



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 11:52 PM UTC

PDB ID : 4NZD / pdb_00004nzd
Title : Interleukin 21 receptor
Authors : Hamming, O.T.; Kang, L.; Siupka, P.; Gad, H.H.; Hartmann, R.
Deposited on : 2013-12-12
Resolution : 2.75 Å(reported)

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

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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

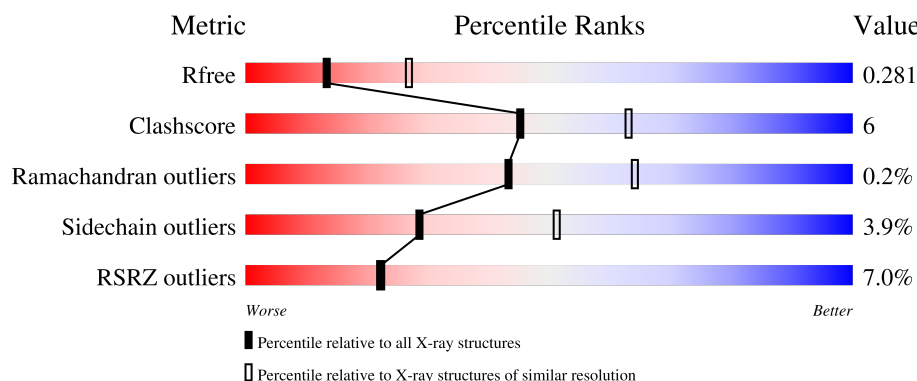
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	219	7% 83% 11% • •
1	B	219	8% 80% 14% 5%
1	C	219	5% 83% 12% • •
2	D	5	20% 80%
2	E	5	80% 20%

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Mol	Chain	Length	Quality of chain
2	F	5	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: green (20%), yellow (20%), and orange (60%).

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
2	FUC	D	5	X	-	-	-
2	FUC	E	5	X	-	-	-
2	FUC	F	5	X	-	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5498 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 Interleukin-21 receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	0	0
			1689	1071	285	322	11			
1	B	208	Total	C	N	O	S	0	0	0
			1686	1070	277	328	11			
1	C	210	Total	C	N	O	S	0	1	0
			1702	1080	290	322	10			

There are 30 discrepancies between the modelled and reference sequences:

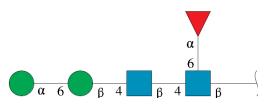
Chain	Residue	Modelled	Actual	Comment	Reference
A	78	GLN	ASN	conflict	UNP Q9HBE5
A	85	GLN	ASN	conflict	UNP Q9HBE5
A	106	ASP	ASN	conflict	UNP Q9HBE5
A	116	GLN	ASN	conflict	UNP Q9HBE5
A	214	HIS	-	expression tag	UNP Q9HBE5
A	215	HIS	-	expression tag	UNP Q9HBE5
A	216	HIS	-	expression tag	UNP Q9HBE5
A	217	HIS	-	expression tag	UNP Q9HBE5
A	218	HIS	-	expression tag	UNP Q9HBE5
A	219	HIS	-	expression tag	UNP Q9HBE5
B	78	GLN	ASN	conflict	UNP Q9HBE5
B	85	GLN	ASN	conflict	UNP Q9HBE5
B	106	ASP	ASN	conflict	UNP Q9HBE5
B	116	GLN	ASN	conflict	UNP Q9HBE5
B	214	HIS	-	expression tag	UNP Q9HBE5
B	215	HIS	-	expression tag	UNP Q9HBE5
B	216	HIS	-	expression tag	UNP Q9HBE5
B	217	HIS	-	expression tag	UNP Q9HBE5
B	218	HIS	-	expression tag	UNP Q9HBE5
B	219	HIS	-	expression tag	UNP Q9HBE5
C	78	GLN	ASN	conflict	UNP Q9HBE5
C	85	GLN	ASN	conflict	UNP Q9HBE5
C	106	ASP	ASN	conflict	UNP Q9HBE5

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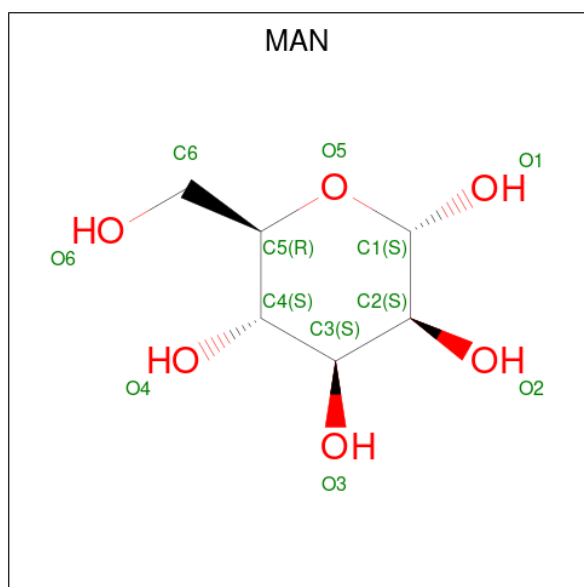
Chain	Residue	Modelled	Actual	Comment	Reference
C	116	GLN	ASN	conflict	UNP Q9HBE5
C	214	HIS	-	expression tag	UNP Q9HBE5
C	215	HIS	-	expression tag	UNP Q9HBE5
C	216	HIS	-	expression tag	UNP Q9HBE5
C	217	HIS	-	expression tag	UNP Q9HBE5
C	218	HIS	-	expression tag	UNP Q9HBE5
C	219	HIS	-	expression tag	UNP Q9HBE5

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranos e-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acet amido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	5	Total	C	N	O	0	0	0
			60	34	2	24			
2	E	5	Total	C	N	O	0	0	0
			60	34	2	24			
2	F	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 3 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 11 6 5	0	0
3	B	1	Total C O 11 6 5	0	0
3	C	1	Total C O 11 6 5	0	0

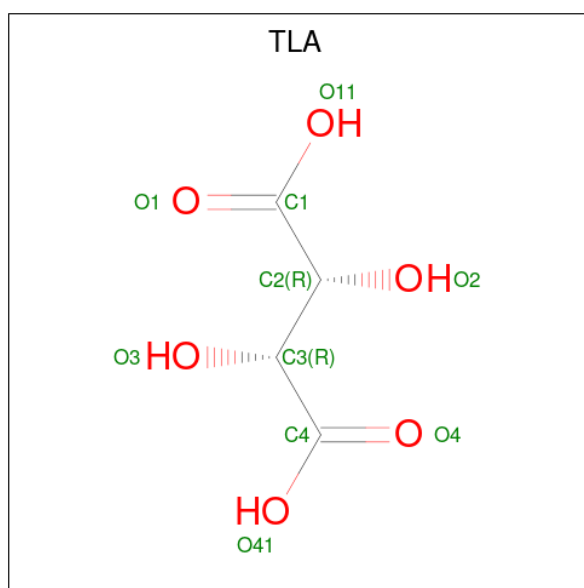
- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total Na 3 3	0	0
4	C	2	Total Na 2 2	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

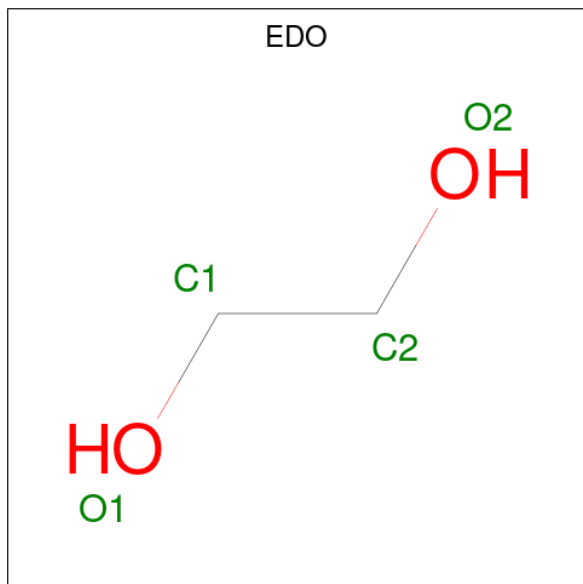
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	4	Total Cl 4 4	0	0
5	B	5	Total Cl 5 5	0	0
5	C	2	Total Cl 2 2	0	0

- Molecule 6 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: C₄H₆O₆).



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

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			4	2	2		

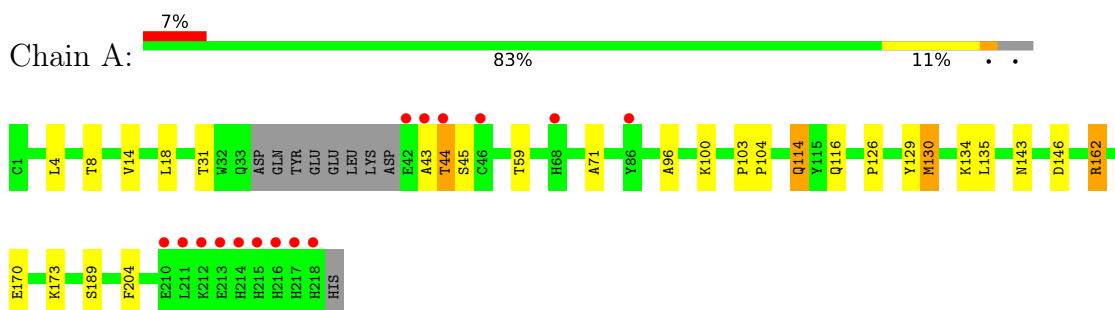
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	39	Total	O	0	0
			39	39		
8	B	59	Total	O	0	0
			59	59		
8	C	60	Total	O	0	0
			60	60		

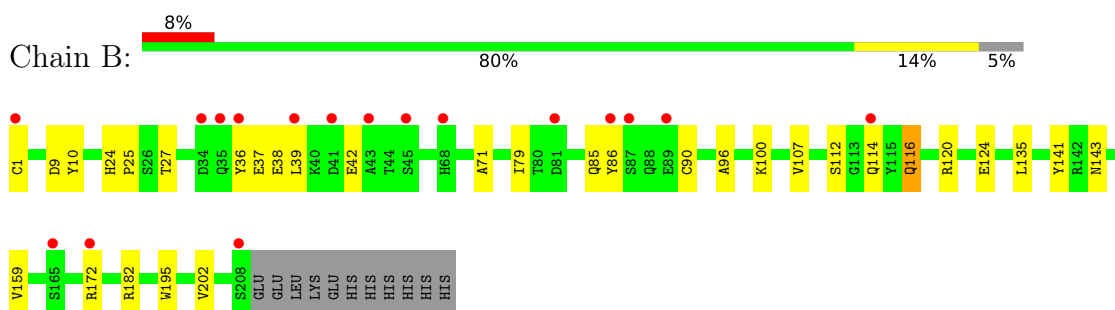
3 Residue-property plots [i](#)

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.

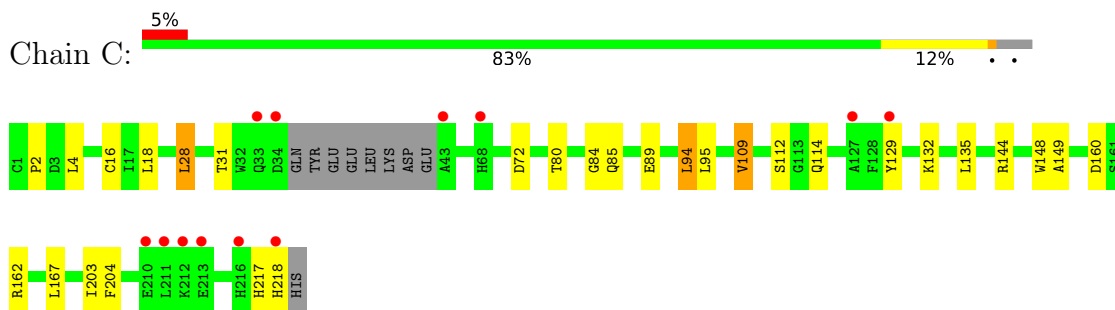
- Molecule 1: Interleukin-21 receptor



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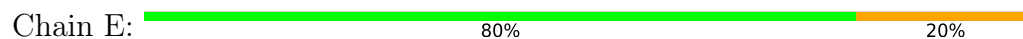


- Molecule 2: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose





- Molecule 2: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	114.33Å 125.26Å 178.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.78 – 2.75 29.78 – 2.75	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.78-2.75) 98.9 (29.78-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.83 (at 2.76Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.239 , 0.275 0.246 , 0.281	Depositor DCC
R_{free} test set	2000 reflections (6.01%)	wwPDB-VP
Wilson B-factor (Å ²)	59.8	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.9	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	0.87	EDS
Total number of atoms	5498	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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, BMA, NA, EDO, MAN, TLA, FUC, CL

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	0.34	0/1741	0.77	0/2373
1	B	0.34	0/1736	0.77	0/2365
1	C	0.34	0/1758	0.77	0/2396
All	All	0.34	0/5235	0.77	0/7134

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	1689	0	1565	19	0
1	B	1686	0	1577	18	0
1	C	1702	0	1585	20	0
2	D	60	0	52	0	0
2	E	60	0	52	2	0
2	F	60	0	52	3	0
3	A	11	0	10	0	0
3	B	11	0	10	2	0
3	C	11	0	10	1	0
4	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	2	0	0	0	0
5	A	4	0	0	0	0
5	B	5	0	0	1	0
5	C	2	0	0	1	0
6	A	20	0	8	2	0
6	B	10	0	4	1	0
7	C	4	0	6	0	0
8	A	39	0	0	4	0
8	B	59	0	0	4	0
8	C	60	0	0	9	0
All	All	5498	0	4931	61	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 6.

The worst 5 of 61 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:B:141:TYR:OH	8:B:447:HOH:O	1.91	0.88
1:C:89:GLU:OE1	8:C:405:HOH:O	1.94	0.84
1:B:1:CYS:SG	8:B:456:HOH:O	2.40	0.80
3:B:301:MAN:H62	2:E:3:BMA:H61	1.68	0.75
1:A:173:LYS:NZ	8:A:432:HOH:O	2.21	0.72

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	206/219 (94%)	197 (96%)	9 (4%)	0	100	100
1	B	206/219 (94%)	195 (95%)	10 (5%)	1 (0%)	24	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	207/219 (94%)	197 (95%)	10 (5%)	0	100	100
All	All	619/657 (94%)	589 (95%)	29 (5%)	1 (0%)	43	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	37	GLU

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	187/201 (93%)	180 (96%)	7 (4%)	30	54
1	B	190/201 (94%)	182 (96%)	8 (4%)	26	49
1	C	189/201 (94%)	182 (96%)	7 (4%)	30	54
All	All	566/603 (94%)	544 (96%)	22 (4%)	28	51

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

Mol	Chain	Res	Type
1	B	159	VAL
1	C	94	LEU
1	C	31	THR
1	C	95	LEU
1	A	162	ARG

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	140	GLN
1	B	180	GLN
1	B	207	GLN
1	A	140	GLN

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Mol	Chain	Res	Type
1	A	136	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 ⓘ

15 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	$\# Z > 2$
2	NAG	D	1	2,1	14,14,15	0.32	0	17,19,21	0.85	1 (5%)
2	NAG	D	2	2	14,14,15	0.39	0	17,19,21	0.83	0
2	BMA	D	3	2	11,11,12	1.11	1 (9%)	15,15,17	1.39	1 (6%)
2	MAN	D	4	2	11,11,12	0.76	0	15,15,17	1.29	2 (13%)
2	FUC	D	5	2	10,10,11	1.17	1 (10%)	14,14,16	1.02	1 (7%)
2	NAG	E	1	2,1	14,14,15	0.31	0	17,19,21	0.43	0
2	NAG	E	2	2	14,14,15	0.40	0	17,19,21	0.61	0
2	BMA	E	3	2	11,11,12	0.68	0	15,15,17	1.20	1 (6%)
2	MAN	E	4	2	11,11,12	0.80	0	15,15,17	0.98	0
2	FUC	E	5	2	10,10,11	0.98	0	14,14,16	0.82	0
2	NAG	F	1	2,1	14,14,15	0.53	0	17,19,21	0.95	1 (5%)
2	NAG	F	2	2	14,14,15	0.25	0	17,19,21	0.48	0
2	BMA	F	3	2	11,11,12	0.97	1 (9%)	15,15,17	1.02	1 (6%)
2	MAN	F	4	2	11,11,12	1.23	2 (18%)	15,15,17	1.75	4 (26%)
2	FUC	F	5	2	10,10,11	1.32	2 (20%)	14,14,16	1.11	2 (14%)

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

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	5	FUC	O5-C1	-2.82	1.39	1.43
2	D	3	BMA	O5-C5	2.80	1.48	1.43
2	F	4	MAN	C2-C3	2.73	1.56	1.52
2	F	3	BMA	O5-C5	2.54	1.48	1.43
2	F	4	MAN	C1-C2	2.54	1.58	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3	BMA	C1-O5-C5	4.36	118.03	112.19
2	F	4	MAN	C1-O5-C5	3.95	117.48	112.19
2	F	4	MAN	C1-C2-C3	3.82	115.20	109.64
2	D	4	MAN	C1-O5-C5	3.76	117.22	112.19
2	E	3	BMA	C1-O5-C5	2.94	116.13	112.19

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	5	FUC	C1
2	E	5	FUC	C1
2	F	5	FUC	C1

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
2	F	4	MAN	C4-C5-C6-O6
2	E	3	BMA	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	F	4	MAN	O5-C5-C6-O6

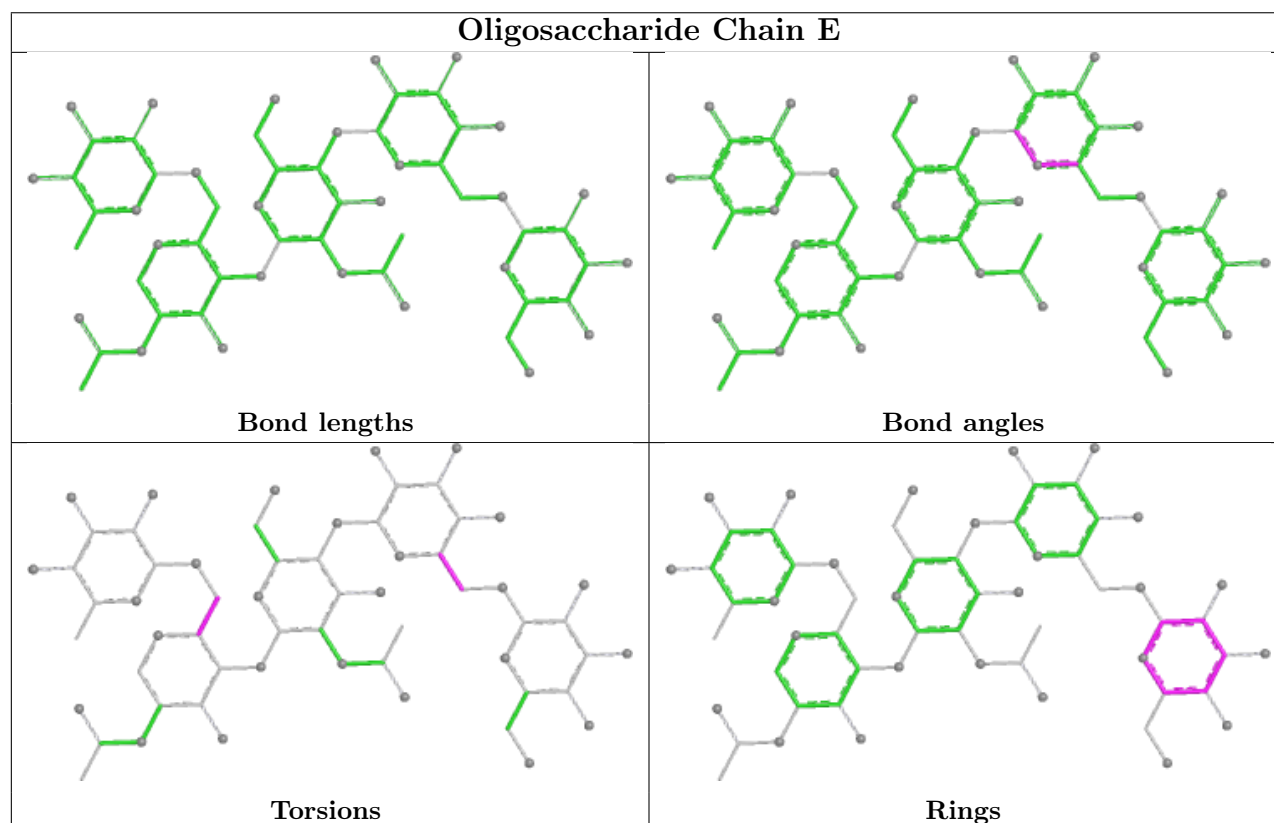
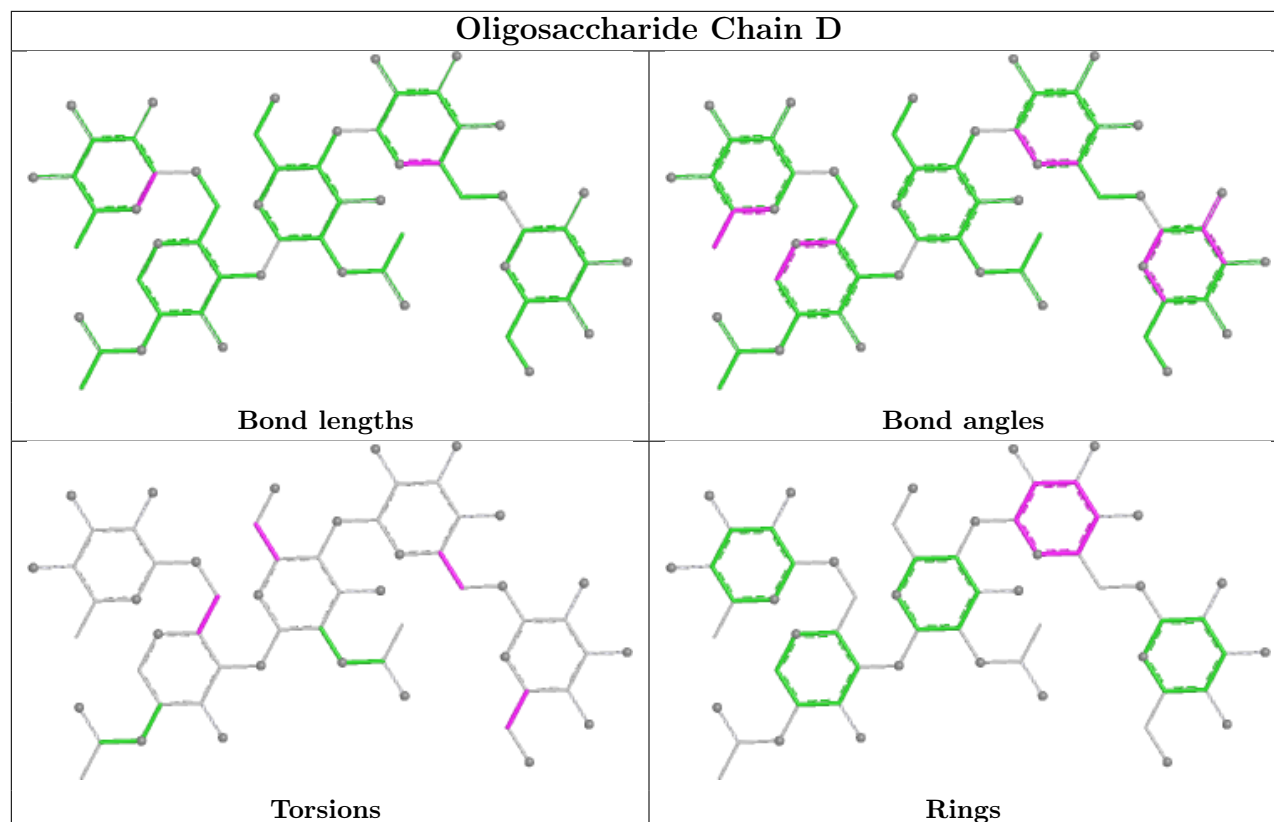
All (2) ring outliers are listed below:

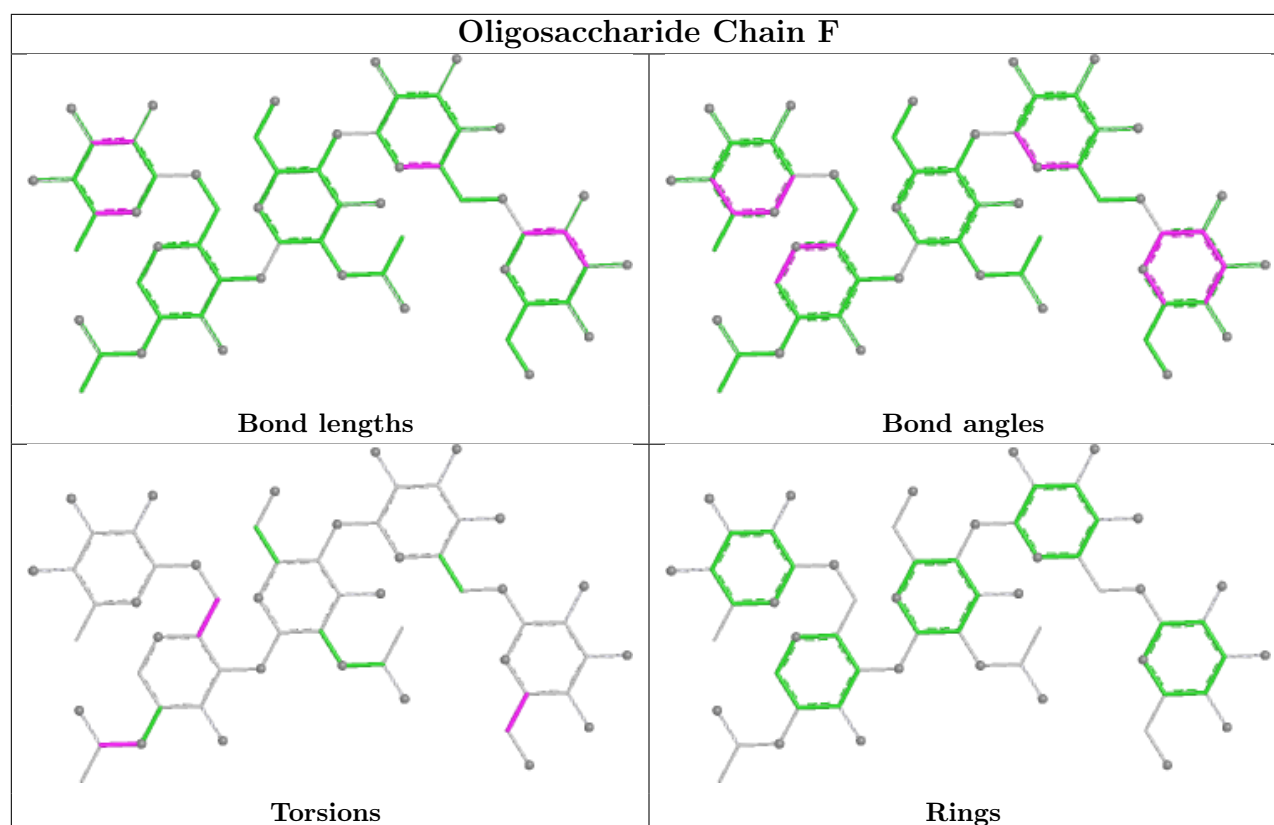
Mol	Chain	Res	Type	Atoms
2	D	3	BMA	C1-C2-C3-C4-C5-O5
2	E	4	MAN	C1-C2-C3-C4-C5-O5

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	NAG	1	0
2	F	3	BMA	1	0
2	F	4	MAN	2	0
2	E	3	BMA	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](#)

Of 23 ligands modelled in this entry, 16 are monoatomic - leaving 7 for Mogul analysis.

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$
6	TLA	A	315	-	9,9,9	0.97	0	12,12,12	1.68	4 (33%)
6	TLA	A	314	-	9,9,9	1.04	0	12,12,12	1.33	2 (16%)
3	MAN	C	301	-	11,11,12	0.78	0	15,15,17	1.00	2 (13%)
3	MAN	B	301	-	11,11,12	1.32	1 (9%)	15,15,17	1.03	1 (6%)
6	TLA	B	312	-	9,9,9	0.99	0	12,12,12	1.34	2 (16%)
7	EDO	C	311	-	3,3,3	0.55	0	2,2,2	0.86	0
3	MAN	A	301	-	11,11,12	1.01	1 (9%)	15,15,17	1.04	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
6	TLA	A	315	-	-	6/12/12/12	-
6	TLA	A	314	-	-	8/12/12/12	-
3	MAN	C	301	-	-	0/2/19/22	0/1/1/1
3	MAN	B	301	-	-	0/2/19/22	0/1/1/1
6	TLA	B	312	-	-	10/12/12/12	-
7	EDO	C	311	-	-	0/1/1/1	-
3	MAN	A	301	-	-	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	MAN	O5-C1	-3.53	1.37	1.43
3	A	301	MAN	O5-C1	-2.01	1.40	1.43

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	315	TLA	O11-C1-C2	2.98	121.59	113.31
3	C	301	MAN	C1-O5-C5	2.69	115.79	112.19
6	A	314	TLA	O41-C4-C3	2.65	120.68	113.31
6	B	312	TLA	O41-C4-C3	2.59	120.50	113.31
6	A	315	TLA	C3-C2-C1	2.57	115.53	109.82

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	314	TLA	C1-C2-C3-O3
6	A	314	TLA	O2-C2-C3-O3
6	A	314	TLA	O2-C2-C3-C4
6	A	315	TLA	C1-C2-C3-C4
6	A	315	TLA	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	314	TLA	2	0
3	C	301	MAN	1	0
3	B	301	MAN	2	0
6	B	312	TLA	1	0

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	210/219 (95%)	0.50	15 (7%) 22 22	24, 41, 72, 103	0
1	B	208/219 (94%)	0.62	17 (8%) 17 18	23, 41, 71, 92	0
1	C	210/219 (95%)	0.53	12 (5%) 29 29	23, 41, 71, 90	1 (0%)
All	All	628/657 (95%)	0.55	44 (7%) 22 22	23, 41, 72, 103	1 (0%)

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	213	GLU	4.9
1	C	43	ALA	4.5
1	A	43	ALA	4.5
1	A	216	HIS	4.4
1	A	212	LYS	4.2

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.

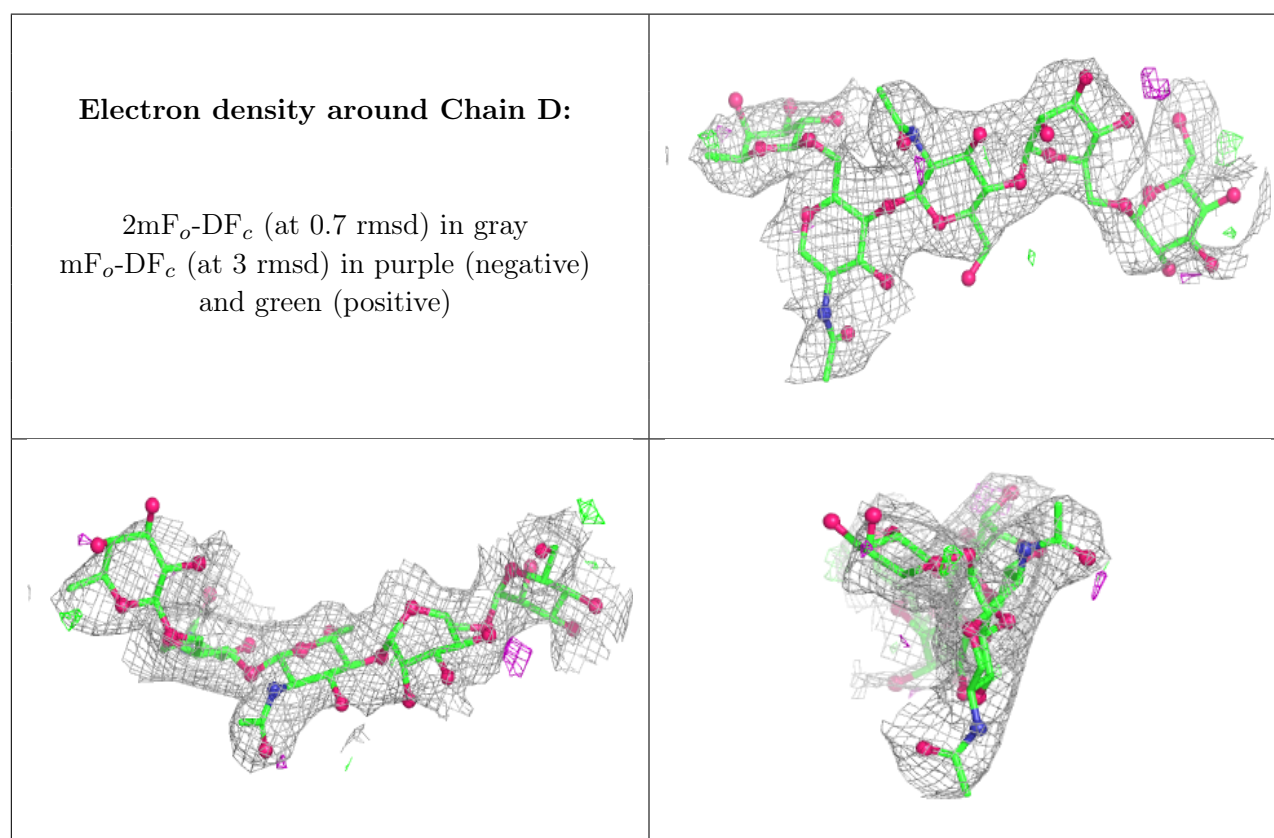
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MAN	D	4	11/12	0.43	0.24	60,99,105,110	0
2	MAN	E	4	11/12	0.55	0.20	58,84,101,102	0
2	MAN	F	4	11/12	0.66	0.17	75,88,101,106	0

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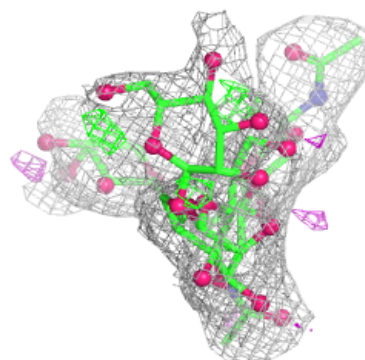
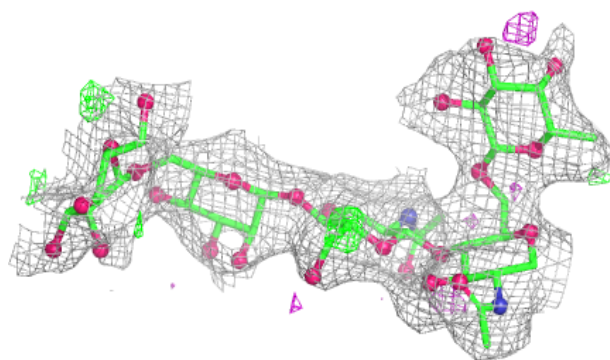
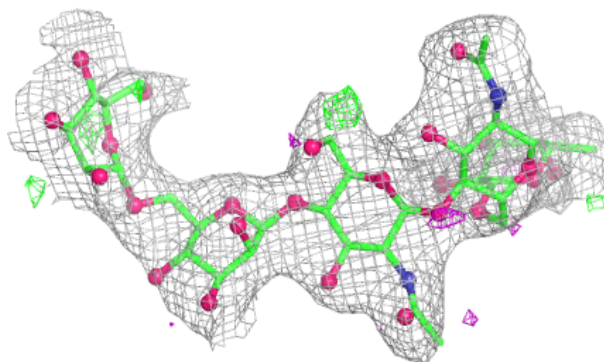
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BMA	F	3	11/12	0.67	0.17	63,78,87,88	0
2	FUC	D	5	10/11	0.76	0.22	63,72,97,99	0
2	BMA	D	3	11/12	0.78	0.14	67,75,91,92	0
2	FUC	E	5	10/11	0.78	0.17	40,56,69,76	0
2	FUC	F	5	10/11	0.82	0.16	49,73,86,97	0
2	NAG	E	2	14/15	0.86	0.13	32,41,49,56	0
2	BMA	E	3	11/12	0.87	0.13	46,65,81,83	0
2	NAG	D	2	14/15	0.88	0.13	46,56,76,82	0
2	NAG	F	2	14/15	0.89	0.12	38,57,68,69	0
2	NAG	E	1	14/15	0.90	0.11	27,46,50,53	0
2	NAG	F	1	14/15	0.92	0.10	33,43,59,65	0
2	NAG	D	1	14/15	0.93	0.10	40,47,61,78	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.

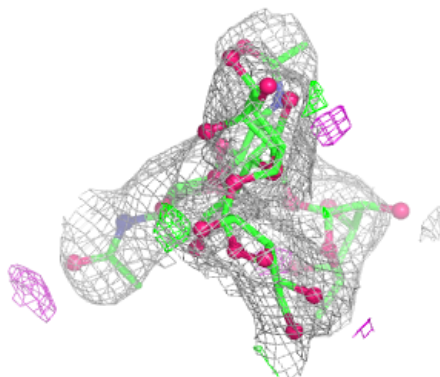
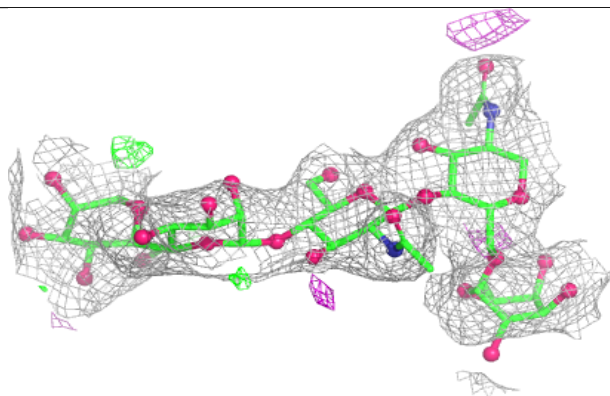
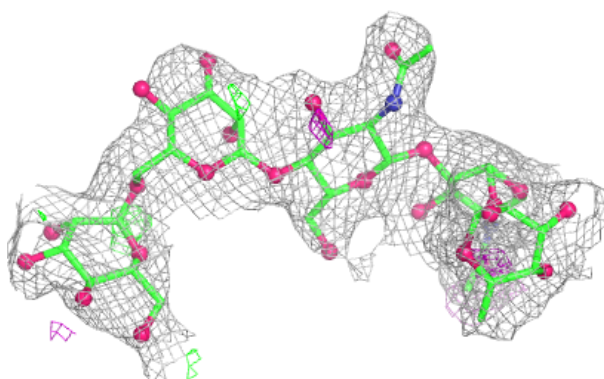


Electron density around Chain E:

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

**Electron density around Chain F:**

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



6.4 Ligands

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
5	CL	A	312	1/1	0.70	0.15	79,79,79,79	0
6	TLA	B	312	10/10	0.74	0.21	42,71,81,82	0
4	NA	C	307	1/1	0.79	0.17	43,43,43,43	0
5	CL	A	313	1/1	0.80	0.23	75,75,75,75	0
5	CL	B	311	1/1	0.80	0.14	68,68,68,68	0
4	NA	A	307	1/1	0.80	0.28	55,55,55,55	0
7	EDO	C	311	4/4	0.80	0.15	45,50,52,63	0
5	CL	B	310	1/1	0.82	0.20	78,78,78,78	0
5	CL	C	310	1/1	0.82	0.09	68,68,68,68	0
4	NA	A	308	1/1	0.83	0.23	50,50,50,50	0
5	CL	A	310	1/1	0.85	0.18	60,60,60,60	0
4	NA	C	308	1/1	0.85	0.21	50,50,50,50	0
6	TLA	A	315	10/10	0.86	0.15	49,67,75,78	0
3	MAN	A	301	11/12	0.86	0.12	39,47,52,65	0
3	MAN	B	301	11/12	0.86	0.12	29,38,45,46	0
5	CL	B	308	1/1	0.87	0.15	72,72,72,72	0
5	CL	B	307	1/1	0.88	0.16	63,63,63,63	0
6	TLA	A	314	10/10	0.89	0.25	50,59,70,72	0
4	NA	A	309	1/1	0.89	0.10	40,40,40,40	0
3	MAN	C	301	11/12	0.91	0.10	37,39,52,52	0
5	CL	A	311	1/1	0.92	0.11	68,68,68,68	0
5	CL	B	309	1/1	0.96	0.09	65,65,65,65	0
5	CL	C	309	1/1	0.98	0.10	53,53,53,53	0

6.5 Other polymers

There are no such residues in this entry.