



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2020 – 11:08 AM BST

PDB ID : 5BOA
Title : Crystal Structure of the Meningitis Pathogen Streptococcus suis adhesion Fhb bound to the disaccharide receptor Gb2
Authors : Zhang, C.; Yu, Y.; Yang, M.; Jiang, Y.
Deposited on : 2015-05-27
Resolution : 2.71 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

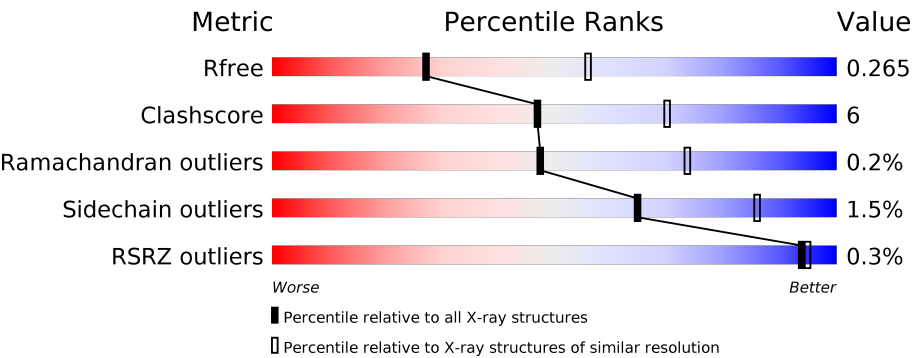
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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	226	<div><div></div><div>68%18%14%</div></div>
1	B	226	<div><div></div><div>77%11%12%</div></div>
1	C	226	<div><div></div><div>74%12%12%</div></div>
1	D	226	<div><div></div><div>75%12%13%</div></div>
1	E	226	<div><div></div><div>75%10%15%</div></div>
1	F	226	<div><div></div><div>65%19%15%</div></div>

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Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	H	2	 100%
2	I	2	 100%
2	J	2	 50%50%
2	K	2	 100%
2	L	2	 50%50%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9415 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 Translation initiation factor 2 (IF-2 GTPase).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	0	0
			1549	975	261	312	1			
1	B	198	Total	C	N	O	S	0	0	0
			1570	987	265	317	1			
1	C	198	Total	C	N	O	S	0	0	0
			1565	982	265	317	1			
1	D	196	Total	C	N	O	S	0	0	0
			1561	983	264	313	1			
1	E	191	Total	C	N	O	S	0	0	0
			1515	954	256	304	1			
1	F	192	Total	C	N	O	S	0	0	0
			1517	953	258	305	1			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	118	MET	-	expression tag	UNP A4VT01
A	119	GLY	-	expression tag	UNP A4VT01
A	120	SER	-	expression tag	UNP A4VT01
A	121	SER	-	expression tag	UNP A4VT01
A	122	HIS	-	expression tag	UNP A4VT01
A	123	HIS	-	expression tag	UNP A4VT01
A	124	HIS	-	expression tag	UNP A4VT01
A	125	HIS	-	expression tag	UNP A4VT01
A	126	HIS	-	expression tag	UNP A4VT01
A	127	HIS	-	expression tag	UNP A4VT01
A	128	SER	-	expression tag	UNP A4VT01
A	129	SER	-	expression tag	UNP A4VT01
A	130	GLY	-	expression tag	UNP A4VT01
A	131	LEU	-	expression tag	UNP A4VT01
A	132	VAL	-	expression tag	UNP A4VT01
A	133	PRO	-	expression tag	UNP A4VT01
A	134	ARG	-	expression tag	UNP A4VT01

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Chain	Residue	Modelled	Actual	Comment	Reference
A	135	GLY	-	expression tag	UNP A4VT01
A	136	SER	-	expression tag	UNP A4VT01
A	137	HIS	-	expression tag	UNP A4VT01
A	138	MET	-	expression tag	UNP A4VT01
B	118	MET	-	expression tag	UNP A4VT01
B	119	GLY	-	expression tag	UNP A4VT01
B	120	SER	-	expression tag	UNP A4VT01
B	121	SER	-	expression tag	UNP A4VT01
B	122	HIS	-	expression tag	UNP A4VT01
B	123	HIS	-	expression tag	UNP A4VT01
B	124	HIS	-	expression tag	UNP A4VT01
B	125	HIS	-	expression tag	UNP A4VT01
B	126	HIS	-	expression tag	UNP A4VT01
B	127	HIS	-	expression tag	UNP A4VT01
B	128	SER	-	expression tag	UNP A4VT01
B	129	SER	-	expression tag	UNP A4VT01
B	130	GLY	-	expression tag	UNP A4VT01
B	131	LEU	-	expression tag	UNP A4VT01
B	132	VAL	-	expression tag	UNP A4VT01
B	133	PRO	-	expression tag	UNP A4VT01
B	134	ARG	-	expression tag	UNP A4VT01
B	135	GLY	-	expression tag	UNP A4VT01
B	136	SER	-	expression tag	UNP A4VT01
B	137	HIS	-	expression tag	UNP A4VT01
B	138	MET	-	expression tag	UNP A4VT01
C	118	MET	-	expression tag	UNP A4VT01
C	119	GLY	-	expression tag	UNP A4VT01
C	120	SER	-	expression tag	UNP A4VT01
C	121	SER	-	expression tag	UNP A4VT01
C	122	HIS	-	expression tag	UNP A4VT01
C	123	HIS	-	expression tag	UNP A4VT01
C	124	HIS	-	expression tag	UNP A4VT01
C	125	HIS	-	expression tag	UNP A4VT01
C	126	HIS	-	expression tag	UNP A4VT01
C	127	HIS	-	expression tag	UNP A4VT01
C	128	SER	-	expression tag	UNP A4VT01
C	129	SER	-	expression tag	UNP A4VT01
C	130	GLY	-	expression tag	UNP A4VT01
C	131	LEU	-	expression tag	UNP A4VT01
C	132	VAL	-	expression tag	UNP A4VT01
C	133	PRO	-	expression tag	UNP A4VT01
C	134	ARG	-	expression tag	UNP A4VT01

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Chain	Residue	Modelled	Actual	Comment	Reference
C	135	GLY	-	expression tag	UNP A4VT01
C	136	SER	-	expression tag	UNP A4VT01
C	137	HIS	-	expression tag	UNP A4VT01
C	138	MET	-	expression tag	UNP A4VT01
D	118	MET	-	expression tag	UNP A4VT01
D	119	GLY	-	expression tag	UNP A4VT01
D	120	SER	-	expression tag	UNP A4VT01
D	121	SER	-	expression tag	UNP A4VT01
D	122	HIS	-	expression tag	UNP A4VT01
D	123	HIS	-	expression tag	UNP A4VT01
D	124	HIS	-	expression tag	UNP A4VT01
D	125	HIS	-	expression tag	UNP A4VT01
D	126	HIS	-	expression tag	UNP A4VT01
D	127	HIS	-	expression tag	UNP A4VT01
D	128	SER	-	expression tag	UNP A4VT01
D	129	SER	-	expression tag	UNP A4VT01
D	130	GLY	-	expression tag	UNP A4VT01
D	131	LEU	-	expression tag	UNP A4VT01
D	132	VAL	-	expression tag	UNP A4VT01
D	133	PRO	-	expression tag	UNP A4VT01
D	134	ARG	-	expression tag	UNP A4VT01
D	135	GLY	-	expression tag	UNP A4VT01
D	136	SER	-	expression tag	UNP A4VT01
D	137	HIS	-	expression tag	UNP A4VT01
D	138	MET	-	expression tag	UNP A4VT01
E	118	MET	-	expression tag	UNP A4VT01
E	119	GLY	-	expression tag	UNP A4VT01
E	120	SER	-	expression tag	UNP A4VT01
E	121	SER	-	expression tag	UNP A4VT01
E	122	HIS	-	expression tag	UNP A4VT01
E	123	HIS	-	expression tag	UNP A4VT01
E	124	HIS	-	expression tag	UNP A4VT01
E	125	HIS	-	expression tag	UNP A4VT01
E	126	HIS	-	expression tag	UNP A4VT01
E	127	HIS	-	expression tag	UNP A4VT01
E	128	SER	-	expression tag	UNP A4VT01
E	129	SER	-	expression tag	UNP A4VT01
E	130	GLY	-	expression tag	UNP A4VT01
E	131	LEU	-	expression tag	UNP A4VT01
E	132	VAL	-	expression tag	UNP A4VT01
E	133	PRO	-	expression tag	UNP A4VT01
E	134	ARG	-	expression tag	UNP A4VT01

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Chain	Residue	Modelled	Actual	Comment	Reference
E	135	GLY	-	expression tag	UNP A4VT01
E	136	SER	-	expression tag	UNP A4VT01
E	137	HIS	-	expression tag	UNP A4VT01
E	138	MET	-	expression tag	UNP A4VT01
F	118	MET	-	expression tag	UNP A4VT01
F	119	GLY	-	expression tag	UNP A4VT01
F	120	SER	-	expression tag	UNP A4VT01
F	121	SER	-	expression tag	UNP A4VT01
F	122	HIS	-	expression tag	UNP A4VT01
F	123	HIS	-	expression tag	UNP A4VT01
F	124	HIS	-	expression tag	UNP A4VT01
F	125	HIS	-	expression tag	UNP A4VT01
F	126	HIS	-	expression tag	UNP A4VT01
F	127	HIS	-	expression tag	UNP A4VT01
F	128	SER	-	expression tag	UNP A4VT01
F	129	SER	-	expression tag	UNP A4VT01
F	130	GLY	-	expression tag	UNP A4VT01
F	131	LEU	-	expression tag	UNP A4VT01
F	132	VAL	-	expression tag	UNP A4VT01
F	133	PRO	-	expression tag	UNP A4VT01
F	134	ARG	-	expression tag	UNP A4VT01
F	135	GLY	-	expression tag	UNP A4VT01
F	136	SER	-	expression tag	UNP A4VT01
F	137	HIS	-	expression tag	UNP A4VT01
F	138	MET	-	expression tag	UNP A4VT01

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	G	2	Total	C	O	0	0	0
			23	12	11			
2	H	2	Total	C	O	0	0	0
			23	12	11			
2	I	2	Total	C	O	0	0	0
			23	12	11			
2	J	2	Total	C	O	0	0	0
			23	12	11			

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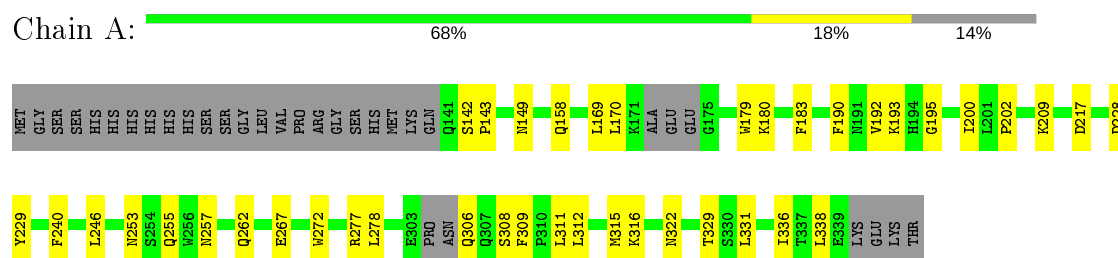
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	K	2	Total	C	O	0	0	0
			23	12	11			
2	L	2	Total	C	O	0	0	0
			23	12	11			

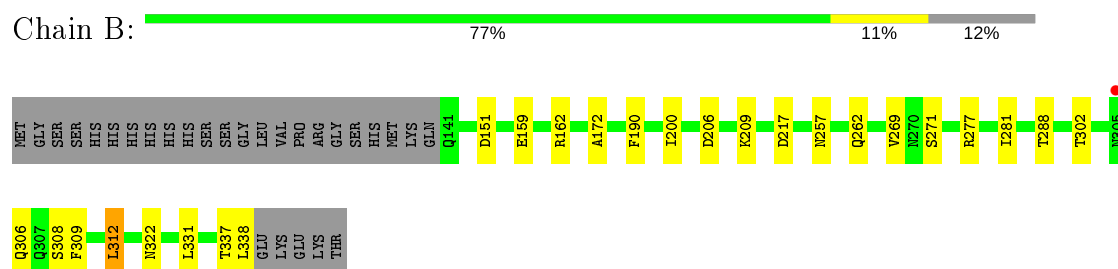
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

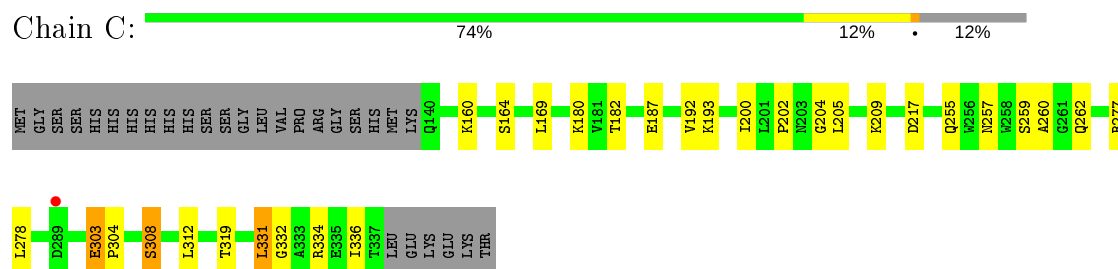
- Molecule 1: Translation initiation factor 2 (IF-2 GTPase)



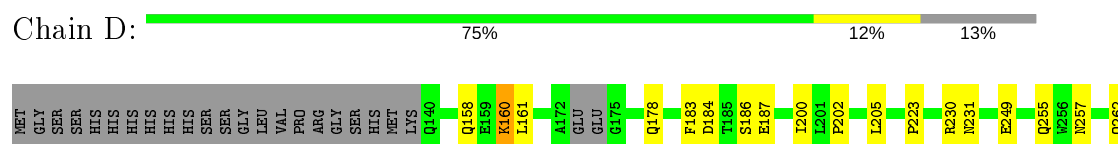
- Molecule 1: Translation initiation factor 2 (IF-2 GTPase)

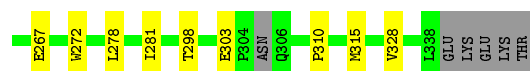


- Molecule 1: Translation initiation factor 2 (IF-2 GTPase)

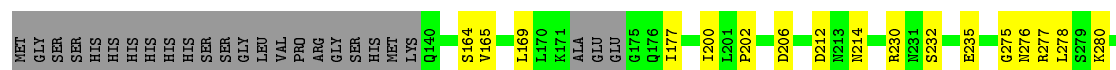


- Molecule 1: Translation initiation factor 2 (IF-2 GTPase)

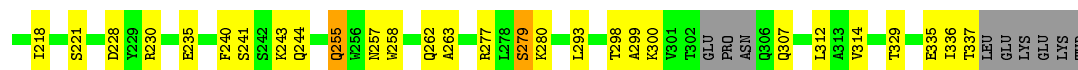
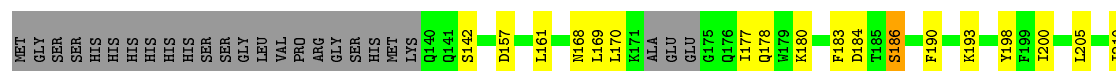




- Molecule 1: Translation initiation factor 2 (IF-2 GTPase)



- Molecule 1: Translation initiation factor 2 (IF-2 GTPase)



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



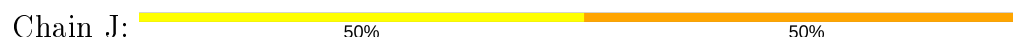
- Molecule 2: alpha-D-galactopyranose-(1-4)-beta-D-galactopyranose



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



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

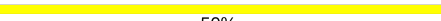



- Molecule 2: alpha-D-galactopyranose-(1-4)-beta-D-galactopyranose

Chain K:  100%

GAL1
GAL2

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

Chain L:  50%  50%

GAL1
GAL2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	126.49 Å 136.57 Å 75.55 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.49 – 2.71 48.50 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.49-2.71) 99.5 (48.50-2.71)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.20 (at 2.73 Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.191 , 0.264 0.195 , 0.265	Depositor DCC
R_{free} test set	1806 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.856	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9415	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% 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: GLA, 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	0.48	0/1580	0.61	0/2140
1	B	0.42	0/1604	0.59	0/2179
1	C	0.43	0/1598	0.62	1/2169 (0.0%)
1	D	0.41	0/1593	0.57	0/2159
1	E	0.44	0/1546	0.61	0/2096
1	F	0.43	0/1547	0.62	0/2097
All	All	0.43	0/9468	0.60	1/12840 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	331	LEU	CA-CB-CG	6.20	129.56	115.30

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	1549	0	1490	25	0
1	B	1570	0	1501	12	0
1	C	1565	0	1496	17	0
1	D	1561	0	1504	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1515	0	1450	15	0
1	F	1517	0	1451	33	0
2	G	23	0	21	0	0
2	H	23	0	20	0	0
2	I	23	0	20	0	0
2	J	23	0	20	1	0
2	K	23	0	20	0	0
2	L	23	0	20	1	0
All	All	9415	0	9013	114	0

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

The worst 5 of 114 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:183:PHE:HD1	1:A:315:MET:HE2	1.36	0.89
1:D:160:LYS:HE3	1:D:187:GLU:HG3	1.68	0.75
1:A:277:ARG:NH2	1:A:308:SER:OG	2.24	0.70
1:B:277:ARG:NH2	1:B:308:SER:OG	2.24	0.70
1:F:184:ASP:OD1	1:F:186:SER:OG	2.09	0.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	188/226 (83%)	177 (94%)	11 (6%)	0	100	100
1	B	196/226 (87%)	182 (93%)	14 (7%)	0	100	100
1	C	196/226 (87%)	178 (91%)	18 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	190/226 (84%)	179 (94%)	10 (5%)	1 (0%)	29	54
1	E	185/226 (82%)	173 (94%)	11 (6%)	1 (0%)	29	54
1	F	186/226 (82%)	172 (92%)	14 (8%)	0	100	100
All	All	1141/1356 (84%)	1061 (93%)	78 (7%)	2 (0%)	47	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	276	ASN
1	D	303	GLU

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	175/204 (86%)	173 (99%)	2 (1%)	73	90
1	B	176/204 (86%)	173 (98%)	3 (2%)	60	84
1	C	175/204 (86%)	172 (98%)	3 (2%)	60	84
1	D	176/204 (86%)	174 (99%)	2 (1%)	73	90
1	E	170/204 (83%)	168 (99%)	2 (1%)	71	88
1	F	170/204 (83%)	166 (98%)	4 (2%)	49	77
All	All	1042/1224 (85%)	1026 (98%)	16 (2%)	65	86

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	334	ARG
1	D	160	LYS
1	F	186	SER
1	C	308	SER
1	F	221	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	255	GLN
1	F	244	GLN
1	E	255	GLN
1	A	306	GLN
1	F	214	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 ⓘ

12 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	GAL	G	1	2	12,12,12	1.19	2 (16%)	17,17,17	1.07	1 (5%)
2	GLA	G	2	2	11,11,12	1.90	3 (27%)	15,15,17	1.34	2 (13%)
2	GAL	H	1	2	12,12,12	1.41	3 (25%)	17,17,17	0.90	0
2	GLA	H	2	2	11,11,12	1.50	2 (18%)	15,15,17	1.43	3 (20%)
2	GAL	I	1	2	12,12,12	1.34	2 (16%)	17,17,17	1.03	0
2	GLA	I	2	2	11,11,12	1.77	3 (27%)	15,15,17	0.79	0
2	GAL	J	1	2	12,12,12	1.34	1 (8%)	17,17,17	1.37	3 (17%)
2	GLA	J	2	2	11,11,12	1.70	3 (27%)	15,15,17	1.26	1 (6%)
2	GAL	K	1	2	12,12,12	1.38	3 (25%)	17,17,17	0.98	0
2	GLA	K	2	2	11,11,12	1.50	1 (9%)	15,15,17	1.02	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GAL	L	1	2	12,12,12	1.31	1 (8%)	17,17,17	0.88	0
2	GLA	L	2	2	11,11,12	1.62	2 (18%)	15,15,17	1.02	1 (6%)

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	GAL	G	1	2	-	0/2/22/22	0/1/1/1
2	GLA	G	2	2	-	0/2/19/22	0/1/1/1
2	GAL	H	1	2	-	0/2/22/22	0/1/1/1
2	GLA	H	2	2	-	0/2/19/22	0/1/1/1
2	GAL	I	1	2	-	2/2/22/22	0/1/1/1
2	GLA	I	2	2	-	1/2/19/22	0/1/1/1
2	GAL	J	1	2	-	0/2/22/22	0/1/1/1
2	GLA	J	2	2	-	0/2/19/22	0/1/1/1
2	GAL	K	1	2	-	0/2/22/22	0/1/1/1
2	GLA	K	2	2	-	0/2/19/22	0/1/1/1
2	GAL	L	1	2	-	0/2/22/22	0/1/1/1
2	GLA	L	2	2	-	0/2/19/22	0/1/1/1

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	2	GLA	C2-C3	-4.62	1.45	1.52
2	I	2	GLA	C2-C3	-4.40	1.46	1.52
2	J	2	GLA	C2-C3	-4.12	1.46	1.52
2	L	2	GLA	C2-C3	-4.06	1.46	1.52
2	K	2	GLA	C2-C3	-3.64	1.47	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	2	GLA	C1-C2-C3	3.39	113.84	109.67
2	H	2	GLA	C1-C2-C3	3.23	113.64	109.67
2	J	1	GAL	C4-C3-C2	3.08	116.20	110.82
2	G	2	GLA	C3-C4-C5	-3.07	104.76	110.24
2	H	2	GLA	O2-C2-C1	-2.95	103.11	109.15

There are no chirality outliers.

All (3) torsion outliers are listed below:

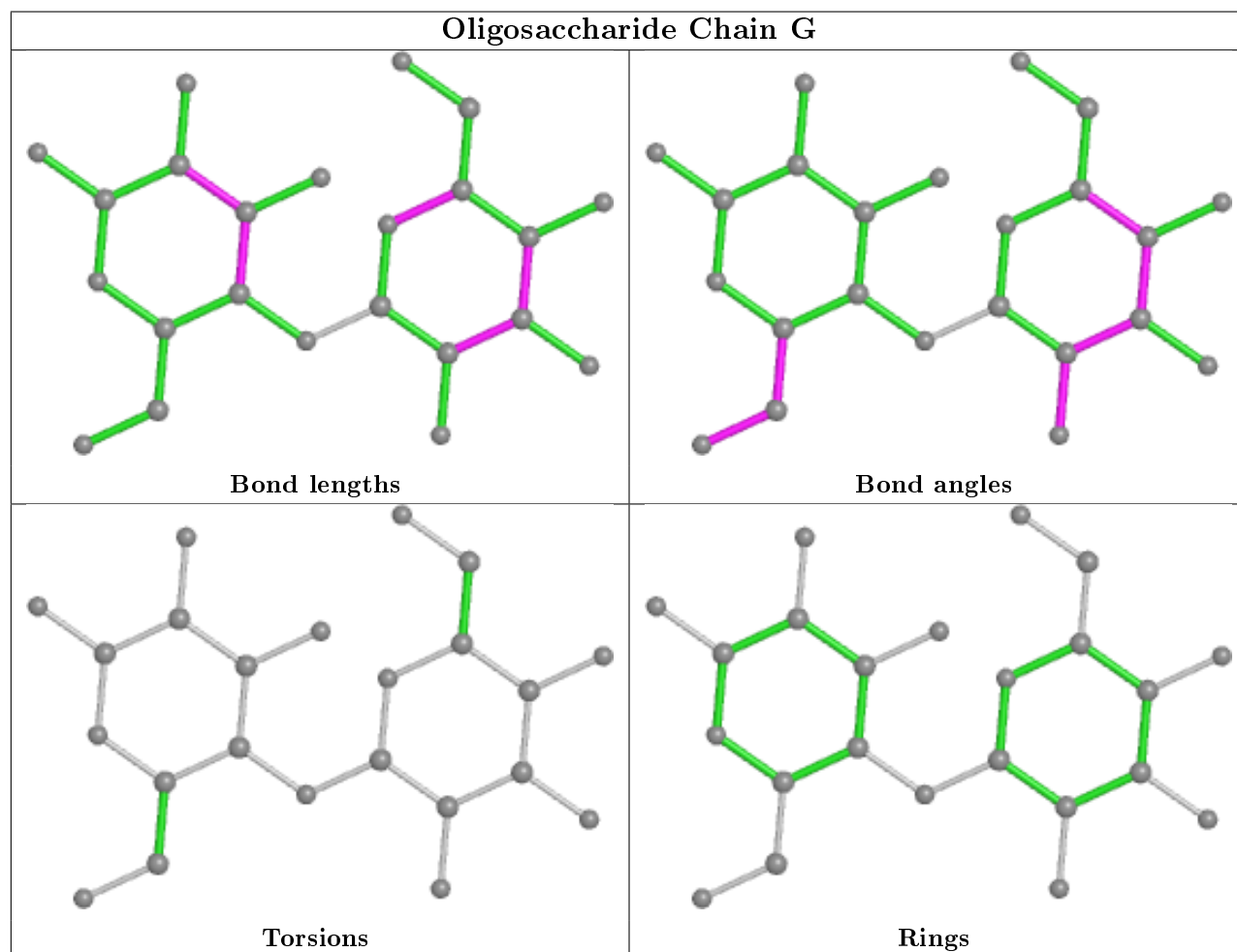
Mol	Chain	Res	Type	Atoms
2	I	1	GAL	C4-C5-C6-O6
2	I	1	GAL	O5-C5-C6-O6
2	I	2	GLA	C4-C5-C6-O6

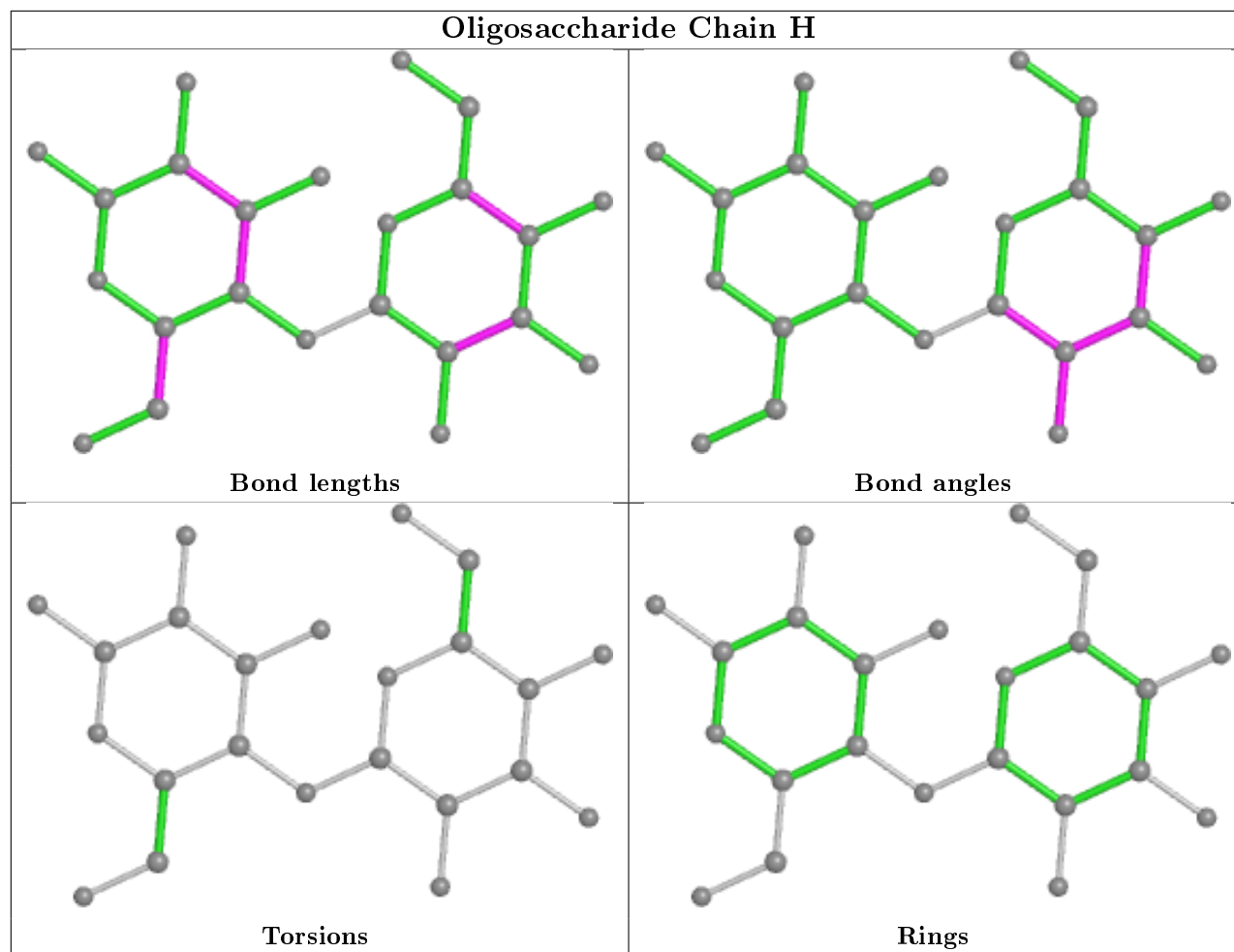
There are no ring outliers.

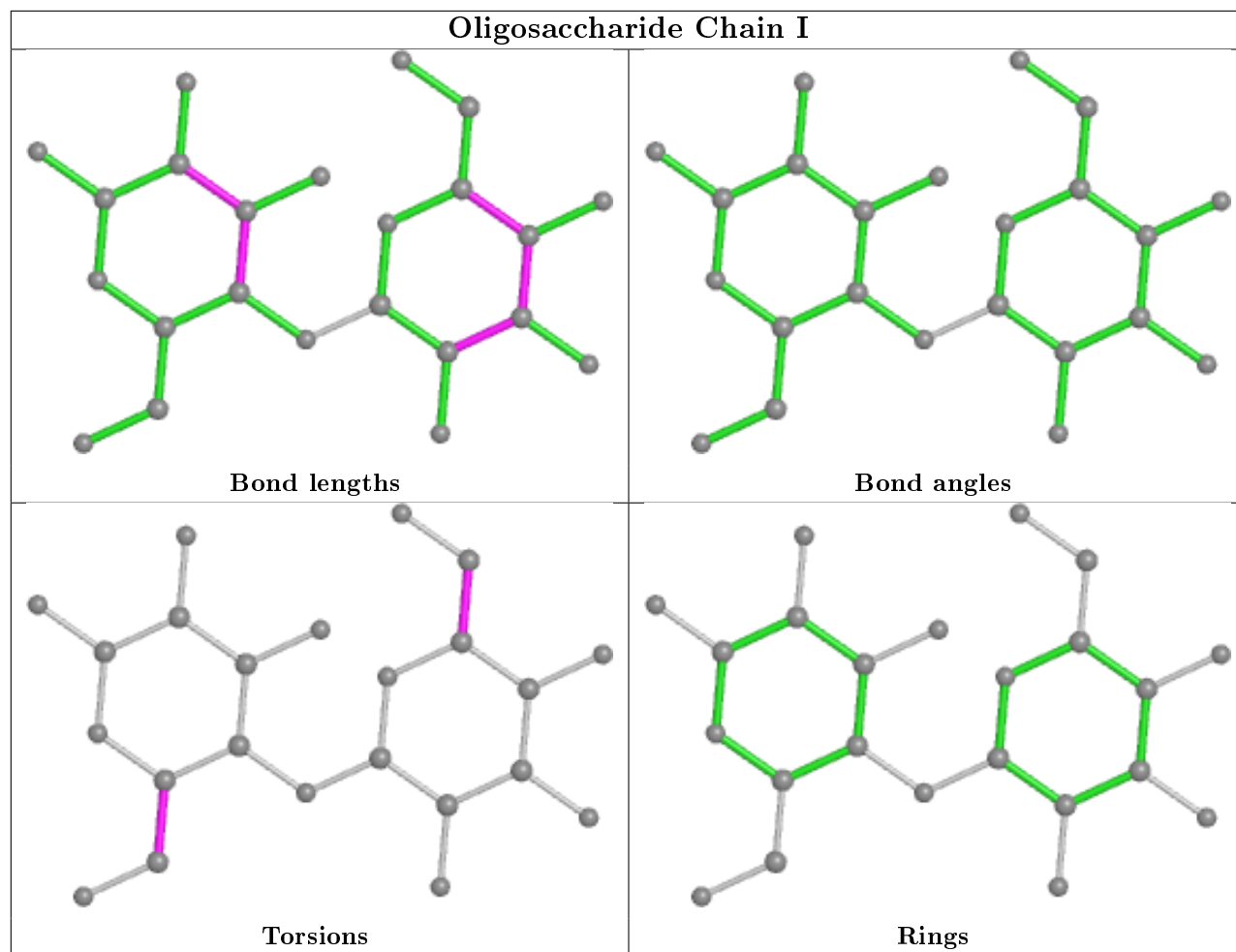
2 monomers are involved in 2 short contacts:

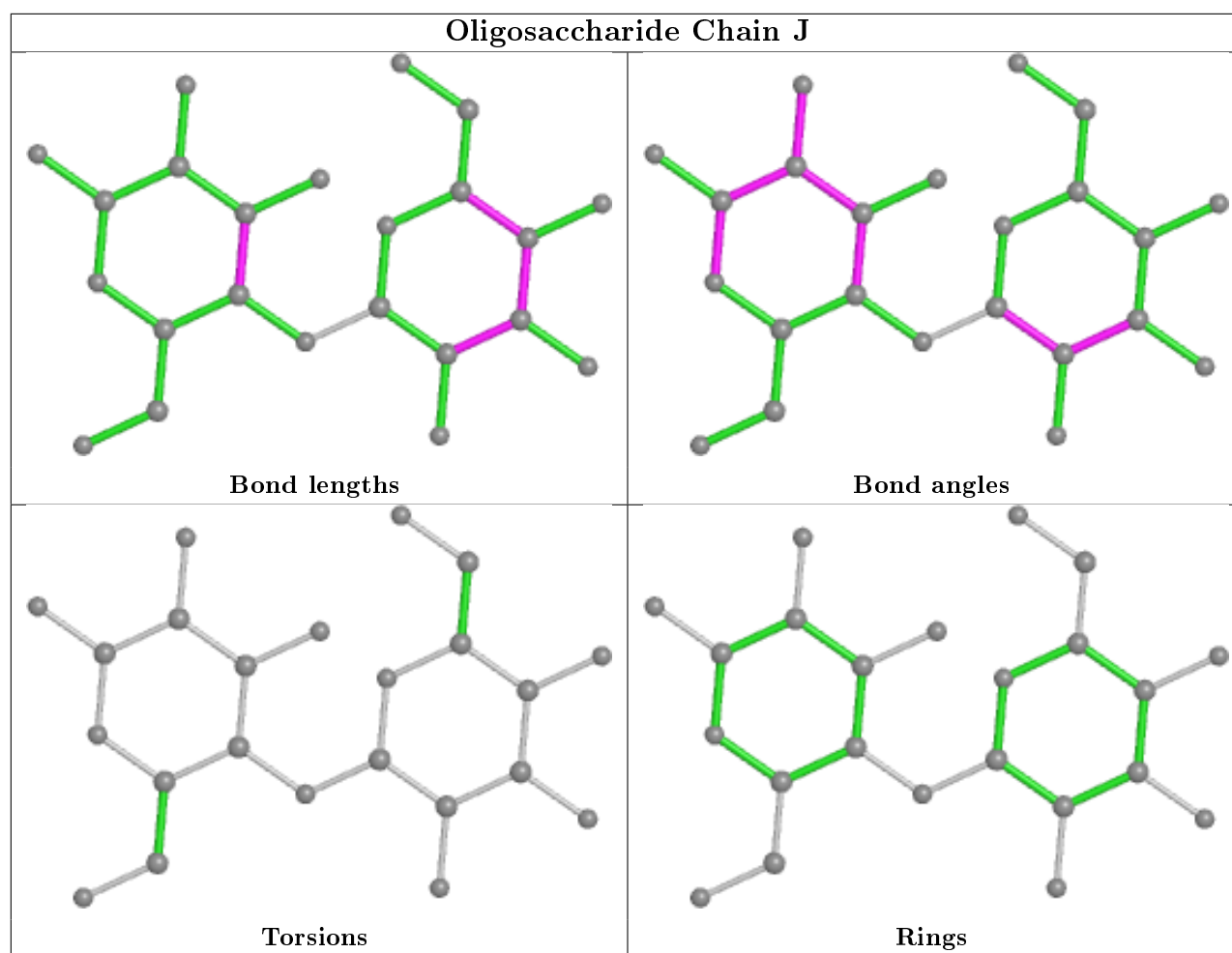
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	1	GAL	1	0
2	J	2	GLA	1	0

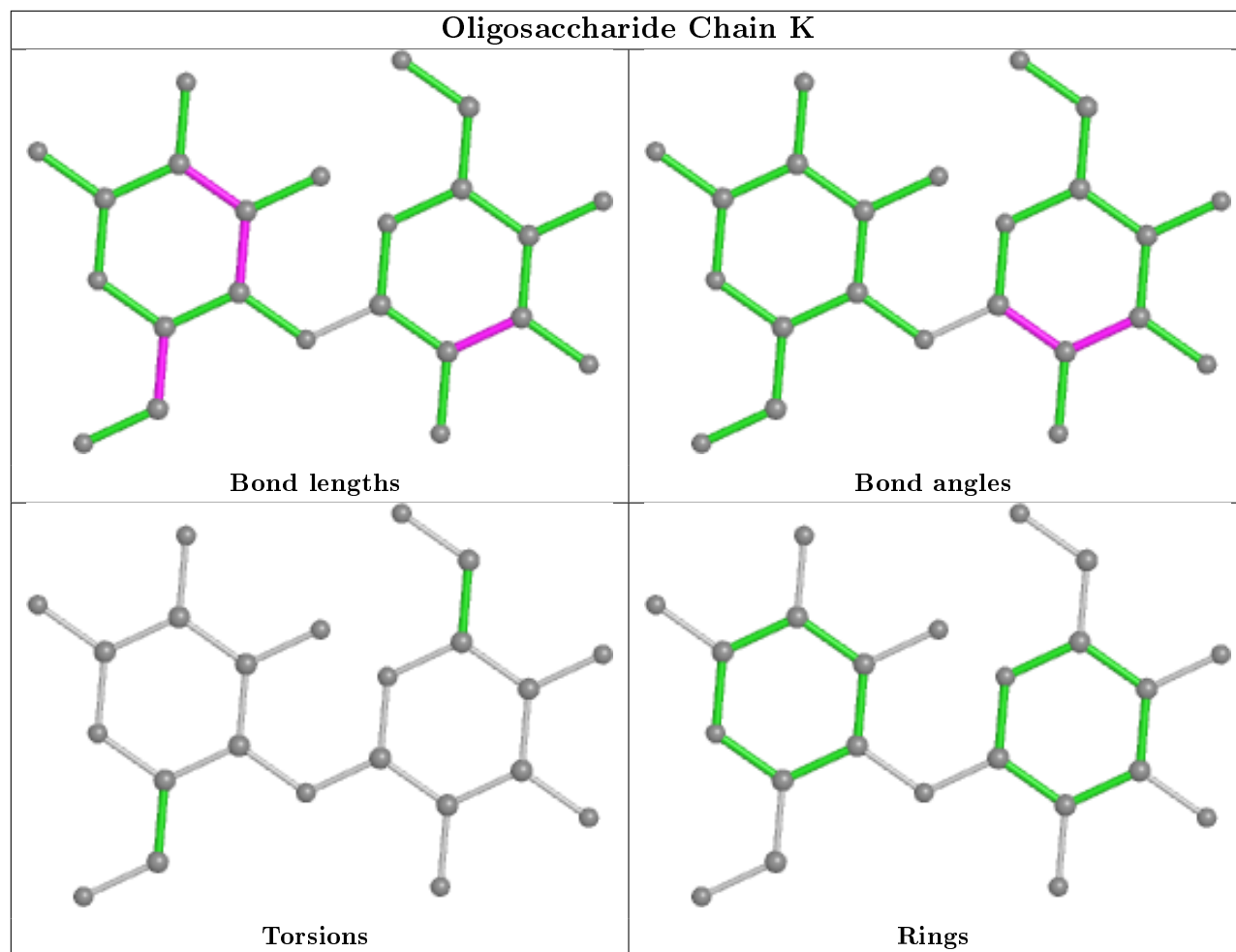
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

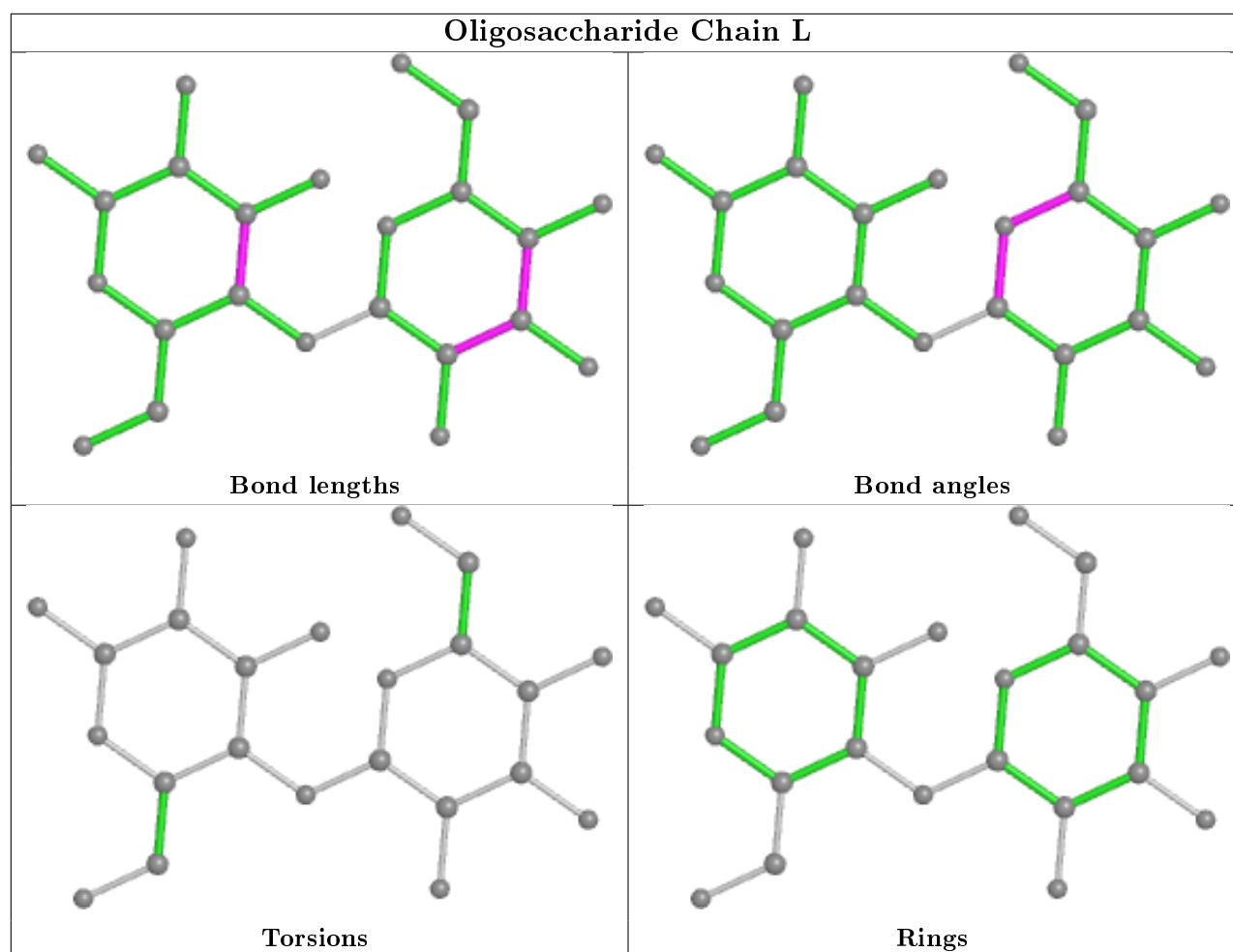












5.6 Ligand geometry [i](#)

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	194/226 (85%)	-0.22	0 100 100	24, 33, 48, 74	0
1	B	198/226 (87%)	-0.17	1 (0%) 91 92	26, 36, 59, 70	0
1	C	198/226 (87%)	-0.12	1 (0%) 91 92	30, 40, 54, 68	0
1	D	196/226 (86%)	-0.19	0 100 100	29, 40, 59, 72	0
1	E	191/226 (84%)	0.08	1 (0%) 91 92	28, 41, 56, 63	0
1	F	192/226 (84%)	-0.13	0 100 100	29, 40, 59, 67	0
All	All	1169/1356 (86%)	-0.13	3 (0%) 94 95	24, 38, 57, 74	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	305	ASN	2.7
1	C	289	ASP	2.3
1	E	311	LEU	2.3

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

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

6.3 Carbohydrates [i](#)

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

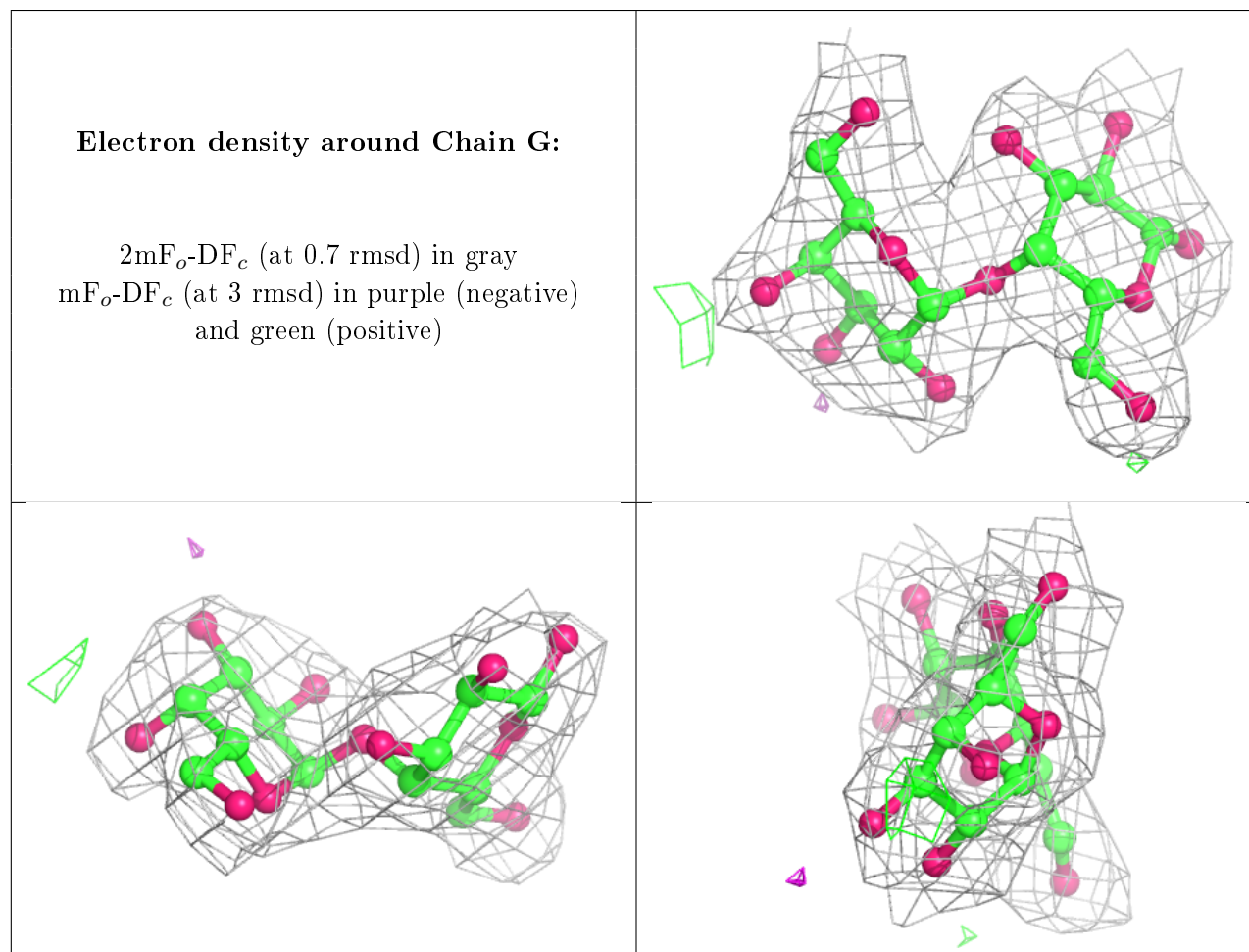
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLA	K	2	11/12	0.93	0.12	35,38,41,42	0

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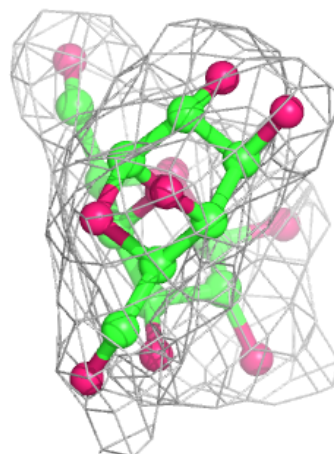
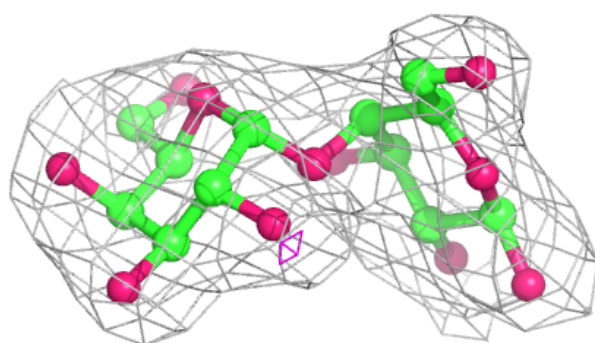
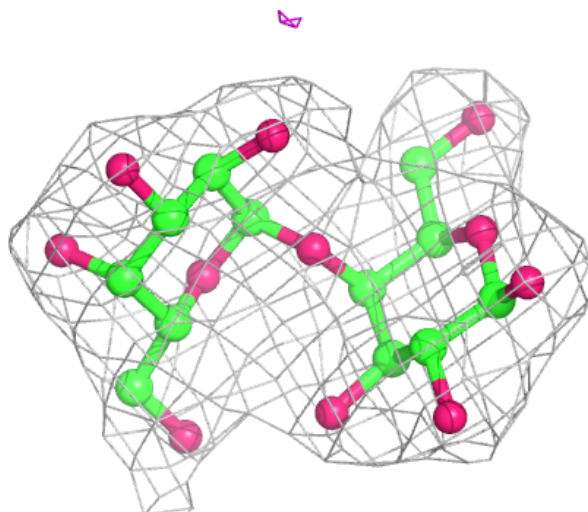
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	GLA	H	2	11/12	0.95	0.14	28,35,39,41	0
2	GLA	J	2	11/12	0.95	0.16	36,39,45,46	0
2	GLA	I	2	11/12	0.95	0.14	36,38,43,44	0
2	GAL	K	1	12/12	0.96	0.15	34,36,41,43	0
2	GAL	I	1	12/12	0.96	0.12	37,42,47,47	0
2	GLA	G	2	11/12	0.97	0.14	27,29,33,37	0
2	GAL	H	1	12/12	0.97	0.15	30,33,35,36	0
2	GAL	L	1	12/12	0.97	0.12	30,36,40,41	0
2	GAL	J	1	12/12	0.97	0.14	33,35,38,39	0
2	GAL	G	1	12/12	0.97	0.14	20,29,31,35	0
2	GLA	L	2	11/12	0.97	0.13	31,35,39,45	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.



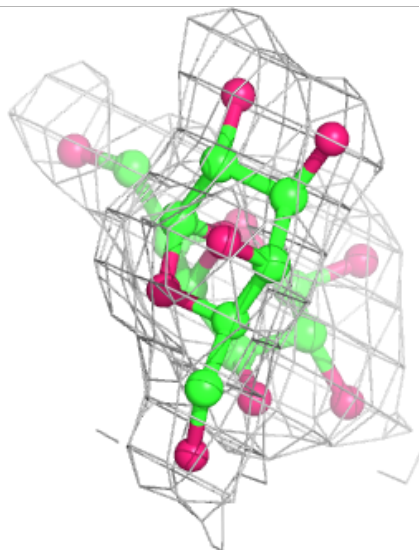
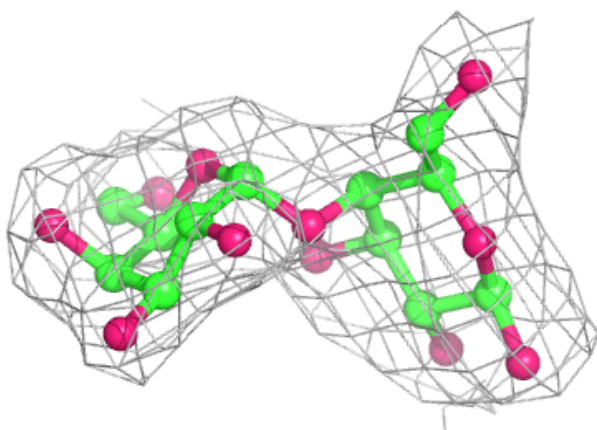
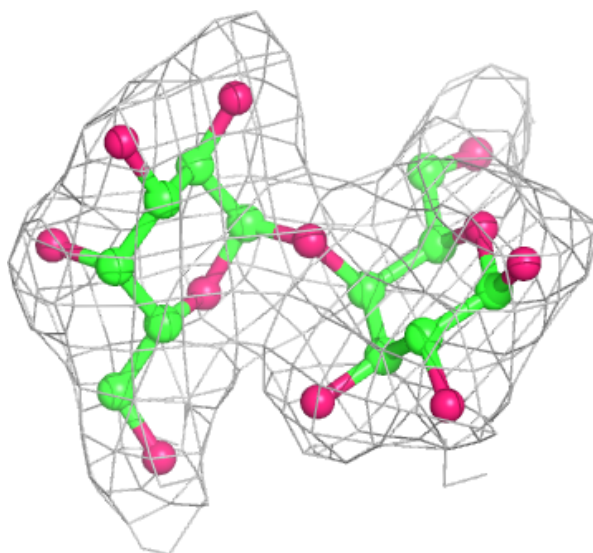
Electron density around Chain H:

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



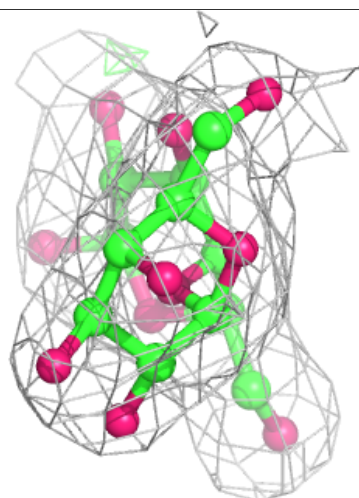
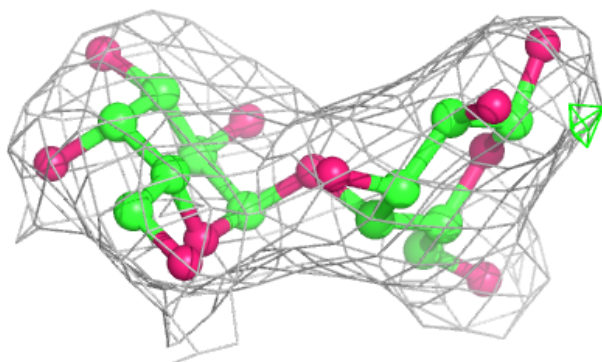
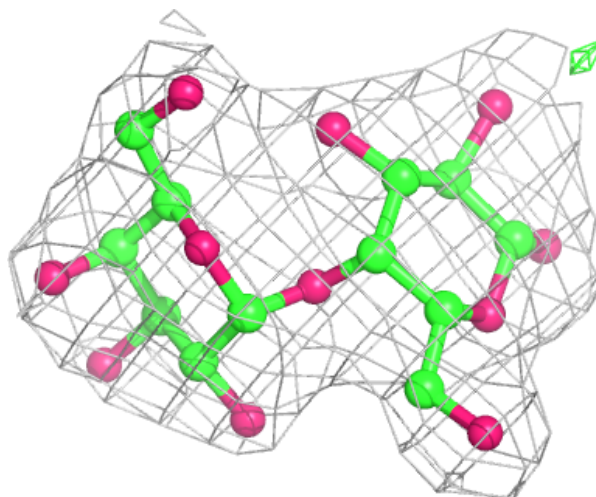
Electron density around Chain I:

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



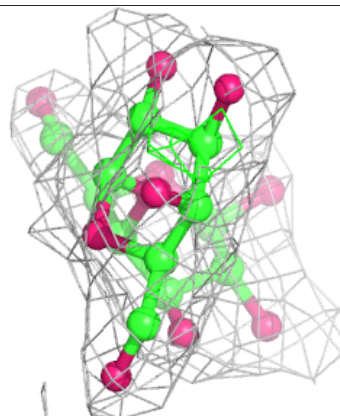
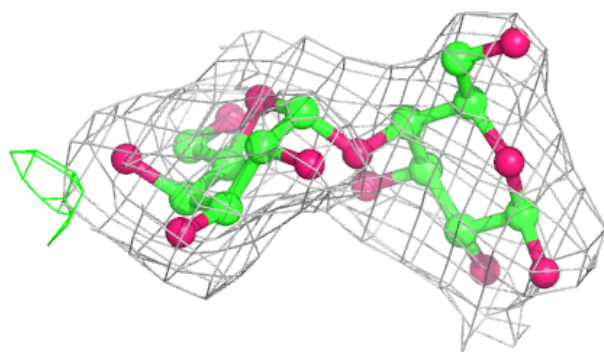
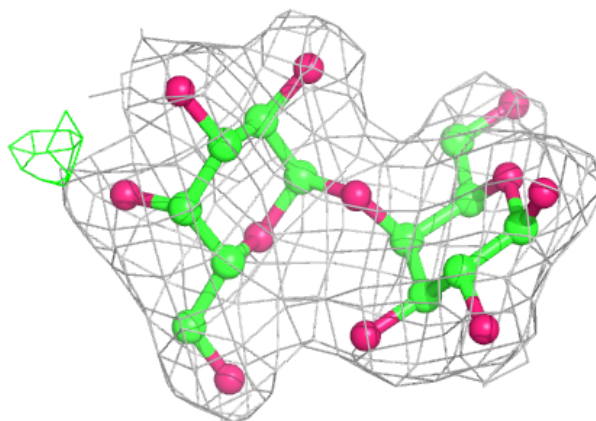
Electron density around Chain J:

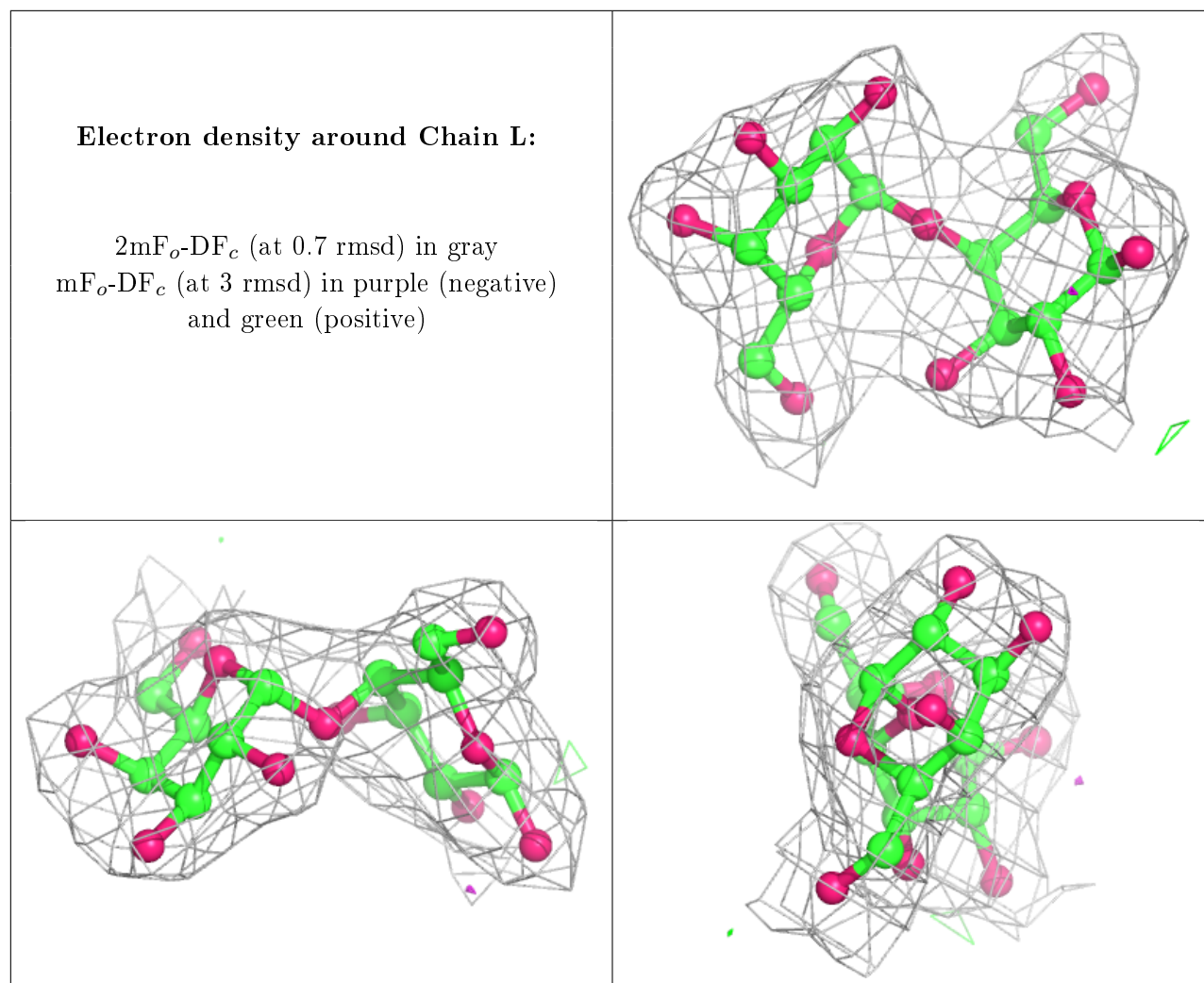
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain K:

$2mF_o - DF_c$ (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.