



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:50 AM UTC

PDB ID : 4S1Q / pdb_00004s1q
Title : Crystal structure of a VRC01-lineage antibody, 45-VRC01.H03+06.D-001739
, in complex with clade A/E HIV-1 gp120 core
Authors : Kwon, Y.D.; Yang, Y.; Zhang, B.; Kwong, P.D.
Deposited on : 2015-01-14
Resolution : 2.40 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

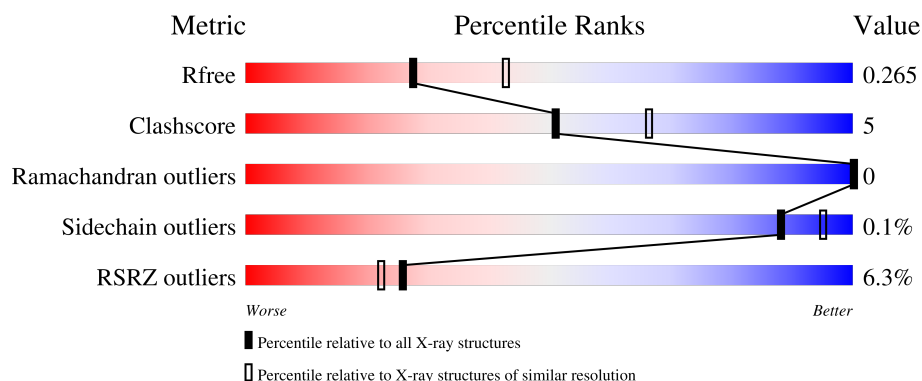
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	G	353	5% 91% 7%
2	H	234	6% 91% 6%
3	L	210	9% 87% 12%

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
4	NAG	G	510	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11855 atoms, of which 5527 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 gp120 core.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	G	344	Total	C	H	N	O	S	0	0	0
			5310	1689	2617	469	512	23			

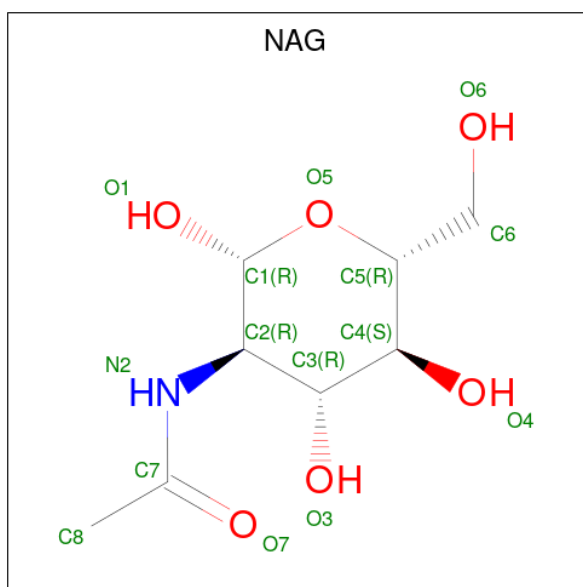
- Molecule 2 is a protein called Fab of VRC01-lineage antibody,45-VRC01.H03+06.D-001739 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	228	Total	C	H	N	O	S	0	0	0
			3261	1102	1525	303	322	9			

- Molecule 3 is a protein called Fab of VRC01 light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	L	209	Total	C	H	N	O	S	0	0	0
			2920	1016	1301	274	325	4			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	G	1	Total 14	C 8	N 1	O 5	0	0	
4	G	1	Total 27	C 8	H 13	N 1	O 5	0	0
4	G	1	Total 27	C 8	H 13	N 1	O 5	0	0
4	G	1	Total 27	C 8	H 13	N 1	O 5	0	0
4	G	1	Total 14	C 8	N 1	O 5	0	0	
4	G	1	Total 26	C 8	H 12	N 1	O 5	0	0
4	G	1	Total 25	C 8	H 11	N 1	O 5	0	0
4	G	1	Total 14	C 8	N 1	O 5	0	0	
4	G	1	Total 25	C 8	H 11	N 1	O 5	0	0
4	G	1	Total 25	C 8	H 11	N 1	O 5	0	0
4	G	1	Total 14	C 8	N 1	O 5	0	0	

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	58	Total	O	0	0
			58	58		

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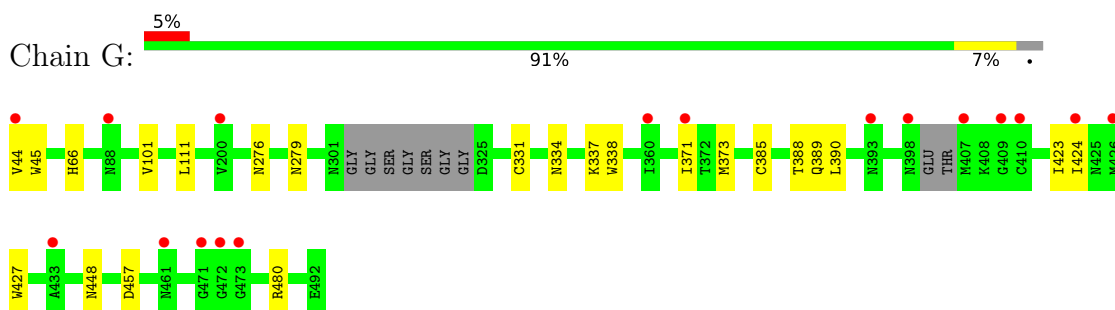
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	42	Total 42	O 42	0	0
5	L	26	Total 26	O 26	0	0

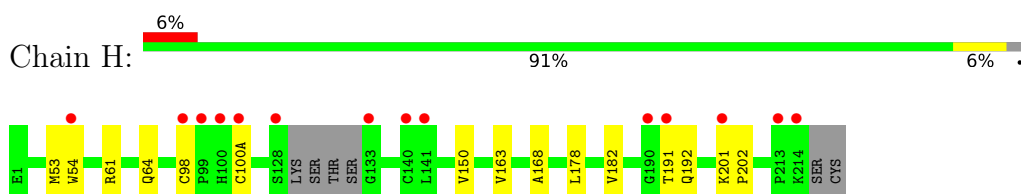
3 Residue-property plots [i](#)

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.

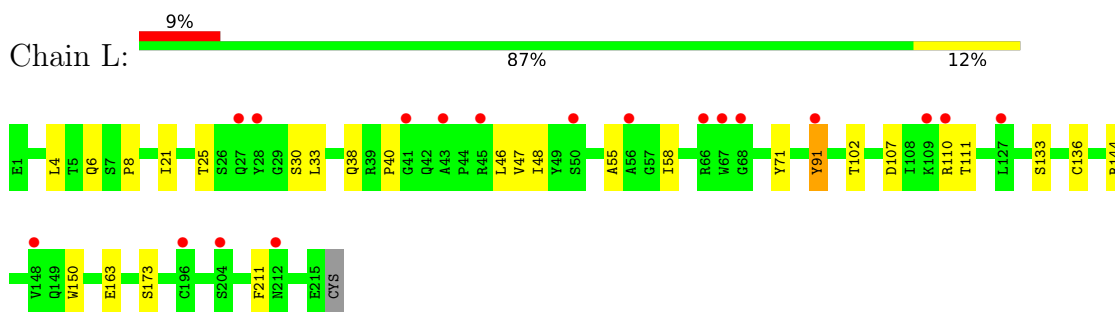
- Molecule 1: HIV-1 gp120 core



- Molecule 2: Fab of VRC01-lineage antibody, 45-VRC01.H03+06.D-001739 heavy chain



- Molecule 3: Fab of VRC01 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.18Å 78.92Å 194.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.35 – 2.40 41.35 – 2.40	Depositor EDS
% Data completeness (in resolution range)	90.5 (41.35-2.40) 89.9 (41.35-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1839)	Depositor
R, R_{free}	0.219 , 0.258 0.229 , 0.265	Depositor DCC
R_{free} test set	2000 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11855	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% 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	G	0.30	0/2749	0.61	0/3730
2	H	0.28	0/1786	0.59	0/2431
3	L	0.28	0/1656	0.59	1/2250 (0.0%)
All	All	0.29	0/6191	0.60	1/8411 (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	L	91	TYR	CB-CA-C	-5.39	110.38	116.63

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	G	2693	2617	2624	23	0
2	H	1736	1525	1692	10	0
3	L	1619	1301	1563	32	0
4	G	154	84	143	17	0
5	G	58	0	0	2	0
5	H	42	0	0	0	0
5	L	26	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6328	5527	6022	64	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 5.

All (64) 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)
3:L:21:ILE:HG23	3:L:102:THR:HG21	1.61	0.82
4:G:505:NAG:H62	3:L:91:TYR:CZ	2.21	0.74
2:H:98:CYS:SG	2:H:100(A):CYS:N	2.60	0.73
3:L:133:SER:O	5:L:318:HOH:O	2.08	0.72
3:L:40:PRO:O	5:L:311:HOH:O	2.08	0.71
3:L:163:GLU:OE2	5:L:325:HOH:O	2.07	0.71
1:G:334:ASN:OD1	4:G:508:NAG:N2	2.24	0.70
1:G:448:ASN:HD22	4:G:511:NAG:H83	1.58	0.69
2:H:53:MET:HG3	2:H:54:TRP:CD1	2.29	0.68
1:G:276:ASN:OD1	5:G:628:HOH:O	2.12	0.67
3:L:33:LEU:HD13	3:L:71:TYR:CG	2.31	0.65
3:L:47:VAL:O	3:L:58:ILE:HD13	1.97	0.65
3:L:4:LEU:CD2	3:L:25:THR:HG22	2.27	0.65
3:L:47:VAL:HG12	3:L:48:ILE:HG12	1.78	0.64
4:G:505:NAG:O4	3:L:30:SER:HB2	1.98	0.64
1:G:389:GLN:HA	4:G:510:NAG:C8	2.29	0.62
3:L:6:GLN:NE2	3:L:102:THR:HG23	2.15	0.61
1:G:389:GLN:HA	4:G:510:NAG:H81	1.84	0.59
3:L:110:ARG:HD3	3:L:173:SER:HB2	1.84	0.59
1:G:389:GLN:CA	4:G:510:NAG:H81	2.33	0.59
4:G:506:NAG:O7	4:G:506:NAG:O3	2.16	0.58
3:L:46:LEU:O	3:L:58:ILE:HD11	2.03	0.58
3:L:144:ARG:NH1	5:L:308:HOH:O	2.37	0.58
2:H:191:THR:OG1	2:H:192:GLN:N	2.36	0.58
1:G:457:ASP:OD2	2:H:64:GLN:NE2	2.37	0.55
3:L:21:ILE:CG2	3:L:102:THR:HG21	2.33	0.55
1:G:338:TRP:NE1	1:G:390:LEU:O	2.40	0.53
3:L:8:PRO:O	3:L:102:THR:HG22	2.08	0.53
4:G:506:NAG:O7	4:G:506:NAG:C3	2.57	0.52
1:G:389:GLN:HG2	4:G:510:NAG:H81	1.93	0.51
2:H:150:VAL:HG23	2:H:178:LEU:HD21	1.93	0.50
1:G:389:GLN:CG	4:G:510:NAG:H81	2.42	0.50
3:L:107:ASP:CG	5:L:319:HOH:O	2.54	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:21:ILE:HD13	3:L:102:THR:OG1	2.11	0.50
1:G:331:CYS:SG	1:G:385:CYS:SG	3.10	0.50
3:L:110:ARG:HG2	3:L:111:THR:H	1.77	0.49
2:H:163:VAL:HA	2:H:182:VAL:HG12	1.96	0.48
3:L:38:GLN:O	3:L:38:GLN:HG3	2.14	0.47
1:G:101:VAL:HG21	1:G:480:ARG:HG2	1.96	0.47
1:G:427:TRP:HA	2:H:54:TRP:CZ2	2.50	0.47
3:L:55:ALA:HB3	3:L:58:ILE:CD1	2.46	0.46
2:H:201:LYS:HB3	2:H:202:PRO:HD3	1.98	0.46
1:G:388:THR:HG22	4:G:510:NAG:C8	2.46	0.46
1:G:334:ASN:HB3	1:G:337:LYS:HB2	1.98	0.45
2:H:168:ALA:HA	2:H:178:LEU:HB3	2.00	0.43
1:G:66:HIS:CD2	1:G:111:LEU:HD21	2.54	0.43
1:G:389:GLN:HG2	4:G:510:NAG:O7	2.19	0.43
3:L:33:LEU:C	3:L:33:LEU:HD23	2.44	0.42
3:L:110:ARG:HG2	3:L:111:THR:N	2.33	0.42
1:G:44:VAL:HG12	1:G:45:TRP:CD2	2.54	0.42
4:G:503:NAG:O7	4:G:503:NAG:O3	2.27	0.42
1:G:371:ILE:HD12	2:H:54:TRP:HB2	2.00	0.42
4:G:505:NAG:H62	3:L:91:TYR:OH	2.20	0.42
4:G:505:NAG:O4	3:L:30:SER:N	2.53	0.42
3:L:33:LEU:HD13	3:L:71:TYR:CD1	2.55	0.41
3:L:6:GLN:HE21	3:L:102:THR:HG23	1.84	0.41
1:G:373:MET:SD	4:G:509:NAG:H82	2.61	0.41
3:L:33:LEU:HD13	3:L:71:TYR:CB	2.51	0.41
3:L:55:ALA:HB3	3:L:58:ILE:HD12	2.03	0.41
3:L:136:CYS:HB2	3:L:150:TRP:CH2	2.56	0.41
1:G:480:ARG:NE	5:G:644:HOH:O	2.43	0.40
3:L:211:PHE:CD1	3:L:211:PHE:C	2.98	0.40
1:G:279:ASN:HB2	3:L:91:TYR:HE1	1.86	0.40
1:G:423:ILE:C	1:G:424:ILE:HG13	2.46	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	G	338/353 (96%)	323 (96%)	15 (4%)	0	100	100
2	H	224/234 (96%)	215 (96%)	9 (4%)	0	100	100
3	L	207/210 (99%)	197 (95%)	10 (5%)	0	100	100
All	All	769/797 (96%)	735 (96%)	34 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	G	307/311 (99%)	307 (100%)	0	100	100
2	H	190/196 (97%)	189 (100%)	1 (0%)	81	91
3	L	181/182 (100%)	181 (100%)	0	100	100
All	All	678/689 (98%)	677 (100%)	1 (0%)	88	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	61	ARG

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

Mol	Chain	Res	Type
1	G	461	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

11 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$
4	NAG	G	507	1	14,14,15	0.30	0	17,19,21	0.55	0
4	NAG	G	511	1	14,14,15	0.41	0	17,19,21	0.74	1 (5%)
4	NAG	G	502	1	14,14,15	0.26	0	17,19,21	0.33	0
4	NAG	G	506	1	14,14,15	0.41	0	17,19,21	0.91	2 (11%)
4	NAG	G	504	1	14,14,15	0.31	0	17,19,21	0.48	0
4	NAG	G	510	1	14,14,15	0.48	0	17,19,21	0.46	0
4	NAG	G	505	1	14,14,15	0.72	1 (7%)	17,19,21	1.10	1 (5%)
4	NAG	G	509	1	14,14,15	0.39	0	17,19,21	0.49	0
4	NAG	G	501	1	14,14,15	0.20	0	17,19,21	1.34	1 (5%)
4	NAG	G	503	1	14,14,15	1.10	2 (14%)	17,19,21	0.79	0
4	NAG	G	508	1	14,14,15	0.47	0	17,19,21	0.50	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	G	507	1	-	2/6/23/26	0/1/1/1
4	NAG	G	511	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	G	502	1	-	0/6/23/26	0/1/1/1
4	NAG	G	506	1	-	1/6/23/26	0/1/1/1
4	NAG	G	504	1	-	2/6/23/26	0/1/1/1
4	NAG	G	510	1	-	0/6/23/26	0/1/1/1
4	NAG	G	505	1	-	2/6/23/26	0/1/1/1
4	NAG	G	509	1	-	0/6/23/26	0/1/1/1
4	NAG	G	501	1	-	0/6/23/26	0/1/1/1
4	NAG	G	503	1	-	1/6/23/26	0/1/1/1
4	NAG	G	508	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)
4	G	503	NAG	C1-C2	2.80	1.56	1.52
4	G	505	NAG	O5-C1	-2.59	1.39	1.43
4	G	503	NAG	O5-C1	-2.54	1.39	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	501	NAG	C1-O5-C5	4.73	118.52	112.19
4	G	505	NAG	C1-O5-C5	3.83	117.31	112.19
4	G	506	NAG	C2-N2-C7	2.74	126.58	122.90
4	G	511	NAG	C1-O5-C5	2.54	115.59	112.19
4	G	506	NAG	C1-O5-C5	2.03	114.91	112.19

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	506	NAG	C3-C2-N2-C7
4	G	511	NAG	C8-C7-N2-C2
4	G	511	NAG	O7-C7-N2-C2
4	G	507	NAG	O5-C5-C6-O6
4	G	505	NAG	O5-C5-C6-O6
4	G	505	NAG	C4-C5-C6-O6
4	G	504	NAG	O5-C5-C6-O6
4	G	504	NAG	C4-C5-C6-O6
4	G	503	NAG	C3-C2-N2-C7
4	G	508	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	G	507	NAG	C4-C5-C6-O6
4	G	508	NAG	O5-C5-C6-O6

There are no ring outliers.

7 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	511	NAG	1	0
4	G	506	NAG	2	0
4	G	510	NAG	7	0
4	G	505	NAG	4	0
4	G	509	NAG	1	0
4	G	503	NAG	1	0
4	G	508	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

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	G	344/353 (97%)	0.32	17 (4%) 35 31	31, 52, 99, 147	0
2	H	228/234 (97%)	0.35	14 (6%) 27 23	27, 54, 106, 158	0
3	L	209/210 (99%)	0.76	18 (8%) 16 13	32, 67, 102, 134	0
All	All	781/797 (97%)	0.44	49 (6%) 26 22	27, 57, 106, 158	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	66	ARG	5.3
3	L	67	TRP	4.6
2	H	98	CYS	4.5
1	G	472	GLY	4.3
3	L	110	ARG	4.0
1	G	407	MET	4.0
3	L	27	GLN	3.7
3	L	212	ASN	3.7
1	G	398	ASN	3.5
3	L	28	TYR	3.5
1	G	424	ILE	3.5
2	H	100	HIS	3.5
3	L	68	GLY	3.4
3	L	204	SER	3.3
3	L	43	ALA	3.1
2	H	213	PRO	3.1
2	H	191	THR	3.1
1	G	410	CYS	3.0
2	H	201	LYS	2.9
1	G	409	GLY	2.9
2	H	54	TRP	2.8
2	H	128	SER	2.7
1	G	44	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
2	H	100(A)	CYS	2.7
1	G	371	ILE	2.6
2	H	99	PRO	2.6
3	L	196	CYS	2.6
1	G	393	ASN	2.5
1	G	426	MET	2.5
3	L	127	LEU	2.5
1	G	473	GLY	2.5
2	H	214	LYS	2.4
3	L	45	ARG	2.3
1	G	200	VAL	2.3
3	L	56	ALA	2.3
3	L	41	GLY	2.3
2	H	140	CYS	2.3
1	G	461	ASN	2.2
1	G	433	ALA	2.2
2	H	133	GLY	2.2
3	L	109	LYS	2.1
1	G	471	GLY	2.1
2	H	190	GLY	2.1
2	H	141	LEU	2.1
1	G	360	ILE	2.1
3	L	91	TYR	2.0
3	L	148	VAL	2.0
1	G	88	ASN	2.0
3	L	50	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](#)

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
4	NAG	G	503	14/15	0.37	0.22	78,96,115,125	0
4	NAG	G	501	14/15	0.40	0.18	40,51,55,59	0
4	NAG	G	511	14/15	0.42	0.18	41,49,56,61	0
4	NAG	G	510	14/15	0.45	0.15	47,63,77,79	0
4	NAG	G	508	14/15	0.56	0.21	62,79,89,93	0
4	NAG	G	505	14/15	0.62	0.22	61,74,78,81	0
4	NAG	G	506	14/15	0.79	0.15	52,77,91,99	0
4	NAG	G	502	14/15	0.83	0.11	45,66,83,91	0
4	NAG	G	509	14/15	0.85	0.09	47,63,77,79	0
4	NAG	G	504	14/15	0.87	0.10	30,43,60,67	0
4	NAG	G	507	14/15	0.88	0.10	40,64,89,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.