



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:43 PM GMT

PDB ID : 4XVT
Title : Crystal structure of HIV-1 93TH057 coreE gp120 with antibody 45-VRC01.H01+07.O-863513/45-VRC01.L01+07.O-110653 (VRC07_1995)
Authors : Joyce, M.G.; Mascola, J.R.; Kwong, P.D.
Deposited on : 2015-01-28
Resolution : 1.69 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
<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

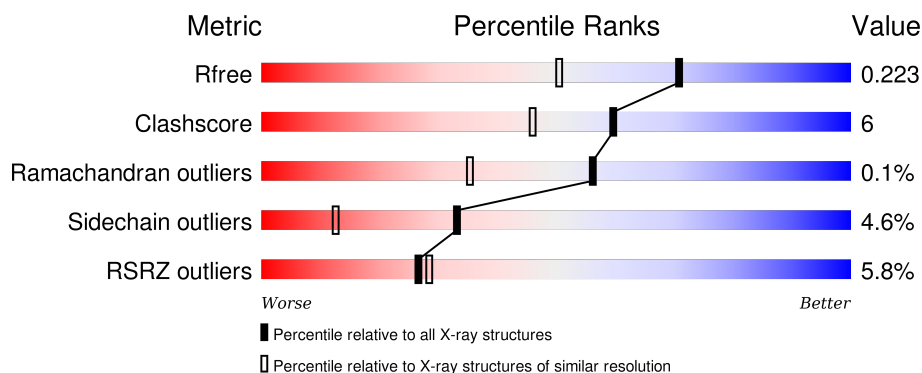
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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}	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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. 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	<div> <div>9%</div> <div>83%</div> <div>12%</div> <div>..</div> </div>
2	H	228	<div> <div>5%</div> <div>85%</div> <div>12%</div> <div>.</div> </div>
3	L	210	<div> <div>%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>

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	501	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6818 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 ENVELOPE GLYCOPROTEIN GP120 OF HIV-1 CLADE A/E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	341	Total	C	N	O	S	0	1	0
			2676	1679	467	508	22			

- Molecule 2 is a protein called donor 45 45-VRC01.H01+07.O-863513/45-VRC01.L01+07.O-110653 (VRC07_1995) Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	228	Total	C	N	O	S	0	0	0
			1734	1091	299	331	13			

- Molecule 3 is a protein called 45-VRC01.H01+07.O-863513/45-VRC01.L01+07.O-110653 (VRC07_1995) Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	208	Total	C	N	O	S	0	2	0
			1629	1020	280	324	5			

- Molecule 4 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	240	Total	O	0	0
			240	240		

Continued on next page...

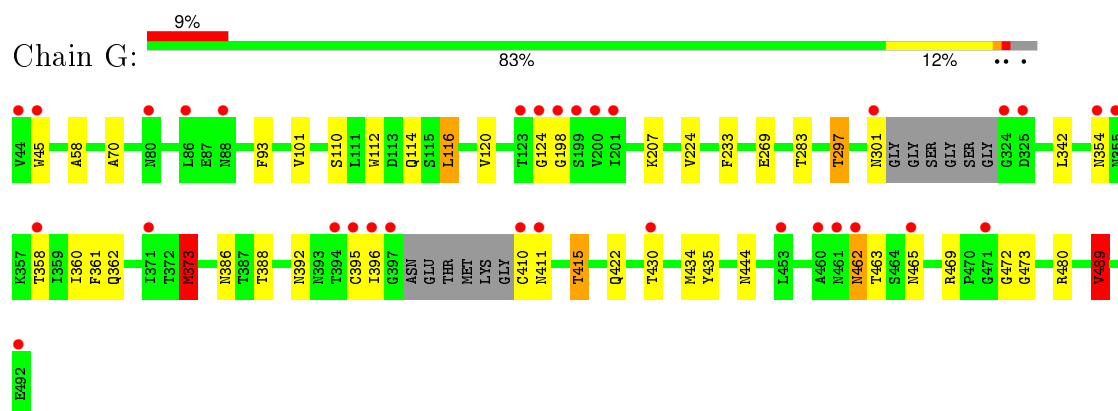
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	203	Total 203	O 203	0	0
5	L	182	Total 182	O 182	0	0

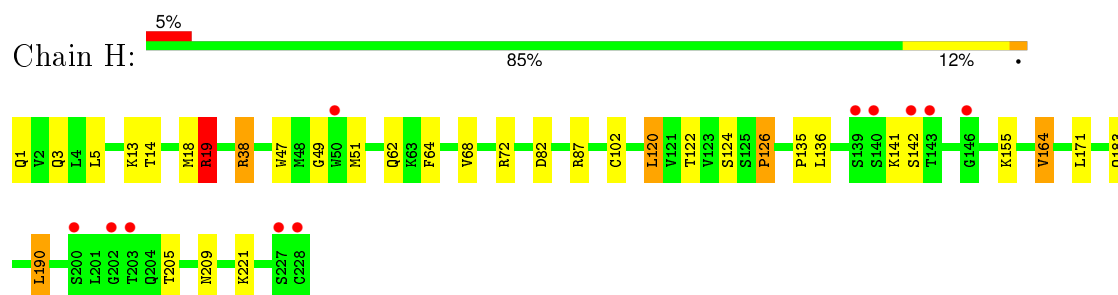
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

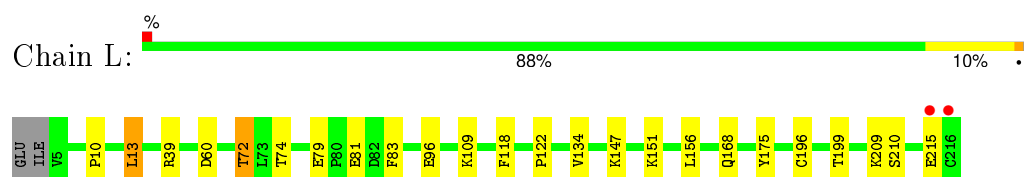
- Molecule 1: ENVELOPE GLYCOPROTEIN GP120 OF HIV-1 CLADE A/E



- Molecule 2: donor 45 45-VRC01.H01+07.O-863513/45-VRC01.L01+07.O-110653 (VRC07_1995) Heavy chain



- Molecule 3: 45-VRC01.H01+07.O-863513/45-VRC01.L01+07.O-110653 (VRC07_1995) 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	64.65Å 67.84Å 199.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.11 – 1.69 34.11 – 1.69	Depositor EDS
% Data completeness (in resolution range)	98.9 (34.11-1.69) 98.9 (34.11-1.69)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 1.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.181 , 0.222 0.182 , 0.223	Depositor DCC
R_{free} test set	4881 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	33.2	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.3	EDS
Estimated twinning fraction	0.023 for k,h,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 97827 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6818	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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, 0.375 respectively for untwinned datasets, and 0.333, 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

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	0.77	1/2735 (0.0%)	0.84	3/3712 (0.1%)
2	H	0.84	1/1779 (0.1%)	1.07	7/2418 (0.3%)
3	L	0.77	1/1671 (0.1%)	0.85	0/2265
All	All	0.79	3/6185 (0.0%)	0.92	10/8395 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	102	CYS	CB-SG	7.20	1.94	1.82
1	G	373	MET	CG-SD	-5.36	1.67	1.81
3	L	196	CYS	CB-SG	-5.15	1.73	1.81

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	38	ARG	NE-CZ-NH1	12.98	126.79	120.30
2	H	51	MET	CG-SD-CE	-12.81	79.71	100.20
2	H	38	ARG	NE-CZ-NH2	-12.10	114.25	120.30
2	H	19	ARG	NE-CZ-NH1	-10.97	114.82	120.30
2	H	19	ARG	NE-CZ-NH2	9.72	125.16	120.30
2	H	190	LEU	CA-CB-CG	8.27	134.32	115.30
1	G	116	LEU	CB-CG-CD1	-5.97	100.84	111.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	38	ARG	CB-CG-CD	5.50	125.91	111.60
1	G	489	VAL	CG1-CB-CG2	5.17	119.18	110.90
1	G	469	ARG	NE-CZ-NH2	-5.13	117.73	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	354	ASN	Peptide

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	2676	0	2612	33	0
2	H	1734	0	1697	21	0
3	L	1629	0	1578	19	0
4	G	154	0	143	6	0
5	G	240	0	0	5	0
5	H	203	0	0	5	0
5	L	182	0	0	4	0
All	All	6818	0	6030	68	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 6.

All (68) 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:39:ARG:HD2	3:L:83[B]:PHE:HE2	1.40	0.86
1:G:283:THR:HG21	1:G:473:GLY:CA	2.19	0.72
2:H:122:THR:HG23	5:H:410:HOH:O	1.89	0.71
1:G:45:TRP:HB2	1:G:489:VAL:HG13	1.73	0.69
2:H:142:SER:HA	3:L:118:PHE:HD2	1.59	0.68
1:G:415:THR:HG23	5:G:743:HOH:O	1.94	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:395:CYS:HG	1:G:410:CYS:HG	0.76	0.64
1:G:373:MET:HE2	1:G:386:ASN:HA	1.79	0.64
2:H:155:LYS:NZ	2:H:183:GLN:OE1	2.32	0.62
1:G:463:THR:HB	1:G:465:ASN:H	1.65	0.61
1:G:410:CYS:SG	4:G:510:NAG:C6	2.91	0.59
3:L:39:ARG:HD2	3:L:83[B]:PHE:CE2	2.30	0.59
1:G:283:THR:HG21	1:G:473:GLY:HA3	1.85	0.59
1:G:392:ASN:O	1:G:396:ILE:HG12	2.01	0.59
3:L:83[B]:PHE:HD1	5:L:377:HOH:O	1.85	0.58
2:H:205:THR:HG23	5:H:404:HOH:O	2.04	0.58
1:G:269:GLU:HG2	4:G:505:NAG:H61	1.86	0.58
3:L:168:GLN:HG3	3:L:175:TYR:CZ	2.38	0.58
2:H:124:SER:OG	2:H:126:PRO:HD2	2.04	0.57
3:L:74:THR:HG23	5:L:411:HOH:O	2.05	0.57
1:G:410:CYS:SG	4:G:510:NAG:H62	2.45	0.57
1:G:415:THR:HG21	5:G:779:HOH:O	2.05	0.57
2:H:141:LYS:NZ	3:L:210:SER:H	2.03	0.56
1:G:110:SER:O	1:G:114:GLN:HG2	2.06	0.56
3:L:151:LYS:HG2	3:L:156:LEU:HD23	1.89	0.55
2:H:141:LYS:HE2	3:L:209:LYS:HD2	1.89	0.54
1:G:462:ASN:HD22	1:G:462:ASN:H	1.55	0.54
3:L:10:PRO:HG3	3:L:13:LEU:HD13	1.89	0.53
2:H:141:LYS:HZ2	3:L:210:SER:H	1.55	0.53
1:G:116:LEU:HD13	1:G:435:TYR:OH	2.09	0.52
2:H:19:ARG:HD3	2:H:82:ASP:OD2	2.10	0.52
2:H:205:THR:HG22	5:H:443:HOH:O	2.10	0.51
1:G:358:THR:HB	1:G:465:ASN:HB3	1.91	0.51
1:G:297:THR:HG22	1:G:444:ASN:OD1	2.11	0.51
2:H:3:GLN:HG3	5:H:446:HOH:O	2.09	0.50
1:G:388:THR:HG22	4:G:510:NAG:H81	1.93	0.50
1:G:422:GLN:HG3	5:G:787:HOH:O	2.10	0.50
3:L:122:PRO:HD3	3:L:134:VAL:HG22	1.94	0.49
1:G:396:ILE:HG22	1:G:396:ILE:O	2.14	0.48
2:H:47:TRP:CZ2	2:H:49:GLY:HA2	2.48	0.48
1:G:124:GLY:HA3	1:G:198:GLY:HA3	1.68	0.47
2:H:64:PHE:HB3	2:H:68:VAL:CG2	2.44	0.47
4:G:511:NAG:H83	5:G:690:HOH:O	2.15	0.47
1:G:101:VAL:HG21	1:G:480:ARG:HG2	1.96	0.47
1:G:283:THR:HG21	1:G:473:GLY:N	2.30	0.47
2:H:13:LYS:HE3	2:H:126:PRO:O	2.15	0.47
2:H:135:PRO:HD3	2:H:221:LYS:HE2	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:395:CYS:O	1:G:396:ILE:HD13	2.16	0.46
3:L:147:LYS:HB3	3:L:199:THR:HB	1.97	0.45
1:G:430:THR:HA	5:G:672:HOH:O	2.17	0.45
1:G:112:TRP:CE3	1:G:116:LEU:HD11	2.52	0.45
2:H:164:VAL:HA	2:H:209:ASN:O	2.16	0.45
1:G:112:TRP:CZ3	1:G:116:LEU:HD11	2.52	0.44
2:H:141:LYS:HZ3	3:L:209:LYS:HA	1.83	0.44
1:G:361:PHE:O	1:G:362:GLN:NE2	2.46	0.43
1:G:395:CYS:SG	4:G:510:NAG:H62	2.58	0.43
2:H:141:LYS:HG3	5:L:466:HOH:O	2.18	0.42
3:L:72:THR:HG23	5:L:301:HOH:O	2.19	0.42
3:L:79:GLU:OE2	3:L:81:GLU:OE1	2.38	0.42
1:G:58:ALA:HB2	1:G:70:ALA:HB3	2.00	0.42
2:H:120:LEU:HD13	5:H:410:HOH:O	2.20	0.41
1:G:93:PHE:HB2	1:G:233:PHE:CZ	2.56	0.41
1:G:342:LEU:HB3	1:G:396:ILE:HD12	2.02	0.41
1:G:207:LYS:HD3	1:G:207:LYS:HA	1.89	0.41
2:H:124:SER:OG	2:H:126:PRO:CD	2.68	0.40
2:H:47:TRP:CE3	3:L:96:GLU:HB2	2.56	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	336/353 (95%)	318 (95%)	17 (5%)	1 (0%)	46	26
2	H	226/228 (99%)	223 (99%)	3 (1%)	0	100	100
3	L	208/210 (99%)	203 (98%)	5 (2%)	0	100	100
All	All	770/791 (97%)	744 (97%)	25 (3%)	1 (0%)	56	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	472	GLY

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	305/311 (98%)	294 (96%)	11 (4%)	42	19
2	H	194/194 (100%)	179 (92%)	15 (8%)	16	3
3	L	181/181 (100%)	176 (97%)	5 (3%)	51	29
All	All	680/686 (99%)	649 (95%)	31 (5%)	33	12

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	120	VAL
1	G	224	VAL
1	G	297	THR
1	G	301	ASN
1	G	360	ILE
1	G	373	MET
1	G	411	ASN
1	G	415	THR
1	G	434	MET
1	G	462	ASN
1	G	489	VAL
2	H	1	GLN
2	H	5	LEU
2	H	14	THR
2	H	18	MET
2	H	19	ARG
2	H	38	ARG
2	H	62	GLN
2	H	72	ARG
2	H	87	ARG
2	H	120	LEU
2	H	126	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	H	136	LEU
2	H	164	VAL
2	H	171	LEU
2	H	190	LEU
3	L	13	LEU
3	L	60	ASP
3	L	72	THR
3	L	109	LYS
3	L	215	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	462	ASN
2	H	1	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	501	1	14,14,15	0.28	0	15,19,21	0.53	0
4	NAG	G	502	1	14,14,15	1.15	1 (7%)	15,19,21	2.52	2 (13%)
4	NAG	G	503	1	14,14,15	0.38	0	15,19,21	0.46	0
4	NAG	G	504	1	14,14,15	0.31	0	15,19,21	0.32	0
4	NAG	G	505	1	14,14,15	0.56	0	15,19,21	0.90	1 (6%)
4	NAG	G	506	1	14,14,15	0.39	0	15,19,21	0.64	0
4	NAG	G	507	1	14,14,15	0.41	0	15,19,21	0.55	0
4	NAG	G	508	1	14,14,15	0.52	0	15,19,21	0.35	0
4	NAG	G	509	1	14,14,15	0.48	0	15,19,21	0.56	0
4	NAG	G	510	1	14,14,15	0.28	0	15,19,21	0.54	0
4	NAG	G	511	1	14,14,15	0.40	0	15,19,21	0.42	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	501	1	-	0/6/23/26	0/1/1/1
4	NAG	G	502	1	-	0/6/23/26	0/1/1/1
4	NAG	G	503	1	-	0/6/23/26	0/1/1/1
4	NAG	G	504	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	506	1	-	0/6/23/26	0/1/1/1
4	NAG	G	507	1	-	0/6/23/26	0/1/1/1
4	NAG	G	508	1	-	0/6/23/26	0/1/1/1
4	NAG	G	509	1	-	0/6/23/26	0/1/1/1
4	NAG	G	510	1	-	0/6/23/26	0/1/1/1
4	NAG	G	511	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	502	NAG	O5-C1	4.28	1.50	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	502	NAG	O5-C5-C4	2.44	114.17	110.13
4	G	505	NAG	C1-O5-C5	2.80	116.26	112.14
4	G	502	NAG	C1-O5-C5	9.13	125.57	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	505	NAG	1	0
4	G	510	NAG	4	0
4	G	511	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	341/353 (96%)	0.43	32 (9%)	11 12	26, 40, 71, 118	0
2	H	228/228 (100%)	0.19	11 (4%)	34 38	23, 37, 58, 119	0
3	L	208/210 (99%)	-0.15	2 (0%)	84 87	25, 39, 58, 115	0
All	All	777/791 (98%)	0.21	45 (5%)	26 28	23, 38, 64, 119	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	228	CYS	12.5
1	G	324	GLY	12.3
1	G	410	CYS	8.5
3	L	216	CYS	8.5
1	G	198	GLY	8.2
1	G	124	GLY	5.7
1	G	397	GLY	5.6
2	H	227	SER	5.1
1	G	396	ILE	4.9
1	G	301	ASN	4.6
1	G	123	THR	4.5
1	G	354	ASN	4.0
2	H	142	SER	3.9
1	G	200	VAL	3.9
1	G	462	ASN	3.6
1	G	199	SER	3.6
1	G	201	ILE	3.3
1	G	355	ASN	3.1
1	G	411	ASN	3.1
1	G	394	THR	3.0
1	G	44	VAL	2.9
1	G	371	ILE	2.8
2	H	202	GLY	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	460	ALA	2.7
2	H	203	THR	2.7
1	G	80	ASN	2.7
2	H	146	GLY	2.7
1	G	471	GLY	2.6
3	L	215	GLU	2.6
1	G	395	CYS	2.6
1	G	358	THR	2.5
2	H	143	THR	2.5
1	G	461	ASN	2.5
1	G	45	TRP	2.5
2	H	200	SER	2.4
1	G	492	GLU	2.4
1	G	453	LEU	2.4
1	G	325	ASP	2.4
1	G	430	THR	2.3
2	H	50	TRP	2.2
1	G	86	LEU	2.2
1	G	88	ASN	2.2
2	H	140	SER	2.1
2	H	139	SER	2.0
1	G	465	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](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	G	501	14/15	0.69	0.19	2.59	44,52,64,66	0
4	NAG	G	508	14/15	0.90	0.19	1.87	61,67,70,75	0
4	NAG	G	507	14/15	0.88	0.17	1.87	53,59,69,70	0
4	NAG	G	511	14/15	0.75	0.29	1.79	66,73,79,81	0
4	NAG	G	505	14/15	0.93	0.17	1.32	42,49,59,60	0
4	NAG	G	504	14/15	0.94	0.20	1.01	60,66,77,77	0
4	NAG	G	510	14/15	0.76	0.28	1.00	111,117,121,122	0
4	NAG	G	502	14/15	0.92	0.10	0.91	42,60,77,80	0
4	NAG	G	506	14/15	0.94	0.10	-0.22	31,38,44,48	0
4	NAG	G	509	14/15	0.93	0.11	-0.37	48,60,65,72	0
4	NAG	G	503	14/15	0.72	0.51	-	125,140,143,146	0

6.5 Other polymers [i](#)

There are no such residues in this entry.