



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:02 PM UTC

PDB ID : 1UMI / pdb_00001umi
Title : Structural basis of sugar-recognizing ubiquitin ligase
Authors : Mizushima, T.; Hirao, T.; Yoshida, Y.; Lee, S.J.; Chiba, T.; Iwai, K.; Yamaguchi, Y.; Kato, K.; Tsukihara, T.; Tanaka, K.
Deposited on : 2003-10-01
Resolution : 2.40 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

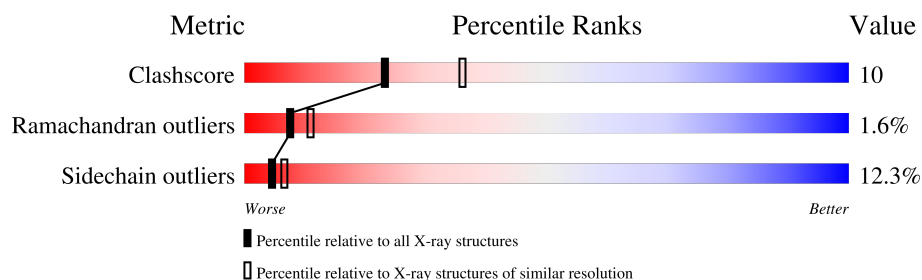
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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	184	
2	B	2	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1562 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 F-box only protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	184	Total	C	N	O	S	0	0	0
			1488	946	249	291	2			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	114	GLY	-	cloning artifact	GB 28436805
A	115	SER	-	cloning artifact	GB 28436805
A	116	HIS	-	cloning artifact	GB 28436805
A	132	ALA	CYS	engineered mutation	GB 28436805
A	151	LYS	ARG	SEE REMARK 999	GB 28436805

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			29	16	2	11			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	45	Total	O	0	0
			45	45		

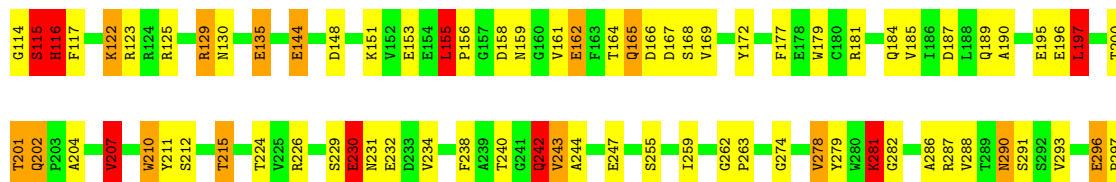
3 Residue-property plots

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.

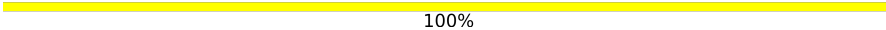
Note EDS was not executed.

- Molecule 1: F-box only protein 2

Chain A: 



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose

Chain B: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.81Å 63.81Å 147.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.72 – 2.40	Depositor
% Data completeness (in resolution range)	99.7 (58.72-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.197 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1562	wwPDB-VP
Average B, all atoms (Å ²)	37.0	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: NDG, NAG

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	2.31	64/1532 (4.2%)	1.96	39/2080 (1.9%)

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	3

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	281	LYS	CE-NZ	11.07	1.82	1.49
1	A	281	LYS	CB-CG	10.49	1.83	1.52
1	A	288	VAL	C-O	8.72	1.33	1.24
1	A	242	GLN	CG-CD	8.67	1.73	1.52
1	A	125	ARG	NE-CZ	8.56	1.42	1.33
1	A	135	GLU	CG-CD	8.32	1.72	1.52
1	A	135	GLU	CD-OE2	8.14	1.40	1.25
1	A	291	SER	N-CA	-8.13	1.36	1.46
1	A	122	LYS	CG-CD	7.95	1.76	1.52
1	A	230	GLU	CG-CD	7.68	1.71	1.52
1	A	114	GLY	N-CA	7.59	1.57	1.45
1	A	242	GLN	CB-CG	7.57	1.75	1.52
1	A	278	VAL	C-O	-7.45	1.15	1.24
1	A	226	ARG	C-O	-7.34	1.14	1.23
1	A	135	GLU	CA-CB	7.24	1.63	1.53
1	A	115	SER	N-CA	7.20	1.54	1.46
1	A	238	PHE	C-O	-7.15	1.15	1.24
1	A	200	THR	CA-CB	6.98	1.62	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	135	GLU	CA-C	6.93	1.63	1.52
1	A	169	VAL	C-O	6.90	1.31	1.24
1	A	181	ARG	CZ-NH1	6.88	1.42	1.32
1	A	197	LEU	CA-C	6.78	1.61	1.52
1	A	281	LYS	CD-CE	6.70	1.72	1.52
1	A	207	VAL	CB-CG1	-6.49	1.31	1.52
1	A	229	SER	CA-C	6.45	1.61	1.53
1	A	116	HIS	N-CA	6.42	1.58	1.46
1	A	215	THR	CA-CB	6.41	1.64	1.53
1	A	201	THR	CA-C	6.35	1.61	1.52
1	A	189	GLN	CG-CD	6.34	1.68	1.52
1	A	290	ASN	C-O	-6.31	1.15	1.23
1	A	230	GLU	CA-CB	6.28	1.63	1.53
1	A	187	ASP	CA-C	6.21	1.60	1.53
1	A	274	GLY	CA-C	-6.03	1.45	1.51
1	A	190	ALA	C-O	-6.02	1.16	1.24
1	A	162	GLU	CA-C	6.00	1.60	1.52
1	A	212	SER	CA-C	-5.98	1.45	1.52
1	A	263	PRO	CA-CB	5.90	1.61	1.53
1	A	244	ALA	C-O	-5.84	1.17	1.24
1	A	122	LYS	CE-NZ	5.76	1.66	1.49
1	A	156	PRO	N-CA	5.76	1.54	1.47
1	A	196	GLU	CA-C	-5.73	1.45	1.52
1	A	114	GLY	C-O	-5.65	1.12	1.23
1	A	202	GLN	N-CA	5.63	1.50	1.46
1	A	123	ARG	N-CA	5.60	1.53	1.46
1	A	204	ALA	CA-CB	5.58	1.62	1.53
1	A	286	ALA	C-O	5.48	1.30	1.23
1	A	148	ASP	N-CA	5.45	1.53	1.46
1	A	156	PRO	CG-CD	5.43	1.69	1.50
1	A	281	LYS	CG-CD	5.43	1.68	1.52
1	A	210	TRP	C-O	5.42	1.30	1.24
1	A	185	VAL	C-O	-5.38	1.18	1.24
1	A	279	TYR	CD2-CE2	5.37	1.54	1.38
1	A	122	LYS	CD-CE	5.34	1.68	1.52
1	A	262	GLY	C-O	-5.30	1.16	1.24
1	A	296	GLU	CD-OE1	5.29	1.35	1.25
1	A	224	THR	C-O	-5.27	1.17	1.24
1	A	200	THR	CA-C	-5.27	1.48	1.53
1	A	234	VAL	C-O	5.18	1.29	1.23
1	A	189	GLN	CA-CB	5.16	1.61	1.53
1	A	125	ARG	CZ-NH1	5.16	1.40	1.32

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	259	ILE	CG1-CD1	5.08	1.71	1.51
1	A	177	PHE	C-O	-5.06	1.17	1.23
1	A	240	THR	C-O	-5.06	1.17	1.24
1	A	162	GLU	CA-CB	5.01	1.61	1.53

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	155	LEU	CA-C-N	-22.13	92.18	119.84
1	A	155	LEU	C-N-CA	-22.13	92.18	119.84
1	A	155	LEU	CA-C-O	-11.87	103.90	120.16
1	A	155	LEU	O-C-N	-11.42	108.19	121.32
1	A	115	SER	N-CA-C	10.78	125.85	110.23
1	A	155	LEU	N-CA-C	10.46	132.93	109.81
1	A	207	VAL	N-CA-CB	-9.41	99.02	111.82
1	A	166	ASP	CB-CA-C	7.83	121.95	111.70
1	A	122	LYS	CA-CB-CG	7.73	129.56	114.10
1	A	116	HIS	N-CA-C	7.06	130.76	111.00
1	A	114	GLY	CA-C-N	7.01	130.66	120.71
1	A	114	GLY	C-N-CA	7.01	130.66	120.71
1	A	195	GLU	CA-CB-CG	6.99	128.09	114.10
1	A	125	ARG	NE-CZ-NH1	6.55	128.05	121.50
1	A	155	LEU	C-N-CD	6.35	151.03	125.00
1	A	201	THR	CA-C-N	-6.25	116.08	122.83
1	A	201	THR	C-N-CA	-6.25	116.08	122.83
1	A	281	LYS	CB-CA-C	6.20	119.15	109.84
1	A	195	GLU	N-CA-C	6.15	118.49	111.11
1	A	189	GLN	CB-CG-CD	6.01	122.82	112.60
1	A	144	GLU	CA-CB-CG	5.94	125.99	114.10
1	A	207	VAL	CB-CA-C	5.87	118.34	110.42
1	A	189	GLN	N-CA-CB	5.78	118.62	110.12
1	A	230	GLU	CB-CG-CD	5.70	122.29	112.60
1	A	129	ARG	CB-CG-CD	5.53	124.03	111.30
1	A	166	ASP	N-CA-C	-5.49	98.26	107.32
1	A	156	PRO	N-CA-CB	5.44	108.96	103.25
1	A	144	GLU	N-CA-C	-5.43	98.51	108.02
1	A	190	ALA	N-CA-C	-5.43	105.92	112.54
1	A	282	GLY	N-CA-C	5.41	119.93	112.52
1	A	242	GLN	N-CA-C	-5.37	101.70	109.59
1	A	169	VAL	O-C-N	5.28	128.75	122.83
1	A	243	VAL	N-CA-C	5.25	116.15	108.53
1	A	200	THR	CA-C-O	-5.15	115.05	120.71

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	SER	CA-C-N	5.13	127.67	120.28
1	A	229	SER	C-N-CA	5.13	127.67	120.28
1	A	162	GLU	CB-CA-C	5.12	117.88	109.90
1	A	296	GLU	N-CA-C	5.08	117.99	110.32
1	A	135	GLU	CA-CB-CG	5.06	124.22	114.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	115	SER	Peptide
1	A	116	HIS	Peptide
1	A	155	LEU	Peptide

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	1488	0	1368	30	0
2	B	29	0	22	0	0
3	A	45	0	0	2	0
All	All	1562	0	1390	30	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 10.

All (30) 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:242:GLN:CB	1:A:242:GLN:CG	1.75	1.65
1:A:122:LYS:CD	1:A:122:LYS:CG	1.76	1.62
1:A:281:LYS:CB	1:A:281:LYS:CG	1.83	1.53
1:A:281:LYS:CE	1:A:281:LYS:NZ	1.82	1.42
1:A:115:SER:HB3	3:A:43:HOH:O	1.37	1.24
1:A:197:LEU:C	1:A:197:LEU:HD12	2.00	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:LEU:HD13	1:A:172:TYR:HD2	1.45	0.80
1:A:122:LYS:CD	1:A:122:LYS:CB	2.60	0.79
1:A:230:GLU:HB3	3:A:10:HOH:O	1.84	0.77
1:A:115:SER:HA	1:A:116:HIS:CB	2.14	0.76
1:A:155:LEU:HD13	1:A:172:TYR:CD2	2.29	0.66
1:A:197:LEU:HD12	1:A:197:LEU:O	1.95	0.65
1:A:231:ASN:O	1:A:232:GLU:HB2	2.05	0.57
1:A:115:SER:HA	1:A:116:HIS:HB2	1.88	0.54
1:A:197:LEU:C	1:A:197:LEU:CD1	2.79	0.54
1:A:210:TRP:CD1	1:A:290:ASN:HD22	2.33	0.46
1:A:117:PHE:CD1	1:A:297:PRO:HB2	2.51	0.46
1:A:117:PHE:CE1	1:A:297:PRO:HB2	2.51	0.45
1:A:159:ASN:HB3	1:A:215:THR:OG1	2.17	0.45
1:A:122:LYS:CD	1:A:122:LYS:HB2	2.48	0.44
1:A:201:THR:O	1:A:202:GLN:C	2.60	0.44
1:A:207:VAL:HG22	1:A:293:VAL:HG22	1.99	0.44
1:A:172:TYR:CD1	1:A:172:TYR:C	2.96	0.43
1:A:281:LYS:CG	1:A:281:LYS:CA	2.86	0.43
1:A:179:TRP:HZ2	1:A:242:GLN:HG3	1.84	0.43
1:A:151:LYS:HE3	1:A:153:GLU:OE2	2.19	0.42
1:A:116:HIS:CD2	1:A:116:HIS:C	2.98	0.41
1:A:164:THR:O	1:A:165:GLN:HB2	2.20	0.41
1:A:130:ASN:ND2	1:A:135:GLU:H	2.19	0.41
1:A:211:TYR:HA	1:A:287:ARG:O	2.21	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	182/184 (99%)	169 (93%)	10 (6%)	3 (2%)	7 11

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	116	HIS
1	A	165	GLN
1	A	167	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	A	155/155 (100%)	136 (88%)	19 (12%)	4 6

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	HIS
1	A	129	ARG
1	A	144	GLU
1	A	155	LEU
1	A	158	ASP
1	A	161	VAL
1	A	162	GLU
1	A	168	SER
1	A	184	GLN
1	A	197	LEU
1	A	207	VAL
1	A	230	GLU
1	A	242	GLN
1	A	243	VAL
1	A	247	GLU
1	A	255	SER
1	A	278	VAL
1	A	281	LYS
1	A	296	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	ASN

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 ⓘ

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	NDG	B	1	2	15,15,15	2.08	6 (40%)	21,21,21	3.42	12 (57%)
2	NAG	B	2	2	14,14,15	1.52	2 (14%)	17,19,21	3.22	9 (52%)

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	NDG	B	1	2	-	2/6/26/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NDG	O1-C1	4.79	1.54	1.39
2	B	2	NAG	O7-C7	-3.55	1.15	1.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NDG	O6-C6	-3.43	1.28	1.42
2	B	2	NAG	O5-C1	-2.80	1.39	1.43
2	B	1	NDG	O5-C5	-2.20	1.39	1.44
2	B	1	NDG	O5-C1	-2.18	1.37	1.42
2	B	1	NDG	C3-C2	-2.14	1.49	1.53
2	B	1	NDG	C8-C7	2.05	1.54	1.50

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NDG	O5-C5-C4	8.44	124.91	109.70
2	B	2	NAG	O7-C7-C8	-6.86	109.84	122.05
2	B	1	NDG	C1-C2-C3	6.52	119.43	110.54
2	B	2	NAG	O5-C5-C4	5.51	124.23	110.83
2	B	1	NDG	C1-C2-N2	5.03	116.55	110.73
2	B	2	NAG	O7-C7-N2	4.88	130.60	121.98
2	B	2	NAG	C1-O5-C5	4.22	117.84	112.19
2	B	1	NDG	O7-C7-N2	4.18	129.37	121.98
2	B	2	NAG	C2-N2-C7	4.07	128.35	122.90
2	B	1	NDG	O5-C5-C6	3.69	115.58	106.44
2	B	1	NDG	C8-C7-N2	-3.65	110.07	116.12
2	B	2	NAG	O4-C4-C3	3.36	118.30	110.38
2	B	1	NDG	O1-C1-O5	-3.31	100.58	110.41
2	B	2	NAG	C4-C3-C2	3.11	115.57	111.02
2	B	1	NDG	O6-C6-C5	2.92	121.28	111.33
2	B	1	NDG	O5-C1-C2	2.83	112.36	109.52
2	B	1	NDG	O4-C4-C5	2.77	116.16	109.32
2	B	1	NDG	O1-C1-C2	-2.76	103.47	109.22
2	B	1	NDG	C4-C3-C2	2.68	114.30	110.40
2	B	2	NAG	O3-C3-C2	2.22	114.02	109.40
2	B	2	NAG	O4-C4-C5	2.07	114.41	109.32

There are no chirality outliers.

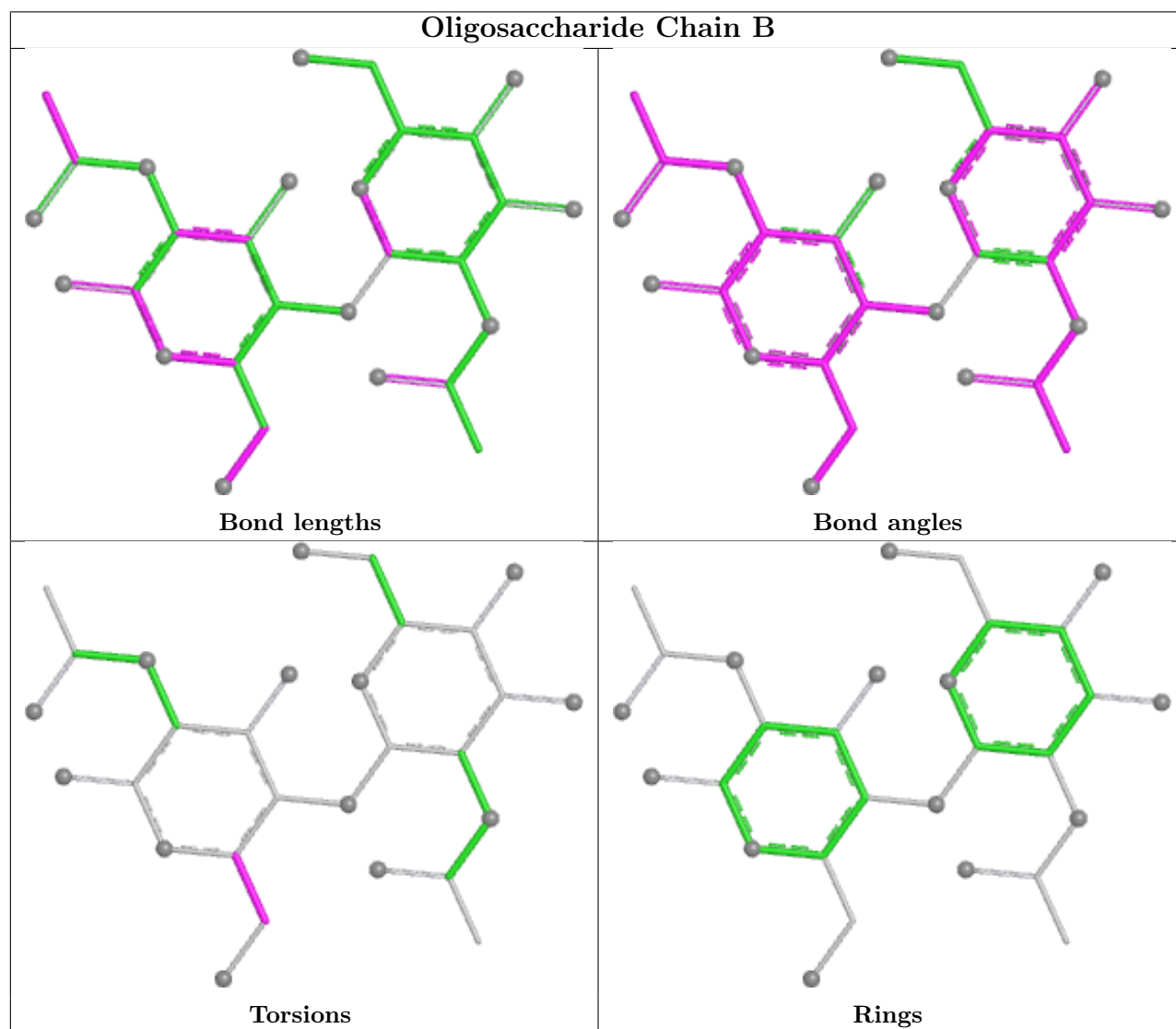
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NDG	C4-C5-C6-O6
2	B	1	NDG	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](#)

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.