



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:47 PM GMT

PDB ID : 1QLR
Title : CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF A HUMAN MON-
OCLONAL IGM COLD AGGLUTININ
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Deposited on : 1999-09-11
Resolution : 2.83 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

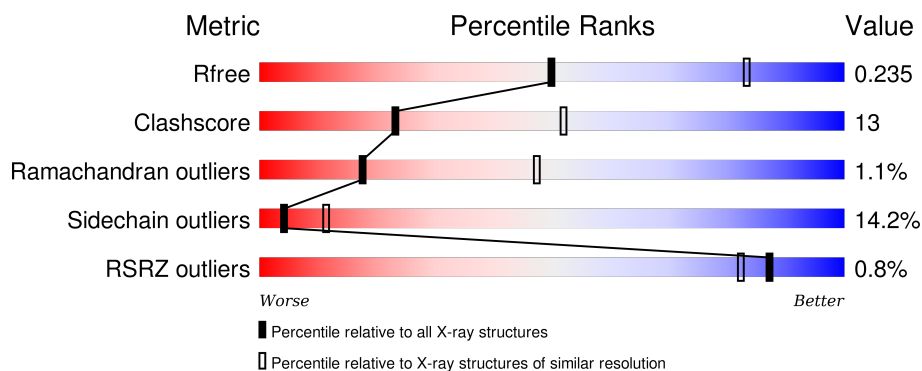
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.83 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3170 (2.88-2.80)
Clashscore	102246	3658 (2.88-2.80)
Ramachandran outliers	100387	3591 (2.88-2.80)
Sidechain outliers	100360	3594 (2.88-2.80)
RSRZ outliers	91569	3184 (2.88-2.80)

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. 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 $\leq 5\%$. 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	215	<div> <div>62%</div> <div>27%</div> <div>8%</div> <div>.</div> </div>
1	C	215	<div> <div>62%</div> <div>28%</div> <div>7%</div> <div>.</div> </div>
2	B	232	<div> <div>51%</div> <div>31%</div> <div>6%</div> <div>.</div> <div>10%</div> </div>
2	D	232	<div> <div>52%</div> <div>29%</div> <div>7%</div> <div>.</div> <div>10%</div> </div>

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	Res	Chirality	Geometry	Clashes	Electron density
3	FUC	B	302	X	-	-	-
3	FUC	D	302	X	-	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6540 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 IGM KAPPA CHAIN V-III (KAU COLD AGGLUTININ).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1638	1023	275	335	5			
1	C	215	Total	C	N	O	S	0	0	0
			1638	1023	275	335	5			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	CYS	GLY	CONFLICT	PIR A23746
C	23	CYS	GLY	CONFLICT	PIR A23746
A	88	CYS	GLY	CONFLICT	PIR A23746
C	88	CYS	GLY	CONFLICT	PIR A23746
A	134	CYS	GLY	CONFLICT	PIR A23746
C	134	CYS	GLY	CONFLICT	PIR A23746
A	194	CYS	GLY	CONFLICT	PIR A23746
C	194	CYS	GLY	CONFLICT	PIR A23746
A	214	CYS	GLY	CONFLICT	PIR A23746
C	214	CYS	GLY	CONFLICT	PIR A23746

- Molecule 2 is a protein called IGM FAB REGION IV-J(H4)-C (KAU COLD AGGLUTININ).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	209	Total	C	N	O	S	0	0	0
			1608	1024	271	308	5			
2	D	209	Total	C	N	O	S	0	0	0
			1608	1024	271	308	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	22	CYS	GLY	CONFLICT	PIR B23746
D	22	CYS	GLY	CONFLICT	PIR B23746

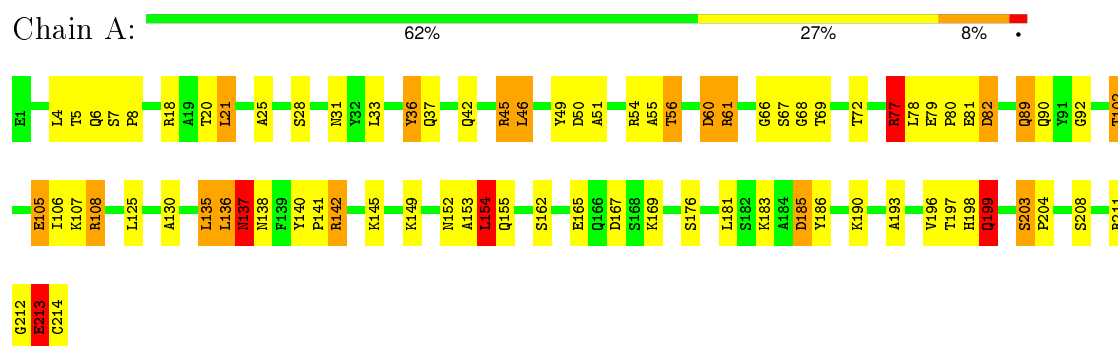
- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	2	Total	C	N	O	0	0
			24	14	1	9		
3	D	2	Total	C	N	O	0	0
			24	14	1	9		

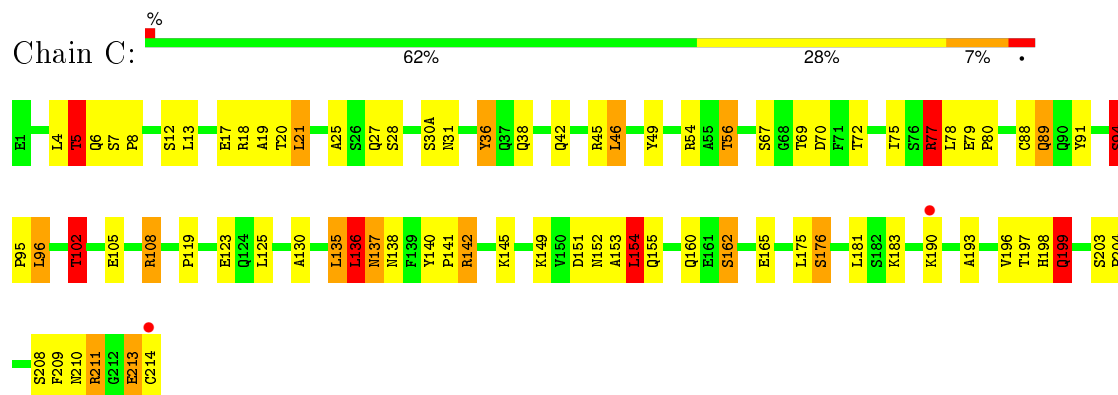
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

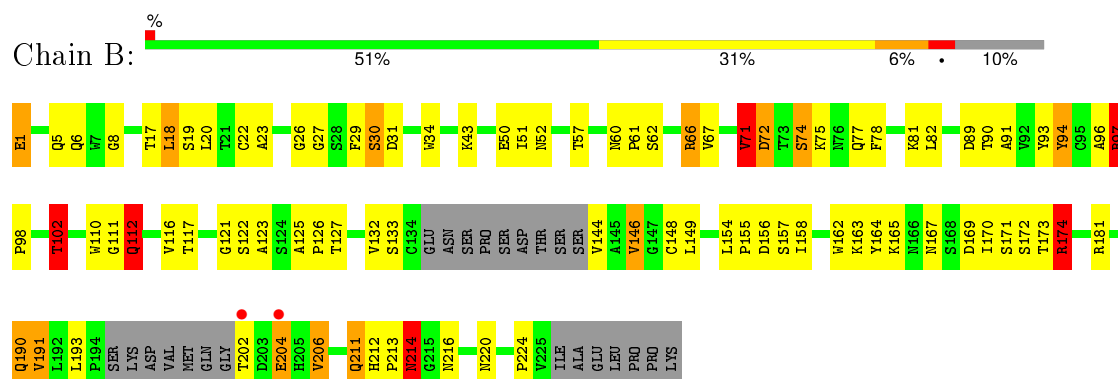
- Molecule 1: IGM KAPPA CHAIN V-III (KAU COLD AGGLUTININ)



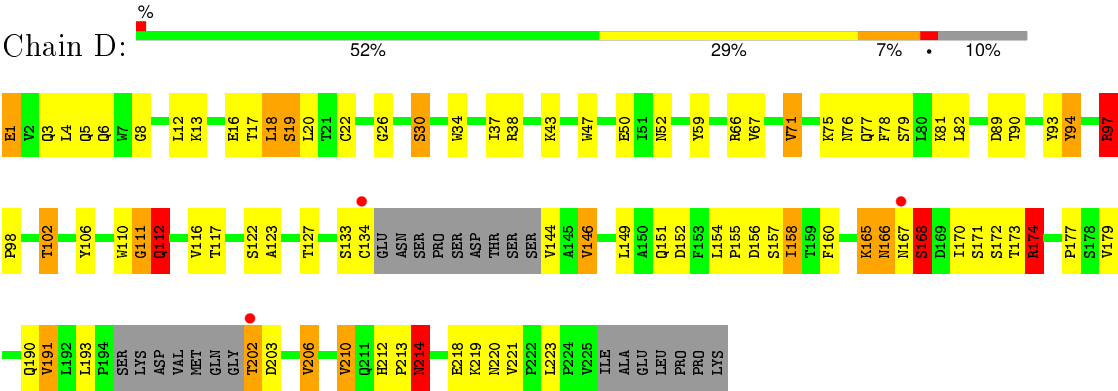
- Molecule 1: IGM KAPPA CHAIN V-III (KAU COLD AGGLUTININ)



- Molecule 2: IGM FAB REGION IV-J(H4)-C (KAU COLD AGGLUTININ)



● Molecule 2: IGM FAB REGION IV-J(H4)-C (KAU COLD AGGLUTININ)



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	115.66Å 115.66Å 174.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	13.10 – 2.83 13.12 – 2.84	Depositor EDS
% Data completeness (in resolution range)	96.8 (13.10-2.83) 96.8 (13.12-2.84)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.84Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.216 , 0.265 0.189 , 0.235	Depositor DCC
R_{free} test set	1578 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 67.6	EDS
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 31328 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6540	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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 lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.78	0/1673	2.06	55/2273 (2.4%)
1	C	0.79	2/1673 (0.1%)	2.09	55/2273 (2.4%)
2	B	0.76	1/1654 (0.1%)	1.82	42/2259 (1.9%)
2	D	0.76	0/1654	1.90	42/2259 (1.9%)
All	All	0.77	3/6654 (0.0%)	1.97	194/9064 (2.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	C	0	3
3	B	1	0
3	D	1	0
All	All	2	5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	36	TYR	CE2-CZ	-6.25	1.30	1.38
2	B	27	GLY	N-CA	5.50	1.54	1.46
1	C	49	TYR	CE1-CZ	-5.33	1.31	1.38

The worst 5 of 194 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	54	ARG	NE-CZ-NH2	-23.10	108.75	120.30
1	A	54	ARG	NE-CZ-NH2	-21.46	109.57	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	97	ARG	NE-CZ-NH2	-16.70	111.95	120.30
1	C	49	TYR	CD1-CG-CD2	-14.71	101.72	117.90
1	C	49	TYR	CB-CG-CD2	14.42	129.65	121.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	302	FUC	C1
3	D	302	FUC	C1

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137	ASN	Mainchain
1	A	60	ASP	Mainchain
1	C	151	ASP	Mainchain
1	C	5	THR	Mainchain
1	C	94	SER	Mainchain

5.2 Too-close contacts

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	1638	0	1586	39	0
1	C	1638	0	1586	39	1
2	B	1608	0	1550	44	1
2	D	1608	0	1550	56	0
3	B	24	0	22	0	0
3	D	24	0	22	1	0
All	All	6540	0	6316	172	1

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 13.

The worst 5 of 172 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:C:137:ASN:HB3	1:C:138:ASN:HD22	1.28	0.98
1:A:137:ASN:HB3	1:A:138:ASN:HD22	1.28	0.93
1:C:79:GLU:HG3	1:C:80:PRO:HD2	1.64	0.80
1:A:79:GLU:HG3	1:A:80:PRO:HD2	1.65	0.79
2:B:18:LEU:HD12	2:B:19:SER:N	2.03	0.73

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:211:GLN:OE1	1:C:27:GLN:NE2[4_456]	2.14	0.06

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	A	213/215 (99%)	195 (92%)	15 (7%)	3 (1%)	14	40
1	C	213/215 (99%)	197 (92%)	15 (7%)	1 (0%)	34	67
2	B	203/232 (88%)	194 (96%)	6 (3%)	3 (2%)	13	38
2	D	203/232 (88%)	185 (91%)	16 (8%)	2 (1%)	19	50
All	All	832/894 (93%)	771 (93%)	52 (6%)	9 (1%)	17	47

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	GLU
2	D	166	ASN
2	D	168	SER
1	A	51	ALA
1	A	154	LEU

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	185/185 (100%)	160 (86%)	25 (14%)	5	13
1	C	185/185 (100%)	159 (86%)	26 (14%)	4	11
2	B	180/201 (90%)	153 (85%)	27 (15%)	3	10
2	D	180/201 (90%)	154 (86%)	26 (14%)	4	11
All	All	730/772 (95%)	626 (86%)	104 (14%)	4	11

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	202	THR
1	C	56	THR
2	D	172	SER
2	B	204	GLU
1	C	5	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	89	GLN
1	C	138	ASN
2	D	112	GLN
2	B	205	HIS
2	B	214	ASN

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 ⓘ

4 carbohydrates 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	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	NAG	B	301	3,2	14,14,15	1.23	1 (7%)	15,19,21	1.86	4 (26%)
3	FUC	B	302	3	10,10,11	0.83	0	14,14,16	2.25	4 (28%)
3	NAG	D	301	3,2	14,14,15	1.38	2 (14%)	15,19,21	2.62	9 (60%)
3	FUC	D	302	3	10,10,11	0.64	0	14,14,16	1.49	2 (14%)

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	B	301	3,2	-	0/6/23/26	0/1/1/1
3	FUC	B	302	3	1/1/4/5	0/0/17/20	0/1/1/1
3	NAG	D	301	3,2	-	0/6/23/26	0/1/1/1
3	FUC	D	302	3	1/1/4/5	0/0/17/20	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	NAG	O7-C7	-3.52	1.15	1.23
3	D	301	NAG	O7-C7	-3.47	1.15	1.23
3	D	301	NAG	C1-C2	2.18	1.55	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	301	NAG	C4-C3-C2	-5.55	102.60	111.23
3	B	301	NAG	C4-C3-C2	-3.86	105.23	111.23
3	D	301	NAG	C6-C5-C4	-3.47	104.47	113.02
3	D	301	NAG	C2-N2-C7	-2.76	119.49	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	301	NAG	C6-C5-C4	-2.35	107.22	113.02

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	D	302	FUC	C1
3	B	302	FUC	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	302	FUC	1	0

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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, 95th 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	OWAB(Å ²)	Q<0.9
1	A	215/215 (100%)	-0.82	0 100 100	16, 39, 76, 94	0
1	C	215/215 (100%)	-0.78	2 (0%) 85 80	16, 39, 76, 93	0
2	B	209/232 (90%)	-0.60	2 (0%) 84 78	17, 37, 90, 100	0
2	D	209/232 (90%)	-0.63	3 (1%) 78 71	17, 37, 90, 100	0
All	All	848/894 (94%)	-0.71	7 (0%) 87 82	16, 39, 85, 100	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	202	THR	4.4
1	C	214	CYS	3.0
2	D	202	THR	2.9
2	B	204	GLU	2.4
1	C	190	LYS	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(\AA^2)	Q<0.9
3	FUC	D	302	10/11	0.85	0.36	-	100,100,100,100	0
3	NAG	D	301	14/15	0.80	0.23	-	98,99,100,100	0
3	FUC	B	302	10/11	0.93	0.25	-	99,100,100,100	0
3	NAG	B	301	14/15	0.78	0.28	-	99,99,100,100	0

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.