



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:25 AM UTC

PDB ID : 7FC6 / pdb_00007fc6
Title : Crystal structure of SARS-CoV RBD and horse ACE2
Authors : Wang, X.Q.; Lan, J.; Ge, J.W.
Deposited on : 2021-07-13
Resolution : 2.65 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

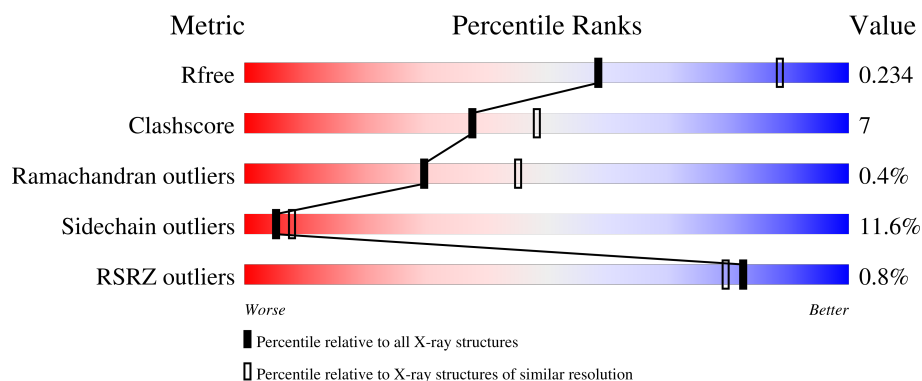
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	597	72%24%.
2	S	192	87%11%.
3	B	2	100%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6465 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 Angiotensin-converting enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	597	Total	C	N	O	S	0	0	0
			4862	3104	805	924	29			

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S	192	Total	C	N	O	S	0	0	0
			1530	989	249	283	9			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

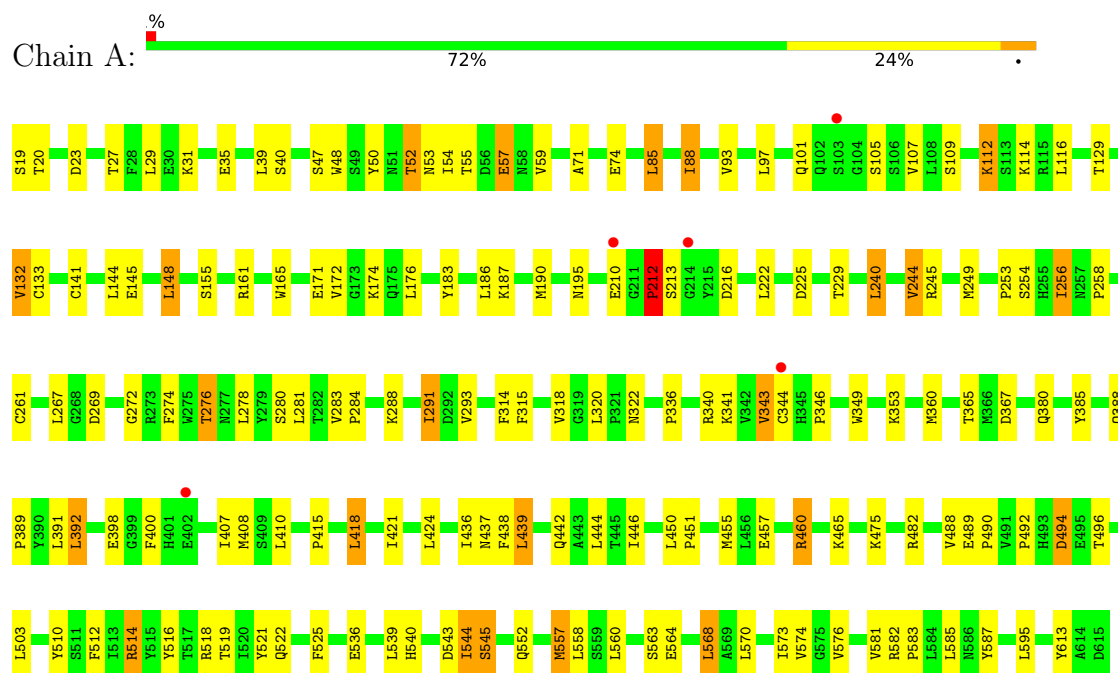
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	12	Total	O	0	0
			12	12		
5	S	5	Total	O	0	0
			5	5		

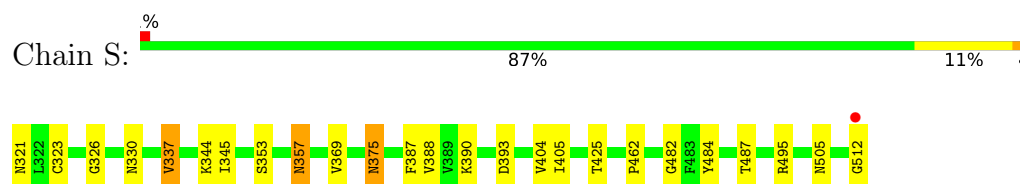
3 Residue-property plots

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.

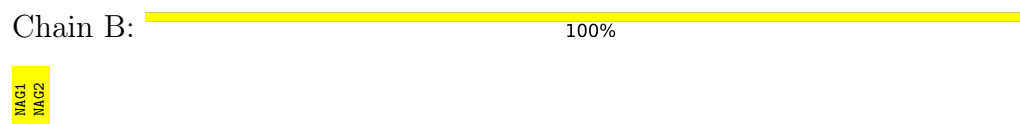
• Molecule 1: Angiotensin-converting enzyme



• Molecule 2: Spike protein S1



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.96Å 126.31Å 171.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.95 – 2.65 17.95 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.7 (17.95-2.65) 99.3 (17.95-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.66Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.185 , 0.235 0.191 , 0.234	Depositor DCC
R_{free} test set	1802 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	58.6	Xtriage
Anisotropy	0.617	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 41.2	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	0.95	EDS
Total number of atoms	6465	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: 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	0.42	0/4998	0.65	2/6786 (0.0%)
2	S	0.40	0/1578	0.59	0/2154
All	All	0.41	0/6576	0.64	2/8940 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	PRO	N-CA-CB	-6.47	96.46	103.25
1	A	212	PRO	N-CA-C	5.56	123.92	112.47

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	A	4862	0	4645	79	0
2	S	1530	0	1451	11	0
3	B	28	0	25	2	0
4	A	14	0	13	2	0
4	S	14	0	13	0	0
5	A	12	0	0	2	0
5	S	5	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6465	0	6147	88	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 (88) 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:A:703:NAG:O4	5:A:801:HOH:O	1.94	0.84
1:A:365:THR:HG22	1:A:367:ASP:H	1.48	0.78
1:A:55:THR:HG21	3:B:1:NAG:H62	1.73	0.70
1:A:272:GLY:O	5:A:802:HOH:O	2.11	0.68
1:A:132:VAL:HG13	1:A:148:LEU:HD21	1.74	0.67
1:A:460:ARG:NH2	1:A:510:TYR:O	2.30	0.65
1:A:388:GLN:HG3	1:A:389:PRO:HD2	1.80	0.64
1:A:340:ARG:HD3	3:B:1:NAG:H82	1.81	0.63
1:A:494:ASP:HB2	1:A:496:THR:HG22	1.80	0.63
1:A:293:VAL:HG11	1:A:418:LEU:HG	1.80	0.62
1:A:116:LEU:HB2	1:A:186:LEU:HD23	1.81	0.62
1:A:229:THR:HG23	1:A:516:TYR:OH	2.01	0.61
1:A:109:SER:HB3	1:A:112:LYS:HB2	1.83	0.60
1:A:291:ILE:HD11	1:A:415:PRO:HG3	1.85	0.58
1:A:31:LYS:NZ	1:A:35:GLU:OE1	2.35	0.58
1:A:55:THR:O	1:A:59:VAL:HG23	2.04	0.58
1:A:365:THR:HG22	1:A:367:ASP:N	2.18	0.57
1:A:400:PHE:HD2	1:A:557:MET:HE3	1.71	0.56
1:A:315:PHE:CZ	1:A:408:MET:HG3	2.41	0.56
1:A:398:GLU:HG3	1:A:514:ARG:HB3	1.91	0.53
1:A:494:ASP:N	1:A:494:ASP:OD1	2.42	0.53
1:A:27:THR:HG21	2:S:462:PRO:HG3	1.91	0.53
1:A:105:SER:HA	1:A:190:MET:HG3	1.91	0.52
1:A:457:GLU:HG2	1:A:512:PHE:HB3	1.92	0.51
2:S:353:SER:O	2:S:357:ASN:ND2	2.45	0.50
1:A:269:ASP:OD1	1:A:272:GLY:N	2.43	0.50
1:A:71:ALA:O	1:A:74:GLU:HG3	2.12	0.50
1:A:47:SER:HB3	1:A:349:TRP:HH2	1.77	0.49
1:A:320:LEU:HB3	1:A:380:GLN:NE2	2.27	0.49
1:A:318:VAL:HG23	1:A:320:LEU:HD23	1.95	0.48
1:A:145:GLU:HG2	1:A:344:CYS:CB	2.44	0.48
1:A:314:PHE:HZ	1:A:544:ILE:HG22	1.77	0.48
1:A:284:PRO:HG2	1:A:436:ILE:HG22	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:337:VAL:HG22	2:S:388:VAL:O	2.13	0.48
1:A:240:LEU:O	1:A:244:VAL:HG13	2.13	0.48
1:A:353:LYS:HE3	2:S:482:GLY:O	2.13	0.48
1:A:450:LEU:HB2	1:A:451:PRO:HD3	1.96	0.48
1:A:132:VAL:CG1	1:A:148:LEU:HD21	2.41	0.47
1:A:48:TRP:O	1:A:52:THR:HB	2.14	0.47
1:A:249:MET:HG2	1:A:256:ILE:HB	1.97	0.47
1:A:145:GLU:HG2	1:A:344:CYS:HB2	1.97	0.46
1:A:543:ASP:OD1	1:A:545:SER:HB2	2.14	0.46
1:A:564:GLU:OE1	1:A:568:LEU:HD13	2.16	0.46
1:A:155:SER:HB3	1:A:161:ARG:HD2	1.97	0.46
2:S:337:VAL:HG13	2:S:387:PHE:CD1	2.50	0.46
1:A:465:LYS:HB2	1:A:465:LYS:HE3	1.72	0.46
1:A:392:LEU:HG	1:A:563:SER:HA	1.98	0.46
1:A:284:PRO:HD2	1:A:437:ASN:OD1	2.16	0.45
1:A:85:LEU:O	1:A:88:ILE:HG12	2.16	0.45
1:A:27:THR:HG21	2:S:462:PRO:CG	2.46	0.45
1:A:57:GLU:H	1:A:57:GLU:HG2	1.51	0.45
1:A:291:ILE:HD12	1:A:291:ILE:HA	1.54	0.45
1:A:261:CYS:HB2	1:A:488:VAL:HB	1.99	0.44
1:A:407:ILE:HD11	1:A:525:PHE:CD2	2.52	0.44
1:A:539:LEU:H	1:A:539:LEU:HD23	1.82	0.44
1:A:97:LEU:O	1:A:101:GLN:HG2	2.18	0.44
1:A:225:ASP:O	1:A:229:THR:HG22	2.17	0.44
1:A:54:ILE:HD11	1:A:343:VAL:HG12	2.00	0.44
1:A:455:MET:HE3	1:A:455:MET:HB3	1.87	0.43
1:A:336:PRO:HB3	1:A:340:ARG:HH11	1.83	0.43
1:A:439:LEU:HD12	1:A:439:LEU:HA	1.73	0.43
1:A:492:PRO:HG3	1:A:613:TYR:CE1	2.52	0.43
2:S:484:TYR:HB2	2:S:487:THR:CG2	2.48	0.43
1:A:253:PRO:O	1:A:254:SER:OG	2.24	0.43
2:S:375:ASN:O	2:S:512:GLY:HA3	2.18	0.43
2:S:393:ASP:HB3	2:S:405:ILE:HG13	2.01	0.43
1:A:545:SER:HB3	4:A:703:NAG:H82	2.00	0.42
1:A:23:ASP:O	1:A:27:THR:HG22	2.18	0.42
1:A:346:PRO:HB3	1:A:360:MET:HG3	2.01	0.42
2:S:425:THR:HG21	2:S:495:ARG:HG3	2.01	0.42
1:A:267:LEU:HD23	1:A:267:LEU:HA	1.83	0.42
1:A:450:LEU:HD23	1:A:450:LEU:HA	1.88	0.42
1:A:438:PHE:O	1:A:442:GLN:HG2	2.19	0.42
1:A:165:TRP:CZ3	1:A:490:PRO:HD2	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:PHE:HB3	1:A:276:THR:HG23	2.01	0.42
1:A:47:SER:HB3	1:A:349:TRP:CH2	2.54	0.41
1:A:540:HIS:HA	1:A:587:TYR:CE1	2.55	0.41
1:A:50:TYR:CE1	1:A:59:VAL:HG22	2.56	0.41
1:A:183:TYR:O	1:A:187:LYS:HB2	2.21	0.41
2:S:326:GLY:O	2:S:330:ASN:HB2	2.20	0.41
1:A:582:ARG:HB3	1:A:583:PRO:HD3	2.02	0.41
1:A:446:ILE:HG23	1:A:519:THR:HG23	2.03	0.41
1:A:410:LEU:HA	1:A:410:LEU:HD23	1.85	0.41
1:A:144:LEU:HA	1:A:148:LEU:HB2	2.02	0.40
1:A:245:ARG:HD3	1:A:258:PRO:HA	2.03	0.40
1:A:482:ARG:HH21	1:A:489:GLU:CD	2.28	0.40
1:A:521:TYR:O	1:A:522:GLN:C	2.65	0.40
1:A:314:PHE:CZ	1:A:544:ILE:HG22	2.54	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	595/597 (100%)	577 (97%)	16 (3%)	2 (0%)	36	52
2	S	190/192 (99%)	177 (93%)	12 (6%)	1 (0%)	24	39
All	All	785/789 (100%)	754 (96%)	28 (4%)	3 (0%)	30	45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	PRO
1	A	53	ASN
2	S	505	ASN

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	525/525 (100%)	455 (87%)	70 (13%)	4	6
2	S	167/167 (100%)	157 (94%)	10 (6%)	17	30
All	All	692/692 (100%)	612 (88%)	80 (12%)	5	8

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	SER
1	A	20	THR
1	A	29	LEU
1	A	39	LEU
1	A	40	SER
1	A	52	THR
1	A	57	GLU
1	A	85	LEU
1	A	88	ILE
1	A	93	VAL
1	A	107	VAL
1	A	112	LYS
1	A	114	LYS
1	A	129	THR
1	A	132	VAL
1	A	133	CYS
1	A	141	CYS
1	A	148	LEU
1	A	171	GLU
1	A	172	VAL
1	A	174	LYS
1	A	176	LEU
1	A	195	ASN
1	A	210	GLU
1	A	212	PRO
1	A	213	SER
1	A	216	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	222	LEU
1	A	240	LEU
1	A	244	VAL
1	A	256	ILE
1	A	276	THR
1	A	278	LEU
1	A	280	SER
1	A	281	LEU
1	A	283	VAL
1	A	288	LYS
1	A	291	ILE
1	A	322	ASN
1	A	341	LYS
1	A	343	VAL
1	A	385	TYR
1	A	391	LEU
1	A	392	LEU
1	A	418	LEU
1	A	421	ILE
1	A	424	LEU
1	A	439	LEU
1	A	444	LEU
1	A	460	ARG
1	A	475	LYS
1	A	494	ASP
1	A	503	LEU
1	A	514	ARG
1	A	518	ARG
1	A	536	GLU
1	A	544	ILE
1	A	545	SER
1	A	552	GLN
1	A	557	MET
1	A	558	LEU
1	A	560	LEU
1	A	568	LEU
1	A	570	LEU
1	A	573	ILE
1	A	574	VAL
1	A	576	VAL
1	A	581	VAL
1	A	585	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	595	LEU
2	S	321	ASN
2	S	323	CYS
2	S	337	VAL
2	S	344	LYS
2	S	345	ILE
2	S	357	ASN
2	S	369	VAL
2	S	375	ASN
2	S	390	LYS
2	S	404	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	255	HIS
2	S	357	ASN

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](#)

2 monosaccharides 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
3	NAG	B	1	1,3	14,14,15	0.68	0	17,19,21	0.75	0
3	NAG	B	2	3	14,14,15	0.54	0	17,19,21	0.72	1 (5%)

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
3	NAG	B	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2	NAG	C1-O5-C5	2.28	115.24	112.19

There are no chirality outliers.

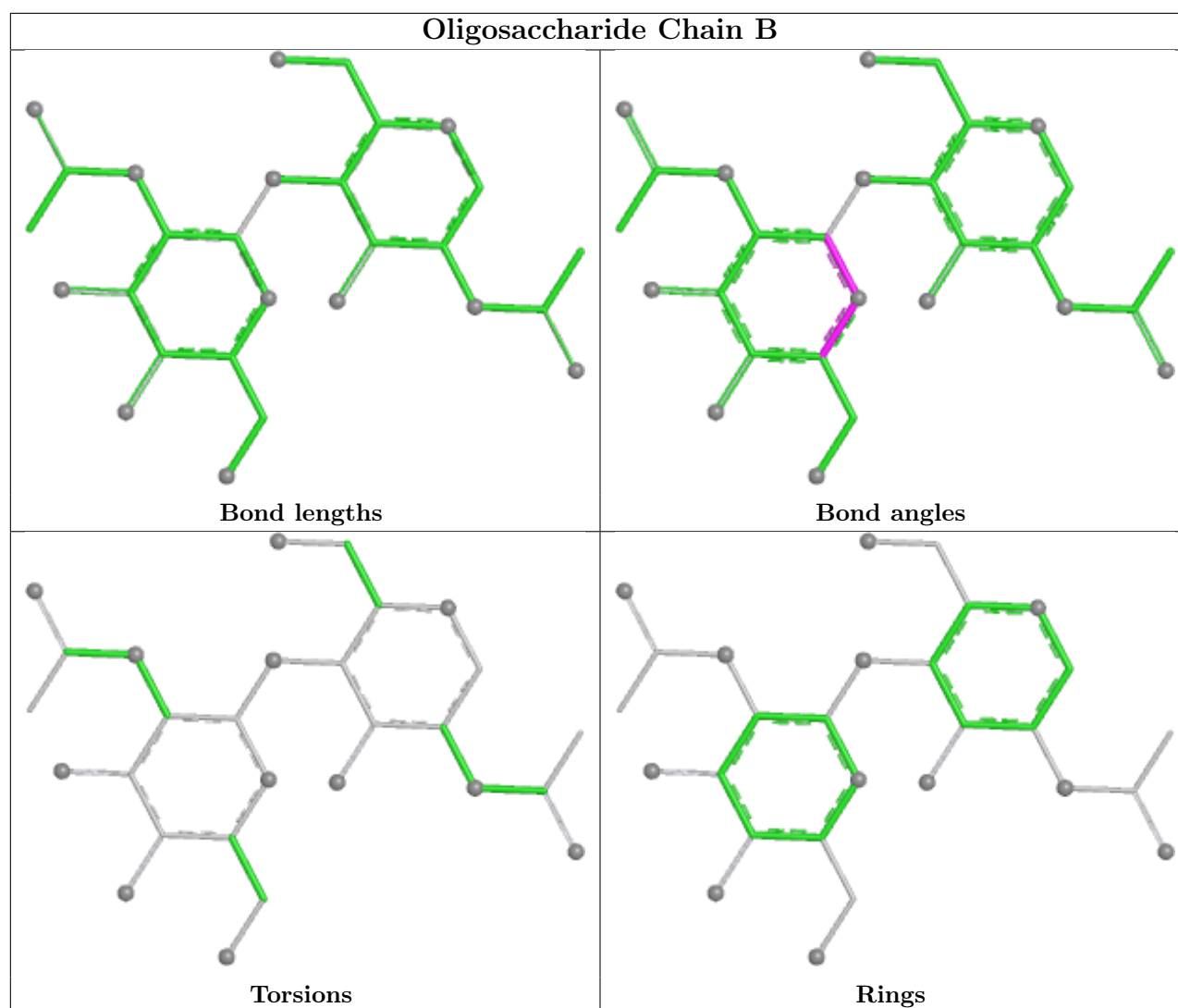
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1	NAG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



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	703	1	14,14,15	0.64	1 (7%)	17,19,21	0.94	1 (5%)
4	NAG	S	601	2	14,14,15	1.01	1 (7%)	17,19,21	1.68	2 (11%)

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	703	1	-	2/6/23/26	0/1/1/1
4	NAG	S	601	2	-	1/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	S	601	NAG	O5-C1	3.56	1.49	1.43
4	A	703	NAG	O5-C1	2.16	1.47	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	S	601	NAG	C1-O5-C5	5.35	119.35	112.19
4	A	703	NAG	C1-O5-C5	3.31	116.62	112.19
4	S	601	NAG	C1-C2-N2	2.71	114.70	110.43

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	703	NAG	C4-C5-C6-O6
4	A	703	NAG	O5-C5-C6-O6
4	S	601	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	703	NAG	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	597/597 (100%)	-0.41	5 (0%) 82 79	37, 58, 95, 133	0
2	S	192/192 (100%)	-0.40	1 (0%) 87 85	39, 59, 93, 112	0
All	All	789/789 (100%)	-0.40	6 (0%) 82 79	37, 58, 94, 133	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	210	GLU	5.4
1	A	402	GLU	4.0
2	S	512	GLY	3.7
1	A	103	SER	2.5
1	A	214	GLY	2.2
1	A	344	CYS	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.

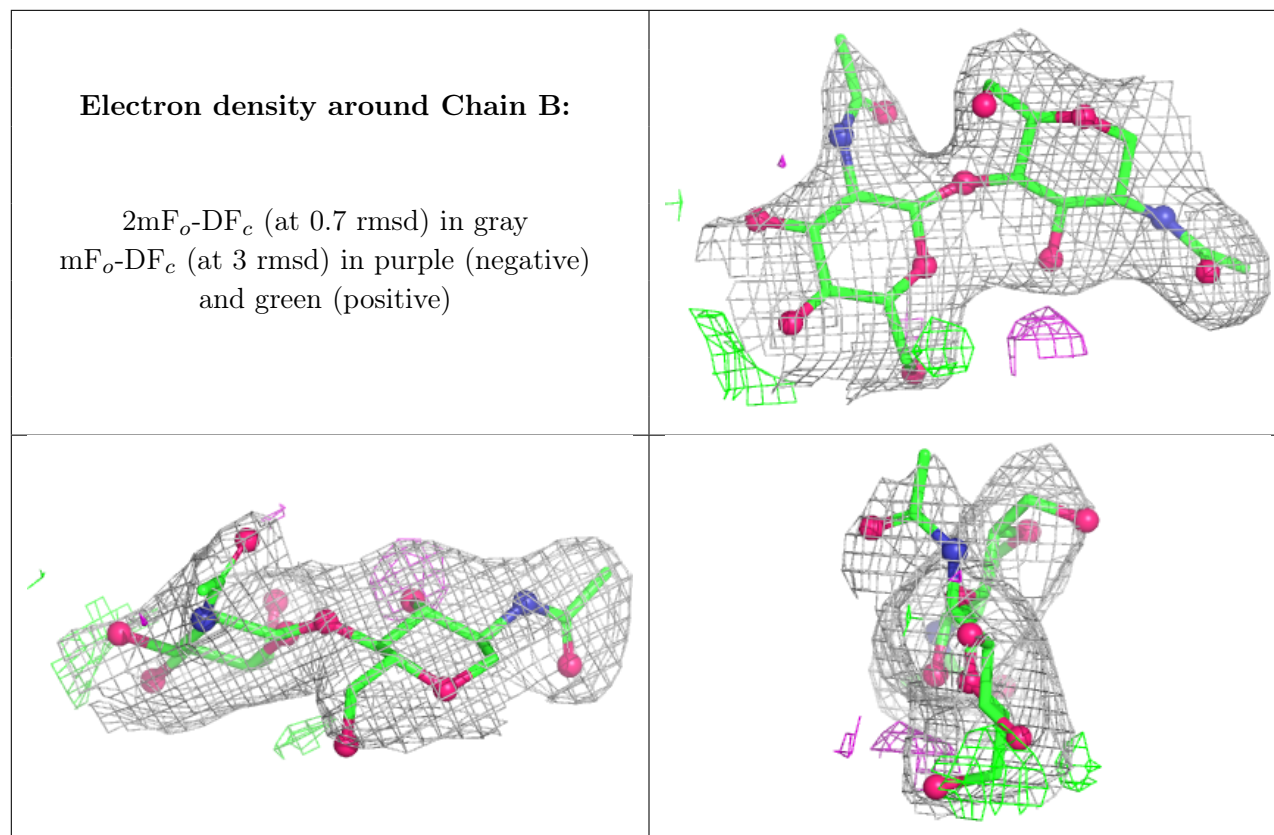
6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
3	NAG	B	1	14/15	-	-	60,75,91,91	0
3	NAG	B	2	14/15	-	-	91,101,106,107	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.



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	703	14/15	0.66	0.17	98,111,125,126	0
4	NAG	S	601	14/15	0.69	0.15	96,106,111,113	0

6.5 Other polymers [i](#)

There are no such residues in this entry.