



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2026 – 07:35 PM UTC

PDB ID : 6IUT / pdb_00006iut
Title : Crystal structure of influenza A virus H5 hemagglutinin globular head in complex with the Fab of antibody AVFluIgG01
Authors : Wang, P.; Zuo, Y.; Sun, J.; Zhang, L.; Wang, X.
Deposited on : 2018-11-30
Resolution : 2.30 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

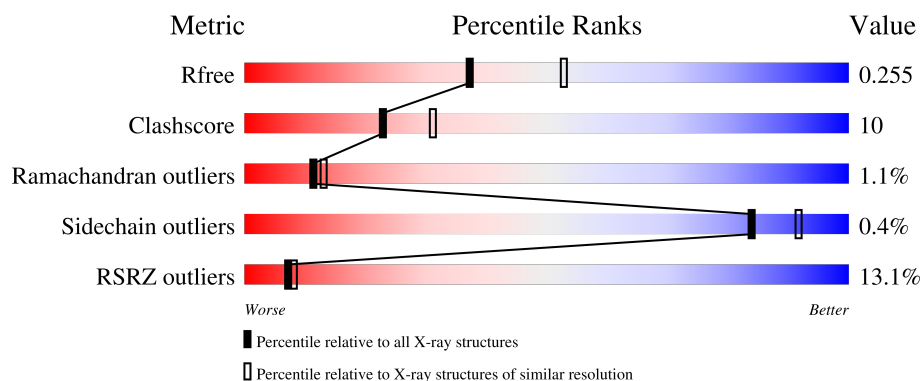
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 $\leq 5\%$. 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	H	219	5% 84% 16% .
2	L	216	6% 90% 8% .
3	A	230	26% 61% 28% . 10%
4	B	3	67% 33%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5141 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 AVFluIgG01 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	219	Total	C	N	O	S	0	1	0
			1635	1039	265	327	4			

- Molecule 2 is a protein called AVFluIgG01 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	0	0
			1620	1005	271	339	5			

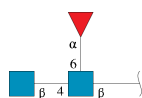
- Molecule 3 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	208	Total	C	N	O	S	3	1	0
			1683	1074	287	316	6			

There are 6 discrepancies between the modelled and reference sequences:

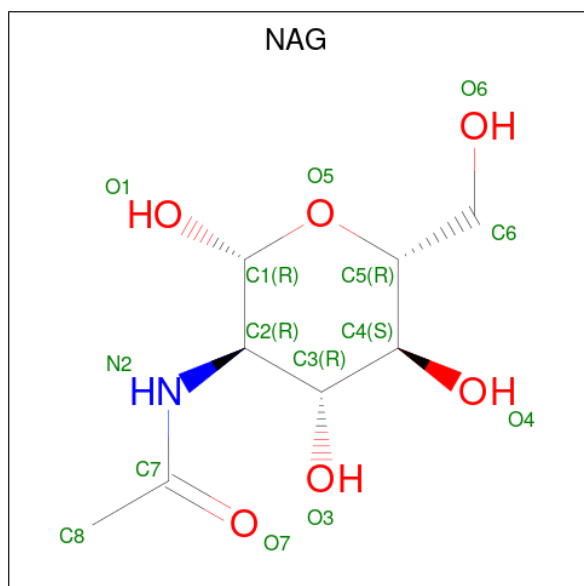
Chain	Residue	Modelled	Actual	Comment	Reference
A	269	HIS	-	expression tag	UNP Q1WDM0
A	270	HIS	-	expression tag	UNP Q1WDM0
A	271	HIS	-	expression tag	UNP Q1WDM0
A	272	HIS	-	expression tag	UNP Q1WDM0
A	273	HIS	-	expression tag	UNP Q1WDM0
A	274	HIS	-	expression tag	UNP Q1WDM0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

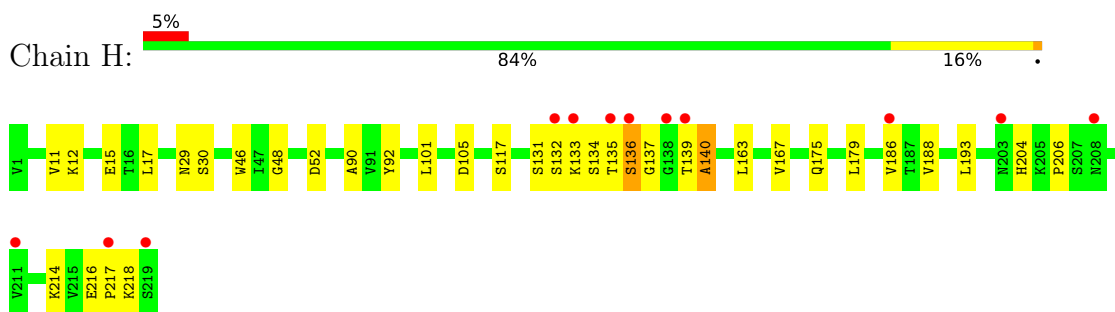
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	49	Total	O	0	0
			49	49		
6	L	72	Total	O	0	0
			72	72		
6	A	30	Total	O	0	0
			30	30		

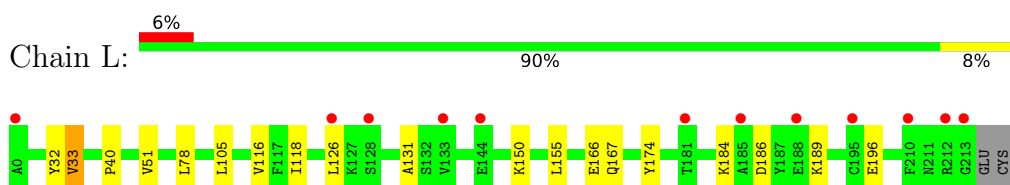
3 Residue-property plots [i](#)

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.

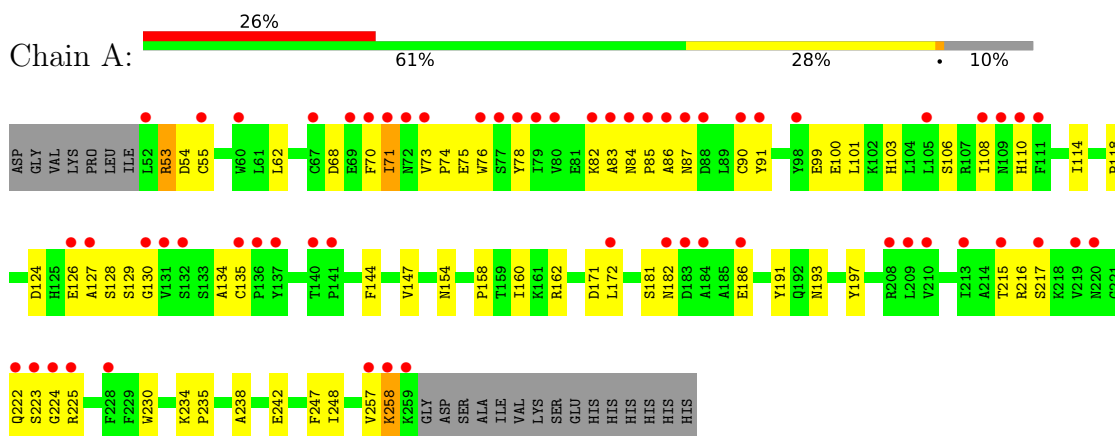
- Molecule 1: AVFluIgG01 Heavy Chain



- Molecule 2: AVFluIgG01 Light Chain



- Molecule 3: Hemagglutinin



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





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	112.10Å 150.05Å 107.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.07 – 2.30 42.07 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.7 (42.07-2.30) 98.0 (42.07-2.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.205 , 0.255 0.210 , 0.255	Depositor DCC
R_{free} test set	2035 reflections (4.09%)	wwPDB-VP
Wilson B-factor (Å ²)	45.4	Xtriage
Anisotropy	0.455	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5141	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	H	0.50	1/1681 (0.1%)	0.66	1/2298 (0.0%)
2	L	0.42	0/1655	0.58	0/2249
3	A	0.41	0/1733	0.68	1/2358 (0.0%)
All	All	0.44	1/5069 (0.0%)	0.64	2/6905 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	101	LEU	C-O	-5.12	1.17	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	134	ALA	N-CA-C	-5.56	105.22	111.28
1	H	101	LEU	N-CA-C	-5.55	104.53	112.13

There are no chirality outliers.

There are no planarity outliers.

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	H	1635	0	1607	40	0
2	L	1620	0	1541	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1683	0	1628	52	0
4	B	38	0	34	2	0
5	A	14	0	13	0	0
6	A	30	0	0	2	0
6	H	49	0	0	0	0
6	L	72	0	0	0	0
All	All	5141	0	4823	102	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 10.

All (102) 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:H:134:SER:CB	1:H:139:THR:HG21	1.27	1.55
1:H:134:SER:HA	1:H:139:THR:CG2	1.39	1.49
1:H:134:SER:CA	1:H:139:THR:CG2	2.02	1.35
1:H:134:SER:OG	1:H:139:THR:HG21	1.21	1.28
1:H:134:SER:CA	1:H:139:THR:HG21	1.63	1.25
1:H:134:SER:CB	1:H:139:THR:CG2	2.17	1.20
1:H:134:SER:HA	1:H:139:THR:HG23	1.14	1.14
1:H:134:SER:OG	1:H:139:THR:CG2	2.04	1.05
1:H:134:SER:CA	1:H:139:THR:HG23	1.78	0.98
2:L:40:PRO:HG2	2:L:166:GLU:HG3	1.50	0.93
3:A:70:PHE:HD1	3:A:71:ILE:HG13	1.39	0.87
3:A:70:PHE:CD1	3:A:71:ILE:HG13	2.14	0.82
1:H:134:SER:HA	1:H:139:THR:HG22	1.61	0.80
1:H:134:SER:HB3	1:H:139:THR:HG21	1.62	0.77
1:H:137:GLY:C	1:H:139:THR:H	1.90	0.77
1:H:135:THR:N	1:H:139:THR:HG23	2.01	0.75
1:H:135:THR:HG21	2:L:116:VAL:H	1.52	0.74
1:H:135:THR:H	1:H:139:THR:HG23	1.53	0.73
1:H:105[A]:ASP:OD2	4:B:3:FUC:O3	2.06	0.72
3:A:154:ASN:O	6:A:401:HOH:O	2.07	0.70
3:A:91:TYR:CE2	3:A:222:GLN:HG2	2.27	0.69
3:A:222:GLN:HG3	3:A:224:GLY:H	1.59	0.67
3:A:110:HIS:HE1	3:A:257:VAL:H	1.43	0.66
1:H:134:SER:C	1:H:139:THR:HG23	2.21	0.65
1:H:12:LYS:HD3	1:H:117:SER:HA	1.78	0.65
2:L:126:LEU:HD21	2:L:131:ALA:HB2	1.82	0.61
3:A:90:CYS:SG	3:A:135:CYS:HB3	2.41	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:147:VAL:CG1	3:A:248:ILE:HG22	2.31	0.61
3:A:126:GLU:OE2	3:A:129:SER:N	2.32	0.60
1:H:137:GLY:C	1:H:139:THR:N	2.57	0.59
3:A:110:HIS:HE1	3:A:257:VAL:N	2.00	0.59
3:A:114:ILE:HD11	3:A:172:LEU:HD21	1.86	0.58
3:A:110:HIS:CE1	3:A:257:VAL:HB	2.38	0.58
1:H:134:SER:HG	1:H:139:THR:HG21	1.59	0.57
3:A:110:HIS:CE1	3:A:257:VAL:H	2.22	0.57
2:L:126:LEU:HD22	2:L:184:LYS:HG3	1.88	0.56
1:H:133:LYS:HE2	2:L:118:ILE:HG22	1.87	0.55
3:A:147:VAL:HG12	3:A:248:ILE:HG22	1.89	0.55
3:A:197:TYR:HE2	3:A:242:GLU:HG2	1.71	0.55
1:H:90:ALA:HB3	1:H:92:TYR:CE1	2.43	0.53
1:H:131:SER:OG	1:H:132:SER:N	2.40	0.53
3:A:124:ASP:HB3	3:A:158:PRO:HG2	1.91	0.53
1:H:167:VAL:HG12	1:H:186:VAL:HG13	1.90	0.53
3:A:191:TYR:O	3:A:193:ASN:N	2.40	0.51
2:L:186:ASP:HA	2:L:189:LYS:HD2	1.91	0.51
3:A:82:LYS:HD2	3:A:84:ASN:H	1.74	0.50
3:A:55:CYS:SG	3:A:87:ASN:ND2	2.75	0.50
3:A:68:ASP:HB3	3:A:70:PHE:HE2	1.77	0.50
2:L:33:VAL:HG13	2:L:51:VAL:HG22	1.93	0.49
3:A:101:LEU:HB2	3:A:230:TRP:CE2	2.47	0.49
1:H:46:TRP:CH2	1:H:48:GLY:HA2	2.47	0.49
3:A:76:TRP:HD1	3:A:78:TYR:N	2.11	0.48
2:L:150:LYS:NZ	2:L:196:GLU:OE1	2.36	0.48
3:A:53:ARG:HG2	3:A:54:ASP:OD1	2.14	0.48
2:L:167:GLN:HG3	2:L:174:TYR:CZ	2.49	0.47
3:A:171:ASP:OD1	3:A:234:LYS:HA	2.14	0.47
1:H:163:LEU:HD21	1:H:186:VAL:HG11	1.96	0.47
2:L:32:TYR:HE2	3:A:118:PRO:HG3	1.80	0.47
3:A:108:ILE:HD13	3:A:258:LYS:HA	1.96	0.46
3:A:74:PRO:O	3:A:76:TRP:N	2.48	0.46
1:H:12:LYS:HB2	1:H:15:GLU:HG3	1.97	0.46
1:H:29:ASN:O	1:H:30:SER:HB2	2.15	0.46
3:A:90:CYS:H	3:A:144:PHE:HZ	1.63	0.46
1:H:193:LEU:HB3	1:H:217:PRO:HG3	1.98	0.46
1:H:137:GLY:O	1:H:139:THR:N	2.43	0.45
2:L:78:LEU:HD11	2:L:105:LEU:HD21	1.98	0.45
3:A:110:HIS:HE1	3:A:257:VAL:HB	1.81	0.45
3:A:160:ILE:O	3:A:242:GLU:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:139:THR:O	1:H:140:ALA:HB3	2.16	0.45
1:H:139:THR:O	1:H:188:VAL:O	2.36	0.44
2:L:126:LEU:O	2:L:184:LYS:HD2	2.17	0.44
1:H:11:VAL:HG21	1:H:17:LEU:HD23	2.00	0.44
1:H:175:GLN:HG2	1:H:179:LEU:O	2.18	0.44
3:A:247:PHE:N	6:A:407:HOH:O	2.51	0.44
1:H:134:SER:HB3	1:H:139:THR:CG2	2.30	0.44
3:A:126:GLU:OE2	3:A:128:SER:N	2.51	0.43
3:A:171:ASP:OD1	3:A:235:PRO:HD3	2.17	0.43
2:L:126:LEU:HA	2:L:126:LEU:HD23	1.56	0.43
3:A:82:LYS:HD2	3:A:83:ALA:N	2.32	0.43
3:A:126:GLU:OE2	3:A:127:ALA:N	2.51	0.43
1:H:52:ASP:OD1	3:A:162:ARG:HB2	2.18	0.43
3:A:182:ASN:ND2	3:A:223:SER:HB2	2.33	0.43
3:A:216:ARG:HH12	3:A:225:ARG:HH21	1.67	0.43
3:A:54:ASP:O	3:A:86:ALA:HB3	2.18	0.43
3:A:238:ALA:HB3	4:B:1:NAG:H82	2.01	0.42
3:A:181:SER:HB2	3:A:186:GLU:HG2	2.02	0.42
3:A:62:LEU:O	3:A:144:PHE:HB3	2.20	0.42
1:H:204:HIS:NE2	1:H:206:PRO:HG2	2.35	0.41
1:H:135:THR:O	1:H:136:SER:HB2	2.19	0.41
1:H:214:LYS:HD3	1:H:216:GLU:OE2	2.21	0.41
2:L:32:TYR:CE2	3:A:118:PRO:HG3	2.55	0.41
2:L:150:LYS:HG2	2:L:155:LEU:HD23	2.02	0.41
3:A:54:ASP:HB3	3:A:86:ALA:HB3	2.03	0.41
3:A:83:ALA:O	3:A:85:PRO:HD3	2.20	0.41
3:A:73:VAL:HA	3:A:74:PRO:HD3	1.97	0.41
3:A:110:HIS:ND1	3:A:110:HIS:O	2.54	0.41
3:A:82:LYS:HE3	3:A:84:ASN:HB2	2.03	0.41
3:A:99:GLU:HG2	3:A:100:GLU:H	1.84	0.41
3:A:103:HIS:O	3:A:106:SER:OG	2.26	0.41
3:A:182:ASN:OD1	3:A:215:THR:HA	2.21	0.41
3:A:216:ARG:HH12	3:A:225:ARG:NH2	2.18	0.40
1:H:217:PRO:O	1:H:218:LYS:HG2	2.21	0.40

There are no symmetry-related clashes.

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	H	218/219 (100%)	203 (93%)	13 (6%)	2 (1%)	14	17
2	L	212/216 (98%)	201 (95%)	11 (5%)	0	100	100
3	A	207/230 (90%)	184 (89%)	18 (9%)	5 (2%)	4	4
All	All	637/665 (96%)	588 (92%)	42 (7%)	7 (1%)	11	13

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	75	GLU
3	A	53	ARG
1	H	140	ALA
3	A	71	ILE
1	H	136	SER
3	A	258	LYS
3	A	130	GLY

5.3.2 Protein sidechains

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	H	189/188 (100%)	189 (100%)	0	100	100
2	L	185/187 (99%)	184 (100%)	1 (0%)	81	90
3	A	188/206 (91%)	186 (99%)	2 (1%)	65	81
All	All	562/581 (97%)	559 (100%)	3 (0%)	84	90

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	33	VAL
3	A	217[A]	SER
3	A	217[B]	SER

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

Mol	Chain	Res	Type
1	H	109	GLN
2	L	190	HIS
3	A	110	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	B	1	3,4	14,14,15	0.50	0	17,19,21	0.66	0
4	NAG	B	2	4	14,14,15	0.79	1 (7%)	17,19,21	0.43	0
4	FUC	B	3	4	10,10,11	0.98	1 (10%)	14,14,16	0.95	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	B	1	3,4	-	0/6/23/26	0/1/1/1
4	NAG	B	2	4	-	1/6/23/26	0/1/1/1
4	FUC	B	3	4	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2	NAG	O5-C1	-2.85	1.38	1.43
4	B	3	FUC	C2-C3	2.31	1.56	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

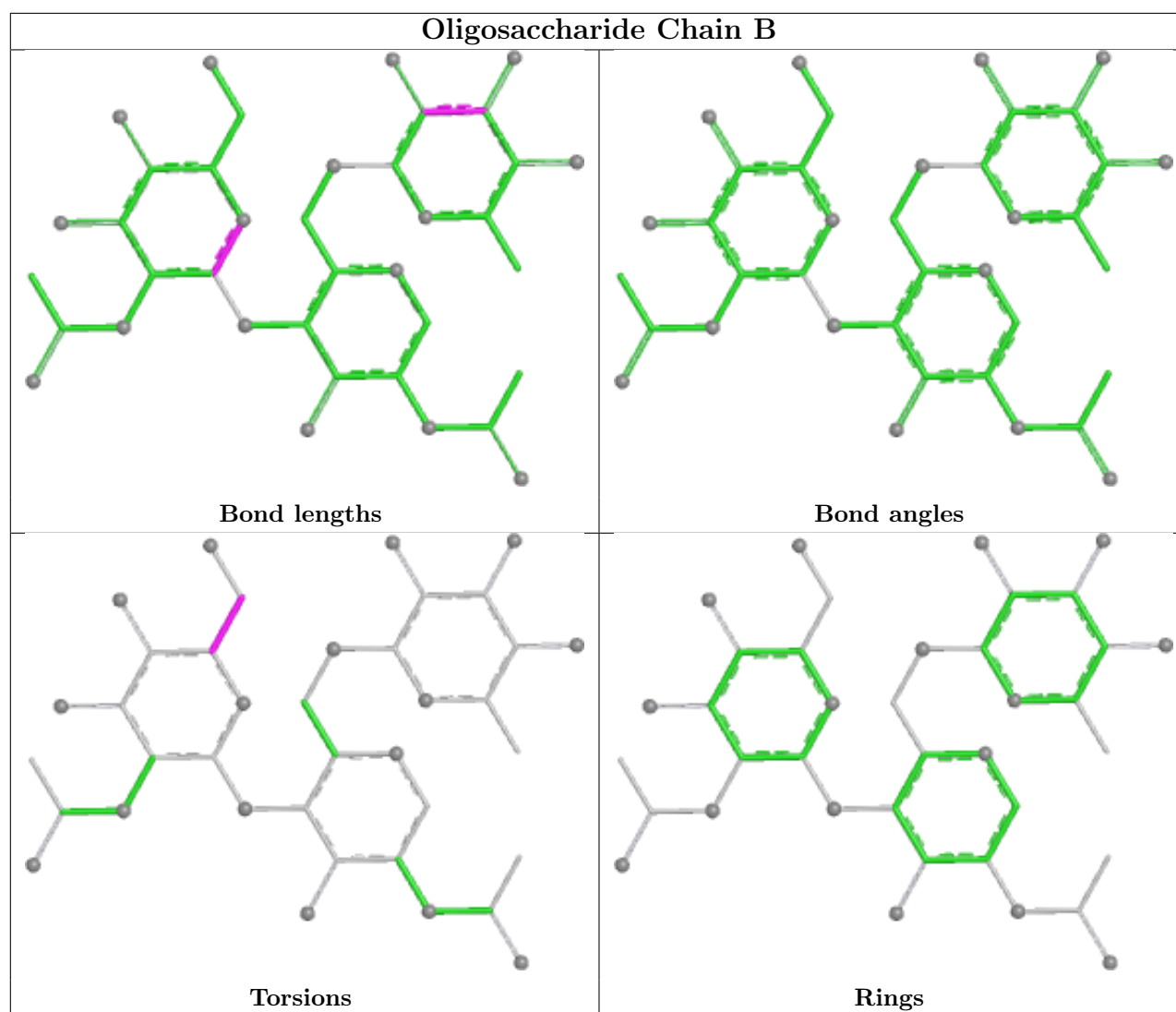
Mol	Chain	Res	Type	Atoms
4	B	2	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1	NAG	1	0
4	B	3	FUC	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](#)

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	A	301	3	14,14,15	0.63	1 (7%)	17,19,21	0.84	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	NAG	A	301	3	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	301	NAG	O5-C1	-2.11	1.40	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	301	NAG	C4-C5-C6-O6
5	A	301	NAG	O5-C5-C6-O6
5	A	301	NAG	C8-C7-N2-C2
5	A	301	NAG	O7-C7-N2-C2

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

6.1 Protein, DNA and RNA chains

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	H	219/219 (100%)	0.64	12 (5%)	30 32	27, 50, 68, 98	1 (0%)
2	L	214/216 (99%)	0.60	12 (5%)	30 32	32, 44, 80, 87	0
3	A	208/230 (90%)	1.55	60 (28%)	1 1	38, 68, 120, 134	1 (0%)
All	All	641/665 (96%)	0.92	84 (13%)	7 8	27, 52, 106, 134	2 (0%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	0	ALA	5.6
3	A	71	ILE	5.3
3	A	84	ASN	5.2
3	A	78	TYR	5.0
3	A	224	GLY	4.5
3	A	111	PHE	4.4
3	A	136	PRO	4.4
3	A	213	ILE	4.3
2	L	213	GLY	4.3
3	A	219	VAL	4.0
3	A	90	CYS	3.9
3	A	91	TYR	3.9
1	H	135	THR	3.7
3	A	70	PHE	3.7
3	A	259	LYS	3.7
1	H	133	LYS	3.7
3	A	55	CYS	3.6
3	A	87	ASN	3.6
3	A	52	LEU	3.5
3	A	127	ALA	3.5
3	A	130	GLY	3.5
3	A	140	THR	3.5
3	A	222	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
3	A	67	CYS	3.5
3	A	137	TYR	3.3
3	A	223	SER	3.3
3	A	88	ASP	3.2
3	A	131	VAL	3.2
1	H	136	SER	3.1
2	L	144	GLU	3.0
3	A	110	HIS	3.0
3	A	225	ARG	3.0
1	H	219	SER	3.0
3	A	135	CYS	3.0
3	A	60	TRP	3.0
3	A	83	ALA	2.9
3	A	79	ILE	2.9
3	A	182	ASN	2.9
3	A	257	VAL	2.8
3	A	69	GLU	2.7
1	H	139	THR	2.7
2	L	188	GLU	2.7
1	H	132	SER	2.6
3	A	105	LEU	2.6
3	A	76	TRP	2.6
3	A	73	VAL	2.5
3	A	228	PHE	2.5
3	A	77	SER	2.4
3	A	72	ASN	2.4
3	A	172	LEU	2.4
3	A	85	PRO	2.4
1	H	138	GLY	2.4
3	A	258	LYS	2.4
2	L	210	PHE	2.4
2	L	212	ARG	2.4
3	A	220	ASN	2.3
3	A	215	THR	2.3
2	L	128	SER	2.3
3	A	82	LYS	2.3
1	H	211	VAL	2.3
3	A	126	GLU	2.3
3	A	141	PRO	2.3
1	H	203	ASN	2.3
1	H	208	ASN	2.3
3	A	132	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	H	186	VAL	2.3
3	A	80	VAL	2.3
3	A	183	ASP	2.2
2	L	185	ALA	2.2
3	A	98	TYR	2.2
3	A	108	ILE	2.2
2	L	181	THR	2.2
3	A	86	ALA	2.2
3	A	217[A]	SER	2.2
2	L	126	LEU	2.1
2	L	195	CYS	2.1
1	H	217	PRO	2.1
2	L	133	VAL	2.1
3	A	184	ALA	2.1
3	A	210	VAL	2.1
3	A	186	GLU	2.0
3	A	209	LEU	2.0
3	A	208	ARG	2.0
3	A	109	ASN	2.0

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

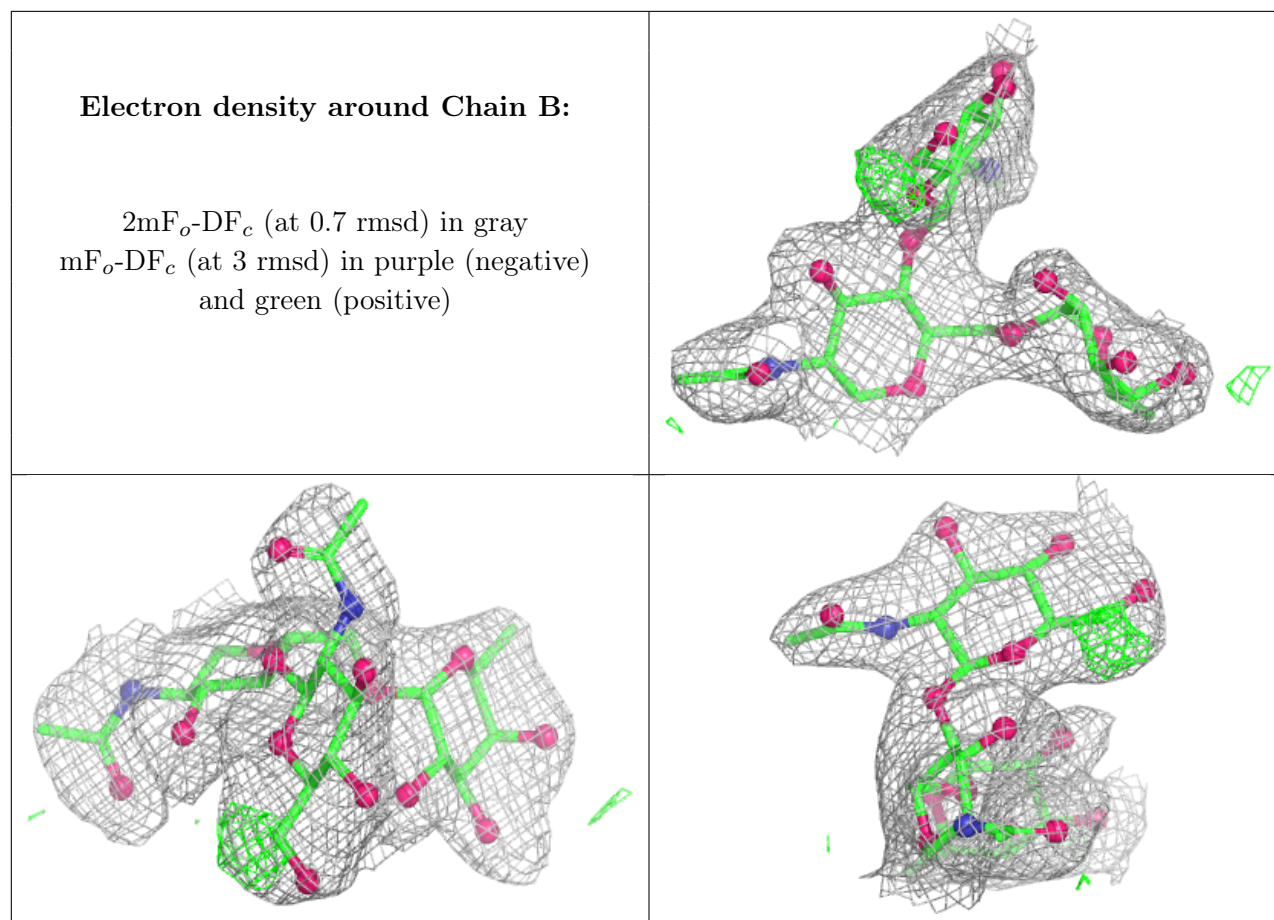
There are no non-standard protein/DNA/RNA residues in this entry.

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, 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	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	B	1	14/15	-	-	41,49,54,57	0
4	NAG	B	2	14/15	-	-	59,67,77,81	0
4	FUC	B	3	10/11	-	-	41,48,54,59	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, 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	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	A	301	14/15	0.47	0.21	79,86,90,95	0

6.5 Other polymers [i](#)

There are no such residues in this entry.