



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 03:38 PM EDT

PDB ID : 6P67 / pdb_00006p67
Title : Crystal Structure of a Complex of human IL-7Ralpha with an anti-IL-7Ralpha 2B8 Fab
Authors : Walsh, S.T.R.; Kashi, L.; Kohnhorst, C.L.
Deposited on : 2019-06-03
Resolution : 2.90 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 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

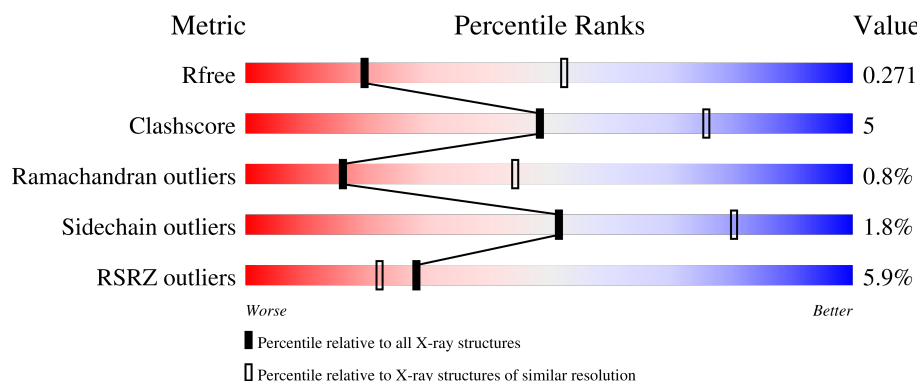
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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.



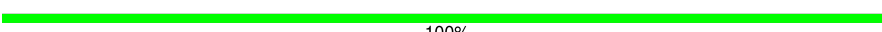
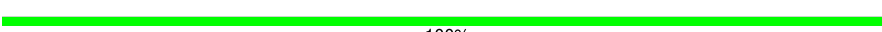
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 ≥ 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	225	10% 89% 9% ..
1	C	225	10% 90% 9% .
1	E	225	14% 84% 13% ..
1	H	225	9% 83% 15% ..
2	B	214	% 92% 7%

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Mol	Chain	Length	Quality of chain
2	D	214	 91% 8%
2	F	214	 85% 14% 4%
2	L	214	 86% 13% %
3	G	223	 70% 17% • 13% 3%
3	I	223	 63% 22% • 13% 8%
3	J	223	 79% 8% 13% 4%
3	K	223	 74% 9% • 16% 4%
4	M	3	 67% 33%
4	N	3	 100%
5	O	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 19325 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 Anti-IL-7R 2B8 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1664	1053	267	336	8			
1	C	223	Total	C	N	O	S	0	0	0
			1667	1055	266	338	8			
1	E	220	Total	C	N	O	S	0	0	0
			1637	1040	261	328	8			
1	H	223	Total	C	N	O	S	0	0	0
			1677	1062	271	336	8			

- Molecule 2 is a protein called anti-IL-7R 2B8 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1652	1037	277	332	6			
2	D	213	Total	C	N	O	S	0	0	0
			1652	1037	277	332	6			
2	F	213	Total	C	N	O	S	0	0	0
			1648	1035	277	330	6			
2	L	213	Total	C	N	O	S	0	0	0
			1652	1037	277	332	6			

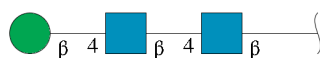
- Molecule 3 is a protein called Interleukin-7 receptor subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	195	Total	C	N	O	S	0	0	0
			1558	1008	252	290	8			
3	I	193	Total	C	N	O	S	0	0	0
			1542	997	250	287	8			
3	J	195	Total	C	N	O	S	0	0	0
			1420	908	235	269	8			
3	K	188	Total	C	N	O	S	0	0	0
			1384	886	232	258	8			

There are 20 discrepancies between the modelled and reference sequences:

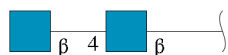
Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	GLY	-	expression tag	UNP P16871
G	-2	SER	-	expression tag	UNP P16871
G	-1	HIS	-	expression tag	UNP P16871
G	0	MET	-	expression tag	UNP P16871
G	46	THR	ILE	conflict	UNP P16871
I	-3	GLY	-	expression tag	UNP P16871
I	-2	SER	-	expression tag	UNP P16871
I	-1	HIS	-	expression tag	UNP P16871
I	0	MET	-	expression tag	UNP P16871
I	46	THR	ILE	conflict	UNP P16871
J	-3	GLY	-	expression tag	UNP P16871
J	-2	SER	-	expression tag	UNP P16871
J	-1	HIS	-	expression tag	UNP P16871
J	0	MET	-	expression tag	UNP P16871
J	46	THR	ILE	conflict	UNP P16871
K	-3	GLY	-	expression tag	UNP P16871
K	-2	SER	-	expression tag	UNP P16871
K	-1	HIS	-	expression tag	UNP P16871
K	0	MET	-	expression tag	UNP P16871
K	46	THR	ILE	conflict	UNP P16871

- Molecule 4 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.



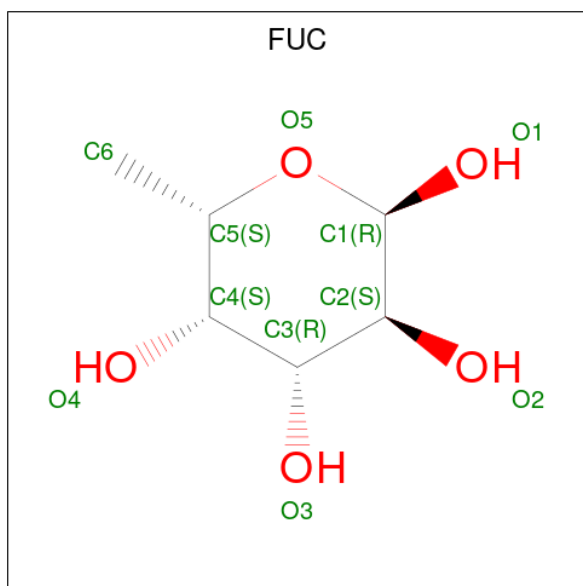
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	M	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	N	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



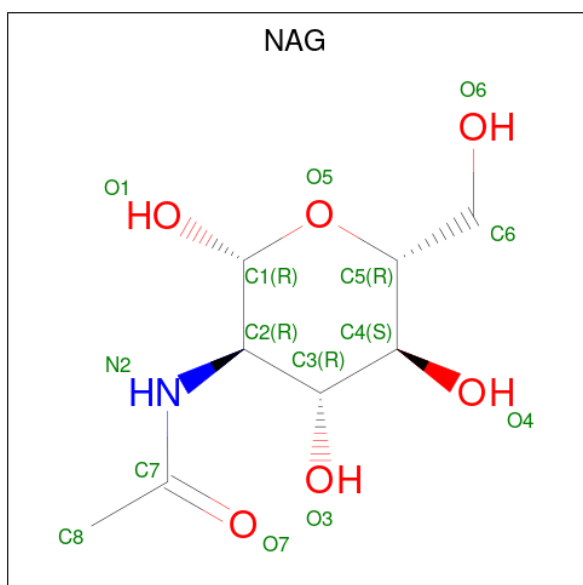
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is alpha-L-fucopyranose (CCD ID: FUC) (formula: $C_6H_{12}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	G	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

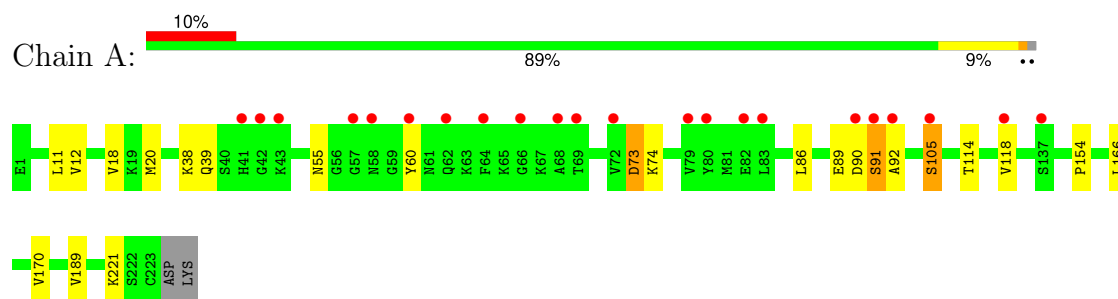


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	G	1	Total	C	N	O	0	0
			14	8	1	5		
7	I	1	Total	C	N	O	0	0
			14	8	1	5		
7	J	1	Total	C	N	O	0	0
			14	8	1	5		
7	K	1	Total	C	N	O	0	0
			14	8	1	5		

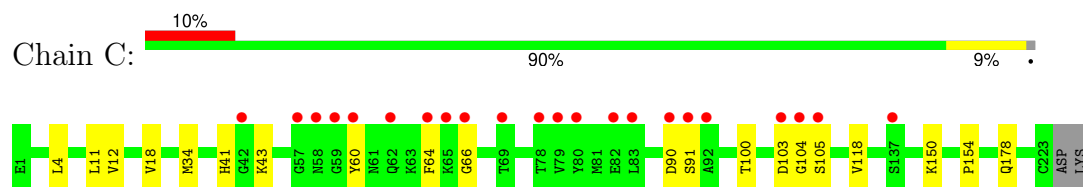
3 Residue-property plots [i](#)

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.

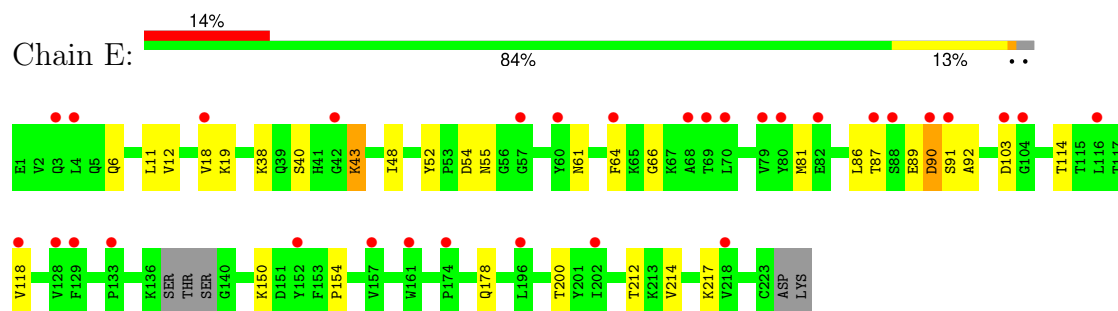
- Molecule 1: Anti-IL-7R 2B8 Fab heavy chain



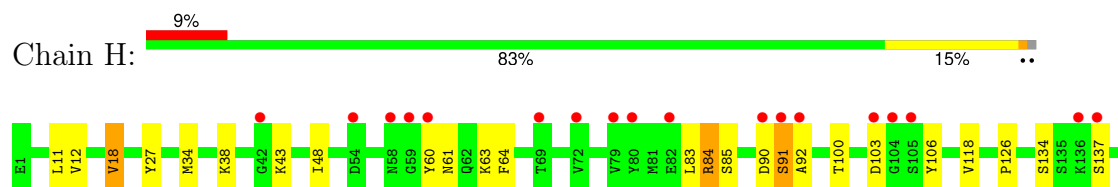
- Molecule 1: Anti-IL-7R 2B8 Fab heavy chain



- Molecule 1: Anti-IL-7R 2B8 Fab heavy chain



- Molecule 1: Anti-IL-7R 2B8 Fab heavy chain





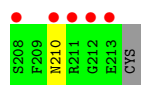
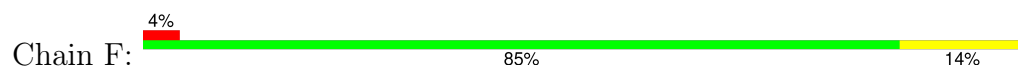
- Molecule 2: anti-IL-7R 2B8 Fab light chain



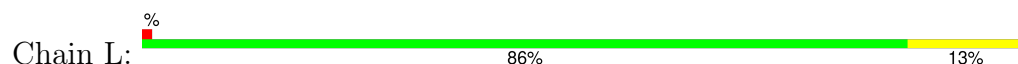
- Molecule 2: anti-IL-7R 2B8 Fab light chain



- Molecule 2: anti-IL-7R 2B8 Fab light chain



- Molecule 2: anti-IL-7R 2B8 Fab light chain

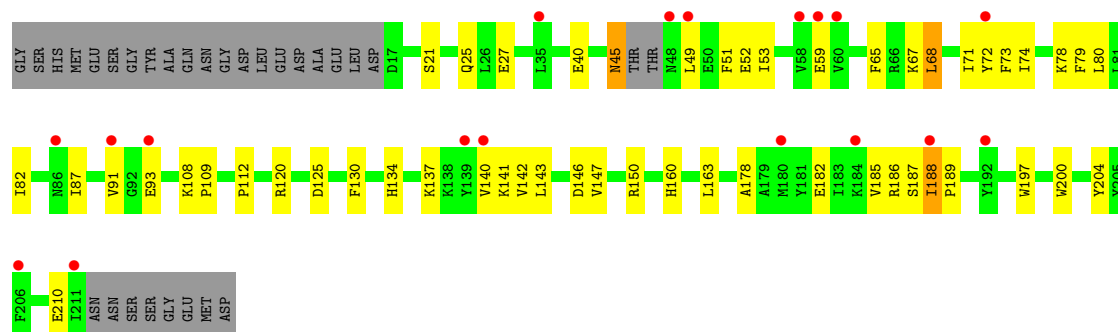


- Molecule 3: Interleukin-7 receptor subunit alpha

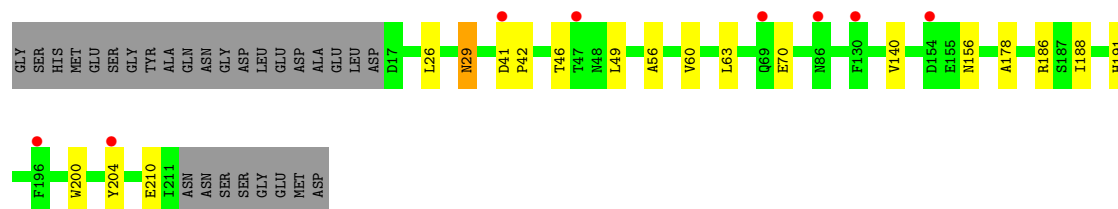
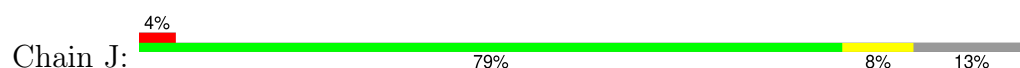


- Molecule 3: Interleukin-7 receptor subunit alpha

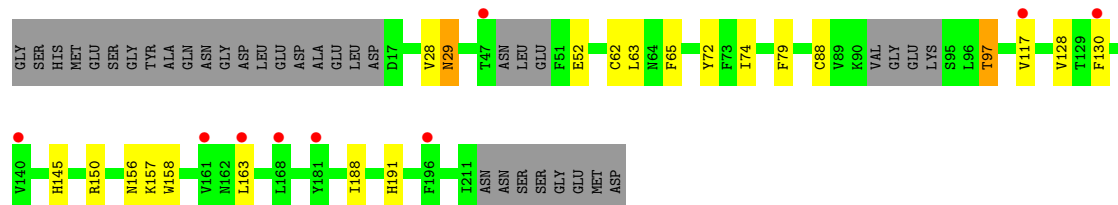
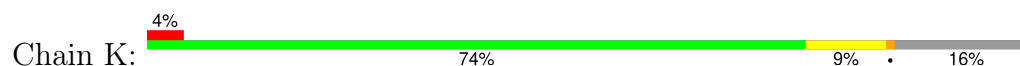




- Molecule 3: Interleukin-7 receptor subunit alpha



- Molecule 3: Interleukin-7 receptor subunit alpha



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



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



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

100%

3AG1
3AG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.90Å 219.68Å 90.35Å 90.00° 104.33° 90.00°	Depositor
Resolution (Å)	43.77 – 2.90 43.77 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (43.77-2.90) 99.3 (43.77-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.90Å)	Xtriage
Refinement program	phenix.refine 1.16rc1_3535, PHENIX 1.16rc1_3535	Depositor
R, R_{free}	0.249 , 0.266 0.250 , 0.271	Depositor DCC
R_{free} test set	1986 reflections (2.83%)	wwPDB-VP
Wilson B-factor (Å ²)	73.1	Xtriage
Anisotropy	0.588	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	19325	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% 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: NAG, FUC, BMA

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	0.14	0/1708	0.39	0/2329
1	C	0.11	0/1712	0.41	0/2335
1	E	0.11	0/1681	0.35	0/2292
1	H	0.13	0/1722	0.43	1/2345 (0.0%)
2	B	0.11	0/1688	0.36	0/2290
2	D	0.12	0/1688	0.37	0/2290
2	F	0.19	0/1684	0.40	1/2285 (0.0%)
2	L	0.11	0/1688	0.35	0/2290
3	G	0.14	0/1597	0.38	0/2171
3	I	0.26	0/1580	0.47	0/2142
3	J	0.13	0/1457	0.39	0/1999
3	K	0.17	0/1419	0.43	0/1942
All	All	0.15	0/19624	0.40	2/26710 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	43	LYS	CB-CA-C	-6.15	108.86	117.23
2	F	18	ARG	NE-CZ-NH1	-5.14	116.36	121.50

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	1664	0	1580	15	0
1	C	1667	0	1578	9	0
1	E	1637	0	1546	16	1
1	H	1677	0	1607	23	2
2	B	1652	0	1606	14	0
2	D	1652	0	1606	13	0
2	F	1648	0	1602	24	0
2	L	1652	0	1606	18	0
3	G	1558	0	1489	25	1
3	I	1542	0	1472	43	1
3	J	1420	0	1200	8	0
3	K	1384	0	1184	12	0
4	M	39	0	34	2	0
4	N	39	0	34	0	0
5	O	28	0	25	0	0
6	G	10	0	10	0	0
7	G	14	0	13	0	0
7	I	14	0	13	0	1
7	J	14	0	13	0	0
7	K	14	0	13	1	0
All	All	19325	0	18231	205	3

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 5.

The worst 5 of 205 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:L:9:LYS:HD3	2:L:9:LYS:H	1.39	0.86
1:H:90:ASP:O	1:H:92:ALA:N	2.16	0.79
3:I:178:ALA:HB2	3:I:210:GLU:HG2	1.65	0.77
2:F:9:LYS:H	2:F:9:LYS:HD3	1.51	0.76
2:B:9:LYS:H	2:B:9:LYS:HD3	1.50	0.75

All (3) 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:H:179:SER:O	7:I:301:NAG:O4[2_646]	1.99	0.21
1:E:103:ASP:OD2	3:I:204:TYR:OH[1_554]	2.00	0.20
3:G:204:TYR:OH	1:H:103:ASP:OD2[1_554]	2.13	0.07

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	221/225 (98%)	210 (95%)	8 (4%)	3 (1%)	9	30
1	C	221/225 (98%)	208 (94%)	10 (4%)	3 (1%)	9	30
1	E	216/225 (96%)	201 (93%)	12 (6%)	3 (1%)	9	30
1	H	221/225 (98%)	208 (94%)	11 (5%)	2 (1%)	14	41
2	B	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
2	D	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
2	F	211/214 (99%)	204 (97%)	7 (3%)	0	100	100
2	L	211/214 (99%)	203 (96%)	6 (3%)	2 (1%)	14	41
3	G	193/223 (86%)	175 (91%)	16 (8%)	2 (1%)	12	39
3	I	189/223 (85%)	172 (91%)	16 (8%)	1 (0%)	24	54
3	J	193/223 (86%)	173 (90%)	18 (9%)	2 (1%)	12	39
3	K	182/223 (82%)	168 (92%)	12 (7%)	2 (1%)	11	36
All	All	2480/2648 (94%)	2332 (94%)	128 (5%)	20 (1%)	16	44

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	TYR
1	C	60	TYR
1	E	91	SER
1	H	84	ARG
1	H	91	SER

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	185/193 (96%)	182 (98%)	3 (2%)	55	83
1	C	186/193 (96%)	183 (98%)	3 (2%)	55	83
1	E	180/193 (93%)	177 (98%)	3 (2%)	53	82
1	H	188/193 (97%)	186 (99%)	2 (1%)	65	88
2	B	188/189 (100%)	186 (99%)	2 (1%)	65	88
2	D	188/189 (100%)	187 (100%)	1 (0%)	81	93
2	F	187/189 (99%)	185 (99%)	2 (1%)	65	88
2	L	188/189 (100%)	185 (98%)	3 (2%)	55	83
3	G	170/204 (83%)	168 (99%)	2 (1%)	63	86
3	I	168/204 (82%)	161 (96%)	7 (4%)	26	60
3	J	132/204 (65%)	128 (97%)	4 (3%)	36	70
3	K	131/204 (64%)	125 (95%)	6 (5%)	24	57
All	All	2091/2344 (89%)	2053 (98%)	38 (2%)	51	80

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	J	188	ILE
2	L	9	LYS
3	K	29	ASN
3	K	97	THR
2	L	96	ARG

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

Mol	Chain	Res	Type
1	H	199	GLN
3	I	172	GLN
3	I	191	HIS
3	I	160	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	42	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

8 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	M	1	3,4	14,14,15	0.30	0	17,19,21	0.52	0
4	NAG	M	2	4	14,14,15	0.43	0	17,19,21	0.41	0
4	BMA	M	3	4	11,11,12	0.60	0	15,15,17	0.71	0
4	NAG	N	1	3,4	14,14,15	0.22	0	17,19,21	0.48	0
4	NAG	N	2	4	14,14,15	0.27	0	17,19,21	0.52	0
4	BMA	N	3	4	11,11,12	0.46	0	15,15,17	0.80	0
5	NAG	O	1	3,5	14,14,15	0.23	0	17,19,21	0.43	0
5	NAG	O	2	5	14,14,15	0.28	0	17,19,21	0.43	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	M	1	3,4	-	2/6/23/26	0/1/1/1
4	NAG	M	2	4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	M	3	4	-	0/2/19/22	0/1/1/1
4	NAG	N	1	3,4	-	2/6/23/26	0/1/1/1
4	NAG	N	2	4	-	2/6/23/26	0/1/1/1
4	BMA	N	3	4	-	1/2/19/22	0/1/1/1
5	NAG	O	1	3,5	-	0/6/23/26	0/1/1/1
5	NAG	O	2	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

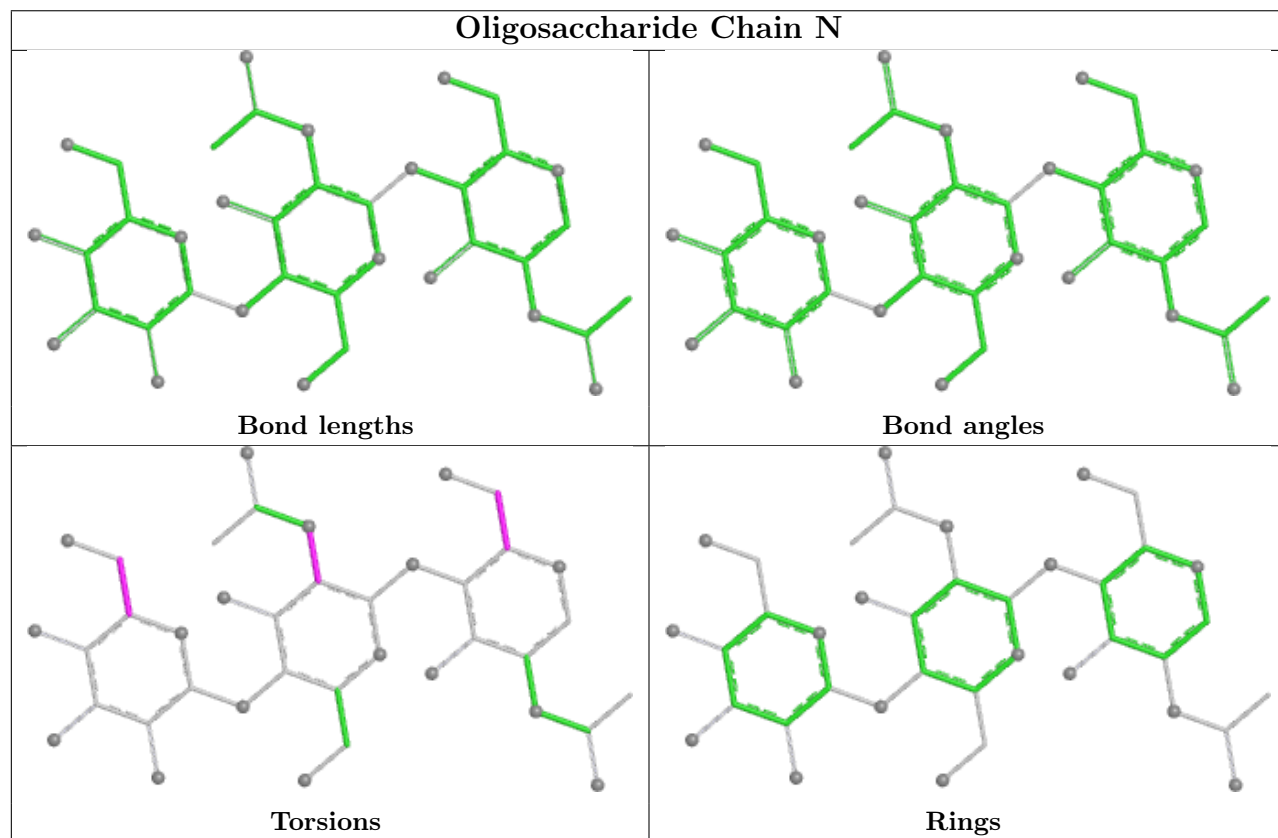
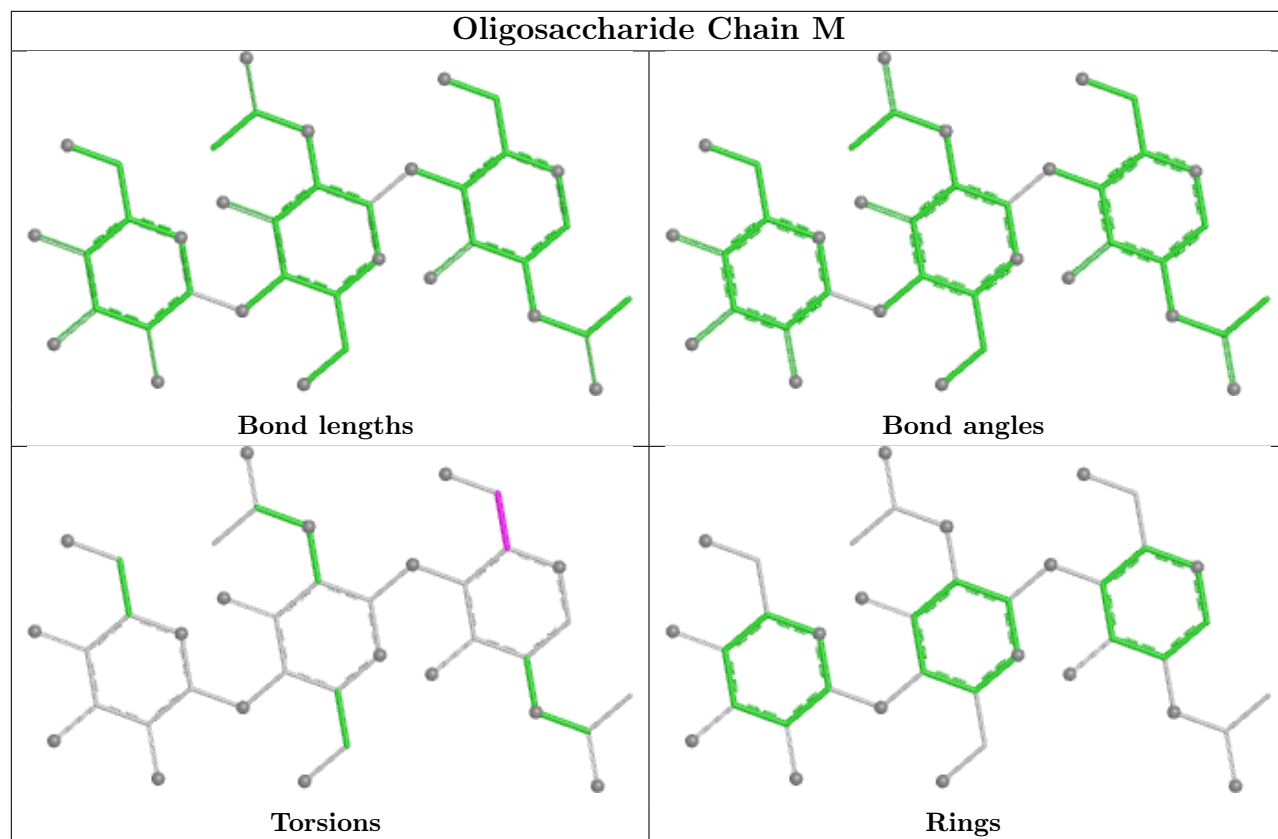
Mol	Chain	Res	Type	Atoms
4	N	1	NAG	O5-C5-C6-O6
4	N	1	NAG	C4-C5-C6-O6
4	N	3	BMA	O5-C5-C6-O6
4	N	2	NAG	C3-C2-N2-C7
4	M	1	NAG	C4-C5-C6-O6

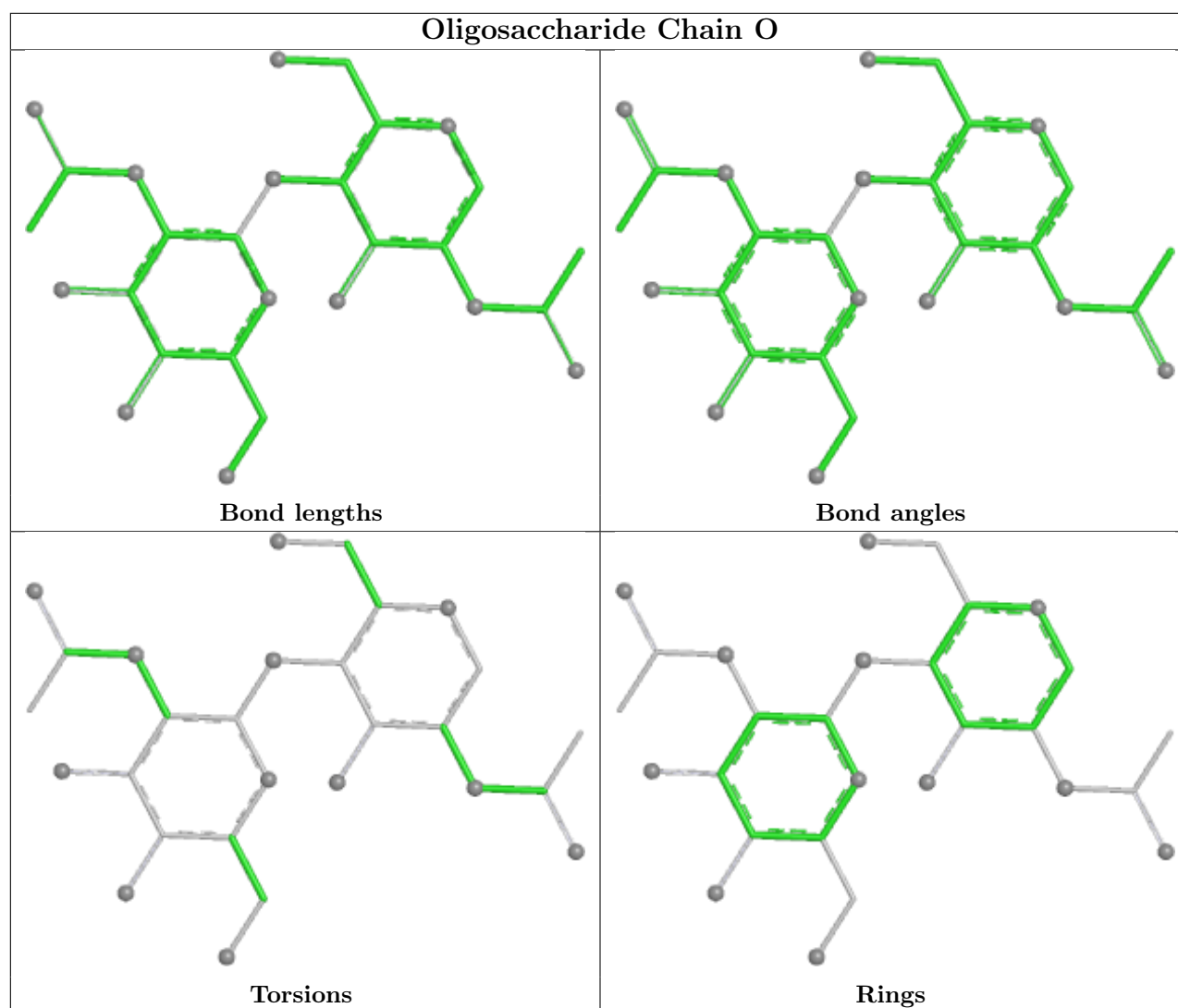
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	1	NAG	2	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](#)

5 ligands 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	$\# Z > 2$
7	NAG	J	303	3	14,14,15	0.35	0	17,19,21	0.59	0
7	NAG	G	305	3	14,14,15	0.29	0	17,19,21	0.35	0
7	NAG	I	301	3	14,14,15	0.15	0	17,19,21	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	K	301	3	14,14,15	0.26	0	17,19,21	0.46	0
6	FUC	G	304	-	10,10,11	0.75	0	14,14,16	0.71	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	J	303	3	-	1/6/23/26	0/1/1/1
7	NAG	G	305	3	-	0/6/23/26	0/1/1/1
7	NAG	I	301	3	-	4/6/23/26	0/1/1/1
7	NAG	K	301	3	-	2/6/23/26	0/1/1/1
6	FUC	G	304	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	K	301	NAG	C4-C5-C6-O6
7	I	301	NAG	O5-C5-C6-O6
7	I	301	NAG	C4-C5-C6-O6
7	K	301	NAG	O5-C5-C6-O6
7	J	303	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	I	301	NAG	0	1
7	K	301	NAG	1	0

5.7 Other polymers ⓘ

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, 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	223/225 (99%)	0.70	22 (9%) 13 11	46, 74, 118, 246	0
1	C	223/225 (99%)	0.60	22 (9%) 13 11	50, 74, 128, 214	0
1	E	220/225 (97%)	1.25	31 (14%) 6 5	69, 106, 137, 206	0
1	H	223/225 (99%)	0.56	20 (8%) 15 13	43, 62, 116, 226	0
2	B	213/214 (99%)	0.04	2 (0%) 81 75	46, 59, 81, 116	0
2	D	213/214 (99%)	0.08	0 100 100	46, 62, 87, 103	0
2	F	213/214 (99%)	0.35	8 (3%) 44 36	50, 66, 121, 137	0
2	L	213/214 (99%)	0.00	2 (0%) 81 75	38, 52, 75, 86	0
3	G	195/223 (87%)	0.57	6 (3%) 51 42	49, 98, 168, 194	0
3	I	193/223 (86%)	0.99	18 (9%) 14 12	68, 126, 191, 227	0
3	J	195/223 (87%)	0.76	8 (4%) 41 33	66, 153, 188, 205	0
3	K	188/223 (84%)	0.88	9 (4%) 35 28	76, 170, 212, 228	0
All	All	2512/2648 (94%)	0.56	148 (5%) 28 22	38, 77, 181, 246	0

The worst 5 of 148 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	91	SER	6.0
1	H	104	GLY	6.0
1	H	42	GLY	4.9
1	A	137	SER	4.8
3	I	48	ASN	4.8

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

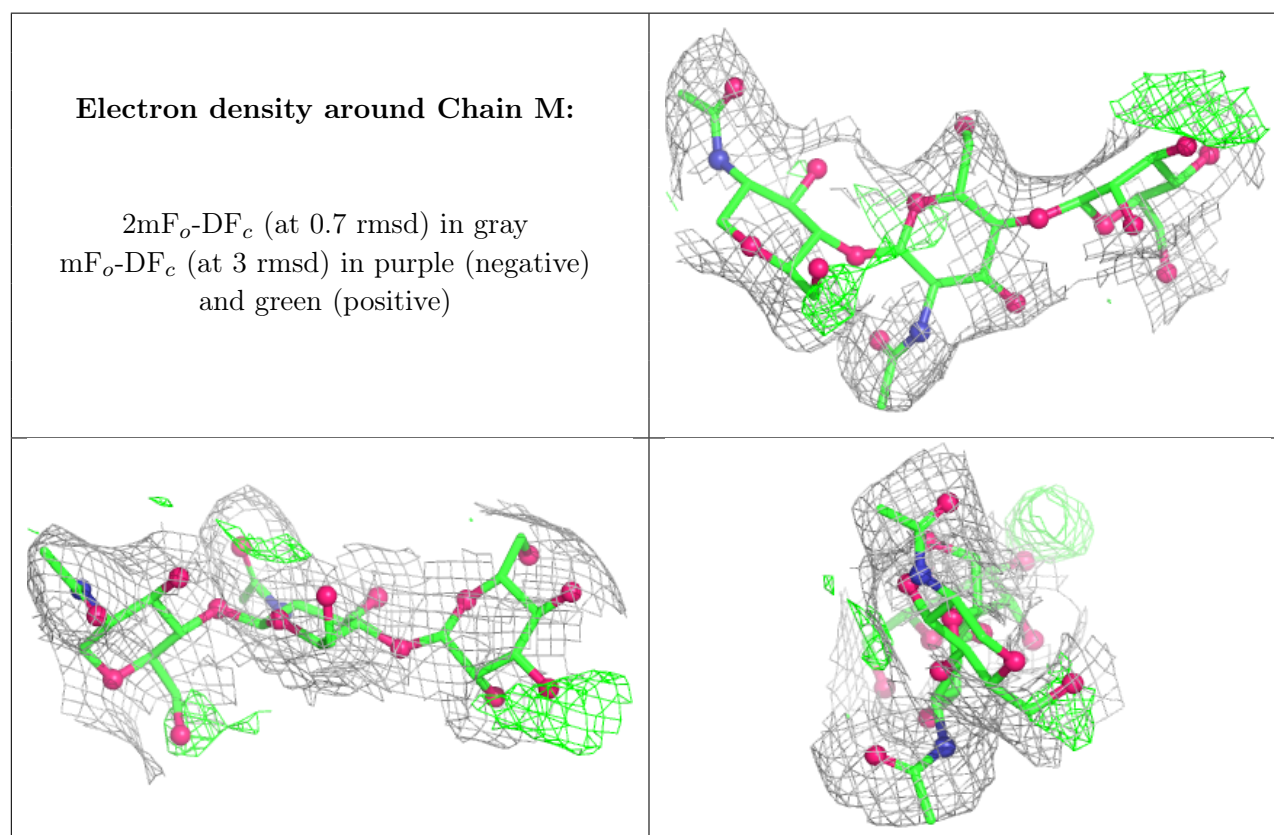
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

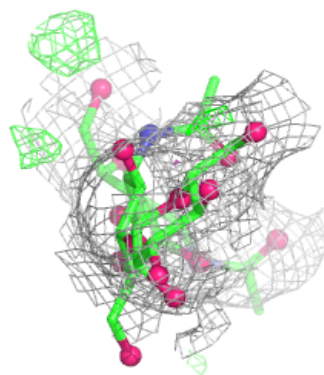
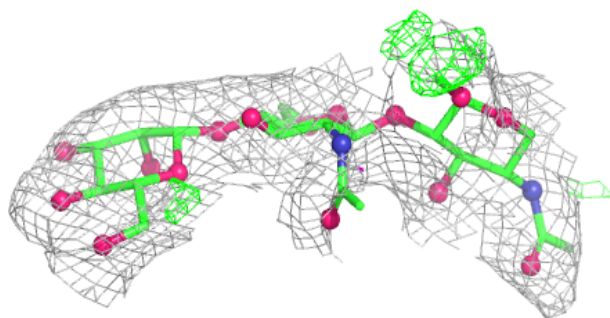
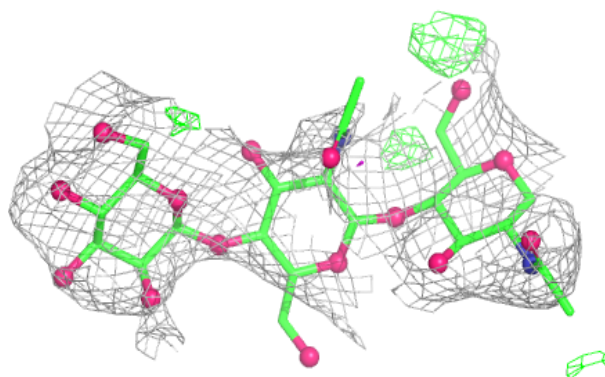
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	N	3	11/12	0.44	0.12	118,122,128,128	0
4	BMA	M	3	11/12	0.51	0.14	99,108,110,112	0
4	NAG	N	2	14/15	0.62	0.15	117,130,132,134	0
5	NAG	O	2	14/15	0.67	0.13	112,121,122,124	0
4	NAG	N	1	14/15	0.70	0.15	88,102,112,118	0
5	NAG	O	1	14/15	0.73	0.15	93,110,116,122	0
4	NAG	M	2	14/15	0.73	0.13	95,101,107,108	0
4	NAG	M	1	14/15	0.84	0.12	67,81,92,93	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.

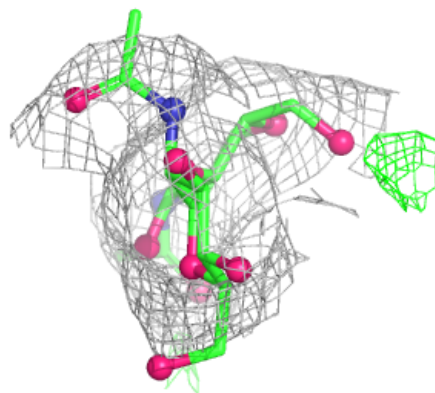
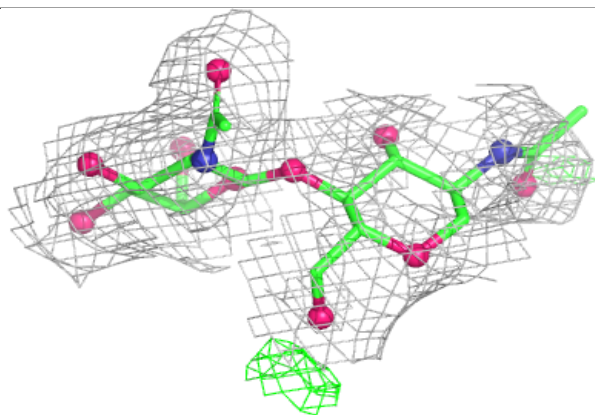
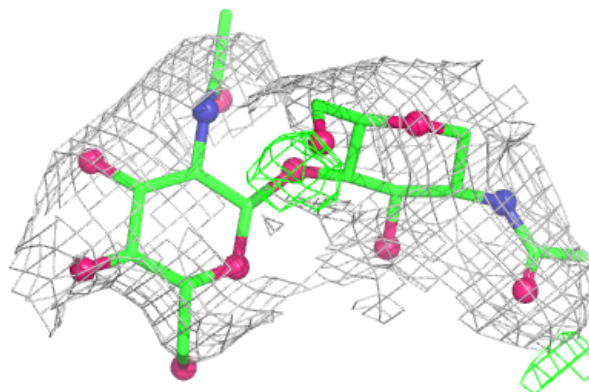


Electron density around Chain N:

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

**Electron density around Chain O:**

$2mF_o-DF_c$ (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, 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
7	NAG	J	303	14/15	0.02	0.17	131,155,165,169	0
7	NAG	G	305	14/15	0.14	0.14	127,143,149,151	0
6	FUC	G	304	10/11	0.61	0.18	93,109,112,112	0
7	NAG	I	301	14/15	0.71	0.15	134,158,181,187	0
7	NAG	K	301	14/15	0.78	0.15	101,113,116,131	0

6.5 Other polymers [i](#)

There are no such residues in this entry.