



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 07:24 PM UTC

PDB ID : 8OG1 / pdb_00008og1
Title : Exostosin-like 3 apo enzyme
Authors : Sammon, D.; Hohenester, E.
Deposited on : 2023-03-17
Resolution : 1.58 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

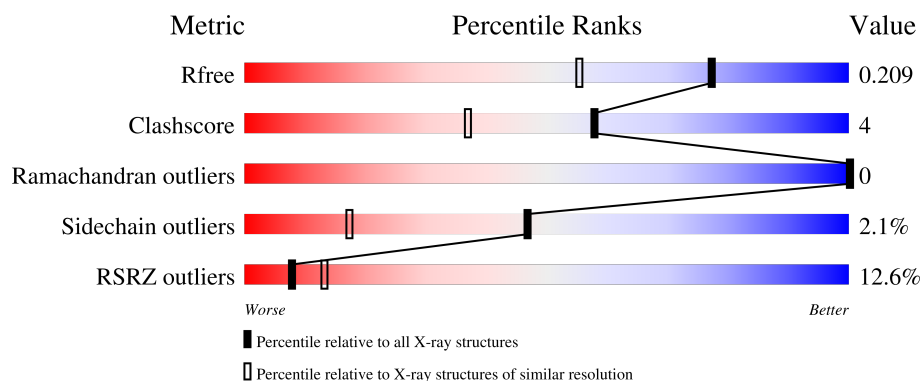
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	891	10% 71% 9% 20%
2	B	3	67% 33%
3	C	6	17% 67% 17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11911 atoms, of which 5720 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 Exostosin-like 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	715	Total	C	H	N	O	S	0	5	0
			11372	3716	5622	978	1024	32			

There are 23 discrepancies between the modelled and reference sequences:

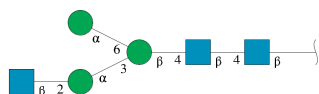
Chain	Residue	Modelled	Actual	Comment	Reference
A	29	ALA	-	expression tag	UNP O43909
A	30	PRO	-	expression tag	UNP O43909
A	31	LEU	-	expression tag	UNP O43909
A	32	VAL	-	expression tag	UNP O43909
A	33	HIS	-	expression tag	UNP O43909
A	34	HIS	-	expression tag	UNP O43909
A	35	HIS	-	expression tag	UNP O43909
A	36	HIS	-	expression tag	UNP O43909
A	37	HIS	-	expression tag	UNP O43909
A	38	HIS	-	expression tag	UNP O43909
A	39	ALA	-	expression tag	UNP O43909
A	40	LEU	-	expression tag	UNP O43909
A	41	ASP	-	expression tag	UNP O43909
A	42	GLU	-	expression tag	UNP O43909
A	43	ASN	-	expression tag	UNP O43909
A	44	LEU	-	expression tag	UNP O43909
A	45	TYR	-	expression tag	UNP O43909
A	46	PHE	-	expression tag	UNP O43909
A	47	GLN	-	expression tag	UNP O43909
A	48	GLY	-	expression tag	UNP O43909
A	49	ALA	-	expression tag	UNP O43909
A	50	LEU	-	expression tag	UNP O43909
A	51	ALA	-	expression tag	UNP O43909

- Molecule 2 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
2	B	3	Total	C	H	N	O	0	0	0
			73	22	34	2	15			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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	C	6	Total	C	H	N	O	0	0	0
			139	42	64	3	30			

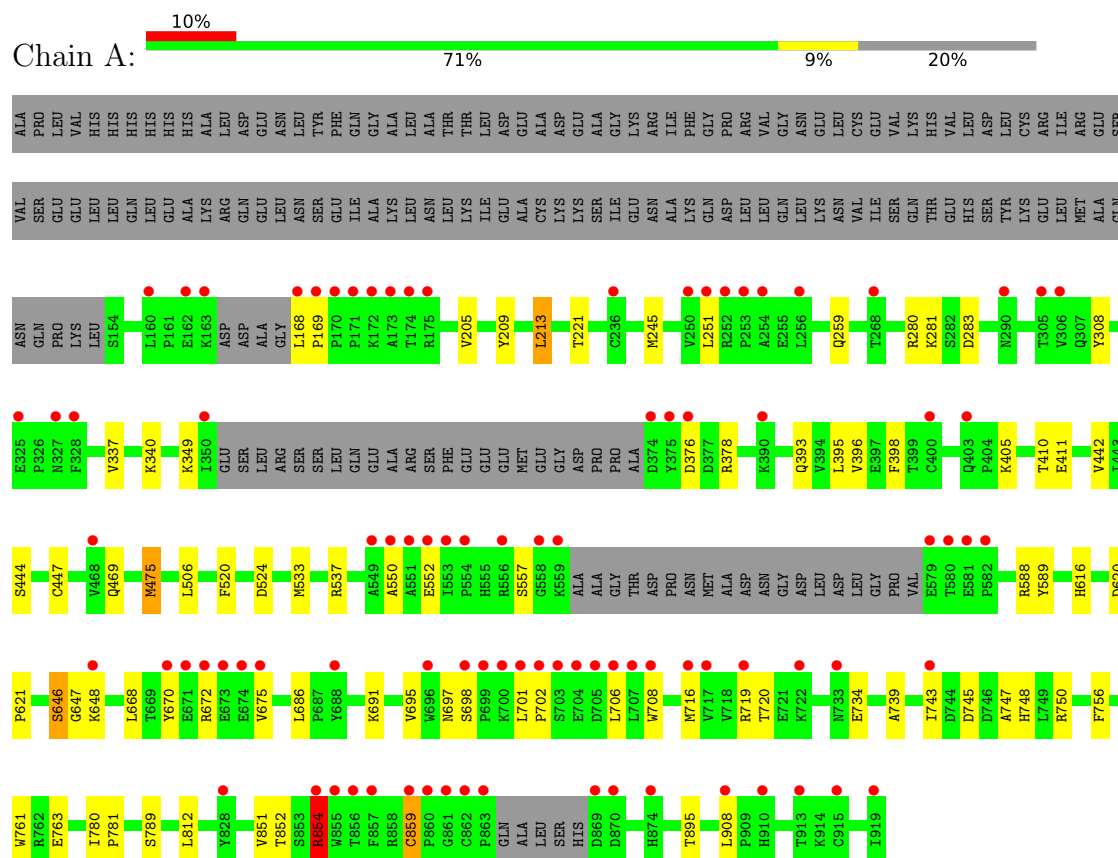
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	327	Total	O	0	0
			327	327		

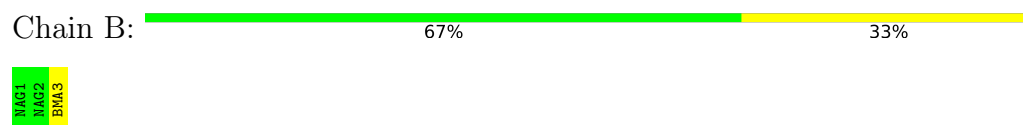
3 Residue-property plots

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.

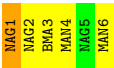
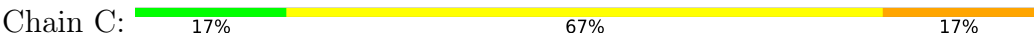
• Molecule 1: Exostosin-like 3



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



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	120.90Å 120.90Å 127.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.76 – 1.58 34.76 – 1.58	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.76-1.58) 99.9 (34.76-1.58)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 1.58Å)	Xtriage
Refinement program	PHENIX 1.18rc1_3769, PHENIX 1.18rc1_3769	Depositor
R, R_{free}	0.184 , 0.211 0.184 , 0.209	Depositor DCC
R_{free} test set	7425 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.267	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 33.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11911	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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, CSO, 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	0.47	0/5922	0.65	1/8064 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	854	ARG	NE-CZ-NH2	5.19	123.88	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	520	PHE	Peptide

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	5750	5622	5633	52	1
2	B	39	34	34	0	0
3	C	75	64	64	1	0
4	A	327	0	0	8	0
All	All	6191	5720	5731	52	1

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 4.

All (52) 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:A:851:VAL:HG12	1:A:852:THR:HG23	1.57	0.87
1:A:854:ARG:HH21	1:A:854:ARG:HG3	1.54	0.73
1:A:308:TYR:OH	4:A:1002:HOH:O	2.08	0.71
1:A:447[B]:CYS:SG	4:A:1288:HOH:O	2.50	0.69
1:A:698:SER:O	1:A:719:ARG:NH1	2.27	0.67
1:A:411:GLU:OE1	1:A:444:SER:OG	2.09	0.62
1:A:589:TYR:OH	4:A:1003:HOH:O	2.13	0.61
1:A:245:MET:HE1	1:A:251:LEU:HD23	1.85	0.59
1:A:205:VAL:HG21	1:A:259[B]:GLN:HG3	1.85	0.57
1:A:205:VAL:HG22	1:A:259[A]:GLN:HG2	1.86	0.57
1:A:395:LEU:C	1:A:395:LEU:HD23	2.32	0.55
1:A:283:ASP:OD2	1:A:405:LYS:HD3	2.09	0.52
1:A:337:VAL:HG22	1:A:506:LEU:HD22	1.90	0.52
1:A:550:ALA:HB3	1:A:734:GLU:CD	2.35	0.52
1:A:756:PHE:CE2	1:A:851:VAL:HG13	2.44	0.51
1:A:646:SER:OG	1:A:647:GLY:N	2.45	0.50
1:A:537:ARG:NH1	4:A:1006:HOH:O	2.30	0.50
1:A:620:ASP:OD1	1:A:621:PRO:HD2	2.12	0.50
1:A:763:GLU:CG	4:A:1044:HOH:O	2.59	0.50
1:A:280:ARG:NH2	1:A:281:LYS:HD2	2.27	0.49
1:A:745:ASP:OD2	4:A:1004:HOH:O	2.19	0.49
1:A:205:VAL:CG2	1:A:259[B]:GLN:HG3	2.43	0.49
1:A:209:TYR:CE2	1:A:251:LEU:HD13	2.49	0.48
1:A:763:GLU:HG2	4:A:1044:HOH:O	2.12	0.48
1:A:552:GLU:CG	1:A:716:MET:HE2	2.43	0.48
1:A:349:LYS:HE3	1:A:410:THR:O	2.14	0.48
1:A:550:ALA:HB3	1:A:734:GLU:OE1	2.14	0.47
1:A:475[A]:MET:HG3	1:A:533:MET:HG2	1.97	0.47
1:A:672:ARG:HB3	1:A:675:VAL:HG22	1.96	0.47
1:A:168:LEU:N	1:A:169:PRO:HD2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:701:LEU:HB3	1:A:702:PRO:CD	2.46	0.46
1:A:221:THR:HG23	1:A:524:ASP:OD1	2.16	0.45
1:A:743:ILE:CG1	1:A:747:ALA:HB3	2.47	0.45
1:A:550:ALA:HB3	1:A:734:GLU:OE2	2.18	0.44
1:A:557:SER:HA	1:A:708:TRP:O	2.18	0.43
1:A:670:TYR:CD1	1:A:698:SER:HA	2.54	0.43
1:A:697:ASN:OD1	1:A:720:THR:HG21	2.19	0.43
1:A:340:LYS:HE2	1:A:393:GLN:OE1	2.19	0.42
1:A:396:VAL:CG1	1:A:398:PHE:CZ	3.02	0.42
1:A:739:ALA:HB2	1:A:761:TRP:CZ3	2.53	0.42
1:A:789:SER:OG	3:C:1:NAG:H81	2.20	0.42
1:A:396:VAL:CG1	1:A:398:PHE:CE2	3.02	0.42
1:A:763:GLU:HG2	1:A:763:GLU:O	2.18	0.42
1:A:780:ILE:HB	1:A:781:PRO:HD3	2.01	0.41
1:A:748:HIS:NE2	1:A:859:CYS:HB3	2.35	0.41
1:A:706:LEU:HD12	1:A:706:LEU:HA	1.86	0.41
1:A:396:VAL:HG12	1:A:398:PHE:CE2	2.55	0.41
1:A:442:VAL:HG12	1:A:469:GLN:HB2	2.03	0.41
1:A:668:LEU:HD12	1:A:695:VAL:HB	2.02	0.41
1:A:588[B]:ARG:NH2	4:A:1015:HOH:O	2.54	0.40
1:A:213:LEU:HD12	1:A:213:LEU:HA	1.91	0.40
1:A:691:LYS:HD3	1:A:716:MET:HG3	2.04	0.40

All (1) 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:A:763:GLU:OE2	1:A:895:THR:HG1[6_555]	1.59	0.01

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	709/891 (80%)	682 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	625/785 (80%)	611 (98%)	14 (2%)	45	15

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	213	LEU
1	A	376	ASP
1	A	378	ARG
1	A	475[A]	MET
1	A	475[B]	MET
1	A	616	HIS
1	A	646	SER
1	A	648	LYS
1	A	686	LEU
1	A	750	ARG
1	A	812	LEU
1	A	854	ARG
1	A	859	CYS
1	A	908	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	277	ASN
1	A	403	GLN
1	A	733	ASN
1	A	872	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	CSO	A	606	1	3,6,7	0.93	0	1,6,8	0.61	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
1	CSO	A	606	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

9 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	B	1	2,1	14,14,15	0.55	0	17,19,21	0.67	0
2	NAG	B	2	2	14,14,15	0.53	0	17,19,21	0.43	0
2	BMA	B	3	2	11,11,12	1.26	2 (18%)	15,15,17	0.80	0
3	NAG	C	1	3,1	14,14,15	0.34	0	17,19,21	0.62	1 (5%)
3	NAG	C	2	3	14,14,15	0.84	1 (7%)	17,19,21	0.51	0
3	BMA	C	3	3	11,11,12	1.16	1 (9%)	15,15,17	0.87	0
3	MAN	C	4	3	11,11,12	1.23	1 (9%)	15,15,17	1.39	3 (20%)
3	NAG	C	5	3	14,14,15	0.24	0	17,19,21	0.53	0
3	MAN	C	6	3	11,11,12	1.16	1 (9%)	15,15,17	1.33	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
2	NAG	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	2/2/19/22	0/1/1/1
3	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	2/2/19/22	0/1/1/1
3	NAG	C	5	3	-	2/6/23/26	0/1/1/1
3	MAN	C	6	3	-	1/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	NAG	O5-C1	-2.80	1.39	1.43
2	B	3	BMA	C2-C3	2.75	1.56	1.52
3	C	6	MAN	C1-C2	2.63	1.58	1.52
3	C	3	BMA	O5-C1	-2.36	1.39	1.43
3	C	4	MAN	O6-C6	2.19	1.51	1.42
2	B	3	BMA	C1-C2	2.17	1.57	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	6	MAN	C1-O5-C5	4.10	117.68	112.19
3	C	4	MAN	O2-C2-C1	2.50	114.95	109.22
3	C	4	MAN	C1-C2-C3	-2.18	106.47	109.64
3	C	4	MAN	O2-C2-C3	-2.13	105.75	110.15
3	C	1	NAG	C1-O5-C5	2.00	114.87	112.19

There are no chirality outliers.

All (7) torsion outliers are listed below:

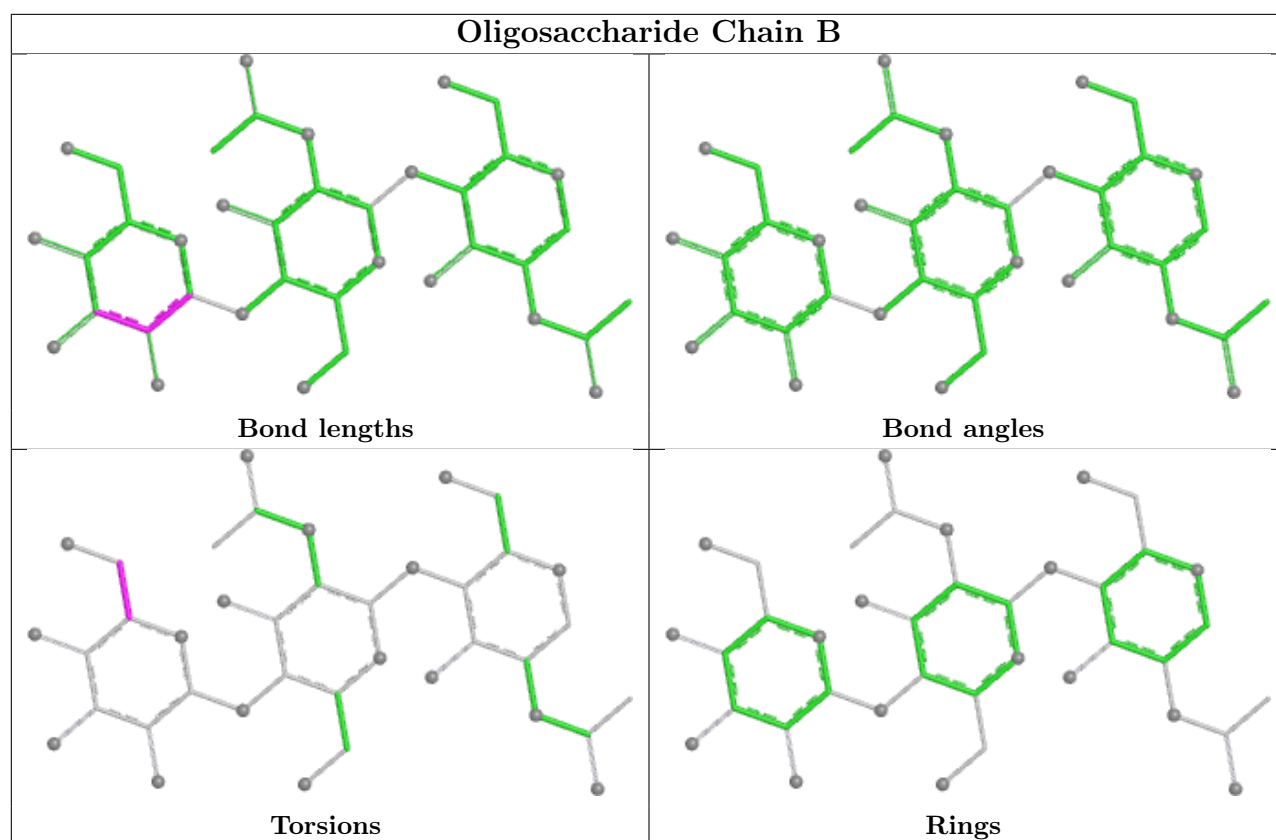
Mol	Chain	Res	Type	Atoms
3	C	5	NAG	C1-C2-N2-C7
3	C	4	MAN	C4-C5-C6-O6
3	C	4	MAN	O5-C5-C6-O6
2	B	3	BMA	C4-C5-C6-O6
3	C	5	NAG	O5-C5-C6-O6
2	B	3	BMA	O5-C5-C6-O6
3	C	6	MAN	O5-C5-C6-O6

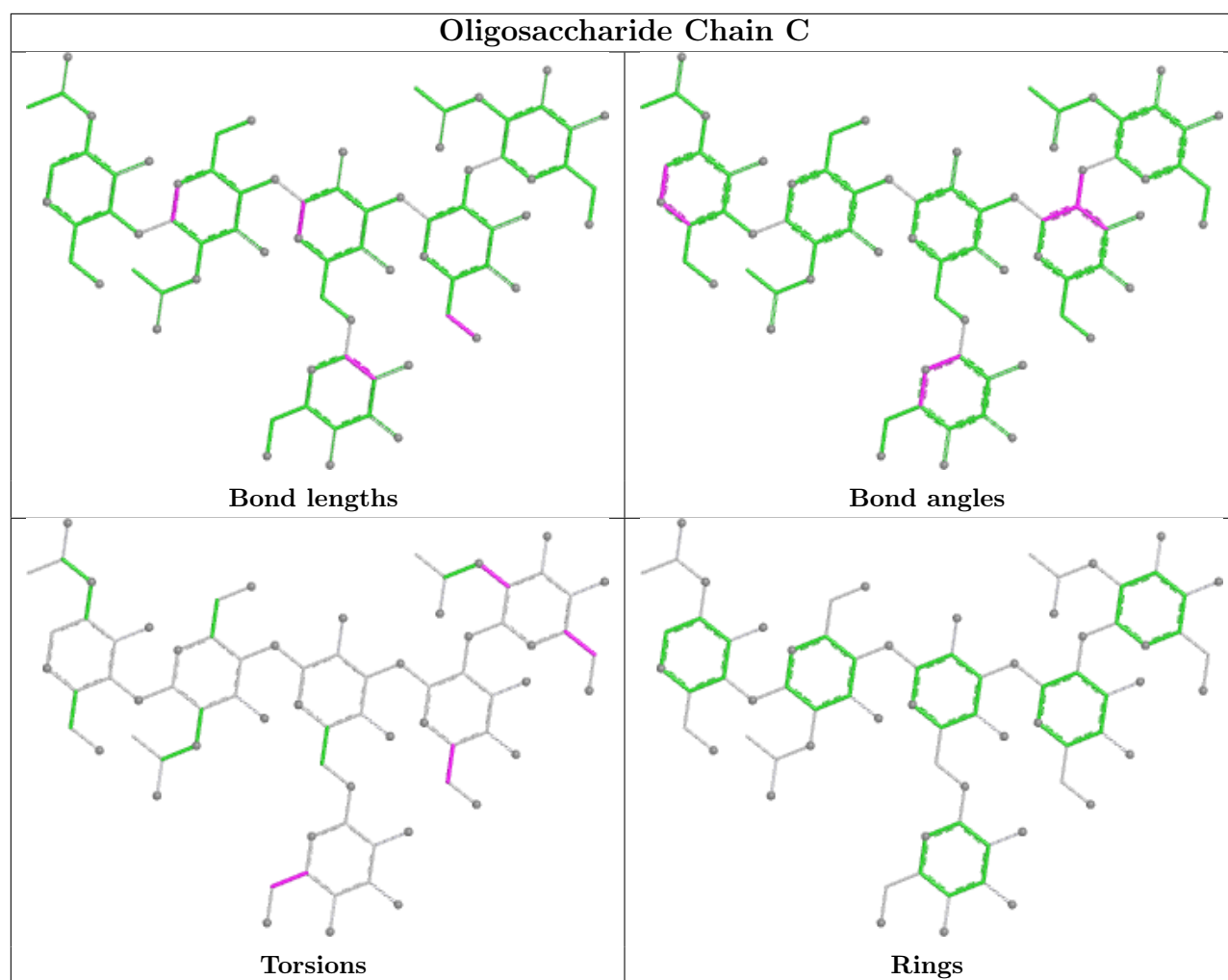
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	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

6.1 Protein, DNA and RNA chains

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	714/891 (80%)	0.57	90 (12%) 8 13	18, 34, 77, 113	5 (0%)

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	350	ILE	7.6
1	A	168	LEU	6.8
1	A	857	PHE	6.5
1	A	163	LYS	5.7
1	A	328	PHE	5.6
1	A	701	LEU	5.3
1	A	374	ASP	5.0
1	A	705	ASP	4.9
1	A	863	PRO	4.7
1	A	699	PRO	4.4
1	A	169	PRO	4.4
1	A	580	THR	4.4
1	A	162	GLU	4.2
1	A	706	LEU	4.2
1	A	172	LYS	4.2
1	A	559	LYS	4.2
1	A	250	VAL	4.2
1	A	675	VAL	4.1
1	A	550	ALA	3.9
1	A	861	GLY	3.7
1	A	251	LEU	3.7
1	A	549	ALA	3.7
1	A	551	ALA	3.7
1	A	160	LEU	3.7
1	A	707	LEU	3.7
1	A	170	PRO	3.6
1	A	855	TRP	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	254	ALA	3.5
1	A	670	TYR	3.4
1	A	327	ASN	3.4
1	A	579	GLU	3.3
1	A	700	LYS	3.3
1	A	703	SER	3.2
1	A	306	VAL	3.2
1	A	688	TYR	3.2
1	A	704	GLU	3.2
1	A	173	ALA	3.2
1	A	325	GLU	3.2
1	A	256	LEU	3.1
1	A	743	ILE	2.9
1	A	696	TRP	2.9
1	A	174	THR	2.9
1	A	252	ARG	2.8
1	A	553	ILE	2.8
1	A	558	GLY	2.8
1	A	919	ILE	2.8
1	A	722	LYS	2.7
1	A	582	PRO	2.7
1	A	672	ARG	2.7
1	A	719	ARG	2.7
1	A	581	GLU	2.7
1	A	305	THR	2.6
1	A	874	HIS	2.6
1	A	268	THR	2.6
1	A	716	MET	2.6
1	A	702	PRO	2.6
1	A	870	ASP	2.6
1	A	674	GLU	2.6
1	A	869	ASP	2.6
1	A	856	THR	2.5
1	A	862	CYS	2.5
1	A	671	GLU	2.4
1	A	648	LYS	2.4
1	A	859	CYS	2.4
1	A	698	SER	2.4
1	A	375	TYR	2.3
1	A	253	PRO	2.3
1	A	860	PRO	2.3
1	A	552	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	175	ARG	2.3
1	A	236	CYS	2.3
1	A	468	VAL	2.3
1	A	290	ASN	2.2
1	A	554	PRO	2.2
1	A	673	GLU	2.2
1	A	171	PRO	2.2
1	A	376	ASP	2.2
1	A	910	HIS	2.2
1	A	913	THR	2.1
1	A	708	TRP	2.1
1	A	908	LEU	2.1
1	A	717	VAL	2.1
1	A	733	ASN	2.1
1	A	915	CYS	2.1
1	A	556	ARG	2.1
1	A	390	LYS	2.0
1	A	400	CYS	2.0
1	A	854	ARG	2.0
1	A	403	GLN	2.0
1	A	828	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSO	A	606	7/8	0.98	0.06	19,24,31,37	0

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.

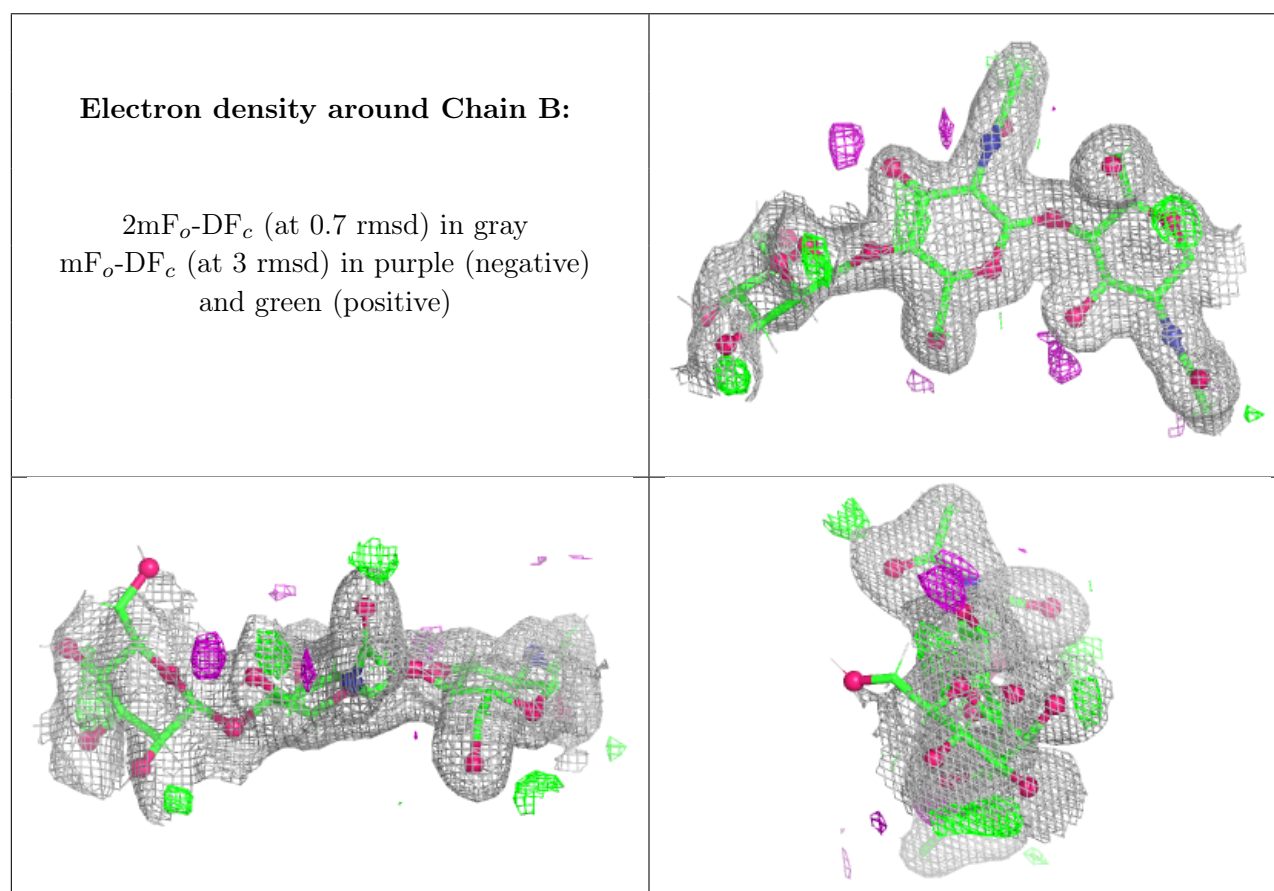
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	C	5	14/15	0.51	0.21	83,116,147,162	0

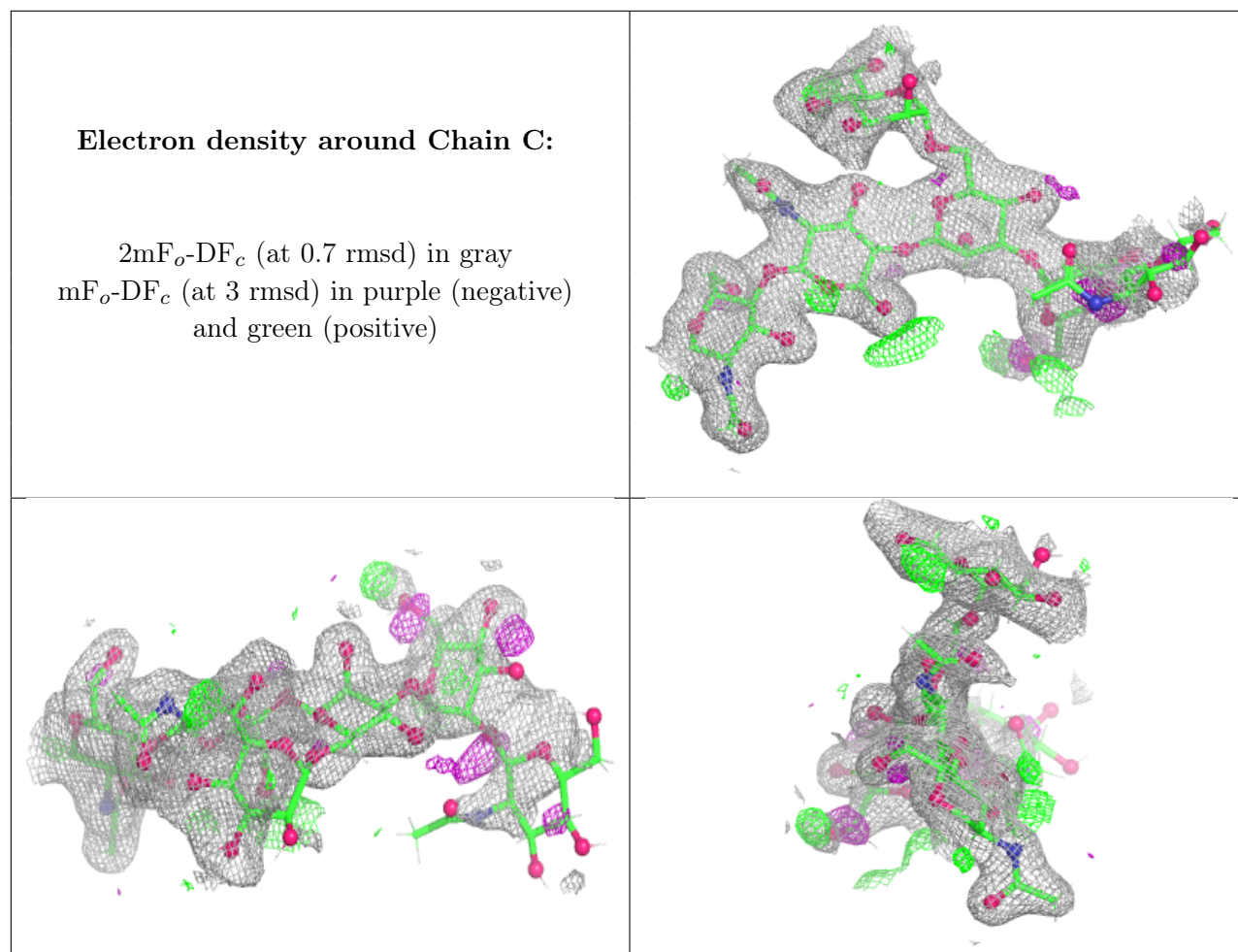
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BMA	B	3	11/12	0.63	0.16	77,99,128,129	0
3	MAN	C	6	11/12	0.70	0.15	60,82,101,121	0
3	MAN	C	4	11/12	0.73	0.20	44,65,99,102	0
2	NAG	B	2	14/15	0.88	0.12	39,57,81,84	0
3	BMA	C	3	11/12	0.90	0.10	43,53,71,72	0
3	NAG	C	2	14/15	0.93	0.10	34,47,59,68	0
3	NAG	C	1	14/15	0.94	0.09	32,39,45,48	0
2	NAG	B	1	14/15	0.96	0.07	26,34,44,44	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.





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.