



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 08:36 PM UTC

PDB ID : 3CPU / pdb_00003cpu
Title : SUBSITE MAPPING OF THE ACTIVE SITE OF HUMAN PANCREATIC ALPHA-AMYLASE USING SUBSTRATES, THE PHARMACOLOGICAL INHIBITOR ACARBOSE, AND AN ACTIVE SITE VARIANT
Authors : Brayer, G.D.; Sidhu, G.; Maurus, R.; Rydberg, E.H.; Braun, C.; Wang, Y.; Nguyen, N.T.; Overall, C.M.; Withers, S.G.
Deposited on : 1999-06-08
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)
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

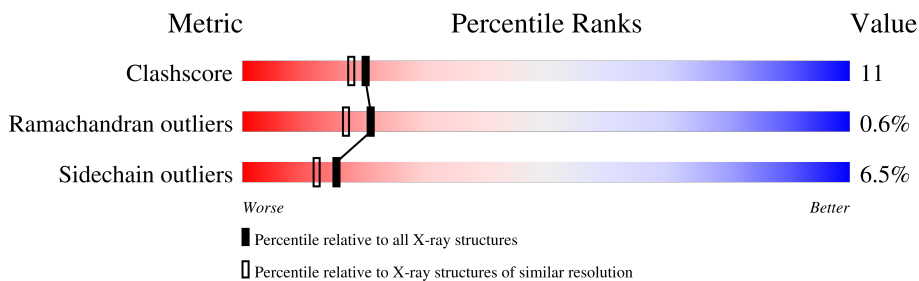
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	496	
2	B	2	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4204 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 Pancreatic alpha-amylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	496	3946	2497	697	732	20	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	300	ASN	ASP	engineered mutation	UNP P04746

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-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 CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	233	Total 233	O 233	0	0

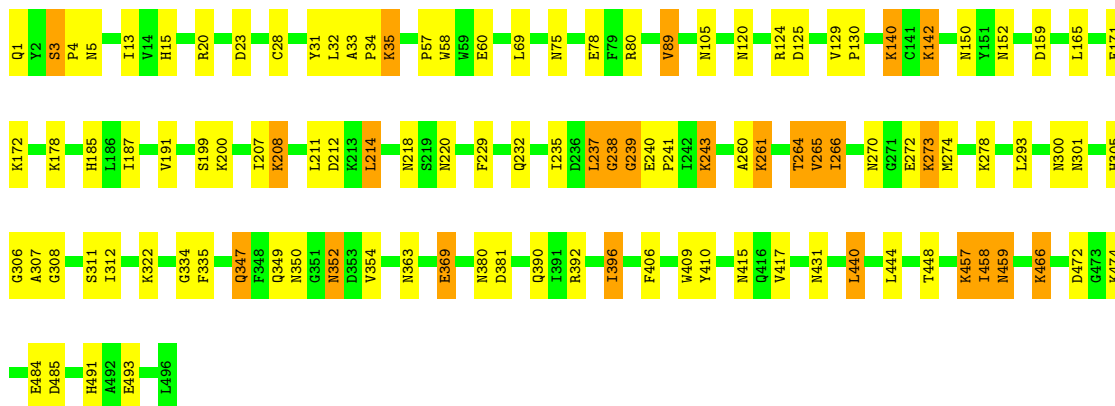
3 Residue-property plots

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: Pancreatic alpha-amylase

Chain A: 



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain B: 

GLC1
GLC2

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.91Å 75.39Å 136.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00	Depositor
% Data completeness (in resolution range)	83.4 (8.00-2.00)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.179 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4204	wwPDB-VP
Average B, all atoms (Å ²)	19.0	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: GLC, CA, CL, PCA

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	0.57	3/4053 (0.1%)	0.95	10/5506 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	240	GLU	C-N	11.22	1.48	1.33
1	A	237	LEU	C-N	6.12	1.42	1.33
1	A	265	VAL	CA-CB	6.07	1.62	1.54

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	240	GLU	CA-C-N	-10.57	107.65	119.28
1	A	240	GLU	C-N-CA	-10.57	107.65	119.28
1	A	306	GLY	N-CA-C	7.67	121.42	110.46
1	A	240	GLU	O-C-N	7.34	127.09	121.88
1	A	3	SER	CB-CA-C	7.06	117.99	109.31
1	A	334	GLY	N-CA-C	6.56	124.22	112.22
1	A	239	GLY	N-CA-C	5.69	126.66	113.18
1	A	3	SER	CA-C-N	5.33	125.66	119.47
1	A	3	SER	C-N-CA	5.33	125.66	119.47
1	A	89	VAL	CG1-CB-CG2	5.19	122.22	110.80

There are no chirality outliers.

There are no planarity outliers.

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	3946	0	3720	87	0
2	B	23	0	21	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	233	0	0	17	0
All	All	4204	0	3741	87	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 11.

All (87) 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:208:LYS:HE2	1:A:212:ASP:OD1	1.76	0.85
1:A:322:LYS:HD2	5:A:618:HOH:O	1.77	0.84
1:A:293:LEU:HD23	5:A:642:HOH:O	1.81	0.79
1:A:218:ASN:HD21	1:A:220:ASN:HD22	1.34	0.75
1:A:235:ILE:HG23	1:A:307:ALA:HB2	1.68	0.74
1:A:261:LYS:HA	1:A:261:LYS:HE2	1.69	0.73
1:A:390:GLN:HG2	5:A:618:HOH:O	1.87	0.72
1:A:31:TYR:OH	1:A:392:ARG:HG3	1.90	0.71
1:A:308:GLY:HA3	1:A:312:ILE:HD11	1.72	0.70
1:A:235:ILE:CG2	1:A:307:ALA:HB2	2.21	0.70
1:A:347:GLN:O	1:A:354:VAL:HG22	1.97	0.65
1:A:472:ASP:OD1	1:A:474:LYS:HB2	1.97	0.65
1:A:363:ASN:HB3	5:A:731:HOH:O	1.96	0.65
1:A:459:ASN:O	1:A:459:ASN:ND2	2.26	0.62
1:A:459:ASN:C	1:A:459:ASN:HD22	2.07	0.61
1:A:466:LYS:HE2	5:A:633:HOH:O	2.00	0.61
1:A:369:GLU:CD	1:A:369:GLU:H	2.07	0.60
1:A:335:PHE:HB3	5:A:642:HOH:O	2.01	0.60
1:A:308:GLY:CA	1:A:312:ILE:HD11	2.32	0.59
1:A:349:GLN:O	1:A:350:ASN:HB2	2.02	0.58
1:A:4:PRO:O	1:A:5:ASN:HB2	2.04	0.58
1:A:208:LYS:HE3	1:A:211:LEU:HB2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:ASN:HB3	1:A:431:ASN:HB3	1.86	0.57
1:A:218:ASN:HD22	1:A:220:ASN:H	1.52	0.57
1:A:265:VAL:HG22	1:A:272:GLU:HB3	1.87	0.57
1:A:15:HIS:HD2	5:A:515:HOH:O	1.91	0.54
1:A:142:LYS:N	1:A:142:LYS:HE3	2.22	0.54
1:A:150:ASN:HD21	1:A:152:ASN:HB2	1.73	0.53
1:A:211:LEU:HA	1:A:214:LEU:HD22	1.90	0.53
1:A:274:MET:HE3	5:A:613:HOH:O	2.10	0.51
1:A:493:GLU:OE1	1:A:493:GLU:HA	2.11	0.51
1:A:274:MET:H	1:A:415:ASN:ND2	2.08	0.51
1:A:380:ASN:O	1:A:381:ASP:HB2	2.10	0.51
1:A:33:ALA:HB3	1:A:34:PRO:HD3	1.92	0.51
1:A:33:ALA:HB2	1:A:89:VAL:HG13	1.93	0.51
1:A:264:THR:HG22	1:A:311:SER:CB	2.41	0.51
1:A:448:THR:HG21	1:A:466:LYS:NZ	2.25	0.50
1:A:485:ASP:OD1	5:A:618:HOH:O	2.19	0.50
1:A:13:ILE:HD13	5:A:555:HOH:O	2.10	0.50
1:A:218:ASN:ND2	1:A:220:ASN:H	2.10	0.50
1:A:235:ILE:HG23	1:A:307:ALA:CB	2.40	0.50
1:A:352:ASN:OD1	1:A:352:ASN:C	2.54	0.50
1:A:57:PRO:O	1:A:60:GLU:HG2	2.11	0.49
1:A:199:SER:OG	1:A:232:GLN:HB3	2.12	0.49
1:A:152:ASN:O	1:A:241:PRO:HG3	2.13	0.49
1:A:150:ASN:ND2	1:A:152:ASN:H	2.10	0.48
1:A:229:PHE:HZ	5:A:642:HOH:O	1.96	0.48
1:A:392:ARG:O	1:A:396:ILE:HD12	2.14	0.48
1:A:273:LYS:HB3	1:A:273:LYS:HE2	1.46	0.48
1:A:80:ARG:NH2	1:A:185:HIS:HE1	2.12	0.47
1:A:15:HIS:CD2	5:A:515:HOH:O	2.67	0.47
1:A:58:TRP:HH2	1:A:300:ASN:OD1	1.97	0.47
1:A:466:LYS:HZ3	1:A:466:LYS:HG2	1.54	0.47
1:A:484:GLU:HB3	5:A:664:HOH:O	2.15	0.46
1:A:243:LYS:HB2	1:A:243:LYS:HE2	1.52	0.46
1:A:369:GLU:HB2	5:A:599:HOH:O	2.14	0.46
1:A:20:ARG:HD3	1:A:23:ASP:OD2	2.15	0.46
1:A:390:GLN:CG	5:A:618:HOH:O	2.56	0.46
1:A:274:MET:H	1:A:415:ASN:HD22	1.64	0.45
1:A:142:LYS:HE3	1:A:142:LYS:H	1.81	0.45
1:A:187:ILE:HA	1:A:191:VAL:HG22	1.97	0.45
1:A:3:SER:HA	1:A:4:PRO:HD3	1.74	0.45
1:A:491:HIS:CE1	1:A:493:GLU:HB2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:ASN:ND2	1:A:459:ASN:C	2.74	0.45
1:A:237:LEU:O	1:A:238:GLY:O	2.36	0.43
1:A:140:LYS:HD3	1:A:159:ASP:CG	2.43	0.43
1:A:457:LYS:C	1:A:458:ILE:HG12	2.44	0.43
1:A:260:ALA:O	1:A:264:THR:CG2	2.66	0.43
1:A:300:ASN:OD1	1:A:305:HIS:HB3	2.18	0.43
1:A:13:ILE:HG21	5:A:555:HOH:O	2.18	0.43
1:A:178:LYS:HA	1:A:178:LYS:HD2	1.77	0.42
1:A:207:ILE:O	1:A:211:LEU:HG	2.18	0.42
1:A:171:GLU:HG2	1:A:172:LYS:N	2.33	0.42
1:A:120:ASN:HB3	1:A:125:ASP:HB3	2.02	0.42
1:A:124:ARG:N	1:A:124:ARG:HD3	2.35	0.42
1:A:235:ILE:HG21	1:A:307:ALA:HB2	1.99	0.41
1:A:28:CYS:HA	1:A:32:LEU:HB2	2.02	0.41
1:A:440:LEU:O	1:A:474:LYS:HA	2.21	0.41
1:A:33:ALA:HB3	1:A:34:PRO:CD	2.51	0.41
1:A:260:ALA:O	1:A:264:THR:HG23	2.20	0.41
1:A:75:ASN:OD1	1:A:78:GLU:HG3	2.21	0.41
1:A:266:ILE:HD11	5:A:613:HOH:O	2.20	0.41
1:A:410:TYR:CD1	1:A:410:TYR:C	2.99	0.41
1:A:35:LYS:HA	1:A:35:LYS:HD2	1.84	0.41
1:A:58:TRP:CH2	1:A:300:ASN:OD1	2.74	0.41
1:A:406:PHE:HZ	1:A:409:TRP:CE3	2.39	0.41
1:A:129:VAL:HB	1:A:130:PRO:HA	2.03	0.40

There are no symmetry-related clashes.

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	A	494/496 (100%)	474 (96%)	17 (3%)	3 (1%)	21 17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	238	GLY
1	A	239	GLY
1	A	301	ASN

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	A	418/418 (100%)	391 (94%)	27 (6%)	15 12

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LYS
1	A	69	LEU
1	A	105	ASN
1	A	140	LYS
1	A	142	LYS
1	A	165	LEU
1	A	200	LYS
1	A	208	LYS
1	A	214	LEU
1	A	243	LYS
1	A	261	LYS
1	A	264	THR
1	A	266	ILE
1	A	270	ASN
1	A	273	LYS
1	A	278	LYS
1	A	347	GLN
1	A	352	ASN
1	A	369	GLU
1	A	396	ILE
1	A	417	VAL
1	A	440	LEU

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Mol	Chain	Res	Type
1	A	444	LEU
1	A	457	LYS
1	A	458	ILE
1	A	459	ASN
1	A	466	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	105	ASN
1	A	150	ASN
1	A	185	HIS
1	A	218	ASN
1	A	270	ASN
1	A	415	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](#)

1 non-standard protein/DNA/RNA residue 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
1	PCA	A	1	1	7,8,9	2.08	2 (28%)	9,10,12	1.99	3 (33%)

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
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	CB-CG	-3.38	1.45	1.53
1	A	1	PCA	CD-N	3.25	1.42	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	PCA	CB-CG-CD	4.36	111.15	104.41
1	A	1	PCA	O-C-CA	-2.43	118.53	124.77
1	A	1	PCA	CB-CA-C	-2.03	109.87	112.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	12,12,12	2.28	4 (33%)	17,17,17	1.71	2 (11%)
2	GLC	B	2	2	11,11,12	2.06	2 (18%)	15,15,17	1.57	3 (20%)

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	-	0/2/22/22	0/1/1/1
2	GLC	B	2	2	-	1/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	GLC	C4-C5	5.27	1.64	1.53
2	B	1	GLC	C1-C2	4.84	1.63	1.52
2	B	1	GLC	O4-C4	-3.72	1.33	1.43
2	B	1	GLC	C3-C2	3.51	1.61	1.52
2	B	2	GLC	C1-C2	2.92	1.59	1.52
2	B	1	GLC	C4-C5	2.44	1.58	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	GLC	C1-O5-C5	5.04	123.41	113.65
2	B	2	GLC	C1-O5-C5	3.30	116.60	112.19
2	B	2	GLC	O5-C5-C6	-2.98	101.86	107.66
2	B	2	GLC	C3-C4-C5	-2.61	105.49	110.23
2	B	1	GLC	C1-C2-C3	-2.27	105.73	110.36

There are no chirality outliers.

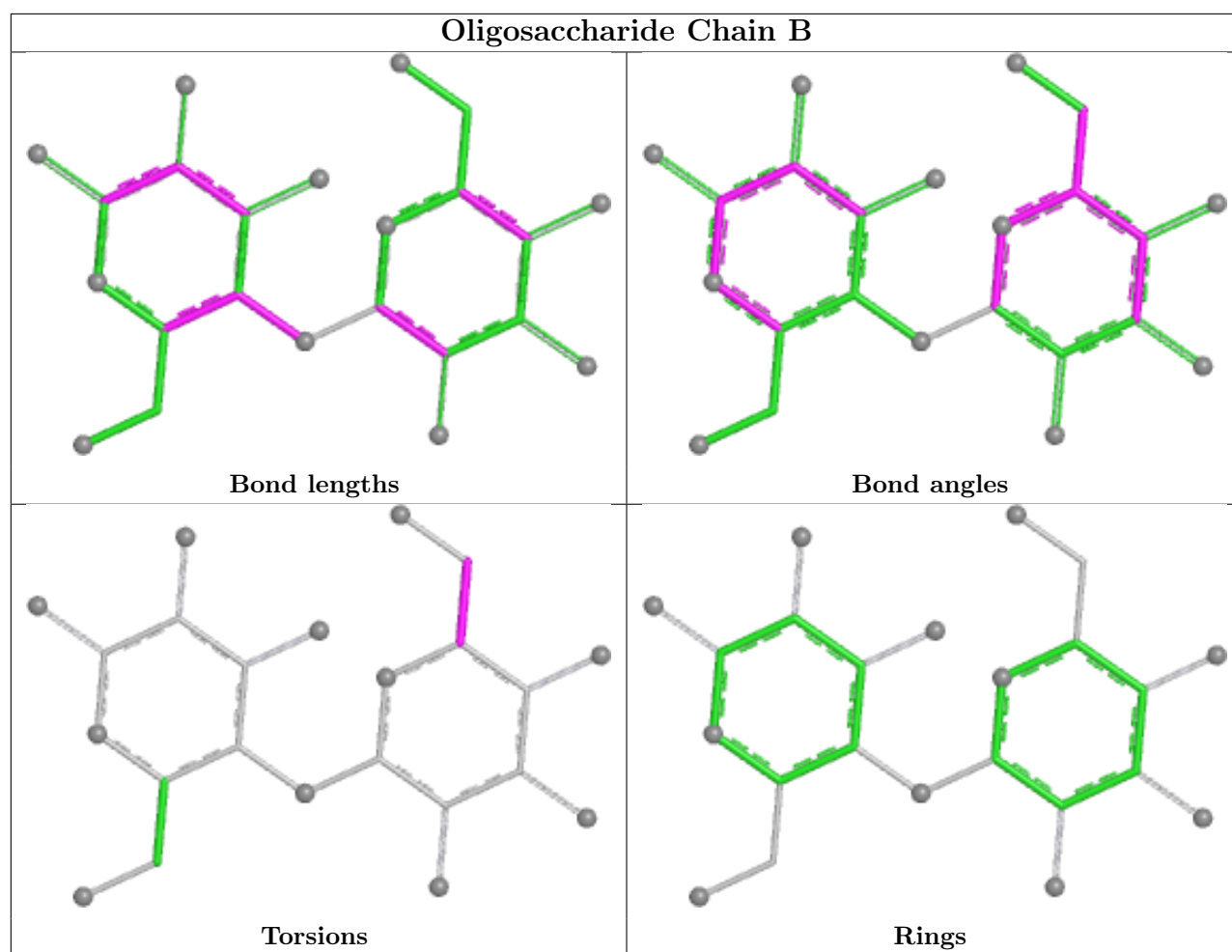
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	GLC	O5-C5-C6-O6

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 [i](#)

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

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.