



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:52 PM UTC

PDB ID : 7B7A / pdb_00007b7a
Title : ENDO-POLY GALACTURONASE FROM ARABIDOPSIS THALIANA
Authors : Safran, J.; Tabi, W.; Habrylo, O.; Bouckaert, J.; Lefebvre, V.; Senechal, F.; Pelloux, J.
Deposited on : 2020-12-10
Resolution : 1.30 Å (reported)

This is a Full wwPDB X-ray Structure Validation 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

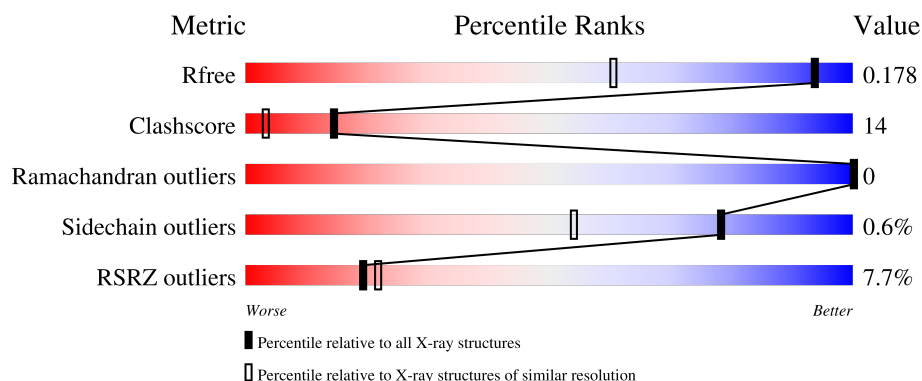
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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	1553 (1.30-1.30)
Clashscore	190562	1595 (1.30-1.30)
Ramachandran outliers	187476	1551 (1.30-1.30)
Sidechain outliers	187428	1551 (1.30-1.30)
RSRZ outliers	180081	1549 (1.30-1.30)

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	429	7% 73% 17% • 9%
2	C	2	100%
3	B	6	100%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6852 atoms, of which 3083 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 Pectin lyase-like superfamily protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	391	6108	1907	3023	529	624	25	0	42	0

There are 23 discrepancies between the modelled and reference sequences:

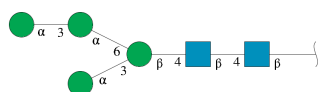
Chain	Residue	Modelled	Actual	Comment	Reference
A	407	PHE	-	expression tag	UNP Q9LYJ5
A	408	LEU	-	expression tag	UNP Q9LYJ5
A	409	GLU	-	expression tag	UNP Q9LYJ5
A	410	GLN	-	expression tag	UNP Q9LYJ5
A	411	LYS	-	expression tag	UNP Q9LYJ5
A	412	LEU	-	expression tag	UNP Q9LYJ5
A	413	ILE	-	expression tag	UNP Q9LYJ5
A	414	SER	-	expression tag	UNP Q9LYJ5
A	415	GLU	-	expression tag	UNP Q9LYJ5
A	416	GLU	-	expression tag	UNP Q9LYJ5
A	417	ASP	-	expression tag	UNP Q9LYJ5
A	418	LEU	-	expression tag	UNP Q9LYJ5
A	419	ASN	-	expression tag	UNP Q9LYJ5
A	420	SER	-	expression tag	UNP Q9LYJ5
A	421	ALA	-	expression tag	UNP Q9LYJ5
A	422	VAL	-	expression tag	UNP Q9LYJ5
A	423	ASP	-	expression tag	UNP Q9LYJ5
A	424	HIS	-	expression tag	UNP Q9LYJ5
A	425	HIS	-	expression tag	UNP Q9LYJ5
A	426	HIS	-	expression tag	UNP Q9LYJ5
A	427	HIS	-	expression tag	UNP Q9LYJ5
A	428	HIS	-	expression tag	UNP Q9LYJ5
A	429	HIS	-	expression tag	UNP Q9LYJ5

- Molecule 2 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
2	C	2	Total	C	H	N	O	0	0	0
			44	16	16	2	10			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	6	Total	C	H	N	O	0	0	0
			116	40	44	2	30			

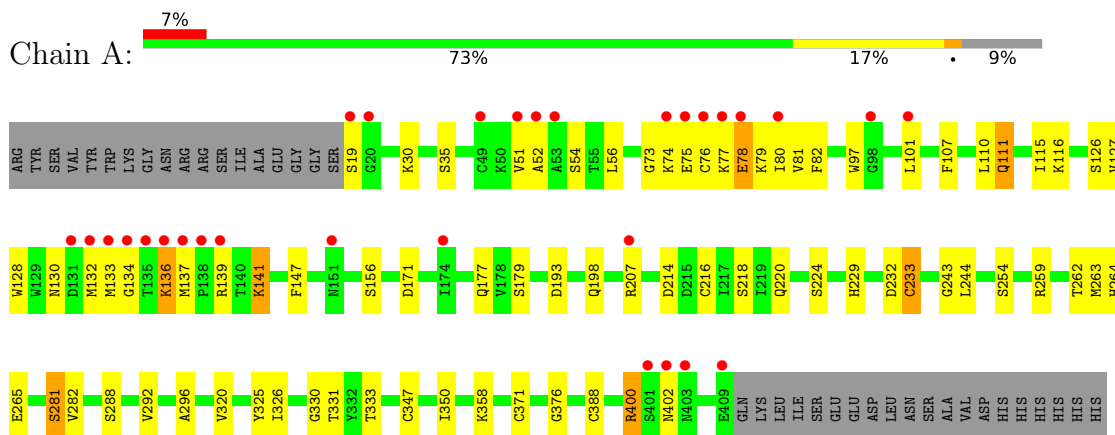
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	582	Total	O	0	2
			584	584		

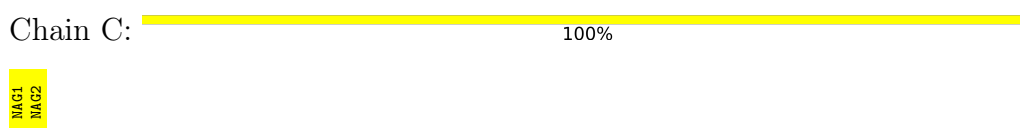
3 Residue-property plots [i](#)

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.

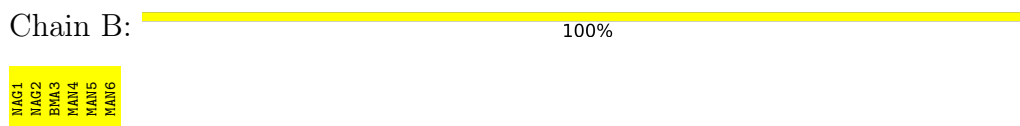
- Molecule 1: Pectin lyase-like superfamily protein



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.97Å 41.83Å 63.33Å 93.25° 99.86° 114.95°	Depositor
Resolution (Å)	34.50 – 1.30 34.50 – 1.30	Depositor EDS
% Data completeness (in resolution range)	96.1 (34.50-1.30) 96.2 (34.50-1.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 1.30Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.142 , 0.177 0.144 , 0.178	Depositor DCC
R_{free} test set	4184 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 56.1	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	0.98	EDS
Total number of atoms	6852	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.55% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, MAN, 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	0.63	1/3268 (0.0%)	0.88	4/4437 (0.1%)

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	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	141	LYS	C-O	-5.08	1.19	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	MET	CA-C-N	-9.61	109.93	121.85
1	A	133	MET	C-N-CA	-9.61	109.93	121.85
1	A	78	GLU	CA-C-O	-6.00	114.20	121.28
1	A	400	ARG	CB-CG-CD	5.13	123.10	111.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	111[A]	GLN	Mainchain
1	A	111[B]	GLN	Mainchain

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Mol	Chain	Res	Type	Group
1	A	233[B]	CYS	Mainchain
1	A	281[B]	SER	Mainchain

5.2 Too-close contacts

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	3085	3023	2846	88	1
2	C	28	16	25	0	0
3	B	72	44	61	0	0
4	A	584	0	0	12	3
All	All	3769	3083	2932	88	4

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 14.

All (88) 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:51:VAL:C	1:A:77:LYS:HE2	1.59	1.26
1:A:52:ALA:HA	1:A:77:LYS:CE	1.70	1.22
1:A:52:ALA:HA	1:A:77:LYS:NZ	1.56	1.18
1:A:52:ALA:N	1:A:77:LYS:HE2	1.58	1.18
1:A:51:VAL:HG13	1:A:54:SER:HB3	1.18	1.13
1:A:127:VAL:HA	1:A:132:MET:HE3	1.17	1.07
1:A:52:ALA:CA	1:A:77:LYS:HE2	1.85	1.06
1:A:52:ALA:CA	1:A:77:LYS:CE	2.42	0.95
1:A:78:GLU:OE1	1:A:111[B]:GLN:HG2	1.67	0.94
1:A:127:VAL:HA	1:A:132:MET:CE	2.00	0.91
1:A:51:VAL:O	1:A:77:LYS:HE2	1.71	0.90
1:A:51:VAL:CG1	1:A:54:SER:HB3	2.00	0.89
1:A:220[A]:GLN:NE2	4:A:501:HOH:O	2.04	0.84
1:A:30:LYS:HD2	1:A:35:SER:CB	2.07	0.84
1:A:51:VAL:C	1:A:77:LYS:CE	2.50	0.83
1:A:139:ARG:HD2	1:A:139:ARG:O	1.89	0.73
1:A:52:ALA:N	1:A:77:LYS:CE	2.46	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ALA:HA	1:A:77:LYS:HE2	1.48	0.72
1:A:259:ARG:NH1	4:A:509:HOH:O	2.22	0.72
1:A:52:ALA:HA	1:A:77:LYS:HZ1	1.51	0.72
1:A:51:VAL:O	1:A:77:LYS:CE	2.37	0.71
1:A:73:GLY:HA2	1:A:76:CYS:HB3	1.74	0.69
1:A:216:CYS:SG	1:A:233[B]:CYS:HB3	2.32	0.69
1:A:51:VAL:HG13	1:A:54:SER:CB	2.12	0.67
1:A:402:ASN:O	4:A:502:HOH:O	2.12	0.66
1:A:127:VAL:CA	1:A:132:MET:HE3	2.10	0.65
1:A:282[B]:VAL:CG2	1:A:320:VAL:HG22	2.28	0.64
1:A:126:SER:O	1:A:130:ASN:HB2	1.97	0.63
1:A:78:GLU:OE1	1:A:111[B]:GLN:CG	2.44	0.62
1:A:52:ALA:HA	1:A:77:LYS:HZ3	1.57	0.61
1:A:19:SER:N	4:A:518:HOH:O	2.36	0.59
1:A:282[B]:VAL:O	1:A:282[B]:VAL:HG23	2.02	0.59
1:A:81:VAL:HG11	1:A:116:LYS:HE2	1.87	0.56
1:A:232:ASP:OD1	1:A:262[A]:THR:OG1	2.23	0.56
1:A:82:PHE:HB3	1:A:115:ILE:HG13	1.87	0.56
1:A:30:LYS:HD2	1:A:35:SER:HB3	1.84	0.55
1:A:115:ILE:HD13	1:A:147:PHE:CZ	2.42	0.55
1:A:244:LEU:CD1	1:A:282[B]:VAL:CG1	2.85	0.55
1:A:198:GLN:OE1	4:A:503:HOH:O	2.18	0.55
1:A:193[C]:ASP:OD1	1:A:214:ASP:HB3	2.08	0.54
1:A:193[C]:ASP:OD1	1:A:193[C]:ASP:N	2.38	0.54
1:A:259:ARG:HA	1:A:288[A]:SER:O	2.09	0.53
1:A:281[A]:SER:OG	1:A:402:ASN:HB3	2.09	0.52
1:A:265:GLU:OE1	4:A:505:HOH:O	2.19	0.52
1:A:111[B]:GLN:HG2	4:A:521:HOH:O	2.09	0.51
1:A:75:GLU:O	1:A:75:GLU:HG2	2.12	0.50
1:A:134:GLY:C	1:A:136:LYS:H	2.20	0.50
1:A:171[B]:ASP:OD1	4:A:507:HOH:O	2.20	0.50
1:A:115:ILE:HD13	1:A:147:PHE:HZ	1.77	0.49
1:A:282[B]:VAL:HG21	1:A:320:VAL:HG22	1.96	0.47
1:A:107:PHE:HB3	1:A:110:LEU:HD12	1.95	0.47
1:A:220[A]:GLN:NE2	1:A:243:GLY:O	2.41	0.46
1:A:218[B]:SER:OG	1:A:220[B]:GLN:OE1	2.33	0.46
1:A:229:HIS:HA	1:A:259:ARG:O	2.17	0.45
1:A:156:SER:HA	1:A:179:SER:O	2.17	0.45
1:A:347[C]:CYS:SG	1:A:350:ILE:HD11	2.57	0.45
1:A:51:VAL:CG1	1:A:54:SER:CB	2.84	0.45
1:A:52:ALA:HB2	1:A:77:LYS:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:LYS:HG3	1:A:75:GLU:N	2.32	0.45
1:A:78:GLU:O	1:A:79:LYS:HB2	2.17	0.44
1:A:224[A]:SER:HA	1:A:254:SER:O	2.18	0.44
1:A:139:ARG:HD2	1:A:139:ARG:C	2.40	0.44
1:A:244:LEU:CD1	1:A:282[A]:VAL:CG2	2.96	0.43
1:A:76:CYS:SG	1:A:80:ILE:CD1	3.06	0.43
1:A:97:TRP:O	1:A:101:LEU:HD22	2.18	0.43
1:A:350:ILE:O	1:A:376:GLY:HA3	2.18	0.43
1:A:371:CYS:HB2	1:A:388[A]:CYS:HB2	1.98	0.43
1:A:137:MET:CG	1:A:141:LYS:HE3	2.49	0.43
1:A:136:LYS:NZ	4:A:542:HOH:O	2.52	0.43
1:A:177:GLN:HG2	4:A:538:HOH:O	2.19	0.43
1:A:77:LYS:HG2	1:A:78:GLU:N	2.33	0.42
1:A:128:TRP:HB3	1:A:141:LYS:HD3	2.01	0.42
1:A:224[B]:SER:HA	1:A:254:SER:O	2.19	0.42
1:A:288[A]:SER:HA	1:A:326:ILE:O	2.20	0.42
1:A:296:ALA:HA	1:A:333:THR:OG1	2.20	0.42
1:A:263:MET:HE2	1:A:263:MET:HB3	1.79	0.42
1:A:30:LYS:HD2	1:A:35:SER:HB2	1.95	0.42
1:A:244:LEU:CD1	1:A:282[B]:VAL:HG11	2.50	0.41
1:A:292:VAL:O	1:A:330:GLY:HA3	2.20	0.41
1:A:282[B]:VAL:CG2	1:A:282[B]:VAL:O	2.66	0.41
1:A:282[B]:VAL:HG22	1:A:320:VAL:HG22	2.00	0.41
1:A:331:THR:HA	1:A:358:LYS:O	2.21	0.40
1:A:262[B]:THR:HG23	4:A:644:HOH:O	2.21	0.40
1:A:402:ASN:OD1	4:A:508:HOH:O	2.22	0.40
1:A:56:LEU:C	1:A:56:LEU:HD23	2.46	0.40

All (4) 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:134:GLY:CA	1:A:207:ARG:NH1[1_655]	2.08	0.12
4:A:612:HOH:O	4:A:845:HOH:O[1_455]	2.08	0.12
4:A:669:HOH:O	4:A:853:HOH:O[1_455]	2.12	0.08
4:A:742:HOH:O	4:A:962:HOH:O[1_655]	2.14	0.06

5.3 Torsion angles

5.3.1 Protein backbone

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	432/429 (101%)	406 (94%)	26 (6%)	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	368/360 (102%)	366 (100%)	2 (0%)	81	60

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	LYS
1	A	264	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	ASN
1	A	177	GLN
1	A	227	ASN
1	A	229	HIS
1	A	297	ASN
1	A	402	ASN

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
3	NAG	B	1	3,1	14,14,15	1.48	2 (14%)	17,19,21	1.47	4 (23%)
3	NAG	B	2	3	14,14,15	1.14	2 (14%)	17,19,21	1.06	1 (5%)
3	BMA	B	3	3	11,11,12	1.06	1 (9%)	15,15,17	1.23	2 (13%)
3	MAN	B	4	3	11,11,12	0.75	0	15,15,17	1.67	4 (26%)
3	MAN	B	5	3	11,11,12	0.91	0	15,15,17	0.97	1 (6%)
3	MAN	B	6	3	11,11,12	0.77	0	15,15,17	1.55	3 (20%)
2	NAG	C	1	2,1	14,14,15	1.05	0	17,19,21	1.55	3 (17%)
2	NAG	C	2	2	14,14,15	1.35	2 (14%)	17,19,21	1.68	4 (23%)

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	B	6	3	-	2/2/19/22	0/1/1/1
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	NAG	O7-C7	-3.28	1.15	1.23
2	C	2	NAG	C1-C2	3.02	1.56	1.52
2	C	2	NAG	O7-C7	-2.94	1.16	1.23
3	B	2	NAG	O7-C7	-2.70	1.17	1.23
3	B	3	BMA	O5-C1	-2.14	1.40	1.43
3	B	1	NAG	C1-C2	-2.12	1.49	1.52
3	B	2	NAG	O5-C1	-2.08	1.40	1.43

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	4	MAN	O2-C2-C1	4.22	118.88	109.22
2	C	2	NAG	C8-C7-N2	3.85	122.50	116.12
2	C	1	NAG	O5-C1-C2	-3.64	105.67	111.29
3	B	6	MAN	C2-C3-C4	-3.42	104.84	110.86
2	C	2	NAG	O4-C4-C3	-3.19	102.87	110.38
3	B	1	NAG	C1-C2-N2	-3.02	105.67	110.43
3	B	5	MAN	C1-O5-C5	2.65	115.74	112.19
3	B	1	NAG	O4-C4-C3	-2.62	104.19	110.38
3	B	4	MAN	O4-C4-C3	-2.59	104.28	110.38
3	B	1	NAG	C2-N2-C7	-2.54	119.50	122.90
2	C	2	NAG	O7-C7-C8	-2.44	117.71	122.05
3	B	4	MAN	O2-C2-C3	-2.37	105.25	110.15
3	B	3	BMA	O5-C1-C2	-2.35	105.18	110.79
3	B	3	BMA	C1-O5-C5	2.35	115.33	112.19
3	B	1	NAG	C8-C7-N2	-2.30	112.30	116.12
2	C	1	NAG	C2-N2-C7	-2.15	120.02	122.90
3	B	2	NAG	O3-C3-C2	-2.14	104.95	109.40
3	B	6	MAN	O3-C3-C2	2.10	114.33	110.05
2	C	1	NAG	O6-C6-C5	-2.08	104.25	111.33
2	C	2	NAG	C2-N2-C7	-2.08	120.11	122.90
3	B	4	MAN	O6-C6-C5	-2.04	104.37	111.33
3	B	6	MAN	O5-C5-C6	2.03	111.61	107.66

There are no chirality outliers.

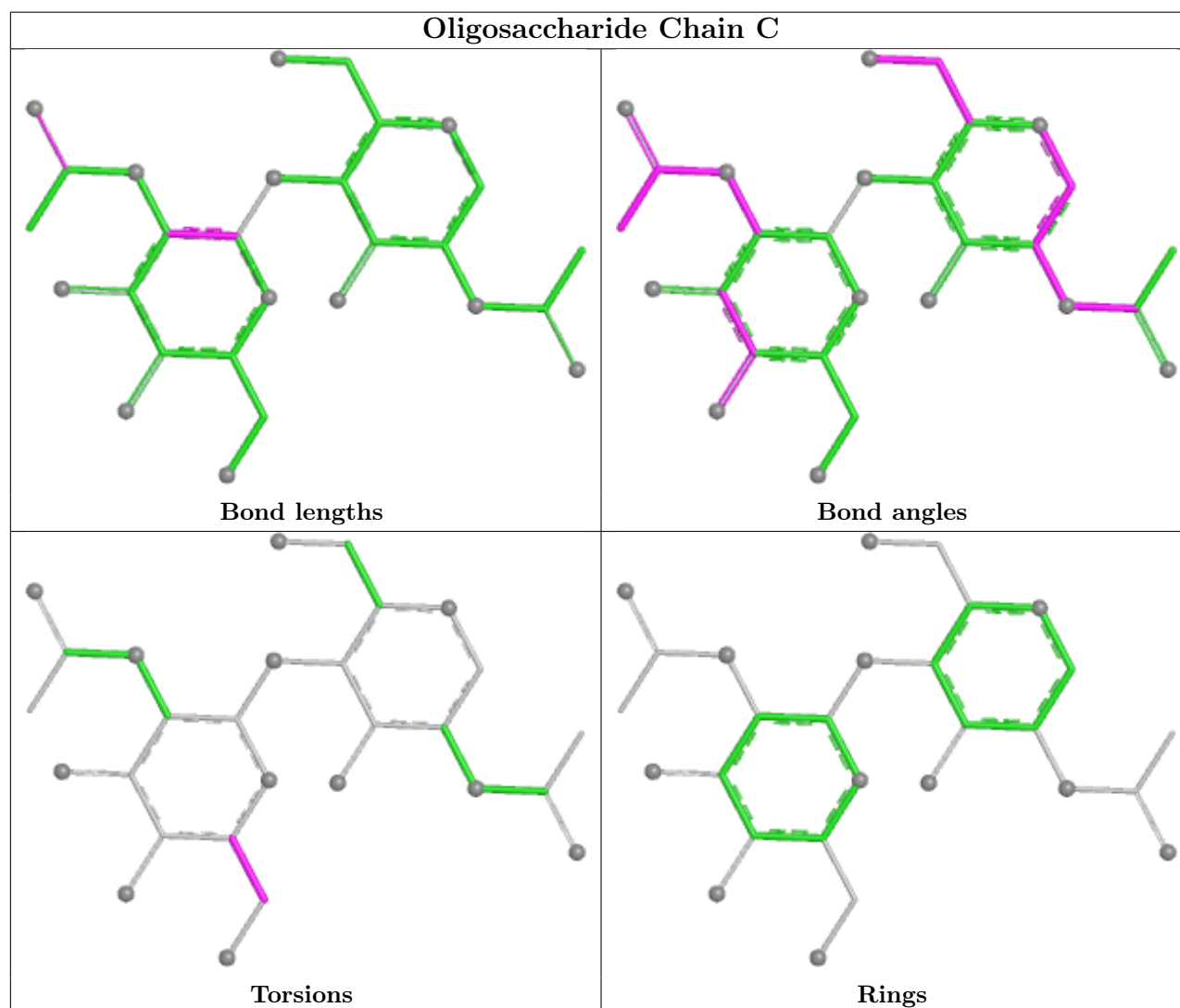
All (6) torsion outliers are listed below:

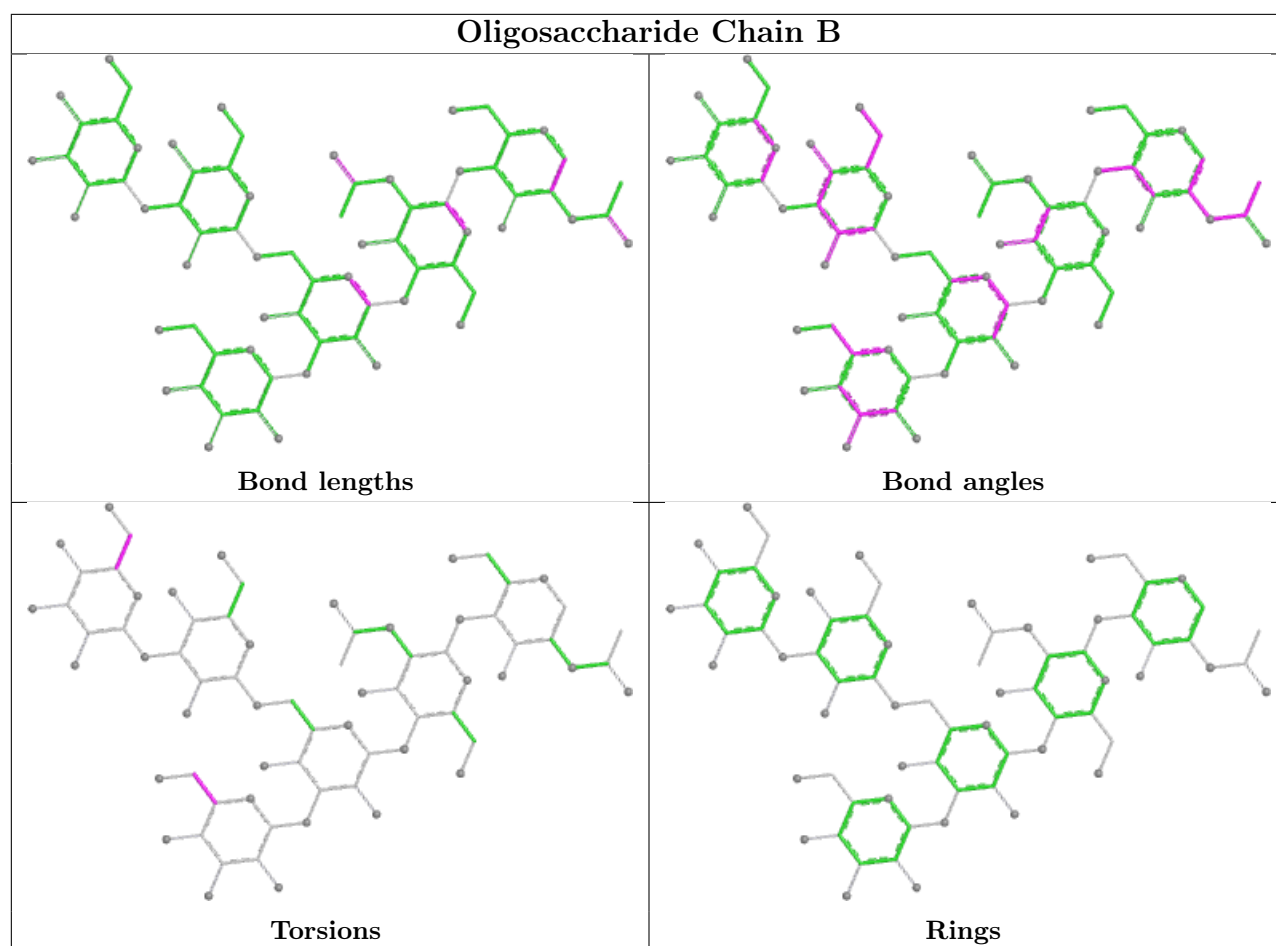
Mol	Chain	Res	Type	Atoms
3	B	6	MAN	O5-C5-C6-O6
3	B	6	MAN	C4-C5-C6-O6
3	B	5	MAN	C4-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
3	B	5	MAN	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	391/429 (91%)	0.33	30 (7%)	19 22	6, 20, 56, 141	28 (7%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	402	ASN	7.2
1	A	138	PRO	6.6
1	A	134	GLY	6.5
1	A	135	THR	6.3
1	A	53	ALA	5.9
1	A	132	MET	5.8
1	A	74	LYS	4.9
1	A	403	ASN	4.8
1	A	77	LYS	4.6
1	A	136	LYS	4.4
1	A	51	VAL	4.4
1	A	52	ALA	4.4
1	A	137	MET	4.0
1	A	401	SER	3.8
1	A	133	MET	3.7
1	A	139	ARG	3.6
1	A	76	CYS	3.5
1	A	98	GLY	3.4
1	A	207	ARG	3.2
1	A	78	GLU	3.1
1	A	131	ASP	3.0
1	A	174	ILE	2.8
1	A	101	LEU	2.6
1	A	80	ILE	2.4
1	A	19	SER	2.2
1	A	409	GLU	2.1
1	A	75	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	49	CYS	2.0
1	A	151	ASN	2.0
1	A	20	GLY	2.0

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](#)

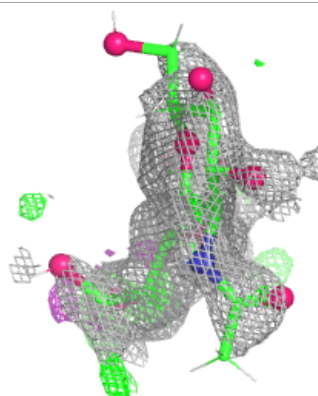
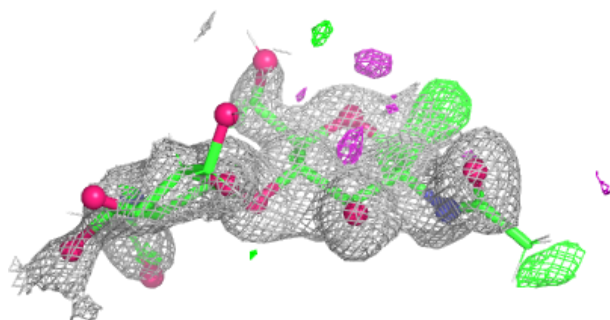
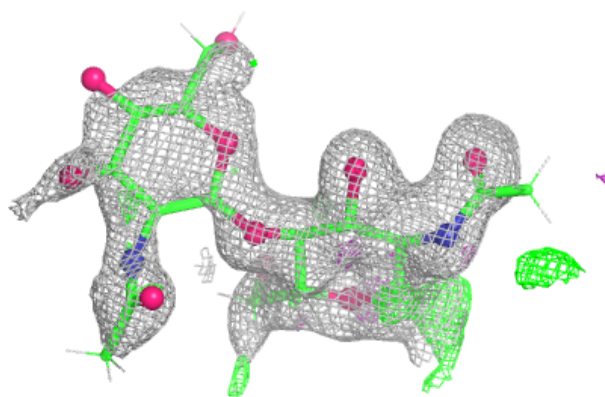
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NAG	B	2	14/15	0.79	0.20	15,20,32,43	0
3	NAG	B	1	14/15	0.88	0.17	15,20,36,36	0
2	NAG	C	2	14/15	0.94	0.09	53,102,141,151	22
2	NAG	C	1	14/15	0.96	0.07	26,60,90,97	0
3	BMA	B	3	11/12	-	-	32,76,137,137	0
3	MAN	B	4	11/12	-	-	33,44,90,105	0
3	MAN	B	5	11/12	-	-	44,82,113,122	0
3	MAN	B	6	11/12	-	-	48,62,87,104	19

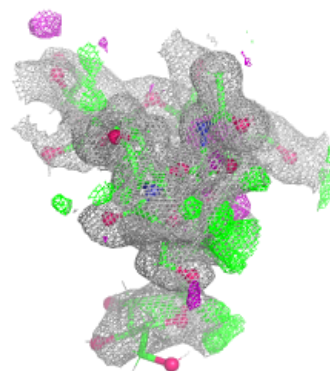
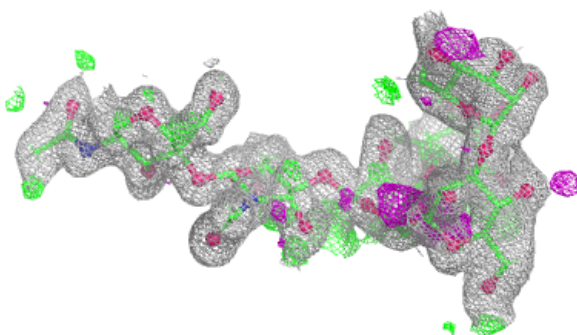
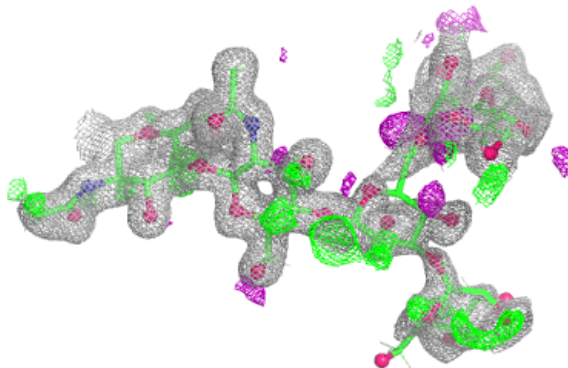
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

**Electron density around Chain B:**

$2mF_o-DF_c$ (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.