



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:47 AM UTC

PDB ID : 6LF3 / pdb\_00006lf3  
Title : 3D domain-swapped dimer of the maltose-binding protein fused to a fragment of the protein-tyrosine kinase 2-beta  
Authors : Momin, A.A.; Shahul Hameed, U.F.; Arold, S.T.  
Deposited on : 2019-11-28  
Resolution : 3.20 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](mailto: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>.

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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

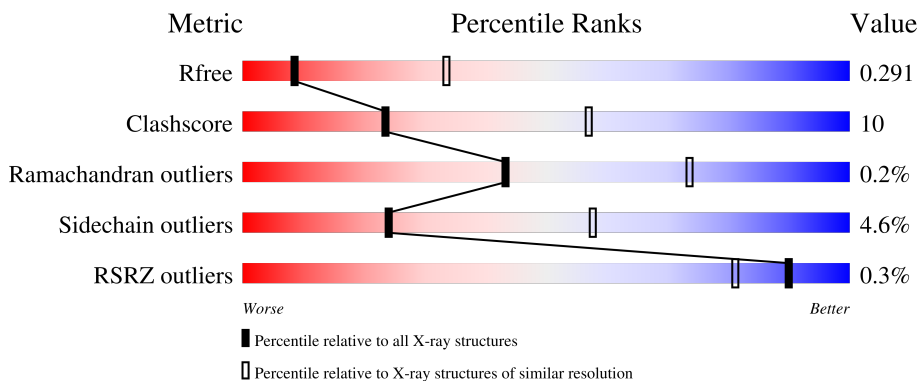
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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  $\geq 3$ , 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	419	 70% 17% • 12%
1	B	419	 71% 15% • 12%
1	C	419	 69% 18% • 12%
1	D	419	 67% 18% • 12%
1	E	419	 71% 16% • 12%

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Mol	Chain	Length	Quality of chain
1	F	419	 72% 14% 12%
2	G	2	 50% 50%
2	H	2	 50% 50%
2	I	2	 100%
2	J	2	 50% 50%
2	K	2	 50% 50%
2	L	2	 50% 50%

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	GLC	J	1	-	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 17124 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 Maltose/maltodextrin-binding periplasmic protein, Protein-tyrosine kinase 2-beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	369	2837	1827	463	541	6	0	0	0
1	B	369	2837	1827	463	541	6	0	0	0
1	C	368	2828	1822	462	538	6	0	0	0
1	D	368	2828	1822	462	538	6	0	0	0
1	E	368	2828	1822	462	538	6	0	0	0
1	F	368	2828	1822	462	538	6	0	0	0

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AEX9
A	83	ALA	ASP	engineered mutation	UNP P0AEX9
A	84	ALA	LYS	engineered mutation	UNP P0AEX9
A	173	ALA	GLU	engineered mutation	UNP P0AEX9
A	174	ALA	ASN	engineered mutation	UNP P0AEX9
A	240	ALA	LYS	engineered mutation	UNP P0AEX9
A	360	ALA	GLU	engineered mutation	UNP P0AEX9
A	363	ALA	LYS	engineered mutation	UNP P0AEX9
A	364	ALA	ASP	engineered mutation	UNP P0AEX9
A	368	ASN	-	linker	UNP P0AEX9
A	369	ALA	-	linker	UNP P0AEX9
B	1	MET	-	initiating methionine	UNP P0AEX9
B	83	ALA	ASP	engineered mutation	UNP P0AEX9
B	84	ALA	LYS	engineered mutation	UNP P0AEX9
B	173	ALA	GLU	engineered mutation	UNP P0AEX9
B	174	ALA	ASN	engineered mutation	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	240	ALA	LYS	engineered mutation	UNP P0AEX9
B	360	ALA	GLU	engineered mutation	UNP P0AEX9
B	363	ALA	LYS	engineered mutation	UNP P0AEX9
B	364	ALA	ASP	engineered mutation	UNP P0AEX9
B	368	ASN	-	linker	UNP P0AEX9
B	369	ALA	-	linker	UNP P0AEX9
C	1	MET	-	initiating methionine	UNP P0AEX9
C	83	ALA	ASP	engineered mutation	UNP P0AEX9
C	84	ALA	LYS	engineered mutation	UNP P0AEX9
C	173	ALA	GLU	engineered mutation	UNP P0AEX9
C	174	ALA	ASN	engineered mutation	UNP P0AEX9
C	240	ALA	LYS	engineered mutation	UNP P0AEX9
C	360	ALA	GLU	engineered mutation	UNP P0AEX9
C	363	ALA	LYS	engineered mutation	UNP P0AEX9
C	364	ALA	ASP	engineered mutation	UNP P0AEX9
C	368	ASN	-	linker	UNP P0AEX9
C	369	ALA	-	linker	UNP P0AEX9
D	1	MET	-	initiating methionine	UNP P0AEX9
D	83	ALA	ASP	engineered mutation	UNP P0AEX9
D	84	ALA	LYS	engineered mutation	UNP P0AEX9
D	173	ALA	GLU	engineered mutation	UNP P0AEX9
D	174	ALA	ASN	engineered mutation	UNP P0AEX9
D	240	ALA	LYS	engineered mutation	UNP P0AEX9
D	360	ALA	GLU	engineered mutation	UNP P0AEX9
D	363	ALA	LYS	engineered mutation	UNP P0AEX9
D	364	ALA	ASP	engineered mutation	UNP P0AEX9
D	368	ASN	-	linker	UNP P0AEX9
D	369	ALA	-	linker	UNP P0AEX9
E	1	MET	-	initiating methionine	UNP P0AEX9
E	83	ALA	ASP	engineered mutation	UNP P0AEX9
E	84	ALA	LYS	engineered mutation	UNP P0AEX9
E	173	ALA	GLU	engineered mutation	UNP P0AEX9
E	174	ALA	ASN	engineered mutation	UNP P0AEX9
E	240	ALA	LYS	engineered mutation	UNP P0AEX9
E	360	ALA	GLU	engineered mutation	UNP P0AEX9
E	363	ALA	LYS	engineered mutation	UNP P0AEX9
E	364	ALA	ASP	engineered mutation	UNP P0AEX9
E	368	ASN	-	linker	UNP P0AEX9
E	369	ALA	-	linker	UNP P0AEX9
F	1	MET	-	initiating methionine	UNP P0AEX9
F	83	ALA	ASP	engineered mutation	UNP P0AEX9
F	84	ALA	LYS	engineered mutation	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	173	ALA	GLU	engineered mutation	UNP P0AEX9
F	174	ALA	ASN	engineered mutation	UNP P0AEX9
F	240	ALA	LYS	engineered mutation	UNP P0AEX9
F	360	ALA	GLU	engineered mutation	UNP P0AEX9
F	363	ALA	LYS	engineered mutation	UNP P0AEX9
F	364	ALA	ASP	engineered mutation	UNP P0AEX9
F	368	ASN	-	linker	UNP P0AEX9
F	369	ALA	-	linker	UNP P0AEX9

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

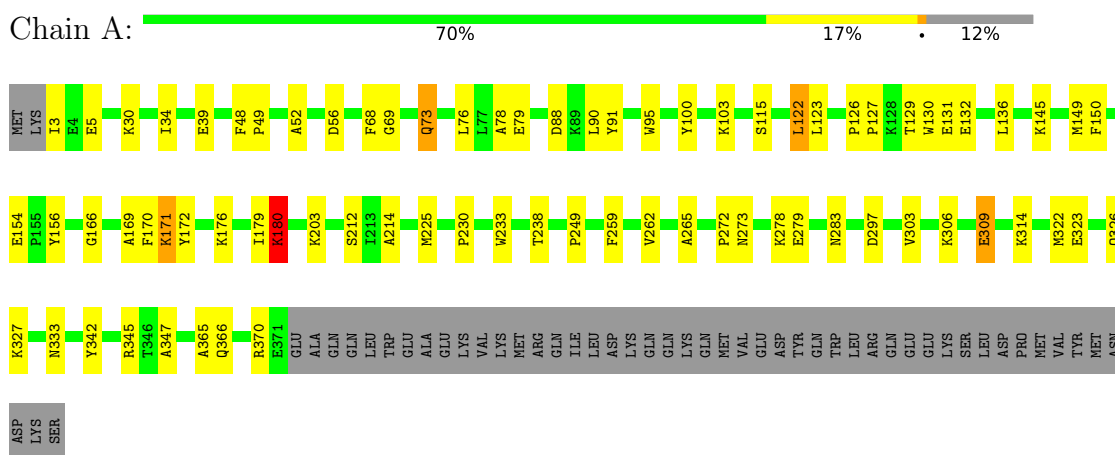


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	G	2	Total	C	O	0	0	0
			23	12	11			
2	H	2	Total	C	O	0	0	0
			23	12	11			
2	I	2	Total	C	O	0	0	0
			23	12	11			
2	J	2	Total	C	O	0	0	0
			23	12	11			
2	K	2	Total	C	O	0	0	0
			23	12	11			
2	L	2	Total	C	O	0	0	0
			23	12	11			

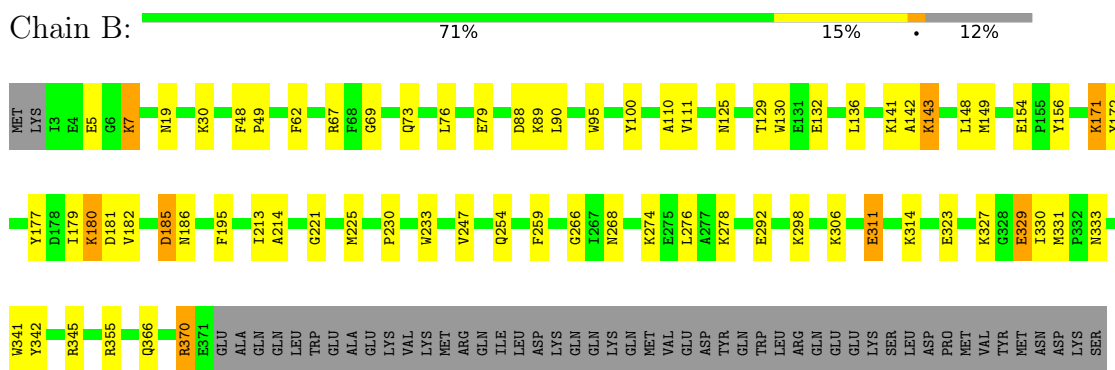
### 3 Residue-property plots [i](#)

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.

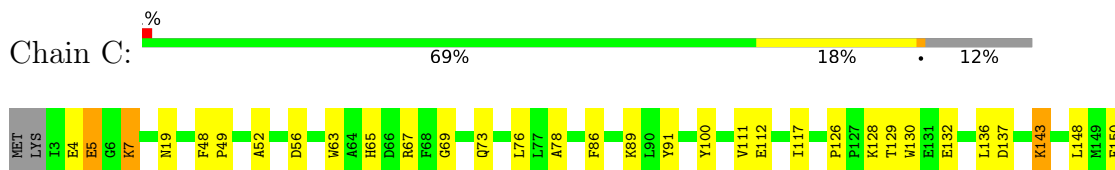
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Protein-tyrosine kinase 2-beta

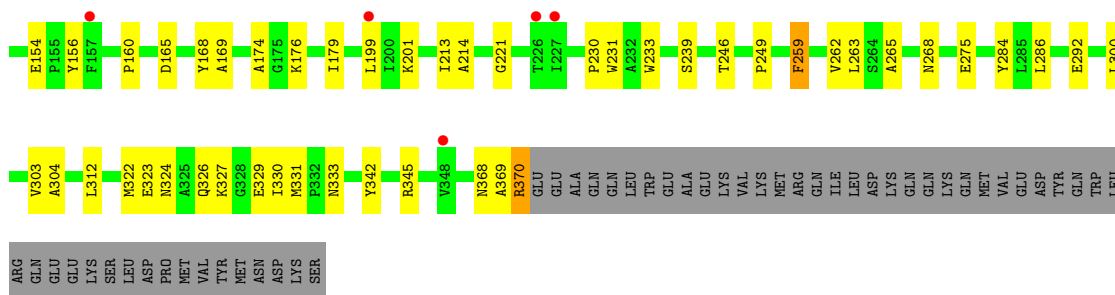


- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Protein-tyrosine kinase 2-beta



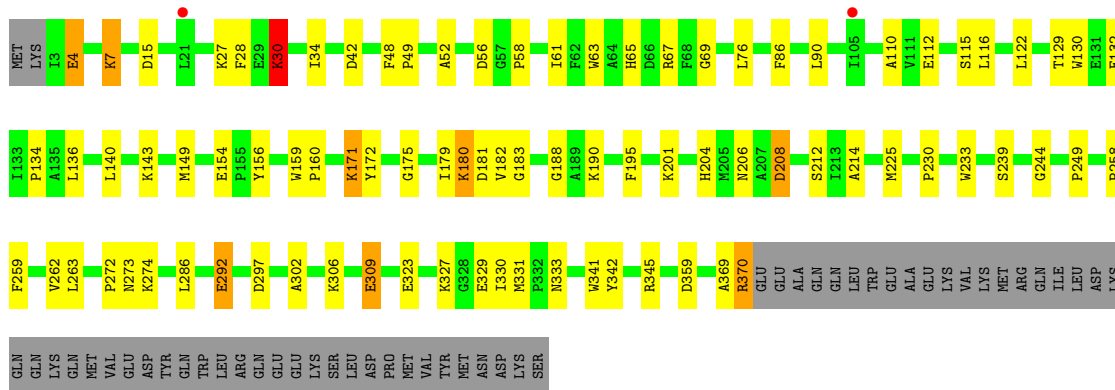
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein, Protein-tyrosine kinase 2-beta





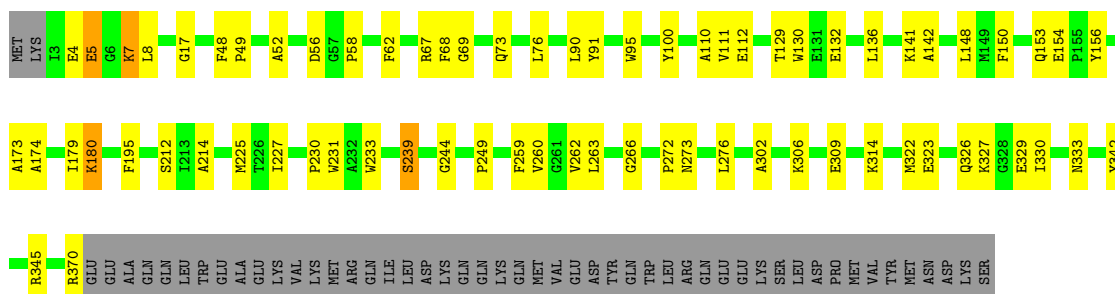
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Protein-tyrosine kinase 2-beta

Chain D: 67% 18% 12%



- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Protein-tyrosine kinase 2-beta

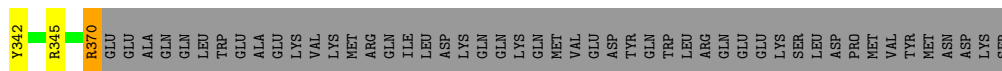
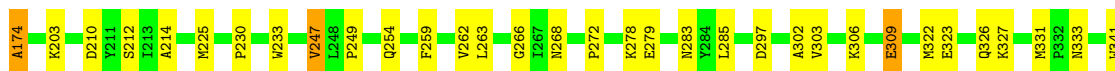
Chain E: 71% 16% 12%



- Molecule 1: Maltose/maltodextrin-binding periplasmic protein,Protein-tyrosine kinase 2-beta

Chain F: 72% 14% 12%





- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain G: 50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain H: 50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain I: 100%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain J: 50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain K: 50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain L: 50% 50%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.78Å 92.74Å 93.61Å 112.46° 101.66° 94.93°	Depositor
Resolution (Å)	47.90 – 3.20 47.90 – 3.21	Depositor EDS
% Data completeness (in resolution range)	97.0 (47.90-3.20) 97.0 (47.90-3.21)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.20 (at 3.19Å)	Xtrriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.244 , 0.284 0.250 , 0.291	Depositor DCC
$R_{free}$ test set	1864 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	99.1	Xtrriage
Anisotropy	0.572	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 102.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	17124	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	129.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.08% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GLC

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	0.54	0/2906	1.06	3/3951 (0.1%)
1	B	0.56	0/2906	1.05	4/3951 (0.1%)
1	C	0.52	0/2897	1.02	2/3939 (0.1%)
1	D	0.54	0/2897	1.06	5/3939 (0.1%)
1	E	0.54	0/2897	1.04	4/3939 (0.1%)
1	F	0.55	0/2897	1.05	3/3939 (0.1%)
All	All	0.54	0/17400	1.05	21/23658 (0.1%)

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	E	0	1
1	F	0	2
All	All	0	3

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	309	GLU	CB-CG-CD	9.05	127.99	112.60
1	D	201	LYS	CB-CG-CD	7.47	128.47	111.30
1	D	30	LYS	CB-CA-C	7.08	122.54	110.79
1	E	239	SER	CA-C-N	-6.02	112.85	122.66
1	E	239	SER	C-N-CA	-6.02	112.85	122.66

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	173	ALA	Peptide
1	F	173	ALA	Peptide
1	F	174	ALA	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	2837	0	2804	90	0
1	B	2837	0	2804	75	1
1	C	2828	0	2798	81	0
1	D	2828	0	2798	91	0
1	E	2828	0	2798	77	1
1	F	2828	0	2798	64	0
2	G	23	0	21	3	0
2	H	23	0	21	4	0
2	I	23	0	21	7	0
2	J	23	0	21	6	0
2	K	23	0	21	4	0
2	L	23	0	21	3	0
All	All	17124	0	16926	348	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 10.

The worst 5 of 348 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:366:GLN:HE21	1:A:370:ARG:NH2	1.38	1.20
1:D:180:LYS:HA	1:D:180:LYS:HE2	1.20	1.15
1:B:185:ASP:OD1	1:B:366:GLN:OE1	1.64	1.15
1:A:203:LYS:CG	1:E:314:LYS:HB3	1.77	1.12
1:F:156:TYR:HB2	2:L:1:GLC:H62	1.19	1.11

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:247:VAL:CG2	1:E:142:ALA:O[1_566]	2.19	0.01

### 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	367/419 (88%)	363 (99%)	4 (1%)	0	100	100
1	B	367/419 (88%)	362 (99%)	5 (1%)	0	100	100
1	C	366/419 (87%)	359 (98%)	6 (2%)	1 (0%)	36	68
1	D	366/419 (87%)	361 (99%)	5 (1%)	0	100	100
1	E	366/419 (87%)	359 (98%)	6 (2%)	1 (0%)	36	68
1	F	366/419 (87%)	360 (98%)	4 (1%)	2 (0%)	24	59
All	All	2198/2514 (87%)	2164 (98%)	30 (1%)	4 (0%)	43	73

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	174	ALA
1	E	174	ALA
1	C	369	ALA
1	F	169	ALA

#### 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	287/335 (86%)	273 (95%)	14 (5%)	22	55
1	B	287/335 (86%)	271 (94%)	16 (6%)	19	52
1	C	286/335 (85%)	275 (96%)	11 (4%)	29	62
1	D	286/335 (85%)	269 (94%)	17 (6%)	18	50
1	E	286/335 (85%)	279 (98%)	7 (2%)	43	70
1	F	286/335 (85%)	272 (95%)	14 (5%)	22	55
All	All	1718/2010 (86%)	1639 (95%)	79 (5%)	24	58

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	370	ARG
1	F	171	LYS
1	E	136	LEU
1	F	5	GLU
1	F	259	PHE

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

Mol	Chain	Res	Type
1	C	366	GLN
1	E	350	ASN
1	D	356	GLN
1	E	356	GLN
1	B	125	ASN

### 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](#)

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	GLC	G	1	2	12,12,12	1.37	2 (16%)	17,17,17	2.01	6 (35%)
2	GLC	G	2	2	11,11,12	0.89	0	15,15,17	2.05	5 (33%)
2	GLC	H	1	2	12,12,12	1.08	2 (16%)	17,17,17	1.78	6 (35%)
2	GLC	H	2	2	11,11,12	0.57	0	15,15,17	1.55	1 (6%)
2	GLC	I	1	2	12,12,12	1.15	1 (8%)	17,17,17	2.21	7 (41%)
2	GLC	I	2	2	11,11,12	0.96	0	15,15,17	1.38	2 (13%)
2	GLC	J	1	2	12,12,12	0.94	0	17,17,17	2.22	9 (52%)
2	GLC	J	2	2	11,11,12	0.71	0	15,15,17	1.40	3 (20%)
2	GLC	K	1	2	12,12,12	0.76	0	17,17,17	1.34	2 (11%)
2	GLC	K	2	2	11,11,12	0.56	0	15,15,17	1.72	3 (20%)
2	GLC	L	1	2	12,12,12	1.02	1 (8%)	17,17,17	1.62	4 (23%)
2	GLC	L	2	2	11,11,12	0.78	0	15,15,17	2.28	4 (26%)

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	GLC	G	1	2	-	1/2/22/22	0/1/1/1
2	GLC	G	2	2	-	2/2/19/22	0/1/1/1
2	GLC	H	1	2	-	0/2/22/22	0/1/1/1
2	GLC	H	2	2	-	2/2/19/22	0/1/1/1
2	GLC	I	1	2	-	2/2/22/22	0/1/1/1
2	GLC	I	2	2	-	1/2/19/22	0/1/1/1
2	GLC	J	1	2	-	2/2/22/22	0/1/1/1
2	GLC	J	2	2	-	1/2/19/22	0/1/1/1
2	GLC	K	1	2	-	0/2/22/22	0/1/1/1
2	GLC	K	2	2	-	2/2/19/22	0/1/1/1
2	GLC	L	1	2	-	0/2/22/22	0/1/1/1
2	GLC	L	2	2	-	2/2/19/22	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)
2	G	1	GLC	O1-C1	2.38	1.47	1.39
2	I	1	GLC	O1-C1	2.35	1.47	1.39
2	H	1	GLC	C1-C2	2.13	1.57	1.52
2	H	1	GLC	O1-C1	2.13	1.46	1.39
2	G	1	GLC	C4-C5	-2.05	1.48	1.53

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	2	GLC	C1-O5-C5	6.48	120.87	112.19
2	H	2	GLC	C1-O5-C5	5.19	119.14	112.19
2	J	1	GLC	C3-C4-C5	-4.59	101.92	110.23
2	K	2	GLC	C1-O5-C5	4.57	118.31	112.19
2	I	1	GLC	C3-C4-C5	-4.38	102.30	110.23

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

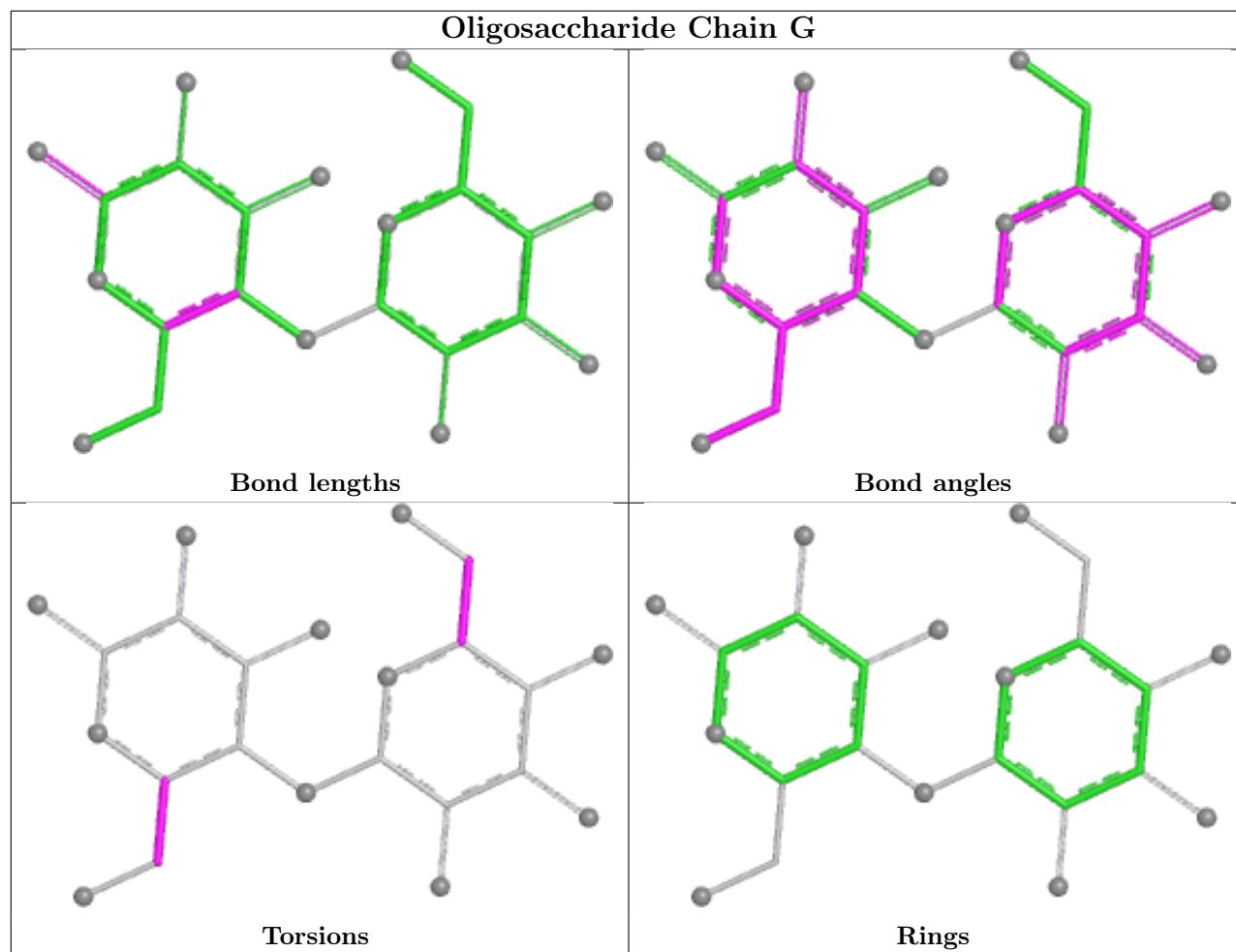
Mol	Chain	Res	Type	Atoms
2	I	1	GLC	O5-C5-C6-O6
2	J	1	GLC	O5-C5-C6-O6
2	K	2	GLC	O5-C5-C6-O6
2	G	2	GLC	O5-C5-C6-O6
2	H	2	GLC	O5-C5-C6-O6

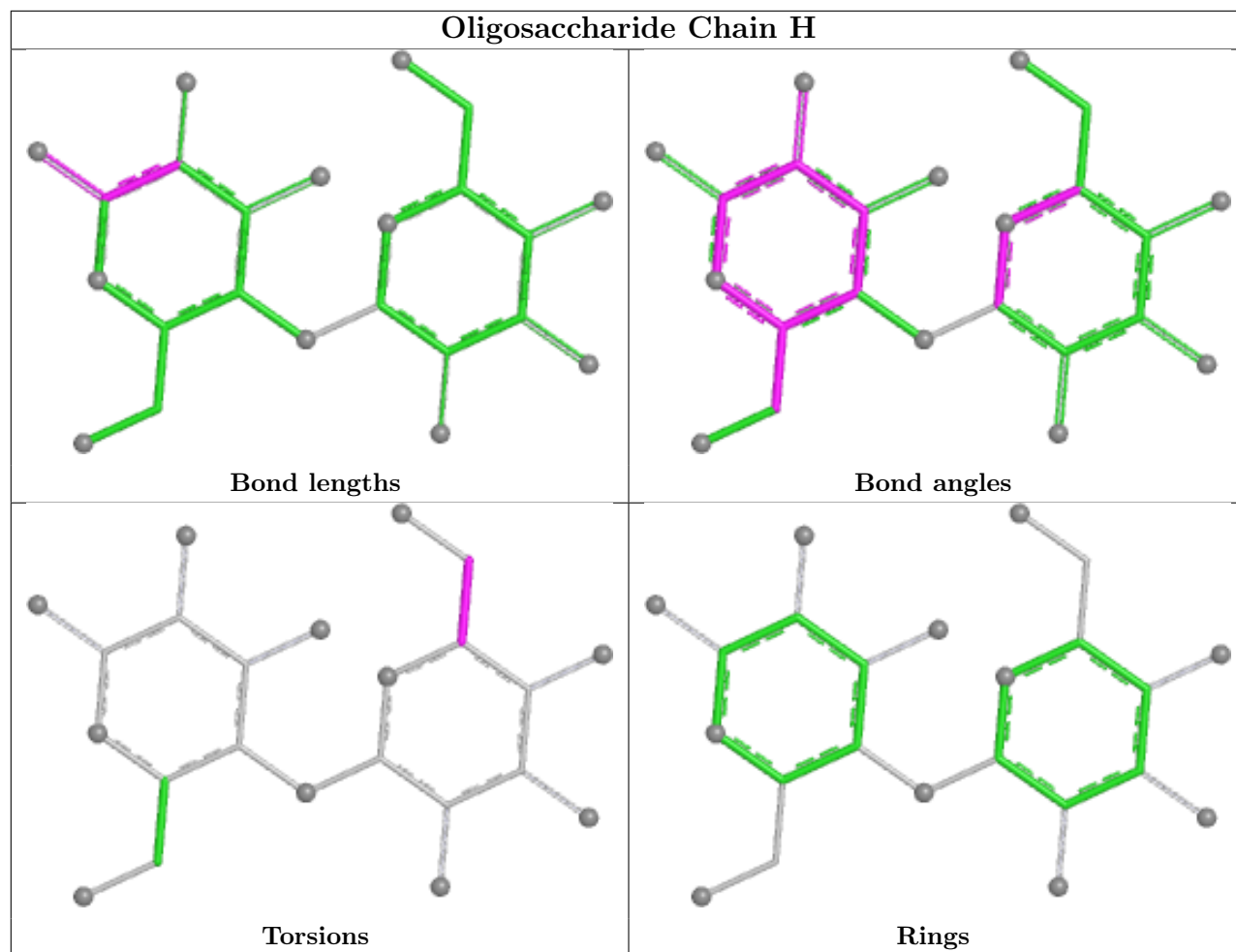
There are no ring outliers.

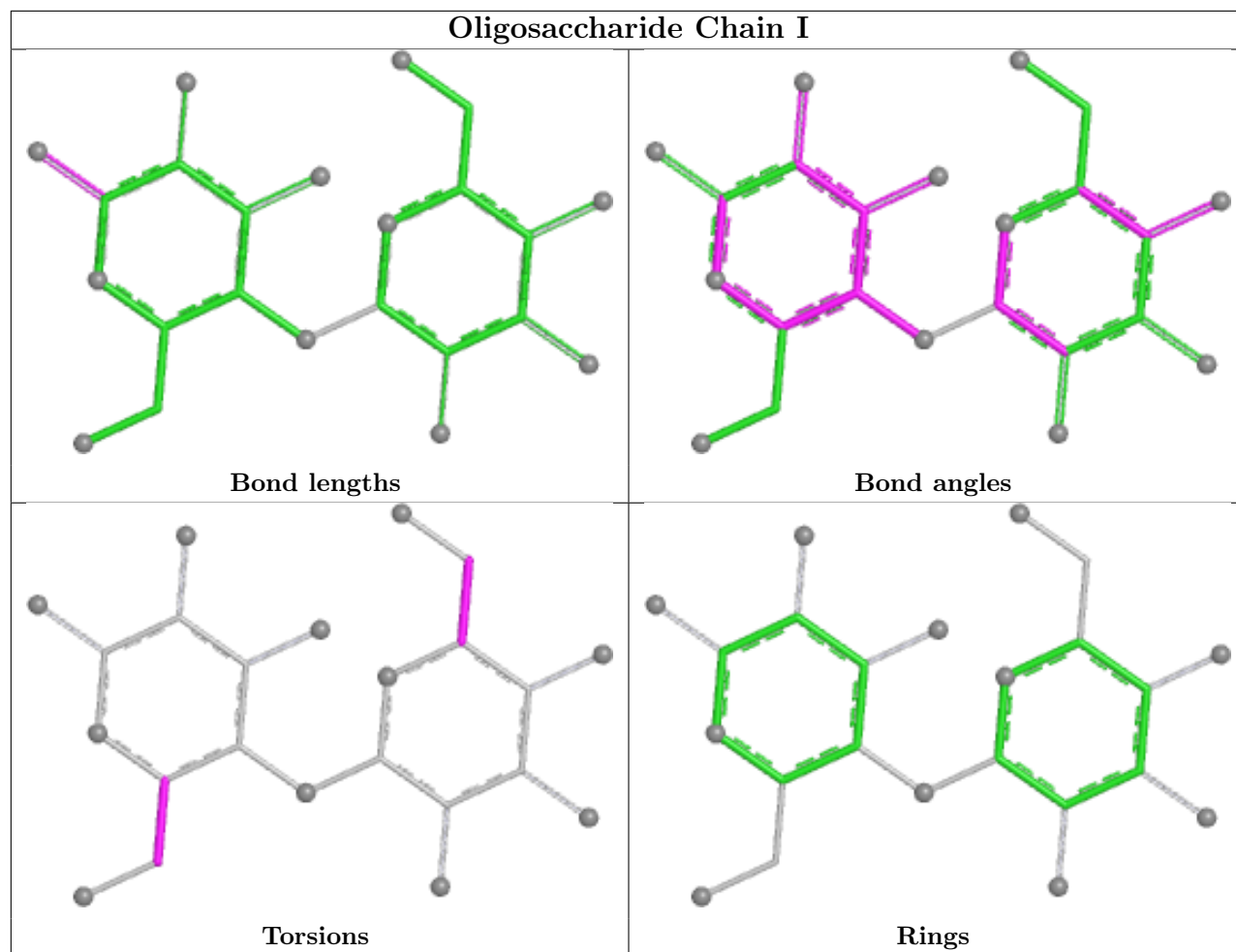
7 monomers are involved in 27 short contacts:

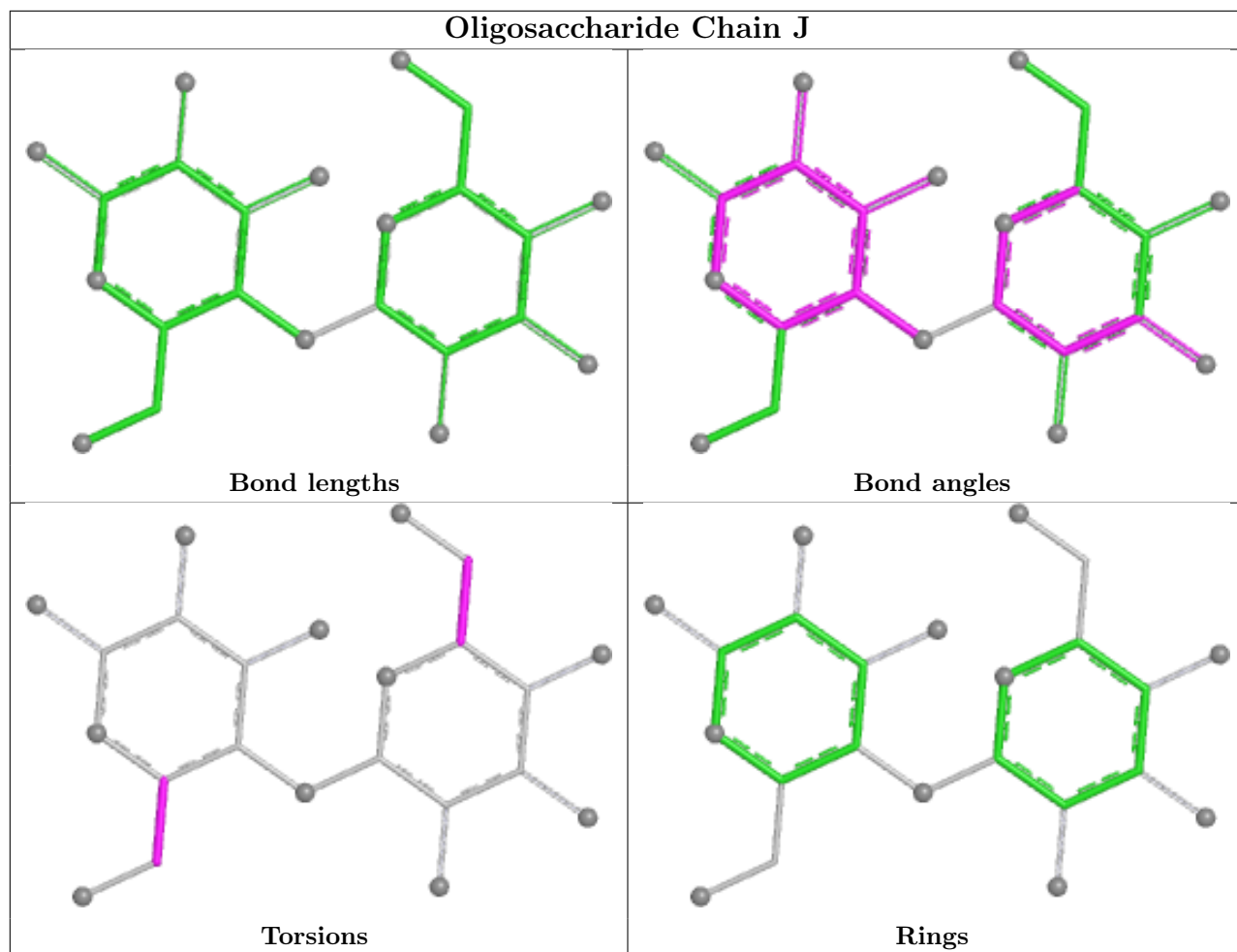
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	1	GLC	4	0
2	J	1	GLC	6	0
2	G	1	GLC	3	0
2	L	1	GLC	3	0
2	I	2	GLC	2	0
2	I	1	GLC	5	0
2	H	1	GLC	4	0

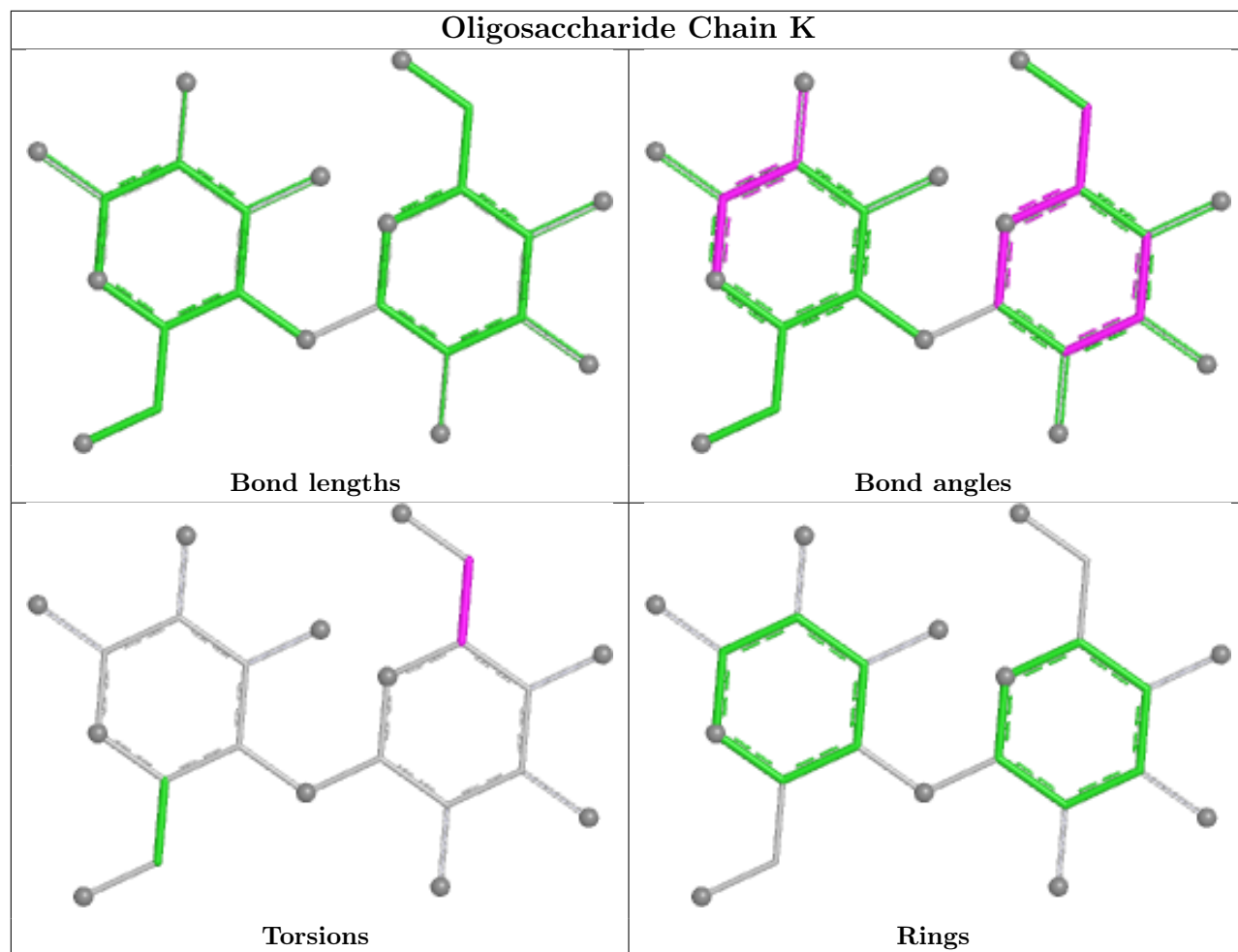
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

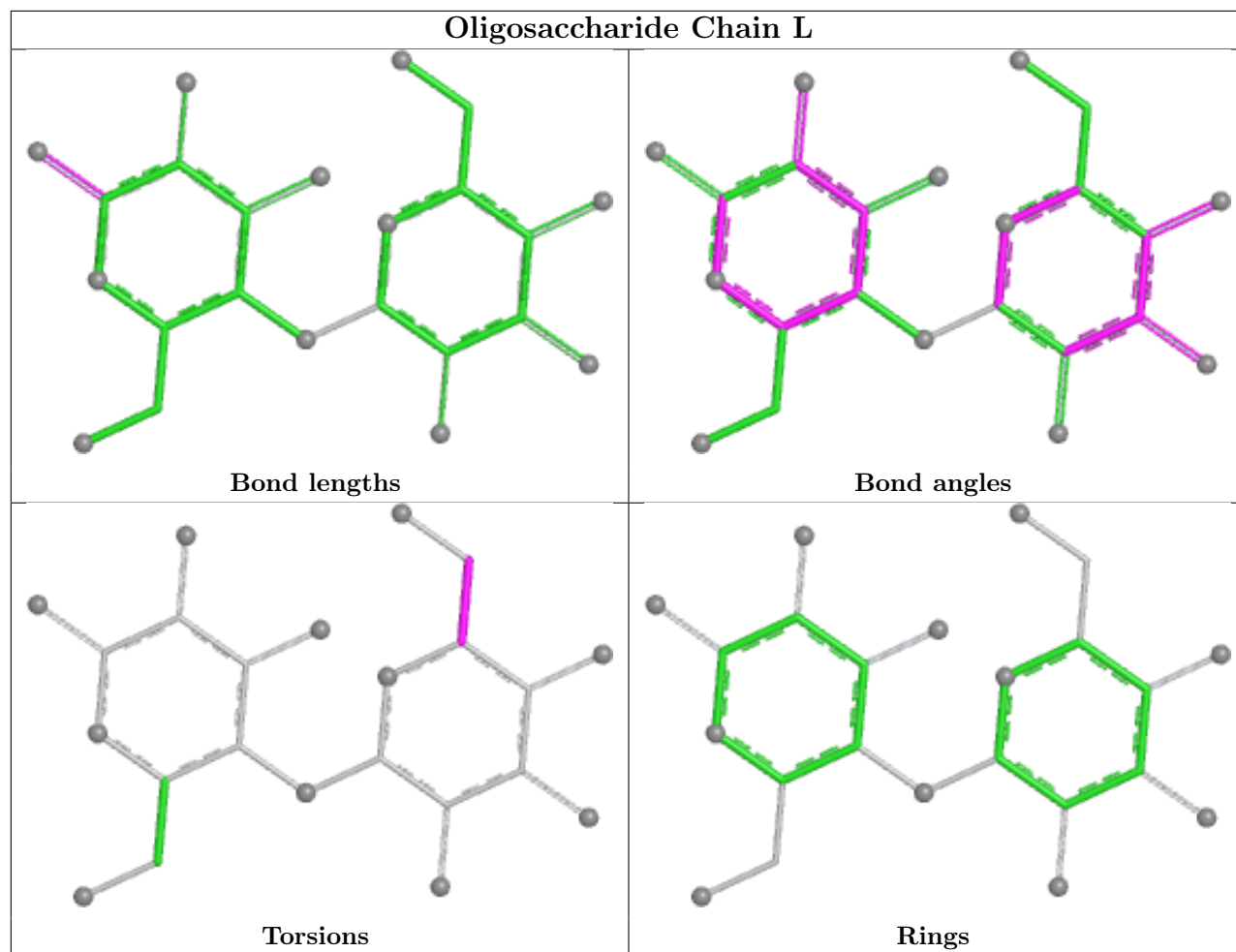












## 5.6 Ligand geometry [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	369/419 (88%)	-0.32	0 <a href="#">100</a> <a href="#">100</a>	66, 106, 175, 204	0
1	B	369/419 (88%)	-0.37	0 <a href="#">100</a> <a href="#">100</a>	59, 102, 184, 227	0
1	C	368/419 (87%)	0.04	5 (1%) <a href="#">73</a> <a href="#">54</a>	72, 144, 215, 256	0
1	D	368/419 (87%)	0.04	2 (0%) <a href="#">87</a> <a href="#">76</a>	68, 147, 212, 239	0
1	E	368/419 (87%)	-0.28	0 <a href="#">100</a> <a href="#">100</a>	48, 108, 237, 283	0
1	F	368/419 (87%)	-0.20	0 <a href="#">100</a> <a href="#">100</a>	50, 121, 247, 292	0
All	All	2210/2514 (87%)	-0.18	7 (0%) <a href="#">90</a> <a href="#">81</a>	48, 120, 216, 292	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	21	LEU	4.2
1	C	157	PHE	3.4
1	C	348	VAL	2.9
1	C	199	LEU	2.4
1	C	226	THR	2.2

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

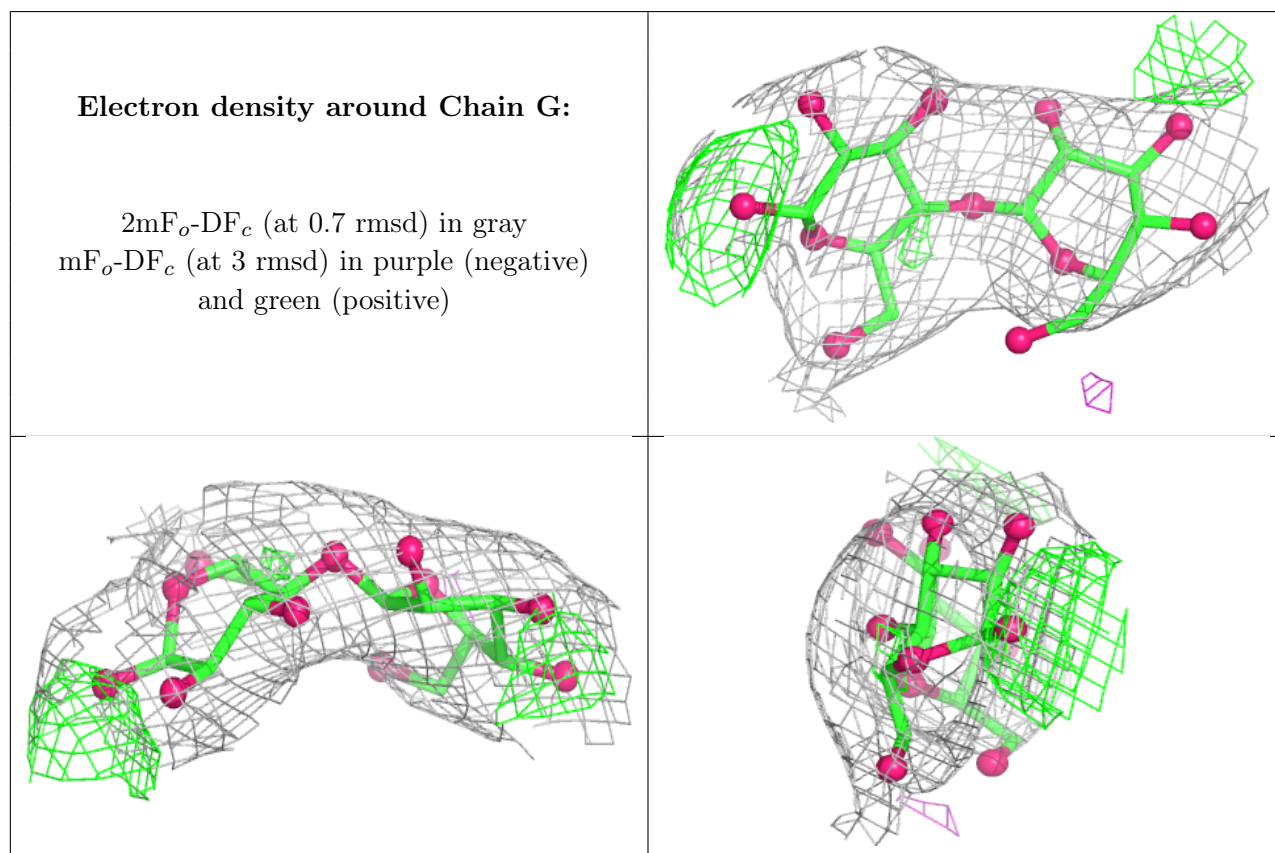
There are no non-standard protein/DNA/RNA residues in this entry.

### 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, 95<sup>th</sup> 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.

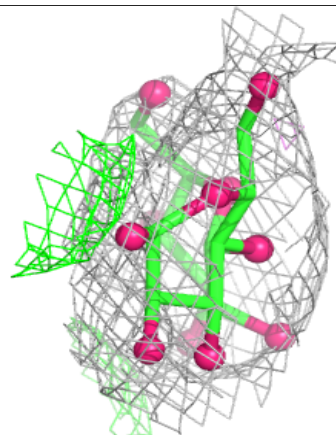
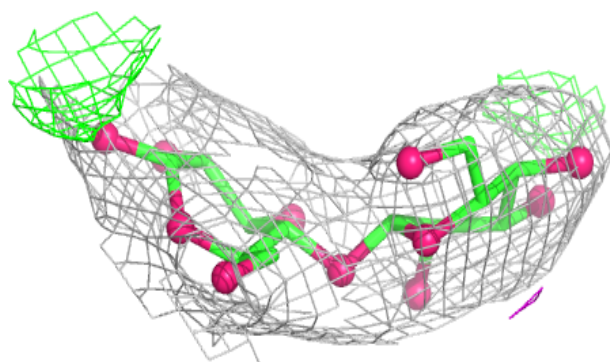
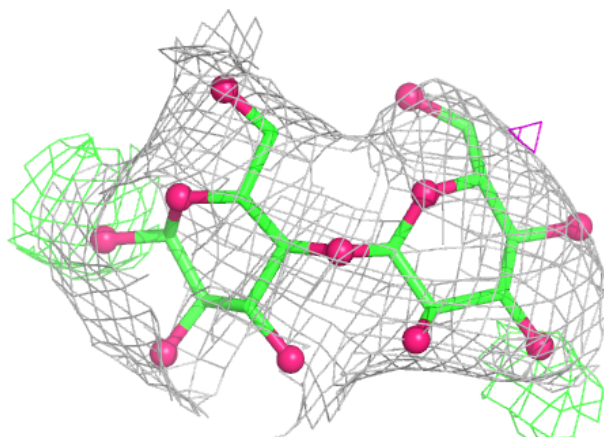
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLC	I	2	11/12	0.66	0.16	113,157,169,173	0
2	GLC	J	1	12/12	0.75	0.12	104,110,118,135	0
2	GLC	J	2	11/12	0.76	0.14	124,165,191,204	0
2	GLC	I	1	12/12	0.77	0.11	99,115,122,131	0
2	GLC	K	2	11/12	0.85	0.10	113,129,140,146	0
2	GLC	H	2	11/12	0.86	0.12	88,99,110,112	0
2	GLC	G	1	12/12	0.86	0.09	55,73,80,80	0
2	GLC	H	1	12/12	0.87	0.08	69,80,94,100	0
2	GLC	K	1	12/12	0.89	0.08	68,78,95,112	0
2	GLC	G	2	11/12	0.91	0.12	62,73,88,90	0
2	GLC	L	1	12/12	0.91	0.08	54,63,74,78	0
2	GLC	L	2	11/12	0.92	0.10	57,65,69,71	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.

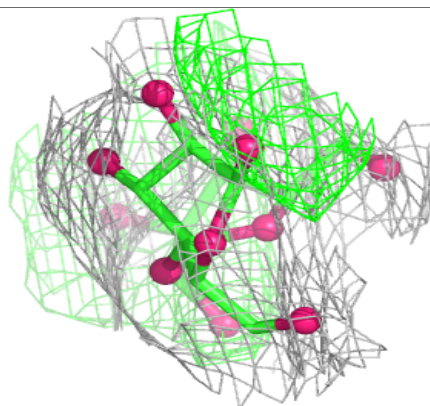
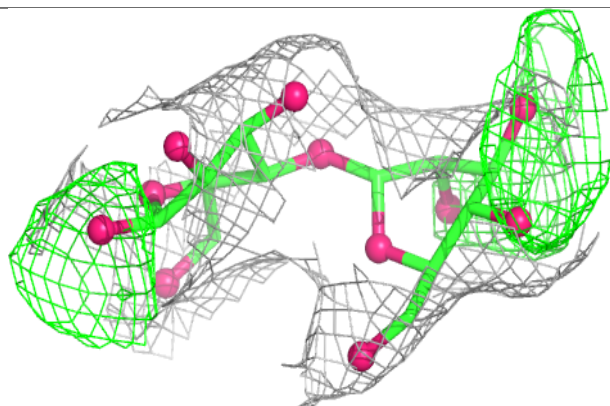
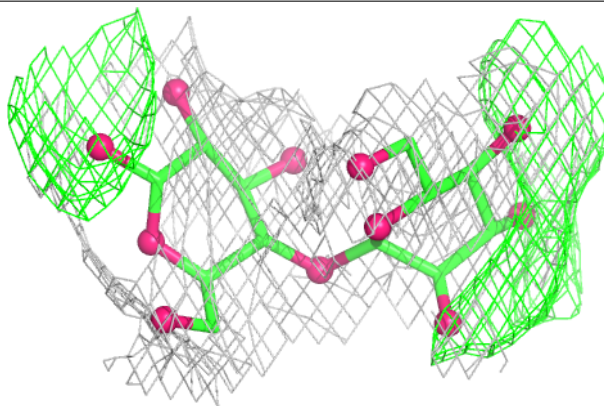


**Electron density around Chain H:**

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

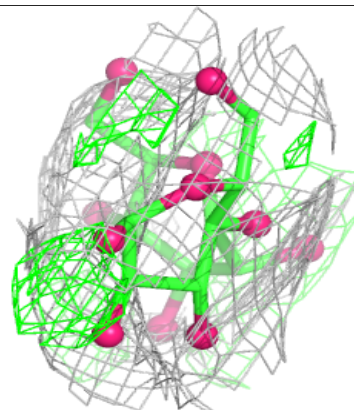
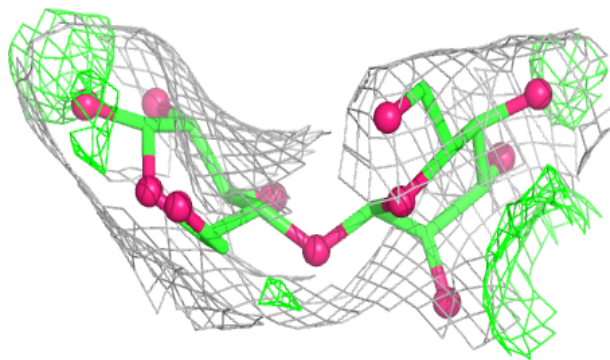
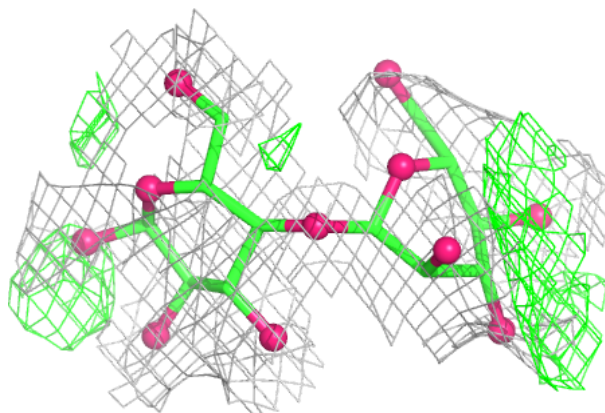
**Electron density around Chain I:**

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



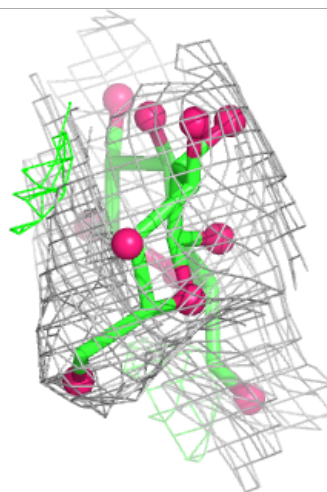
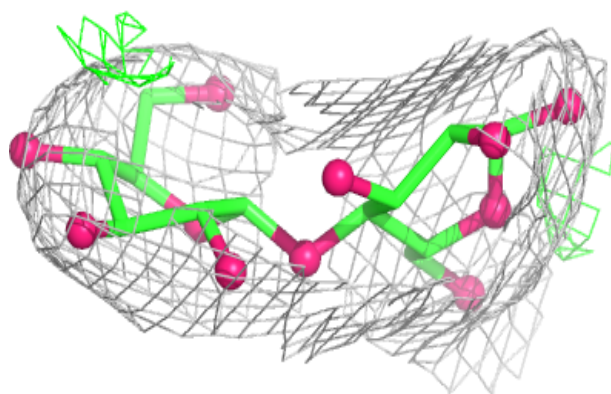
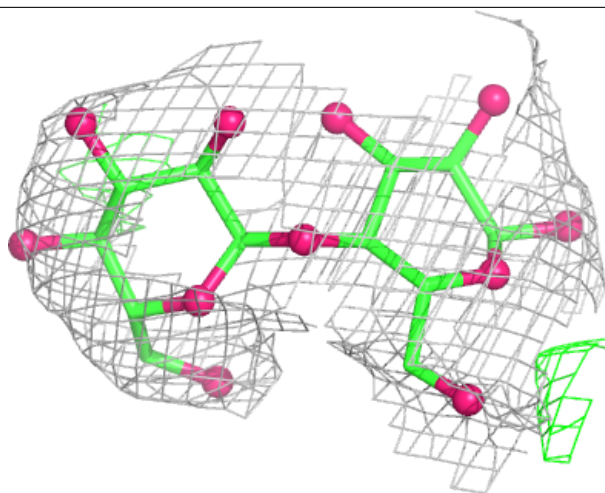
**Electron density around Chain J:**

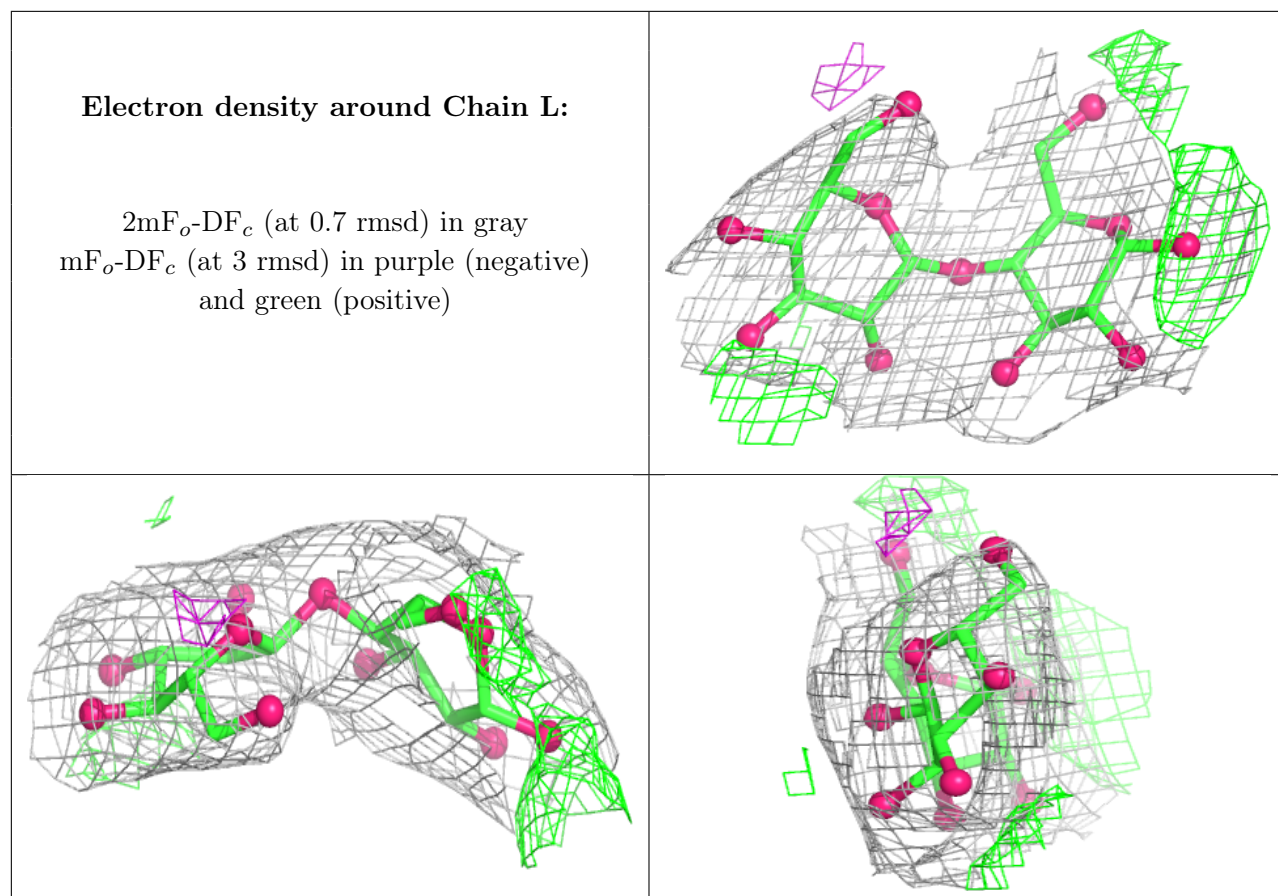
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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.