

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

#### Aug 2, 2023 – 12:09 PM EDT

PDB ID	:	1C39
Title	:	STRUCTURE OF CATION-DEPENDENT MANNOSE 6-PHOSPHATE RE-
		CEPTOR BOUND TO PENTAMANNOSYL PHOSPHATE
Authors	:	Olson, L.J.; Zhang, J.; Lee, Y.C.; Dahms, N.M.; Kim, J.JP.
Deposited on		
Resolution	:	1.85  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:

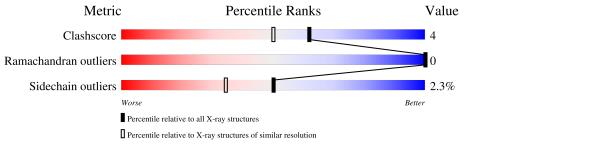
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
$\mathrm{EDS}$	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

# 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 1.85 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	Similar resolution
Metric	$(\# {\rm Entries})$	$(\# { m Entries},  { m resolution}  { m range}({ m \AA}))$
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592(1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	А	152	91%	89	%•
1	В	152	90%	10	%
2	С	2	50%	50%	
2	D	2	100%		
3	Е	3	100%		
3	F	3	67%	33%	



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2711 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 CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	152	Total 1203	-		O 236	S 10	0	0	0
1	В	152	Total 1203	-		O 236	S 10	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	31	GLN	ASN	engineered mutation	UNP P11456
А	57	GLN	ASN	engineered mutation	UNP P11456
А	68	GLN	ASN	engineered mutation	UNP P11456
А	87	GLN	ASN	engineered mutation	UNP P11456
В	31	GLN	ASN	engineered mutation	UNP P11456
В	57	GLN	ASN	engineered mutation	UNP P11456
В	68	GLN	ASN	engineered mutation	UNP P11456
В	87	GLN	ASN	engineered mutation	UNP P11456

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

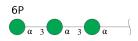


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	2 C	2	Total C N O		0	0			
		2	28	16	2	10	0	0	0
0	П	2	Total	С	Ν	0	0	0	0
	2 D	2	28	16	2	10	0	0	U

• Molecule 3 is an oligosaccharide called 6-O-phosphono-alpha-D-mannopyranose-(1-3)-alpha-



D-mannopyranose-(1-3)-alpha-D-mannopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	2	Total	С	Ο	Р	0	0	0
5 E	5	38	18	19	1	0	0	0	
9	Б	9	Total	С	0	Р	0	0	0
0	Г	3	38	18	19	1			

• Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Mn 1 1	0	0
4	В	1	Total Mn 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	78	Total         O           78         78	0	0
5	В	93	Total O 93 93	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. 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. 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.

Note EDS was not executed.

• Molecule 1: CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR

Chain A:	91%	8% •	:
E3 K4 Q31 G3 E35 E35 E35 E35 C37 K72 K72	E82 E83 688 688 688 688 688 688 688 688 688 6		
• Molecule 1: CATI	ON-DEPENDENT MANNOS	SE-6-PHOSPHATE RECI	EPTOR
Chain B:	90%	10%	•
E3 K18 K18 E35 E35 E35 E35 K17 K79	P100 P100 P100 P130 P130 P130 P130 P130		
• Molecule 2: 2-acet opyranose	tamido-2-deoxy-beta-D-glucop	oyranose-(1-4)-2-acetamid	lo-2-deoxy-beta-D-gluc
Chain C:	50%	50%	
NAG2 NAG2			
• Molecule 2: 2-acet opyranose	tamido-2-deoxy-beta-D-glucop	oyranose-(1-4)-2-acetamid	lo-2-deoxy-beta-D-gluc
Chain D:	100%		•

VAG1 VAG2

• Molecule 3: 6-O-phosphono-alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-3)-alpha -D-mannopyranose

Chain E:

100%

MAN1 MAN2 M6P3



 $\bullet$  Molecule 3: 6-O-phosphono-alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-3)-alpha -D-mannopyranose

67%

Chain F:

33%

MAN1 MAN2 M6P3



## 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	42.84Å 79.31Å 55.57Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $100.33^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	40.00 - 1.85	Depositor
% Data completeness	88.4 (40.00-1.85)	Depositor
(in resolution range)	00.4 (40.00 1.00)	Depositor
$R_{merge}$	0.05	Depositor
R <sub>sym</sub>	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
$R, R_{free}$	0.210 , $0.246$	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2711	wwPDB-VP
Average B, all atoms $(Å^2)$	28.0	wwPDB-VP



# 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, MAN, MN, M6P  $\,$ 

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		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.34	0/1223	0.58	0/1638	
1	В	0.35	0/1223	0.60	0/1638	
All	All	0.35	0/2446	0.59	0/3276	

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	1203	0	1156	13	0
1	В	1203	0	1156	9	0
2	С	28	0	24	1	0
2	D	28	0	24	0	0
3	Е	38	0	29	0	0
3	F	38	0	29	2	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
5	А	78	0	0	1	0
5	В	93	0	0	0	0
All	All	2711	0	2418	22	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 4.

All (22) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:68:GLN:NE2	1:A:73:LYS:HB3	1.66	1.10
1:A:68:GLN:HE21	1:A:73:LYS:HB3	1.13	1.06
1:A:68:GLN:NE2	5:A:626:HOH:O	2.30	0.64
1:A:3:GLU:HG2	1:A:4:LYS:H	1.67	0.59
1:B:111:ARG:HH12	3:F:3:M6P:H4	1.66	0.59
1:B:25:ARG:NH1	1:B:87:GLN:HE22	2.03	0.55
1:A:88:GLY:HA3	1:A:91:TRP:CE2	2.44	0.53
1:A:68:GLN:HE21	1:A:73:LYS:CB	2.04	0.52
1:A:3:GLU:HG2	1:A:4:LYS:N	2.25	0.51
1:A:35:GLU:HA	1:A:47:TYR:O	2.10	0.50
1:B:111:ARG:NH1	3:F:3:M6P:H4	2.26	0.50
1:B:60:SER:HB3	1:B:79:ARG:HH21	1.76	0.49
1:A:67:ILE:HA	1:A:73:LYS:O	2.14	0.48
1:B:25:ARG:HH12	1:B:87:GLN:HE22	1.63	0.47
1:B:35:GLU:HA	1:B:47:TYR:O	2.17	0.44
1:A:82:GLU:HG2	2:C:1:NAG:H82	1.99	0.44
1:A:134:GLU:O	1:A:141:CYS:HB3	2.19	0.42
1:B:134:GLU:O	1:B:141:CYS:HB3	2.18	0.42
1:A:71:ASN:ND2	1:A:73:LYS:HB2	2.35	0.42
1:A:68:GLN:HE21	1:A:68:GLN:HB2	1.66	0.41
1:B:100:ASP:O	1:B:111:ARG:HG3	2.21	0.40
1:B:129:ASN:HA	1:B:130:PRO:HD3	1.83	0.40

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	Perce	ntiles
1	А	150/152~(99%)	144 (96%)	6 (4%)	0	100	100
1	В	150/152~(99%)	144 (96%)	6 (4%)	0	100	100
All	All	300/304~(99%)	288~(96%)	12~(4%)	0	100	100

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains (i)

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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	133/133~(100%)	130~(98%)	3~(2%)	50	34	
1	В	133/133~(100%)	130~(98%)	3~(2%)	50	34	
All	All	266/266~(100%)	260~(98%)	6(2%)	50	34	

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	31	GLN
1	А	35	GLU
1	А	68	GLN
1	В	3	GLU
1	В	18	LYS
1	В	144	LEU

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

Mol	Chain	Res	Type
1	А	68	GLN
1	А	104	ASN
1	В	66	GLN
1	В	87	GLN



#### 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)

10 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	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	NAG	С	1	1,2	$14,\!14,\!15$	0.68	0	17,19,21	0.94	1 (5%)
2	NAG	С	2	2	14,14,15	1.35	2 (14%)	17,19,21	2.07	5 (29%)
2	NAG	D	1	1,2	14,14,15	0.62	0	17,19,21	0.80	1 (5%)
2	NAG	D	2	2	14,14,15	1.24	1 (7%)	17,19,21	1.99	4 (23%)
3	MAN	Е	1	3	12,12,12	1.17	1 (8%)	17,17,17	0.53	0
3	MAN	Е	2	3	11,11,12	1.26	2 (18%)	$15,\!15,\!17$	0.95	1 (6%)
3	M6P	Е	3	3	15,15,16	1.33	1 (6%)	22,22,24	0.96	1 (4%)
3	MAN	F	1	3	12,12,12	1.77	1 (8%)	17,17,17	2.08	4 (23%)
3	MAN	F	2	3	11,11,12	1.51	2 (18%)	$15,\!15,\!17$	1.03	1 (6%)
3	M6P	F	3	4,3	15, 15, 16	1.38	2 (13%)	22,22,24	1.89	3 (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	С	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	С	2	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
3	MAN	Е	1	3	-	0/2/22/22	0/1/1/1
3	MAN	Е	2	3	-	0/2/19/22	0/1/1/1
3	M6P	Ε	3	3	-	0/6/23/26	0/1/1/1
3	MAN	F	1	3	-	1/2/22/22	0/1/1/1
3	MAN	F	2	3	-	0/2/19/22	0/1/1/1
3	M6P	F	3	4,3	-	5/6/23/26	0/1/1/1

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All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1	MAN	C1-C2	5.09	1.64	1.52
2	С	2	NAG	C1-C2	4.10	1.58	1.52
2	D	2	NAG	C1-C2	3.50	1.57	1.52
3	Е	3	M6P	P-O1P	3.29	1.61	1.50
3	F	2	MAN	C2-C3	3.21	1.57	1.52
3	F	3	M6P	O6-C6	-2.98	1.33	1.44
3	F	3	M6P	P-O1P	2.60	1.58	1.50
3	Ε	2	MAN	C2-C3	2.27	1.55	1.52
3	F	2	MAN	O5-C1	2.25	1.47	1.43
3	Е	2	MAN	O5-C1	2.20	1.47	1.43
3	Е	1	MAN	O5-C1	2.12	1.48	1.42
2	С	2	NAG	O5-C1	2.02	1.46	1.43

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
3	F	3	M6P	P-O6-C6	7.31	138.44	118.30
2	С	2	NAG	O5-C1-C2	-5.57	102.49	111.29
2	D	2	NAG	O5-C1-C2	-5.31	102.90	111.29
3	F	1	MAN	C1-O5-C5	4.59	122.33	113.66
3	F	1	MAN	O5-C1-C2	-4.35	102.52	110.28
2	С	2	NAG	C1-C2-N2	-3.91	103.80	110.49
2	D	2	NAG	C1-C2-N2	-3.62	104.30	110.49
3	Ε	2	MAN	C1-O5-C5	3.30	116.67	112.19
3	F	1	MAN	O1-C1-O5	3.04	119.51	110.38
3	F	2	MAN	C1-O5-C5	2.90	116.12	112.19
3	Ε	3	M6P	C1-O5-C5	2.76	115.94	112.19
3	F	3	M6P	O6-C6-C5	2.57	117.82	108.99
2	С	2	NAG	C1-O5-C5	2.47	115.54	112.19
3	F	1	MAN	O5-C5-C4	-2.38	105.36	109.69

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Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
2	D	2	NAG	O4-C4-C5	2.33	115.08	109.30
3	F	3	M6P	C2-C3-C4	-2.31	106.89	110.89
2	D	1	NAG	C4-C3-C2	-2.16	107.85	111.02
2	С	2	NAG	O4-C4-C5	2.11	114.54	109.30
2	D	2	NAG	C1-O5-C5	2.11	115.05	112.19
2	С	1	NAG	C4-C3-C2	-2.05	108.02	111.02
2	С	2	NAG	O3-C3-C2	2.02	113.65	109.47

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There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
3	F	3	M6P	C4-C5-C6-O6
3	F	3	M6P	O5-C5-C6-O6
3	F	3	M6P	C6-O6-P-O1P
3	F	3	M6P	C6-O6-P-O2P
3	F	3	M6P	C6-O6-P-O3P
2	С	1	NAG	C4-C5-C6-O6
2	С	1	NAG	O5-C5-C6-O6
3	F	1	MAN	O5-C5-C6-O6

All (8) torsion outliers are listed below:

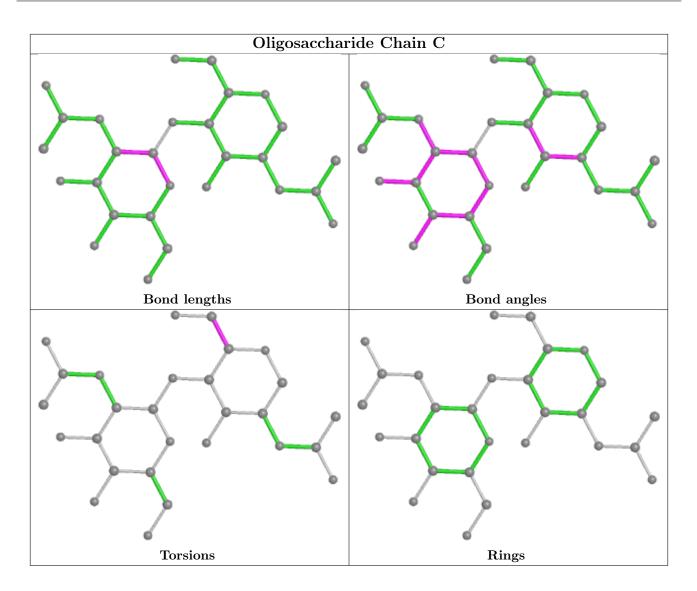
There are no ring outliers.

2 monomers are involved in 3 short contacts:

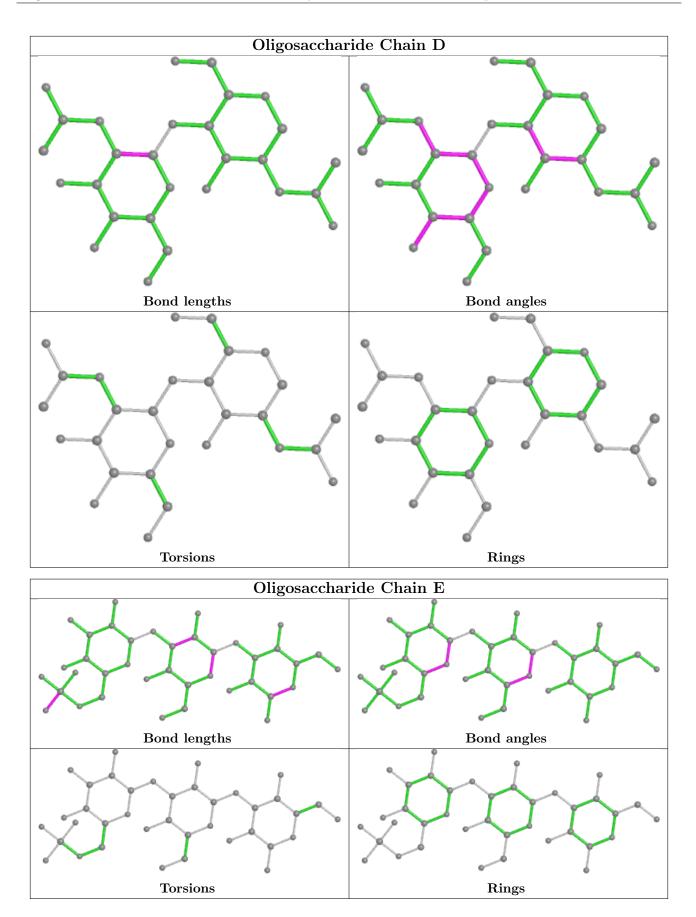
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	3	M6P	2	0
2	С	1	NAG	1	0

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



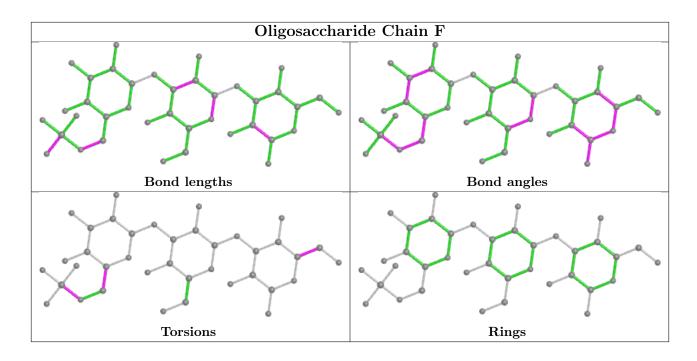












## 5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

### 5.7 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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

#### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

