



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 21, 2021 – 06:10 PM EDT

PDB ID : 7JIX
Title : Murine antibody that engages the influenza hemagglutinin receptor binding site
Authors : Bajic, G.; Schmidt, A.G.
Deposited on : 2020-07-23
Resolution : 3.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.22
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)	:	2.22

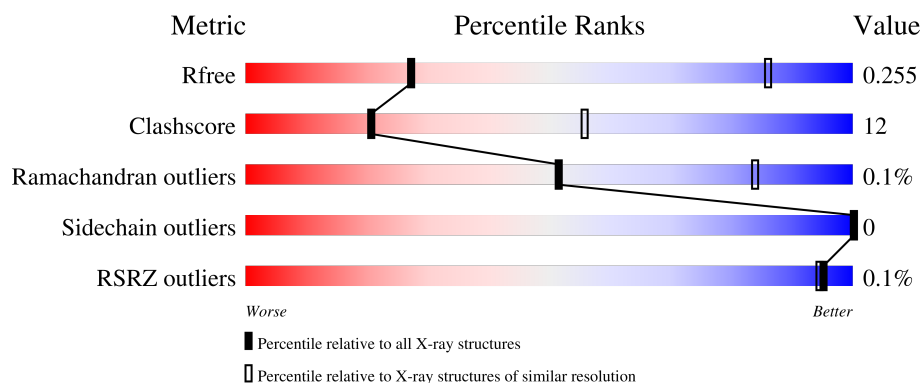
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.90 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	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)

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 ≥ 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	334	
2	B	177	
3	L	220	
4	H	227	
5	C	5	

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Mol	Chain	Length	Quality of chain
6	D	3	 100%
6	E	3	 67% 33%

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
6	NAG	D	2	-	-	-	X
6	BMA	D	3	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7365 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 Hemagglutinin HA1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2535	1597	441	486	11			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	ALA	-	expression tag	UNP A7Y8A6
A	-2	ASP	-	expression tag	UNP A7Y8A6
A	-1	PRO	-	expression tag	UNP A7Y8A6
A	0	GLY	-	expression tag	UNP A7Y8A6
A	1	TYR	-	expression tag	UNP A7Y8A6
A	2	LEU	-	expression tag	UNP A7Y8A6
A	3	LEU	-	expression tag	UNP A7Y8A6
A	4	GLU	-	expression tag	UNP A7Y8A6

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1394	874	238	275	7			

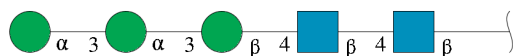
- Molecule 3 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	216	Total	C	N	O	S	0	0	0
			1665	1034	277	348	6			

- Molecule 4 is a protein called Fab heavy chain.

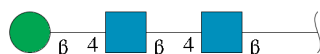
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	219	Total	C	N	O	S	0	0	0
			1632	1030	272	322	8			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

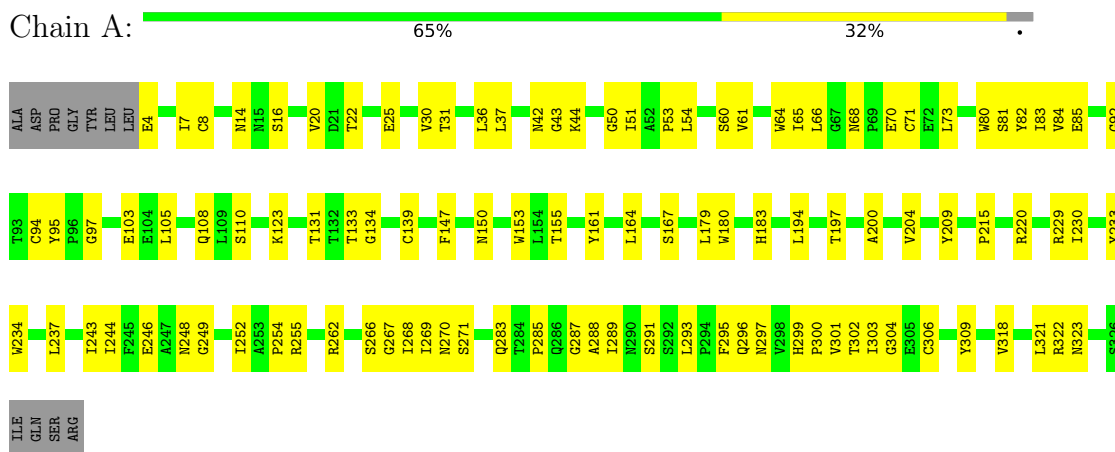


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	D	3	Total	C	N	O	0	0	0
			39	22	2	15			
6	E	3	Total	C	N	O	0	0	0
			39	22	2	15			

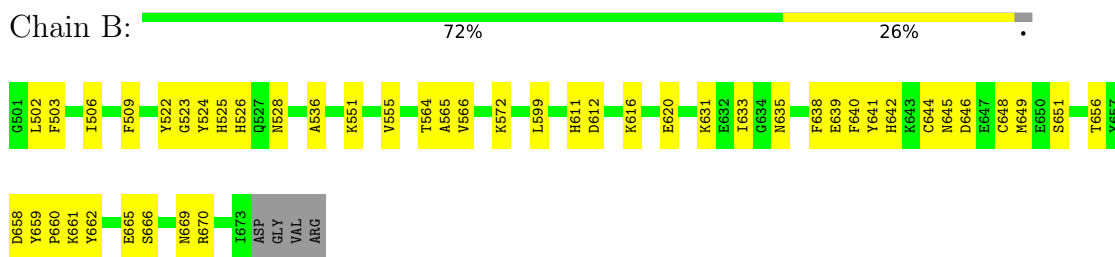
3 Residue-property plots [i](#)

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.

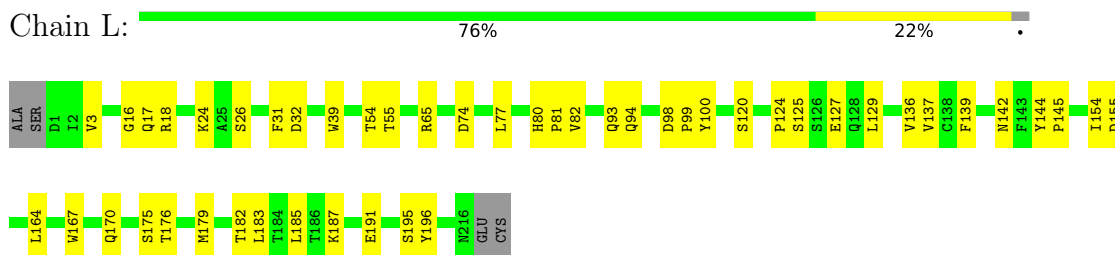
- Molecule 1: Hemagglutinin HA1 chain



- Molecule 2: Hemagglutinin HA2 chain



- Molecule 3: Fab light chain



- Molecule 4: Fab heavy chain

Y148	ALA
F149	SER
P150	E1
E151	V2
P152	
	P9
T156	V18
W157	
V166	Y27
	A28
A171	F29
	S30
L177	R31
Y178	S32
T179	W33
L180	A34
	N35
W184	Q39
	R40
T197	
C198	L45
N199	E46
	W47
K211	L48
K212	G49
I213	R50
G219	D57
HIS	
HIS	F64
HIS	
HIS	T69
HIS	
HIS	M81
	Q82
	L83
	L86
	E89
	L111
	S115
	P122
	Y125
	P126
	T135
	L141
	L144
	V145
	L146
	G147

- NAG1
NAG2
BMA3
MAN4
MAN5

- NAG1
NAG2
BMA3

- | NAG1 | NAG2 | BMA3 |
|------|------|------|
|------|------|------|

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	198.51Å 198.51Å 198.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.15 – 3.90 48.15 – 3.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (48.15-3.90) 90.0 (48.15-3.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 3.88Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.215 , 0.255 0.215 , 0.255	Depositor DCC
R_{free} test set	1211 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	84.1	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 69.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.037 for l,-k,h	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	7365	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, MAN

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	0/2601	0.53	0/3540
2	B	0.26	0/1421	0.44	0/1909
3	L	0.25	0/1703	0.51	0/2315
4	H	0.27	0/1675	0.53	0/2285
All	All	0.27	0/7400	0.51	0/10049

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	2535	0	2443	80	0
2	B	1394	0	1326	45	0
3	L	1665	0	1576	32	0
4	H	1632	0	1597	37	0
5	C	61	0	52	5	0
6	D	39	0	34	0	0
6	E	39	0	34	0	0
All	All	7365	0	7062	178	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 12.

The worst 5 of 178 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)
2:B:648:CYS:HA	2:B:651:SER:HB3	1.40	1.03
1:A:51:ILE:HG13	1:A:81:SER:HB2	1.61	0.82
4:H:166:VAL:HG12	4:H:184:VAL:HG12	1.61	0.80
1:A:134:GLY:HA3	1:A:153:TRP:HB3	1.63	0.80
1:A:110:SER:O	1:A:266:SER:OG	2.02	0.77

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	321/334 (96%)	302 (94%)	18 (6%)	1 (0%)	41	75
2	B	171/177 (97%)	159 (93%)	12 (7%)	0	100	100
3	L	214/220 (97%)	205 (96%)	9 (4%)	0	100	100
4	H	217/227 (96%)	205 (94%)	12 (6%)	0	100	100
All	All	923/958 (96%)	871 (94%)	51 (6%)	1 (0%)	51	84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	50	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	283/292 (97%)	283 (100%)	0	100	100
2	B	149/152 (98%)	149 (100%)	0	100	100
3	L	190/193 (98%)	190 (100%)	0	100	100
4	H	183/190 (96%)	183 (100%)	0	100	100
All	All	805/827 (97%)	805 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	42	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](#)

11 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	$\# Z > 2$
5	NAG	C	1	5,1	14,14,15	0.28	0	17,19,21	0.54	0
5	NAG	C	2	5	14,14,15	0.18	0	17,19,21	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BMA	C	3	5	11,11,12	0.69	0	15,15,17	0.97	1 (6%)
5	MAN	C	4	5	11,11,12	1.28	2 (18%)	15,15,17	2.36	4 (26%)
5	MAN	C	5	5	11,11,12	0.57	0	15,15,17	1.10	2 (13%)
6	NAG	D	1	6,1	14,14,15	0.38	0	17,19,21	0.60	0
6	NAG	D	2	6	14,14,15	0.34	0	17,19,21	0.41	0
6	BMA	D	3	6	11,11,12	0.72	0	15,15,17	0.73	0
6	NAG	E	1	6,1	14,14,15	0.35	0	17,19,21	0.36	0
6	NAG	E	2	6	14,14,15	0.52	0	17,19,21	0.68	0
6	BMA	E	3	6	11,11,12	1.16	2 (18%)	15,15,17	1.45	2 (13%)

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
5	NAG	C	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	C	2	5	-	1/6/23/26	0/1/1/1
5	BMA	C	3	5	-	2/2/19/22	0/1/1/1
5	MAN	C	4	5	-	2/2/19/22	0/1/1/1
5	MAN	C	5	5	-	1/2/19/22	0/1/1/1
6	NAG	D	1	6,1	-	3/6/23/26	0/1/1/1
6	NAG	D	2	6	-	0/6/23/26	0/1/1/1
6	BMA	D	3	6	-	1/2/19/22	0/1/1/1
6	NAG	E	1	6,1	-	0/6/23/26	0/1/1/1
6	NAG	E	2	6	-	2/6/23/26	0/1/1/1
6	BMA	E	3	6	-	2/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	4	MAN	C1-C2	3.58	1.60	1.52
6	E	3	BMA	C1-C2	2.24	1.57	1.52
6	E	3	BMA	C4-C5	2.17	1.57	1.53
5	C	4	MAN	O5-C1	2.05	1.47	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	4	MAN	C1-O5-C5	5.89	120.17	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	4	MAN	C1-C2-C3	4.36	115.03	109.67
5	C	4	MAN	O5-C1-C2	4.24	117.32	110.77
6	E	3	BMA	O5-C1-C2	-3.04	106.08	110.77
5	C	5	MAN	C1-O5-C5	2.88	116.10	112.19

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

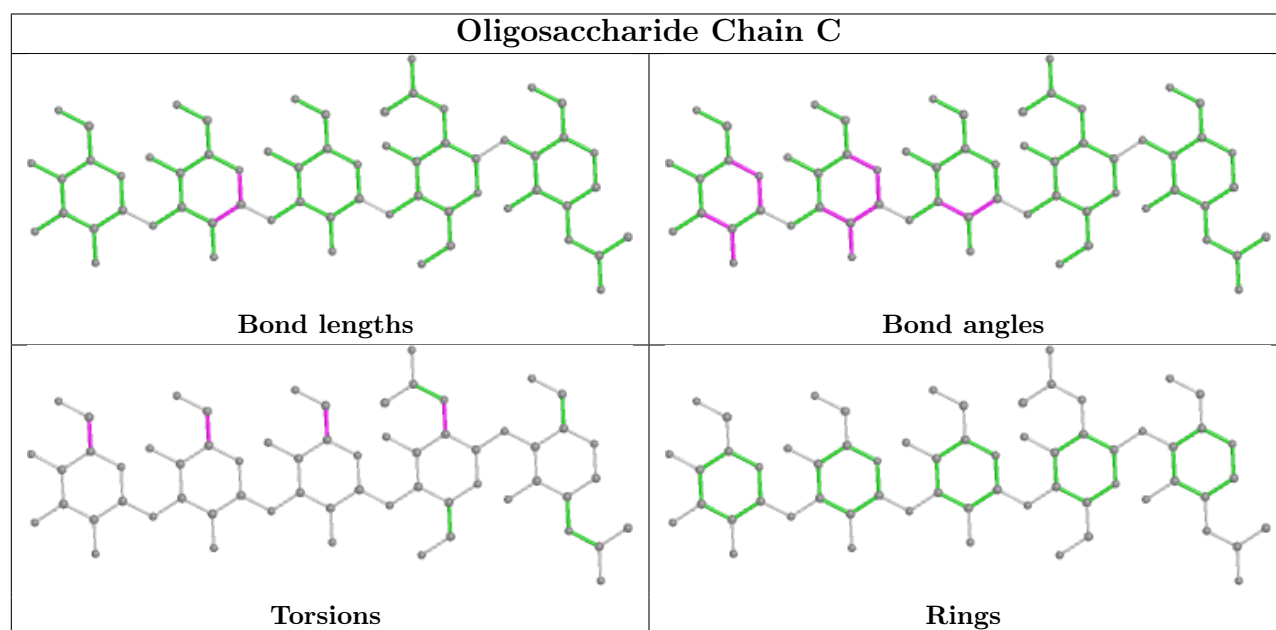
Mol	Chain	Res	Type	Atoms
6	E	3	BMA	O5-C5-C6-O6
5	C	4	MAN	C4-C5-C6-O6
5	C	4	MAN	O5-C5-C6-O6
5	C	3	BMA	C4-C5-C6-O6
6	E	3	BMA	C4-C5-C6-O6

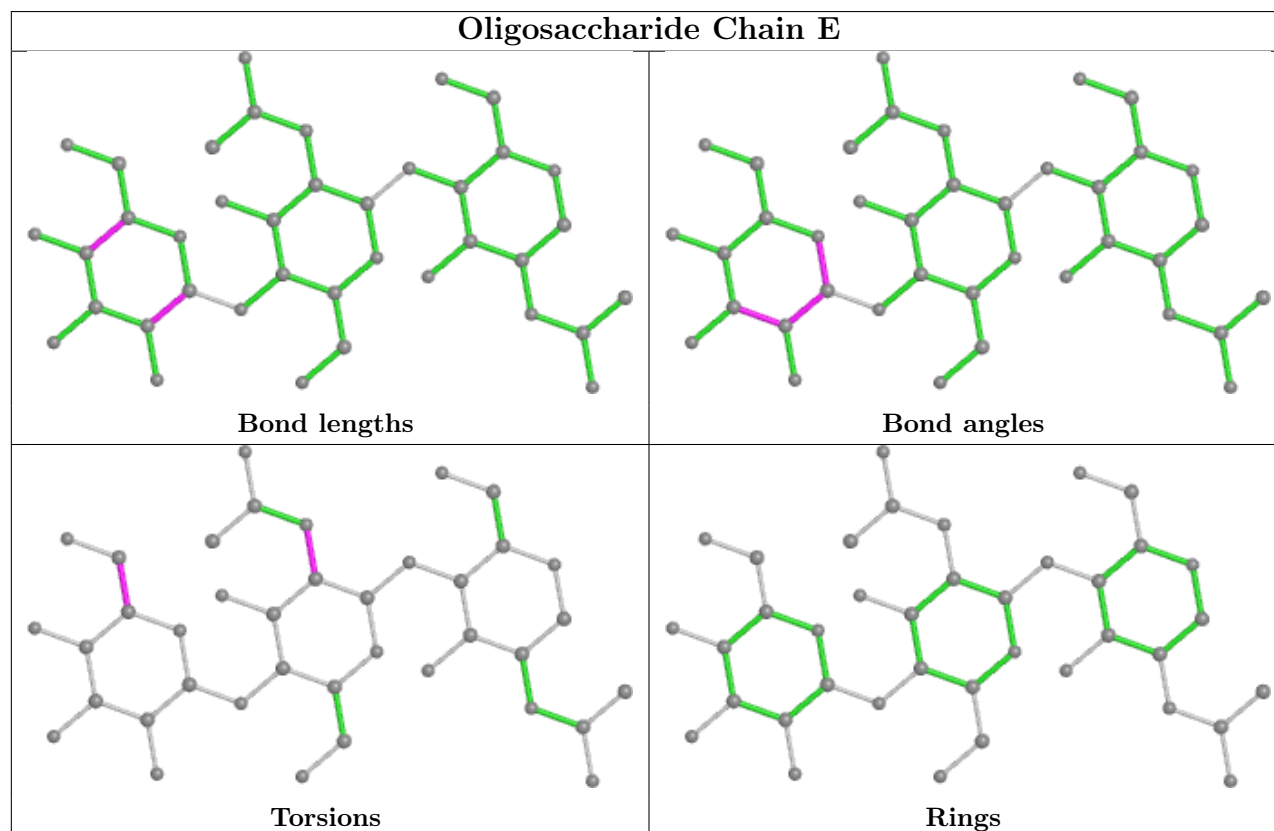
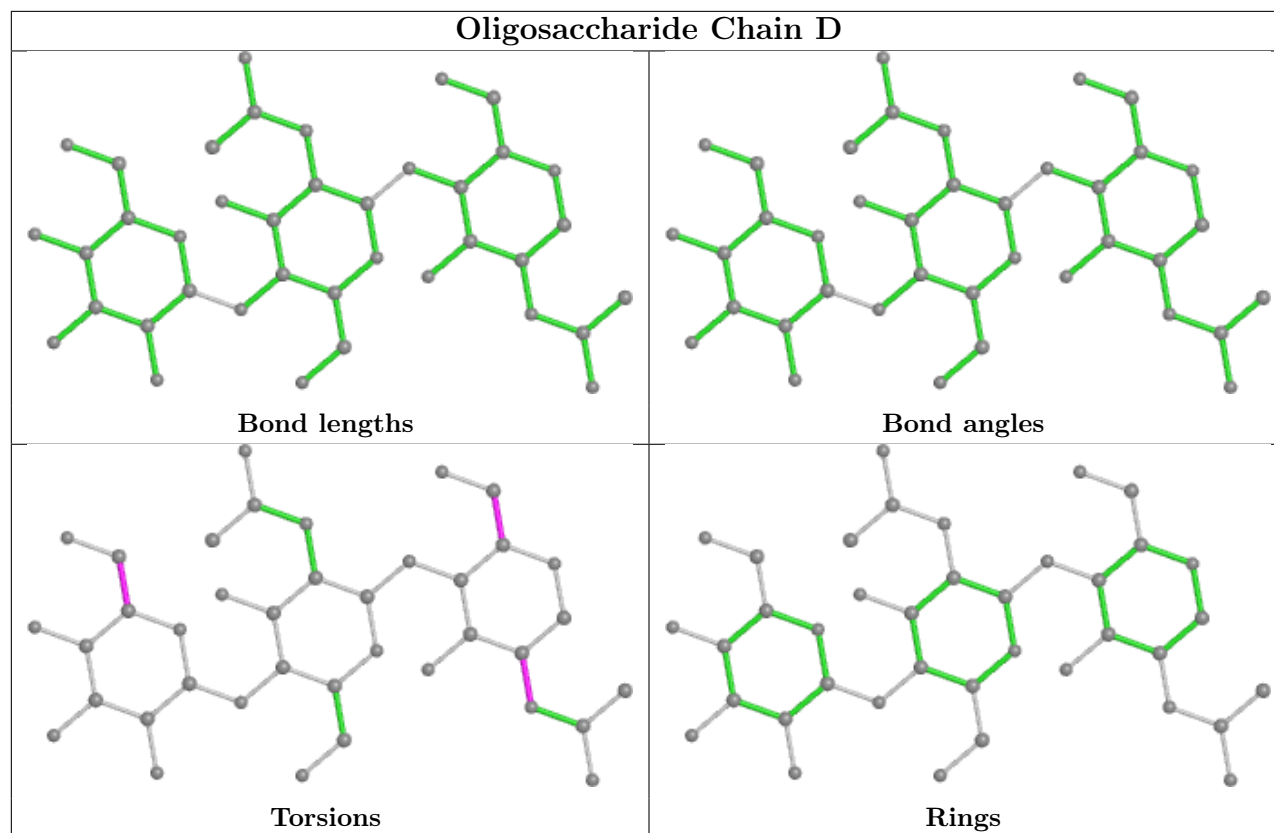
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1	NAG	4	0
5	C	2	NAG	1	0
5	C	4	MAN	1	0

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





5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	323/334 (96%)	-0.27	0	100 100	49, 83, 123, 156	0
2	B	173/177 (97%)	-0.13	0	100 100	52, 112, 166, 181	0
3	L	216/220 (98%)	-0.13	0	100 100	66, 94, 122, 137	0
4	H	219/227 (96%)	-0.06	1 (0%)	91 85	64, 100, 149, 192	0
All	All	931/958 (97%)	-0.16	1 (0%)	95 94	49, 93, 149, 192	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	H	135	THR	3.2

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

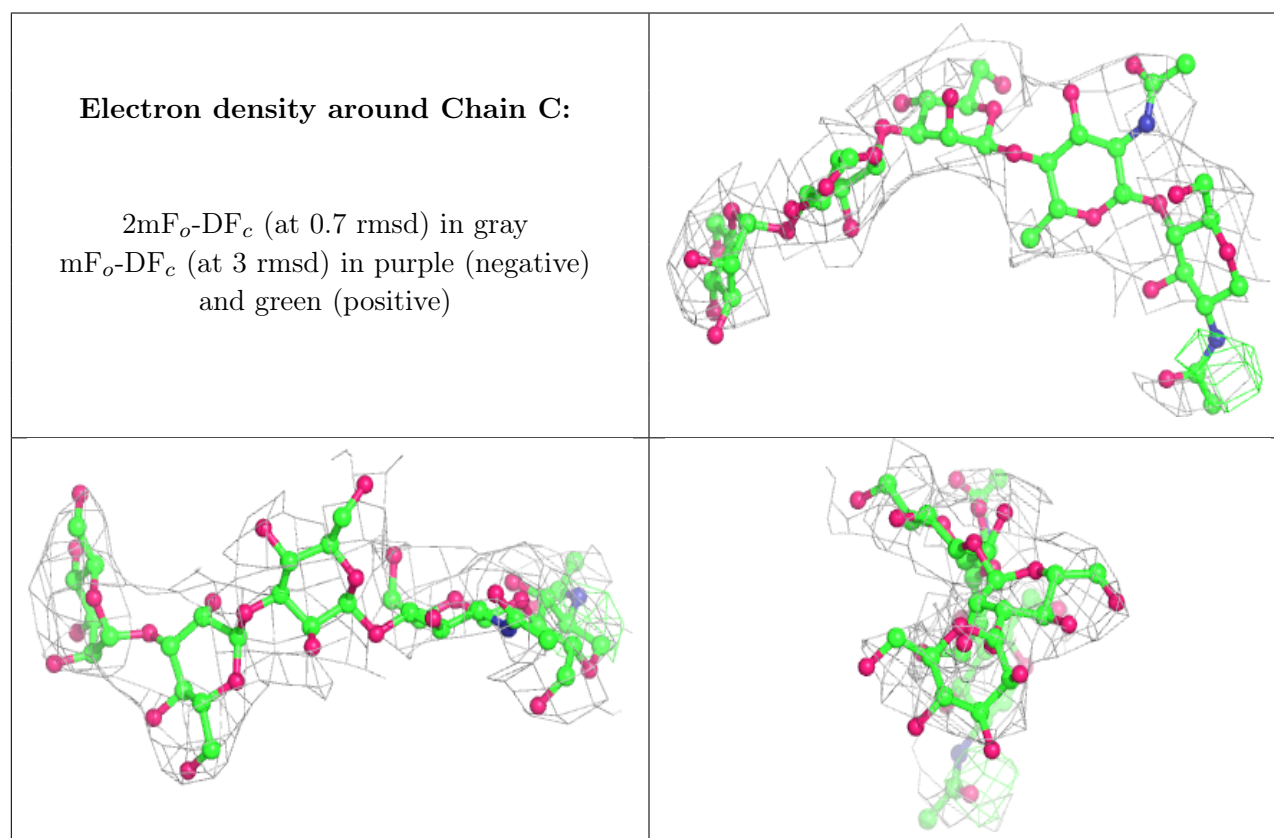
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	BMA	D	3	11/12	0.57	0.66	154,202,235,240	0
6	NAG	D	2	14/15	0.66	0.60	145,212,231,239	0
6	BMA	E	3	11/12	0.66	0.36	112,180,216,223	0
6	NAG	E	2	14/15	0.77	0.35	116,169,203,230	0
6	NAG	D	1	14/15	0.80	0.34	101,167,213,225	0
5	BMA	C	3	11/12	0.82	0.22	100,146,162,177	0

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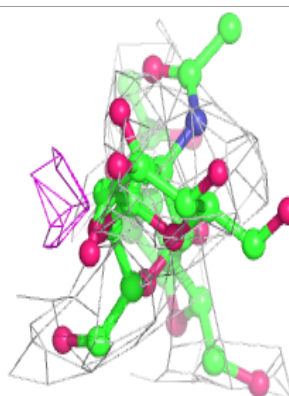
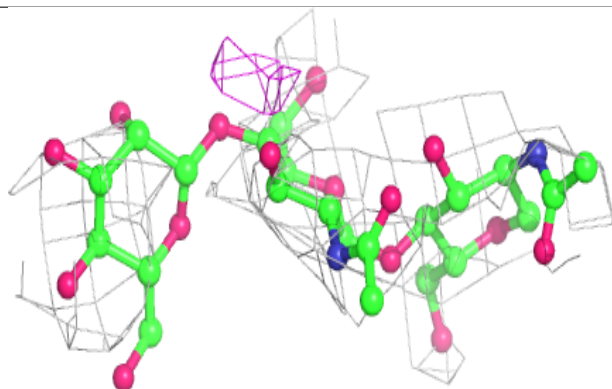
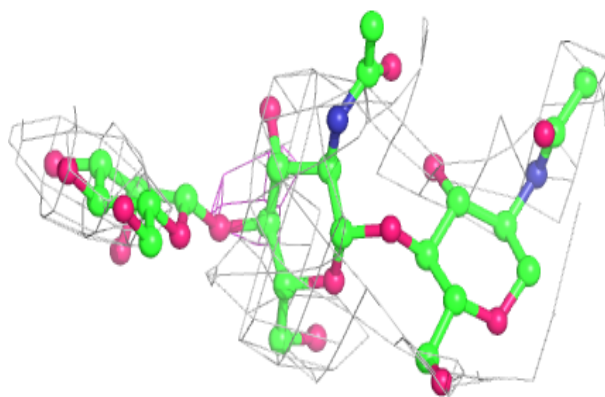
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	MAN	C	5	11/12	0.90	0.41	132,161,176,182	0
6	NAG	E	1	14/15	0.90	0.19	50,122,159,179	0
5	MAN	C	4	11/12	0.91	0.25	107,160,172,173	0
5	NAG	C	2	14/15	0.92	0.17	100,109,138,158	0
5	NAG	C	1	14/15	0.94	0.16	72,88,100,127	0

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.

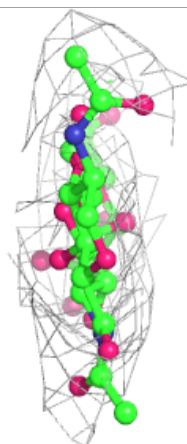
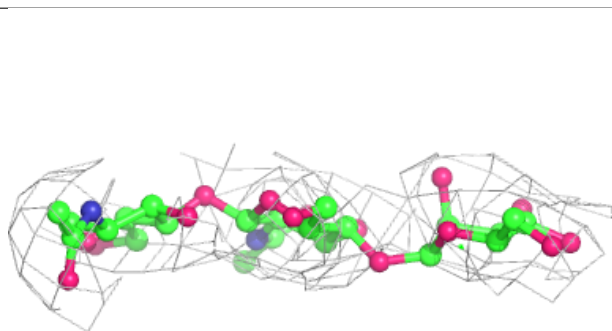
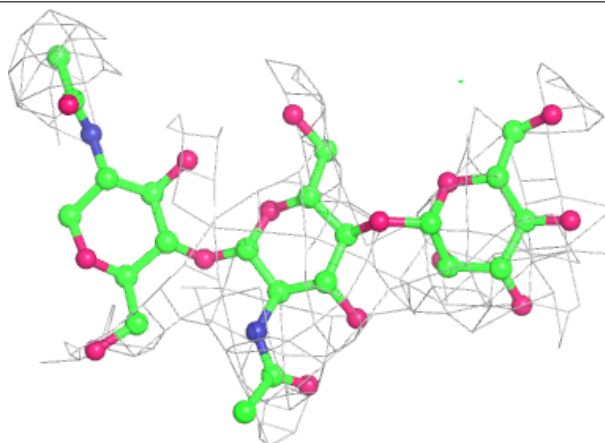


Electron density around Chain D:

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

**Electron density around Chain E:**

$2mF_o-DF_c$ (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.