



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 04:07 am GMT

PDB ID : 4LSP
Title : Crystal structure of broadly and potently neutralizing antibody VRC-CH31 in complex with HIV-1 clade A/E gp120 93TH057
Authors : Zhou, T.; Moquin, S.; Kwong, P.D.
Deposited on : 2013-07-23
Resolution : 2.15 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

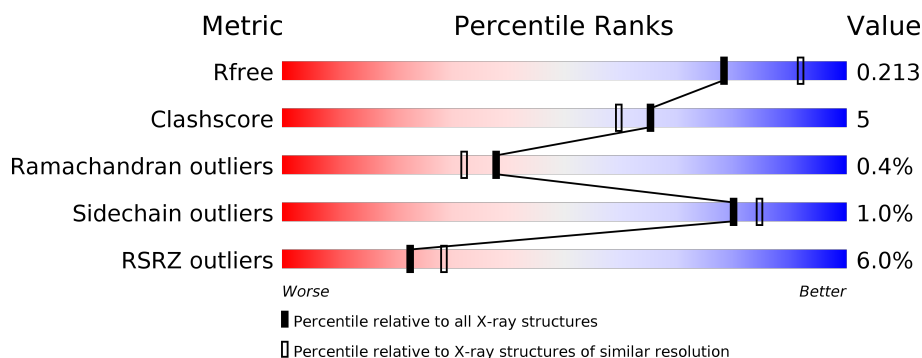
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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>7%</div> <div>89%</div> <div>9%</div> <div>.</div> </div>
2	H	236	<div> <div>%</div> <div>86%</div> <div>6%</div> <div>8%</div> </div>
3	L	210	<div> <div>10%</div> <div>86%</div> <div>13%</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
4	NAG	G	503	-	-	-	X
4	NAG	G	508	-	-	-	X
4	NAG	G	511	-	-	X	X
4	NAG	G	512	-	-	-	X
5	SO4	L	304	-	-	-	X
6	EDO	G	515	-	-	-	X
6	EDO	G	516	-	-	X	X
6	EDO	H	305	-	-	-	X
7	PEG	G	520	-	-	-	X
7	PEG	G	521	-	-	-	X
8	NA	G	522	-	-	-	X
8	NA	G	523	-	-	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 12393 atoms, of which 5895 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 CLADE A/E STRAIN 93TH057 GP120.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	G	347	5363	1700	2650	472	518	23	0	0	0

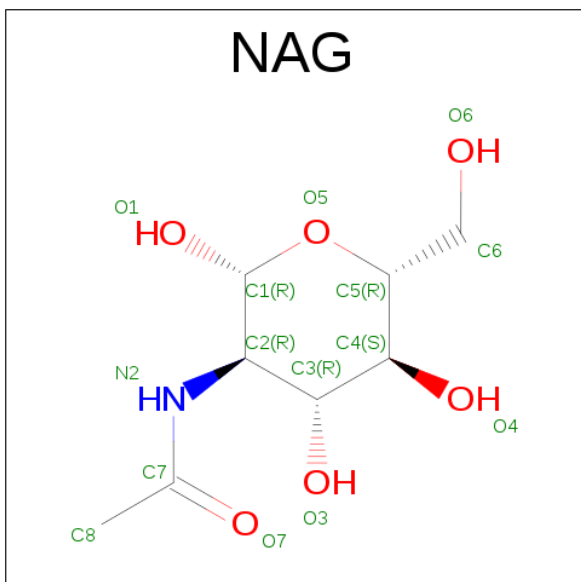
- Molecule 2 is a protein called HEAVY CHAIN OF ANTIBODY VRC-CH31.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	H	216	3261	1043	1614	287	311	6	0	0	0

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

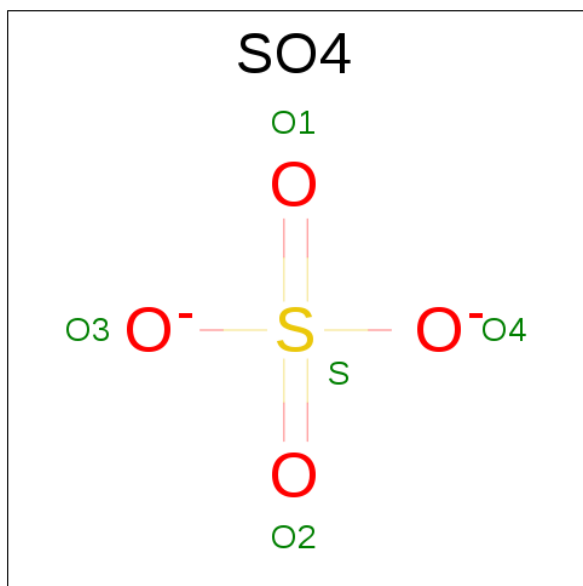
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	L	208	3134	989	1545	271	324	5	0	0	0

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



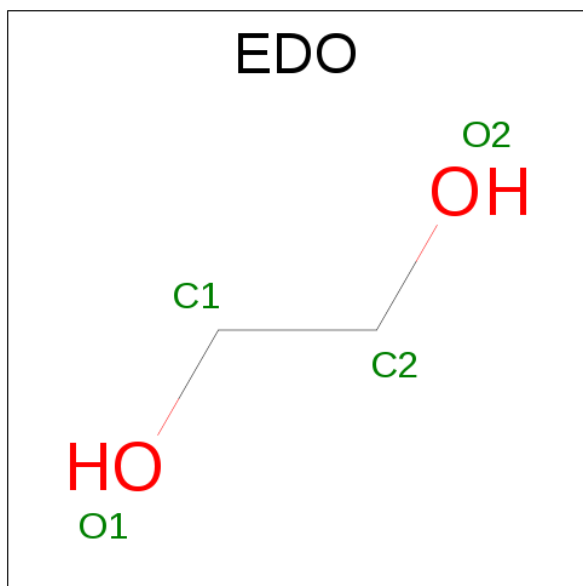
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total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

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	G	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



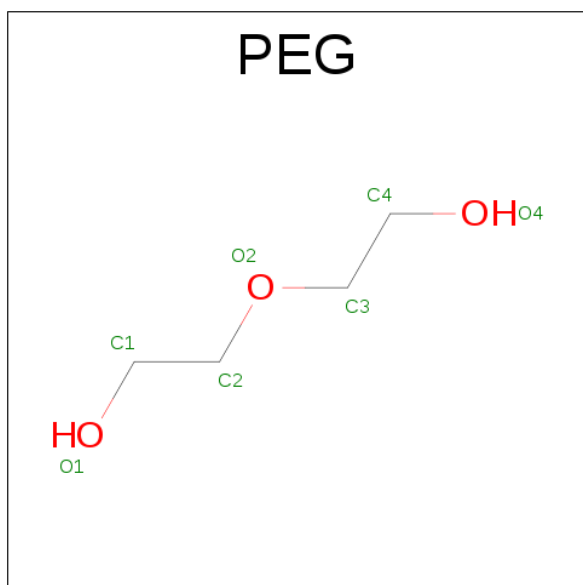
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	G	1	Total	C	H	O	0	0
			10	2	6	2		
6	G	1	Total	C	H	O	0	0
			10	2	6	2		
6	G	1	Total	C	H	O	0	0
			10	2	6	2		
6	G	1	Total	C	H	O	0	0
			10	2	6	2		
6	G	1	Total	C	H	O	0	0
			10	2	6	2		
6	H	1	Total	C	H	O	0	0
			10	2	6	2		
6	H	1	Total	C	H	O	0	0
			10	2	6	2		
6	H	1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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	H	1	Total	C	H	O	0	0
			10	2	6	2		
6	L	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	G	1	Total	C	H	O	0	0
			17	4	10	3		
7	G	1	Total	C	H	O	0	0
			17	4	10	3		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	1	Total	Na	0	0
			1	1		
8	G	2	Total	Na	0	0
			2	2		

- Molecule 9 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	L	3	Total	C	N	O	0	0
			39	22	2	15		

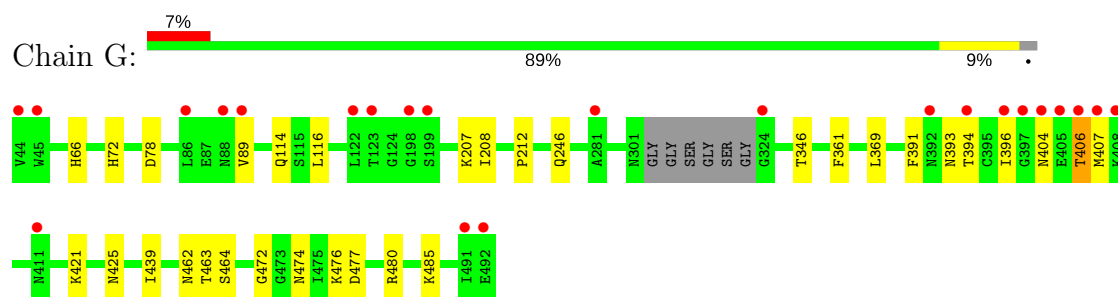
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	G	142	Total 142	O 142	0	0
10	H	78	Total 78	O 78	0	0
10	L	46	Total 46	O 46	0	0

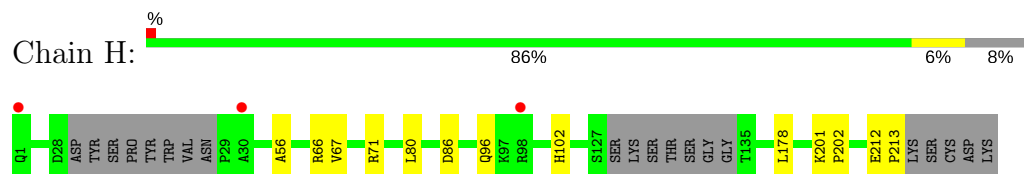
3 Residue-property plots [i](#)

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

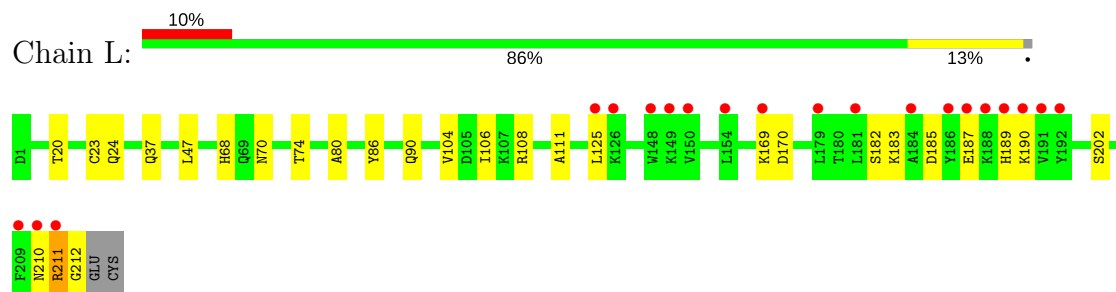
- Molecule 1: HIV-1 CLADE A/E STRAIN 93TH057 GP120



- Molecule 2: HEAVY CHAIN OF ANTIBODY VRC-CH31



- Molecule 3: LIGHT CHAIN OF ANTIBODY VRC-CH31



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.39Å 83.96Å 175.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.04 – 2.15 48.04 – 2.15	Depositor EDS
% Data completeness (in resolution range)	95.6 (48.04-2.15) 95.4 (48.04-2.15)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.16Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: DEV_1317)	Depositor
R, R_{free}	0.180 , 0.214 0.180 , 0.213	Depositor DCC
R_{free} test set	2662 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.441	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.8	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	0.96	EDS
Total number of atoms	12393	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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: BMA, NAG, NA, EDO, SO4, PEG

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	0.28	0/2770	0.47	0/3760
2	H	0.30	0/1691	0.49	0/2309
3	L	0.30	0/1619	0.48	0/2192
All	All	0.29	0/6080	0.48	0/8261

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	2713	2650	2641	21	1
2	H	1647	1614	1609	9	0
3	L	1589	1545	1546	16	0
4	G	168	0	156	12	0
5	G	10	0	0	0	0
5	L	5	0	0	0	0
6	G	20	30	29	5	0
6	H	20	30	30	0	0
6	L	4	6	6	0	0
7	G	14	20	20	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	G	2	0	0	0	0
8	H	1	0	0	0	0
9	L	39	0	34	3	0
10	G	142	0	0	6	1
10	H	78	0	0	0	0
10	L	46	0	0	1	0
All	All	6498	5895	6071	58	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 5.

All (58) 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:G:501:NAG:O3	4:G:501:NAG:H82	1.63	0.95
3:L:189:HIS:O	3:L:211:ARG:NH1	2.17	0.78
1:G:391:PHE:O	10:G:706:HOH:O	2.05	0.73
4:G:511:NAG:H83	4:G:511:NAG:C3	2.19	0.73
4:G:511:NAG:C8	4:G:511:NAG:C3	2.69	0.71
1:G:406:THR:HA	4:G:511:NAG:H62	1.73	0.69
4:G:511:NAG:C8	4:G:511:NAG:H3	2.22	0.69
4:G:511:NAG:O3	4:G:511:NAG:H83	1.95	0.67
6:G:516:EDO:O1	10:G:677:HOH:O	2.13	0.67
3:L:70:ASN:ND2	9:L:301:NAG:H83	2.11	0.65
2:H:66:ARG:NH2	2:H:86:ASP:OD2	2.32	0.63
3:L:24:GLN:NE2	3:L:70:ASN:OD1	2.33	0.61
1:G:407:MET:O	4:G:511:NAG:O6	2.19	0.60
4:G:501:NAG:C8	4:G:501:NAG:O3	2.45	0.59
1:G:369:LEU:HB2	7:G:521:PEG:H31	1.85	0.59
4:G:512:NAG:H83	10:G:639:HOH:O	2.04	0.57
1:G:246:GLN:NE2	10:G:681:HOH:O	2.39	0.55
4:G:511:NAG:H83	4:G:511:NAG:H3	1.83	0.53
3:L:182:SER:OG	3:L:185:ASP:OD1	2.25	0.53
2:H:96:GLN:OE1	2:H:102:HIS:NE2	2.41	0.52
3:L:210:ASN:O	3:L:212:GLY:N	2.43	0.52
6:G:516:EDO:H22	2:H:56:ALA:HB1	1.92	0.52
3:L:183:LYS:NZ	3:L:187:GLU:OE2	2.44	0.50
3:L:70:ASN:HD22	9:L:301:NAG:H83	1.76	0.50
1:G:472:GLY:HA2	6:G:516:EDO:H21	1.93	0.49
1:G:207:LYS:HE2	1:G:439:ILE:HG23	1.94	0.49
1:G:394:THR:CG2	1:G:407:MET:SD	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:485:LYS:NZ	10:G:732:HOH:O	2.40	0.48
3:L:190:LYS:NZ	10:L:431:HOH:O	2.44	0.48
1:G:421:LYS:NZ	7:G:521:PEG:H21	2.29	0.47
1:G:114:GLN:NE2	10:G:709:HOH:O	2.38	0.47
1:G:393:ASN:HA	1:G:396:ILE:HD13	1.96	0.47
2:H:67:VAL:CG1	2:H:80:LEU:HD11	2.44	0.47
1:G:462:ASN:O	1:G:464:SER:N	2.47	0.46
4:G:511:NAG:H82	4:G:511:NAG:H3	1.94	0.46
3:L:80:ALA:HA	3:L:106:ILE:HD11	1.98	0.46
3:L:20:THR:HG22	3:L:74:THR:HG23	1.98	0.46
1:G:346:THR:HG21	1:G:396:ILE:HG21	1.97	0.45
1:G:477:ASP:OD1	1:G:480:ARG:NH1	2.43	0.45
1:G:474:ASN:OD1	1:G:476:LYS:HB2	2.16	0.45
1:G:425:ASN:CG	7:G:521:PEG:H11	2.37	0.45
3:L:169:LYS:HG3	3:L:170:ASP:N	2.33	0.44
4:G:501:NAG:H82	4:G:501:NAG:HO3	1.73	0.43
6:G:516:EDO:H22	2:H:56:ALA:CB	2.47	0.43
1:G:346:THR:HG22	1:G:361:PHE:HE2	1.82	0.43
9:L:301:NAG:O3	9:L:302:NAG:O5	2.37	0.43
3:L:86:TYR:HE1	3:L:104:VAL:CG1	2.32	0.42
1:G:66:HIS:CG	1:G:212:PRO:HA	2.54	0.42
3:L:37:GLN:HB2	3:L:47:LEU:HD11	2.00	0.42
1:G:78:ASP:HB3	6:G:518:EDO:H12	2.02	0.42
3:L:86:TYR:HE1	3:L:104:VAL:HG11	1.85	0.42
2:H:212:GLU:HB2	2:H:213:PRO:HD2	2.01	0.41
1:G:116:LEU:HD21	1:G:208:ILE:HD11	2.03	0.41
3:L:125:LEU:O	3:L:183:LYS:HD2	2.21	0.41
3:L:108:ARG:NH2	3:L:111:ALA:HB2	2.36	0.41
2:H:178:LEU:HD12	2:H:178:LEU:C	2.41	0.40
2:H:201:LYS:N	2:H:202:PRO:CD	2.84	0.40
2:H:66:ARG:HH22	2:H:86:ASP:CG	2.24	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)
1:G:72:HIS:O	10:G:738:HOH:O[4_555]	2.14	0.06

5.3 Torsion angles

5.3.1 Protein backbone

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	343/353 (97%)	327 (95%)	15 (4%)	1 (0%)	44	41
2	H	210/236 (89%)	206 (98%)	4 (2%)	0	100	100
3	L	206/210 (98%)	199 (97%)	5 (2%)	2 (1%)	18	11
All	All	759/799 (95%)	732 (96%)	24 (3%)	3 (0%)	38	32

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	463	THR
3	L	211	ARG
3	L	68	HIS

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	309/311 (99%)	306 (99%)	3 (1%)	80	84
2	H	180/198 (91%)	179 (99%)	1 (1%)	89	92
3	L	180/182 (99%)	177 (98%)	3 (2%)	66	71
All	All	669/691 (97%)	662 (99%)	7 (1%)	80	84

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	89	VAL
1	G	404	ASN
1	G	406	THR
2	H	71	ARG
3	L	23	CYS
3	L	90	GLN
3	L	202	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	85	HIS
1	G	432	GLN
3	L	90	GLN
3	L	189	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 carbohydrates 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	$\# Z > 2$
9	NAG	L	301	9,3	14,14,15	0.76	0	15,19,21	0.63	0
9	NAG	L	302	9	14,14,15	0.92	1 (7%)	15,19,21	0.78	0
9	BMA	L	303	9	11,11,12	0.79	0	13,15,17	0.92	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
9	NAG	L	301	9,3	-	0/6/23/26	0/1/1/1
9	NAG	L	302	9	-	0/6/23/26	0/1/1/1
9	BMA	L	303	9	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	L	302	NAG	O5-C1	-3.16	1.38	1.43

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	L	301	NAG	3	0
9	L	302	NAG	1	0

5.6 Ligand geometry

Of 31 ligands modelled in this entry, 3 are monoatomic - leaving 28 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	501	1	14,14,15	1.24	1 (7%)	15,19,21	1.39	2 (13%)
4	NAG	G	502	1	14,14,15	0.39	0	15,19,21	0.61	0
4	NAG	G	503	1	14,14,15	0.57	0	15,19,21	0.51	0
4	NAG	G	504	1	14,14,15	0.65	0	15,19,21	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	G	505	1	14,14,15	0.22	0	15,19,21	0.49	0
4	NAG	G	506	1	14,14,15	0.28	0	15,19,21	0.38	0
4	NAG	G	507	1	14,14,15	0.24	0	15,19,21	0.39	0
4	NAG	G	508	1	14,14,15	0.43	0	15,19,21	1.04	1 (6%)
4	NAG	G	509	1	14,14,15	0.59	0	15,19,21	0.44	0
4	NAG	G	510	1	14,14,15	1.01	1 (7%)	15,19,21	0.73	0
4	NAG	G	511	1	14,14,15	0.55	0	15,19,21	1.72	4 (26%)
4	NAG	G	512	1	14,14,15	0.45	0	15,19,21	0.63	0
5	SO4	G	513	-	4,4,4	0.16	0	6,6,6	0.12	0
5	SO4	G	514	-	4,4,4	0.16	0	6,6,6	0.05	0
6	EDO	G	515	-	3,3,3	0.42	0	2,2,2	0.25	0
6	EDO	G	516	-	3,3,3	0.40	0	2,2,2	0.42	0
6	EDO	G	517	8	3,3,3	0.40	0	2,2,2	0.39	0
6	EDO	G	518	-	3,3,3	0.41	0	2,2,2	0.33	0
6	EDO	G	519	-	3,3,3	0.47	0	2,2,2	0.24	0
7	PEG	G	520	-	6,6,6	0.64	0	5,5,5	0.97	1 (20%)
7	PEG	G	521	-	6,6,6	0.56	0	5,5,5	1.13	0
6	EDO	H	301	-	3,3,3	0.48	0	2,2,2	0.31	0
6	EDO	H	302	-	3,3,3	0.48	0	2,2,2	0.20	0
6	EDO	H	303	-	3,3,3	0.45	0	2,2,2	0.35	0
6	EDO	H	304	-	3,3,3	0.44	0	2,2,2	0.45	0
6	EDO	H	305	-	3,3,3	0.38	0	2,2,2	0.55	0
5	SO4	L	304	-	4,4,4	0.13	0	6,6,6	0.10	0
6	EDO	L	305	-	3,3,3	0.43	0	2,2,2	0.35	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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	G	512	1	-	0/6/23/26	0/1/1/1
5	SO4	G	513	-	-	0/0/0/0	0/0/0/0
5	SO4	G	514	-	-	0/0/0/0	0/0/0/0
6	EDO	G	515	-	-	0/1/1/1	0/0/0/0
6	EDO	G	516	-	-	0/1/1/1	0/0/0/0
6	EDO	G	517	8	-	0/1/1/1	0/0/0/0
6	EDO	G	518	-	-	0/1/1/1	0/0/0/0
6	EDO	G	519	-	-	0/1/1/1	0/0/0/0
7	PEG	G	520	-	-	0/4/4/4	0/0/0/0
7	PEG	G	521	-	-	0/4/4/4	0/0/0/0
6	EDO	H	301	-	-	0/1/1/1	0/0/0/0
6	EDO	H	302	-	-	0/1/1/1	0/0/0/0
6	EDO	H	303	-	-	0/1/1/1	0/0/0/0
6	EDO	H	304	-	-	0/1/1/1	0/0/0/0
6	EDO	H	305	-	-	0/1/1/1	0/0/0/0
5	SO4	L	304	-	-	0/0/0/0	0/0/0/0
6	EDO	L	305	-	-	0/1/1/1	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	501	NAG	O5-C1	-4.34	1.36	1.43
4	G	510	NAG	C1-C2	2.77	1.56	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	511	NAG	C4-C3-C2	-2.44	107.45	111.02
4	G	508	NAG	C4-C3-C2	-2.15	107.86	111.02
7	G	520	PEG	C3-O2-C2	2.03	122.11	113.30
4	G	511	NAG	C1-O5-C5	2.33	115.37	112.17
4	G	501	NAG	O3-C3-C2	2.79	115.36	109.39
4	G	511	NAG	C1-C2-N2	2.80	115.27	110.49
4	G	501	NAG	C2-N2-C7	3.41	127.92	122.94
4	G	511	NAG	C2-N2-C7	4.18	129.04	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	501	NAG	3	0
4	G	511	NAG	8	0
4	G	512	NAG	1	0
6	G	516	EDO	4	0
6	G	518	EDO	1	0
7	G	521	PEG	3	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	347/353 (98%)	0.43	23 (6%) 19 24	35, 53, 106, 136	0
2	H	216/236 (91%)	0.08	3 (1%) 75 80	34, 52, 101, 122	0
3	L	208/210 (99%)	0.53	20 (9%) 9 12	37, 68, 106, 126	0
All	All	771/799 (96%)	0.36	46 (5%) 23 29	34, 57, 105, 136	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	404	ASN	7.8
1	G	406	THR	6.0
1	G	324	GLY	5.5
1	G	44	VAL	5.1
3	L	181	LEU	4.7
1	G	397	GLY	4.6
1	G	407	MET	4.1
1	G	492	GLU	3.9
3	L	188	LYS	3.9
3	L	125	LEU	3.6
3	L	184	ALA	3.5
1	G	199	SER	3.4
3	L	189	HIS	3.3
1	G	396	ILE	3.3
1	G	408	LYS	3.2
1	G	122	LEU	3.2
3	L	191	VAL	3.2
1	G	394	THR	3.1
3	L	190	LYS	3.1
3	L	148	TRP	3.1
2	H	98	ARG	3.1
1	G	198	GLY	3.1
2	H	30	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
3	L	187	GLU	3.0
1	G	491	ILE	2.8
3	L	150	VAL	2.8
1	G	411	ASN	2.8
1	G	86	LEU	2.8
3	L	179	LEU	2.8
1	G	392	ASN	2.7
3	L	186	TYR	2.5
1	G	405	GLU	2.5
3	L	192	TYR	2.4
3	L	210	ASN	2.4
3	L	154	LEU	2.4
2	H	1	GLN	2.3
3	L	211	ARG	2.3
1	G	281	ALA	2.2
3	L	209	PHE	2.2
1	G	88	ASN	2.2
3	L	126	LYS	2.2
1	G	123	THR	2.1
1	G	89	VAL	2.1
3	L	169	LYS	2.1
3	L	149	LYS	2.1
1	G	45	TRP	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](#)

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(Å ²)	Q<0.9
9	NAG	L	301	14/15	0.69	0.15	1.63	59,82,97,123	0
9	NAG	L	302	14/15	0.73	0.35	-	127,137,160,162	0
9	BMA	L	303	11/12	0.26	0.33	-	134,153,160,162	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. 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(Å ²)	Q<0.9
7	PEG	G	521	7/7	0.63	0.46	15.11	56,86,104,104	0
8	NA	G	523	1/1	0.92	0.38	11.58	83,83,83,83	0
6	EDO	G	516	4/4	0.71	0.37	9.24	59,85,92,102	0
8	NA	G	522	1/1	0.96	0.31	8.13	69,69,69,69	0
4	NAG	G	512	14/15	0.81	0.26	5.64	95,110,127,138	0
6	EDO	H	305	4/4	0.80	0.30	3.60	78,94,109,109	0
4	NAG	G	501	14/15	0.84	0.40	3.13	100,115,126,128	0
7	PEG	G	520	7/7	0.78	0.25	3.09	49,67,82,82	0
5	SO4	L	304	5/5	0.88	0.18	2.55	115,118,119,122	0
4	NAG	G	508	14/15	0.80	0.29	2.42	79,108,114,121	0
6	EDO	G	515	4/4	0.95	0.24	2.39	43,52,56,56	0
4	NAG	G	503	14/15	0.95	0.20	2.06	26,45,52,62	0
6	EDO	H	301	4/4	0.92	0.17	1.93	46,70,83,84	0
6	EDO	G	519	4/4	0.89	0.16	1.49	49,66,79,90	0
4	NAG	G	510	14/15	0.77	0.35	1.18	105,129,138,143	0
4	NAG	G	511	14/15	0.63	0.47	0.97	108,119,146,152	0
6	EDO	H	303	4/4	0.91	0.15	0.72	86,104,108,116	0
6	EDO	G	518	4/4	0.93	0.14	0.43	63,78,94,94	0
5	SO4	G	514	5/5	0.95	0.14	0.30	95,98,103,112	0
6	EDO	H	304	4/4	0.94	0.15	0.29	46,63,84,91	0
4	NAG	G	505	14/15	0.93	0.14	0.03	53,67,73,77	0
4	NAG	G	502	14/15	0.93	0.13	0.00	44,58,65,80	0
6	EDO	H	302	4/4	0.94	0.18	-0.17	37,52,71,85	0
4	NAG	G	504	14/15	0.92	0.12	-0.63	37,60,76,86	0
8	NA	H	306	1/1	0.90	0.09	-1.01	81,81,81,81	0
4	NAG	G	509	14/15	0.94	0.11	-1.26	56,68,78,81	0
4	NAG	G	506	14/15	0.94	0.09	-1.30	61,76,81,87	0
6	EDO	G	517	4/4	0.97	0.10	-1.99	48,60,72,73	0
5	SO4	G	513	5/5	0.98	0.13	-2.09	63,66,81,83	0
6	EDO	L	305	4/4	0.81	0.25	-	79,95,103,114	0
4	NAG	G	507	14/15	0.87	0.17	-	66,78,97,106	0

6.5 Other polymers ⓘ

There are no such residues in this entry.