



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 05:08 PM BST

PDB ID : 6IUT
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 following versions of software and data (see [references ⓘ](#)) 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)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

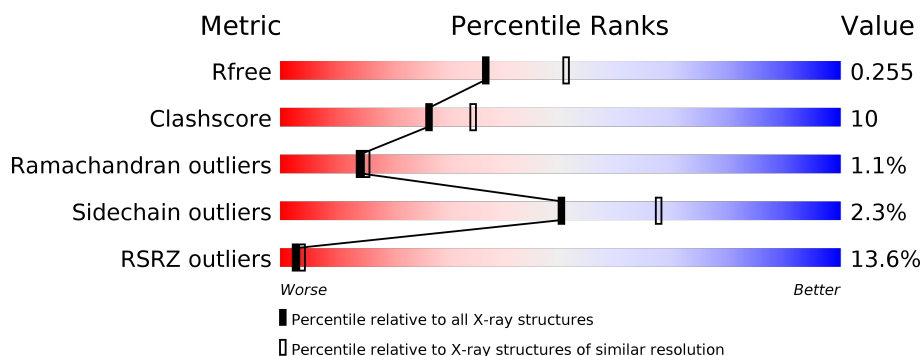
1 Overall quality at a glance

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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 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 $\leq 5\%$. 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	 3% 84% 16% •
2	L	216	 5% 89% 10% •
3	A	230	 30% 60% 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			

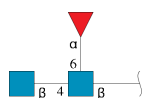
- Molecule 3 is a protein called Hemagglutinin.

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 (three-letter code: 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		

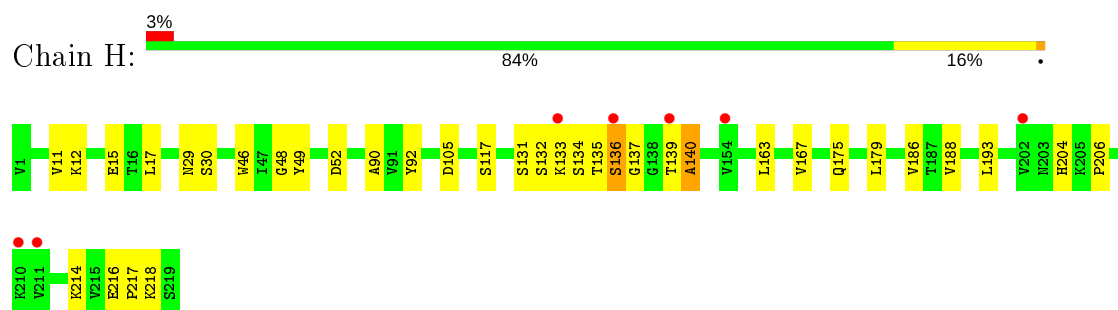
- Molecule 6 is water.

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		

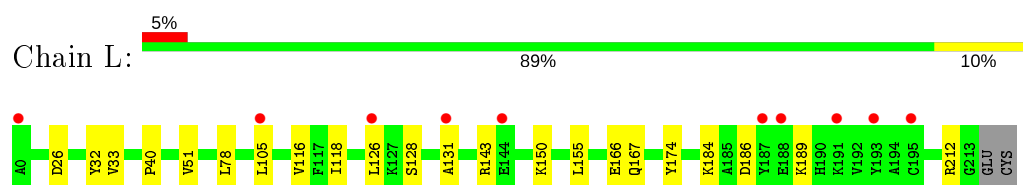
3 Residue-property plots

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.

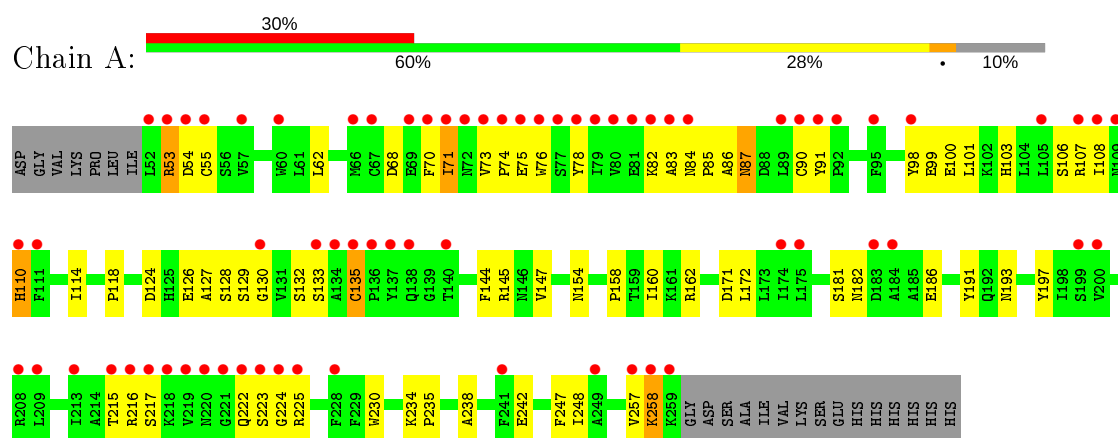
• Molecule 1: AVFluIG01 Heavy Chain



• Molecule 2: AVFluIG01 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) 97.7 (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 0.207 , 0.255	Depositor DCC
R_{free} test set	2035 reflections (5.09%)	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)	0.33 , 41.5	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 [i](#)

5.1 Standard geometry [i](#)

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	0.51	0/1681	0.67	0/2298
2	L	0.49	0/1655	0.62	0/2249
3	A	0.44	0/1733	0.64	1/2358 (0.0%)
All	All	0.48	0/5069	0.64	1/6905 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	135	CYS	CA-CB-SG	-5.92	103.35	114.00

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	H	1635	0	1607	40	0
2	L	1620	0	1541	14	0
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	L	72	0	0	0	0
All	All	5141	0	4823	101	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 (101) 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: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:137:GLY:C	1:H:139:THR:H	1.90	0.72
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: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
1:H:134:SER:C	1:H:139:THR:HG23	2.21	0.61
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:H:137:GLY:C	1:H:139:THR:N	2.57	0.55
3:A:197:TYR:HE2	3:A:242:GLU:HG2	1.71	0.55
3:A:147:VAL:HG12	3:A:248:ILE:HG22	1.89	0.55
1:H:131:SER:OG	1:H:132:SER:N	2.40	0.54
1:H:90:ALA:HB3	1:H:92:TYR:CE1	2.43	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
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:103:HIS:O	3:A:106:SER:OG	2.26	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
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
3:A:247:PHE:N	6:A:407:HOH:O	2.51	0.44
1:H:11:VAL:HG21	1:H:17:LEU:HD23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:175:GLN:HG2	1:H:179:LEU:O	2.18	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
3:A:126:GLU:OE2	3:A:127:ALA:N	2.51	0.43
3:A:82:LYS:HD2	3:A:83:ALA:N	2.32	0.43
2:L:126:LEU:HA	2:L:126:LEU:HD23	1.56	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:150:LYS:HG2	2:L:155:LEU:HD23	2.02	0.41
2:L:32:TYR:CE2	3:A:118:PRO:HG3	2.55	0.41
3:A:83:ALA:O	3:A:85:PRO:HD3	2.20	0.41
3:A:54:ASP:HB3	3:A:86:ALA:HB3	2.03	0.41
3:A:110:HIS:ND1	3:A:110:HIS:O	2.54	0.41
3:A:73:VAL:HA	3:A:74:PRO:HD3	1.97	0.41
3:A:99:GLU:HG2	3:A:100:GLU:H	1.84	0.41
3:A:182:ASN:OD1	3:A:215:THR:HA	2.21	0.41
3:A:82:LYS:HE3	3:A:84:ASN:HB2	2.03	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 [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	H	218/219 (100%)	203 (93%)	13 (6%)	2 (1%)	17	20
2	L	212/216 (98%)	201 (95%)	11 (5%)	0	100	100
3	A	207/230 (90%)	184 (89%)	18 (9%)	5 (2%)	6	4
All	All	637/665 (96%)	588 (92%)	42 (7%)	7 (1%)	14	15

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%)	188 (100%)	1 (0%)	88	95
2	L	185/187 (99%)	181 (98%)	4 (2%)	52	69
3	A	188/206 (91%)	179 (95%)	9 (5%)	25	36
All	All	562/581 (97%)	548 (98%)	14 (2%)	50	65

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	49	TYR
2	L	26	ASP
2	L	128	SER
2	L	143	ARG
2	L	212	ARG
3	A	87	ASN

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Mol	Chain	Res	Type
3	A	98	TYR
3	A	107	ARG
3	A	110	HIS
3	A	132	SER
3	A	133	SER
3	A	145	ARG
3	A	217[A]	SER
3	A	217[B]	SER

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

Mol	Chain	Res	Type
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	0.46	0	17,19,21	0.64	0
4	NAG	B	2	4	14,14,15	0.83	1 (7%)	17,19,21	0.40	0
4	FUC	B	3	4	10,10,11	1.00	1 (10%)	14,14,16	1.01	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	-3.01	1.38	1.43
4	B	3	FUC	C2-C3	2.39	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

5.6 Ligand geometry

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	0.66	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	-2.24	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%)	0.43	7 (3%) 47 54	35, 50, 68, 98	0
2	L	214/216 (99%)	0.44	10 (4%) 31 38	32, 44, 80, 87	0
3	A	208/230 (90%)	1.72	70 (33%) 0 0	38, 68, 120, 134	0
All	All	641/665 (96%)	0.85	87 (13%) 3 4	32, 52, 106, 134	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	220	ASN	9.8
3	A	80	VAL	7.8
3	A	259	LYS	7.4
3	A	223	SER	7.2
3	A	78	TYR	7.1
3	A	215	THR	7.0
3	A	136	PRO	6.4
3	A	72	ASN	6.3
3	A	111	PHE	6.0
3	A	221	GLY	5.9
3	A	258	LYS	5.5
3	A	222	GLN	4.9
3	A	105	LEU	4.8
3	A	217[A]	SER	4.7
3	A	81	GLU	4.7
3	A	84	ASN	4.5
3	A	218	LYS	4.4
3	A	219	VAL	4.4
3	A	75	GLU	4.4
3	A	76	TRP	4.3
3	A	70	PHE	4.1
3	A	108	ILE	4.0
3	A	52	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
3	A	60	TRP	3.6
3	A	135	CYS	3.6
3	A	133	SER	3.6
3	A	213	ILE	3.5
3	A	109	ASN	3.5
2	L	188	GLU	3.3
3	A	67	CYS	3.3
3	A	83	ALA	3.3
3	A	77	SER	3.3
3	A	98	TYR	3.2
3	A	110	HIS	3.2
3	A	71	ILE	3.1
3	A	257	VAL	3.1
3	A	137	TYR	3.1
3	A	228	PHE	3.1
2	L	0	ALA	3.1
3	A	140	THR	3.1
3	A	134	ALA	3.1
3	A	200	VAL	3.1
3	A	91	TYR	3.1
3	A	225	ARG	3.0
1	H	211	VAL	2.9
3	A	69	GLU	2.8
2	L	191	LYS	2.8
3	A	174	ILE	2.8
3	A	82	LYS	2.8
3	A	209	LEU	2.7
1	H	139	THR	2.7
3	A	224	GLY	2.7
1	H	202	VAL	2.7
2	L	193	TYR	2.6
3	A	90	CYS	2.6
1	H	133	LYS	2.6
1	H	154	VAL	2.6
3	A	54	ASP	2.6
1	H	136	SER	2.5
2	L	144	GLU	2.5
3	A	74	PRO	2.4
3	A	53	ARG	2.4
3	A	241	PHE	2.4
3	A	66	MET	2.4
3	A	138	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
3	A	73	VAL	2.4
2	L	105	LEU	2.3
3	A	208	ARG	2.3
2	L	195	CYS	2.3
2	L	131	ALA	2.3
2	L	126	LEU	2.3
3	A	89	LEU	2.3
3	A	175	LEU	2.3
3	A	183	ASP	2.2
3	A	95	PHE	2.2
3	A	216	ARG	2.2
2	L	187	TYR	2.2
3	A	249	ALA	2.1
1	H	210	LYS	2.1
3	A	107	ARG	2.1
3	A	55	CYS	2.1
3	A	92	PRO	2.1
3	A	79	ILE	2.0
3	A	57	VAL	2.0
3	A	130	GLY	2.0
3	A	199	SER	2.0
3	A	184	ALA	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(Å ²)	Q<0.9
4	NAG	B	2	14/15	0.90	0.18	59,67,77,81	0
4	NAG	B	1	14/15	0.94	0.12	41,49,54,57	0
4	FUC	B	3	10/11	0.94	0.16	41,48,54,59	0

6.4 Ligands

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(\AA^2)	Q<0.9
5	NAG	A	301	14/15	0.62	0.31	79,86,90,95	0

6.5 Other polymers

There are no such residues in this entry.