wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2023 – 06:00 PM EDT

PDB ID	:	1QQP
Title	:	FOOT-AND-MOUTH DISEASE VIRUS/ OLIGOSACCHARIDE RECEPTOR COMPLEX.
Authors	:	Fry, E.E.; Lea, S.M.; Jackson, T.; Newman, J.W.I.; Ellard, F.M.; Blakemore, W.E.; Abu-Ghazaleh, R.; Samuel, A.; King, A.M.Q.; Stuart, D.I.
Deposited on	:	1999-05-20
Resolution	:	1.90 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 (i) 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 (i)) were used in the production of this report:

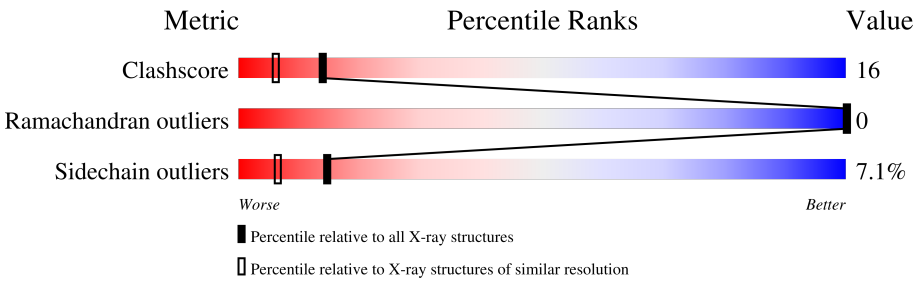
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1	213	78% 7% • 12%
2	2	218	78% 16% 6% •
3	3	220	89% 8% •
4	4	85	49% • • 46%
5	A	5	20% 80%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6002 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 PROTEIN (GENOME POLYPROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1	188	1471	931	260	275	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	56	VAL	ILE	SEE REMARK 999	UNP P03305
1	137	SER	ASN	conflict	UNP P03305

- Molecule 2 is a protein called PROTEIN (GENOME POLYPROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	2	216	1698	1080	290	321	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	130	CYS	TYR	SEE REMARK 999	UNP P03305

- Molecule 3 is a protein called PROTEIN (GENOME POLYPROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	3	220	1680	1075	275	321	9	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	85	HIS	GLN	SEE REMARK 999	UNP P03305
3	168	THR	ALA	SEE REMARK 999	UNP P03305

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
3	173	ASP	GLY	SEE REMARK 999	UNP P03305

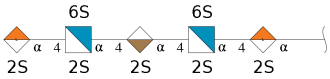
- Molecule 4 is a protein called PROTEIN (GENOME POLYPROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	4	46	352	222	57	71	2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	40	ASN	ASP	conflict	UNP P03305
4	41	ASP	ASN	conflict	UNP P03305

- Molecule 5 is an oligosaccharide called 2-O-sulfo-alpha-L-gulopyranuronic acid-(1-4)-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-(1-4)-2-O-sulfo-alpha-L-gulopyranuronic acid.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	A	5	170	60	4	92	14	0	5	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	1	250	250	250	0	0
6	2	212	212	212	0	0
6	3	152	152	152	0	0
6	4	17	17	17	0	0

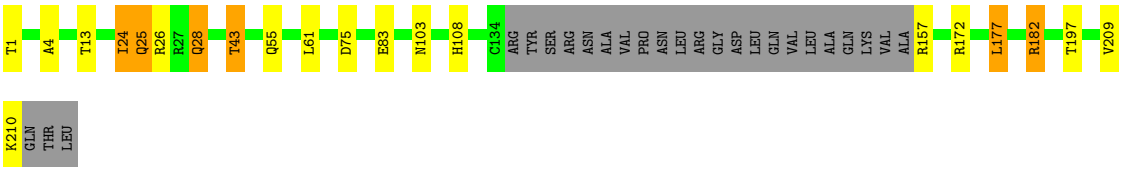
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

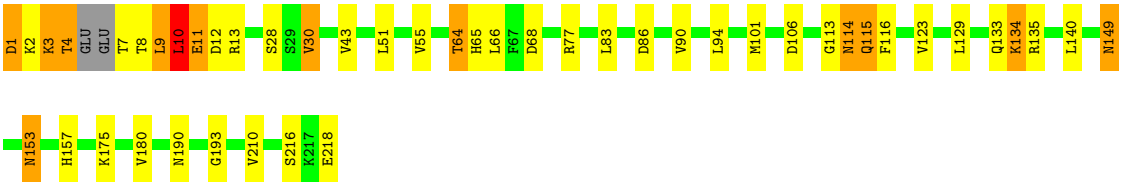
• Molecule 1: PROTEIN (GENOME POLYPROTEIN)

Chain 1:



• Molecule 2: PROTEIN (GENOME POLYPROTEIN)

Chain 2:



• Molecule 3: PROTEIN (GENOME POLYPROTEIN)

Chain 3:

• Molecule 4: PROTEIN (GENOME POLYPROTEIN)

Chain 4:

• Molecule 5: 2-O-sulfo-alpha-L-gulopyranuronic acid-(1-4)-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-(1-4)-2-O-sulfo-alpha-L-gulopyranuronic acid

Chain A:

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α, β, γ	345.00Å 345.00Å 345.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 1.90	Depositor
% Data completeness (in resolution range)	91.0 (12.00-1.90)	Depositor
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.161 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6002	wwPDB-VP
Average B, all atoms ($Å^2$)	23.0	wwPDB-VP

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: IDX, SGN, IDS

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	0.60	0/1505	0.94	4/2055 (0.2%)
2	2	0.67	0/1740	0.98	6/2374 (0.3%)
3	3	0.60	0/1728	1.08	11/2361 (0.5%)
4	4	0.71	0/358	0.85	0/481
All	All	0.64	0/5331	0.99	21/7271 (0.3%)

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
3	3	0	1

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	3	34	ARG	NE-CZ-NH2	-19.68	110.46	120.30
3	3	34	ARG	NE-CZ-NH1	16.30	128.45	120.30
1	1	182	ARG	NE-CZ-NH1	-13.89	113.36	120.30
1	1	182	ARG	NE-CZ-NH2	13.56	127.08	120.30
2	2	135	ARG	NE-CZ-NH1	-9.74	115.43	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	34	ARG	Sidechain

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	1	1471	0	1471	20	0
2	2	1698	0	1662	109	3
3	3	1680	0	1616	27	0
4	4	352	0	324	14	0
5	A	170	0	60	7	0
6	1	250	0	0	6	0
6	2	212	0	0	18	4
6	3	152	0	0	9	0
6	4	17	0	0	2	0
All	All	6002	0	5133	166	4

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 16.

The worst 5 of 166 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)
2:2:4:THR:CG2	2:2:10:LEU:HD11	1.31	1.56
2:2:4:THR:CG2	2:2:10:LEU:CD1	2.12	1.27
2:2:3:LYS:HE2	6:2:235:HOH:O	1.37	1.22
2:2:2:LYS:HG2	4:4:80:PHE:CE2	1.76	1.20
2:2:10:LEU:HG	2:2:11:GLU:N	1.42	1.17

All (4) 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)
2:2:90:VAL:CG2	6:2:390:HOH:O[2_555]	0.77	1.43
2:2:90:VAL:CB	6:2:391:HOH:O[2_555]	1.59	0.61
6:2:325:HOH:O	6:2:325:HOH:O[2_555]	1.74	0.46
2:2:90:VAL:CB	6:2:390:HOH:O[2_555]	1.79	0.41

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	184/213 (86%)	180 (98%)	4 (2%)	0	100	100
2	2	212/218 (97%)	201 (95%)	11 (5%)	0	100	100
3	3	218/220 (99%)	212 (97%)	6 (3%)	0	100	100
4	4	42/85 (49%)	41 (98%)	1 (2%)	0	100	100
All	All	656/736 (89%)	634 (97%)	22 (3%)	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	1	160/183 (87%)	153 (96%)	7 (4%)	28	19
2	2	189/191 (99%)	165 (87%)	24 (13%)	4	1
3	3	176/176 (100%)	169 (96%)	7 (4%)	31	22
4	4	37/67 (55%)	35 (95%)	2 (5%)	22	13
All	All	562/617 (91%)	522 (93%)	40 (7%)	14	6

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	149	ASN
3	3	130	MET
2	2	153	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	3	81	LEU
3	3	168	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
3	3	181	GLN
4	4	31	GLN
4	4	32	ASN
4	4	24	ASN
2	2	157	HIS

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)

10 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	IDX	A	1[A]	5	16,16,17	1.99	2 (12%)	17,24,26	1.03	2 (11%)
5	IDX	A	1[B]	5	16,16,17	1.98	2 (12%)	17,24,26	1.00	2 (11%)
5	SGN	A	2[A]	5	18,19,20	3.99	4 (22%)	22,29,31	1.27	1 (4%)
5	SGN	A	2[B]	5	18,19,20	3.95	4 (22%)	22,29,31	1.24	2 (9%)
5	IDS	A	3[A]	5	16,16,17	1.95	2 (12%)	17,24,26	0.93	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	IDS	A	3[B]	5	16,16,17	1.95	2 (12%)	17,24,26	1.84	3 (17%)
5	SGN	A	4[A]	5	18,19,20	3.91	4 (22%)	22,29,31	1.27	2 (9%)
5	SGN	A	4[B]	5	18,19,20	3.91	4 (22%)	22,29,31	1.32	2 (9%)
5	IDX	A	5[A]	5	15,15,17	2.06	2 (13%)	15,22,26	1.04	1 (6%)
5	IDX	A	5[B]	5	15,15,17	2.01	2 (13%)	15,22,26	1.12	1 (6%)

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	IDX	A	1[A]	5	-	5/9/26/29	0/1/1/1
5	IDX	A	1[B]	5	-	2/9/26/29	0/1/1/1
5	SGN	A	2[A]	5	-	4/11/28/31	0/1/1/1
5	SGN	A	2[B]	5	-	0/11/28/31	0/1/1/1
5	IDS	A	3[A]	5	-	3/9/26/29	0/1/1/1
5	IDS	A	3[B]	5	-	6/9/26/29	0/1/1/1
5	SGN	A	4[A]	5	-	8/11/28/31	0/1/1/1
5	SGN	A	4[B]	5	-	5/11/28/31	0/1/1/1
5	IDX	A	5[A]	5	-	8/9/22/29	0/1/1/1
5	IDX	A	5[B]	5	-	3/9/22/29	0/1/1/1

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2[A]	SGN	S1-N2	12.57	1.76	1.59
5	A	2[B]	SGN	S1-N2	12.36	1.76	1.59
5	A	4[A]	SGN	S1-N2	12.36	1.76	1.59
5	A	4[B]	SGN	S1-N2	12.31	1.76	1.59
5	A	4[A]	SGN	O6-S2	7.80	1.78	1.56

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	3[B]	IDS	O2-C2-C3	4.86	113.74	106.95
5	A	2[A]	SGN	O1S-S1-O2S	-4.50	109.53	120.16
5	A	2[B]	SGN	O1S-S1-O2S	-4.48	109.57	120.16
5	A	4[A]	SGN	O1S-S1-O2S	-4.45	109.63	120.16

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	4[B]	SGN	O1S-S1-O2S	-4.16	110.34	120.16

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

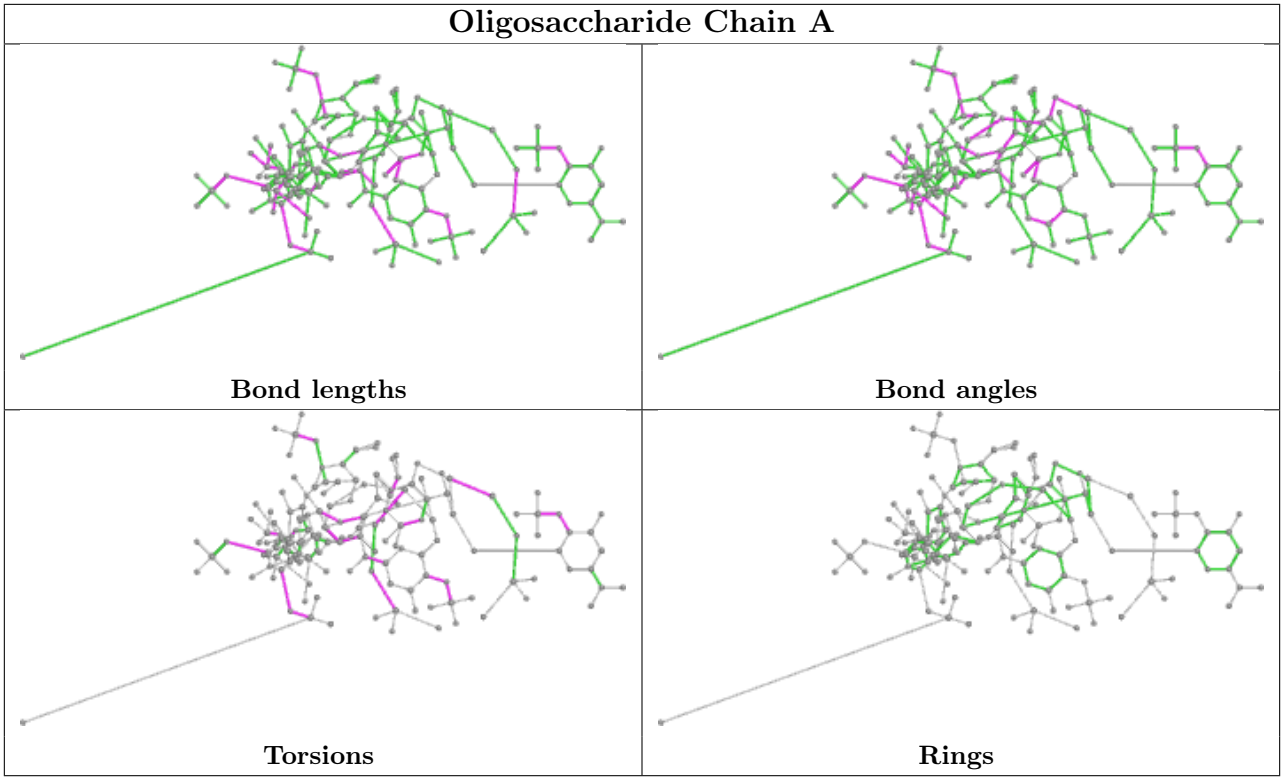
Mol	Chain	Res	Type	Atoms
5	A	1[A]	IDX	C1-C2-O2-S
5	A	1[A]	IDX	C3-C2-O2-S
5	A	1[A]	IDX	C2-O2-S-O1S
5	A	1[A]	IDX	C2-O2-S-O2S
5	A	1[A]	IDX	C2-O2-S-O3S

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	3[B]	IDS	2	0
5	A	4[A]	SGN	3	0
5	A	1[A]	IDX	1	0
5	A	1[B]	IDX	1	0
5	A	4[B]	SGN	1	0
5	A	5[A]	IDX	3	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)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.