

wwPDB X-ray Structure Validation Summary Report (i)

Aug 7, 2020 – 08:36 PM BST

PDB ID	:	4F JP
Title	:	Crystal Structure of C-lobe of Bovine lactoferrin Complexed with Naproxen
		at 1.68 A Resolution
Authors	:	Shukla, P.K.; Gautam, L.; Sinha, M.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on	:	2012-06-12
$\operatorname{Resolution}$:	1.68 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 following versions of software and data (see references (1)) were used in the production of this report:

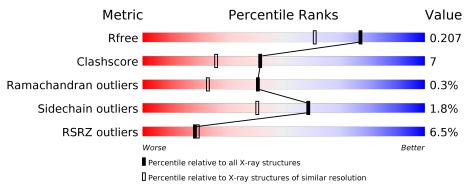
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\rm CCP4$:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.68 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	$6780 \ (1.70-1.66)$
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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 >=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%	18% •
2	В	6	67%	33%
3	С	2	100%	
3	D	2	100%	

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 crite-



ria:

Mol	Type	Chain	\mathbf{Res}	Chirality	Geometry	Clashes	Electron density
9	NPS	А	711	-	-	-	Х



2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 3042 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	A	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
А	565	LYS	ASN	SEE REMARK 999	UNP P24627
А	608	GLU	LYS	SEE REMARK 999	UNP P24627

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

Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf	Trace
2	В	6	Total 45	C 29	N 6	0 9	S 1	0	0	0

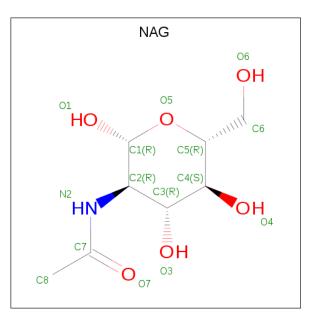
• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



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: $C_8H_{15}NO_6$).





I	Mol	Chain	Residues	A	ton	ns		ZeroOcc	AltConf
	4	А	1	Total 14	С 8	N 1	0 5	0	0

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

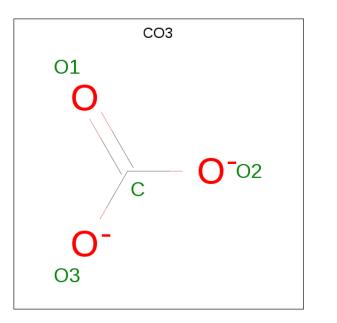
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total Fe 1 1	0	0

• 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

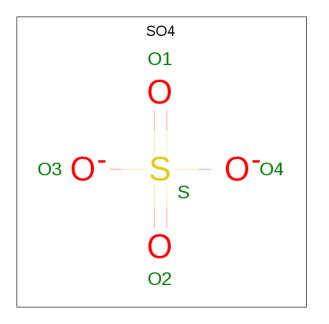
• Molecule 7 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).





Mol	Chain	Residues	Ate	oms		ZeroOcc	AltConf
7	А	1	Total 4	$\begin{array}{c} \mathrm{C} \\ 1 \end{array}$	O 3	0	0

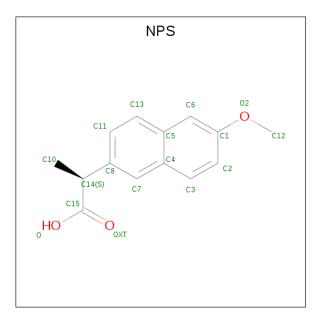
• Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Ato	\mathbf{ms}		ZeroOcc	AltConf
8	А	1	Total 5	0 4	S 1	0	0

• Molecule 9 is (2S)-2-(6-methoxynaphthalen-2-yl) propanoic acid (three-letter code: NPS) (formula: $C_{14}H_{14}O_3$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
9	А	1	Total 17	C 14	O 3	0	0

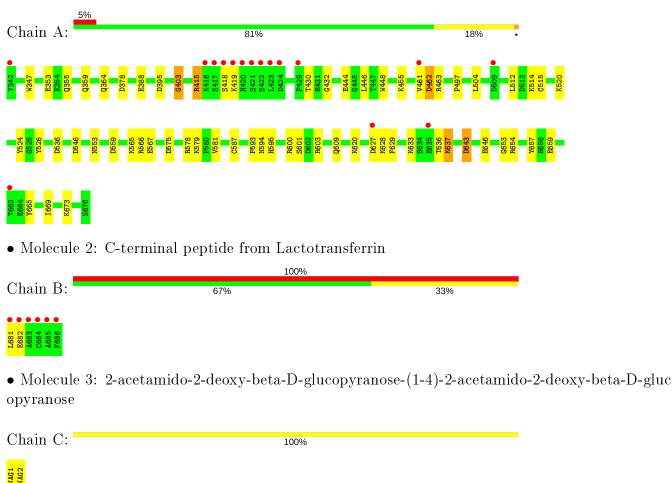
• Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	336	Total O 336 336	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.



• Molecule 1: Lactotransferrin

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

Chain D:

100%

NAG 1 NAG 2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	62.28Å 49.95 Å 65.30 Å	Depositor
a, b, c, α , β , γ	90.00° 107.00° 90.00°	Depositor
Resolution (Å)	62.45 - 1.68	Depositor
Resolution (A)	31.73 - 1.68	EDS
% Data completeness	$99.7\ (62.45 ext{-} 1.68)$	Depositor
(in resolution range)	$99.8 \ (31.73 \text{-} 1.68)$	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) > 1$	$4.79 ({\rm at}1.68{ m \AA})$	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.163 , 0.208	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.162 , 0.207	DCC
R_{free} test set	2208 reflections (5.04%)	wwPDB-VP
Wilson B-factor $(Å^2)$	17.6	Xtriage
Anisotropy	0.608	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.38 , 45.7	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3042	wwPDB-VP
Average B, all atoms $(Å^2)$	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.29% 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: ZN, NAG, CO3, SO4, NPS, FE

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		Boı	nd lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.25	7/2608~(0.3%)	1.24	17/3533~(0.5%)	
2	В	0.85	0/45	0.83	0/58	
All	All	1.24	7/2653~(0.3%)	1.23	17/3591~(0.5%)	

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	А	603	ARG	CZ-NH1	6.47	1.41	1.33
1	А	347	TRP	CD2-CE2	6.06	1.48	1.41
1	А	524	TYR	CE1-CZ	-5.86	1.30	1.38
1	А	403	GLY	C-O	5.71	1.32	1.23
1	А	659	GLU	CD-OE1	-5.54	1.19	1.25

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	600	ARG	NE-CZ-NH2	-11.00	114.80	120.30
1	А	526	TYR	CB-CG-CD2	-7.94	116.24	121.00
1	А	575	ASP	CB-CG-OD1	7.41	124.97	118.30
1	А	415	ARG	NE-CZ-NH2	-6.83	116.89	120.30
1	А	643	ASP	CB-CG-OD1	6.42	124.07	118.30

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	2560	0	2480	35	0
2	В	45	0	39	0	0
3	С	28	0	25	0	0
3	D	28	0	25	0	0
4	А	14	0	13	0	0
5	А	1	0	0	0	0
6	А	2	0	0	0	0
7	А	4	0	0	0	0
8	А	5	0	0	0	0
9	А	17	0	13	4	0
10	А	336	0	0	3	0
10	В	2	0	0	0	0
All	All	3042	0	2595	37	0

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.

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 7.

The worst 5 of 37 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:359:GLN:HG2	10:A:990:HOH:O	1.46	1.12
1:A:627:ASP:OD2	1:A:628:LYS:HG3	1.74	0.88
1:A:565:LYS:HE3	1:A:567:GLU:H	1.42	0.83
1:A:565:LYS:HE3	1:A:567:GLU:N	2.02	0.73
1:A:355:GLN:HG2	10:A:969:HOH:O	1.89	0.72

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	333/335~(99%)	324~(97%)	9~(3%)	0	100	100
2	В	4/6~(67%)	3~(75%)	0	1 (25%)	0	0
All	All	337/341~(99%)	327~(97%)	9~(3%)	1 (0%)	41	23

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	682	GLU

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	А	278/278~(100%)	274~(99%)	4 (1%)	67 51		
2	В	4/4~(100%)	3~(75%)	1 (25%)	0 0		
All	All	282/282~(100%)	277 (98%)	5 (2%)	59 40		

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	418	SER
1	А	419	LYS
1	А	515	CYS
1	А	609	GLN
2	В	681	LEU

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

Mol	Chain	Res	Type
1	А	360	GLN
1	А	551	ASN
1	А	594	ASN
1	А	613	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	ol Type Chain Re		Res	Link	Bond lengths			Bond angles		
	туре	Cham	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	NAG	С	1	1,3	14,14,15	0.82	0	$17,\!19,\!21$	1.33	3 (17%)
3	NAG	С	2	3	14,14,15	0.78	1 (7%)	$17,\!19,\!21$	1.64	4 (23%)
3	NAG	D	1	1,3	14,14,15	0.86	0	$17,\!19,\!21$	1.99	<mark>6 (35%)</mark>
3	NAG	D	2	3	14,14,15	0.66	0	$17,\!19,\!21$	1.54	3 (17%)

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	1,3	-	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	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
3	С	2	NAG	O5-C1	-2.26	1.40	1.43



Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	D	1	NAG	C1-O5-C5	4.60	118.43	112.19
3	D	2	NAG	C3-C4-C5	-4.02	103.07	110.24
3	С	2	NAG	C2-N2-C7	3.79	128.30	122.90
3	D	1	NAG	O3-C3-C2	-3.49	102.24	109.47
3	D	1	NAG	C2-N2-C7	-3.32	118.17	122.90

The worst 5 of 16 bond angle outliers are listed below:

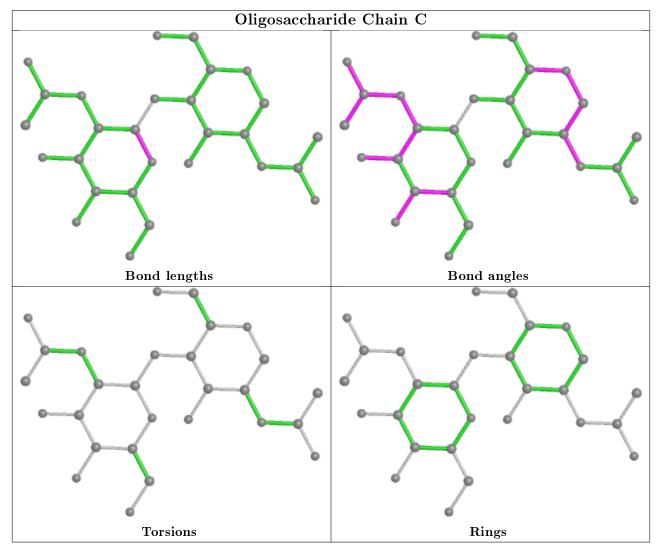
There are no chirality outliers.

There are no torsion outliers.

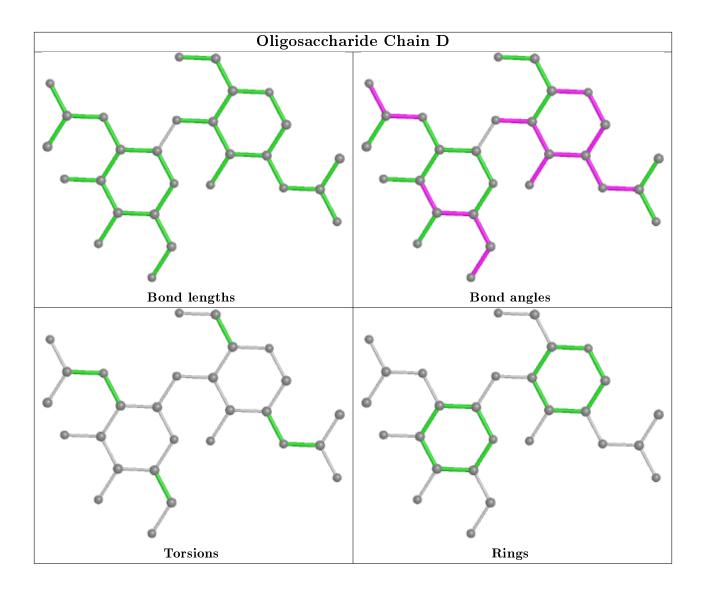
There are no ring outliers.

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 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).

Mal	Mol Type Chain Res		Res	Link	Bo	Bond lengths			Bond angles		
INIOI	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
8	SO4	А	710	-	4,4,4	0.42	0	6,6,6	3.01	$\frac{3}{50\%}$	
9	NPS	А	711	-	15,18,18	1.37	2 (13%)	21,25,25	0.87	0	
7	CO3	А	709	5	$0,\!3,\!3$	0.00	-	0,3,3	0.00	-	



Mal	Mol Type Chain		hain Res		Bond lengths			Bond angles		
			nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	NAG	А	701	1	14,14,15	0.93	1 (7%)	$17,\!19,\!21$	2.76	<mark>6 (35%)</mark>

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	\mathbf{Res}	Link	Chirals	Torsions	Rings
9	NPS	А	711	-	-	2/6/10/10	0/2/2/2
4	NAG	А	701	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
9	А	711	NPS	C5-C4	2.78	1.48	1.42
9	А	711	NPS	C8-C14	-2.56	1.48	1.52
4	А	701	NAG	O7-C7	2.06	1.27	1.23

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
4	А	701	NAG	O5-C1-C2	-6.87	100.44	111.29
8	А	710	SO4	O4-S-O2	-5.45	80.85	109.31
4	А	701	NAG	C1-O5-C5	4.72	118.59	112.19
4	A	701	NAG	C2-N2-C7	4.70	129.59	122.90
4	А	701	NAG	C8-C7-N2	-3.50	110.17	116.10

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	А	711	NPS	C2-C1-O2-C12
9	А	711	NPS	C6-C1-O2-C12

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes	
9	А	711	NPS	4	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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	$\mathbf{Q}{<}0.9$
1	А	335/335~(100%)	0.02	16 (4%) 30 32	11, 20, 47, 100	1 (0%)
2	В	6/6~(100%)	6.71	6 (100%) 0 0	40, 50, 112, 114	0
All	All	341/341~(100%)	0.14	22 (6%) 18 19	11, 20, 48, 114	1 (0%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	RSRZ
2	В	681	LEU	16.4
1	А	342	TYR	10.6
2	В	682	GLU	10.0
1	А	419	LYS	6.4
1	А	422	SER	6.2

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

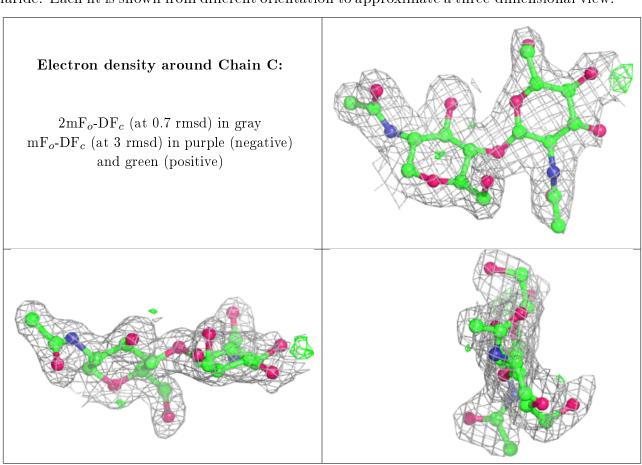
There are no non-standard protein/DNA/RNA residues in this entry.

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.

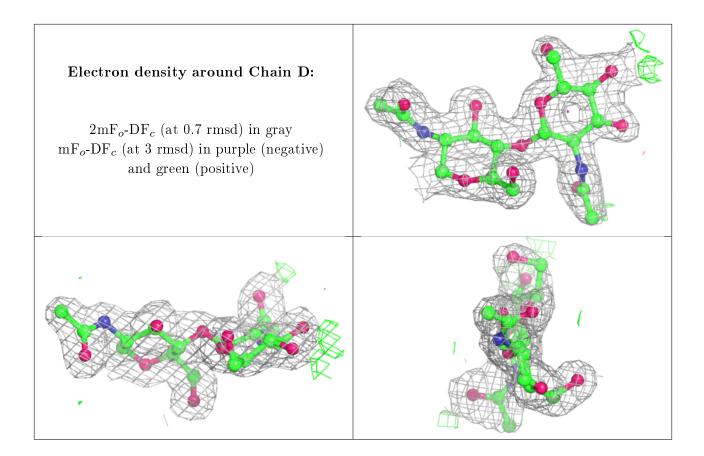
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
3	NAG	D	2	14/15	0.88	0.17	$35,\!40,\!49,\!54$	0
3	NAG	С	1	14/15	0.89	0.12	$28,\!32,\!39,\!43$	0
3	NAG	С	2	14/15	0.91	0.23	$37,\!45,\!48,\!59$	0
3	NAG	D	1	14/15	0.96	0.06	$23,\!27,\!31,\!35$	0





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	$\mathbf{B} extsf{-}\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{A}^2)$	Q<0.9
9	NPS	А	711	17/17	0.46	0.43	$33,\!58,\!63,\!65$	17
4	NAG	А	701	14/15	0.77	0.19	$38,\!46,\!55,\!64$	0
8	SO4	А	710	5/5	0.98	0.16	$37,\!38,\!40,\!49$	0
6	ZN	А	708	1/1	0.98	0.06	$20,\!20,\!20,\!20$	0
7	CO3	А	709	4/4	0.98	0.12	$12,\!12,\!12,\!13$	0
6	ZN	А	707	1/1	0.99	0.04	$18,\!18,\!18,\!18$	0
5	FE	А	706	1/1	1.00	0.08	11,11,11,11	0

6.5 Other polymers (i)

There are no such residues in this entry.

