



# Full wwPDB X-ray Structure Validation Report ⓘ

May 5, 2022 – 04:28 pm BST

PDB ID : 7Z0Y  
Title : THSC20.HVTR04 Fab bound to SARS-CoV-2 Receptor Binding Domain  
Authors : Wibmer, C.K.  
Deposited on : 2022-02-23  
Resolution : 2.95 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.28.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.28.1

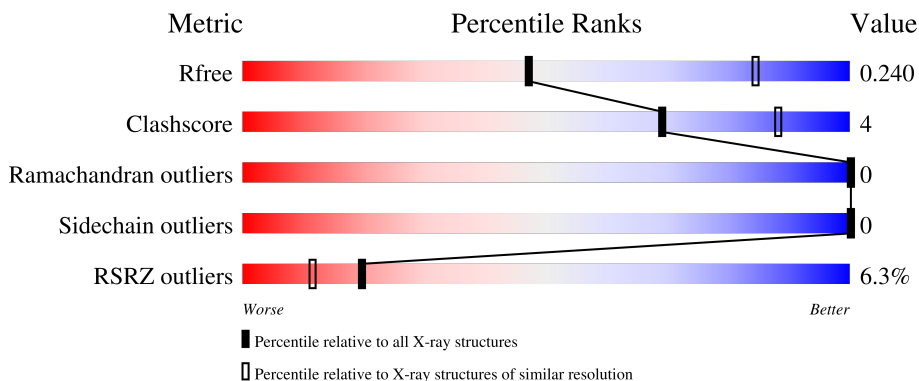
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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  $\geq 3$ , 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	H	233	 2% 85% 9% 6%
2	L	214	 7% 93% 6%
3	R	205	 10% 93% 5%
4	A	3	 33% 33% 33%

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
1	PCA	H	1	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9593 atoms, of which 4662 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 THSC20.HVTR04 Fab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	H	219	3260	1046	1613	274	320	7	0	0	0

- Molecule 2 is a protein called THSC20.HVTR04 Fab light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	L	212	3080	983	1509	261	321	6	0	0	0

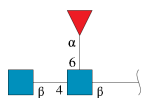
- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	R	202	3117	1027	1517	265	300	8	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

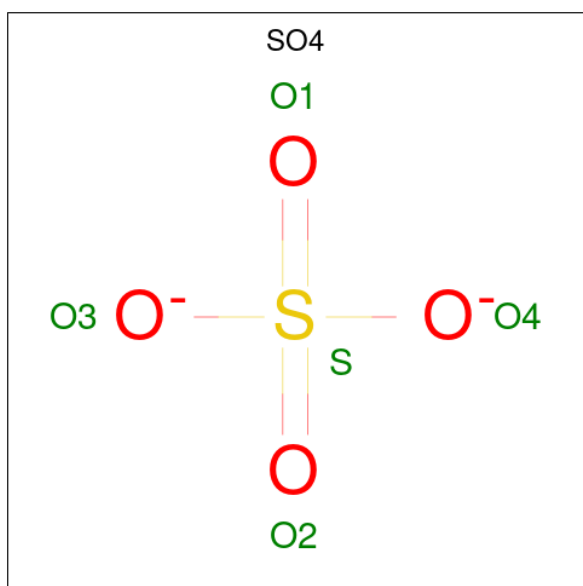
Chain	Residue	Modelled	Actual	Comment	Reference
R	330	GLN	-	expression tag	UNP P0DTC2
R	528	GLY	-	expression tag	UNP P0DTC2
R	529	LEU	-	expression tag	UNP P0DTC2
R	530	GLU	-	expression tag	UNP P0DTC2
R	531	VAL	-	expression tag	UNP P0DTC2
R	532	LEU	-	expression tag	UNP P0DTC2
R	533	PHE	-	expression tag	UNP P0DTC2
R	534	GLN	-	expression tag	UNP P0DTC2

- 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	H	N				O
4	A	3	61	22	23	2	14	0	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

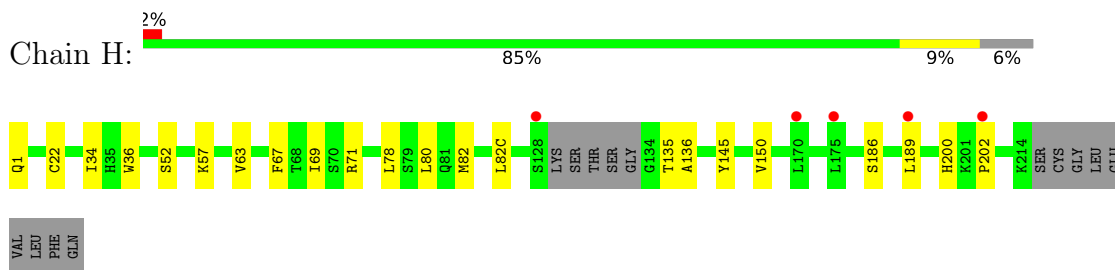
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	15	Total	O	0	0
			15	15		
6	L	19	Total	O	0	0
			19	19		
6	R	31	Total	O	0	0
			31	31		

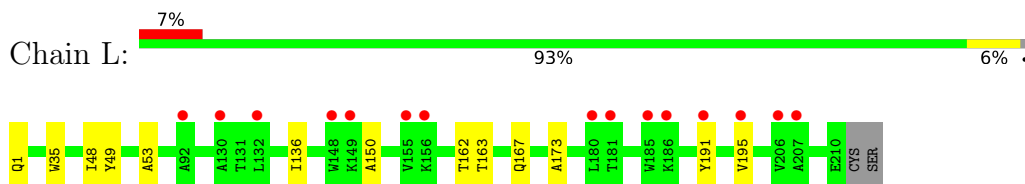
### 3 Residue-property plots [i](#)

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.

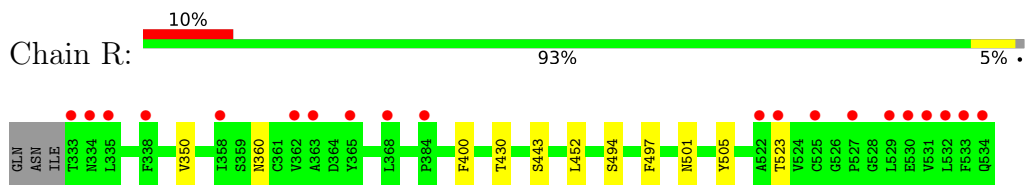
- Molecule 1: THSC20.HVTR04 Fab heavy chain



- Molecule 2: THSC20.HVTR04 Fab light chain



- Molecule 3: Spike protein S1



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.16Å 126.16Å 167.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.95 59.03 – 2.94	Depositor EDS
% Data completeness (in resolution range)	78.5 (50.00-2.95) 78.5 (59.03-2.94)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.219 , 0.241 0.226 , 0.240	Depositor DCC
$R_{free}$ test set	1141 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.1	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	9593	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SO4, NAG, FUC, PCA

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	H	0.35	0/1681	0.57	0/2295
2	L	0.31	0/1604	0.52	0/2193
3	R	0.31	0/1645	0.53	0/2238
All	All	0.33	0/4930	0.54	0/6726

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	H	1647	1613	1613	22	0
2	L	1571	1509	1510	6	0
3	R	1600	1517	1516	6	0
4	A	38	23	34	1	0
5	L	5	0	0	0	0
5	R	5	0	0	0	0
6	H	15	0	0	0	0
6	L	19	0	0	0	0
6	R	31	0	0	0	0
All	All	4931	4662	4673	35	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 4.

All (35) 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)
1:H:145:TYR:CE2	1:H:150:VAL:HG23	2.12	0.85
2:L:136:ILE:HG12	2:L:195:VAL:HG11	1.66	0.78
1:H:145:TYR:CE2	1:H:150:VAL:CG2	2.80	0.65
1:H:34:ILE:HG21	1:H:78:LEU:HD23	1.81	0.62
3:R:452:LEU:HD23	3:R:494:SER:HA	1.84	0.60
1:H:145:TYR:CD2	1:H:150:VAL:CG2	2.86	0.58
1:H:145:TYR:CD2	1:H:150:VAL:HG23	2.40	0.57
3:R:501:ASN:HB3	3:R:505:TYR:HB2	1.86	0.56
1:H:57:LYS:HE2	1:H:69:ILE:O	2.08	0.54
2:L:167:GLN:OE1	2:L:173:ALA:HB2	2.07	0.53
1:H:186:SER:O	1:H:189:LEU:HD23	2.09	0.53
2:L:150:ALA:HB2	2:L:191:TYR:HE1	1.74	0.53
4:A:1:NAG:O7	4:A:1:NAG:H3	2.09	0.52
1:H:78:LEU:HD12	1:H:78:LEU:C	2.33	0.50
3:R:443:SER:HB3	3:R:497:PHE:HB3	1.93	0.49
3:R:360:ASN:H	3:R:523:THR:HB	1.78	0.48
1:H:52:SER:O	1:H:71:ARG:NH1	2.45	0.48
1:H:22:CYS:HB3	1:H:78:LEU:HD11	1.95	0.48
1:H:34:ILE:HG21	1:H:78:LEU:CD2	2.44	0.47
1:H:63:VAL:HG13	1:H:67:PHE:CG	2.49	0.47
1:H:82:MET:HE3	1:H:82(C):LEU:HD11	1.95	0.47
3:R:430:THR:HG23	3:R:430:THR:O	2.15	0.47
1:H:200:HIS:CD2	1:H:202:PRO:HD2	2.51	0.45
1:H:34:ILE:HD13	1:H:78:LEU:HD23	2.00	0.44
1:H:34:ILE:HD13	1:H:78:LEU:CD2	2.47	0.44
1:H:22:CYS:HB3	1:H:78:LEU:CD1	2.48	0.43
2:L:49:TYR:O	2:L:53:ALA:HB3	2.19	0.43
2:L:162:THR:HG22	2:L:163:THR:O	2.18	0.43
1:H:145:TYR:CD2	1:H:150:VAL:HG21	2.54	0.43
2:L:35:TRP:HB2	2:L:48:ILE:HB	2.00	0.42
1:H:63:VAL:CG1	1:H:67:PHE:HB2	2.50	0.41
3:R:350:VAL:HG23	3:R:400:PHE:CD1	2.55	0.41
1:H:135:THR:HG22	1:H:136:ALA:N	2.35	0.41
1:H:34:ILE:CG2	1:H:78:LEU:CD2	2.99	0.40
1:H:36:TRP:NE1	1:H:80:LEU:HB2	2.36	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	H	215/233 (92%)	210 (98%)	5 (2%)	0	100	100
2	L	210/214 (98%)	198 (94%)	12 (6%)	0	100	100
3	R	200/205 (98%)	187 (94%)	13 (6%)	0	100	100
All	All	625/652 (96%)	595 (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	H	184/196 (94%)	184 (100%)	0	100	100
2	L	175/178 (98%)	175 (100%)	0	100	100
3	R	174/177 (98%)	174 (100%)	0	100	100
All	All	533/551 (97%)	533 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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
1	PCA	H	1	1	7,8,9	0.51	0	9,10,12	0.83	1 (11%)
2	PCA	L	1	2	7,8,9	2.27	2 (28%)	9,10,12	1.94	4 (44%)

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
1	PCA	H	1	1	-	0/0/11/13	0/1/1/1
2	PCA	L	1	2	-	0/0/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	1	PCA	CD-N	4.69	1.47	1.34
2	L	1	PCA	CA-N	3.59	1.50	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	1	PCA	OE-CD-CG	-2.91	121.68	126.76
2	L	1	PCA	CA-N-CD	-2.87	103.76	113.58
2	L	1	PCA	CG-CD-N	2.42	114.67	108.39
1	H	1	PCA	O-C-CA	-2.40	118.50	124.78
2	L	1	PCA	CB-CA-N	2.24	109.72	103.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates

3 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	4,3	14,14,15	0.16	0	17,19,21	0.78	1 (5%)
4	NAG	A	2	4	14,14,15	0.20	0	17,19,21	0.52	0
4	FUC	A	3	4	10,10,11	0.85	0	14,14,16	1.00	1 (7%)

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	4,3	-	3/6/23/26	0/1/1/1
4	NAG	A	2	4	-	0/6/23/26	0/1/1/1
4	FUC	A	3	4	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1	NAG	C1-O5-C5	2.34	115.36	112.19
4	A	3	FUC	O5-C5-C4	2.14	113.36	109.52

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1	NAG	C3-C2-N2-C7

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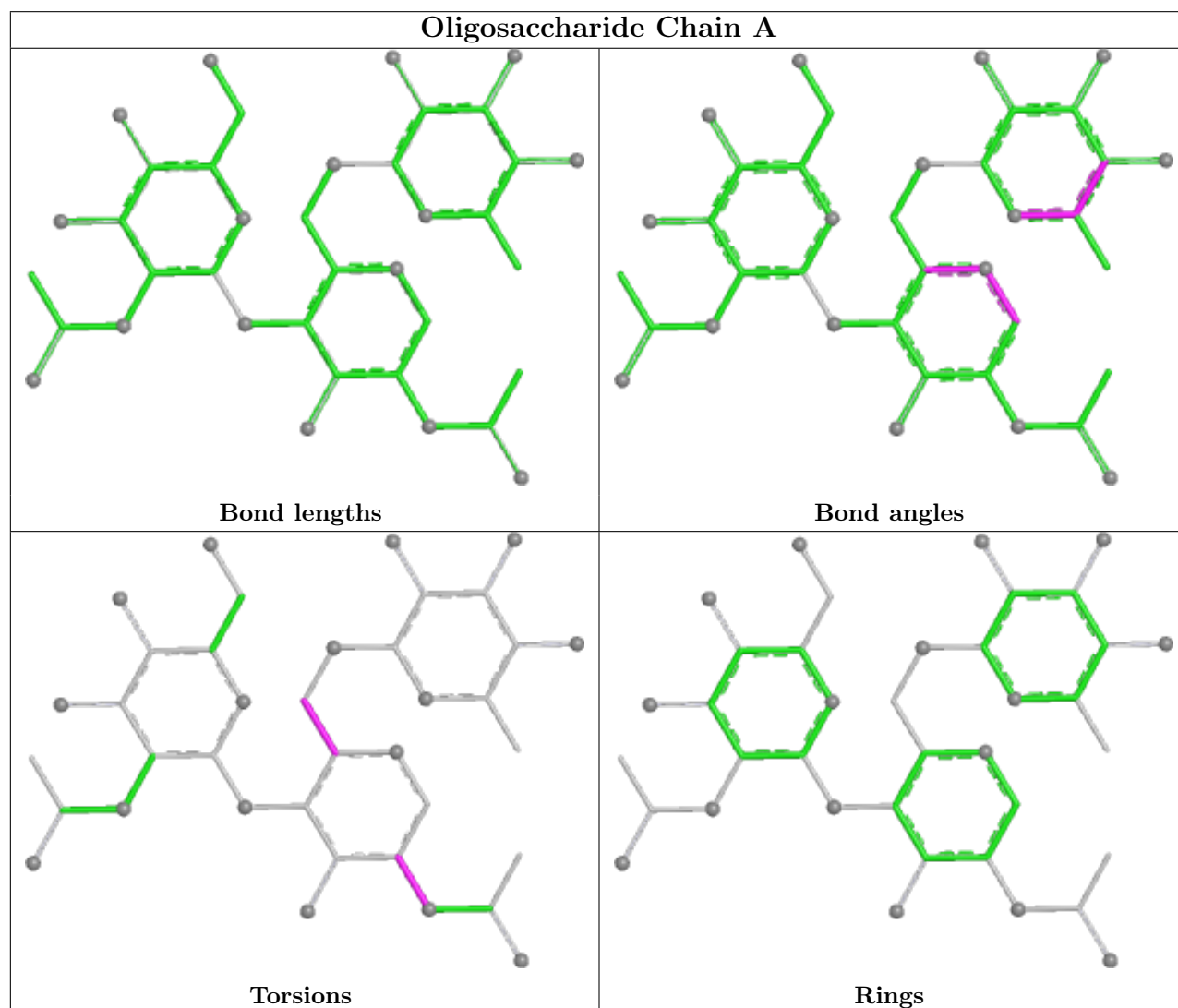
Mol	Chain	Res	Type	Atoms
4	A	1	NAG	C4-C5-C6-O6
4	A	1	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1	NAG	1	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	$\# Z  > 2$
5	SO4	R	601	-	4,4,4	0.44	0	6,6,6	0.04	0
5	SO4	L	301	-	4,4,4	0.13	0	6,6,6	0.09	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	H	218/233 (93%)	0.54	5 (2%) 60 43	31, 61, 97, 115	0
2	L	211/214 (98%)	0.64	15 (7%) 16 9	34, 60, 144, 296	0
3	R	202/205 (98%)	0.74	20 (9%) 7 4	32, 50, 115, 158	0
All	All	631/652 (96%)	0.64	40 (6%) 20 11	31, 59, 126, 296	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	149	LYS	5.2
3	R	334	ASN	5.1
3	R	534	GLN	4.7
3	R	529	LEU	4.6
2	L	155	VAL	4.6
3	R	532	LEU	4.6
3	R	358	ILE	4.2
2	L	186	LYS	4.1
2	L	185	TRP	4.0
3	R	335	LEU	3.9
3	R	522	ALA	3.5
2	L	148	TRP	3.4
3	R	525	CYS	3.4
1	H	128	SER	3.2
2	L	180	LEU	3.0
3	R	523	THR	3.0
1	H	175	LEU	2.8
3	R	333	THR	2.8
3	R	365	TYR	2.6
2	L	191	TYR	2.5
3	R	533	PHE	2.5
3	R	384	PRO	2.4
2	L	206	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
3	R	527	PRO	2.4
2	L	130	ALA	2.3
2	L	156	LYS	2.3
2	L	132	LEU	2.3
3	R	363	ALA	2.2
3	R	531	VAL	2.2
3	R	368	LEU	2.1
2	L	207	ALA	2.1
1	H	170	LEU	2.1
2	L	181	THR	2.1
1	H	202	PRO	2.1
2	L	195	VAL	2.0
3	R	530	GLU	2.0
3	R	362	VAL	2.0
2	L	92	ALA	2.0
3	R	338	PHE	2.0
1	H	189	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	PCA	H	1	8/9	0.66	0.44	72,118,142,142	0
2	PCA	L	1	8/9	0.90	0.21	80,88,100,107	0

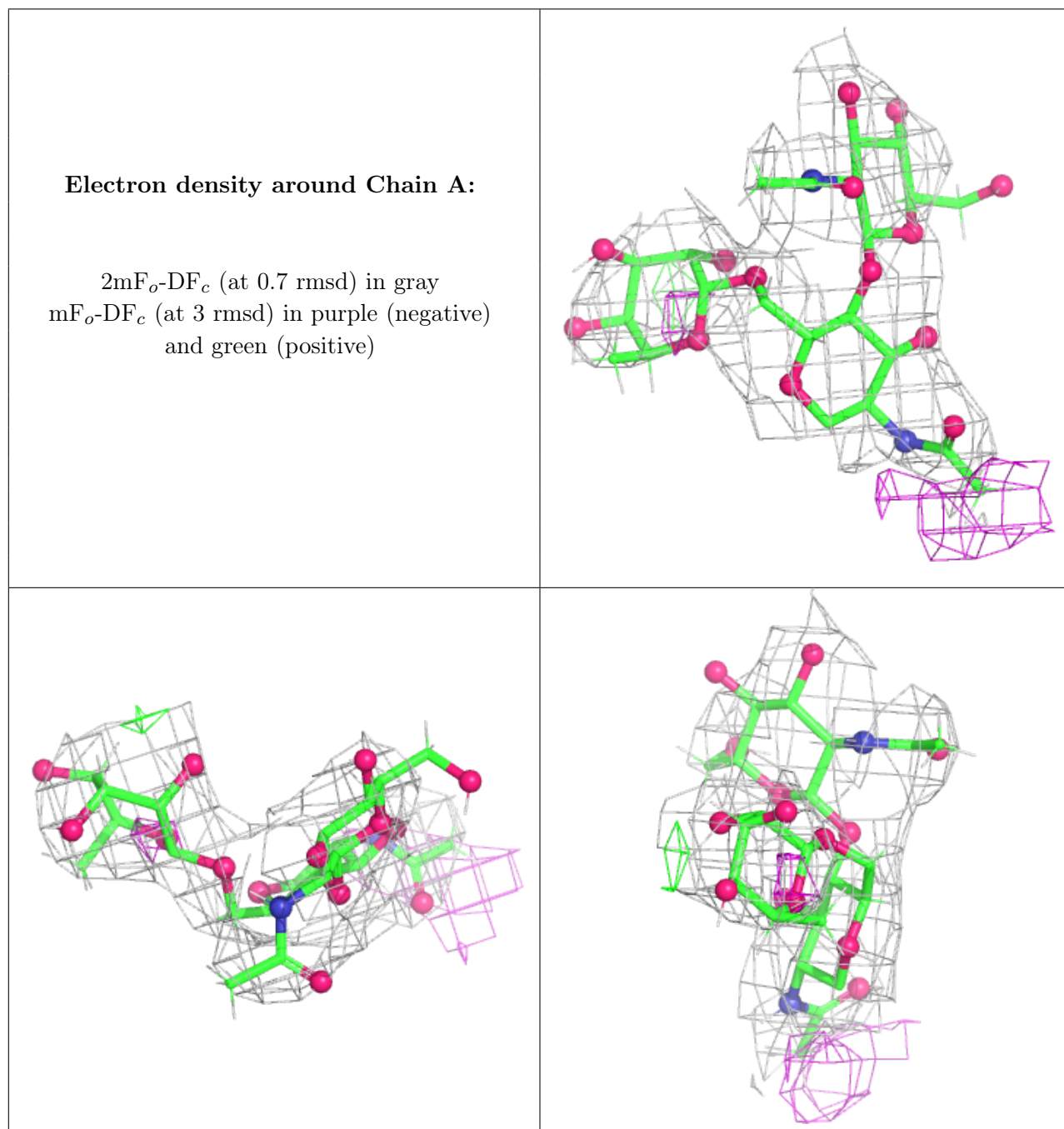
## 6.3 Carbohydrates [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	NAG	A	2	14/15	0.80	0.37	95,115,143,153	0
4	NAG	A	1	14/15	0.89	0.24	77,93,113,123	0
4	FUC	A	3	10/11	0.89	0.41	102,112,134,136	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.



## 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<sup>th</sup> 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
5	SO4	R	601	5/5	0.88	0.30	73,83,94,100	0
5	SO4	L	301	5/5	0.95	0.14	67,70,76,80	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.