



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 09:17 AM BST

PDB ID : 6GFJ  
Title : Structure of RIP2 CARD domain fused to crystallisable MBP tag  
Authors : Pellegrini, E.; Cusack, S.  
Deposited on : 2018-04-30  
Resolution : 3.30 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.

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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

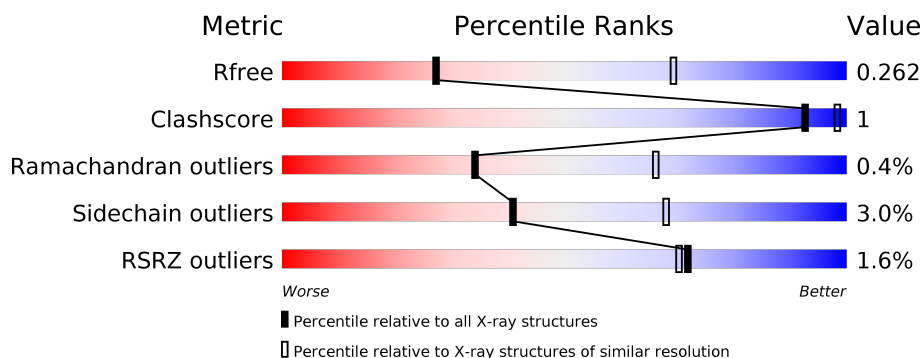
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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.



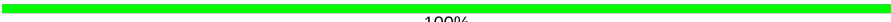

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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  $\geq 3$ , 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	477	<div> <div style="width: 90%;"></div> <div style="width: 5%;"></div> <div style="width: 5%;"></div> </div>
1	B	477	<div>2%</div> <div> <div style="width: 91%;"></div> <div style="width: 6%;"></div> <div style="width: 3%;"></div> </div>
1	C	477	<div>2%</div> <div> <div style="width: 89%;"></div> <div style="width: 6%;"></div> <div style="width: 5%;"></div> </div>
1	D	477	<div>2%</div> <div> <div style="width: 90%;"></div> <div style="width: 5%;"></div> <div style="width: 5%;"></div> </div>
2	E	2	<div>100%</div>
2	F	2	<div>100%</div>

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Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	H	2	 50%50%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14252 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 Sugar ABC transporter substrate-binding protein, Receptor-interacting serine/threonine-protein kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	457	Total	C	N	O	S	0	0	0
			3553	2273	584	686	10			
1	B	457	Total	C	N	O	S	0	0	0
			3553	2273	584	686	10			
1	C	456	Total	C	N	O	S	0	0	0
			3544	2268	583	683	10			
1	D	452	Total	C	N	O	S	0	0	0
			3514	2249	578	677	10			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ILE	THR	conflict	UNP A0A0F8NYV9
A	239	ALA	LYS	conflict	UNP A0A0F8NYV9
A	359	ALA	GLU	conflict	UNP A0A0F8NYV9
A	362	ALA	LYS	conflict	UNP A0A0F8NYV9
A	363	ALA	ASP	conflict	UNP A0A0F8NYV9
A	368	ALA	SER	conflict	UNP A0A0F8NYV9
A	369	ALA	SER	conflict	UNP A0A0F8NYV9
A	370	ALA	SER	linker	UNP A0A0F8NYV9
B	2	ILE	THR	conflict	UNP A0A0F8NYV9
B	239	ALA	LYS	conflict	UNP A0A0F8NYV9
B	359	ALA	GLU	conflict	UNP A0A0F8NYV9
B	362	ALA	LYS	conflict	UNP A0A0F8NYV9
B	363	ALA	ASP	conflict	UNP A0A0F8NYV9
B	368	ALA	SER	conflict	UNP A0A0F8NYV9
B	369	ALA	SER	conflict	UNP A0A0F8NYV9
B	370	ALA	SER	linker	UNP A0A0F8NYV9
C	2	ILE	THR	conflict	UNP A0A0F8NYV9
C	239	ALA	LYS	conflict	UNP A0A0F8NYV9
C	359	ALA	GLU	conflict	UNP A0A0F8NYV9
C	362	ALA	LYS	conflict	UNP A0A0F8NYV9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	363	ALA	ASP	conflict	UNP A0A0F8NYV9
C	368	ALA	SER	conflict	UNP A0A0F8NYV9
C	369	ALA	SER	conflict	UNP A0A0F8NYV9
C	370	ALA	SER	linker	UNP A0A0F8NYV9
D	2	ILE	THR	conflict	UNP A0A0F8NYV9
D	239	ALA	LYS	conflict	UNP A0A0F8NYV9
D	359	ALA	GLU	conflict	UNP A0A0F8NYV9
D	362	ALA	LYS	conflict	UNP A0A0F8NYV9
D	363	ALA	ASP	conflict	UNP A0A0F8NYV9
D	368	ALA	SER	conflict	UNP A0A0F8NYV9
D	369	ALA	SER	conflict	UNP A0A0F8NYV9
D	370	ALA	SER	linker	UNP A0A0F8NYV9

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



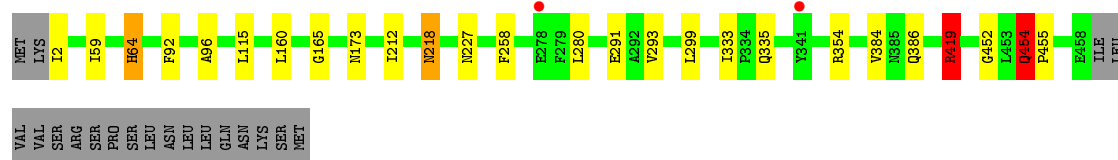
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			22	12	10			
2	F	2	Total	C	O	0	0	0
			22	12	10			
2	G	2	Total	C	O	0	0	0
			22	12	10			
2	H	2	Total	C	O	0	0	0
			22	12	10			

### 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.

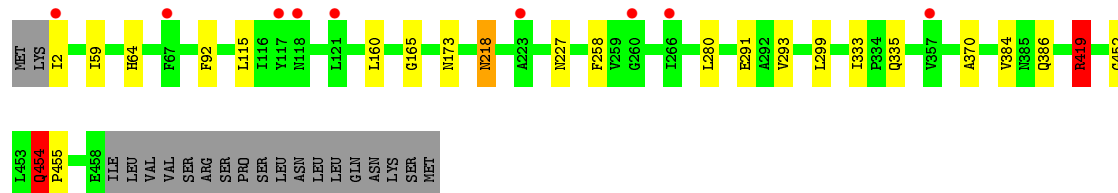
- Molecule 1: Sugar ABC transporter substrate-binding protein, Receptor-interacting serine/threonine-protein kinase 2

Chain A: 




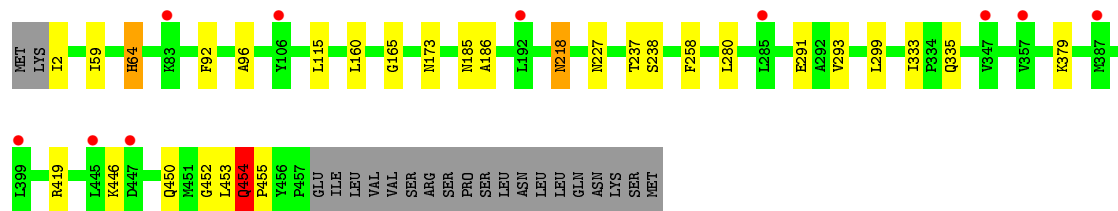
- Molecule 1: Sugar ABC transporter substrate-binding protein, Receptor-interacting serine/threonine-protein kinase 2

Chain B: 




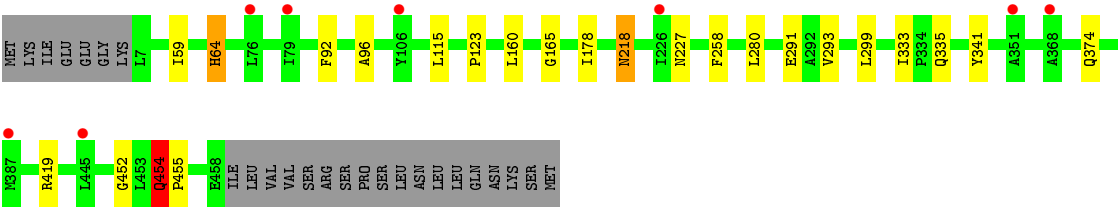
- Molecule 1: Sugar ABC transporter substrate-binding protein, Receptor-interacting serine/threonine-protein kinase 2

Chain C: 



- Molecule 1: Sugar ABC transporter substrate-binding protein, Receptor-interacting serine/threonine-protein kinase 2

Chain D: 



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

Chain E: 100%



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

Chain F: 100%



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

Chain G: 100%



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

Chain H: 50% 50%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.46 Å 121.57 Å 123.16 Å 90.00° 109.04° 90.00°	Depositor
Resolution (Å)	46.98 – 3.30 49.36 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (46.98-3.30) 99.1 (49.36-3.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.53 (at 3.33 Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, $R_{free}$	0.235 , 0.266 0.240 , 0.262	Depositor DCC
$R_{free}$ test set	1540 reflections (4.13%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	108.7	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 78.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.038 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	14252	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% 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	0.40	0/3630	0.54	2/4927 (0.0%)
1	B	0.41	1/3630 (0.0%)	0.54	2/4927 (0.0%)
1	C	0.44	1/3621 (0.0%)	0.56	3/4915 (0.1%)
1	D	0.44	1/3591 (0.0%)	0.55	2/4876 (0.0%)
All	All	0.42	3/14472 (0.0%)	0.55	9/19645 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	452	GLY	C-N	13.10	1.64	1.34
1	C	452	GLY	C-N	13.00	1.64	1.34
1	B	370	ALA	C-N	-5.06	1.22	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	452	GLY	O-C-N	-7.08	111.37	122.70
1	D	452	GLY	O-C-N	-7.08	111.38	122.70
1	A	419	ARG	CG-CD-NE	-5.26	100.75	111.80
1	B	419	ARG	CG-CD-NE	-5.25	100.77	111.80
1	C	454	GLN	C-N-CD	5.21	139.35	128.40

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	3553	0	3532	13	0
1	B	3553	0	3532	9	0
1	C	3544	0	3526	13	0
1	D	3514	0	3493	10	0
2	E	22	0	18	0	0
2	F	22	0	18	0	0
2	G	22	0	18	0	0
2	H	22	0	18	0	0
All	All	14252	0	14155	42	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 1.

The worst 5 of 42 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:B:454:GLN:HB3	1:B:455:PRO:CD	1.99	0.93
1:D:454:GLN:HB3	1:D:455:PRO:CD	1.99	0.93
1:A:454:GLN:HB3	1:A:455:PRO:CD	1.99	0.92
1:C:454:GLN:HB3	1:C:455:PRO:CD	1.99	0.91
1:C:454:GLN:HB3	1:C:455:PRO:HD3	1.63	0.80

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	455/477 (95%)	433 (95%)	20 (4%)	2 (0%)	34 66
1	B	455/477 (95%)	434 (95%)	19 (4%)	2 (0%)	34 66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	454/477 (95%)	434 (96%)	18 (4%)	2 (0%)	34 66
1	D	450/477 (94%)	430 (96%)	18 (4%)	2 (0%)	34 66
All	All	1814/1908 (95%)	1731 (95%)	75 (4%)	8 (0%)	34 66

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	454	GLN
1	B	454	GLN
1	C	454	GLN
1	D	454	GLN
1	A	165	GLY

### 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	371/391 (95%)	360 (97%)	11 (3%)	41 68
1	B	371/391 (95%)	360 (97%)	11 (3%)	41 68
1	C	370/391 (95%)	358 (97%)	12 (3%)	39 67
1	D	367/391 (94%)	357 (97%)	10 (3%)	44 71
All	All	1479/1564 (95%)	1435 (97%)	44 (3%)	41 68

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	258	PHE
1	C	92	PHE
1	D	258	PHE
1	B	291	GLU
1	C	2	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	100	ASN
1	C	218	ASN
1	D	218	ASN
1	B	385	ASN
1	D	335	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 ⓘ

8 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	E	1	2	11,11,12	0.56	0	15,16,17	0.84	0
2	GLC	E	2	2	11,11,12	0.30	0	15,15,17	0.85	0
2	GLC	F	1	2	11,11,12	0.59	0	15,16,17	1.02	1 (6%)
2	GLC	F	2	2	11,11,12	0.42	0	15,15,17	0.94	1 (6%)
2	GLC	G	1	2	11,11,12	0.56	0	15,16,17	0.96	0
2	GLC	G	2	2	11,11,12	0.39	0	15,15,17	0.92	0
2	GLC	H	1	2	11,11,12	0.67	0	15,16,17	1.20	2 (13%)
2	GLC	H	2	2	11,11,12	0.41	0	15,15,17	0.88	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	E	1	2	-	-	0/1/1/1
2	GLC	E	2	2	-	0/2/19/22	0/1/1/1
2	GLC	F	1	2	-	-	0/1/1/1
2	GLC	F	2	2	-	0/2/19/22	0/1/1/1
2	GLC	G	1	2	-	-	0/1/1/1
2	GLC	G	2	2	-	0/2/19/22	0/1/1/1
2	GLC	H	1	2	-	-	0/1/1/1
2	GLC	H	2	2	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	GLC	C1-C2-C3	2.66	115.83	110.31
2	H	1	GLC	C4-C3-C2	2.47	115.14	110.82
2	F	2	GLC	O5-C1-C2	-2.39	107.08	110.77
2	F	1	GLC	C1-C2-C3	2.27	115.03	110.31

There are no chirality outliers.

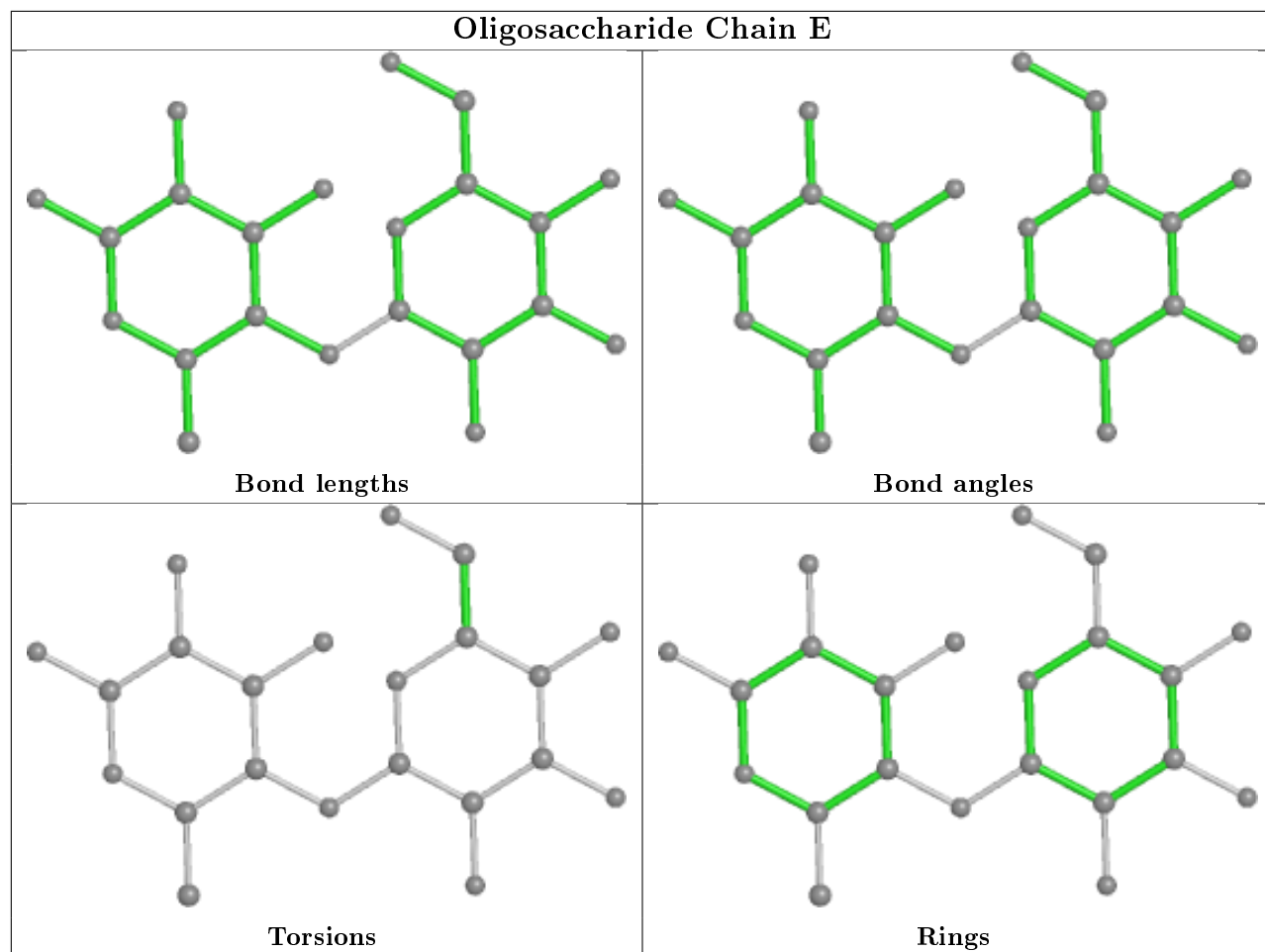
All (1) torsion outliers are listed below:

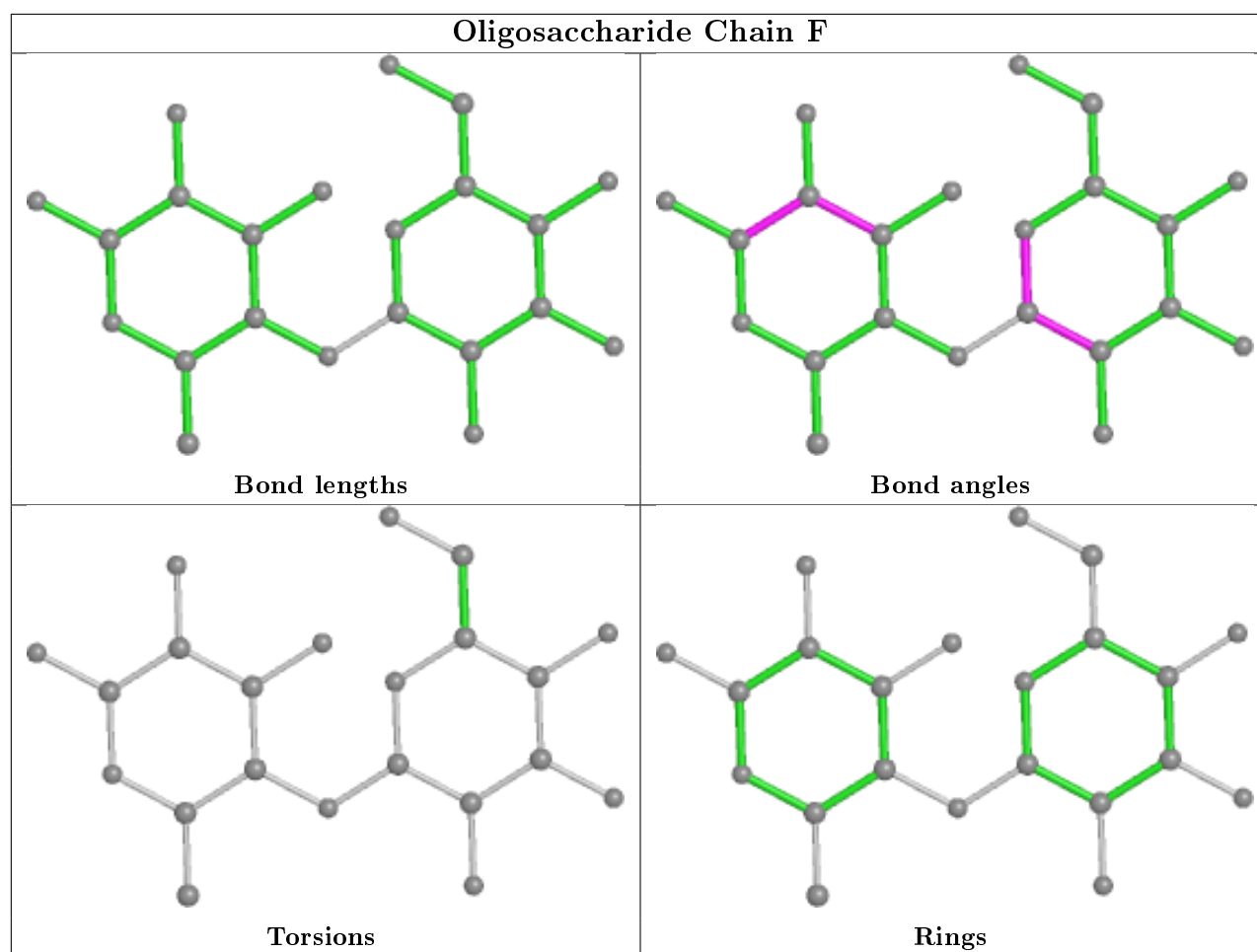
Mol	Chain	Res	Type	Atoms
2	H	2	GLC	O5-C5-C6-O6

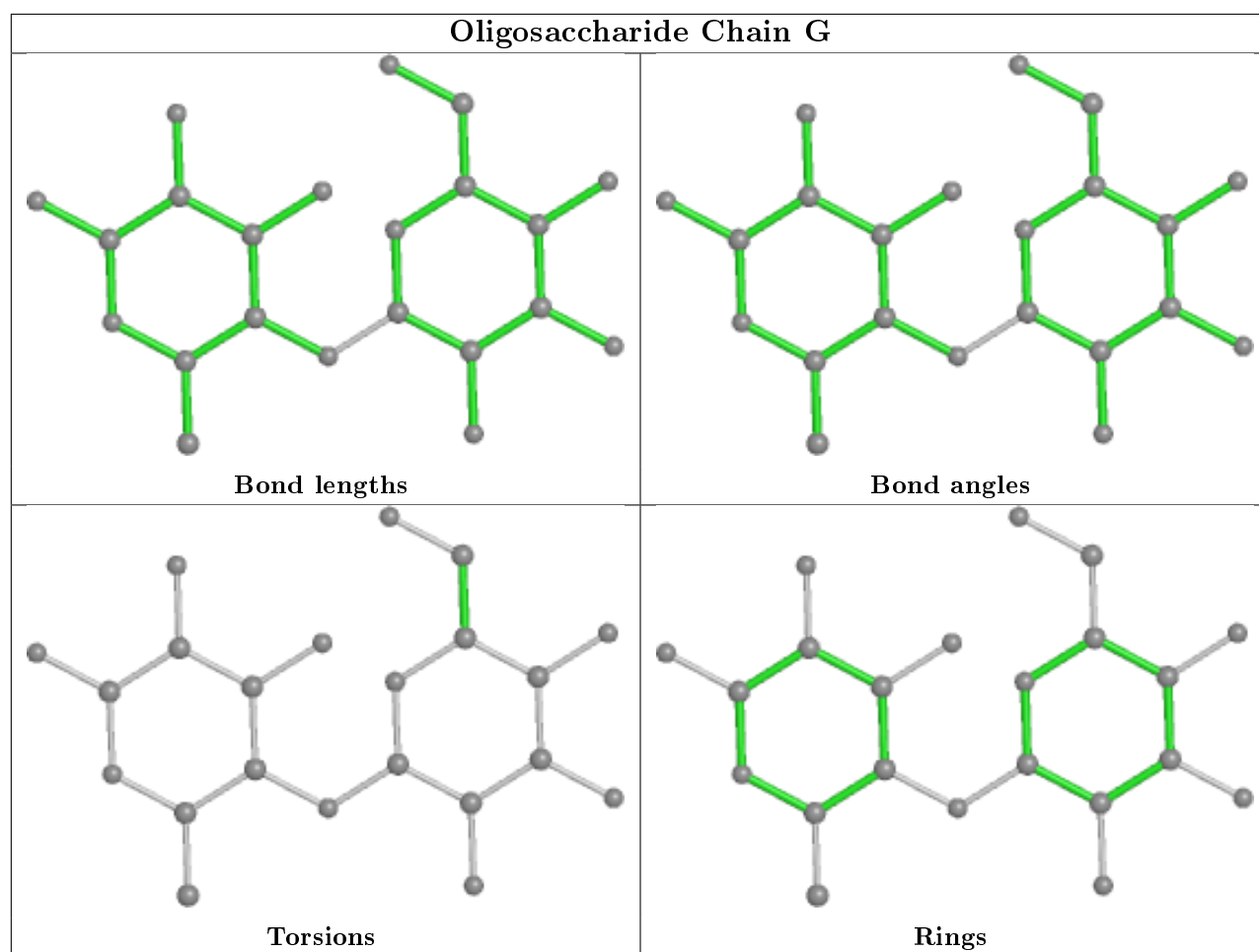
There are no ring outliers.

No monomer is involved in short contacts.

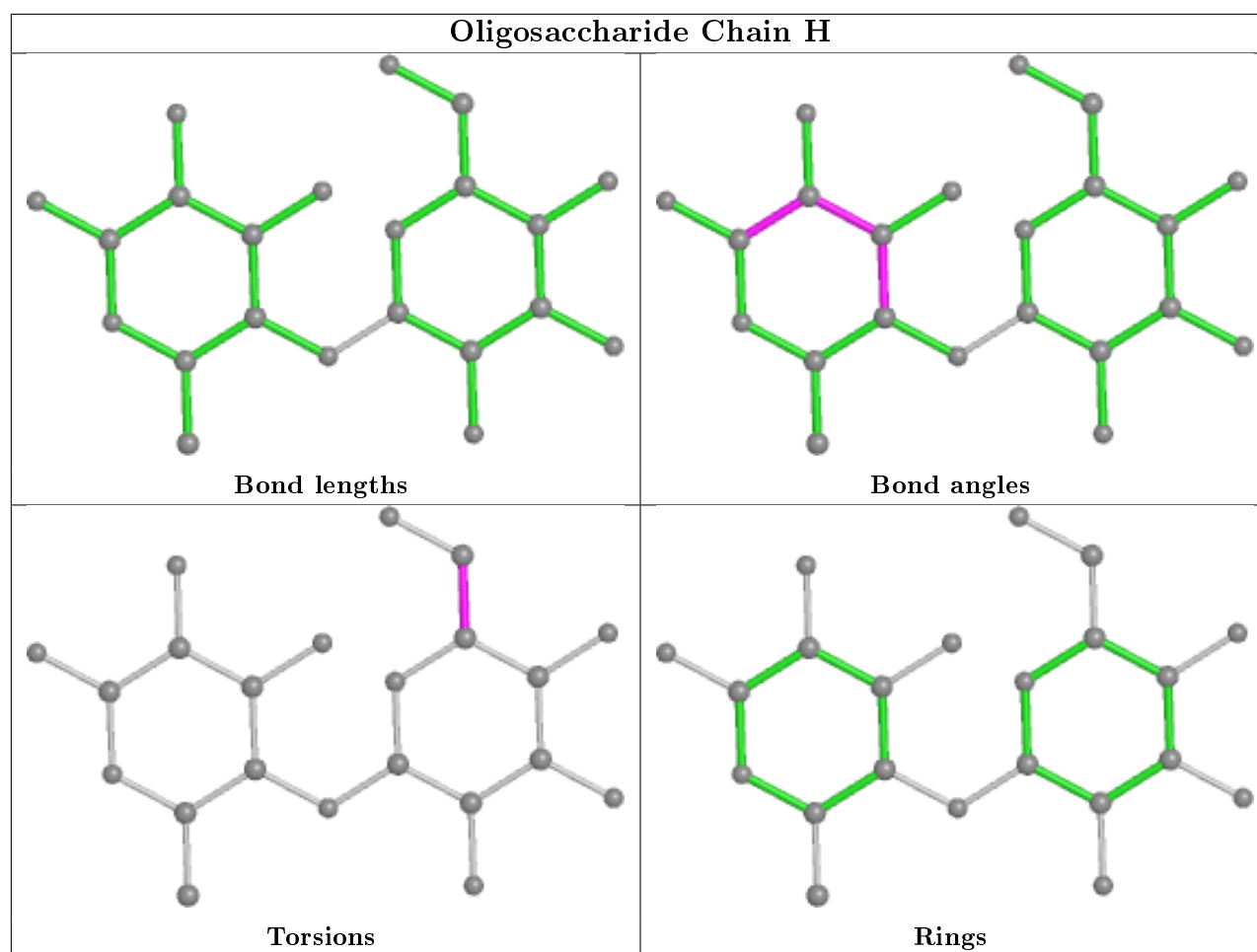
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











## 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	452:GLY	C	453:LEU	N	1.64
1	D	452:GLY	C	453:LEU	N	1.64

## 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	457/477 (95%)	0.10	2 (0%) 92 93	95, 123, 160, 186	0
1	B	457/477 (95%)	0.14	9 (1%) 65 64	94, 130, 165, 196	0
1	C	456/477 (95%)	0.15	10 (2%) 62 60	86, 133, 172, 199	0
1	D	452/477 (94%)	0.14	8 (1%) 68 67	96, 134, 171, 189	0
All	All	1822/1908 (95%)	0.13	29 (1%) 72 70	86, 130, 169, 199	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	106	TYR	3.6
1	D	351	ALA	3.5
1	C	357	VAL	3.3
1	C	445	LEU	2.9
1	D	226	ILE	2.8

### 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.

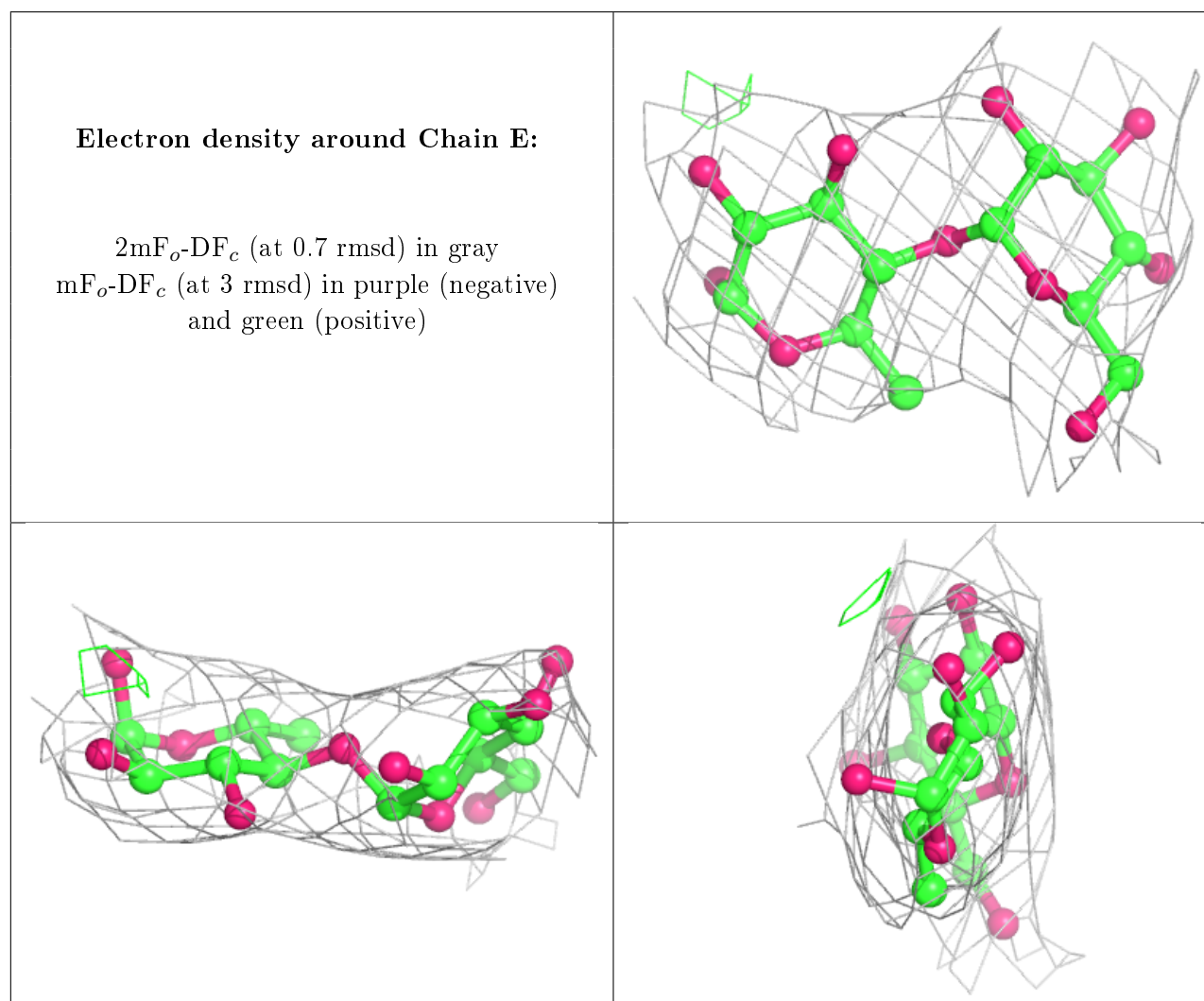
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	GLC	E	2	11/12	0.96	0.23	94,98,101,102	0
2	GLC	F	2	11/12	0.96	0.19	104,108,111,111	0

*Continued on next page...*

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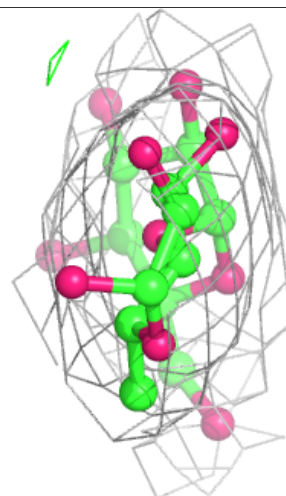
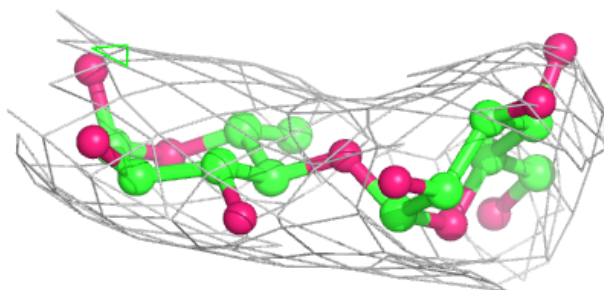
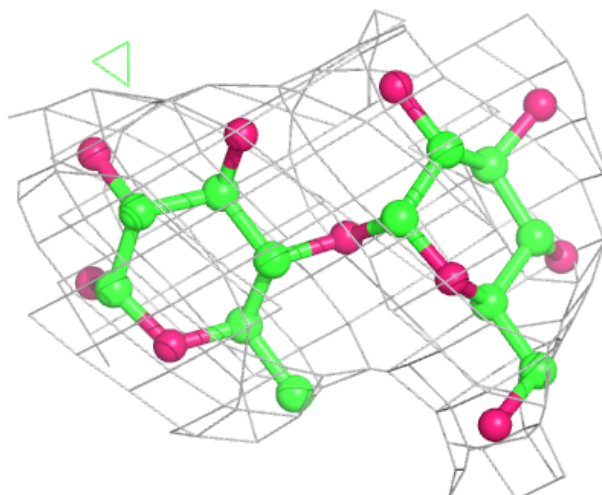
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLC	H	1	11/12	0.96	0.23	117,119,121,124	0
2	GLC	H	2	11/12	0.96	0.21	111,117,119,119	0
2	GLC	G	2	11/12	0.97	0.19	100,104,106,107	0
2	GLC	G	1	11/12	0.98	0.23	96,97,98,100	0
2	GLC	F	1	11/12	0.98	0.22	100,103,106,106	0
2	GLC	E	1	11/12	0.98	0.20	89,92,94,94	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.



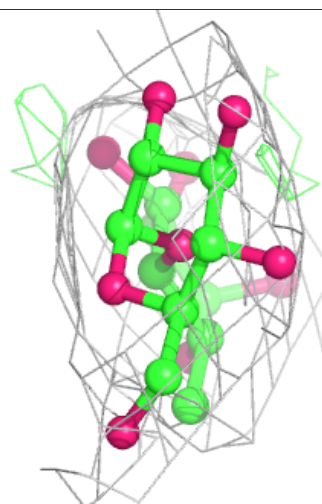
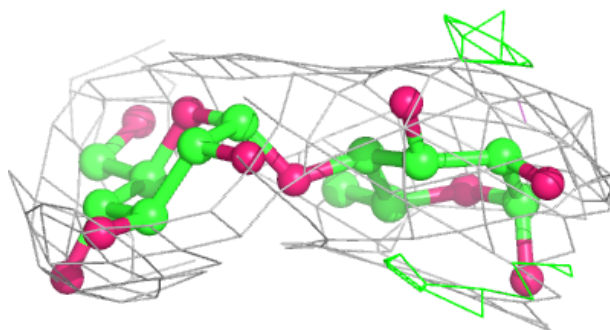
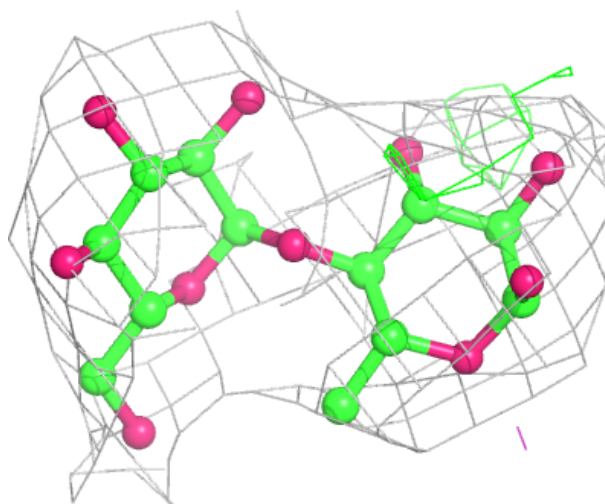
**Electron density around Chain F:**

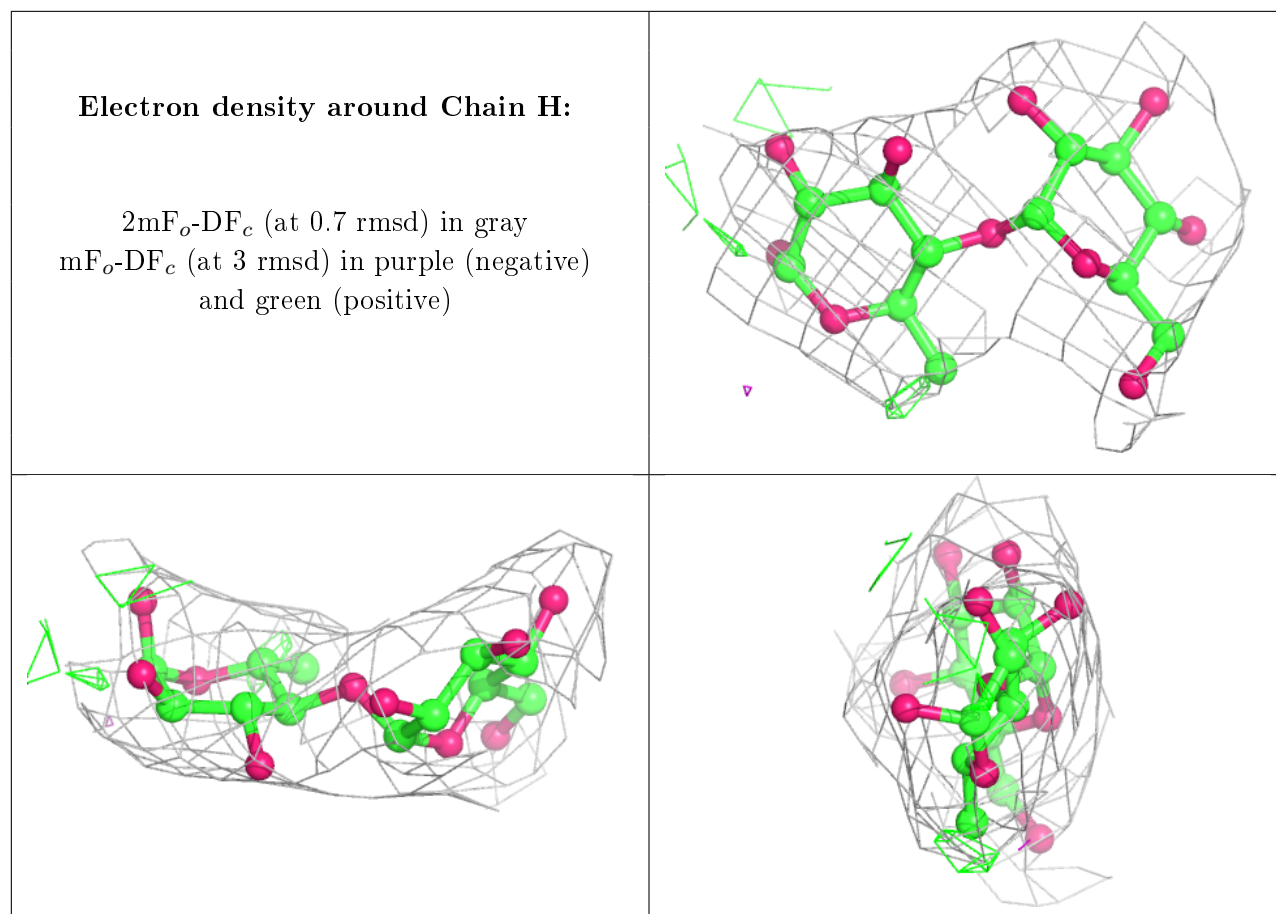
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain G:**

$2mF_o-DF_c$  (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.