

Full wwPDB X-ray Structure Validation Report (i)

Aug 8, 2020 – 12:06 AM BST

PDB ID : 5TZU

Title: Crystal structure of human CD47 ECD bound to Fab of B6H12.2

Authors : Cardoso, R.M.F.

Deposited on : 2016-11-22

Resolution : 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 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

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

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

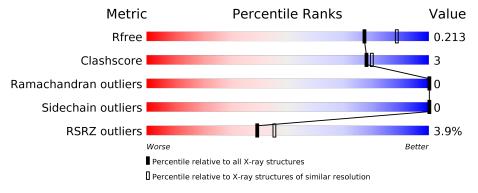
Validation Pipeline (wwPDB-VP) : 2.13.1

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 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
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 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 c	hain	
1	L	214	20%	93%		7%
2	Н	227	7%	88%		7% 6%
3	С	129	% •	84%	5%	11%
4	A	2	5	50%	50%	
5	В	5	20%	40%	40%	
6	D	3		67%	33%	



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
5	BMA	В	3	-	-	-	X
5	MAN	В	4	-	-	-	X
5	MAN	В	5	-	-	-	X
6	NAG	D	2	-	-	-	X
6	BMA	D	3	-	-	-	X
8	ACT	Н	302	-	-	X	-
9	NAG	С	201	-	-	-	X



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 4553 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 Light Chain of Fab B6H12.2.

Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf	Trace
1	T.	213	Total	С	N	О	S	0	2	0
1		210	1601	1005	270	321	5			

• Molecule 2 is a protein called Heavy Chain of Fab B6H12.2.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	Н	214	Total	С	N	О	S	0	0	0
_			1555	991	253	305	6			9

• Molecule 3 is a protein called Leukocyte surface antigen CD47.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	С	115	Total 880	C 563	N 136	O 177	S 4	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	15	GLY	CYS	engineered mutation	UNP Q08722
С	124	HIS	-	expression tag	UNP Q08722
С	125	HIS	-	expression tag	UNP Q08722
С	126	HIS	-	expression tag	UNP Q08722
С	127	HIS	-	expression tag	UNP Q08722
С	128	HIS	_	expression tag	UNP Q08722
С	129	HIS	-	expression tag	UNP Q08722

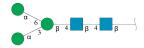
• Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.





Mol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf	Trace
4	A	2	Total 28	C 16	N 2	O 10	0	0	0

• Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



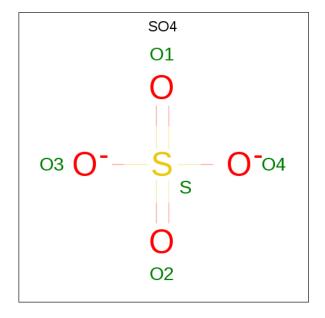
Mol	Chain	Residues	A	\ton	ns	ZeroOcc	AltConf	Trace
5	В	5	Total 61	C 34		0	0	0

• Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	D	3	Total 39	C 22	N 2	O 15	0	0	0

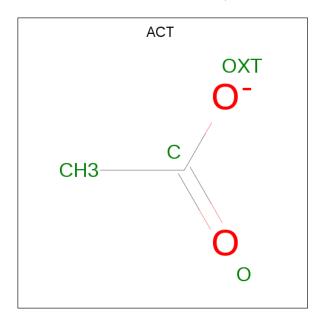
• Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	1	Total O S 5 4 1	0	0
7	Н	1	Total O S 5 4 1	0	0

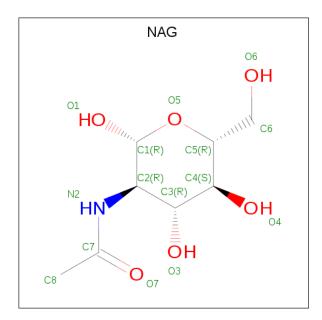
 \bullet Molecule 8 is ACETATE ION (three-letter code: ACT) (formula: $\mathrm{C_2H_3O_2}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	Н	1	Total C O 4 2 2	0	0
8	Н	1	Total C O 4 2 2	0	0
8	С	1	Total C O 4 2 2	0	0

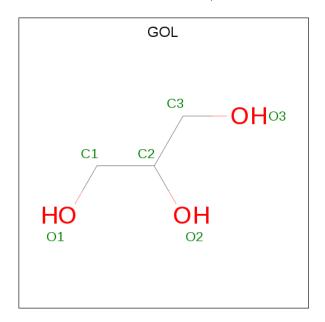
• Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	С	1	Total 14				0	0
9	С	1	Total 14		N 1	O 5	0	0

• Molecule 10 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	C	1	Total C O 6 3 3	0	0

• Molecule 11 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	L	123	Total O 123 123	0	0
11	Н	125	Total O 125 125	0	0
11	С	85	Total O 85 85	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 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 20% 40% 40%





 $\bullet \ \, Molecule \ 6: \ beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose$

Chain D: 67% 33%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	161.76Å 54.53Å 83.49Å	Depositor
a, b, c, α , β , γ	90.00° 95.89° 90.00°	Depositor
Resolution (Å)	37.76 - 2.10	Depositor
resolution (A)	38.55 - 2.10	EDS
% Data completeness	98.6 (37.76-2.10)	Depositor
(in resolution range)	98.4 (38.55-2.10)	EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.19 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
P. P.	0.177 , 0.213	Depositor
R, R_{free}	0.179 , 0.213	DCC
R_{free} test set	2129 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	1.494	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33 , 49.0	EDS
L-test for twinning ²	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4553	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.80% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: GOL, BMA, NAG, SO4, ACT, MAN

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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	L	0.29	0/1643	0.53	0/2237	
2	Н	0.30	0/1592	0.51	0/2177	
3	С	0.28	0/895	0.51	0/1216	
All	All	0.29	0/4130	0.52	0/5630	

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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	L	1601	0	1509	8	0
2	Н	1555	0	1463	8	0
3	С	880	0	828	5	0
4	A	28	0	25	1	0
5	В	61	0	52	4	0
6	D	39	0	34	2	0
7	Н	5	0	0	0	0
7	L	5	0	0	0	0
8	С	4	0	3	0	0
8	Н	8	0	6	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	С	28	0	26	1	0
10	С	6	0	8	0	0
11	С	85	0	0	1	0
11	Н	125	0	0	0	0
11	L	123	0	0	0	0
All	All	4553	0	3954	24	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 3.

All (24) 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:L:38:GLN:HE22	2:H:39:GLN:HE22	1.32	0.75
11:C:355:HOH:O	5:B:1:NAG:H83	1.85	0.74
2:H:68:PHE:CE1	2:H:83:ILE:HG23	2.33	0.62
2:H:17:SER:OG	2:H:82:GLN:NE2	2.34	0.59
3:C:13:THR:HG22	3:C:114:ARG:O	2.03	0.58
8:H:302:ACT:H1	5:B:2:NAG:HN2	1.69	0.57
3:C:12:PHE:HB3	4:A:1:NAG:H82	1.87	0.55
8:H:302:ACT:CH3	5:B:2:NAG:HN2	2.21	0.53
1:L:21:LEU:HD12	1:L:73:LEU:HD23	1.93	0.51
1:L:80:PRO:HA	1:L:106:ILE:HG13	1.92	0.51
2:H:91:THR:HG23	2:H:115:THR:HA	1.97	0.46
1:L:83[A]:VAL:HG23	1:L:104:LEU:O	2.16	0.45
2:H:124:PRO:HB3	2:H:150:TYR:HB3	1.98	0.45
3:C:40:TRP:CE2	3:C:80:LEU:HB2	2.52	0.45
2:H:29:PHE:CD2	2:H:77:ASN:HA	2.52	0.45
1:L:90:ASN:HD21	1:L:97:THR:HB	1.82	0.44
2:H:53:SER:HA	2:H:72:ARG:NH1	2.32	0.44
3:C:55:ASN:ND2	6:D:1:NAG:H83	2.34	0.43
1:L:120:PRO:HD3	1:L:132:VAL:HG22	2.02	0.42
1:L:125:LEU:O	1:L:183:LYS:HG3	2.20	0.42
3:C:93:ASN:OD1	9:C:212:NAG:H83	2.20	0.41
1:L:115:VAL:HG12	1:L:207:LYS:HG3	2.00	0.41
5:B:2:NAG:C8	6:D:1:NAG:H82	2.50	0.41
2:H:6:GLU:OE2	2:H:109:GLY:HA3	2.20	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	Perce	\mathbf{ntiles}
1	L	$213/214 \ (100\%)$	207 (97%)	6 (3%)	0	100	100
2	Н	210/227 (92%)	209 (100%)	1 (0%)	0	100	100
3	С	113/129 (88%)	111 (98%)	2 (2%)	0	100	100
All	All	536/570 (94%)	527 (98%)	9 (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	${ m L}$	175/189~(93%)	175 (100%)	0	100	100	
2	Н	160/192~(83%)	160 (100%)	0	100	100	
3	С	93/118 (79%)	93 (100%)	0	100	100	
All	All	$428/499 \ (86\%)$	428 (100%)	0	100	100	

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	L	38	GLN
1	L	89	GLN
2	Н	82	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)

10 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	Trno	Chain	Res	Link	Вс	nd leng	ths	Bond angles		
IVIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1	3,4	14,14,15	0.36	0	17,19,21	0.60	0
4	NAG	A	2	4	14,14,15	0.53	0	17,19,21	0.43	0
5	NAG	В	1	3,5	14,14,15	0.65	1 (7%)	17,19,21	0.58	0
5	NAG	В	2	5	14,14,15	0.65	0	17,19,21	0.77	1 (5%)
5	BMA	В	3	5	11,11,12	0.27	0	15,15,17	1.12	1 (6%)
5	MAN	В	4	5	11,11,12	0.79	0	15,15,17	0.90	1 (6%)
5	MAN	В	5	5	11,11,12	0.30	0	15,15,17	0.69	0
6	NAG	D	1	3,6	14,14,15	0.50	0	17,19,21	0.62	0
6	NAG	D	2	6	14,14,15	0.53	0	17,19,21	0.43	0
6	BMA	D	3	6	11,11,12	0.24	0	15,15,17	0.69	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	NAG	A	1	3,4	-	0/6/23/26	0/1/1/1
4	NAG	A	2	4	-	0/6/23/26	0/1/1/1
5	NAG	В	1	3,5	-	3/6/23/26	0/1/1/1
5	NAG	В	2	5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BMA	В	3	5	-	1/2/19/22	0/1/1/1
5	MAN	В	4	5	1	0/2/19/22	0/1/1/1
5	MAN	В	5	5	-	2/2/19/22	0/1/1/1
6	NAG	D	1	3,6	-	2/6/23/26	0/1/1/1
6	NAG	D	2	6	-	0/6/23/26	0/1/1/1
6	BMA	D	3	6	_	2/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$Ideal(\AA)$
5	В	1	NAG	O5-C1	-2.02	1.40	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
5	В	2	NAG	O4-C4-C5	-2.54	102.98	109.30
5	В	4	MAN	O2-C2-C3	-2.34	105.45	110.14
5	В	3	BMA	O3-C3-C4	-2.09	105.52	110.35

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	1	NAG	C8-C7-N2-C2
6	D	1	NAG	O7-C7-N2-C2
5	В	1	NAG	C8-C7-N2-C2
5	В	1	NAG	O7-C7-N2-C2
5	В	5	MAN	C4-C5-C6-O6
5	В	5	MAN	O5-C5-C6-O6
5	В	1	NAG	O5-C5-C6-O6
6	D	3	BMA	C4-C5-C6-O6
5	В	3	BMA	O5-C5-C6-O6
6	D	3	BMA	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	В	2	NAG	3	0
6	D	1	NAG	2	0

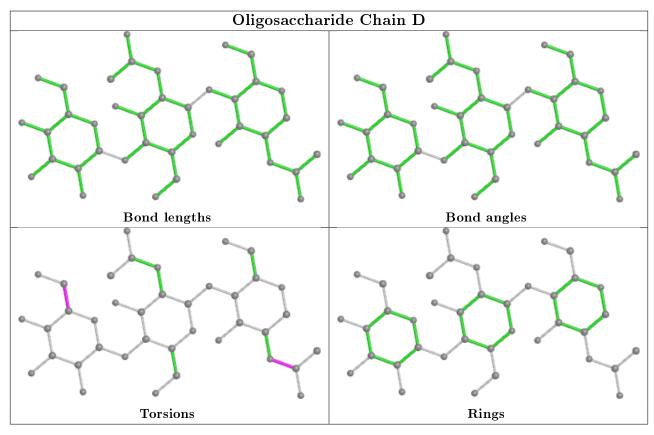
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	В	1	NAG	1	0
4	A	1	NAG	1	0

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)

8 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	Type	Chain	Res	Link	Bo	Bond lengths			ond ang	les
MIGI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	ACT	Н	302	_	1,3,3	0.82	0	0,3,3	0.00	-
8	ACT	Н	303	-	1,3,3	1.39	0	0,3,3	0.00	-



Mol	Trino	Chain	Res	Link	Bo	nd leng	ths	Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	С	212	3	14,14,15	0.36	0	17,19,21	1.11	1 (5%)
7	SO4	Н	301	-	4,4,4	0.15	0	6,6,6	0.07	0
8	ACT	С	214	-	1,3,3	1.42	0	0,3,3	0.00	_
7	SO4	L	301	_	4,4,4	0.14	0	6,6,6	0.05	0
10	GOL	С	213	-	5,5,5	0.37	0	5,5,5	0.22	0
9	NAG	С	201	3	14,14,15	0.33	0	17,19,21	0.68	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
9	NAG	С	212	3	-	4/6/23/26	0/1/1/1
10	GOL	С	213	-	-	2/4/4/4	-
9	NAG	С	201	3	_	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^o)$
9	С	212	NAG	C1-O5-C5	3.80	117.35	112.19
9	С	201	NAG	C1-O5-C5	2.42	115.47	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	С	213	GOL	O1-C1-C2-C3
9	С	212	NAG	C8-C7-N2-C2
9	С	212	NAG	O7-C7-N2-C2
9	С	212	NAG	O5-C5-C6-O6
10	С	213	GOL	O1-C1-C2-O2
9	С	212	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

\mathbf{Mol}	Chain	${f Res}$	Type	Clashes	Symm-Clashes
8	Н	302	ACT	2	0

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\mathbf{Mol}	Chain	Res	Type	Clashes	Symm-Clashes
9	С	212	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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(m \AA^2)$	Q<0.9
1	L	213/214~(99%)	0.27	5 (2%) 60 65	16, 37, 56, 67	0
2	Н	214/227 (94%)	0.59	15 (7%) 16 20	16, 31, 51, 65	0
3	С	115/129 (89%)	0.10	1 (0%) 84 86	20, 31, 51, 60	0
All	All	542/570 (95%)	0.36	21 (3%) 39 45	16, 33, 53, 67	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	С	7	THR	4.1
2	Н	139	GLY	3.6
2	Н	132	SER	3.5
2	Н	140	THR	3.1
1	L	1	ASP	3.0
1	L	59	PRO	3.0
2	Н	183	LEU	2.9
1	L	152	ASN	2.9
2	Н	161	SER	2.5
2	Н	162	GLY	2.5
2	Н	163	ALA	2.4
2	Н	165	THR	2.4
2	Н	52	THR	2.3
2	Н	196	THR	2.3
2	Н	66	GLY	2.3
2	Н	51	ILE	2.3
1	L	157	GLY	2.2
2	Н	57	TYR	2.2
2	Н	147	VAL	2.1
2	Н	195	GLY	2.0
1	L	203[A]	SER	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.

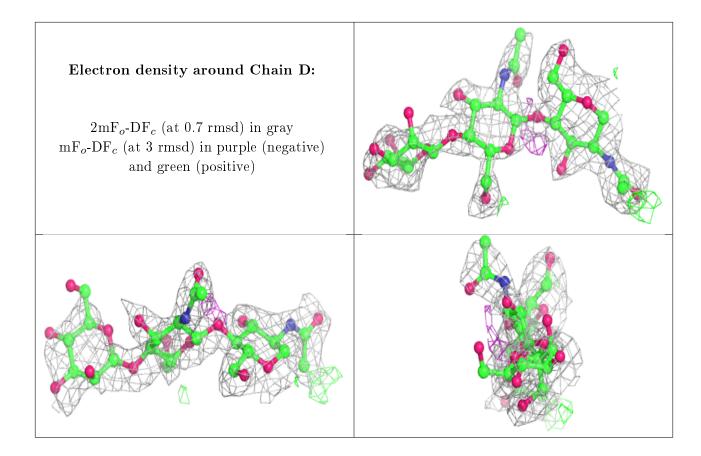
6.3 Carbohydrates (i)

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	$\operatorname{\textbf{B-factors}}(\mathring{\mathbf{A}}^2)$	Q < 0.9
6	NAG	D	2	14/15	0.61	0.45	80,90,100,108	0
5	BMA	В	3	11/12	0.66	0.51	79,87,95,102	0
5	MAN	В	4	11/12	0.68	0.69	111,115,121,122	0
5	MAN	В	5	11/12	0.70	0.60	103,106,109,111	0
6	BMA	D	3	11/12	0.72	0.53	114,116,118,121	0
6	NAG	D	1	14/15	0.80	0.26	48,58,68,77	0
4	NAG	A	2	14/15	0.82	0.36	47,57,64,69	0
5	NAG	В	2	14/15	0.86	0.45	$45,\!51,\!55,\!67$	0
4	NAG	A	1	14/15	0.91	0.12	22,34,51,52	0
5	NAG	В	1	14/15	0.91	0.13	24,42,55,62	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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
9	NAG	С	201	14/15	0.46	0.45	64,80,83,83	0
10	GOL	С	213	6/6	0.73	0.26	61,63,66,70	0
8	ACT	Н	302	4/4	0.80	0.22	44,52,53,66	0
9	NAG	С	212	14/15	0.81	0.29	59,70,78,83	0
8	ACT	Н	303	4/4	0.89	0.14	69,75,75,79	0
8	ACT	С	214	4/4	0.90	0.25	59,63,64,65	0
7	SO4	L	301	5/5	0.91	0.29	79,85,88,91	0
7	SO4	Н	301	5/5	0.96	0.17	95,96,97,98	0

6.5 Other polymers (i)

There are no such residues in this entry.

