



## wwPDB EM Validation Summary Report ⓘ

Aug 27, 2023 – 12:28 AM JST

PDB ID : 7WHD  
EMDB ID : EMD-32499  
Title : SARS-CoV-2 spike in complex with the ZB8 neutralizing antibody Fab (2u1d)  
Authors : Zeng, J.W.; Wang, X.W.; Ge, J.W.; Wang, Z.Y.  
Deposited on : 2021-12-30  
Resolution : 2.65 Å (reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev50  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35

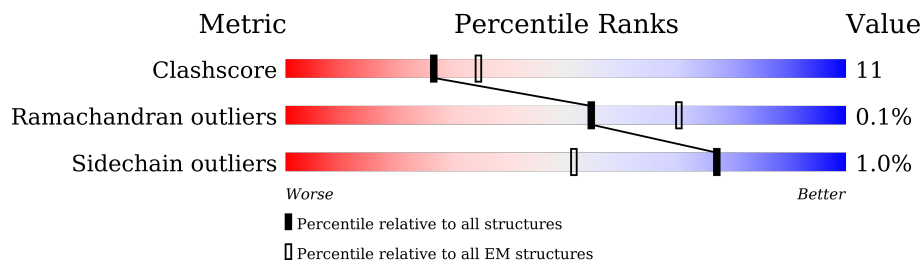
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.65 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.




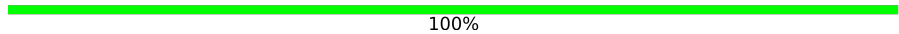


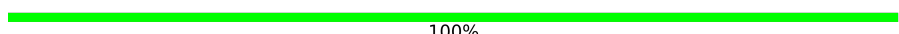

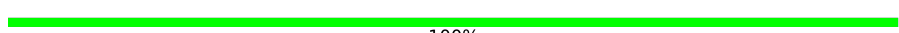



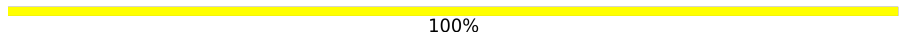
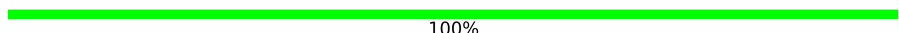

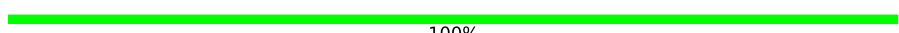
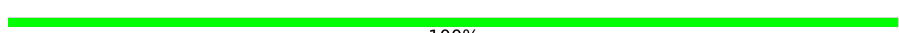



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	
2	G	224	
2	J	224	
3	E	214	
3	H	214	

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Mol	Chain	Length	Quality of chain
3	K	214	 64% 36%
4	F	2	 100%
4	I	2	 50% 50%
4	L	2	 50% 50%
4	M	2	 100%
4	N	2	 50% 50%
4	O	2	 100%
4	P	2	 100%
4	Q	2	 100%
4	R	2	 50% 50%
4	S	2	 100%
4	T	2	 100%
4	U	2	 50% 50%
4	V	2	 100%
4	W	2	 100%
4	X	2	 50% 50%
4	Y	2	 50% 50%
4	Z	2	 100%

## 2 Entry composition i

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

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
			Total	C	N	O	S		
2	D	224	1646	1034	276	328	8	0	0
2	G	224	1646	1034	276	328	8	0	0
2	J	224	1646	1034	276	328	8	0	0

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

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

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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.



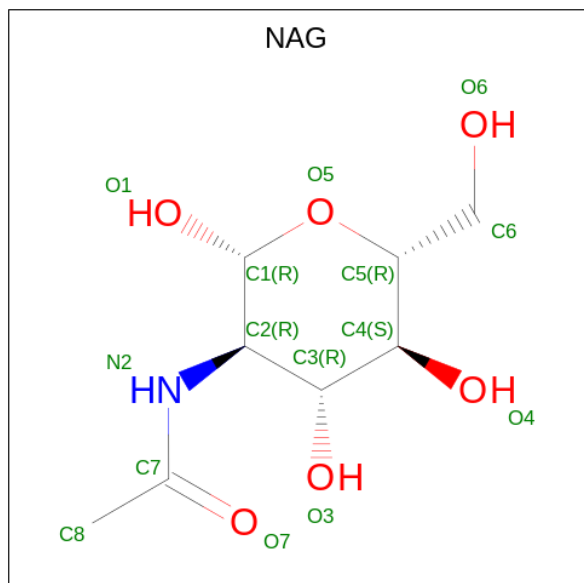
Mol	Chain	Residues	Atoms				AltConf	Trace
4	F	2	Total	C	N	O	0	0
			28	16	2	10		
4	I	2	Total	C	N	O	0	0
			28	16	2	10		
4	L	2	Total	C	N	O	0	0
			28	16	2	10		
4	M	2	Total	C	N	O	0	0
			28	16	2	10		
4	N	2	Total	C	N	O	0	0
			28	16	2	10		
4	O	2	Total	C	N	O	0	0
			28	16	2	10		
4	P	2	Total	C	N	O	0	0
			28	16	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
			Total	C	N	O		
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		

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



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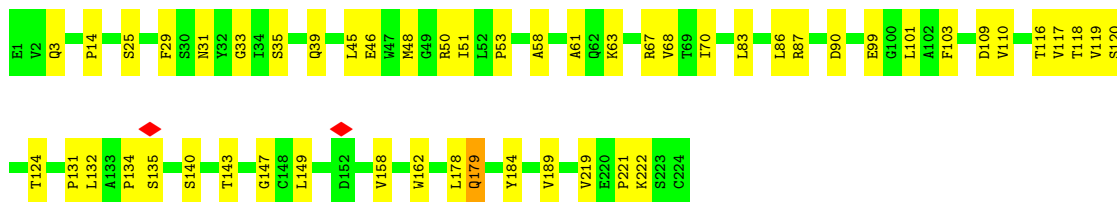
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	B	1	Total 14	8	1	5	0
5	B	1	Total 14	8	1	5	0
5	B	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1	5	0
5	C	1	Total 14	8	1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



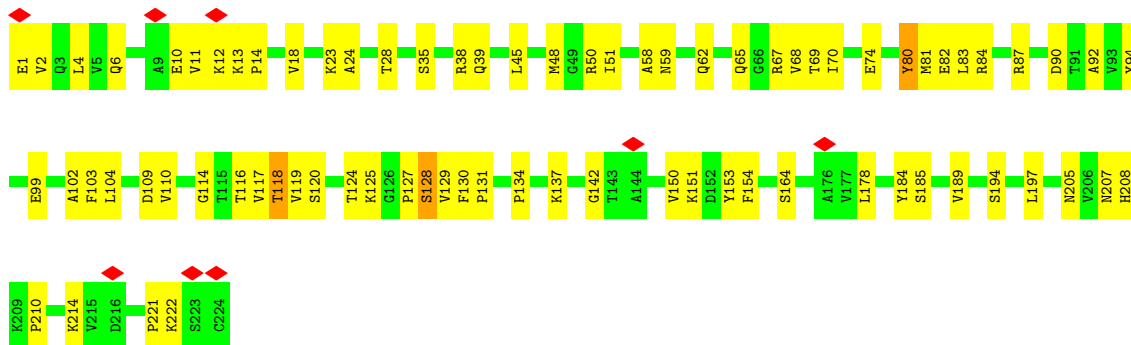




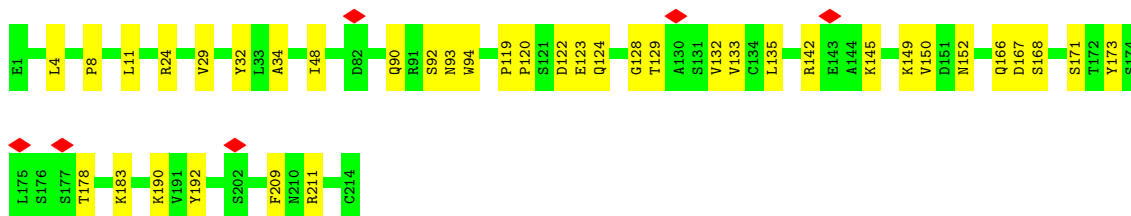
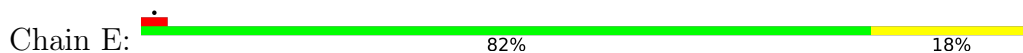




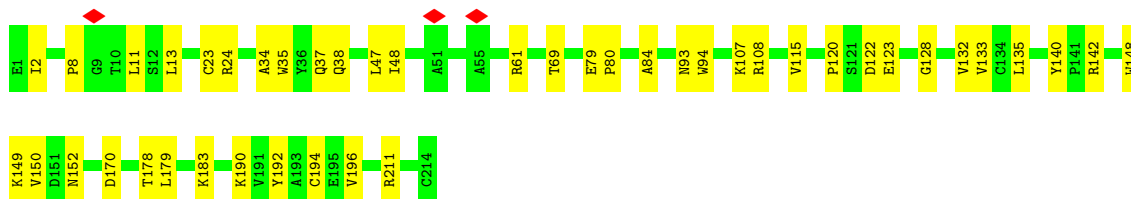
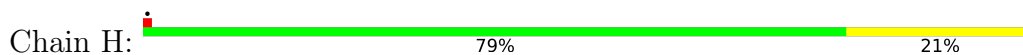
• Molecule 2: antibody ZB8 heavy chain



• Molecule 3: antibody ZB8 light chain

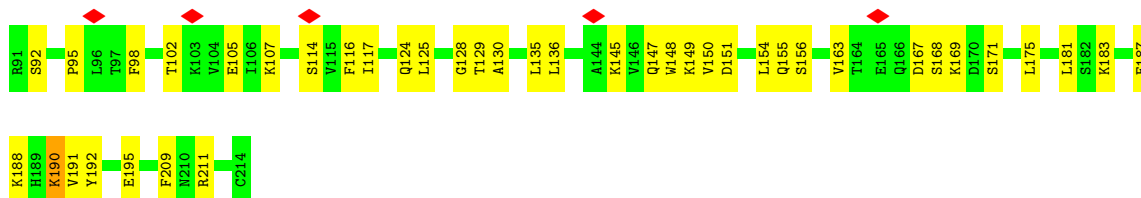


• Molecule 3: antibody ZB8 light chain



• Molecule 3: antibody ZB8 light chain





- 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:  100%



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

Chain N:  50%



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

Chain O:  100%

MAG1  
MAG2

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

Chain P:  100%MAG1  
MAG2

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

Chain Q:  100%MAG1  
MAG2

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

Chain R:  50%MAG1  
MAG2

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

Chain S:  100%MAG1  
MAG2

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

Chain T:  100%MAG1  
MAG2

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

Chain U:  50%MAG1  
MAG2

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

Chain V:  100%

MAG1  
MAG2

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

Chain W:  100%


MAG1  
MAG2

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

Chain X:  50% 50%

MAG1  
MAG2

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

Chain Y:  50% 50%

MAG1  
MAG2

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

Chain Z:  100%

MAG1  
MAG2

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	616779	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	0.107	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.006	Depositor
Map size ( $\text{\AA}$ )	397.43982, 397.43982, 397.43982	wwPDB
Map dimensions	362, 362, 362	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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.35	0/8039	0.51	0/10936
1	B	0.34	0/8045	0.52	0/10942
1	C	0.35	0/8028	0.52	0/10919
2	D	0.33	0/1682	0.51	0/2287
2	G	0.35	0/1682	0.52	0/2287
2	J	0.30	0/1682	0.50	0/2287
3	E	0.32	0/1679	0.51	0/2280
3	H	0.33	0/1679	0.52	0/2280
3	K	0.29	0/1679	0.54	0/2280
All	All	0.34	0/34195	0.52	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 [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	7863	0	7661	188	0
1	B	7870	0	7675	177	0
1	C	7853	0	7655	168	0
2	D	1646	0	1627	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	1646	0	1627	33	0
2	J	1646	0	1627	69	0
3	E	1643	0	1601	28	0
3	H	1643	0	1601	31	0
3	K	1643	0	1601	63	0
4	F	28	0	25	0	0
4	I	28	0	25	1	0
4	L	28	0	25	2	0
4	M	28	0	25	0	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	2	0
4	S	28	0	25	2	0
4	T	28	0	25	0	0
4	U	28	0	25	1	0
4	V	28	0	25	0	0
4	W	28	0	25	0	0
4	X	28	0	25	1	0
4	Y	28	0	25	2	0
4	Z	28	0	25	0	0
5	A	98	0	91	1	0
5	B	70	0	65	0	0
5	C	112	0	104	4	0
All	All	34209	0	33360	752	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 752 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:117:LEU:CD1	1:C:233:ILE:HG21	1.53	1.36
1:A:660:TYR:HE2	1:A:675:GLN:OE1	1.00	1.32
2:J:14:PRO:HD3	2:J:120:SER:O	1.27	1.31
2:D:14:PRO:HD3	2:D:120:SER:O	1.31	1.24
1:A:660:TYR:CE2	1:A:675:GLN:OE1	1.89	1.23

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 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%)	913 (92%)	74 (8%)	1 (0%)	51	69
1	B	989/1120 (88%)	913 (92%)	76 (8%)	0	100	100
1	C	986/1120 (88%)	908 (92%)	76 (8%)	2 (0%)	47	64
2	D	222/224 (99%)	192 (86%)	30 (14%)	0	100	100
2	G	222/224 (99%)	188 (85%)	33 (15%)	1 (0%)	29	43
2	J	222/224 (99%)	192 (86%)	30 (14%)	0	100	100
3	E	212/214 (99%)	197 (93%)	15 (7%)	0	100	100
3	H	212/214 (99%)	183 (86%)	29 (14%)	0	100	100
3	K	212/214 (99%)	188 (89%)	24 (11%)	0	100	100
All	All	4265/4674 (91%)	3874 (91%)	387 (9%)	4 (0%)	54	69

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	230	PRO
1	C	231	ILE
2	G	124	THR
1	A	811	LYS

### 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 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%)	870 (99%)	11 (1%)	71	84
1	B	881/971 (91%)	878 (100%)	3 (0%)	92	96
1	C	879/971 (90%)	871 (99%)	8 (1%)	78	87
2	D	184/184 (100%)	180 (98%)	4 (2%)	52	70
2	G	184/184 (100%)	181 (98%)	3 (2%)	62	78
2	J	184/184 (100%)	178 (97%)	6 (3%)	38	54
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%)	183 (99%)	2 (1%)	73	85
All	All	3748/4020 (93%)	3711 (99%)	37 (1%)	77	86

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	179	GLN
3	K	188	LYS
2	J	13	LYS
2	J	118	THR
1	B	675	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	690	GLN
1	B	125	ASN
1	C	474	GLN
1	A	658	ASN
1	A	121	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates i

34 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	0.24	0	17,19,21	0.46	0
4	NAG	F	2	4	14,14,15	0.25	0	17,19,21	0.44	0
4	NAG	I	1	4,1	14,14,15	0.24	0	17,19,21	0.47	0
4	NAG	I	2	4	14,14,15	0.38	0	17,19,21	1.23	1 (5%)
4	NAG	L	1	4,1	14,14,15	0.43	0	17,19,21	0.60	0
4	NAG	L	2	4	14,14,15	0.40	0	17,19,21	1.27	1 (5%)
4	NAG	M	1	4,1	14,14,15	0.28	0	17,19,21	0.47	0
4	NAG	M	2	4	14,14,15	0.25	0	17,19,21	0.52	0
4	NAG	N	1	4,1	14,14,15	0.30	0	17,19,21	0.69	1 (5%)
4	NAG	N	2	4	14,14,15	0.23	0	17,19,21	0.41	0
4	NAG	O	1	4,1	14,14,15	0.27	0	17,19,21	0.31	0
4	NAG	O	2	4	14,14,15	0.22	0	17,19,21	0.45	0
4	NAG	P	1	4,1	14,14,15	0.18	0	17,19,21	0.59	0
4	NAG	P	2	4	14,14,15	0.22	0	17,19,21	0.49	0
4	NAG	Q	1	4,1	14,14,15	0.23	0	17,19,21	0.47	0
4	NAG	Q	2	4	14,14,15	0.22	0	17,19,21	0.40	0
4	NAG	R	1	4,1	14,14,15	0.67	0	17,19,21	0.93	1 (5%)
4	NAG	R	2	4	14,14,15	0.26	0	17,19,21	0.37	0
4	NAG	S	1	4,1	14,14,15	0.41	0	17,19,21	0.52	0
4	NAG	S	2	4	14,14,15	0.44	0	17,19,21	0.48	0
4	NAG	T	1	4,1	14,14,15	0.24	0	17,19,21	0.46	0
4	NAG	T	2	4	14,14,15	0.19	0	17,19,21	0.43	0
4	NAG	U	1	4,1	14,14,15	0.38	0	17,19,21	1.28	2 (11%)
4	NAG	U	2	4	14,14,15	0.21	0	17,19,21	0.44	0
4	NAG	V	1	4,1	14,14,15	0.25	0	17,19,21	0.46	0
4	NAG	V	2	4	14,14,15	0.24	0	17,19,21	0.37	0
4	NAG	W	1	4,1	14,14,15	0.25	0	17,19,21	0.43	0
4	NAG	W	2	4	14,14,15	0.28	0	17,19,21	0.56	0
4	NAG	X	1	4,1	14,14,15	0.28	0	17,19,21	0.55	0
4	NAG	X	2	4	14,14,15	0.50	0	17,19,21	1.24	1 (5%)
4	NAG	Y	1	4,1	14,14,15	0.38	0	17,19,21	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	Y	2	4	14,14,15	0.40	0	17,19,21	1.26	2 (11%)
4	NAG	Z	1	4,1	14,14,15	0.21	0	17,19,21	0.43	0
4	NAG	Z	2	4	14,14,15	0.22	0	17,19,21	0.36	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	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	3/6/23/26	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	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	P	2	4	-	2/6/23/26	0/1/1/1
4	NAG	Q	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	2/6/23/26	0/1/1/1
4	NAG	R	1	4,1	-	2/6/23/26	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	-	1/6/23/26	0/1/1/1
4	NAG	T	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	T	2	4	-	0/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	5/6/23/26	0/1/1/1
4	NAG	U	2	4	-	0/6/23/26	0/1/1/1
4	NAG	V	1	4,1	-	2/6/23/26	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

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

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	U	1	NAG	C2-N2-C7	4.38	129.14	122.90
4	X	2	NAG	C2-N2-C7	4.33	129.06	122.90
4	I	2	NAG	C2-N2-C7	4.30	129.03	122.90
4	Y	2	NAG	C2-N2-C7	4.26	128.97	122.90
4	L	2	NAG	C2-N2-C7	4.26	128.97	122.90

There are no chirality outliers.

5 of 69 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	2	NAG	C4-C5-C6-O6
4	Z	1	NAG	O5-C5-C6-O6
4	Y	2	NAG	C4-C5-C6-O6
4	L	2	NAG	O5-C5-C6-O6
4	T	1	NAG	O5-C5-C6-O6

There are no ring outliers.

10 monomers are involved in 11 short contacts:

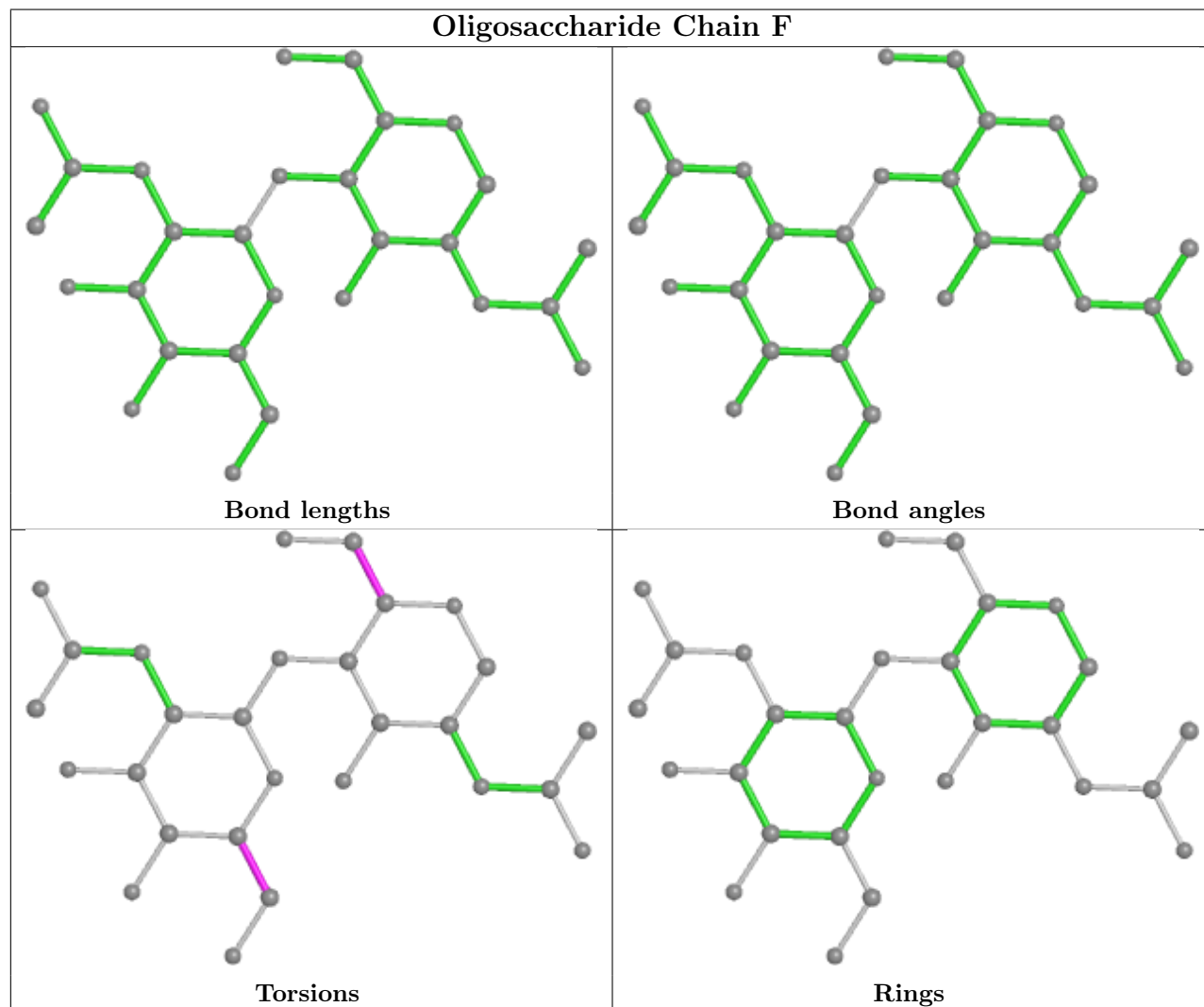
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	U	1	NAG	1	0
4	S	2	NAG	1	0
4	Y	1	NAG	1	0
4	R	1	NAG	2	0
4	X	2	NAG	1	0
4	I	2	NAG	1	0
4	L	2	NAG	1	0
4	L	1	NAG	1	0

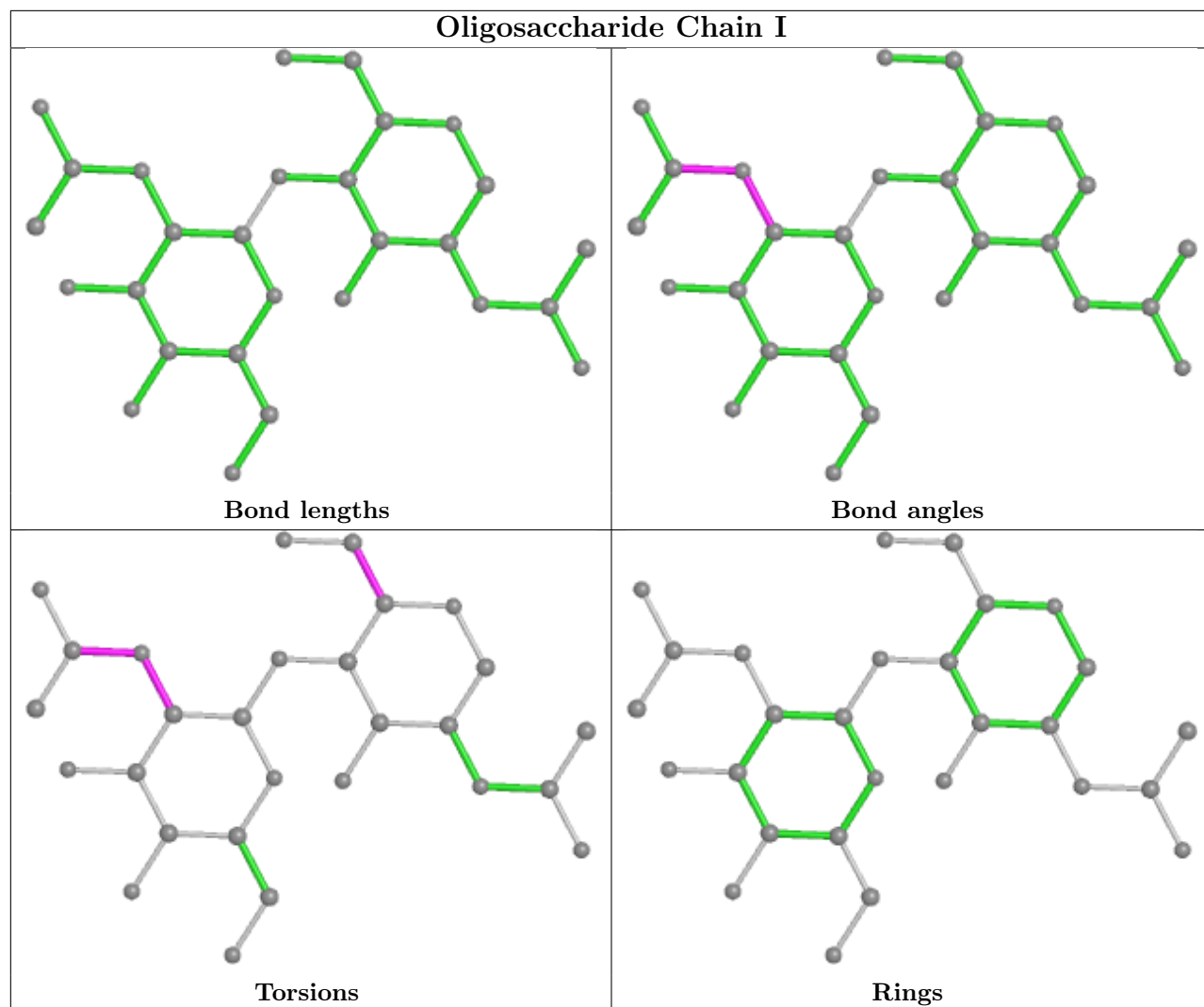
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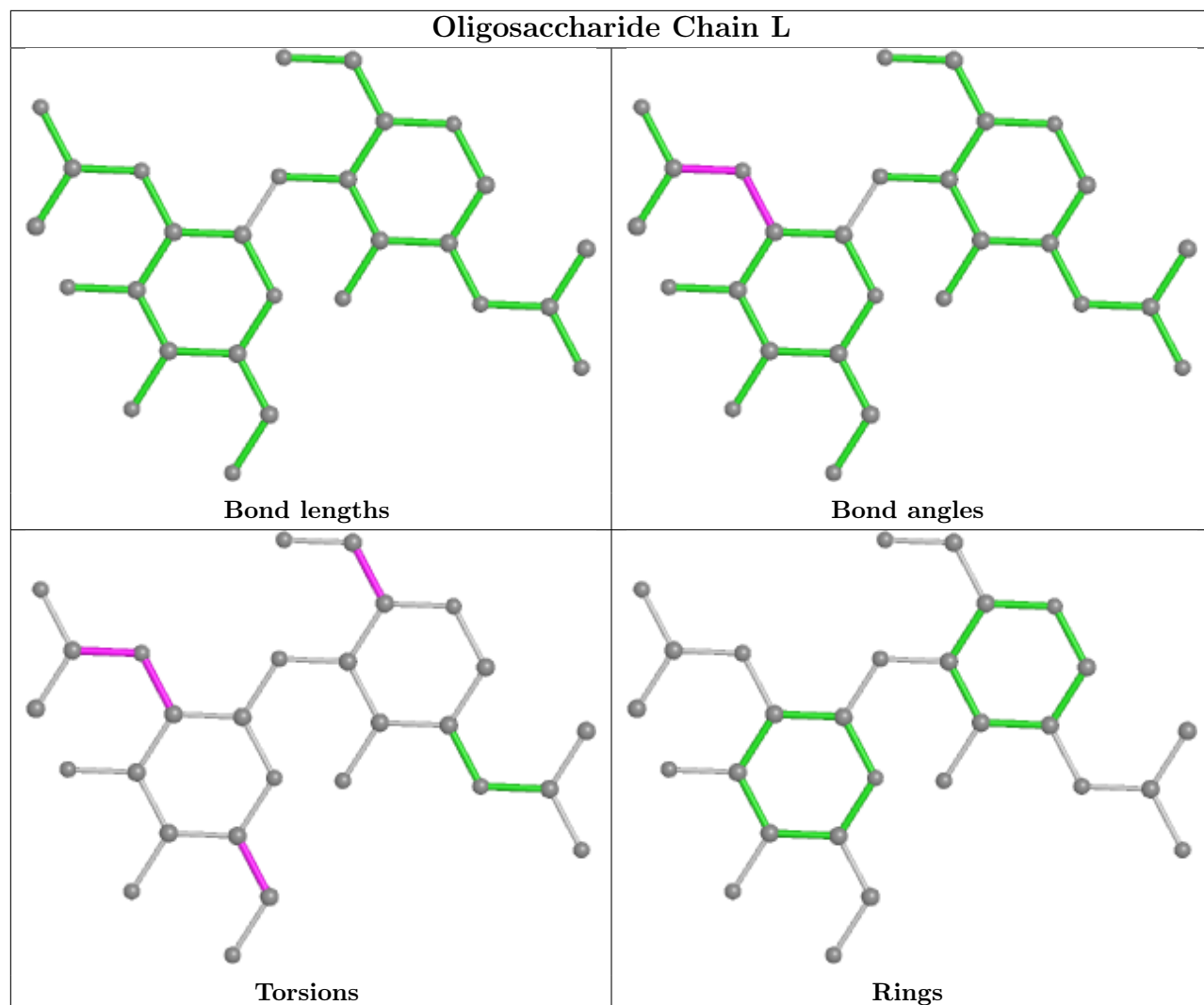
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Y	2	NAG	1	0
4	S	1	NAG	2	0

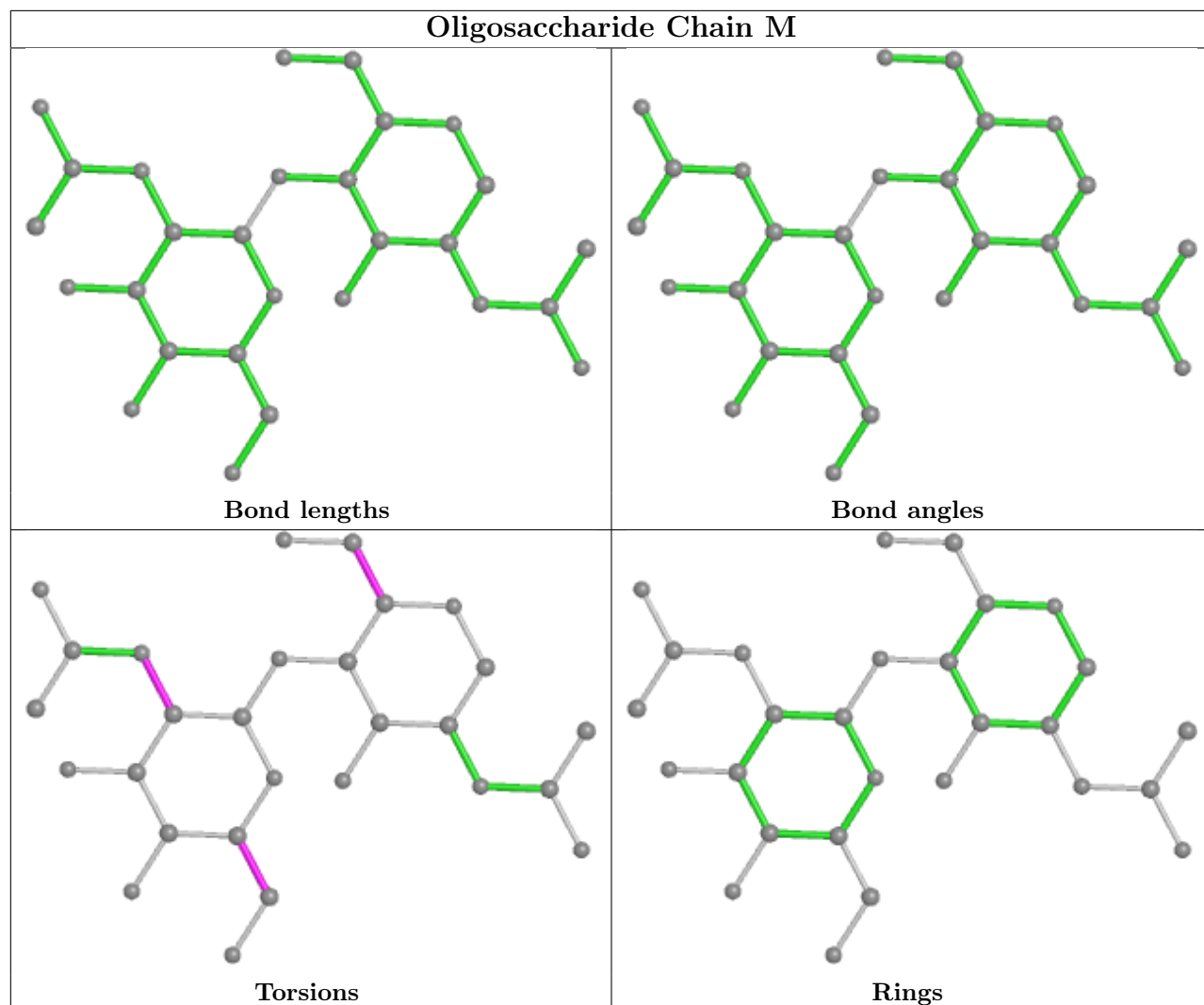
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

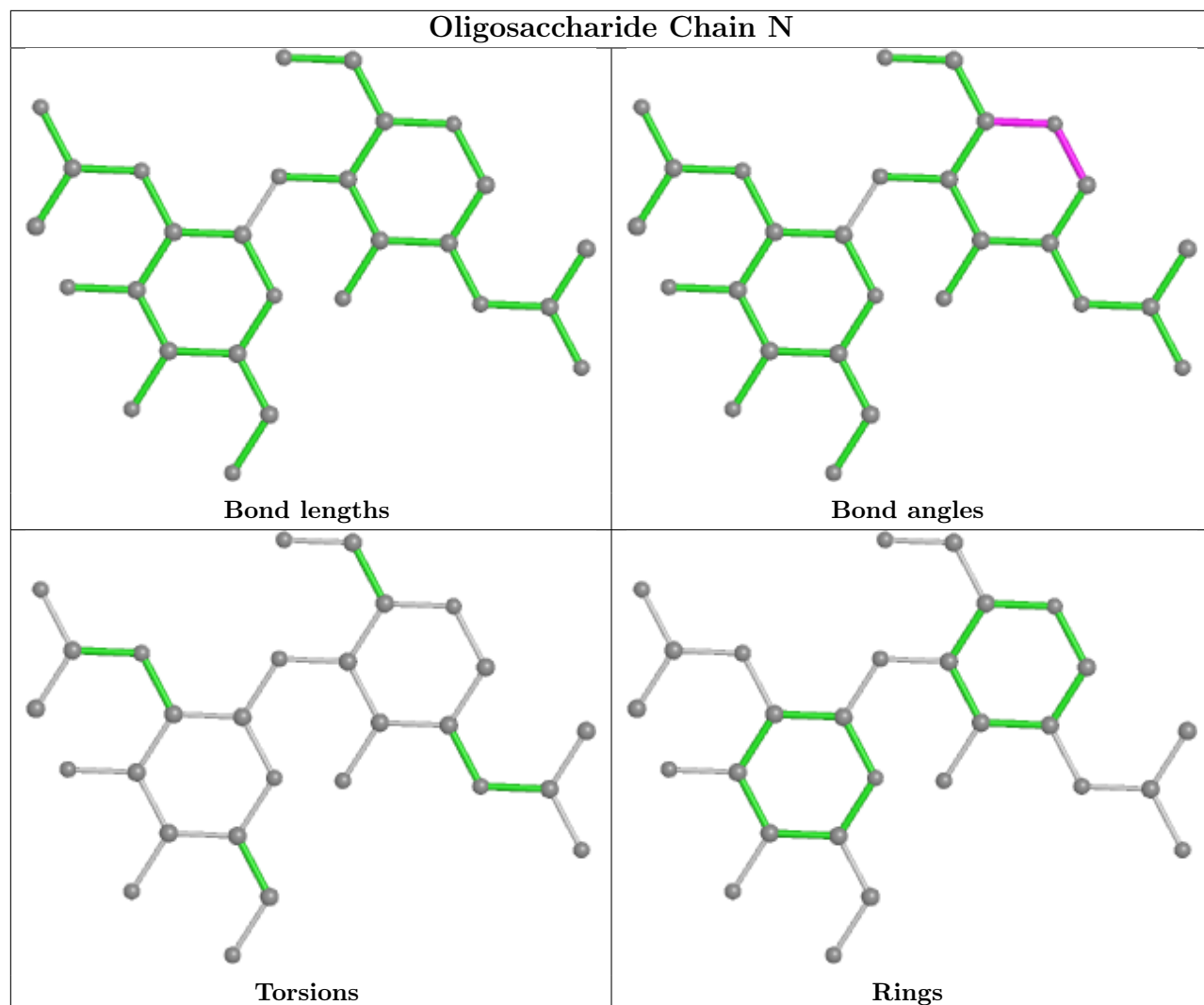


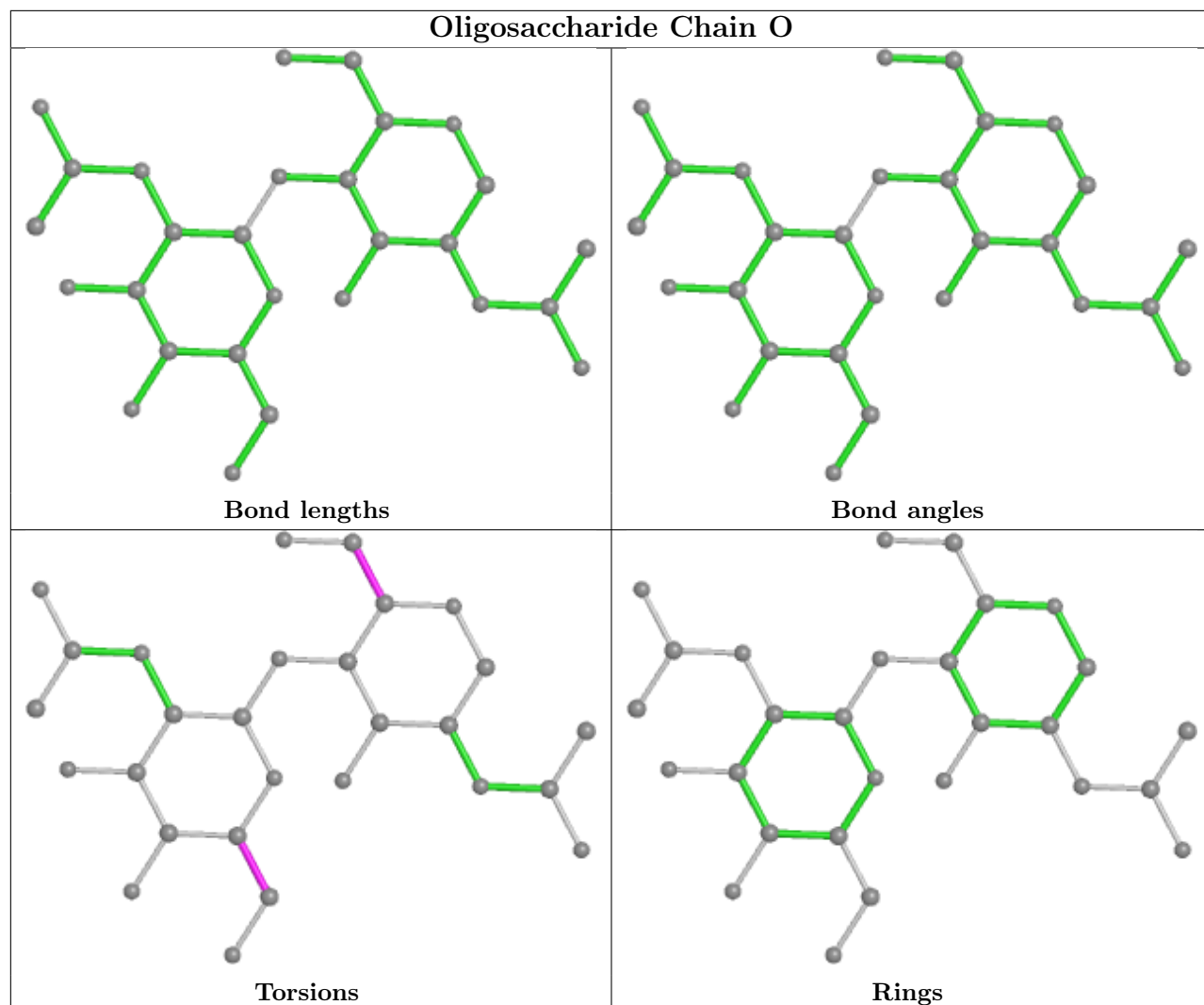


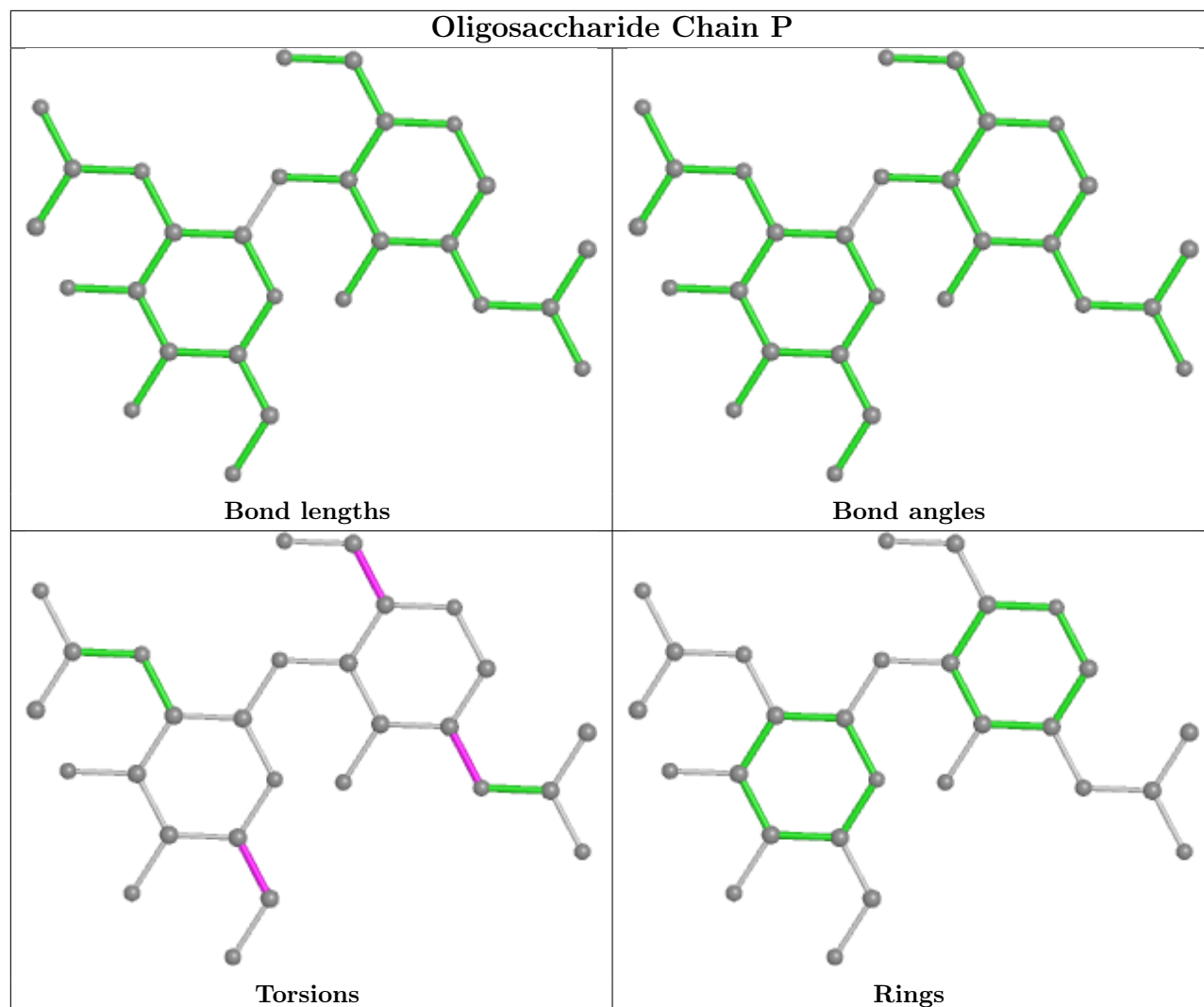


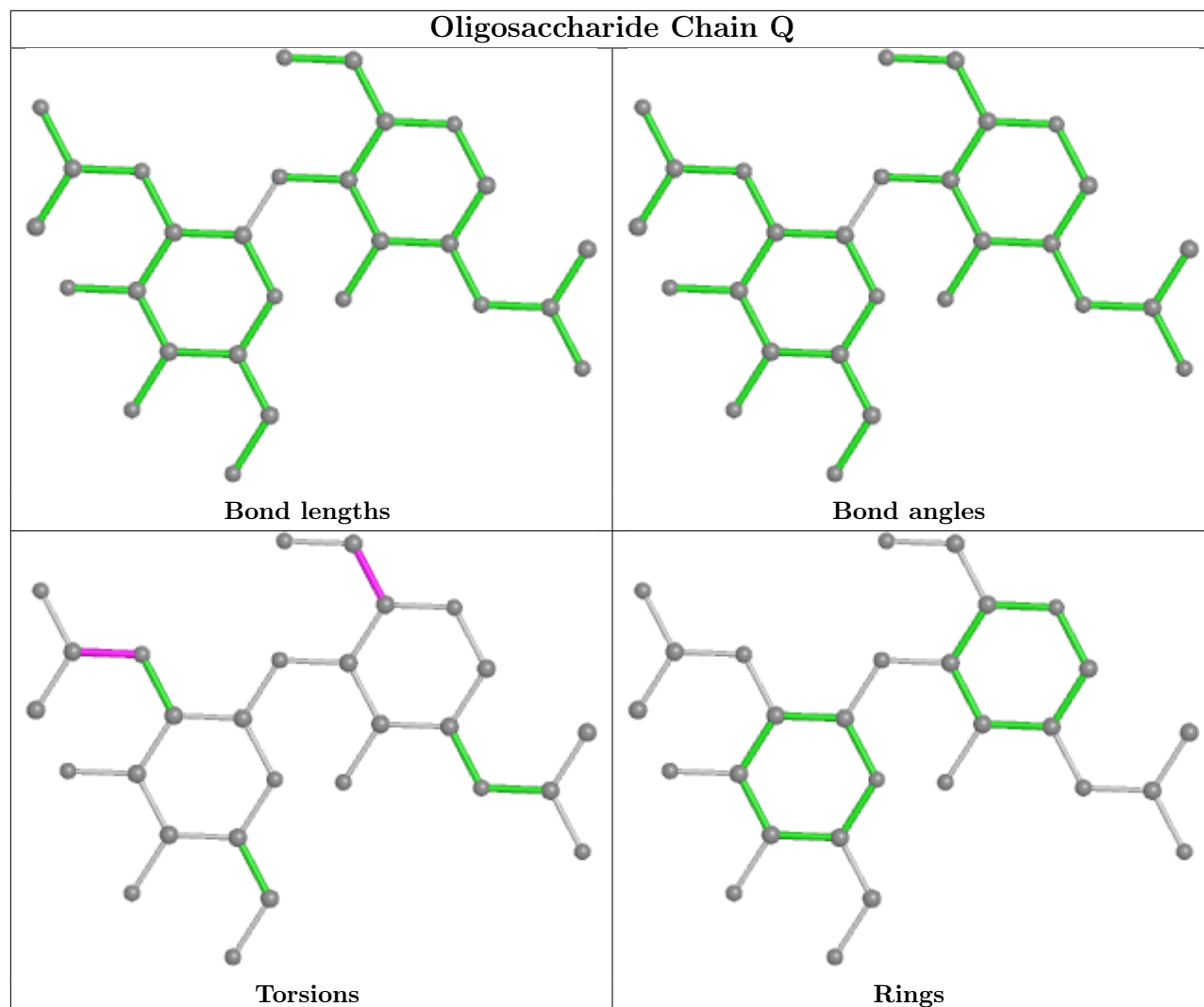


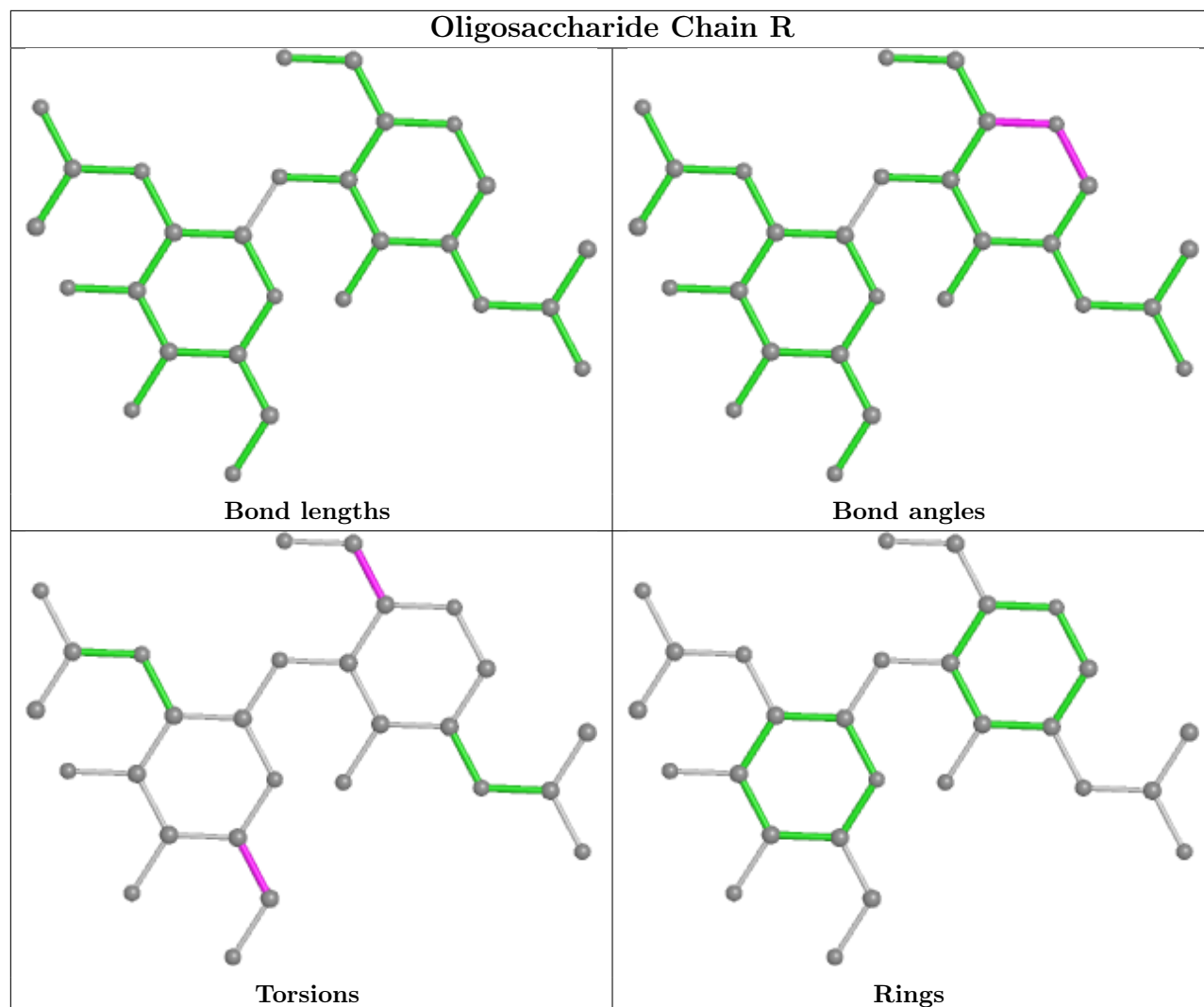


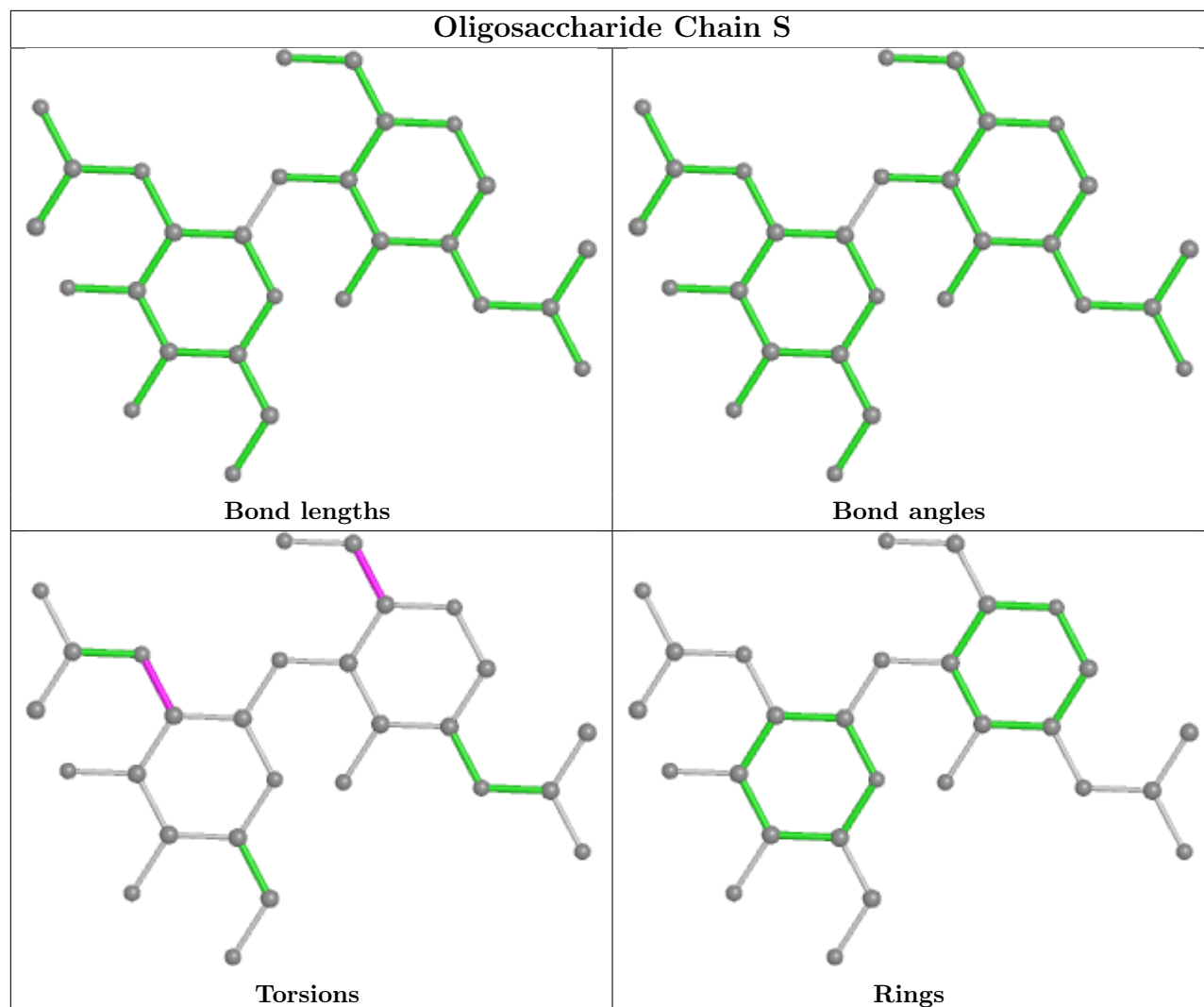




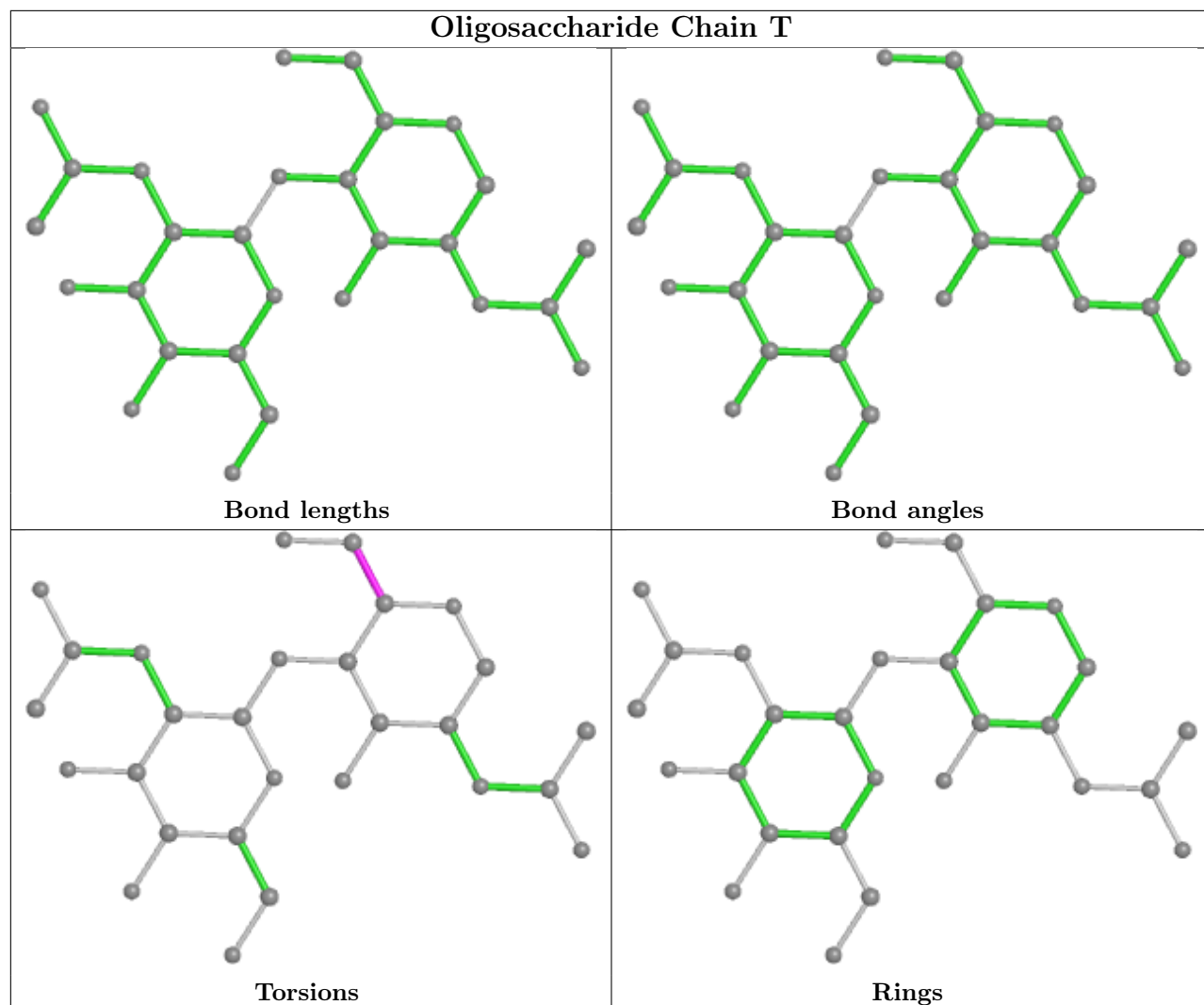


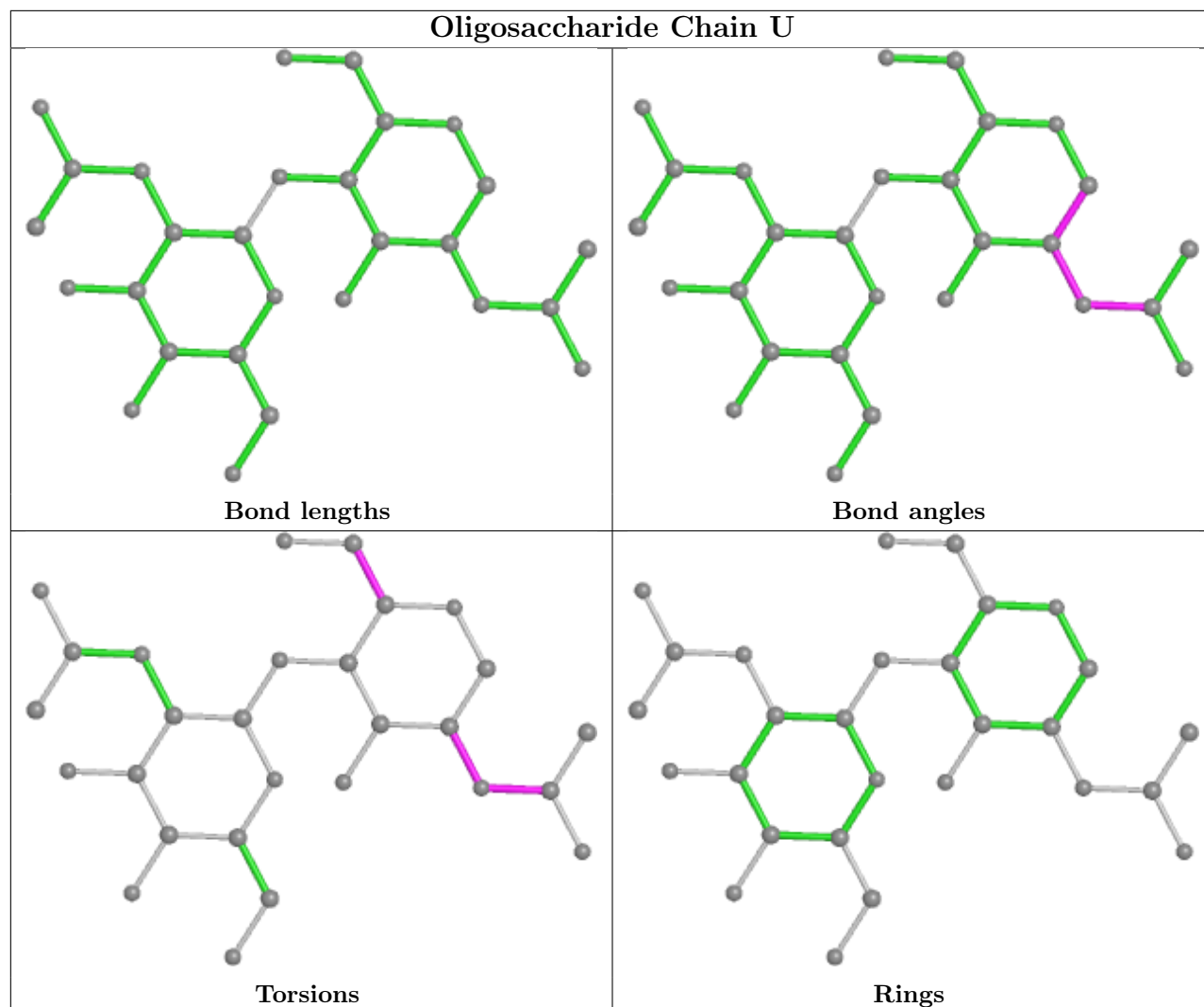


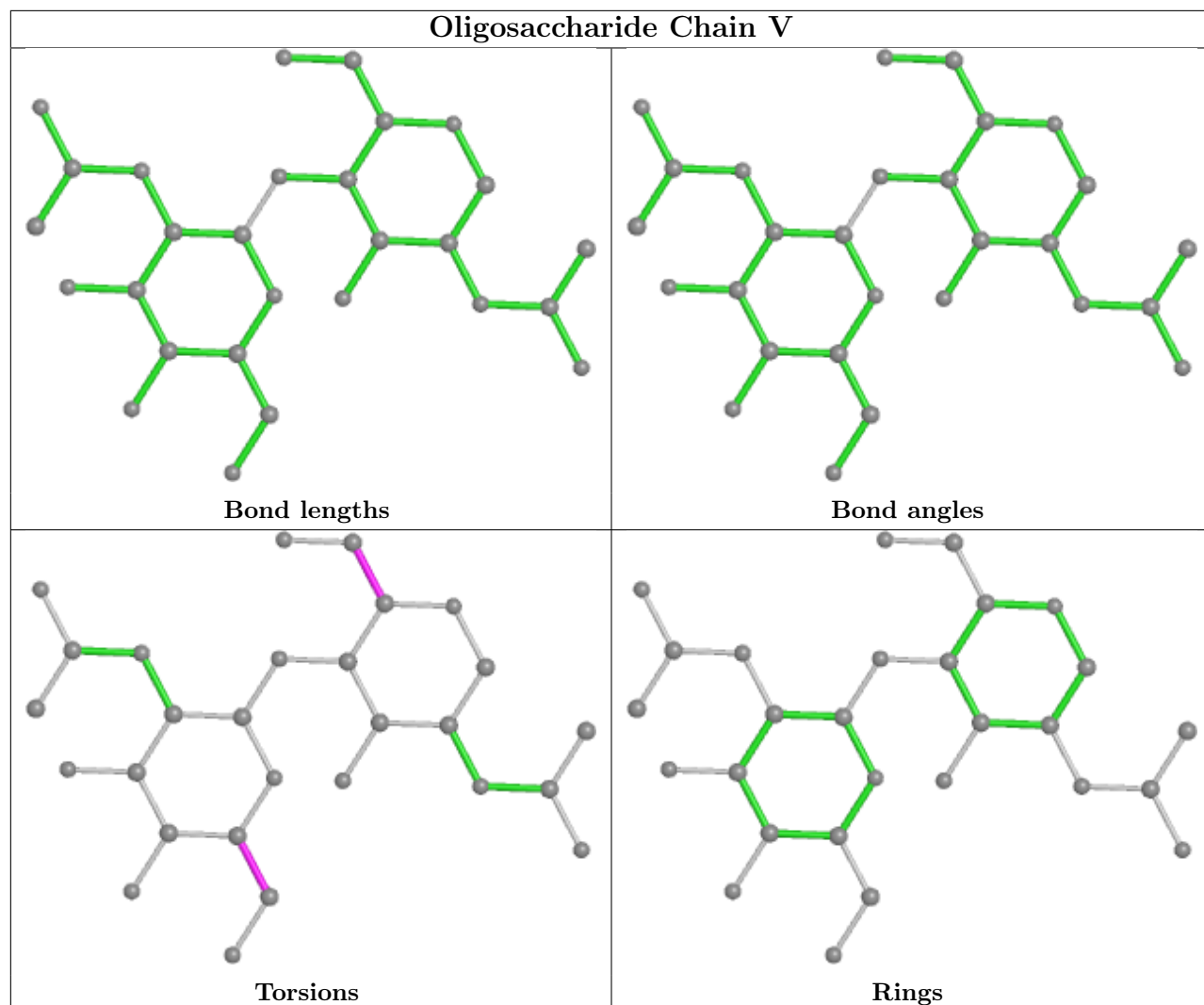


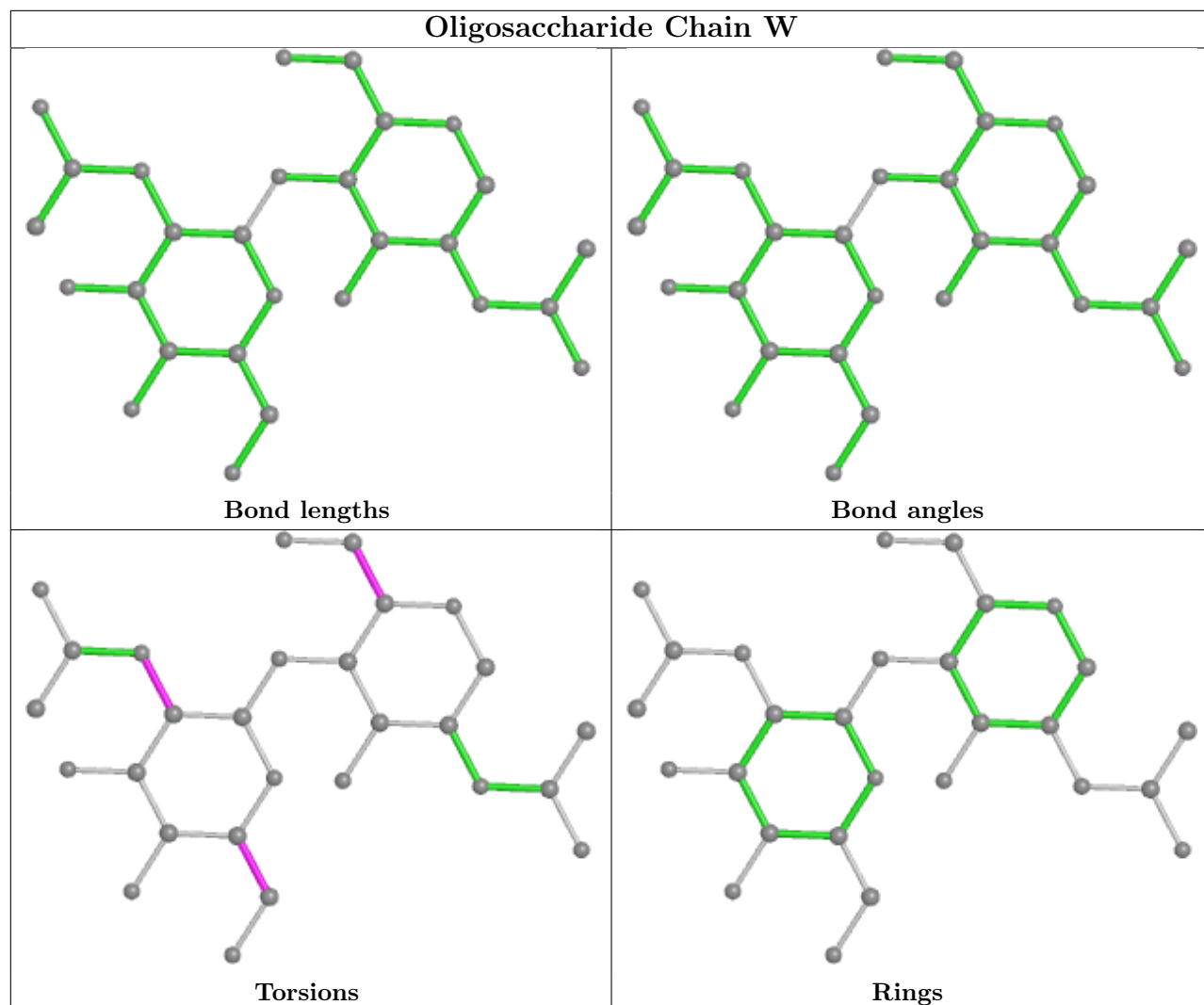


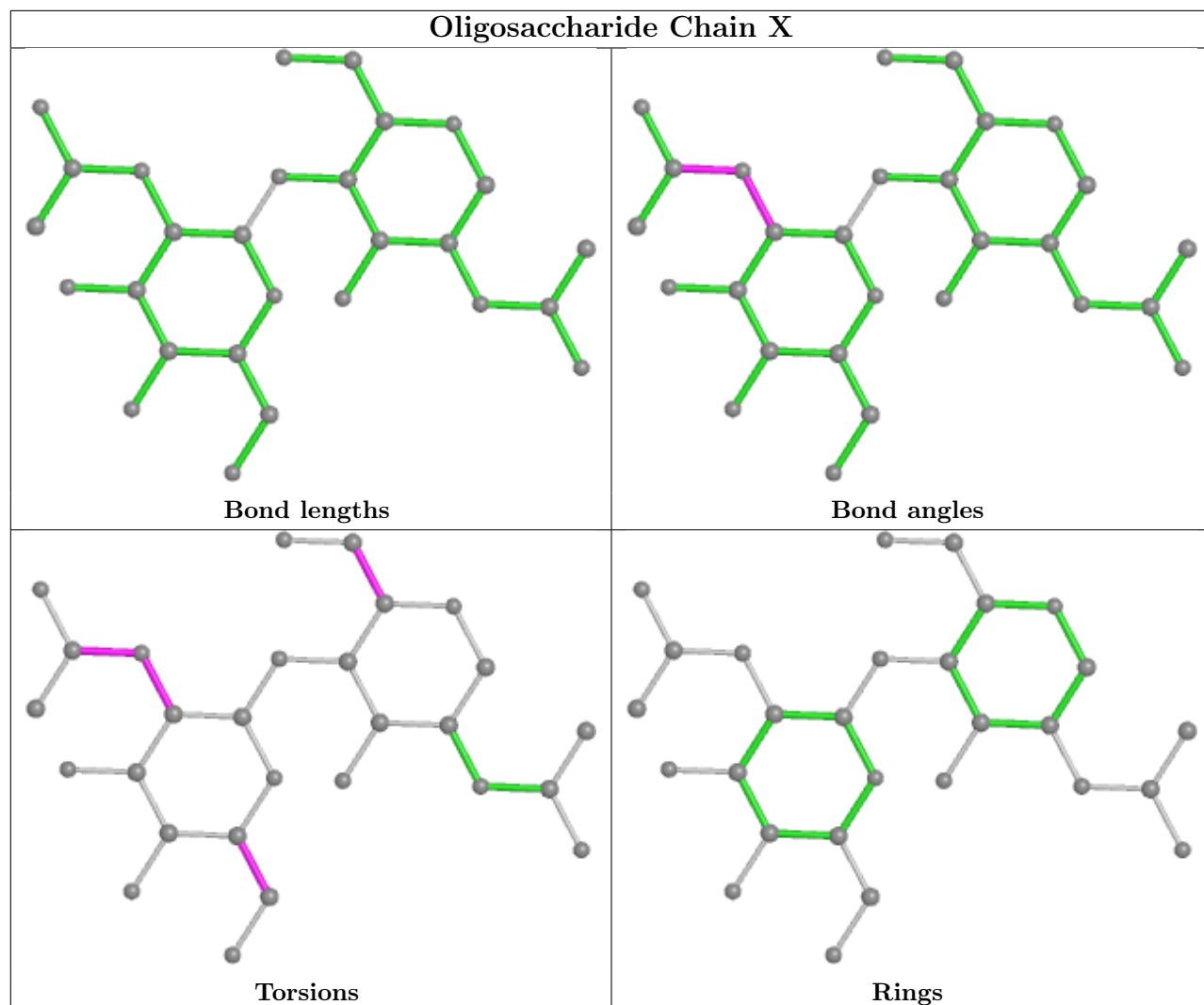


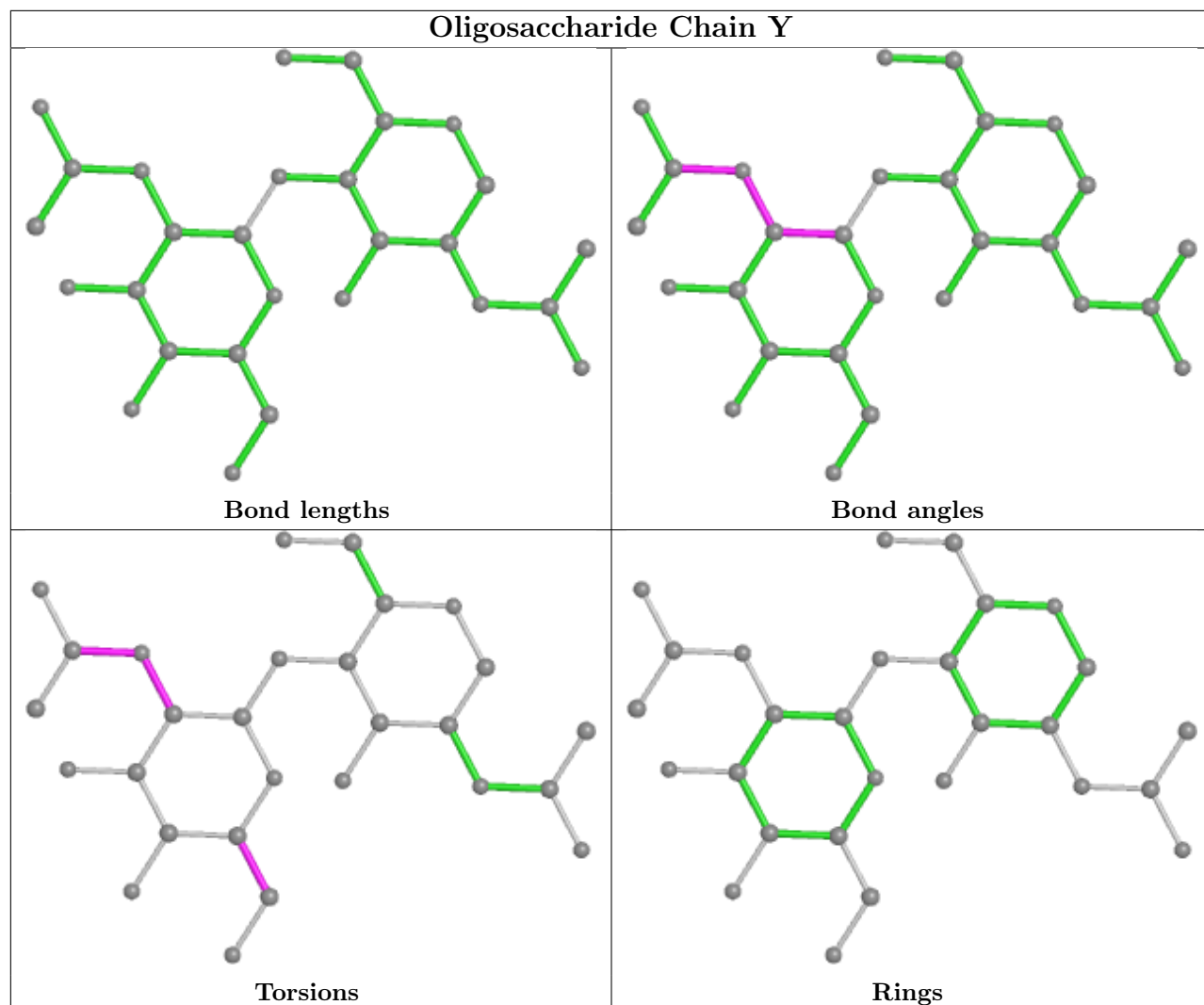


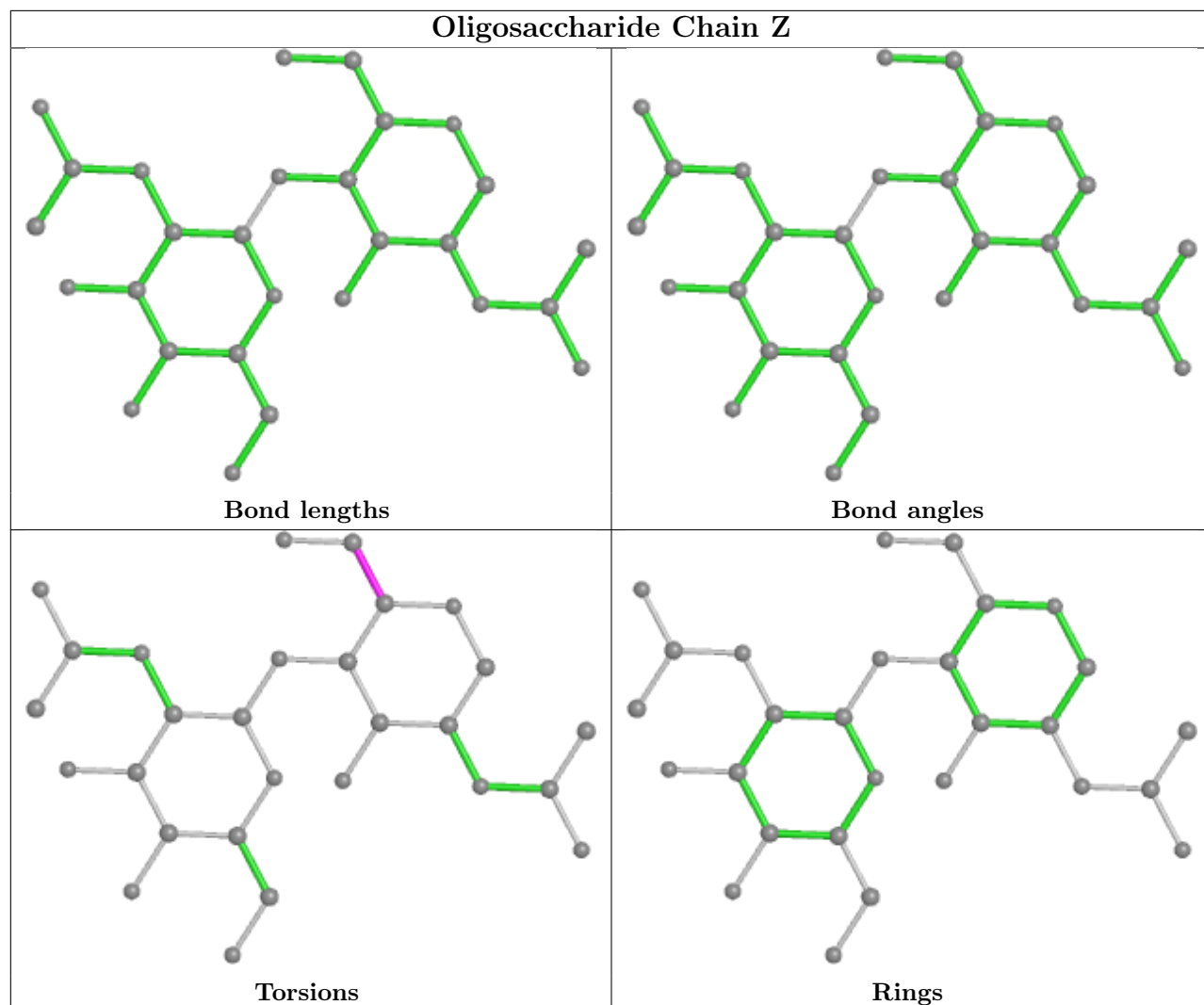












## 5.6 Ligand geometry [i](#)

20 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	A	1401	1	14,14,15	0.19	0	17,19,21	0.41	0
5	NAG	C	1401	1	14,14,15	0.21	0	17,19,21	0.45	0
5	NAG	A	1405	1	14,14,15	0.17	0	17,19,21	0.47	0
5	NAG	C	1402	1	14,14,15	0.23	0	17,19,21	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	NAG	C	1405	1	14,14,15	0.20	0	17,19,21	0.46	0
5	NAG	C	1403	1	14,14,15	0.23	0	17,19,21	0.45	0
5	NAG	B	1404	1	14,14,15	0.31	0	17,19,21	0.46	0
5	NAG	B	1402	1	14,14,15	0.24	0	17,19,21	0.35	0
5	NAG	C	1408	1	14,14,15	0.37	0	17,19,21	1.28	1 (5%)
5	NAG	A	1402	1	14,14,15	0.40	0	17,19,21	1.22	1 (5%)
5	NAG	A	1404	1	14,14,15	0.29	0	17,19,21	0.60	1 (5%)
5	NAG	C	1404	1	14,14,15	0.57	0	17,19,21	1.22	1 (5%)
5	NAG	B	1405	1	14,14,15	0.19	0	17,19,21	0.50	0
5	NAG	A	1407	1	14,14,15	0.27	0	17,19,21	0.56	0
5	NAG	C	1407	1	14,14,15	0.27	0	17,19,21	0.44	0
5	NAG	C	1406	1	14,14,15	0.25	0	17,19,21	0.64	0
5	NAG	A	1403	1	14,14,15	0.25	0	17,19,21	0.47	0
5	NAG	B	1401	1	14,14,15	0.28	0	17,19,21	0.40	0
5	NAG	B	1403	1	14,14,15	0.34	0	17,19,21	0.58	0
5	NAG	A	1406	1	14,14,15	0.24	0	17,19,21	0.46	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	A	1401	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1401	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1405	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1402	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1405	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1404	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1402	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1408	1	-	3/6/23/26	0/1/1/1
5	NAG	A	1402	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1404	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1404	1	-	5/6/23/26	0/1/1/1
5	NAG	B	1405	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1407	1	-	3/6/23/26	0/1/1/1
5	NAG	C	1407	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1406	1	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	1403	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1401	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1403	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1406	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1402	NAG	C2-N2-C7	4.32	129.05	122.90
5	C	1408	NAG	C2-N2-C7	4.31	129.04	122.90
5	C	1404	NAG	C2-N2-C7	4.18	128.85	122.90
5	A	1404	NAG	C1-O5-C5	2.04	114.96	112.19

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1403	NAG	O5-C5-C6-O6
5	A	1405	NAG	O5-C5-C6-O6
5	C	1403	NAG	C4-C5-C6-O6
5	A	1405	NAG	C4-C5-C6-O6
5	A	1406	NAG	C4-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	1408	NAG	1	0
5	A	1402	NAG	1	0
5	C	1404	NAG	2	0
5	C	1406	NAG	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

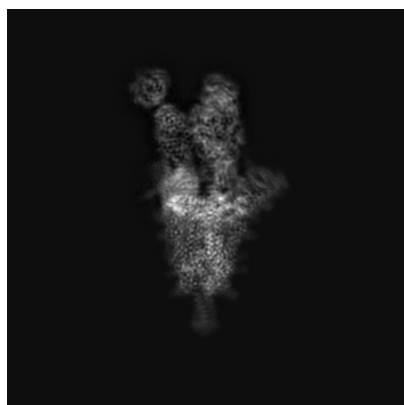
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32499. These allow visual inspection of the internal detail of the map and identification of artifacts.

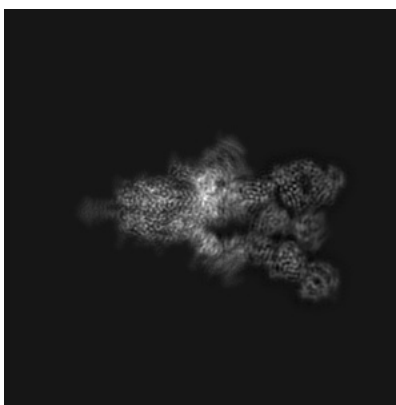
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

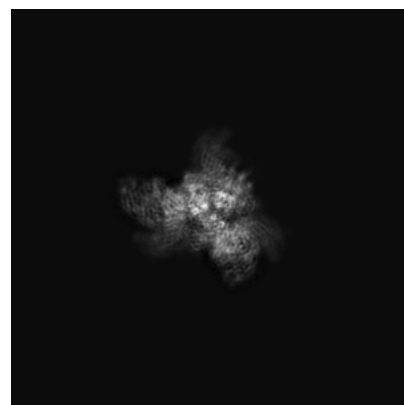
#### 6.1.1 Primary map



X



Y



Z

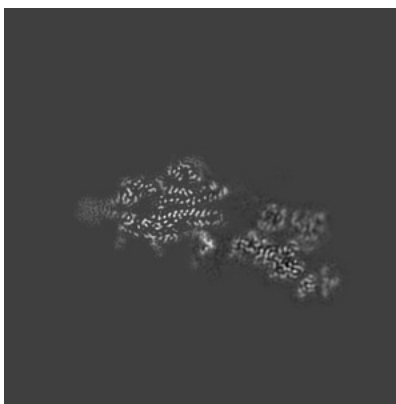
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



X Index: 181



Y Index: 181



Z Index: 181

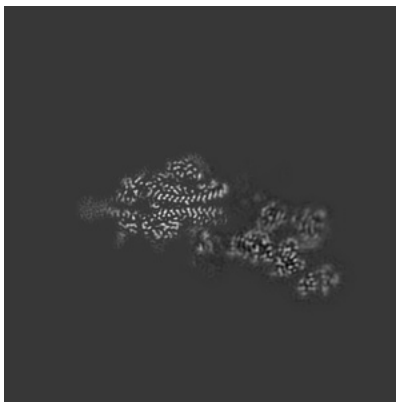
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [\(i\)](#)

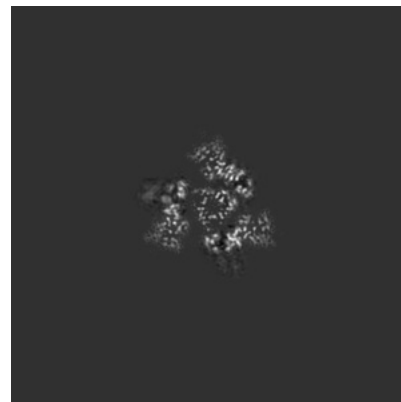
### 6.3.1 Primary map



X Index: 188



Y Index: 183

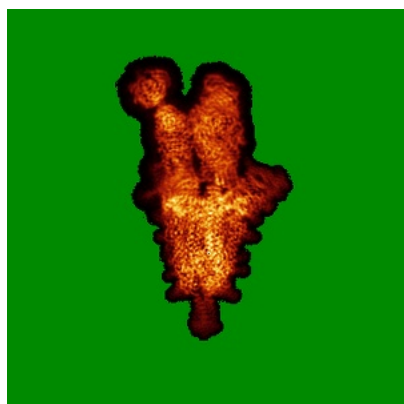


Z Index: 188

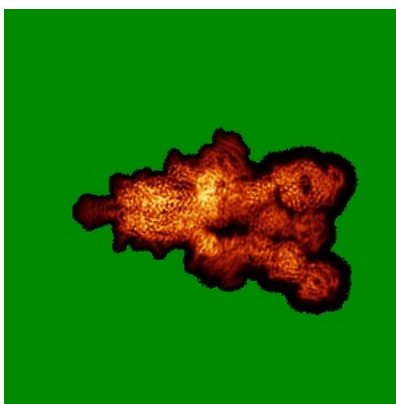
The images above show the largest variance slices of the map in three orthogonal directions.

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

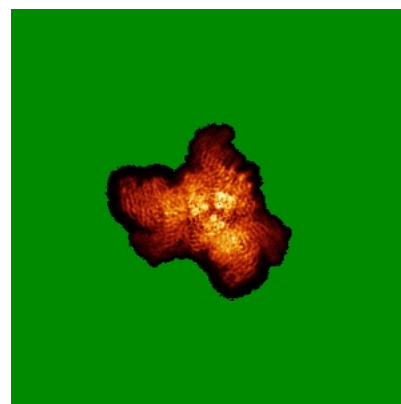
### 6.4.1 Primary map



X



Y

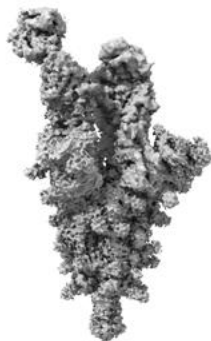


Z

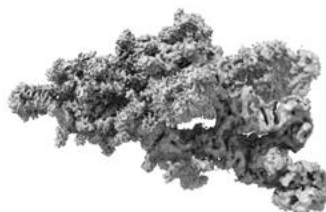
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

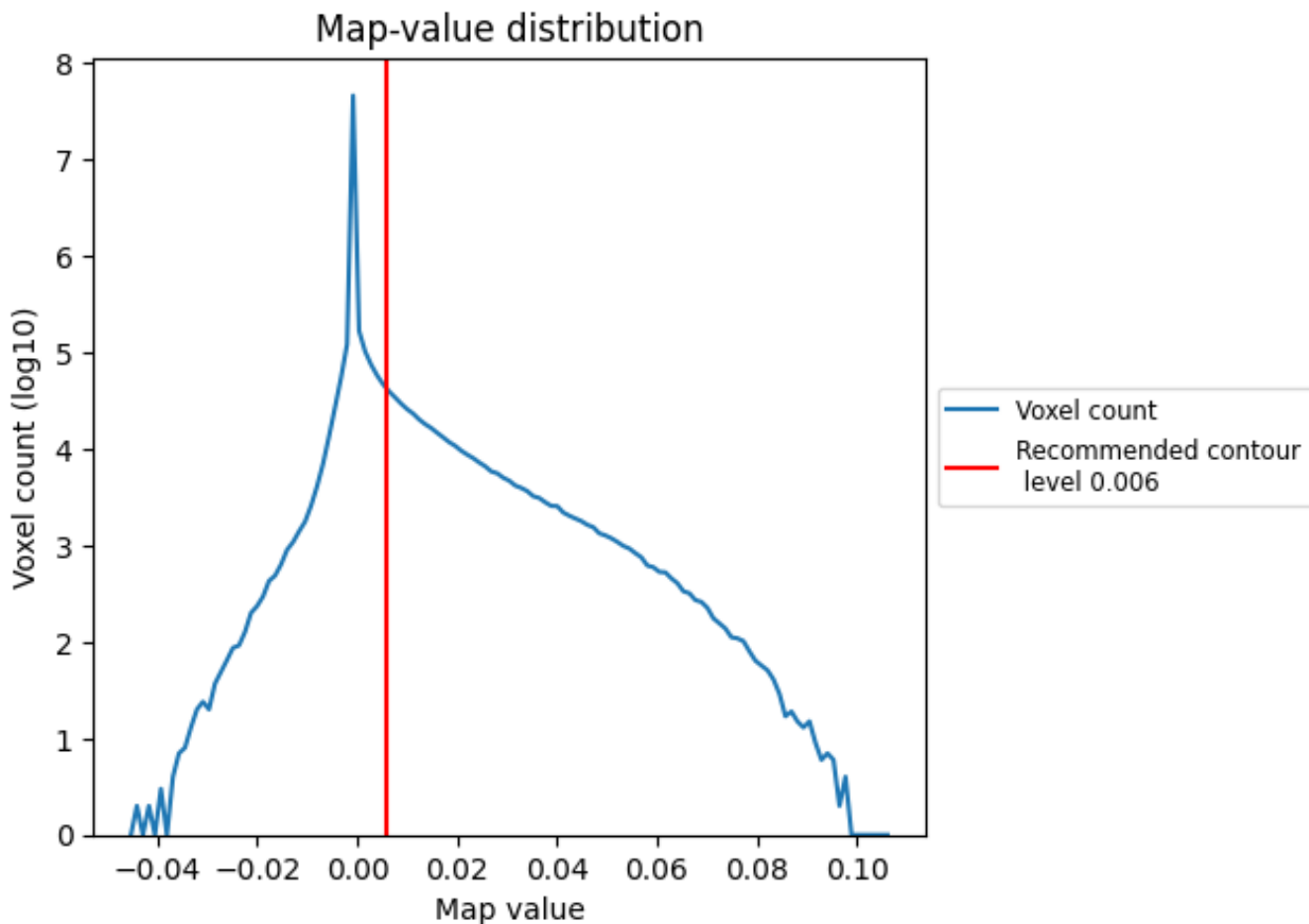
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

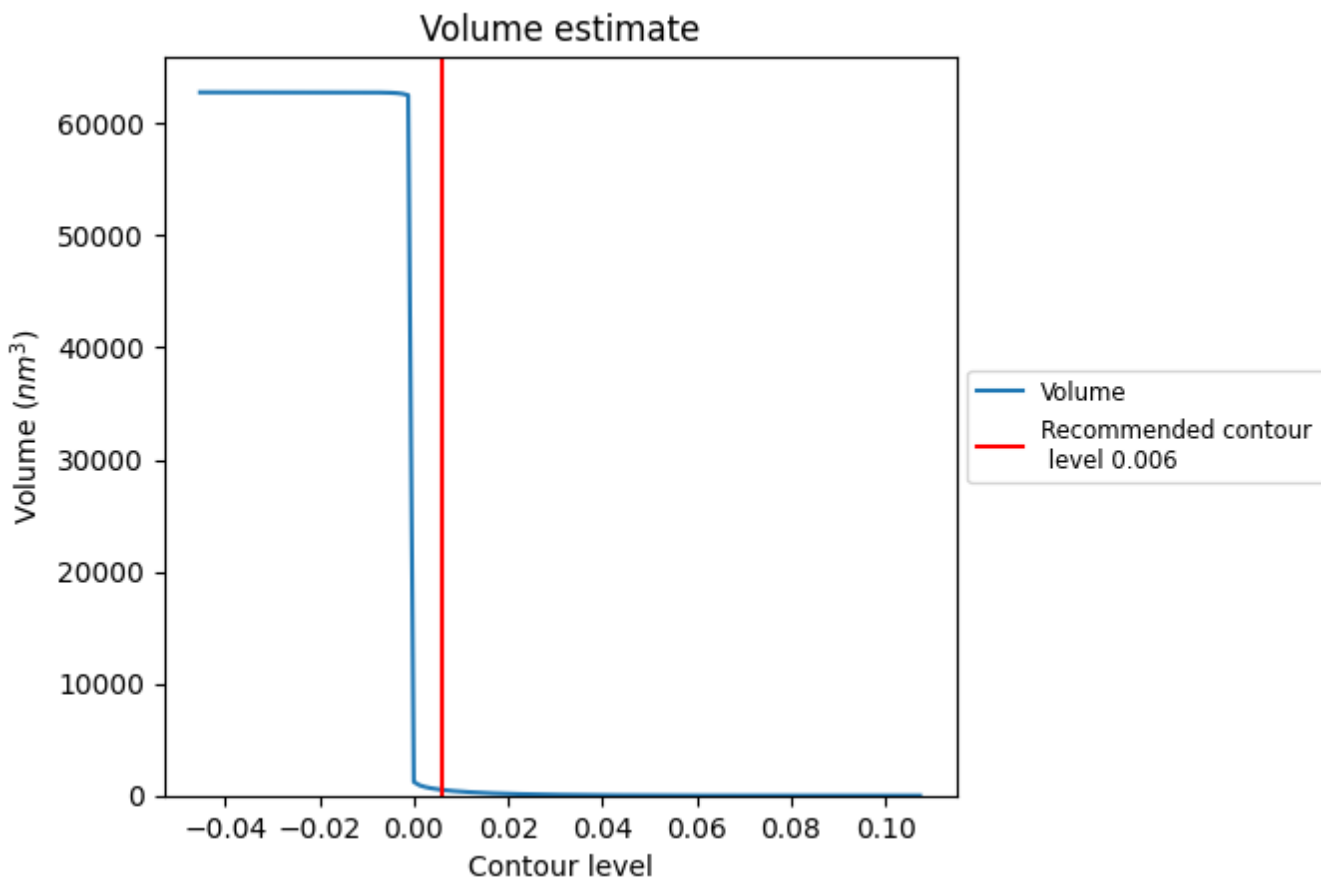
This section contains the results of statistical analysis of the map.

### 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.

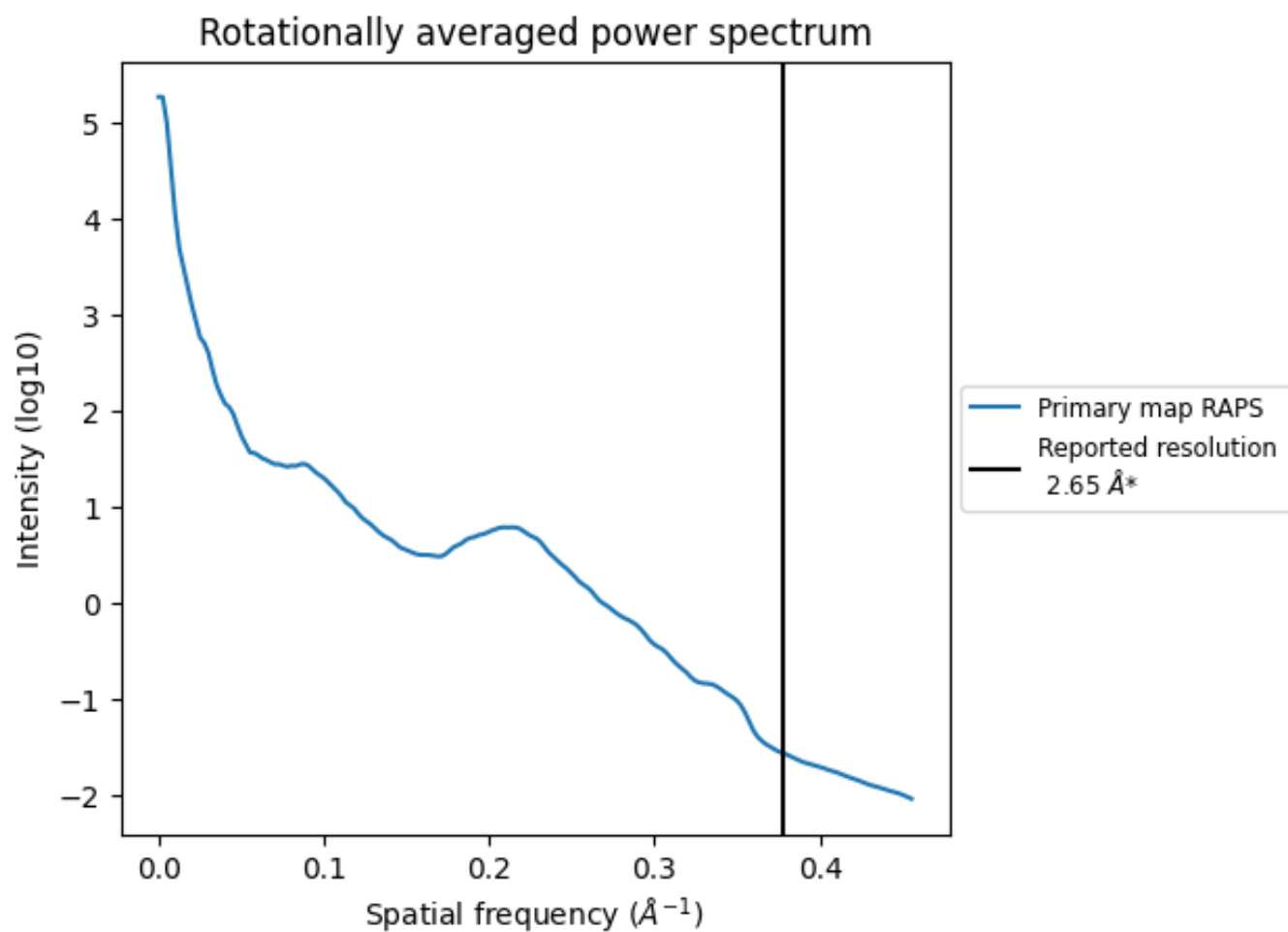
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 511  $\text{nm}^3$ ; this corresponds to an approximate mass of 461 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 i



\*Reported resolution corresponds to spatial frequency of  $0.377 \text{ \AA}^{-1}$



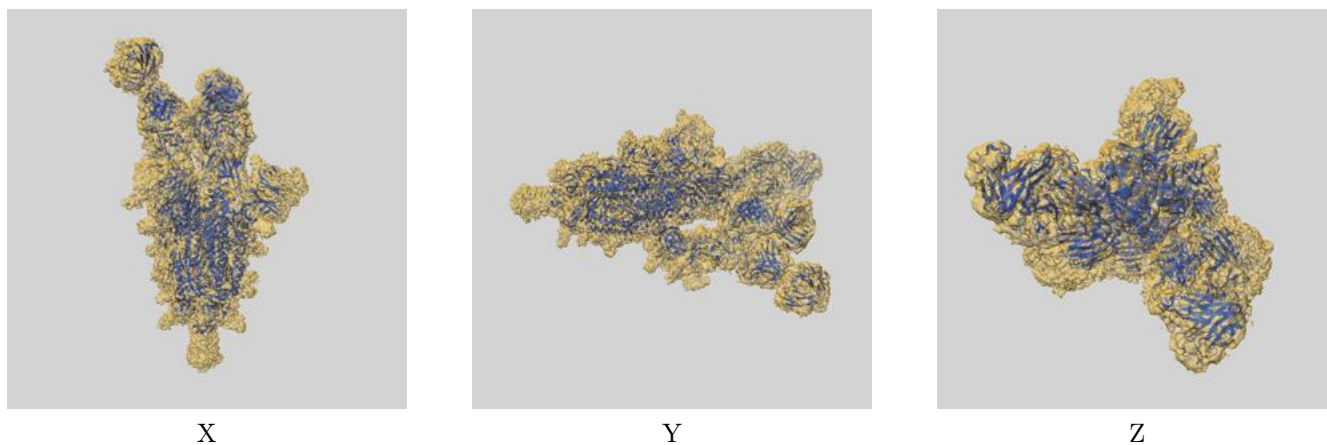
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

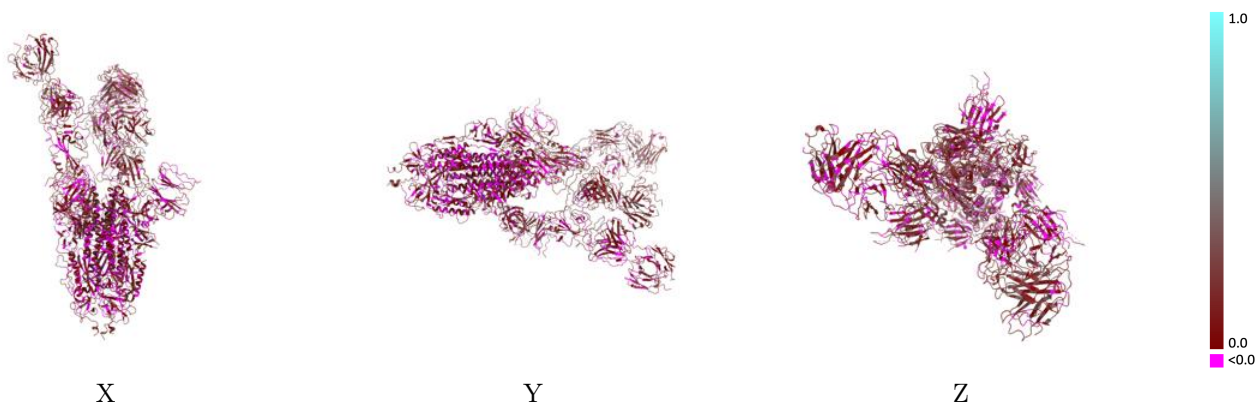
This section contains information regarding the fit between EMDB map EMD-32499 and PDB model 7WHD. Per-residue inclusion information can be found in section 3 on page 8.

### 9.1 Map-model overlay [i](#)



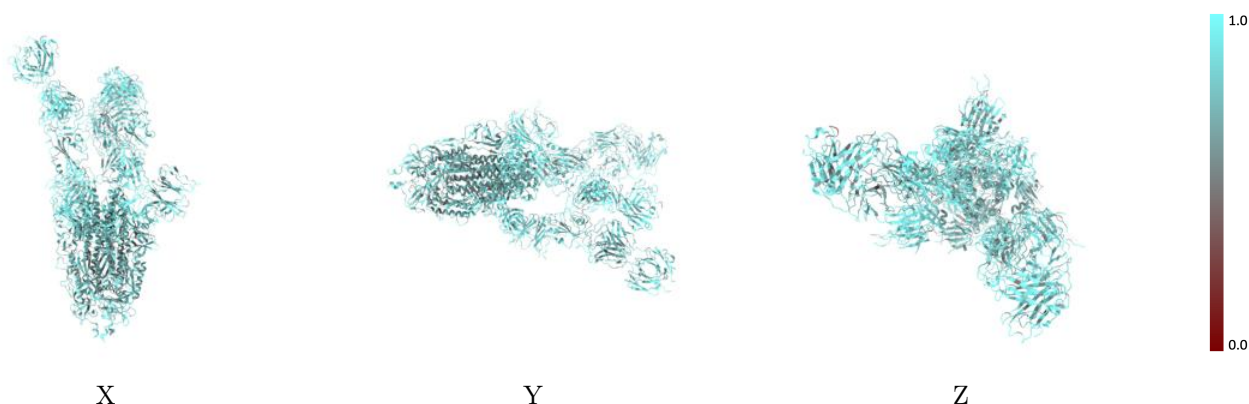
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



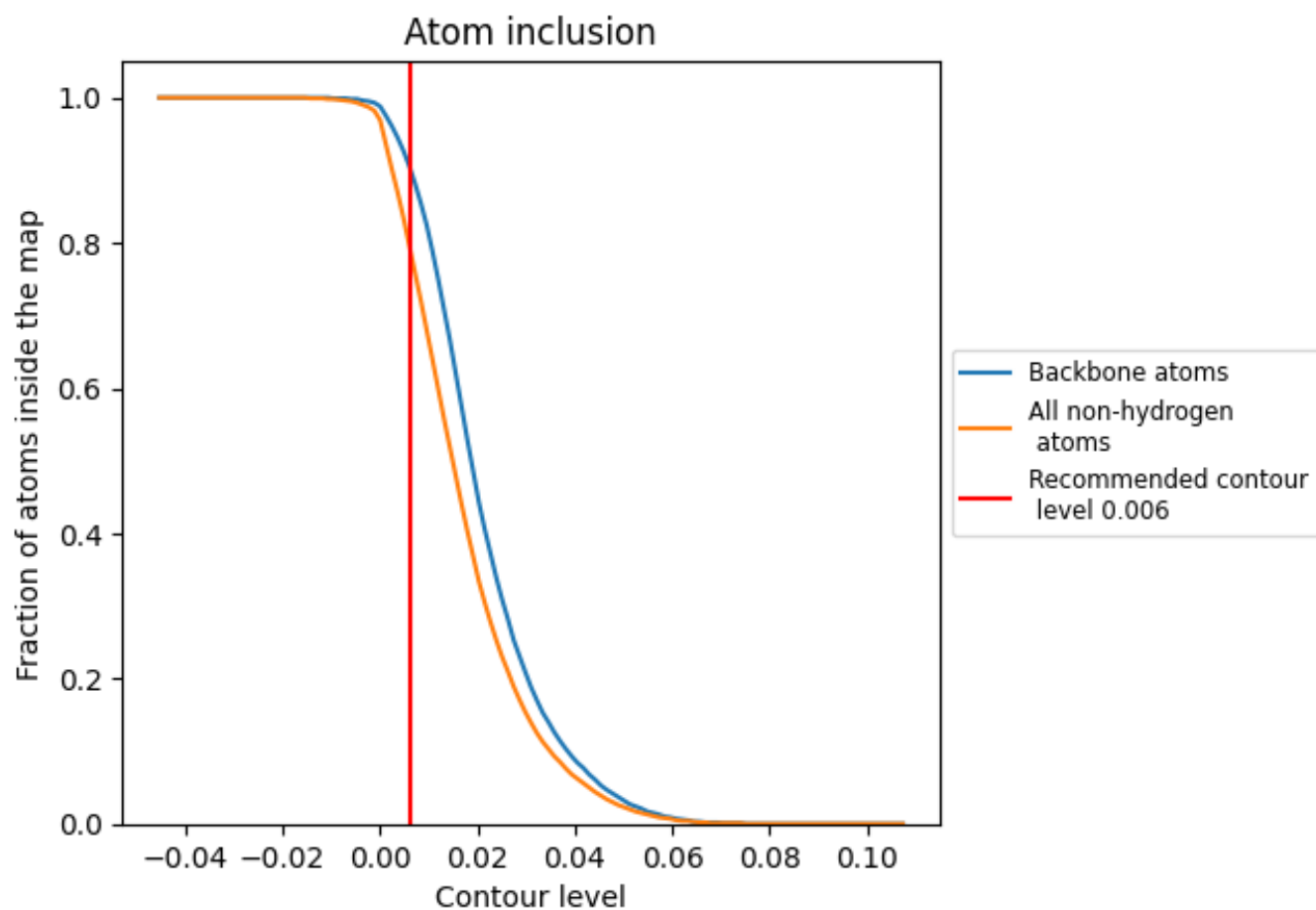
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).























































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 80% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.1280
A	 0.7900	 0.1150
B	 0.8070	 0.1220
C	 0.7790	 0.0920
D	 0.7670	 0.1070
E	 0.7870	 0.1020
F	 0.8570	 0.2260
G	 0.8160	 0.1980
H	 0.8010	 0.1780
I	 0.8210	 0.1670
J	 0.8390	 0.2100
K	 0.8390	 0.2150
L	 0.5000	 -0.0040
M	 0.7140	 0.0330
N	 0.8570	 0.1790
O	 0.7500	 0.2430
P	 0.7500	 0.0870
Q	 0.8210	 0.2010
R	 0.6070	 0.1740
S	 0.8930	 0.2630
T	 0.8570	 0.3360
U	 0.7500	 0.1400
V	 0.8210	 0.3010
W	 0.7860	 0.0890
X	 0.6790	 0.3070
Y	 0.8570	 0.2200
Z	 0.9640	 0.2980

