



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 08:29 PM EDT

PDB ID : 7CHO / pdb_00007cho
Title : Crystal structure of SARS-CoV-2 antibody P5A-1D2 with RBD
Authors : Wang, X.; Zhang, L.; Ge, J.; Wang, R.; Zhang, Q.
Deposited on : 2020-07-06
Resolution : 2.56 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

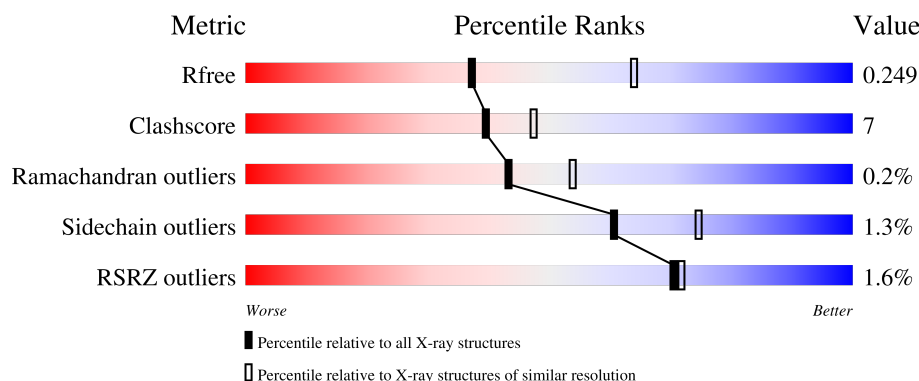
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.56 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1853 (2.58-2.54)
Clashscore	190562	1897 (2.58-2.54)
Ramachandran outliers	187476	1875 (2.58-2.54)
Sidechain outliers	187428	1875 (2.58-2.54)
RSRZ outliers	180081	1853 (2.58-2.54)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	217	4% 72% 18% 11%
1	E	217	2% 74% 15% 11%
2	B	222	83% 16%
2	H	222	82% 16% .
3	C	217	% 83% 13% .

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Mol	Chain	Length	Quality of chain
3	L	217	2% 83% 14%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9571 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
1	E	194	Total	C	N	O	S	0	0	0
			1536	984	256	288	8			
1	A	194	Total	C	N	O	S	0	0	0
			1536	984	256	288	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	530	HIS	-	expression tag	UNP P0DTC2
E	531	HIS	-	expression tag	UNP P0DTC2
E	532	HIS	-	expression tag	UNP P0DTC2
E	533	HIS	-	expression tag	UNP P0DTC2
E	534	HIS	-	expression tag	UNP P0DTC2
E	535	HIS	-	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

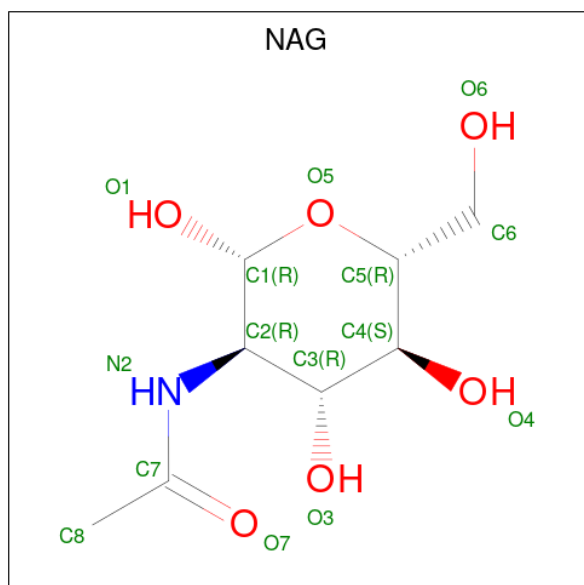
- Molecule 2 is a protein called antibody P5A-1D2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	217	Total	C	N	O	S	0	0	0
			1619	1023	269	321	6			
2	B	221	Total	C	N	O	S	0	0	0
			1642	1036	274	326	6			

- Molecule 3 is a protein called antibody P5A-1D2 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	4	0
			1568	979	261	323	5			
3	C	209	Total	C	N	O	S	0	3	0
			1545	964	258	318	5			

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



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	14	Total	O	0	0
			14	14		
5	H	18	Total	O	0	0
			18	18		
5	L	16	Total	O	0	0
			16	16		
5	A	14	Total	O	0	0
			14	14		
5	B	18	Total	O	0	0
			18	18		

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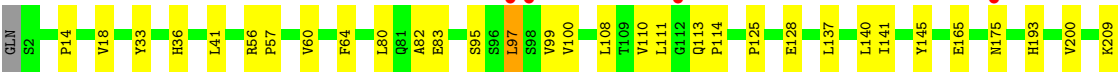
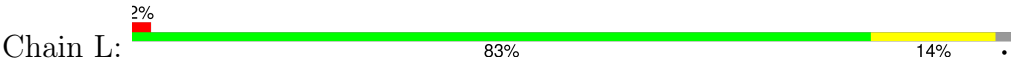
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	17	Total	O	0	0
			17	17		

- Molecule 1: Spike protein S1

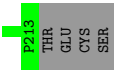
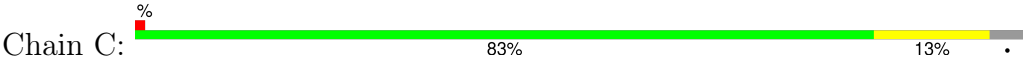




• Molecule 3: antibody P5A-1D2 light chain



• Molecule 3: antibody P5A-1D2 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	158.75Å 67.51Å 154.37Å 90.00° 112.18° 90.00°	Depositor
Resolution (Å)	36.52 – 2.56 36.52 – 2.56	Depositor EDS
% Data completeness (in resolution range)	96.0 (36.52-2.56) 96.0 (36.52-2.56)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.202 , 0.247 0.206 , 0.249	Depositor DCC
R_{free} test set	2394 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	50.1	Xtriage
Anisotropy	0.495	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9571	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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

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	A	0.52	0/1579	0.64	1/2149 (0.0%)
1	E	0.38	0/1579	0.64	0/2149
2	B	0.36	0/1680	0.60	0/2290
2	H	0.41	0/1656	0.63	0/2257
3	C	0.35	0/1593	0.58	0/2176
3	L	0.46	0/1621	0.70	0/2215
All	All	0.42	0/9708	0.63	1/13236 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	445	VAL	N-CA-C	5.52	120.83	109.34

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	1536	0	1452	30	0
1	E	1536	0	1452	21	0
2	B	1642	0	1607	29	0
2	H	1619	0	1582	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1545	0	1497	21	0
3	L	1568	0	1524	21	0
4	A	14	0	13	0	0
4	E	14	0	13	0	0
5	A	14	0	0	1	0
5	B	18	0	0	1	0
5	C	17	0	0	0	0
5	E	14	0	0	0	0
5	H	18	0	0	1	0
5	L	16	0	0	1	0
All	All	9571	0	9140	124	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 7.

All (124) 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:C:41:LEU:O	3:C:44:THR:OG1	2.07	0.73
3:L:165:GLU:OE2	5:L:301:HOH:O	2.08	0.71
1:A:403:ARG:HD2	1:A:505:TYR:CE1	2.25	0.71
2:H:2:VAL:CG1	2:H:27:PHE:CE2	2.76	0.69
2:H:171:VAL:HG22	2:H:190:VAL:HG22	1.78	0.66
2:B:199:THR:OG1	2:B:200:GLN:N	2.29	0.66
1:A:403:ARG:HH21	1:A:405:ASP:HB2	1.61	0.66
1:A:493:GLN:NE2	2:B:101:VAL:O	2.23	0.65
2:B:97:ARG:NH2	2:B:109:ASP:OD2	2.27	0.65
2:B:47:TRP:CD2	3:C:100:VAL:CG1	2.81	0.64
2:H:2:VAL:HG13	2:H:27:PHE:CE2	2.32	0.63
2:B:47:TRP:CG	3:C:100:VAL:CG1	2.81	0.63
2:H:88:GLU:HB2	2:B:88:GLU:OE1	1.99	0.63
2:H:75:ASN:ND2	5:H:301:HOH:O	2.26	0.61
2:B:12:ILE:HG21	2:B:85:LEU:HD13	1.81	0.61
3:L:113:GLN:HG3	3:L:114:PRO:HD2	1.83	0.61
3:C:13:ALA:HB3	3:C:16:GLN:HG3	1.83	0.60
1:E:516:GLU:HG2	1:E:518:LEU:HD13	1.82	0.60
2:H:131:PRO:HD3	2:H:217:LYS:HD3	1.84	0.60
2:H:88:GLU:CD	2:B:88:GLU:HB2	2.27	0.59
1:A:364:ASP:O	1:A:367:VAL:HG12	2.03	0.59
3:C:92:SER:O	3:C:100:VAL:HG23	2.03	0.58
1:E:441:LEU:HD22	1:E:509:ARG:NH2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:339:GLY:O	1:E:343:ASN:HB2	2.04	0.57
2:H:82:MET:HB3	2:H:85:LEU:HD21	1.85	0.57
1:E:364:ASP:OD1	1:E:366:SER:HB3	2.03	0.57
2:B:47:TRP:CG	3:C:100:VAL:HG13	2.39	0.57
1:A:368:LEU:O	1:A:374:PHE:HE2	1.89	0.55
2:H:205:ASN:ND2	2:H:216:ASP:OD1	2.35	0.55
3:L:141:ILE:HG12	3:L:200:VAL:HG21	1.88	0.55
1:A:335:LEU:HD23	1:A:362:VAL:O	2.07	0.55
1:A:382:VAL:HB	1:A:387:LEU:HD13	1.89	0.55
1:E:403:ARG:NH2	3:L:33:TYR:OH	2.40	0.54
2:B:47:TRP:CD2	3:C:100:VAL:HG12	2.42	0.54
3:L:56:ARG:HD3	3:L:64:PHE:O	2.08	0.54
2:H:69:ILE:HD11	2:H:78:LEU:HD11	1.89	0.54
1:A:403:ARG:NH2	3:C:33:TYR:OH	2.40	0.54
2:B:22:CYS:HB3	2:B:78:LEU:HB3	1.90	0.53
1:E:433:VAL:HG22	1:E:512:VAL:HG22	1.91	0.53
1:E:350:VAL:HA	1:E:400:PHE:HB2	1.91	0.53
3:L:193:HIS:NE2	3:C:193:HIS:NE2	2.57	0.53
3:C:199:GLN:NE2	3:C:208:GLU:OE2	2.42	0.53
2:H:2:VAL:HG11	2:H:27:PHE:CE2	2.44	0.52
1:A:383:SER:HG	1:A:386:LYS:HB2	1.75	0.52
2:B:222:LYS:O	5:B:301:HOH:O	2.18	0.51
1:A:383:SER:OG	1:A:386:LYS:HB2	2.12	0.50
3:C:137:LEU:HD12	3:C:183:LEU:HD23	1.93	0.50
1:A:477:SER:N	2:B:26:GLY:O	2.45	0.50
1:E:477:SER:HA	2:H:28:ILE:HD11	1.93	0.50
2:H:218:LYS:HE2	2:H:220:GLU:OE2	2.11	0.50
1:E:403:ARG:HD3	1:E:406:GLU:OE2	2.10	0.50
3:L:14:PRO:HA	3:L:80:LEU:O	2.11	0.50
3:C:124:PRO:HA	3:C:137:LEU:HD23	1.93	0.50
2:B:97:ARG:NH2	2:B:99:LEU:HD11	2.27	0.49
1:A:350:VAL:HA	1:A:400:PHE:HB2	1.92	0.49
2:B:40:ALA:HB3	2:B:43:LYS:HB2	1.94	0.49
1:A:359:SER:OG	1:A:394:ASN:OD1	2.15	0.49
3:L:113:GLN:HG3	3:L:114:PRO:CD	2.42	0.49
3:L:125:PRO:HD3	3:L:137[A]:LEU:HD23	1.95	0.49
1:A:431:GLY:HA3	1:A:513:LEU:O	2.13	0.49
3:L:18:VAL:HG11	3:L:108:LEU:HD11	1.95	0.48
1:A:437:ASN:ND2	1:A:439:ASN:H	2.11	0.48
2:B:178:LEU:HD13	2:B:184:TYR:CE1	2.49	0.48
1:E:371:SER:C	1:E:373:SER:H	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:128:GLU:OE1	3:L:128:GLU:N	2.43	0.48
3:C:14:PRO:HD3	3:C:111:LEU:O	2.12	0.48
1:E:505:TYR:CZ	2:H:104:THR:HB	2.49	0.48
3:L:57:PRO:HG2	3:L:60:VAL:HG21	1.96	0.48
1:E:392:PHE:CE1	1:E:515:PHE:HB3	2.49	0.47
1:A:374:PHE:HB2	5:A:708:HOH:O	2.15	0.47
1:A:342:PHE:CZ	1:A:368:LEU:HD21	2.49	0.47
1:A:353:TRP:H	1:A:353:TRP:CD1	2.31	0.47
2:H:107:TYR:HB3	3:L:36:HIS:CD2	2.49	0.47
2:H:88:GLU:OE2	2:B:88:GLU:HB2	2.15	0.47
2:H:197:LEU:HD23	2:H:197:LEU:HA	1.73	0.47
1:A:403:ARG:HH21	1:A:405:ASP:CB	2.27	0.47
2:B:30:SER:HA	2:B:71:ARG:HD2	1.98	0.46
3:C:63:ARG:HB3	3:C:78:THR:O	2.15	0.46
2:B:97:ARG:HG2	2:B:98:ALA:N	2.30	0.46
2:H:90:THR:HG23	2:H:118:THR:HA	1.98	0.46
2:H:189:VAL:HG11	3:L:140:LEU:HD22	1.99	0.45
1:A:364:ASP:OD2	1:A:367:VAL:HB	2.17	0.45
3:L:82:ALA:HA	3:L:110:VAL:HG21	1.99	0.45
1:A:347:PHE:CE2	1:A:399:SER:HB2	2.51	0.45
2:B:175:PRO:HG2	3:C:170:SER:OG	2.17	0.45
1:A:347:PHE:CD2	1:A:399:SER:HB2	2.52	0.45
1:E:455:LEU:HD11	2:H:100:GLN:HB3	1.98	0.45
1:A:437:ASN:HD21	1:A:439:ASN:HB2	1.82	0.44
2:B:36:TRP:NE1	2:B:80:LEU:HB2	2.32	0.44
1:E:393:THR:O	1:E:523:THR:OG1	2.35	0.44
3:C:56:ARG:HD3	3:C:64:PHE:O	2.17	0.44
1:E:395:VAL:HA	1:E:514:SER:O	2.17	0.44
1:A:421:TYR:OH	2:B:52:TYR:HB3	2.17	0.44
2:B:82:MET:HB3	2:B:85:LEU:HD21	1.99	0.44
2:H:124:THR:HG22	2:H:211:SER:HB3	2.00	0.44
1:A:396:TYR:O	1:A:513:LEU:HA	2.17	0.43
3:L:33:TYR:HE2	3:L:95:SER:HB3	1.83	0.43
1:E:392:PHE:CD1	1:E:515:PHE:HB3	2.53	0.43
1:E:443:SER:HB3	1:E:499:PRO:HD3	1.99	0.43
2:B:13:GLN:H	2:B:13:GLN:CD	2.26	0.43
1:E:425:LEU:HD21	1:E:512:VAL:HG11	2.01	0.43
1:E:403:ARG:HD2	1:E:505:TYR:CE1	2.53	0.42
1:A:449:TYR:CD1	1:A:449:TYR:N	2.87	0.42
2:B:39:GLN:HB2	2:B:45:LEU:HD23	2.01	0.42
3:L:209:LYS:HA	3:L:209:LYS:HD3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:32:ASN:OD1	2:B:97:ARG:HD2	2.19	0.42
3:C:155:ALA:HB2	3:C:196:TYR:CE2	2.54	0.42
2:H:47:TRP:CG	3:L:100:VAL:HG22	2.54	0.42
1:E:520:ALA:HB1	1:E:521:PRO:HD2	2.01	0.42
2:B:135:SER:OG	2:B:136:SER:N	2.52	0.42
3:L:113:GLN:HB3	3:L:145:TYR:CZ	2.54	0.41
2:H:207:ASN:OD1	2:H:214:LYS:HD3	2.20	0.41
1:A:387:LEU:HD12	1:A:387:LEU:HA	1.85	0.41
3:L:97:LEU:H	3:L:97:LEU:HG	1.58	0.41
1:E:364:ASP:O	1:E:367:VAL:HG22	2.21	0.41
1:A:392:PHE:CE1	1:A:515:PHE:HB3	2.56	0.41
3:C:54:SER:HB3	3:C:66:GLY:O	2.21	0.41
2:H:152:ASP:HB3	2:H:183:LEU:HD13	2.03	0.41
1:A:418:ILE:HD13	1:A:418:ILE:HA	1.87	0.41
1:A:447:GLY:HA3	1:A:449:TYR:HE1	1.85	0.41
3:C:62:ASP:OD1	3:C:62:ASP:N	2.47	0.40
3:L:14:PRO:HD3	3:L:111:LEU:O	2.22	0.40
2:B:102:GLY:HA3	3:C:51:TYR:HE1	1.87	0.40
2:B:179:GLN:HG2	3:C:165:GLU:HG3	2.02	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	A	192/217 (88%)	178 (93%)	13 (7%)	1 (0%)	24	33
1	E	192/217 (88%)	174 (91%)	17 (9%)	1 (0%)	24	33
2	B	219/222 (99%)	210 (96%)	8 (4%)	1 (0%)	24	33
2	H	213/222 (96%)	209 (98%)	4 (2%)	0	100	100
3	C	208/217 (96%)	199 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	L	214/217 (99%)	199 (93%)	15 (7%)	0	100	100
All	All	1238/1312 (94%)	1169 (94%)	66 (5%)	3 (0%)	43	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	195	SER
1	E	497	PHE
1	A	457	ARG

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	A	167/190 (88%)	165 (99%)	2 (1%)	63	76
1	E	167/190 (88%)	166 (99%)	1 (1%)	78	85
2	B	184/185 (100%)	183 (100%)	1 (0%)	81	87
2	H	181/185 (98%)	177 (98%)	4 (2%)	45	61
3	C	177/182 (97%)	175 (99%)	2 (1%)	65	77
3	L	181/182 (100%)	176 (97%)	5 (3%)	38	54
All	All	1057/1114 (95%)	1042 (99%)	15 (1%)	61	73

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	388	ASN
2	H	12	ILE
2	H	18	LEU
2	H	151	LYS
2	H	185	SER
3	L	41	LEU
3	L	83	GLU
3	L	97	LEU

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Mol	Chain	Res	Type
3	L	99	VAL
3	L	175	ASN
1	A	346	ARG
1	A	373	SER
2	B	2	VAL
3	C	206[A]	THR
3	C	206[B]	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	334	ASN
1	E	409	GLN
1	E	414	GLN
1	E	493	GLN
2	H	179	GLN
2	H	207	ASN
1	A	370	ASN
1	A	437	ASN
1	A	474	GLN
1	A	501	ASN
2	B	179	GLN
3	C	91	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	A	601	1	14,14,15	0.64	0	17,19,21	0.54	0
4	NAG	E	601	1	14,14,15	0.75	0	17,19,21	0.64	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	A	601	1	-	0/6/23/26	0/1/1/1
4	NAG	E	601	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	601	NAG	O5-C5-C6-O6
4	E	601	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	A	194/217 (89%)	0.18	8 (4%) 41 42	42, 61, 91, 103	0
1	E	194/217 (89%)	0.10	5 (2%) 57 59	40, 55, 81, 94	0
2	B	221/222 (99%)	-0.32	1 (0%) 87 89	34, 46, 65, 82	0
2	H	217/222 (97%)	-0.17	0 100 100	37, 50, 70, 81	0
3	C	209/217 (96%)	-0.25	2 (0%) 79 81	27, 50, 63, 74	3 (1%)
3	L	212/217 (97%)	-0.11	4 (1%) 66 67	32, 51, 68, 87	4 (1%)
All	All	1247/1312 (95%)	-0.10	20 (1%) 70 72	27, 51, 77, 103	7 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	368	LEU	4.5
1	E	389	ASP	4.0
1	A	389	ASP	3.3
1	A	449	TYR	3.2
1	E	391	CYS	2.9
1	A	384	PRO	2.8
3	C	2	SER	2.5
1	A	526	GLY	2.4
1	E	388	ASN	2.4
3	L	97	LEU	2.3
1	A	365	TYR	2.3
1	A	372	ALA	2.2
3	L	112	GLY	2.2
3	C	95	SER	2.2
1	E	335	LEU	2.2
3	L	98	SER	2.1
2	B	137	LYS	2.1
1	E	392	PHE	2.1
3	L	175	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	447	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	A	601	14/15	0.63	0.14	88,120,130,130	0
4	NAG	E	601	14/15	0.67	0.15	92,113,124,127	0

6.5 Other polymers [i](#)

There are no such residues in this entry.