



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:14 AM UTC

PDB ID : 7MZM / pdb_00007mzm
Title : SARS-CoV-2 receptor binding domain bound to Fab PDI 215
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Deposited on : 2021-05-24
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)
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

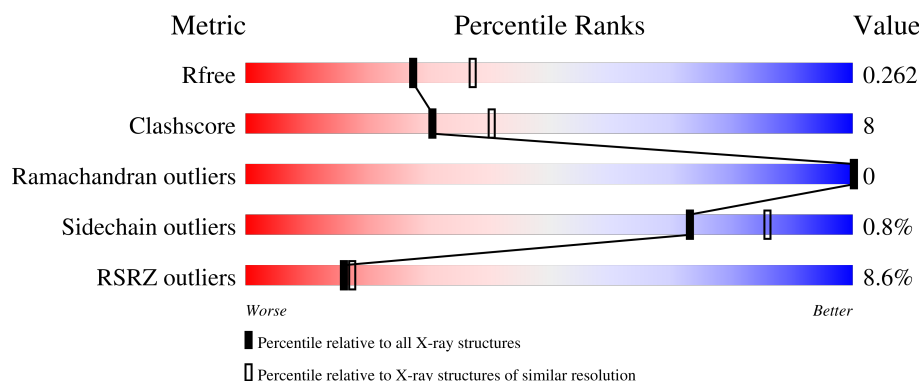
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	H	239	5% 85% 10% .
2	L	216	5% 81% 19%
3	A	205	16% 78% 16% 6%
4	B	2	100%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4996 atoms, of which 16 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 PDI 215 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	230	Total	C	N	O	S	0	3	0
			1738	1098	285	342	13			

- Molecule 2 is a protein called PDI 215 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	215	Total	C	N	O	S	0	1	0
			1616	1014	269	329	4			

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	192	Total	C	N	O	S	0	0	0
			1487	950	250	279	8			

There are 8 discrepancies between the modelled and reference sequences:

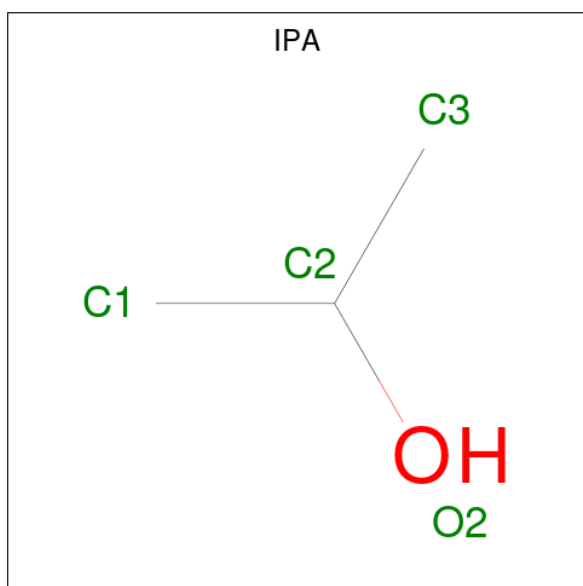
Chain	Residue	Modelled	Actual	Comment	Reference
A	528	GLY	-	expression tag	UNP P0DTC2
A	529	SER	-	expression tag	UNP P0DTC2
A	530	HIS	-	expression tag	UNP P0DTC2
A	531	HIS	-	expression tag	UNP P0DTC2
A	532	HIS	-	expression tag	UNP P0DTC2
A	533	HIS	-	expression tag	UNP P0DTC2
A	534	HIS	-	expression tag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

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 5 is ISOPROPYL ALCOHOL (CCD ID: IPA) (formula: C₃H₈O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			12	3	8	1		
5	A	1	Total	C	H	O	0	0
			12	3	8	1		

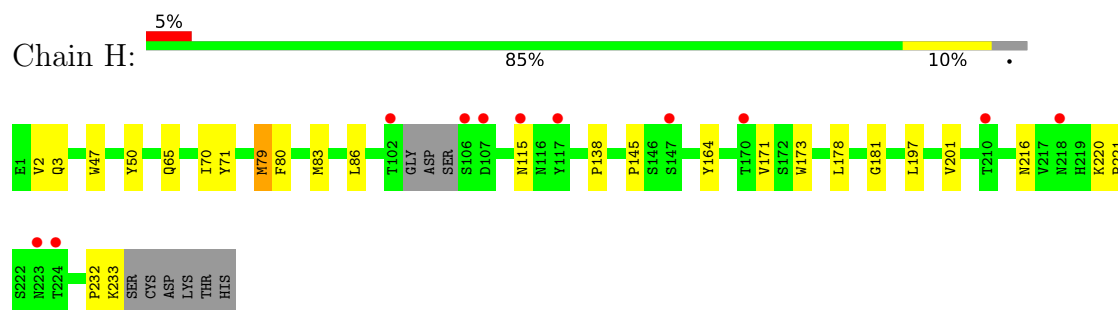
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	36	Total	O	0	0
			36	36		
6	L	41	Total	O	0	0
			41	41		
6	A	30	Total	O	0	0
			30	30		

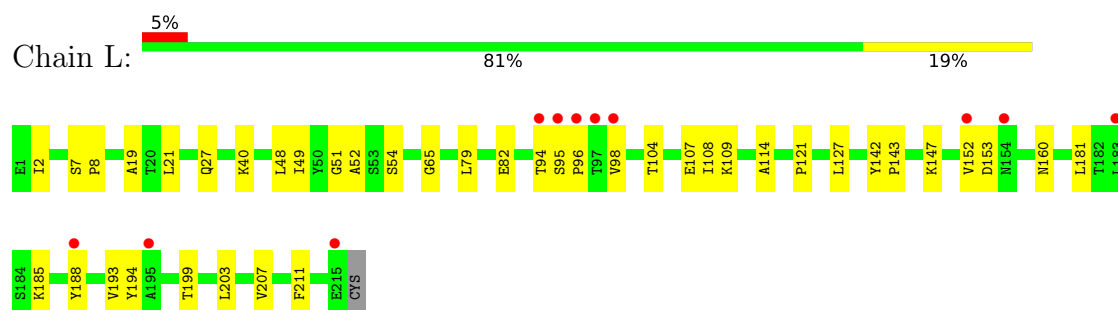
3 Residue-property plots [i](#)

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.

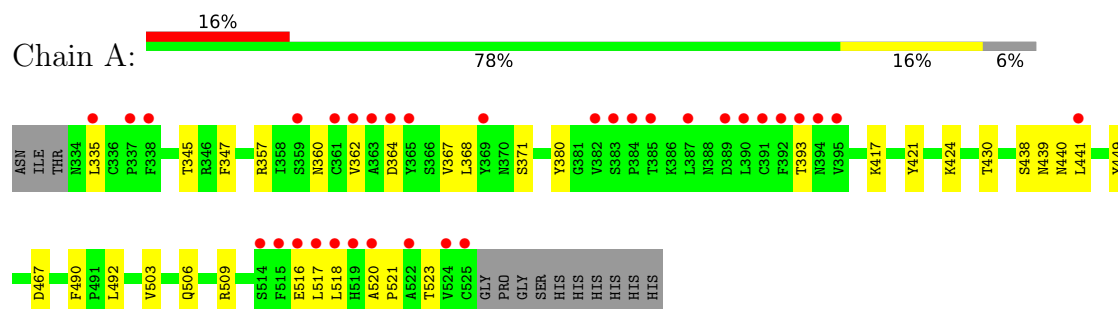
- Molecule 1: PDI 215 heavy chain



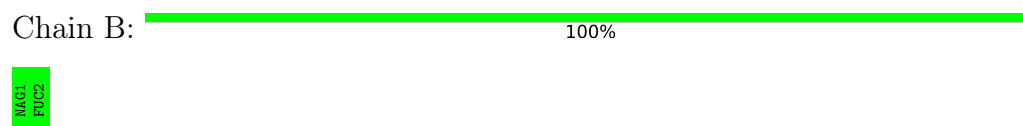
- Molecule 2: PDI 215 light chain



- Molecule 3: Spike protein S1



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



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	95.80Å 120.33Å 128.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.90 – 2.30 47.90 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.90-2.30) 100.0 (47.90-2.30)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.29Å)	Xtriage
Refinement program	PHENIX dev_3965	Depositor
R, R_{free}	0.216 , 0.257 0.220 , 0.262	Depositor DCC
R_{free} test set	1998 reflections (6.00%)	wwPDB-VP
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 31.5	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	0.94	EDS
Total number of atoms	4996	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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: IPA, NAG, FUC

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	0.26	0/1785	0.48	0/2438
2	L	0.24	0/1654	0.44	0/2256
3	A	0.22	0/1528	0.45	0/2083
All	All	0.24	0/4967	0.46	0/6777

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	1738	0	1625	20	0
2	L	1616	0	1533	32	0
3	A	1487	0	1361	32	0
4	B	24	0	22	0	0
5	A	8	16	16	1	0
6	A	30	0	0	2	0
6	H	36	0	0	2	0
6	L	41	0	0	0	0
All	All	4980	16	4557	78	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 8.

All (78) 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:A:516:GLU:HG2	3:A:518:LEU:CD1	1.70	1.22
3:A:516:GLU:CG	3:A:518:LEU:HD11	1.79	1.12
3:A:516:GLU:HG2	3:A:518:LEU:HD11	1.04	1.03
2:L:203:LEU:HD13	2:L:207:VAL:HG23	1.65	0.79
3:A:424:LYS:HD3	6:A:706:HOH:O	1.83	0.78
1:H:173:TRP:HB3	1:H:178:LEU:HD23	1.73	0.70
2:L:2:ILE:HG12	2:L:27:GLN:HG2	1.73	0.69
3:A:364:ASP:OD2	3:A:367:VAL:HG23	1.93	0.67
6:H:308:HOH:O	3:A:345:THR:HG22	1.94	0.67
3:A:393:THR:HB	3:A:518:LEU:HD13	1.77	0.67
1:H:47:TRP:CG	2:L:98[B]:VAL:CG2	2.79	0.65
2:L:94:THR:O	2:L:94:THR:HG22	1.97	0.64
2:L:109:LYS:NZ	2:L:109:LYS:HB3	2.12	0.64
1:H:145:PRO:HG2	1:H:232:PRO:HA	1.79	0.63
2:L:8:PRO:O	2:L:104:THR:HG23	2.00	0.62
3:A:516:GLU:CD	3:A:518:LEU:HD11	2.25	0.60
2:L:147:LYS:HB3	2:L:199:THR:HB	1.85	0.59
3:A:335:LEU:HG	3:A:362:VAL:O	2.03	0.58
3:A:360:ASN:HA	3:A:523:THR:OG1	2.04	0.58
1:H:83:MET:HE2	1:H:86:LEU:HD21	1.86	0.56
6:H:308:HOH:O	3:A:345:THR:CG2	2.52	0.56
3:A:368:LEU:HA	3:A:371:SER:OG	2.06	0.55
2:L:109:LYS:HB3	2:L:109:LYS:HZ1	1.71	0.55
1:H:47:TRP:CB	2:L:98[B]:VAL:HG23	2.39	0.53
3:A:517:LEU:C	3:A:518:LEU:HD12	2.34	0.53
1:H:65:GLN:HG3	3:A:449:TYR:HD1	1.74	0.53
2:L:203:LEU:HD13	2:L:207:VAL:CG2	2.36	0.52
3:A:503:VAL:HA	3:A:506:GLN:NE2	2.25	0.52
3:A:380:TYR:O	3:A:430:THR:HA	2.09	0.52
2:L:127:LEU:O	2:L:185:LYS:HD2	2.10	0.51
1:H:171:VAL:HA	1:H:216:ASN:O	2.09	0.51
2:L:160:ASN:O	2:L:181:LEU:HD12	2.11	0.50
3:A:440:ASN:ND2	3:A:441:LEU:HG	2.27	0.50
1:H:197:LEU:C	1:H:197:LEU:HD12	2.37	0.50
1:H:70:ILE:HD11	1:H:79[A]:MET:HE1	1.94	0.49
2:L:95:SER:OG	2:L:96:PRO:HD2	2.13	0.48
2:L:40:LYS:NZ	2:L:82:GLU:O	2.44	0.48
1:H:47:TRP:CG	2:L:98[B]:VAL:HG21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:2:VAL:C	1:H:3:GLN:HG2	2.39	0.47
1:H:79[A]:MET:HE2	1:H:79[A]:MET:HB2	1.84	0.47
2:L:153:ASP:OD1	2:L:193:VAL:HG23	2.15	0.47
3:A:393:THR:CB	3:A:518:LEU:HD13	2.44	0.47
3:A:518:LEU:HD12	3:A:518:LEU:N	2.29	0.47
1:H:71:TYR:CE1	1:H:80:PHE:HB2	2.50	0.46
1:H:232:PRO:O	1:H:233:LYS:HB3	2.15	0.46
2:L:152:VAL:O	2:L:153:ASP:HB2	2.15	0.46
2:L:114:ALA:HB1	2:L:203:LEU:HD21	1.99	0.45
2:L:142:TYR:CD1	2:L:143:PRO:HA	2.52	0.45
2:L:49:ILE:HD13	2:L:65:GLY:N	2.32	0.45
2:L:114:ALA:HB1	2:L:203:LEU:CD2	2.47	0.44
3:A:520:ALA:HB1	3:A:521:PRO:HD2	1.99	0.44
1:H:50:TYR:C	1:H:50:TYR:CD1	2.95	0.44
2:L:188:TYR:HA	2:L:194:TYR:OH	2.18	0.44
2:L:142:TYR:CG	2:L:143:PRO:HA	2.53	0.43
3:A:417:LYS:HZ1	5:A:602:IPA:C3	2.31	0.43
1:H:138:PRO:HB3	1:H:164:TYR:HB3	1.99	0.43
1:H:65:GLN:OE1	3:A:449:TYR:HB2	2.18	0.43
3:A:467:ASP:HB3	6:A:708:HOH:O	2.18	0.43
1:H:220:LYS:N	1:H:221:PRO:HD2	2.34	0.43
2:L:121:PRO:HB3	2:L:211:PHE:CE1	2.54	0.43
2:L:48:LEU:C	2:L:49:ILE:HG13	2.44	0.43
2:L:19:ALA:HB2	2:L:79:LEU:HD11	2.00	0.42
2:L:51:GLY:O	2:L:52:ALA:HB3	2.19	0.42
1:H:65:GLN:HG3	3:A:449:TYR:CD1	2.55	0.42
3:A:417:LYS:HD3	3:A:417:LYS:HA	1.72	0.42
3:A:490:PHE:CE2	3:A:492:LEU:HB2	2.55	0.42
2:L:121:PRO:HB3	2:L:211:PHE:CZ	2.54	0.42
3:A:417:LYS:O	3:A:421:TYR:HB2	2.20	0.42
3:A:438:SER:HB3	3:A:509:ARG:HG3	2.02	0.42
2:L:7:SER:HA	2:L:8:PRO:C	2.46	0.41
3:A:347:PHE:CE2	3:A:509:ARG:HB3	2.56	0.41
2:L:21:LEU:HD12	2:L:21:LEU:N	2.35	0.41
3:A:357:ARG:HG3	3:A:357:ARG:HH11	1.86	0.41
3:A:357:ARG:HG3	3:A:357:ARG:NH1	2.36	0.40
2:L:49:ILE:HA	2:L:54:SER:O	2.21	0.40
2:L:109:LYS:HA	2:L:142:TYR:OH	2.22	0.40
1:H:181:GLY:O	1:H:201:VAL:HA	2.22	0.40
3:A:439:ASN:ND2	3:A:506:GLN:OE1	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	231/239 (97%)	225 (97%)	6 (3%)	0	100	100
2	L	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
3	A	190/205 (93%)	178 (94%)	12 (6%)	0	100	100
All	All	635/660 (96%)	608 (96%)	27 (4%)	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	H	189/202 (94%)	186 (98%)	3 (2%)	55	73
2	L	176/188 (94%)	174 (99%)	2 (1%)	65	81
3	A	154/177 (87%)	154 (100%)	0	100	100
All	All	519/567 (92%)	514 (99%)	5 (1%)	73	82

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	79[A]	MET
1	H	79[B]	MET
1	H	115	ASN
2	L	107	GLU
2	L	108	ILE

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

Mol	Chain	Res	Type
1	H	39	GLN
2	L	39	GLN
2	L	149	GLN

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 ⓘ

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	$\# Z > 2$
4	NAG	B	1	3,4	14,14,15	0.42	0	17,19,21	0.40	0
4	FUC	B	2	4	10,10,11	0.59	0	14,14,16	0.61	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	B	1	3,4	-	0/6/23/26	0/1/1/1
4	FUC	B	2	4	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

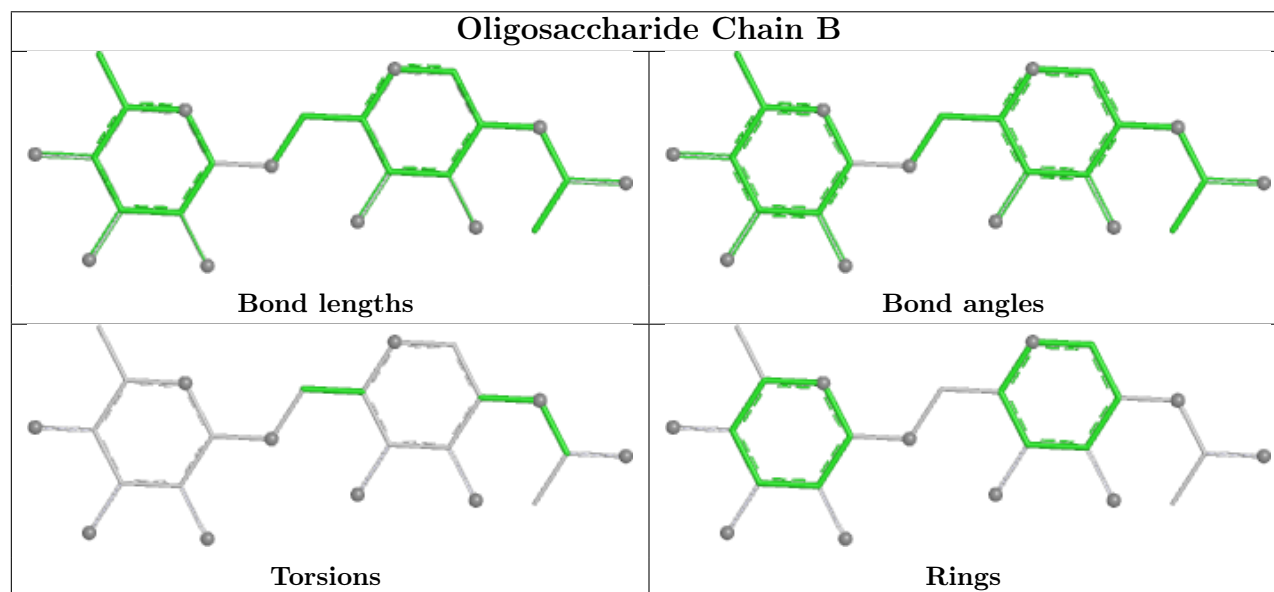
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	IPA	A	601	-	3,3,3	0.53	0	3,3,3	0.35	0
5	IPA	A	602	-	3,3,3	0.58	0	3,3,3	0.42	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	602	IPA	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, 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	H	230/239 (96%)	0.51	11 (4%) 35 37	17, 47, 68, 81	3 (1%)
2	L	215/216 (99%)	0.50	11 (5%) 33 35	34, 47, 67, 84	1 (0%)
3	A	192/205 (93%)	1.04	33 (17%) 4 4	36, 61, 97, 104	0
All	All	637/660 (96%)	0.67	55 (8%) 16 17	17, 50, 84, 104	4 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	96	PRO	4.4
3	A	383	SER	4.0
3	A	363	ALA	4.0
3	A	362	VAL	3.8
3	A	519	HIS	3.7
3	A	389	ASP	3.7
2	L	195	ALA	3.4
2	L	94	THR	3.3
3	A	392	PHE	3.3
2	L	97	THR	3.2
1	H	147	SER	3.1
3	A	382	VAL	3.1
3	A	524	VAL	3.1
3	A	515	PHE	3.1
1	H	115	ASN	3.1
2	L	98[A]	VAL	3.0
3	A	335	LEU	2.9
1	H	117	TYR	2.9
3	A	514	SER	2.9
3	A	391	CYS	2.8
3	A	522	ALA	2.8
3	A	338	PHE	2.8
3	A	365	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
3	A	385	THR	2.7
3	A	369	TYR	2.7
1	H	102	THR	2.7
3	A	525	CYS	2.7
3	A	387	LEU	2.7
3	A	394	ASN	2.7
3	A	390	LEU	2.7
2	L	215	GLU	2.4
3	A	518	LEU	2.4
1	H	218	ASN	2.4
1	H	106	SER	2.4
3	A	516	GLU	2.3
3	A	520	ALA	2.2
3	A	395	VAL	2.2
1	H	170	THR	2.2
1	H	224	THR	2.2
2	L	95	SER	2.2
3	A	393	THR	2.2
2	L	183	LEU	2.1
3	A	517	LEU	2.1
2	L	188	TYR	2.1
1	H	223	ASN	2.1
3	A	384	PRO	2.1
3	A	359	SER	2.1
3	A	364	ASP	2.1
2	L	152	VAL	2.1
1	H	210	THR	2.0
3	A	361	CYS	2.0
1	H	107	ASP	2.0
2	L	154	ASN	2.0
3	A	441	LEU	2.0
3	A	337	PRO	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.

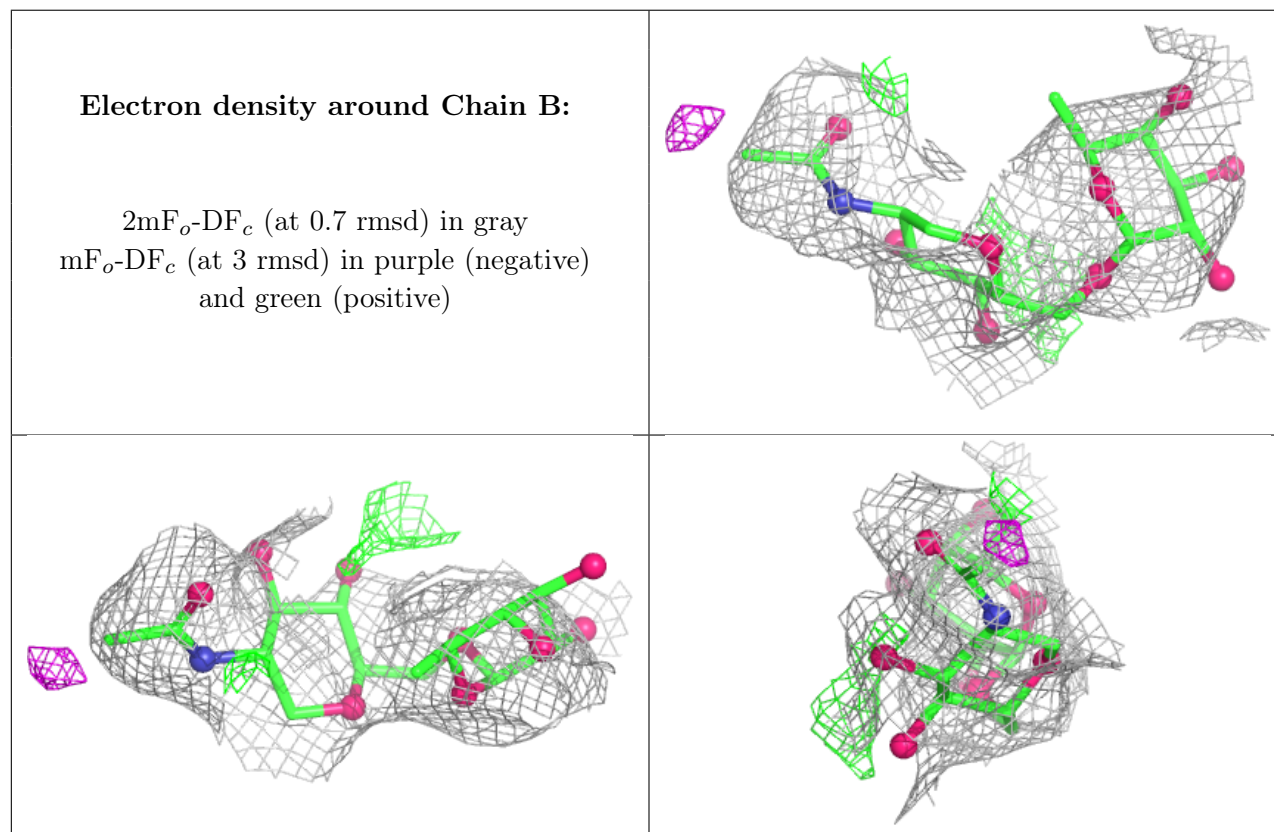
6.3 Carbohydrates [i](#)

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	B	1	14/15	-	-	77,102,118,125	0
4	FUC	B	2	10/11	-	-	119,124,127,130	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 ⓘ

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	IPA	A	602	4/4	0.77	0.21	44,53,70,70	0
5	IPA	A	601	4/4	0.81	0.18	53,64,84,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.