

wwPDB X-ray Structure Validation Summary Report (i)

Sep 26, 2023 – 06:21 PM EDT

PDB ID	:	6BZ4
Title	:	Human IgG1 lacking complement-dependent cytotoxicity: hu3S193 Fc mutant
		K322A
Authors	:	Farrugia, W.; Burvenich, I.G.J.; Scott, A.M.; Ramsland, P.A.
Deposited on	:	2017-12-22
Resolution	:	2.40 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:

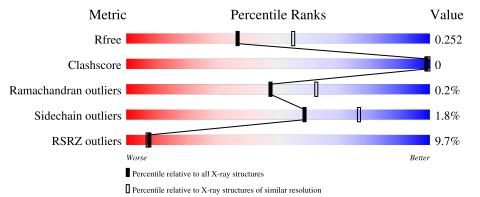
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	208	5% 97%		.
1	В	208	97%		
2	С	7	71%	29%	
3	D	6	50%	50%	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	D	1	-	-	-	Х



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3506 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 Immunoglobulin gamma-1 heavy chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	207	Total	С	Ν	0	S	0	0	0
	A	207	1654	1053	278	317	6	0	0	0
1	В	206	Total	С	Ν	0	S	0	0	0
	D	200	1630	1035	274	315	6	0	U	0

There are 2 discrepancies between the modelled and reference sequences:

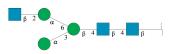
Chain	Residue	Modelled	Actual	Comment	Reference
А	322	ALA	LYS	engineered mutation	UNP P0DOX5
В	322	ALA	LYS	engineered mutation	UNP P0DOX5

• Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alp ha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-de oxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	С	7	Total 85	C 48	N 3	0 34	0	0	0

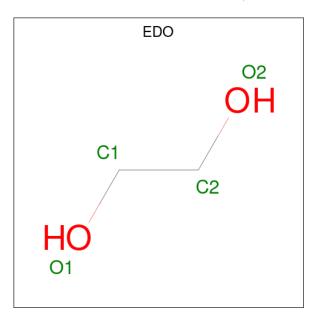
• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alp ha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
3	D	6	Total 75	C 42	N 3	O 30	0	0	0

• Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 5 is water.

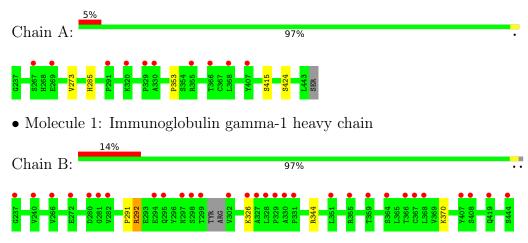
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	24	Total O 24 24	0	0
5	В	34	Total O 34 34	0	0



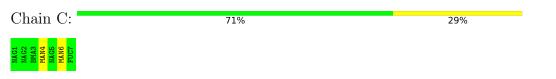
3 Residue-property plots (i)

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: Immunoglobulin gamma-1 heavy chain



 $\label{eq:2.2} \bullet \mbox{Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)]2-acetamido-2-deo$



 $\label{eq:mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]} beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2$

Chain D:	50%	50%
NAG1 NAG2 MAN4 MAN6 MAN6		



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	49.32Å 79.50Å 138.22Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.30 - 2.40	Depositor
Resolution (A)	28.30 - 2.40	EDS
% Data completeness	98.8 (28.30-2.40)	Depositor
(in resolution range)	98.8 (28.30-2.40)	EDS
R _{merge}	0.05	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.30 (at 2.39 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
D D.	0.212 , 0.249	Depositor
R, R_{free}	0.217 , 0.252	DCC
R_{free} test set	2000 reflections $(9.22%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	54.4	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31,46.3	EDS
L-test for twinning ²	$ \langle L \rangle = 0.48, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3506	wwPDB-VP
Average B, all atoms $(Å^2)$	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.73% 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: BMA, EDO, MAN, NAG, FUC

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 RMSZ	lengths	Bond angles		
	Moi Chain		# Z > 5	RMSZ	# Z > 5	
1	А	0.26	0/1700	0.45	0/2318	
1	В	0.27	0/1673	0.47	0/2280	
All	All	0.27	0/3373	0.46	0/4598	

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	1654	0	1617	0	0
1	В	1630	0	1592	3	0
2	С	85	0	73	0	0
3	D	75	0	64	0	0
4	В	4	0	6	0	0
5	А	24	0	0	0	0
5	В	34	0	0	1	0
All	All	3506	0	3352	3	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 0.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:370:LYS:NZ	5:B:601:HOH:O	2.36	0.57
1:B:291:PRO:CB	1:B:292:ARG:HB2	2.37	0.54
1:B:291:PRO:CA	1:B:292:ARG:HB2	2.44	0.47

All (3) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	entiles	
1	А	205/208~(99%)	204 (100%)	1 (0%)	0	100	100
1	В	202/208~(97%)	199~(98%)	2(1%)	1 (0%)	29	41
All	All	407/416~(98%)	403 (99%)	3 (1%)	1 (0%)	47	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type ABG		
1	В	292	ARG		

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	192/193~(100%)	187~(97%)	5(3%)	46 66

Continued on next page...



Continued from previous page...

Mol	Chain	Analysed Rotameric Outlier		Outliers	Percentiles	
1	В	190/193~(98%)	188 (99%)	2(1%)	73 87	
All	All	382/386~(99%)	375~(98%)	7 (2%)	59 76	

5 of 7 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	А	415	SER
1	А	424	SER
1	В	344	ARG
1	В	326	LYS
1	А	353	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

13 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	Chain	Chain	Chain Res	Link	Bo	Bond lengths			Bond angles		
	туре	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2		
2	NAG	С	1	2,1	$14,\!14,\!15$	0.30	0	17,19,21	0.35	0		
2	NAG	С	2	2	14,14,15	0.20	0	17,19,21	0.45	0		
2	BMA	С	3	2	11,11,12	0.54	0	$15,\!15,\!17$	0.81	0		



Mol	Turne	Chain	Res	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
N101	Type	Ullaili	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	MAN	С	4	2	11,11,12	0.84	1 (9%)	$15,\!15,\!17$	1.03	2 (13%)
2	NAG	С	5	2	14,14,15	0.20	0	17,19,21	0.39	0
2	MAN	С	6	2	11,11,12	0.70	0	$15,\!15,\!17$	1.10	2 (13%)
2	FUC	С	7	2	10,10,11	0.72	0	14,14,16	0.85	0
3	NAG	D	1	3,1	14,14,15	0.17	0	17,19,21	0.46	0
3	NAG	D	2	3	14,14,15	0.21	0	17,19,21	0.40	0
3	BMA	D	3	3	$11,\!11,\!12$	0.77	0	$15,\!15,\!17$	0.73	0
3	MAN	D	4	3	11,11,12	0.68	0	$15,\!15,\!17$	1.25	2 (13%)
3	NAG	D	5	3	14,14,15	0.75	0	$17,\!19,\!21$	1.47	2 (11%)
3	MAN	D	6	3	11,11,12	0.70	0	$15,\!15,\!17$	1.08	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	NAG	С	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	С	2	2	-	0/6/23/26	0/1/1/1
2	BMA	С	3	2	-	0/2/19/22	0/1/1/1
2	MAN	С	4	2	-	0/2/19/22	0/1/1/1
2	NAG	С	5	2	-	2/6/23/26	0/1/1/1
2	MAN	С	6	2	-	0/2/19/22	0/1/1/1
2	FUC	С	7	2	-	-	0/1/1/1
3	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	MAN	D	4	3	_	2/2/19/22	0/1/1/1
3	NAG	D	5	3	-	2/6/23/26	0/1/1/1
3	MAN	D	6	3	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	С	4	MAN	O5-C1	-2.00	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
3	D	5	NAG	O5-C5-C6	3.66	112.94	107.20

Continued on next page...



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	D	5	NAG	C2-N2-C7	-3.00	118.63	122.90
2	С	6	MAN	C1-O5-C5	2.85	116.06	112.19
3	D	6	MAN	C1-O5-C5	2.47	115.54	112.19
3	D	4	MAN	C1-O5-C5	2.44	115.50	112.19

Continued from previous page...

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

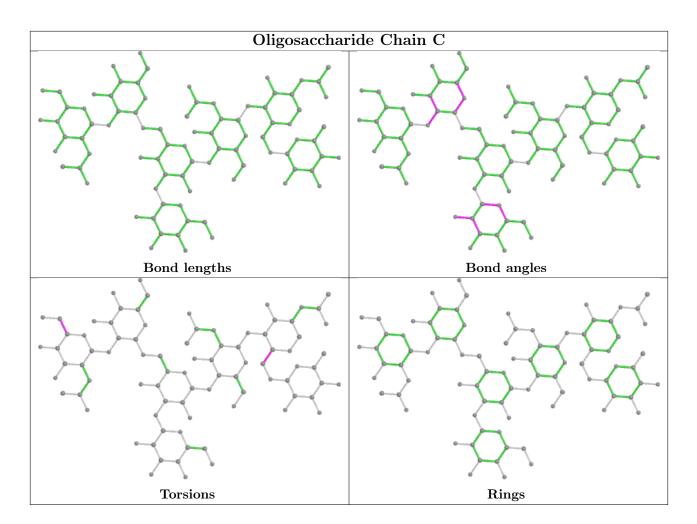
Mol	Chain	Res	Type	Atoms
2	С	1	NAG	O5-C5-C6-O6
3	D	5	NAG	O5-C5-C6-O6
2	С	5	NAG	O5-C5-C6-O6
2	С	5	NAG	C4-C5-C6-O6
2	С	1	NAG	C4-C5-C6-O6

There are no ring outliers.

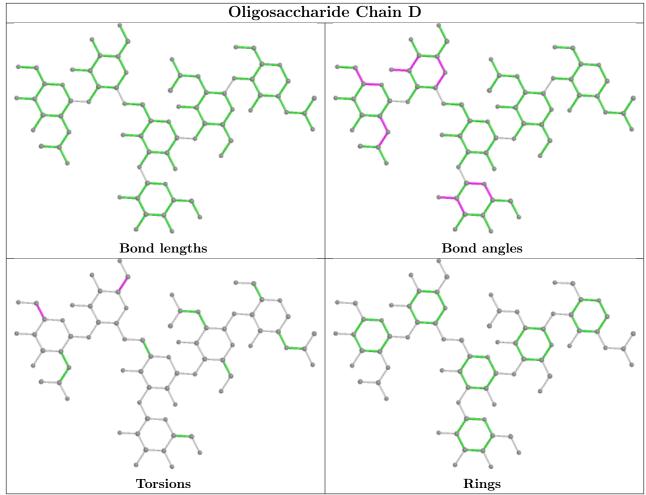
No monomer is involved in short contacts.

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)

1 ligand is 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).

Mal	Turne	Chain	Res	Link	B	ond leng	gths	Bond angles		
	Mol Type Chair	Chain	nes	LINK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
4	EDO	В	507	-	3,3,3	0.48	0	$2,\!2,\!2$	0.26	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
4	EDO	В	507	-	-	0/1/1/1	-

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)

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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	207/208~(99%)	0.21	10 (4%) 30 29	37, 72, 117, 154	0
1	В	206/208~(99%)	0.65	30 (14%) 2 2	36, 80, 141, 174	0
All	All	413/416~(99%)	0.43	40 (9%) 7 7	36, 75, 132, 174	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	237	GLY	5.1
1	В	330	ALA	5.0
1	В	326	LYS	4.7
1	В	329	PRO	4.6
1	А	355	ARG	4.1

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	$B-factors(Å^2)$	Q<0.9
3	NAG	D	2	14/15	0.53	0.37	131,140,146,147	0
3	NAG	D	1	14/15	0.60	0.47	121,137,140,140	0
3	MAN	D	6	11/12	0.66	0.40	120,121,124,125	0
2	FUC	С	7	10/11	0.80	0.28	129,134,137,139	0
2	MAN	С	6	11/12	0.80	0.25	113,119,121,123	0

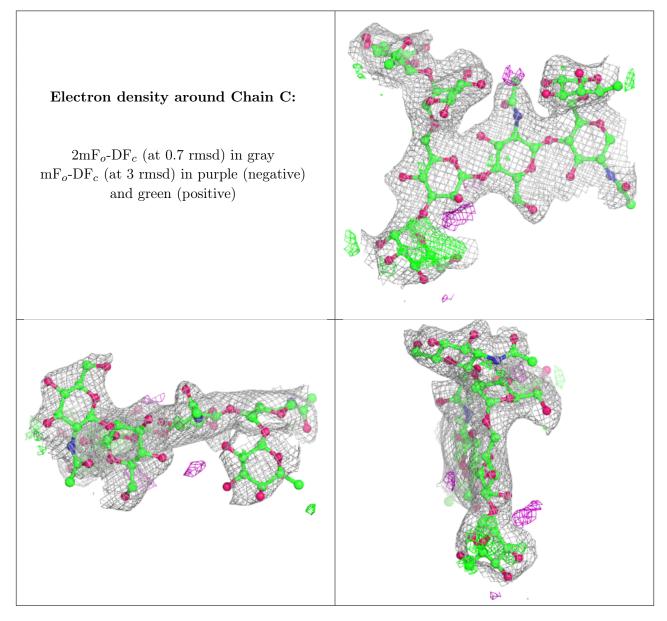
Continued on next page...



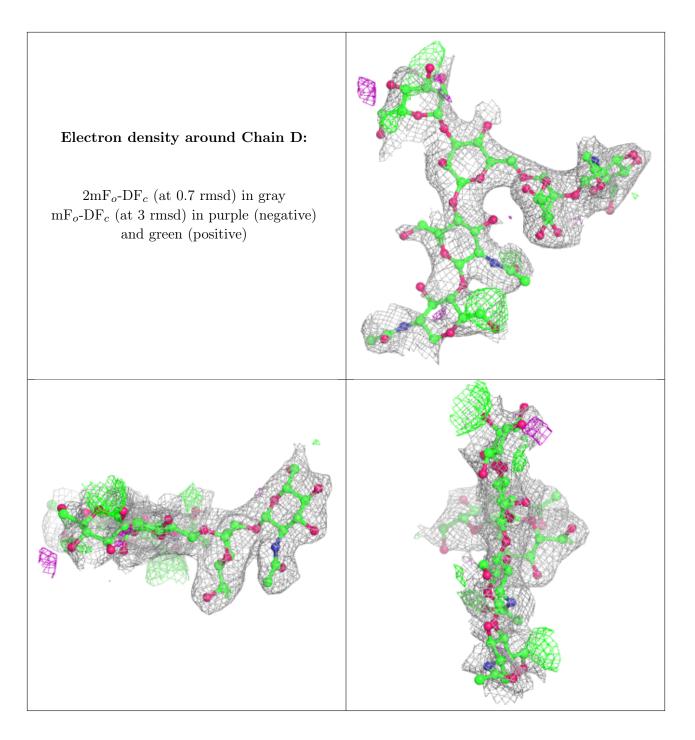
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	$Q{<}0.9$
3	BMA	D	3	11/12	0.83	0.16	109,119,121,124	0
3	MAN	D	4	11/12	0.86	0.19	99,102,104,105	0
2	NAG	С	5	14/15	0.87	0.20	91,92,98,98	0
2	MAN	С	4	11/12	0.87	0.15	87,91,92,93	0
3	NAG	D	5	14/15	0.89	0.14	94,96,97,98	0
2	NAG	С	1	14/15	0.89	0.12	89,101,112,120	0
2	BMA	С	3	11/12	0.92	0.12	93,97,102,107	0
2	NAG	С	2	14/15	0.96	0.13	93,96,99,100	0

Continued from previous page...

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
4	EDO	В	507	4/4	0.94	0.10	$52,\!53,\!53,\!54$	0



6.5 Other polymers (i)

There are no such residues in this entry.

