



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:49 PM UTC

PDB ID : 1FC2 / pdb_00001fc2
Title : Crystallographic Refinement and Atomic Models of a Human FC Fragment and its Complex with Fragment B of Protein A from Staphylococcus Aureus at 2.9-and 2.8-Angstroms Resolution
Authors : Deisenhofer, J.
Deposited on : 1981-05-21
Resolution : 2.80 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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

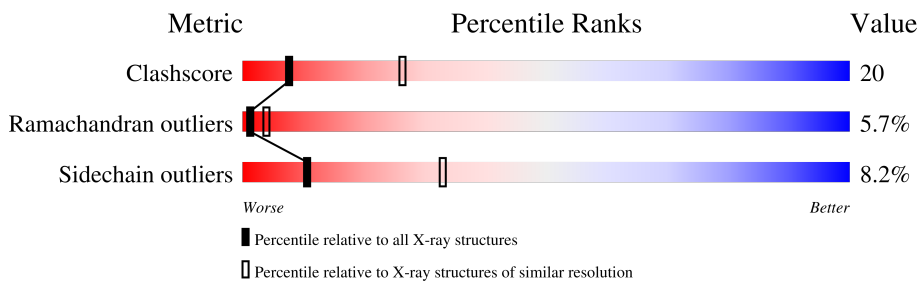
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	58	26% 38% 10% 24%
2	D	224	45% 37% 10% 8%
3	A	9	78% 22%

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
3	MAN	A	3	X	-	-	-
3	FUC	A	9	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2125 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 FRAGMENT B OF PROTEIN A COMPLEX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	C	44	354	220	62	72	25	0	1

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	175	UNK	ALA	conflict	UNP P02976
C	176	UNK	PRO	conflict	UNP P02976

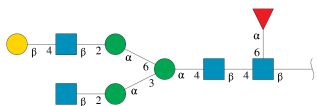
- Molecule 2 is a protein called IMMUNOGLOBULIN FC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	207	1656	1054	282	313	7	279	0	1

There are 5 discrepancies between the modelled and reference sequences:

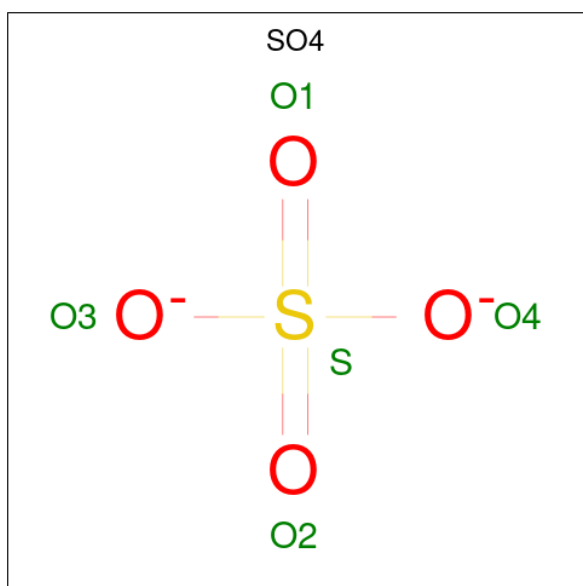
Chain	Residue	Modelled	Actual	Comment	Reference
D	272	GLN	GLU	conflict	EMBL Y14737
D	283	GLN	GLU	conflict	EMBL Y14737
D	294	GLN	GLU	conflict	EMBL Y14737
D	312	ASN	ASP	conflict	EMBL Y14737
D	315	ASP	ASN	conflict	EMBL Y14737

- Molecule 3 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-4)-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
3	A	9	110	62	4	44	68	0	0

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



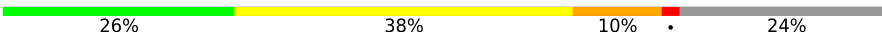
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	C	1	5	4	1	0	0

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.

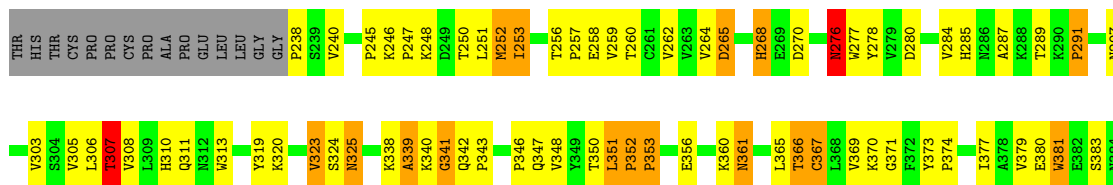
- Molecule 1: FRAGMENT B OF PROTEIN A COMPLEX

Chain C: 




- Molecule 2: IMMUNOGLOBULIN FC

Chain D: 



- Molecule 3: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	70.60Å 70.60Å 147.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2125	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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: NAG, FUC, GAL, SO4, MAN

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	C	1.28	2/360 (0.6%)	1.98	14/486 (2.9%)
2	D	1.40	16/1702 (0.9%)	1.81	27/2318 (1.2%)
All	All	1.38	18/2062 (0.9%)	1.84	41/2804 (1.5%)

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
1	C	0	4
2	D	0	14
All	All	0	18

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	310	HIS	CE1-NE2	9.72	1.42	1.32
1	C	137	HIS	ND1-CE1	9.36	1.42	1.32
2	D	435	HIS	ND1-CE1	9.27	1.41	1.32
2	D	417	TRP	NE1-CE2	-9.24	1.27	1.37
2	D	381	TRP	NE1-CE2	-9.15	1.27	1.37

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	351	LEU	CA-C-N	9.28	126.43	119.66
2	D	351	LEU	C-N-CA	9.28	126.43	119.66
2	D	389	ASN	CA-CB-CG	-6.73	105.87	112.60
1	C	140	ASN	CA-CB-CG	-6.71	105.89	112.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	366	THR	CA-C-N	-6.70	113.67	123.05

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	125	ASN	Sidechain
1	C	127	GLU	Sidechain
1	C	140	ASN	Sidechain
1	C	154	LYS	Mainchain
2	D	252	MET	Mainchain

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	C	354	0	330	12	3
2	D	1656	0	1629	59	7
3	A	110	0	94	2	0
4	C	5	0	0	0	0
All	All	2125	0	2053	68	7

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 20.

The worst 5 of 68 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:D:388:GLU:HG2	2:D:410:LEU:HD11	1.53	0.88
2:D:248:LYS:HG3	2:D:428:MET:HE1	1.57	0.86
2:D:284:VAL:HB	2:D:287:ALA:HB2	1.59	0.83
1:C:135:ILE:HD13	1:C:149:PHE:HB3	1.63	0.79
2:D:238:PRO:HA	2:D:265:ASP:CB	2.17	0.74

The worst 5 of 7 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:D:356:GLU:OE2	2:D:439:LYS:NZ[6_555]	0.71	1.49
1:C:159:GLN:NE2	2:D:390:ASN:ND2[5_665]	1.56	0.64
2:D:356:GLU:CD	2:D:439:LYS:NZ[6_555]	1.59	0.61
1:C:159:GLN:NE2	2:D:390:ASN:CG[5_665]	1.89	0.31
2:D:356:GLU:OE2	2:D:439:LYS:CE[6_555]	2.08	0.12

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	C	42/58 (72%)	33 (79%)	3 (7%)	6 (14%)	0	0
2	D	205/224 (92%)	180 (88%)	17 (8%)	8 (4%)	2	8
All	All	247/282 (88%)	213 (86%)	20 (8%)	14 (6%)	1	4

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	125	ASN
1	C	158	SER
1	C	160	SER
1	C	161	ALA
2	D	265	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	C	39/49 (80%)	35 (90%)	4 (10%)	7	23
2	D	193/207 (93%)	178 (92%)	15 (8%)	11	35
All	All	232/256 (91%)	213 (92%)	19 (8%)	10	33

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	367	CYS
2	D	437	THR
2	D	439	LYS
2	D	425	CYS
2	D	289	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	361	ASN
2	D	384	ASN
2	D	438	GLN
2	D	389	ASN
1	C	162	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](#)

9 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	$\# Z > 2$
3	NAG	A	1	3,2	14,14,15	0.76	0	17,19,21	1.43	2 (11%)
3	NAG	A	2	3	14,14,15	1.12	1 (7%)	17,19,21	1.43	2 (11%)
3	MAN	A	3	3	11,11,12	0.65	0	15,15,17	1.36	1 (6%)
3	MAN	A	4	3	11,11,12	0.71	0	15,15,17	1.69	1 (6%)
3	NAG	A	5	3	14,14,15	0.77	0	17,19,21	1.52	1 (5%)
3	GAL	A	6	3	11,11,12	0.65	0	15,15,17	1.61	1 (6%)
3	MAN	A	7	3	11,11,12	0.55	0	15,15,17	1.60	1 (6%)
3	NAG	A	8	3	14,14,15	0.75	0	17,19,21	1.57	1 (5%)
3	FUC	A	9	3	10,10,11	0.76	0	14,14,16	1.01	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
3	NAG	A	1	3,2	-	4/6/23/26	0/1/1/1
3	NAG	A	2	3	-	0/6/23/26	0/1/1/1
3	MAN	A	3	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	A	4	3	-	0/2/19/22	0/1/1/1
3	NAG	A	5	3	-	0/6/23/26	0/1/1/1
3	GAL	A	6	3	-	1/2/19/22	0/1/1/1
3	MAN	A	7	3	-	0/2/19/22	0/1/1/1
3	NAG	A	8	3	-	0/6/23/26	0/1/1/1
3	FUC	A	9	3	2/2/4/5	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	2	NAG	C1-C2	2.37	1.55	1.52

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	8	NAG	C1-O5-C5	5.85	120.03	112.19
3	A	7	MAN	C1-O5-C5	5.71	119.83	112.19
3	A	4	MAN	C1-O5-C5	5.58	119.67	112.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	6	GAL	C1-O5-C5	5.18	119.13	112.19
3	A	5	NAG	C1-O5-C5	4.97	118.84	112.19

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	3	MAN	C1
3	A	9	FUC	C1
3	A	9	FUC	C5

All (5) torsion outliers are listed below:

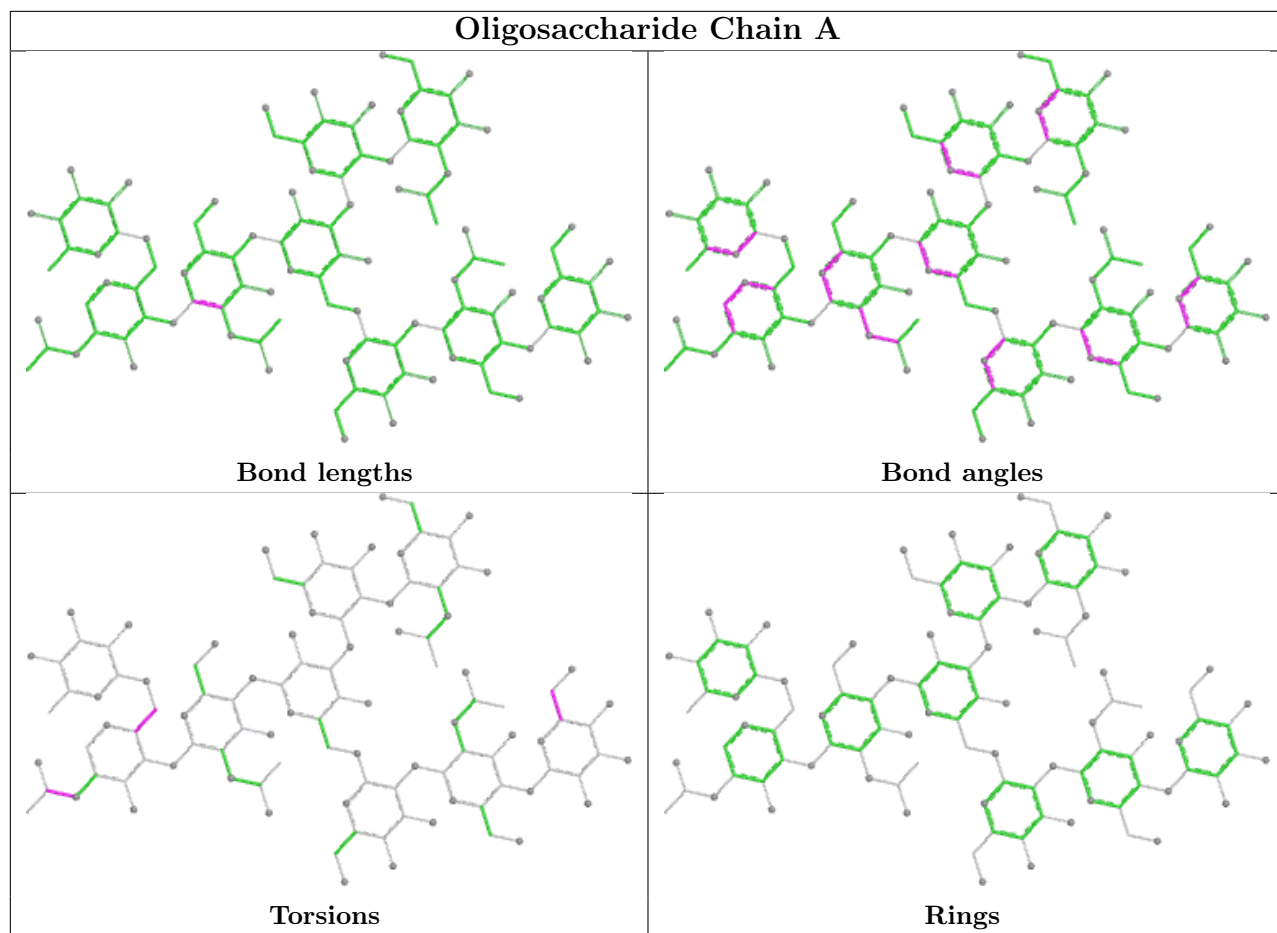
Mol	Chain	Res	Type	Atoms
3	A	1	NAG	C8-C7-N2-C2
3	A	1	NAG	O7-C7-N2-C2
3	A	6	GAL	O5-C5-C6-O6
3	A	1	NAG	C4-C5-C6-O6
3	A	1	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	6	GAL	2	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](#)

1 ligand is 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	SO4	C	201	-	4,4,4	1.02	0	6,6,6	0.21	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

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 [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.