

Full wwPDB X-ray Structure Validation Report (i)

Sep 5, 2023 – 06:21 AM EDT

:	3THM
:	Crystal structure of Fas receptor extracellular domain in complex with Fab
	EP6b_B01
:	Zuger, S.; Stirnimann, C.; Briand, C.; Grutter, M.G.
:	2011-08-19
:	2.10 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:

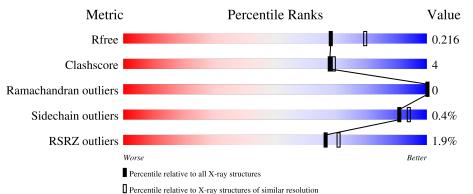
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 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 2.10 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	5197(2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	L	216	92%	7% •
2	Н	245	% 8 4%	9% 7%
3	F	156	4% 42% 6% • 51%	
4	А	3	100%	



$3 \mathrm{THM}$

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 8192 atoms, of which 3867 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 Fab EP6b_B01, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	L	214	Total 3212	C 1024	Н 1580	N 271	O 333	S 4	0	1	0

• Molecule 2 is a protein called Fab EP6b_B01, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	Н	228	Total 3364	C 1065	Н 1667	N 286	O 340	S 6	0	1	0

• Molecule 3 is a protein called Tumor necrosis factor receptor superfamily member 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
3	F	77	Total 1155	C 356	Н 554	N 120	0 113	S 12	0	0	0

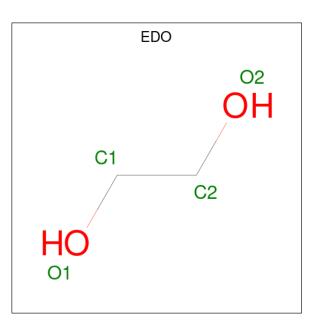
• Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[al pha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
4	А	3	Total 74	C 22	Н 36	N 2	0 14	0	0	0

• Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
5	L	1	Total C H O	0	0	
		Ĩ	10 2 6 2	Ŭ	0	
5	T.	1	Total C H O	0	0	
0	Ľ	1	10 2 6 2	0	0	
5	L	1	Total C H O	0	0	
0	Ľ	1	10 2 6 2	0	0	
5	т	1	Total C H O	0	0	
0	L	1	10 2 6 2	0	0	
5	т	1	Total C H O	0	0	
0	L	1	10 2 6 2	0	U	

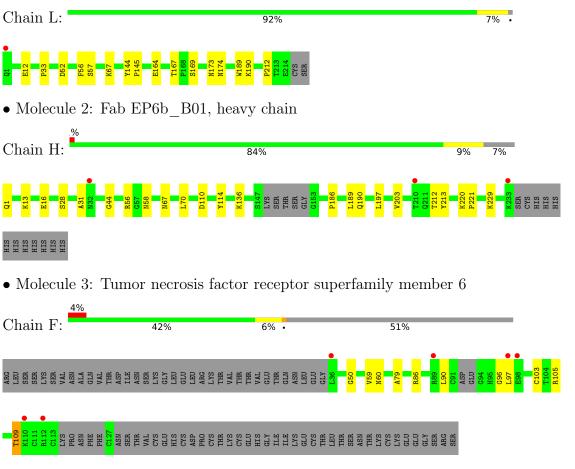
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	L	181	Total O 181 181	0	0
6	Н	126	Total O 126 126	0	0
6	F	30	Total O 30 30	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: Fab EP6b_B01, light chain

• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-ace tamido-2-deoxy-beta-D-glucopyranose

Chain A:

100%

NAG1 NAG2 FUC3



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	94.51Å 94.51Å 139.20Å	Deperitor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.26 - 2.10	Depositor
Resolution (A)	47.26 - 2.10	EDS
% Data completeness	$100.0 \ (47.26-2.10)$	Depositor
(in resolution range)	99.9 (47.26-2.10)	EDS
R _{merge}	0.10	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.75 (at 2.10 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.7.1_743	Depositor
B B.	0.183 , 0.221	Depositor
R, R_{free}	0.177 , 0.216	DCC
R_{free} test set	2129 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	29.5	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.38 , 35.4	EDS
L-test for twinning ²	$< L > = 0.45, < L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.112 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8192	wwPDB-VP
Average B, all atoms $(Å^2)$	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.63% 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: FUC, NAG, EDO

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	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	L	0.46	0/1673	0.52	0/2287	
2	Н	0.37	0/1735	0.50	0/2369	
3	F	0.39	0/611	0.47	0/816	
All	All	0.41	0/4019	0.51	0/5472	

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	L	1632	1580	1578	11	0
2	Н	1697	1667	1666	17	0
3	F	601	554	553	7	0
4	А	38	36	34	0	0
5	L	20	30	30	0	0
6	F	30	0	0	0	0
6	Н	126	0	0	3	0
6	L	181	0	0	1	0
All	All	4325	3867	3861	30	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 4.

All (30) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A + a 1	A + a	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:L:190:LYS:NZ	6:L:247:HOH:O	2.35	0.55
2:H:114:TYR:HB2	3:F:86:ARG:NH2	2.22	0.55
1:L:164:GLU:HG3	2:H:190:GLN:HG2	1.89	0.55
3:F:96:GLY:C	3:F:97:LEU:HD12	2.30	0.52
2:H:212:THR:HG23	2:H:229:LYS:HE3	1.91	0.52
3:F:90:LEU:N	3:F:90:LEU:HD22	2.26	0.51
2:H:197:LEU:C	2:H:197:LEU:HD12	2.32	0.50
3:F:103:CYS:HB2	3:F:109:THR:OG1	2.12	0.50
2:H:136:LYS:NZ	6:H:339:HOH:O	2.45	0.49
2:H:220:LYS:N	2:H:221:PRO:CD	2.74	0.49
1:L:189:TRP:CZ2	1:L:212:PRO:HA	2.47	0.48
2:H:110:ASP:OD1	2:H:114:TYR:CD2	2.66	0.48
2:H:28:SER:HB3	2:H:31:ALA:HB2	1.94	0.48
2:H:203:VAL:HG11	2:H:213:TYR:CE1	2.50	0.46
1:L:167:THR:HG22	6:H:277:HOH:O	2.16	0.46
2:H:203:VAL:HG11	2:H:213:TYR:CZ	2.51	0.46
2:H:67:ASN:HB3	2:H:70:LEU:HD23	1.97	0.46
1:L:169:SER:OG	2:H:186:PRO:HG2	2.15	0.46
2:H:189:LEU:C	2:H:189:LEU:HD13	2.37	0.45
3:F:50:GLY:HA2	3:F:105:ARG:O	2.17	0.45
2:H:13:LYS:O	2:H:16:GLU:HB2	2.18	0.44
1:L:33:PRO:HD3	3:F:79:ALA:HB3	1.99	0.43
1:L:173:ASN:O	1:L:174:ASN:HB2	2.17	0.43
2:H:1:GLN:HB3	6:H:351:HOH:O	2.19	0.43
3:F:59:VAL:HG13	3:F:60:ASN:CG	2.39	0.43
2:H:56:ARG:HH11	2:H:58:ASN:HB3	1.85	0.41
1:L:52:ASP:OD2	1:L:67:LYS:HD3	2.21	0.41
1:L:167:THR:CG2	2:H:44:GLY:HA3	2.51	0.41
1:L:144:TYR:HA	1:L:145:PRO:C	2.40	0.41
1:L:56:PHE:CG	1:L:57:SER:N	2.88	0.40

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	L	213/216~(99%)	208~(98%)	5(2%)	0	100 100
2	Н	225/245~(92%)	218 (97%)	7 (3%)	0	100 100
3	F	72/156~(46%)	71 (99%)	1 (1%)	0	100 100
All	All	510/617~(83%)	497 (98%)	13 (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 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	L	185/186~(100%)	184 (100%)	1 (0%)	88 92
2	Н	193/208~(93%)	193 (100%)	0	100 100
3	F	69/143~(48%)	68~(99%)	1 (1%)	67 73
All	All	447/537~(83%)	445 (100%)	2(0%)	91 94

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

Mol	Chain	Res	Type		
1	L	12	GLU		
3	F	109	THR		

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



Mol	Chain	Res	Type
2	Н	183	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)

3 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	Mol Type	Chain	Res	Link	Bo	Bond lengths			Bond angles		
IVIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
4	NAG	А	1	1,4	14,14,15	1.45	3 (21%)	17,19,21	<mark>3.12</mark>	8 (47%)	
4	NAG	А	2	4	14,14,15	1.12	1 (7%)	17,19,21	1.23	1 (5%)	
4	FUC	А	3	4	10,10,11	1.72	2 (20%)	14,14,16	2.04	<mark>5 (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	Res	Link	Chirals	Torsions	Rings
4	NAG	А	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	А	2	4	-	2/6/23/26	0/1/1/1
4	FUC	А	3	4	-	-	0/1/1/1

All (6) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(\text{\AA})$	Ideal(Å)
4	А	3	FUC	O5-C5	-3.55	1.35	1.43
4	А	3	FUC	O5-C1	-3.20	1.38	1.43
4	А	1	NAG	C2-N2	-3.12	1.41	1.46
4	А	1	NAG	O7-C7	-2.22	1.18	1.23
4	А	2	NAG	C2-N2	-2.18	1.42	1.46
4	А	1	NAG	O5-C1	-2.07	1.40	1.43

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	А	1	NAG	C1-O5-C5	6.85	121.47	112.19
4	А	1	NAG	O5-C5-C6	6.64	117.61	107.20
4	А	3	FUC	C1-C2-C3	4.80	115.56	109.67
4	А	1	NAG	C2-N2-C7	4.53	129.35	122.90
4	А	1	NAG	C6-C5-C4	-3.62	104.53	113.00
4	А	2	NAG	O5-C5-C6	3.42	112.57	107.20
4	А	1	NAG	C3-C4-C5	3.07	115.71	110.24
4	А	3	FUC	O4-C4-C3	-2.96	103.50	110.35
4	А	3	FUC	O3-C3-C4	-2.94	103.56	110.35
4	А	1	NAG	C8-C7-N2	-2.54	111.80	116.10
4	А	3	FUC	C3-C4-C5	2.49	113.65	109.77
4	А	1	NAG	O3-C3-C4	-2.19	105.28	110.35
4	А	1	NAG	O4-C4-C5	-2.15	103.95	109.30
4	А	3	FUC	O5-C5-C6	-2.01	103.01	107.33

There are no chirality outliers.

All (3) torsion outliers are listed below:

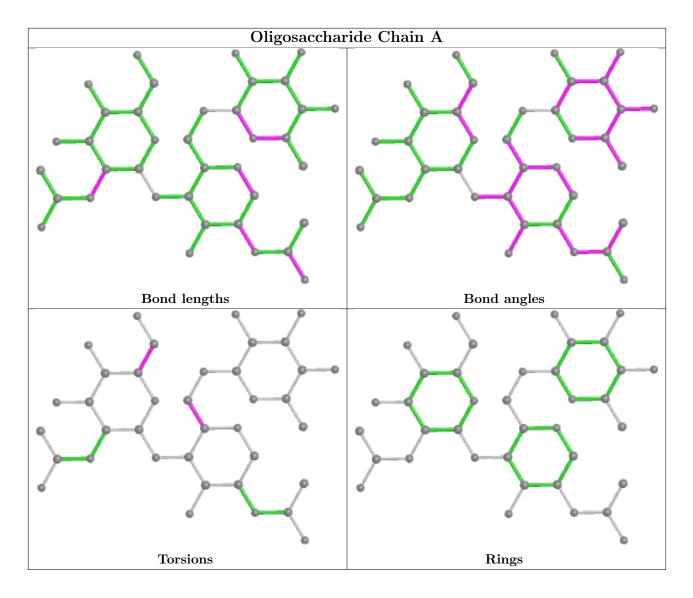
Mol	Chain	Res	Type	Atoms
4	А	2	NAG	O5-C5-C6-O6
4	А	2	NAG	C4-C5-C6-O6
4	А	1	NAG	O5-C5-C6-O6

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)

5 ligands 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	Turne	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Res	Link	B	ond leng	gths	В	ond ang	gles
	Type	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2									
5	EDO	L	220	-	3,3,3	0.48	0	2,2,2	0.18	0									
5	EDO	L	218	-	3,3,3	0.48	0	2,2,2	0.23	0									
5	EDO	L	221	-	3,3,3	0.41	0	2,2,2	0.47	0									



Mal	Mol Type Chain Res L	Chain	Dec	Link	Bond lengths			Bond angles		
MOI		LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2		
5	EDO	L	219	-	3,3,3	0.43	0	$2,\!2,\!2$	0.33	0
5	EDO	L	217	-	3,3,3	0.47	0	$2,\!2,\!2$	0.31	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
5	EDO	L	220	-	-	0/1/1/1	-
5	EDO	L	218	-	-	0/1/1/1	-
5	EDO	L	221	-	-	1/1/1/1	-
5	EDO	L	219	-	-	0/1/1/1	-
5	EDO	L	217	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	221	EDO	O1-C1-C2-O2

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	lysed $ $ <rsrz> $$ $#$RSRZ>2 $$</rsrz>		$OWAB(Å^2)$	Q < 0.9
1	L	214/216~(99%)	-0.36	1 (0%) 91 92	15, 24, 43, 94	0
2	Н	228/245~(93%)	-0.19	3 (1%) 77 80	19, 36, 68, 100	0
3	F	77/156~(49%)	0.20	6 (7%) 13 17	23, 50, 116, 145	0
All	All	519/617~(84%)	-0.20	10 (1%) 66 71	15, 32, 73, 145	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	36	LEU	5.3
3	F	97	LEU	4.2
3	F	98	GLU	4.0
2	Н	32	ASN	2.9
3	F	112	ARG	2.9
2	Н	233	LYS	2.5
3	F	110	LYS	2.5
2	Н	210	THR	2.3
3	F	89	ARG	2.3
1	L	1	GLN	2.3

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

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

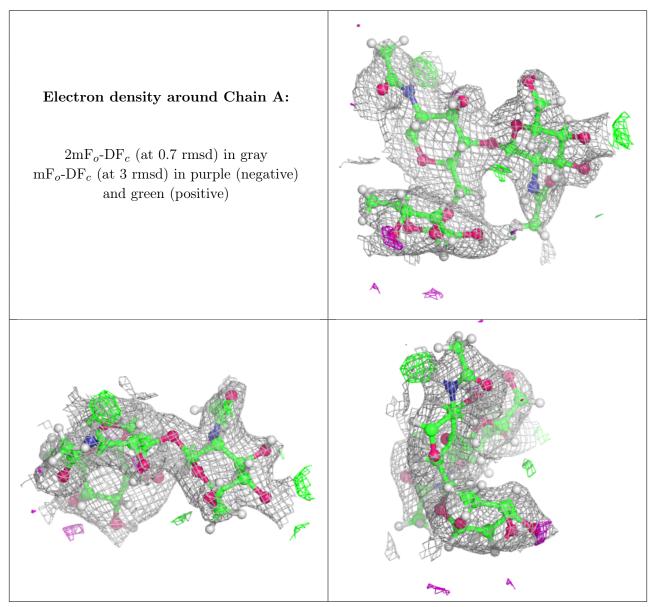
6.3 Carbohydrates (i)

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
4	NAG	А	2	14/15	0.88	0.19	42,63,77,81	0
4	NAG	А	1	14/15	0.92	0.12	29,40,50,66	0
4	FUC	А	3	10/11	0.92	0.12	49,68,83,94	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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
5	EDO	L	220	4/4	0.82	0.17	42,52,63,68	0
5	EDO	L	219	4/4	0.84	0.26	42,55,66,66	0
5	EDO	L	221	4/4	0.92	0.17	32,46,69,83	0
5	EDO	L	218	4/4	0.95	0.11	33,52,61,62	0
5	EDO	L	217	4/4	0.97	0.09	15,21,39,39	0

6.5 Other polymers (i)

There are no such residues in this entry.

