

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

Jan 7, 2024 – 06:59 am GMT

PDB ID : 5OXS

Title: Crystal structure of human lung surfactant protein D trimeric fragment with

bound ligand Salmonella enterica Minnesota R5 oligosaccharide

Authors: Shrive, A.K.; Greenhough, T.J.

Deposited on : 2017-09-07

Resolution : 1.65 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 : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

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

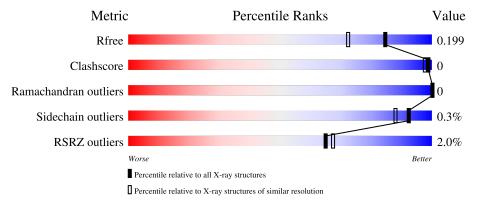
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.65 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
$R_{free}$	130704	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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 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	177	86%	14%			
1	В	177	2%	• 14%			
1	С	177	84%	• 14%			
2	D	4	25%	75%			
2	Е	4	50%	50%			

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Mol	Chain	Length	Quality of chain				
2	F	4	25%	75%			



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4175 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 Pulmonary surfactant-associated protein D.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	152	Total	С	N	О	S	0	2	0
1	A	152	1178	738	200	235	5	0	3	U
1	D	153	Total	С	N	О	S	0	2	0
1	Ъ	199	1190	744	201	240	5	0	3	U
1	С	153	Total	С	N	О	S	0	0	0
1		199	1169	732	199	233	5		U	U

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	GLY	-	expression tag	UNP P35247
A	180	SER	-	expression tag	UNP P35247
В	179	GLY	-	expression tag	UNP P35247
В	180	SER	-	expression tag	UNP P35247
С	179	GLY	-	expression tag	UNP P35247
С	180	SER	-	expression tag	UNP P35247

• Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-3)-L-glycero-alpha-D-man no-heptopyranose-(1-3)-L-glycero-alpha-D-manno-heptopyranose-(1-5)-4,7-anhydro-3-deoxy-D-gluco-oct-2-ulosonic acid.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	D	4	Total C O 52 28 24	0	0	0
2	E	4	Total C O 52 28 24	0	0	0
2	F	4	Total C O 52 28 24	0	0	0



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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Ca 2 2	0	0
3	В	2	Total Ca 2 2	0	0
3	С	1	Total Ca 1 1	0	0

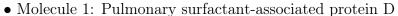
• Molecule 4 is water.

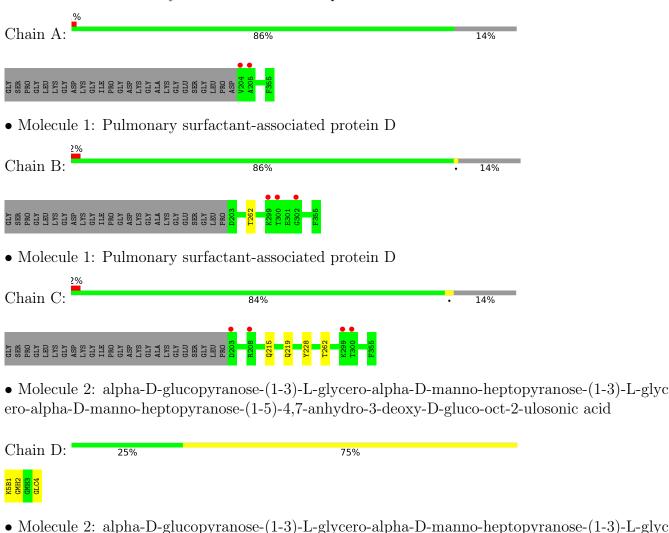
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	174	Total O 174 174	0	0
4	В	167	Total O 167 167	0	0
4	С	136	Total O 136 136	0	0



# 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.





Chain E: 50% 50%

ero-alpha-D-manno-heptopyranose-(1-5)-4,7-anhydro-3-deoxy-D-gluco-oct-2-ulosonic acid





 $\bullet \ \, Molecule \ 2: \ alpha-D-glucopyranose-(1-3)-L-glycero-alpha-D-manno-heptopyranose-(1-3)-L-glycero-alpha-D-manno-heptopyranose-(1-5)-4,7-anhydro-3-deoxy-D-gluco-oct-2-ulosonic acid$ 

Chain F: 25% 75%





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	55.68Å 108.51Å 56.17Å	Donositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $92.89^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	56.10 - 1.65	Depositor
Resolution (A)	56.10 - 1.65	EDS
% Data completeness	92.8 (56.10-1.65)	Depositor
(in resolution range)	92.8 (56.10-1.65)	EDS
$R_{merge}$	0.05	Depositor
Rogum	(Not available)	Depositor
$ < I/\sigma(I) > 1 $	2.23  (at  1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
$R, R_{free}$	0.165 , $0.187$	Depositor
it, it free	0.177 , $0.199$	DCC
$R_{free}$ test set	3647  reflections  (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.1	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 48.4	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.48, < L^2> = 0.31$	Xtriage
	0.011 for l,k,-h	
Estimated twinning fraction	0.043  for h,-k,-l	Xtriage
	0.033  for  l,-k,h	
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4175	wwPDB-VP
Average B, all atoms $(Å^2)$	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.72% 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: GLC, K5B, GMH, CA

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	
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.51	0/1203	0.65	0/1626
1	В	0.52	0/1215	0.62	0/1641
1	С	0.52	0/1191	0.63	0/1609
All	All	0.52	0/3609	0.63	0/4876

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	A	1178	0	1136	0	0
1	В	1190	0	1138	1	0
1	С	1169	0	1123	2	0
2	D	52	0	30	0	0
2	Е	52	0	30	0	0
2	F	52	0	30	0	0
3	A	2	0	0	0	0
3	В	2	0	0	0	0
3	С	1	0	0	0	0
4	A	174	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	В	167	0	0	1	0
4	С	136	0	0	1	0
All	All	4175	0	3487	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.

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

Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:C:215:GLN:O	1:C:219:GLN:HG2	2.15	0.47
1:B:262:THR:HG23	4:B:531:HOH:O	2.16	0.45
1:C:262:THR:HG22	4:C:565:HOH:O	2.19	0.42

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	153/177 (86%)	150 (98%)	3 (2%)	0	100	100
1	В	154/177 (87%)	151 (98%)	3 (2%)	0	100	100
1	С	151/177 (85%)	147 (97%)	4 (3%)	0	100	100
All	All	458/531 (86%)	448 (98%)	10 (2%)	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	Percentiles		
1	A	125/138 (91%)	125 (100%)	0	100 100		
1	В	126/138 (91%)	126 (100%)	0	100 100		
1	С	123/138 (89%)	122 (99%)	1 (1%)	81 70		
All	All	374/414 (90%)	373 (100%)	1 (0%)	92 88		

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	228	TYR

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

Mol	Chain	Res	Type
1	С	209	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)

12 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).



Mal	Trino	Chain	Dag	Link	Во	ond leng	ths	В	ond ang	les
Mol	Type	Chain	Res	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	K5B	D	1	2	15,15,15	1.44	1 (6%)	18,21,21	1.11	1 (5%)
2	GMH	D	2	2	13,13,14	0.59	0	17,18,20	0.97	2 (11%)
2	GMH	D	3	2	13,13,14	0.43	0	17,18,20	0.94	0
2	GLC	D	4	3,2	11,11,12	0.68	0	15,15,17	1.82	4 (26%)
2	K5B	Е	1	2	15,15,15	1.97	1 (6%)	18,21,21	1.62	5 (27%)
2	GMH	Е	2	3,2	13,13,14	0.49	0	17,18,20	1.19	2 (11%)
2	GMH	Е	3	2	13,13,14	0.52	0	17,18,20	0.79	0
2	GLC	Е	4	2	11,11,12	0.55	0	15,15,17	0.91	0
2	K5B	F	1	2	15,15,15	1.79	2 (13%)	18,21,21	1.15	2 (11%)
2	GMH	F	2	3,2	13,13,14	0.36	0	17,18,20	1.24	1 (5%)
2	GMH	F	3	2	13,13,14	0.54	0	17,18,20	1.33	2 (11%)
2	GLC	F	4	2	11,11,12	0.29	0	15,15,17	0.77	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
2	K5B	D	1	2	-	3/10/26/26	0/1/1/1
2	GMH	D	2	2	-	4/6/23/26	0/1/1/1
2	GMH	D	3	2	=	0/6/23/26	0/1/1/1
2	GLC	D	4	3,2	-	0/2/19/22	0/1/1/1
2	K5B	${ m E}$	1	2	-	3/10/26/26	0/1/1/1
2	GMH	Ε	2	3,2	-	0/6/23/26	0/1/1/1
2	GMH	Ε	3	2	-	0/6/23/26	0/1/1/1
2	GLC	Ε	4	2	-	0/2/19/22	0/1/1/1
2	K5B	F	1	2	-	3/10/26/26	0/1/1/1
2	GMH	F	2	3,2	-	0/6/23/26	0/1/1/1
2	GMH	F	3	2	-	4/6/23/26	0/1/1/1
2	GLC	F	4	2	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}( ext{\AA})$
2	Е	1	K5B	C2-C1	-7.29	1.43	1.53
2	F	1	K5B	C2-C1	-6.41	1.45	1.53
2	D	1	K5B	C2-C1	-4.93	1.47	1.53
2	F	1	K5B	O1B-C1	-2.09	1.24	1.30



All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	Е	1	K5B	O1A-C1-C2	-4.08	116.28	121.72
2	D	4	GLC	O3-C3-C2	3.69	117.07	109.99
2	D	4	GLC	O4-C4-C5	3.24	117.33	109.30
2	Е	1	K5B	O7-C7-C8	-3.14	102.42	109.21
2	D	4	GLC	O3-C3-C4	-3.08	103.23	110.35
2	D	4	GLC	O4-C4-C3	-3.02	103.37	110.35
2	F	3	GMH	C6-C5-C4	2.57	118.28	114.03
2	Е	2	GMH	O6-C6-C5	2.54	115.23	109.14
2	D	1	K5B	O7-C7-C8	-2.47	103.87	109.21
2	D	2	GMH	C1-O5-C5	2.47	115.52	111.48
2	D	2	GMH	C6-C5-C4	-2.37	110.10	114.03
2	F	2	GMH	O6-C6-C5	2.31	114.69	109.14
2	F	3	GMH	C1-O5-C5	2.30	115.25	111.48
2	Е	1	K5B	O7-C4-C3	-2.24	104.42	109.09
2	Е	2	GMH	O6-C6-C7	-2.15	104.09	109.14
2	Е	1	K5B	O1B-C1-C2	2.15	119.85	113.97
2	Е	1	K5B	O2-C2-C3	2.08	125.70	121.53
2	F	1	K5B	O7-C4-C5	-2.02	101.11	105.11
2	F	1	K5B	C8-C7-C6	-2.01	110.23	115.09

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	K5B	O1B-C1-C2-C3
2	D	2	GMH	C4-C5-C6-C7
2	D	2	GMH	C4-C5-C6-O6
2	D	2	GMH	O5-C5-C6-C7
2	D	2	GMH	O5-C5-C6-O6
2	Е	1	K5B	O1A-C1-C2-C3
2	Е	1	K5B	O1B-C1-C2-C3
2	F	1	K5B	O1B-C1-C2-C3
2	F	3	GMH	C4-C5-C6-C7
2	F	3	GMH	C4-C5-C6-O6
2	F	3	GMH	O5-C5-C6-C7
2	F	3	GMH	O5-C5-C6-O6
2	D	1	K5B	O2-C2-C3-C4
2	D	1	K5B	C1-C2-C3-C4
2	Е	1	K5B	O1A-C1-C2-O2
2	F	1	K5B	O1A-C1-C2-O2
2	F	1	K5B	O1A-C1-C2-C3

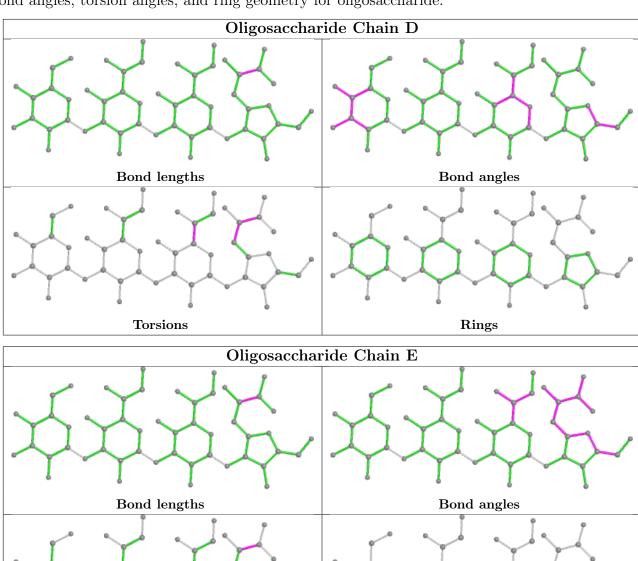


There are no ring outliers.

No monomer is involved in short contacts.

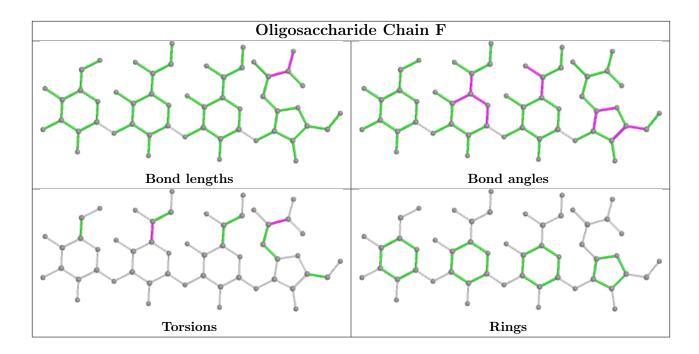
Torsions

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





Rings



## 5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

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	<rsrz></rsrz>	#RS	SRZ>	>2	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	152/177~(85%)	-0.35	2 (1%)	77	80	13, 20, 31, 64	0
1	В	153/177 (86%)	-0.21	3 (1%)	65	67	13, 19, 45, 64	0
1	С	153/177 (86%)	-0.22	4 (2%)	56	56	12, 21, 42, 67	0
All	All	458/531 (86%)	-0.26	9 (1%)	65	67	12, 20, 42, 67	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	302	GLY	4.8
1	A	205	ALA	4.7
1	С	299	LYS	4.1
1	В	300	THR	3.1
1	A	204	VAL	3.0
1	С	300	THR	2.9
1	С	208	ARG	2.6
1	С	203	ASP	2.2
1	В	299	LYS	2.0

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

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

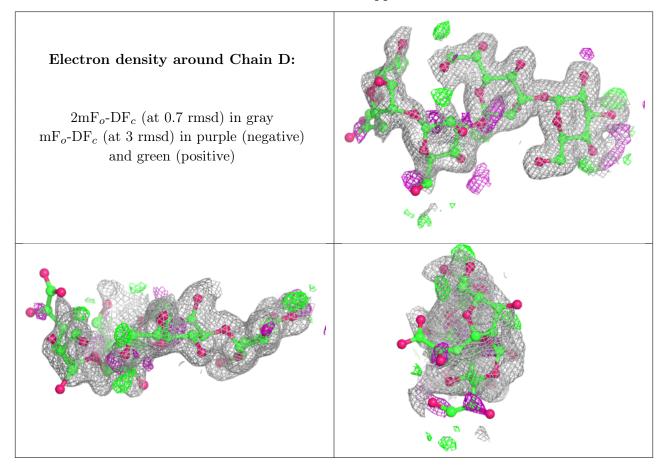
## 6.3 Carbohydrates (i)

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.

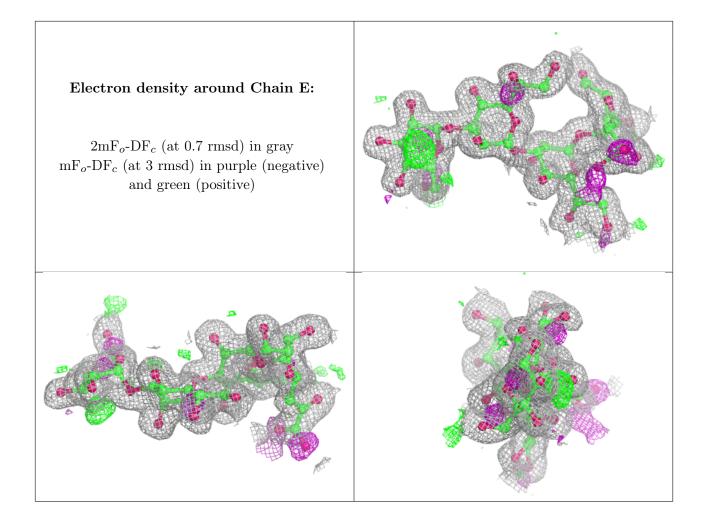


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	K5B	D	1	15/15	0.54	0.34	79,87,97,98	0
2	GMH	D	2	13/14	0.60	0.36	52,69,81,82	0
2	GLC	F	4	11/12	0.86	0.14	42,46,48,51	0
2	GLC	Е	4	11/12	0.88	0.11	30,32,33,33	0
2	K5B	F	1	15/15	0.88	0.12	27,36,45,50	0
2	GMH	F	3	13/14	0.88	0.11	33,39,44,50	0
2	GMH	D	3	13/14	0.88	0.11	27,35,43,47	0
2	GMH	Е	3	13/14	0.91	0.10	26,30,37,41	0
2	K5B	Е	1	15/15	0.92	0.11	19,25,46,48	0
2	GLC	D	4	11/12	0.94	0.08	20,22,24,24	0
2	GMH	Е	2	13/14	0.96	0.07	15,17,20,24	0
2	GMH	F	2	13/14	0.96	0.06	18,23,25,28	0

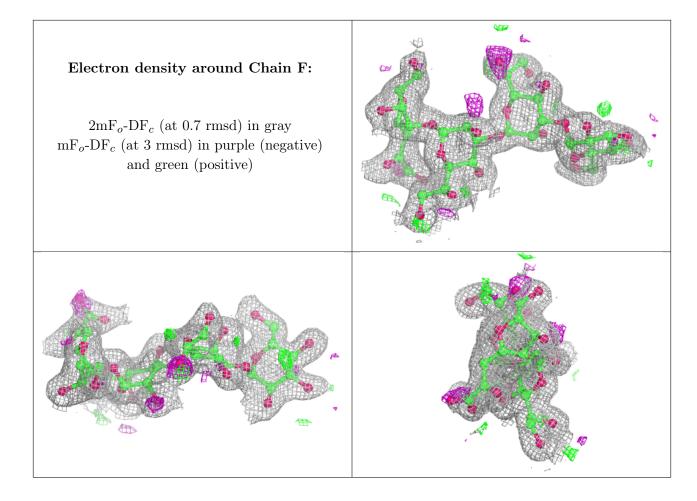
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.











## 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	${f B-factors}({f A}^2)$	Q < 0.9
3	CA	В	402	1/1	0.98	0.09	33,33,33,33	0
3	CA	A	401	1/1	0.99	0.09	17,17,17,17	0
3	CA	С	402	1/1	0.99	0.10	17,17,17,17	0
3	CA	A	402	1/1	1.00	0.09	16,16,16,16	0
3	CA	В	401	1/1	1.00	0.10	14,14,14,14	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

