



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 19, 2024 – 09:41 PM EDT

PDB ID : 3UEZ
Title : Crystal structure of the human Colony-Stimulating Factor 1 (hCSF-1) cytokine
in complex with the viral receptor BARF1
Authors : Elegheert, J.; Bracke, N.; Savvides, S.N.
Deposited on : 2011-10-31
Resolution : 3.41 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

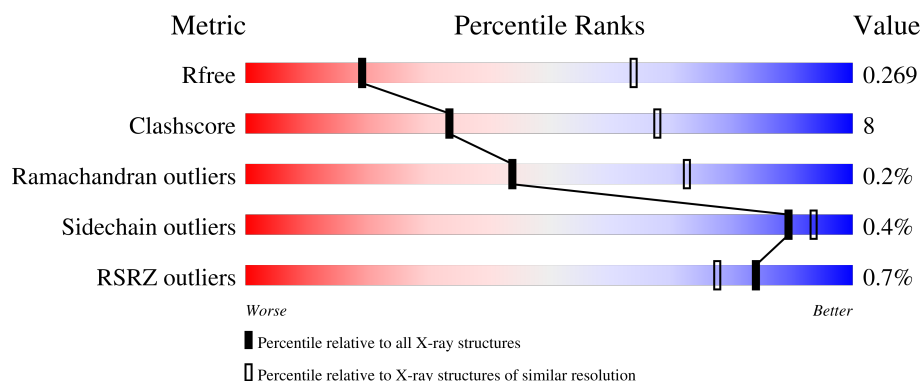
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.41 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}	164625	1112 (3.48-3.36)
Clashscore	180529	1144 (3.48-3.36)
Ramachandran outliers	177936	1146 (3.48-3.36)
Sidechain outliers	177891	1146 (3.48-3.36)
RSRZ outliers	164620	1112 (3.48-3.36)

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	208	 77% 12% 11%
1	B	208	 74% 15% 11%
1	C	208	 70% 20% 11%
1	D	208	 68% 21% 11%
2	E	153	 79% 14% 7%

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Mol	Chain	Length	Quality of chain
2	F	153	<div><div>%</div><div><div></div><div>75%</div><div>17%</div><div>8%</div></div></div>
2	G	153	<div><div></div><div>80%</div><div>13%</div><div>7%</div></div>
2	H	153	<div><div>3%</div><div><div></div><div>71%</div><div>20%</div><div>9%</div></div></div>
3	I	3	<div><div></div><div>100%</div></div>
3	J	3	<div><div></div><div>67%</div><div>33%</div></div>
3	K	3	<div><div></div><div>67%</div><div>33%</div></div>
3	L	3	<div><div></div><div>33%</div><div>67%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10693 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 Secreted protein BARF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	185	Total	C	N	O	S	0	0	0
			1477	955	251	264	7			
1	B	185	Total	C	N	O	S	0	0	0
			1481	958	252	264	7			
1	C	186	Total	C	N	O	S	0	0	0
			1483	958	252	266	7			
1	D	186	Total	C	N	O	S	0	0	0
			1487	961	253	266	7			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	SER	THR	engineered mutation	UNP P03228
A	222	LYS	-	expression tag	UNP P03228
A	223	HIS	-	expression tag	UNP P03228
A	224	HIS	-	expression tag	UNP P03228
A	225	HIS	-	expression tag	UNP P03228
A	226	HIS	-	expression tag	UNP P03228
A	227	HIS	-	expression tag	UNP P03228
A	228	HIS	-	expression tag	UNP P03228
B	169	SER	THR	engineered mutation	UNP P03228
B	222	LYS	-	expression tag	UNP P03228
B	223	HIS	-	expression tag	UNP P03228
B	224	HIS	-	expression tag	UNP P03228
B	225	HIS	-	expression tag	UNP P03228
B	226	HIS	-	expression tag	UNP P03228
B	227	HIS	-	expression tag	UNP P03228
B	228	HIS	-	expression tag	UNP P03228
C	169	SER	THR	engineered mutation	UNP P03228
C	222	LYS	-	expression tag	UNP P03228
C	223	HIS	-	expression tag	UNP P03228
C	224	HIS	-	expression tag	UNP P03228
C	225	HIS	-	expression tag	UNP P03228

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Chain	Residue	Modelled	Actual	Comment	Reference
C	226	HIS	-	expression tag	UNP P03228
C	227	HIS	-	expression tag	UNP P03228
C	228	HIS	-	expression tag	UNP P03228
D	169	SER	THR	engineered mutation	UNP P03228
D	222	LYS	-	expression tag	UNP P03228
D	223	HIS	-	expression tag	UNP P03228
D	224	HIS	-	expression tag	UNP P03228
D	225	HIS	-	expression tag	UNP P03228
D	226	HIS	-	expression tag	UNP P03228
D	227	HIS	-	expression tag	UNP P03228
D	228	HIS	-	expression tag	UNP P03228

- Molecule 2 is a protein called Macrophage colony-stimulating factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	142	Total	C	N	O	S	0	0	0
			1159	730	193	225	11			
2	F	141	Total	C	N	O	S	0	0	0
			1150	723	192	224	11			
2	G	143	Total	C	N	O	S	0	1	0
			1174	739	195	229	11			
2	H	139	Total	C	N	O	S	0	0	0
			1126	708	189	218	11			

There are 16 discrepancies between the modelled and reference sequences:

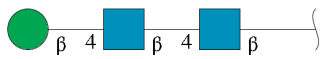
Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	GLY	-	expression tag	UNP P09603
E	-2	SER	-	expression tag	UNP P09603
E	-1	HIS	-	expression tag	UNP P09603
E	0	MET	-	expression tag	UNP P09603
F	-3	GLY	-	expression tag	UNP P09603
F	-2	SER	-	expression tag	UNP P09603
F	-1	HIS	-	expression tag	UNP P09603
F	0	MET	-	expression tag	UNP P09603
G	-3	GLY	-	expression tag	UNP P09603
G	-2	SER	-	expression tag	UNP P09603
G	-1	HIS	-	expression tag	UNP P09603
G	0	MET	-	expression tag	UNP P09603
H	-3	GLY	-	expression tag	UNP P09603
H	-2	SER	-	expression tag	UNP P09603
H	-1	HIS	-	expression tag	UNP P09603

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Chain	Residue	Modelled	Actual	Comment	Reference
H	0	MET	-	expression tag	UNP P09603

- Molecule 3 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.

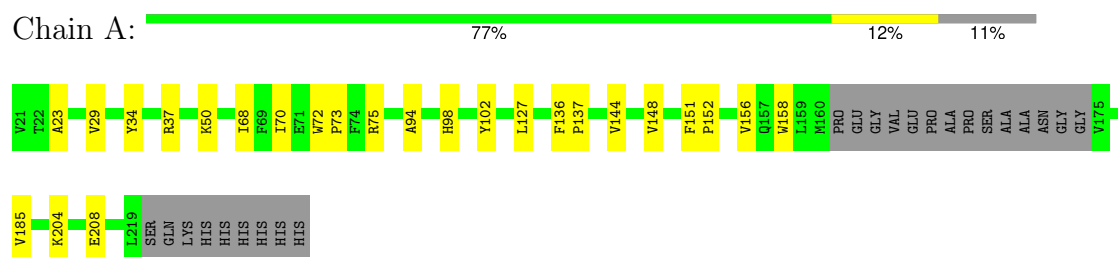


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	K	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	L	3	Total	C	N	O	0	0	0
			39	22	2	15			

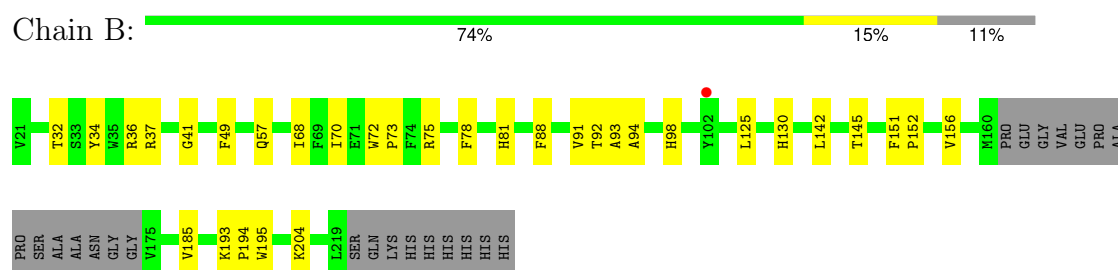
3 Residue-property plots

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.

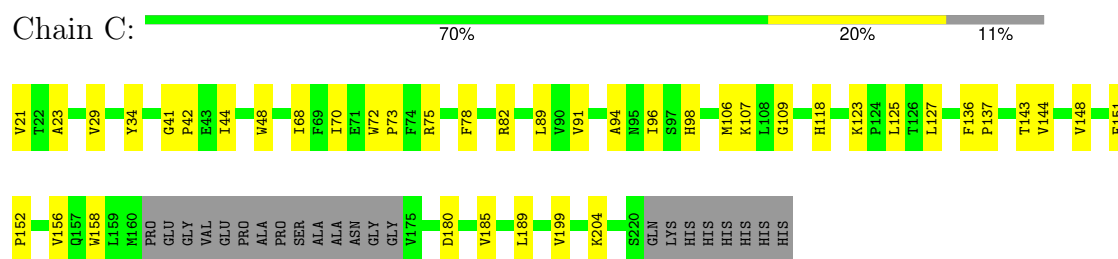
• Molecule 1: Secreted protein BARF1



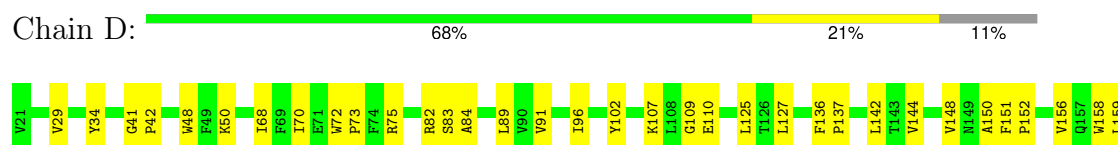
• Molecule 1: Secreted protein BARF1



• Molecule 1: Secreted protein BARF1

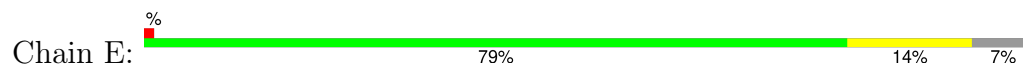


• Molecule 1: Secreted protein BARF1

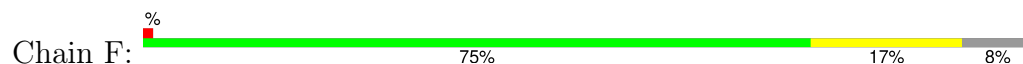




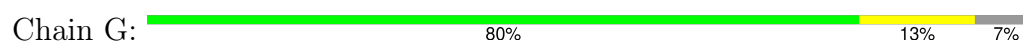
- Molecule 2: Macrophage colony-stimulating factor 1



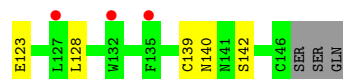
- Molecule 2: Macrophage colony-stimulating factor 1



- Molecule 2: Macrophage colony-stimulating factor 1



- Molecule 2: Macrophage colony-stimulating factor 1



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  67% 33%



- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  33% 67%



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	235.24Å 235.24Å 95.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 3.41 40.00 – 3.41	Depositor EDS
% Data completeness (in resolution range)	96.4 (40.00-3.41) 96.4 (40.00-3.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 3.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_874)	Depositor
R, R_{free}	0.231 , 0.274 0.223 , 0.269	Depositor DCC
R_{free} test set	1294 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	70.5	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 28.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.039 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10693	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.16% 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

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	0.22	0/1520	0.41	0/2069
1	B	0.22	0/1524	0.41	0/2073
1	C	0.23	0/1526	0.41	0/2077
1	D	0.22	0/1530	0.40	0/2081
2	E	0.22	0/1179	0.36	0/1589
2	F	0.22	0/1168	0.37	0/1572
2	G	0.23	0/1197	0.36	0/1613
2	H	0.22	0/1143	0.37	0/1538
All	All	0.22	0/10787	0.39	0/14612

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	1477	0	1445	16	0
1	B	1481	0	1456	18	0
1	C	1483	0	1450	29	0
1	D	1487	0	1461	25	0
2	E	1159	0	1122	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1150	0	1113	20	0
2	G	1174	0	1136	17	0
2	H	1126	0	1094	26	0
3	I	39	0	34	1	0
3	J	39	0	34	0	0
3	K	39	0	34	0	0
3	L	39	0	34	0	0
All	All	10693	0	10413	161	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 8.

The worst 5 of 161 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:F:5:GLU:N	2:F:5:GLU:OE1	2.29	0.65
2:G:52:LYS:NZ	2:G:101:ALA:O	2.32	0.63
2:E:51:LYS:NZ	2:E:137:LYS:O	2.34	0.61
1:C:70:ILE:O	1:C:75:ARG:NH1	2.35	0.59
2:F:134:ILE:HG23	2:F:135:PHE:CD2	2.39	0.57

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	181/208 (87%)	177 (98%)	4 (2%)	0	100	100
1	B	181/208 (87%)	173 (96%)	7 (4%)	1 (1%)	22	51
1	C	182/208 (88%)	178 (98%)	3 (2%)	1 (0%)	25	55
1	D	182/208 (88%)	174 (96%)	7 (4%)	1 (0%)	25	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	140/153 (92%)	136 (97%)	4 (3%)	0	100	100
2	F	137/153 (90%)	133 (97%)	4 (3%)	0	100	100
2	G	142/153 (93%)	139 (98%)	3 (2%)	0	100	100
2	H	135/153 (88%)	128 (95%)	7 (5%)	0	100	100
All	All	1280/1444 (89%)	1238 (97%)	39 (3%)	3 (0%)	44	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	41	GLY
1	D	41	GLY
1	C	41	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	165/183 (90%)	165 (100%)	0	100	100
1	B	166/183 (91%)	165 (99%)	1 (1%)	84	90
1	C	166/183 (91%)	165 (99%)	1 (1%)	84	90
1	D	167/183 (91%)	165 (99%)	2 (1%)	67	79
2	E	134/145 (92%)	134 (100%)	0	100	100
2	F	133/145 (92%)	133 (100%)	0	100	100
2	G	136/145 (94%)	136 (100%)	0	100	100
2	H	130/145 (90%)	129 (99%)	1 (1%)	79	87
All	All	1197/1312 (91%)	1192 (100%)	5 (0%)	89	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	204	LYS

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Mol	Chain	Res	Type
1	C	204	LYS
1	D	110	GLU
1	D	193	LYS
2	H	90	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	118	HIS
1	B	130	HIS
1	C	57	GLN
1	A	101	ASN
1	A	81	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 ⓘ

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	$\# Z > 2$
3	NAG	I	1	1,3	14,14,15	0.48	0	17,19,21	0.94	1 (5%)
3	NAG	I	2	3	14,14,15	0.48	0	17,19,21	0.83	0
3	BMA	I	3	3	11,11,12	0.60	0	15,15,17	0.59	0
3	NAG	J	1	1,3	14,14,15	0.66	0	17,19,21	0.90	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	J	2	3	14,14,15	0.48	0	17,19,21	0.68	0
3	BMA	J	3	3	11,11,12	0.59	0	15,15,17	0.66	0
3	NAG	K	1	1,3	14,14,15	0.48	0	17,19,21	1.04	1 (5%)
3	NAG	K	2	3	14,14,15	0.50	0	17,19,21	0.63	0
3	BMA	K	3	3	11,11,12	0.57	0	15,15,17	0.65	0
3	NAG	L	1	1,3	14,14,15	0.64	0	17,19,21	1.09	1 (5%)
3	NAG	L	2	3	14,14,15	0.54	0	17,19,21	0.83	0
3	BMA	L	3	3	11,11,12	0.62	0	15,15,17	1.00	1 (6%)

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	NAG	I	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	3/6/23/26	0/1/1/1
3	BMA	I	3	3	-	0/2/19/22	0/1/1/1
3	NAG	J	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	1/6/23/26	0/1/1/1
3	BMA	J	3	3	-	0/2/19/22	0/1/1/1
3	NAG	K	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	K	2	3	-	0/6/23/26	0/1/1/1
3	BMA	K	3	3	-	0/2/19/22	0/1/1/1
3	NAG	L	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
3	BMA	L	3	3	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	1	NAG	C4-C3-C2	3.40	116.00	111.02
3	K	1	NAG	C1-O5-C5	3.20	116.47	112.19
3	L	3	BMA	C1-C2-C3	2.99	113.99	109.64
3	J	1	NAG	C4-C3-C2	2.67	114.94	111.02
3	I	1	NAG	C1-O5-C5	2.12	115.03	112.19

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

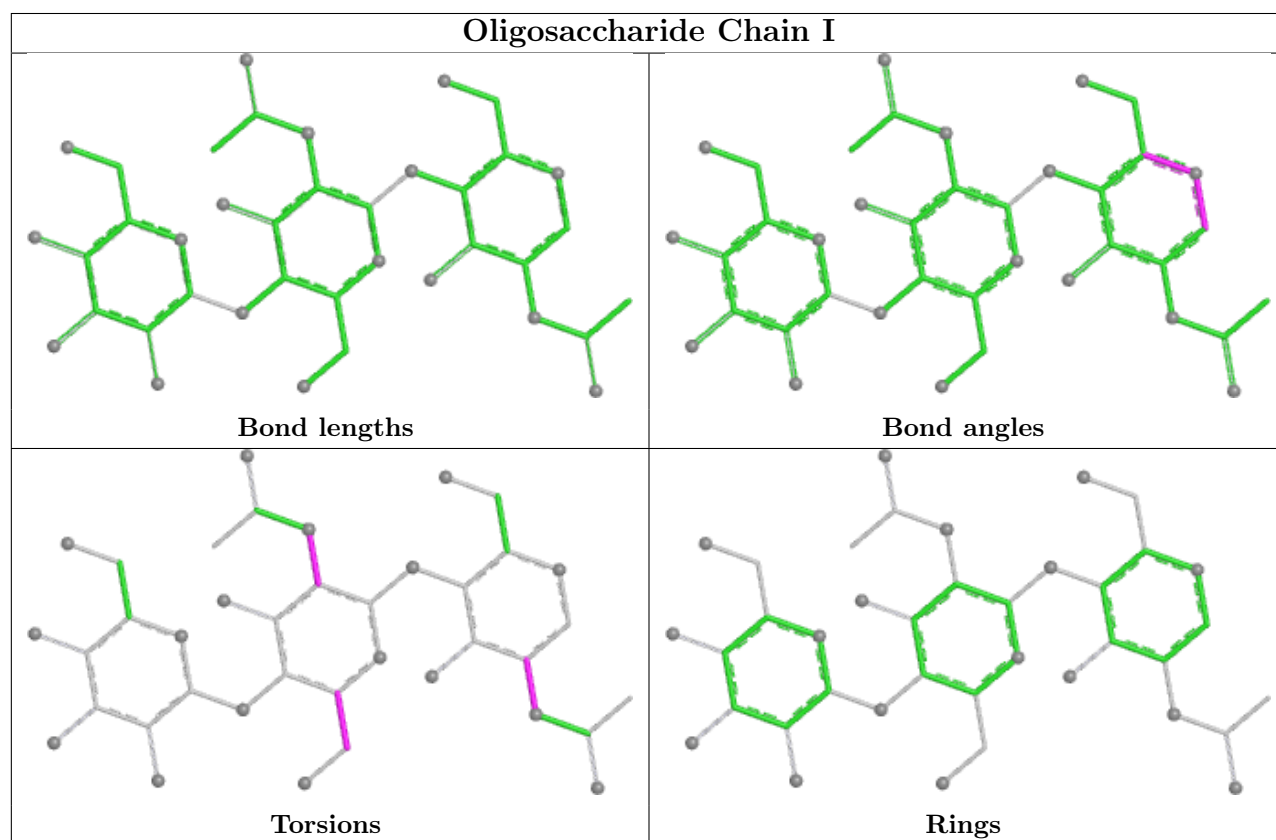
Mol	Chain	Res	Type	Atoms
3	K	1	NAG	C1-C2-N2-C7
3	I	2	NAG	O5-C5-C6-O6
3	I	2	NAG	C4-C5-C6-O6
3	I	2	NAG	C3-C2-N2-C7
3	J	2	NAG	O5-C5-C6-O6

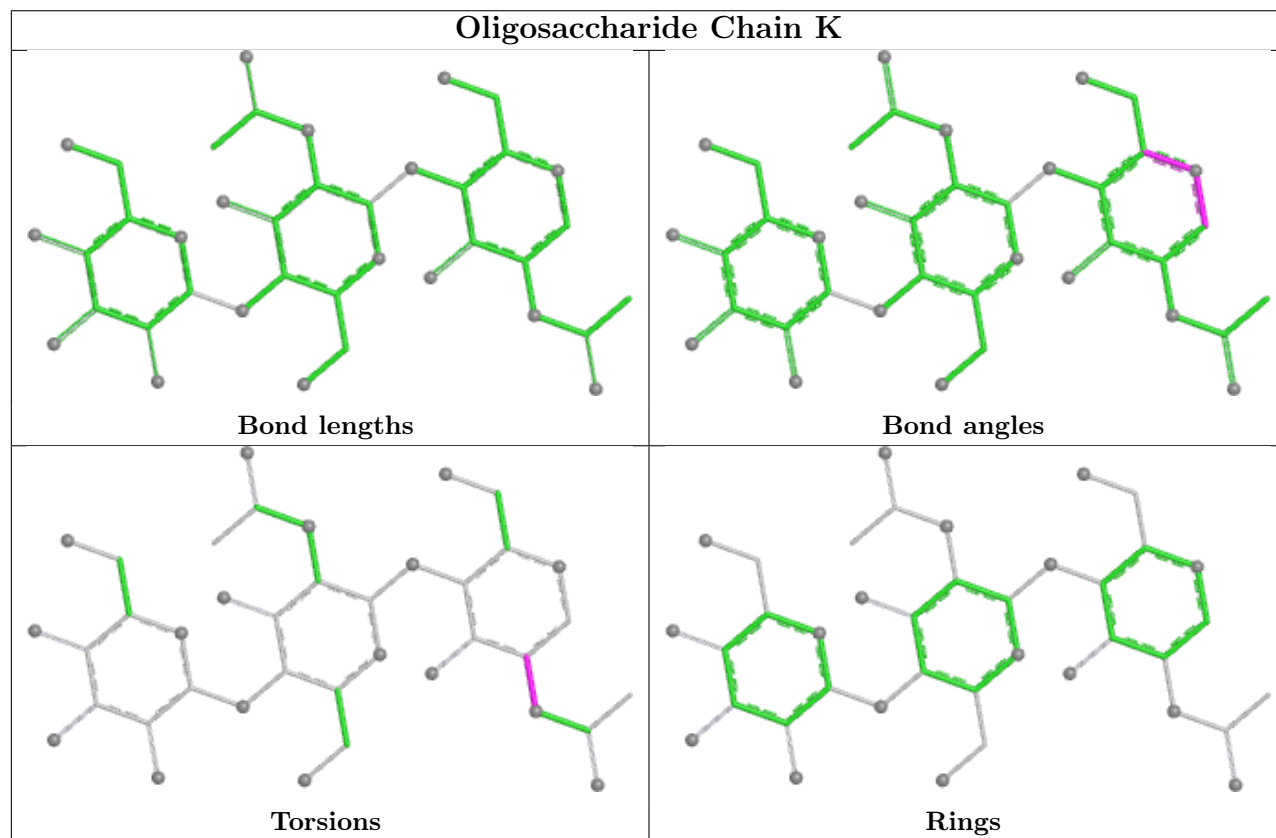
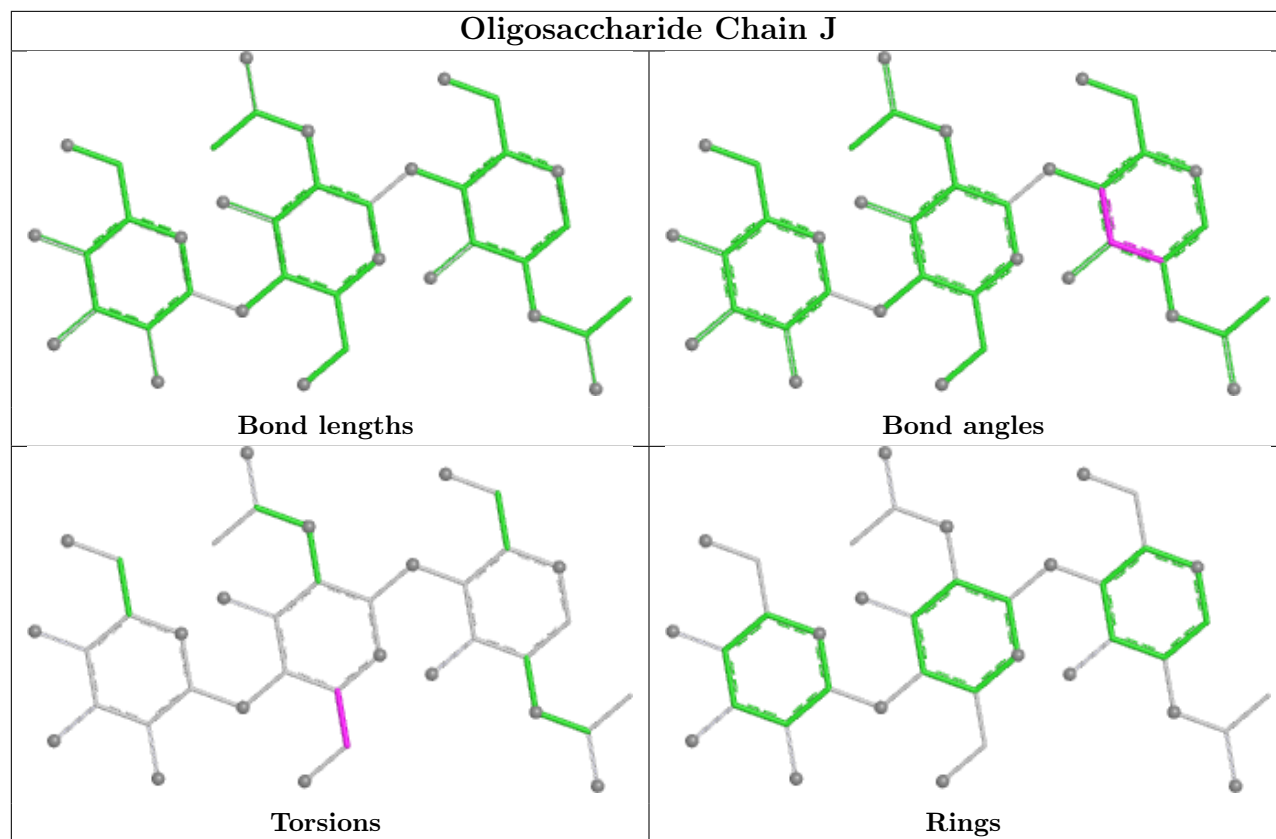
There are no ring outliers.

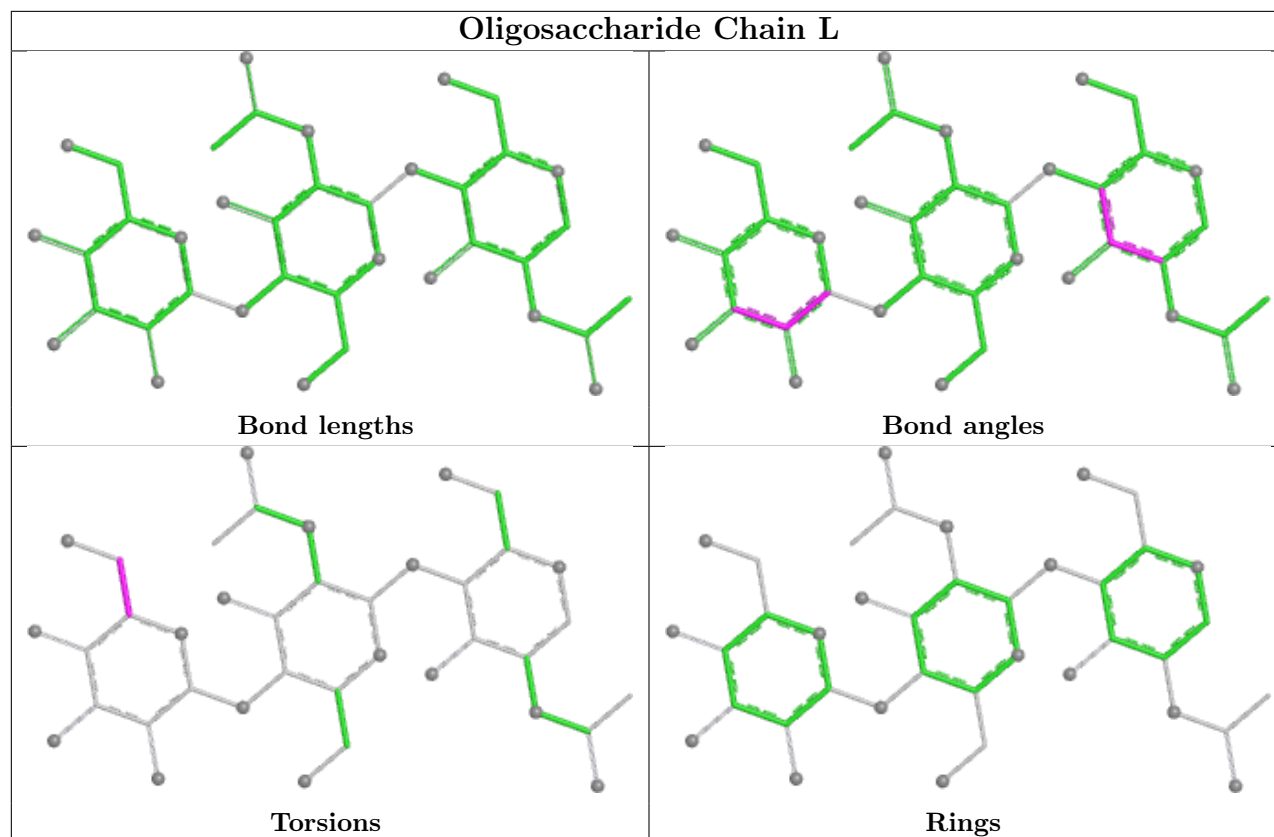
2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	3	BMA	1	0
3	I	2	NAG	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	185/208 (88%)	-0.33	0 100 100	45, 60, 81, 94	0
1	B	185/208 (88%)	-0.21	1 (0%) 87 83	46, 64, 80, 102	0
1	C	186/208 (89%)	-0.23	0 100 100	50, 63, 89, 108	0
1	D	186/208 (89%)	-0.25	0 100 100	45, 62, 85, 115	0
2	E	142/153 (92%)	-0.01	1 (0%) 84 78	57, 85, 111, 119	0
2	F	141/153 (92%)	0.20	2 (1%) 73 64	61, 105, 153, 170	0
2	G	143/153 (93%)	0.03	0 100 100	53, 90, 113, 138	1 (0%)
2	H	139/153 (90%)	0.32	5 (3%) 46 39	56, 110, 148, 168	0
All	All	1307/1444 (90%)	-0.09	9 (0%) 84 78	45, 72, 133, 170	1 (0%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	58	GLN	3.5
2	F	54	PHE	3.2
2	H	132	TRP	2.4
2	H	135	PHE	2.4
1	B	102	TYR	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.

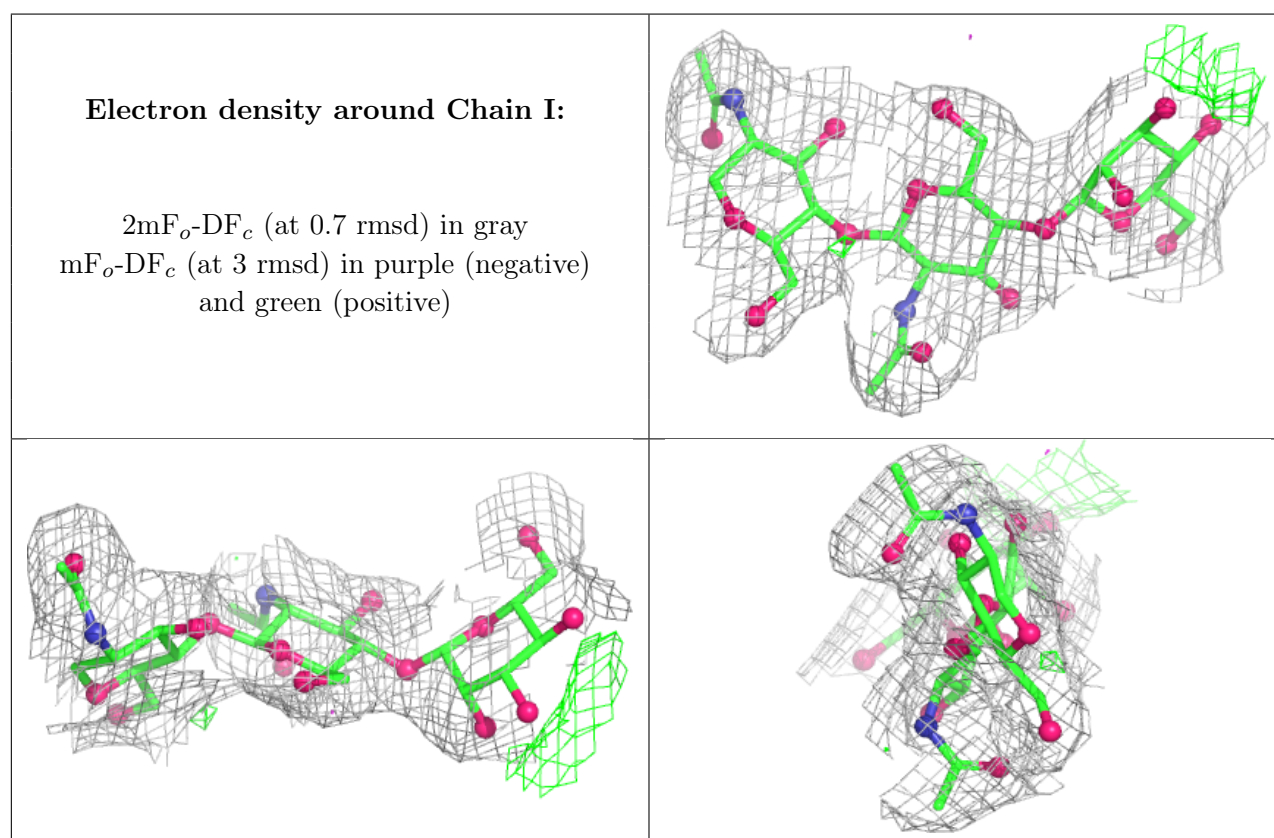
6.3 Carbohydrates [i](#)

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, 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.

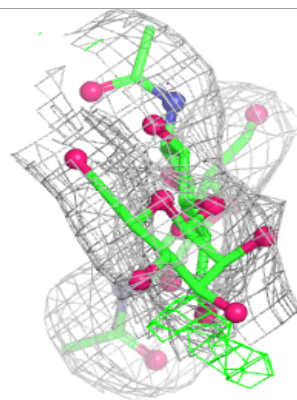
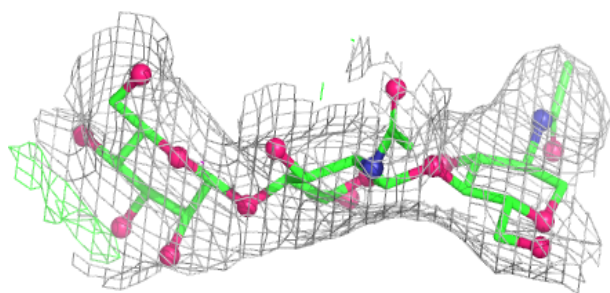
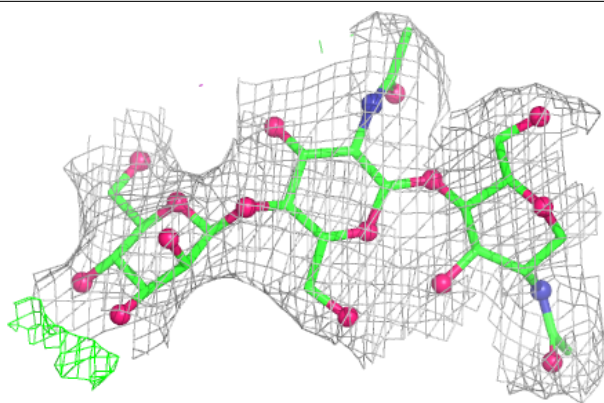
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BMA	J	3	11/12	0.71	0.11	67,75,94,96	0
3	BMA	I	3	11/12	0.79	0.10	74,80,89,91	0
3	BMA	K	3	11/12	0.80	0.09	71,80,88,93	0
3	BMA	L	3	11/12	0.80	0.09	70,80,91,97	0
3	NAG	I	2	14/15	0.85	0.11	63,70,80,81	0
3	NAG	J	2	14/15	0.89	0.10	60,64,70,71	0
3	NAG	J	1	14/15	0.90	0.10	42,60,63,69	0
3	NAG	K	2	14/15	0.91	0.08	61,68,72,73	0
3	NAG	K	1	14/15	0.92	0.08	50,65,72,74	0
3	NAG	I	1	14/15	0.92	0.08	49,61,70,78	0
3	NAG	L	2	14/15	0.95	0.06	52,64,80,85	0
3	NAG	L	1	14/15	0.95	0.07	50,62,66,68	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.

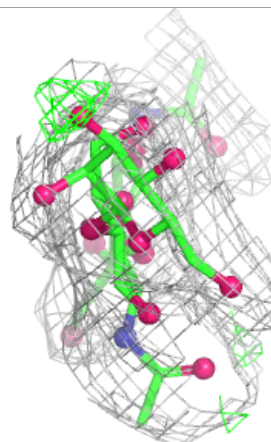
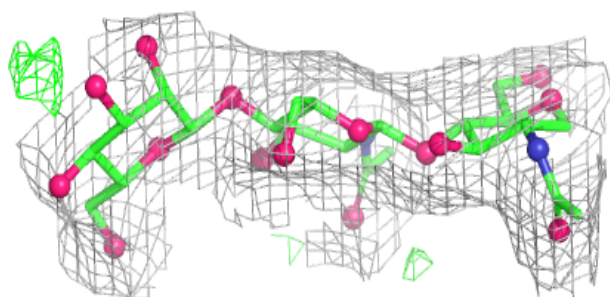
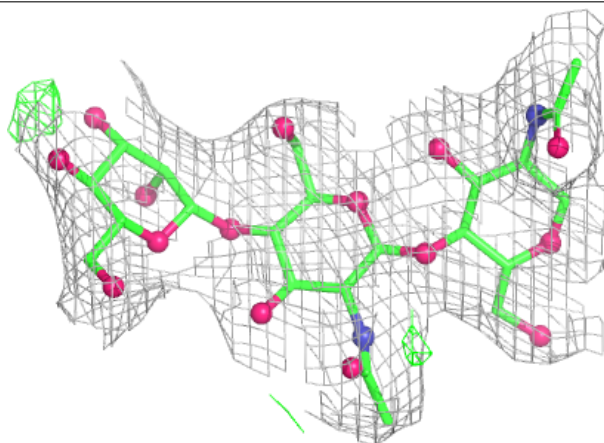


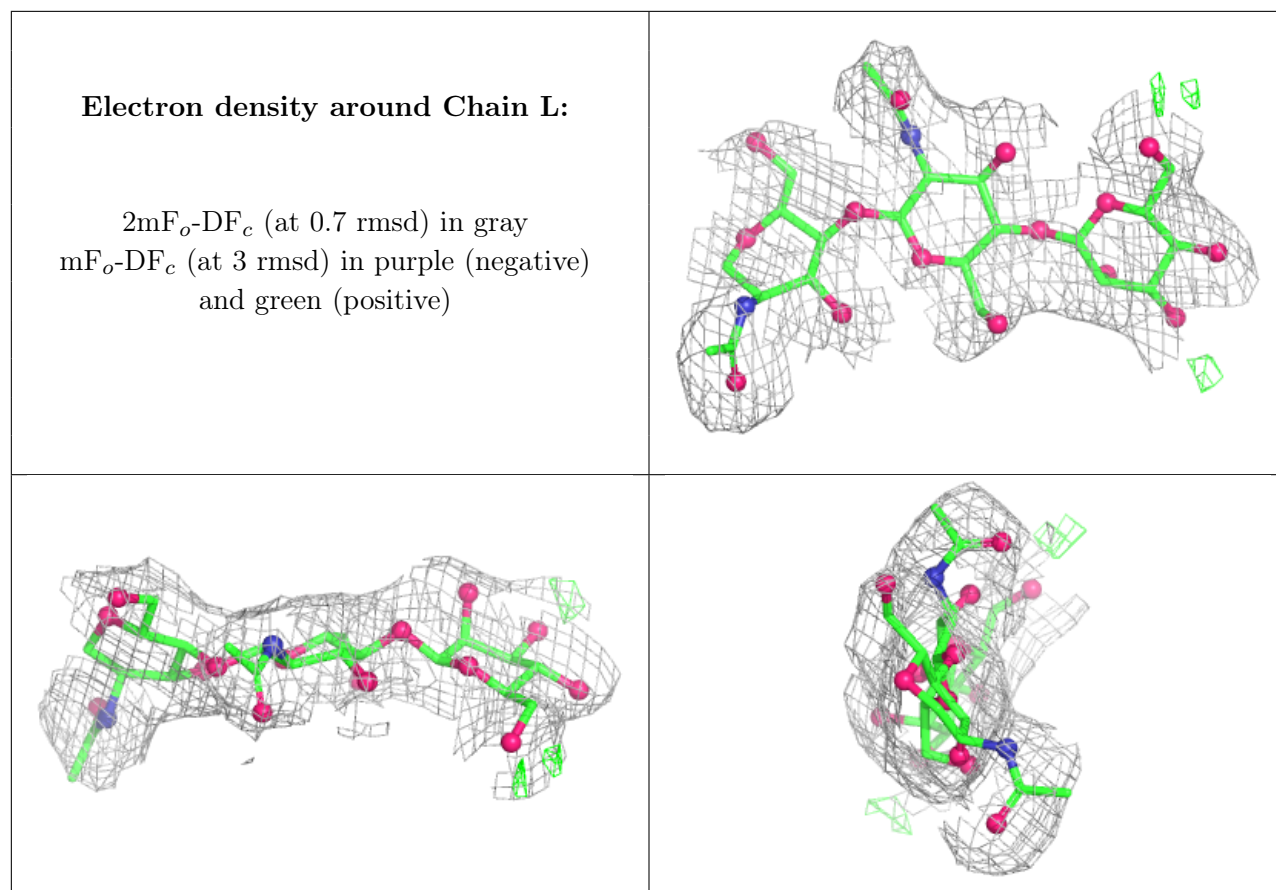
Electron density around Chain J:

$2mF_o-DF_c$ (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.