Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2023 – 05:27 PM EDT

PDB ID	:	7U8E
Title	:	Crystal structure of antibody Ab246 in complex with SARS-CoV-2 receptor binding domain
Authors	:	Sankhala, R.S.; Joyce, M.G.
Deposited on	:	2022-03-08
Resolution	:	2.29 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:

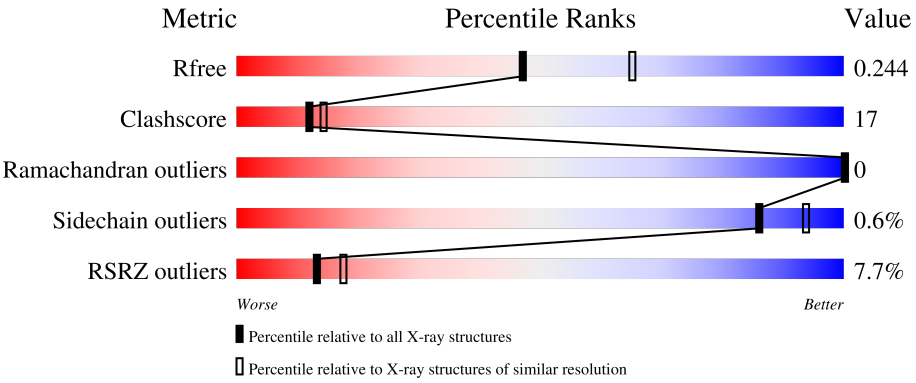
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	205	13% 65% 32% .
2	H	227	7% 73% 25% .
3	L	221	3% 72% 26% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	L	302	-	-	X	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5100 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	198	1569	1003	265	293	8	0	1	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	528	GLY	-	expression tag	UNP P0DTC2
A	529	SER	-	expression tag	UNP P0DTC2
A	530	HIS	-	expression tag	UNP P0DTC2
A	531	HIS	-	expression tag	UNP P0DTC2
A	532	HIS	-	expression tag	UNP P0DTC2
A	533	HIS	-	expression tag	UNP P0DTC2
A	534	HIS	-	expression tag	UNP P0DTC2
A	535	HIS	-	expression tag	UNP P0DTC2

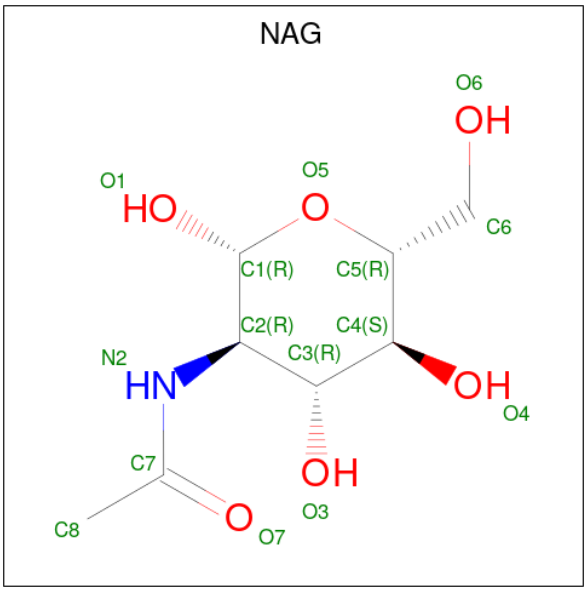
- Molecule 2 is a protein called Antibody Ab246 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	222	1661	1050	275	329	7	0	0	0

- Molecule 3 is a protein called Antibody Ab246 Fab light chain.

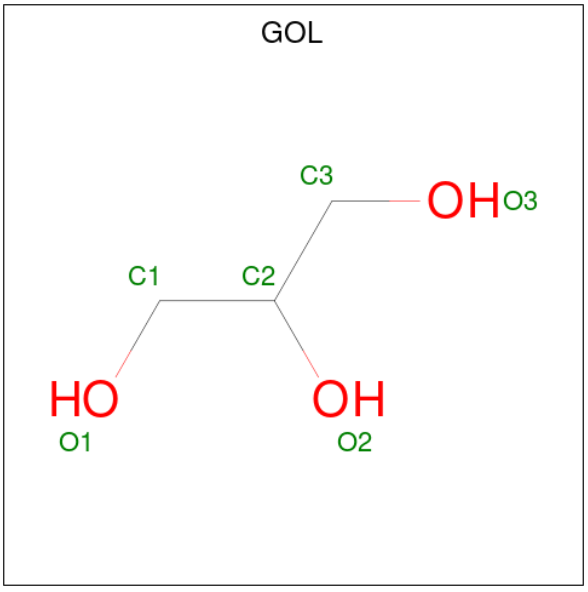
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	216	1619	1019	271	323	6	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	H	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	1	Total C O 6 3 3	0	0
5	L	1	Total C O 6 3 3	0	0
5	L	1	Total C O 6 3 3	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	1	Total Cl 1 1	0	0

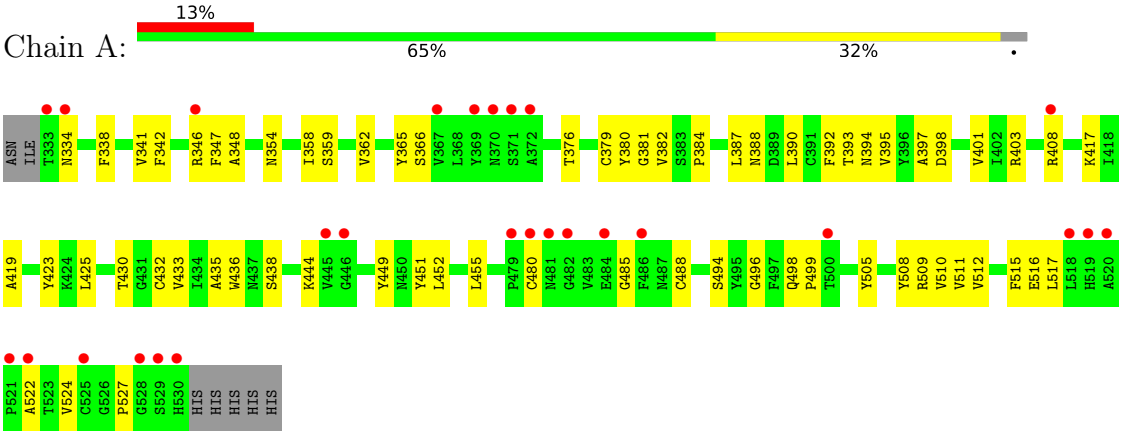
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	28	Total O 28 28	0	0
7	H	91	Total O 91 91	0	0
7	L	81	Total O 81 81	0	0

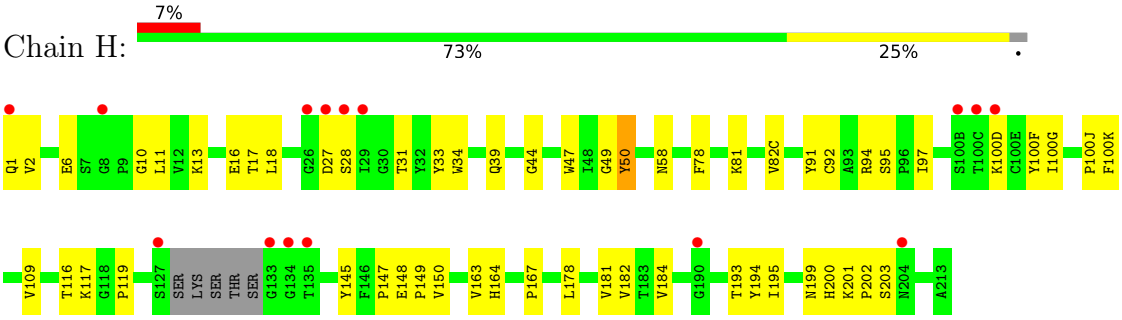
3 Residue-property plots (i)

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.

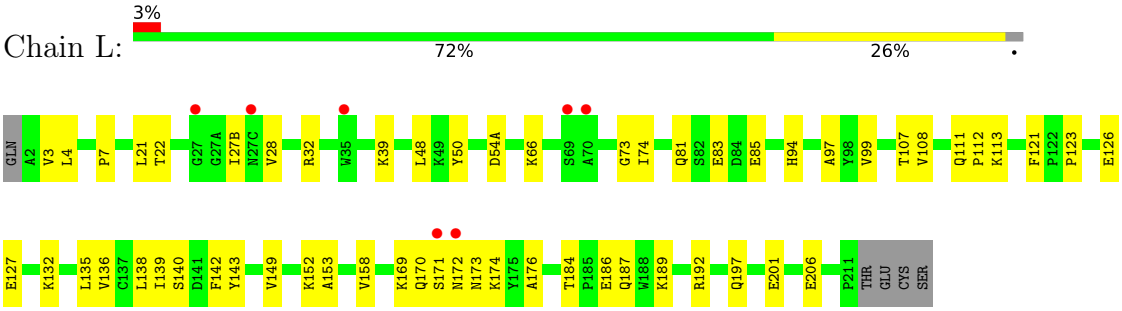
• Molecule 1: Spike protein S1



• Molecule 2: Antibody Ab246 Fab heavy chain



• Molecule 3: Antibody Ab246 Fab light chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	194.80Å 41.60Å 98.99Å 90.00° 107.03° 90.00°	Depositor
Resolution (Å)	19.90 – 2.29 19.90 – 2.29	Depositor EDS
% Data completeness (in resolution range)	82.4 (19.90-2.29) 82.4 (19.90-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	3.65 (at 2.28Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.204 , 0.247 0.207 , 0.244	Depositor DCC
R_{free} test set	1433 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	27.5	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 49.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5100	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: CL, GOL, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.32	0/1617	0.48	0/2199
2	H	0.37	0/1702	0.56	0/2322
3	L	0.32	0/1659	0.51	0/2258
All	All	0.34	0/4978	0.52	0/6779

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

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1569	0	1479	64	0
2	H	1661	0	1625	52	0
3	L	1619	0	1566	58	0
4	A	14	0	13	2	0
5	A	12	0	16	1	0
5	H	12	0	16	3	0
5	L	12	0	16	5	0
6	H	1	0	0	0	0
7	A	28	0	0	6	0
7	H	91	0	0	1	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	L	81	0	0	4	0
All	All	5100	0	4731	166	3

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 17.

All (166) 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:3:VAL:HG12	3:L:4:LEU:HD13	1.50	0.94
2:H:2:VAL:HG11	2:H:94:ARG:NH1	1.90	0.87
3:L:170:GLN:OE1	3:L:171:SER:N	2.08	0.85
1:A:433:VAL:HG11	7:A:714:HOH:O	1.77	0.83
3:L:121:PHE:HB2	3:L:136:VAL:HG22	1.61	0.83
3:L:192:ARG:NH2	5:L:301:GOL:O3	2.12	0.82
1:A:505:TYR:O	7:A:701:HOH:O	1.99	0.80
2:H:181:VAL:HG21	3:L:138:LEU:HD13	1.65	0.78
1:A:342:PHE:CZ	1:A:511:VAL:HG21	2.19	0.76
1:A:388:ASN:HB3	1:A:527:PRO:HD2	1.67	0.76
1:A:358:ILE:HB	1:A:395:VAL:HG23	1.70	0.73
2:H:164:HIS:NE2	3:L:170:GLN:HG3	2.04	0.72
3:L:73:GLY:C	3:L:74:ILE:HD12	2.11	0.70
1:A:395:VAL:HG13	1:A:524:VAL:HG11	1.72	0.70
1:A:417:LYS:H	5:A:602:GOL:H11	1.55	0.70
1:A:384:PRO:HA	1:A:387:LEU:HG	1.73	0.69
2:H:181:VAL:HG21	3:L:138:LEU:CD1	2.22	0.68
3:L:113:LYS:HD3	3:L:201:GLU:HG2	1.76	0.66
1:A:403:ARG:HD3	1:A:505:TYR:CD1	2.30	0.66
1:A:452:LEU:HD22	1:A:494:SER:HA	1.78	0.65
3:L:107:THR:HG23	5:L:302:GOL:H12	1.77	0.65
1:A:394:ASN:O	1:A:516:GLU:HB3	1.98	0.64
3:L:126:GLU:OE1	3:L:126:GLU:N	2.29	0.64
1:A:517:LEU:HD23	1:A:517:LEU:H	1.62	0.64
3:L:85:GLU:HG3	3:L:108:VAL:HG23	1.79	0.63
3:L:27(B):ILE:CD1	3:L:94:HIS:CE1	2.81	0.62
2:H:47:TRP:CZ2	2:H:49:GLY:HA2	2.33	0.62
2:H:181:VAL:CG2	3:L:138:LEU:HD13	2.30	0.62
2:H:16:GLU:O	2:H:82(C):VAL:HG22	2.00	0.61
1:A:359:SER:HB3	1:A:394:ASN:OD1	2.00	0.61
2:H:116:THR:HG21	2:H:203:SER:HA	1.82	0.61
2:H:164:HIS:CE1	3:L:170:GLN:HG3	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:186:GLU:OE1	3:L:189:LYS:HE2	2.01	0.59
1:A:365:TYR:HB2	1:A:388:ASN:OD1	2.02	0.59
3:L:149:VAL:HG22	7:L:426:HOH:O	2.00	0.59
1:A:408:ARG:HG3	7:A:722:HOH:O	2.02	0.59
1:A:403:ARG:HG3	1:A:505:TYR:HA	1.85	0.59
3:L:113:LYS:HD3	3:L:201:GLU:CG	2.33	0.59
2:H:167:PRO:HD2	7:L:427:HOH:O	2.03	0.58
1:A:348:ALA:HB2	1:A:354:ASN:OD1	2.02	0.58
3:L:123:PRO:HD3	3:L:135:LEU:CD2	2.33	0.58
2:H:18:LEU:HD12	2:H:109:VAL:HG11	1.87	0.57
3:L:3:VAL:HG12	3:L:4:LEU:CD1	2.32	0.56
3:L:139:ILE:HG22	3:L:142:PHE:CE2	2.41	0.56
2:H:17:THR:HG21	2:H:81:LYS:HE3	1.86	0.56
3:L:127:GLU:HG2	3:L:132:LYS:O	2.05	0.56
2:H:18:LEU:CD1	2:H:109:VAL:HG11	2.36	0.55
3:L:50:TYR:HE2	3:L:66:LYS:HG3	1.72	0.55
3:L:169:LYS:HA	3:L:174:LYS:O	2.06	0.55
2:H:184:VAL:HG11	2:H:194:TYR:CE1	2.41	0.55
2:H:163:VAL:HG22	2:H:182:VAL:HG22	1.89	0.55
1:A:496:GLY:O	1:A:498:GLN:HG3	2.07	0.55
2:H:148:GLU:HB3	2:H:149:PRO:HA	1.89	0.54
3:L:27(B):ILE:HD13	3:L:94:HIS:CE1	2.43	0.54
1:A:505:TYR:HB3	7:A:701:HOH:O	2.06	0.54
2:H:2:VAL:CG1	2:H:27:ASP:O	2.56	0.54
1:A:358:ILE:HB	1:A:395:VAL:CG2	2.38	0.53
2:H:1:GLN:H2	2:H:27:ASP:H	1.53	0.53
1:A:342:PHE:CE2	1:A:511:VAL:HG21	2.44	0.53
1:A:394:ASN:HB2	1:A:516:GLU:OE2	2.09	0.52
2:H:11:LEU:HD12	2:H:147:PRO:HG3	1.91	0.52
3:L:107:THR:CG2	5:L:302:GOL:H12	2.40	0.52
1:A:438:SER:HB3	1:A:509:ARG:HG3	1.90	0.52
1:A:338:PHE:HB3	4:A:601:NAG:H81	1.91	0.52
2:H:95:SER:HB2	2:H:100(J):PRO:HA	1.91	0.52
2:H:199:ASN:ND2	2:H:201:LYS:HE2	2.25	0.52
1:A:376:THR:OG1	1:A:435:ALA:HB3	2.10	0.52
3:L:85:GLU:HG3	3:L:108:VAL:CG2	2.40	0.52
3:L:27(B):ILE:HD11	3:L:94:HIS:CE1	2.44	0.51
3:L:197:GLN:HG3	3:L:206:GLU:HG3	1.91	0.51
1:A:452:LEU:HD22	1:A:494:SER:CA	2.39	0.51
1:A:398:ASP:O	1:A:511:VAL:HA	2.11	0.51
1:A:430:THR:O	1:A:430:THR:HG23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:6:GLU:OE1	2:H:91:TYR:HA	2.11	0.50
1:A:392:PHE:O	1:A:524:VAL:HG12	2.11	0.50
2:H:10:GLY:HA3	5:H:303:GOL:O3	2.11	0.50
3:L:74:ILE:HD12	3:L:74:ILE:N	2.26	0.50
1:A:388:ASN:CB	1:A:527:PRO:HD2	2.41	0.50
2:H:117:LYS:HE2	7:H:426:HOH:O	2.12	0.49
3:L:28:VAL:O	3:L:66:LYS:NZ	2.38	0.49
1:A:438:SER:CB	1:A:509:ARG:HG3	2.43	0.49
2:H:6:GLU:HG3	2:H:92:CYS:SG	2.52	0.49
3:L:4:LEU:HD22	3:L:99:VAL:HG23	1.94	0.49
3:L:121:PHE:HB2	3:L:136:VAL:CG2	2.37	0.49
3:L:152:LYS:HD3	3:L:197:GLN:NE2	2.28	0.49
1:A:452:LEU:CD2	1:A:494:SER:HA	2.43	0.49
1:A:401:VAL:HG11	1:A:451:TYR:CD1	2.48	0.48
3:L:48:LEU:HD12	3:L:48:LEU:C	2.34	0.48
3:L:169:LYS:HE2	3:L:173:ASN:HA	1.94	0.48
2:H:2:VAL:HG12	2:H:27:ASP:O	2.12	0.48
3:L:39:LYS:HE2	3:L:83:GLU:OE1	2.13	0.48
1:A:338:PHE:CB	4:A:601:NAG:H81	2.44	0.48
2:H:100(D):LYS:HD3	2:H:100(F):TYR:CZ	2.49	0.48
3:L:111:GLN:HG3	3:L:112:PRO:HD2	1.96	0.48
2:H:116:THR:CG2	2:H:203:SER:HB3	2.44	0.48
1:A:444:LYS:O	1:A:499:PRO:HD3	2.14	0.48
2:H:119:PRO:HB3	2:H:145:TYR:HB3	1.95	0.47
1:A:347:PHE:O	1:A:451:TYR:HE1	1.97	0.47
1:A:346:ARG:HG2	7:A:706:HOH:O	2.15	0.47
1:A:417:LYS:HE3	1:A:455:LEU:O	2.14	0.47
2:H:31:THR:CG2	2:H:97:ILE:HD12	2.45	0.47
1:A:517:LEU:HG	1:A:517:LEU:O	2.14	0.47
2:H:13:LYS:HB2	2:H:16:GLU:HG3	1.96	0.47
2:H:10:GLY:CA	5:H:303:GOL:O3	2.63	0.47
3:L:27(B):ILE:HD11	3:L:94:HIS:NE2	2.30	0.47
3:L:85:GLU:CG	3:L:108:VAL:H	2.28	0.47
1:A:366:SER:H	1:A:388:ASN:HD21	1.61	0.46
3:L:143:TYR:HE2	5:L:302:GOL:O3	1.97	0.46
1:A:403:ARG:CG	1:A:505:TYR:HA	2.45	0.46
1:A:401:VAL:HG23	1:A:508:TYR:O	2.16	0.46
3:L:81:GLN:O	3:L:108:VAL:HG21	2.15	0.46
3:L:172:ASN:OD1	3:L:172:ASN:C	2.54	0.46
2:H:116:THR:HG21	2:H:203:SER:CA	2.45	0.46
2:H:10:GLY:N	5:H:303:GOL:O3	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:21:LEU:HD12	3:L:21:LEU:N	2.32	0.45
3:L:123:PRO:HD3	3:L:135:LEU:HD23	1.97	0.45
1:A:393:THR:HA	1:A:522:ALA:HA	1.98	0.45
2:H:150:VAL:HG23	2:H:178:LEU:HD21	1.98	0.45
1:A:334:ASN:O	1:A:362:VAL:HG12	2.17	0.44
1:A:436:TRP:CE2	1:A:509:ARG:HB2	2.52	0.44
1:A:358:ILE:HA	7:A:709:HOH:O	2.18	0.44
2:H:34:TRP:O	2:H:50:TYR:HA	2.17	0.44
2:H:50:TYR:CE1	2:H:58:ASN:HB2	2.51	0.44
1:A:342:PHE:CZ	1:A:511:VAL:CG2	2.97	0.44
3:L:32:ARG:NH1	7:L:409:HOH:O	2.45	0.43
3:L:48:LEU:HD12	3:L:48:LEU:O	2.18	0.43
3:L:7:PRO:HD3	3:L:22:THR:HG23	1.99	0.43
1:A:401:VAL:CG1	1:A:451:TYR:CD1	3.01	0.43
1:A:433:VAL:HG13	1:A:433:VAL:O	2.18	0.43
2:H:33:TYR:CD2	2:H:100(G):ILE:HD11	2.53	0.43
1:A:417:LYS:HE2	1:A:455:LEU:HD22	1.99	0.43
1:A:517:LEU:HD23	1:A:517:LEU:N	2.30	0.43
1:A:379:CYS:HA	1:A:432:CYS:HA	2.01	0.43
2:H:47:TRP:CZ3	3:L:97:ALA:HA	2.53	0.43
3:L:184:THR:OG1	3:L:187:GLN:HG3	2.19	0.43
1:A:449:TYR:O	1:A:452:LEU:HD21	2.17	0.43
1:A:381:GLY:HA2	2:H:97:ILE:HG22	2.00	0.43
2:H:150:VAL:CG2	2:H:178:LEU:HD21	2.49	0.43
2:H:164:HIS:HE2	3:L:170:GLN:HG3	1.82	0.43
1:A:451:TYR:C	1:A:452:LEU:HD23	2.38	0.42
3:L:153:ALA:HB2	3:L:158:VAL:HG21	2.01	0.42
1:A:392:PHE:CD1	1:A:515:PHE:HB3	2.54	0.42
2:H:150:VAL:HG12	2:H:200:HIS:CD2	2.54	0.42
2:H:201:LYS:HB2	2:H:202:PRO:HD3	2.01	0.42
2:H:28:SER:O	2:H:28:SER:OG	2.36	0.42
2:H:193:THR:HG22	2:H:195:ILE:HG13	2.02	0.42
1:A:401:VAL:HG11	1:A:451:TYR:CE1	2.55	0.42
2:H:116:THR:CG2	2:H:203:SER:CB	2.98	0.42
3:L:50:TYR:CE2	3:L:66:LYS:HG3	2.53	0.42
3:L:186:GLU:CD	3:L:189:LYS:HE2	2.40	0.42
3:L:54(A):ASP:OD1	3:L:54(A):ASP:C	2.57	0.41
3:L:136:VAL:O	3:L:136:VAL:HG23	2.20	0.41
1:A:382:VAL:HG21	1:A:390:LEU:CD1	2.50	0.41
1:A:341:VAL:HG11	1:A:397:ALA:HB1	2.02	0.41
1:A:419:ALA:HA	1:A:423:TYR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:107:THR:OG1	5:L:302:GOL:H12	2.21	0.41
1:A:485:GLY:H	1:A:488:CYS:HB2	1.86	0.41
3:L:140:SER:HA	3:L:176:ALA:HA	2.02	0.41
2:H:95:SER:HB3	2:H:100(K):PHE:H	1.86	0.41
2:H:178:LEU:C	2:H:178:LEU:HD12	2.41	0.41
1:A:382:VAL:HG21	1:A:390:LEU:HD12	2.01	0.41
2:H:39:GLN:HA	2:H:44:GLY:O	2.21	0.40
1:A:425:LEU:HD21	1:A:512:VAL:HG11	2.03	0.40
1:A:380:TYR:O	1:A:430:THR:HA	2.20	0.40
2:H:78:PHE:CZ	2:H:92:CYS:HB2	2.57	0.40
2:H:167:PRO:HG2	7:L:457:HOH:O	2.21	0.40

All (3) 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)
7:H:434:HOH:O	7:H:452:HOH:O[1_545]	2.02	0.18
7:H:413:HOH:O	7:H:434:HOH:O[1_565]	2.11	0.09
7:H:452:HOH:O	7:H:476:HOH:O[1_565]	2.14	0.06

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	197/205 (96%)	193 (98%)	4 (2%)	0	100	100
2	H	218/227 (96%)	213 (98%)	5 (2%)	0	100	100
3	L	214/221 (97%)	211 (99%)	3 (1%)	0	100	100
All	All	629/653 (96%)	617 (98%)	12 (2%)	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	A	170/177 (96%)	168 (99%)	2 (1%)	71 84
2	H	192/197 (98%)	191 (100%)	1 (0%)	88 95
3	L	179/186 (96%)	179 (100%)	0	100 100
All	All	541/560 (97%)	538 (99%)	3 (1%)	86 94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	480	CYS
1	A	510	VAL
2	H	50	TYR

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

Mol	Chain	Res	Type
2	H	199	ASN
3	L	94	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

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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	$\#\|Z\| > 2$
5	GOL	L	301	-	5,5,5	0.36	0	5,5,5	0.24	0
4	NAG	A	601	1	14,14,15	0.26	0	17,19,21	0.47	0
5	GOL	H	302	-	5,5,5	0.08	0	5,5,5	0.31	0
5	GOL	L	302	-	5,5,5	0.09	0	5,5,5	0.32	0
5	GOL	H	303	-	5,5,5	0.09	0	5,5,5	0.32	0
5	GOL	A	603	-	5,5,5	0.09	0	5,5,5	0.32	0
5	GOL	A	602	-	5,5,5	0.34	0	5,5,5	0.40	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
5	GOL	L	301	-	-	2/4/4/4	-
4	NAG	A	601	1	-	0/6/23/26	0/1/1/1
5	GOL	H	302	-	-	3/4/4/4	-
5	GOL	L	302	-	-	0/4/4/4	-
5	GOL	H	303	-	-	3/4/4/4	-
5	GOL	A	603	-	-	3/4/4/4	-
5	GOL	A	602	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	602	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
5	A	603	GOL	C1-C2-C3-O3
5	H	302	GOL	O1-C1-C2-C3
5	H	303	GOL	C1-C2-C3-O3
5	L	301	GOL	O1-C1-C2-C3
5	A	602	GOL	O1-C1-C2-O2
5	A	603	GOL	O2-C2-C3-O3
5	H	302	GOL	O1-C1-C2-O2
5	L	301	GOL	O1-C1-C2-O2
5	A	603	GOL	O1-C1-C2-O2
5	H	302	GOL	O2-C2-C3-O3
5	A	602	GOL	O2-C2-C3-O3
5	H	303	GOL	O1-C1-C2-O2
5	A	602	GOL	C1-C2-C3-O3
5	H	303	GOL	O2-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	301	GOL	1	0
4	A	601	NAG	2	0
5	L	302	GOL	4	0
5	H	303	GOL	3	0
5	A	602	GOL	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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	198/205 (96%)	0.84	27 (13%) 3 4	30, 56, 101, 131	0
2	H	222/227 (97%)	0.20	15 (6%) 17 22	13, 30, 63, 97	0
3	L	216/221 (97%)	0.18	7 (3%) 47 54	18, 42, 64, 97	0
All	All	636/653 (97%)	0.40	49 (7%) 13 17	13, 42, 84, 131	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	27	ASP	9.3
1	A	530	HIS	8.0
1	A	521	PRO	6.8
1	A	369	TYR	6.6
1	A	370	ASN	6.1
2	H	133	GLY	5.2
1	A	445	VAL	5.0
2	H	127	SER	4.9
1	A	333	THR	4.8
1	A	519	HIS	4.8
1	A	479	PRO	4.8
1	A	334	ASN	4.7
3	L	172	ASN	4.5
1	A	529	SER	4.2
2	H	204	ASN	4.1
2	H	100(C)	THR	4.0
1	A	528	GLY	3.7
1	A	518	LEU	3.7
2	H	134	GLY	3.7
1	A	372	ALA	3.6
3	L	27	GLY	3.6
1	A	346	ARG	3.6
1	A	522	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
2	H	1	GLN	3.3
1	A	408	ARG	3.3
2	H	29	ILE	3.2
1	A	481	ASN	3.2
3	L	70	ALA	3.1
1	A	446	GLY	3.1
1	A	482	GLY	2.9
1	A	520	ALA	2.9
1	A	500	THR	2.9
1	A	484	GLU	2.8
1	A	486	PHE	2.8
3	L	69	SER	2.7
2	H	135	THR	2.6
2	H	100(D)	LYS	2.5
2	H	28	SER	2.5
3	L	35	TRP	2.5
2	H	190	GLY	2.4
1	A	480	CYS	2.4
1	A	367	VAL	2.2
1	A	371	SER	2.1
2	H	26	GLY	2.1
2	H	100(B)	SER	2.1
2	H	8	GLY	2.1
1	A	525	CYS	2.0
3	L	27(C)	ASN	2.0
3	L	171	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 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^{th} 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^2)	Q<0.9
5	GOL	H	303	6/6	0.46	0.39	59,63,75,87	0
5	GOL	L	302	6/6	0.72	0.44	20,20,20,20	0
5	GOL	A	602	6/6	0.77	0.19	39,43,44,44	0
4	NAG	A	601	14/15	0.82	0.31	59,70,75,76	0
5	GOL	H	302	6/6	0.84	0.16	53,60,63,65	0
5	GOL	A	603	6/6	0.87	0.27	20,20,20,20	0
5	GOL	L	301	6/6	0.89	0.11	48,56,58,58	0
6	CL	H	301	1/1	0.94	0.21	58,58,58,58	0

6.5 Other polymers (i)

There are no such residues in this entry.