

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

#### Nov 20, 2024 – 03:07 pm GMT

PDB ID : 9G3R

Title: LecA from Pseudomonas aeruginosa in complex with a synthetic thiogalacto-

side

Authors: Melicher, F.; Faltinek, L.; Wimmerova, M.

Deposited on : 2024-07-12

Resolution : 1.70 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:

Mol Probity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 3.0

Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)

CCP4 : 9.0.003 (Gargrove)

Density-Fitness : 1.0.11

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

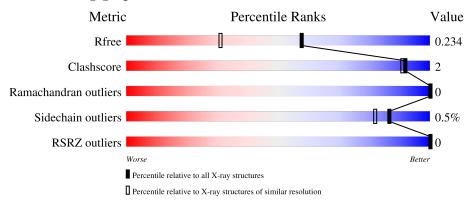
Validation Pipeline (wwPDB-VP) : 2.39

## 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.70 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	164625	5161 (1.70-1.70)
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (1.70-1.70)

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	A	121	97%	•
1	В	121	96%	<del>.</del>
1	С	121	98%	••
1	D	121	92% 7%	
1	Е	121	97%	•



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Mol		Length	Quality of chain					
1	F	121	96%					
1	G	121	96%					
1	Н	121	93%	7% •				
2	I	2	50% 50%					
2	J	2	100%					
2	K	2	50% 50%					
2	L	2	50% 50%					
2	M	2	50%					



## 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7758 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 PA-I galactophilic lectin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	121	Total	С	N	О	S	0	1	0
1	A	121	890	562	153	172	3	U	1	U
1	В	121	Total	С	N	О	S	0	2	0
1	Б	121	902	569	156	174	3	0	<u> </u>	0
1	С	121	Total	С	N	О	S	0	3	0
1		121	906	572	155	176	3	0	3	U
1	D	121	Total	С	N	О	S	0	2	0
1	D	121	903	573	154	173	3			
1	E	121	Total	С	N	Ο	S	0	3	0
1	Ľ	121	909	576	156	174	3	0		
1	F	121	Total	С	N	О	S	0	2	0
1	Г	121	906	571	157	175	3	0	<u> </u>	0
1	G	121	Total	С	N	О	S	0	3	0
1	G	121	910	577	155	175	3	0	3	0
1	Н	120	Total	С	N	О	S	0	3	0
1	11	120	910	575	157	175	3	U		U

• Molecule 2 is an oligosaccharide called 1-thio-beta-D-galactopyranose-(1-1)-alpha-L-fucopyr anose.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	Ţ	2	Total	С	О	S	0	0	0
2	1	2	22	12	9	1	U	0	U
2	J	2	Total	С	О	S	0	0	0
2	J	2	22	12	9	1			
2	K	2	Total	С	О	S	0	0	0
	11	2	22	12	9	1	U		
2	Т	2	Total	С	О	S	0	0	0
	П	2	22	12	9	1	0	U	U
2	M	2	Total	С	О	S	0	0	0
	1/1	2	22	12	9	1		U	U

• Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

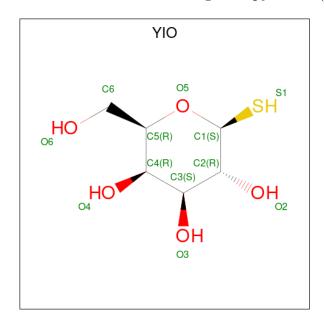


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	В	1	Total Ca 1 1	0	0
3	С	1	Total Ca 1 1	0	0
3	D	1	Total Ca 1 1	0	0
3	Е	1	Total Ca 1 1	0	0
3	F	1	Total Ca 1 1	0	0
3	G	1	Total Ca 1 1	0	0
3	Н	1	Total Ca 1 1	0	0

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0

 $\bullet$  Molecule 5 is 1-thio-beta-D-galactopy ranose (three-letter code: YIO) (formula:  $\rm C_6H_{12}O_5S).$ 



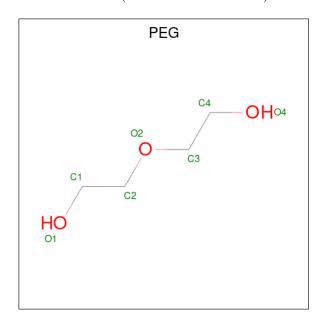
$\mathbf{Mol}$	Chain	Residues	Ato	ms		ZeroOcc	AltConf
5	С	1	Total C	O 5	S 1	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Е	1	Total C O S 12 6 5 1	0	0
5	F	1	Total C O S 12 6 5 1	0	0

• Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	1	Total C O 7 4 3	0	0
6	Н	1	Total C O 7 4 3	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	53	Total O 53 53	0	0
7	В	27	Total O 27 27	0	0
7	С	42	Total O 42 42	0	0
7	D	59	Total O 59 59	0	0
7	Е	54	Total O 54 54	0	0



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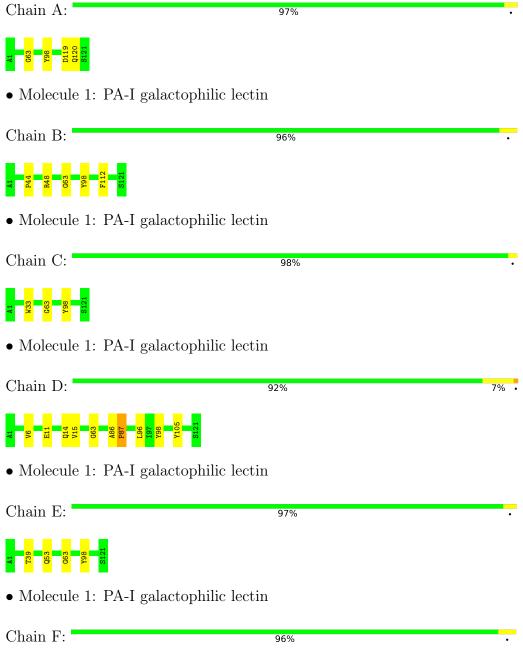
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	F	35	Total O 35 35	0	0
7	G	44	Total O 44 44	0	0
7	Н	39	Total O 39 39	0	0



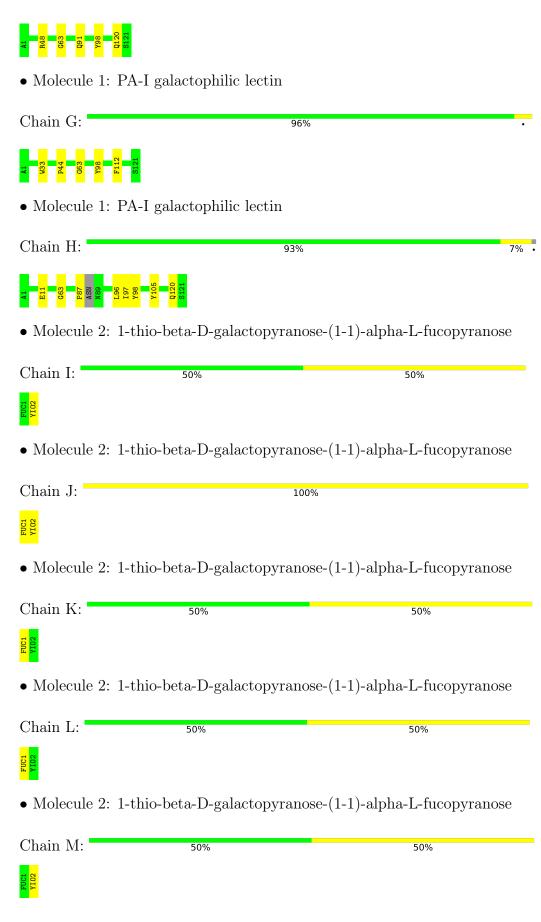
## 3 Residue-property plots (i)

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.

• Molecule 1: PA-I galactophilic lectin









# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	50.90Å 99.82Å 86.84Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	45.39 - 1.70	Depositor
resolution (A)	45.39 - 1.70	EDS
% Data completeness	98.2 (45.39-1.70)	Depositor
(in resolution range)	98.2 (45.39-1.70)	EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.47  (at  1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
Ρ. Р.	0.196 , 0.227	Depositor
$R, R_{free}$	0.206 , $0.234$	DCC
$R_{free}$ test set	4735 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.5	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.32 , 15.1	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.136 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7758	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.28% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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: PEG, YIO, CA, FUC, CL

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	Mol Chain		lengths	Bond angles	
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.46	0/916	0.82	1/1253~(0.1%)
1	В	0.43	0/931	0.73	0/1272
1	С	0.46	0/938	0.75	0/1283
1	D	0.51	0/932	0.82	0/1274
1	Е	0.45	0/941	0.81	0/1286
1	F	0.45	0/935	0.79	0/1277
1	G	0.45	0/942	0.77	0/1287
1	Н	0.48	0/939	0.82	1/1281 (0.1%)
All	All	0.46	0/7474	0.79	$2/10213 \ (0.0\%)$

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

$\mathbf{Mol}$	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
1	Н	120	GLN	N-CA-CB	-5.09	101.44	110.60
1	A	120	GLN	N-CA-CB	-5.04	101.52	110.60

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	D	86	ALA	Peptide
1	D	87	PRO	Peptide

#### 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

1 1 1 1	A B	890	0	0.49	0	6
1		000		843	2	0
		902	0	864	3	0
1	С	906	0	866	2	0
	D	903	0	871	7	0
1	Е	909	0	882	1	0
1	F	906	0	870	4	0
1	G	910	0	882	3	0
1	Н	910	0	874	3	0
2	I	22	0	19	0	0
2	J	22	0	19	0	0
2	K	22	0	19	0	0
2	L	22	0	19	0	0
2	M	22	0	19	0	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
3	С	1	0	0	0	0
3	D	1	0	0	0	0
3	Е	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	Н	1	0	0	0	0
4	A	1	0	0	0	0
5	С	12	0	10	0	0
5	Е	12	0	10	0	0
5	F	12	0	10	0	0
6	Е	7	0	10	0	0
6	Н	7	0	10	0	0
7	A	53	0	0	0	0
7	В	27	0	0	0	0
7	С	42	0	0	0	0
7	D	59	0	0	1	0
7	Е	54	0	0	0	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	F	35	0	0	1	0
7	G	44	0	0	0	0
7	Н	39	0	0	0	0
All	All	7758	0	7097	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 2.

All (22) 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:D:15[B]:VAL:HG22	7:D:330:HOH:O	2.09	0.53
1:D:11:GLU:HG2	1:D:105:TYR:CD1	2.45	0.52
1:D:6[B]:VAL:HG12	1:D:14:GLN:HB3	1.93	0.49
1:B:63:GLY:HA2	1:B:98:TYR:CZ	2.47	0.49
1:A:119:ASP:HA	1:F:120[A]:GLN:HG2	1.95	0.48
1:H:63:GLY:HA2	1:H:98:TYR:CZ	2.49	0.48
1:D:63:GLY:HA2	1:D:98:TYR:CZ	2.50	0.47
1:F:63:GLY:HA2	1:F:98:TYR:CZ	2.51	0.46
1:A:63:GLY:HA2	1:A:98:TYR:CZ	2.52	0.45
1:D:6[B]:VAL:HG11	1:D:96:LEU:HB2	1.97	0.45
1:D:6[B]:VAL:HG11	1:D:96:LEU:CB	2.47	0.45
1:H:11:GLU:HG2	1:H:105:TYR:CD1	2.53	0.43
1:E:63:GLY:HA2	1:E:98:TYR:CZ	2.53	0.43
1:B:44:PRO:HA	1:B:112:PHE:CZ	2.55	0.42
1:G:44:PRO:HA	1:G:112:PHE:CZ	2.55	0.42
1:H:96:LEU:C	1:H:97:ILE:HG13	2.41	0.41
1:F:91:GLN:HG3	7:F:329:HOH:O	2.20	0.41
1:D:11:GLU:HG2	1:D:105:TYR:CG	2.55	0.41
1:G:63:GLY:HA2	1:G:98:TYR:CZ	2.56	0.41
1:C:63:GLY:HA2	1:C:98:TYR:CZ	2.56	0.40
1:F:48:ARG:HD2	1:G:33:TRP:CE3	2.57	0.40
1:B:48:ARG:HD2	1:C:33:TRP:CE3	2.56	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	A	120/121 (99%)	117 (98%)	3 (2%)	0	100	100
1	В	$121/121 \; (100\%)$	117 (97%)	4 (3%)	0	100	100
1	C	122/121 (101%)	119 (98%)	3 (2%)	0	100	100
1	D	121/121 (100%)	115 (95%)	6 (5%)	0	100	100
1	E	122/121 (101%)	119 (98%)	3 (2%)	0	100	100
1	F	121/121 (100%)	117 (97%)	4 (3%)	0	100	100
1	G	122/121 (101%)	119 (98%)	3 (2%)	0	100	100
1	Н	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
All	All	968/968 (100%)	939 (97%)	29 (3%)	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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	A	91/94 (97%)	91 (100%)	0	100	100
1	В	94/94 (100%)	94 (100%)	0	100	100
1	С	95/94 (101%)	95 (100%)	0	100	100
1	D	94/94 (100%)	93 (99%)	1 (1%)	70	60
1	E	96/94 (102%)	94 (98%)	2 (2%)	48	32
1	F	95/94 (101%)	95 (100%)	0	100	100



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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	G	96/94 (102%)	96 (100%)	0	100	100	
1	Н	96/94 (102%)	95 (99%)	1 (1%)	73	64	
All	All	757/752 (101%)	753 (100%)	4 (0%)	86	82	

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	87	PRO
1	Ε	39	THR
1	Е	53	GLN
1	Н	87	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	Н	40	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	Type	Chain	Res	Link	Вс	ond leng	ths	В	ond ang	les
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FUC	I	1	2	10,10,11	0.22	0	14,14,16	0.83	0
2	YIO	I	2	2,3	11,12,12	0.23	0	15,17,17	1.07	1 (6%)
2	FUC	J	1	2	10,10,11	0.27	0	14,14,16	1.04	1 (7%)
2	YIO	J	2	2,3	11,12,12	0.41	0	15,17,17	1.13	1 (6%)
2	FUC	K	1	2	10,10,11	0.49	0	14,14,16	1.51	2 (14%)
2	YIO	K	2	2,3	11,12,12	0.48	0	15,17,17	0.93	0
2	FUC	L	1	2	10,10,11	0.34	0	14,14,16	0.76	1 (7%)
2	YIO	L	2	2,3	11,12,12	0.39	0	15,17,17	0.92	0
2	FUC	M	1	2	10,10,11	0.56	0	14,14,16	1.11	0
2	YIO	M	2	2,3	11,12,12	0.29	0	15,17,17	1.11	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	FUC	I	1	2	-	-	0/1/1/1
2	YIO	I	2	2,3	-	0/2/22/22	0/1/1/1
2	FUC	J	1	2	-	-	0/1/1/1
2	YIO	J	2	2,3	-	0/2/22/22	0/1/1/1
2	FUC	K	1	2	-	-	0/1/1/1
2	YIO	K	2	2,3	-	0/2/22/22	0/1/1/1
2	FUC	L	1	2	-	-	0/1/1/1
2	YIO	L	2	2,3	-	0/2/22/22	0/1/1/1
2	FUC	M	1	2	-	-	0/1/1/1
2	YIO	M	2	2,3	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
2	K	1	FUC	O2-C2-C3	-3.60	102.93	110.14
2	I	2	YIO	O4-C4-C5	2.86	116.40	109.30
2	M	2	YIO	O5-C1-C2	-2.72	106.89	110.31
2	K	1	FUC	O2-C2-C1	2.39	114.05	109.15
2	J	1	FUC	O2-C2-C3	-2.39	105.36	110.14
2	L	1	FUC	O5-C1-C2	-2.29	107.23	110.77
2	J	2	YIO	O4-C4-C5	2.13	114.58	109.30
2	M	2	YIO	O4-C4-C5	2.08	114.47	109.30



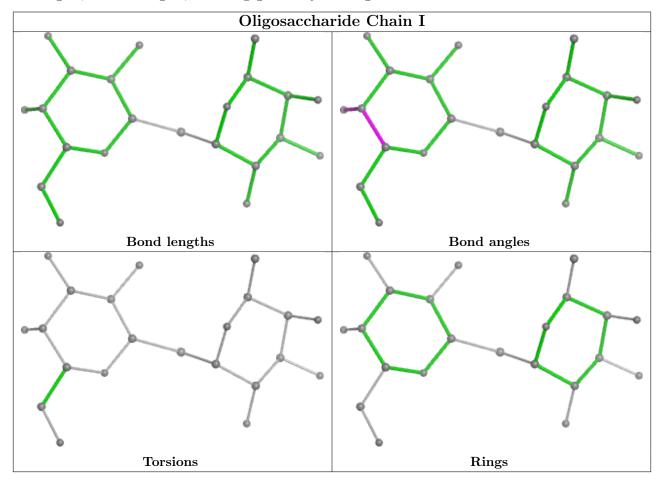
There are no chirality outliers.

There are no torsion outliers.

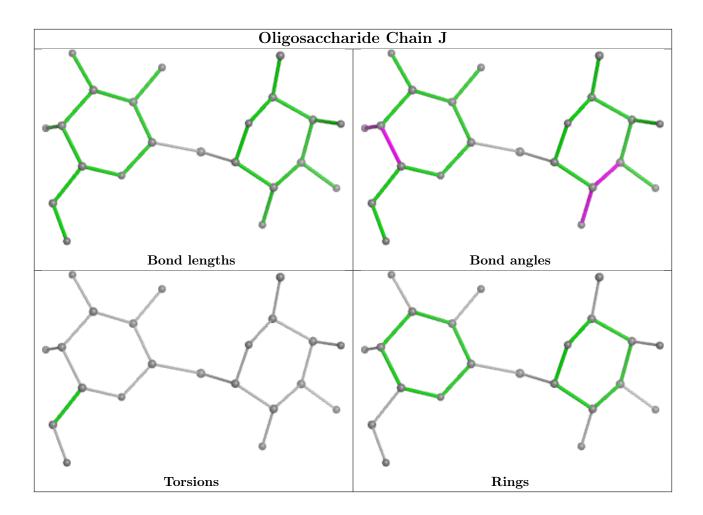
There are no ring outliers.

No monomer is involved in short contacts.

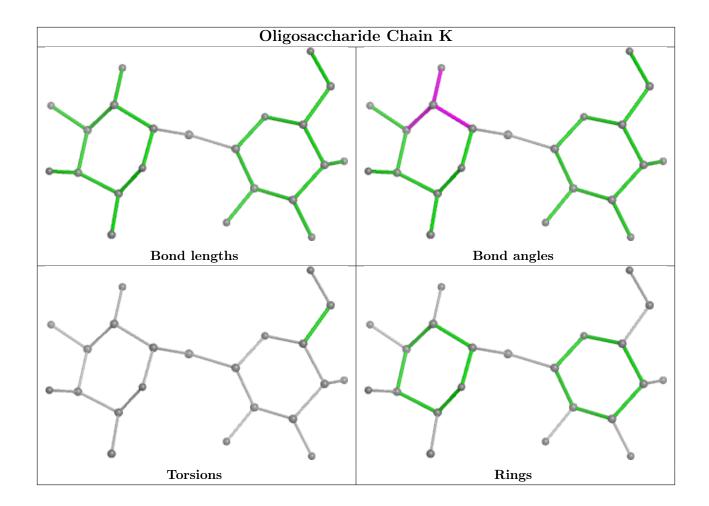
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



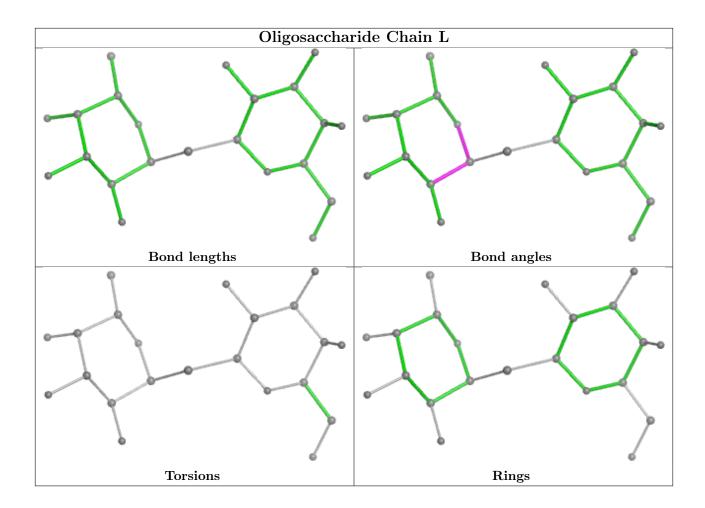




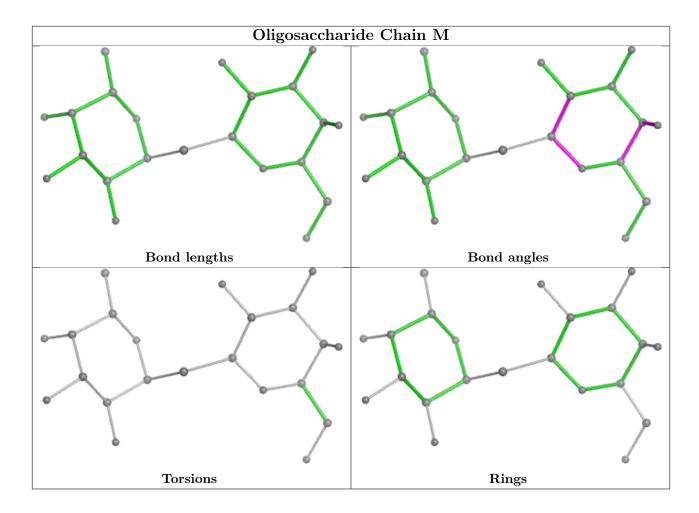












#### 5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 9 are monoatomic - leaving 5 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	Mol Type	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	PEG	Е	203	-	6,6,6	0.41	0	5,5,5	0.30	0
5	YIO	Е	202	3	11,12,12	0.37	0	15,17,17	1.13	1 (6%)
5	YIO	F	202	3	11,12,12	0.51	0	15,17,17	1.46	2 (13%)
6	PEG	Н	202	-	6,6,6	0.33	0	5,5,5	0.37	0
5	YIO	С	202	3	11,12,12	0.34	0	15,17,17	0.78	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
6	PEG	Е	203	-	-	2/4/4/4	-
5	YIO	Е	202	3	-	0/2/22/22	0/1/1/1
5	YIO	F	202	3	-	0/2/22/22	0/1/1/1
6	PEG	Н	202	-	-	2/4/4/4	-
5	YIO	С	202	3	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	Е	202	YIO	O4-C4-C5	2.95	116.61	109.30
5	F	202	YIO	O5-C1-C2	-2.71	106.90	110.31
5	F	202	YIO	O4-C4-C5	2.24	114.85	109.30

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	Е	203	PEG	O1-C1-C2-O2
6	Н	202	PEG	C1-C2-O2-C3
6	Н	202	PEG	O1-C1-C2-O2
6	Е	203	PEG	C1-C2-O2-C3

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)

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	Analysed	<rsrz></rsrz>	7	#RSF	ZZ>2	$OWAB(A^2)$	Q<0.9
1	A	121/121 (100%)	-1.24	0	100	100	9, 19, 30, 43	1 (0%)
1	В	121/121 (100%)	-1.13	0	100	100	11, 21, 36, 44	2 (1%)
1	С	121/121 (100%)	-1.23	0	100	100	10, 18, 34, 40	3 (2%)
1	D	121/121 (100%)	-1.27	0	100	100	10, 16, 28, 50	2 (1%)
1	E	121/121 (100%)	-1.24	0	100	100	10, 18, 28, 46	3 (2%)
1	F	121/121 (100%)	-1.18	0	100	100	11, 19, 34, 48	2 (1%)
1	G	121/121 (100%)	-1.24	0	100	100	11, 18, 30, 38	3 (2%)
1	Н	120/121 (99%)	-1.25	0	100	100	7, 17, 30, 43	3 (2%)
All	All	967/968 (99%)	-1.22	0	100	100	7, 18, 33, 50	19 (1%)

There are no RSRZ outliers to report.

#### 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.

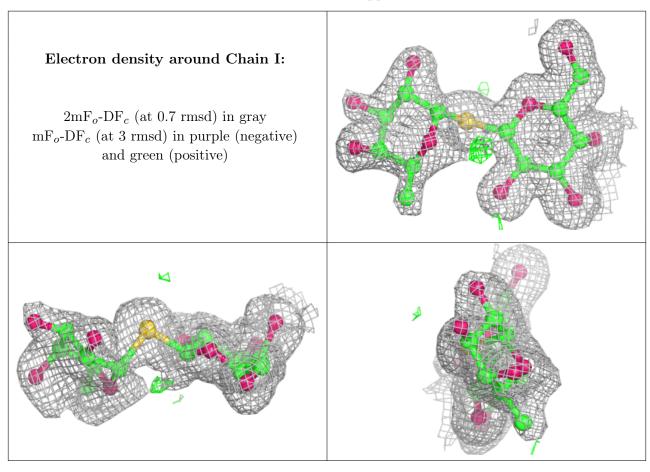
Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
2	FUC	I	1	10/11	0.97	0.05	32,35,38,41	0
2	FUC	J	1	10/11	0.97	0.06	34,36,39,39	0
2	YIO	J	2	12/12	0.98	0.05	31,35,40,43	0



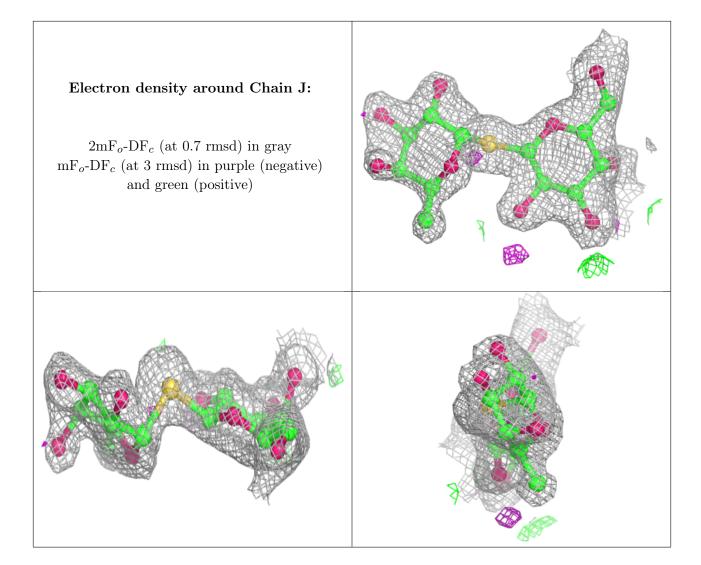
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	FUC	M	1	10/11	0.98	0.05	26,28,31,33	0
2	FUC	K	1	10/11	0.99	0.04	26,28,31,32	0
2	YIO	K	2	12/12	0.99	0.03	18,20,22,23	0
2	FUC	L	1	10/11	0.99	0.04	35,38,42,47	0
2	YIO	L	2	12/12	0.99	0.03	21,22,25,28	0
2	YIO	I	2	12/12	0.99	0.03	19,21,23,24	0
2	YIO	M	2	12/12	0.99	0.04	17,20,23,24	0

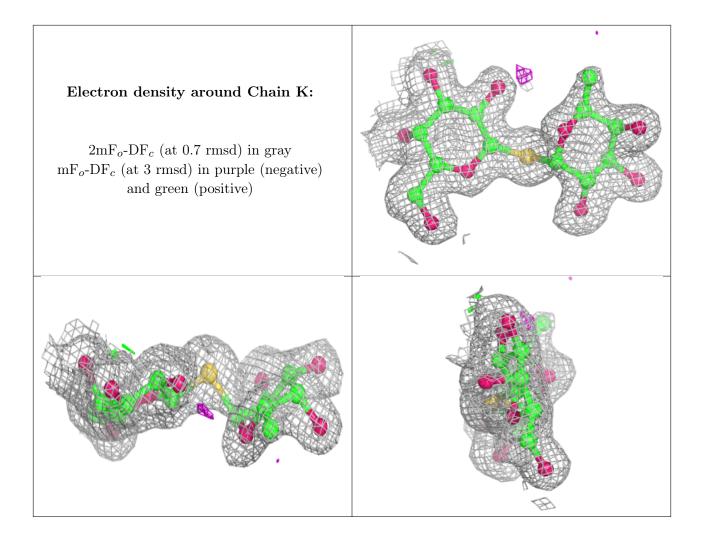
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.







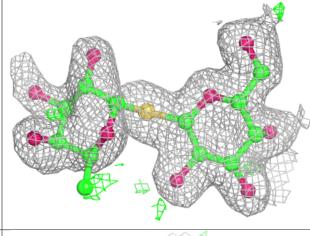


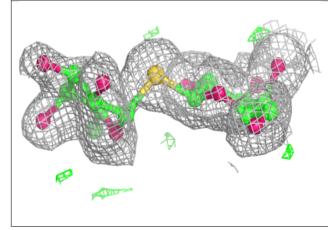


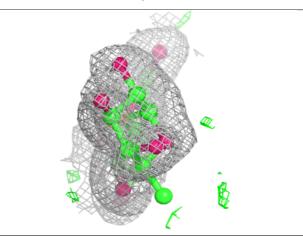


# Electron density around Chain L:

 $2 {
m mF}_o {
m -DF}_c$  (at 0.7 rmsd) in gray  ${
m mF}_o {
m -DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)

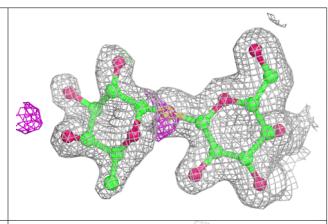


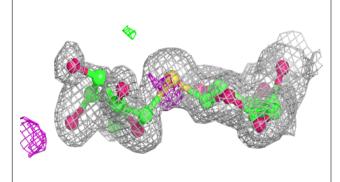


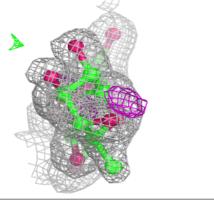


#### Electron density around Chain M:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 0.7 rmsd) in gray  $\mathrm{mF}_o\text{-}\mathrm{DF}_c$  (at 3 rmsd) in purple (negative) and green (positive)









#### 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
6	PEG	Е	203	7/7	0.98	0.05	35,40,43,47	0
6	PEG	Н	202	7/7	0.98	0.06	32,40,42,45	0
5	YIO	С	202	12/12	0.99	0.04	23,27,33,34	0
5	YIO	Е	202	12/12	0.99	0.03	21,24,27,29	0
5	YIO	F	202	12/12	0.99	0.03	24,26,30,31	0
3	CA	В	201	1/1	0.99	0.04	29,29,29,29	0
3	CA	F	201	1/1	0.99	0.02	24,24,24,24	0
3	CA	Н	201	1/1	1.00	0.01	15,15,15,15	0
4	CL	A	202	1/1	1.00	0.05	28,28,28,28	0
3	CA	С	201	1/1	1.00	0.01	23,23,23,23	0
3	CA	D	201	1/1	1.00	0.01	15,15,15,15	0
3	CA	Е	201	1/1	1.00	0.01	19,19,19,19	0
3	CA	A	201	1/1	1.00	0.03	18,18,18,18	0
3	CA	G	201	1/1	1.00	0.03	18,18,18,18	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

