

wwPDB X-ray Structure Validation Summary Report (i)

Oct 31, 2023 – 11:41 PM EDT

PDB ID	:	3U8Q
Title	:	Crystal Structure of C-lobe of Bovine lactoferrin Complexed with Phenyl-
		Propanolamine at 1.97 A Resolution
Authors	:	Shukla, P.K.; Gautam, L.; Sinha, M.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on	:	2011-10-17
Resolution	:	1.97 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 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:

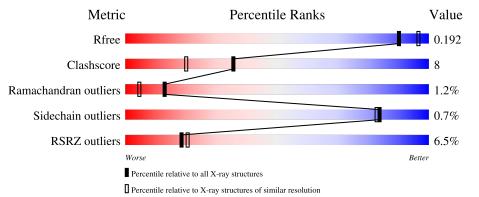
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.97 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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	335	5% 84%	16%
2	В	6	67%	17%
3	С	2	50%	50%
3	D	2	100%	



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2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 2974 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 Lactotransferrin.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	335	Total 2560	C 1593	N 448	O 499	S 20	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	565	LYS	ASN	conflict	UNP P24627
А	608	GLU	LYS	conflict	UNP P24627

• Molecule 2 is a protein called C-terminal peptide of Lactotransferrin.

Mol	Chain	Residues		Ato	\mathbf{ms}			ZeroOcc	AltConf	Trace
2	В	6	Total 44	C 29	N 6	0 8	S 1	0	0	0

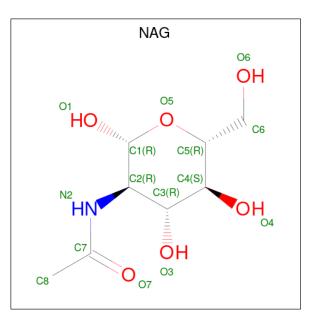
• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



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

• Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	А	1	Total	С	Ν	Ο	0	0
	11	1	14	8	1	5		Ŭ

• Molecule 5 is FE (III) ION (three-letter code: FE) (formula: Fe).

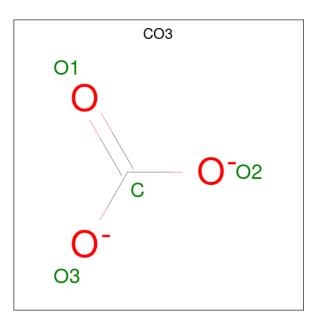
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total Fe 1 1	0	0

• Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	2	Total Zn 2 2	0	0

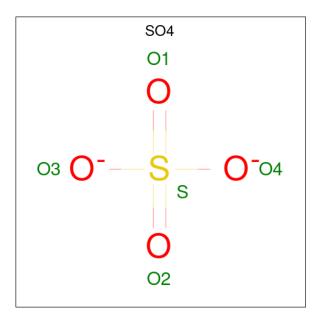
• Molecule 7 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	А	1	Total 4	C 1	O 3	0	0

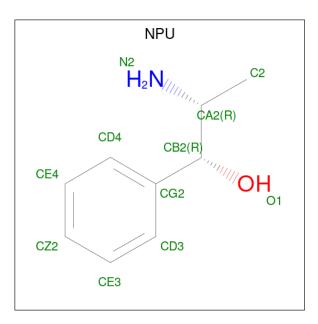
• Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
8	А	1	Total 5	0 4	S 1	0	0

• Molecule 9 is (1R,2R)-2-amino-1-phenyl propan-1-ol (three-letter code: NPU) (formula: $\rm C_9H_{13}NO).$





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	А	1	Total C N Q 11 9 1 2) 1	0	0

• Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	275	Total O 275 275	0	0
10	В	2	Total O 2 2	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.

5%		
Chain A:	84%	16%
Y342 T343 R344 P352 Q364 1373 T373 D395	K404 K416 K413 K420 K420 K420 K420 K420 K420 K420 K420 K420 K426 K456 K456 <th< td=""><td>V461 1462 R463 R463 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A466 A464 A464 A466 A464 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A6 A5 A6 A5 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A7 A7 A7 A7 A7 A7 A7</td></th<>	V461 1462 R463 R463 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A464 A466 A464 A464 A466 A464 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A466 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A46 A6 A5 A6 A5 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A6 A7 A7 A7 A7 A7 A7 A7 A7
N553 N553 K565 R566 E567 L572 L572 A552 A552 R593 N594 H593	H666 H666 N621 P626 N622 F628 F629 F629 F629 F629 F629 F629 F629 F634 F653 F654 F654 F653 F654 F653 F654 F653 F654 F657 F657 F657 F657 F657 F657 F657 F657	1669 18673 18676
• Molecule 2: C-t	erminal peptide of Lactotransferrin	
	67%	
Chain B:	83%	17%
L681 E662 C663 C6683 A685 F685 F686		
• Molecule 3: 2-a opyranose	cetamido-2-deoxy-beta-D-glucopyra	nose-(1-4)-2-acetamido
Chain C:	50%	50%

• Molecule 1: Lactotransferrin

NAG1 NAG2

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:

100%

NAG1 NAG2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	62.44Å 49.92 Å 65.49 Å	Depositor
a, b, c, α , β , γ	90.00° 107.26° 90.00°	Depositor
Resolution (Å)	39.01 - 1.97	Depositor
nesolution (A)	39.01 - 1.97	EDS
% Data completeness	99.5 (39.01 - 1.97)	Depositor
(in resolution range)	99.7 (39.01 - 1.97)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.05	Depositor
$< I/\sigma(I) > 1$	2.48 (at 1.97 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
B B.	0.179 , 0.198	Depositor
R, R_{free}	0.176 , 0.192	DCC
R_{free} test set	1376 reflections (5.03%)	wwPDB-VP
Wilson B-factor $(Å^2)$	27.7	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 59.2	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.020 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2974	wwPDB-VP
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.02% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: CO3, NPU, ZN, FE, SO4, NAG

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	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.37	0/2608	0.69	1/3533~(0.0%)
2	В	0.41	0/44	0.79	0/58
All	All	0.37	0/2652	0.69	1/3591~(0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	А	444	GLU	N-CA-C	5.49	125.83	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	А	2560	0	2480	43	0
2	В	44	0	39	1	0
3	С	28	0	25	1	0
3	D	28	0	25	0	0
4	А	14	0	13	1	0
5	А	1	0	0	0	0
6	А	2	0	0	0	0
7	А	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes		
8	А	5	0	0	0	0		
9	А	11	0	13	5	0		
10	А	275	0	0	0	0		
10	В	2	0	0	0	0		
All	All	2974	0	2595	43	0		

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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 8.

The worst 5 of 43 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:565:LYS:HE3	1:A:567:GLU:H	1.24	0.99
1:A:342:TYR:HA	1:A:606:HIS:CE1	2.07	0.87
1:A:342:TYR:HA	1:A:606:HIS:HE1	1.37	0.86
1:A:565:LYS:HE3	1:A:567:GLU:N	2.02	0.73
1:A:663:THR:O	1:A:667:THR:HG23	1.89	0.73

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	333/335~(99%)	314 (94%)	16~(5%)	3~(1%)	17 8
2	В	4/6~(67%)	2 (50%)	1 (25%)	1 (25%)	0 0
All	All	337/341~(99%)	316~(94%)	17~(5%)	4 (1%)	13 4

All (4) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	А	416	LYS
1	А	420	HIS
1	А	634	SER
2	В	682	GLU

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	278/278~(100%)	276~(99%)	2(1%)	84 83		
2	В	4/4~(100%)	4 (100%)	0	100 100		
All	All	282/282~(100%)	280~(99%)	2(1%)	84 83		

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	342	TYR
1	А	515	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	360	GLN
1	А	551	ASN
1	А	606	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)

4 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	Bo	Bond lengths			Bond angles		
10101		Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2	
3	NAG	С	1	3,1	14,14,15	1.19	2 (14%)	17,19,21	1.59	4 (23%)	
3	NAG	С	2	3	14,14,15	0.88	0	17,19,21	1.10	1 (5%)	
3	NAG	D	1	3,1	14,14,15	1.26	2 (14%)	17,19,21	1.99	5 (29%)	
3	NAG	D	2	3	14,14,15	0.65	0	17,19,21	1.00	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
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	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
3	D	1	NAG	O5-C1	-2.42	1.39	1.43
3	С	1	NAG	C2-N2	-2.30	1.42	1.46
3	С	1	NAG	O5-C1	-2.29	1.40	1.43
3	D	1	NAG	O7-C7	-2.10	1.18	1.23

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	D	1	NAG	C1-O5-C5	5.04	119.03	112.19
3	D	1	NAG	C3-C4-C5	-4.05	103.01	110.24
3	С	1	NAG	C1-O5-C5	3.67	117.16	112.19

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	С	2	NAG	O4-C4-C5	2.81	116.26	109.30
3	С	1	NAG	C1-C2-N2	-2.79	105.73	110.49

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	2	NAG	C4-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6

There are no ring outliers.

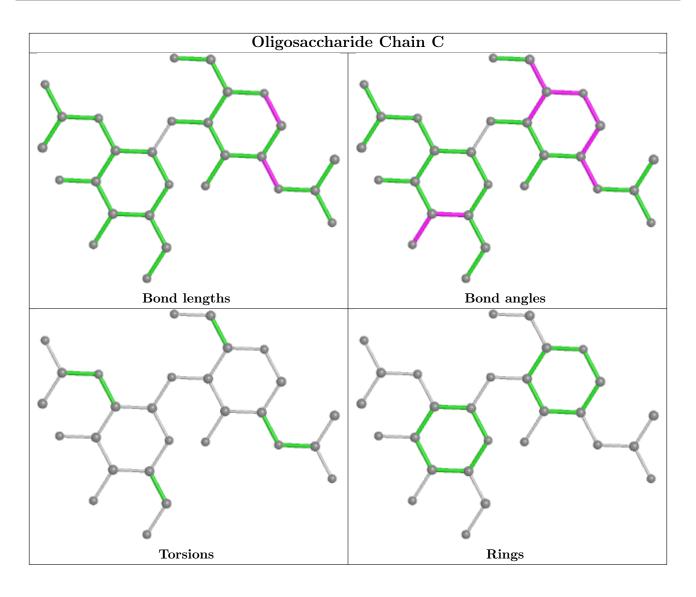
1 monomer is involved in 1 short contact:

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

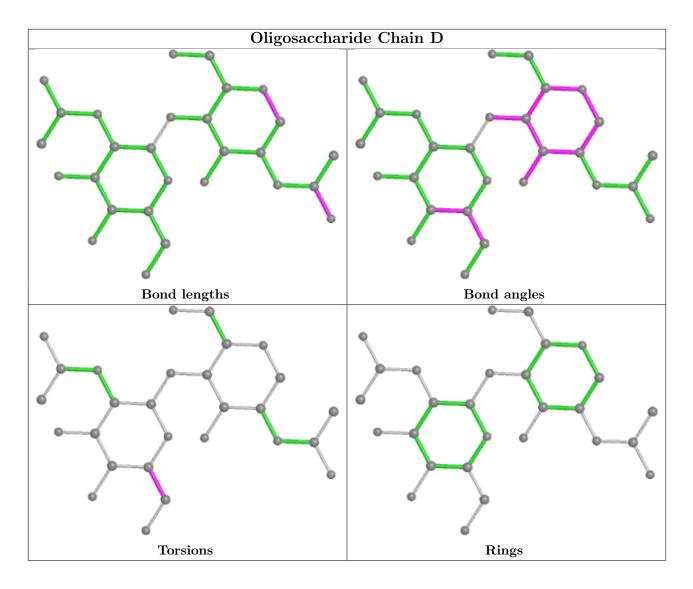
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	s Link	Bo	Bond lengths			Bond angles		
IVIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
9	NPU	А	7231	-	11,11,11	1.67	3 (27%)	12,14,14	2.91	5 (41%)	
7	CO3	А	697	5	2,3,3	0.54	0	2,3,3	0.24	0	
8	SO4	А	698	-	4,4,4	0.25	0	$6,\!6,\!6$	0.05	0	



Γ	Mol	Туре	Chain	Res Link	Bond lengths			Bond angles			
					LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
	4	NAG	А	687	1	$14,\!14,\!15$	0.91	1 (7%)	$17,\!19,\!21$	1.90	5 (29%)

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
9	NPU	А	7231	-	-	4/8/8/8	0/1/1/1
4	NAG	А	687	1	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
9	А	7231	NPU	CD3-CG2	2.79	1.43	1.39
9	А	7231	NPU	CG2-CB2	2.77	1.55	1.51
4	А	687	NAG	O5-C1	-2.42	1.39	1.43
9	А	7231	NPU	O1-CB2	-2.12	1.38	1.42

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
9	А	7231	NPU	CG2-CB2-CA2	6.94	123.36	112.34
9	А	7231	NPU	CD3-CG2-CB2	4.44	127.35	120.73
4	А	687	NAG	O5-C1-C2	-4.41	104.33	111.29
4	А	687	NAG	C1-O5-C5	3.45	116.87	112.19
9	А	7231	NPU	CD4-CG2-CD3	-3.10	114.42	118.29

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	А	7231	NPU	O1-CB2-CG2-CD4
9	А	7231	NPU	O1-CB2-CG2-CD3
9	А	7231	NPU	CA2-CB2-CG2-CD4
9	А	7231	NPU	CA2-CB2-CG2-CD3

There are no ring outliers.

2 monomers are involved in 6 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	А	7231	NPU	5	0
4	А	687	NAG	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 (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 > 2	$OWAB(Å^2)$	$\mathbf{Q}{<}0.9$
1	А	335/335~(100%)	0.35	18 (5%) 25 28	19, 31, 66, 100	1 (0%)
2	В	6/6~(100%)	4.25	4 (66%) 0 0	62, 68, 95, 97	0
All	All	341/341 (100%)	0.42	22 (6%) 18 20	19, 31, 68, 100	1 (0%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	420	HIS	11.5
1	А	418	SER	11.4
1	А	422	SER	11.1
1	А	423	LEU	9.8
1	А	342	TYR	8.9

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

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

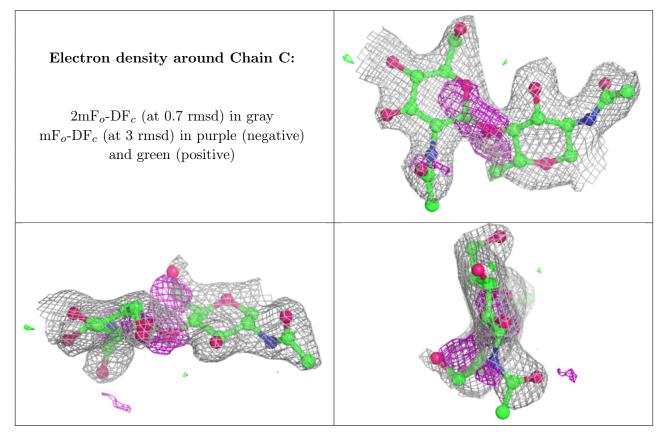
6.3 Carbohydrates (i)

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.

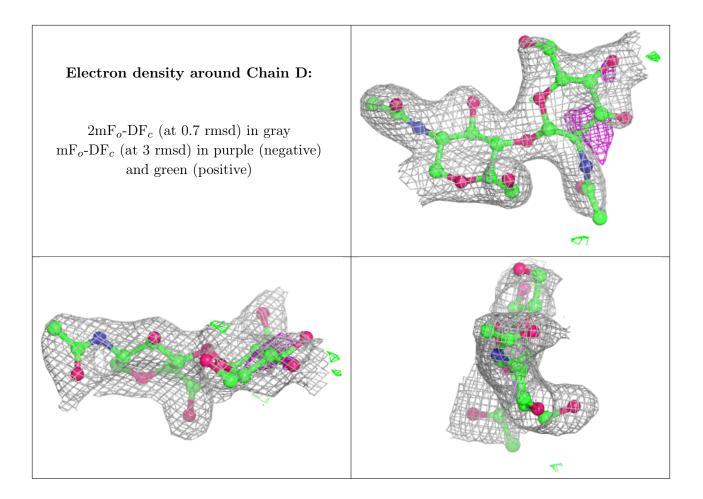
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	NAG	D	2	14/15	0.80	0.29	44,53,57,58	0
3	NAG	С	2	14/15	0.84	0.36	47,51,53,56	0
3	NAG	С	1	14/15	0.84	0.24	$45,\!46,\!56,\!56$	0
3	NAG	D	1	14/15	0.93	0.10	36,42,51,56	0



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
9	NPU	А	7231	11/11	0.67	0.32	43,47,52,53	0
4	NAG	А	687	14/15	0.79	0.32	45,52,57,58	0
6	ZN	А	696	1/1	0.97	0.13	33,33,33,33	0
8	SO4	А	698	5/5	0.98	0.08	61,62,62,64	0
7	CO3	А	697	4/4	0.98	0.09	19,20,20,23	0
6	ZN	А	695	1/1	0.99	0.13	29,29,29,29	0
5	FE	А	694	1/1	1.00	0.14	22,22,22,22	0

6.5 Other polymers (i)

There are no such residues in this entry.

