



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2025 – 08:10 AM EDT

PDB ID : 9N3S / pdb\_00009n3s  
Title : Crystal structure of the fungal mannosyltransferase Och1 reveals active site primed for N-glycan binding  
Authors : Kelly, E.T.R.; Rodionov, D.; Berghuis, A.M.  
Deposited on : 2025-01-31  
Resolution : 2.01 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

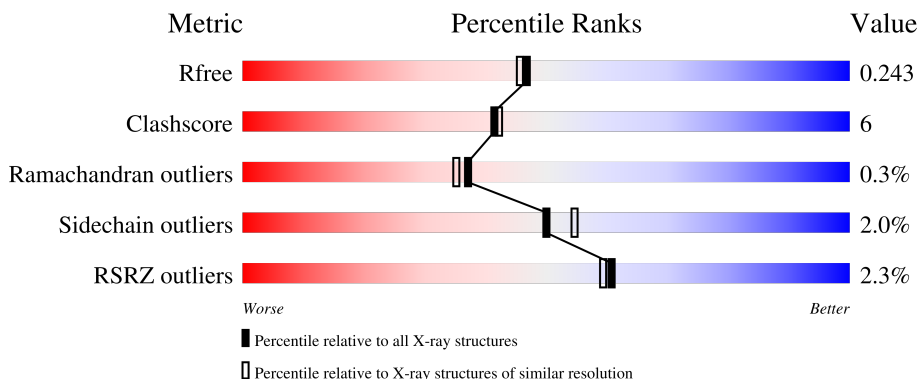
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


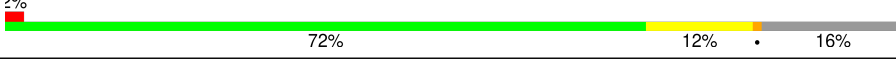
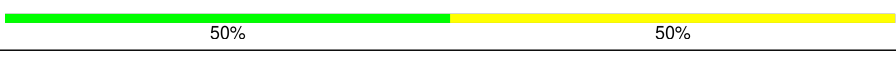

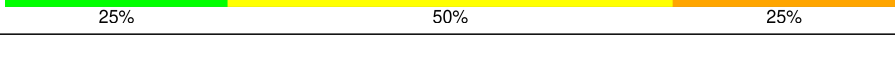
The reported resolution of this entry is 2.01 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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  $\geq 3$ , 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	431	
1	B	431	
2	C	2	
3	D	5	
4	E	4	

## 2 Entry composition [i](#)

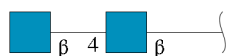
There are 6 unique types of molecules in this entry. The entry contains 6190 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Initiation-specific alpha-1,6-mannosyltransferase.

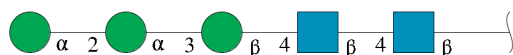
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	0	0
			2931	1888	484	547	12			
1	B	362	Total	C	N	O	S	0	0	0
			2881	1859	472	539	11			

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



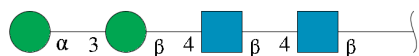
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-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	D	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is an oligosaccharide called 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
4	E	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	135	Total	O	0	0
			135	135		
6	B	90	Total	O	0	0
			90	90		





- Molecule 3: alpha-D-mannopyranose-(1-2)-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



- Molecule 4: 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, $\alpha$ , $\beta$ , $\gamma$	43.45Å 57.09Å 84.09Å 85.57° 75.31° 75.13°	Depositor
Resolution (Å)	24.46 – 2.01 24.46 – 2.01	Depositor EDS
% Data completeness (in resolution range)	89.8 (24.46-2.01) 89.7 (24.46-2.01)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.17 (at 2.01Å)	Xtriage
Refinement program	PHENIX DEV_4694	Depositor
R, $R_{free}$	0.198 , 0.243 0.198 , 0.243	Depositor DCC
$R_{free}$ test set	1999 reflections (3.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.006 for -h,-k,-h+l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6190	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.38	0/3009	0.54	0/4100
1	B	0.31	0/2954	0.50	0/4019
All	All	0.35	0/5963	0.52	0/8119

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

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	2931	0	2837	43	0
1	B	2881	0	2802	33	0
2	C	28	0	25	1	0
3	D	61	0	52	0	0
4	E	50	0	43	1	0
5	B	14	0	13	0	0
6	A	135	0	0	2	0
6	B	90	0	0	3	0
All	All	6190	0	5772	74	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.



All (74) 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:147:GLU:HA	1:A:157:ILE:HD13	1.64	0.79
1:A:354:GLU:OE1	6:A:501:HOH:O	2.06	0.74
1:A:126:GLY:HA3	1:B:122:LYS:HE3	1.79	0.64
1:B:51:THR:C	1:B:52:LEU:HG	2.22	0.63
1:B:149:LEU:O	6:B:601:HOH:O	2.16	0.60
1:A:52:LEU:HG	1:A:53:LEU:N	2.17	0.59
1:B:158:GLN:O	1:B:162:LEU:HD23	2.03	0.58
1:B:103:THR:HG21	1:B:173:LEU:HD21	1.87	0.56
1:B:239:VAL:HB	1:B:267:GLN:HB3	1.87	0.56
1:B:96:ILE:H	1:B:235:GLN:NE2	2.02	0.56
1:B:256:ALA:HA	1:B:340:MET:HE3	1.86	0.56
1:B:256:ALA:HB2	1:B:340:MET:HG2	1.89	0.55
1:A:278:LEU:HD21	1:A:348:PHE:HA	1.88	0.55
1:A:259:ILE:HG21	1:A:353:PHE:HE2	1.73	0.54
1:A:454:SER:OG	1:B:462:LYS:HE2	2.08	0.53
1:B:94:ALA:HB2	6:B:607:HOH:O	2.08	0.53
1:B:402:LYS:HE2	1:B:403:PHE:CZ	2.43	0.53
1:B:222:SER:HB2	1:B:227:LEU:HD11	1.90	0.53
1:A:119:THR:HB	6:A:523:HOH:O	2.09	0.52
1:A:68:ILE:HD13	1:A:82:ASP:OD2	2.09	0.52
1:A:278:LEU:HD11	1:A:348:PHE:CD1	2.44	0.52
4:E:2:NAG:O3	4:E:3:BMA:H2	2.10	0.52
1:B:147:GLU:OE2	1:B:161:LYS:NZ	2.31	0.52
1:B:58:HIS:ND1	1:B:308:ASP:OD2	2.44	0.51
1:B:77:LEU:HD13	1:B:82:ASP:HB3	1.93	0.51
1:A:356:MET:HG2	1:A:431:VAL:HG11	1.94	0.50
1:A:65:LYS:HG3	1:A:359:VAL:HG12	1.92	0.50
1:A:278:LEU:HD11	1:A:348:PHE:HD1	1.77	0.49
1:B:230:ASP:O	1:B:233:SER:HB3	2.12	0.49
1:A:184:ILE:HD11	1:A:196:ILE:HG21	1.95	0.49
1:A:219:TYR:CE1	1:A:222:SER:HB3	2.47	0.49
1:B:258:ARG:NH2	6:B:602:HOH:O	2.46	0.49
1:A:246:PRO:HB3	1:A:259:ILE:HG12	1.95	0.48
1:A:239:VAL:HB	1:A:267:GLN:HB3	1.96	0.48
1:A:103:THR:HG22	1:A:185:TYR:OH	2.14	0.48
1:A:246:PRO:HB2	1:A:419:TRP:CE3	2.49	0.48
1:A:462:LYS:HD3	1:A:464:MET:SD	2.54	0.48
1:B:441:SER:HA	1:B:458:MET:O	2.14	0.48
1:A:81:ARG:HA	1:A:280:LEU:HD21	1.95	0.47
1:A:253:GLU:OE1	1:A:256:ALA:HA	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:MET:HE2	1:B:431:VAL:HB	1.96	0.47
1:B:167:ILE:HG23	1:B:339:ILE:HD12	1.97	0.47
1:A:441:SER:HA	1:A:458:MET:O	2.15	0.46
1:B:219:TYR:CE1	1:B:222:SER:HB3	2.50	0.46
1:A:119:THR:HG21	1:B:192:LEU:O	2.15	0.45
1:A:77:LEU:O	1:A:83:GLN:NE2	2.41	0.45
1:A:228:SER:OG	1:A:230:ASP:OD1	2.31	0.45
1:A:150:TYR:HB2	1:A:157:ILE:HG12	1.99	0.45
1:B:197:ASP:HA	1:B:202:GLN:HG2	1.99	0.45
1:A:347:ILE:O	1:A:351:ILE:HG12	2.17	0.45
1:A:372:ASN:O	1:A:401:ARG:HB2	2.17	0.44
1:B:118:ARG:O	1:B:122:LYS:HG2	2.18	0.44
1:B:352:ILE:O	1:B:356:MET:HG3	2.18	0.44
1:B:157:ILE:HG22	1:B:161:LYS:HE3	2.00	0.43
1:A:273:PRO:O	1:A:277:GLU:HG2	2.18	0.43
1:B:159:ALA:O	1:B:286:THR:HG21	2.19	0.43
1:B:103:THR:HG21	1:B:173:LEU:CD2	2.49	0.42
1:A:259:ILE:HG21	1:A:353:PHE:CE2	2.53	0.42
1:A:246:PRO:HG3	1:A:259:ILE:HD11	2.01	0.42
1:A:158:GLN:O	1:A:162:LEU:HG	2.19	0.42
1:A:120:TYR:CZ	1:A:464:MET:HG3	2.55	0.42
1:A:445:ASP:OD2	1:A:462:LYS:HE2	2.20	0.42
1:A:142:ILE:HD12	1:A:173:LEU:HD21	2.02	0.42
1:B:339:ILE:H	1:B:339:ILE:HG12	1.64	0.41
1:B:211:ILE:HG12	1:B:229:SER:O	2.21	0.41
1:A:182:GLY:HA3	1:A:270:PRO:HD3	2.02	0.41
1:A:118:ARG:O	1:A:122:LYS:HG2	2.20	0.41
1:A:301:ILE:HB	1:A:309:TYR:CZ	2.56	0.41
1:A:143:ILE:O	1:A:147:GLU:HG3	2.21	0.40
1:A:373:LEU:HD23	1:A:401:ARG:HB3	2.03	0.40
1:B:179:PHE:CE1	1:B:271:GLY:HA2	2.55	0.40
1:B:308:ASP:OD1	2:C:2:NAG:O6	2.39	0.40
1:A:120:TYR:CE1	1:A:464:MET:HG3	2.57	0.40
1:A:307:GLU:HA	1:A:313:TYR:CE2	2.57	0.40

There are no symmetry-related clashes.

## 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	358/431 (83%)	349 (98%)	8 (2%)	1 (0%)	37	35
1	B	348/431 (81%)	340 (98%)	7 (2%)	1 (0%)	37	35
All	All	706/862 (82%)	689 (98%)	15 (2%)	2 (0%)	37	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	235	GLN
1	B	235	GLN

### 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	327/396 (83%)	321 (98%)	6 (2%)	54	59
1	B	323/396 (82%)	316 (98%)	7 (2%)	47	51
All	All	650/792 (82%)	637 (98%)	13 (2%)	50	55

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	A	77	LEU
1	A	129	SER
1	A	139	ASP

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Mol	Chain	Res	Type
1	A	332	LYS
1	A	448	GLN
1	B	135	SER
1	B	202	GLN
1	B	233	SER
1	B	240	ILE
1	B	297	VAL
1	B	326	SER
1	B	410	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	312	ASN
1	A	331	ASN
1	A	341	ASN
1	A	448	GLN
1	B	60	GLN
1	B	71	ASN
1	B	133	GLN
1	B	263	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 ⓘ

11 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	C	1	2,1	14,14,15	0.38	0	17,19,21	0.60	0
2	NAG	C	2	2	14,14,15	0.33	0	17,19,21	0.55	0
3	NAG	D	1	1,3	14,14,15	0.31	0	17,19,21	0.61	0
3	NAG	D	2	3	14,14,15	0.60	0	17,19,21	0.56	0
3	BMA	D	3	3	11,11,12	0.81	0	15,15,17	0.80	0
3	MAN	D	4	3	11,11,12	0.71	0	15,15,17	1.05	2 (13%)
3	MAN	D	5	3	11,11,12	1.11	1 (9%)	15,15,17	0.87	0
4	NAG	E	1	1,4	14,14,15	0.51	0	17,19,21	0.52	0
4	NAG	E	2	4	14,14,15	0.57	0	17,19,21	0.71	0
4	BMA	E	3	4	11,11,12	1.73	3 (27%)	15,15,17	1.34	2 (13%)
4	MAN	E	4	4	11,11,12	1.10	1 (9%)	15,15,17	1.77	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	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
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	MAN	D	4	3	-	2/2/19/22	0/1/1/1
3	MAN	D	5	3	-	1/2/19/22	0/1/1/1
4	NAG	E	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	E	2	4	-	1/6/23/26	0/1/1/1
4	BMA	E	3	4	-	2/2/19/22	0/1/1/1
4	MAN	E	4	4	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	3	BMA	C4-C5	2.76	1.58	1.53
4	E	4	MAN	O5-C5	2.71	1.48	1.43
4	E	3	BMA	O5-C5	2.37	1.48	1.43
3	D	5	MAN	C4-C5	2.23	1.57	1.53
4	E	3	BMA	C4-C3	2.04	1.57	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	4	MAN	C1-O5-C5	6.29	120.61	112.19
3	D	4	MAN	C1-O5-C5	2.91	116.09	112.19
4	E	3	BMA	O3-C3-C4	2.73	116.82	110.38
4	E	3	BMA	O2-C2-C3	-2.50	104.97	110.15
3	D	4	MAN	O2-C2-C3	-2.14	105.72	110.15

There are no chirality outliers.

All (11) torsion outliers are listed below:

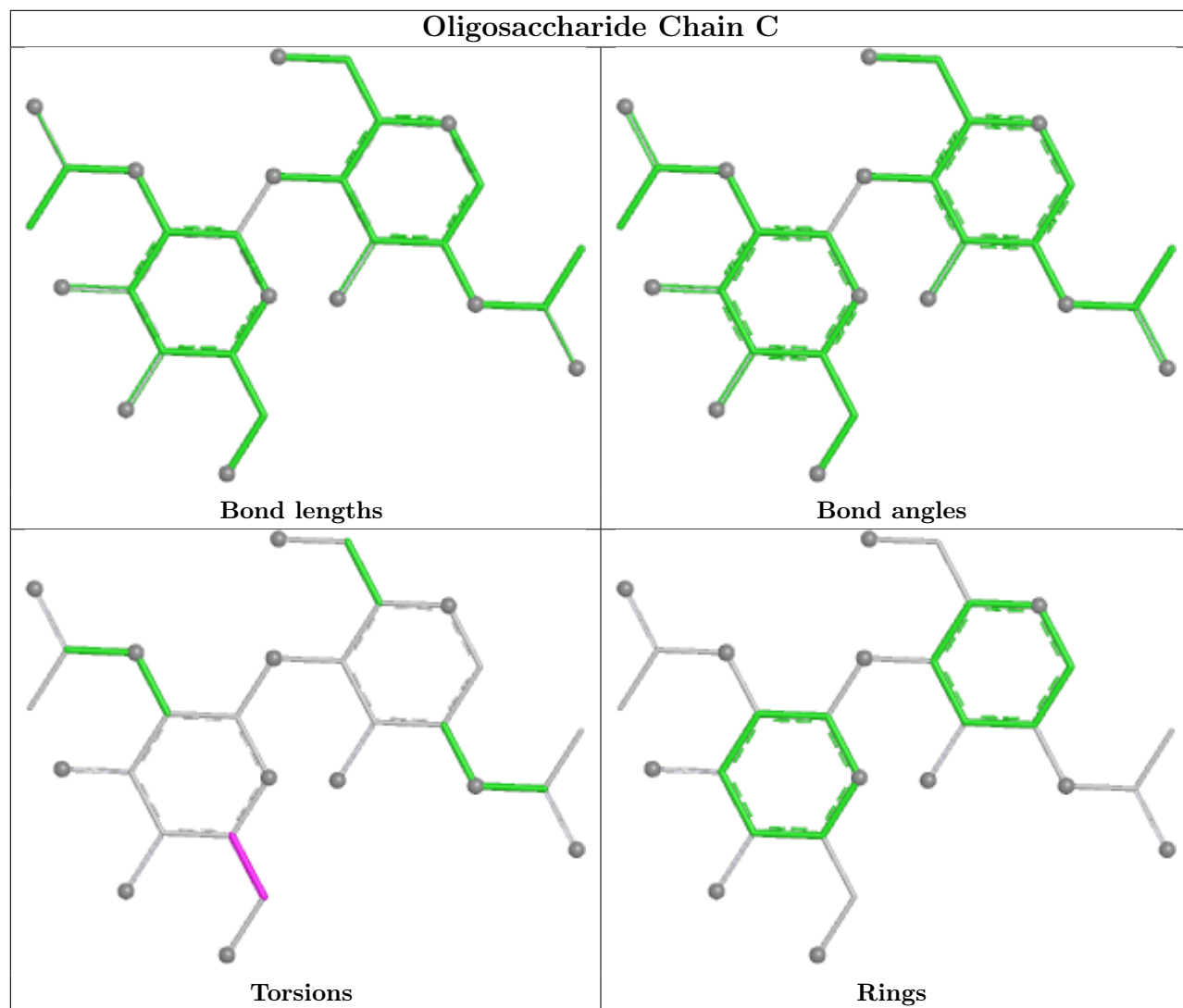
Mol	Chain	Res	Type	Atoms
3	D	2	NAG	O5-C5-C6-O6
3	D	4	MAN	O5-C5-C6-O6
4	E	3	BMA	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	4	MAN	C4-C5-C6-O6
4	E	3	BMA	O5-C5-C6-O6
4	E	1	NAG	C1-C2-N2-C7
2	C	2	NAG	C4-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
3	D	5	MAN	O5-C5-C6-O6

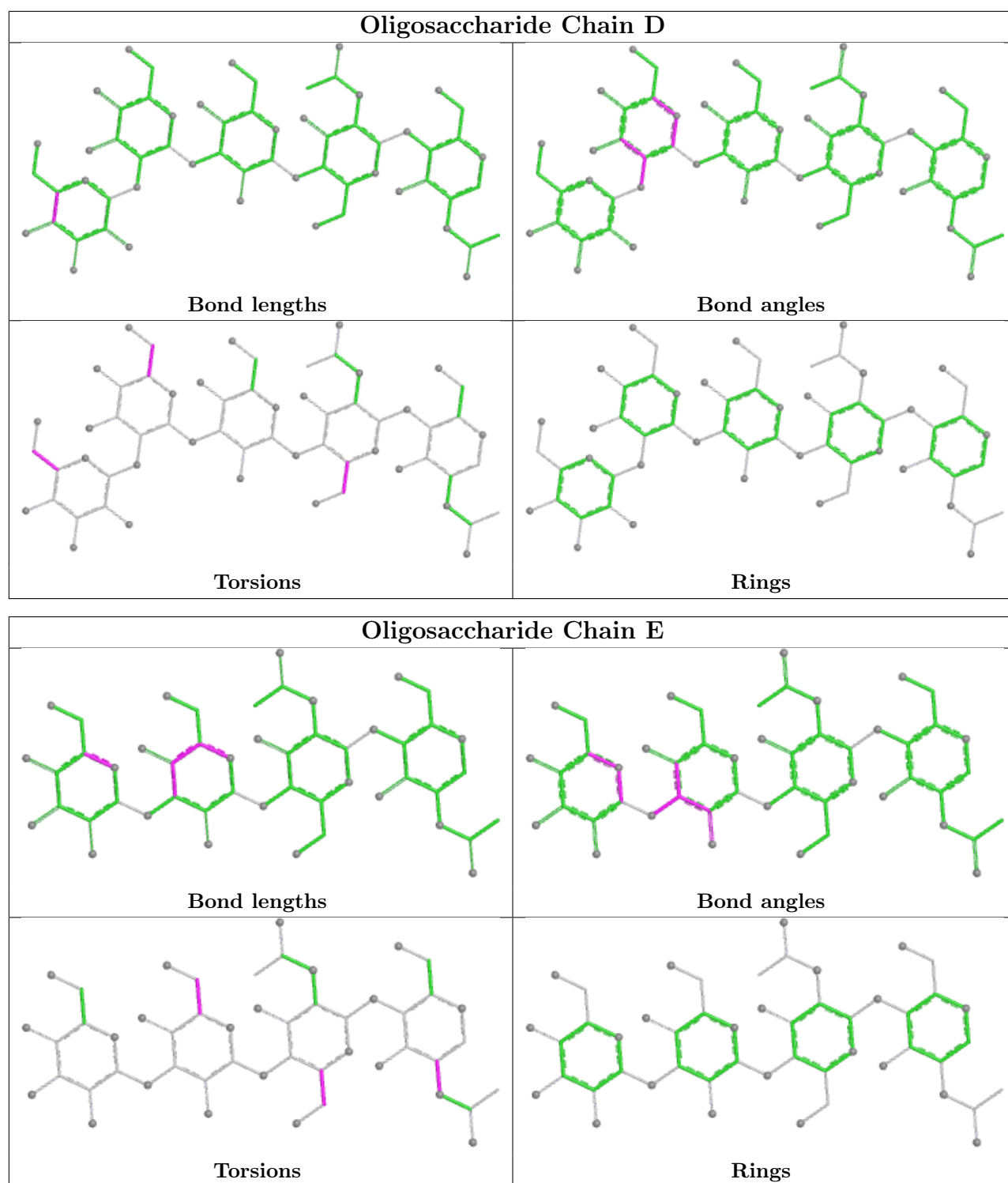
There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	3	BMA	1	0
2	C	2	NAG	1	0
4	E	2	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





## 5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z  > 2$
5	NAG	B	501	1	14,14,15	0.48	0	17,19,21	0.42	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
5	NAG	B	501	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	NAG	C4-C5-C6-O6
5	B	501	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	368/431 (85%)	-0.08	9 (2%) 59 58	12, 26, 47, 62	0
1	B	362/431 (83%)	0.15	8 (2%) 62 60	15, 31, 51, 63	0
All	All	730/862 (84%)	0.03	17 (2%) 61 59	12, 28, 50, 63	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	256	ALA	4.6
1	A	341	ASN	2.9
1	B	336	GLY	2.7
1	B	132	TYR	2.6
1	B	451	ALA	2.6
1	B	86	PHE	2.6
1	A	108	ALA	2.6
1	A	106	VAL	2.5
1	A	254	TRP	2.5
1	B	337	SER	2.4
1	A	77	LEU	2.4
1	A	258	ARG	2.3
1	B	232	ILE	2.2
1	B	400	THR	2.2
1	A	448	GLN	2.1
1	B	231	GLU	2.0
1	A	251	TRP	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

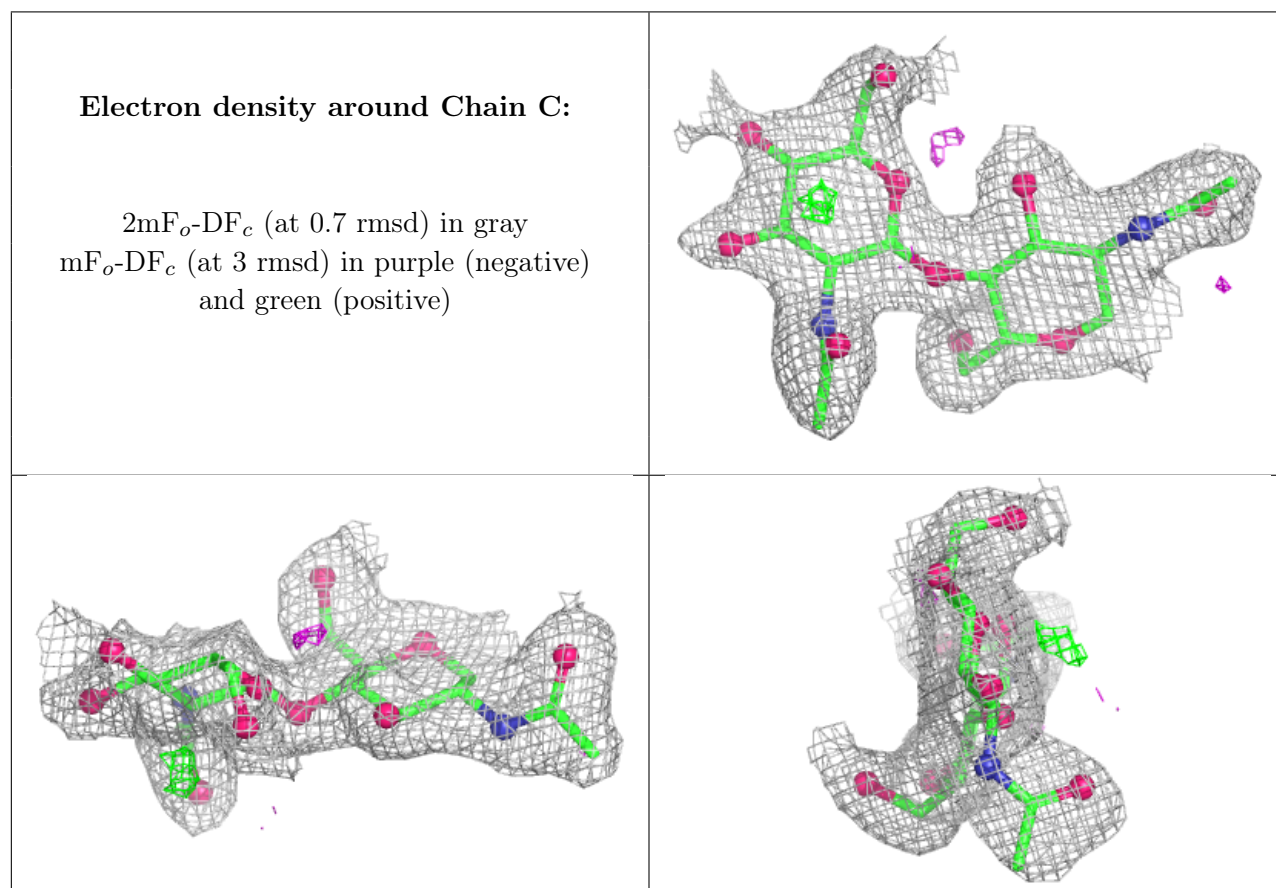
There are no non-standard protein/DNA/RNA residues in this entry.

## 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, 95<sup>th</sup> 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.

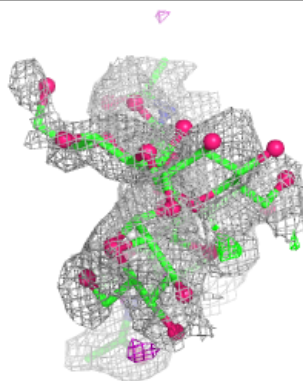
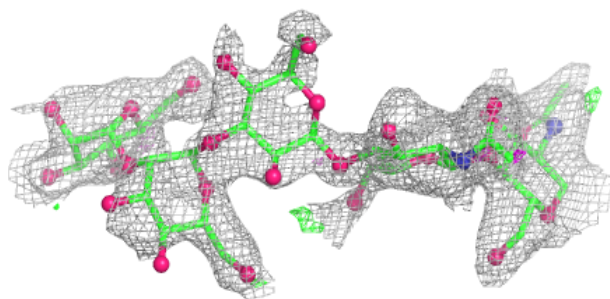
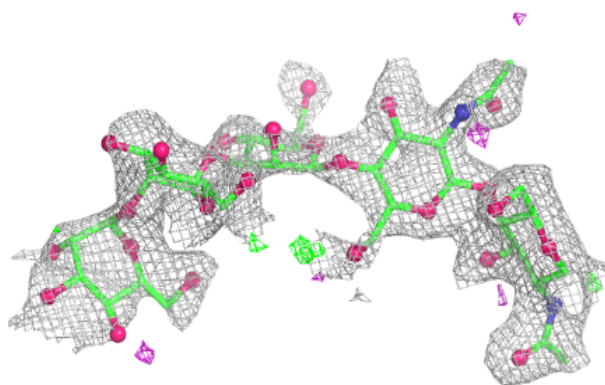
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MAN	D	4	11/12	0.46	0.16	73,74,78,82	0
3	MAN	D	5	11/12	0.62	0.12	60,66,70,71	0
3	BMA	D	3	11/12	0.65	0.13	67,69,71,72	0
4	BMA	E	3	11/12	0.67	0.14	50,57,61,63	0
4	MAN	E	4	11/12	0.70	0.12	48,54,60,64	0
3	NAG	D	2	14/15	0.75	0.12	46,50,61,62	0
2	NAG	C	2	14/15	0.85	0.10	36,40,46,54	0
3	NAG	D	1	14/15	0.87	0.09	26,32,41,42	0
4	NAG	E	2	14/15	0.90	0.09	27,34,44,47	0
4	NAG	E	1	14/15	0.92	0.08	18,24,28,30	0
2	NAG	C	1	14/15	0.96	0.06	21,28,33,35	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.

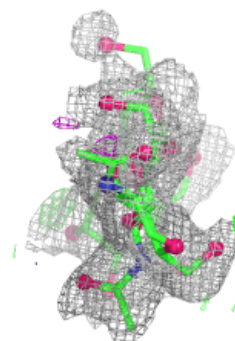
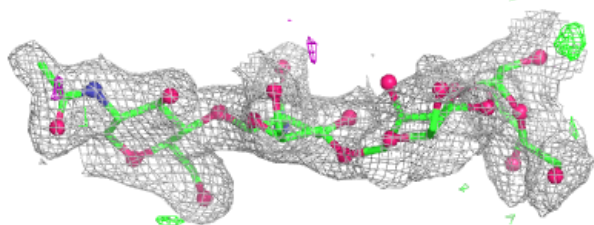
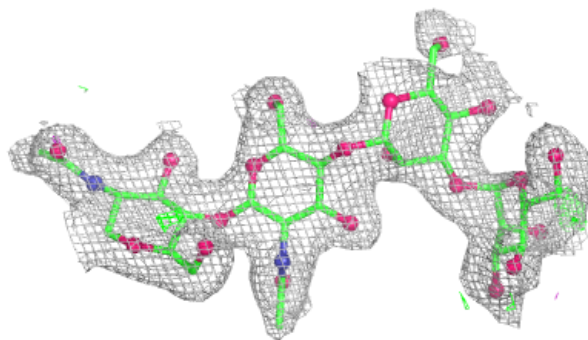


**Electron density around Chain D:**

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

**Electron density around Chain E:**

$2mF_o-DF_c$  (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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
5	NAG	B	501	14/15	0.74	0.14	40,48,60,65	0

## 6.5 Other polymers

There are no such residues in this entry.