 % 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 7.3770e-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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BGC, GAL

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	0.25	0/1039	0.51	1/1395 (0.1%)
1	B	0.13	0/1033	0.39	0/1387
1	C	0.21	0/1039	0.45	0/1395
1	D	0.21	0/1036	0.44	0/1391
1	E	0.21	0/1039	0.48	0/1395
1	F	0.21	0/1039	0.43	0/1395
1	G	0.14	0/1039	0.41	0/1395
1	H	0.19	0/1039	0.45	0/1395
1	I	0.20	0/1039	0.41	0/1395
1	J	0.24	0/1039	0.43	0/1395
1	K	0.15	0/1039	0.45	0/1395
1	L	0.16	0/1039	0.45	0/1395
1	M	0.18	0/1039	0.44	0/1395
1	N	0.28	0/1039	0.45	0/1395
1	O	0.15	0/1039	0.42	0/1395
1	P	0.16	0/1039	0.49	0/1395
All	All	0.20	0/16615	0.45	1/22308 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	K	0	1
1	P	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	LYS	CG-CD-CE	5.71	124.42	111.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	K	114	HIS	Peptide
1	P	114	HIS	Peptide

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	1017	0	988	43	0
1	B	1012	0	983	25	0
1	C	1017	0	988	40	0
1	D	1014	0	986	25	0
1	E	1017	0	988	29	0
1	F	1017	0	988	25	0
1	G	1017	0	988	24	0
1	H	1017	0	988	26	0
1	I	1017	0	988	25	0
1	J	1017	0	988	23	0
1	K	1017	0	988	34	0
1	L	1017	0	988	28	0
1	M	1017	0	988	32	0
1	N	1017	0	988	50	0
1	O	1017	0	988	34	0
1	P	1017	0	988	21	0
2	Q	23	0	20	1	0
2	R	23	0	20	3	0
2	S	23	0	20	0	0
2	T	23	0	20	5	0
2	U	23	0	20	1	0
2	V	23	0	20	5	0
2	W	23	0	20	9	0
2	X	23	0	20	3	0
3	A	29	0	0	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	22	0	0	8	0
3	C	24	0	0	5	0
3	D	28	0	0	4	0
3	E	29	0	0	13	0
3	F	16	0	0	6	0
3	G	25	0	0	4	0
3	H	27	0	0	2	0
3	I	40	0	0	7	0
3	J	32	0	0	5	0
3	K	24	0	0	8	0
3	L	21	0	0	9	1
3	M	36	0	0	8	0
3	N	34	0	0	7	1
3	O	23	0	0	10	0
3	P	15	0	0	4	0
All	All	16873	0	15961	461	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 14.

The worst 5 of 461 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:O:93:SER:HB2	1:O:114:HIS:HB2	1.44	0.98
1:A:43:ASP:OD2	1:A:44:LYS:HE3	1.65	0.94
1:I:132:LYS:HG2	1:O:130:SER:HB2	1.54	0.89
1:A:55:GLU:HG2	2:R:1:BGC:H6C2	1.58	0.84
1:M:52:ARG:NH2	2:W:2:GAL:O4	2.10	0.83

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)
3:L:212:HOH:O	3:N:311:HOH:O[1_454]	1.76	0.44

5.3 Torsion angles

5.3.1 Protein backbone

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	129/134 (96%)	125 (97%)	4 (3%)	0	100	100
1	B	129/134 (96%)	126 (98%)	3 (2%)	0	100	100
1	C	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
1	D	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
1	E	129/134 (96%)	124 (96%)	4 (3%)	1 (1%)	16	11
1	F	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
1	G	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
1	H	129/134 (96%)	128 (99%)	1 (1%)	0	100	100
1	I	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
1	J	129/134 (96%)	126 (98%)	3 (2%)	0	100	100
1	K	129/134 (96%)	123 (95%)	4 (3%)	2 (2%)	7	3
1	L	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
1	M	129/134 (96%)	126 (98%)	3 (2%)	0	100	100
1	N	129/134 (96%)	127 (98%)	2 (2%)	0	100	100
1	O	129/134 (96%)	128 (99%)	1 (1%)	0	100	100
1	P	129/134 (96%)	126 (98%)	3 (2%)	0	100	100
All	All	2064/2144 (96%)	2021 (98%)	40 (2%)	3 (0%)	48	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	114	HIS
1	E	116	HIS
1	K	115	SER

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	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	B	115/118 (98%)	115 (100%)	0	100	100
1	C	116/118 (98%)	113 (97%)	3 (3%)	40	44
1	D	115/118 (98%)	115 (100%)	0	100	100
1	E	116/118 (98%)	116 (100%)	0	100	100
1	F	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	G	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	H	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	I	116/118 (98%)	116 (100%)	0	100	100
1	J	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	K	116/118 (98%)	116 (100%)	0	100	100
1	L	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	M	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	N	116/118 (98%)	115 (99%)	1 (1%)	70	78
1	O	116/118 (98%)	116 (100%)	0	100	100
1	P	116/118 (98%)	113 (97%)	3 (3%)	40	44
All	All	1854/1888 (98%)	1840 (99%)	14 (1%)	73	80

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	26	SER
1	L	43	ASP
1	P	61	ASN
1	P	16	LYS
1	P	19	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	40	GLN
1	M	40	GLN
1	K	67	ASN
1	L	40	GLN
1	N	70	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 ⓘ

16 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	BGC	Q	1	2	12,12,12	2.34	6 (50%)	17,17,17	0.83	1 (5%)
2	GAL	Q	2	2	11,11,12	1.69	3 (27%)	15,15,17	3.07	6 (40%)
2	BGC	R	1	2	12,12,12	2.32	5 (41%)	17,17,17	1.00	1 (5%)
2	GAL	R	2	2	11,11,12	1.63	2 (18%)	15,15,17	2.41	6 (40%)
2	BGC	S	1	2	12,12,12	2.27	6 (50%)	17,17,17	0.69	0
2	GAL	S	2	2	11,11,12	1.62	2 (18%)	15,15,17	1.04	1 (6%)
2	BGC	T	1	2	12,12,12	2.23	5 (41%)	17,17,17	1.09	2 (11%)
2	GAL	T	2	2	11,11,12	1.60	2 (18%)	15,15,17	2.47	6 (40%)
2	BGC	U	1	2	12,12,12	2.26	5 (41%)	17,17,17	0.84	0
2	GAL	U	2	2	11,11,12	1.61	2 (18%)	15,15,17	2.95	6 (40%)
2	BGC	V	1	2	12,12,12	2.31	5 (41%)	17,17,17	0.92	1 (5%)
2	GAL	V	2	2	11,11,12	1.65	3 (27%)	15,15,17	2.41	7 (46%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BGC	W	1	2	12,12,12	1.99	4 (33%)	17,17,17	1.57	4 (23%)
2	GAL	W	2	2	11,11,12	1.97	3 (27%)	15,15,17	2.70	6 (40%)
2	BGC	X	1	2	12,12,12	2.29	5 (41%)	17,17,17	0.96	1 (5%)
2	GAL	X	2	2	11,11,12	1.59	2 (18%)	15,15,17	2.49	7 (46%)

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	BGC	Q	1	2	-	2/2/22/22	0/1/1/1
2	GAL	Q	2	2	-	0/2/19/22	0/1/1/1
2	BGC	R	1	2	-	2/2/22/22	0/1/1/1
2	GAL	R	2	2	-	0/2/19/22	0/1/1/1
2	BGC	S	1	2	-	0/2/22/22	0/1/1/1
2	GAL	S	2	2	-	0/2/19/22	0/1/1/1
2	BGC	T	1	2	-	0/2/22/22	0/1/1/1
2	GAL	T	2	2	-	2/2/19/22	0/1/1/1
2	BGC	U	1	2	-	0/2/22/22	0/1/1/1
2	GAL	U	2	2	-	0/2/19/22	0/1/1/1
2	BGC	V	1	2	-	2/2/22/22	0/1/1/1
2	GAL	V	2	2	-	2/2/19/22	0/1/1/1
2	BGC	W	1	2	-	2/2/22/22	0/1/1/1
2	GAL	W	2	2	-	1/2/19/22	0/1/1/1
2	BGC	X	1	2	-	2/2/22/22	0/1/1/1
2	GAL	X	2	2	-	1/2/19/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Q	1	BGC	O5-C1	4.49	1.53	1.42
2	R	1	BGC	O5-C1	4.37	1.53	1.42
2	W	2	GAL	C2-C3	-4.34	1.45	1.52
2	V	1	BGC	O5-C1	4.34	1.53	1.42
2	S	1	BGC	O5-C1	4.32	1.53	1.42

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	W	2	GAL	C1-C2-C3	8.01	121.31	109.64
2	Q	2	GAL	C1-C2-C3	7.97	121.25	109.64
2	U	2	GAL	C1-C2-C3	6.96	119.78	109.64
2	X	2	GAL	C1-C2-C3	6.24	118.73	109.64
2	R	2	GAL	C1-C2-C3	6.04	118.44	109.64

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

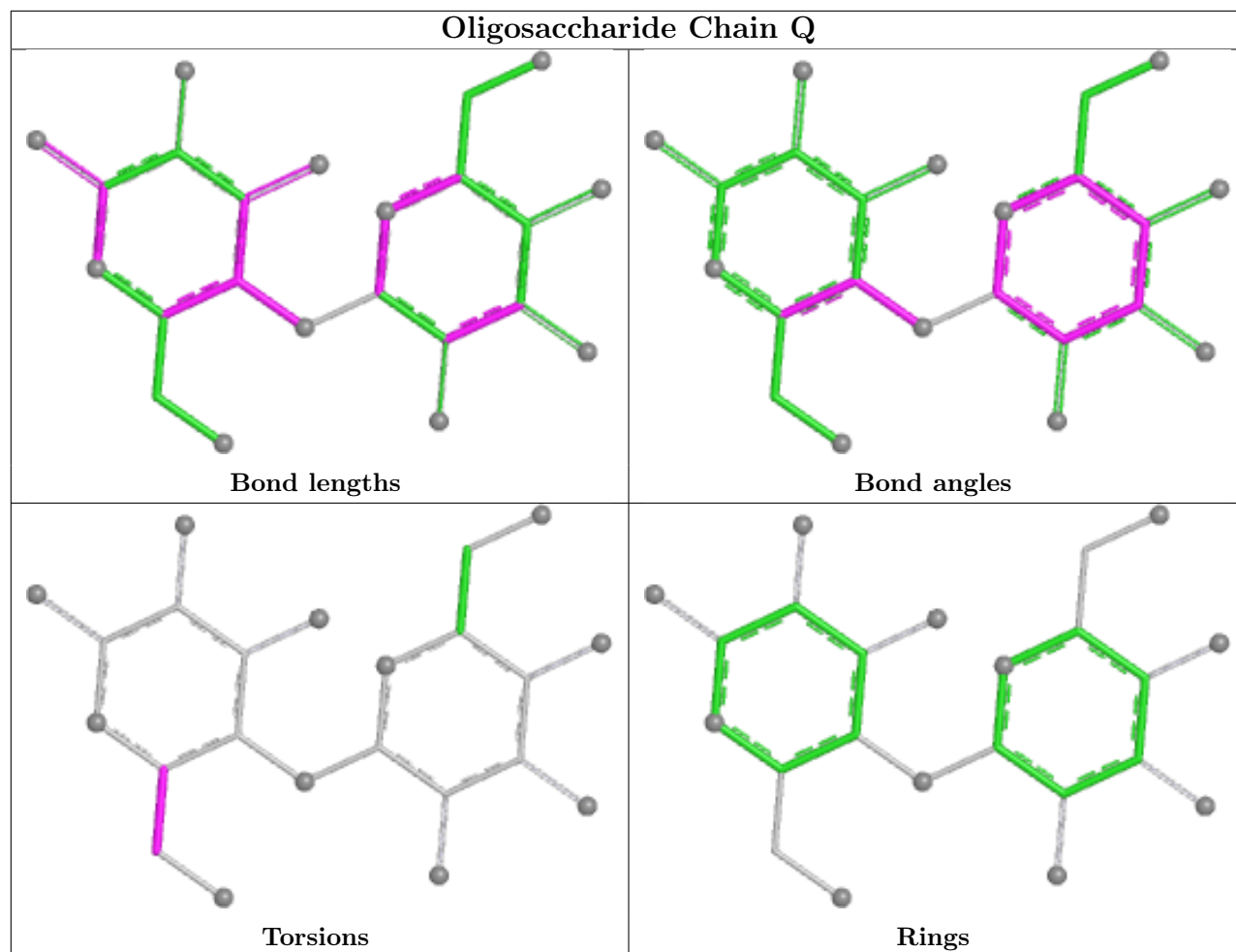
Mol	Chain	Res	Type	Atoms
2	R	1	BGC	O5-C5-C6-O6
2	V	2	GAL	C4-C5-C6-O6
2	R	1	BGC	C4-C5-C6-O6
2	W	1	BGC	C4-C5-C6-O6
2	T	2	GAL	O5-C5-C6-O6

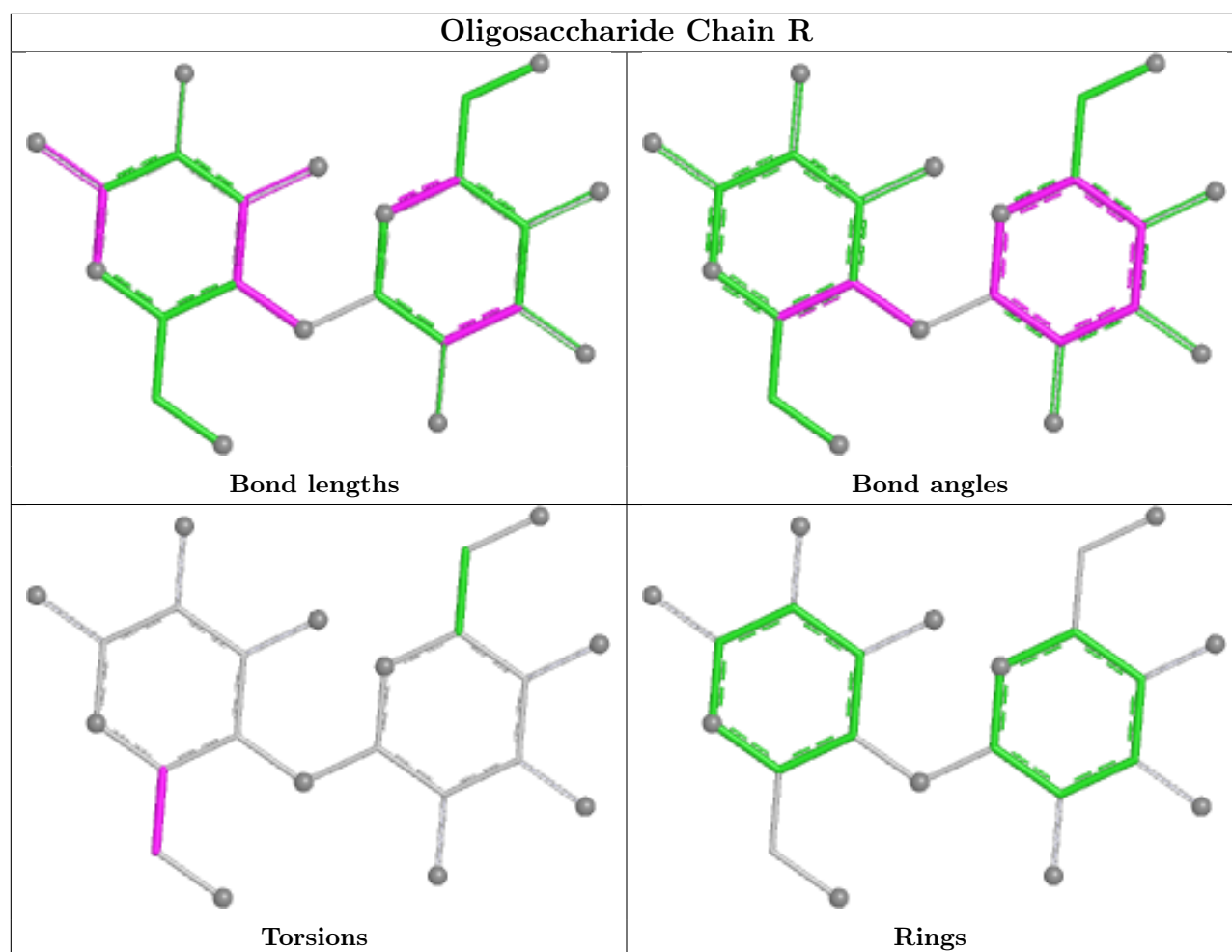
There are no ring outliers.

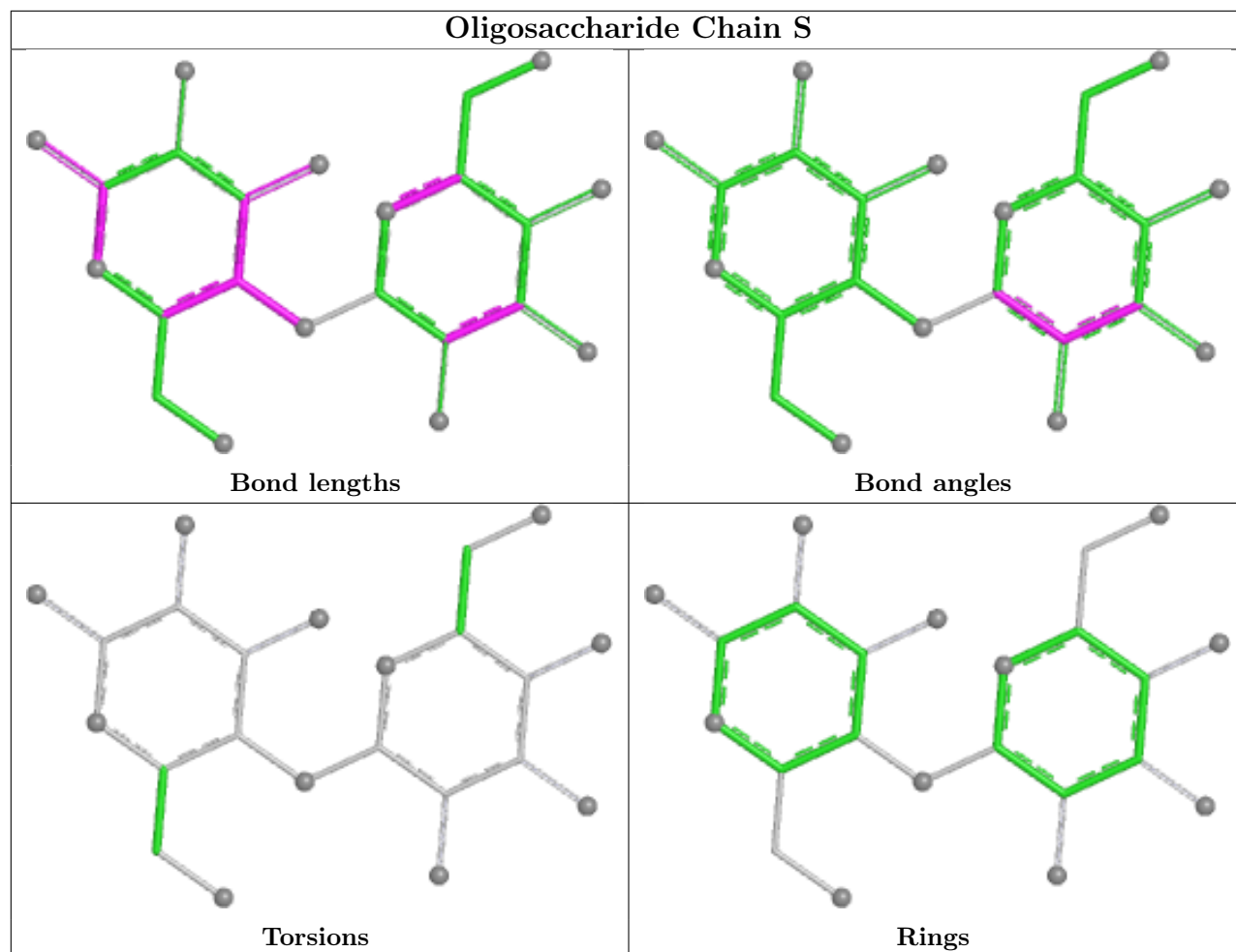
14 monomers are involved in 27 short contacts:

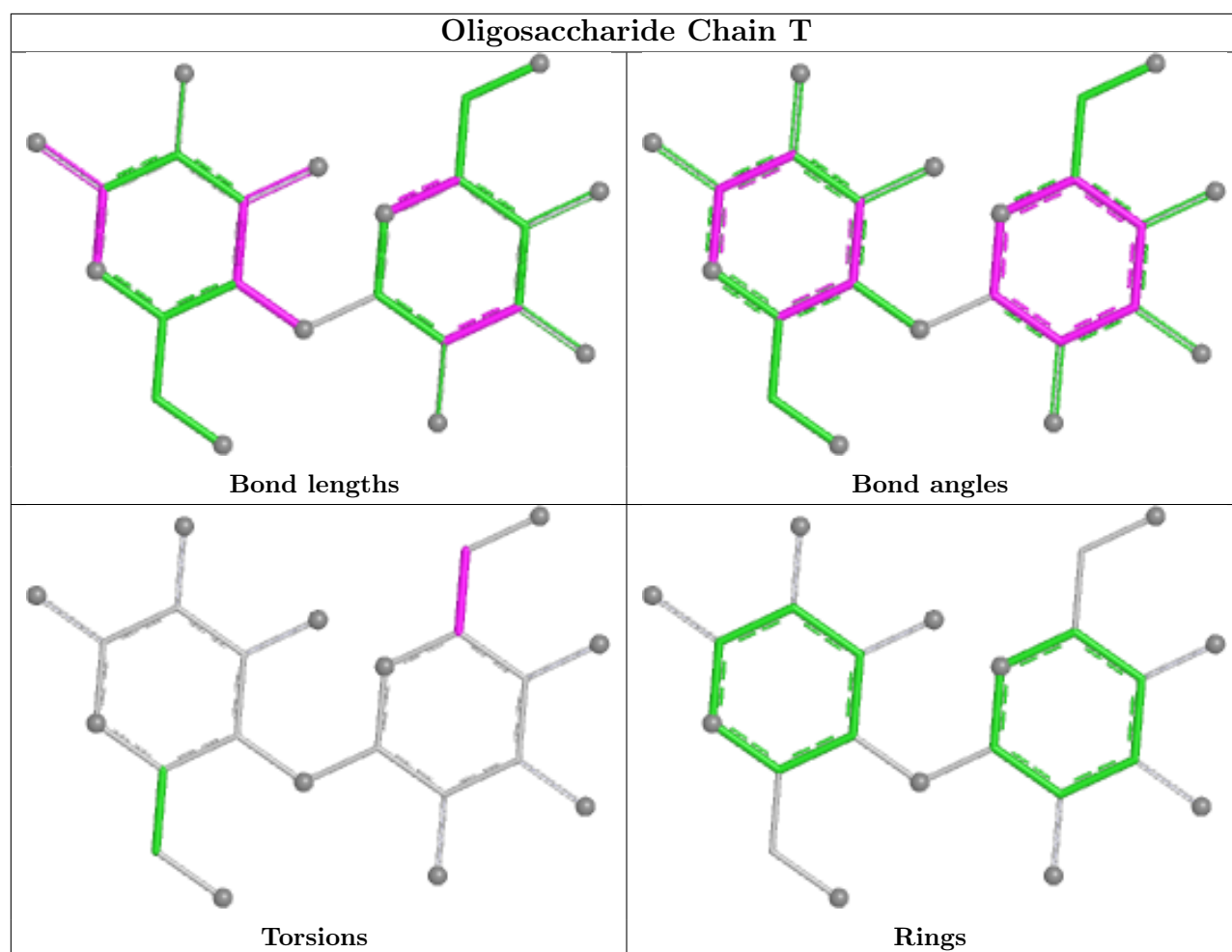
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	R	2	GAL	2	0
2	Q	1	BGC	1	0
2	T	1	BGC	1	0
2	U	2	GAL	1	0
2	W	2	GAL	4	0
2	X	1	BGC	2	0
2	V	1	BGC	3	0
2	V	2	GAL	3	0
2	R	1	BGC	3	0
2	W	1	BGC	6	0
2	Q	2	GAL	1	0
2	T	2	GAL	4	0
2	U	1	BGC	1	0
2	X	2	GAL	3	0

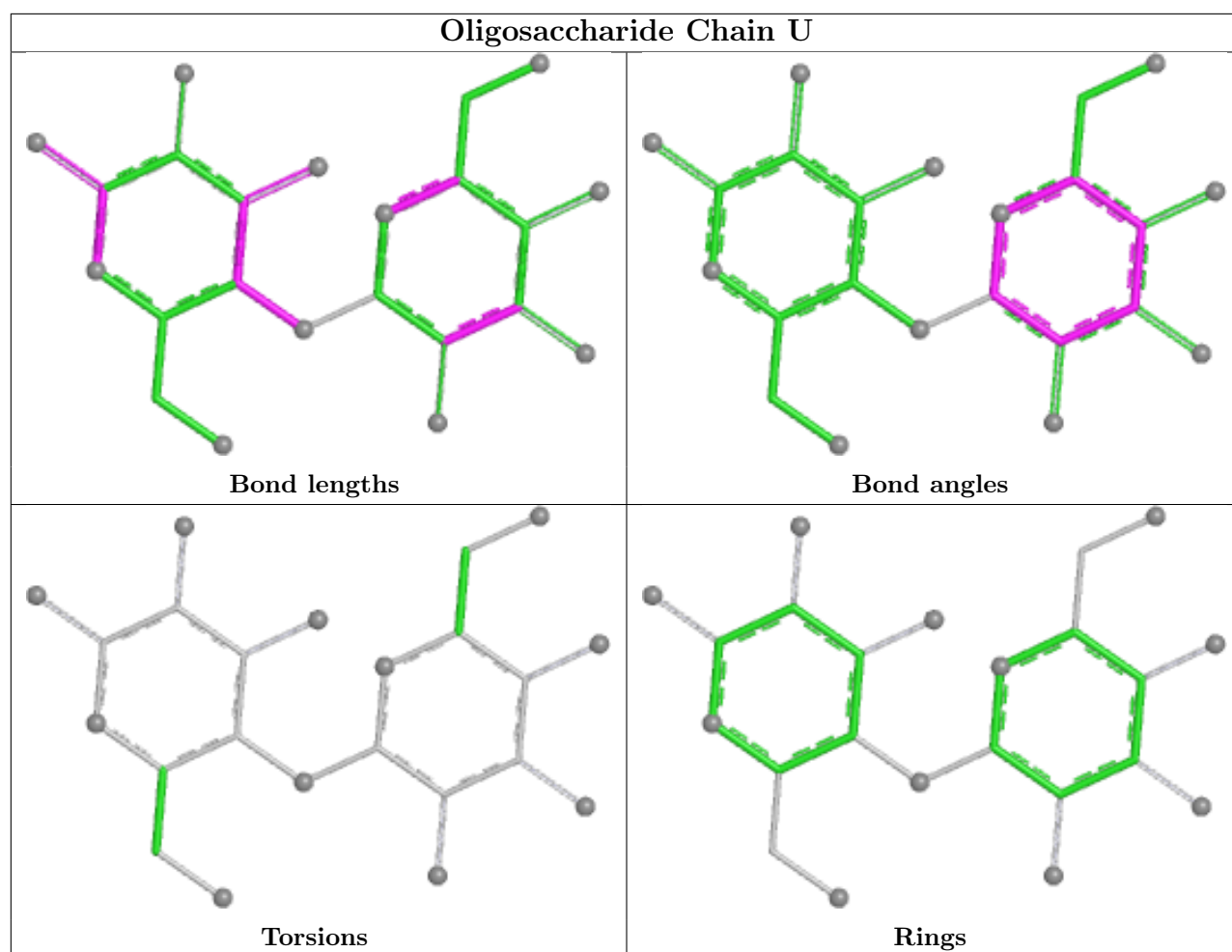
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

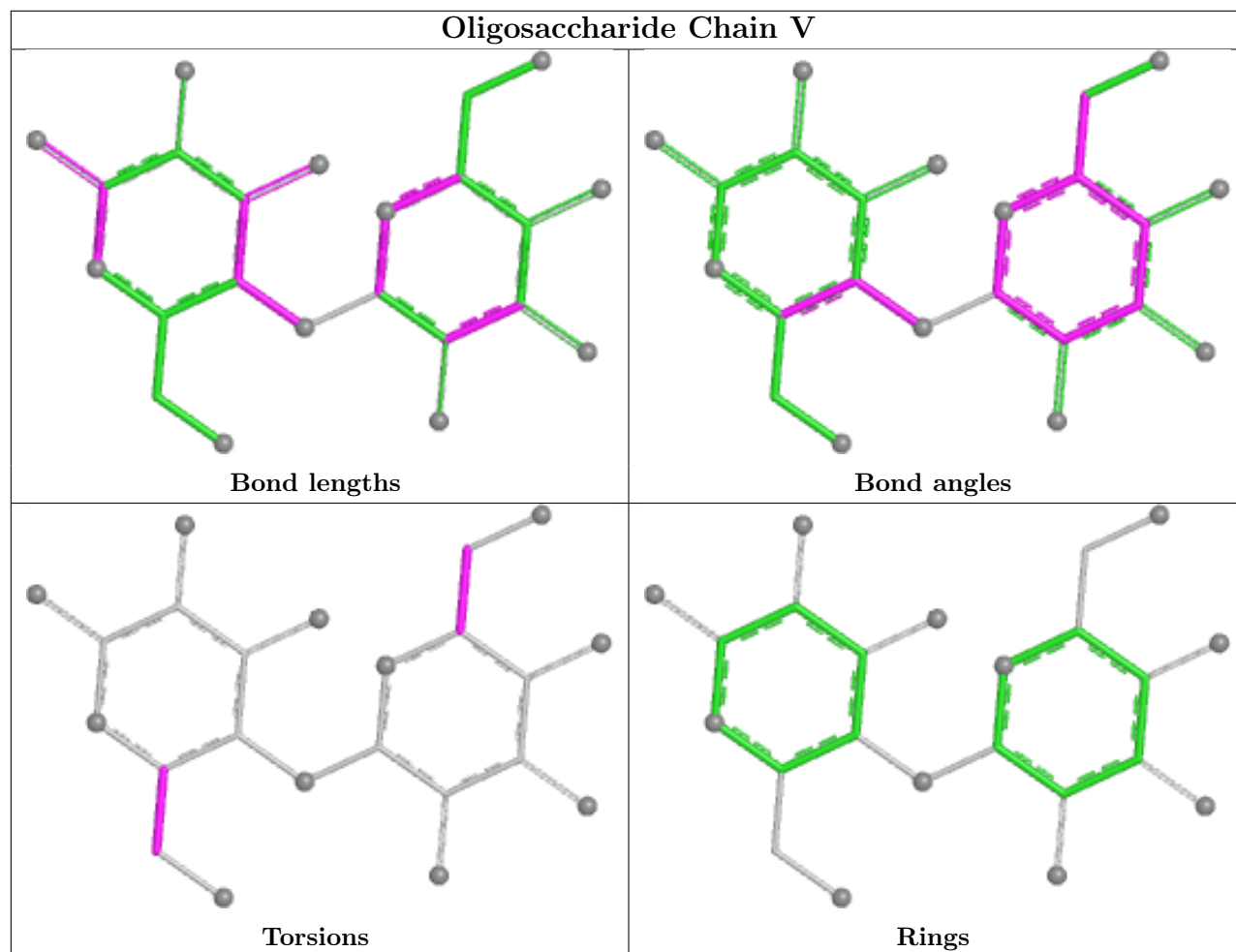


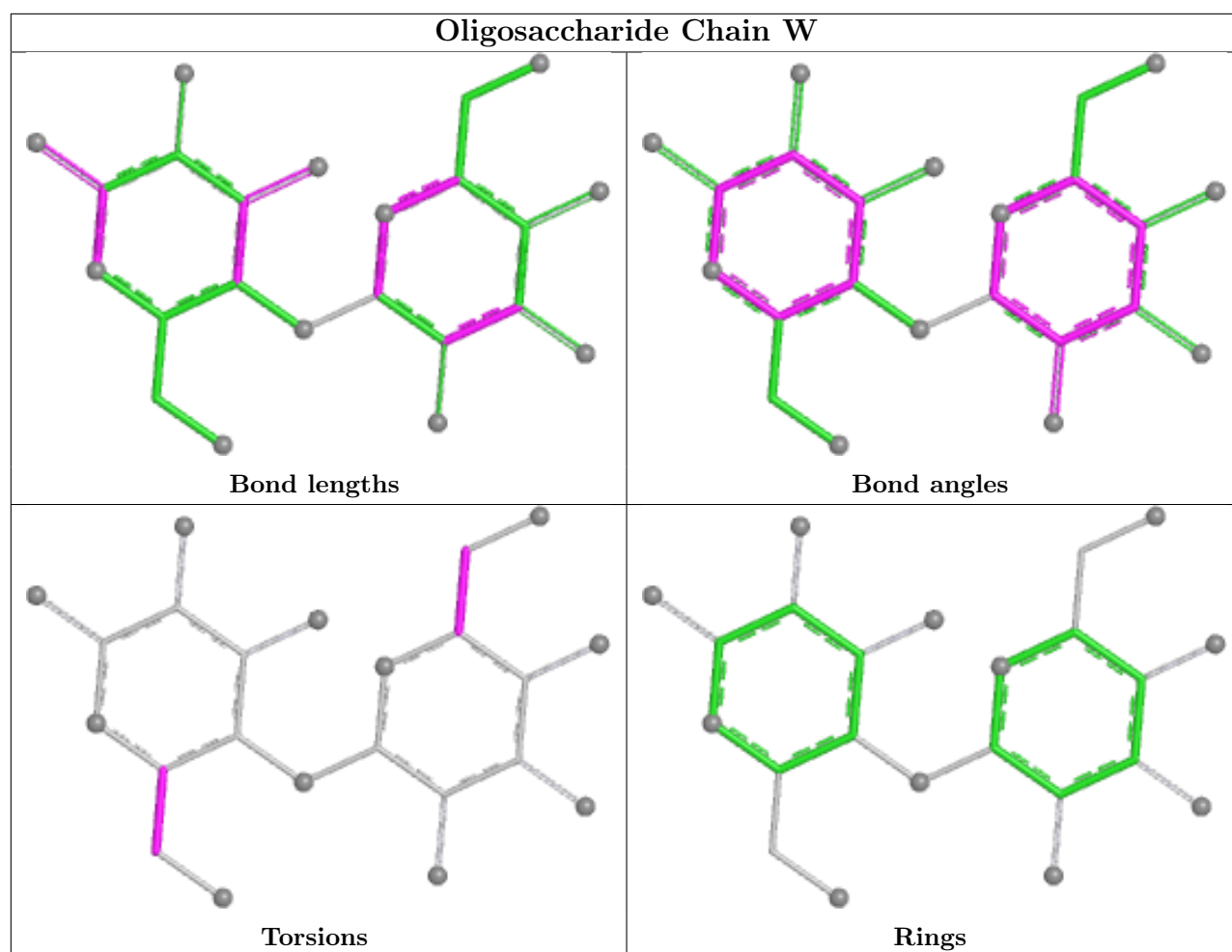


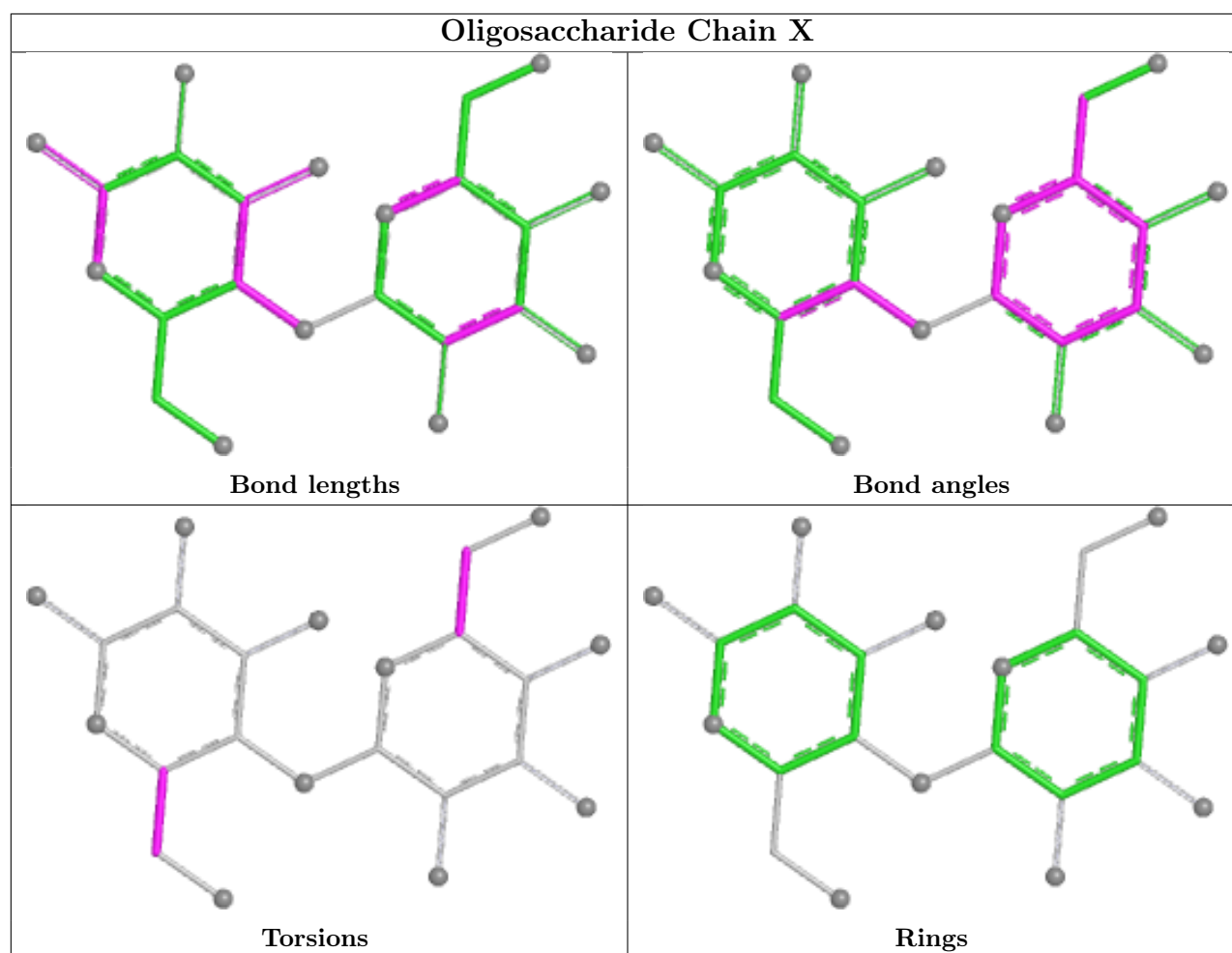












5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	131/134 (97%)	-1.38	0 100 100	19, 34, 48, 60	0
1	B	131/134 (97%)	-1.41	0 100 100	16, 31, 41, 47	0
1	C	131/134 (97%)	-1.45	0 100 100	17, 30, 43, 49	0
1	D	131/134 (97%)	-1.39	0 100 100	20, 32, 43, 54	0
1	E	131/134 (97%)	-1.47	0 100 100	16, 28, 41, 60	0
1	F	131/134 (97%)	-1.38	0 100 100	17, 35, 48, 52	0
1	G	131/134 (97%)	-1.41	0 100 100	20, 31, 44, 59	0
1	H	131/134 (97%)	-1.42	0 100 100	19, 30, 42, 50	0
1	I	131/134 (97%)	-1.47	0 100 100	18, 29, 39, 47	0
1	J	131/134 (97%)	-1.44	0 100 100	20, 32, 45, 52	0
1	K	131/134 (97%)	-1.44	0 100 100	14, 28, 40, 60	0
1	L	131/134 (97%)	-1.35	0 100 100	18, 36, 50, 53	0
1	M	131/134 (97%)	-1.48	0 100 100	18, 29, 40, 45	0
1	N	131/134 (97%)	-1.41	0 100 100	21, 32, 45, 53	0
1	O	131/134 (97%)	-1.37	0 100 100	19, 34, 49, 59	0
1	P	131/134 (97%)	-1.44	0 100 100	16, 31, 43, 51	0
All	All	2096/2144 (97%)	-1.42	0 100 100	14, 31, 46, 60	0

There are no RSRZ outliers to report.

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

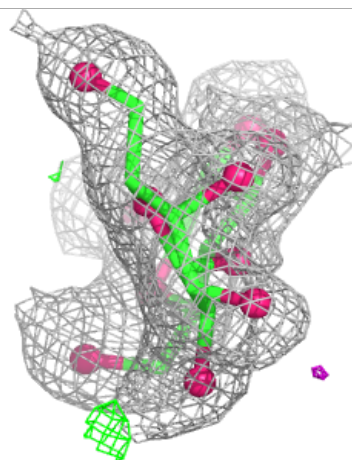
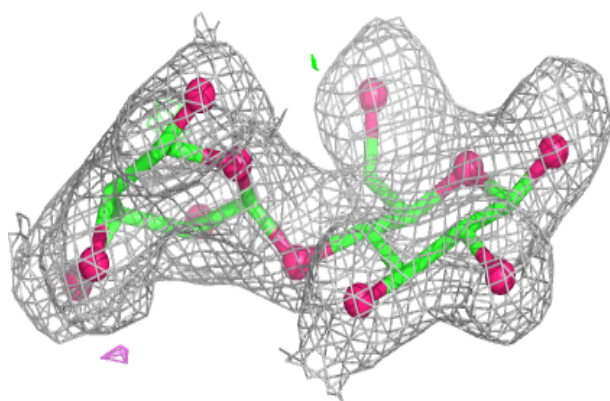
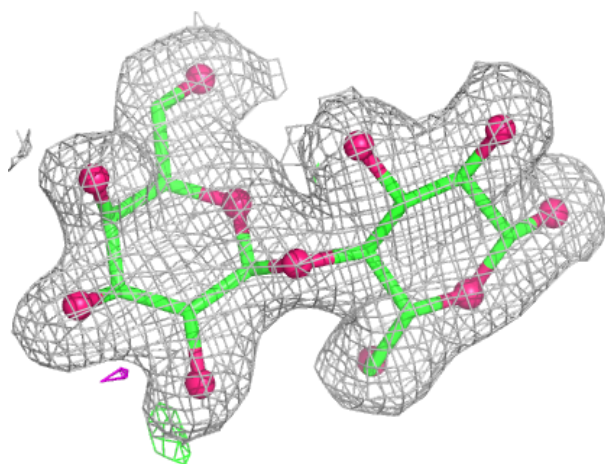
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BGC	V	1	12/12	0.98	0.04	40,47,49,52	0
2	BGC	X	1	12/12	0.98	0.04	42,50,55,59	0
2	GAL	R	2	11/12	0.99	0.03	29,36,43,45	0
2	BGC	S	1	12/12	0.99	0.03	19,29,34,41	0
2	GAL	S	2	11/12	0.99	0.02	14,17,21,25	0
2	BGC	T	1	12/12	0.99	0.04	38,43,46,47	0
2	GAL	T	2	11/12	0.99	0.05	38,42,46,50	0
2	BGC	U	1	12/12	0.99	0.03	29,34,37,38	0
2	GAL	U	2	11/12	0.99	0.03	25,28,31,32	0
2	GAL	Q	2	11/12	0.99	0.02	23,27,32,33	0
2	GAL	V	2	11/12	0.99	0.04	33,37,44,47	0
2	BGC	W	1	12/12	0.99	0.04	37,44,51,54	0
2	GAL	W	2	11/12	0.99	0.03	21,35,40,40	0
2	BGC	R	1	12/12	0.99	0.03	34,40,47,49	0
2	GAL	X	2	11/12	0.99	0.04	33,40,47,48	0
2	BGC	Q	1	12/12	1.00	0.02	24,32,35,36	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.

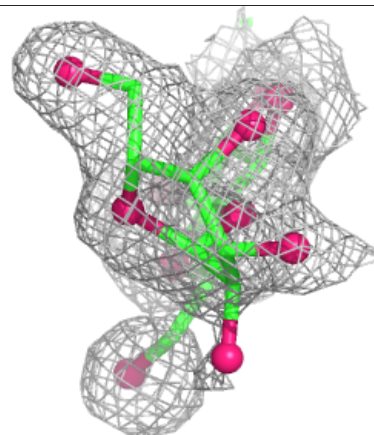
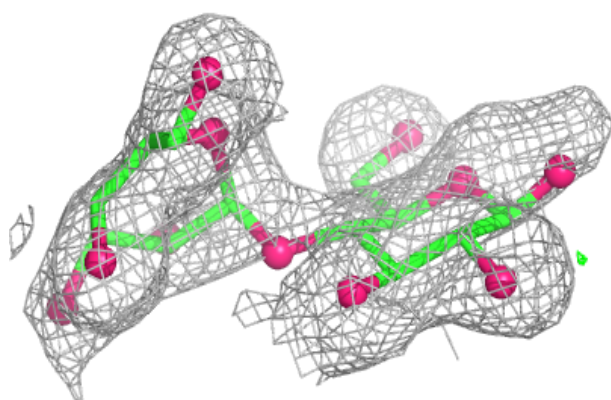
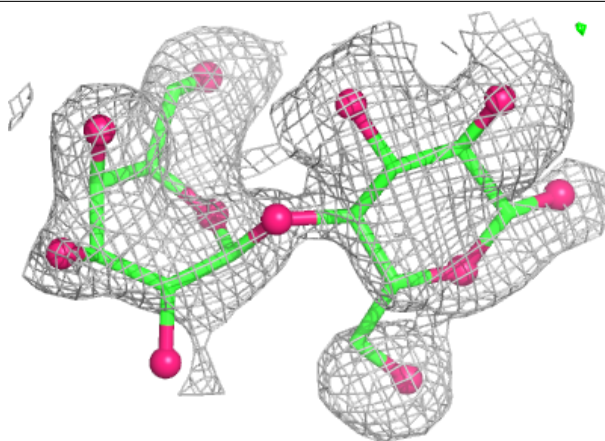
Electron density around Chain Q:

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

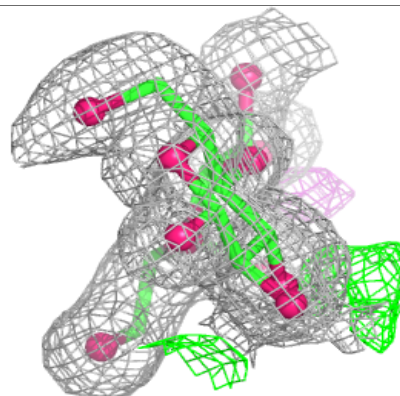
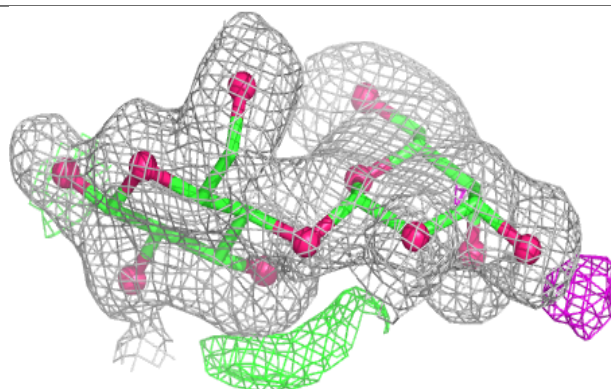
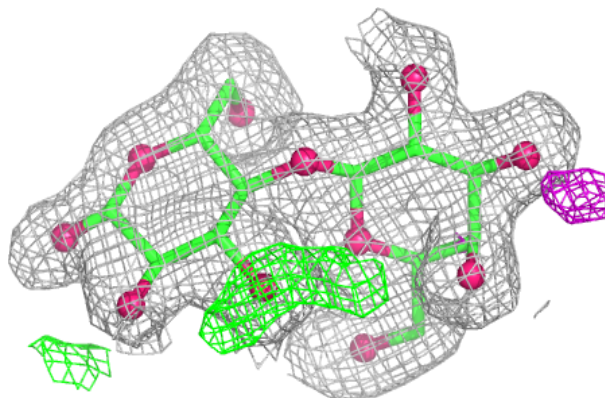


Electron density around Chain R:

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

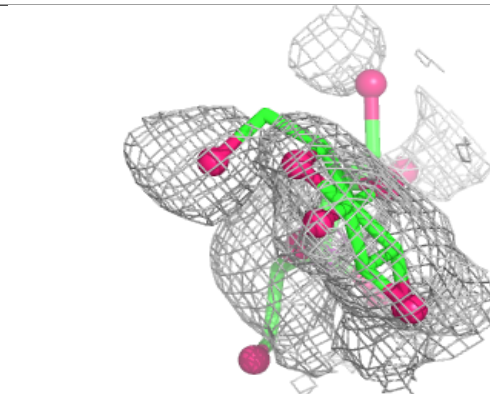
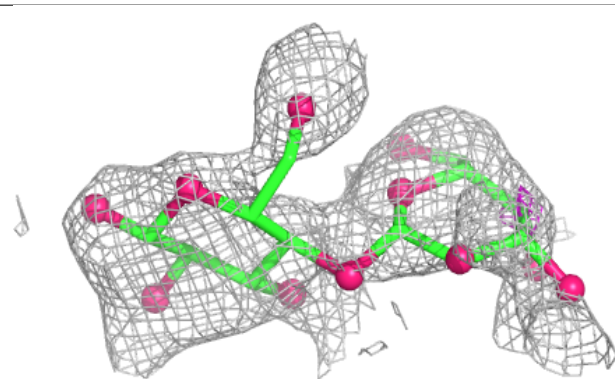
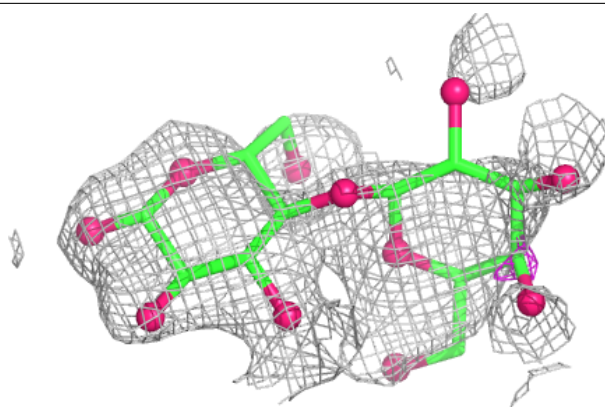
**Electron density around Chain S:**

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

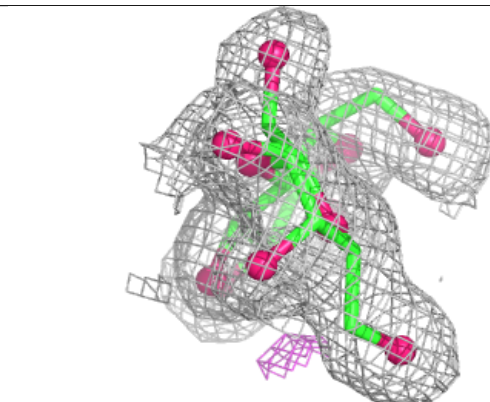
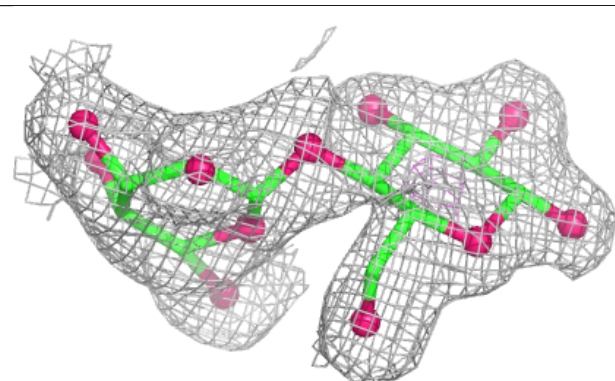
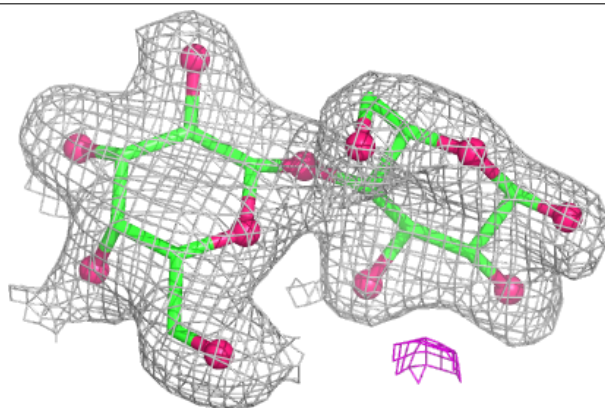


Electron density around Chain T:

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

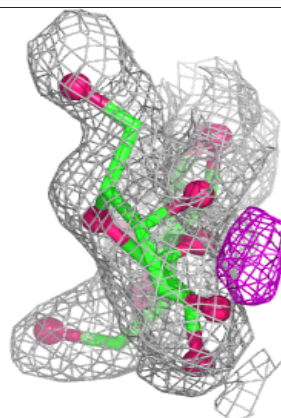
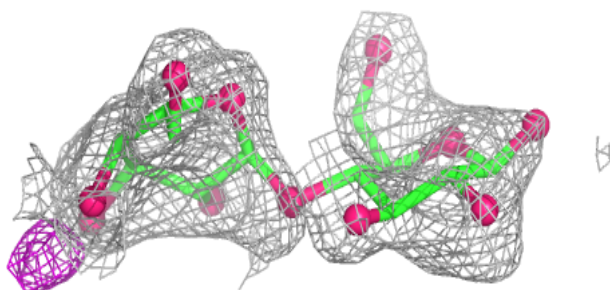
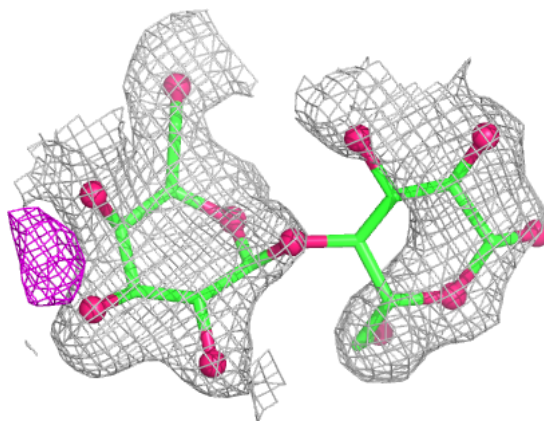
**Electron density around Chain U:**

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



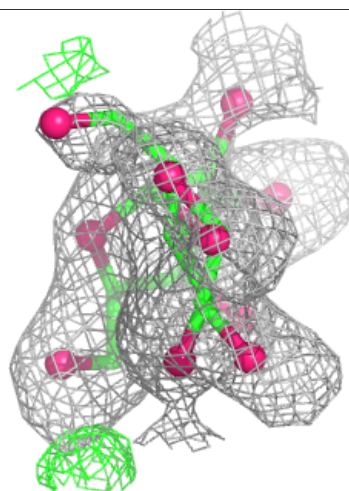
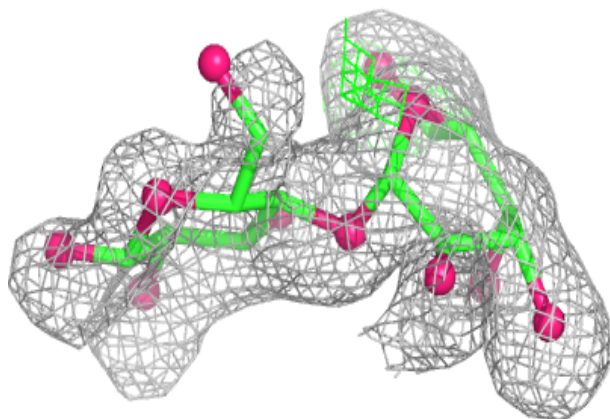
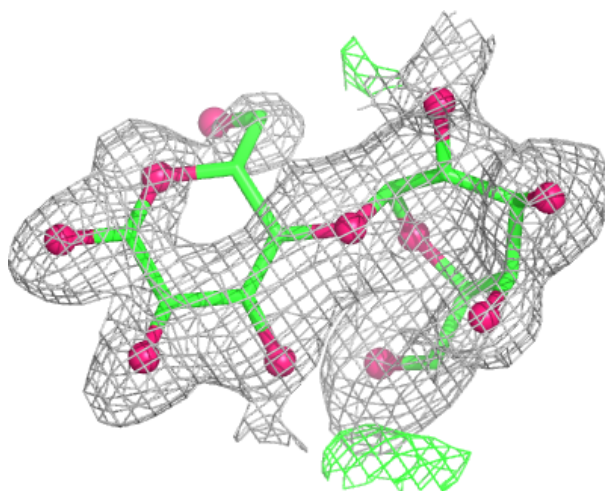
Electron density around Chain V:

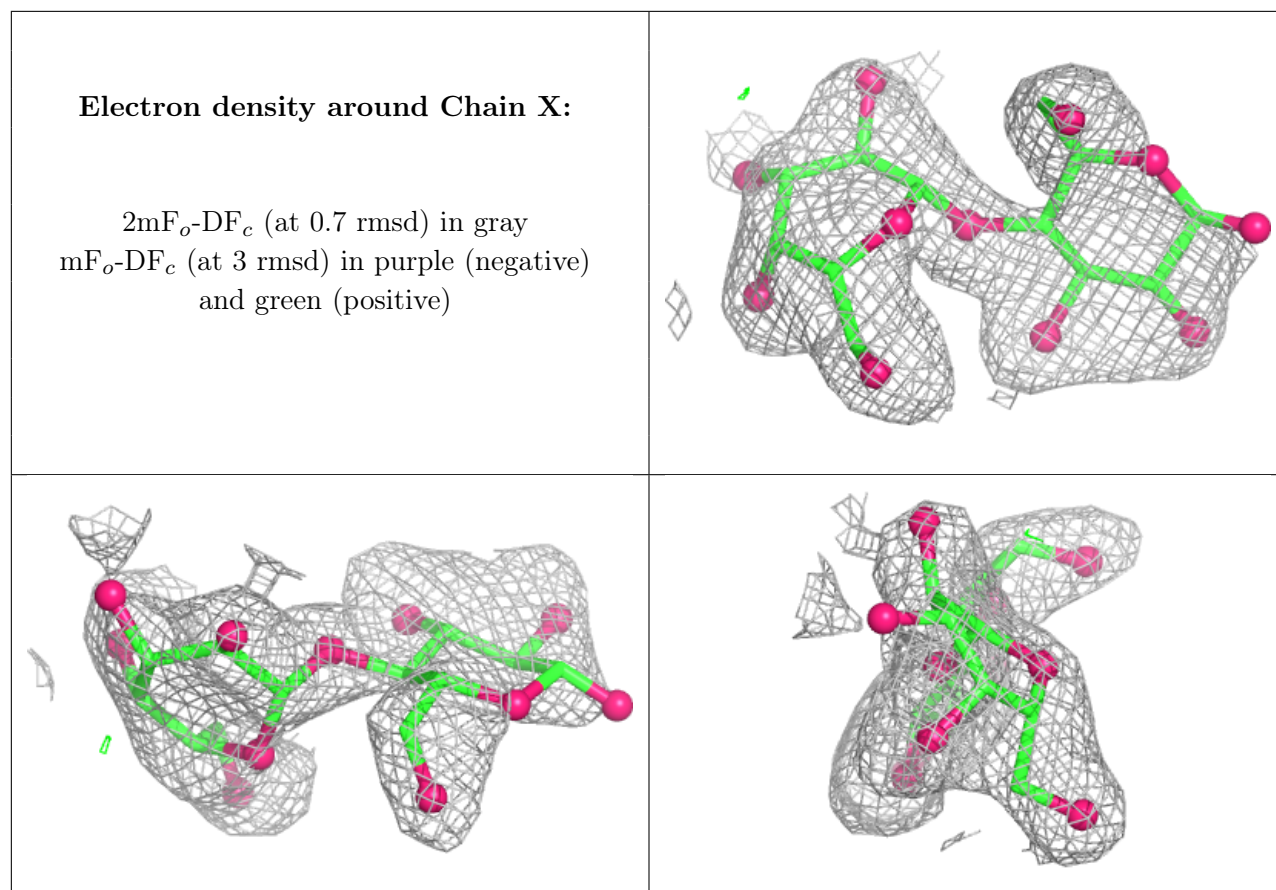
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain W:

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.