



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:37 PM UTC

PDB ID : 7BEH / pdb_00007beh
Title : Crystal structure of the receptor binding domain of SARS-CoV-2 Spike glycoprotein in complex with COVOX-316 Fab
Authors : Zhou, D.; Zhao, Y.; Ren, J.; Stuart, D.
Deposited on : 2020-12-23
Resolution : 2.30 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)
Xtrriage (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

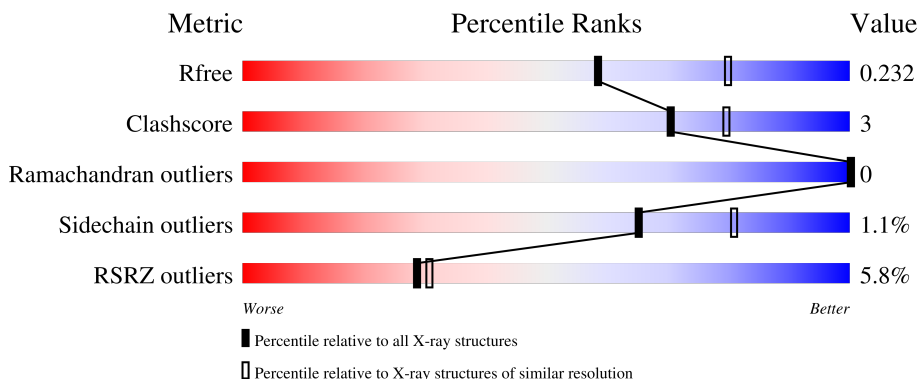
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 $\leq 5\%$. 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	E	205	 11% 86% 8% 5%
2	H	240	 4% 83% 8% 9%
3	L	229	 % 84% 9% 7%
4	A	3	 67% 33%
4	B	3	 67% 33%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4967 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 glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	195	1541	987	257	289	8	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	324	GLU	-	expression tag	UNP P0DTC2
E	325	THR	-	expression tag	UNP P0DTC2
E	326	GLY	-	expression tag	UNP P0DTC2
E	327	HIS	-	expression tag	UNP P0DTC2
E	328	HIS	-	expression tag	UNP P0DTC2
E	329	HIS	-	expression tag	UNP P0DTC2
E	330	HIS	-	expression tag	UNP P0DTC2
E	331	HIS	-	expression tag	UNP P0DTC2
E	332	HIS	-	expression tag	UNP P0DTC2
E	527	LYS	PRO	engineered mutation	UNP P0DTC2

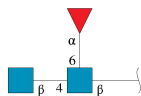
- Molecule 2 is a protein called COVOX-316 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	219	1649	1038	279	322	10	0	1	0

- Molecule 3 is a protein called COVOX-316 light chain.

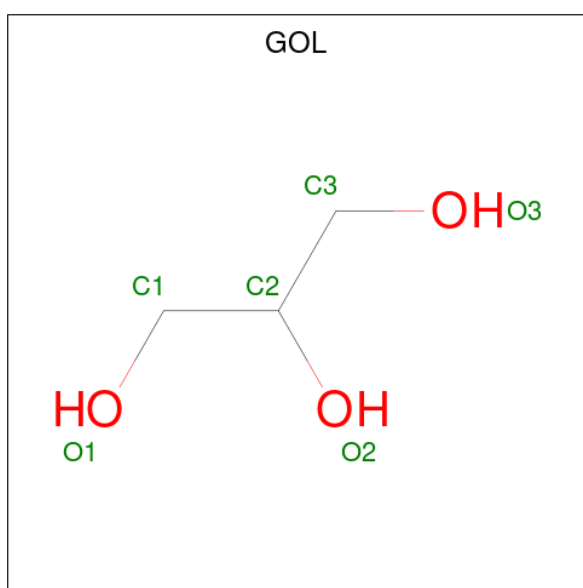
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	212	1573	985	262	321	5	0	0	0

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	A	3	38	22	2	14	0	0	0
4	B	3	38	22	2	14	0	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	H	1	Total	C	N	O	0	0
			8	4	1	3		
6	L	1	Total	C	N	O	0	0
			8	4	1	3		

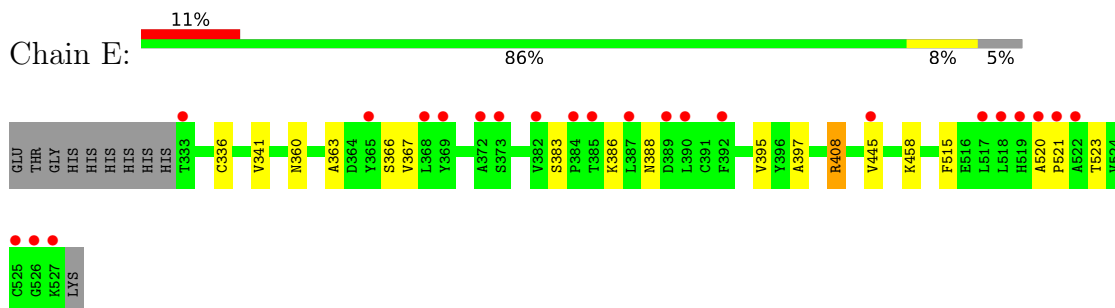
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	E	36	Total	O	0	0
			36	36		
7	H	38	Total	O	0	0
			38	38		
7	L	26	Total	O	0	0
			26	26		

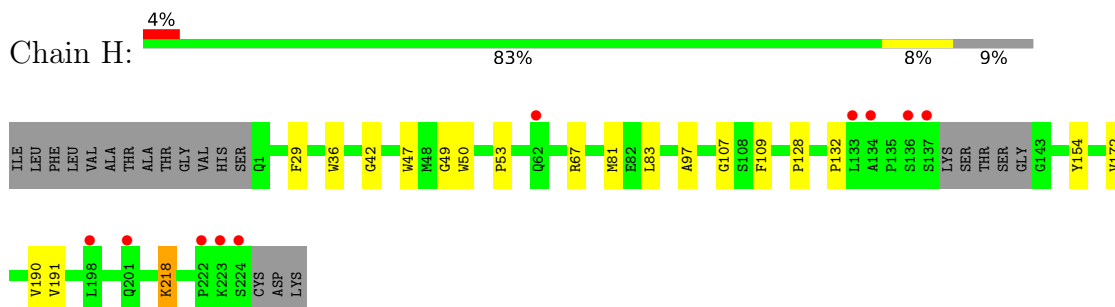
3 Residue-property plots

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.

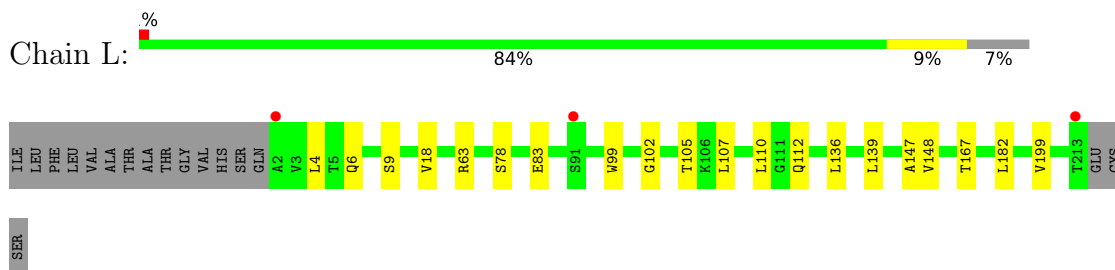
- Molecule 1: Spike glycoprotein



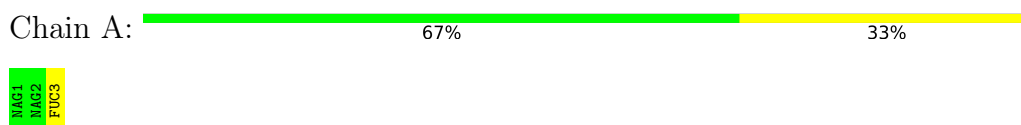
- Molecule 2: COVOX-316 heavy chain



- Molecule 3: COVOX-316 light chain



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:  67% 33%

 MAG1
MAG2
FUC3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	104.02Å 150.86Å 46.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.27 – 2.30 45.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	85.5 (45.27-2.30) 85.5 (45.27-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.18.1_3865	Depositor
R, R_{free}	0.213 , 0.230 0.216 , 0.232	Depositor DCC
R_{free} test set	1392 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	50.8	Xtrriage
Anisotropy	0.526	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 29.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4967	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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: FUC, NAG, GOL, TRS

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	E	0.13	0/1584	0.29	0/2156
2	H	0.13	0/1692	0.31	0/2302
3	L	0.11	0/1615	0.30	0/2207
All	All	0.12	0/4891	0.30	0/6665

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	E	1541	0	1454	10	0
2	H	1649	0	1607	13	0
3	L	1573	0	1512	12	0
4	A	38	0	34	0	0
4	B	38	0	34	0	0
5	E	6	0	8	0	0
5	H	6	0	8	0	0
6	H	8	0	12	0	0
6	L	8	0	12	0	0
7	E	36	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	H	38	0	0	1	0
7	L	26	0	0	1	0
All	All	4967	0	4681	32	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 3.

All (32) 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:9:SER:HB2	3:L:147:ALA:HB3	1.67	0.75
1:E:383:SER:HB3	1:E:386:LYS:HG2	1.76	0.67
2:H:190:VAL:HG21	3:L:139:LEU:HD13	1.81	0.62
1:E:366:SER:HB2	1:E:388:ASN:HD22	1.65	0.61
2:H:128:PRO:HB3	2:H:154:TYR:HB3	1.84	0.60
3:L:136:LEU:HD12	3:L:182:LEU:HD23	1.83	0.60
2:H:172:VAL:HG22	2:H:191:VAL:HG22	1.85	0.59
3:L:18:VAL:HG11	3:L:107:LEU:HD11	1.89	0.54
2:H:132:PRO:HD3	2:H:218:LYS:HD3	1.91	0.52
1:E:408:ARG:N	7:E:801:HOH:O	2.24	0.51
3:L:4:LEU:HB2	3:L:102:GLY:HA2	1.94	0.49
2:H:42:GLY:HA3	3:L:167:THR:HG21	1.95	0.48
1:E:366:SER:HB2	1:E:388:ASN:ND2	2.30	0.46
1:E:360:ASN:HA	1:E:523:THR:HB	1.98	0.46
1:E:341:VAL:HG11	1:E:397:ALA:HB1	1.96	0.46
2:H:107:GLY:HA3	3:L:99:TRP:NE1	2.30	0.46
1:E:336:CYS:HB2	1:E:363:ALA:HB2	1.98	0.45
1:E:458:LYS:HD3	1:E:458:LYS:HA	1.84	0.45
2:H:36:TRP:CE2	2:H:81:MET:HB2	2.51	0.45
2:H:47:TRP:HZ2	2:H:50:TRP:HD1	1.65	0.44
1:E:395:VAL:HG22	1:E:515:PHE:HD1	1.81	0.44
1:E:520:ALA:HB1	1:E:521:PRO:HD2	2.00	0.44
3:L:83:GLU:H	3:L:83:GLU:CD	2.25	0.44
3:L:112:GLN:NE2	7:L:403:HOH:O	2.33	0.43
2:H:29:PHE:CE2	2:H:53:PRO:HB3	2.54	0.42
2:H:81:MET:HE3	2:H:81:MET:HB3	1.93	0.42
3:L:6:GLN:HG2	3:L:105:THR:OG1	2.19	0.42
3:L:148:VAL:HG21	3:L:199:VAL:HG13	2.02	0.42
3:L:63:ARG:HB3	3:L:78:SER:O	2.20	0.41
2:H:67:ARG:NH2	7:H:609:HOH:O	2.53	0.41
2:H:47:TRP:CH2	2:H:49:GLY:HA2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:97:ALA:HB1	2:H:109:PHE:HB3	2.03	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	E	193/205 (94%)	179 (93%)	14 (7%)	0	100	100
2	H	216/240 (90%)	207 (96%)	9 (4%)	0	100	100
3	L	210/229 (92%)	203 (97%)	7 (3%)	0	100	100
All	All	619/674 (92%)	589 (95%)	30 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	E	167/177 (94%)	164 (98%)	3 (2%)	51	70
2	H	185/202 (92%)	183 (99%)	2 (1%)	65	81
3	L	176/190 (93%)	175 (99%)	1 (1%)	78	89
All	All	528/569 (93%)	522 (99%)	6 (1%)	65	81

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	367	VAL
1	E	408	ARG
1	E	445	VAL
2	H	83	LEU
2	H	218	LYS
3	L	110	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	394	ASN
1	E	450	ASN
1	E	493	GLN
2	H	180	GLN
3	L	174	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](#)

6 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	$\# Z > 2$
4	NAG	A	1	1,4	14,14,15	0.43	0	17,19,21	0.50	0
4	NAG	A	2	4	14,14,15	0.34	0	17,19,21	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	FUC	A	3	4	10,10,11	0.79	0	14,14,16	0.98	1 (7%)
4	NAG	B	1	4,2	14,14,15	0.38	0	17,19,21	0.52	0
4	NAG	B	2	4	14,14,15	0.17	0	17,19,21	0.49	0
4	FUC	B	3	4	10,10,11	0.92	1 (10%)	14,14,16	0.95	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	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	A	2	4	-	4/6/23/26	0/1/1/1
4	FUC	A	3	4	-	-	0/1/1/1
4	NAG	B	1	4,2	-	2/6/23/26	0/1/1/1
4	NAG	B	2	4	-	3/6/23/26	0/1/1/1
4	FUC	B	3	4	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	3	FUC	C1-C2	2.30	1.57	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	3	FUC	O5-C5-C4	2.09	113.31	109.55

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1	NAG	O5-C5-C6-O6
4	B	2	NAG	O5-C5-C6-O6
4	A	1	NAG	C4-C5-C6-O6
4	B	2	NAG	C4-C5-C6-O6
4	A	2	NAG	C4-C5-C6-O6
4	A	2	NAG	O5-C5-C6-O6
4	B	1	NAG	C4-C5-C6-O6
4	B	1	NAG	O5-C5-C6-O6

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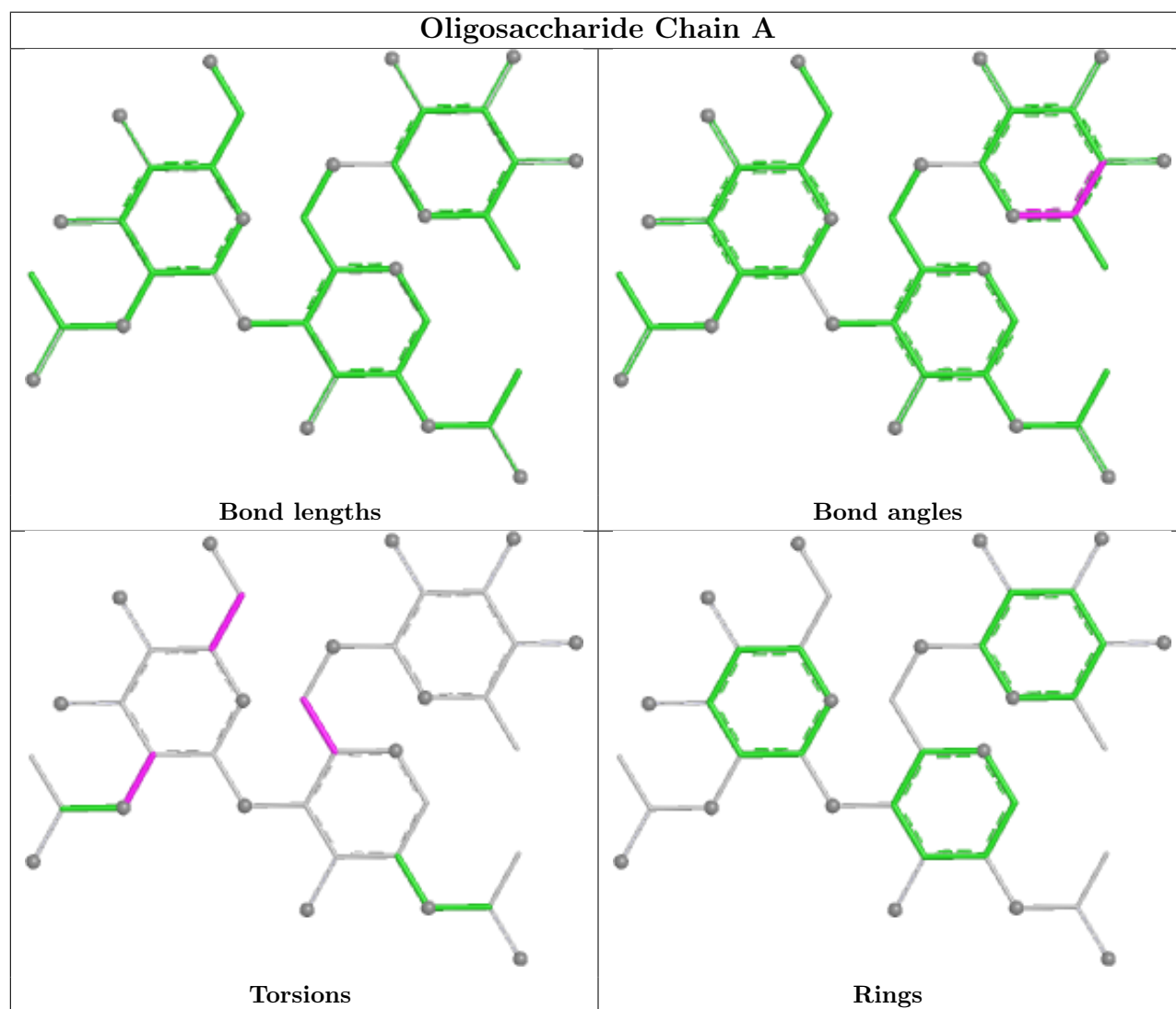
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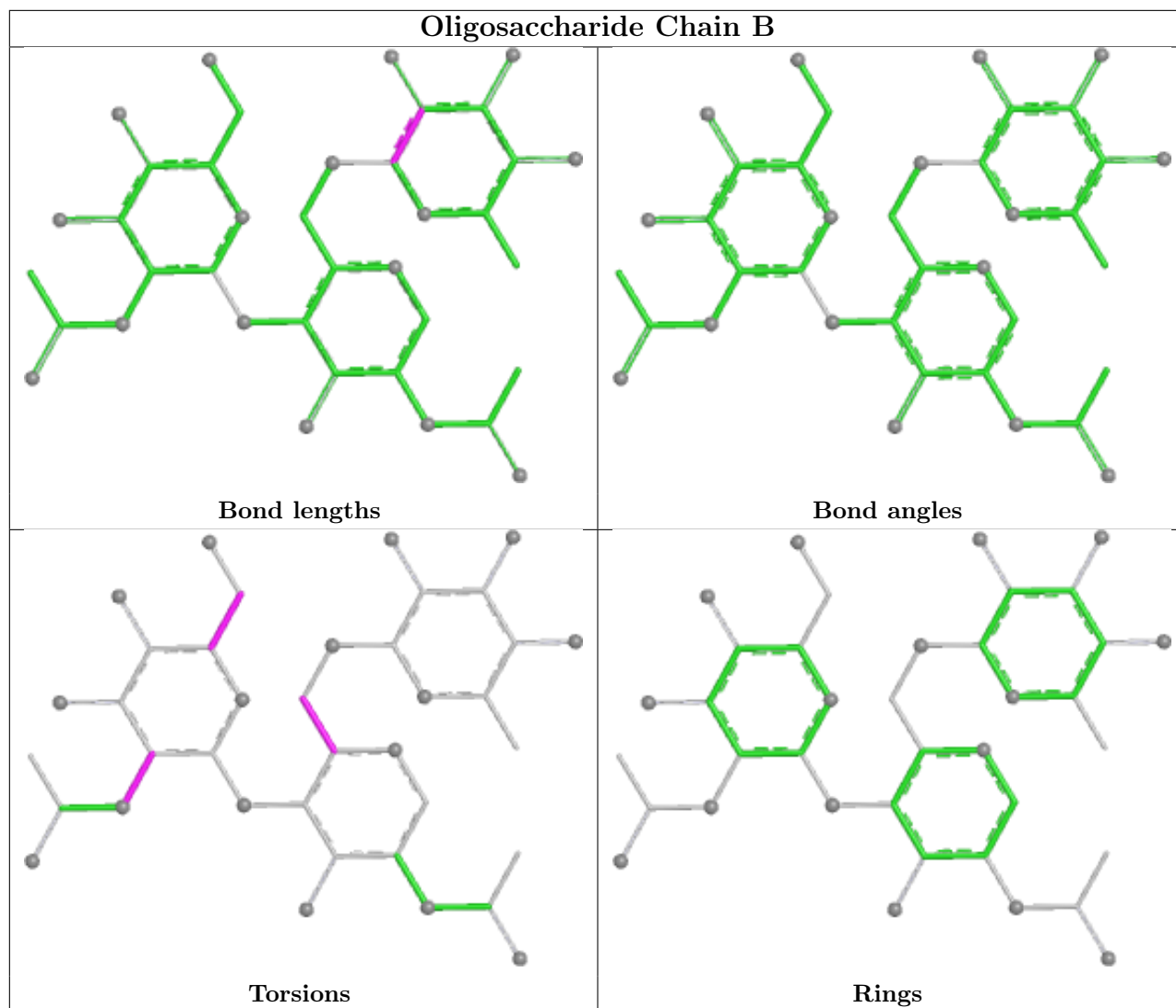
Mol	Chain	Res	Type	Atoms
4	A	2	NAG	C1-C2-N2-C7
4	A	2	NAG	C3-C2-N2-C7
4	B	2	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

4 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	$\# Z > 2$
5	GOL	H	501	-	5,5,5	1.01	0	5,5,5	0.88	0
5	GOL	E	701	-	5,5,5	0.87	0	5,5,5	1.11	0
6	TRS	L	301	-	7,7,7	0.32	0	9,9,9	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	TRS	H	502	-	7,7,7	0.30	0	9,9,9	0.21	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	H	501	-	-	4/4/4/4	-
5	GOL	E	701	-	-	0/4/4/4	-
6	TRS	L	301	-	-	2/9/9/9	-
6	TRS	H	502	-	-	6/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	H	501	GOL	C1-C2-C3-O3
5	H	501	GOL	O1-C1-C2-O2
5	H	501	GOL	O2-C2-C3-O3
5	H	501	GOL	O1-C1-C2-C3
6	H	502	TRS	C2-C-C1-O1
6	H	502	TRS	C2-C-C3-O3
6	H	502	TRS	N-C-C1-O1
6	H	502	TRS	N-C-C3-O3
6	H	502	TRS	C3-C-C1-O1
6	H	502	TRS	C1-C-C3-O3
6	L	301	TRS	C1-C-C3-O3
6	L	301	TRS	N-C-C3-O3

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

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	E	195/205 (95%)	0.75	23 (11%) 9 10	41, 57, 118, 153	0
2	H	219/240 (91%)	0.34	10 (4%) 37 39	34, 50, 77, 106	1 (0%)
3	L	212/229 (92%)	0.41	3 (1%) 73 75	44, 60, 78, 88	0
All	All	626/674 (92%)	0.49	36 (5%) 29 31	34, 55, 92, 153	1 (0%)

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	390	LEU	4.1
1	E	445	VAL	3.6
1	E	384	PRO	3.6
1	E	527	LYS	3.5
1	E	333	THR	3.5
1	E	518	LEU	3.3
1	E	521	PRO	3.3
3	L	213	THR	3.3
1	E	392	PHE	3.3
1	E	365	TYR	3.1
3	L	91	SER	3.0
1	E	525	CYS	3.0
1	E	387	LEU	2.9
1	E	517	LEU	2.8
1	E	519	HIS	2.7
1	E	385	THR	2.7
2	H	224	SER	2.6
1	E	520	ALA	2.6
2	H	222	PRO	2.5
1	E	368	LEU	2.4
2	H	198	LEU	2.4
3	L	2	ALA	2.3
1	E	372	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
2	H	136	SER	2.3
2	H	133	LEU	2.2
1	E	389	ASP	2.2
2	H	201	GLN	2.2
2	H	223	LYS	2.2
1	E	369	TYR	2.2
1	E	382	VAL	2.2
2	H	137	SER	2.2
1	E	373	SER	2.1
2	H	62	GLN	2.1
1	E	526	GLY	2.1
1	E	522	ALA	2.0
2	H	134	ALA	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](#)

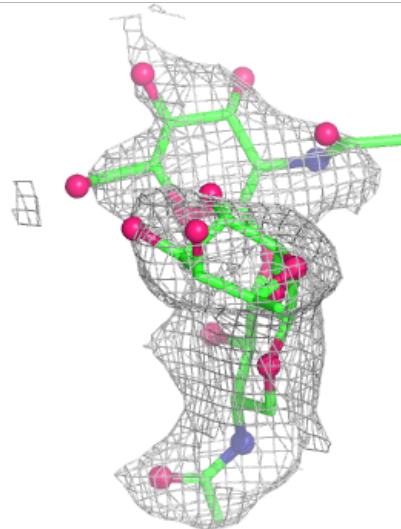
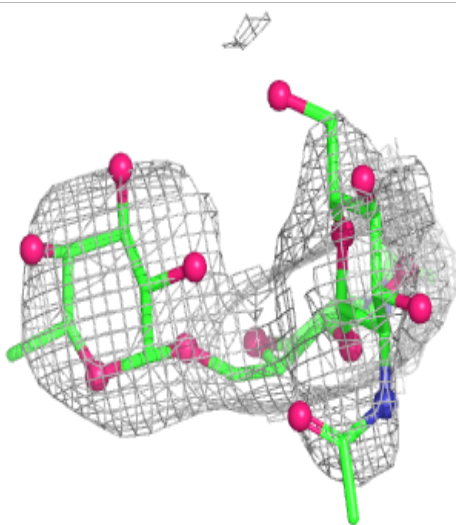
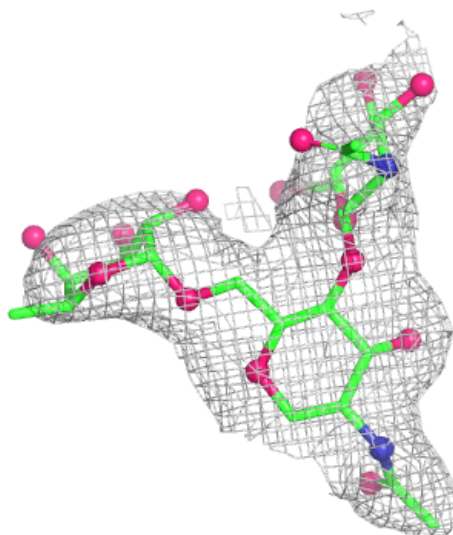
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

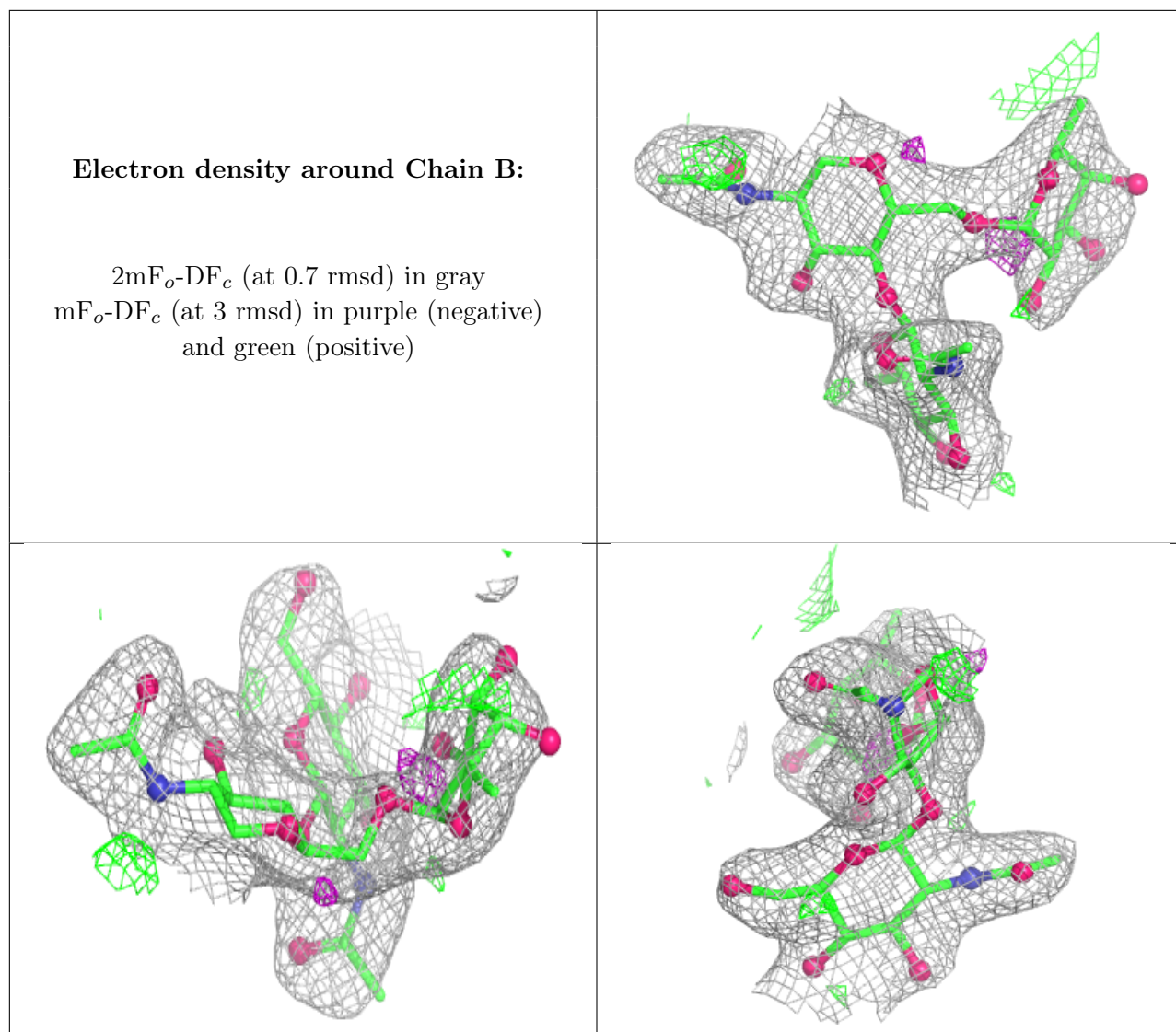
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	1	14/15	-	-	61,67,77,78	0
4	NAG	A	2	14/15	-	-	87,96,102,103	0
4	FUC	A	3	10/11	-	-	77,81,88,90	0
4	NAG	B	1	14/15	-	-	35,49,59,62	0
4	NAG	B	2	14/15	-	-	53,61,69,71	0
4	FUC	B	3	10/11	-	-	58,65,70,72	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain A:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





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(Å ²)	Q<0.9
5	GOL	H	501	6/6	0.56	0.21	69,76,77,83	0
6	TRS	H	502	8/8	0.71	0.16	50,58,67,68	0
6	TRS	L	301	8/8	0.73	0.17	63,70,72,76	0
5	GOL	E	701	6/6	0.85	0.12	64,67,68,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.