



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1ZBA / pdb_00001zba
Title : Foot-and-Mouth Disease virus serotype A1061 complexed with oligosaccharide receptor.
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Deposited on : 2005-04-08
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

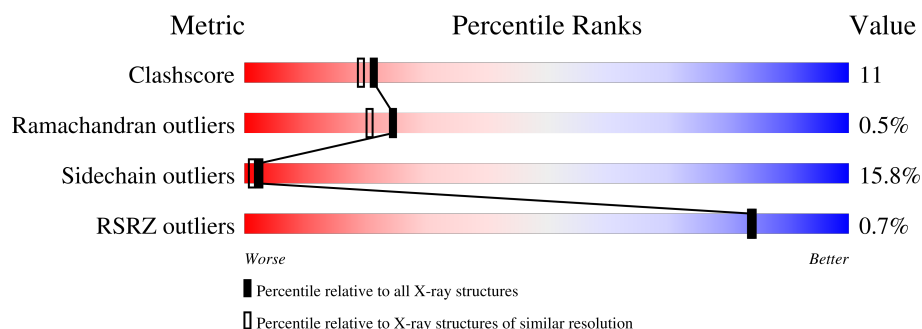
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	1	212	
2	2	218	
3	3	221	
4	4	85	
5	A	3	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5732 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 Coat protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	191	Total	C	N	O	S	0	0	0
			1492	944	266	278	4			

- Molecule 2 is a protein called Coat protein VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	207	Total	C	N	O	S	0	0	0
			1652	1061	280	306	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	14	LEU	ILE	engineered mutation	UNP Q84769

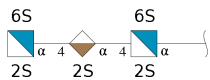
- Molecule 3 is a protein called Coat protein VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	221	Total	C	N	O	S	0	0	0
			1708	1089	277	335	7			

- Molecule 4 is a protein called Coat protein VP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	4	49	Total	C	N	O	S	0	0	0
			375	235	62	76	2			

- Molecule 5 is an oligosaccharide called 2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	A	3	Total	C	N	O	S	0	0	0
			55	18	2	30	5			

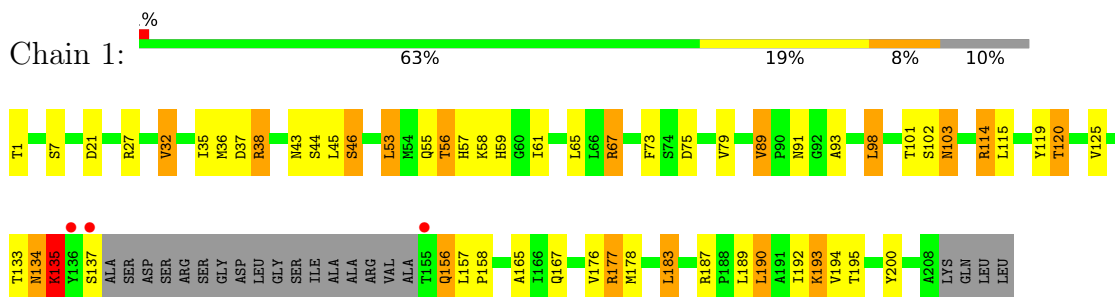
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	1	154	Total	O	0	0
			154	154		
6	2	109	Total	O	0	0
			109	109		
6	3	157	Total	O	0	0
			157	157		
6	4	30	Total	O	0	0
			30	30		

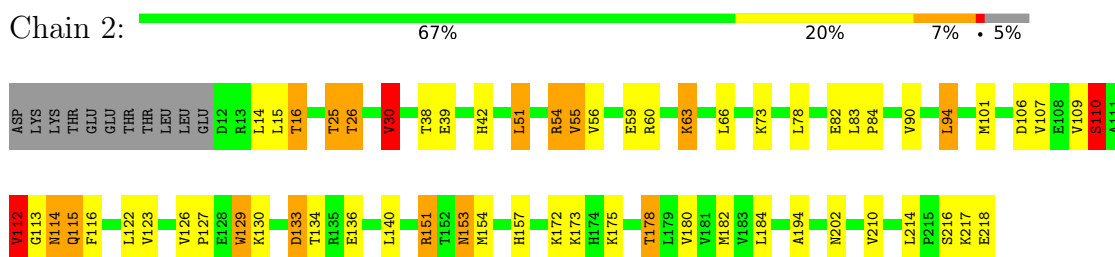
3 Residue-property plots [i](#)

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.

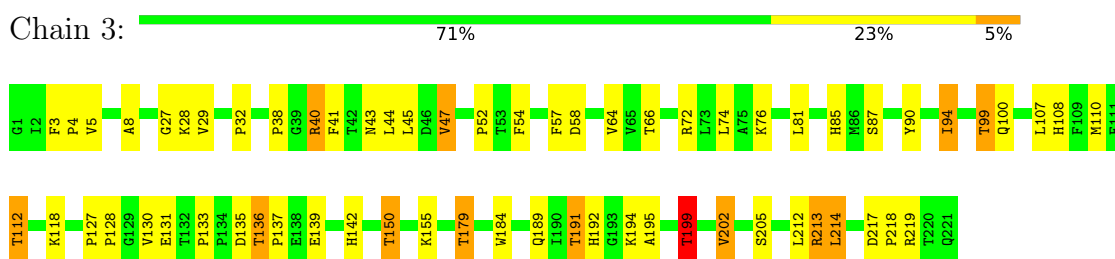
• Molecule 1: Coat protein VP1



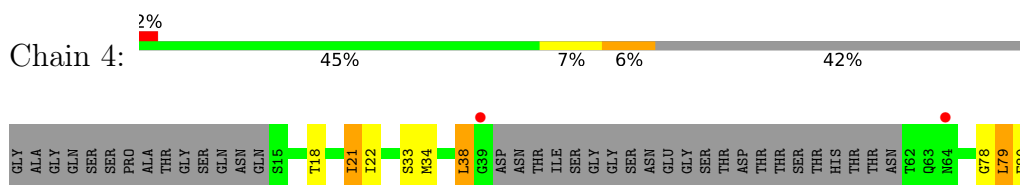
• Molecule 2: Coat protein VP2



• Molecule 3: Coat protein VP3



• Molecule 4: Coat protein VP4



- Molecule 5: 2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose

Chain A:

67%

33%



SGN1
IDS2
SGN3

4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	307.00Å 307.00Å 715.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.00 30.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.00) 23.9 (30.00-2.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 2.01Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.183 , (Not available) 0.177 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.017 for -h,1/3*h-1/3*k-1/3*l,-4/3*h-8/3*k +1/3*l 0.016 for -1/3*h+1/3*k+1/3*l,-k,8/3*h+4/ 3*k+1/3*l 0.017 for -2/3*h-1/3*k-1/3*l,-1/3*h-2/3*k+ 1/3*l,-4/3*h+4/3*k+1/3*l 0.017 for 1/3*h+2/3*k-1/3*l,-k,-8/3*h-4/3* k-1/3*l 0.017 for -1/3*h-2/3*k+1/3*l,-2/3*h-1/3*k- 1/3*l,4/3*h-4/3*k-1/3*l 0.015 for -h,2/3*h+1/3*k+1/3*l,4/3*h+8/3 *k-1/3*l 0.074 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.52	EDS
Total number of atoms	5732	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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: IDS, SGN

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	1	0.68	2/1527 (0.1%)	1.07	9/2083 (0.4%)
2	2	0.66	1/1701 (0.1%)	1.17	17/2322 (0.7%)
3	3	0.67	1/1757 (0.1%)	1.12	12/2405 (0.5%)
4	4	0.60	0/381	1.08	2/513 (0.4%)
All	All	0.66	4/5366 (0.1%)	1.12	40/7323 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	2	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	182	MET	SD-CE	-14.11	1.44	1.79
3	3	110	MET	SD-CE	-12.09	1.49	1.79
1	1	178	MET	SD-CE	-9.95	1.54	1.79
1	1	36	MET	SD-CE	-8.04	1.59	1.79

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	110	SER	O-C-N	-8.76	112.96	123.29
3	3	54	PHE	N-CA-C	8.70	123.35	110.48
2	2	109	VAL	CA-C-N	8.65	134.93	123.00
2	2	109	VAL	C-N-CA	8.65	134.93	123.00
2	2	109	VAL	O-C-N	-8.03	114.68	123.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	110	SER	Mainchain

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	1	1492	0	1485	45	0
2	2	1652	0	1607	39	0
3	3	1708	0	1631	32	0
4	4	375	0	348	6	1
5	A	55	0	23	1	0
6	1	154	0	0	5	2
6	2	109	0	0	5	3
6	3	157	0	0	2	0
6	4	30	0	0	2	0
All	All	5732	0	5094	113	3

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 11.

The worst 5 of 113 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)
2:2:129:TRP:HB2	2:2:178:THR:HG21	1.52	0.91
1:1:57:HIS:HD2	1:1:59:HIS:H	1.18	0.88
1:1:156:GLN:HE21	1:1:156:GLN:HA	1.42	0.84
1:1:135:LYS:NZ	1:1:158:PRO:HA	1.93	0.83
2:2:115:GLN:NE2	2:2:115:GLN:H	1.78	0.81

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1:525:HOH:O	6:2:235:HOH:O[2_555]	0.77	1.43
4:4:80:PHE:O	6:2:236:HOH:O[2_555]	1.93	0.27
6:1:653:HOH:O	6:2:221:HOH:O[2_555]	2.12	0.08

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	1	187/212 (88%)	179 (96%)	7 (4%)	1 (0%)	24	21
2	2	205/218 (94%)	195 (95%)	10 (5%)	0	100	100
3	3	219/221 (99%)	208 (95%)	10 (5%)	1 (0%)	24	21
4	4	45/85 (53%)	41 (91%)	3 (7%)	1 (2%)	5	2
All	All	656/736 (89%)	623 (95%)	30 (5%)	3 (0%)	24	21

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	4	78	GLY
1	1	135	LYS
3	3	58	ASP

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	1	161/176 (92%)	134 (83%)	27 (17%)	2	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	2	181/192 (94%)	150 (83%)	31 (17%)	2	1
3	3	183/183 (100%)	157 (86%)	26 (14%)	3	2
4	4	40/68 (59%)	35 (88%)	5 (12%)	4	2
All	All	565/619 (91%)	476 (84%)	89 (16%)	2	1

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	180	VAL
3	3	135	ASP
3	3	29	VAL
3	3	76	LYS
3	3	191	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	2	202	ASN
3	3	85	HIS
4	4	24	ASN
3	3	43	ASN
3	3	108	HIS

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 ⓘ

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
5	SGN	A	1	5	20,20,20	3.94	4 (20%)	25,31,31	1.18	2 (8%)
5	IDS	A	2	5	16,16,17	1.93	2 (12%)	16,24,26	1.23	2 (12%)
5	SGN	A	3	5	19,19,20	4.19	4 (21%)	23,29,31	1.24	1 (4%)

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	SGN	A	1	5	-	4/11/31/31	0/1/1/1
5	IDS	A	2	5	-	3/9/26/29	0/1/1/1
5	SGN	A	3	5	-	5/11/28/31	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	3	SGN	S1-N2	14.30	1.77	1.59
5	A	1	SGN	S1-N2	13.76	1.76	1.59
5	A	3	SGN	O6-S2	7.74	1.77	1.56
5	A	1	SGN	O6-S2	7.23	1.76	1.56
5	A	2	IDS	O2-S	6.60	1.77	1.57

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	3	SGN	O1S-S1-O2S	-4.81	109.67	120.36
5	A	1	SGN	O1S-S1-O2S	-4.72	109.86	120.36
5	A	2	IDS	C3-C4-C5	3.01	114.47	109.30
5	A	1	SGN	C6-C5-C4	-2.20	107.45	112.07
5	A	2	IDS	O2-C2-C3	2.07	109.84	106.95

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

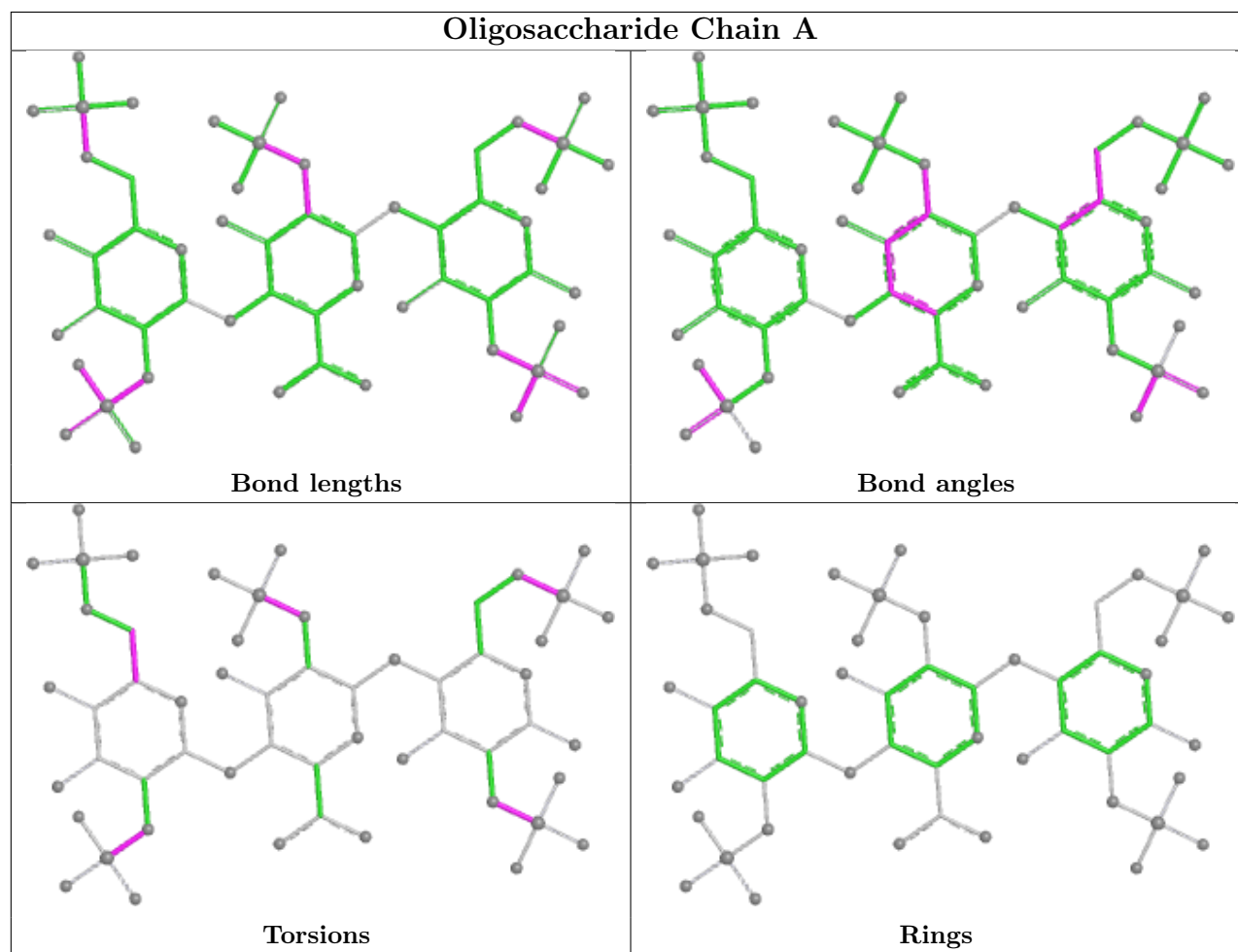
Mol	Chain	Res	Type	Atoms
5	A	2	IDS	C2-O2-S-O1S
5	A	2	IDS	C2-O2-S-O3S
5	A	3	SGN	C4-C5-C6-O6
5	A	3	SGN	O5-C5-C6-O6
5	A	3	SGN	C2-N2-S1-O1S

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1	SGN	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](#)

There are no ligands in this entry.

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 [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	1	191/212 (90%)	-1.29	3 (1%) 70 70	13, 21, 59, 151	0
2	2	207/218 (94%)	-1.42	0 100 100	14, 21, 44, 104	0
3	3	221/221 (100%)	-1.43	0 100 100	14, 20, 48, 86	0
4	4	49/85 (57%)	-0.75	2 (4%) 41 40	17, 43, 109, 138	0
All	All	668/736 (90%)	-1.34	5 (0%) 84 84	13, 21, 61, 151	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1	137	SER	4.6
1	1	155	THR	3.1
1	1	136	TYR	2.8
4	4	64	ASN	2.5
4	4	39	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](#)

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.

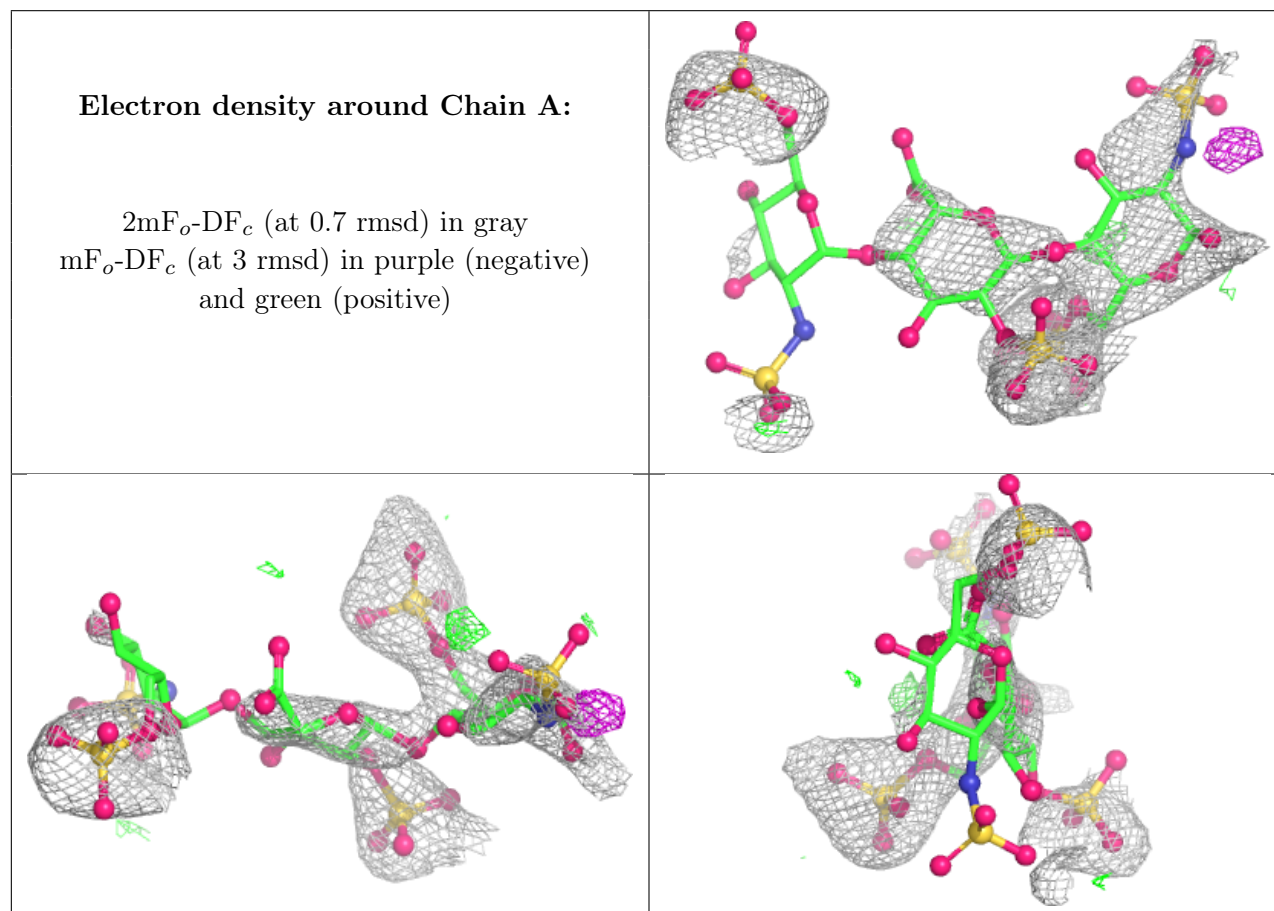
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SGN	A	1	20/20	-	-	10,42,81,86	20
5	IDS	A	2	16/17	-	-	34,61,83,91	16

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	SGN	A	3	19/20	-	-	66,78,118,125	19

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.