



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:48 AM UTC

PDB ID : 1JGI / pdb_00001jgi
Title : Crystal Structure of the Active Site Mutant Glu328Gln of Amylosucrase from *Neisseria polysaccharea* in Complex with the Natural Substrate Sucrose
Authors : Mirza, O.; Skov, L.K.; Gajhede, M.
Deposited on : 2001-06-25
Resolution : 2.00 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)	:	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

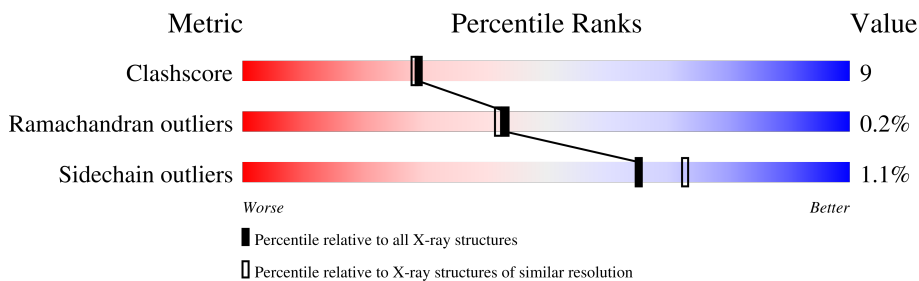
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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)

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	A	628	 83% 15% .
2	B	2	 50% 50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5699 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.

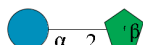
- Molecule 1 is a protein called amylosucrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	628	5054	3214	880	939	21	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	cloning artifact	UNP Q9ZEU2
A	2	PRO	-	cloning artifact	UNP Q9ZEU2
A	3	ASN	-	cloning artifact	UNP Q9ZEU2
A	4	SER	-	cloning artifact	UNP Q9ZEU2
A	131	TYR	HIS	SEE REMARK 999	UNP Q9ZEU2
A	328	GLN	GLU	engineered mutation	UNP Q9ZEU2
A	537	ASP	GLY	SEE REMARK 999	UNP Q9ZEU2

- Molecule 2 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	B	2	23	12	11	0	0	0

- Molecule 3 is water.

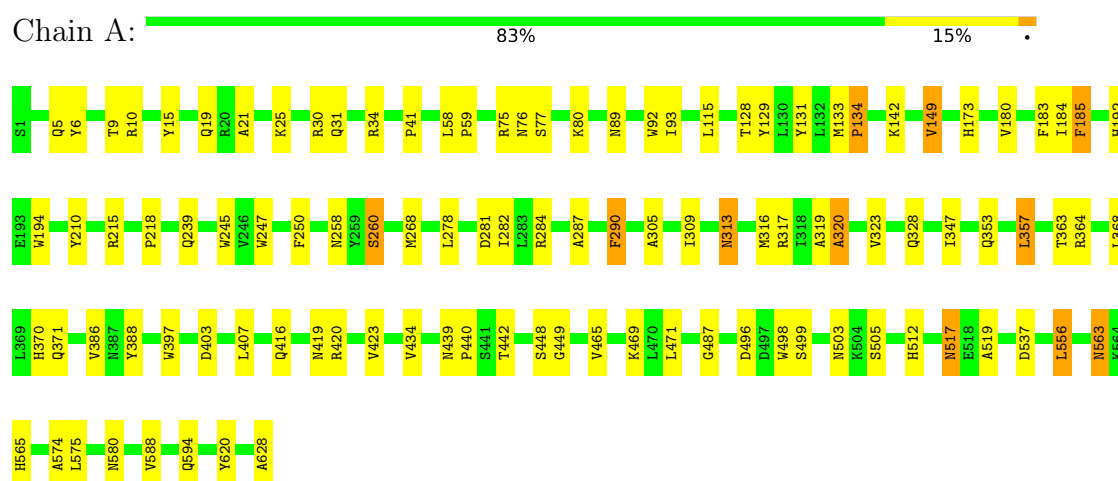
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	622	Total	O	0	0
			622	622		

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: amylosucrase



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.59Å 116.74Å 60.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.91 – 2.00	Depositor
% Data completeness (in resolution range)	79.7 (27.91-2.00)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.186 , 0.226	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5699	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FRU, GLC

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	A	0.36	0/5192	0.85	14/7062 (0.2%)

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	A	0	1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	386	VAL	N-CA-C	-7.17	96.77	107.37
1	A	487	GLY	N-CA-C	-6.70	106.41	113.58
1	A	149	VAL	N-CA-C	6.04	116.86	108.89
1	A	320	ALA	CA-C-N	5.78	126.18	119.47
1	A	320	ALA	C-N-CA	5.78	126.18	119.47
1	A	260	SER	N-CA-C	-5.63	106.37	113.18
1	A	594	GLN	N-CA-C	5.57	118.12	111.71
1	A	278	LEU	N-CA-C	-5.50	106.53	113.18
1	A	588	VAL	N-CA-C	-5.20	99.67	107.37
1	A	505	SER	N-CA-C	5.14	118.33	111.75
1	A	290	PHE	N-CA-C	5.13	119.63	113.17
1	A	357	LEU	N-CA-C	-5.13	105.77	111.36
1	A	319	ALA	N-CA-C	5.07	119.61	113.38
1	A	128	THR	N-CA-C	-5.01	105.97	113.89

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	129	TYR	Sidechain

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	A	5054	0	4833	86	0
2	B	23	0	21	1	0
3	A	622	0	0	4	0
All	All	5699	0	4854	86	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 9.

All (86) 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:A:316:MET:HE2	1:A:323:VAL:HB	1.32	1.12
1:A:284:ARG:NH2	1:A:328:GLN:HG3	1.85	0.92
1:A:142:LYS:HZ2	1:A:503:ASN:HA	1.46	0.79
1:A:316:MET:CE	1:A:320:ALA:HB3	2.16	0.76
1:A:316:MET:HE1	1:A:320:ALA:HB3	1.68	0.75
1:A:31:GLN:HE22	1:A:34:ARG:HH21	1.36	0.73
1:A:173:HIS:HE1	1:A:281:ASP:OD2	1.71	0.73
1:A:192:HIS:HD2	1:A:194:TRP:H	1.34	0.73
1:A:316:MET:HE2	1:A:323:VAL:CB	2.16	0.73
1:A:563:ASN:HD22	1:A:565:HIS:H	1.36	0.71
1:A:580:ASN:O	1:A:620:TYR:HA	1.92	0.69
1:A:284:ARG:CZ	1:A:328:GLN:HG3	2.24	0.67
1:A:58:LEU:HB3	1:A:59:PRO:HD3	1.77	0.66
1:A:258:ASN:HD22	1:A:260:SER:H	1.44	0.66
1:A:21:ALA:O	1:A:25:LYS:HD3	1.97	0.64
1:A:556:LEU:HD12	1:A:556:LEU:C	2.23	0.64
1:A:30:ARG:HH12	1:A:34:ARG:HE	1.47	0.63
1:A:258:ASN:HD22	1:A:258:ASN:C	2.05	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ASN:O	1:A:423:VAL:HG22	1.99	0.61
1:A:563:ASN:HD22	1:A:563:ASN:C	2.11	0.59
1:A:180:VAL:HG22	1:A:282:ILE:HB	1.84	0.58
1:A:397:TRP:HE1	1:A:419:ASN:ND2	2.02	0.57
1:A:30:ARG:HD2	1:A:30:ARG:C	2.29	0.57
1:A:25:LYS:HD2	1:A:25:LYS:N	2.21	0.54
1:A:517:ASN:C	1:A:517:ASN:HD22	2.16	0.54
1:A:469:LYS:HD3	1:A:537:ASP:HB3	1.90	0.53
1:A:563:ASN:ND2	1:A:565:HIS:H	2.06	0.53
1:A:258:ASN:ND2	1:A:260:SER:H	2.05	0.53
1:A:357:LEU:HB3	1:A:471:LEU:HD22	1.91	0.53
1:A:30:ARG:NH1	1:A:34:ARG:HE	2.06	0.52
1:A:465:VAL:HG12	1:A:469:LYS:HE2	1.90	0.52
1:A:363:THR:O	1:A:364:ARG:HB2	2.09	0.52
1:A:76:ASN:OD1	1:A:77:SER:N	2.43	0.51
1:A:30:ARG:HD2	1:A:30:ARG:O	2.10	0.51
1:A:434:VAL:HG23	1:A:448:SER:HB2	1.91	0.51
1:A:574:ALA:HA	1:A:628:ALA:HB3	1.92	0.50
1:A:250:PHE:CD1	2:B:1:GLC:H62	2.46	0.50
1:A:434:VAL:CG2	1:A:448:SER:HB2	2.41	0.50
1:A:5:GLN:O	1:A:9:THR:HG23	2.11	0.50
1:A:287:ALA:HA	3:A:1123:HOH:O	2.11	0.50
1:A:115:LEU:C	1:A:115:LEU:HD13	2.37	0.49
1:A:371:GLN:OE1	1:A:403:ASP:HB3	2.13	0.49
1:A:469:LYS:HE3	1:A:537:ASP:OD1	2.12	0.49
1:A:210:TYR:HB2	1:A:247:TRP:HB2	1.95	0.49
1:A:133:MET:HB3	1:A:134:PRO:HD2	1.94	0.49
1:A:6:TYR:CZ	1:A:10:ARG:HD2	2.47	0.48
1:A:316:MET:HE3	1:A:320:ALA:HB3	1.93	0.48
1:A:305:ALA:O	1:A:309:ILE:HG13	2.13	0.48
1:A:31:GLN:NE2	1:A:34:ARG:HH21	2.08	0.48
1:A:89:ASN:ND2	1:A:92:TRP:HB3	2.30	0.47
1:A:149:VAL:CG2	1:A:184:ILE:HD12	2.44	0.47
1:A:287:ALA:HB1	1:A:290:PHE:HD2	1.80	0.47
1:A:313:ASN:ND2	1:A:317:ARG:HH11	2.14	0.46
1:A:15:TYR:HB3	1:A:19:GLN:HB2	1.97	0.46
1:A:183:PHE:CE2	1:A:185:PHE:HB3	2.51	0.46
1:A:370:HIS:HD2	3:A:1210:HOH:O	1.97	0.46
1:A:75:ARG:HB3	1:A:80:LYS:HE3	1.98	0.46
1:A:416:GLN:O	1:A:420:ARG:HG3	2.16	0.45
1:A:258:ASN:C	1:A:258:ASN:ND2	2.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:GLY:C	1:A:512:HIS:HB3	2.41	0.45
1:A:131:TYR:HA	1:A:180:VAL:HB	1.98	0.44
1:A:185:PHE:HA	1:A:268:MET:CE	2.47	0.44
1:A:239:GLN:HB2	1:A:245:TRP:CZ2	2.53	0.44
1:A:239:GLN:HB2	1:A:245:TRP:CE2	2.53	0.44
1:A:465:VAL:CG1	1:A:469:LYS:NZ	2.81	0.43
1:A:439:ASN:HB3	1:A:442:THR:OG1	2.18	0.43
1:A:353:GLN:O	1:A:357:LEU:HG	2.18	0.43
1:A:498:TRP:CG	1:A:499:SER:N	2.86	0.43
1:A:368:LEU:HD23	1:A:407:LEU:HD12	2.01	0.43
1:A:575:LEU:C	1:A:575:LEU:HD13	2.43	0.43
1:A:215:ARG:C	1:A:218:PRO:HD2	2.44	0.43
1:A:41:PRO:HB2	3:A:1331:HOH:O	2.19	0.42
1:A:313:ASN:C	1:A:313:ASN:HD22	2.27	0.42
1:A:574:ALA:CB	1:A:628:ALA:HB3	2.49	0.42
1:A:439:ASN:HA	1:A:440:PRO:HD2	1.93	0.42
1:A:142:LYS:NZ	1:A:503:ASN:HD22	2.18	0.42
1:A:284:ARG:NH2	1:A:328:GLN:CG	2.71	0.41
1:A:517:ASN:HD21	1:A:519:ALA:HB3	1.86	0.41
1:A:556:LEU:C	1:A:556:LEU:CD1	2.93	0.41
1:A:115:LEU:HD13	1:A:115:LEU:O	2.21	0.41
1:A:364:ARG:O	1:A:565:HIS:HD2	2.04	0.40
1:A:370:HIS:HE1	3:A:1494:HOH:O	2.04	0.40
1:A:388:TYR:CD1	1:A:388:TYR:N	2.88	0.40
1:A:287:ALA:HB1	1:A:290:PHE:CD2	2.55	0.40
1:A:93:ILE:HD12	1:A:347:ILE:HG22	2.03	0.40
1:A:316:MET:HE3	1:A:316:MET:HA	2.03	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	A	626/628 (100%)	606 (97%)	19 (3%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	PRO

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	A	533/533 (100%)	527 (99%)	6 (1%)	65	73

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	185	PHE
1	A	313	ASN
1	A	496	ASP
1	A	517	ASN
1	A	556	LEU
1	A	563	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	70	GLN
1	A	98	GLN
1	A	173	HIS
1	A	192	HIS
1	A	196	GLN
1	A	220	GLN
1	A	258	ASN
1	A	301	ASN

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Mol	Chain	Res	Type
1	A	313	ASN
1	A	338	GLN
1	A	342	GLN
1	A	370	HIS
1	A	416	GLN
1	A	419	ASN
1	A	463	HIS
1	A	503	ASN
1	A	517	ASN
1	A	523	GLN
1	A	525	ASN
1	A	560	ASN
1	A	563	ASN
1	A	565	HIS
1	A	601	HIS
1	A	613	GLN

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](#)

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	$\# Z > 2$
2	GLC	B	1	2	11,11,12	1.54	2 (18%)	15,15,17	1.08	1 (6%)
2	FRU	B	2	2	11,12,12	1.69	1 (9%)	10,18,18	0.65	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
2	GLC	B	1	2	-	0/2/19/22	0/1/1/1
2	FRU	B	2	2	-	0/5/24/24	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	FRU	O2-C2	5.27	1.49	1.40
2	B	1	GLC	C2-C3	3.11	1.57	1.52
2	B	1	GLC	O5-C1	2.44	1.47	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	GLC	C1-O5-C5	2.53	115.58	112.19

There are no chirality outliers.

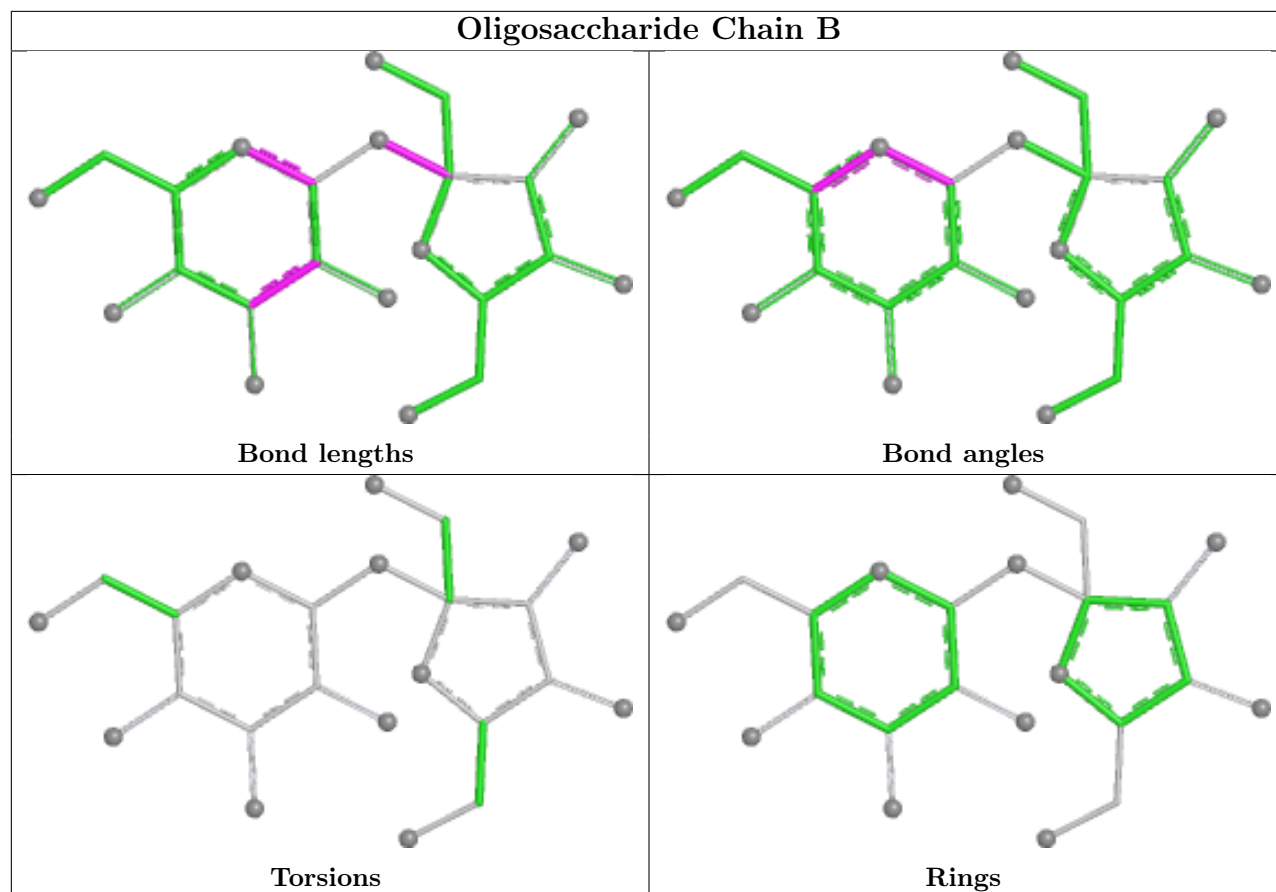
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	GLC	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.