



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:46 AM UTC

PDB ID : 4R4H / pdb_00004r4h
Title : Crystal structure of non-neutralizing, A32-like antibody 2.2c in complex with HIV-1 Env gp120
Authors : McLellan, J.; Acharya, P.; Huang, C.-C.; Kwong, P.D.
Deposited on : 2014-08-19
Resolution : 4.28 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

<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

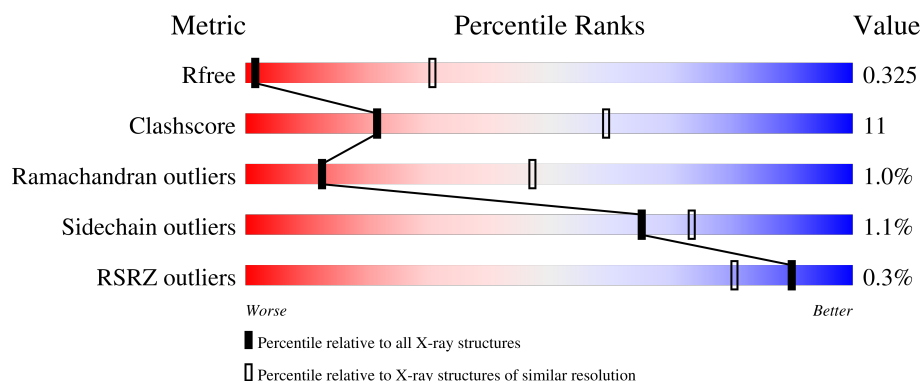
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.28 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	1036 (4.66-3.90)
Clashscore	190562	1081 (4.66-3.90)
Ramachandran outliers	187476	1007 (4.68-3.88)
Sidechain outliers	187428	1034 (4.70-3.86)
RSRZ outliers	180081	1033 (4.66-3.90)

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	A	433	 59% 18% 22%
2	B	178	 83% 16% 1%
3	L	210	 87% 13%
4	H	220	 75% 24% 1%

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	NAG	A	604	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7415 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 HIV-1 Env gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	337	Total	C	N	O	S	0	0	0
			2629	1644	461	503	21			

- Molecule 2 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	178	Total	C	N	O	S	0	3	0
			1391	868	243	276	4			

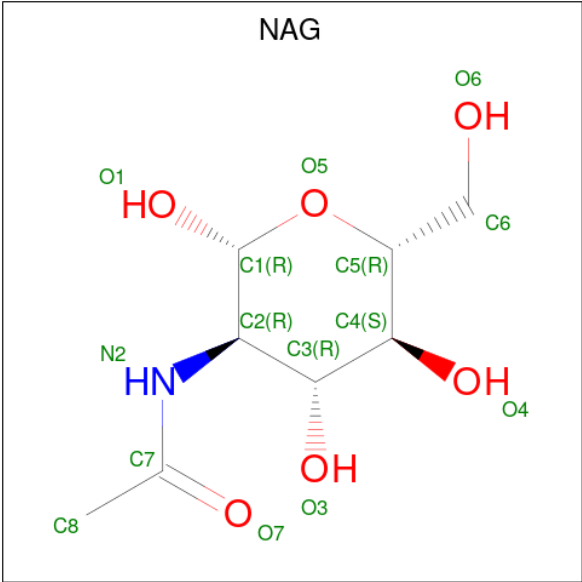
- Molecule 3 is a protein called Antibody 2.2c, Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	210	Total	C	N	O	S	0	0	0
			1612	1012	272	323	5			

- Molecule 4 is a protein called Antibody 2.2c, Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	220	Total	C	N	O	S	0	0	0
			1671	1064	283	319	5			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

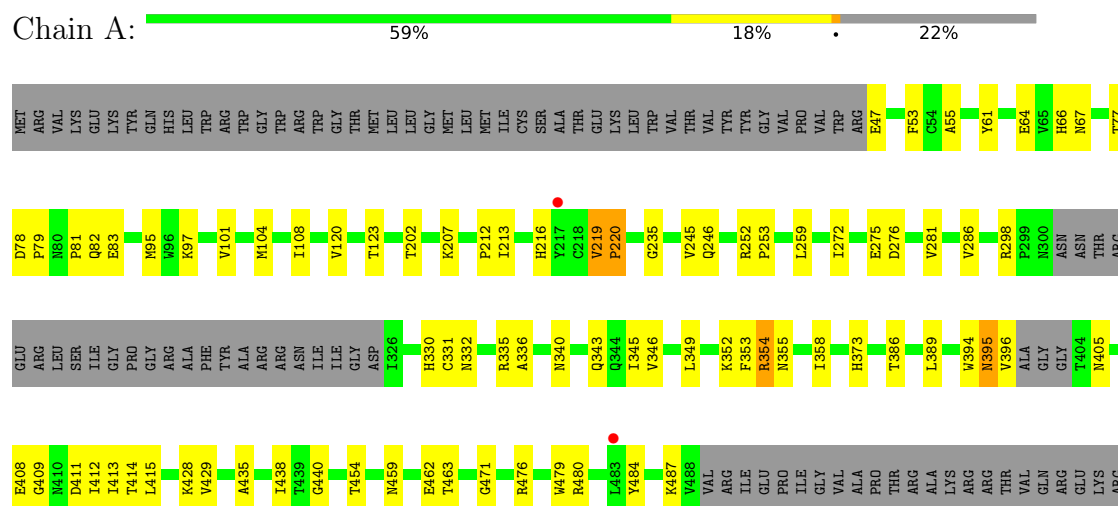


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	H	1	Total	C	N	O	0	0
			14	8	1	5		

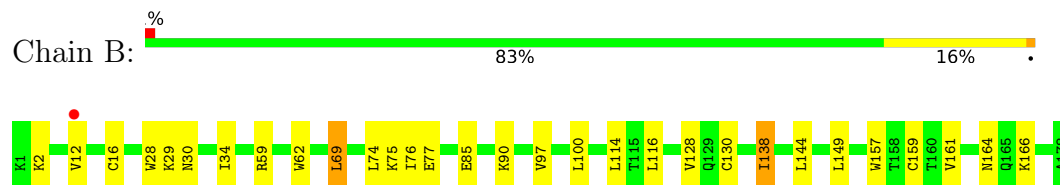
3 Residue-property plots

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.

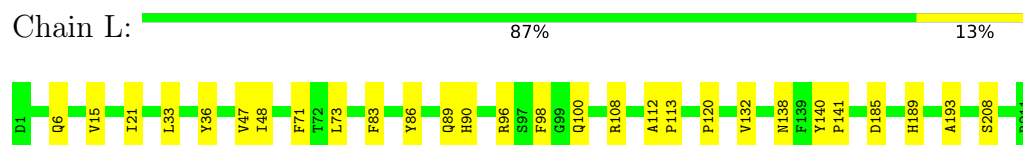
• Molecule 1: HIV-1 Env gp120



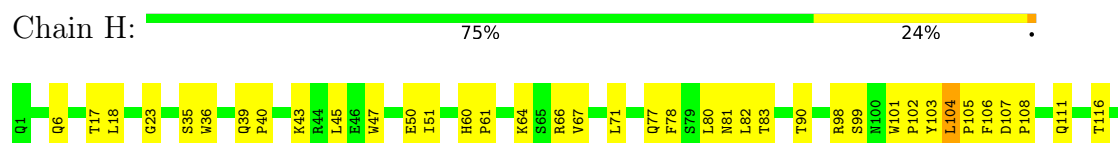
• Molecule 2: T-cell surface glycoprotein CD4



• Molecule 3: Antibody 2.2c, Light chain



• Molecule 4: Antibody 2.2c, Heavy chain



G124	P125		F128	P129		P132		K135		L165		V188	T189	V190		T199	Y200		H206	K207	P208		K216	V217	E218	P219	K220
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.36Å 69.43Å 328.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.73 – 4.28 47.73 – 4.28	Depositor EDS
% Data completeness (in resolution range)	76.8 (47.73-4.28) 67.9 (47.73-4.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 4.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.309 , 0.320 0.317 , 0.325	Depositor DCC
R_{free} test set	424 reflections (4.10%)	wwPDB-VP
Wilson B-factor (Å ²)	120.6	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 144.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	7415	wwPDB-VP
Average B, all atoms (Å ²)	166.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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

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	0.36	0/2681	0.76	0/3642
2	B	0.27	0/1424	0.66	0/1921
3	L	0.28	0/1646	0.68	0/2231
4	H	0.30	0/1720	0.71	0/2352
All	All	0.31	0/7471	0.71	0/10146

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	A	2629	0	2555	84	0
2	B	1391	0	1417	26	0
3	L	1612	0	1583	18	0
4	H	1671	0	1648	42	0
5	A	98	0	89	20	0
5	H	14	0	13	5	0
All	All	7415	0	7305	158	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 11.

The worst 5 of 158 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)
4:H:81:ASN:HD21	5:H:301:NAG:C1	1.32	1.43
4:H:81:ASN:ND2	5:H:301:NAG:O5	1.63	1.30
1:A:332:ASN:HD21	5:A:604:NAG:H2	1.07	1.10
1:A:332:ASN:OD1	5:A:604:NAG:C1	2.06	1.04
1:A:340:ASN:HA	1:A:343:GLN:HG3	1.40	1.03

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	A	331/433 (76%)	288 (87%)	36 (11%)	7 (2%)	5	30
2	B	179/178 (101%)	170 (95%)	9 (5%)	0	100	100
3	L	208/210 (99%)	196 (94%)	11 (5%)	1 (0%)	24	62
4	H	218/220 (99%)	201 (92%)	16 (7%)	1 (0%)	24	62
All	All	936/1041 (90%)	855 (91%)	72 (8%)	9 (1%)	12	47

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	354	ARG
1	A	395	ASN
1	A	405	ASN
3	L	138	ASN
1	A	97	LYS

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	298/379 (79%)	295 (99%)	3 (1%)	68	75
2	B	164/161 (102%)	161 (98%)	3 (2%)	51	66
3	L	183/183 (100%)	182 (100%)	1 (0%)	81	81
4	H	191/191 (100%)	189 (99%)	2 (1%)	68	75
All	All	836/914 (92%)	827 (99%)	9 (1%)	65	73

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	98	ARG
4	H	135	LYS
2	B	2	LYS
2	B	69	LEU
2	B	138	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	189	HIS
4	H	81	ASN
4	H	170	HIS
2	B	110	GLN
2	B	164	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	NAG	A	602	1	14,14,15	0.57	0	17,19,21	3.38	1 (5%)
5	NAG	A	607	1	14,14,15	0.66	0	17,19,21	1.21	2 (11%)
5	NAG	H	301	4	14,14,15	0.44	0	17,19,21	1.02	0
5	NAG	A	606	1	14,14,15	0.45	0	17,19,21	0.78	0
5	NAG	A	603	1	14,14,15	0.54	0	17,19,21	0.52	0
5	NAG	A	604	-	14,14,15	1.06	1 (7%)	17,19,21	0.90	0
5	NAG	A	601	1	14,14,15	0.57	0	17,19,21	0.74	1 (5%)
5	NAG	A	605	1	14,14,15	1.80	2 (14%)	17,19,21	2.39	4 (23%)

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	602	1	-	5/6/23/26	0/1/1/1
5	NAG	A	607	1	-	1/6/23/26	0/1/1/1
5	NAG	H	301	4	-	2/6/23/26	0/1/1/1
5	NAG	A	606	1	-	2/6/23/26	0/1/1/1
5	NAG	A	603	1	-	0/6/23/26	0/1/1/1
5	NAG	A	604	-	-	0/6/23/26	0/1/1/1
5	NAG	A	601	1	-	0/6/23/26	0/1/1/1
5	NAG	A	605	1	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	605	NAG	O5-C1	-5.62	1.34	1.43
5	A	604	NAG	O5-C1	-3.26	1.38	1.43
5	A	605	NAG	C1-C2	-2.89	1.48	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	NAG	C2-N2-C7	13.42	140.89	122.90
5	A	605	NAG	C2-N2-C7	7.21	132.56	122.90
5	A	605	NAG	C1-C2-N2	-3.71	104.58	110.43
5	A	605	NAG	C4-C3-C2	-3.55	105.82	111.02
5	A	607	NAG	C4-C3-C2	-2.92	106.73	111.02

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	602	NAG	C1-C2-N2-C7
5	A	602	NAG	C8-C7-N2-C2
5	A	602	NAG	O7-C7-N2-C2
5	A	605	NAG	C8-C7-N2-C2
5	A	605	NAG	O7-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	607	NAG	2	0
5	H	301	NAG	5	0
5	A	604	NAG	17	0
5	A	601	NAG	2	0
5	A	605	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, 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	337/433 (77%)	-0.15	2 (0%) 85 73	89, 150, 183, 214	0
2	B	178/178 (100%)	-0.28	1 (0%) 85 73	102, 180, 273, 288	3 (1%)
3	L	210/210 (100%)	-0.32	0 100 100	138, 171, 213, 232	0
4	H	220/220 (100%)	-0.24	0 100 100	132, 157, 208, 226	0
All	All	945/1041 (90%)	-0.23	3 (0%) 90 80	89, 160, 226, 288	3 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	TYR	2.8
2	B	12	VAL	2.6
1	A	483	LEU	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](#)

There are no oligosaccharides in this entry.

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	607	14/15	0.39	0.14	144,151,156,156	0
5	NAG	A	605	14/15	0.44	0.12	175,181,185,187	0
5	NAG	A	606	14/15	0.57	0.11	161,164,168,168	0
5	NAG	A	604	14/15	0.67	0.09	153,163,170,170	0
5	NAG	H	301	14/15	0.68	0.10	166,171,178,179	0
5	NAG	A	603	14/15	0.70	0.13	154,158,162,163	0
5	NAG	A	602	14/15	0.74	0.10	167,172,178,178	0
5	NAG	A	601	14/15	0.82	0.12	135,138,141,141	0

6.5 Other polymers [i](#)

There are no such residues in this entry.