

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 22, 2023 – 09:42 PM JST

PDB ID	:	7X2X
Title	:	Crystal Structure of hetero-Diels-Alderase PycR1 in complex with 10-hydrox
		y-8E-humulene
Authors	:	Zhou, J.; Lu, J.
Deposited on		
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 (i) 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 (1)) were used in the production of this report:

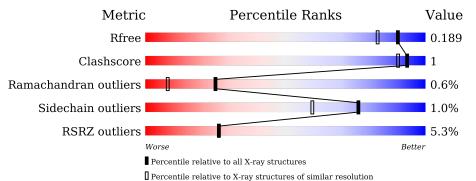
MolProbity Mogul Xtriage (Phenix) EDS	:	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.36
buster-report Percentile statistics Refmac	: : :	1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\;DIFFRACTION$ 

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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

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 <=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	А	388	5% 84%	• 12%
2	В	8	100%	
3	С	5	60%	40%

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
3	BMA	С	3	-	-	-	Х
4	GOL	А	401	-	Х	-	-



# 2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 3370 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 PycR1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	340	Total 2694	C 1724	N 466	0 499	${ m S}{ m 5}$	0	0	0

• Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyran ose-(1-6)-[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		
2	В	8	Total 94	C 52	-	O 40	0	0	0

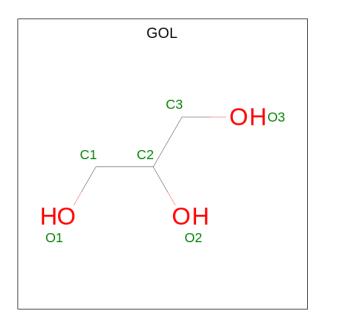
• Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyran ose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
3	С	5	Total 61	C 34	N 2	O 25	0	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).

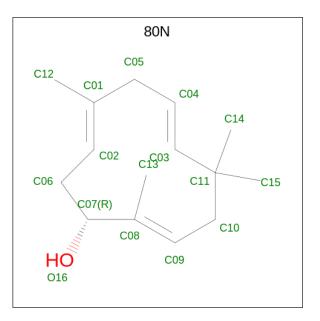






Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	А	1	Total 6	${ m C} { m 3}$	O 3	0	0

• Molecule 5 is (1R, 2E, 6E, 9E)-2,5,5,9-tetramethylcycloundeca-2,6,9-trien-1-ol (three-letter code: 80N) (formula:  $C_{15}H_{24}O$ ) (labeled as "Ligand of Interest" by depositor).



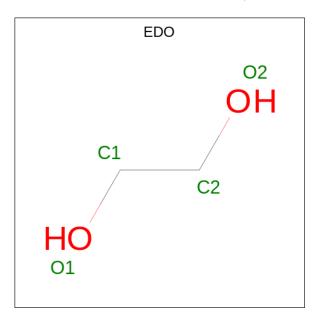
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	А	1	Total 16	C 15	0 1	0	0

• Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).



Mol	Chain	Residues	Aton	ns	ZeroOcc	AltConf
6	А	1	Total 1	Ca 1	0	0

• Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
7	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	5	Total Cl 5 5	0	0

• Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	А	457	Total 457	O 457	0	0



# 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.

Chain A: 5% Chain A: 84% 12% State of the point of the

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

Chain B:

• Molecule 1: PycR1

100%

#### NAG1 NAG2 BMA3 MAN4 MAN5 MAN5 MAN5 BMA8 BMA8

 $\bullet$  Molecule 3: 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

Chain C:

60%

40%



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	78.62Å 78.62Å 163.06Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	45.93 - 1.58	Depositor
Resolution (A)	45.93 - 1.58	EDS
% Data completeness	$100.0 \ (45.93 \text{-} 1.58)$	Depositor
(in resolution range)	$100.0 \ (45.93 - 1.58)$	EDS
R <sub>merge</sub>	0.09	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.96 (at 1.58 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D D.	0.164 , $0.189$	Depositor
$R, R_{free}$	0.165 , $0.189$	DCC
$R_{free}$ test set	3565 reflections $(5.04%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	23.4	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33, $50.0$	EDS
L-test for twinning <sup>2</sup>	$ \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	0.97	EDS
Total number of atoms	3370	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 4.93% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: MAN, 80N, GOL, CL, BMA, NAG, EDO, CA

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		lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.54	0/2778	0.72	0/3804	

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	А	2694	0	2588	7	0
2	В	94	0	78	1	0
3	С	61	0	52	0	0
4	А	6	0	7	3	0
5	А	16	0	0	0	0
6	А	1	0	0	0	0
7	А	36	0	54	1	0
8	А	5	0	0	0	0
9	А	457	0	0	0	0
All	All	3370	0	2779	8	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 1.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:PRO:HD2	4:A:401:GOL:H11	1.68	0.75
4:A:401:GOL:H32	7:A:412:EDO:O1	2.08	0.54
1:A:250:LEU:HD21	1:A:258:ALA:HB2	2.01	0.42
1:A:152:PRO:CD	4:A:401:GOL:H11	2.42	0.42
1:A:210:ALA:HB3	2:B:1:NAG:H82	2.02	0.42
1:A:54:PRO:HD2	1:A:104:ASP:OD1	2.21	0.40
1:A:127:PHE:CE2	1:A:156:LEU:HA	2.56	0.40
1:A:340:GLY:HA3	1:A:357:TRP:CE2	2.57	0.40

All (8) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	А	338/388~(87%)	324 (96%)	12 (4%)	2(1%)	25 8	

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	176	TYR
1	А	96	ILE

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	288/324~(89%)	285~(99%)	3(1%)	76 59	

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	46	TRP
1	А	104	ASP
1	А	251	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	79	GLN
1	А	367	HIS

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates (i)

13 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		n Res Link		Bond lengths			Bond angles			
	туре	e Cham Re	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	NAG	В	1	2,1	14,14,15	0.36	0	17,19,21	0.73	0
2	NAG	В	2	2	14,14,15	0.84	1 (7%)	17,19,21	0.58	0
2	BMA	В	3	2	11,11,12	1.02	0	$15,\!15,\!17$	0.88	1 (6%)



Mol	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
1VIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	MAN	В	4	2	11,11,12	1.39	1 (9%)	$15,\!15,\!17$	1.18	1 (6%)
2	MAN	В	5	2	11,11,12	0.78	0	$15,\!15,\!17$	1.11	2 (13%)
2	MAN	В	6	2	11,11,12	0.70	0	$15,\!15,\!17$	1.02	1 (6%)
2	MAN	В	7	2	11,11,12	0.85	0	$15,\!15,\!17$	1.28	2 (13%)
2	BMA	В	8	2	11,11,12	0.87	0	15, 16, 17	1.23	1 (6%)
3	NAG	С	1	3,1	14,14,15	0.50	0	17,19,21	0.52	0
3	NAG	С	2	3	14,14,15	0.52	0	17,19,21	0.46	0
3	BMA	С	3	3	11,11,12	0.70	0	$15,\!15,\!17$	0.65	0
3	MAN	С	4	3	11,11,12	1.06	1 (9%)	$15,\!15,\!17$	1.59	2 (13%)
3	MAN	С	5	3	11,11,12	1.05	1 (9%)	$15,\!15,\!17$	1.12	2 (13%)

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	В	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	В	2	2	-	0/6/23/26	0/1/1/1
2	BMA	В	3	2	-	0/2/19/22	0/1/1/1
2	MAN	В	4	2	-	0/2/19/22	0/1/1/1
2	MAN	В	5	2	-	0/2/19/22	0/1/1/1
2	MAN	В	6	2	-	0/2/19/22	0/1/1/1
2	MAN	В	7	2	-	0/2/19/22	0/1/1/1
2	BMA	В	8	2	-	-	0/1/1/1
3	NAG	С	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	С	2	3	-	0/6/23/26	0/1/1/1
3	BMA	С	3	3	-	2/2/19/22	0/1/1/1
3	MAN	С	4	3	-	1/2/19/22	0/1/1/1
3	MAN	С	5	3	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
2	В	4	MAN	O5-C1	-3.72	1.37	1.43
2	В	2	NAG	O5-C1	-2.84	1.39	1.43
3	С	5	MAN	O5-C5	2.35	1.48	1.43
3	С	4	MAN	C1-C2	2.09	1.57	1.52

All (12) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	С	4	MAN	C1-O5-C5	4.56	118.37	112.19
2	В	7	MAN	C1-O5-C5	3.42	116.82	112.19
2	В	4	MAN	C1-O5-C5	3.16	116.47	112.19
3	С	5	MAN	C1-O5-C5	3.16	116.47	112.19
2	В	5	MAN	C1-O5-C5	2.85	116.05	112.19
2	В	6	MAN	C1-O5-C5	2.51	115.59	112.19
3	С	4	MAN	C1-C2-C3	2.44	112.66	109.67
2	В	7	MAN	O2-C2-C3	-2.33	105.47	110.14
2	В	5	MAN	O2-C2-C3	-2.24	105.65	110.14
2	В	8	BMA	C3-C4-C5	2.13	113.08	109.77
3	С	5	MAN	O2-C2-C3	-2.06	106.01	110.14
2	В	3	BMA	O2-C2-C3	-2.05	106.04	110.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	С	3	BMA	O5-C5-C6-O6
3	С	3	BMA	C4-C5-C6-O6
3	С	4	MAN	O5-C5-C6-O6

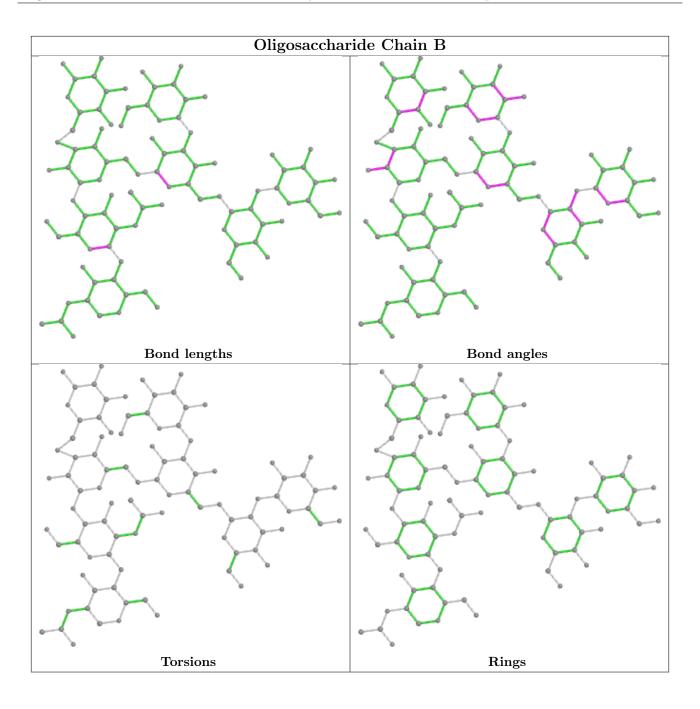
There are no ring outliers.

1 monomer is involved in 1 short contact:

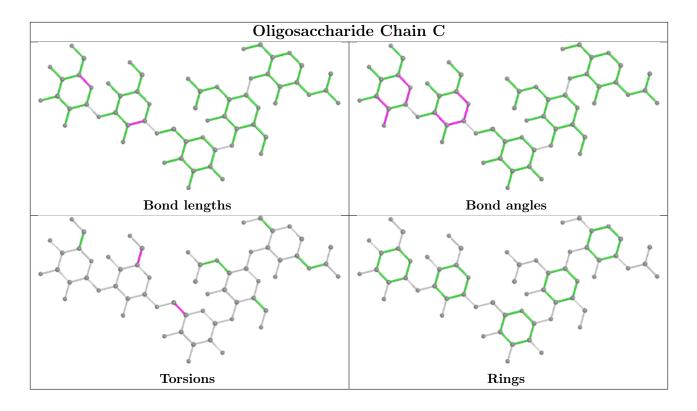
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	1	NAG	1	0

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)

Of 17 ligands modelled in this entry, 6 are monoatomic - leaving 11 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
7	EDO	А	407	-	$3,\!3,\!3$	0.34	0	2,2,2	0.70	0
7	EDO	А	406	-	3,3,3	0.34	0	2,2,2	0.84	0
4	GOL	А	401	-	$5,\!5,\!5$	3.30	2 (40%)	$5,\!5,\!5$	1.08	0
5	80N	А	402	-	16, 16, 16	1.23	2 (12%)	20,22,22	1.67	4 (20%)
7	EDO	А	412	-	3,3,3	0.61	0	2,2,2	0.12	0
7	EDO	А	405	-	3,3,3	0.24	0	2,2,2	0.78	0
7	EDO	А	404	-	3, 3, 3	0.35	0	$2,\!2,\!2$	0.52	0
7	EDO	А	410	-	$3,\!3,\!3$	0.64	0	2,2,2	0.24	0
7	EDO	А	411	-	3, 3, 3	0.59	0	2,2,2	1.03	0
7	EDO	А	408	-	3,3,3	0.46	0	2,2,2	0.48	0
7	EDO	А	409	-	3, 3, 3	0.43	0	2,2,2	0.45	0



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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	А	407	-	-	1/1/1/1	-
7	EDO	А	406	-	-	0/1/1/1	-
4	GOL	А	401	-	-	4/4/4/4	-
5	80N	А	402	-	-	0/22/22/22	0/0/1/1
7	EDO	А	412	-	-	1/1/1/1	-
7	EDO	А	405	-	-	1/1/1/1	-
7	EDO	А	404	-	-	0/1/1/1	-
7	EDO	А	410	-	-	0/1/1/1	-
7	EDO	А	411	-	-	1/1/1/1	-
7	EDO	А	408	-	-	1/1/1/1	-
7	EDO	А	409	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	А	401	GOL	O1-C1	-6.38	1.15	1.42
4	А	401	GOL	C1-C2	-3.48	1.37	1.51
5	А	402	80N	C10-C09	2.15	1.55	1.50
5	А	402	80N	C07-C08	2.13	1.54	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
5	А	402	80N	C07-C06-C02	-4.73	104.05	112.66
5	А	402	80N	C11-C10-C09	-3.78	107.75	113.48
5	А	402	80N	C12-C01-C05	2.25	120.13	114.88
5	А	402	80N	C10-C11-C03	-2.06	104.06	106.32

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	401	GOL	O1-C1-C2-C3
4	А	401	GOL	C1-C2-C3-O3
4	А	401	GOL	O2-C2-C3-O3
4	А	401	GOL	O1-C1-C2-O2
7	А	408	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
7	А	405	EDO	O1-C1-C2-O2
7	А	407	EDO	O1-C1-C2-O2
7	А	412	EDO	O1-C1-C2-O2
7	А	411	EDO	O1-C1-C2-O2

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There are no ring outliers.

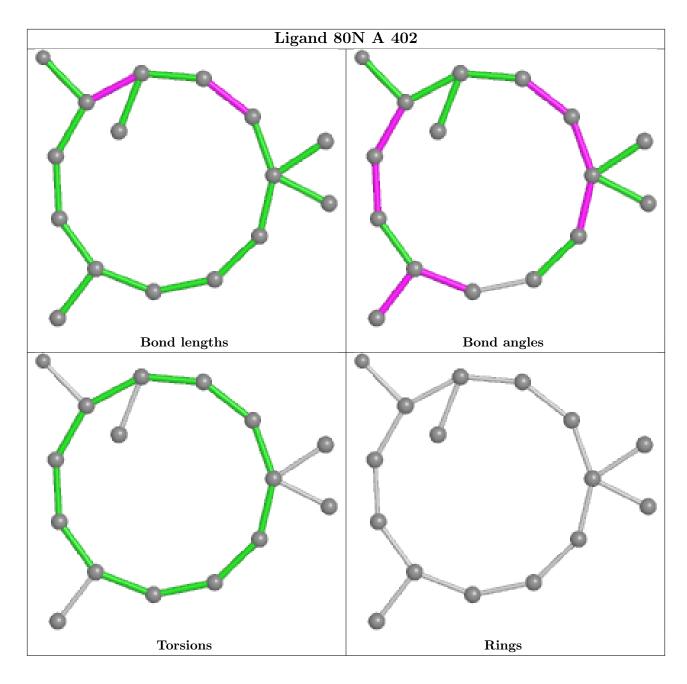
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	401	GOL	3	0
7	А	412	EDO	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







### 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,  $95^{th}$  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	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$		-2	$OWAB(Å^2)$	Q<0.9		
1	А	340/388~(87%)	0.26	18 (5%)	26	26	16, 25, 45, 63	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	29	VAL	8.3
1	А	368	PHE	5.7
1	А	138	ALA	5.1
1	А	367	HIS	4.8
1	А	137	SER	4.7
1	А	236	TRP	4.2
1	А	261	PRO	4.1
1	А	234	ARG	3.4
1	А	141	ASP	3.4
1	А	259	VAL	2.9
1	А	30	LYS	2.7
1	А	136	GLY	2.5
1	А	366	PHE	2.4
1	А	142	LYS	2.2
1	А	140	LYS	2.2
1	А	123	VAL	2.0
1	А	300	PRO	2.0
1	А	283	HIS	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.



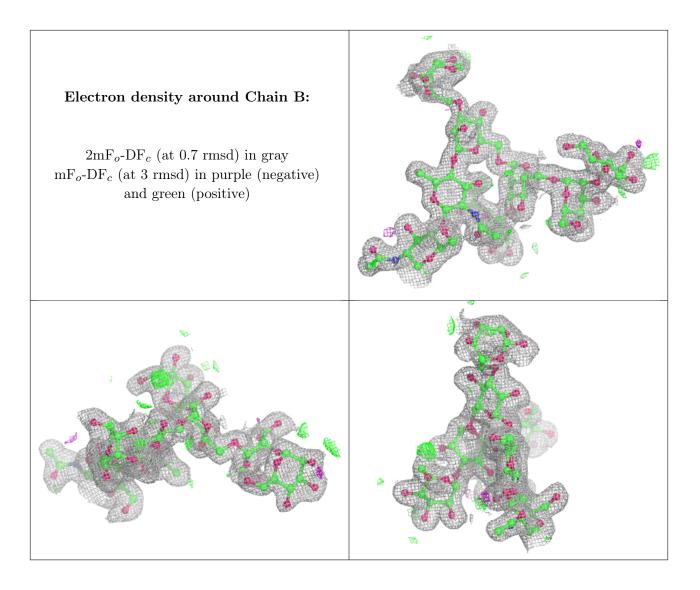
### 6.3 Carbohydrates (i)

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,  $95^{th}$  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.

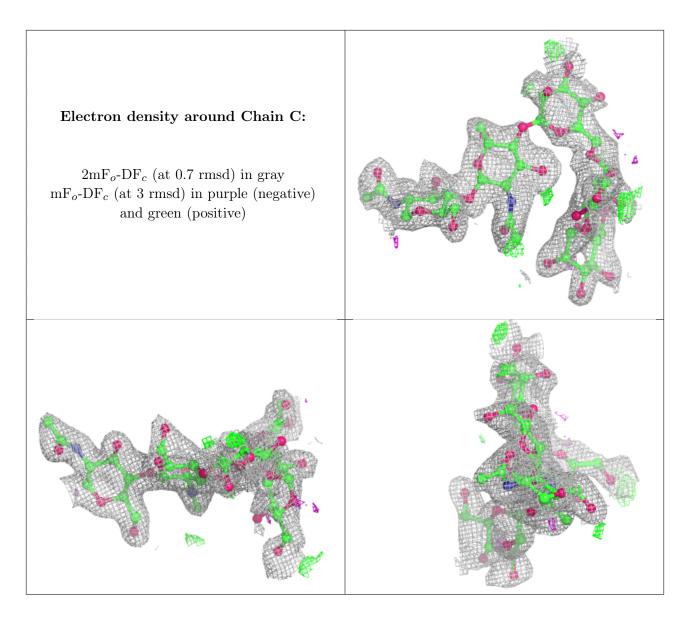
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	$Q{<}0.9$
2	BMA	В	8	11/12	0.48	0.32	62,71,78,79	0
3	MAN	С	4	11/12	0.49	0.35	66,69,73,74	0
3	BMA	С	3	11/12	0.63	0.40	77,84,87,92	0
3	MAN	С	5	11/12	0.73	0.35	$50,\!60,\!67,\!67$	0
3	NAG	С	2	14/15	0.80	0.29	$46,\!59,\!73,\!86$	0
2	BMA	В	3	11/12	0.84	0.15	$27,\!33,\!52,\!59$	0
2	MAN	В	6	11/12	0.85	0.18	$35,\!41,\!50,\!53$	0
2	NAG	В	2	14/15	0.86	0.14	$33,\!37,\!43,\!52$	0
3	NAG	С	1	14/15	0.89	0.21	29,39,46,51	0
2	NAG	В	1	14/15	0.92	0.09	$28,\!33,\!40,\!43$	0
2	MAN	В	5	11/12	0.94	0.08	$24,\!26,\!34,\!44$	0
2	MAN	В	7	11/12	0.94	0.08	24,26,39,48	0
2	MAN	В	4	11/12	0.95	0.05	24,25,28,28	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)

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,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q < 0.9
7	EDO	А	412	4/4	0.74	0.19	$37,\!38,\!48,\!50$	0
7	EDO	А	410	4/4	0.78	0.13	31,38,40,46	0
5	80N	А	402	16/16	0.81	0.15	24,27,34,35	0
8	CL	А	416	1/1	0.82	0.13	74,74,74,74	0
8	CL	А	415	1/1	0.84	0.09	$65,\!65,\!65,\!65$	0
7	EDO	А	411	4/4	0.86	0.18	18,28,36,48	0
8	CL	А	414	1/1	0.87	0.08	64,64,64,64	0

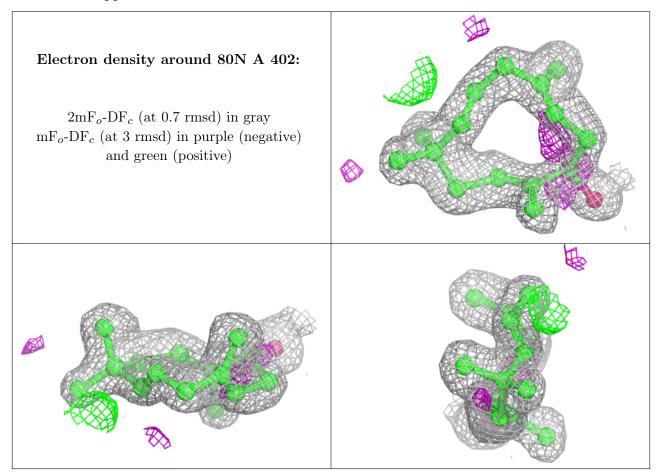
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
7	EDO	А	409	4/4	0.88	0.19	$45,\!51,\!52,\!56$	0
8	CL	А	417	1/1	0.88	0.23	59, 59, 59, 59, 59	0
4	GOL	А	401	6/6	0.90	0.20	21,35,51,53	0
7	EDO	А	408	4/4	0.90	0.35	43,43,51,65	0
7	EDO	А	407	4/4	0.91	0.09	45,48,49,54	0
7	EDO	А	405	4/4	0.92	0.12	$27,\!32,\!43,\!61$	0
7	EDO	А	406	4/4	0.94	0.06	33,46,49,51	0
7	EDO	А	404	4/4	0.96	0.15	33,34,37,38	0
8	CL	А	413	1/1	0.98	0.08	33,33,33,33	0
6	CA	А	403	1/1	1.00	0.08	19,19,19,19	0

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The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



### 6.5 Other polymers (i)

There are no such residues in this entry.

