



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:38 AM UTC

PDB ID : 7WHB / pdb_00007whb
EMDB ID : EMD-32498
Title : SARS-CoV-2 spike in complex with the ZB8 neutralizing antibody Fab (3U)
Authors : Zeng, J.W.; Ge, J.W.; Wang, X.Q.
Deposited on : 2021-12-30
Resolution : 2.67 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

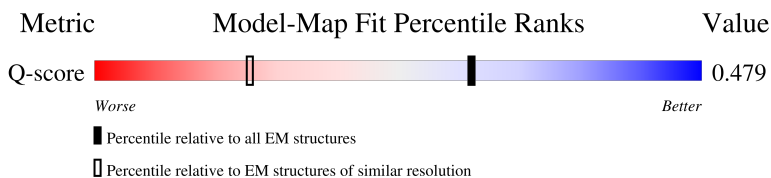
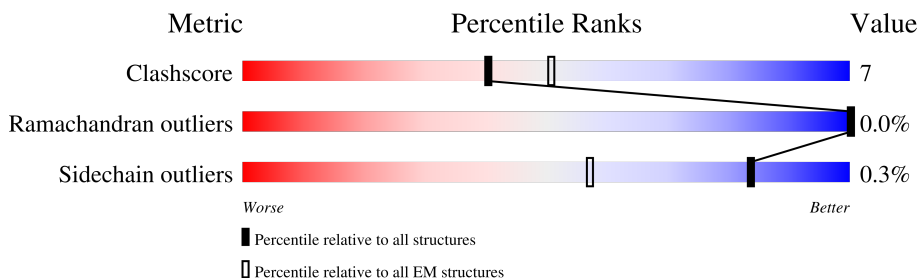
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.67 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.



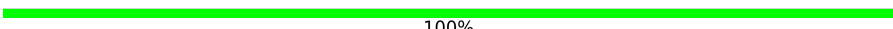
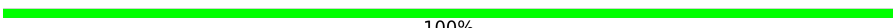
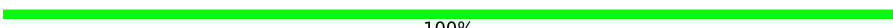
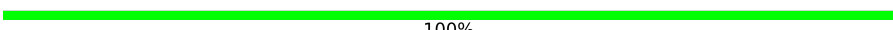
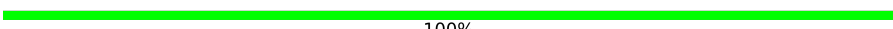
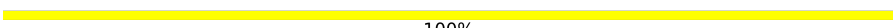
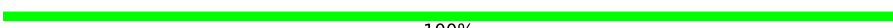
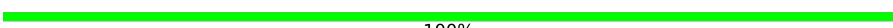
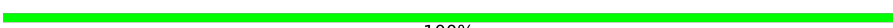
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	9182 (2.17 - 3.17)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1120	
1	B	1120	
1	C	1120	
2	D	224	

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Mol	Chain	Length	Quality of chain
2	G	224	 79%21%
2	J	224	 84%16%
3	E	214	 84%16%
3	H	214	 82%18%
3	K	214	 81%19%
4	F	2	 100%
4	I	2	 50%50%
4	L	2	 50%50%
4	M	2	 50%50%
4	N	2	 100%
4	O	2	 100%
4	P	2	 100%
4	Q	2	 100%
4	R	2	 100%
4	S	2	 50%50%
4	T	2	 100%
4	U	2	 100%
4	V	2	 50%50%
4	W	2	 100%
4	X	2	 100%
4	Y	2	 50%50%
4	Z	2	 50%50%
4	a	2	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 34209 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1006	Total	C	N	O	S	0	0
			7863	5019	1308	1500	36		
1	B	1007	Total	C	N	O	S	0	0
			7870	5023	1310	1501	36		
1	C	1004	Total	C	N	O	S	0	0
			7853	5014	1307	1496	36		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2

- Molecule 2 is a protein called antibody ZB8 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	224	Total	C	N	O	S	0	0
			1646	1034	276	328	8		
2	G	224	Total	C	N	O	S	0	0
			1646	1034	276	328	8		
2	J	224	Total	C	N	O	S	0	0
			1646	1034	276	328	8		

- Molecule 3 is a protein called antibody ZB8 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	214	Total	C	N	O	S	0	0
			1643	1029	279	330	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	214	Total	C	N	O	S	0	0
			1643	1029	279	330	5		
3	K	214	Total	C	N	O	S	0	0
			1643	1029	279	330	5		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
4	F	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	L	2	Total	C	N	O	0	0
			28	16	2	10		
4	M	2	Total	C	N	O	0	0
			28	16	2	10		
4	N	2	Total	C	N	O	0	0
			28	16	2	10		
4	O	2	Total	C	N	O	0	0
			28	16	2	10		
4	P	2	Total	C	N	O	0	0
			28	16	2	10		
4	Q	2	Total	C	N	O	0	0
			28	16	2	10		
4	R	2	Total	C	N	O	0	0
			28	16	2	10		
4	S	2	Total	C	N	O	0	0
			28	16	2	10		
4	T	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		
4	V	2	Total	C	N	O	0	0
			28	16	2	10		
4	W	2	Total	C	N	O	0	0
			28	16	2	10		
4	X	2	Total	C	N	O	0	0
			28	16	2	10		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	Y	2	Total	C	N	O	0	0
			28	16	2	10		
4	Z	2	Total	C	N	O	0	0
			28	16	2	10		
4	a	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	

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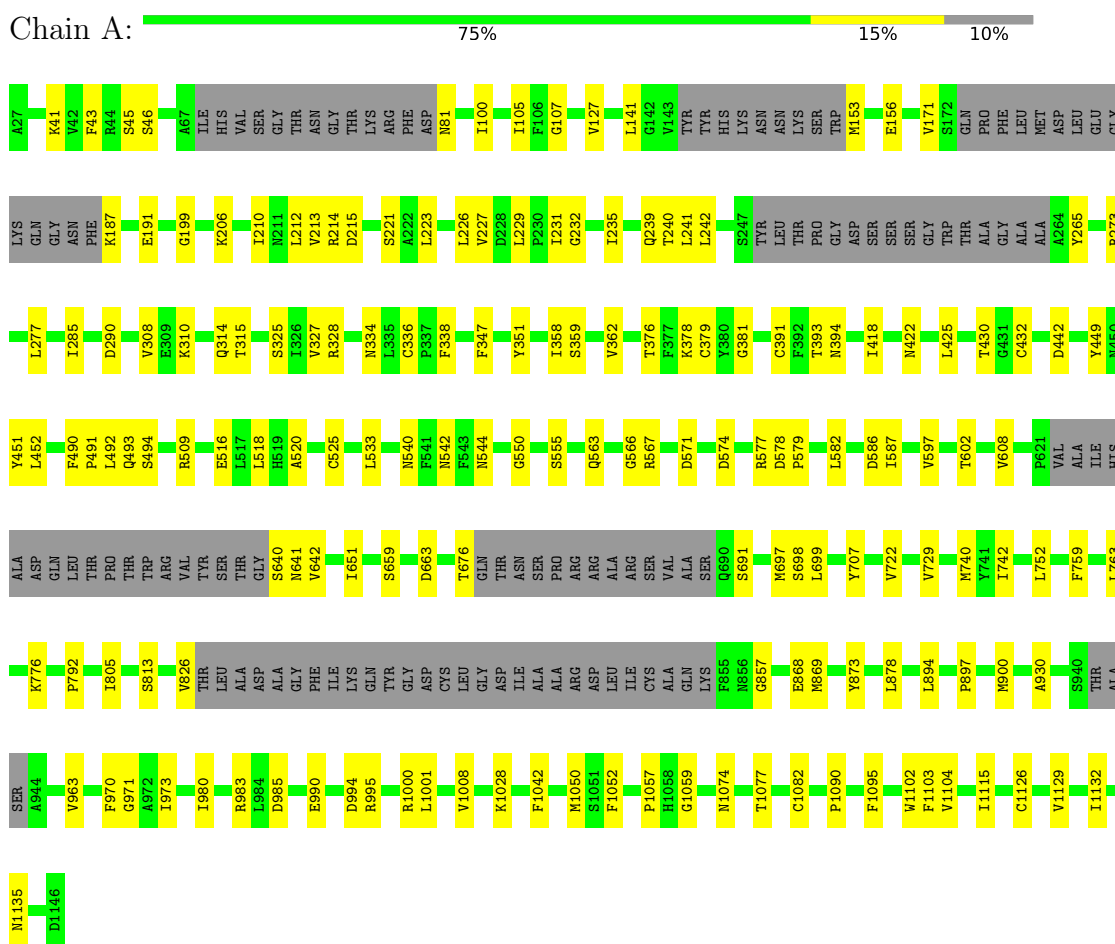
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Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	

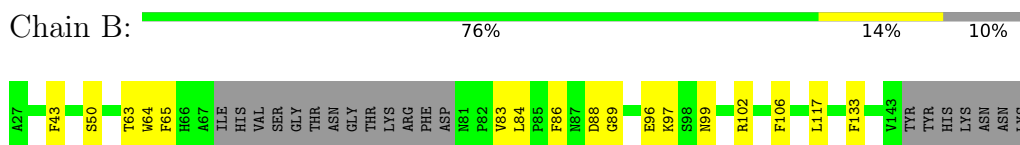
3 Residue-property plots [i](#)

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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

• Molecule 1: Spike glycoprotein



• Molecule 1: Spike glycoprotein

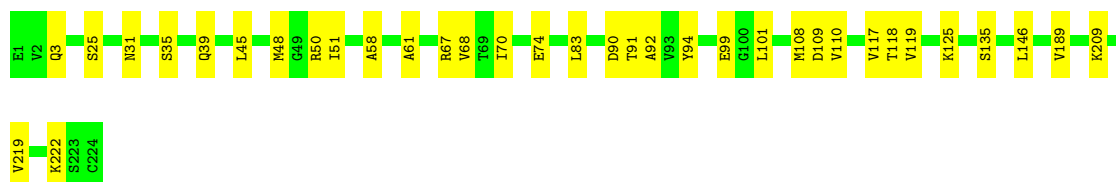




A944	S813	SER	L518	T285	S162	A27
D950	K814	M641	L519	T286	C166	R34
V951	V826	N658	A520	D287	T167	K41
G971	THR	S659	P521	A298		V42
	LEU	Y660	A522	V289	S172	F43
L977	ALA	E661	A522		GLN	S50
	ASP	C662	C525	T299	PRD	F65
L981	ALA				PHE	H66
L981	GLY	Y674	L533	T302	LEU	A67
E990	PHE	Q675	V534	L303	MET	ILE
	ILE	T676	K535	Y313	ASP	HIS
	LYS	GLN			LEU	VAL
R995	GLN	THR	N542	R319	GLU	SER
	TYR	ASN	F543	L303	GLY	GLY
L1001	GLY	SER	N544	P322	LYS	THR
K1028	ASP	PRO	G545		GLN	GLY
	CYS	ARG	L546	V327	ASN	ARG
F1042	LEU	ARG		R328	PHE	ASP
	GLY	ALA	L560			N81
L1049	ILE	ARG	P561	C336	K187	L84
M1050	ASP	SER	F562	P337	N188	K97
S1051	ALA	VAL	Q563	F338	L189	S98
F1052	ALA	ALA				N99
	ARG	SER	G566	F347	N196	R102
V1061	ASP	Q690	R567			F106
V1065	ILE	S691	A570	C379	F201	L117
E1072	CYS	I692	D571	S383	L212	L117
T1077	ALA	I693				M121
	GLN	M697	D574	K386	D215	M122
C1082	K854	S698	R577	C391	L216	V130
	T866	L699	D578	F392	P217	C131
C1082	D867	Y707	P579	T393	Q239	E132
F1095	E868			N394	T240	F133
	M869	A713	L582	V395		V143
W1102	Y873	I714			S247	TYR
F1103		P715	V597	Q404	TYR	LEU
V1104	L878	V722	V620	K417	THR	M121
I1115	M902	I726	PRO	I418	PRO	M122
C1126	F906	L752	VAL	N422	GLY	V130
N1135	N907	I15	ALA		ASP	C131
	G908	HIS	ILE	C432	SER	E132
	I909	F759	ALA		SER	F133
D1146		Q762	ASP	D442	GLY	
	L916	R765	GLN		TRP	V143
	G932	Q774	THR	Y451	THR	TYR
	Q935		PRO	F491	ALA	THR
		T778	THR	L492	ALA	HIS
	S939	K790	TRP		ALA	LYS
	THR		ARG	G504	ALA	ASN
	ALA		VAL		A264	ASN
	SER		TYR	V508	L276	LYS
			SER	R509	L277	LYS
			THR		K278	TRP
			GLY			M153

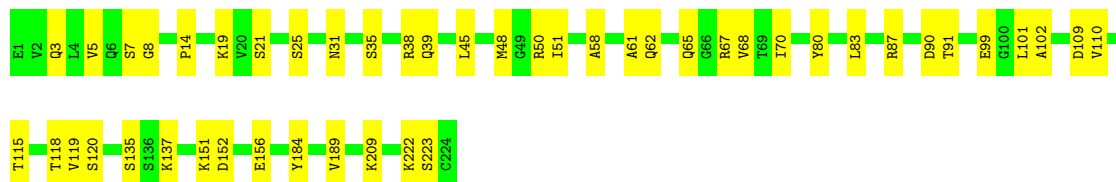
- Molecule 2: antibody ZB8 heavy chain





- Molecule 2: antibody ZB8 heavy chain

Chain G: 79% 21%



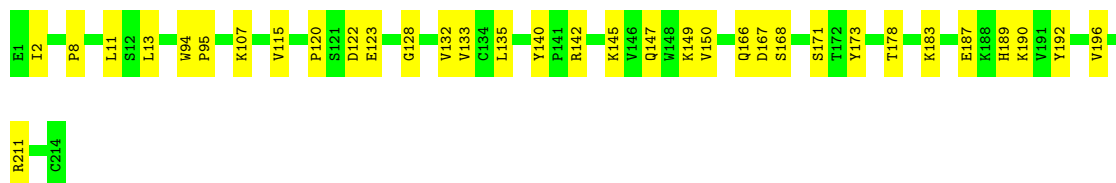
- Molecule 2: antibody ZB8 heavy chain

Chain J: 84% 16%



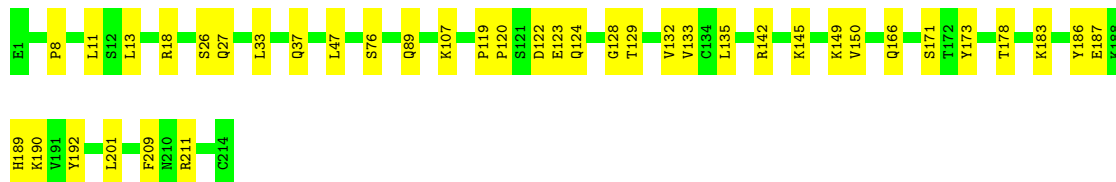
- Molecule 3: antibody ZB8 light chain

Chain E: 84% 16%



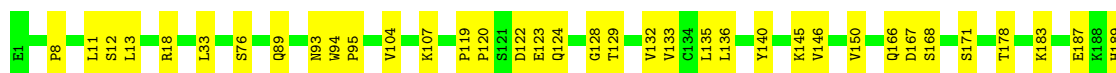
- Molecule 3: antibody ZB8 light chain

Chain H: 82% 18%

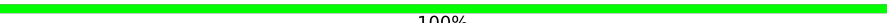


- Molecule 3: antibody ZB8 light chain

Chain K: 81% 19%



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

Chain F:  100%



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

Chain I:  50%



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

Chain L:  50%



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

Chain M:  50%



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

Chain N:  100%



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

Chain O:  100%



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

Chain P:  100%



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

Chain Q:  100%



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

Chain R:  100%



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

Chain S:  50% 50%



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

Chain T:  100%



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

Chain U:  100%



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

Chain V:  50% 50%

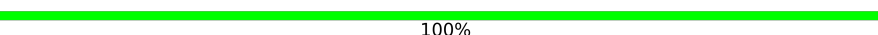


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W:  100%



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

Chain X:  100%



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

Chain Y:  50% 50%

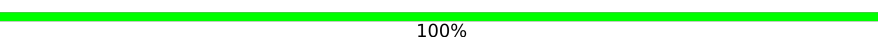


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:  50% 50%



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

Chain a:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	351095	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.100	Depositor
Minimum map value	-0.048	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size ($\text{\AA}$)	395.24402, 395.24402, 395.24402	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0979, 1.0979, 1.0979	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.12	0/8039	0.31	0/10936
1	B	0.12	0/8045	0.31	0/10942
1	C	0.12	0/8028	0.32	0/10919
2	D	0.16	0/1682	0.37	0/2287
2	G	0.15	0/1682	0.37	0/2287
2	J	0.15	0/1682	0.37	0/2287
3	E	0.13	0/1679	0.30	0/2280
3	H	0.12	0/1679	0.30	0/2280
3	K	0.12	0/1679	0.31	0/2280
All	All	0.13	0/34195	0.32	0/46498

There are no bond length outliers.

There are no bond angle outliers.

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	7863	0	7661	110	0
1	B	7870	0	7672	106	0
1	C	7853	0	7655	122	0
2	D	1646	0	1627	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	1646	0	1627	31	0
2	J	1646	0	1627	21	0
3	E	1643	0	1601	25	0
3	H	1643	0	1601	29	0
3	K	1643	0	1601	27	0
4	F	28	0	25	0	0
4	I	28	0	25	1	0
4	L	28	0	25	1	0
4	M	28	0	25	1	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
4	Q	28	0	25	0	0
4	R	28	0	25	0	0
4	S	28	0	25	0	0
4	T	28	0	25	2	0
4	U	28	0	25	0	0
4	V	28	0	25	1	0
4	W	28	0	25	0	0
4	X	28	0	25	0	0
4	Y	28	0	25	1	0
4	Z	28	0	25	2	0
4	a	28	0	25	0	0
5	A	84	0	78	1	0
5	B	70	0	65	0	0
5	C	98	0	90	4	0
All	All	34209	0	33355	472	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 7.

The worst 5 of 472 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:C:674:TYR:CZ	1:C:690:GLN:N	2.22	1.07
1:C:811:LYS:HB2	1:C:812:PRO:HD2	1.50	0.91
1:C:811:LYS:HB2	1:C:812:PRO:CD	2.11	0.79
1:A:199:GLY:HA2	1:A:232:GLY:HA2	1.66	0.76
1:B:327:VAL:HG12	1:B:542:ASN:HB3	1.67	0.76

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 PDB entries followed by that with respect to all EM entries.

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	988/1120 (88%)	932 (94%)	56 (6%)	0	100	100
1	B	989/1120 (88%)	933 (94%)	56 (6%)	0	100	100
1	C	986/1120 (88%)	926 (94%)	59 (6%)	1 (0%)	48	71
2	D	222/224 (99%)	199 (90%)	23 (10%)	0	100	100
2	G	222/224 (99%)	193 (87%)	29 (13%)	0	100	100
2	J	222/224 (99%)	195 (88%)	27 (12%)	0	100	100
3	E	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
3	H	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
3	K	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
All	All	4265/4674 (91%)	3975 (93%)	289 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	813	SER

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 PDB entries followed by that with respect to all EM entries.

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	881/971 (91%)	881 (100%)	0	100	100
1	B	881/971 (91%)	881 (100%)	0	100	100
1	C	879/971 (90%)	877 (100%)	2 (0%)	87	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	184/184 (100%)	182 (99%)	2 (1%)	65	83
2	G	184/184 (100%)	183 (100%)	1 (0%)	81	91
2	J	184/184 (100%)	179 (97%)	5 (3%)	39	67
3	E	185/185 (100%)	185 (100%)	0	100	100
3	H	185/185 (100%)	185 (100%)	0	100	100
3	K	185/185 (100%)	185 (100%)	0	100	100
All	All	3748/4020 (93%)	3738 (100%)	10 (0%)	84	94

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	118	THR
2	J	121	SER
2	J	128	SER
2	D	125	LYS
2	G	118	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	949	GLN
3	E	147	GLN
1	C	957	GLN
2	D	65	GLN
3	E	166	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 ⓘ

36 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	$\# Z > 2$
4	NAG	F	1	4,1	14,14,15	0.25	0	17,19,21	0.48	0
4	NAG	F	2	4	14,14,15	0.22	0	17,19,21	0.42	0
4	NAG	I	1	4,1	14,14,15	0.25	0	17,19,21	0.42	0
4	NAG	I	2	4	14,14,15	0.46	0	17,19,21	1.34	2 (11%)
4	NAG	L	1	4,1	14,14,15	0.67	1 (7%)	17,19,21	0.75	0
4	NAG	L	2	4	14,14,15	0.44	0	17,19,21	1.36	2 (11%)
4	NAG	M	1	4,1	14,14,15	0.21	0	17,19,21	0.42	0
4	NAG	M	2	4	14,14,15	0.27	0	17,19,21	0.53	0
4	NAG	N	1	4,1	14,14,15	0.24	0	17,19,21	0.49	0
4	NAG	N	2	4	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	O	1	4,1	14,14,15	0.19	0	17,19,21	0.44	0
4	NAG	O	2	4	14,14,15	0.23	0	17,19,21	0.48	0
4	NAG	P	1	4,1	14,14,15	0.19	0	17,19,21	0.41	0
4	NAG	P	2	4	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	Q	1	4,1	14,14,15	0.23	0	17,19,21	0.57	0
4	NAG	Q	2	4	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	R	1	4,1	14,14,15	0.25	0	17,19,21	0.50	0
4	NAG	R	2	4	14,14,15	0.23	0	17,19,21	0.41	0
4	NAG	S	1	4,1	14,14,15	0.36	0	17,19,21	0.63	1 (5%)
4	NAG	S	2	4	14,14,15	0.27	0	17,19,21	0.43	0
4	NAG	T	1	4,1	14,14,15	0.33	0	17,19,21	0.51	0
4	NAG	T	2	4	14,14,15	0.53	0	17,19,21	0.56	0
4	NAG	U	1	4,1	14,14,15	0.18	0	17,19,21	0.46	0
4	NAG	U	2	4	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	V	1	4,1	14,14,15	0.40	0	17,19,21	1.34	2 (11%)
4	NAG	V	2	4	14,14,15	0.23	0	17,19,21	0.46	0
4	NAG	W	1	4,1	14,14,15	0.24	0	17,19,21	0.46	0
4	NAG	W	2	4	14,14,15	0.22	0	17,19,21	0.40	0
4	NAG	X	1	4,1	14,14,15	0.20	0	17,19,21	0.43	0
4	NAG	X	2	4	14,14,15	0.26	0	17,19,21	0.55	0
4	NAG	Y	1	4,1	14,14,15	0.25	0	17,19,21	0.47	0
4	NAG	Y	2	4	14,14,15	0.53	0	17,19,21	1.35	2 (11%)
4	NAG	Z	1	4,1	14,14,15	0.21	0	17,19,21	0.42	0
4	NAG	Z	2	4	14,14,15	0.47	0	17,19,21	1.33	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	a	1	4,1	14,14,15	0.19	0	17,19,21	0.44	0
4	NAG	a	2	4	14,14,15	0.22	0	17,19,21	0.44	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
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	6/6/23/26	0/1/1/1
4	NAG	L	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	L	2	4	-	5/6/23/26	0/1/1/1
4	NAG	M	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	M	2	4	-	3/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	N	2	4	-	2/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
4	NAG	Q	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	2/6/23/26	0/1/1/1
4	NAG	R	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	R	2	4	-	2/6/23/26	0/1/1/1
4	NAG	S	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	S	2	4	-	2/6/23/26	0/1/1/1
4	NAG	T	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	T	2	4	-	2/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	U	2	4	-	2/6/23/26	0/1/1/1
4	NAG	V	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	V	2	4	-	2/6/23/26	0/1/1/1
4	NAG	W	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	W	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	X	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	X	2	4	-	2/6/23/26	0/1/1/1
4	NAG	Y	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	Y	2	4	-	5/6/23/26	0/1/1/1
4	NAG	Z	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	Z	2	4	-	6/6/23/26	0/1/1/1
4	NAG	a	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	a	2	4	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	L	1	NAG	O5-C1	-2.26	1.39	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	2	NAG	C2-N2-C7	4.62	129.09	122.90
4	V	1	NAG	C2-N2-C7	4.61	129.08	122.90
4	Y	2	NAG	C2-N2-C7	4.60	129.06	122.90
4	L	2	NAG	C2-N2-C7	4.58	129.04	122.90
4	Z	2	NAG	C2-N2-C7	4.56	129.01	122.90

There are no chirality outliers.

5 of 83 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	S	2	NAG	C4-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
4	N	1	NAG	O5-C5-C6-O6
4	S	1	NAG	O5-C5-C6-O6
4	S	2	NAG	O5-C5-C6-O6

There are no ring outliers.

9 monomers are involved in 9 short contacts:

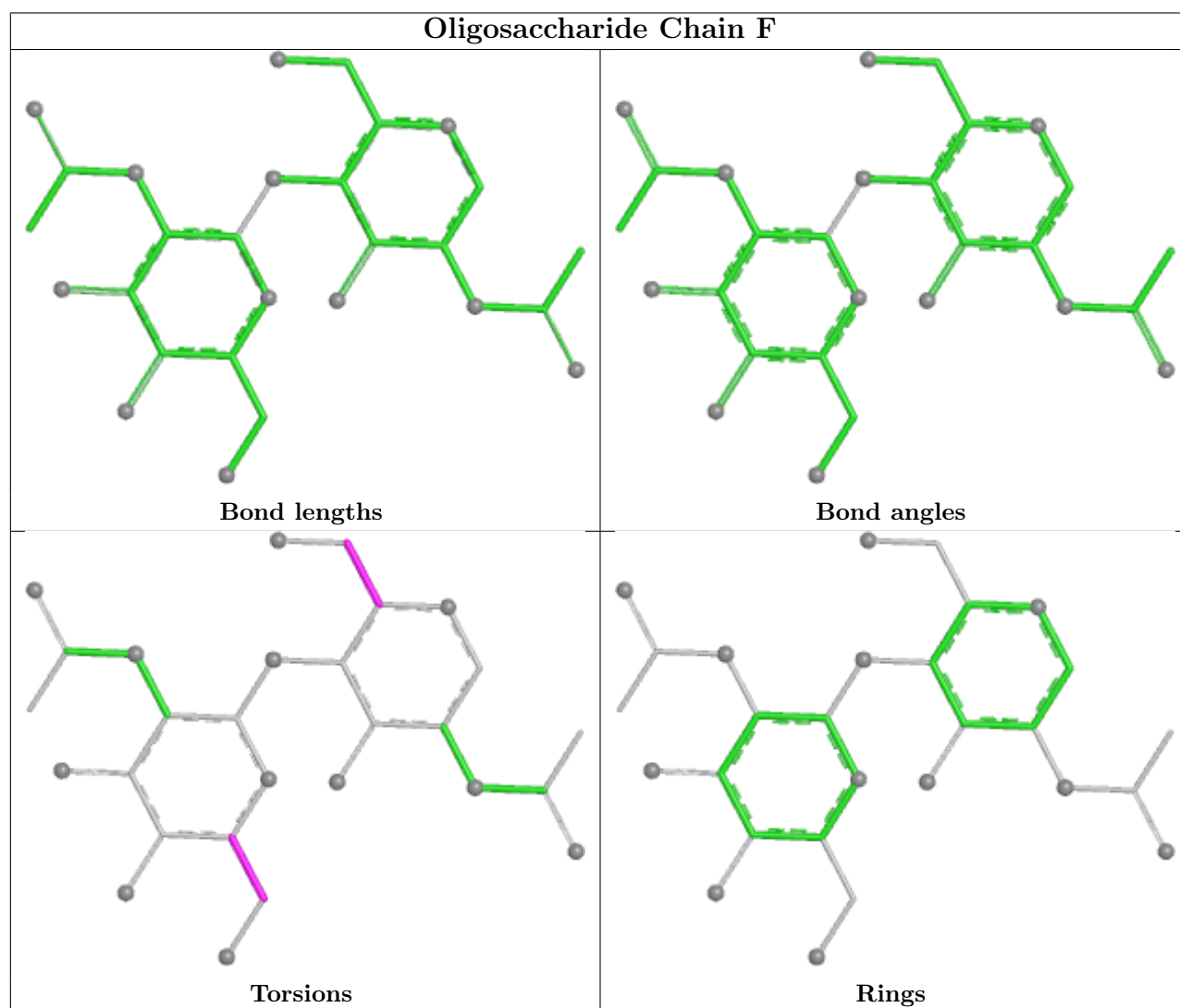
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	2	NAG	1	0
4	T	1	NAG	2	0

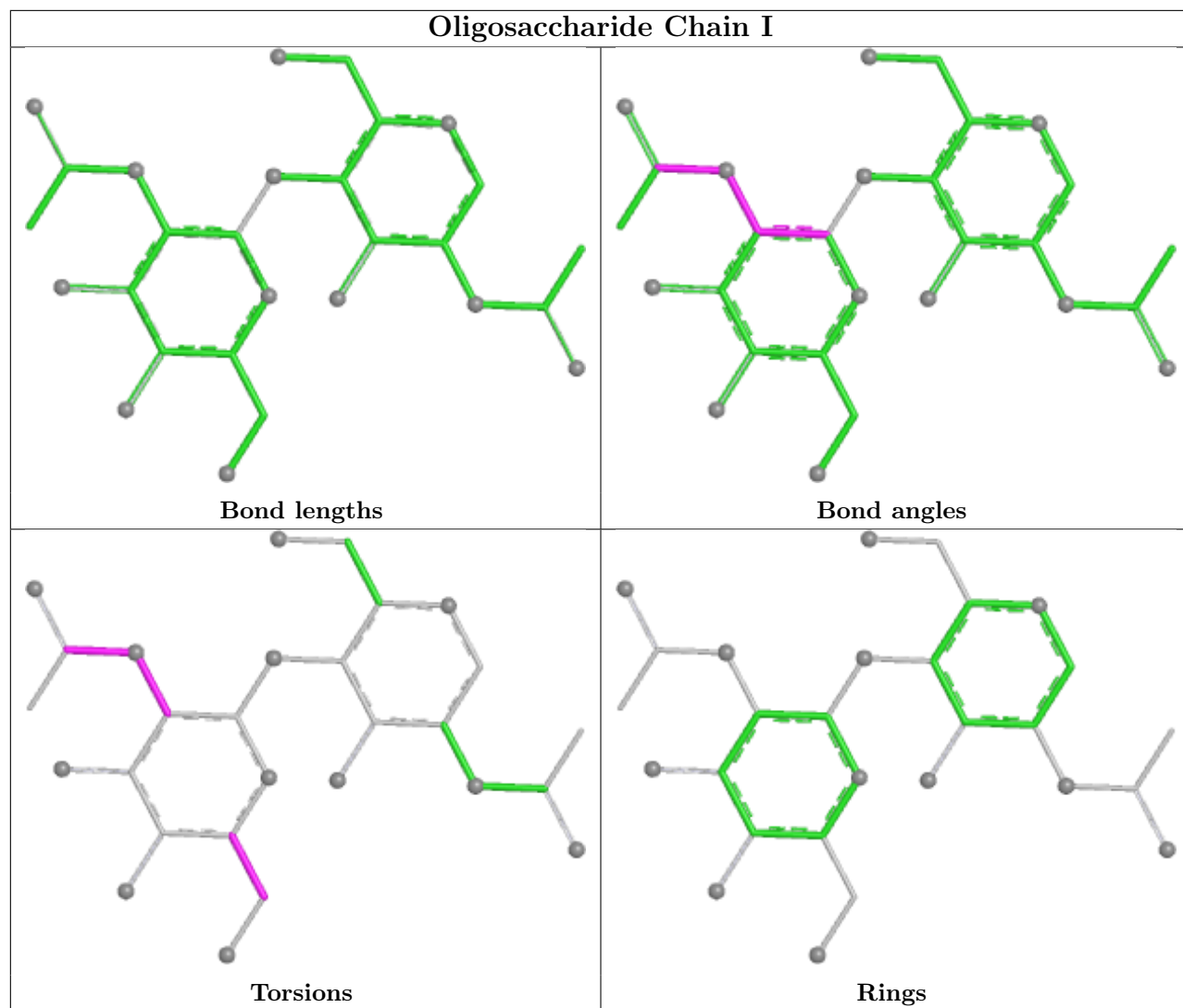
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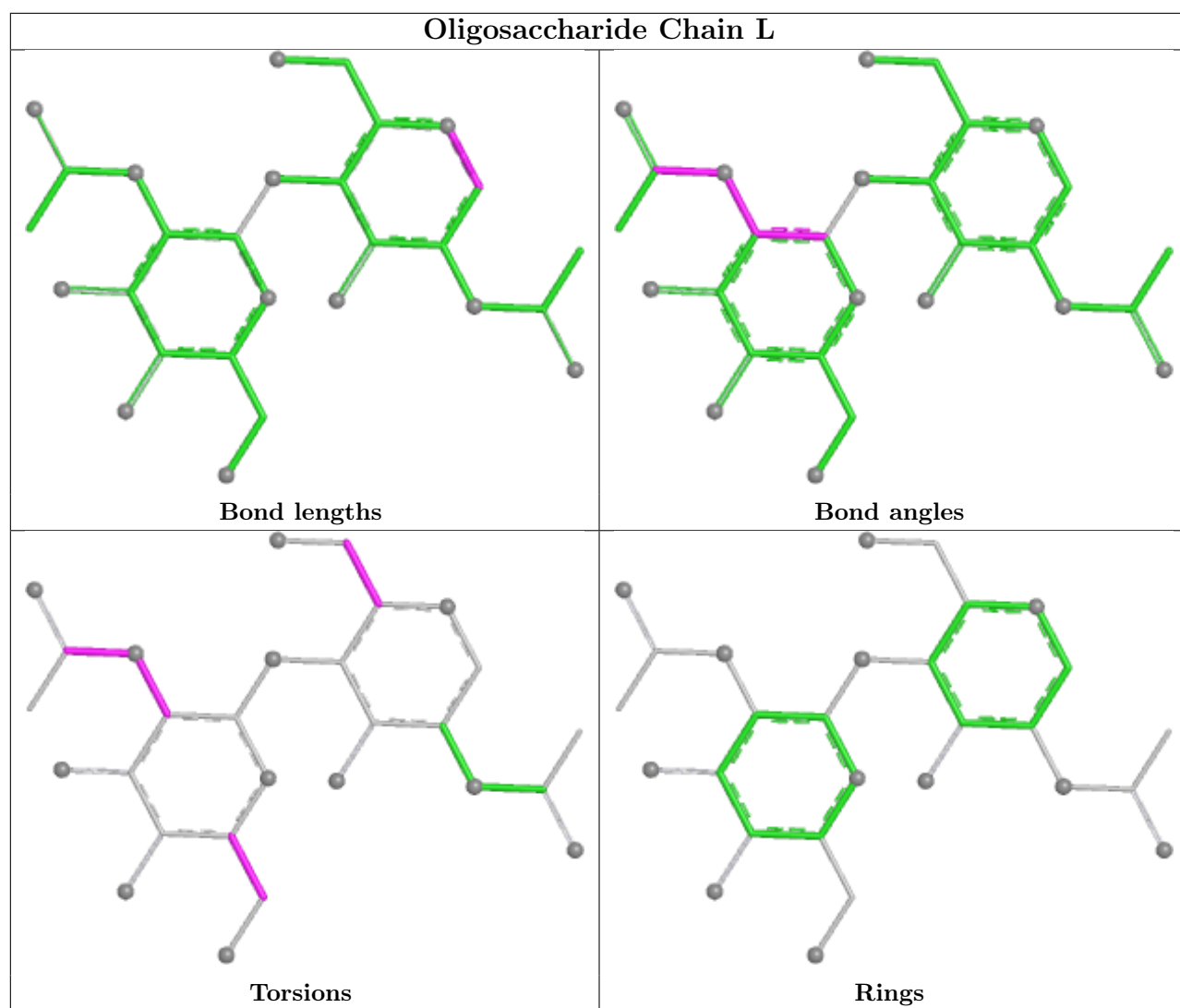
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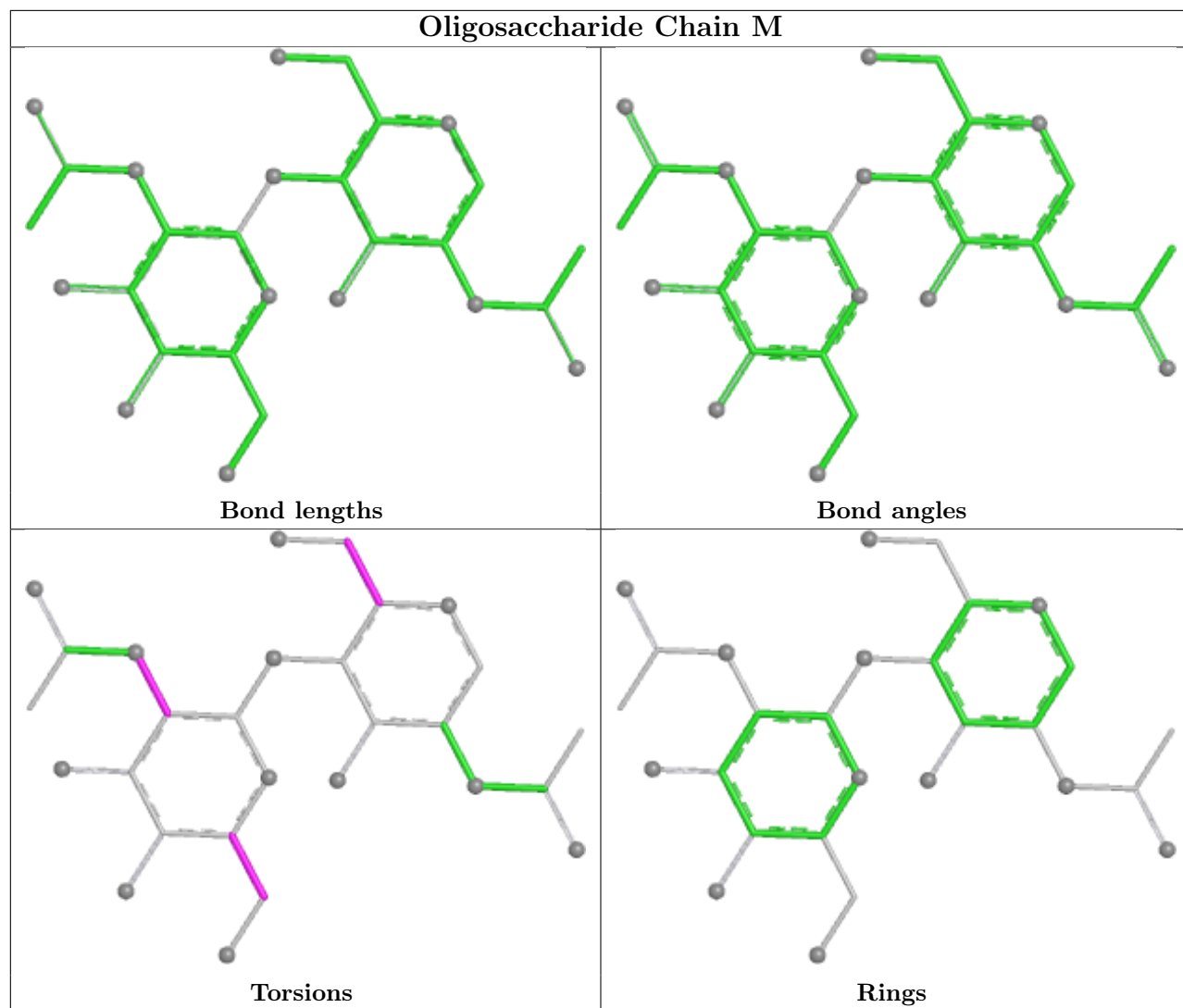
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Z	2	NAG	1	0
4	T	2	NAG	1	0
4	Y	2	NAG	1	0
4	M	1	NAG	1	0
4	Z	1	NAG	1	0
4	I	2	NAG	1	0
4	V	1	NAG	1	0

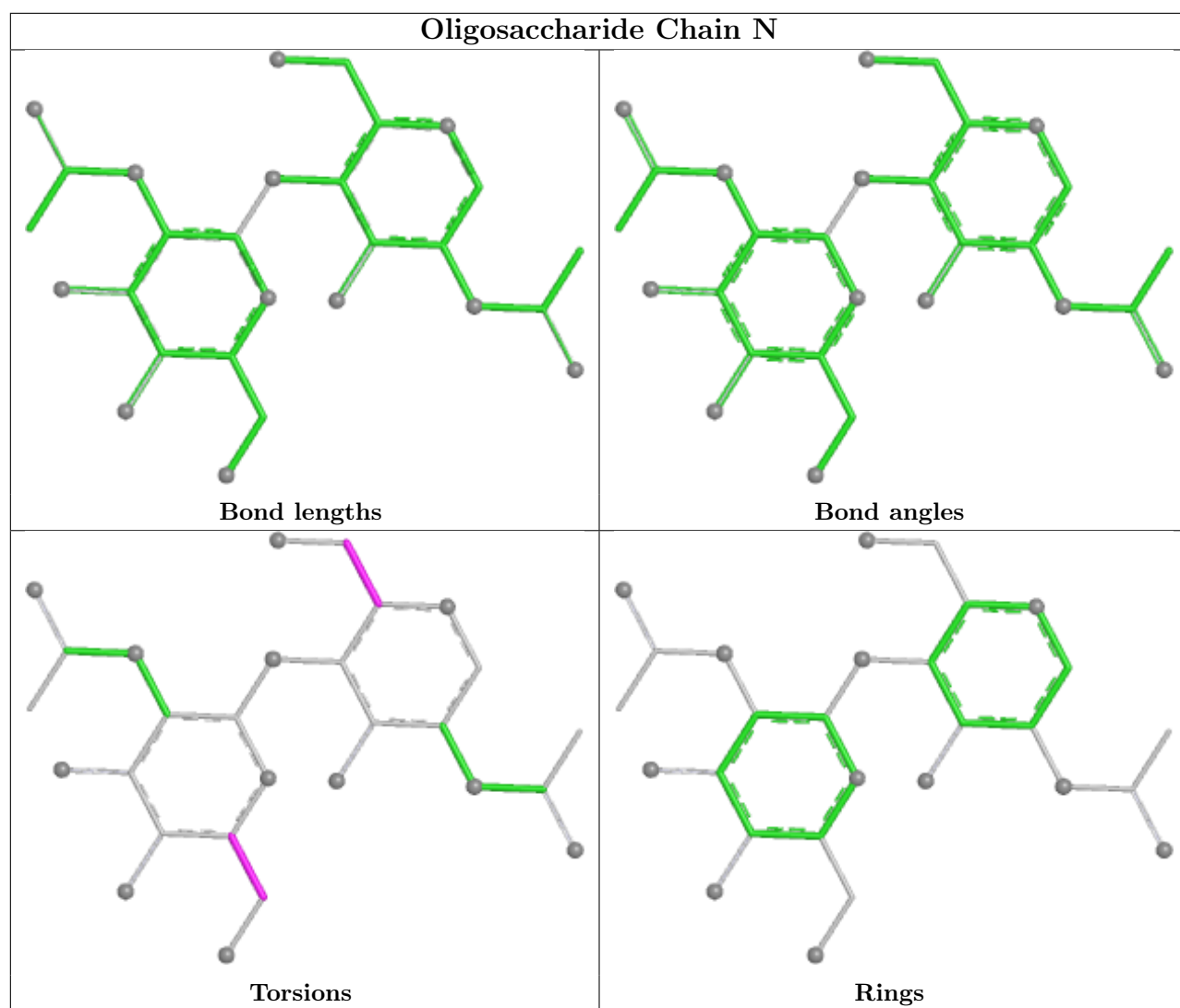
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

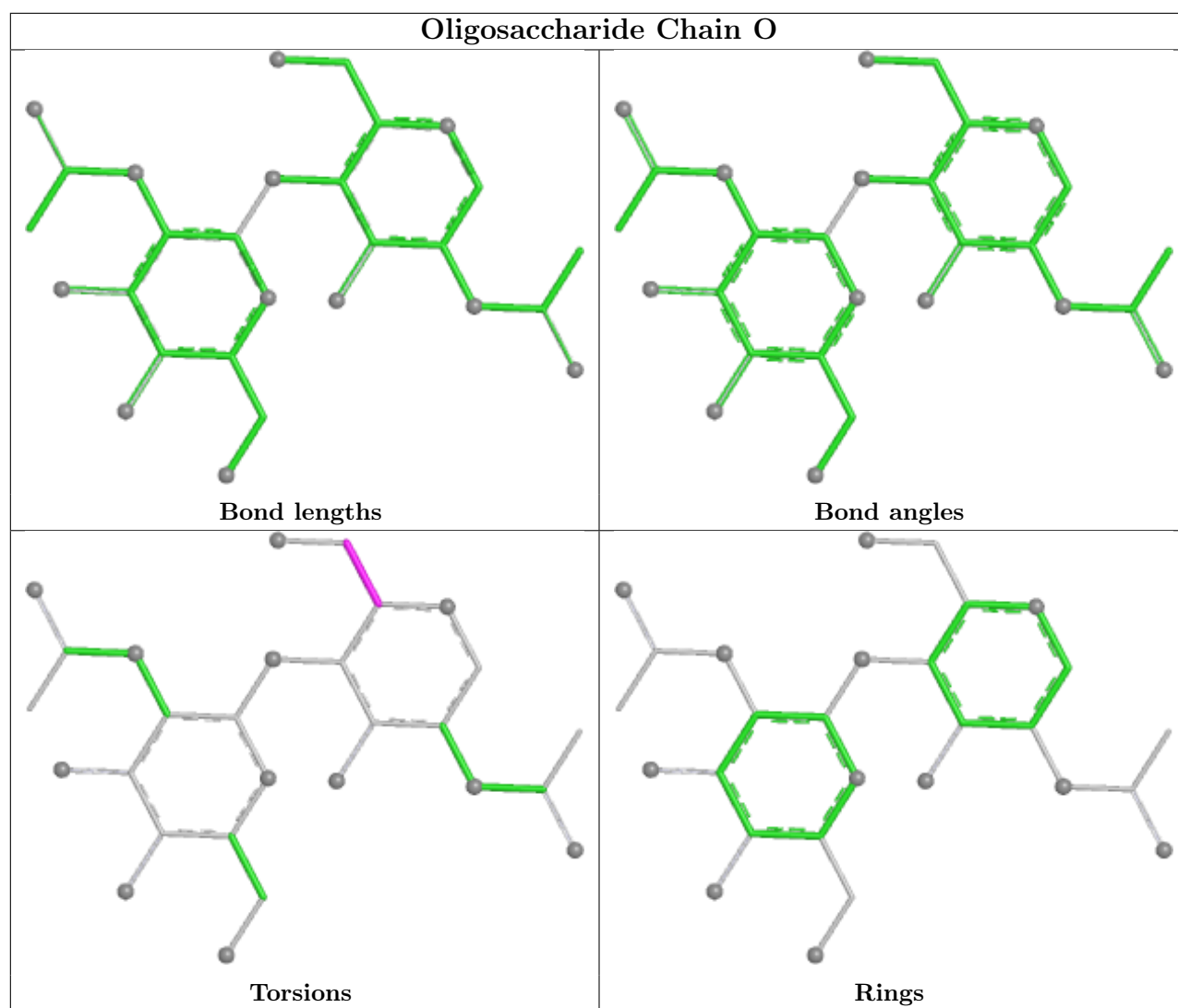


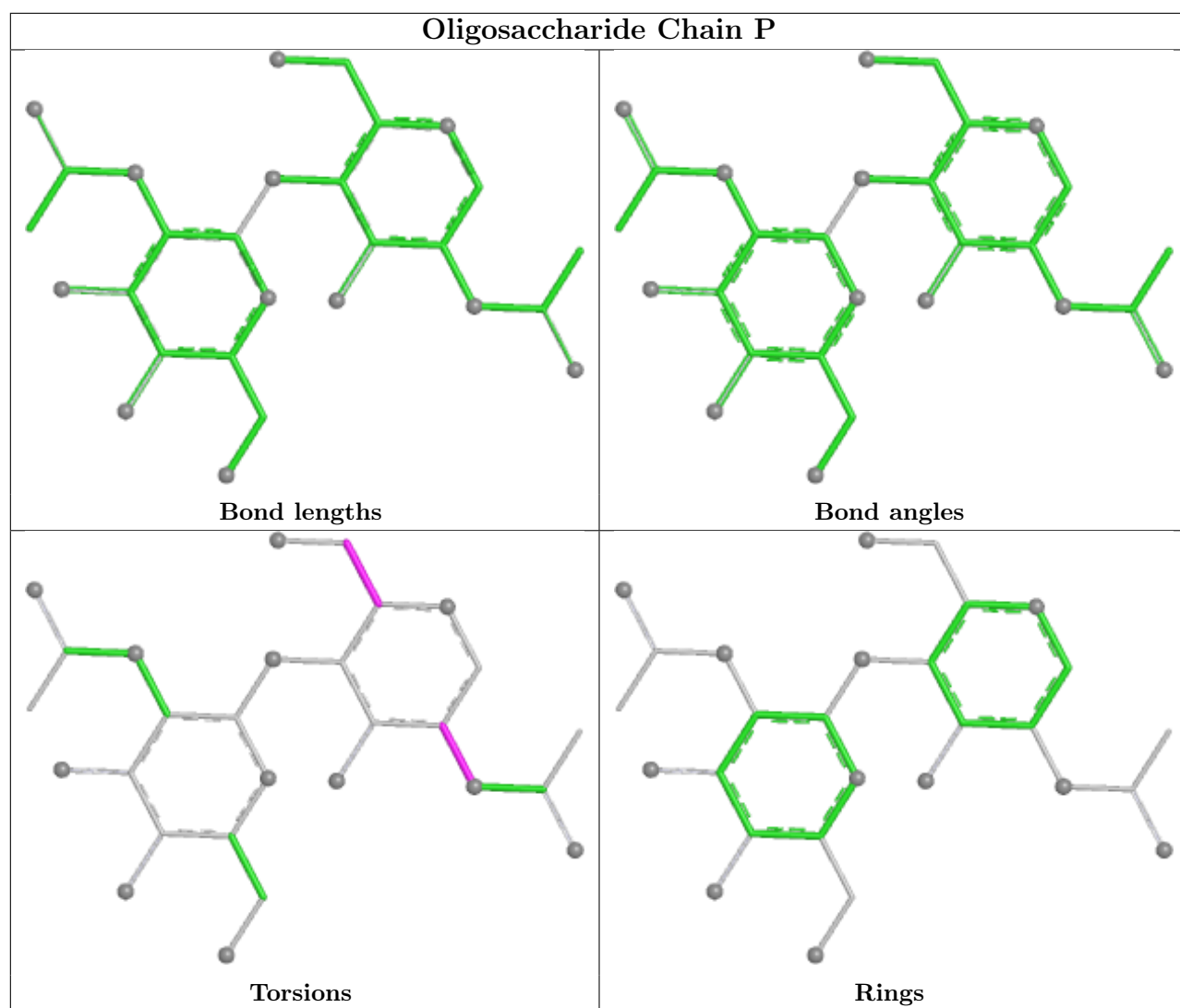


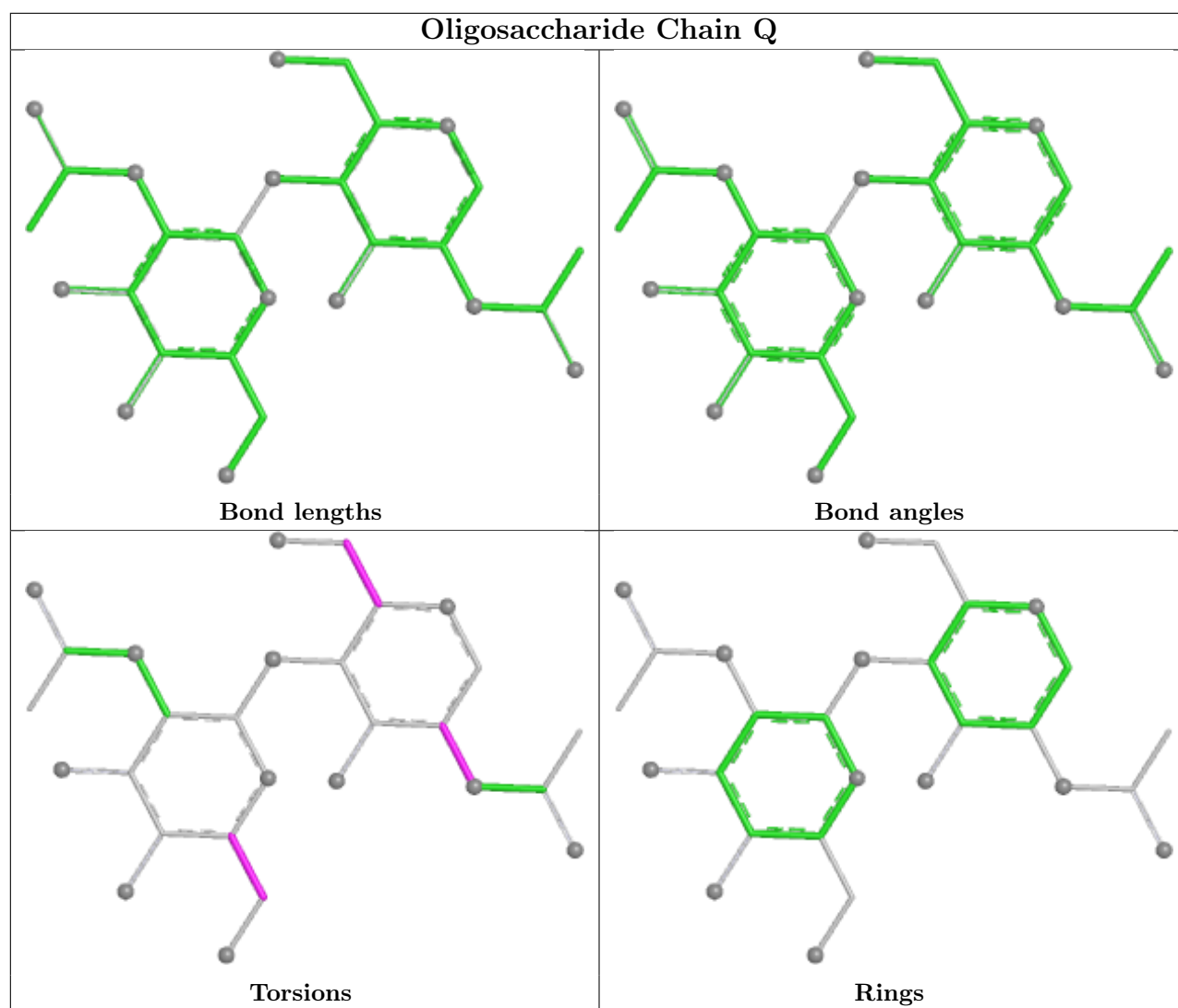


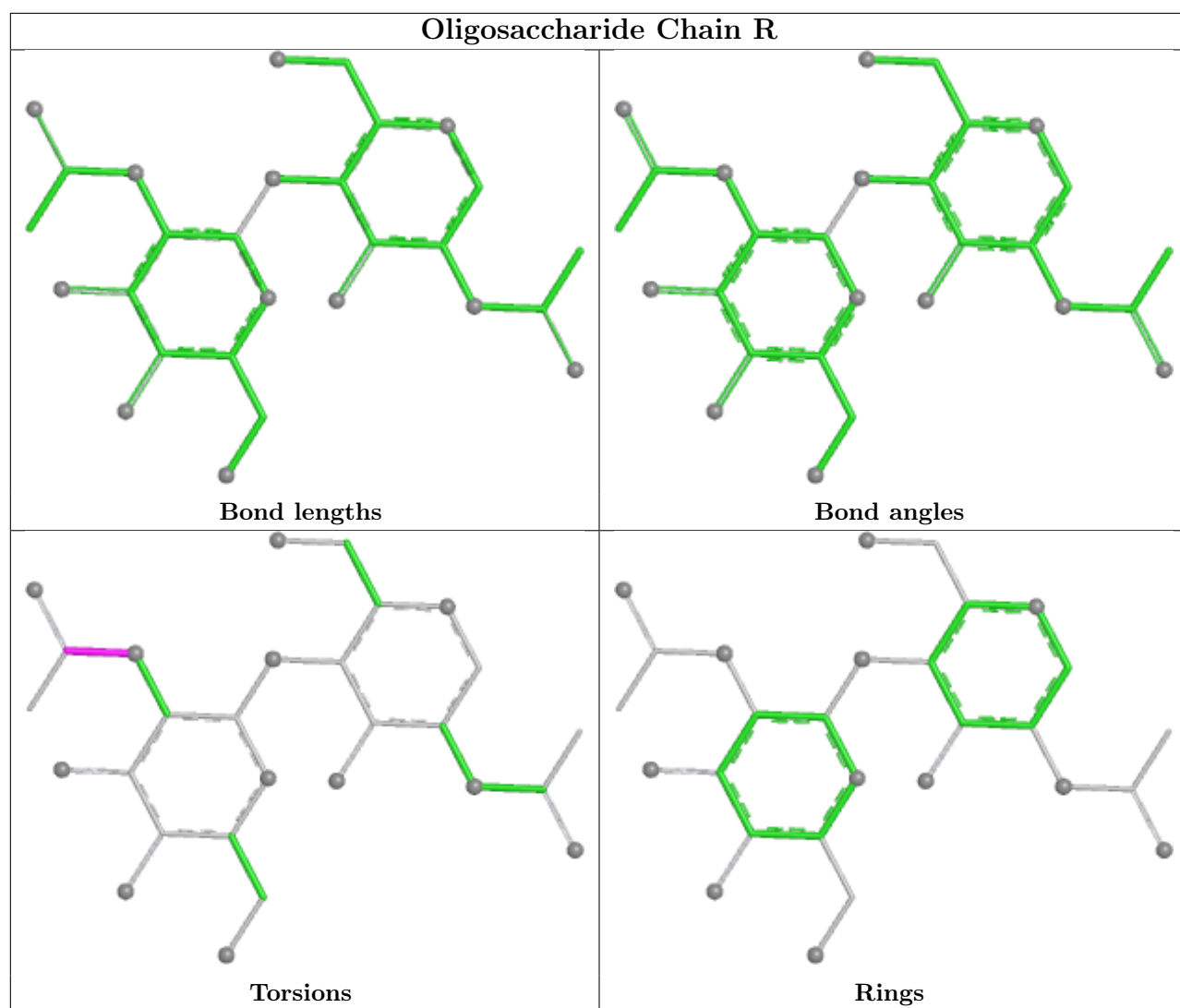


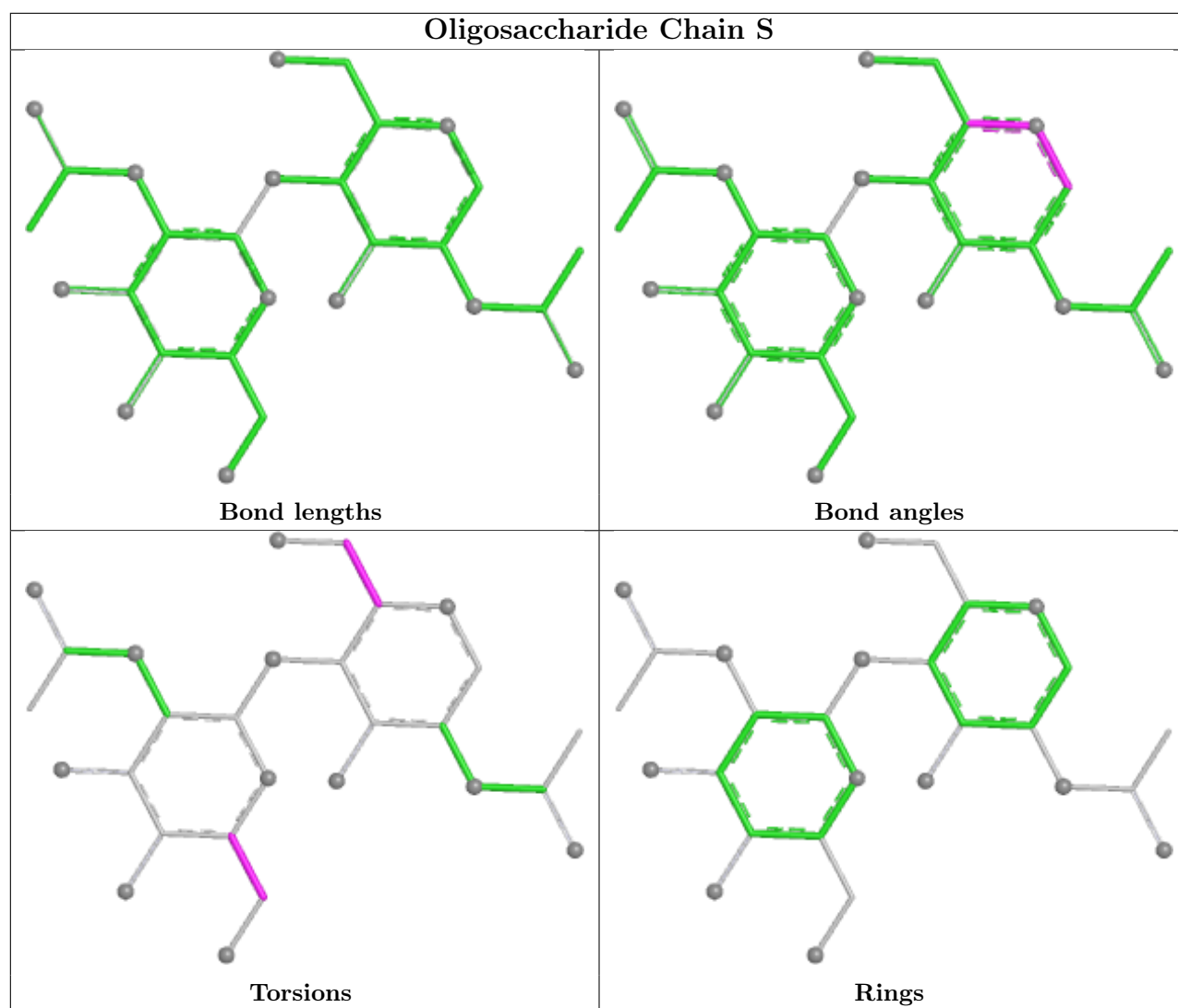


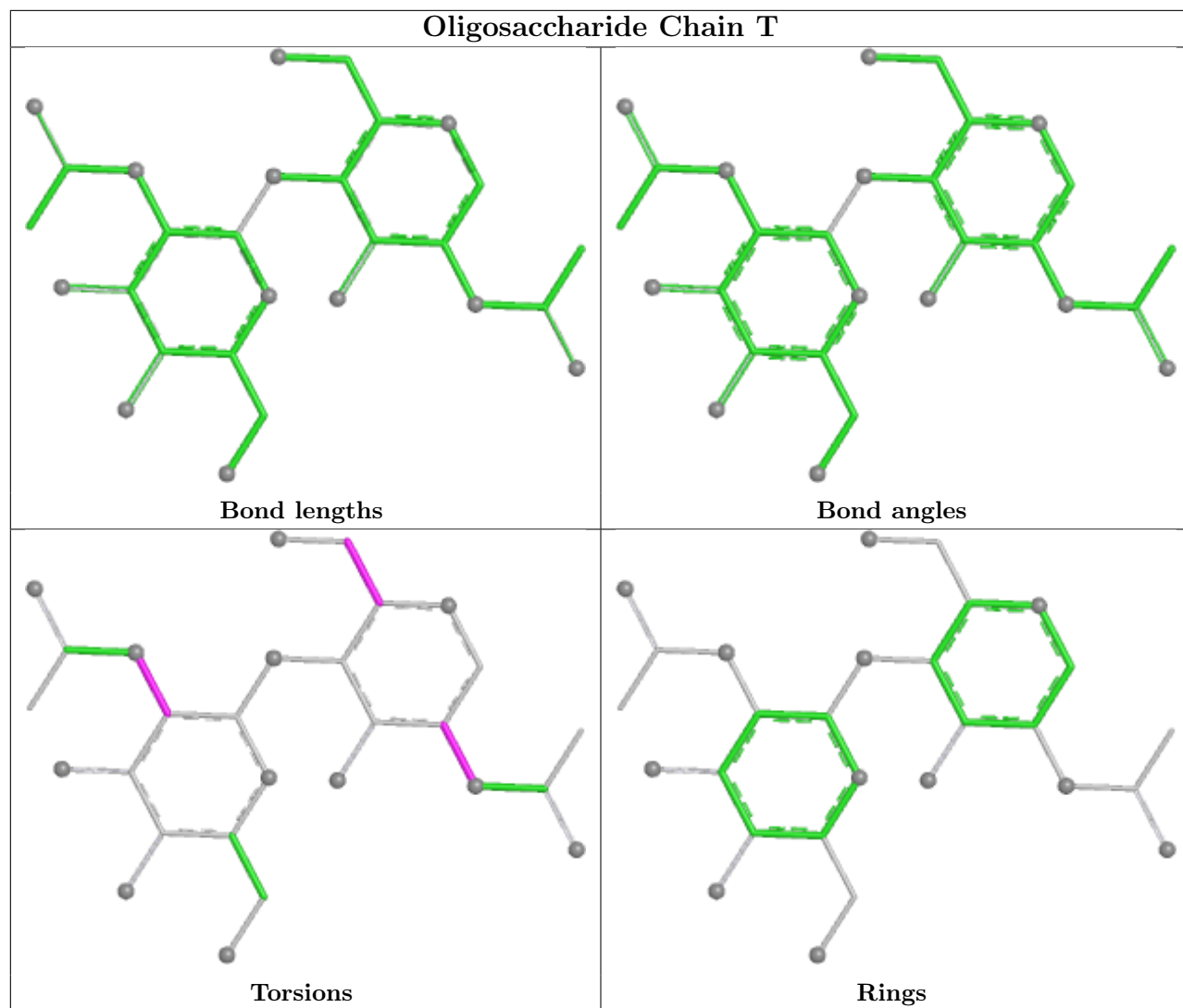


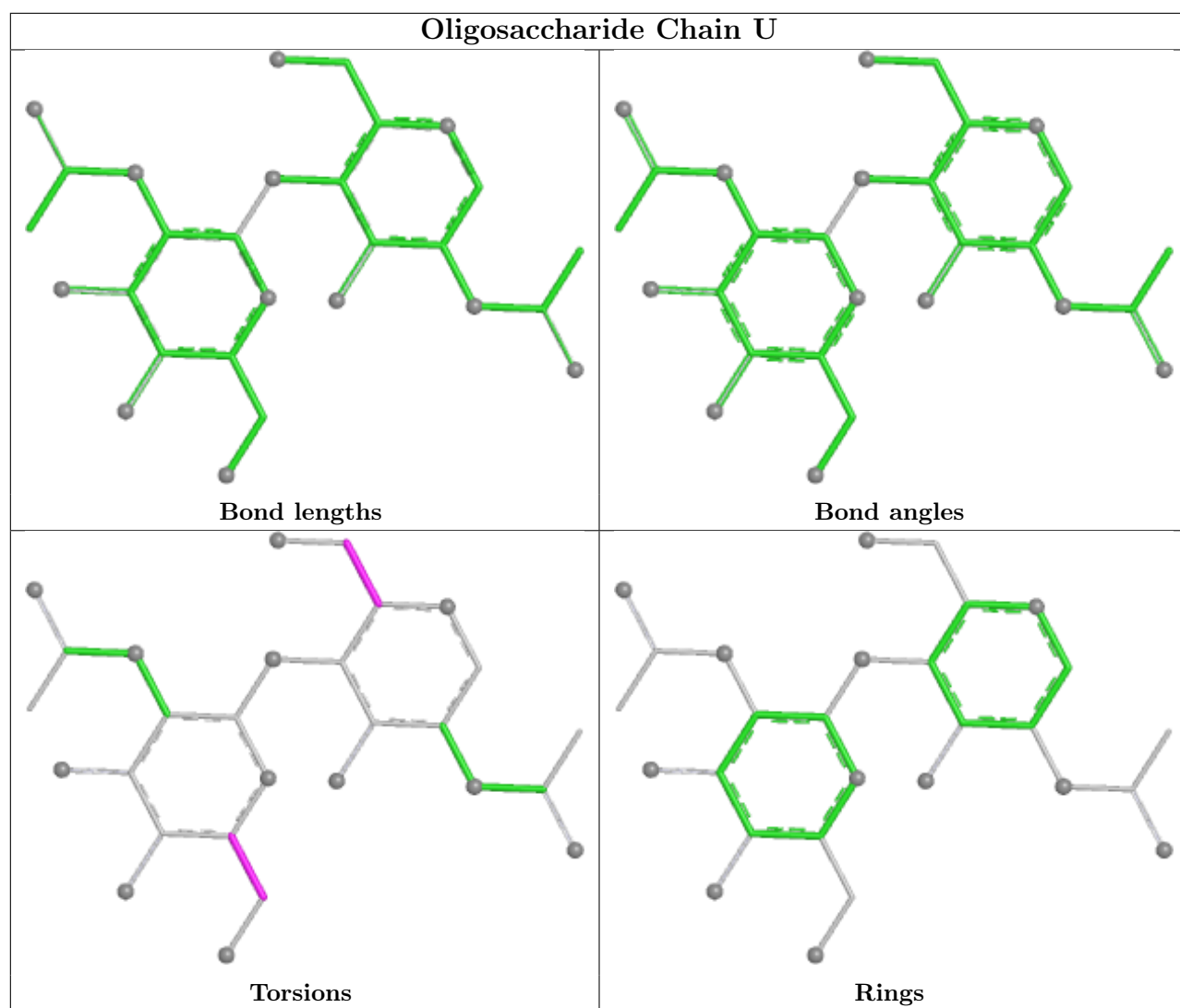


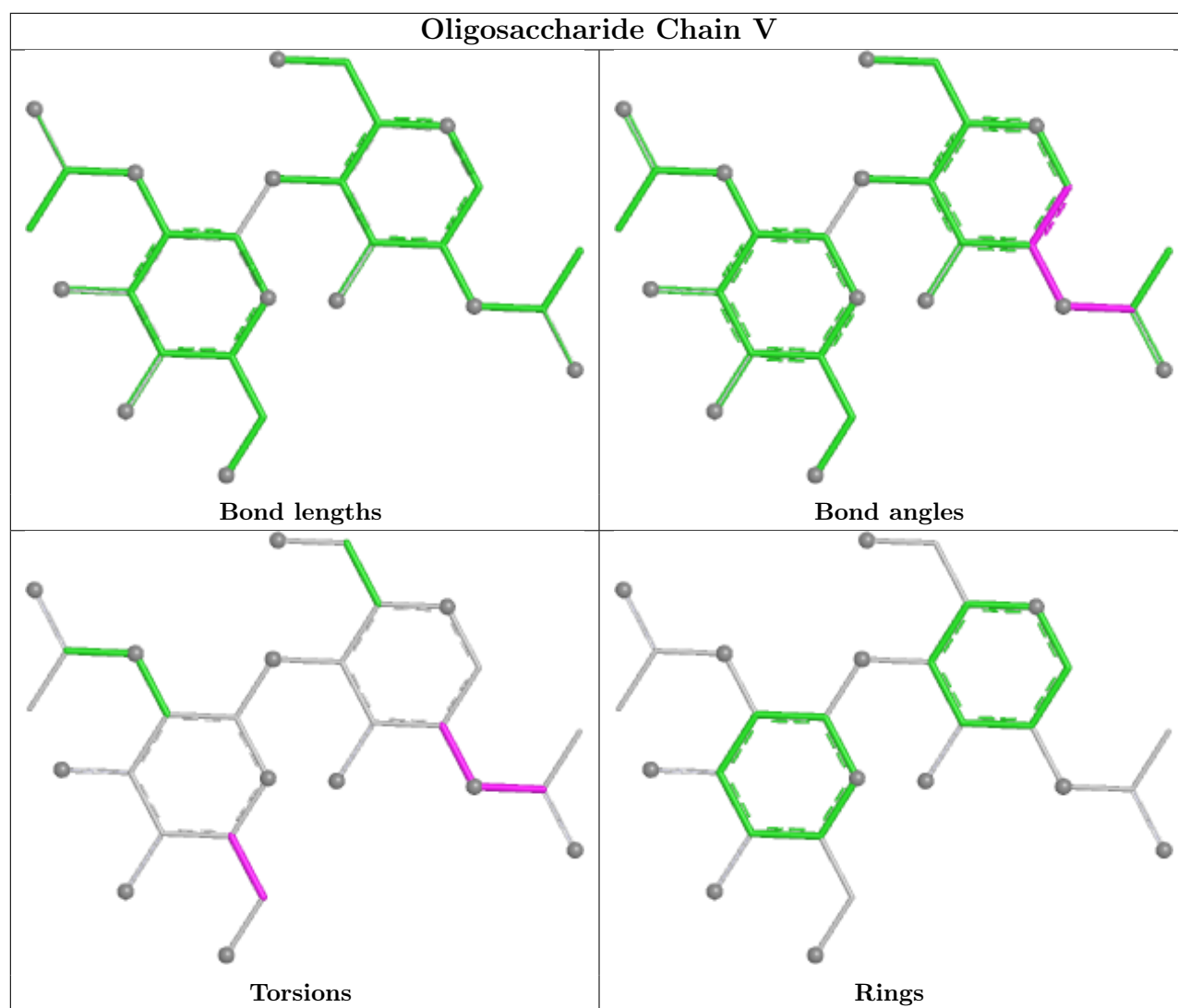


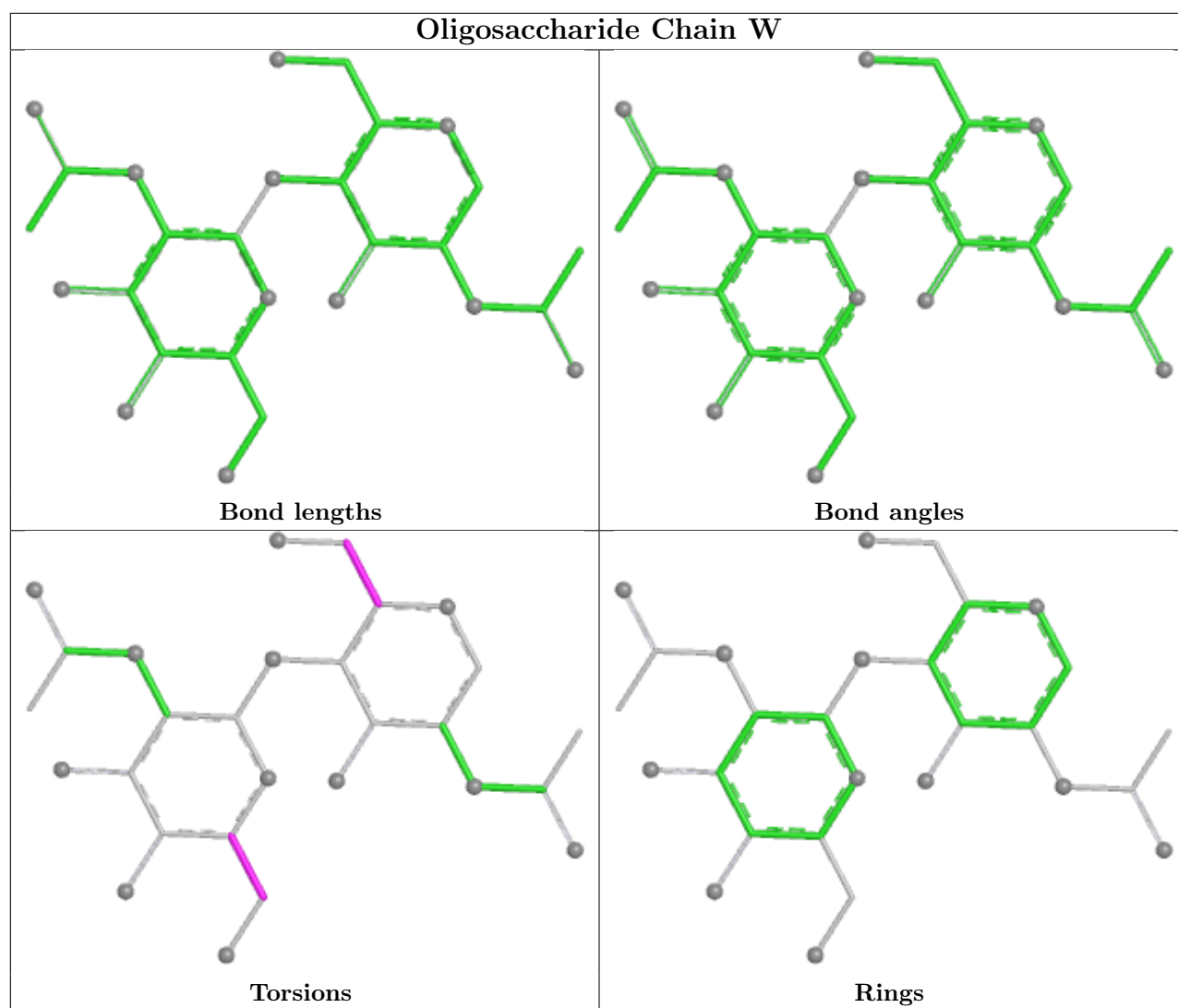


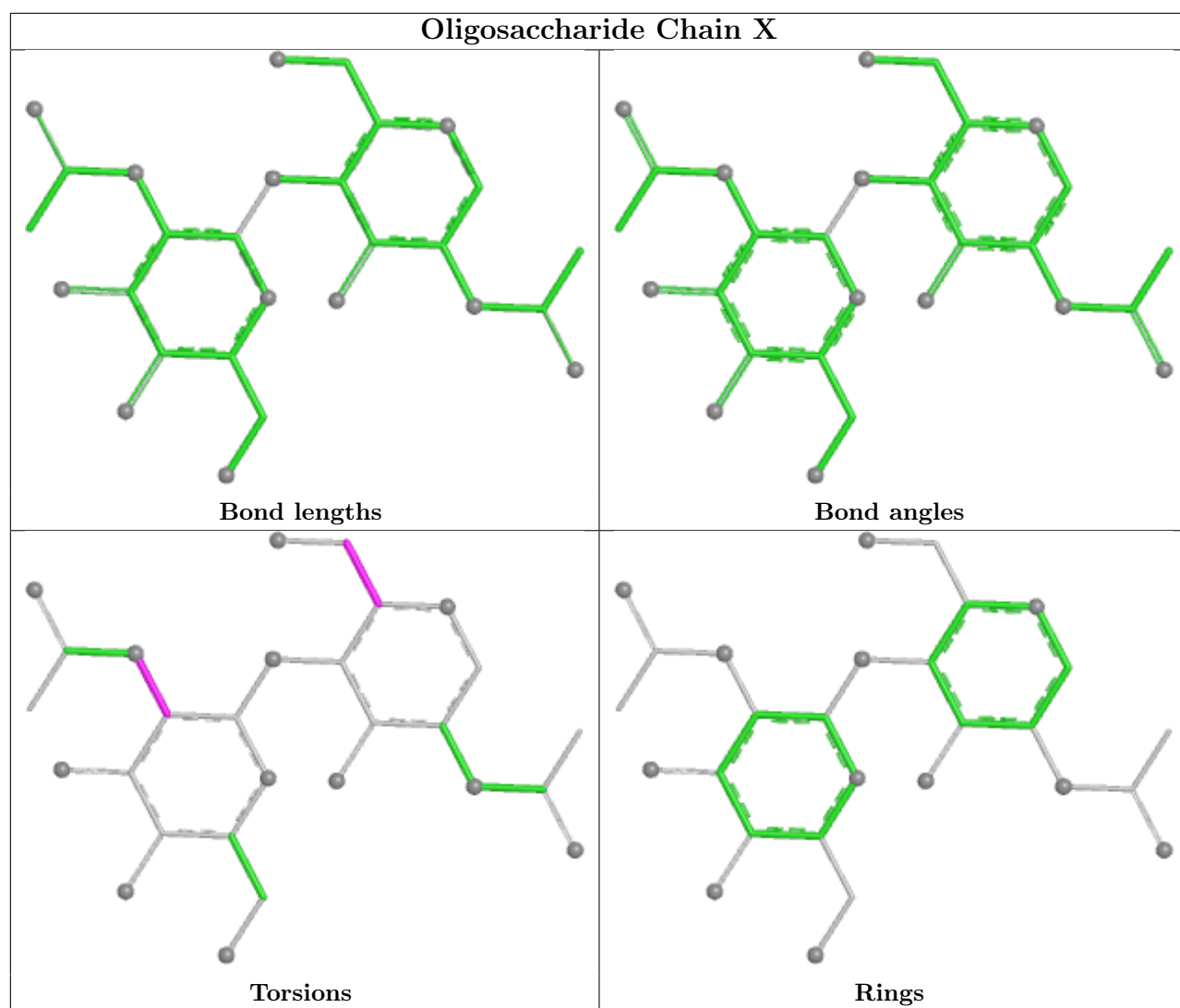


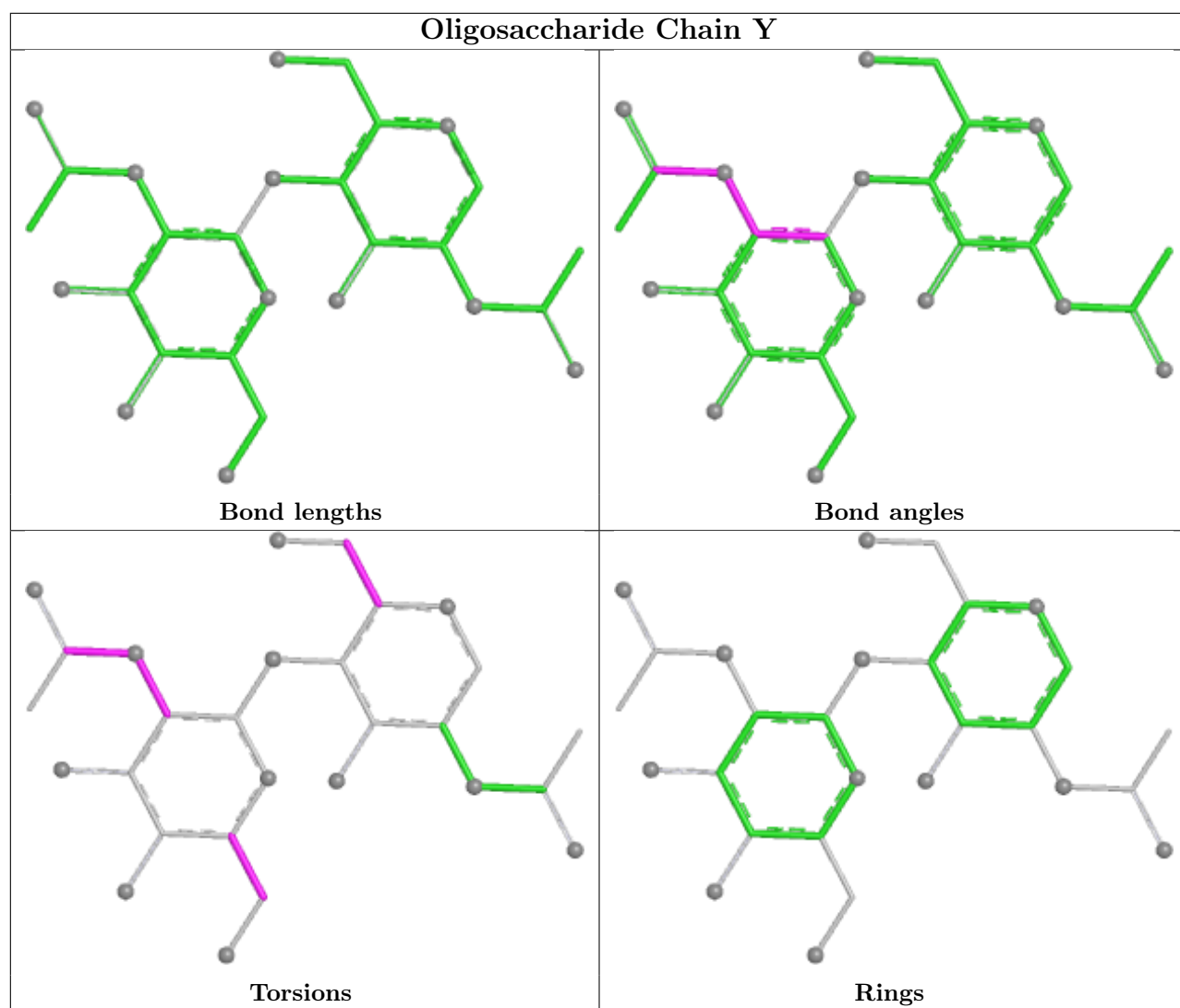


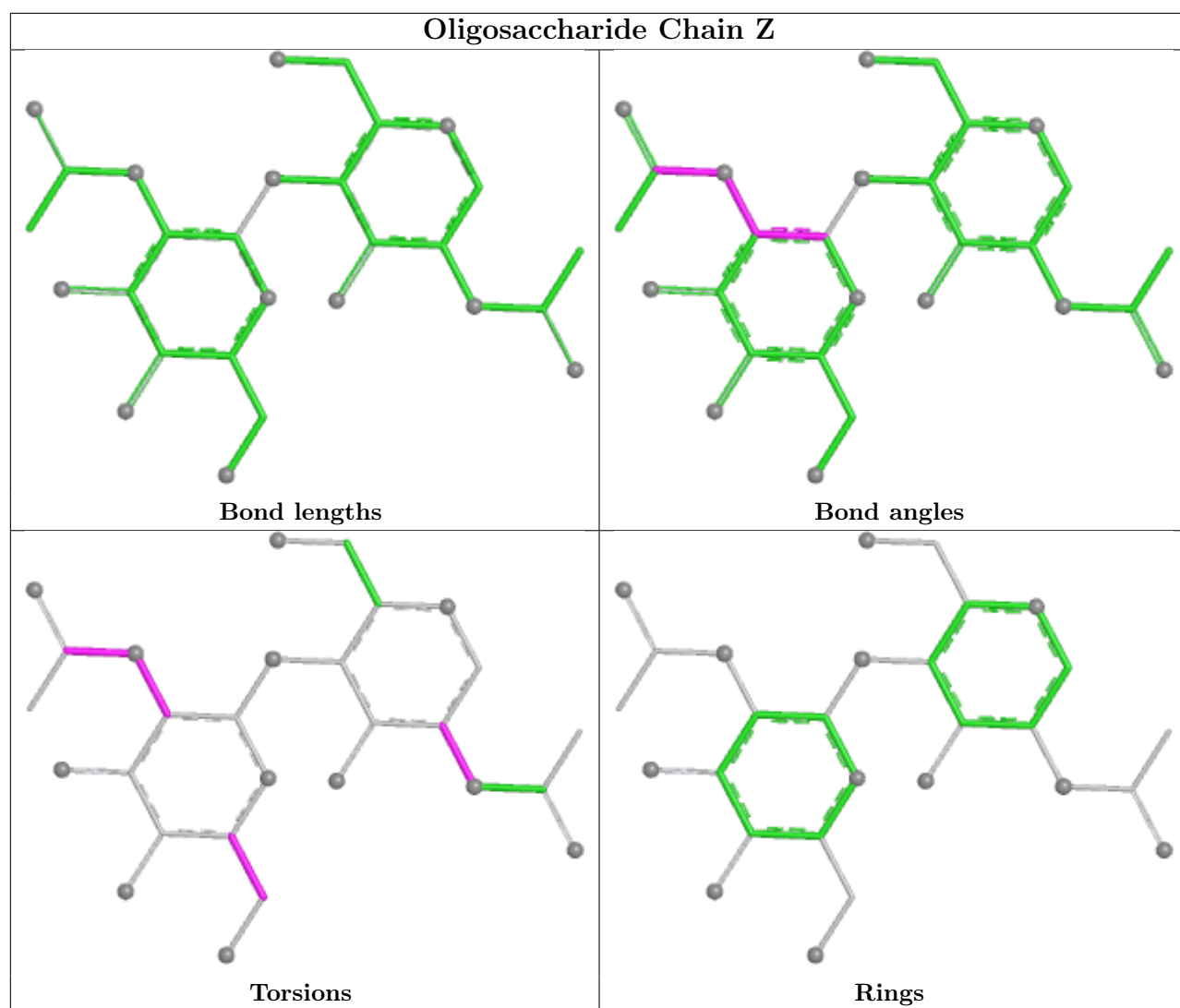


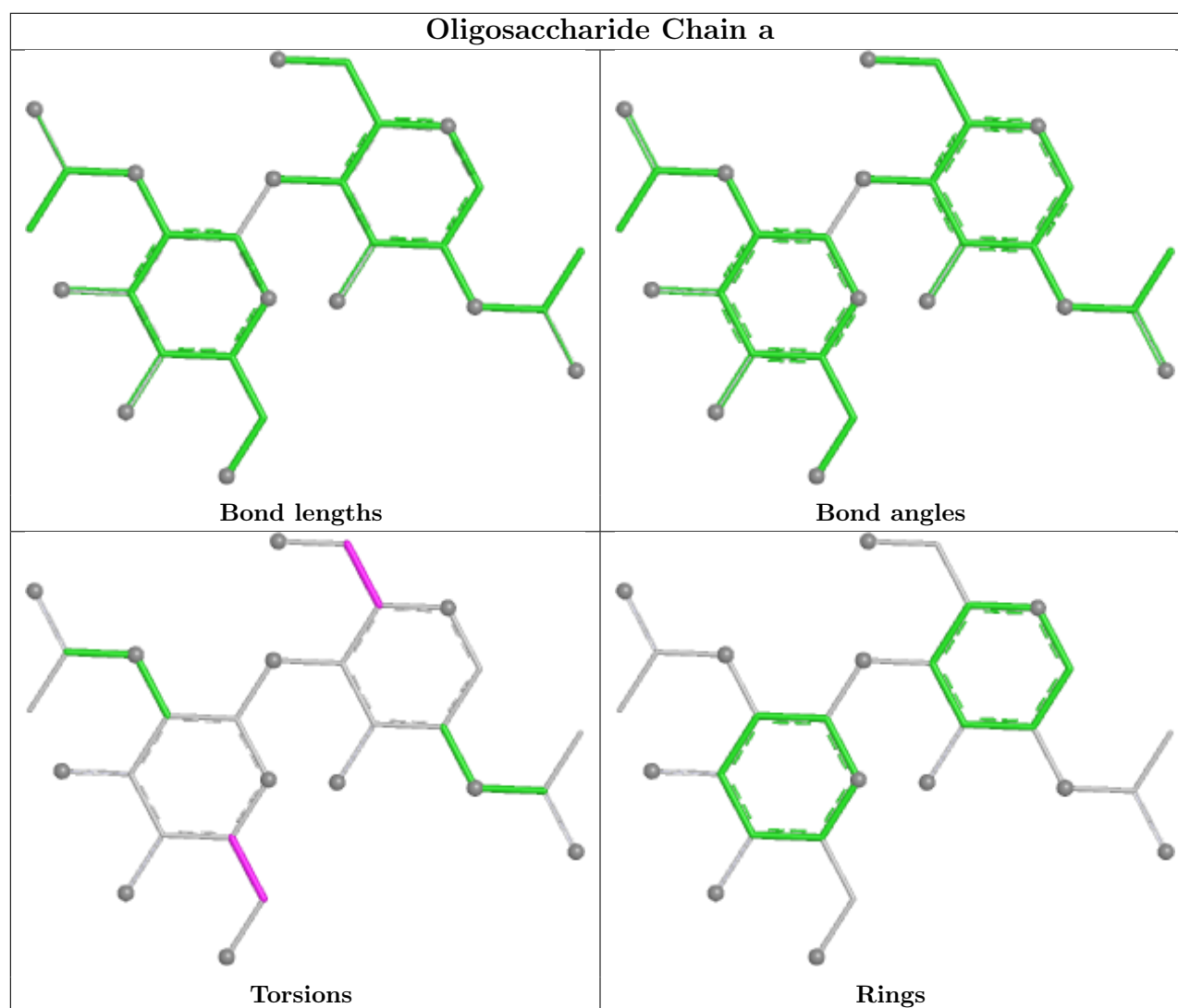












5.6 Ligand geometry [i](#)

18 ligands 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	$\# Z > 2$
5	NAG	C	1201	1	14,14,15	0.51	0	17,19,21	1.33	2 (11%)
5	NAG	B	1401	1	14,14,15	0.23	0	17,19,21	0.47	0
5	NAG	A	1405	1	14,14,15	0.22	0	17,19,21	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	1403	1	14,14,15	0.29	0	17,19,21	0.49	0
5	NAG	C	1204	1	14,14,15	0.49	0	17,19,21	1.31	2 (11%)
5	NAG	B	1403	1	14,14,15	0.36	0	17,19,21	0.64	0
5	NAG	B	1405	1	14,14,15	0.22	0	17,19,21	0.44	0
5	NAG	A	1404	1	14,14,15	0.26	0	17,19,21	0.45	0
5	NAG	A	1402	1	14,14,15	0.22	0	17,19,21	0.54	0
5	NAG	C	1206	1	14,14,15	0.28	0	17,19,21	0.59	0
5	NAG	C	1207	1	14,14,15	0.23	0	17,19,21	0.43	0
5	NAG	B	1404	1	14,14,15	0.21	0	17,19,21	0.41	0
5	NAG	B	1402	1	14,14,15	0.19	0	17,19,21	0.43	0
5	NAG	A	1406	1	14,14,15	0.21	0	17,19,21	0.44	0
5	NAG	A	1401	1	14,14,15	0.22	0	17,19,21	0.47	0
5	NAG	C	1202	1	14,14,15	0.20	0	17,19,21	0.43	0
5	NAG	C	1203	1	14,14,15	0.75	1 (7%)	17,19,21	0.78	1 (5%)
5	NAG	C	1205	1	14,14,15	0.22	0	17,19,21	0.43	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
5	NAG	C	1201	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1401	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1405	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1204	1	-	6/6/23/26	0/1/1/1
5	NAG	B	1403	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1405	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1404	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1402	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1206	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1207	1	-	3/6/23/26	0/1/1/1
5	NAG	B	1404	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1402	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1406	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1401	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1202	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1203	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	C	1205	1	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1203	NAG	C1-C2	2.62	1.55	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1204	NAG	C2-N2-C7	4.56	129.01	122.90
5	C	1201	NAG	C2-N2-C7	4.55	129.00	122.90
5	C	1203	NAG	C1-O5-C5	2.44	115.46	112.19
5	C	1201	NAG	C1-C2-N2	2.25	113.97	110.43
5	C	1204	NAG	C1-C2-N2	2.18	113.87	110.43

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1405	NAG	C4-C5-C6-O6
5	A	1401	NAG	C4-C5-C6-O6
5	A	1402	NAG	C4-C5-C6-O6
5	C	1204	NAG	C4-C5-C6-O6
5	B	1405	NAG	O5-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1201	NAG	1	0
5	C	1204	NAG	1	0
5	A	1402	NAG	1	0
5	C	1203	NAG	2	0

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.

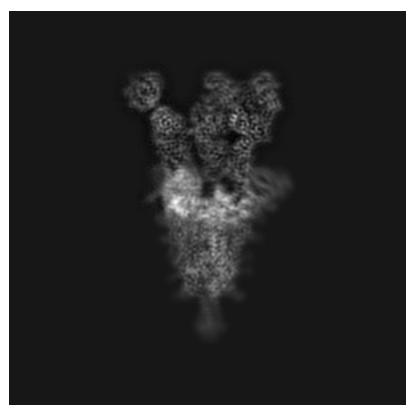
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32498. These allow visual inspection of the internal detail of the map and identification of artifacts.

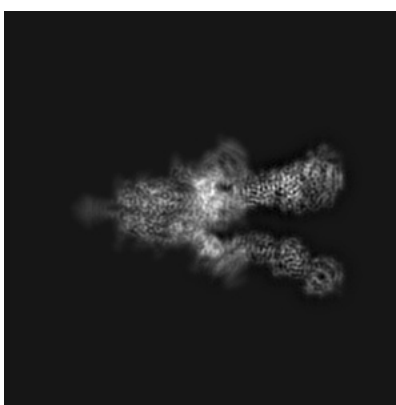
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

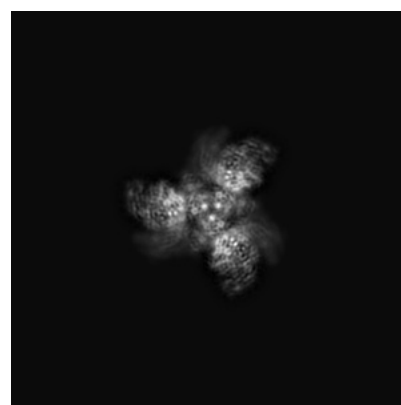
6.1.1 Primary map



X



Y



Z

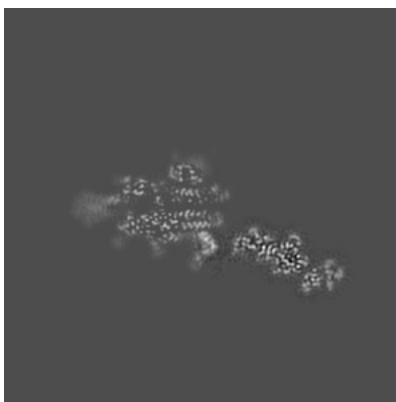
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

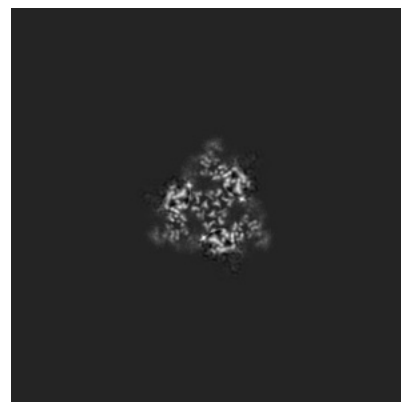
6.2.1 Primary map



X Index: 180



Y Index: 180

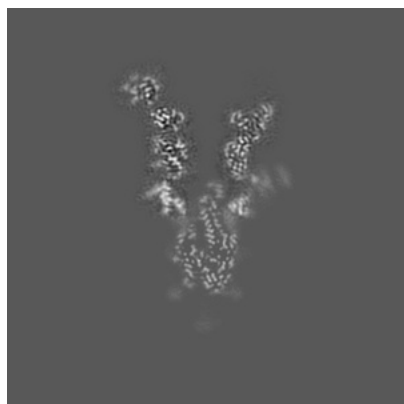


Z Index: 180

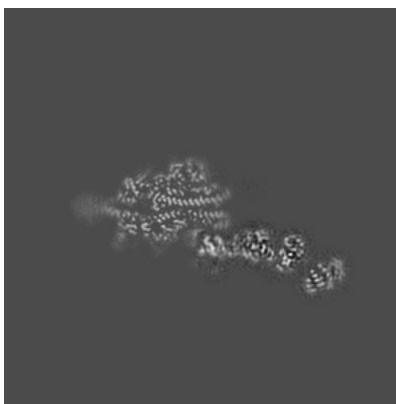
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

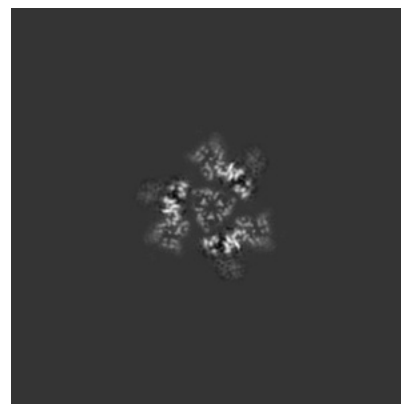
6.3.1 Primary map



X Index: 194



Y Index: 185

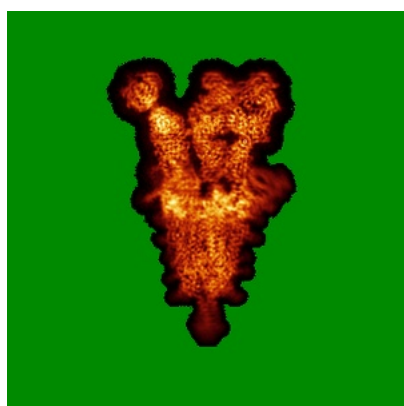


Z Index: 187

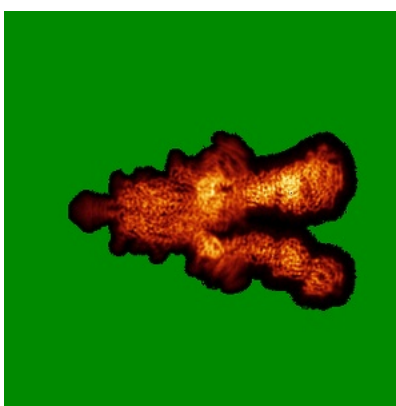
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

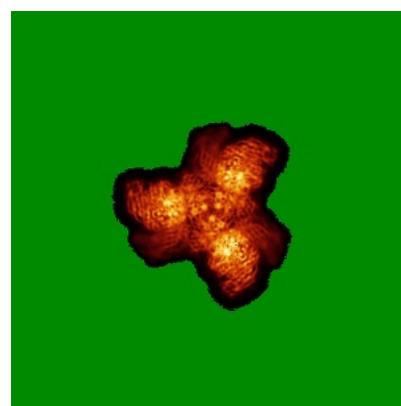
6.4.1 Primary map



X



Y

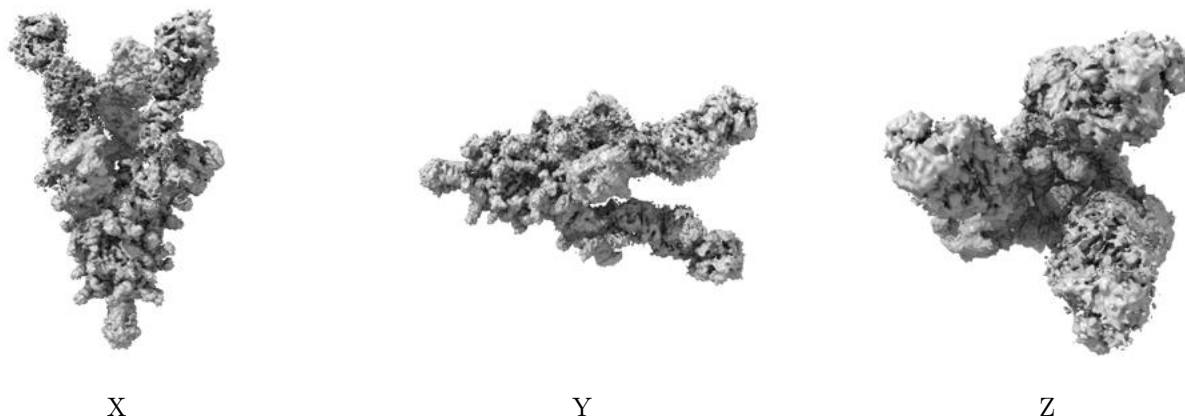


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

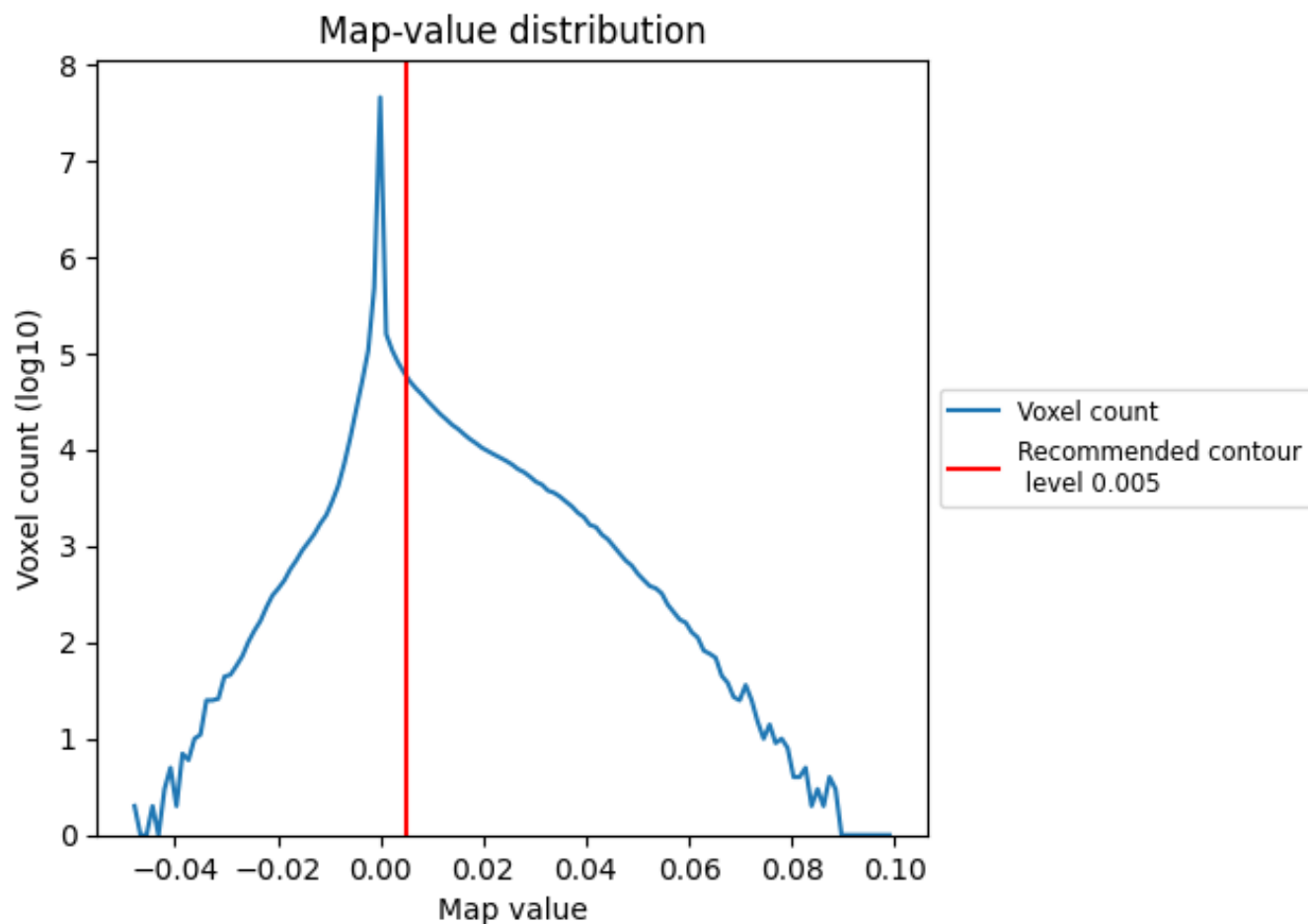
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

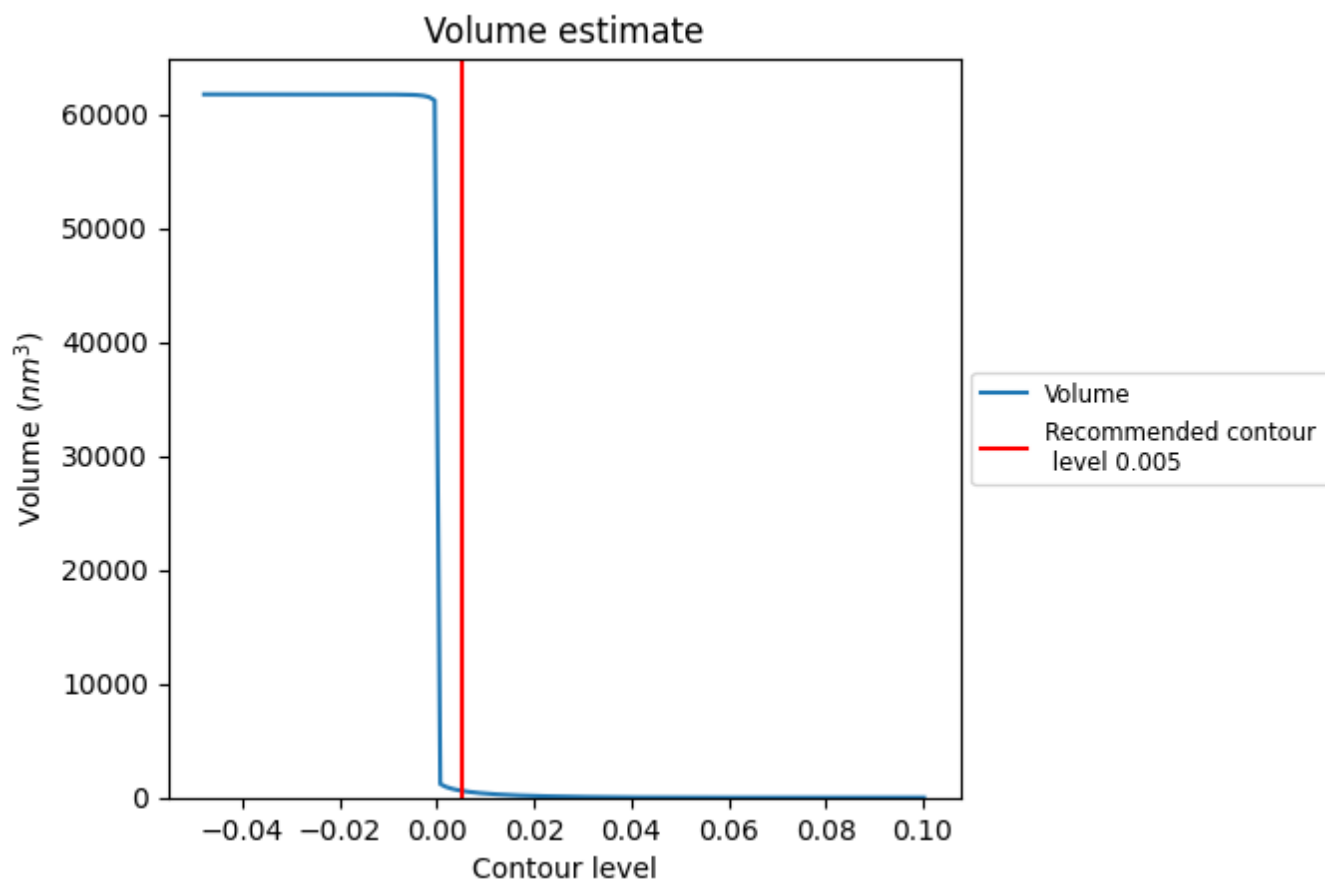
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

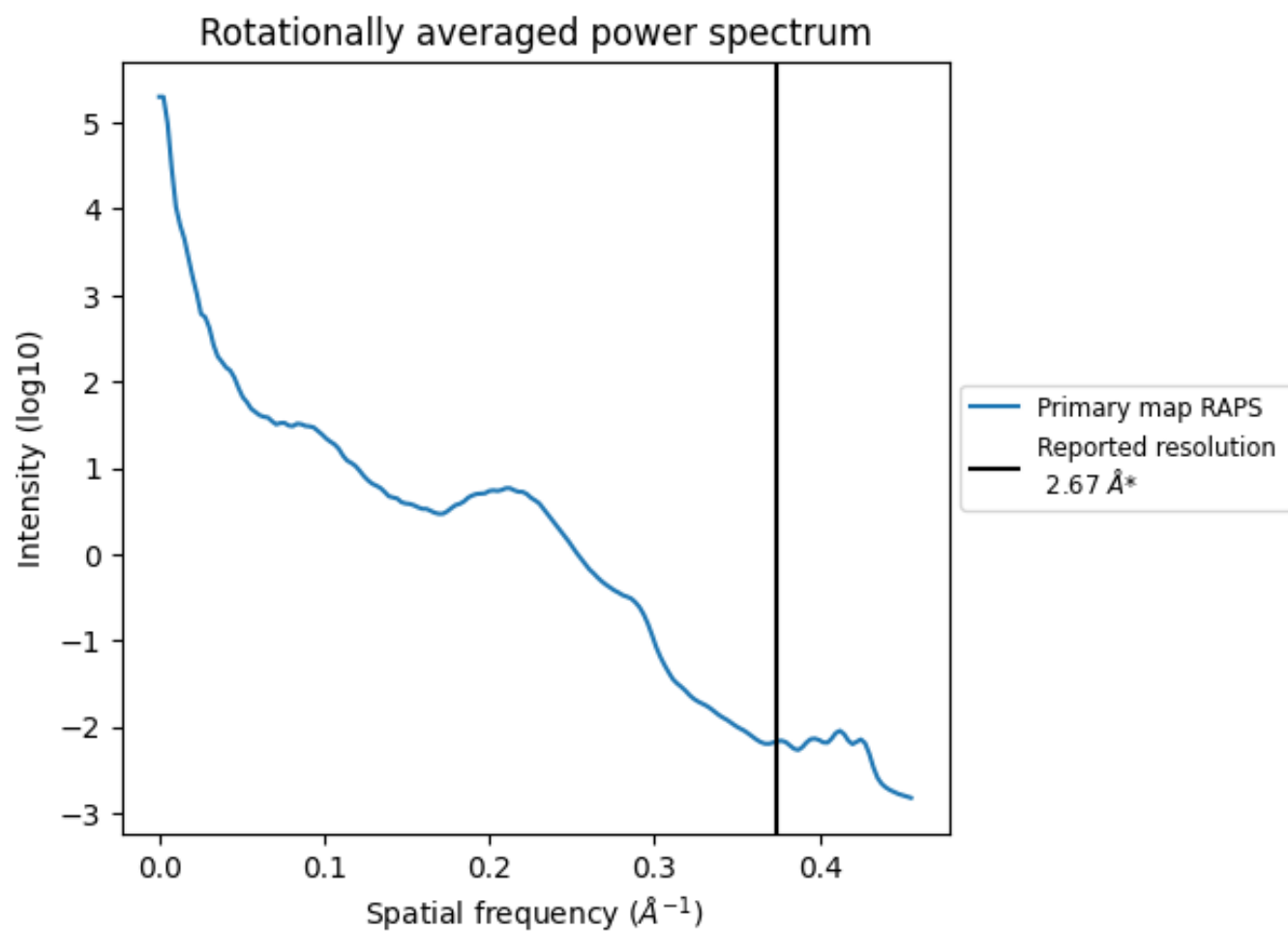
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 608 nm³; this corresponds to an approximate mass of 549 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.375 $\text{\AA}^{-1}$

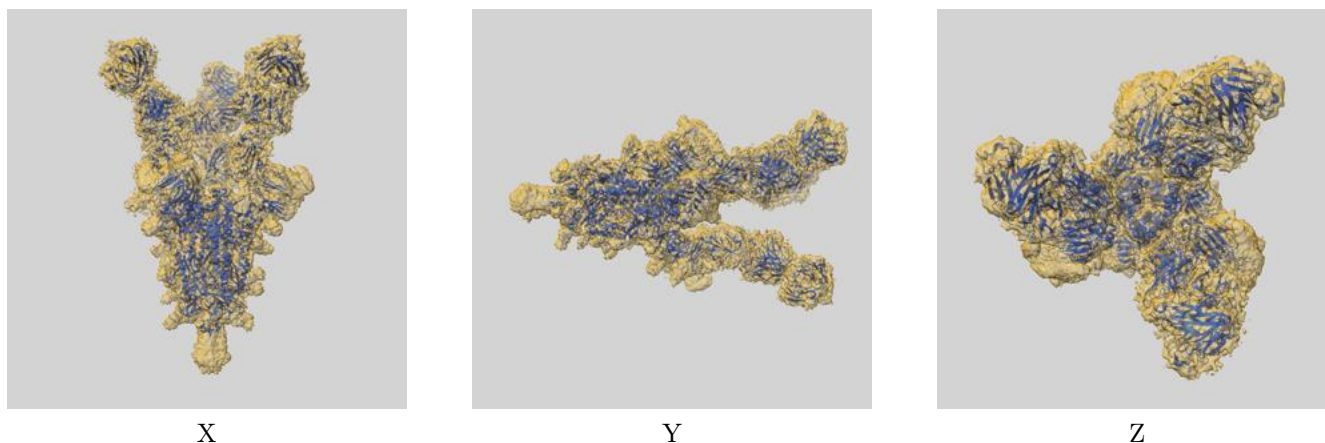
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

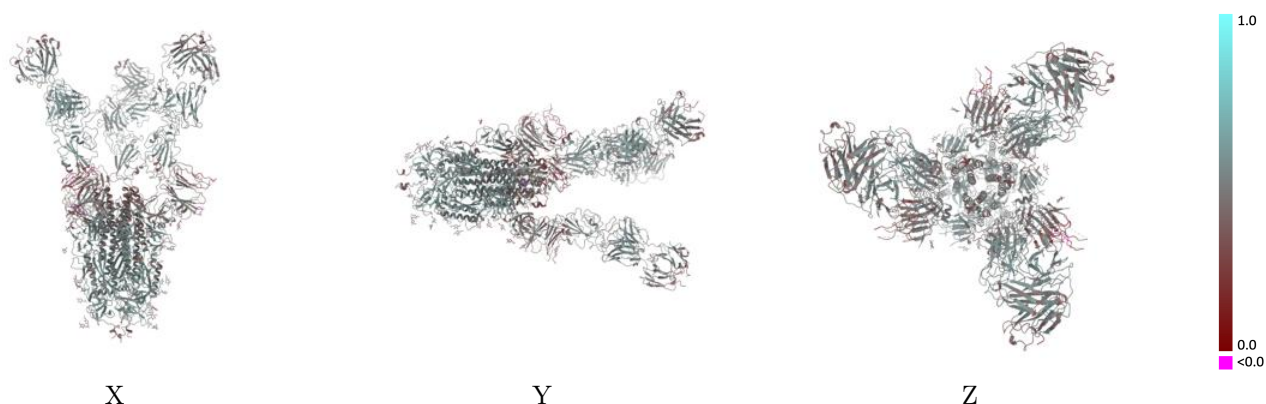
This section contains information regarding the fit between EMDB map EMD-32498 and PDB model 7WHB. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



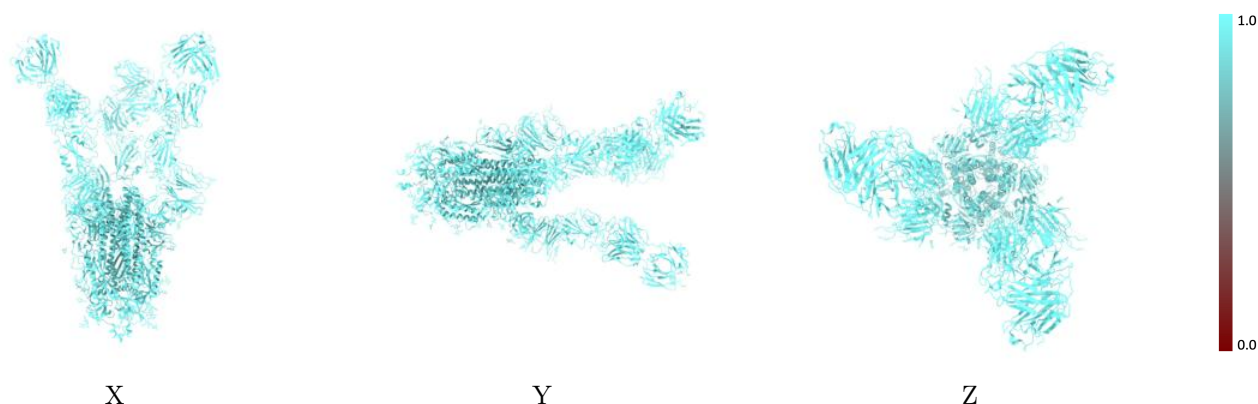
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



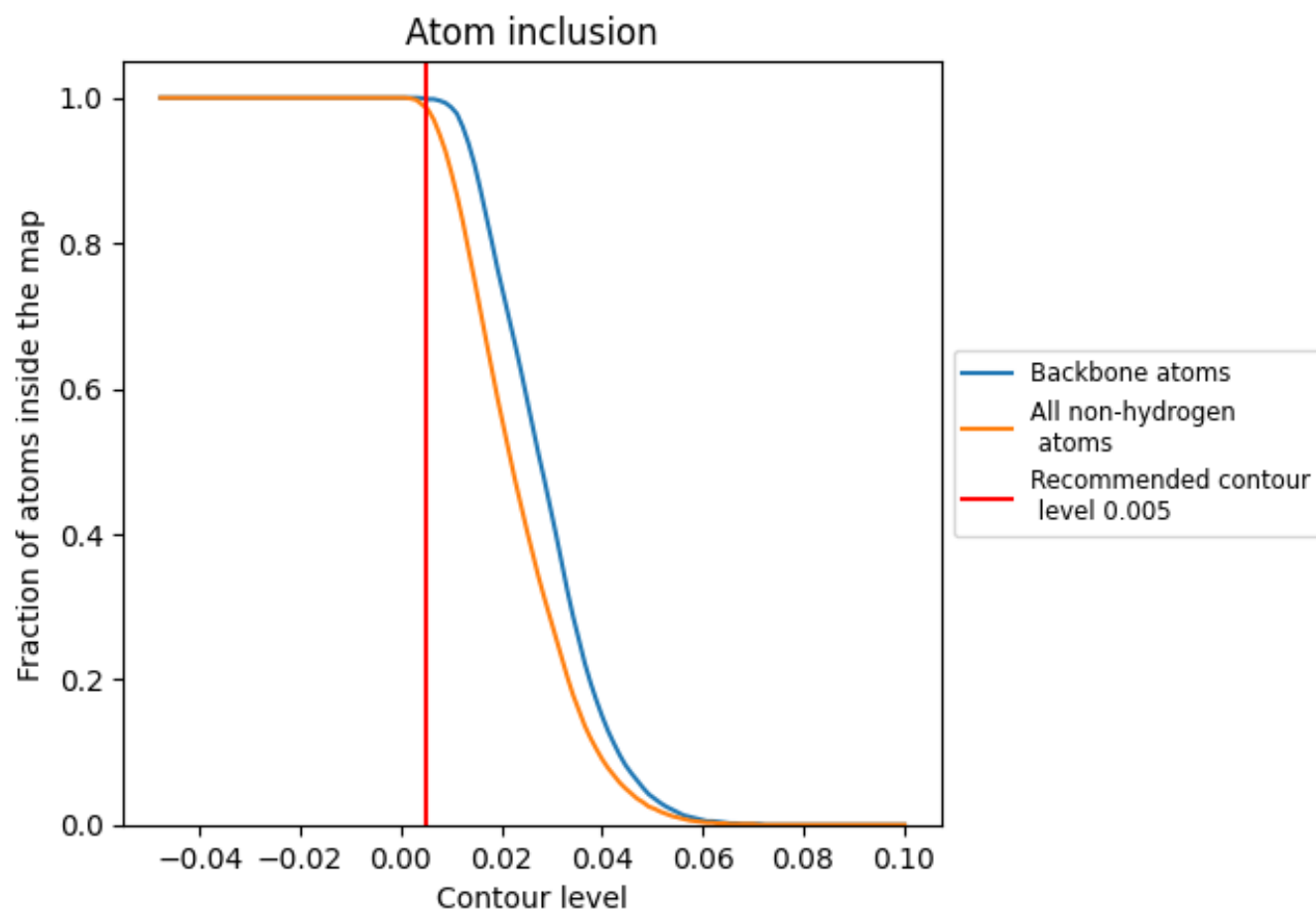
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9860	 0.4790
A	 0.9870	 0.4820
B	 0.9870	 0.4680
C	 0.9880	 0.4740
D	 0.9860	 0.5010
E	 0.9900	 0.5020
F	 1.0000	 0.5030
G	 0.9800	 0.4860
H	 0.9880	 0.4890
I	 1.0000	 0.4160
J	 0.9810	 0.4900
K	 0.9860	 0.4890
L	 0.7860	 0.4070
M	 1.0000	 0.4650
N	 1.0000	 0.3800
O	 1.0000	 0.4300
P	 0.9290	 0.3750
Q	 1.0000	 0.5010
R	 0.9640	 0.3880
S	 0.8210	 0.3940
T	 1.0000	 0.4150
U	 1.0000	 0.4270
V	 0.9290	 0.4090
W	 1.0000	 0.5050
X	 1.0000	 0.4410
Y	 0.8930	 0.3870
Z	 1.0000	 0.4650
a	 1.0000	 0.4120

