



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 07:47 AM BST

PDB ID : 4LSQ  
Title : Crystal structure of broadly and potently neutralizing antibody VRC-CH31 in complex with HIV-1 clade A/E gp120 93TH057 with LOOP D and Loop V5 from clade A strain 3415\_v1\_c1  
Authors : Zhou, T.; Moquin, S.; Kwong, P.D.  
Deposited on : 2013-07-23  
Resolution : 2.25 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](mailto: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.

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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

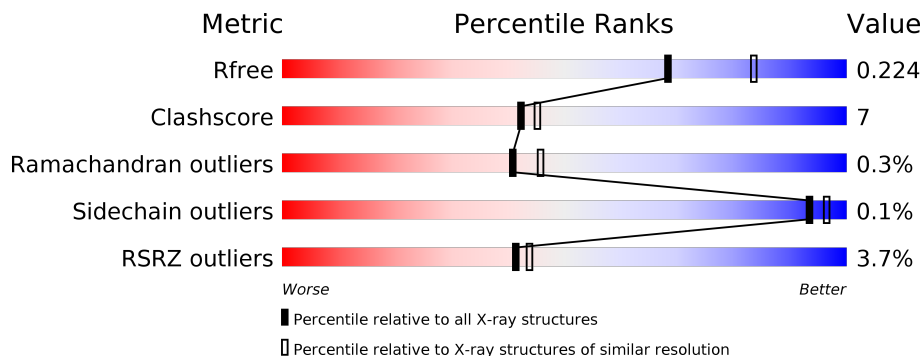
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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  $\geq 3$ , 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	352	 3% 85% 13%
2	H	236	 2% 81% 13% 6%
3	L	210	 7% 84% 15%

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
8	NA	G	515	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 12356 atoms, of which 5841 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 ENVELOPE GLYCOPROTEIN GP120 WITH LOOP D AND V5 FROM STRAIN 3415\_V1\_C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	G	344	5332	1699	2627	467	516	23	0	1	0

- Molecule 2 is a protein called HEAVY CHAIN OF ANTIBODY VRC-CH31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	H	222	3340	1064	1654	295	320	7	0	0	0

- Molecule 3 is a protein called LIGHT CHAIN OF ANTIBODY VRC-CH31 WITH N70D MUTATION.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	L	209	3148	994	1550	271	328	5	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).

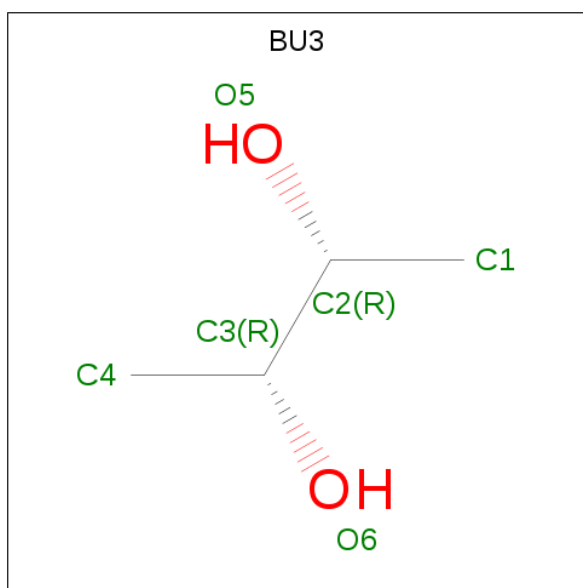


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	2	Total	Cd	0	0
			2	2		
5	G	2	Total	Cd	0	0
			2	2		
5	L	1	Total	Cd	0	0
			1	1		

- Molecule 6 is (R,R)-2,3-BUTANEDIOL (three-letter code: BU3) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
6	G	1	16	4	10	2	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
7	H	2	2	2	0	0
7	G	1	1	1	0	0

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
8	G	4	4	4	0	0

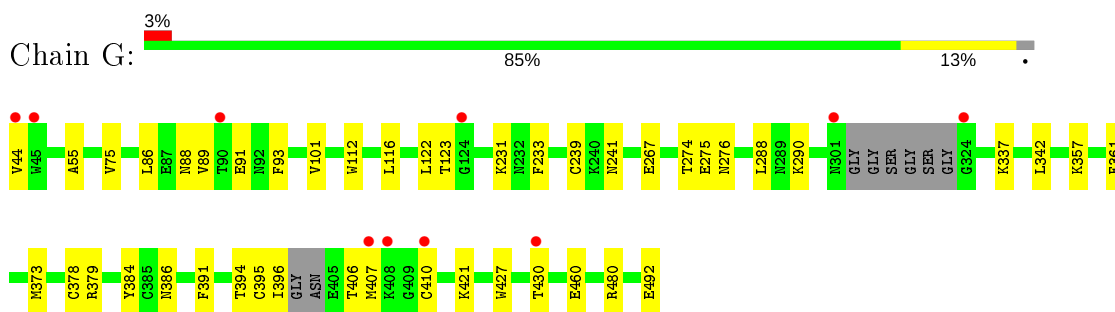
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	G	231	231	231	0	0
9	H	95	95	95	0	0
9	L	56	56	56	0	0

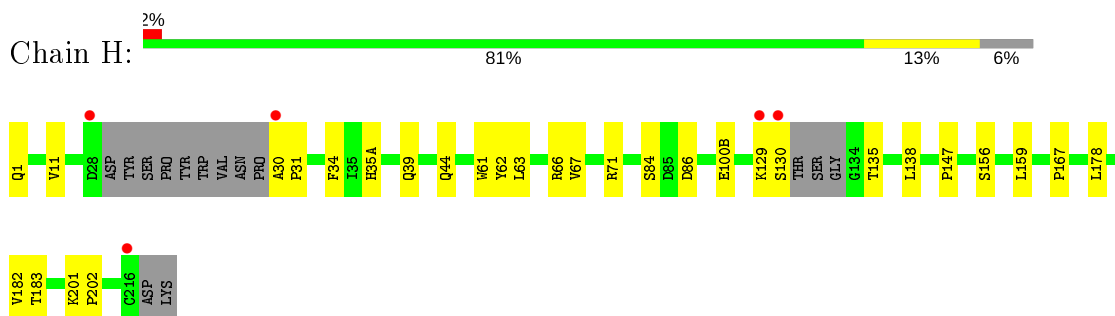
### 3 Residue-property plots [i](#)

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.

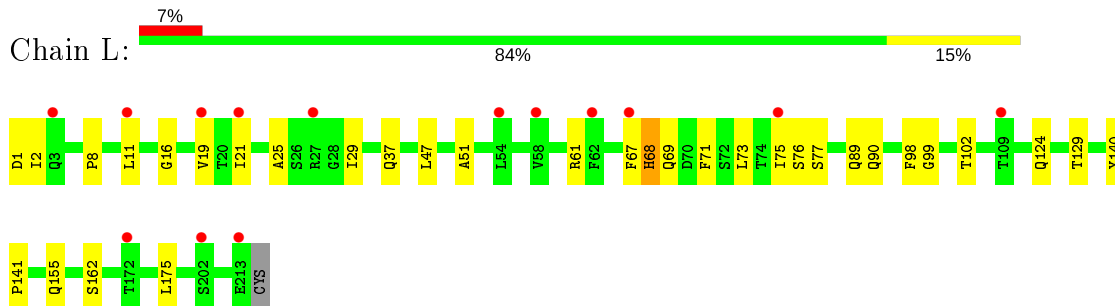
- Molecule 1: ENVELOPE GLYCOPROTEIN GP120 WITH LOOP D AND V5 FROM STRAIN 3415\_V1\_C1



- Molecule 2: HEAVY CHAIN OF ANTIBODY VRC-CH31



- Molecule 3: LIGHT CHAIN OF ANTIBODY VRC-CH31 WITH N70D MUTATION



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.51Å 67.62Å 221.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.38 – 2.25 49.38 – 2.25	Depositor EDS
% Data completeness (in resolution range)	98.4 (49.38-2.25) 98.4 (49.38-2.25)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.01 (at 2.25Å)	Xtrriage
Refinement program	PHENIX 1.7.1_743	Depositor
R, $R_{free}$	0.192 , 0.229 0.188 , 0.224	Depositor DCC
$R_{free}$ test set	2412 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.3	Xtrriage
Anisotropy	0.338	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.025 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12356	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: BU3, CD, NAG, NA, CL

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	0.37	0/2764	0.48	0/3750
2	H	0.30	0/1729	0.47	0/2357
3	L	0.27	0/1628	0.43	0/2204
All	All	0.33	0/6121	0.46	0/8311

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	G	2705	2627	2642	36	0
2	H	1686	1654	1650	22	1
3	L	1598	1550	1551	27	0
4	G	126	0	117	2	0
5	G	2	0	0	0	0
5	H	2	0	0	0	0
5	L	1	0	0	0	0
6	G	6	10	10	1	0
7	G	1	0	0	0	0
7	H	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	G	4	0	0	0	0
9	G	231	0	0	10	0
9	H	95	0	0	5	0
9	L	56	0	0	8	1
All	All	6515	5841	5970	82	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 7.

All (82) 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:G:395:CYS:HG	1:G:410:CYS:HG	1.10	0.90
3:L:155:GLN:NE2	9:L:420:HOH:O	2.05	0.89
3:L:69:GLN:O	9:L:411:HOH:O	1.90	0.88
1:G:274:THR:HG22	1:G:276:ASN:H	1.45	0.82
3:L:25:ALA:N	9:L:411:HOH:O	2.13	0.82
1:G:391:PHE:O	9:G:815:HOH:O	1.99	0.80
2:H:1:GLN:NE2	9:H:1068:HOH:O	2.14	0.79
1:G:357:LYS:NZ	3:L:1:ASP:OD1	2.16	0.78
1:G:274:THR:HG22	1:G:276:ASN:N	2.03	0.74
1:G:88:ASN:ND2	9:G:766:HOH:O	2.21	0.74
9:G:825:HOH:O	7:H:904:CL:CL	2.43	0.73
3:L:75:ILE:O	9:L:424:HOH:O	2.07	0.72
3:L:19:VAL:N	9:L:424:HOH:O	2.23	0.71
3:L:76:SER:O	9:L:407:HOH:O	2.13	0.65
3:L:51:ALA:O	9:L:412:HOH:O	2.14	0.65
1:G:239:CYS:O	9:G:735:HOH:O	2.14	0.64
1:G:274:THR:HG22	1:G:275:GLU:N	2.13	0.63
1:G:357:LYS:HZ3	3:L:1:ASP:CG	2.01	0.62
1:G:112:TRP:CE3	1:G:116:LEU:HD22	2.38	0.59
3:L:37:GLN:HB2	3:L:47:LEU:HD11	1.87	0.56
2:H:84:SER:N	9:H:1043:HOH:O	2.41	0.53
2:H:62:TYR:OH	9:H:1037:HOH:O	2.17	0.53
2:H:44:GLN:NE2	3:L:99:GLY:O	2.41	0.53
1:G:122:LEU:N	1:G:122:LEU:HD12	2.24	0.52
1:G:342:LEU:HD23	1:G:396:ILE:HD11	1.90	0.52
1:G:460:GLU:O	2:H:61:TRP:NE1	2.31	0.52
3:L:140:TYR:CG	3:L:141:PRO:HA	2.45	0.52
1:G:274:THR:HG21	9:G:648:HOH:O	2.10	0.51
2:H:30:ALA:N	2:H:31:PRO:CD	2.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:91:GLU:N	9:G:735:HOH:O	2.36	0.50
2:H:178:LEU:HD12	2:H:178:LEU:C	2.32	0.49
1:G:44:VAL:HG13	1:G:492:GLU:HB2	1.94	0.49
2:H:167:PRO:HG2	3:L:162:SER:OG	2.13	0.49
1:G:241:ASN:ND2	4:G:502:NAG:C7	2.76	0.48
2:H:66:ARG:NH2	2:H:86:ASP:OD2	2.47	0.48
1:G:239:CYS:HB3	9:G:735:HOH:O	2.13	0.47
3:L:61:ARG:NH1	9:L:418:HOH:O	2.21	0.47
3:L:16:GLY:HA2	3:L:77:SER:HB2	1.97	0.47
1:G:112:TRP:CE3	1:G:116:LEU:CD2	2.97	0.47
1:G:427:TRP:HA	6:G:512:BU3:H2	1.96	0.47
1:G:101:VAL:HG21	1:G:480:ARG:HG2	1.96	0.47
1:G:86:LEU:HB3	1:G:89:VAL:HG21	1.96	0.47
1:G:91:GLU:OE2	9:G:750:HOH:O	2.20	0.47
2:H:35(A):HIS:NE2	2:H:100(B):GLU:HG3	2.31	0.46
3:L:21:ILE:HD11	3:L:73:LEU:HD23	1.97	0.46
2:H:201:LYS:HB2	2:H:202:PRO:HD3	1.97	0.46
1:G:123:THR:HG22	1:G:430:THR:O	2.16	0.46
1:G:274:THR:CG2	1:G:275:GLU:N	2.79	0.45
2:H:11:VAL:HG21	2:H:147:PRO:HG3	1.98	0.45
3:L:2:ILE:HD13	3:L:90:GLN:HG2	1.99	0.45
4:G:504:NAG:H83	9:G:637:HOH:O	2.16	0.44
2:H:84:SER:OG	9:H:1043:HOH:O	2.21	0.44
3:L:124:GLN:HG2	3:L:129:THR:O	2.18	0.43
3:L:2:ILE:CD1	3:L:29:ILE:HG21	2.48	0.43
3:L:29:ILE:HD11	3:L:71:PHE:CE1	2.53	0.43
1:G:93:PHE:HB2	1:G:233:PHE:CZ	2.53	0.43
1:G:384:TYR:CE1	1:G:421:LYS:HB2	2.54	0.43
3:L:67:PHE:CG	3:L:68:HIS:N	2.87	0.43
1:G:373:MET:HE2	1:G:386:ASN:HA	2.01	0.43
2:H:201:LYS:N	2:H:202:PRO:CD	2.82	0.43
1:G:290:LYS:HE2	1:G:337:LYS:HE3	2.01	0.42
1:G:288:LEU:HB3	9:G:733:HOH:O	2.19	0.42
1:G:361:PHE:HB3	1:G:391:PHE:HB3	2.01	0.42
2:H:39:GLN:OE1	9:H:1025:HOH:O	2.21	0.42
2:H:30:ALA:N	2:H:31:PRO:HD3	2.35	0.42
1:G:55:ALA:HA	1:G:75:VAL:O	2.20	0.42
2:H:63:LEU:HD13	2:H:67:VAL:HG21	2.02	0.42
3:L:175:LEU:HD23	3:L:175:LEU:C	2.40	0.42
1:G:378:CYS:SG	1:G:379:ARG:HG2	2.60	0.41
1:G:112:TRP:CZ3	1:G:116:LEU:HD21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:129:LYS:O	2:H:130:SER:C	2.58	0.41
2:H:135:THR:CG2	2:H:183:THR:HB	2.51	0.41
3:L:8:PRO:O	3:L:102:THR:HG23	2.21	0.41
2:H:34:PHE:HB2	2:H:100(B):GLU:OE2	2.21	0.41
3:L:21:ILE:CG2	3:L:102:THR:HG21	2.51	0.41
3:L:11:LEU:C	3:L:11:LEU:HD12	2.40	0.41
2:H:159:LEU:HD21	2:H:182:VAL:HG11	2.02	0.41
2:H:138:LEU:HD12	2:H:138:LEU:C	2.42	0.40
1:G:231:LYS:NZ	1:G:267:GLU:OE2	2.27	0.40
3:L:90:GLN:O	3:L:90:GLN:HG3	2.22	0.40
1:G:394:THR:CG2	1:G:407:MET:HG3	2.51	0.40
3:L:89:GLN:HG3	3:L:98:PHE:CE1	2.56	0.40

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:H:156:SER:OG	9:L:444:HOH:O[4_465]	2.04	0.16

## 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	339/352 (96%)	326 (96%)	12 (4%)	1 (0%)	41	46
2	H	216/236 (92%)	211 (98%)	5 (2%)	0	100	100
3	L	207/210 (99%)	198 (96%)	8 (4%)	1 (0%)	29	29
All	All	762/798 (96%)	735 (96%)	25 (3%)	2 (0%)	41	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	406	THR
3	L	68	HIS

### 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	G	309/311 (99%)	309 (100%)	0	100	100
2	H	185/198 (93%)	184 (100%)	1 (0%)	88	92
3	L	181/182 (100%)	181 (100%)	0	100	100
All	All	675/691 (98%)	674 (100%)	1 (0%)	93	96

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

Mol	Chain	Res	Type
2	H	71	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 22 ligands modelled in this entry, 12 are monoatomic - leaving 10 for Mogul analysis.

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	504	1	14,14,15	0.60	0	17,19,21	0.75	0
4	NAG	G	503	1	14,14,15	0.59	0	17,19,21	1.14	2 (11%)
4	NAG	G	507	1	14,14,15	0.43	0	17,19,21	1.22	2 (11%)
6	BU3	G	512	-	4,5,5	1.20	0	6,6,6	0.54	0
4	NAG	G	506	1	14,14,15	0.58	0	17,19,21	0.85	1 (5%)
4	NAG	G	509	1	14,14,15	0.51	0	17,19,21	0.73	0
4	NAG	G	501	1	14,14,15	0.48	0	17,19,21	0.78	1 (5%)
4	NAG	G	508	1	14,14,15	0.54	0	17,19,21	0.63	0
4	NAG	G	505	1	14,14,15	0.47	0	17,19,21	1.31	2 (11%)
4	NAG	G	502	1	14,14,15	0.48	0	17,19,21	1.23	3 (17%)

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	504	1	-	2/6/23/26	0/1/1/1
4	NAG	G	503	1	-	0/6/23/26	0/1/1/1
4	NAG	G	507	1	-	2/6/23/26	0/1/1/1
6	BU3	G	512	-	-	0/4/4/4	-
4	NAG	G	506	1	-	0/6/23/26	0/1/1/1
4	NAG	G	509	1	-	2/6/23/26	0/1/1/1
4	NAG	G	501	1	-	4/6/23/26	0/1/1/1
4	NAG	G	508	1	-	0/6/23/26	0/1/1/1
4	NAG	G	505	1	-	0/6/23/26	0/1/1/1
4	NAG	G	502	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	505	NAG	C1-O5-C5	3.78	117.31	112.19
4	G	507	NAG	C1-O5-C5	3.30	116.66	112.19
4	G	502	NAG	C1-O5-C5	2.60	115.71	112.19
4	G	503	NAG	O5-C5-C6	2.51	111.15	107.20
4	G	501	NAG	C1-O5-C5	2.30	115.31	112.19
4	G	506	NAG	C2-N2-C7	-2.23	119.73	122.90
4	G	502	NAG	C1-C2-N2	2.17	114.19	110.49
4	G	503	NAG	C4-C3-C2	-2.15	107.87	111.02
4	G	505	NAG	O5-C5-C6	2.15	110.57	107.20
4	G	507	NAG	C6-C5-C4	-2.13	108.01	113.00
4	G	502	NAG	C4-C3-C2	-2.03	108.04	111.02

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	502	NAG	C1-C2-N2-C7
4	G	502	NAG	C8-C7-N2-C2
4	G	502	NAG	O7-C7-N2-C2
4	G	501	NAG	C8-C7-N2-C2
4	G	501	NAG	O7-C7-N2-C2
4	G	504	NAG	C8-C7-N2-C2
4	G	504	NAG	O7-C7-N2-C2
4	G	507	NAG	C8-C7-N2-C2
4	G	507	NAG	O7-C7-N2-C2
4	G	509	NAG	C8-C7-N2-C2
4	G	501	NAG	C4-C5-C6-O6
4	G	501	NAG	O5-C5-C6-O6
4	G	509	NAG	O7-C7-N2-C2
4	G	502	NAG	C4-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	504	NAG	1	0
6	G	512	BU3	1	0
4	G	502	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	G	344/352 (97%)	0.23	10 (2%) 51 55	24, 38, 85, 151	0
2	H	222/236 (94%)	0.11	5 (2%) 60 63	26, 51, 95, 149	0
3	L	209/210 (99%)	0.42	14 (6%) 17 19	45, 70, 98, 116	0
All	All	775/798 (97%)	0.25	29 (3%) 41 44	24, 51, 96, 151	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	324	GLY	5.6
2	H	28	ASP	4.0
2	H	216	CYS	3.7
3	L	202	SER	3.6
1	G	44	VAL	3.6
2	H	129	LYS	3.5
1	G	408	LYS	3.4
1	G	301	ASN	3.1
3	L	75	ILE	3.1
3	L	172	THR	3.0
3	L	213	GLU	2.8
3	L	27	ARG	2.8
3	L	62	PHE	2.8
3	L	11	LEU	2.8
1	G	124	GLY	2.7
3	L	67	PHE	2.6
3	L	54	LEU	2.6
3	L	3	GLN	2.6
3	L	109	THR	2.4
2	H	30	ALA	2.4
1	G	45	TRP	2.4
1	G	90	THR	2.4
1	G	407	MET	2.2

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Mol	Chain	Res	Type	RSRZ
3	L	21	ILE	2.2
2	H	130	SER	2.2
3	L	58	VAL	2.1
1	G	410	CYS	2.1
3	L	19	VAL	2.1
1	G	430	THR	2.1

## 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 monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	CD	G	511	1/1	0.33	0.21	193,193,193,193	0
8	NA	G	515	1/1	0.59	0.52	77,77,77,77	0
7	CL	H	904	1/1	0.59	0.17	72,72,72,72	0
8	NA	G	517	1/1	0.74	0.20	64,64,64,64	0
4	NAG	G	509	14/15	0.75	0.26	125,140,158,160	0
7	CL	H	903	1/1	0.78	0.18	80,80,80,80	0
5	CD	H	902	1/1	0.79	0.12	159,159,159,159	0
4	NAG	G	507	14/15	0.88	0.13	43,53,61,65	0
4	NAG	G	504	14/15	0.90	0.13	38,60,71,72	0
4	NAG	G	502	14/15	0.90	0.18	49,70,82,84	0
4	NAG	G	508	14/15	0.92	0.16	41,51,54,58	0
5	CD	G	510	1/1	0.93	0.05	102,102,102,102	0
4	NAG	G	501	14/15	0.94	0.09	45,56,62,62	0
6	BU3	G	512	6/6	0.94	0.25	46,55,62,63	0
8	NA	G	514	1/1	0.95	0.14	51,51,51,51	0
5	CD	L	301	1/1	0.95	0.08	117,117,117,117	0
4	NAG	G	506	14/15	0.95	0.13	42,52,62,62	0

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Atoms</b>	<b>RSCC</b>	<b>RSR</b>	<b>B-factors(<math>\text{\AA}^2</math>)</b>	<b>Q&lt;0.9</b>
4	NAG	G	505	14/15	0.96	0.10	39,58,65,70	0
4	NAG	G	503	14/15	0.97	0.12	27,32,40,48	0
8	NA	G	516	1/1	0.98	0.17	53,53,53,53	0
5	CD	H	901	1/1	0.99	0.12	49,49,49,49	0
7	CL	G	513	1/1	1.00	0.12	37,37,37,37	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.