



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2020 – 02:07 PM BST

PDB ID : 1JXN  
Title : Crystal Structure of the Lectin I from Ulex europaeus in complex with the methyl glycoside of alpha-L-fucose  
Authors : Audette, G.F.; Olson, D.J.H.; Ross, A.R.S.; Quail, J.W.; Delbaere, L.T.J.  
Deposited on : 2001-09-07  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

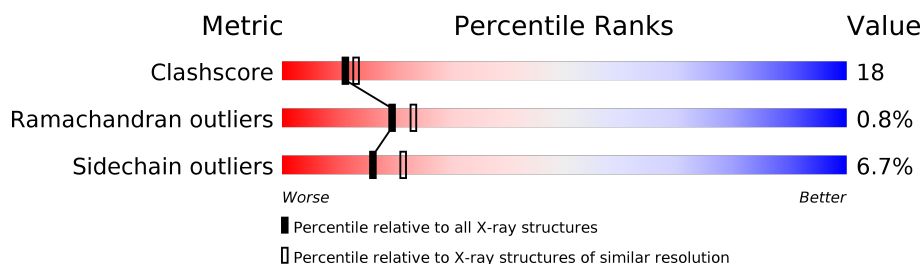
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	242	
1	B	242	
1	C	242	
1	D	242	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7773 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 anti-H(O) lectin I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	0	0
			1864	1191	303	366	4			
1	B	240	Total	C	N	O	S	0	0	0
			1862	1192	302	364	4			
1	C	240	Total	C	N	O	S	0	0	0
			1866	1193	304	365	4			
1	D	239	Total	C	N	O	S	0	0	0
			1851	1185	300	362	4			

There are 40 discrepancies between the modelled and reference sequences:

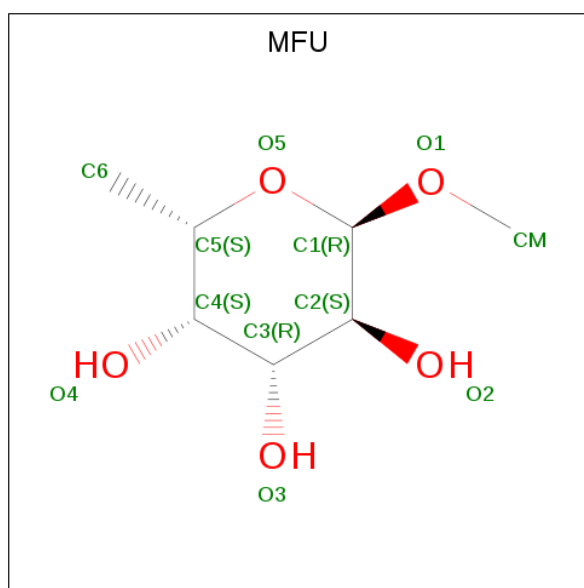
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	ASN	ASP	conflict	UNP P22972
A	65	LEU	VAL	conflict	UNP P22972
A	111	ASN	GLU	conflict	UNP P22972
A	?	-	ASP	deletion	UNP P22972
A	115	CYS	ASN	conflict	UNP P22972
A	136	TRP	ASP	conflict	UNP P22972
A	149	CYS	ARG	conflict	UNP P22972
A	217	SER	GLY	conflict	UNP P22972
A	236	THR	ASN	conflict	UNP P22972
A	237	PHE	LEU	conflict	UNP P22972
B	23	ASN	ASP	conflict	UNP P22972
B	65	LEU	VAL	conflict	UNP P22972
B	111	ASN	GLU	conflict	UNP P22972
B	?	-	ASP	deletion	UNP P22972
B	115	CYS	ASN	conflict	UNP P22972
B	136	TRP	ASP	conflict	UNP P22972
B	149	CYS	ARG	conflict	UNP P22972
B	217	SER	GLY	conflict	UNP P22972
B	236	THR	ASN	conflict	UNP P22972
B	237	PHE	LEU	conflict	UNP P22972
C	23	ASN	ASP	conflict	UNP P22972

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	65	LEU	VAL	conflict	UNP P22972
C	111	ASN	GLU	conflict	UNP P22972
C	?	-	ASP	deletion	UNP P22972
C	115	CYS	ASN	conflict	UNP P22972
C	136	TRP	ASP	conflict	UNP P22972
C	149	CYS	ARG	conflict	UNP P22972
C	217	SER	GLY	conflict	UNP P22972
C	236	THR	ASN	conflict	UNP P22972
C	237	PHE	LEU	conflict	UNP P22972
D	23	ASN	ASP	conflict	UNP P22972
D	65	LEU	VAL	conflict	UNP P22972
D	111	ASN	GLU	conflict	UNP P22972
D	?	-	ASP	deletion	UNP P22972
D	115	CYS	ASN	conflict	UNP P22972
D	136	TRP	ASP	conflict	UNP P22972
D	149	CYS	ARG	conflict	UNP P22972
D	217	SER	GLY	conflict	UNP P22972
D	236	THR	ASN	conflict	UNP P22972
D	237	PHE	LEU	conflict	UNP P22972

- Molecule 2 is methyl alpha-L-fucopyranoside (three-letter code: MFU) (formula: C<sub>7</sub>H<sub>14</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	7	5		
2	B	1	Total	C	O	0	0
			12	7	5		

Continued on next page...

*Continued from previous page...*

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			12	7	5		
2	D	1	Total	C	O	0	0
			12	7	5		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		
3	D	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		
4	D	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			8	6	2		

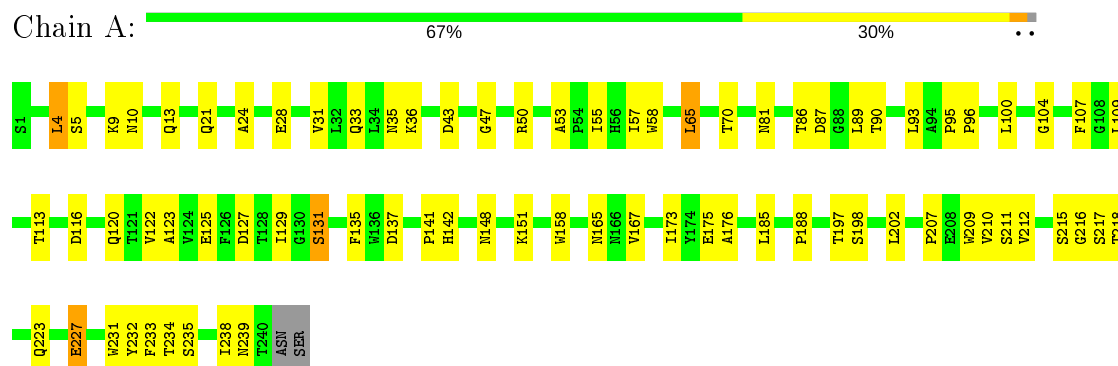
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	73	Total	O	0	0
			73	73		
6	B	80	Total	O	0	0
			80	80		
6	C	62	Total	O	0	0
			62	62		
6	D	51	Total	O	0	0
			51	51		

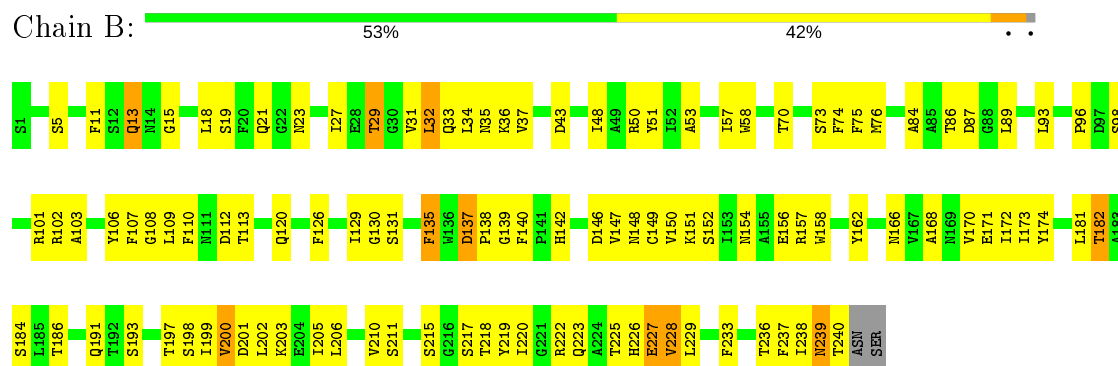
### 3 Residue-property plots

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.

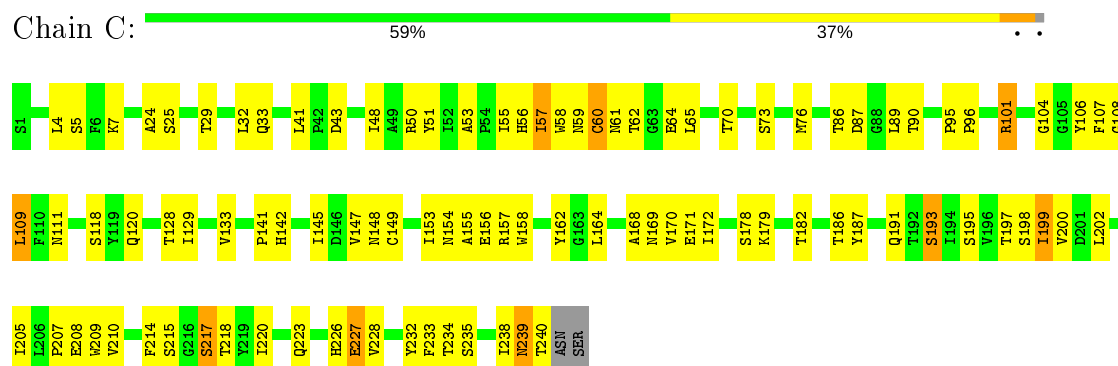
#### • Molecule 1: anti-H(O) lectin I



#### • Molecule 1: anti-H(O) lectin I



#### • Molecule 1: anti-H(O) lectin I



● Molecule 1: anti-H(O) lectin I

Chain D: 

68%

31%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.81Å 69.00Å 119.02Å 90.00° 106.76° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 33.02 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.30) 82.5 (33.02-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 2.29Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.202 , 0.289 0.263 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.7	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 47.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7773	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 62.18 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1708e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MRD, CA, MN, MFU

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	0.50	0/1913	0.74	1/2609 (0.0%)
1	B	0.49	0/1911	0.71	0/2605
1	C	0.50	0/1915	0.74	0/2610
1	D	0.48	0/1900	0.74	1/2591 (0.0%)
All	All	0.49	0/7639	0.74	2/10415 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100	LEU	CA-CB-CG	5.40	127.71	115.30
1	D	91	PHE	N-CA-C	-5.31	96.67	111.00

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	A	1864	0	1775	60	0
1	B	1862	0	1778	86	0
1	C	1866	0	1781	69	0
1	D	1851	0	1760	56	0
2	A	12	0	14	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	12	0	14	4	0
2	C	12	0	14	0	0
2	D	12	0	14	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	C	8	0	14	3	0
6	A	73	0	0	3	0
6	B	80	0	0	10	0
6	C	62	0	0	3	0
6	D	51	0	0	4	0
All	All	7773	0	7164	262	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 18.

The worst 5 of 262 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:B:50:ARG:HH22	1:B:98:SER:HB2	1.26	0.96
1:C:60:CYS:SG	5:C:901:MRD:H3C1	2.11	0.91
1:C:153:ILE:HG23	6:C:957:HOH:O	1.82	0.79
1:C:60:CYS:SG	5:C:901:MRD:O4	2.40	0.75
1:D:136:TRP:HB2	1:D:151:LYS:HG2	1.70	0.74

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	A	238/242 (98%)	219 (92%)	18 (8%)	1 (0%)	34	42
1	B	238/242 (98%)	218 (92%)	17 (7%)	3 (1%)	12	12
1	C	238/242 (98%)	213 (90%)	22 (9%)	3 (1%)	12	12
1	D	237/242 (98%)	221 (93%)	15 (6%)	1 (0%)	34	42
All	All	951/968 (98%)	871 (92%)	72 (8%)	8 (1%)	19	23

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	107	PHE
1	C	239	ASN
1	C	107	PHE
1	D	40	ASN
1	B	135	PHE

### 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	Percentiles	
1	A	206/209 (99%)	194 (94%)	12 (6%)	20	27
1	B	205/209 (98%)	190 (93%)	15 (7%)	14	18
1	C	206/209 (99%)	189 (92%)	17 (8%)	11	14
1	D	203/209 (97%)	192 (95%)	11 (5%)	22	30
All	All	820/836 (98%)	765 (93%)	55 (7%)	16	21

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	227	GLU
1	C	60	CYS
1	D	173	ILE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	228	VAL
1	C	29	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	134	ASN
1	C	33	GLN
1	C	239	ASN
1	B	61	ASN
1	D	23	ASN

### 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](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 8 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	MRD	C	901	-	7,7,7	0.63	0	9,10,10	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MFU	B	602	-	12,12,12	1.52	2 (16%)	17,17,17	3.12	1 (5%)
2	MFU	A	501	-	12,12,12	1.75	2 (16%)	17,17,17	3.22	1 (5%)
2	MFU	D	804	-	12,12,12	1.68	2 (16%)	17,17,17	3.13	2 (11%)
2	MFU	C	703	-	12,12,12	1.66	2 (16%)	17,17,17	3.07	1 (5%)

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	MRD	C	901	-	-	2/5/5/5	-
2	MFU	B	602	-	-	2/2/22/22	0/1/1/1
2	MFU	A	501	-	-	2/2/22/22	0/1/1/1
2	MFU	D	804	-	-	2/2/22/22	0/1/1/1
2	MFU	C	703	-	-	0/2/22/22	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	MFU	O1-C1	4.73	1.48	1.40
2	D	804	MFU	O1-C1	4.65	1.48	1.40
2	C	703	MFU	O1-C1	4.48	1.47	1.40
2	B	602	MFU	O1-C1	4.09	1.47	1.40
2	A	501	MFU	O5-C1	2.75	1.48	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	MFU	CM-O1-C1	12.98	133.31	113.27
2	B	602	MFU	CM-O1-C1	12.49	132.56	113.27
2	D	804	MFU	CM-O1-C1	12.39	132.40	113.27
2	C	703	MFU	CM-O1-C1	12.35	132.34	113.27
2	D	804	MFU	O1-C1-C2	2.42	110.99	108.15

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	MFU	O5-C1-O1-CM

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	B	602	MFU	O5-C1-O1-CM
2	B	602	MFU	C2-C1-O1-CM
2	A	501	MFU	C2-C1-O1-CM
2	D	804	MFU	C2-C1-O1-CM

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	901	MRD	3	0
2	B	602	MFU	4	0
2	A	501	MFU	1	0
2	D	804	MFU	1	0

## 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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.