



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2023 – 10:07 PM EDT

PDB ID : 7JTR  
Title : Complex of maltose-binding protein (MBP) with single-chain Fv (scFv)  
Authors : Loll, P.J.  
Deposited on : 2020-08-18  
Resolution : 2.50 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

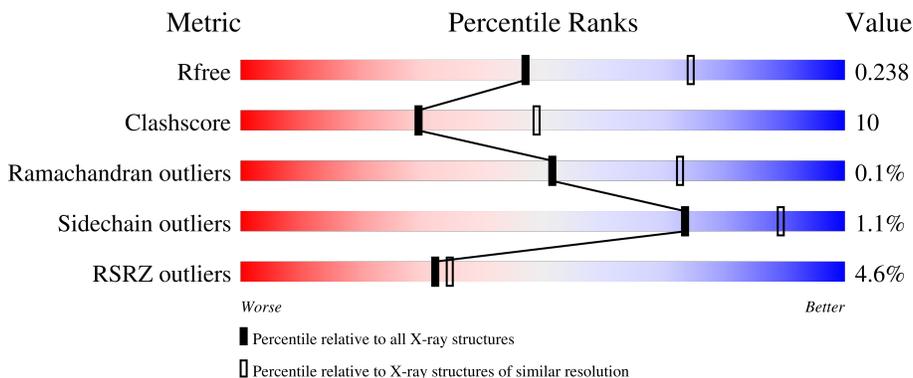
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	369	 3% 80% 18% .
1	C	369	 5% 76% 22% .
1	E	369	 4% 84% 15% .
1	G	369	 6% 78% 20% .
2	B	251	 4% 69% 20% . 10%

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Mol	Chain	Length	Quality of chain
2	D	251	<p>4% 69% 19% 11%</p>
2	F	251	<p>6% 67% 21% 11%</p>
2	H	251	<p>4% 71% 18% 11%</p>
3	J	2	<p>50% 50%</p>
3	K	2	<p>50% 50%</p>
3	L	2	<p>100%</p>
3	M	2	<p>50% 50%</p>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18514 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	369	2871	1849	467	549	6	0	0	0
1	C	369	2871	1849	467	549	6	0	0	0
1	E	369	2871	1849	467	549	6	0	0	0
1	G	369	2871	1849	467	549	6	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	312	VAL	ALA	variant	UNP P0AEX9
C	312	VAL	ALA	variant	UNP P0AEX9
E	312	VAL	ALA	variant	UNP P0AEX9
G	312	VAL	ALA	variant	UNP P0AEX9

- Molecule 2 is a protein called single-chain Fv antibody fragment (scFv).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	225	1734	1096	288	341	9	0	0	0
2	D	223	1721	1089	285	338	9	0	0	0
2	F	224	1731	1094	289	339	9	0	0	0
2	H	224	1731	1094	289	339	9	0	0	0

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	F	1	Total	Cl	0	0
			1	1		
4	H	1	Total	Cl	0	0
			1	1		

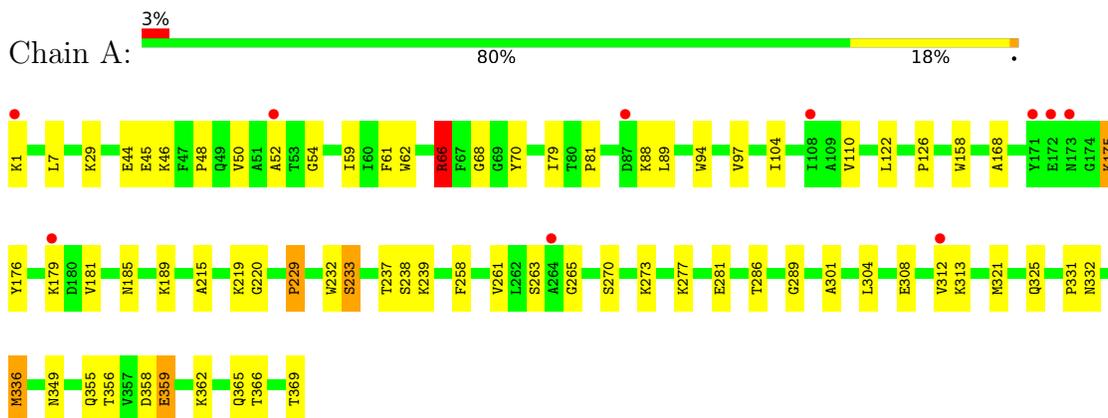
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	O	0	0
			4	4		
5	C	2	Total	O	0	0
			2	2		
5	D	1	Total	O	0	0
			1	1		
5	E	4	Total	O	0	0
			4	4		
5	F	2	Total	O	0	0
			2	2		
5	G	4	Total	O	0	0
			4	4		
5	H	1	Total	O	0	0
			1	1		

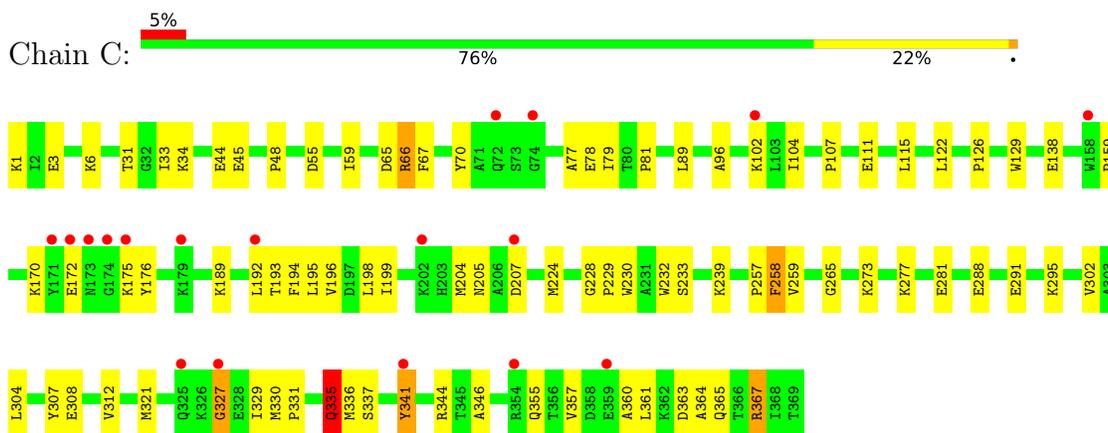
### 3 Residue-property plots

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.

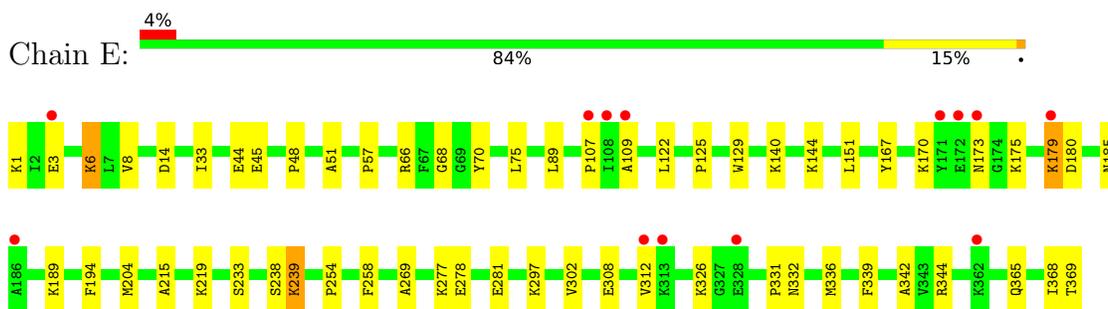
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein



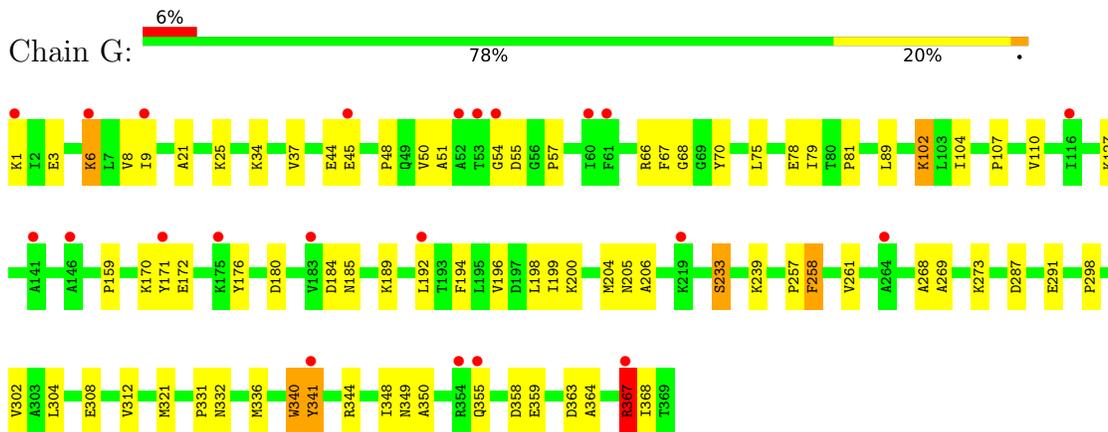
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein



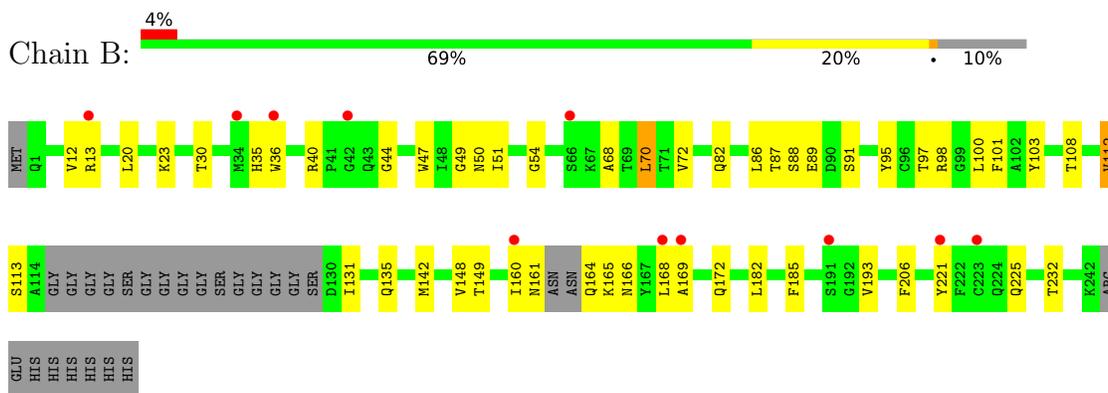
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein



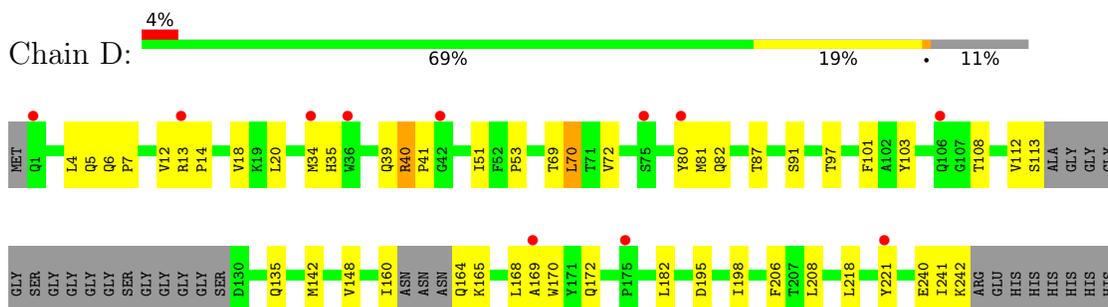
- Molecule 1: Maltose/maltodextrin-binding periplasmic protein



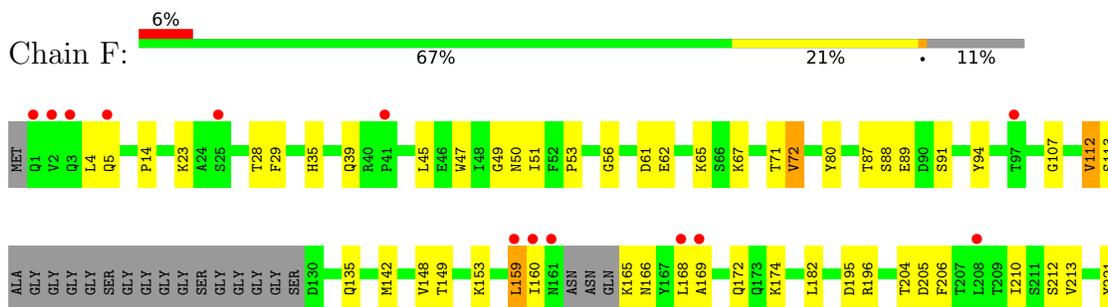
- Molecule 2: single-chain Fv antibody fragment (scFv)



- Molecule 2: single-chain Fv antibody fragment (scFv)



- Molecule 2: single-chain Fv antibody fragment (scFv)





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.20Å 91.70Å 174.63Å 90.00° 91.44° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (20.00-2.50) 98.4 (20.00-2.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.33 (at 2.50Å)	Xtrriage
Refinement program	PHENIX v1.11.1	Depositor
R, $R_{free}$	0.201 , 0.237 0.201 , 0.238	Depositor DCC
$R_{free}$ test set	1980 reflections (1.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.3	Xtrriage
Anisotropy	0.851	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 40.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.009 for k,h,-l 0.004 for -k,-h,-l 0.026 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	18514	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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: CL, 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	0.51	2/2940 (0.1%)	0.74	9/3990 (0.2%)
1	C	0.53	1/2940 (0.0%)	0.83	12/3990 (0.3%)
1	E	0.50	1/2940 (0.0%)	0.73	5/3990 (0.1%)
1	G	0.51	1/2940 (0.0%)	0.77	13/3990 (0.3%)
2	B	0.49	0/1773	0.72	3/2403 (0.1%)
2	D	0.50	0/1760	0.96	8/2385 (0.3%)
2	F	0.51	0/1770	0.83	5/2398 (0.2%)
2	H	0.49	0/1770	0.75	3/2398 (0.1%)
All	All	0.51	5/18833 (0.0%)	0.79	58/25544 (0.2%)

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	C	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	179	LYS	CD-CE	6.21	1.66	1.51
1	A	359	GLU	CD-OE2	5.97	1.32	1.25
1	A	359	GLU	CD-OE1	5.72	1.31	1.25
1	C	34	LYS	CD-CE	5.67	1.65	1.51
1	G	367	ARG	CB-CG	-5.07	1.38	1.52

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	40	ARG	NE-CZ-NH1	-16.17	112.22	120.30
2	D	40	ARG	NE-CZ-NH2	13.70	127.15	120.30
2	D	70	LEU	CB-CG-CD2	-13.24	88.49	111.00
1	G	341	TYR	CA-CB-CG	-10.55	93.35	113.40
2	D	40	ARG	CG-CD-NE	9.56	131.88	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	335	GLN	Sidechain

## 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	2871	0	2850	44	0
1	C	2871	0	2850	62	2
1	E	2871	0	2850	37	2
1	G	2871	0	2850	64	0
2	B	1734	0	1676	37	0
2	D	1721	0	1665	50	0
2	F	1731	0	1675	40	0
2	H	1731	0	1676	24	0
3	J	23	0	21	0	0
3	K	23	0	21	4	0
3	L	23	0	21	1	0
3	M	23	0	21	2	0
4	B	1	0	0	0	0
4	F	1	0	0	1	0
4	H	1	0	0	0	0
5	A	4	0	0	1	0
5	C	2	0	0	0	0
5	D	1	0	0	0	0
5	E	4	0	0	0	0
5	F	2	0	0	0	0
5	G	4	0	0	0	0
5	H	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18514	0	18176	350	2

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 350 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:G:1:LYS:HD2	1:G:54:GLY:C	1.72	1.09
1:C:170:LYS:HE2	1:C:172:GLU:CG	1.83	1.08
1:G:1:LYS:HD2	1:G:54:GLY:O	1.53	1.07
2:D:13:ARG:HG2	2:D:14:PRO:HD2	1.43	1.01
1:C:170:LYS:HE2	1:C:172:GLU:HG3	1.02	1.01

All (2) 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:C:175:LYS:NZ	1:E:219:LYS:NZ[2_957]	1.06	1.14
1:C:175:LYS:NZ	1:E:219:LYS:CE[2_957]	2.14	0.06

## 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	367/369 (100%)	359 (98%)	8 (2%)	0	100 100
1	C	367/369 (100%)	359 (98%)	7 (2%)	1 (0%)	41 61
1	E	367/369 (100%)	360 (98%)	7 (2%)	0	100 100
1	G	367/369 (100%)	359 (98%)	8 (2%)	0	100 100
2	B	219/251 (87%)	209 (95%)	9 (4%)	1 (0%)	29 48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	217/251 (86%)	207 (95%)	9 (4%)	1 (0%)	29	48
2	F	218/251 (87%)	211 (97%)	7 (3%)	0	100	100
2	H	218/251 (87%)	207 (95%)	11 (5%)	0	100	100
All	All	2340/2480 (94%)	2271 (97%)	66 (3%)	3 (0%)	51	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	337	SER
2	D	165	LYS
2	B	44	GLY

### 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	297/297 (100%)	291 (98%)	6 (2%)	55	79
1	C	297/297 (100%)	294 (99%)	3 (1%)	76	90
1	E	297/297 (100%)	294 (99%)	3 (1%)	76	90
1	G	297/297 (100%)	291 (98%)	6 (2%)	55	79
2	B	192/206 (93%)	192 (100%)	0	100	100
2	D	191/206 (93%)	191 (100%)	0	100	100
2	F	192/206 (93%)	190 (99%)	2 (1%)	76	90
2	H	192/206 (93%)	190 (99%)	2 (1%)	76	90
All	All	1955/2012 (97%)	1933 (99%)	22 (1%)	73	89

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	3	GLU
1	G	258	PHE
1	G	233	SER

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Mol	Chain	Res	Type
1	G	358	ASP
1	C	233	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	59	ASN
1	G	355	GLN
2	H	214	GLN
2	H	50	ASN
2	F	50	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](#)

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	$\# Z  > 2$
3	GLC	J	1	3	12,12,12	0.57	0	17,17,17	0.64	0
3	GLC	J	2	3	11,11,12	0.60	0	15,15,17	1.16	1 (6%)
3	GLC	K	1	3	12,12,12	0.65	0	17,17,17	1.05	1 (5%)
3	GLC	K	2	3	11,11,12	1.11	0	15,15,17	2.82	5 (33%)
3	GLC	L	1	3	12,12,12	0.58	0	17,17,17	1.27	2 (11%)
3	GLC	L	2	3	11,11,12	0.57	0	15,15,17	0.96	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GLC	M	1	3	12,12,12	0.62	0	17,17,17	1.05	1 (5%)
3	GLC	M	2	3	11,11,12	0.92	0	15,15,17	1.84	3 (20%)

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
3	GLC	J	1	3	-	0/2/22/22	0/1/1/1
3	GLC	J	2	3	-	0/2/19/22	0/1/1/1
3	GLC	K	1	3	-	0/2/22/22	0/1/1/1
3	GLC	K	2	3	-	1/2/19/22	0/1/1/1
3	GLC	L	1	3	-	0/2/22/22	0/1/1/1
3	GLC	L	2	3	-	2/2/19/22	0/1/1/1
3	GLC	M	1	3	-	0/2/22/22	0/1/1/1
3	GLC	M	2	3	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	2	GLC	O3-C3-C2	-8.00	94.67	109.99
3	K	2	GLC	O5-C5-C6	-4.63	99.94	107.20
3	M	2	GLC	O4-C4-C3	-3.90	101.34	110.35
3	M	2	GLC	O4-C4-C5	3.07	116.91	109.30
3	K	2	GLC	C1-C2-C3	2.90	113.23	109.67

There are no chirality outliers.

All (5) torsion outliers are listed below:

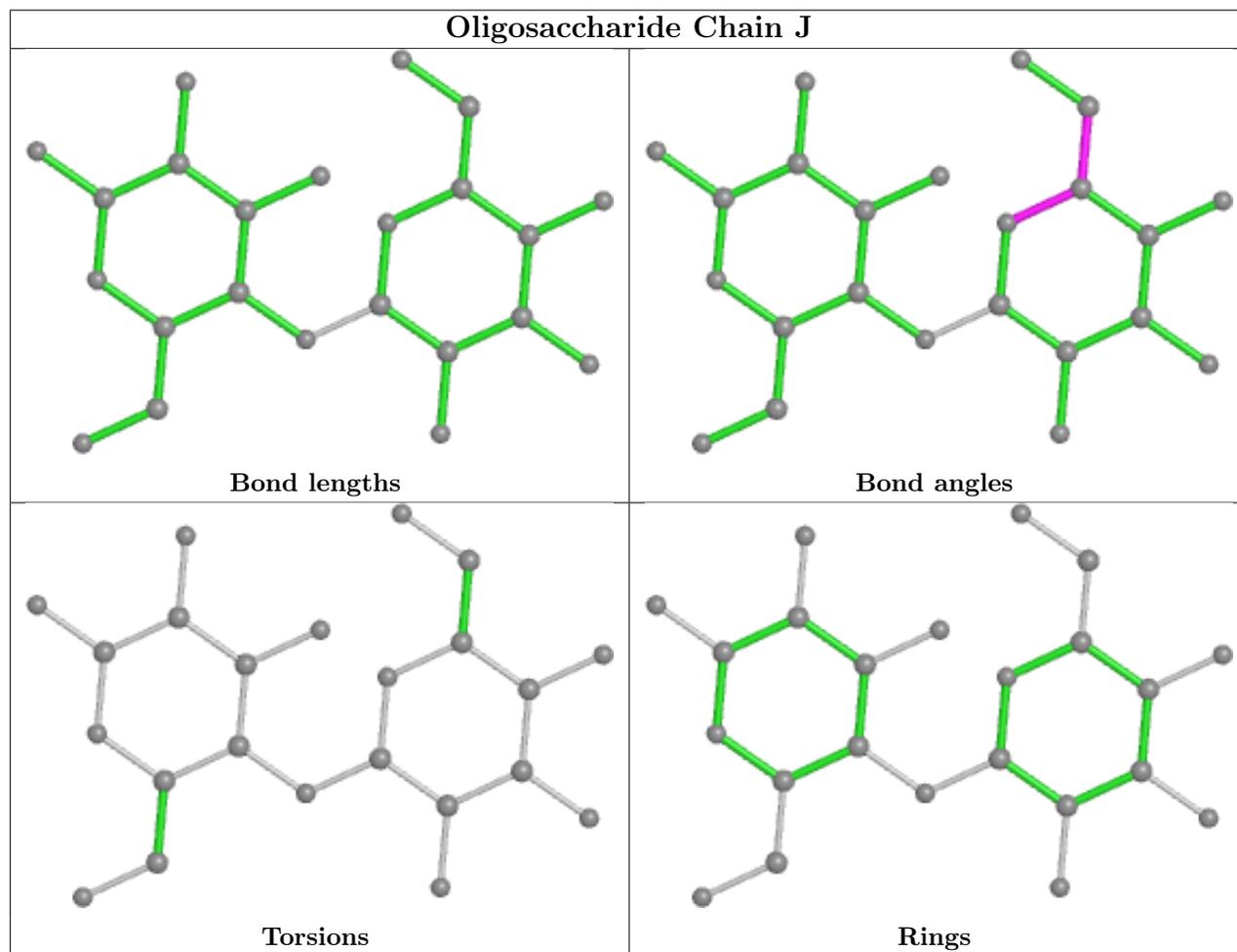
Mol	Chain	Res	Type	Atoms
3	M	2	GLC	C4-C5-C6-O6
3	M	2	GLC	O5-C5-C6-O6
3	L	2	GLC	C4-C5-C6-O6
3	K	2	GLC	O5-C5-C6-O6
3	L	2	GLC	O5-C5-C6-O6

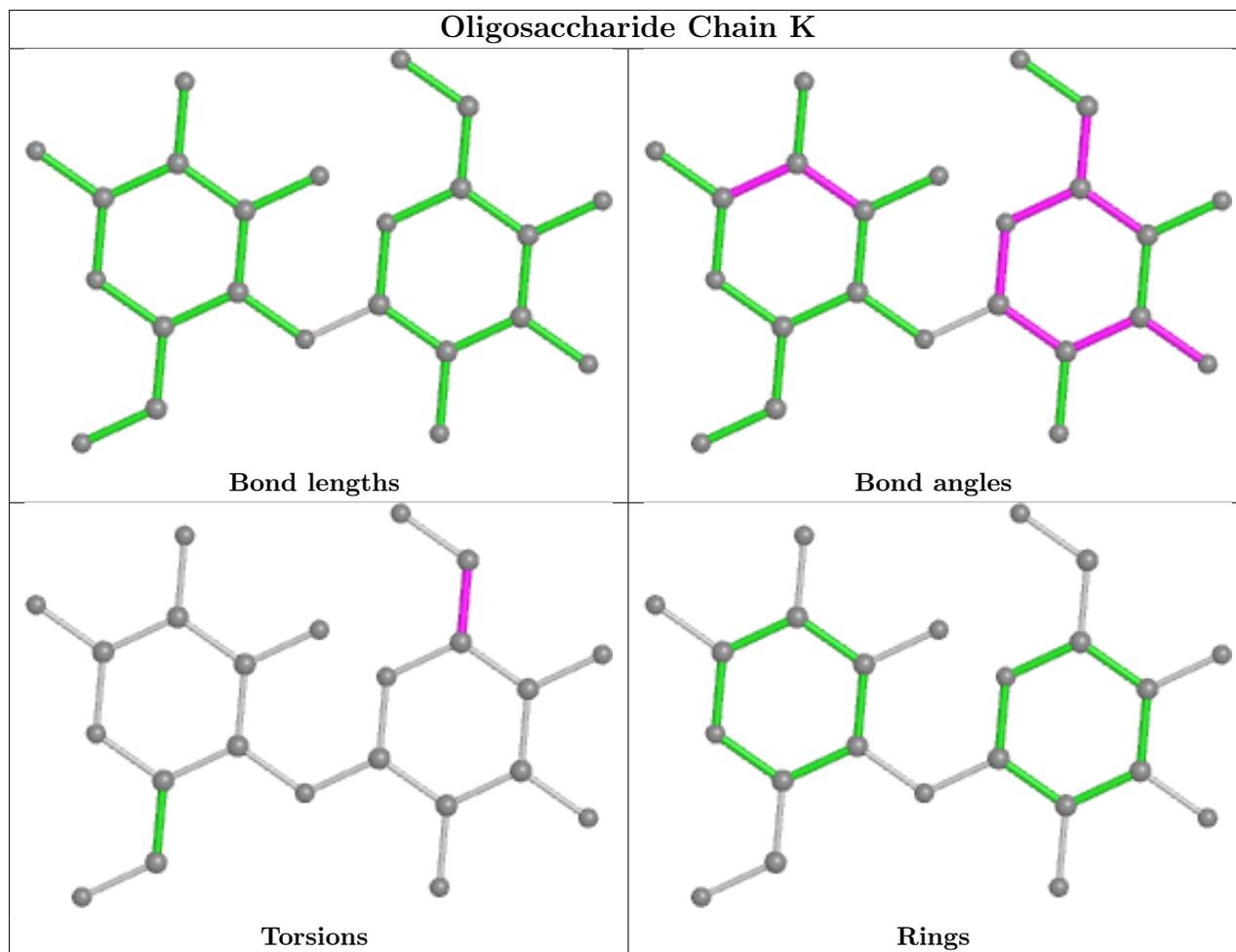
There are no ring outliers.

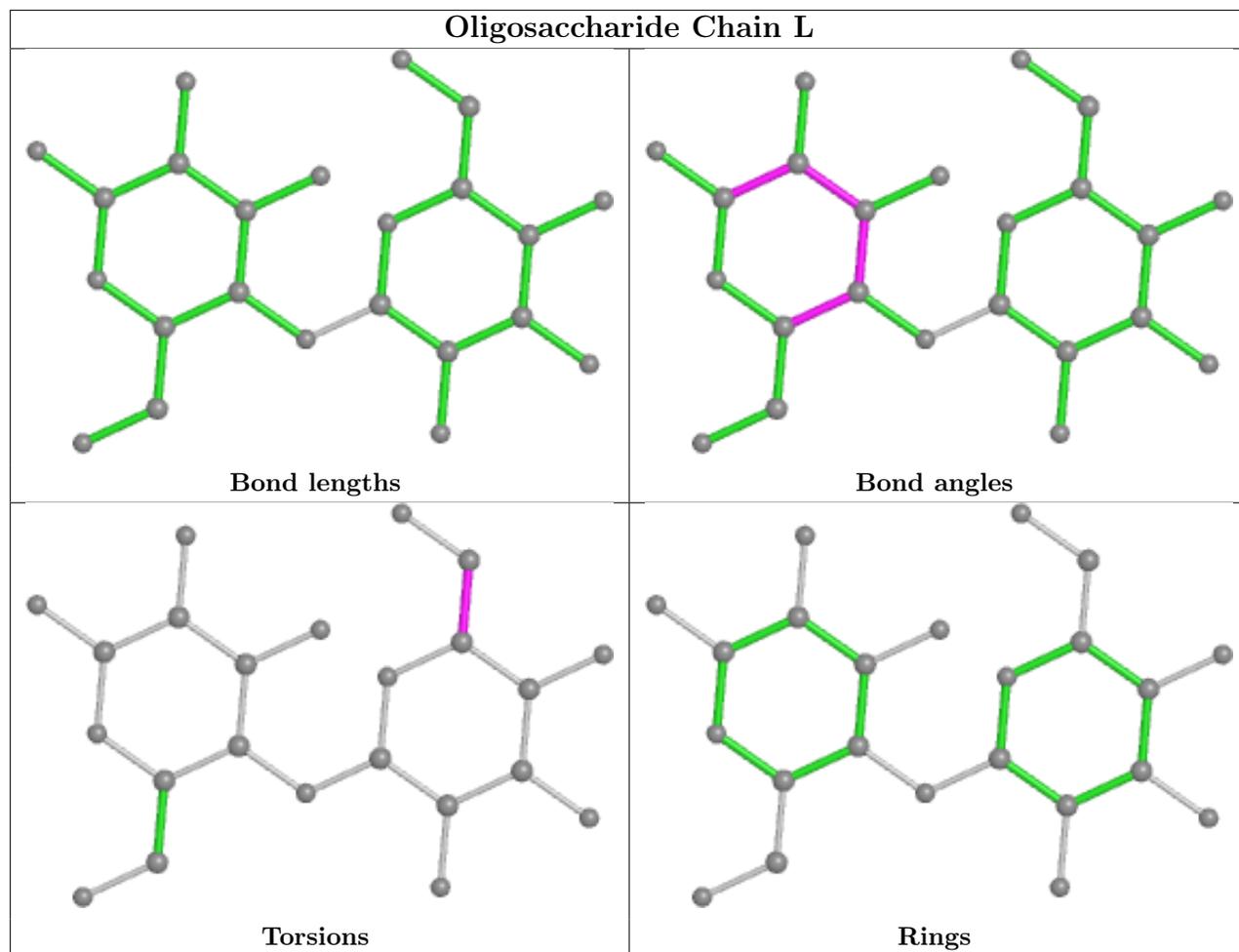
3 monomers are involved in 7 short contacts:

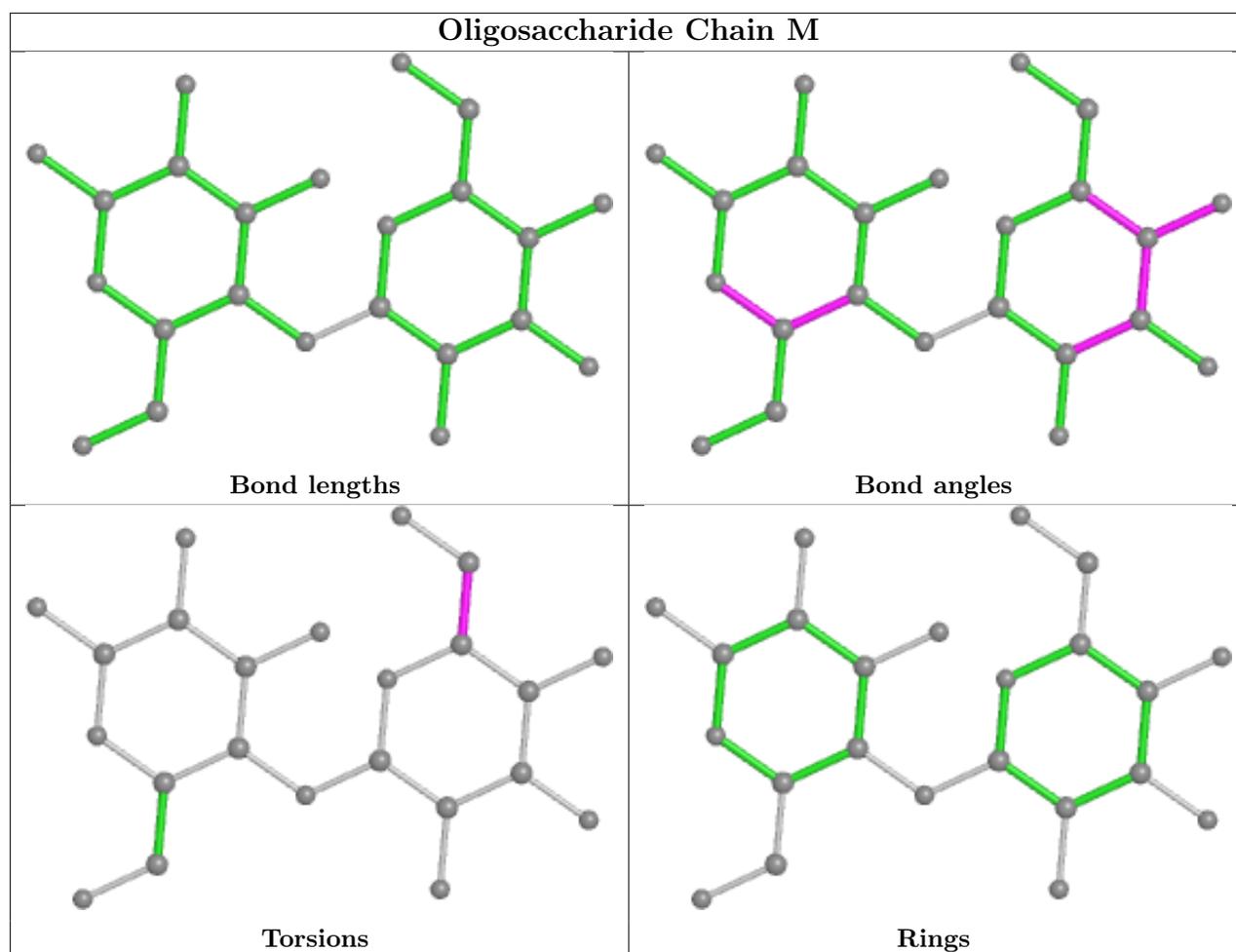
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	M	2	GLC	2	0
3	L	2	GLC	1	0
3	K	2	GLC	4	0

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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

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

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	369/369 (100%)	0.02	10 (2%) 54 58	47, 61, 78, 106	0
1	C	369/369 (100%)	0.21	18 (4%) 29 31	50, 66, 97, 110	0
1	E	369/369 (100%)	0.02	13 (3%) 44 47	45, 59, 77, 101	0
1	G	369/369 (100%)	0.12	22 (5%) 21 22	49, 68, 88, 97	0
2	B	225/251 (89%)	0.19	11 (4%) 29 31	53, 65, 83, 97	0
2	D	223/251 (88%)	0.35	11 (4%) 29 31	54, 69, 90, 113	0
2	F	224/251 (89%)	0.20	14 (6%) 20 21	50, 65, 82, 111	0
2	H	224/251 (89%)	0.27	11 (4%) 29 31	55, 69, 84, 113	0
All	All	2372/2480 (95%)	0.15	110 (4%) 32 34	45, 65, 87, 113	0

The worst 5 of 110 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	341	TYR	5.1
2	F	243	ARG	4.7
2	D	13	ARG	4.3
2	H	1	GLN	4.3
1	G	1	LYS	4.3

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

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

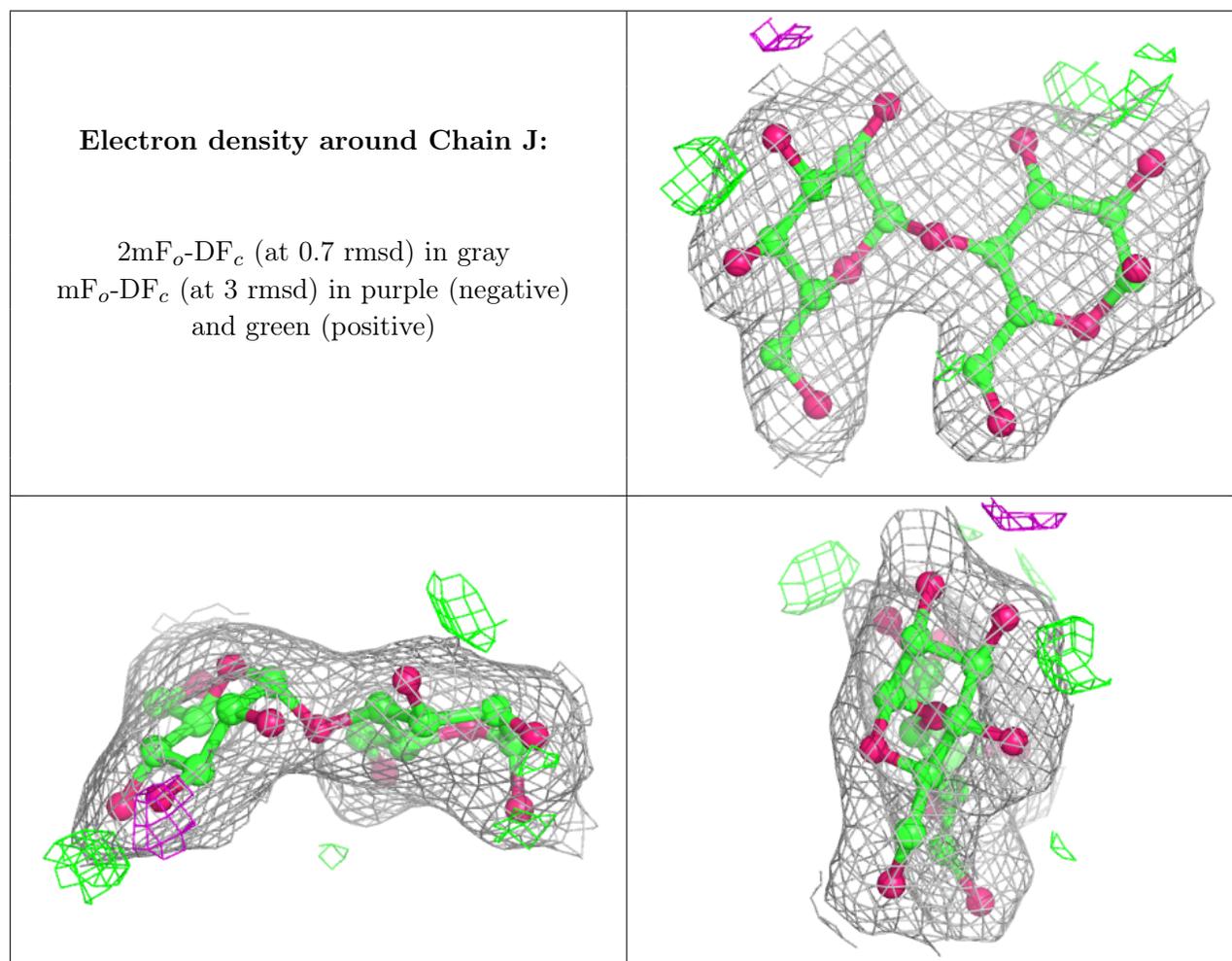
### 6.3 Carbohydrates [i](#)

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.

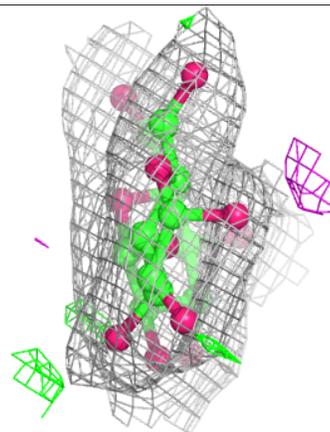
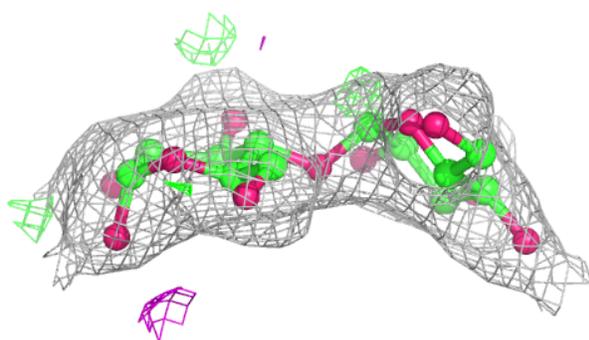
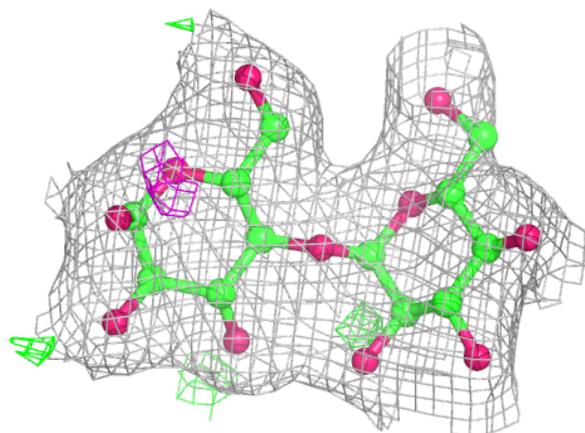
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GLC	K	2	11/12	0.90	0.14	53,65,77,78	0
3	GLC	K	1	12/12	0.96	0.12	54,56,61,64	0
3	GLC	L	1	12/12	0.96	0.10	47,52,58,59	0
3	GLC	L	2	11/12	0.96	0.13	52,54,59,64	0
3	GLC	M	1	12/12	0.96	0.11	60,63,67,69	0
3	GLC	M	2	11/12	0.96	0.12	62,65,71,73	0
3	GLC	J	2	11/12	0.97	0.13	51,58,61,61	0
3	GLC	J	1	12/12	0.98	0.09	51,58,62,62	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.



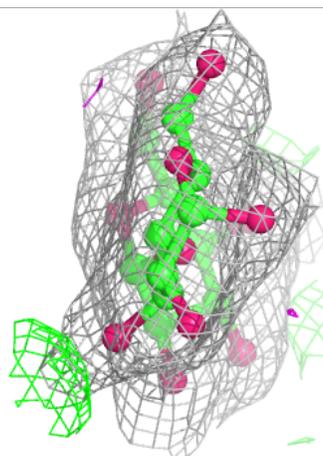
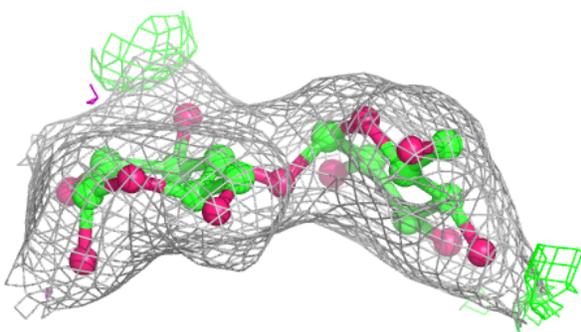
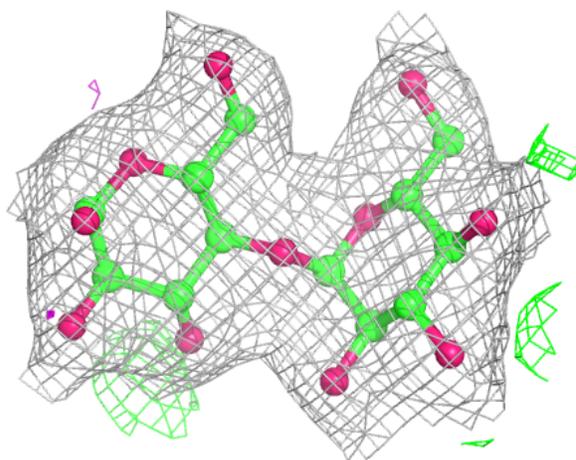
**Electron density around Chain K:**

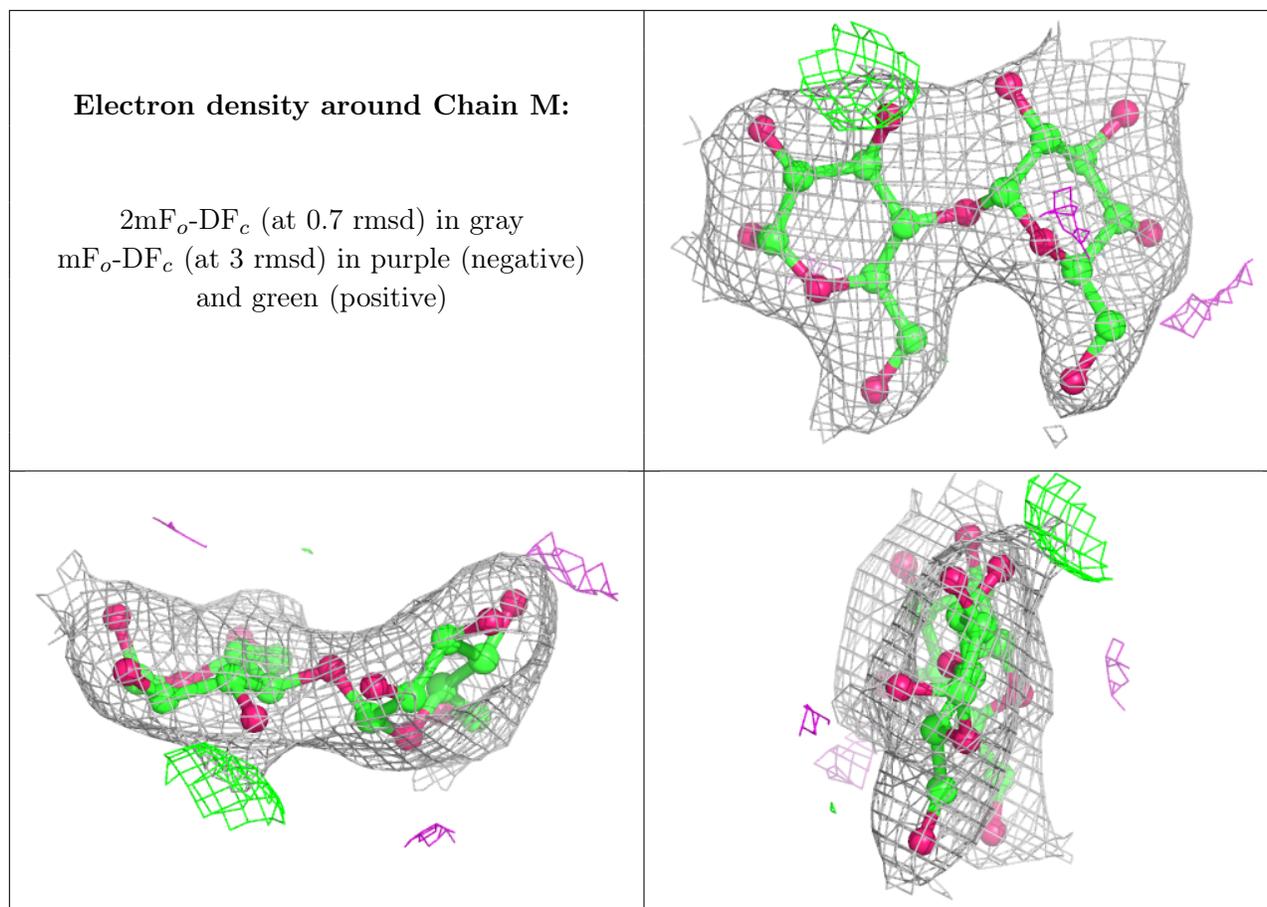
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain L:**

$2mF_o-DF_c$  (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(Å <sup>2</sup> )	Q<0.9
4	CL	H	301	1/1	0.90	0.18	75,75,75,75	0
4	CL	F	301	1/1	0.91	0.07	81,81,81,81	0
4	CL	B	301	1/1	0.91	0.08	79,79,79,79	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.