



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 21, 2022 – 02:38 AM JST

PDB ID : 7WDA  
Title : Crystal structure LpqY in complex with Trehalose from Mycobacterium tuberculosis  
Authors : Sharma, D.; Das, U.  
Deposited on : 2021-12-21  
Resolution : 1.91 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	:	4.02b-467
Mogul	:	?? (??), CSD ??CSD?? (????)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
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)	:	2.29

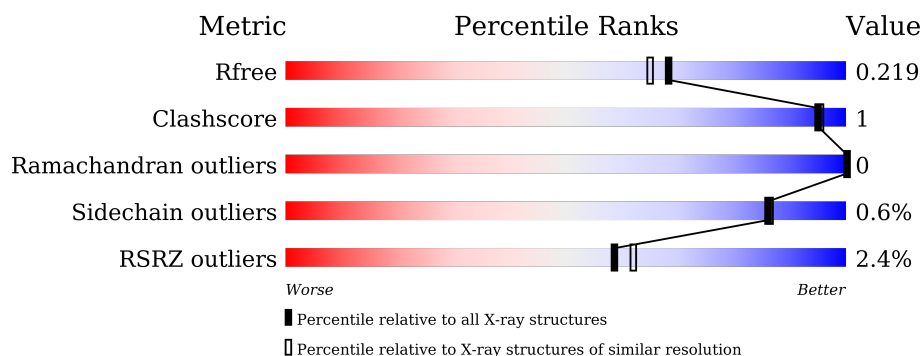
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.91 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	443	<div> <div>4%</div> <div>93%</div> <div>5%</div> <div>• •</div> </div>
1	B	443	<div> <div>2%</div> <div>93%</div> <div>5%</div> <div>•</div> </div>
1	C	443	<div> <div>2%</div> <div>93%</div> <div>• •</div> </div>
1	D	443	<div> <div>%</div> <div>92%</div> <div>• •</div> </div>
2	F	2	<div> <div>100%</div> </div>
2	G	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
2	H	2	 100%
2	I	2	 100%

## 2 Entry composition

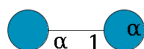
There are 4 unique types of molecules in this entry. The entry contains 14015 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Trehalose-binding lipoprotein LpqY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	432	Total	C	N	O	S	0	1	0
			3257	2061	570	620	6			
1	B	433	Total	C	N	O	S	0	0	0
			3265	2064	573	622	6			
1	C	426	Total	C	N	O	S	0	1	0
			3218	2037	567	608	6			
1	D	426	Total	C	N	O	S	0	1	0
			3222	2039	569	607	7			

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



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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

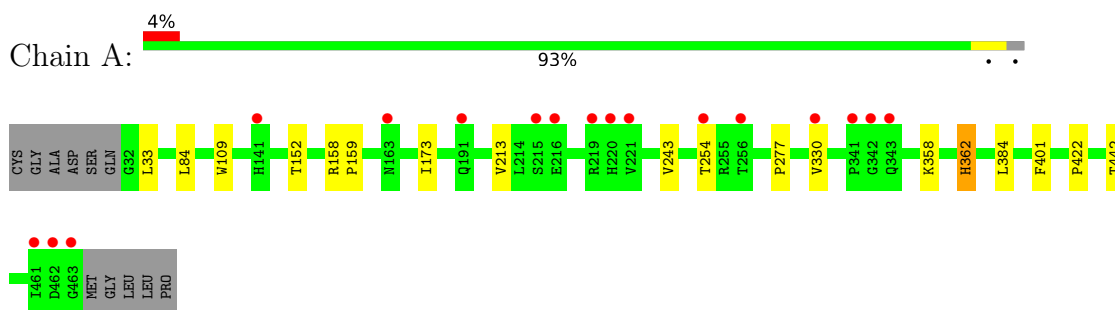
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	219	Total	O	0	0
			219	219		
4	B	253	Total	O	0	0
			253	253		
4	C	207	Total	O	0	0
			207	207		
4	D	262	Total	O	0	0
			262	262		

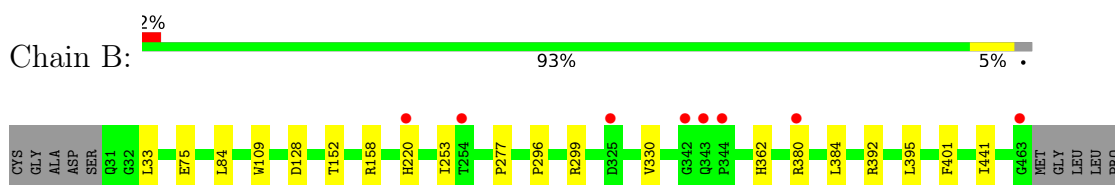
### 3 Residue-property plots [i](#)

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.

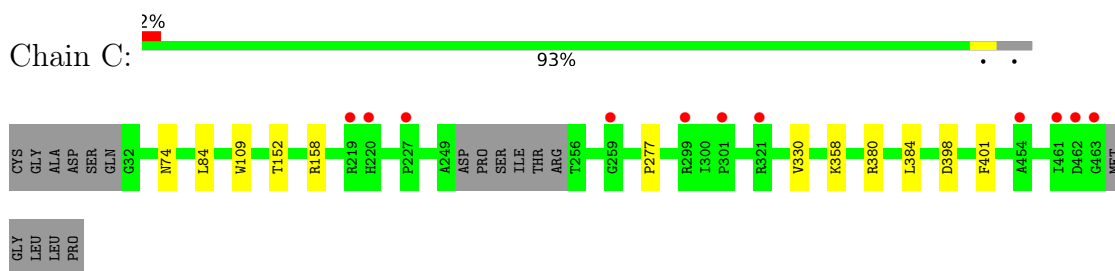
- Molecule 1: Trehalose-binding lipoprotein LpqY



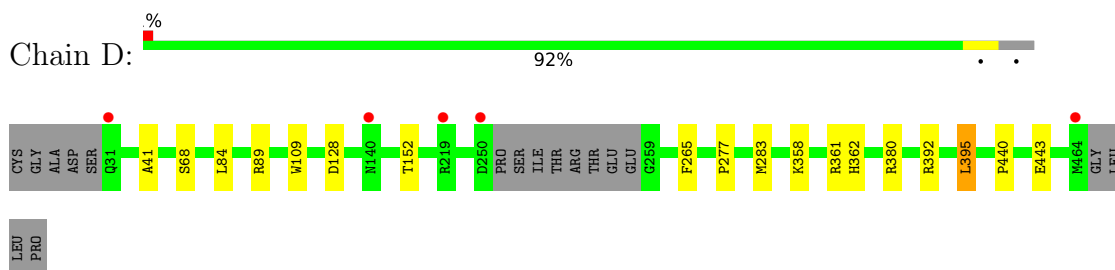
- Molecule 1: Trehalose-binding lipoprotein LpqY



- Molecule 1: Trehalose-binding lipoprotein LpqY



- Molecule 1: Trehalose-binding lipoprotein LpqY



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

Chain F:  100%



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

Chain G:  100%



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

Chain H:  100%



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

Chain I:  100%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	154.30Å 162.13Å 142.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.03 – 1.91 48.03 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.03-1.91) 85.0 (48.03-1.90)	Depositor EDS
$R_{merge}$	0.24	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	-0.32 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.199 , 0.220 0.199 , 0.219	Depositor DCC
$R_{free}$ test set	1994 reflections (1.44%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.9	Xtriage
Anisotropy	0.423	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 42.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14015	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	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 37.16 % 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 4.4720e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, SO4

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	0.29	0/3339	0.52	0/4576
1	B	0.29	0/3343	0.51	0/4580
1	C	0.27	0/3298	0.51	0/4516
1	D	0.31	0/3302	0.52	0/4520
All	All	0.29	0/13282	0.51	0/18192

There are no bond length outliers.

There are no bond angle outliers.

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	3257	0	3191	9	0
1	B	3265	0	3203	10	0
1	C	3218	0	3161	5	0
1	D	3222	0	3169	8	0
2	F	23	0	21	0	0
2	G	23	0	21	0	0
2	H	23	0	21	0	0
2	I	23	0	21	0	0
3	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	0	0	0
3	C	10	0	0	0	0
4	A	219	0	0	0	0
4	B	253	0	0	1	0
4	C	207	0	0	0	0
4	D	262	0	0	0	0
All	All	14015	0	12808	32	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 32 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:D:440:PRO:HG2	1:D:443:GLU:HG3	1.66	0.78
1:A:173:ILE:HD11	1:A:243:VAL:HG22	1.83	0.60
1:B:296:PRO:HB2	1:B:299:ARG:HD3	1.84	0.60
1:C:84:LEU:HD13	1:C:109:TRP:HB3	1.88	0.55
1:A:384:LEU:HD21	1:A:401:PHE:HA	1.92	0.51

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	431/443 (97%)	421 (98%)	10 (2%)	0	100	100
1	B	431/443 (97%)	423 (98%)	8 (2%)	0	100	100
1	C	423/443 (96%)	415 (98%)	8 (2%)	0	100	100
1	D	423/443 (96%)	415 (98%)	8 (2%)	0	100	100
All	All	1708/1772 (96%)	1674 (98%)	34 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	334/344 (97%)	331 (99%)	3 (1%)	78	78
1	B	335/344 (97%)	334 (100%)	1 (0%)	92	93
1	C	329/344 (96%)	327 (99%)	2 (1%)	86	86
1	D	330/344 (96%)	326 (99%)	4 (1%)	71	69
All	All	1328/1376 (96%)	1318 (99%)	10 (1%)	86	81

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	362[A]	HIS
1	D	362[B]	HIS
1	D	395	LEU
1	B	220	HIS
1	C	74	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	180	HIS

### 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.

There are no bond length outliers.

There are no bond angle outliers.

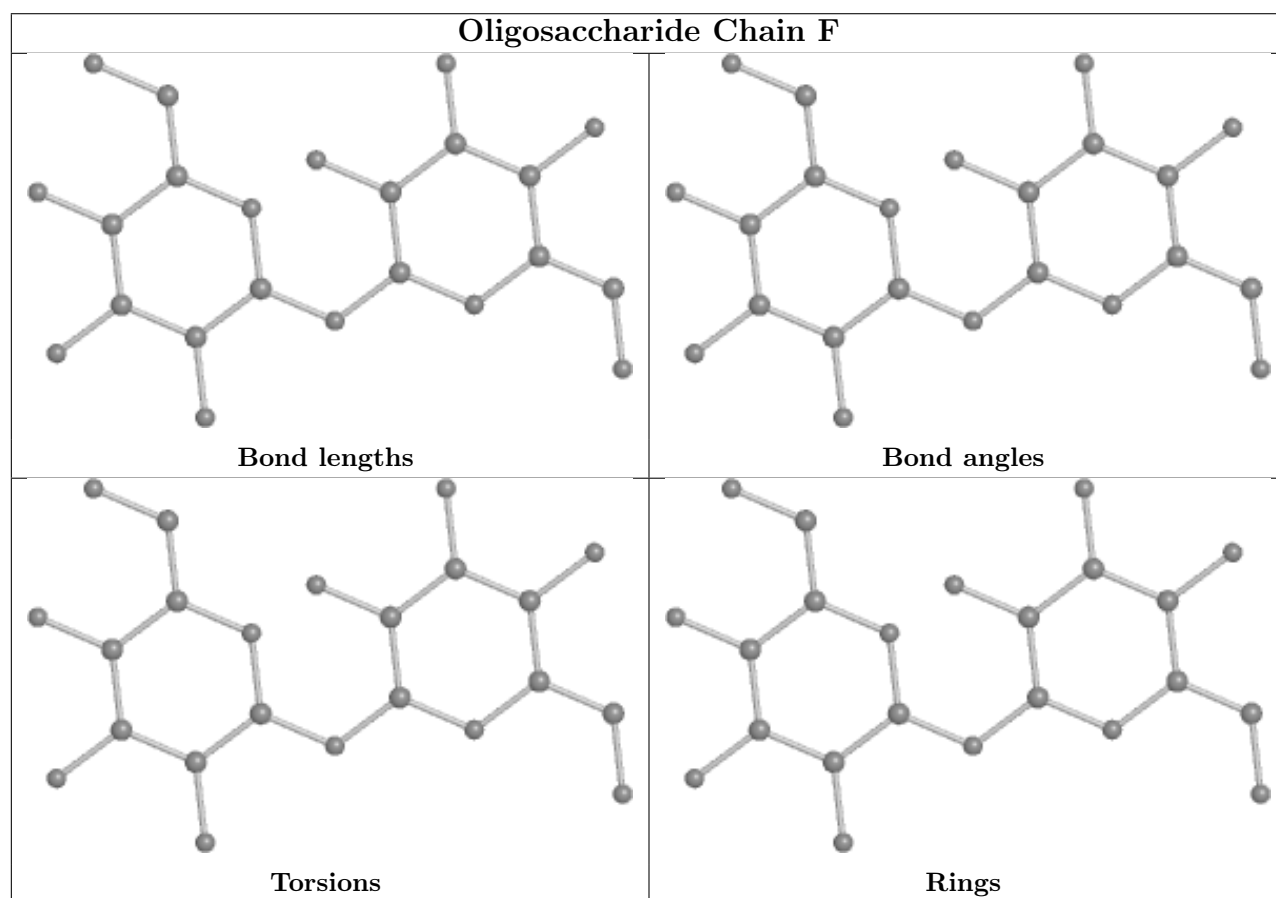
There are no chirality outliers.

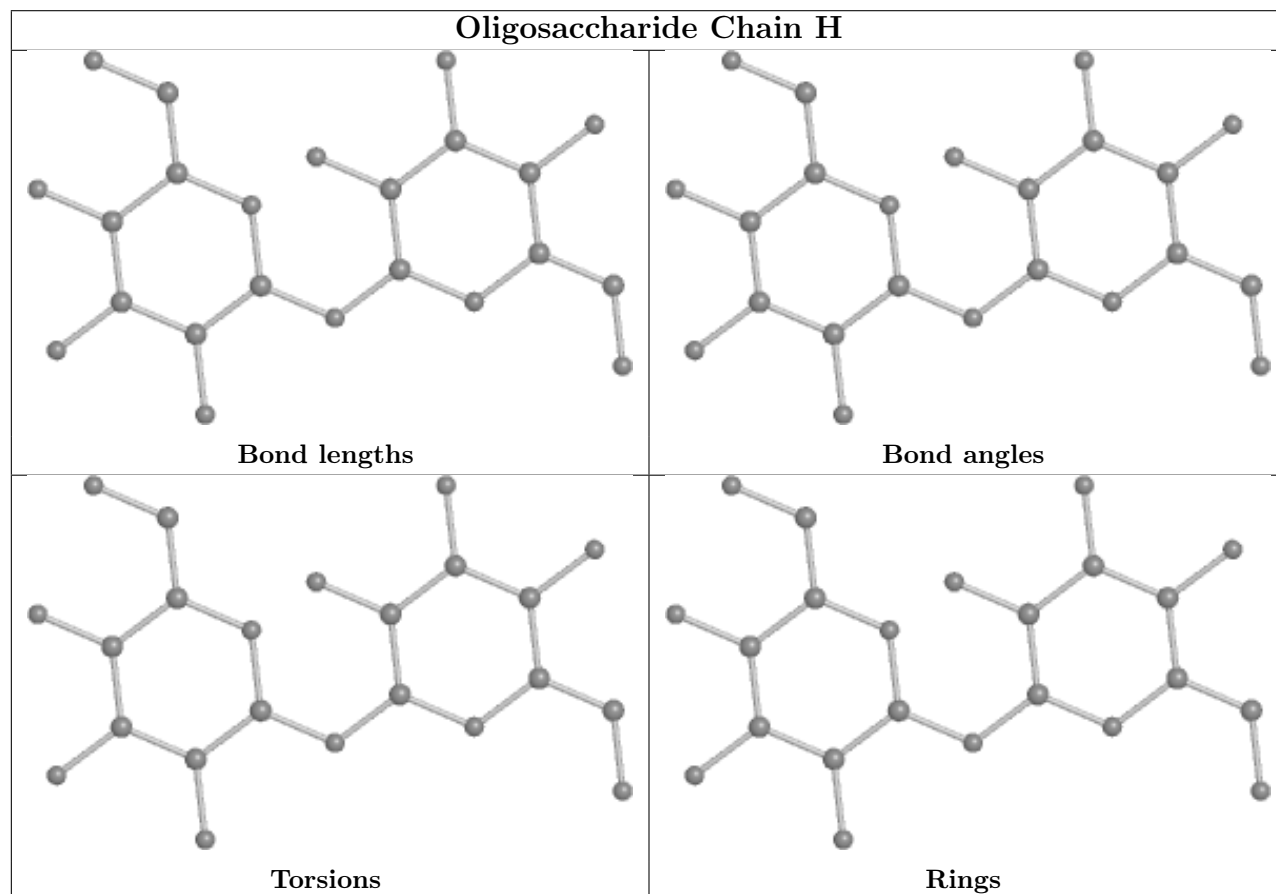
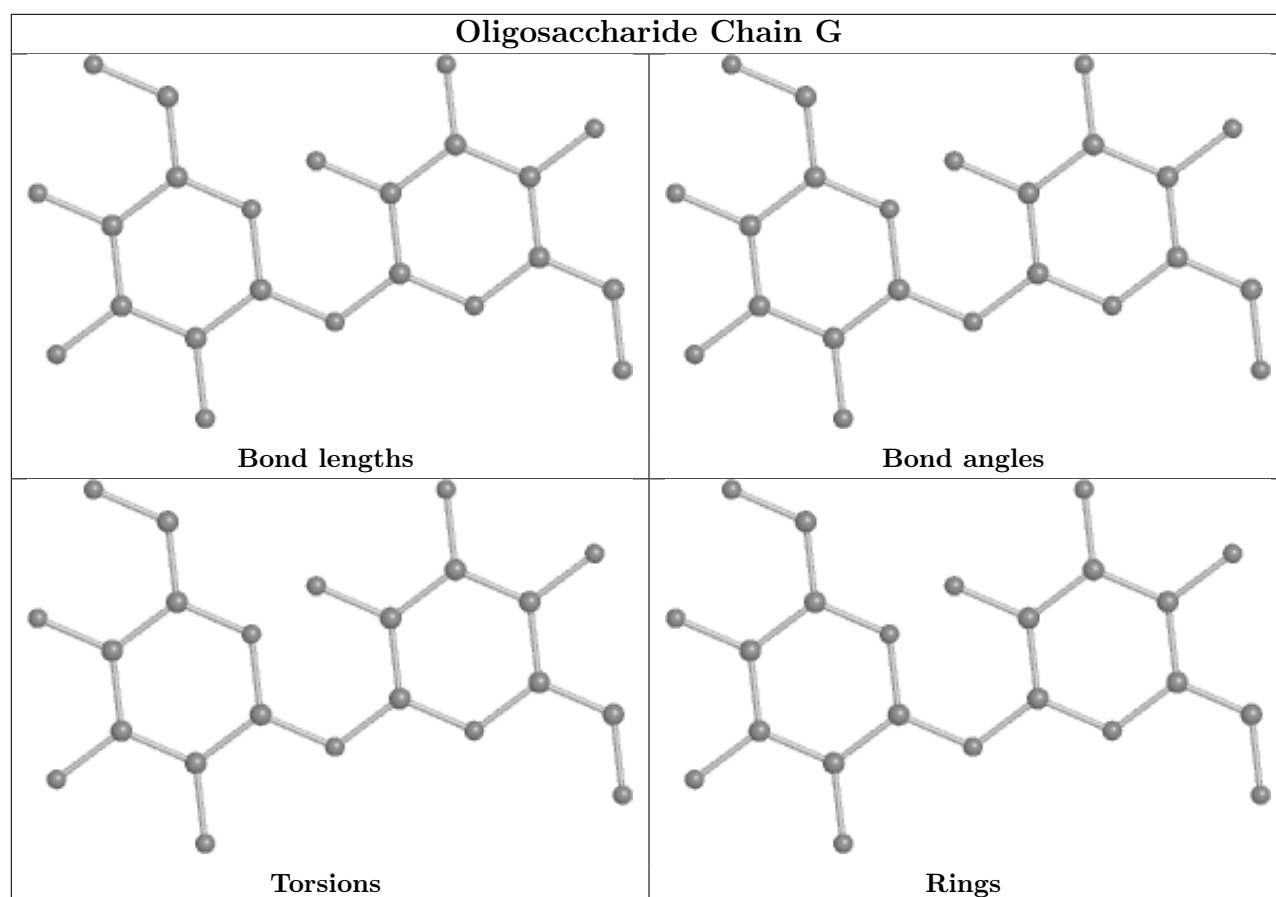
There are no torsion outliers.

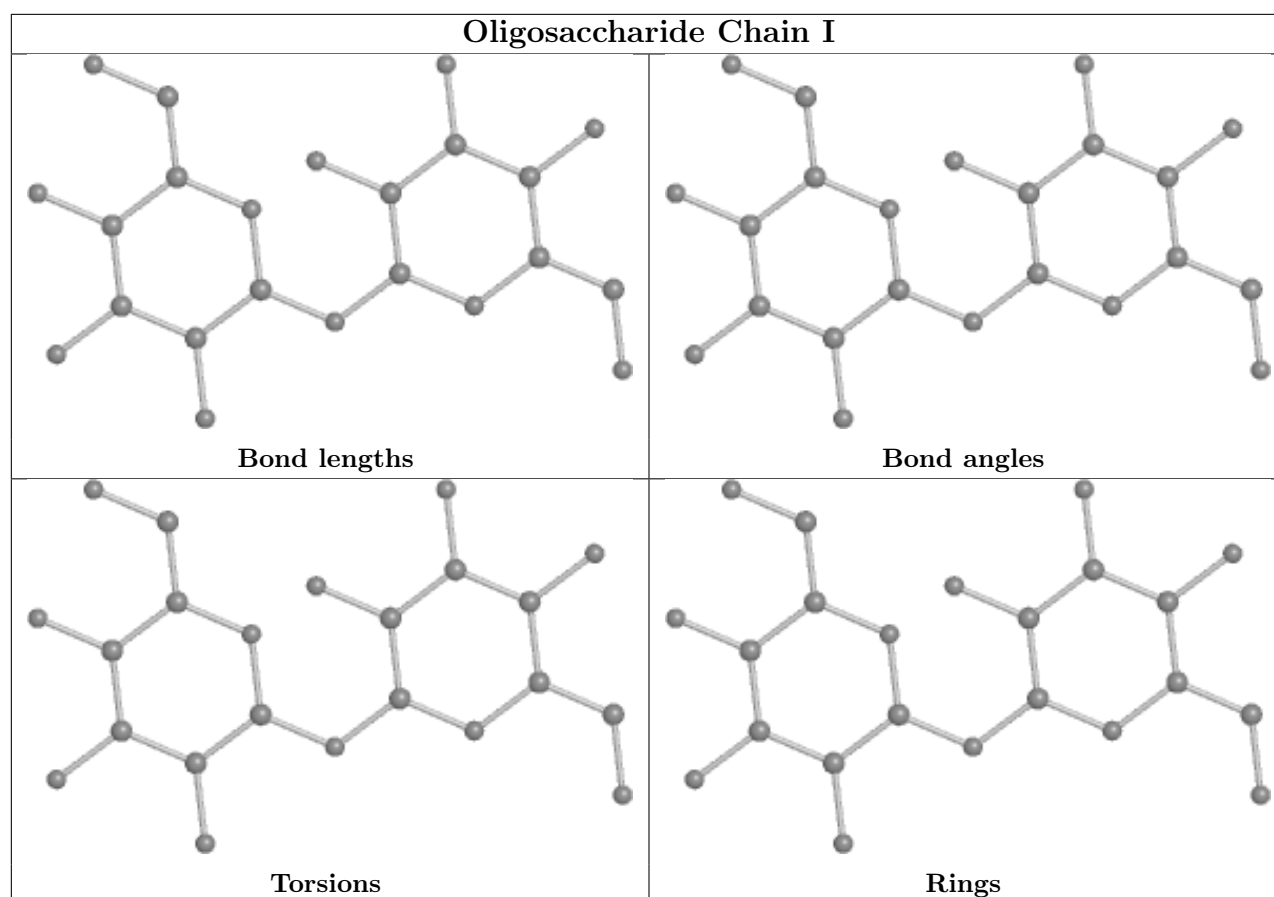
There are no ring outliers.

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](#)

4 ligands are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	432/443 (97%)	0.14	17 (3%) 39 42	25, 36, 58, 86	0
1	B	433/443 (97%)	0.09	8 (1%) 68 71	23, 33, 53, 83	0
1	C	426/443 (96%)	0.10	11 (2%) 56 59	28, 37, 59, 85	0
1	D	426/443 (96%)	0.03	5 (1%) 79 81	25, 32, 48, 81	0
All	All	1717/1772 (96%)	0.09	41 (2%) 59 62	23, 35, 56, 86	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	464	MET	4.5
1	A	191	GLN	3.7
1	A	342	GLY	3.4
1	D	31	GLN	3.3
1	B	342	GLY	3.3

### 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, 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.

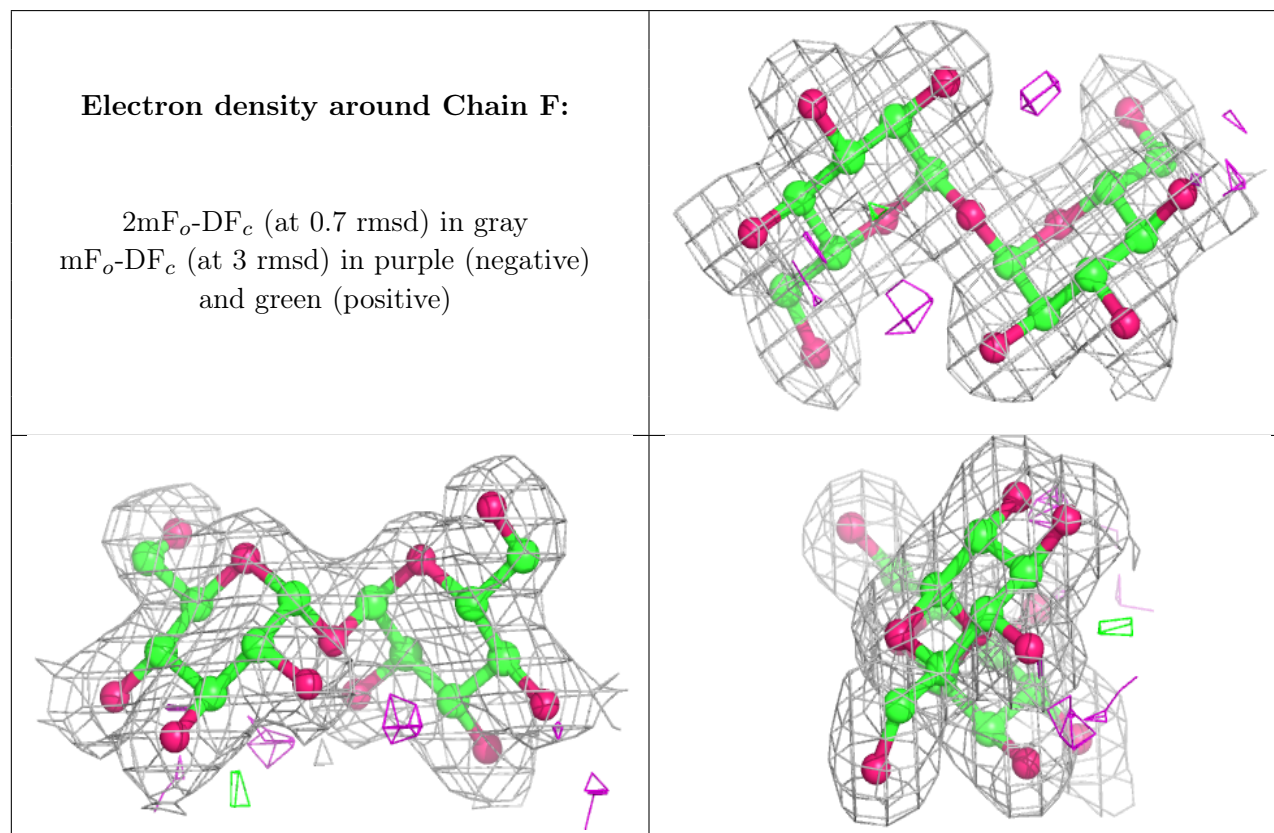
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	GLC	F	1	11/12	0.94	0.12	28,29,31,33	0
2	GLC	G	1	11/12	0.94	0.12	28,29,30,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GLC	I	1	11/12	0.94	0.11	21,25,30,31	0
2	GLC	G	2	12/12	0.96	0.13	28,29,31,31	0
2	GLC	H	1	11/12	0.97	0.09	31,31,33,33	0
2	GLC	H	2	12/12	0.97	0.13	30,30,32,33	0
2	GLC	F	2	12/12	0.97	0.11	28,30,31,32	0
2	GLC	I	2	12/12	0.97	0.12	21,27,31,31	0

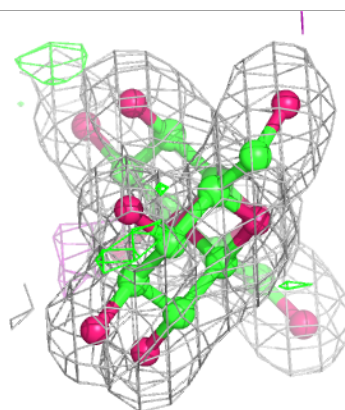
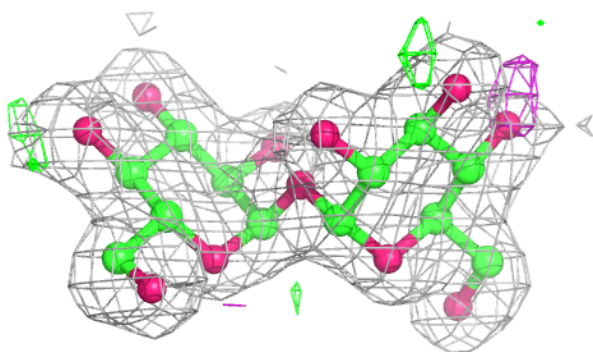
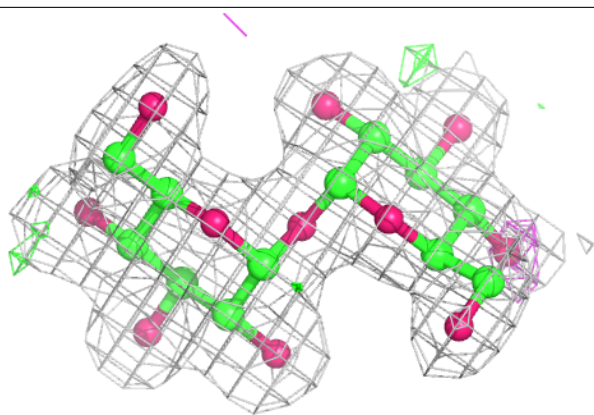
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



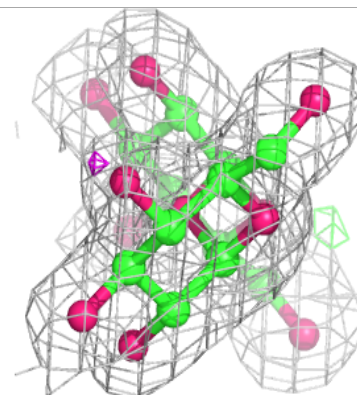
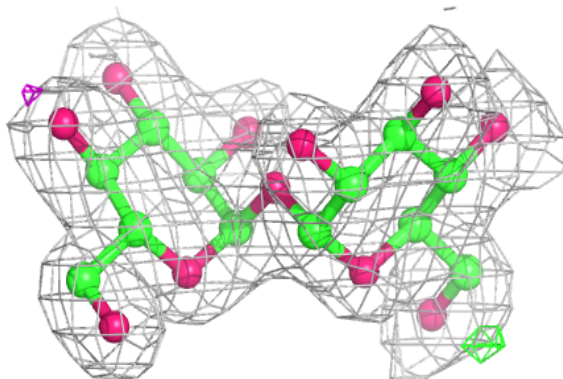
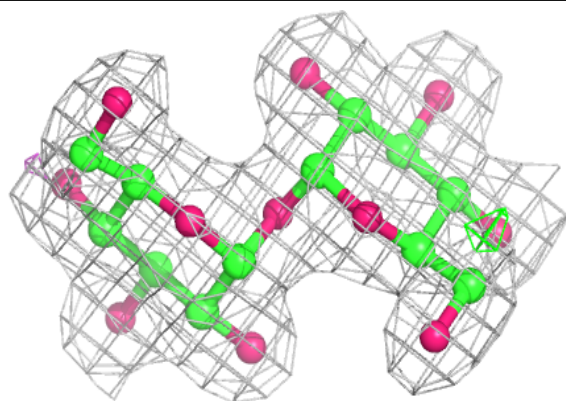


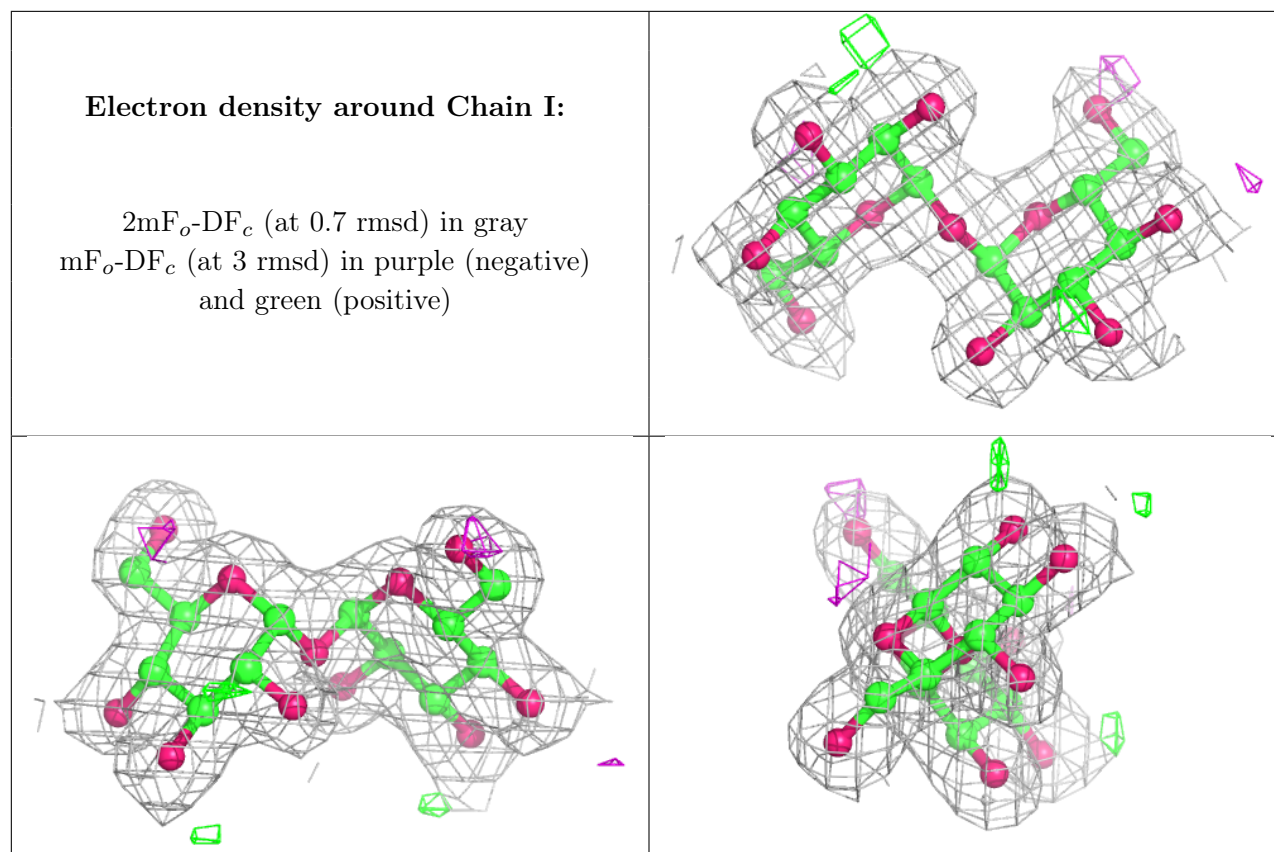
**Electron density around Chain G:**

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

**Electron density around Chain H:**

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





## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
3	SO4	C	501	5/5	0.92	0.12	44,47,60,72	0
3	SO4	A	501	5/5	0.94	0.09	41,43,63,67	0
3	SO4	C	502	5/5	0.94	0.11	44,46,61,62	0
3	SO4	B	501	5/5	0.96	0.11	43,44,60,74	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.