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Mol	Chain	Res	Type	Atoms
2	R	2	NAG	C4-C5-C6-O6
4	Q	4	MAN	O5-C5-C6-O6
2	D	3	BMA	O5-C5-C6-O6
8	W	1	NAG	C3-C2-N2-C7
7	V	3	MAN	O5-C5-C6-O6
10	h	2	NAG	O5-C5-C6-O6
12	k	2	NAG	C4-C5-C6-O6
3	b	2	NAG	O5-C5-C6-O6
11	j	1	NAG	C4-C5-C6-O6
4	Q	1	NAG	O5-C5-C6-O6
2	g	1	NAG	C4-C5-C6-O6
5	I	5	MAN	O5-C5-C6-O6
3	P	1	NAG	C4-C5-C6-O6
2	M	2	NAG	C1-C2-N2-C7
2	d	1	NAG	C1-C2-N2-C7
2	f	2	NAG	C1-C2-N2-C7
3	b	1	NAG	C1-C2-N2-C7
3	c	2	NAG	C1-C2-N2-C7
4	H	1	NAG	C1-C2-N2-C7
12	k	1	NAG	C1-C2-N2-C7
5	I	1	NAG	C4-C5-C6-O6
8	W	2	NAG	O5-C5-C6-O6
2	g	1	NAG	O5-C5-C6-O6
2	M	2	NAG	C3-C2-N2-C7
2	d	1	NAG	C3-C2-N2-C7
2	f	1	NAG	C3-C2-N2-C7
3	b	1	NAG	C3-C2-N2-C7
3	b	2	NAG	C3-C2-N2-C7
3	c	2	NAG	C3-C2-N2-C7
6	U	2	NAG	C3-C2-N2-C7
8	W	2	NAG	C3-C2-N2-C7
12	k	1	NAG	C3-C2-N2-C7
5	L	3	BMA	C4-C5-C6-O6
2	R	2	NAG	O5-C5-C6-O6
3	c	2	NAG	O5-C5-C6-O6
4	S	4	MAN	C4-C5-C6-O6
2	R	1	NAG	C1-C2-N2-C7
2	f	1	NAG	C1-C2-N2-C7
2	g	2	NAG	C1-C2-N2-C7
3	b	2	NAG	C1-C2-N2-C7
3	c	1	NAG	C1-C2-N2-C7
6	K	2	NAG	C1-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
2	M	1	NAG	C3-C2-N2-C7
2	T	2	NAG	C3-C2-N2-C7
2	Y	2	NAG	C3-C2-N2-C7
2	f	2	NAG	C3-C2-N2-C7
4	H	1	NAG	C3-C2-N2-C7
4	a	1	NAG	C3-C2-N2-C7
4	a	2	NAG	C3-C2-N2-C7
6	K	1	NAG	C3-C2-N2-C7
10	h	2	NAG	C3-C2-N2-C7
2	M	2	NAG	C4-C5-C6-O6
5	I	4	MAN	C4-C5-C6-O6
12	k	1	NAG	O5-C5-C6-O6
5	I	4	MAN	O5-C5-C6-O6
6	K	2	NAG	C4-C5-C6-O6
3	X	1	NAG	C4-C5-C6-O6
2	f	2	NAG	O5-C5-C6-O6
12	k	1	NAG	C4-C5-C6-O6

All (4) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	O	4	MAN	C1-C2-C3-C4-C5-O5
5	I	5	MAN	C1-C2-C3-C4-C5-O5
4	i	4	MAN	C1-C2-C3-C4-C5-O5
10	h	4	MAN	C1-C2-C3-C4-C5-O5

66 monomers are involved in 132 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	j	1	NAG	7	0
2	f	2	NAG	2	0
3	F	2	NAG	1	0
10	h	2	NAG	4	0
2	J	1	NAG	2	0
4	H	3	BMA	1	0
3	E	2	NAG	4	0
4	a	4	MAN	1	0
2	g	3	BMA	3	0
5	L	2	NAG	2	0
11	j	2	FUC	5	0
12	k	2	NAG	8	0
7	V	2	NAG	1	0

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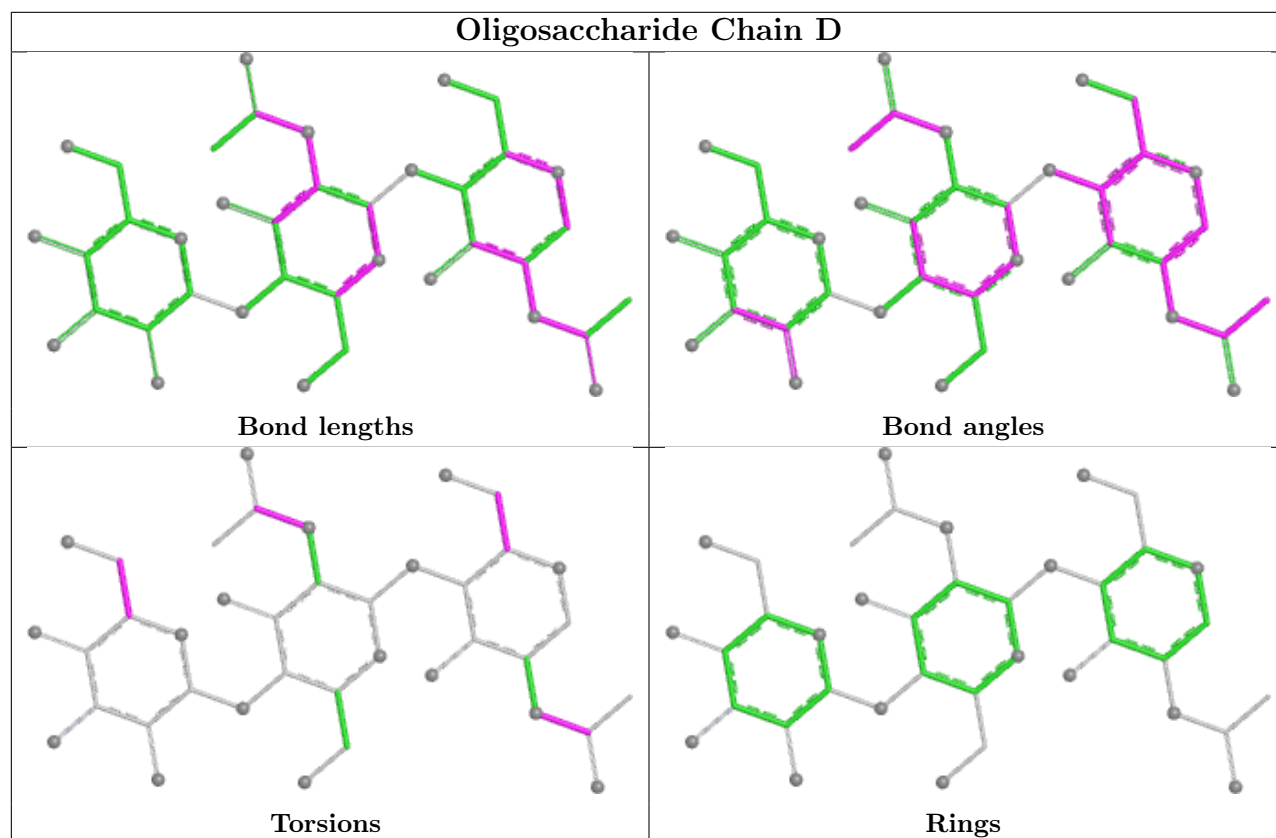
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	f	3	BMA	1	0
2	f	1	NAG	3	0
4	H	1	NAG	5	0
4	H	2	NAG	1	0
4	a	1	NAG	2	0
3	E	1	NAG	2	0
2	D	3	BMA	1	0
5	L	5	MAN	4	0
4	O	1	NAG	1	0
6	U	3	FUC	1	0
4	Q	2	NAG	6	0
12	k	5	MAN	2	0
12	k	1	NAG	11	0
8	W	3	MAN	1	0
2	g	2	NAG	5	0
3	c	1	NAG	1	0
8	W	2	NAG	1	0
2	T	2	NAG	2	0
4	Q	1	NAG	4	0
2	M	1	NAG	1	0
4	O	4	MAN	1	0
3	b	2	NAG	3	0
9	e	1	NAG	1	0
2	G	2	NAG	1	0
6	K	3	FUC	2	0
2	D	2	NAG	3	0
3	b	1	NAG	1	0
10	h	1	NAG	3	0
3	P	1	NAG	3	0
2	T	1	NAG	1	0
12	k	6	FUC	10	0
2	R	2	NAG	7	0
2	d	2	NAG	8	0
2	G	1	NAG	2	0
2	d	1	NAG	5	0
5	L	1	NAG	12	0
5	L	4	MAN	3	0
2	D	1	NAG	4	0
4	O	3	BMA	1	0
2	T	3	BMA	2	0
12	k	3	BMA	4	0
3	N	1	NAG	2	0

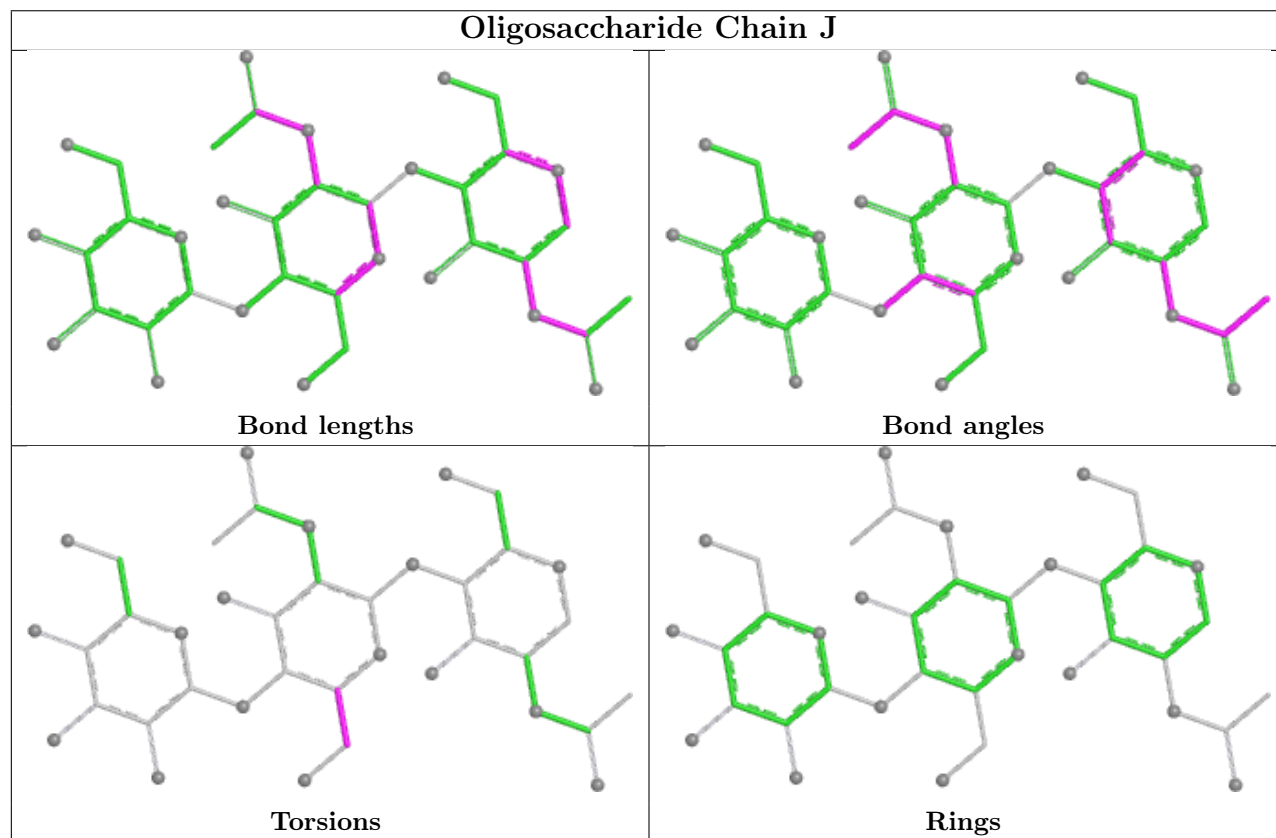
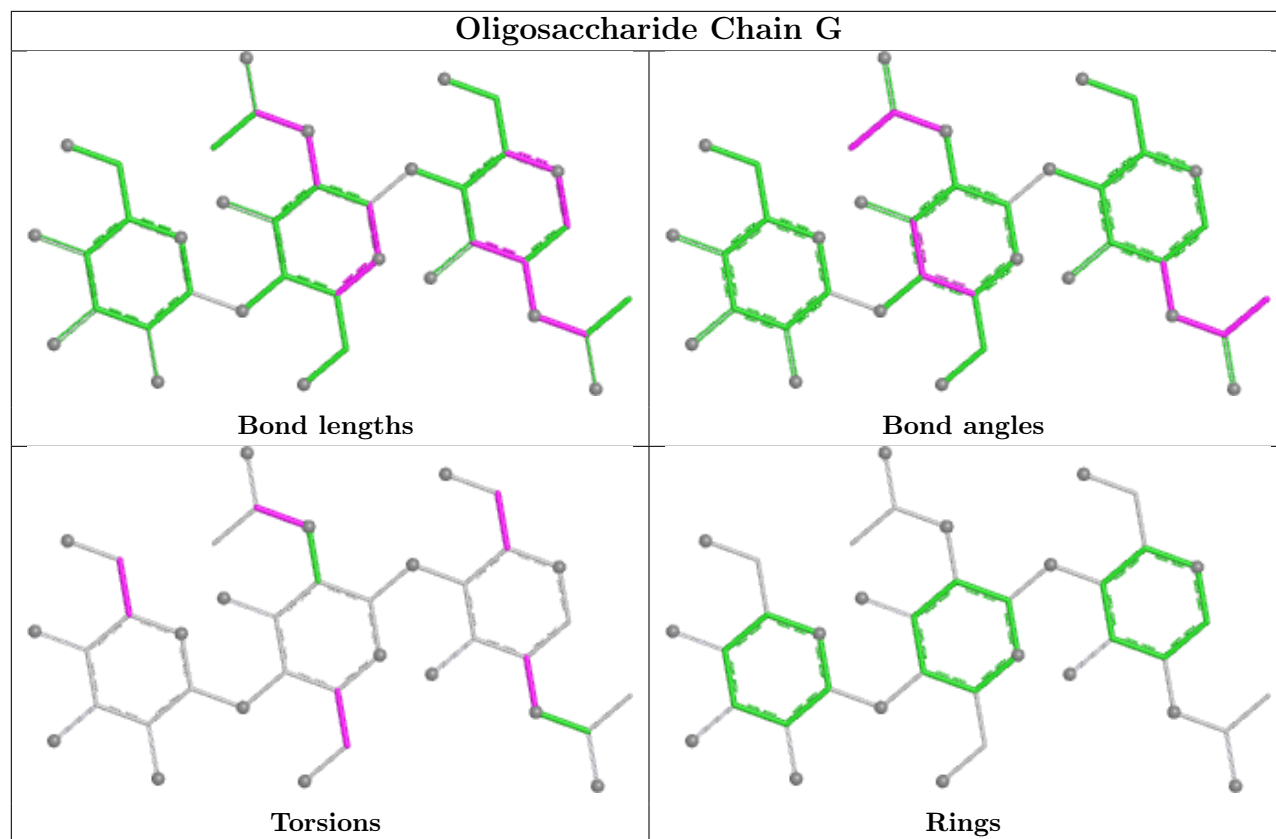
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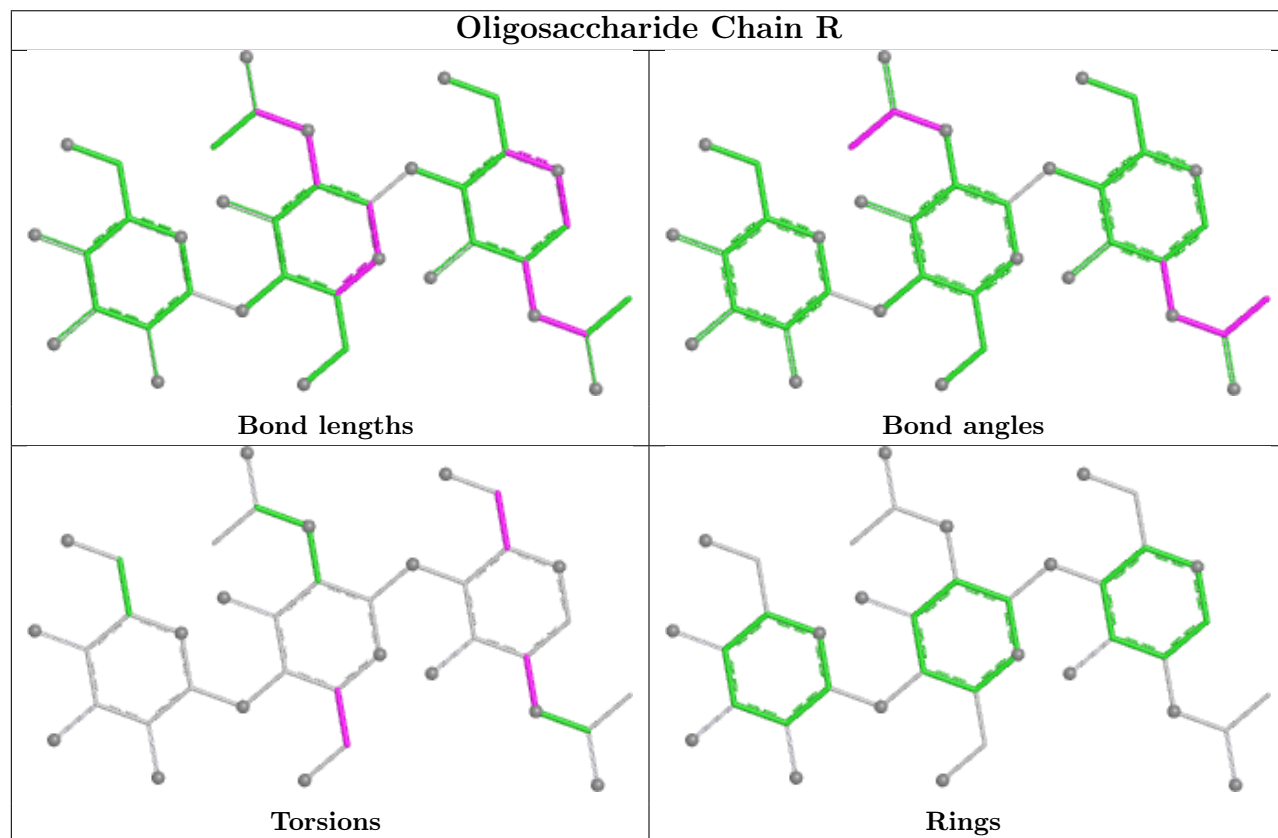
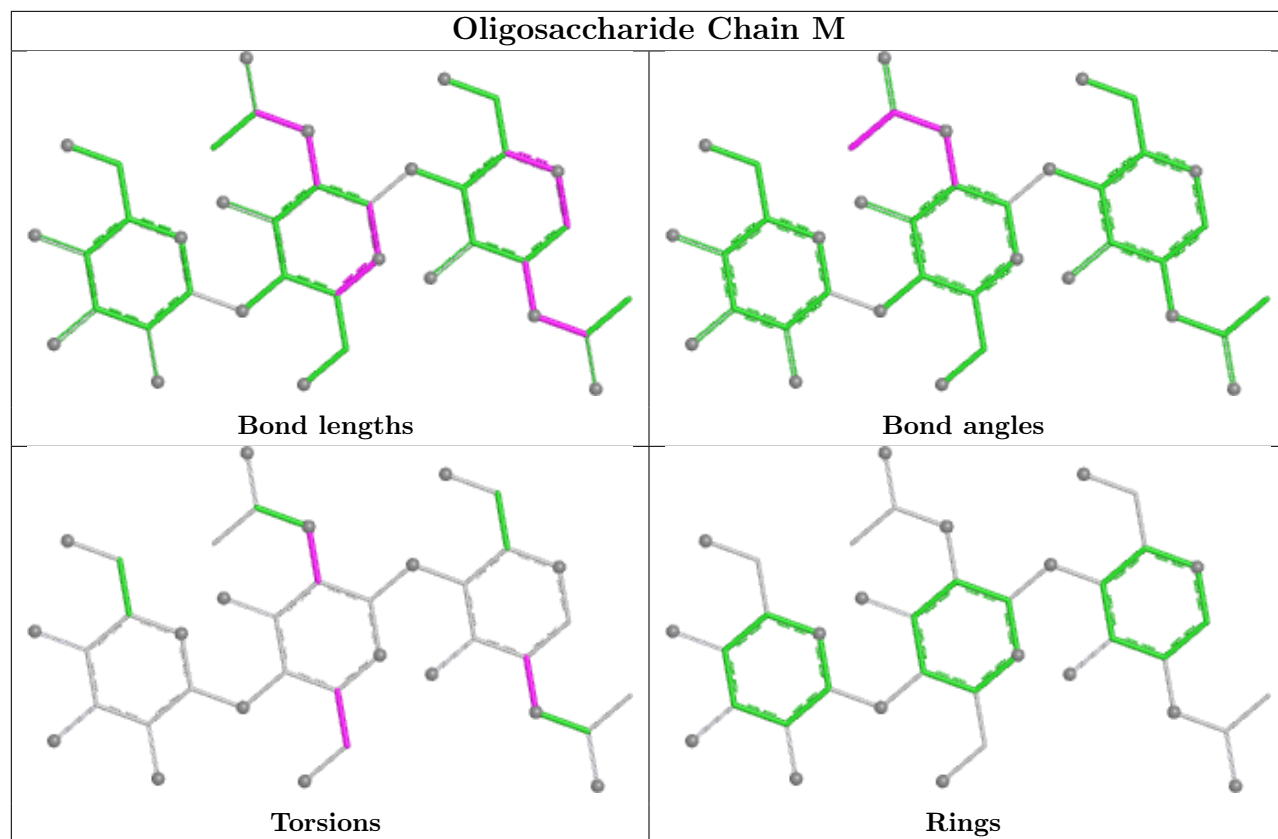
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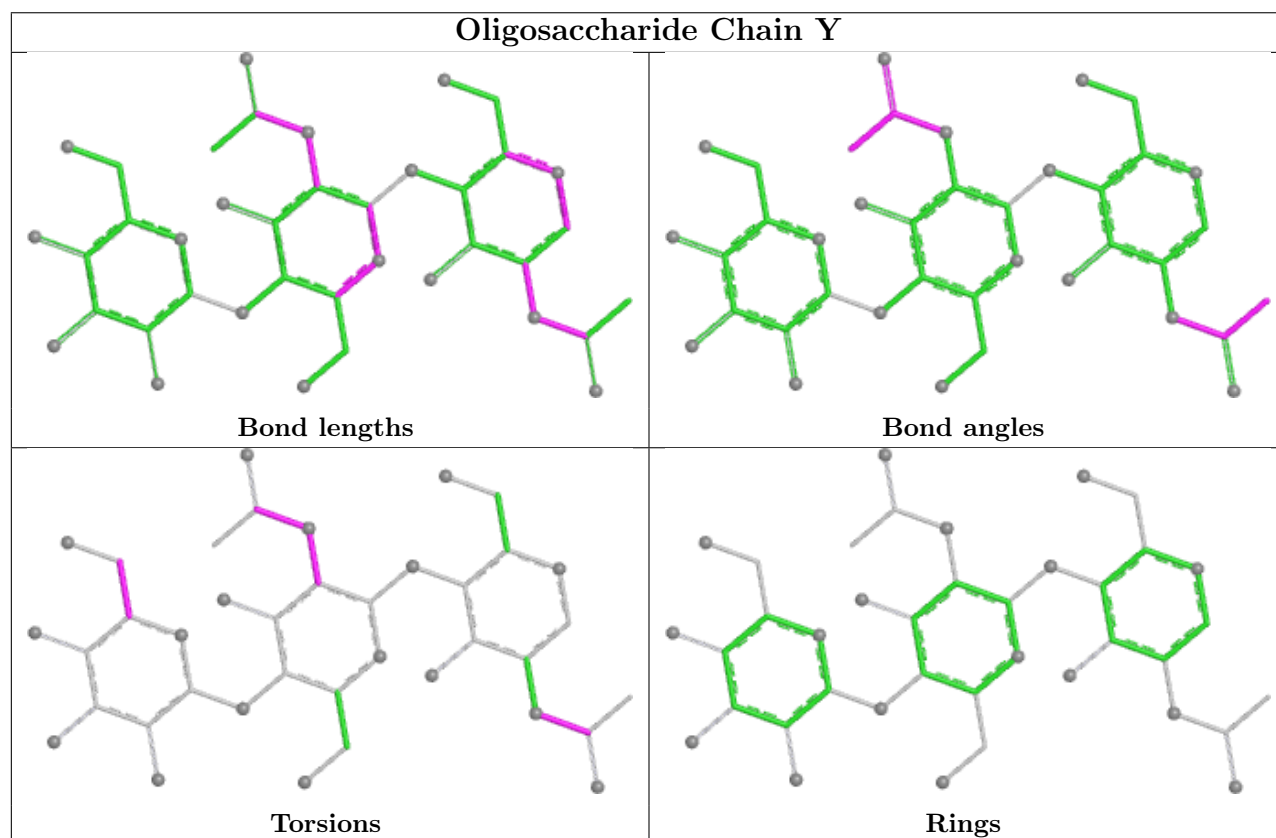
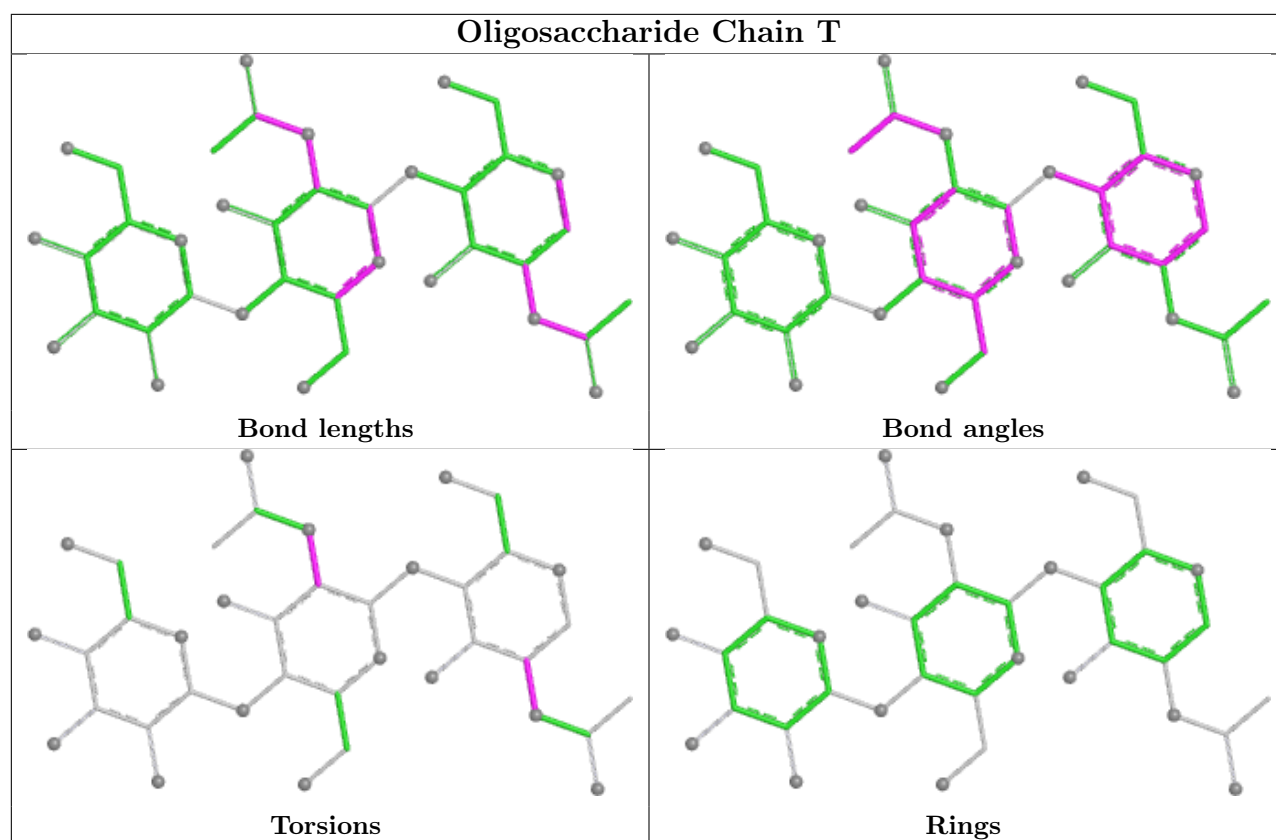
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	R	3	BMA	3	0
2	R	1	NAG	5	0
2	d	3	BMA	6	0
5	L	3	BMA	7	0
2	g	1	NAG	2	0
4	a	3	BMA	1	0
7	V	1	NAG	1	0
12	k	4	MAN	2	0
3	F	1	NAG	1	0
4	Q	3	BMA	4	0
6	U	1	NAG	1	0

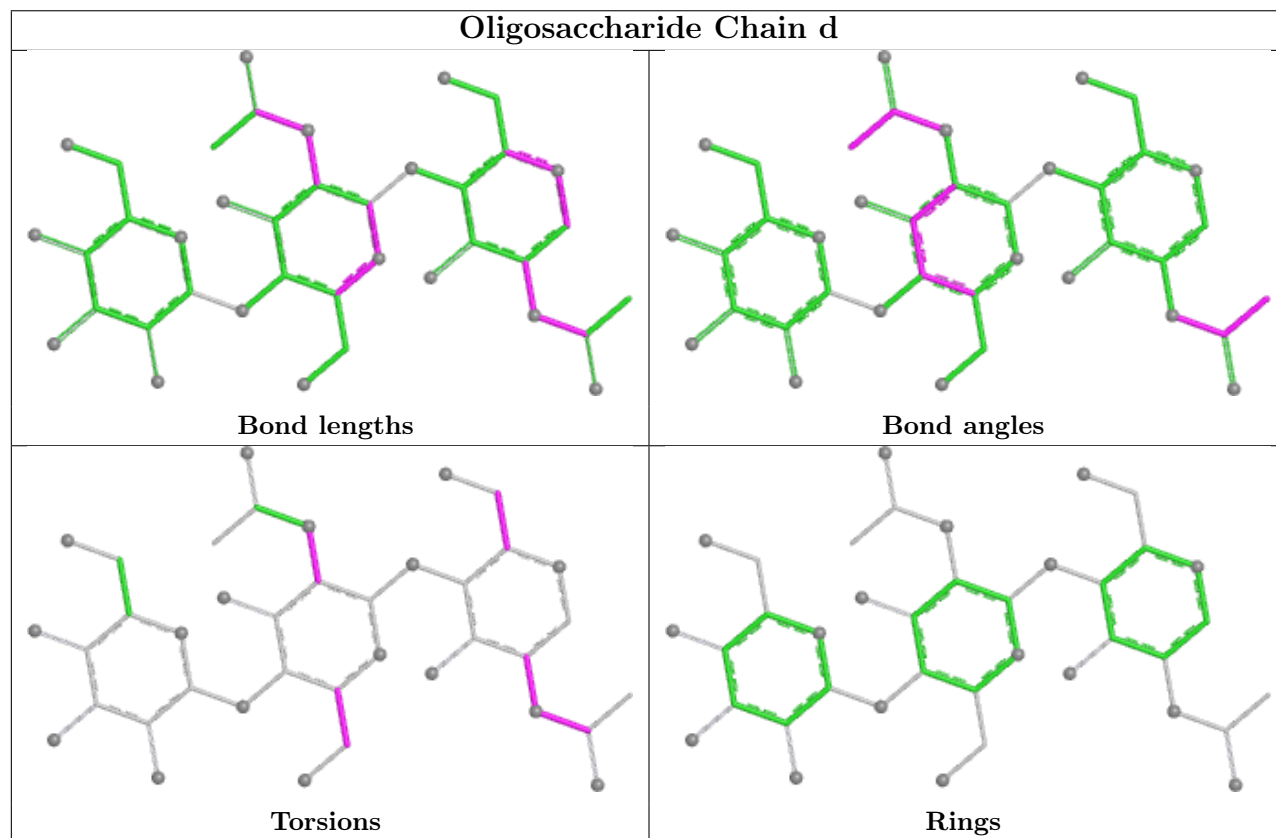
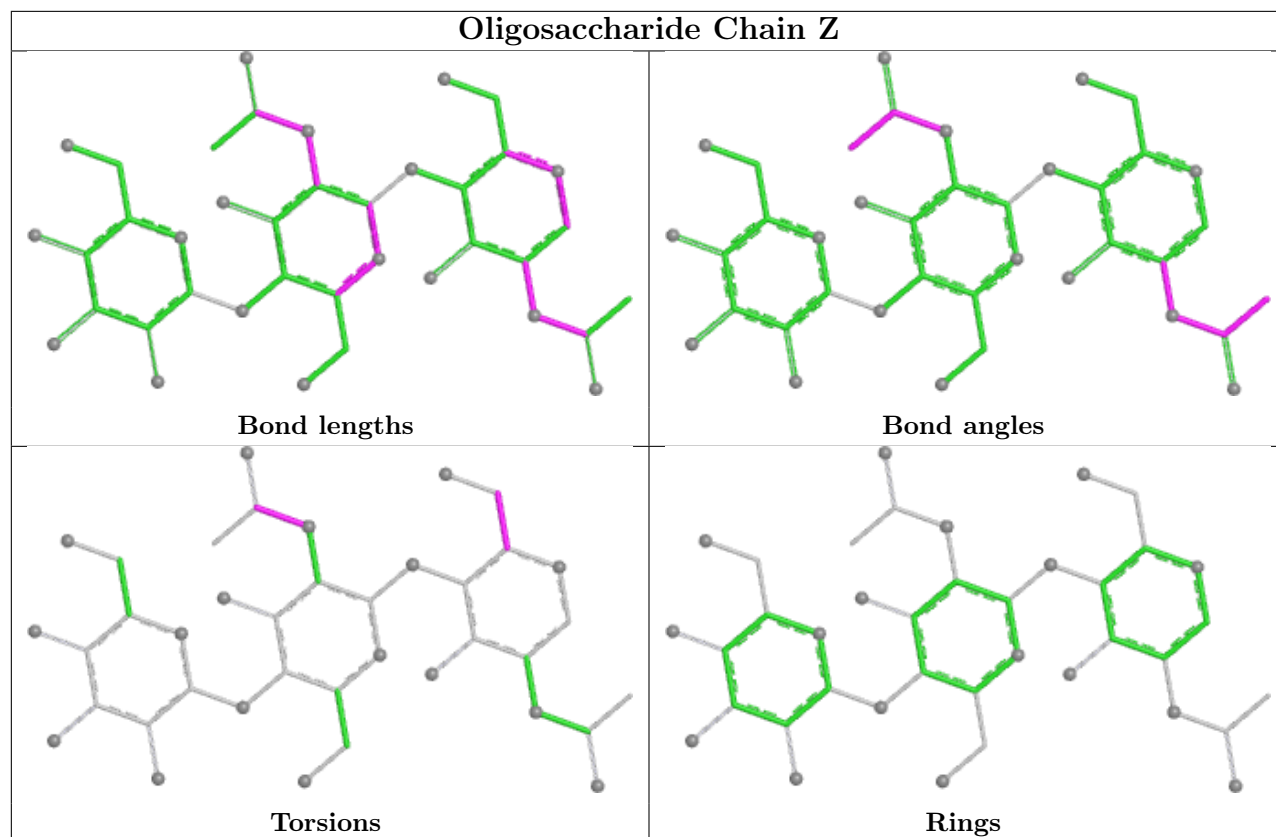
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

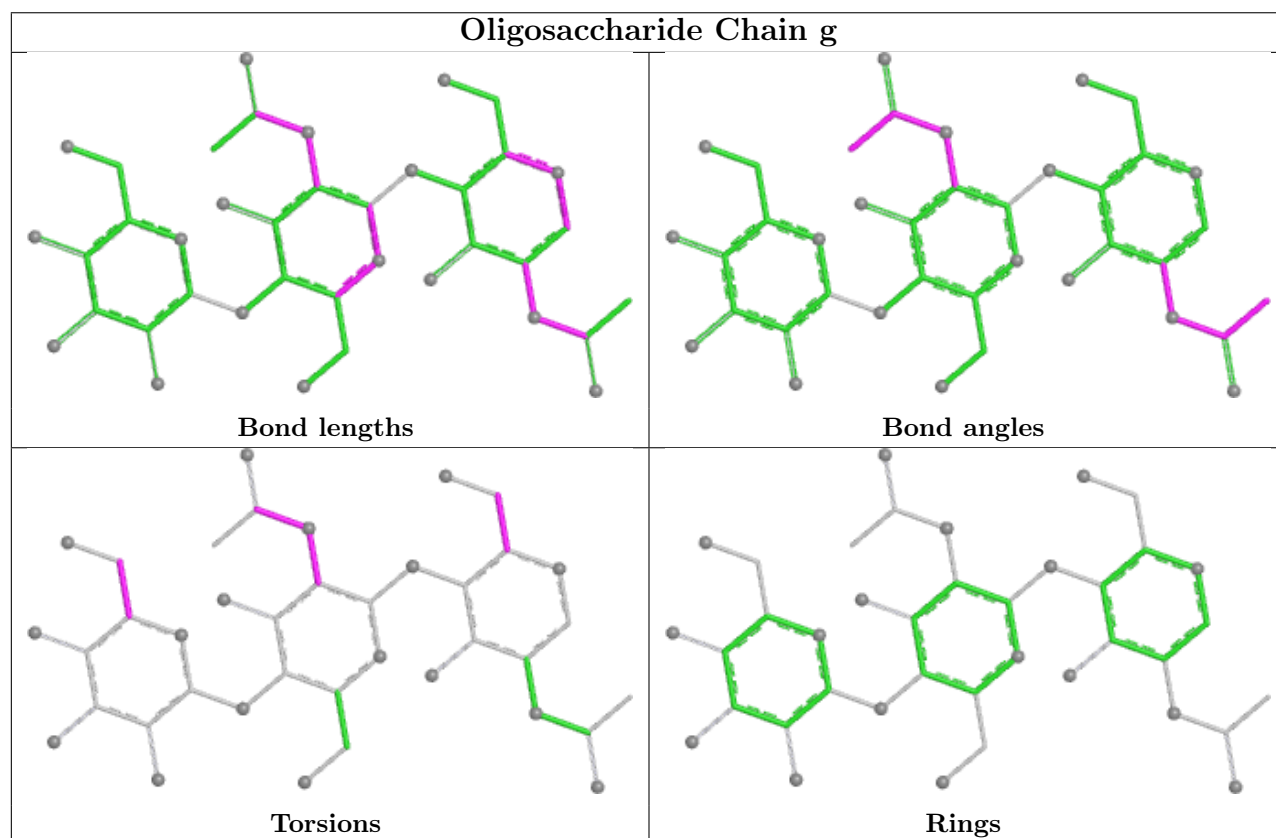
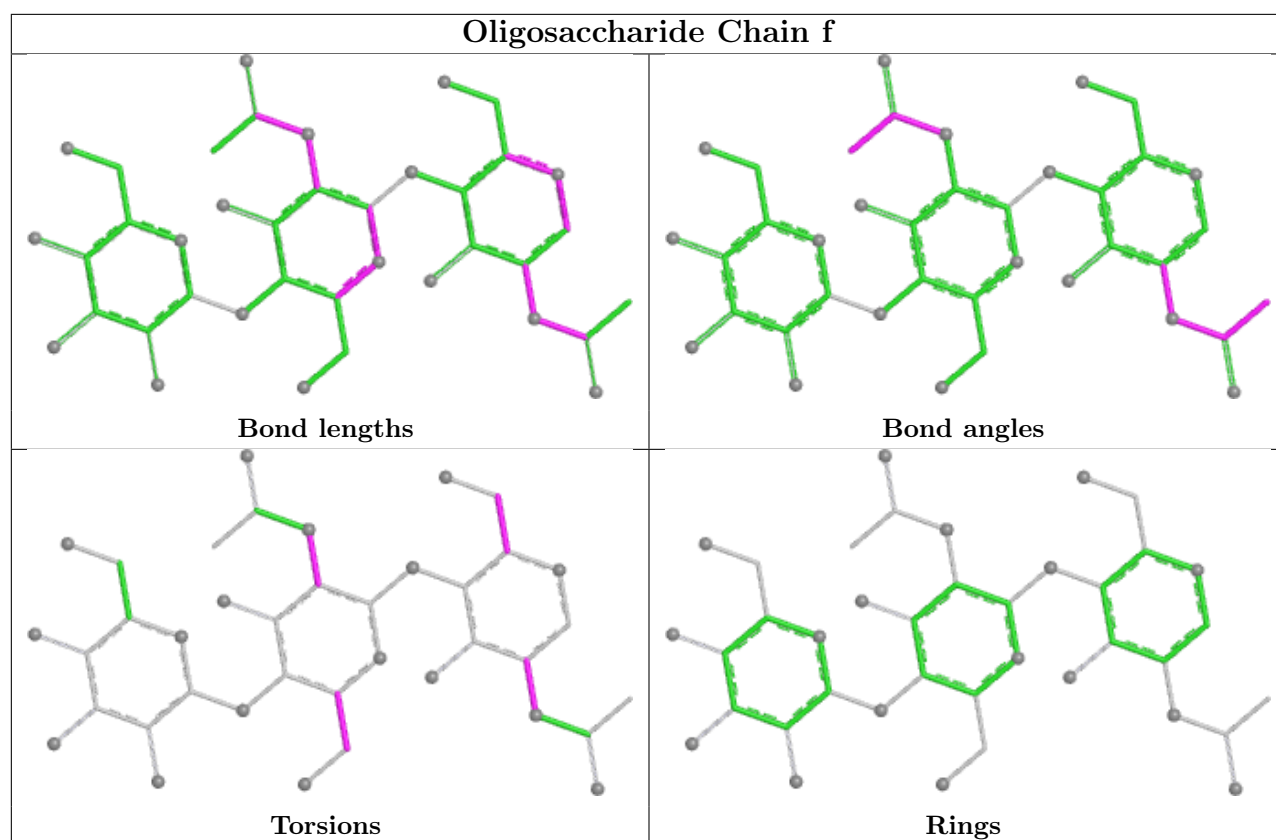


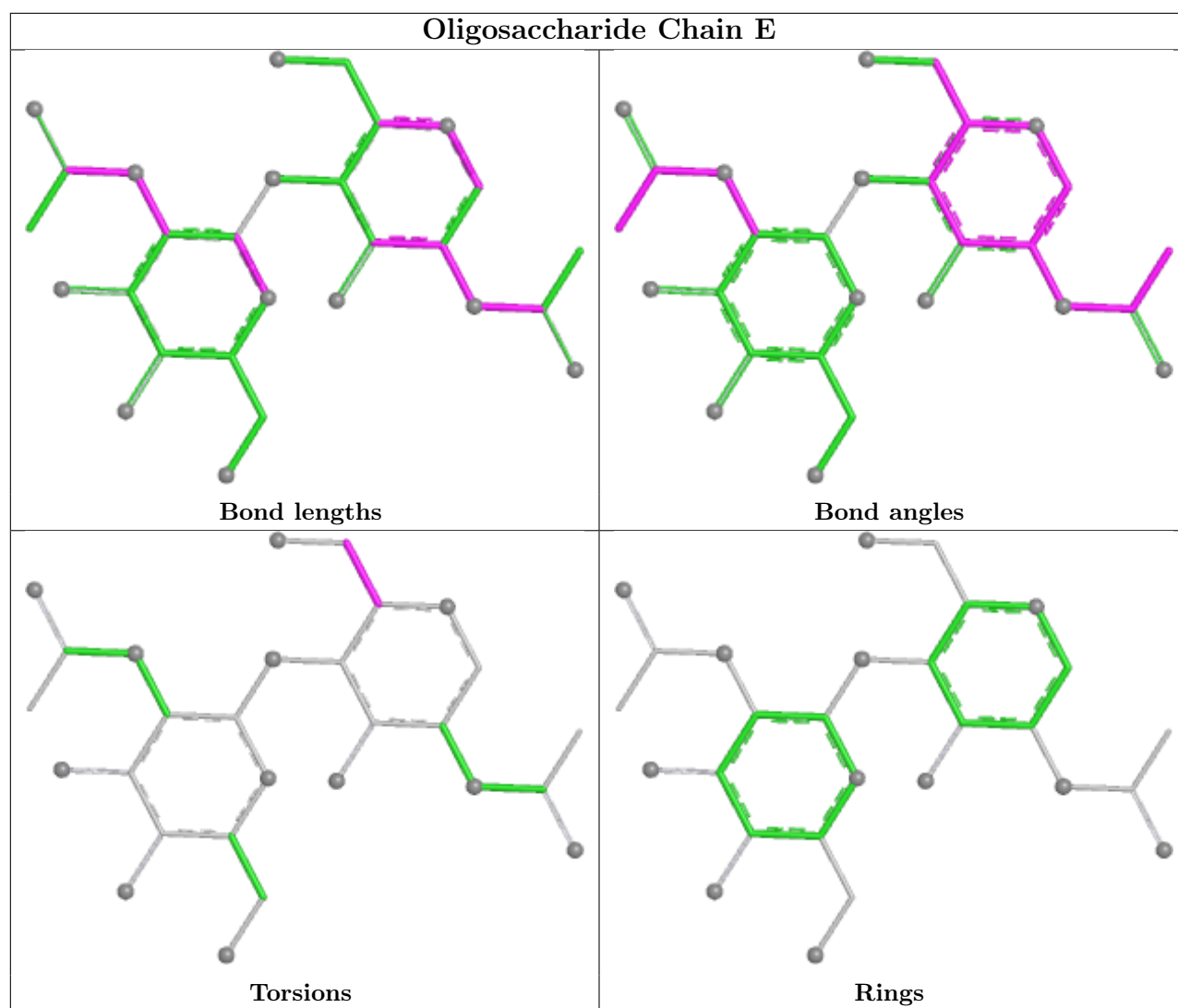


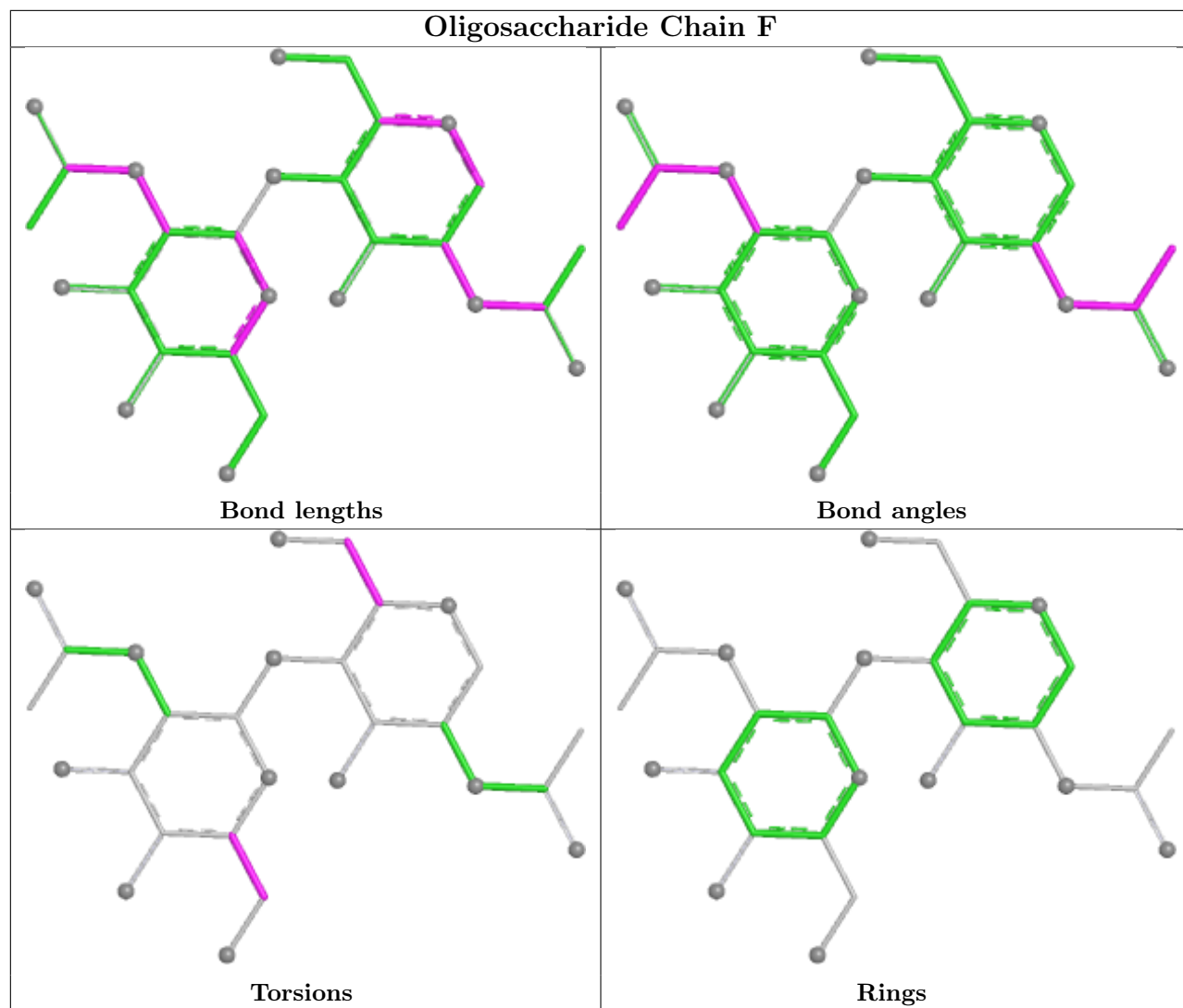


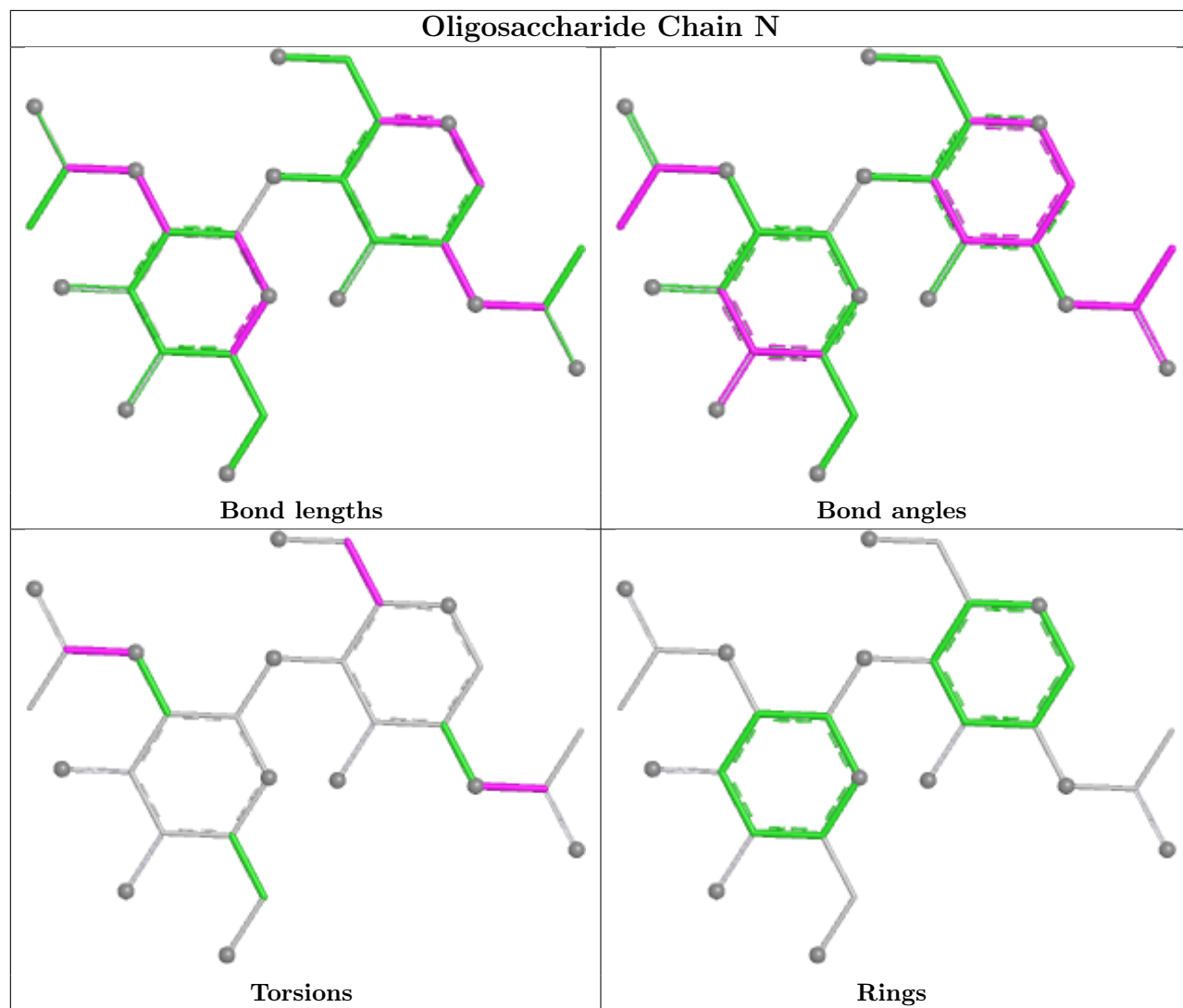


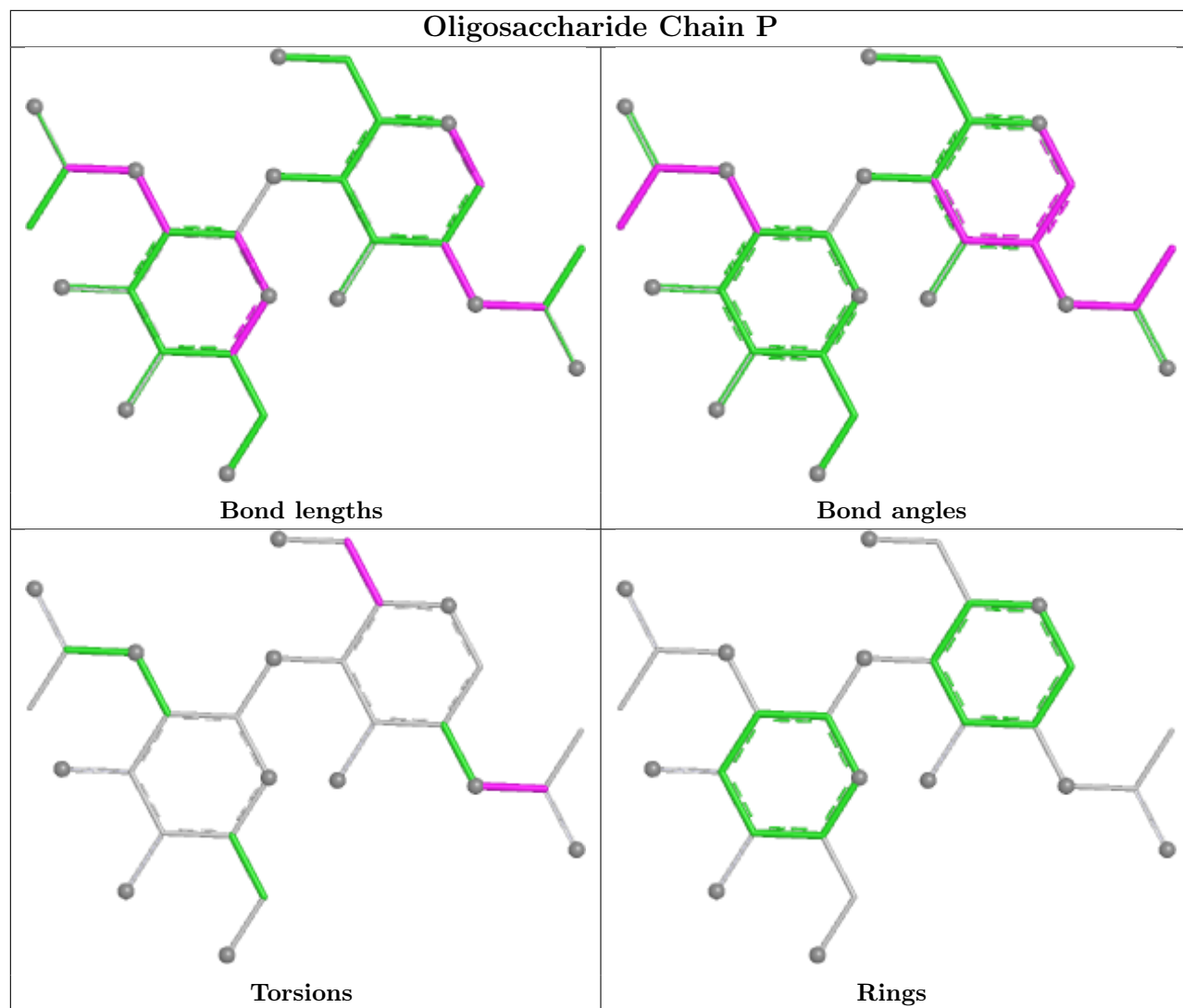


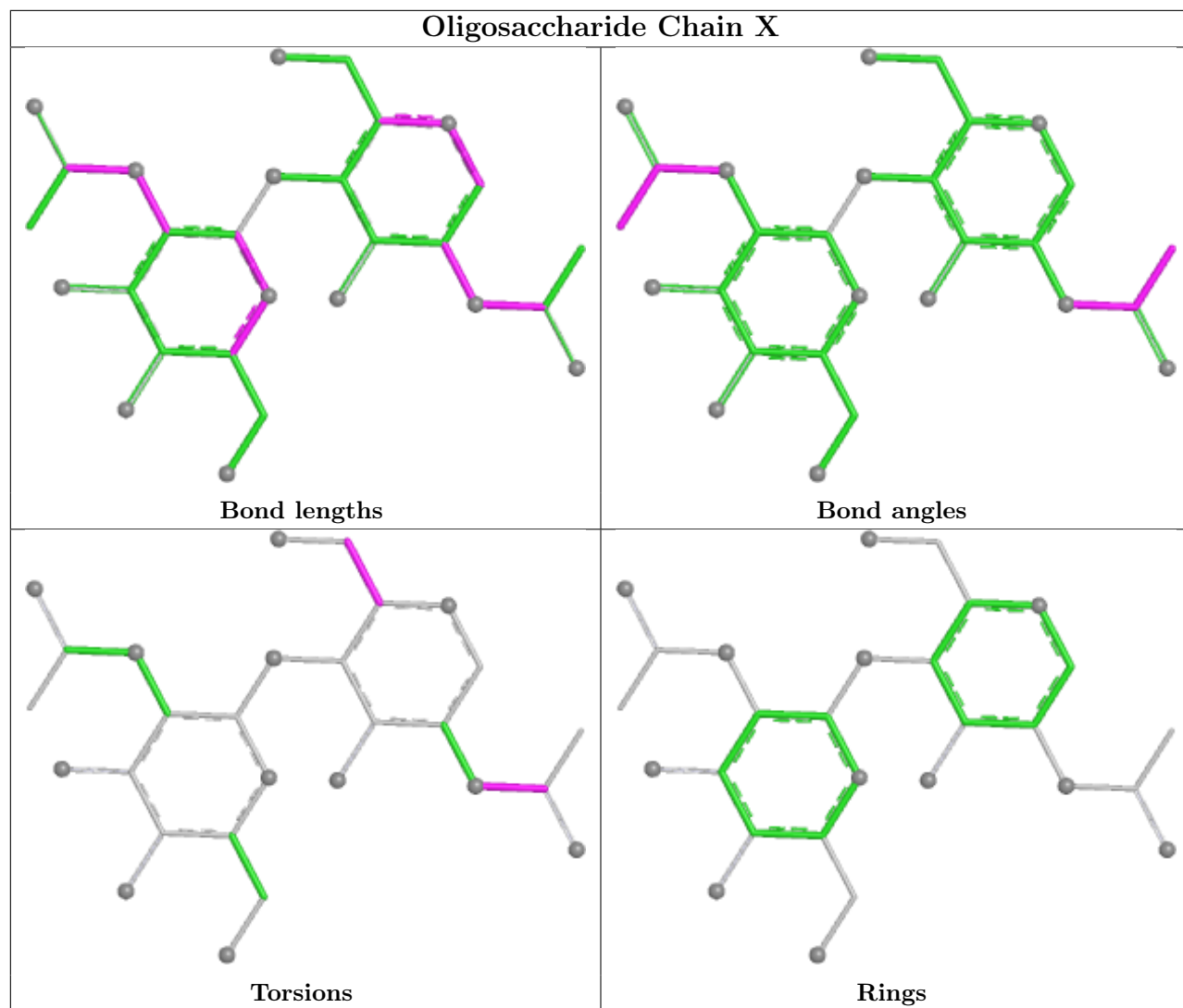


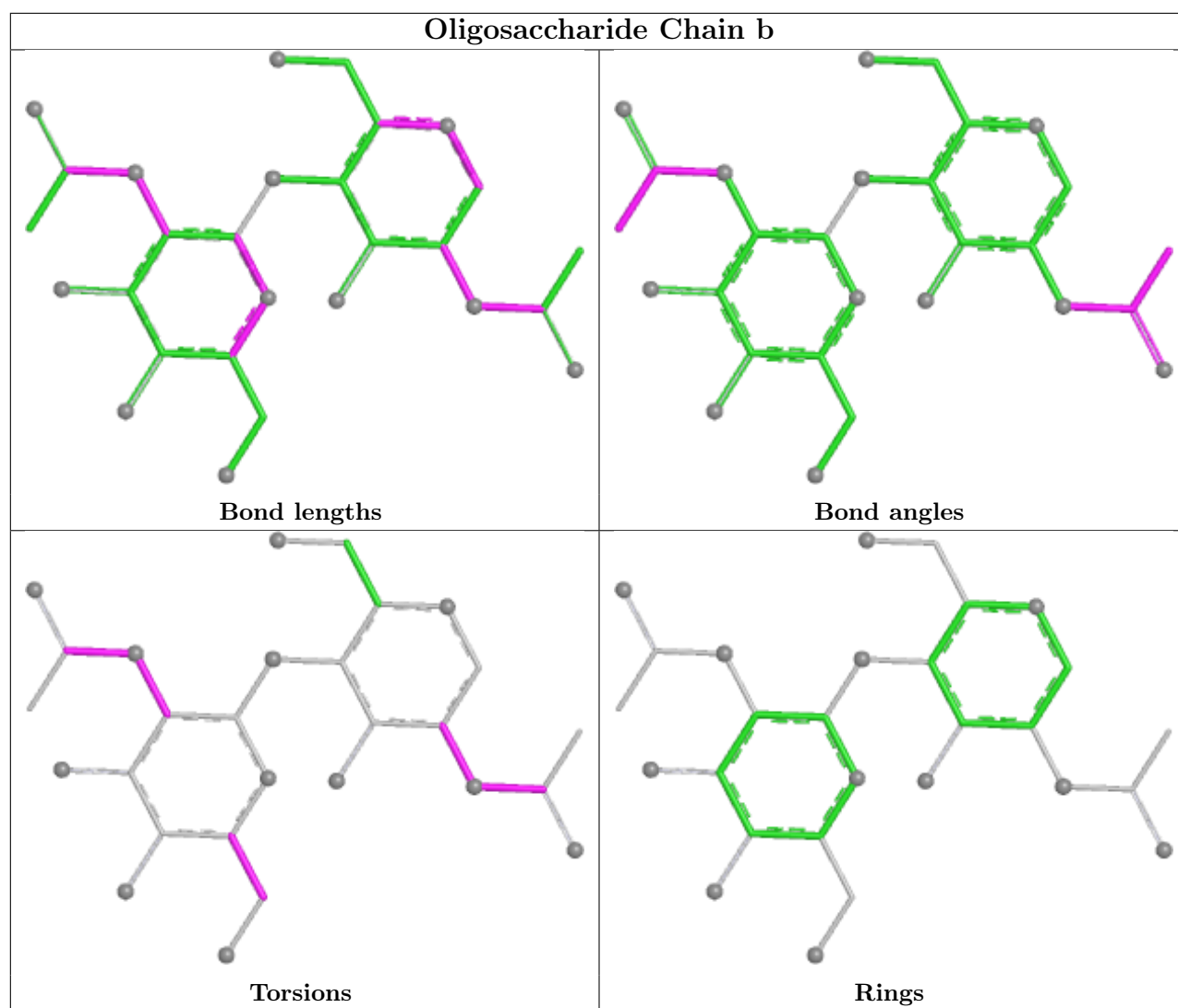


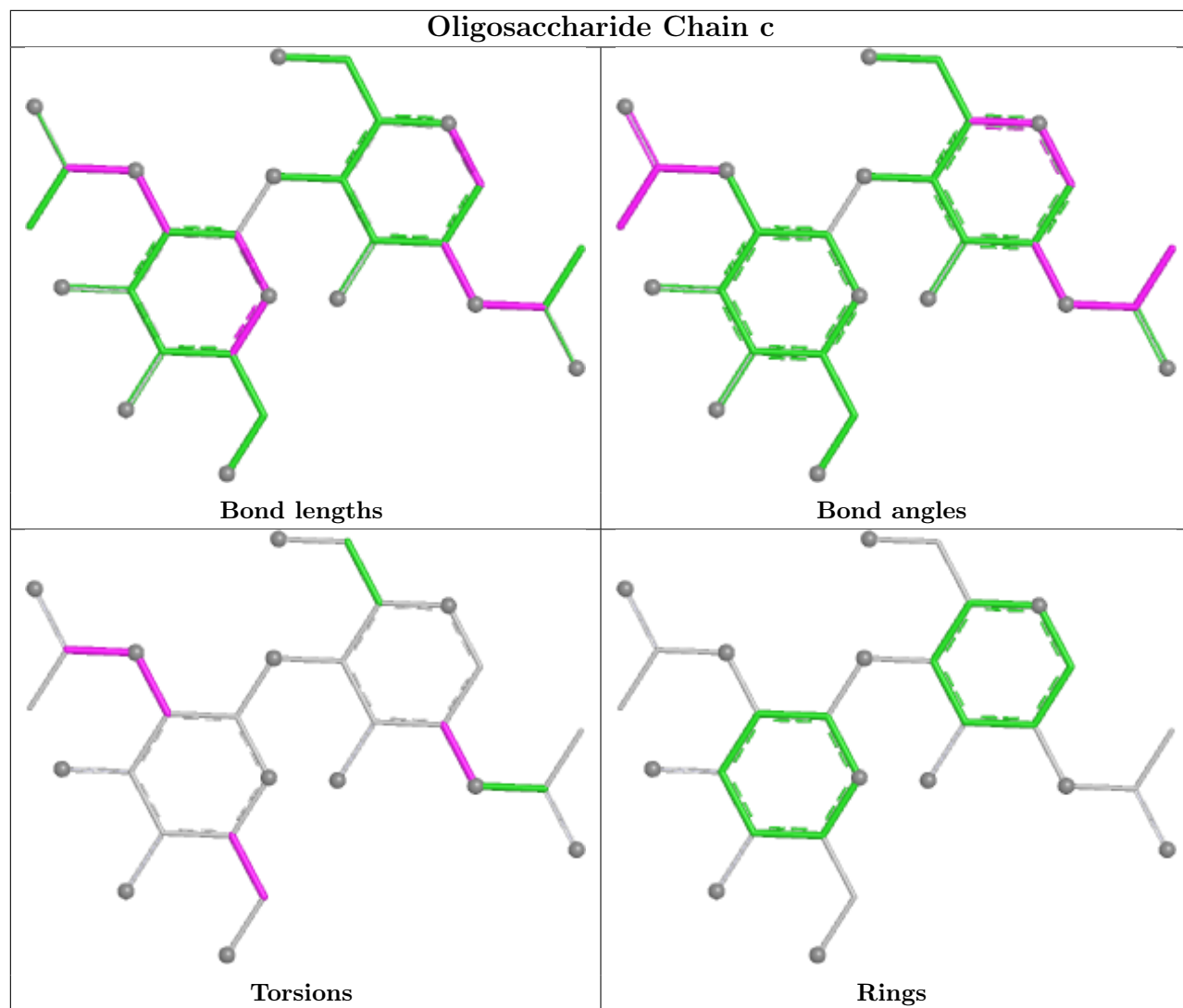


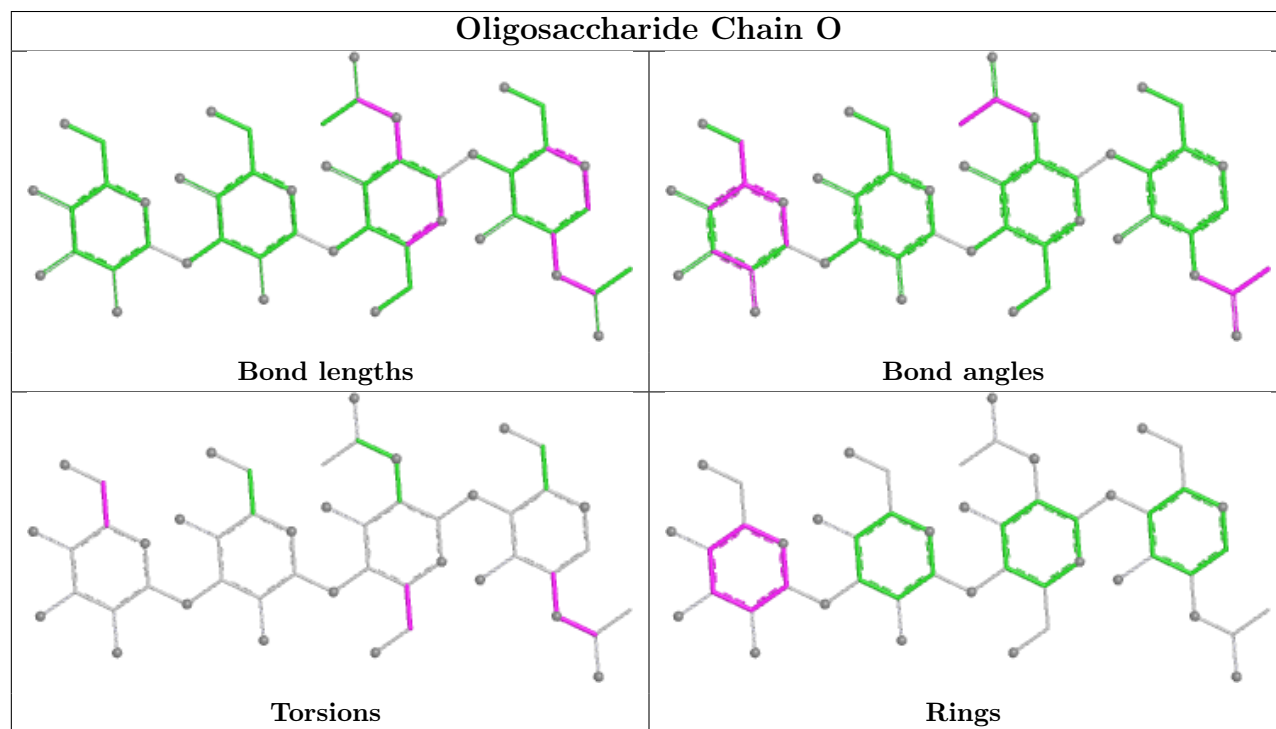
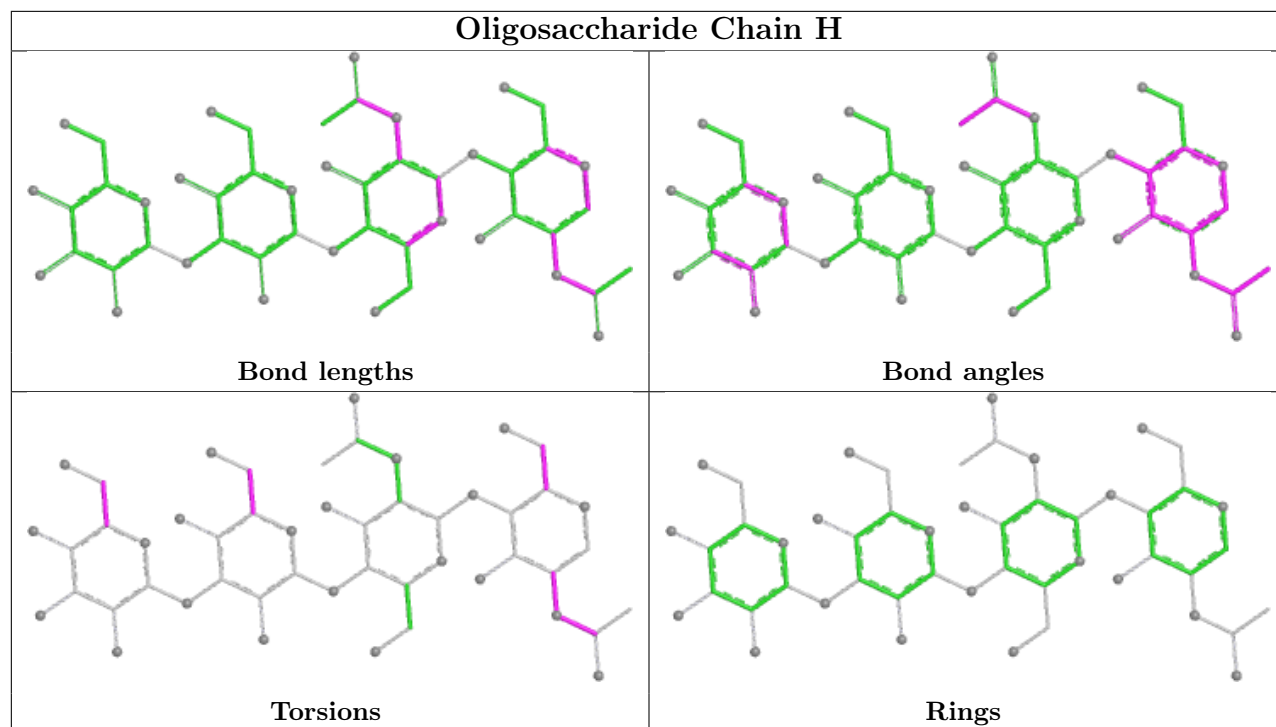




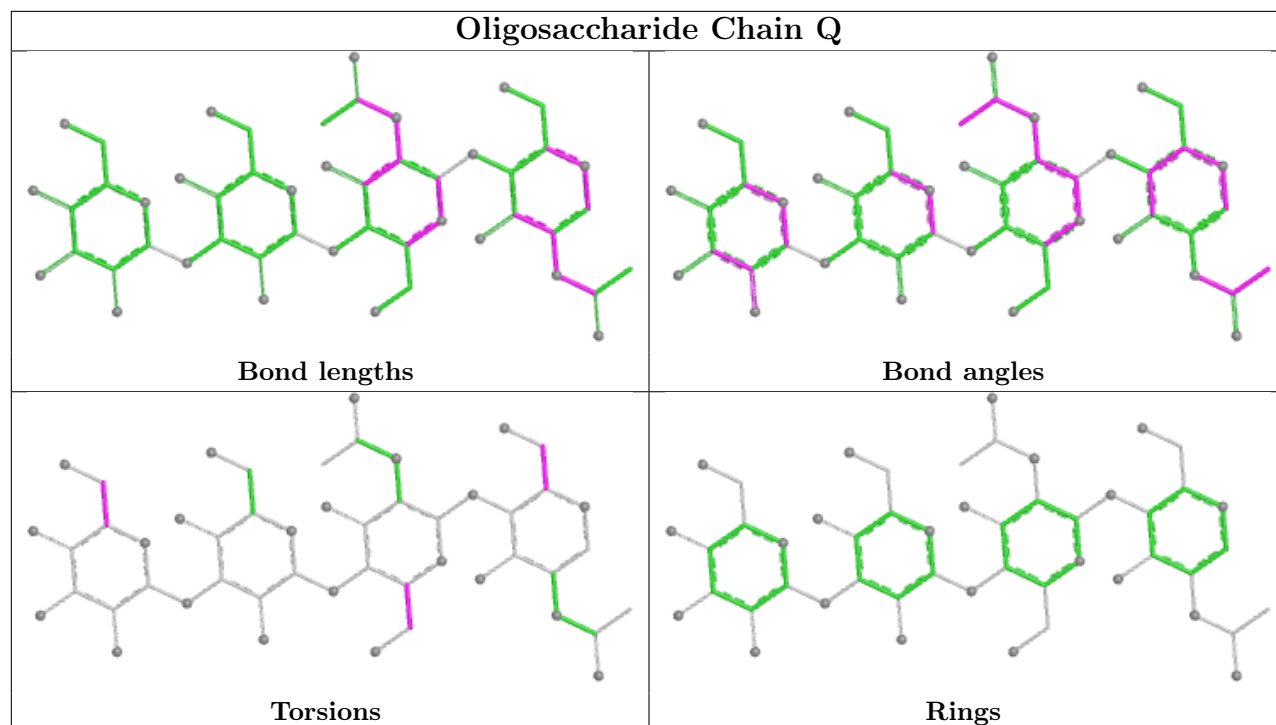




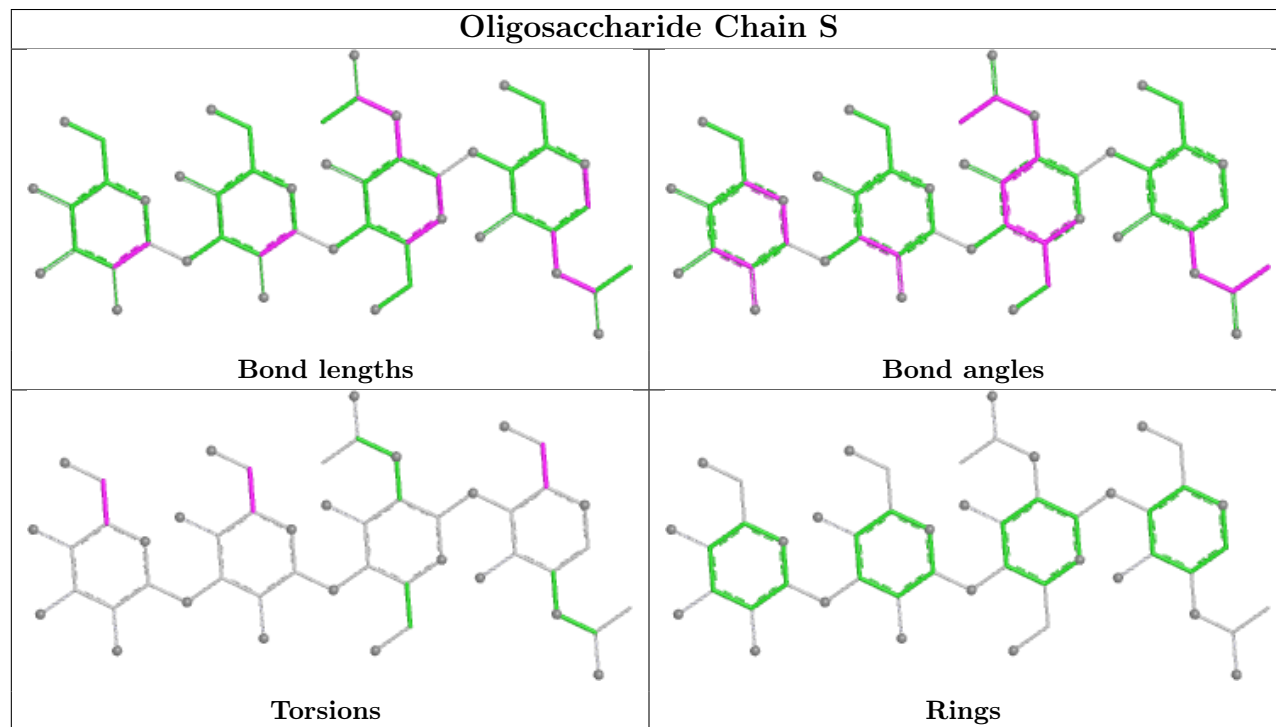


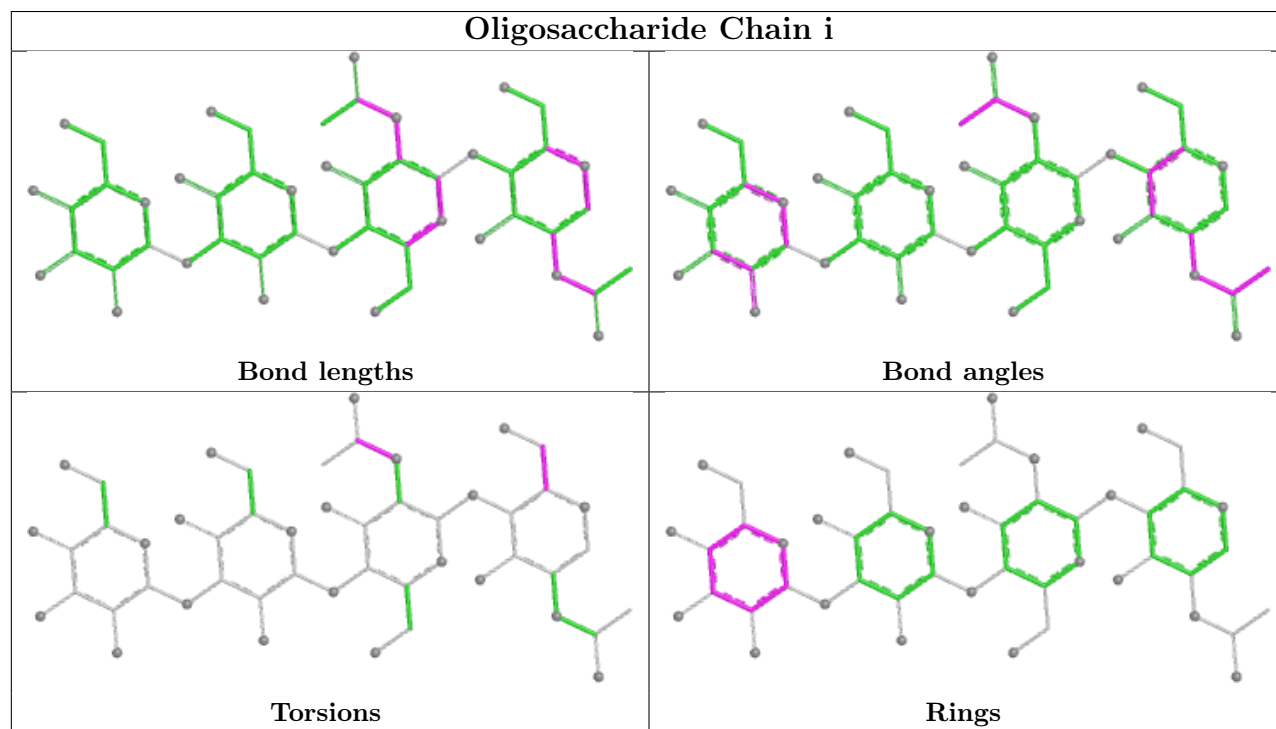
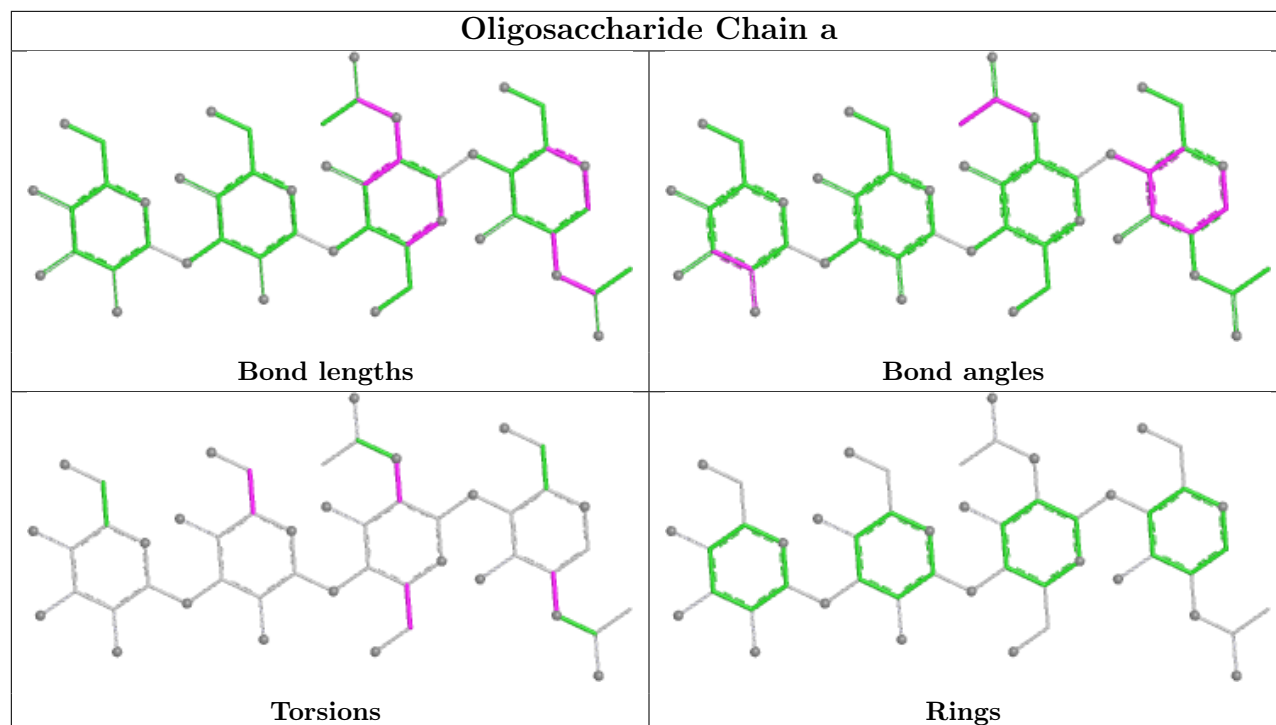


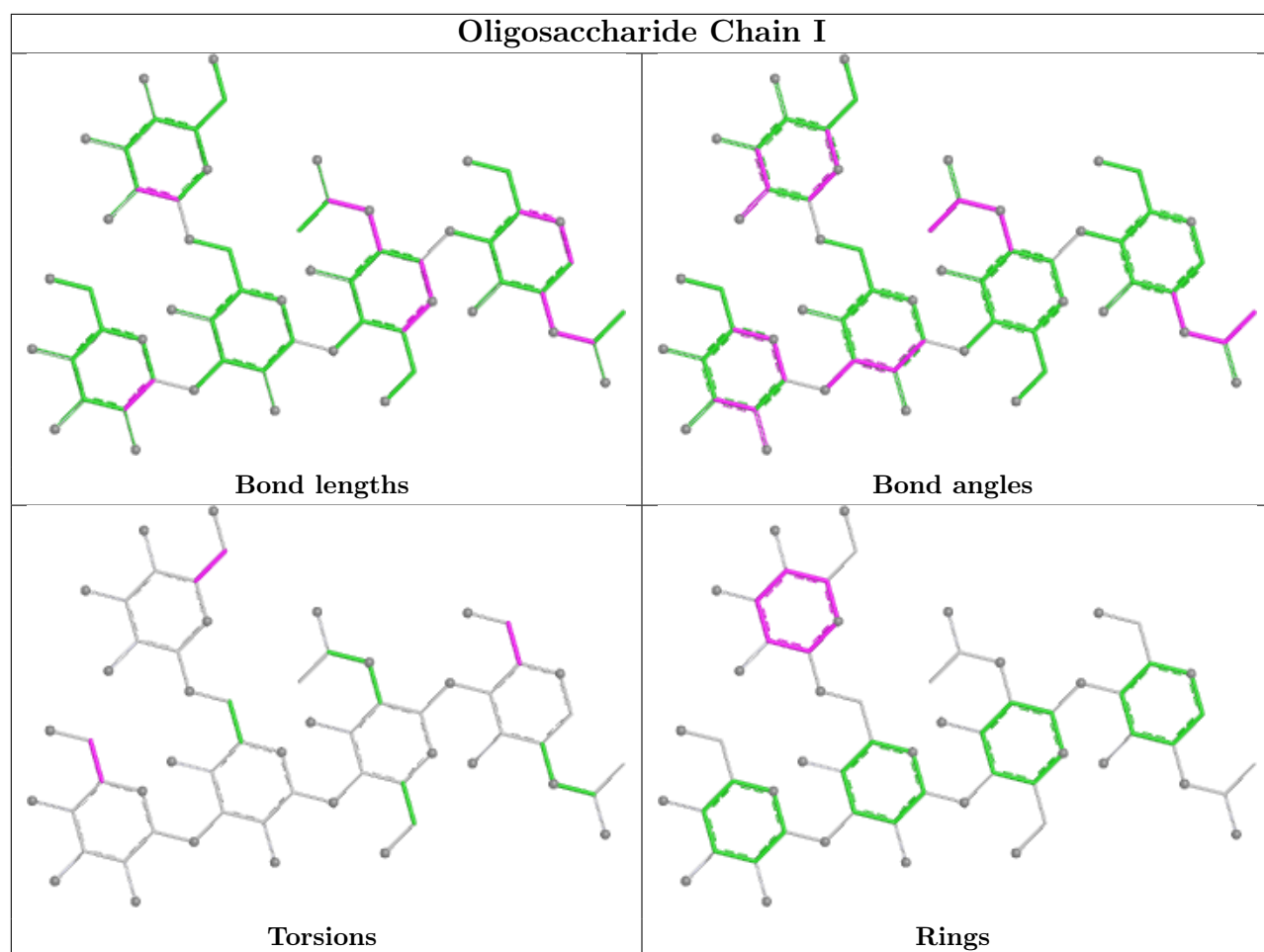
Oligosaccharide Chain Q

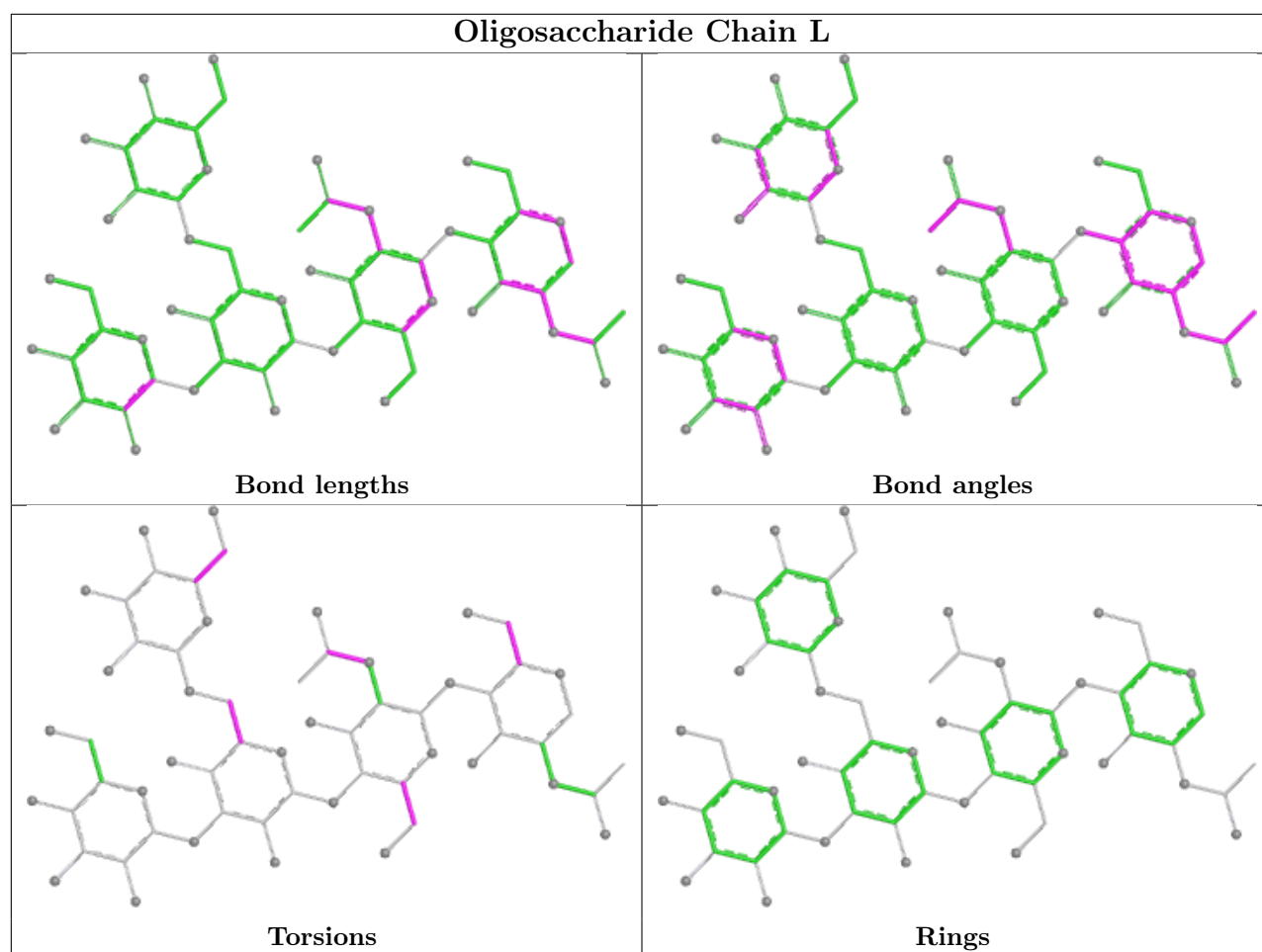


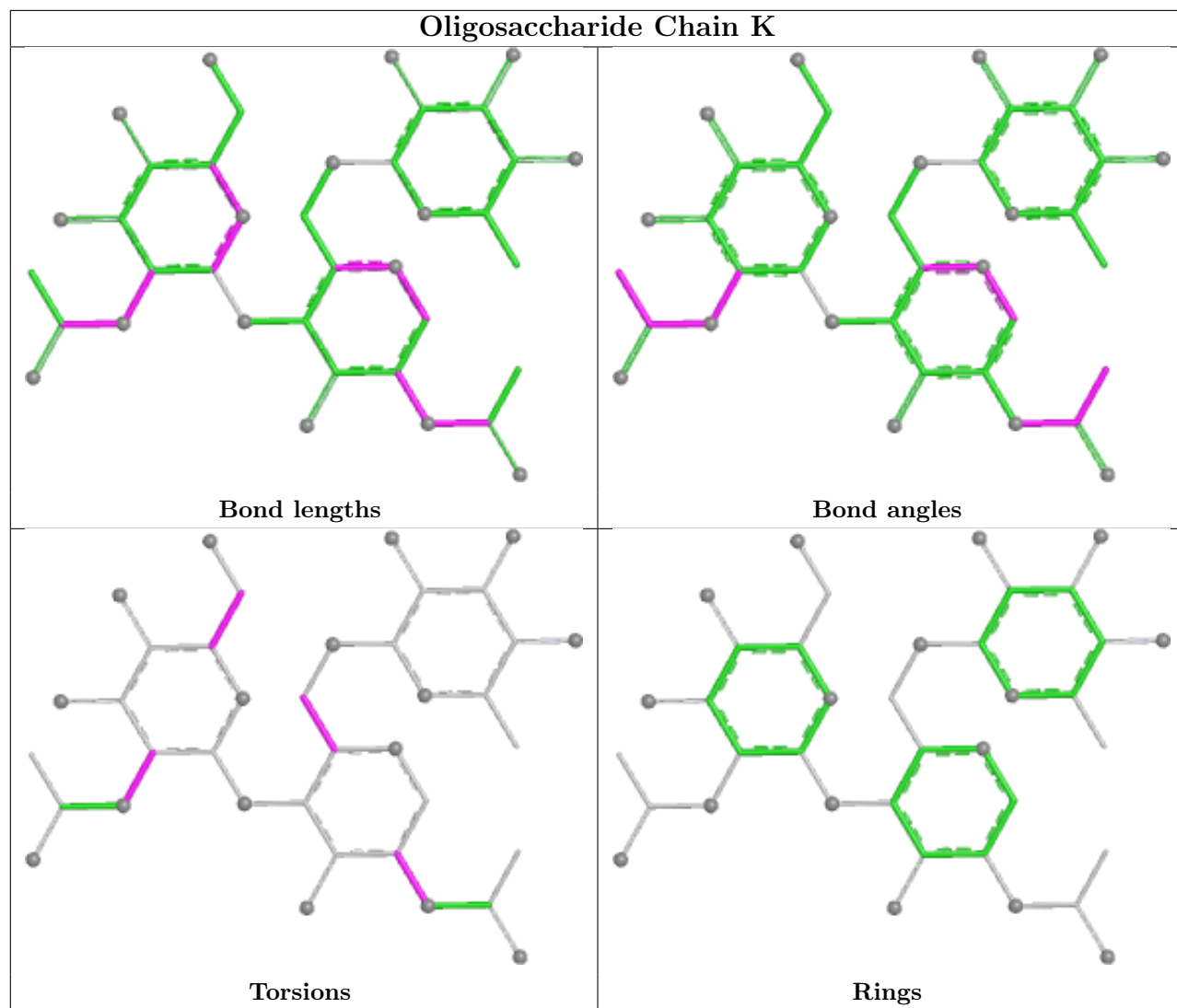
Oligosaccharide Chain S

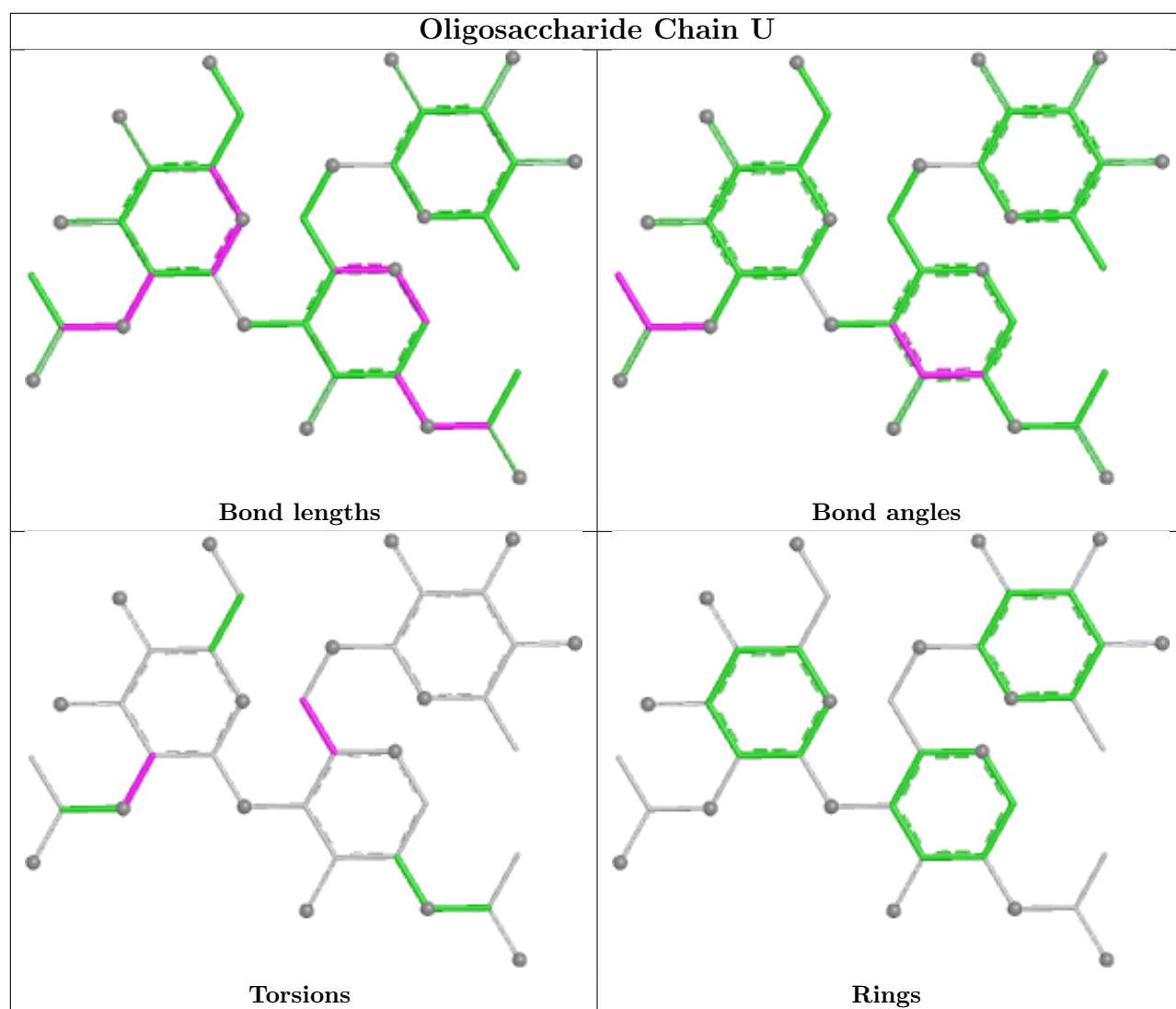


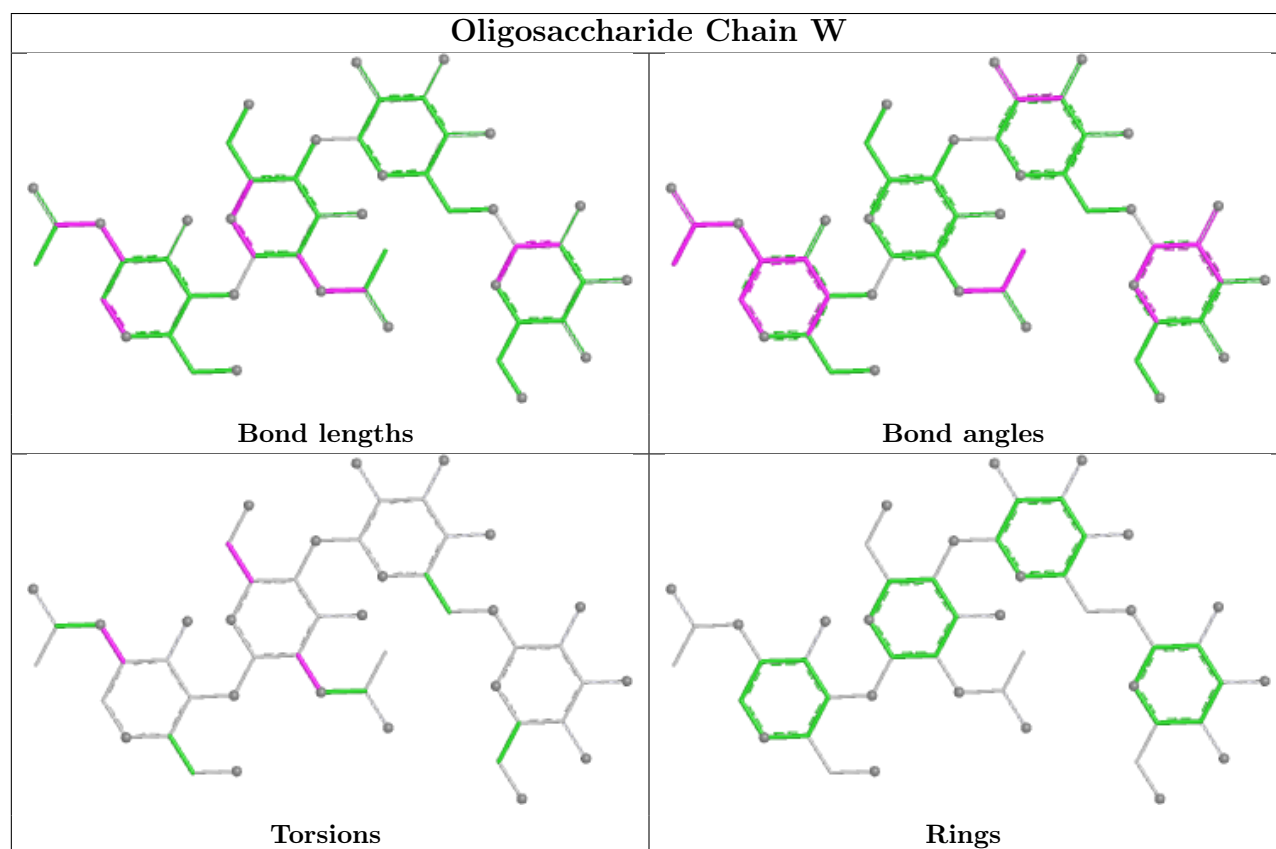
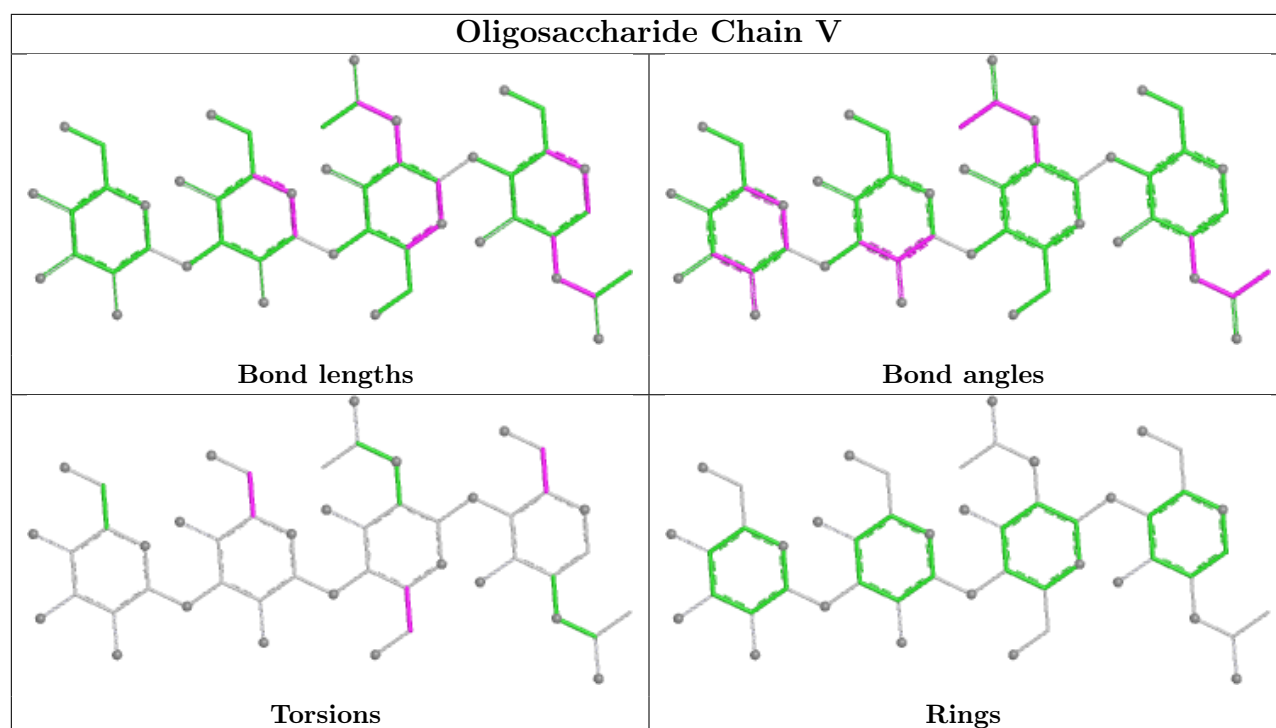


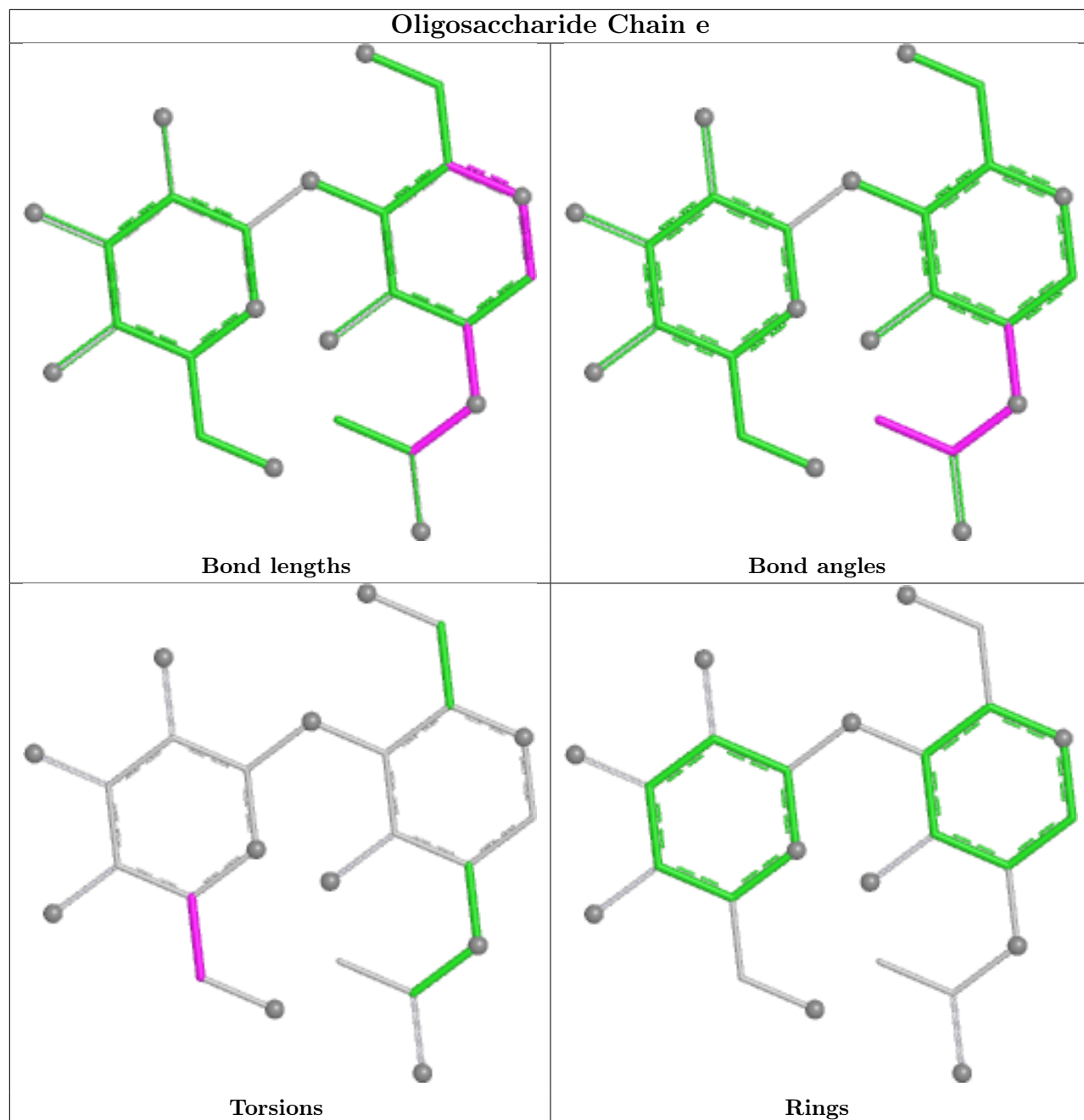


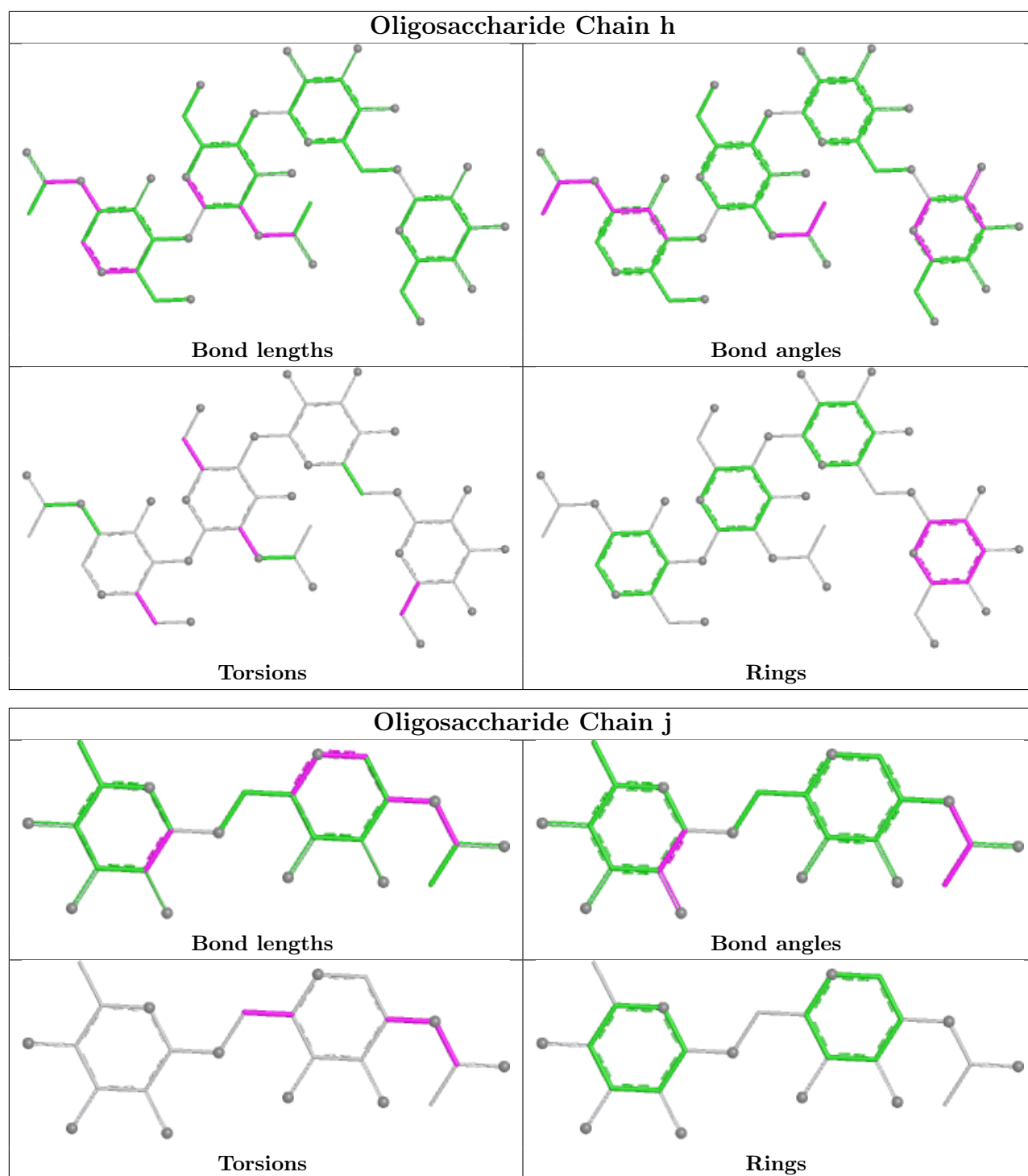


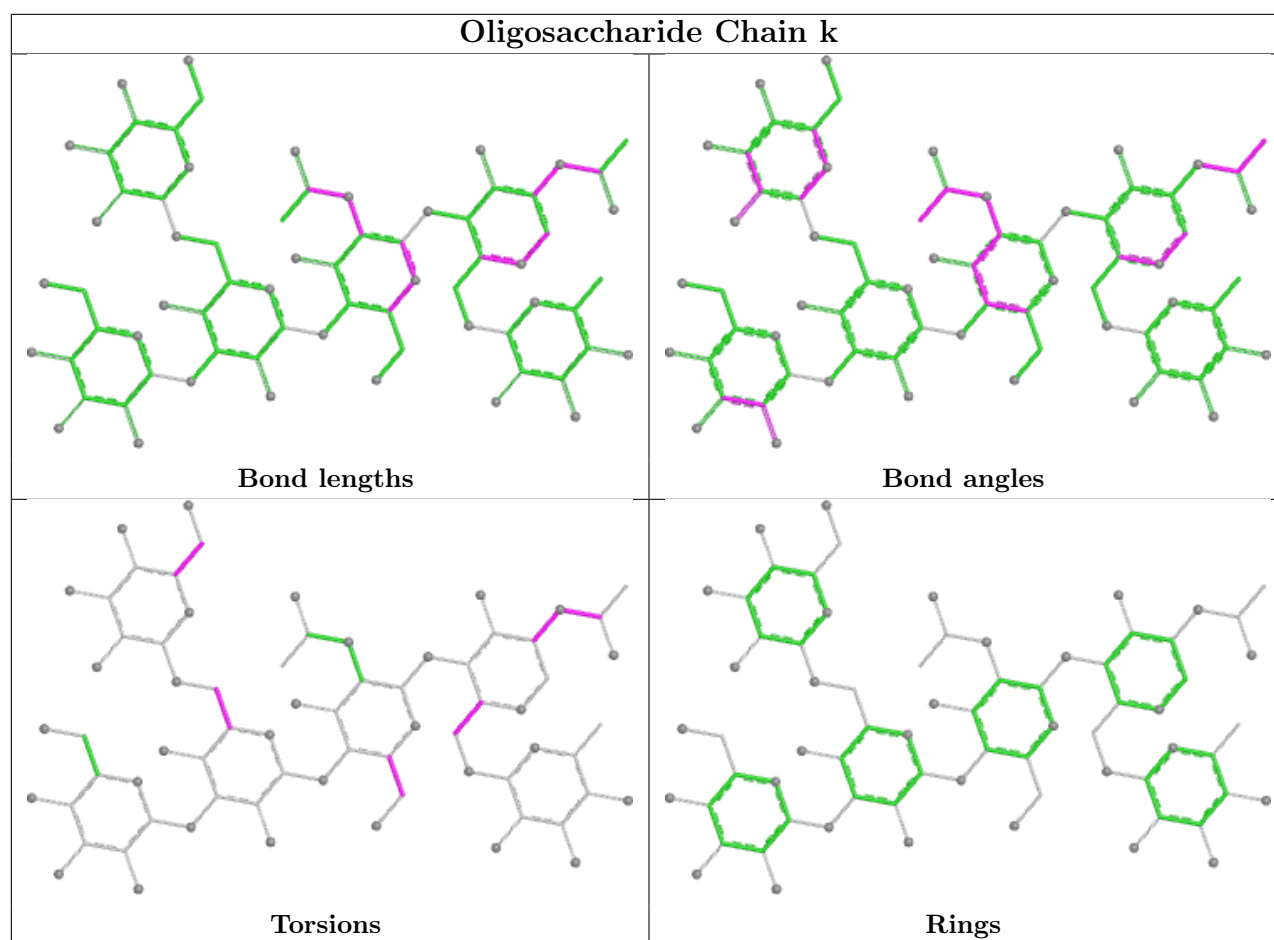












5.6 Ligand geometry [i](#)

15 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$
13	NAG	C	1302	1	14,14,15	2.03	4 (28%)	17,19,21	1.16	1 (5%)
13	NAG	A	1301	1	14,14,15	2.11	5 (35%)	17,19,21	1.40	2 (11%)
13	NAG	B	1304	1	14,14,15	2.35	4 (28%)	17,19,21	2.58	7 (41%)
13	NAG	A	1306	1	14,14,15	1.93	3 (21%)	17,19,21	1.36	2 (11%)
13	NAG	C	1303	1	14,14,15	2.19	5 (35%)	17,19,21	1.92	4 (23%)
13	NAG	B	1303	1	14,14,15	2.02	4 (28%)	17,19,21	1.47	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	NAG	A	1304	1	14,14,15	1.98	4 (28%)	17,19,21	1.02	1 (5%)
13	NAG	B	1306	1	14,14,15	2.14	5 (35%)	17,19,21	1.87	4 (23%)
13	NAG	A	1303	1	14,14,15	2.03	4 (28%)	17,19,21	2.48	7 (41%)
13	NAG	C	1301	1	14,14,15	2.11	4 (28%)	17,19,21	1.35	3 (17%)
13	NAG	B	1301	1	14,14,15	1.98	4 (28%)	17,19,21	1.09	2 (11%)
13	NAG	A	1302	1	14,14,15	2.10	4 (28%)	17,19,21	2.39	9 (52%)
13	NAG	B	1305	1	14,14,15	2.09	4 (28%)	17,19,21	1.72	4 (23%)
13	NAG	A	1305	1	14,14,15	2.04	4 (28%)	17,19,21	1.33	3 (17%)
13	NAG	B	1302	1	14,14,15	2.01	4 (28%)	17,19,21	1.15	2 (11%)

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
13	NAG	C	1302	1	-	3/6/23/26	0/1/1/1
13	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
13	NAG	B	1304	1	-	4/6/23/26	0/1/1/1
13	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
13	NAG	C	1303	1	-	3/6/23/26	0/1/1/1
13	NAG	B	1303	1	-	1/6/23/26	0/1/1/1
13	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
13	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
13	NAG	A	1303	1	1/1/6/7	1/6/23/26	0/1/1/1
13	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
13	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
13	NAG	A	1302	1	1/1/6/7	2/6/23/26	0/1/1/1
13	NAG	B	1305	1	-	1/6/23/26	0/1/1/1
13	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
13	NAG	B	1302	1	-	3/6/23/26	0/1/1/1

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	B	1304	NAG	O5-C1	5.24	1.52	1.43
13	C	1303	NAG	O5-C1	5.08	1.52	1.43
13	B	1303	NAG	O5-C1	4.78	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	C	1301	NAG	O5-C1	4.77	1.51	1.43
13	A	1301	NAG	O5-C1	4.59	1.51	1.43
13	A	1303	NAG	O5-C1	4.38	1.51	1.43
13	A	1305	NAG	O5-C1	4.35	1.51	1.43
13	B	1301	NAG	O5-C1	4.35	1.51	1.43
13	B	1305	NAG	O5-C1	4.33	1.51	1.43
13	B	1302	NAG	O5-C1	4.27	1.50	1.43
13	A	1304	NAG	O5-C1	4.25	1.50	1.43
13	A	1306	NAG	O5-C1	4.22	1.50	1.43
13	C	1302	NAG	O5-C1	4.19	1.50	1.43
13	A	1302	NAG	C7-N2	4.16	1.47	1.34
13	B	1304	NAG	C7-N2	4.16	1.47	1.34
13	A	1302	NAG	O5-C1	4.14	1.50	1.43
13	B	1306	NAG	O5-C1	4.12	1.50	1.43
13	C	1303	NAG	C7-N2	4.07	1.47	1.34
13	B	1305	NAG	C7-N2	4.02	1.47	1.34
13	B	1306	NAG	C7-N2	3.97	1.47	1.34
13	B	1302	NAG	C7-N2	3.95	1.47	1.34
13	C	1302	NAG	C7-N2	3.95	1.47	1.34
13	C	1301	NAG	C7-N2	3.91	1.47	1.34
13	A	1305	NAG	C7-N2	3.90	1.46	1.34
13	A	1303	NAG	C7-N2	3.89	1.46	1.34
13	A	1304	NAG	C7-N2	3.87	1.46	1.34
13	A	1301	NAG	C7-N2	3.85	1.46	1.34
13	A	1306	NAG	C7-N2	3.81	1.46	1.34
13	B	1301	NAG	C7-N2	3.81	1.46	1.34
13	B	1303	NAG	C7-N2	3.70	1.46	1.34
13	B	1304	NAG	O5-C5	3.33	1.49	1.43
13	B	1304	NAG	C2-N2	3.17	1.51	1.46
13	A	1302	NAG	C2-N2	3.08	1.51	1.46
13	B	1306	NAG	O5-C5	2.96	1.49	1.43
13	A	1302	NAG	O5-C5	2.91	1.49	1.43
13	B	1305	NAG	C2-N2	2.86	1.51	1.46
13	B	1306	NAG	C2-N2	2.85	1.51	1.46
13	C	1302	NAG	C2-N2	2.69	1.50	1.46
13	C	1303	NAG	O5-C5	2.66	1.48	1.43
13	B	1302	NAG	C2-N2	2.54	1.50	1.46
13	C	1301	NAG	C2-N2	2.54	1.50	1.46
13	A	1301	NAG	C2-N2	2.53	1.50	1.46
13	A	1305	NAG	C2-N2	2.48	1.50	1.46
13	A	1304	NAG	C2-N2	2.46	1.50	1.46
13	A	1303	NAG	C2-N2	2.42	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	A	1305	NAG	O5-C5	2.42	1.48	1.43
13	A	1303	NAG	O5-C5	2.39	1.48	1.43
13	C	1303	NAG	C2-N2	2.36	1.50	1.46
13	C	1301	NAG	O5-C5	2.36	1.48	1.43
13	B	1301	NAG	O5-C5	2.34	1.48	1.43
13	A	1306	NAG	C2-N2	2.34	1.50	1.46
13	B	1302	NAG	O5-C5	2.31	1.47	1.43
13	B	1305	NAG	O5-C5	2.29	1.47	1.43
13	B	1303	NAG	O5-C5	2.29	1.47	1.43
13	A	1301	NAG	O5-C5	2.26	1.47	1.43
13	B	1301	NAG	C2-N2	2.26	1.50	1.46
13	B	1303	NAG	C2-N2	2.23	1.50	1.46
13	A	1304	NAG	O5-C5	2.16	1.47	1.43
13	C	1302	NAG	O5-C5	2.06	1.47	1.43
13	C	1303	NAG	C3-C2	-2.04	1.48	1.52
13	A	1301	NAG	C1-C2	2.02	1.55	1.52
13	B	1306	NAG	C3-C2	-2.02	1.48	1.52

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A	1303	NAG	C3-C4-C5	6.94	122.81	110.23
13	C	1303	NAG	C1-O5-C5	5.66	119.77	112.19
13	B	1306	NAG	C1-O5-C5	-5.26	105.13	112.19
13	B	1304	NAG	C8-C7-N2	5.15	124.66	116.12
13	A	1302	NAG	C8-C7-N2	4.72	123.95	116.12
13	A	1302	NAG	C1-C2-N2	4.70	117.83	110.43
13	B	1304	NAG	C1-O5-C5	-4.64	105.97	112.19
13	B	1304	NAG	O5-C5-C6	4.43	116.29	107.66
13	B	1304	NAG	C1-C2-N2	-4.40	103.50	110.43
13	A	1303	NAG	O4-C4-C5	3.51	117.96	109.32
13	B	1305	NAG	C8-C7-N2	3.42	121.78	116.12
13	C	1301	NAG	C1-O5-C5	3.34	116.66	112.19
13	B	1305	NAG	C1-O5-C5	3.27	116.57	112.19
13	A	1303	NAG	O4-C4-C3	3.21	117.94	110.38
13	A	1306	NAG	C4-C3-C2	3.03	115.45	111.02
13	A	1302	NAG	C2-N2-C7	-2.95	118.94	122.90
13	B	1303	NAG	C4-C3-C2	2.93	115.31	111.02
13	A	1301	NAG	C2-N2-C7	-2.92	118.98	122.90
13	A	1303	NAG	C2-N2-C7	-2.81	119.13	122.90
13	B	1305	NAG	C2-N2-C7	-2.81	119.13	122.90
13	A	1305	NAG	C1-O5-C5	-2.79	108.45	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	1306	NAG	C3-C4-C5	2.77	115.25	110.23
13	C	1302	NAG	C8-C7-N2	2.71	120.61	116.12
13	A	1303	NAG	C8-C7-N2	2.65	120.51	116.12
13	A	1301	NAG	C8-C7-N2	2.61	120.45	116.12
13	C	1303	NAG	C8-C7-N2	2.56	120.36	116.12
13	A	1302	NAG	O4-C4-C5	-2.56	103.03	109.32
13	B	1304	NAG	O7-C7-C8	-2.53	117.55	122.05
13	A	1302	NAG	O5-C5-C6	2.53	112.59	107.66
13	A	1302	NAG	C3-C4-C5	2.48	114.72	110.23
13	C	1303	NAG	O5-C1-C2	2.43	115.05	111.29
13	B	1306	NAG	C8-C7-N2	2.42	120.13	116.12
13	A	1306	NAG	C1-C2-N2	-2.42	106.62	110.43
13	B	1303	NAG	C3-C4-C5	2.42	114.61	110.23
13	B	1304	NAG	O7-C7-N2	-2.38	117.78	121.98
13	C	1301	NAG	C8-C7-N2	2.35	120.02	116.12
13	A	1302	NAG	C4-C3-C2	2.35	114.46	111.02
13	A	1305	NAG	C8-C7-N2	2.32	119.96	116.12
13	A	1302	NAG	O7-C7-N2	-2.29	117.94	121.98
13	A	1303	NAG	C1-O5-C5	2.27	115.23	112.19
13	A	1304	NAG	C8-C7-N2	2.27	119.88	116.12
13	B	1302	NAG	C8-C7-N2	2.26	119.86	116.12
13	A	1302	NAG	O7-C7-C8	-2.22	118.10	122.05
13	A	1305	NAG	C2-N2-C7	-2.17	120.00	122.90
13	B	1305	NAG	C6-C5-C4	-2.16	107.71	113.02
13	B	1306	NAG	C6-C5-C4	-2.15	107.73	113.02
13	A	1303	NAG	C6-C5-C4	-2.14	107.77	113.02
13	B	1304	NAG	C4-C3-C2	2.11	114.11	111.02
13	B	1301	NAG	C2-N2-C7	-2.10	120.08	122.90
13	C	1301	NAG	C2-N2-C7	-2.07	120.12	122.90
13	C	1303	NAG	O4-C4-C3	-2.06	105.52	110.38
13	B	1302	NAG	C3-C4-C5	2.06	113.96	110.23
13	B	1301	NAG	C8-C7-N2	2.06	119.53	116.12

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
13	A	1302	NAG	C2
13	A	1303	NAG	C4

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	B	1302	NAG	C1-C2-N2-C7
13	B	1303	NAG	C1-C2-N2-C7
13	A	1301	NAG	C4-C5-C6-O6
13	B	1301	NAG	C4-C5-C6-O6
13	A	1304	NAG	O5-C5-C6-O6
13	B	1301	NAG	O5-C5-C6-O6
13	A	1302	NAG	O5-C5-C6-O6
13	A	1302	NAG	C4-C5-C6-O6
13	A	1301	NAG	O5-C5-C6-O6
13	B	1304	NAG	C8-C7-N2-C2
13	B	1304	NAG	O7-C7-N2-C2
13	C	1302	NAG	C8-C7-N2-C2
13	C	1302	NAG	O7-C7-N2-C2
13	A	1304	NAG	C4-C5-C6-O6
13	B	1306	NAG	C4-C5-C6-O6
13	B	1306	NAG	O5-C5-C6-O6
13	C	1301	NAG	C4-C5-C6-O6
13	C	1302	NAG	O5-C5-C6-O6
13	B	1302	NAG	C4-C5-C6-O6
13	C	1303	NAG	O5-C5-C6-O6
13	C	1303	NAG	C3-C2-N2-C7
13	C	1301	NAG	O5-C5-C6-O6
13	B	1304	NAG	C1-C2-N2-C7
13	C	1303	NAG	C1-C2-N2-C7
13	B	1302	NAG	O5-C5-C6-O6
13	B	1305	NAG	C4-C5-C6-O6
13	A	1303	NAG	C3-C2-N2-C7
13	B	1304	NAG	C3-C2-N2-C7

There are no ring outliers.

13 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	C	1302	NAG	1	0
13	A	1301	NAG	1	0
13	B	1304	NAG	1	0
13	A	1306	NAG	1	0
13	C	1303	NAG	2	0
13	B	1303	NAG	2	0
13	A	1303	NAG	1	0
13	C	1301	NAG	1	0
13	B	1301	NAG	1	0
13	A	1302	NAG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	B	1305	NAG	3	0
13	A	1305	NAG	3	0
13	B	1302	NAG	2	0

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.

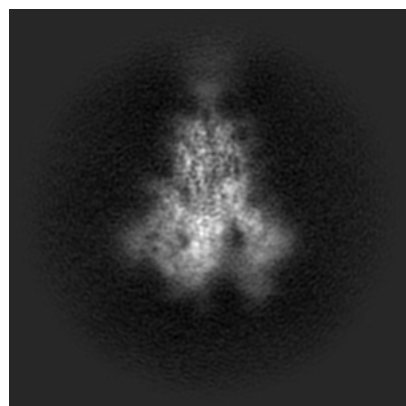
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44475. These allow visual inspection of the internal detail of the map and identification of artifacts.

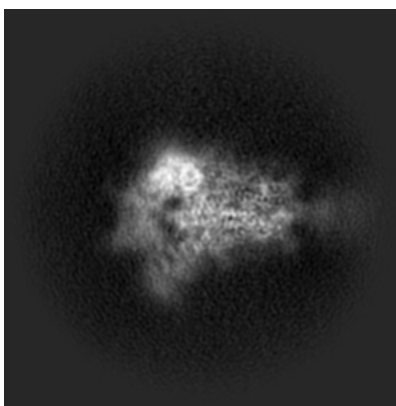
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

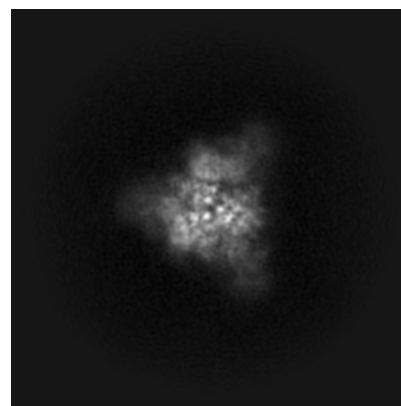
6.1.1 Primary map



X

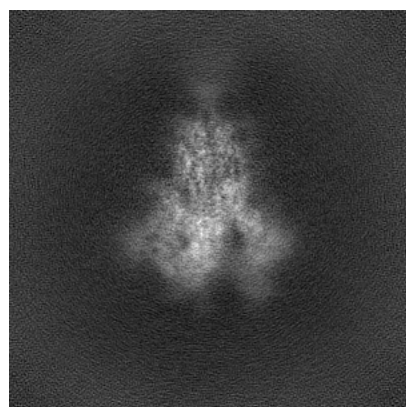


Y

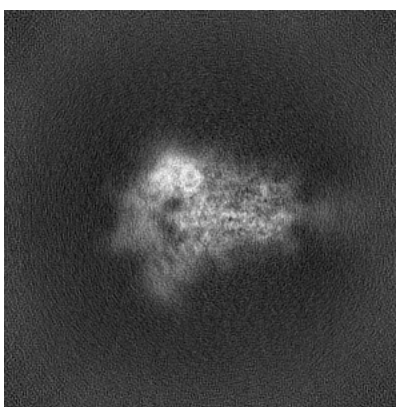


Z

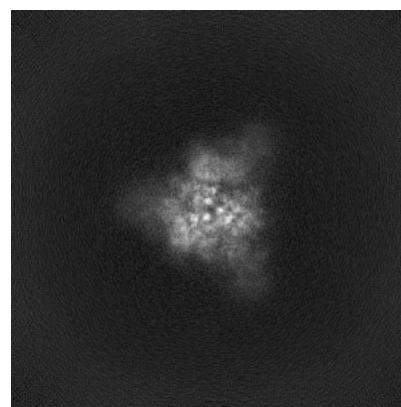
6.1.2 Raw map



X



Y

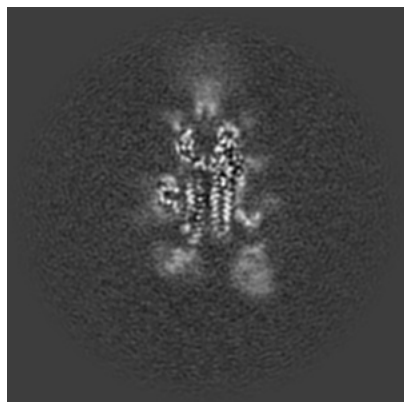


Z

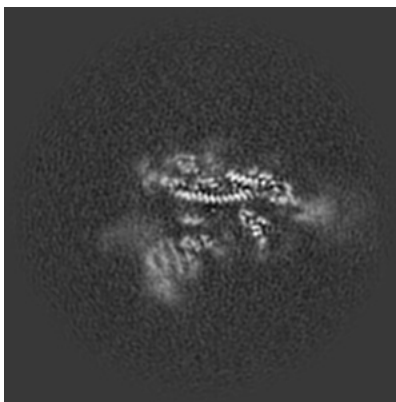
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

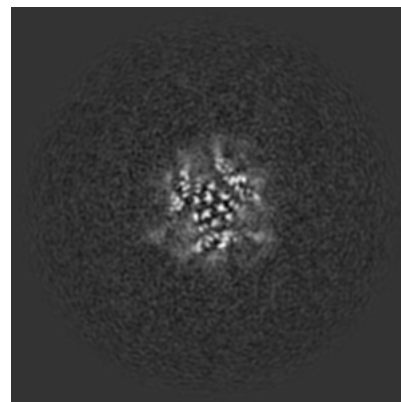
6.2.1 Primary map



X Index: 150

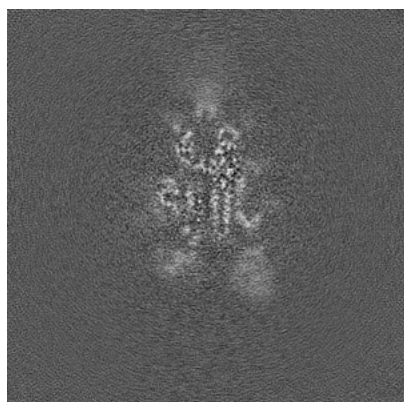


Y Index: 150



Z Index: 150

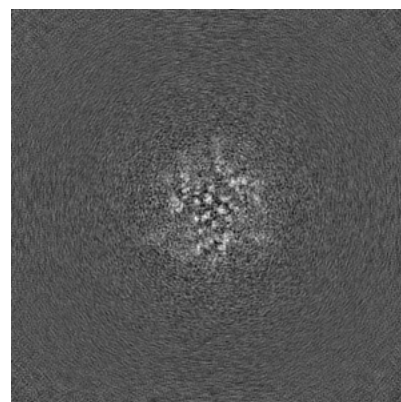
6.2.2 Raw map



X Index: 150



Y Index: 150

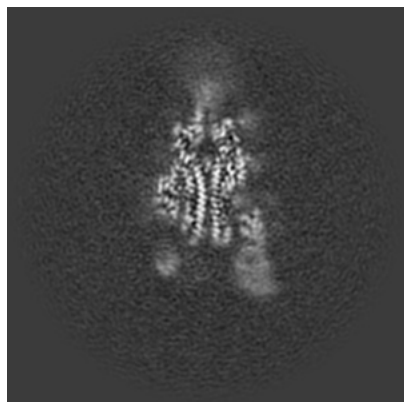


Z Index: 150

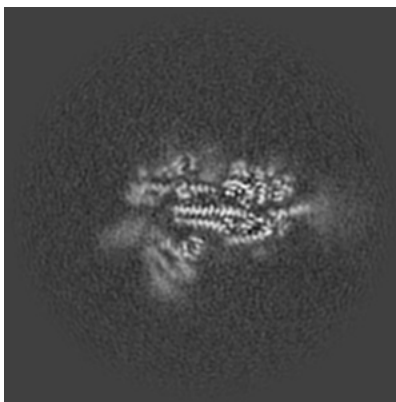
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

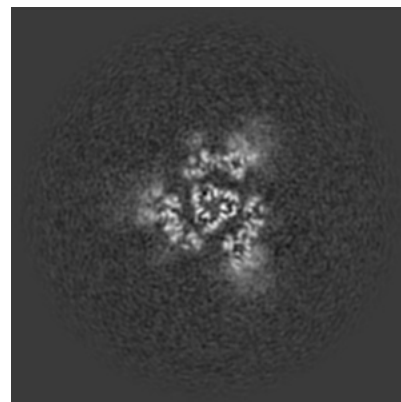
6.3.1 Primary map



X Index: 146

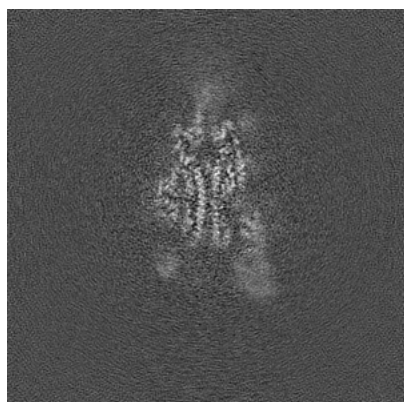


Y Index: 144

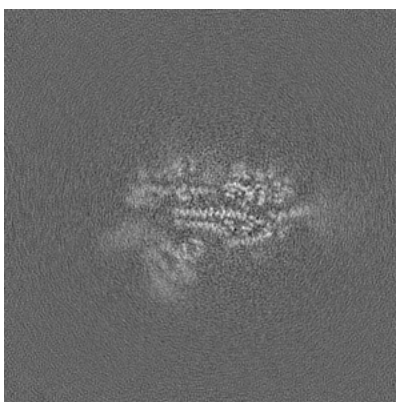


Z Index: 135

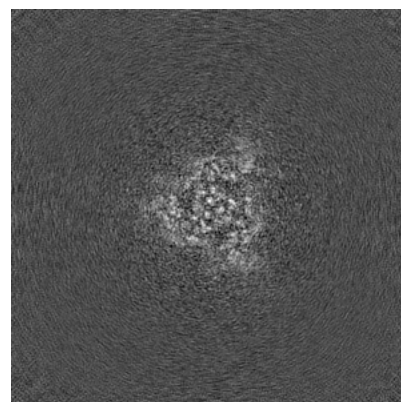
6.3.2 Raw map



X Index: 146



Y Index: 144

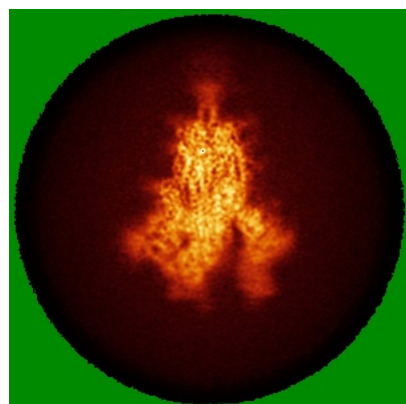


Z Index: 143

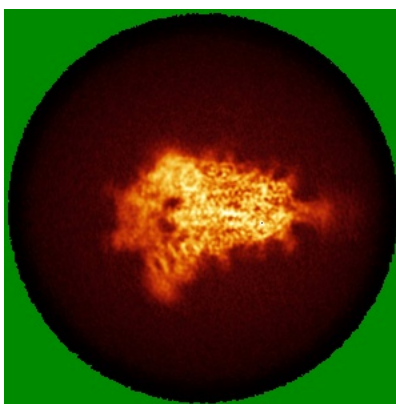
The images above show the largest variance slices of the map in three orthogonal directions.

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

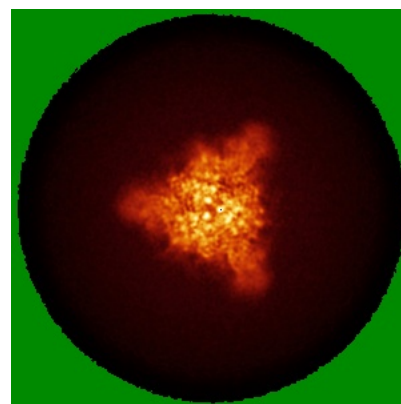
6.4.1 Primary map



X

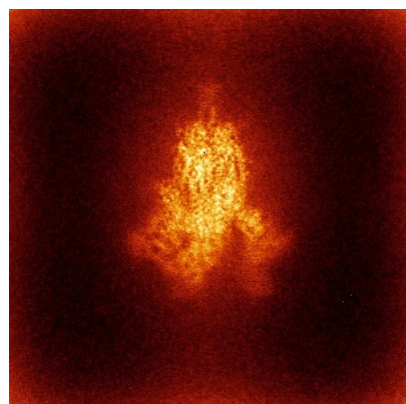


Y

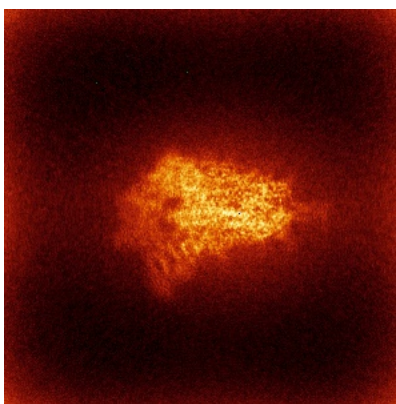


Z

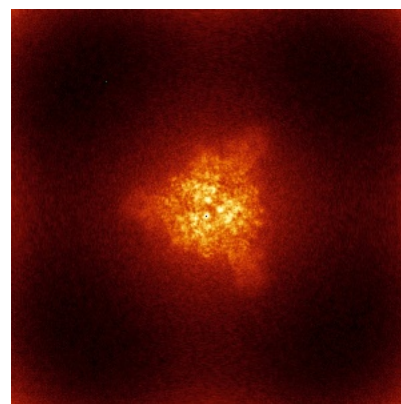
6.4.2 Raw map



X



Y

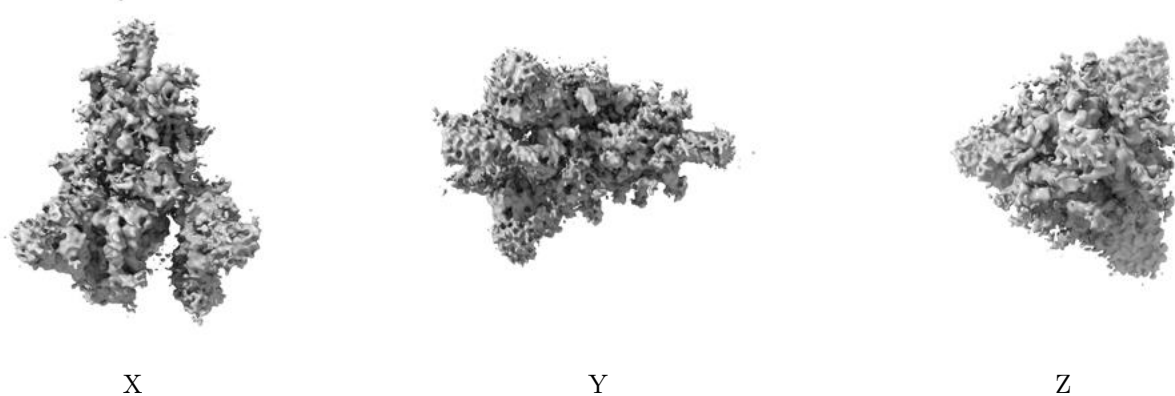


Z

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.

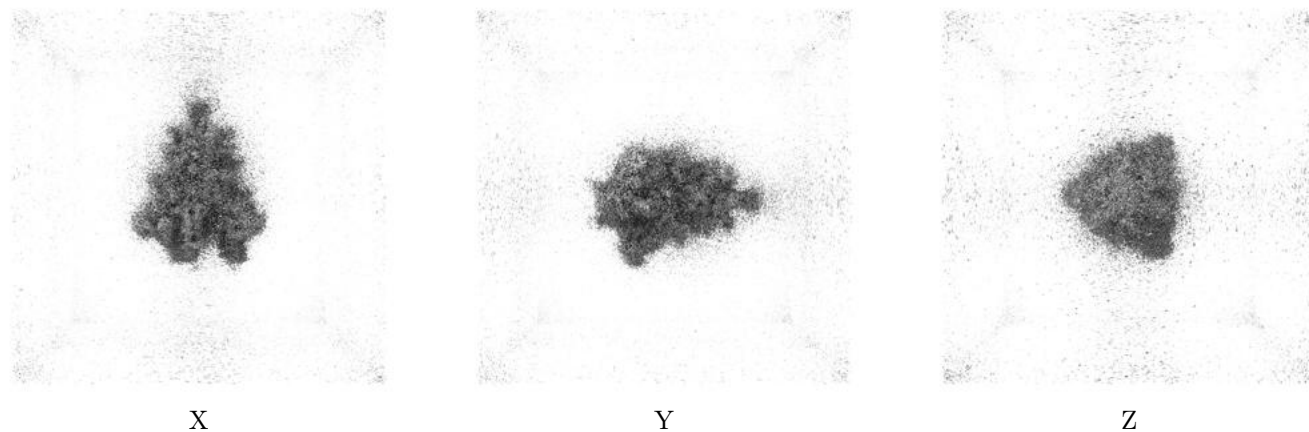
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0916. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

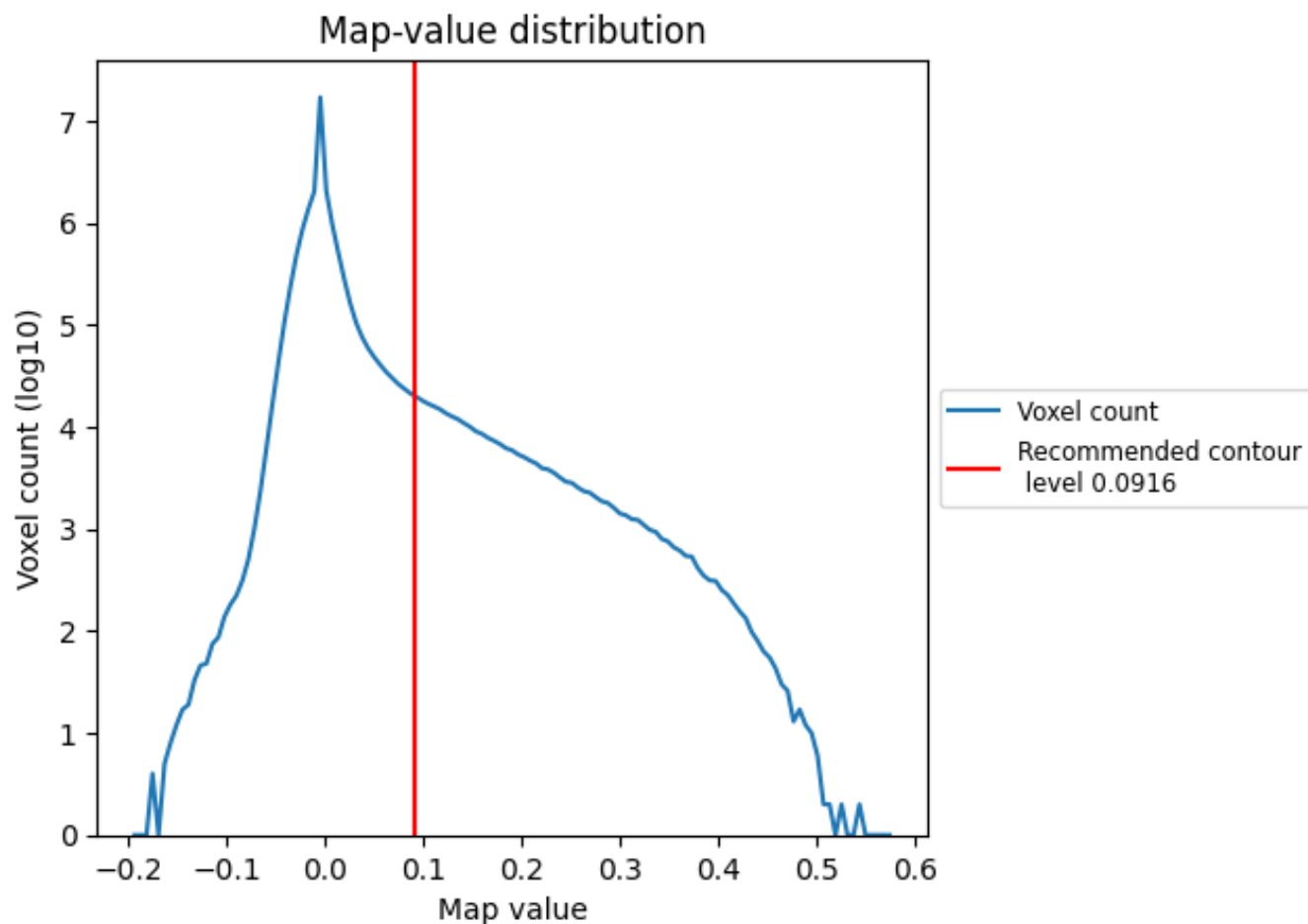
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

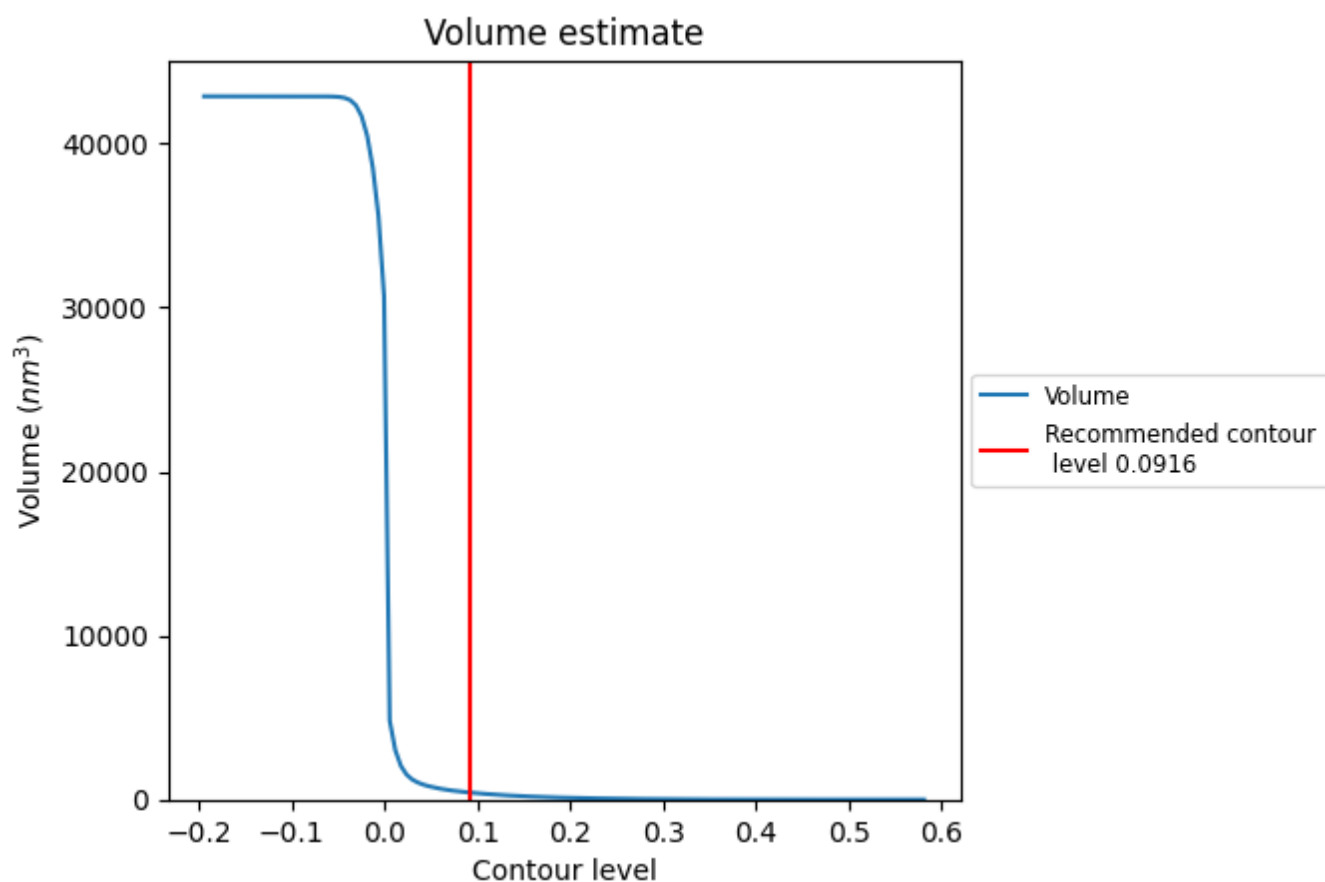
This section contains the results of statistical analysis of the map.

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.

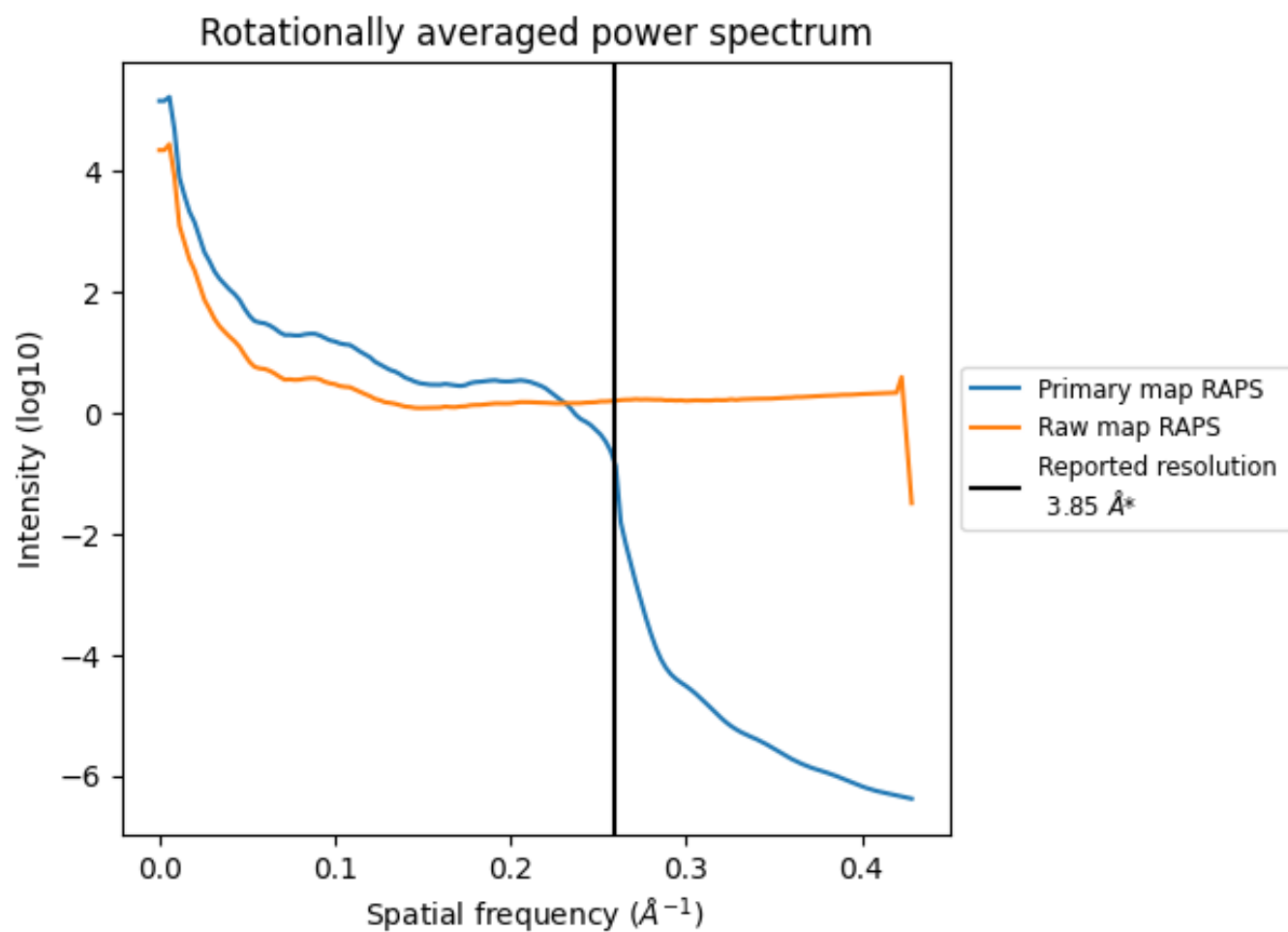
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 429 nm³; this corresponds to an approximate mass of 387 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 ⓘ

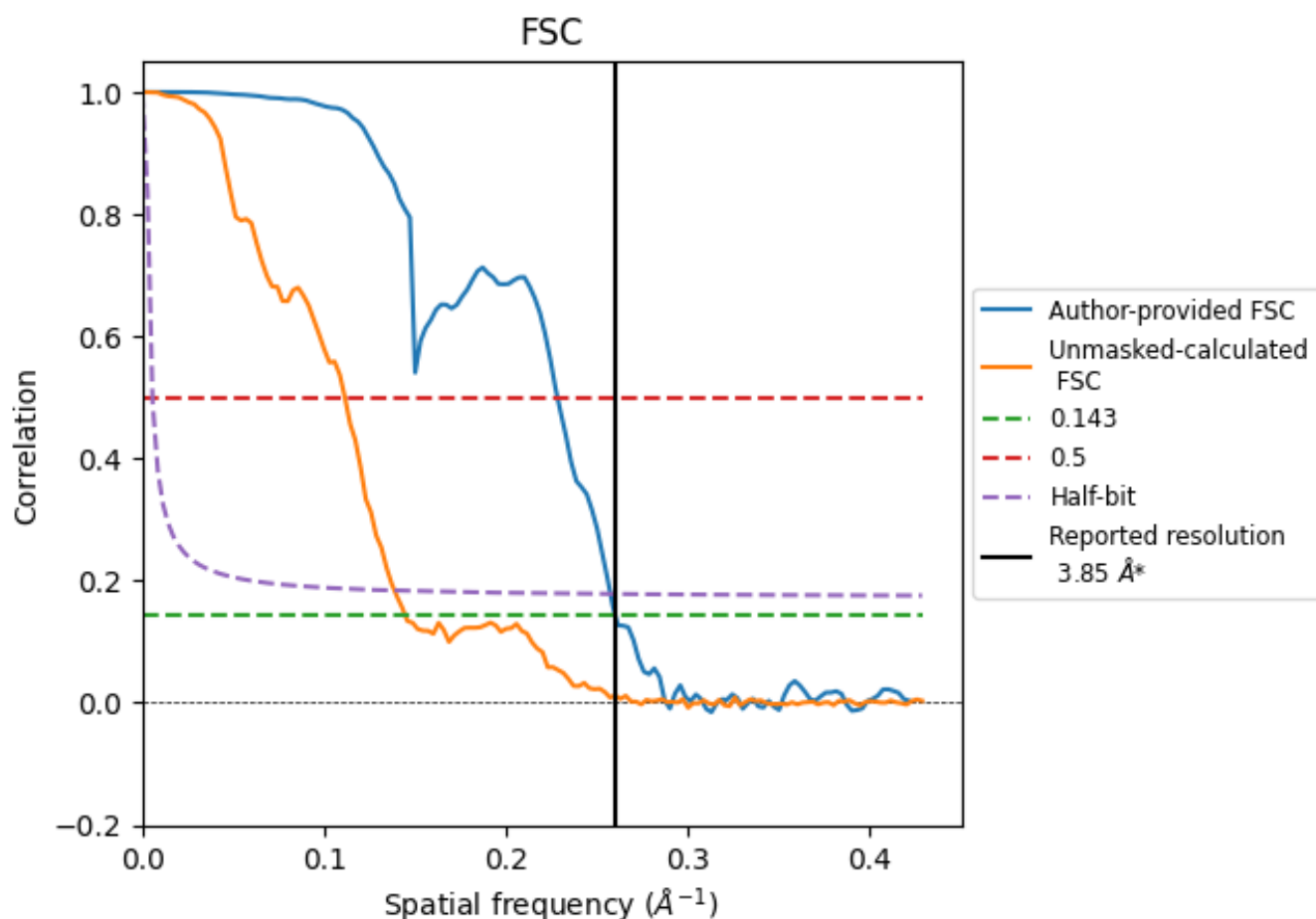


*Reported resolution corresponds to spatial frequency of 0.260 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.260 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

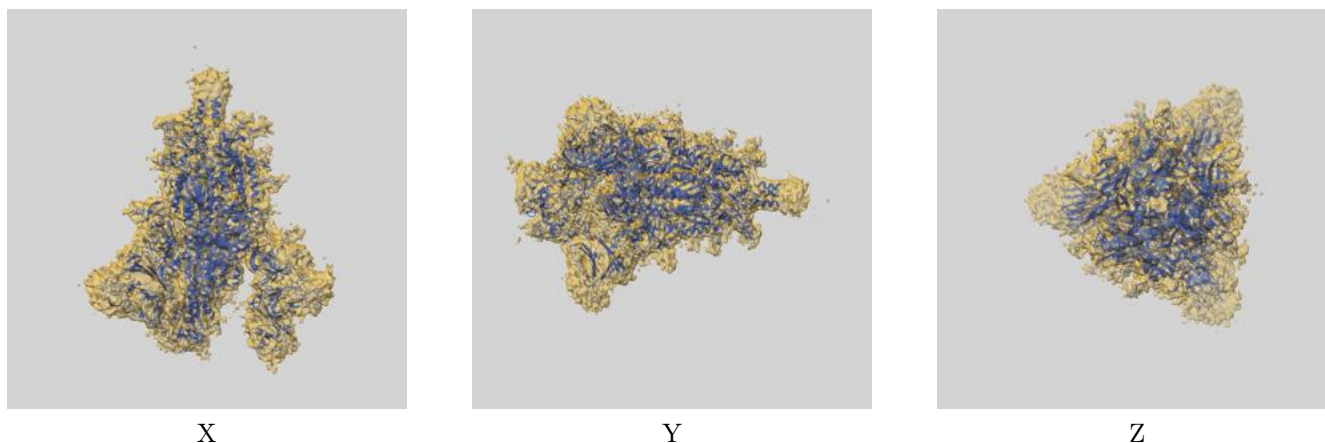
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.85	-	-
Author-provided FSC curve	3.85	4.38	3.89
Unmasked-calculated*	6.92	8.98	7.21

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.92 differs from the reported value 3.85 by more than 10 %

9 Map-model fit [i](#)

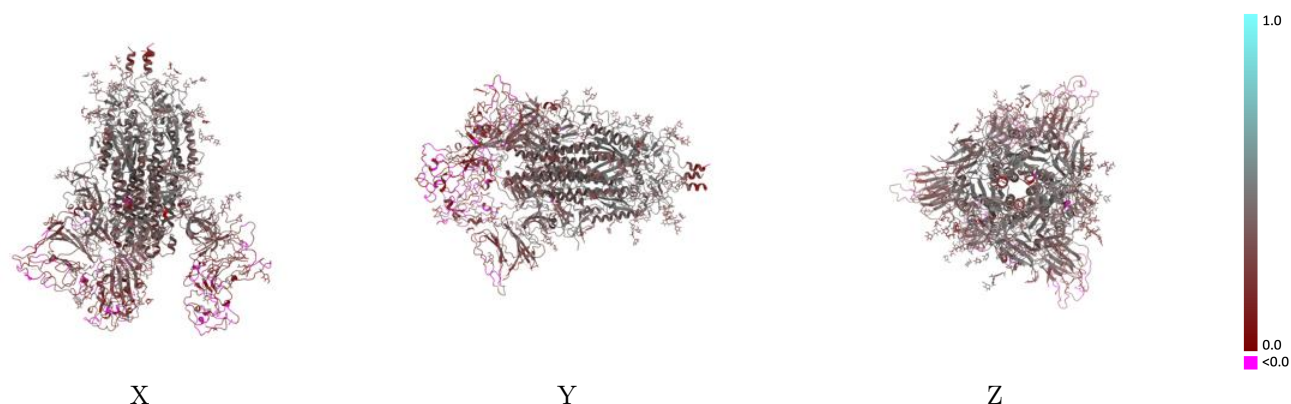
This section contains information regarding the fit between EMDB map EMD-44475 and PDB model 9BEA. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0916 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](#)



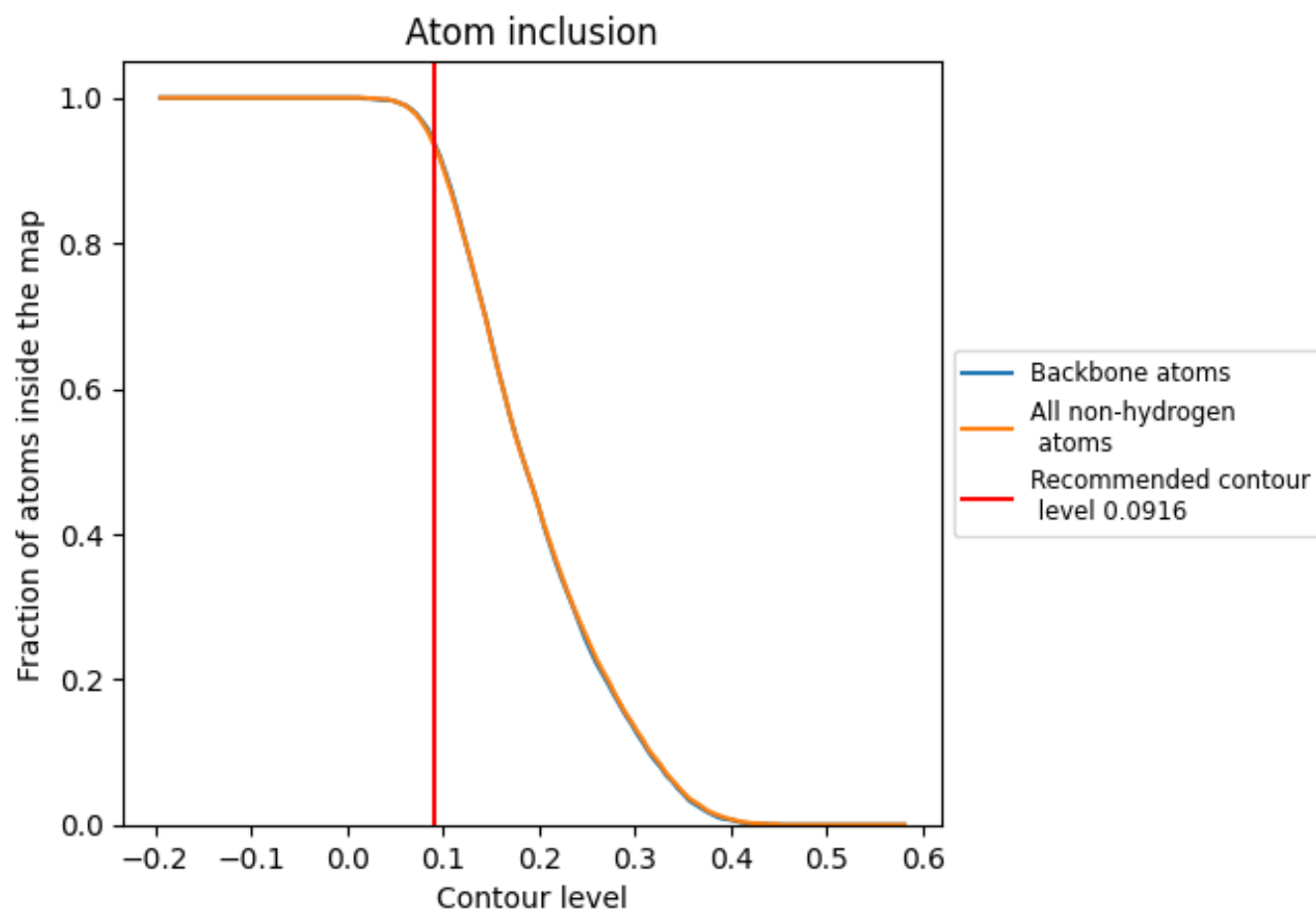
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0916).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.0916) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.3240
A	 0.9310	 0.3160
B	 0.9540	 0.3390
C	 0.9280	 0.3180
D	 0.9230	 0.3220
E	 0.8930	 0.3080
F	 0.8570	 0.3210
G	 0.9490	 0.3030
H	 0.8600	 0.2300
I	 0.8850	 0.3280
J	 0.9230	 0.2890
K	 0.8950	 0.3120
L	 0.9670	 0.3000
M	 0.9740	 0.3490
N	 0.8210	 0.2410
O	 0.8800	 0.2760
P	 0.8570	 0.2430
Q	 0.8200	 0.2790
R	 0.9230	 0.3370
S	 0.8000	 0.2980
T	 0.9740	 0.3070
U	 0.8160	 0.3320
V	 0.8800	 0.3140
W	 0.8000	 0.2990
X	 0.7500	 0.2210
Y	 0.8210	 0.3750
Z	 0.8210	 0.3610
a	 0.9400	 0.3380
b	 0.8570	 0.3730
c	 0.8210	 0.2310
d	 0.8210	 0.3300
e	 0.6800	 0.2480
f	 1.0000	 0.3930
g	 0.8970	 0.3290
h	 0.9000	 0.3020



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Chain	Atom inclusion	Q-score
i	 0.9400	 0.3590
j	 0.9170	 0.3730
k	 0.9010	 0.3330