



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:39 AM UTC

PDB ID : 1OWQ / pdb_00001owq
Title : Crystal structure of a 40 kDa signalling protein (SPC-40) secreted during involution
Authors : Kumar, J.; Sharma, S.; Jasti, J.; Bhushan, A.; Singh, T.P.
Deposited on : 2003-03-29
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

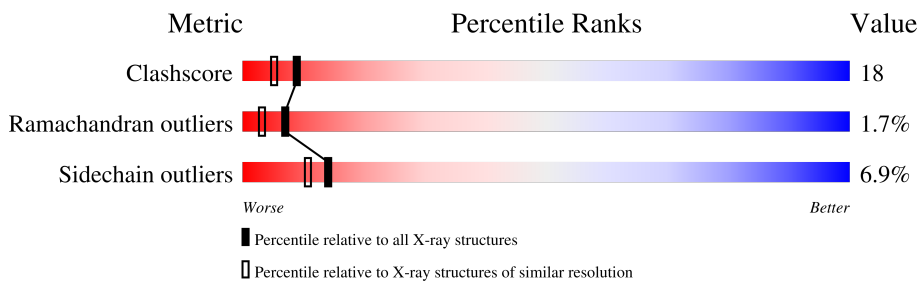
1 Overall quality at a glance

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	361	 71% 24% . .
2	B	3	 67% 33%

2 Entry composition [i](#)

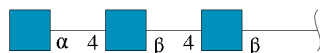
There are 3 unique types of molecules in this entry. The entry contains 3154 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 signal processing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	361	Total	C	N	O	S	0	0	0
			2873	1834	501	529	9			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			42	24	3	15			

- Molecule 3 is water.

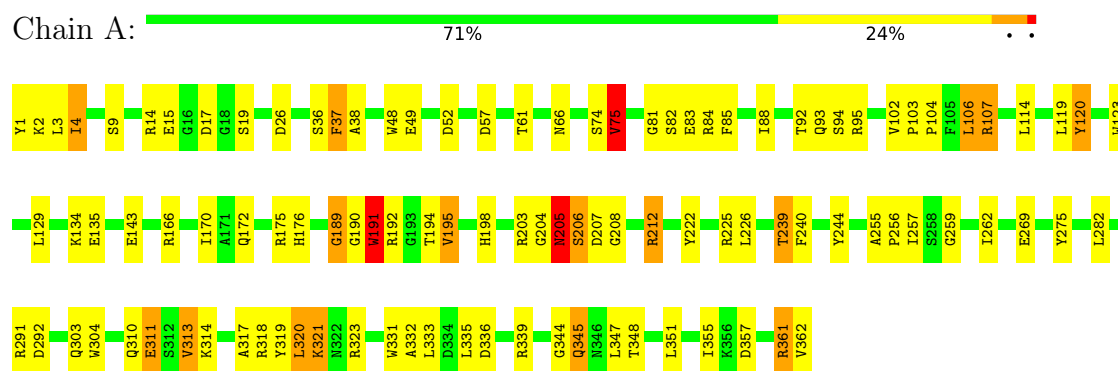
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	239	Total	O	0	0
			239	239		

3 Residue-property plots

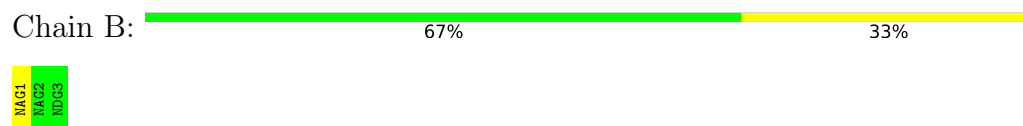
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: signal processing protein



- Molecule 2: 2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-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 21	Depositor
Cell constants a, b, c, α , β , γ	62.15Å 67.02Å 107.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	95.3 (20.00-2.00)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.203 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3154	wwPDB-VP
Average B, all atoms (Å ²)	35.0	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: 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	0.39	0/2951	0.95	13/4003 (0.3%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	36	SER	N-CA-C	8.33	121.82	108.41
1	A	37	PHE	N-CA-C	7.78	127.36	110.80
1	A	361	ARG	N-CA-C	-6.76	103.83	111.14
1	A	38	ALA	N-CA-C	-6.61	100.18	110.42
1	A	336	ASP	N-CA-C	-6.06	102.71	110.53
1	A	333	LEU	N-CA-C	-5.92	104.91	111.71
1	A	66	ASN	CA-C-N	5.62	125.30	119.56
1	A	66	ASN	C-N-CA	5.62	125.30	119.56
1	A	170	ILE	N-CA-C	5.42	116.05	110.36
1	A	26	ASP	CA-C-N	5.32	125.13	119.28
1	A	26	ASP	C-N-CA	5.32	125.13	119.28
1	A	212	ARG	N-CA-C	-5.32	106.75	113.18
1	A	75	VAL	CB-CA-C	-5.24	103.59	110.98

There are no chirality outliers.

There are no planarity outliers.

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	A	2873	0	2792	106	0
2	B	42	0	36	0	0
3	A	239	0	0	14	0
All	All	3154	0	2828	106	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 18.

All (106) 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:321:LYS:NZ	1:A:362:VAL:HB	1.83	0.93
1:A:192:ARG:NE	1:A:192:ARG:HA	1.91	0.84
1:A:192:ARG:HA	1:A:192:ARG:HE	1.45	0.81
1:A:204:GLY:HA2	1:A:292:ASP:HB3	1.61	0.80
1:A:222:TYR:O	1:A:226:LEU:HD23	1.82	0.80
1:A:321:LYS:HZ3	1:A:362:VAL:HB	1.51	0.74
1:A:57:ASP:O	1:A:61:THR:HG23	1.88	0.73
1:A:321:LYS:HG3	1:A:362:VAL:OXT	1.88	0.73
1:A:348:THR:HG22	3:A:473:HOH:O	1.90	0.71
1:A:321:LYS:HZ2	1:A:362:VAL:HB	1.56	0.70
1:A:203:ARG:HB3	1:A:212:ARG:HH11	1.56	0.70
1:A:348:THR:HG21	3:A:562:HOH:O	1.91	0.70
1:A:83:GLU:H	1:A:83:GLU:CD	1.99	0.69
1:A:357:ASP:O	1:A:361:ARG:HD3	1.94	0.68
1:A:212:ARG:O	1:A:212:ARG:HD2	1.94	0.68
1:A:319:TYR:CZ	1:A:323:ARG:HD2	2.30	0.66
1:A:317:ALA:HA	1:A:320:LEU:CD1	2.26	0.65
1:A:120:TYR:CD2	1:A:120:TYR:N	2.61	0.65
1:A:292:ASP:HB2	3:A:448:HOH:O	1.96	0.65
1:A:92:THR:HG22	1:A:95:ARG:HH22	1.62	0.65
1:A:134:LYS:HG2	1:A:176:HIS:NE2	2.12	0.64
1:A:189:GLY:HA2	1:A:244:TYR:OH	1.99	0.63
1:A:82:SER:HB2	3:A:457:HOH:O	1.98	0.63
1:A:313:VAL:HG13	1:A:355:ILE:CG1	2.30	0.62
1:A:4:ILE:HD12	1:A:4:ILE:N	2.15	0.61
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.30	0.61
1:A:1:TYR:CE2	1:A:362:VAL:O	2.55	0.59
1:A:205:ASN:HD22	1:A:205:ASN:N	2.00	0.59
1:A:239:THR:HG21	1:A:332:ALA:O	2.03	0.59
1:A:48:TRP:HB3	3:A:464:HOH:O	2.02	0.58
1:A:313:VAL:CG1	1:A:355:ILE:HG13	2.34	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:ARG:HD3	1:A:212:ARG:CZ	2.33	0.58
1:A:203:ARG:HD3	1:A:212:ARG:NH1	2.19	0.58
1:A:190:GLY:H	1:A:244:TYR:HE2	1.53	0.57
1:A:240:PHE:HB3	1:A:335:LEU:HD13	1.87	0.57
1:A:103:PRO:HB2	1:A:104:PRO:HD3	1.87	0.56
1:A:198:HIS:H	1:A:198:HIS:CD2	2.24	0.56
1:A:102:VAL:HG12	1:A:106:LEU:HD22	1.86	0.55
1:A:191:TRP:H	1:A:191:TRP:CD1	2.24	0.55
1:A:239:THR:HG22	1:A:335:LEU:HB2	1.88	0.55
1:A:323:ARG:NH1	3:A:467:HOH:O	2.39	0.55
1:A:15:GLU:HG2	3:A:425:HOH:O	2.07	0.54
1:A:190:GLY:O	1:A:192:ARG:N	2.40	0.54
1:A:37:PHE:HA	1:A:74:SER:O	2.08	0.53
1:A:205:ASN:N	1:A:205:ASN:ND2	2.56	0.52
1:A:262:ILE:H	1:A:303:GLN:HE22	1.56	0.52
1:A:84:ARG:O	1:A:88:ILE:HG12	2.10	0.52
1:A:314:LYS:O	1:A:318:ARG:HG3	2.11	0.51
1:A:291:ARG:HG3	1:A:292:ASP:N	2.26	0.50
1:A:135:GLU:HG2	3:A:546:HOH:O	2.11	0.50
1:A:2:LYS:HB3	1:A:4:ILE:HD11	1.94	0.50
1:A:317:ALA:O	1:A:320:LEU:HD13	2.12	0.50
1:A:195:VAL:HG23	1:A:257:ILE:HD11	1.95	0.49
1:A:311:GLU:HB2	3:A:471:HOH:O	2.12	0.49
1:A:195:VAL:HG22	1:A:304:TRP:CE3	2.48	0.49
1:A:212:ARG:O	1:A:212:ARG:CD	2.61	0.49
1:A:332:ALA:HB3	1:A:335:LEU:HD12	1.95	0.48
1:A:75:VAL:HG22	1:A:114:LEU:HD11	1.94	0.48
1:A:262:ILE:H	1:A:303:GLN:NE2	2.11	0.48
1:A:344:GLY:O	1:A:345:GLN:C	2.56	0.48
1:A:190:GLY:C	1:A:192:ARG:N	2.72	0.48
1:A:321:LYS:HG3	1:A:362:VAL:C	2.39	0.48
1:A:61:THR:HG22	3:A:553:HOH:O	2.13	0.48
1:A:313:VAL:HG13	1:A:355:ILE:HG13	1.94	0.48
1:A:134:LYS:HG2	1:A:176:HIS:CD2	2.49	0.47
1:A:207:ASP:HA	3:A:578:HOH:O	2.14	0.47
1:A:123:TRP:HA	1:A:166:ARG:O	2.13	0.47
1:A:269:GLU:HG3	3:A:561:HOH:O	2.13	0.47
1:A:332:ALA:HB1	1:A:335:LEU:HG	1.95	0.47
1:A:49:GLU:N	1:A:52:ASP:OD2	2.46	0.47
1:A:291:ARG:NH1	1:A:292:ASP:OD1	2.47	0.47
1:A:320:LEU:HD22	1:A:321:LYS:N	2.29	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:GLY:O	1:A:206:SER:N	2.48	0.46
1:A:313:VAL:HG13	1:A:355:ILE:HG12	1.96	0.46
1:A:244:TYR:HB3	1:A:257:ILE:HD12	1.97	0.46
1:A:320:LEU:HD22	1:A:320:LEU:C	2.40	0.46
1:A:75:VAL:CG2	1:A:114:LEU:HD11	2.46	0.46
1:A:190:GLY:C	1:A:192:ARG:H	2.22	0.46
1:A:192:ARG:C	1:A:194:THR:H	2.24	0.46
1:A:102:VAL:HB	1:A:103:PRO:HD3	1.97	0.45
1:A:102:VAL:CG1	1:A:106:LEU:HD22	2.47	0.45
1:A:319:TYR:OH	1:A:323:ARG:HD2	2.17	0.45
1:A:189:GLY:O	1:A:191:TRP:CD1	2.71	0.44
1:A:4:ILE:N	1:A:4:ILE:CD1	2.81	0.44
1:A:361:ARG:O	1:A:362:VAL:HG22	2.17	0.44
1:A:361:ARG:HG2	3:A:540:HOH:O	2.16	0.44
1:A:257:ILE:CG2	1:A:259:GLY:H	2.31	0.44
1:A:317:ALA:HA	1:A:320:LEU:HD13	2.00	0.43
1:A:49:GLU:HB2	1:A:52:ASP:OD1	2.19	0.43
1:A:361:ARG:C	1:A:362:VAL:CG2	2.92	0.43
1:A:92:THR:HG22	1:A:95:ARG:NH2	2.32	0.43
1:A:203:ARG:HG2	3:A:461:HOH:O	2.18	0.43
1:A:107:ARG:HD3	1:A:143:GLU:OE2	2.19	0.42
1:A:172:GLN:O	1:A:175:ARG:HG2	2.19	0.42
1:A:17:ASP:HB3	1:A:339:ARG:HD2	2.00	0.42
1:A:83:GLU:CD	1:A:83:GLU:N	2.75	0.42
1:A:81:GLY:O	1:A:84:ARG:HB2	2.19	0.42
1:A:345:GLN:HE21	1:A:345:GLN:HB3	1.51	0.41
1:A:93:GLN:HG3	1:A:94:SER:N	2.35	0.41
1:A:2:LYS:HB3	1:A:4:ILE:CD1	2.51	0.41
1:A:331:TRP:O	1:A:332:ALA:HB3	2.20	0.41
1:A:310:GLN:O	1:A:314:LYS:HG3	2.20	0.41
1:A:255:ALA:HA	1:A:256:PRO:HD3	1.91	0.41
1:A:119:LEU:HA	1:A:119:LEU:HD23	1.76	0.40
1:A:14:ARG:O	1:A:19:SER:HB2	2.21	0.40
1:A:239:THR:O	1:A:275:TYR:HB2	2.22	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	359/361 (99%)	337 (94%)	16 (4%)	6 (2%)	7 3

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
1	A	191	TRP
1	A	206	SER
1	A	120	TYR
1	A	208	GLY
1	A	189	GLY

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	303/303 (100%)	282 (93%)	21 (7%)	14 11

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	4	ILE
1	A	9	SER
1	A	75	VAL
1	A	85	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	106	LEU
1	A	107	ARG
1	A	129	LEU
1	A	191	TRP
1	A	195	VAL
1	A	205	ASN
1	A	225	ARG
1	A	239	THR
1	A	282	LEU
1	A	311	GLU
1	A	313	VAL
1	A	320	LEU
1	A	321	LYS
1	A	345	GLN
1	A	347	LEU
1	A	351	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	128	HIS
1	A	150	GLN
1	A	198	HIS
1	A	205	ASN
1	A	265	GLN
1	A	294	GLN
1	A	303	GLN
1	A	310	GLN
1	A	345	GLN

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

3 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	NAG	B	1	2,1	14,14,15	0.53	0	17,19,21	0.77	1 (5%)
2	NAG	B	2	2	14,14,15	0.66	0	17,19,21	0.73	0
2	NDG	B	3	2	14,14,15	0.56	0	17,19,21	0.68	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	NAG	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	NDG	B	3	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	C2-N2-C7	-2.01	120.20	122.90

There are no chirality outliers.

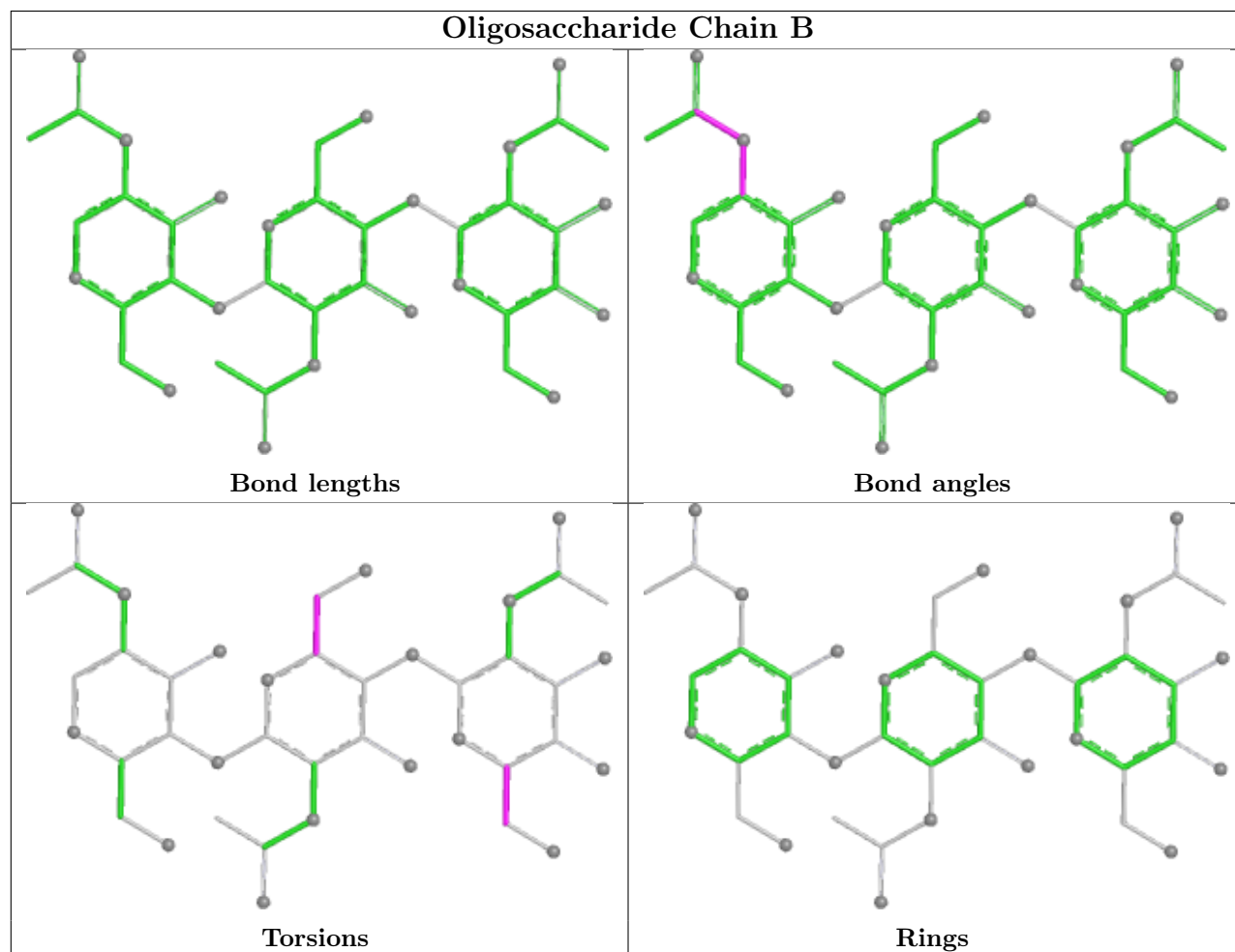
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	3	NDG	O5-C5-C6-O6
2	B	3	NDG	C4-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
2	B	2	NAG	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.