



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:36 PM UTC

PDB ID : 8CYB / pdb_00008cyb
EMDB ID : EMD-27073
Title : SARS-CoV-2 Spike protein in complex with a pan-sarbecovirus nanobody 1-8
Authors : Huang, W.; Taylor, D.
Deposited on : 2022-05-23
Resolution : 2.70 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:

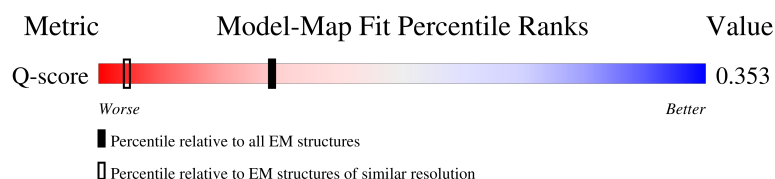
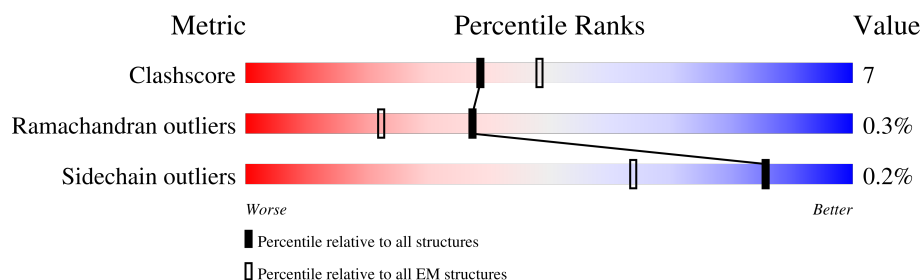
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.70 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	10327 (2.20 - 3.20)

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	1273	
1	B	1273	
1	C	1273	
2	D	127	

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Mol	Chain	Length	Quality of chain
3	E	2	100%
3	K	2	50%
3	S	2	50%
3	T	2	100%
4	F	5	60%
4	G	5	20%
4	H	5	80%
4	J	5	20%
4	M	5	20%
4	O	5	80%
4	V	5	20%
5	I	6	33%
6	L	3	33%
6	P	3	67%
6	Q	3	100%
6	R	3	67%
6	U	3	100%
6	Y	3	67%
6	Z	3	33%
7	N	4	25%
8	W	4	50%
9	X	3	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NAG	H	1	-	-	X	-
4	BMA	M	3	-	-	X	-
6	NAG	R	1	-	-	X	-
7	NAG	N	2	-	-	X	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 54126 atoms, of which 25897 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	1102	Total	C	H	N	O	S	0	0
			16912	5471	8326	1435	1641	39		
1	B	1102	Total	C	H	N	O	S	0	0
			16923	5473	8333	1436	1642	39		
1	C	1102	Total	C	H	N	O	S	0	0
			16900	5471	8313	1436	1641	39		

There are 6 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called pan-sarbecovirus nanobody 1-8.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	D	126	Total	C	H	N	O	S	0	0
			1913	615	925	172	197	4		

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



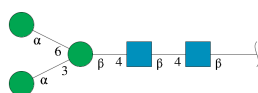
Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	2	Total	C	N	O	0	0
			28	16	2	10		

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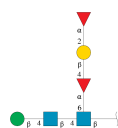
Mol	Chain	Residues	Atoms				AltConf	Trace
3	K	2	Total	C	N	O	0	0
			28	16	2	10		
3	S	2	Total	C	N	O	0	0
			28	16	2	10		
3	T	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



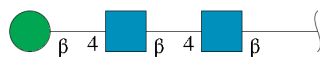
Mol	Chain	Residues	Atoms				AltConf	Trace
4	F	5	Total	C	N	O	0	0
			61	34	2	25		
4	G	5	Total	C	N	O	0	0
			61	34	2	25		
4	H	5	Total	C	N	O	0	0
			61	34	2	25		
4	J	5	Total	C	N	O	0	0
			61	34	2	25		
4	M	5	Total	C	N	O	0	0
			61	34	2	25		
4	O	5	Total	C	N	O	0	0
			61	34	2	25		
4	V	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 5 is an oligosaccharide called alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-4)-alpha-L-fucopyranose-(1-6)-[beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose.



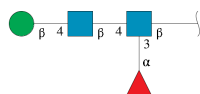
Mol	Chain	Residues	Atoms				AltConf	Trace
5	I	6	Total	C	N	O	0	0
			70	40	2	28		

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
6	L	3	Total	C	N	O	0	0
			39	22	2	15		
6	P	3	Total	C	N	O	0	0
			39	22	2	15		
6	Q	3	Total	C	N	O	0	0
			39	22	2	15		
6	R	3	Total	C	N	O	0	0
			39	22	2	15		
6	U	3	Total	C	N	O	0	0
			39	22	2	15		
6	Y	3	Total	C	N	O	0	0
			39	22	2	15		
6	Z	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 7 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose.



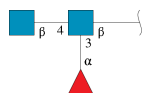
Mol	Chain	Residues	Atoms				AltConf	Trace
7	N	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



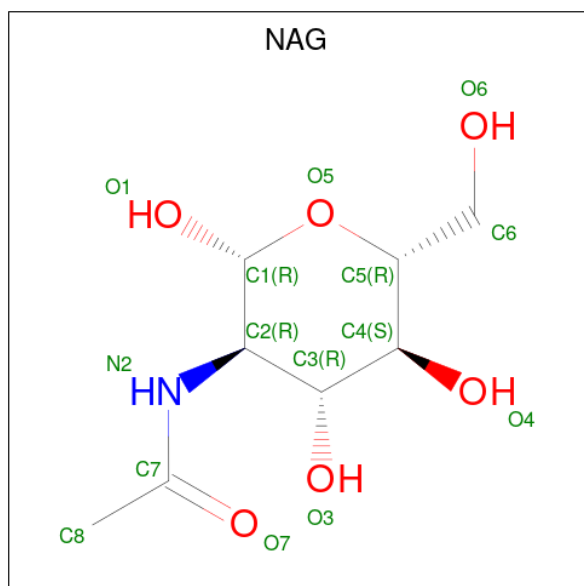
Mol	Chain	Residues	Atoms				AltConf	Trace
8	W	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 9 is an oligosaccharide called alpha-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
9	X	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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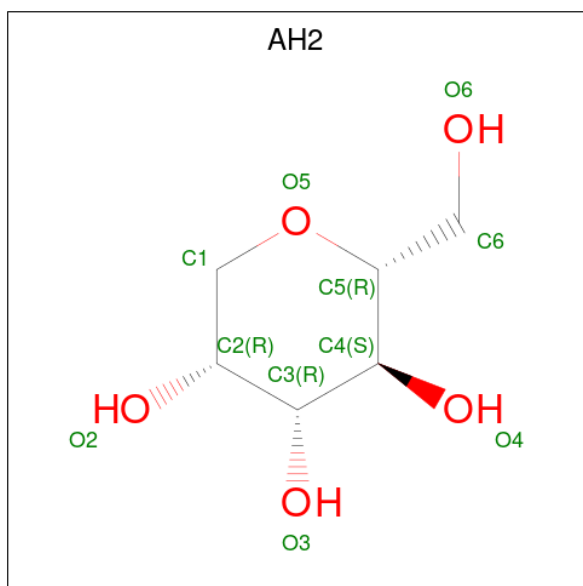
Mol	Chain	Residues	Atoms				AltConf
10	A	1	Total 14	C 8	N 1	O 5	0
10	A	1	Total 14	C 8	N 1	O 5	0
10	A	1	Total 14	C 8	N 1	O 5	0
10	A	1	Total 14	C 8	N 1	O 5	0
10	A	1	Total 14	C 8	N 1	O 5	0
10	A	1	Total 14	C 8	N 1	O 5	0
10	A	1	Total 14	C 8	N 1	O 5	0
10	B	1	Total 14	C 8	N 1	O 5	0
10	B	1	Total 14	C 8	N 1	O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

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

- Molecule 11 is 1-deoxy-alpha-D-mannopyranose (CCD ID: AH2) (formula: C₆H₁₂O₅).

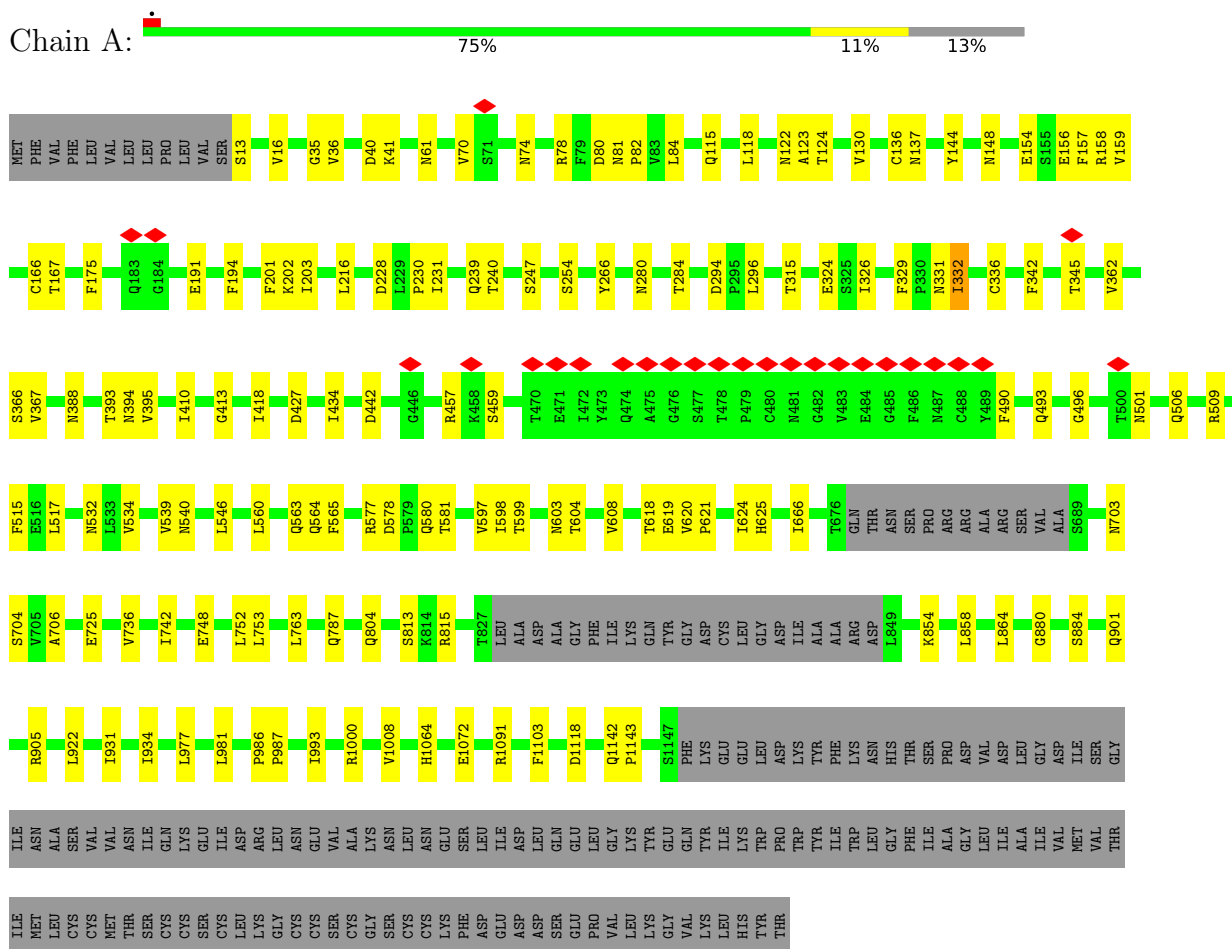


Mol	Chain	Residues	Atoms			AltConf
11	A	1	Total	C	O	0
			11	6	5	

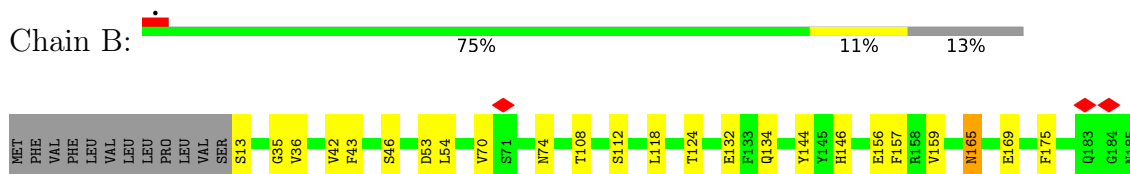
3 Residue-property plots

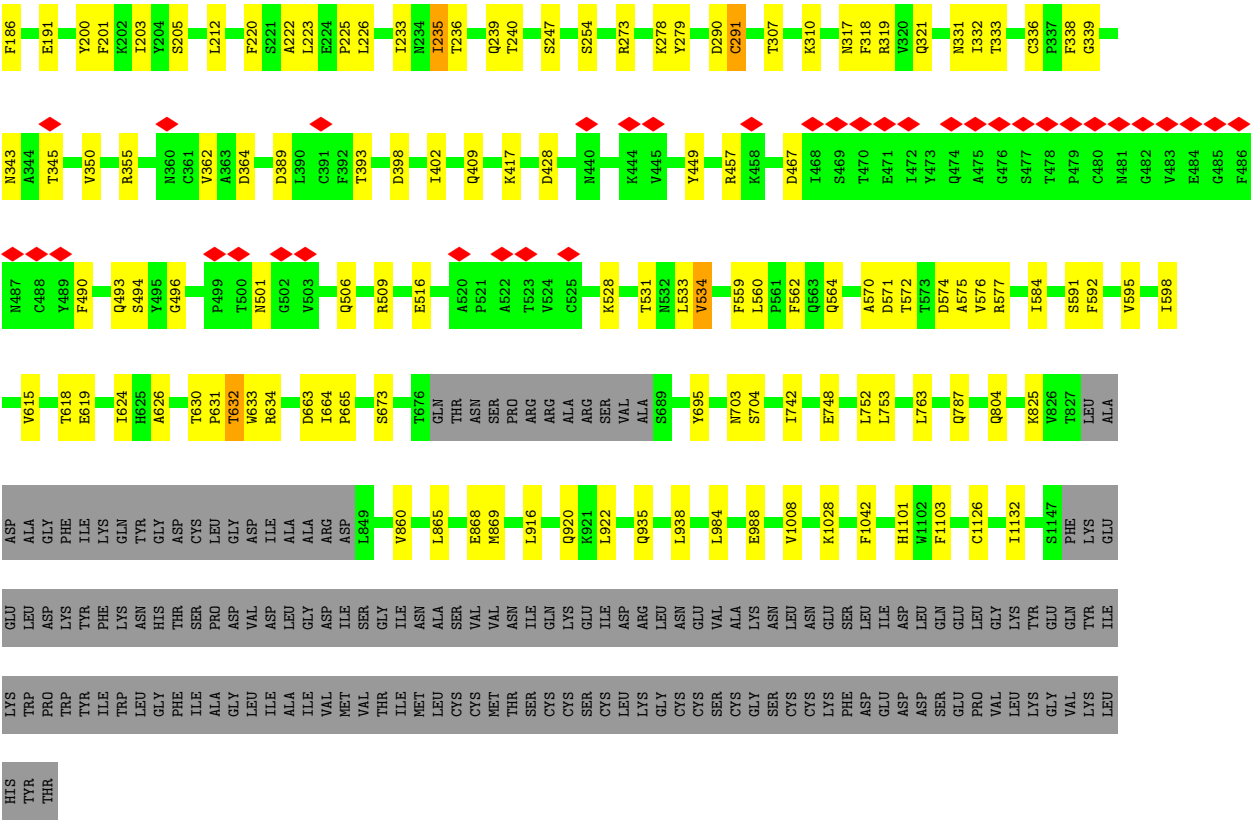
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

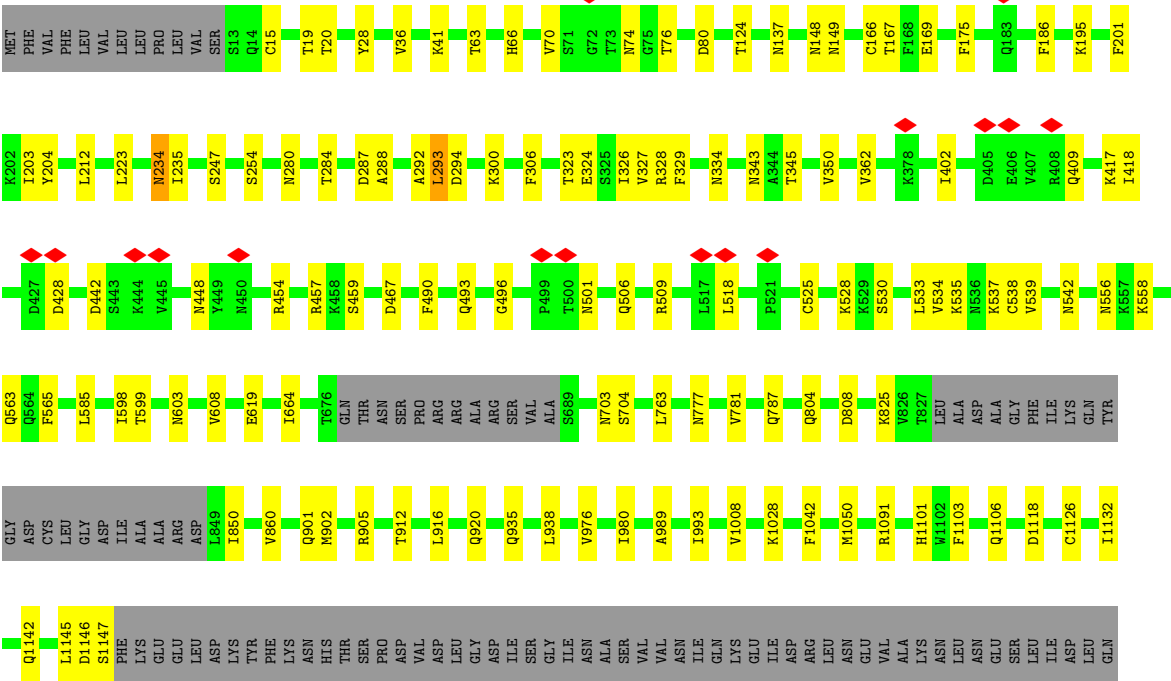
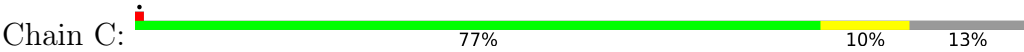


• Molecule 1: Spike glycoprotein





● Molecule 1: Spike glycoprotein



GLU LEU GLY LYS TYR GLU GLN TYR ILE LYS TRP PRO TRP TYR ILE TRP LEU GLY PHE ILE ALA GLY LEU ILE ALA ILE VAL MET THR ILE MET CYS CYS MET THR SER CYS CYS SER CYS LEU LYS GLY CYS CYS SER CYS GLY SER CYS CYS LYS PHE ASP GLU ASP ASP SER

GLU PRO VAL LEU LYS GLY VAL LYS LEU HIS TYR THR

- Molecule 2: pan-sarbecovirus nanobody 1-8

Chain D: 18% 85% 14%

H15 L27 V28 Q29 T30 G31 G32 R43 T44 R50 R54 R55 A56 P57 G58 K59 E60 R61 E62 E68 V69 N70 S71 E72 N73 A77 N78 S79 V80 R88 D89 N90 A91 V95 S101 L102 K103 A104 E105 C112 R116 T123 R124 A125 S126 S140 SER

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 100%

NAG1
NAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K: 50% 50%

NAG1
NAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S: 50% 50%

NAG1
NAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T: 100%

NAG1
NAG2

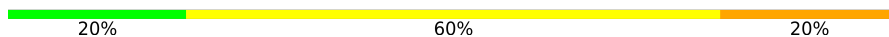
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 60% 40%



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



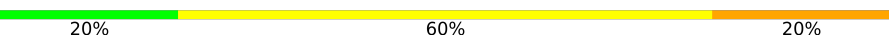
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:

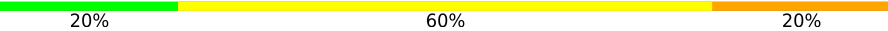


- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

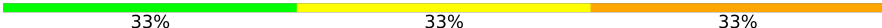


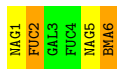
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:  20% 60% 20%



- Molecule 5: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-4)-alpha-L-fucopyranose-(1-6)-[beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  33% 33% 33%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  33% 67%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  67% 33%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  100%

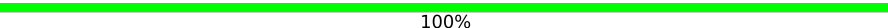


- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:  67% 33%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:  100%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y: 67% 33%



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z: 33% 33% 33%



- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N: 25% 75%



- Molecule 8: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W: 50% 50%



- Molecule 9: alpha-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X: 100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4210888	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 ($e^-/\text{\AA}^2$)	31.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.051	Depositor
Minimum map value	-0.770	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	425.28, 425.28, 425.28	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.329, 1.329, 1.329	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: FUC, NAG, AH2, GAL, MAN, BMA

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	0.09	0/8789	0.24	0/11972
1	B	0.08	0/8793	0.24	0/11977
1	C	0.09	0/8790	0.25	0/11972
2	D	0.07	0/1009	0.22	0/1365
All	All	0.09	0/27381	0.24	0/37286

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	149	ASN	Peptide

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	8586	8326	8331	105	0
1	B	8590	8333	8339	99	0
1	C	8587	8313	8335	95	0
2	D	988	925	925	12	0
3	E	28	0	25	2	0
3	K	28	0	25	4	0
3	S	28	0	25	8	0
3	T	28	0	25	1	0
4	F	61	0	52	9	0
4	G	61	0	52	2	0
4	H	61	0	52	14	0
4	J	61	0	52	2	0
4	M	61	0	52	10	0
4	O	61	0	52	5	0
4	V	61	0	52	3	0
5	I	70	0	61	6	0
6	L	39	0	34	1	0
6	P	39	0	34	1	0
6	Q	39	0	34	0	0
6	R	39	0	34	10	0
6	U	39	0	34	0	0
6	Y	39	0	34	3	0
6	Z	39	0	34	4	0
7	N	49	0	43	7	0
8	W	50	0	43	3	0
9	X	38	0	34	6	0
10	A	154	0	143	8	0
10	B	154	0	143	14	0
10	C	140	0	130	11	0
11	A	11	0	0	0	0
All	All	28229	25897	27229	403	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 403 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)
4:M:3:BMA:H4	4:M:4:MAN:H5	1.39	1.05
9:X:2:FUC:H3	9:X:3:NAG:H83	1.49	0.95
10:B:1311:NAG:H3	10:B:1311:NAG:H83	1.55	0.88
4:H:1:NAG:H83	4:H:1:NAG:H3	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R:1:NAG:H83	6:R:1:NAG:H3	1.56	0.87

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	1096/1273 (86%)	1032 (94%)	62 (6%)	2 (0%)	43	68
1	B	1096/1273 (86%)	1046 (95%)	44 (4%)	6 (0%)	24	48
1	C	1096/1273 (86%)	1033 (94%)	62 (6%)	1 (0%)	48	73
2	D	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
All	All	3412/3946 (86%)	3231 (95%)	172 (5%)	9 (0%)	37	60

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	332	ILE
1	B	534	VAL
1	C	293	LEU
1	B	291	CYS
1	B	591	SER

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	957/1112 (86%)	956 (100%)	1 (0%)	88	96
1	B	958/1112 (86%)	955 (100%)	3 (0%)	86	94
1	C	957/1112 (86%)	955 (100%)	2 (0%)	87	95
2	D	104/105 (99%)	104 (100%)	0	100	100
All	All	2976/3441 (86%)	2970 (100%)	6 (0%)	85	95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	331	ASN
1	C	234	ASN
1	C	603	ASN
1	B	165	ASN
1	A	603	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	658	ASN
1	C	74	ASN
1	C	607	GLN
1	B	919	ASN
1	C	137	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

81 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$
3	NAG	E	1	1,3	14,14,15	0.18	0	17,19,21	0.43	0
3	NAG	E	2	3	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	F	1	1,4	14,14,15	0.24	0	17,19,21	0.55	0
4	NAG	F	2	4	14,14,15	0.23	0	17,19,21	0.46	0
4	BMA	F	3	4	11,11,12	0.75	0	15,15,17	0.74	0
4	MAN	F	4	4	11,11,12	0.71	0	15,15,17	1.06	2 (13%)
4	MAN	F	5	4	11,11,12	0.62	0	15,15,17	0.95	2 (13%)
4	NAG	G	1	1,4	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	G	2	4	14,14,15	0.22	0	17,19,21	0.41	0
4	BMA	G	3	4	11,11,12	0.53	0	15,15,17	0.71	0
4	MAN	G	4	4	11,11,12	0.62	0	15,15,17	1.06	2 (13%)
4	MAN	G	5	4	11,11,12	0.62	0	15,15,17	0.95	2 (13%)
4	NAG	H	1	1,4	14,14,15	0.25	0	17,19,21	0.57	0
4	NAG	H	2	4	14,14,15	0.37	0	17,19,21	0.49	0
4	BMA	H	3	4	11,11,12	0.54	0	15,15,17	0.69	0
4	MAN	H	4	4	11,11,12	1.10	1 (9%)	15,15,17	1.53	3 (20%)
4	MAN	H	5	4	11,11,12	0.62	0	15,15,17	1.09	2 (13%)
5	NAG	I	1	5,1	14,14,15	0.29	0	17,19,21	0.46	0
5	FUC	I	2	5	10,10,11	0.91	0	14,14,16	1.16	1 (7%)
5	GAL	I	3	5	11,11,12	0.79	0	15,15,17	0.87	0
5	FUC	I	4	5	10,10,11	0.63	0	14,14,16	0.75	0
5	NAG	I	5	5	14,14,15	0.30	0	17,19,21	0.49	0
5	BMA	I	6	5	11,11,12	0.96	1 (9%)	15,15,17	0.87	1 (6%)
4	NAG	J	1	1,4	14,14,15	0.25	0	17,19,21	0.48	0
4	NAG	J	2	4	14,14,15	0.22	0	17,19,21	0.41	0
4	BMA	J	3	4	11,11,12	0.63	0	15,15,17	0.80	0
4	MAN	J	4	4	11,11,12	0.64	0	15,15,17	1.02	2 (13%)
4	MAN	J	5	4	11,11,12	0.65	0	15,15,17	0.97	2 (13%)
3	NAG	K	1	1,3	14,14,15	0.21	0	17,19,21	0.43	0
3	NAG	K	2	3	14,14,15	0.26	0	17,19,21	0.56	0
6	NAG	L	1	1,6	14,14,15	0.22	0	17,19,21	0.44	0
6	NAG	L	2	6	14,14,15	0.23	0	17,19,21	0.42	0
6	BMA	L	3	6	11,11,12	0.54	0	15,15,17	0.70	0
4	NAG	M	1	1,4	14,14,15	0.20	0	17,19,21	0.41	0
4	NAG	M	2	4	14,14,15	0.20	0	17,19,21	0.42	0
4	BMA	M	3	4	11,11,12	0.82	0	15,15,17	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	M	4	4	11,11,12	1.53	2 (18%)	15,15,17	2.10	4 (26%)
4	MAN	M	5	4	11,11,12	0.62	0	15,15,17	0.96	2 (13%)
7	NAG	N	1	1,7	14,14,15	0.26	0	17,19,21	0.54	0
7	NAG	N	2	7	14,14,15	0.41	0	17,19,21	0.61	0
7	BMA	N	3	7	11,11,12	0.54	0	15,15,17	0.72	0
7	FUC	N	4	7	10,10,11	0.63	0	14,14,16	0.77	0
4	NAG	O	1	1,4	14,14,15	0.21	0	17,19,21	0.44	0
4	NAG	O	2	4	14,14,15	0.22	0	17,19,21	0.43	0
4	BMA	O	3	4	11,11,12	0.51	0	15,15,17	0.72	0
4	MAN	O	4	4	11,11,12	0.62	0	15,15,17	1.05	2 (13%)
4	MAN	O	5	4	11,11,12	0.67	0	15,15,17	0.98	2 (13%)
6	NAG	P	1	1,6	14,14,15	0.22	0	17,19,21	0.43	0
6	NAG	P	2	6	14,14,15	0.22	0	17,19,21	0.42	0
6	BMA	P	3	6	11,11,12	0.53	0	15,15,17	0.71	0
6	NAG	Q	1	1,6	14,14,15	0.21	0	17,19,21	0.43	0
6	NAG	Q	2	6	14,14,15	0.22	0	17,19,21	0.43	0
6	BMA	Q	3	6	11,11,12	0.54	0	15,15,17	0.70	0
6	NAG	R	1	1,6	14,14,15	0.42	0	17,19,21	0.74	1 (5%)
6	NAG	R	2	6	14,14,15	0.25	0	17,19,21	0.40	0
6	BMA	R	3	6	11,11,12	0.54	0	15,15,17	0.72	0
3	NAG	S	1	1,3	14,14,15	0.26	0	17,19,21	0.55	0
3	NAG	S	2	3	14,14,15	0.30	0	17,19,21	0.91	1 (5%)
3	NAG	T	1	1,3	14,14,15	0.20	0	17,19,21	0.43	0
3	NAG	T	2	3	14,14,15	0.23	0	17,19,21	0.44	0
6	NAG	U	1	1,6	14,14,15	0.22	0	17,19,21	0.43	0
6	NAG	U	2	6	14,14,15	0.22	0	17,19,21	0.42	0
6	BMA	U	3	6	11,11,12	0.55	0	15,15,17	0.71	0
4	NAG	V	1	1,4	14,14,15	0.21	0	17,19,21	0.41	0
4	NAG	V	2	4	14,14,15	0.24	0	17,19,21	0.43	0
4	BMA	V	3	4	11,11,12	0.54	0	15,15,17	0.70	0
4	MAN	V	4	4	11,11,12	0.63	0	15,15,17	1.06	2 (13%)
4	MAN	V	5	4	11,11,12	0.62	0	15,15,17	0.96	2 (13%)
8	NAG	W	1	8,1	14,14,15	0.23	0	17,19,21	0.47	0
8	NAG	W	2	8	14,14,15	0.23	0	17,19,21	0.45	0
8	BMA	W	3	8	11,11,12	1.17	2 (18%)	15,15,17	1.22	2 (13%)
8	MAN	W	4	8	11,11,12	0.61	0	15,15,17	0.98	2 (13%)
9	NAG	X	1	1,9	14,14,15	0.23	0	17,19,21	0.54	0
9	FUC	X	2	9	10,10,11	0.64	0	14,14,16	0.76	0
9	NAG	X	3	9	14,14,15	0.38	0	17,19,21	0.50	0
6	NAG	Y	1	1,6	14,14,15	0.21	0	17,19,21	0.43	0
6	NAG	Y	2	6	14,14,15	0.22	0	17,19,21	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	BMA	Y	3	6	11,11,12	0.54	0	15,15,17	0.71	0
6	NAG	Z	1	1,6	14,14,15	0.19	0	17,19,21	0.41	0
6	NAG	Z	2	6	14,14,15	0.23	0	17,19,21	0.49	0
6	BMA	Z	3	6	11,11,12	0.97	1 (9%)	15,15,17	0.86	1 (6%)

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
3	NAG	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	6/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	1/2/19/22	1/1/1/1
4	MAN	F	5	4	-	1/2/19/22	0/1/1/1
4	NAG	G	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	BMA	G	3	4	-	2/2/19/22	0/1/1/1
4	MAN	G	4	4	-	0/2/19/22	1/1/1/1
4	MAN	G	5	4	-	1/2/19/22	0/1/1/1
4	NAG	H	1	1,4	-	6/6/23/26	0/1/1/1
4	NAG	H	2	4	-	4/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
4	MAN	H	4	4	-	1/2/19/22	0/1/1/1
4	MAN	H	5	4	-	0/2/19/22	1/1/1/1
5	NAG	I	1	5,1	-	4/6/23/26	0/1/1/1
5	FUC	I	2	5	-	-	0/1/1/1
5	GAL	I	3	5	-	0/2/19/22	0/1/1/1
5	FUC	I	4	5	-	-	0/1/1/1
5	NAG	I	5	5	-	2/6/23/26	0/1/1/1
5	BMA	I	6	5	-	1/2/19/22	0/1/1/1
4	NAG	J	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
4	BMA	J	3	4	-	2/2/19/22	0/1/1/1
4	MAN	J	4	4	-	0/2/19/22	1/1/1/1
4	MAN	J	5	4	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	K	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	K	2	3	-	4/6/23/26	0/1/1/1
6	NAG	L	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	L	2	6	-	2/6/23/26	0/1/1/1
6	BMA	L	3	6	-	0/2/19/22	0/1/1/1
4	NAG	M	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	4/6/23/26	0/1/1/1
4	BMA	M	3	4	-	0/2/19/22	0/1/1/1
4	MAN	M	4	4	-	1/2/19/22	0/1/1/1
4	MAN	M	5	4	-	0/2/19/22	0/1/1/1
7	NAG	N	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	N	2	7	-	6/6/23/26	0/1/1/1
7	BMA	N	3	7	-	0/2/19/22	0/1/1/1
7	FUC	N	4	7	-	-	0/1/1/1
4	NAG	O	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
4	BMA	O	3	4	-	2/2/19/22	0/1/1/1
4	MAN	O	4	4	-	0/2/19/22	1/1/1/1
4	MAN	O	5	4	-	1/2/19/22	0/1/1/1
6	NAG	P	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	P	2	6	-	2/6/23/26	0/1/1/1
6	BMA	P	3	6	-	0/2/19/22	0/1/1/1
6	NAG	Q	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	Q	2	6	-	0/6/23/26	0/1/1/1
6	BMA	Q	3	6	-	0/2/19/22	0/1/1/1
6	NAG	R	1	1,6	-	6/6/23/26	0/1/1/1
6	NAG	R	2	6	-	2/6/23/26	0/1/1/1
6	BMA	R	3	6	-	0/2/19/22	0/1/1/1
3	NAG	S	1	1,3	-	6/6/23/26	0/1/1/1
3	NAG	S	2	3	-	2/6/23/26	0/1/1/1
3	NAG	T	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	T	2	3	-	4/6/23/26	0/1/1/1
6	NAG	U	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	U	2	6	-	2/6/23/26	0/1/1/1
6	BMA	U	3	6	-	1/2/19/22	0/1/1/1
4	NAG	V	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	V	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	V	3	4	-	2/2/19/22	0/1/1/1
4	MAN	V	4	4	-	0/2/19/22	1/1/1/1
4	MAN	V	5	4	-	0/2/19/22	0/1/1/1
8	NAG	W	1	8,1	-	2/6/23/26	0/1/1/1
8	NAG	W	2	8	-	2/6/23/26	0/1/1/1
8	BMA	W	3	8	-	1/2/19/22	0/1/1/1
8	MAN	W	4	8	-	0/2/19/22	0/1/1/1
9	NAG	X	1	1,9	-	3/6/23/26	0/1/1/1
9	FUC	X	2	9	-	-	0/1/1/1
9	NAG	X	3	9	-	4/6/23/26	0/1/1/1
6	NAG	Y	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	Y	2	6	-	0/6/23/26	0/1/1/1
6	BMA	Y	3	6	-	0/2/19/22	0/1/1/1
6	NAG	Z	1	1,6	-	3/6/23/26	0/1/1/1
6	NAG	Z	2	6	-	3/6/23/26	0/1/1/1
6	BMA	Z	3	6	-	0/2/19/22	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	4	MAN	C1-C2	3.91	1.61	1.52
4	H	4	MAN	C1-C2	3.11	1.59	1.52
4	M	4	MAN	O5-C1	2.81	1.48	1.43
6	Z	3	BMA	C1-C2	2.58	1.58	1.52
8	W	3	BMA	C2-C3	2.55	1.56	1.52

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	4	MAN	C1-O5-C5	6.41	120.78	112.19
4	H	4	MAN	C1-O5-C5	4.44	118.13	112.19
3	S	2	NAG	C1-O5-C5	3.40	116.75	112.19
4	M	4	MAN	C1-C2-C3	3.01	114.03	109.64
4	V	4	MAN	C1-O5-C5	2.93	116.12	112.19

There are no chirality outliers.

5 of 125 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	J	2	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	V	2	NAG	C4-C5-C6-O6
6	R	1	NAG	O5-C5-C6-O6
3	T	2	NAG	C4-C5-C6-O6
4	V	2	NAG	O5-C5-C6-O6

5 of 6 ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	5	MAN	C1-C2-C3-C4-C5-O5
4	J	4	MAN	C1-C2-C3-C4-C5-O5
4	V	4	MAN	C1-C2-C3-C4-C5-O5
4	G	4	MAN	C1-C2-C3-C4-C5-O5
4	O	4	MAN	C1-C2-C3-C4-C5-O5

56 monomers are involved in 101 short contacts:

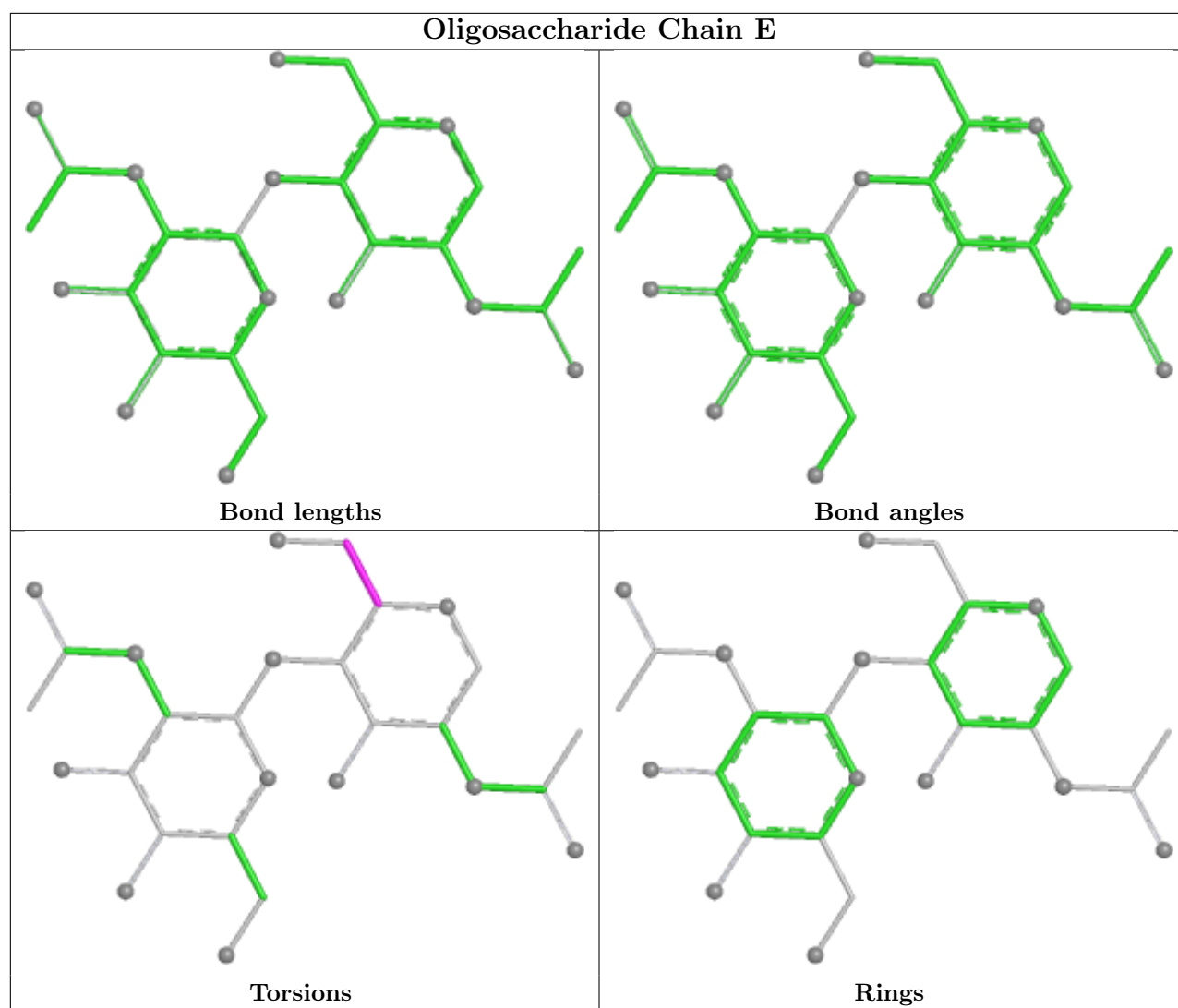
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	2	NAG	1	0
9	X	3	NAG	6	0
6	R	2	NAG	5	0
6	Z	3	BMA	4	0
4	O	1	NAG	2	0
4	J	1	NAG	1	0
4	J	3	BMA	1	0
5	I	5	NAG	4	0
4	J	5	MAN	1	0
4	V	3	BMA	3	0
6	Z	2	NAG	4	0
3	T	2	NAG	1	0
4	F	4	MAN	3	0
3	S	1	NAG	6	0
4	H	2	NAG	3	0
8	W	4	MAN	1	0
6	R	3	BMA	1	0
4	G	3	BMA	1	0
4	H	1	NAG	8	0
4	M	4	MAN	5	0
7	N	4	FUC	1	0
3	S	2	NAG	4	0
4	H	3	BMA	5	0
5	I	1	NAG	2	0
4	O	3	BMA	3	0

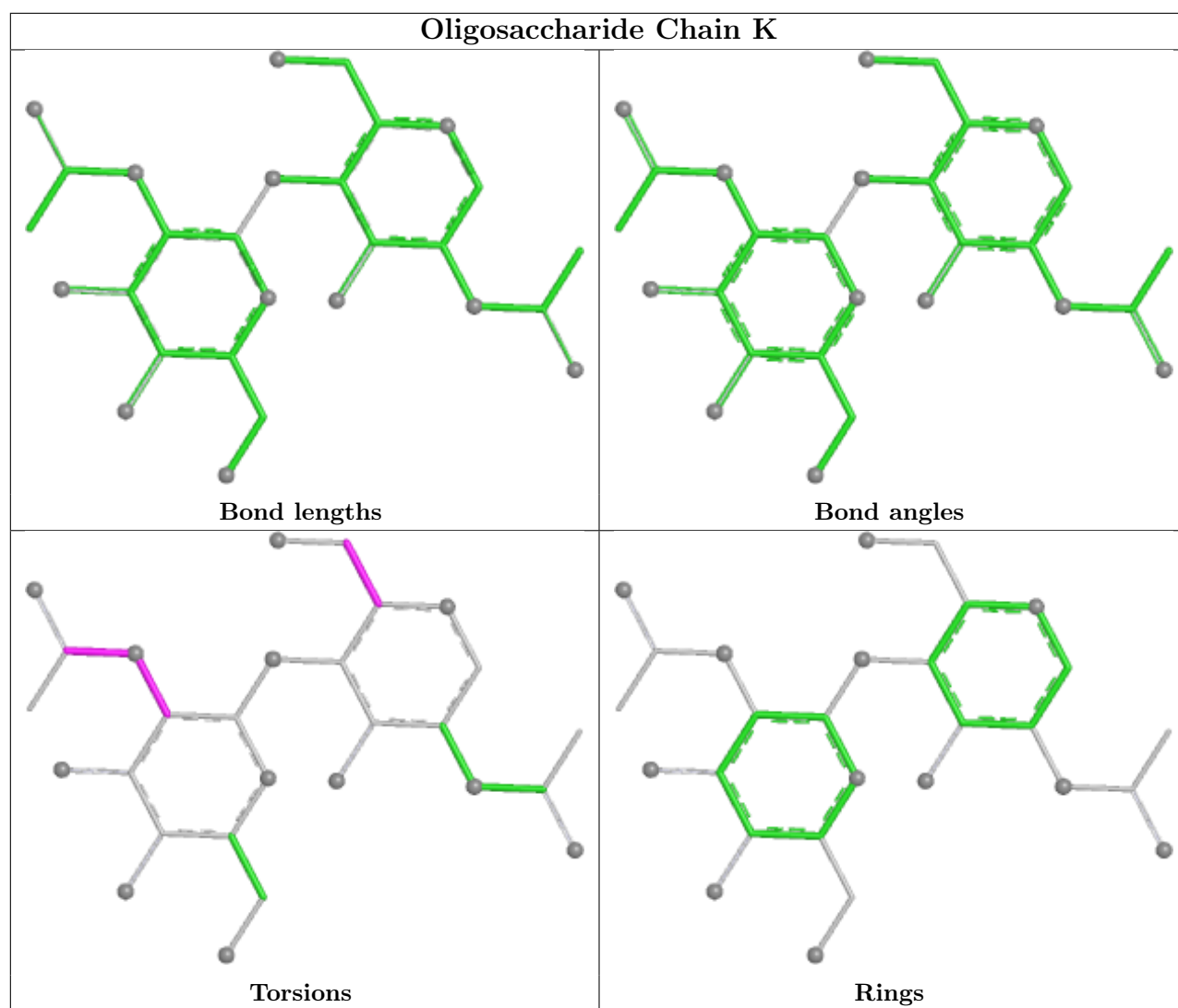
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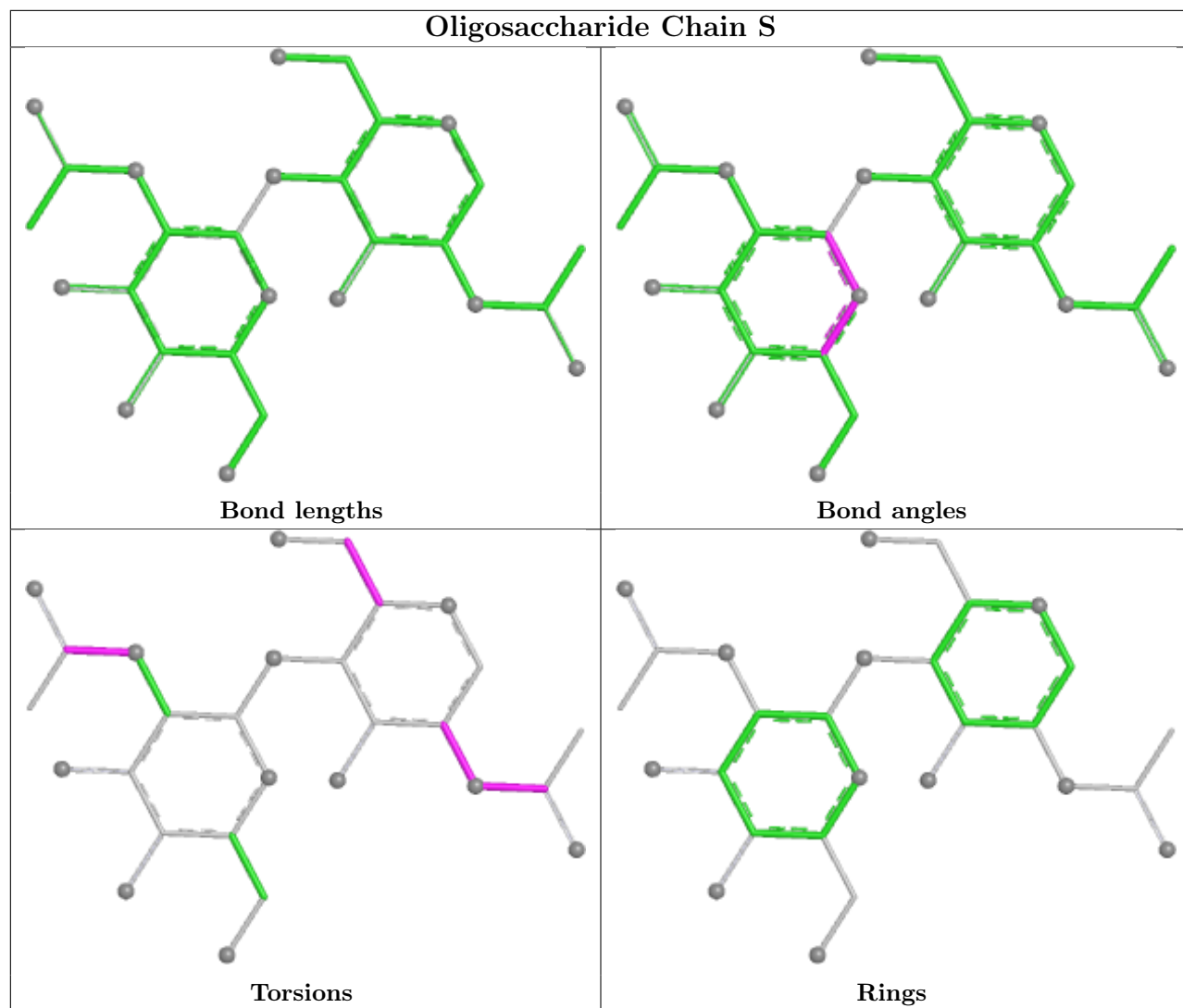
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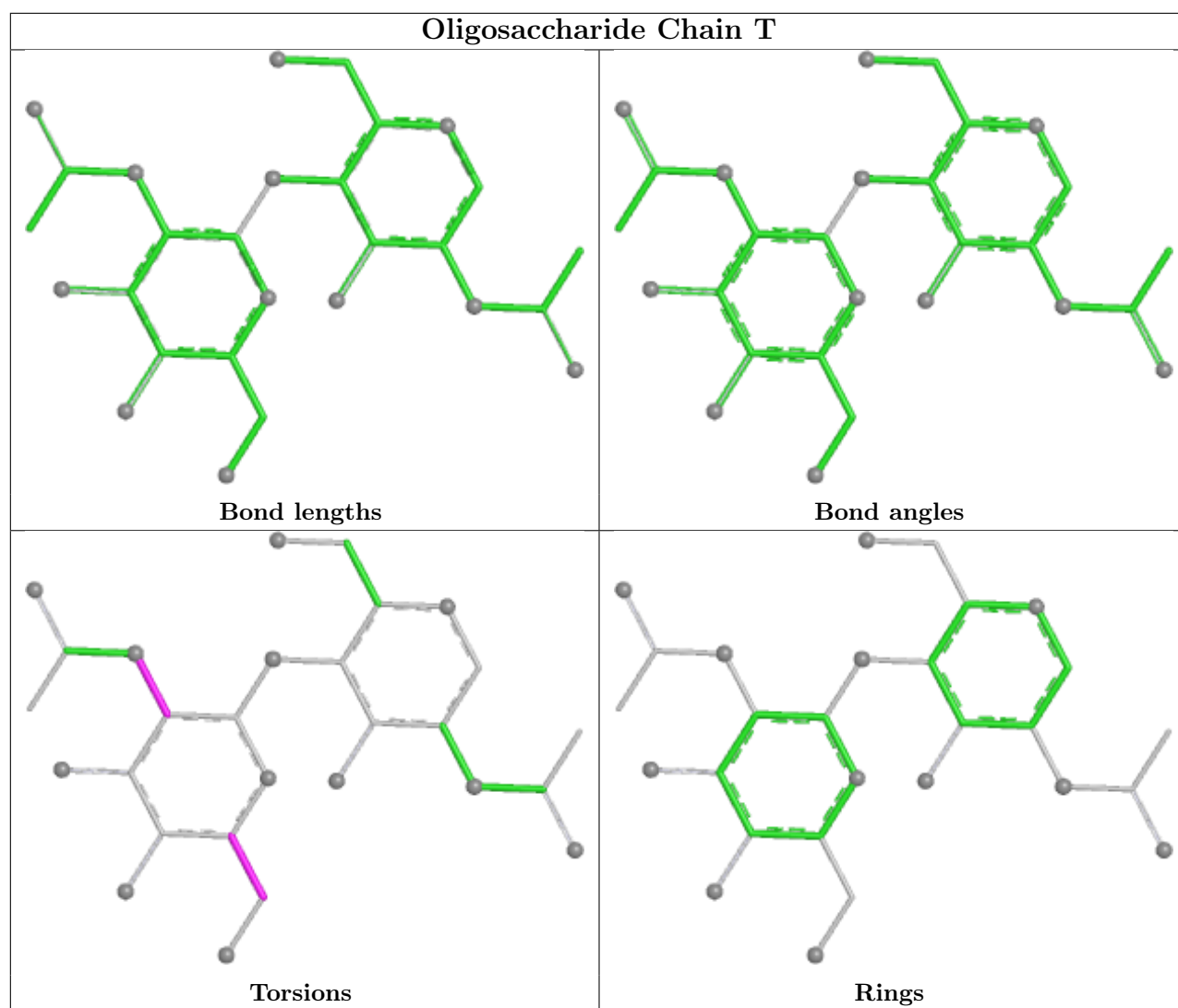
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	Y	1	NAG	3	0
6	P	2	NAG	1	0
4	F	1	NAG	5	0
4	F	2	NAG	1	0
4	F	3	BMA	4	0
3	E	2	NAG	1	0
7	N	2	NAG	7	0
4	M	3	BMA	6	0
4	V	5	MAN	2	0
3	E	1	NAG	2	0
5	I	6	BMA	4	0
4	V	2	NAG	1	0
6	L	1	NAG	1	0
8	W	2	NAG	2	0
4	H	4	MAN	5	0
4	G	5	MAN	1	0
3	T	1	NAG	1	0
4	O	2	NAG	2	0
3	K	2	NAG	4	0
6	R	1	NAG	9	0
9	X	2	FUC	2	0
5	I	2	FUC	1	0
4	O	5	MAN	2	0
9	X	1	NAG	4	0
8	W	1	NAG	1	0
8	W	3	BMA	2	0
4	F	5	MAN	1	0
4	M	1	NAG	4	0
6	L	2	NAG	1	0
7	N	1	NAG	2	0
4	M	5	MAN	1	0

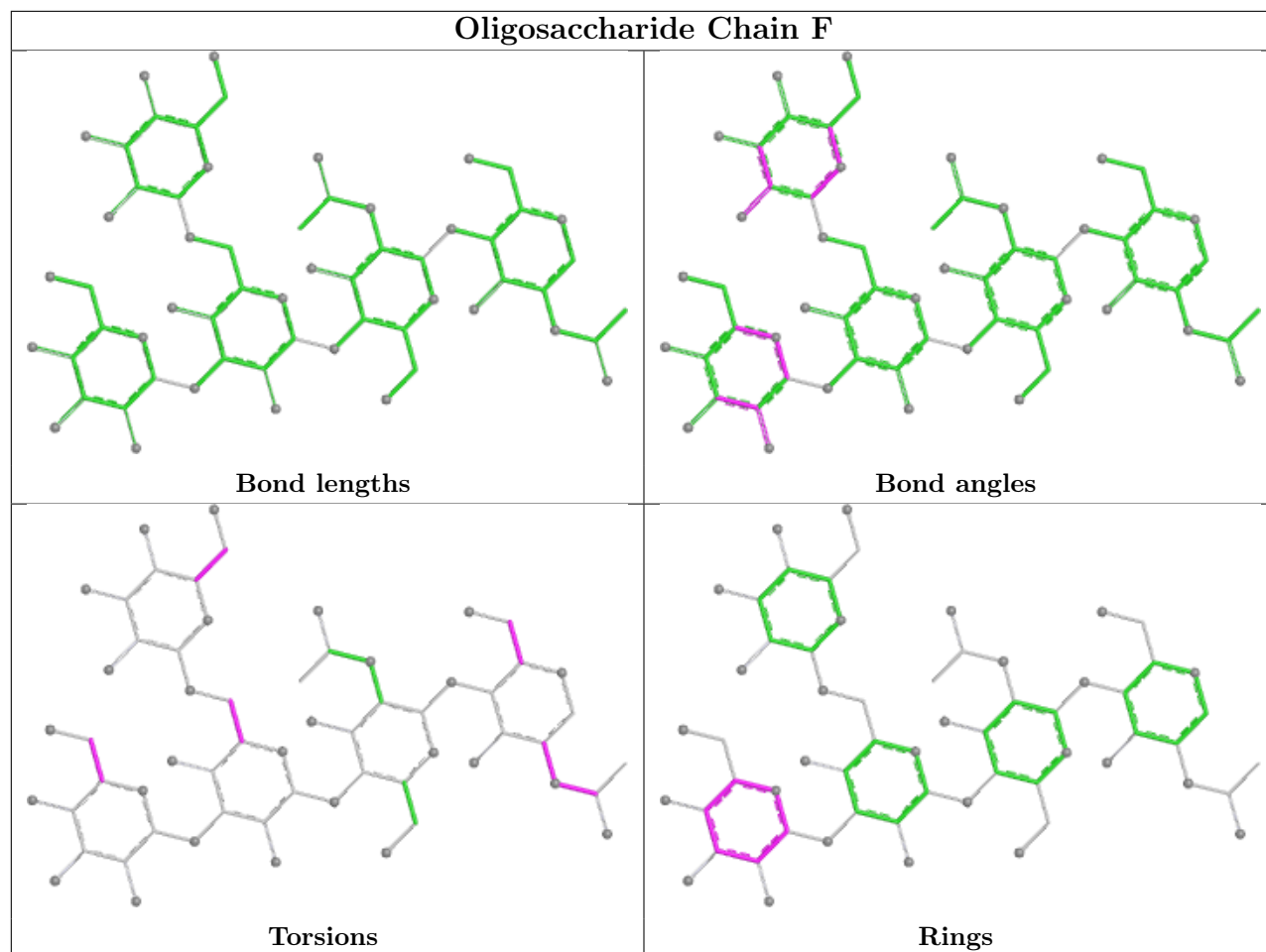
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

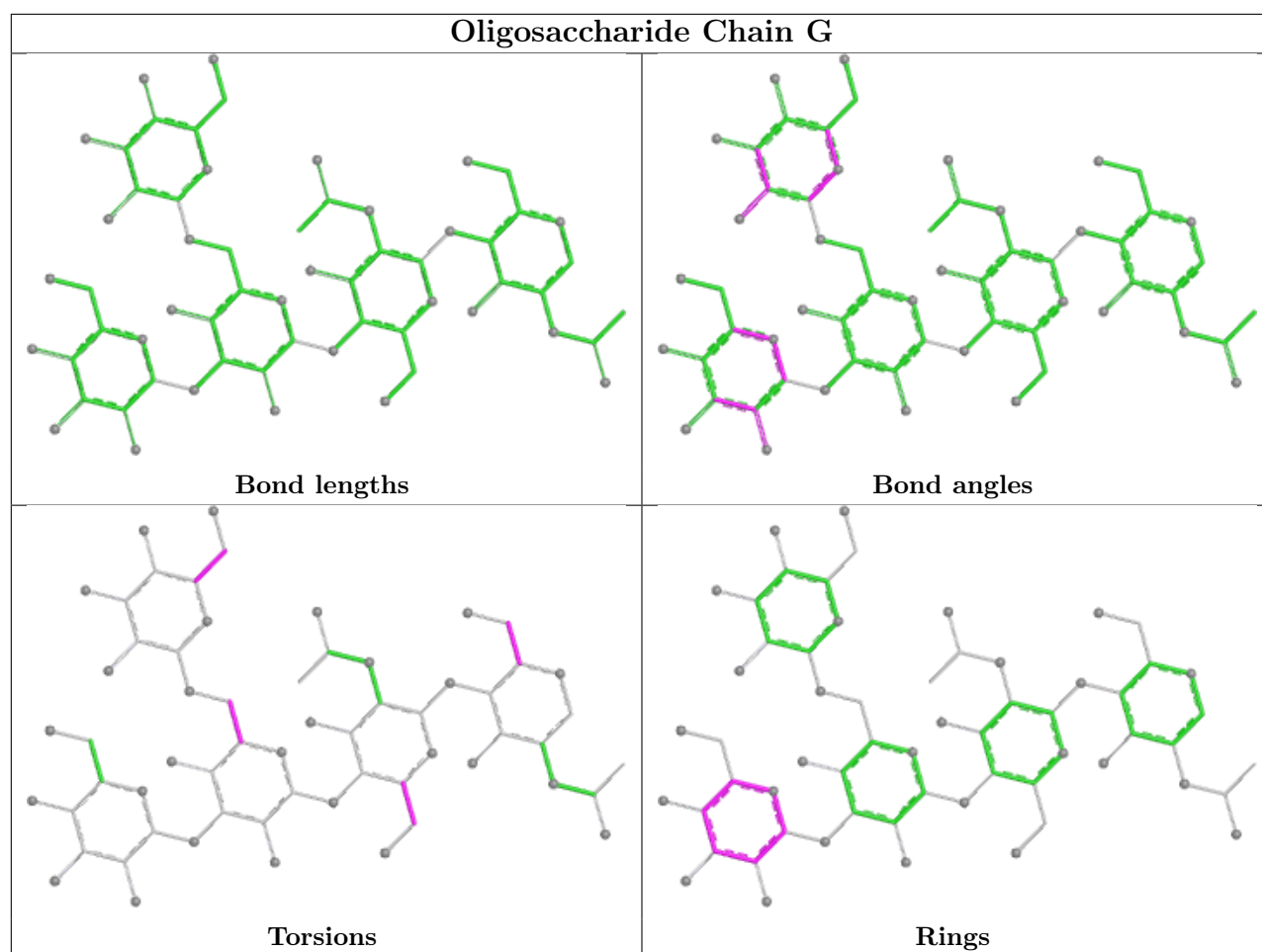


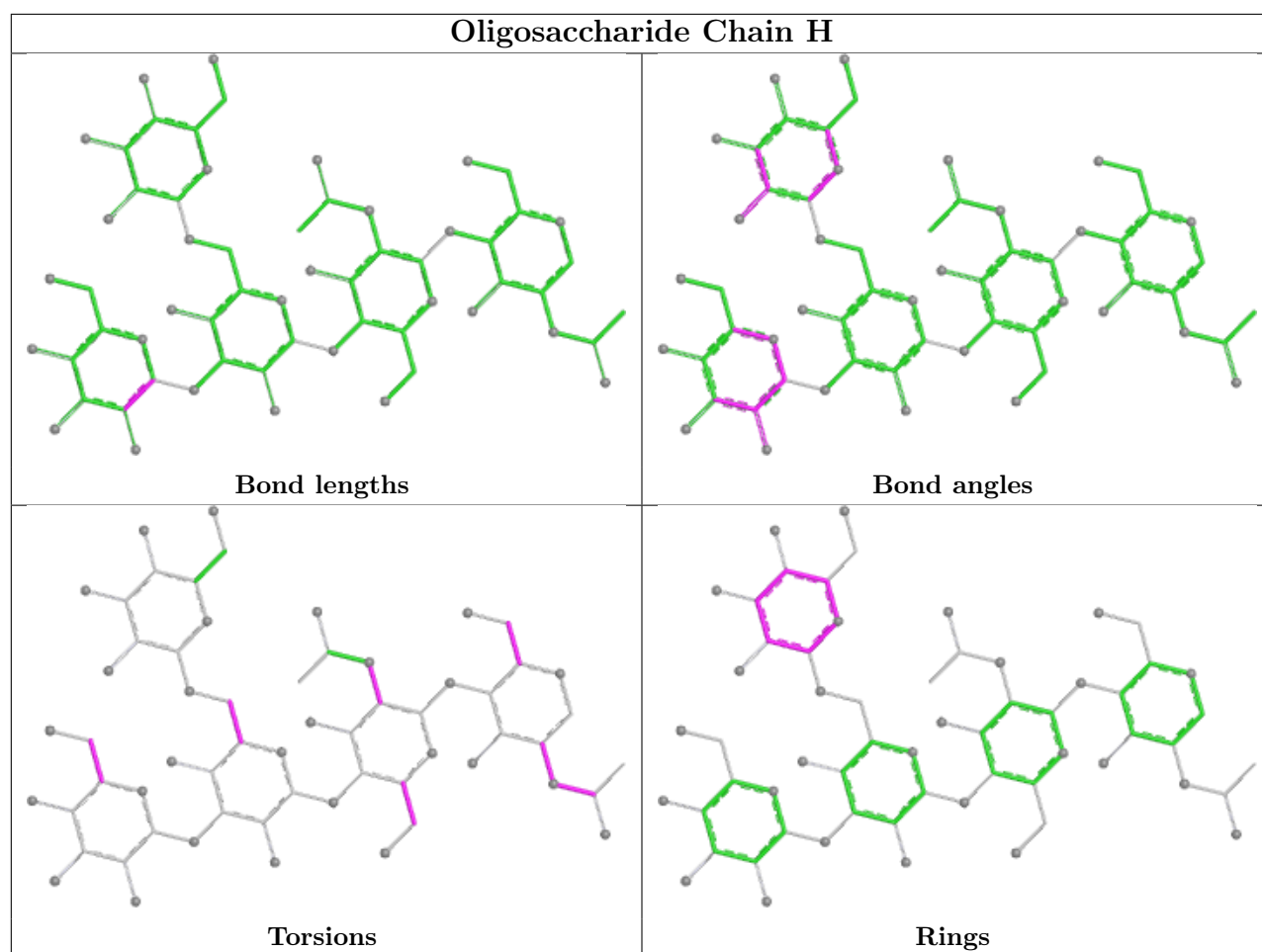


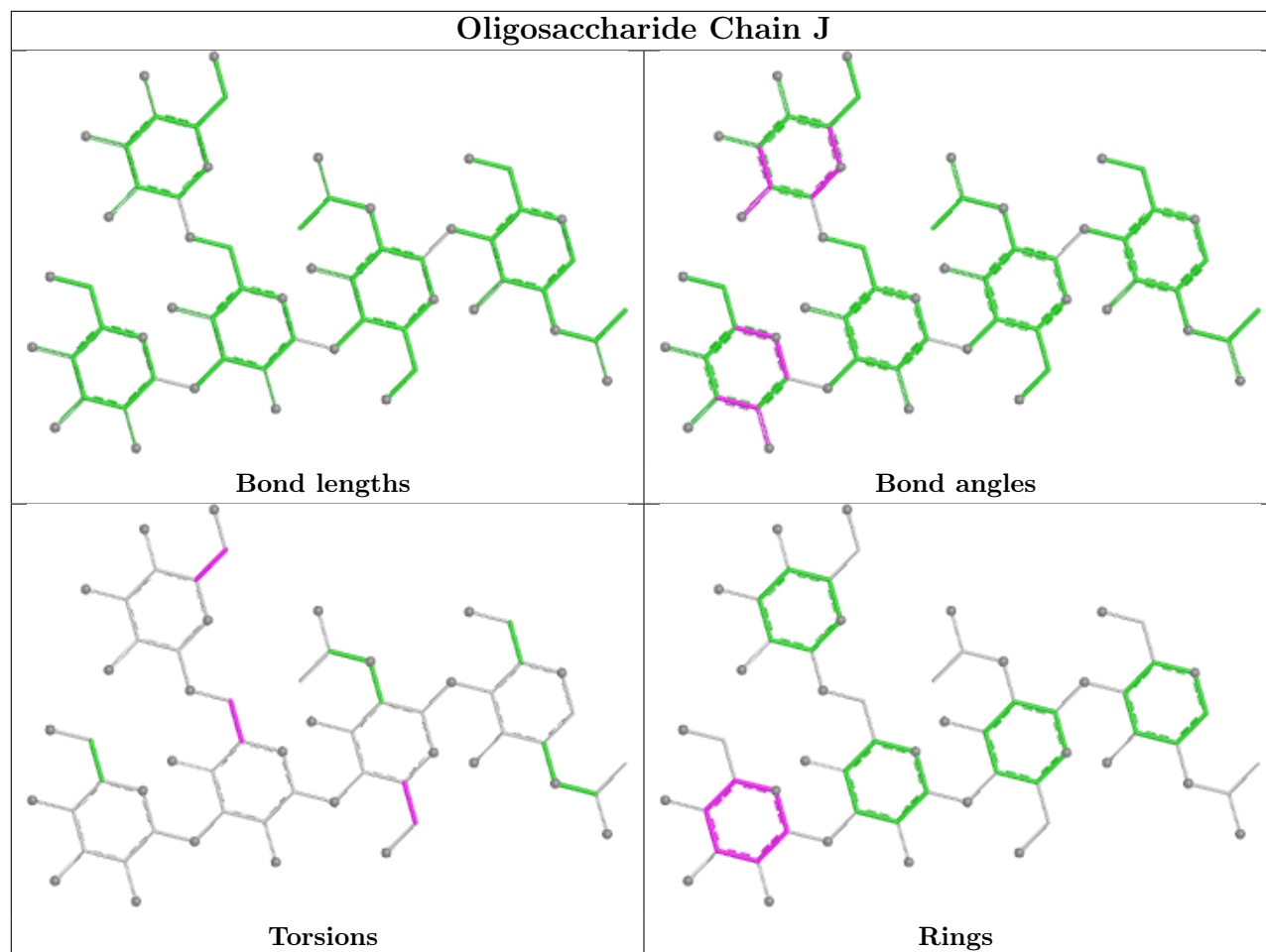


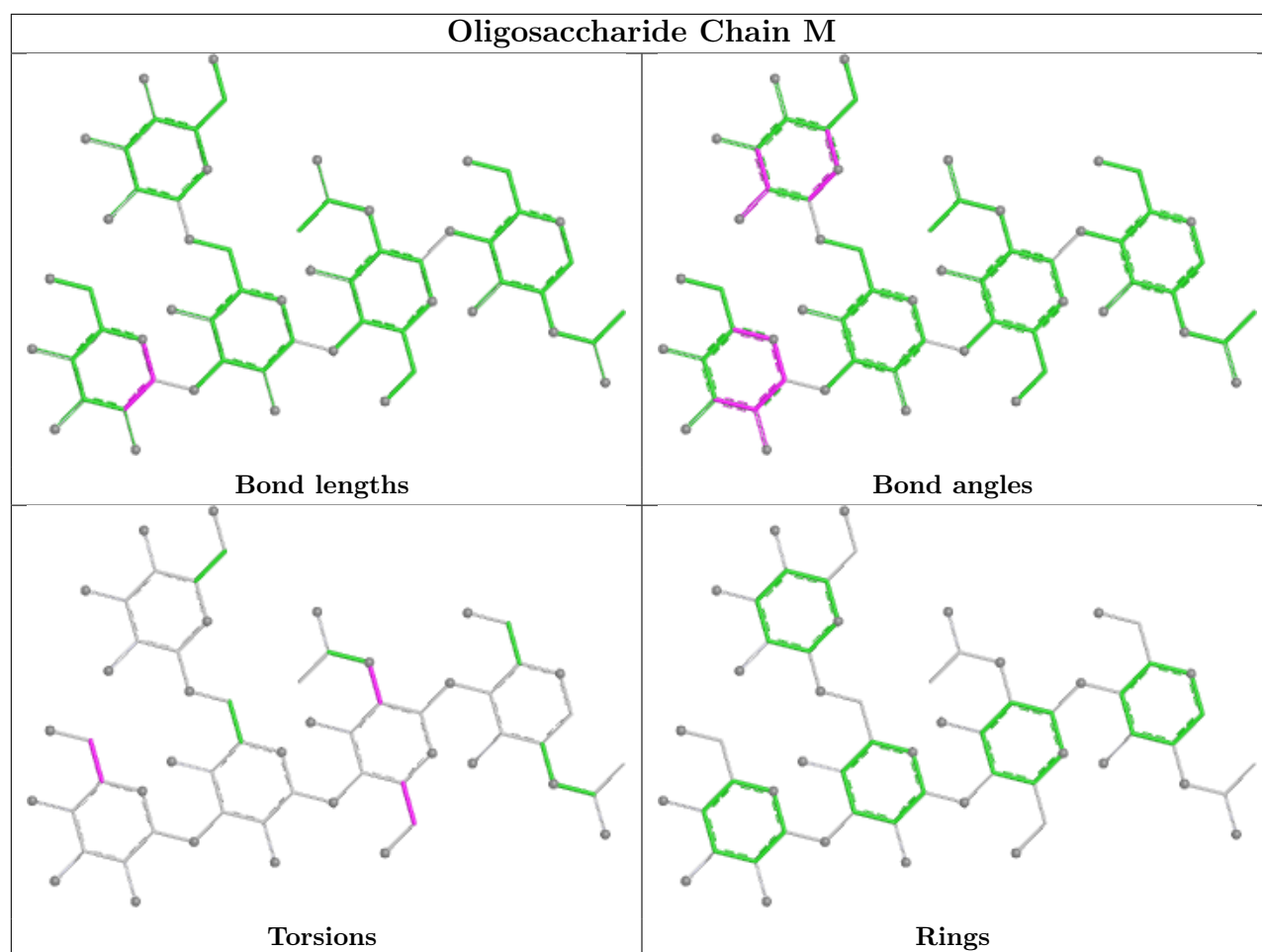


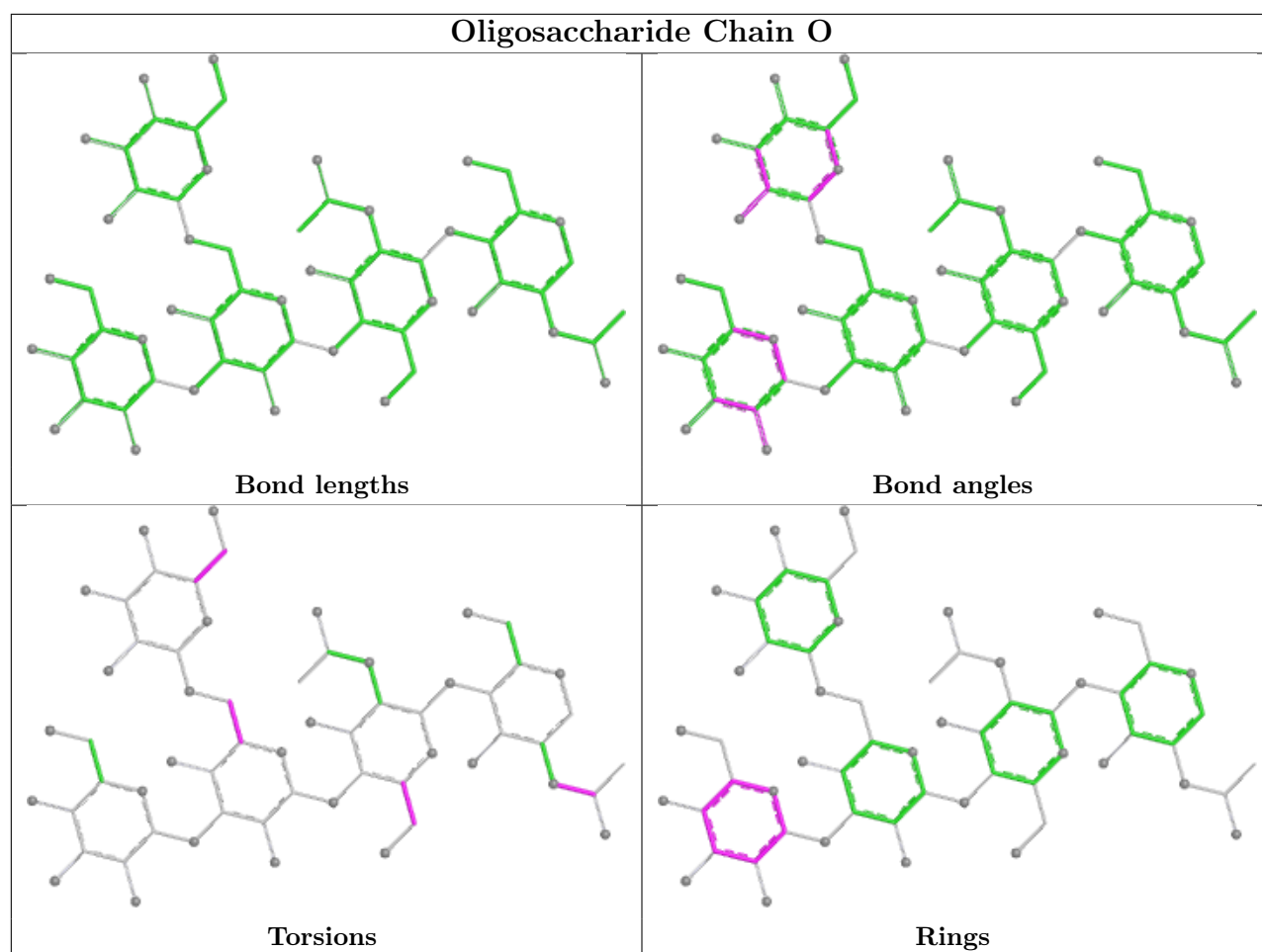


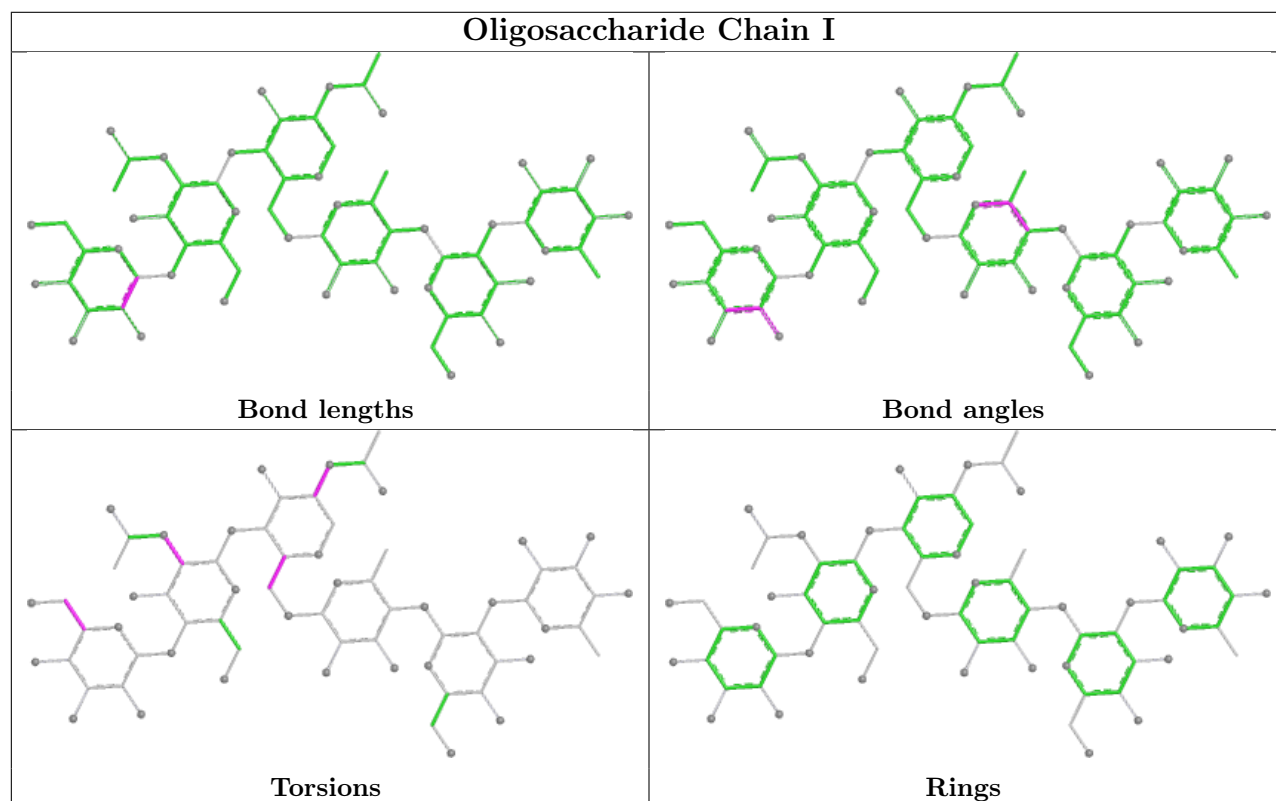
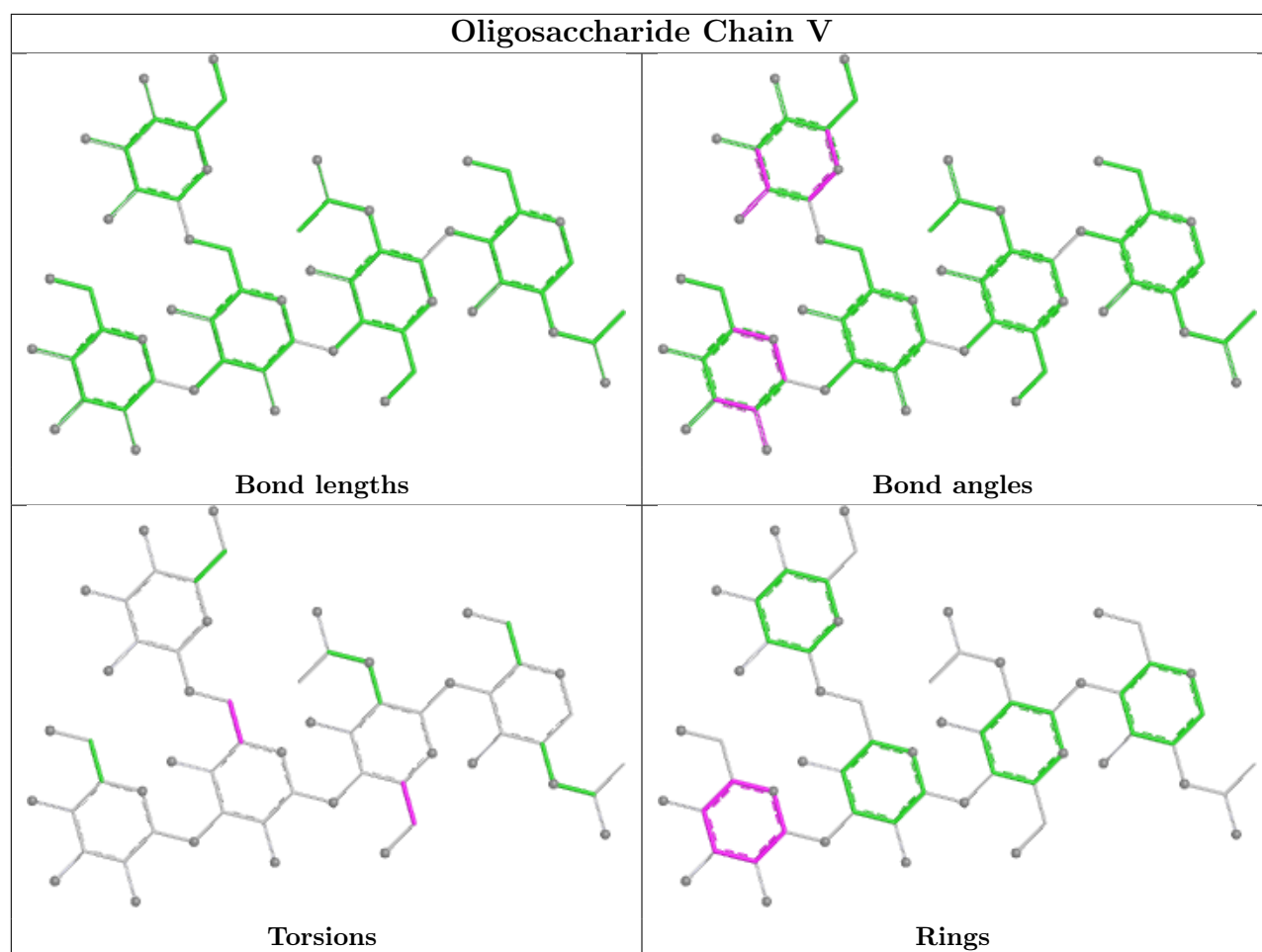


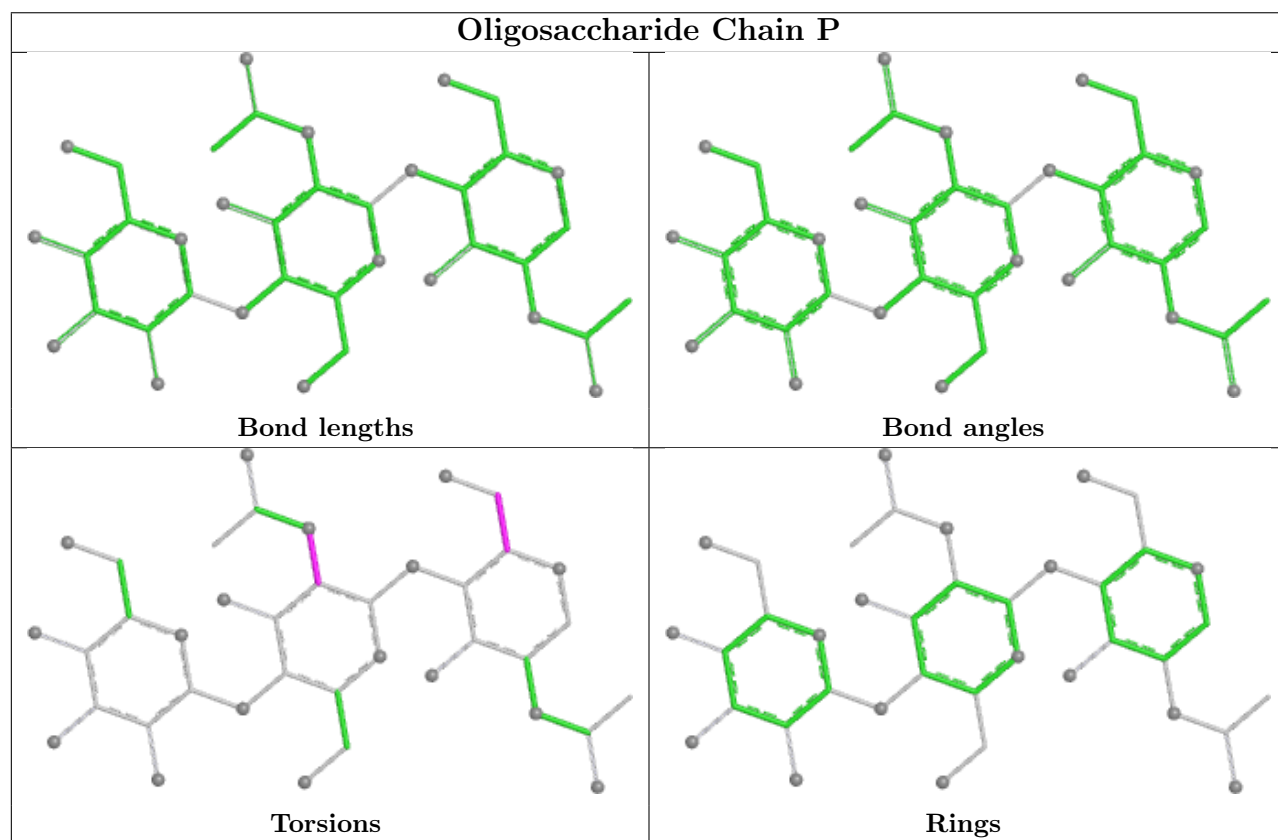
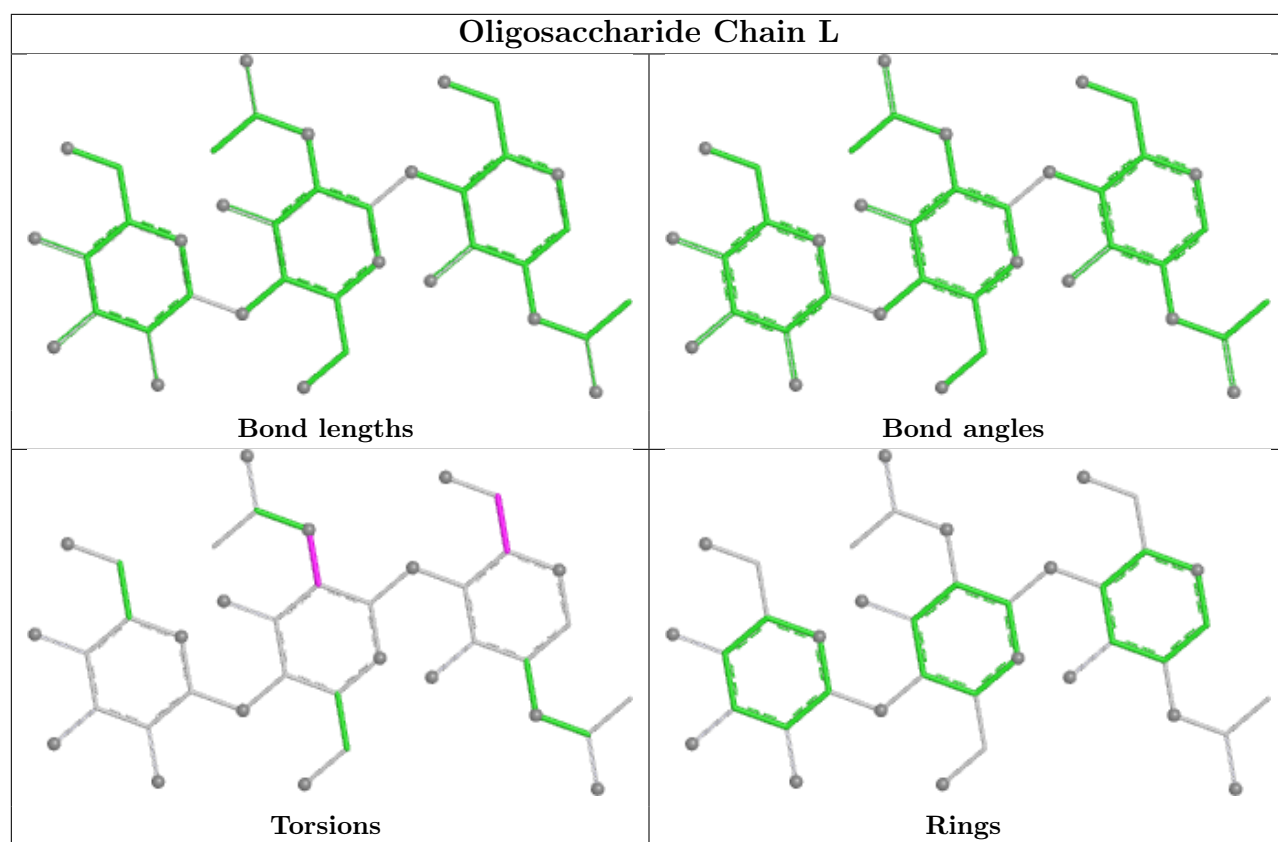


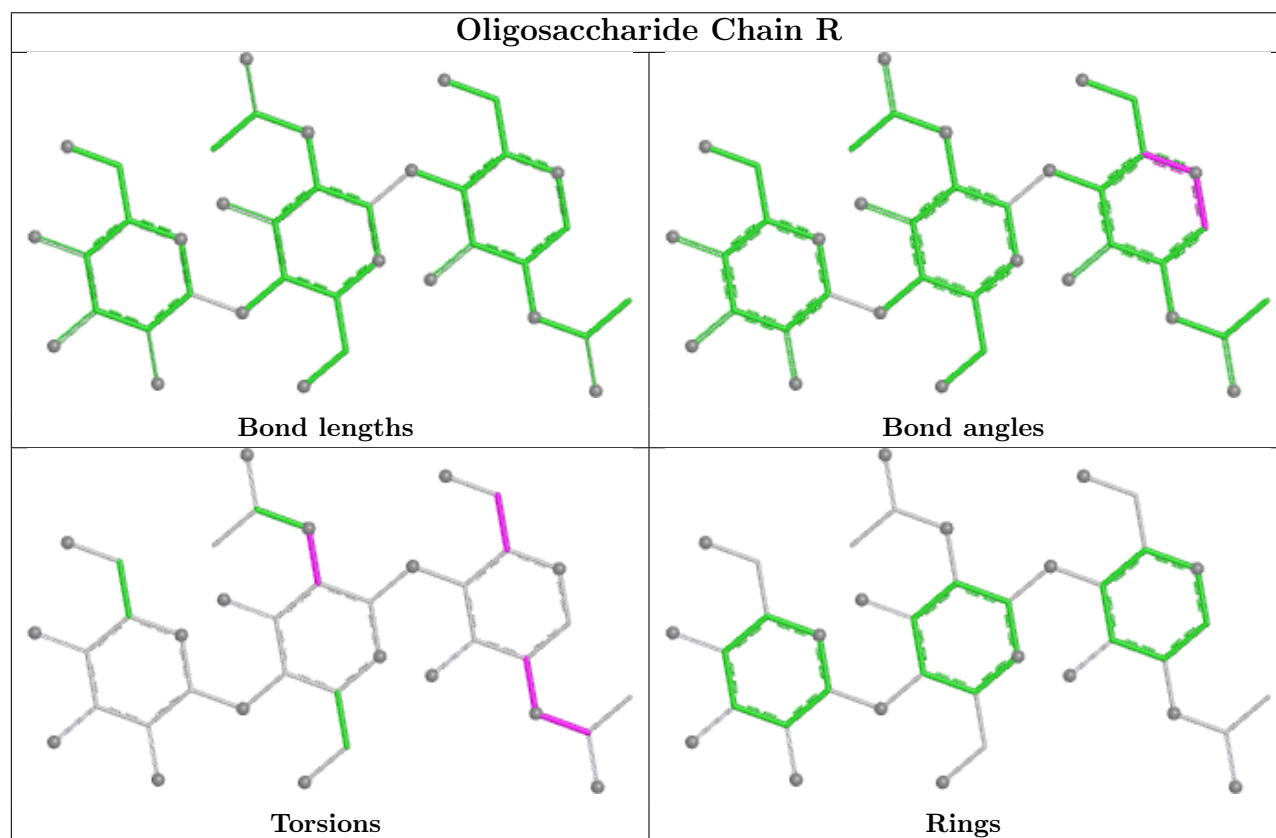
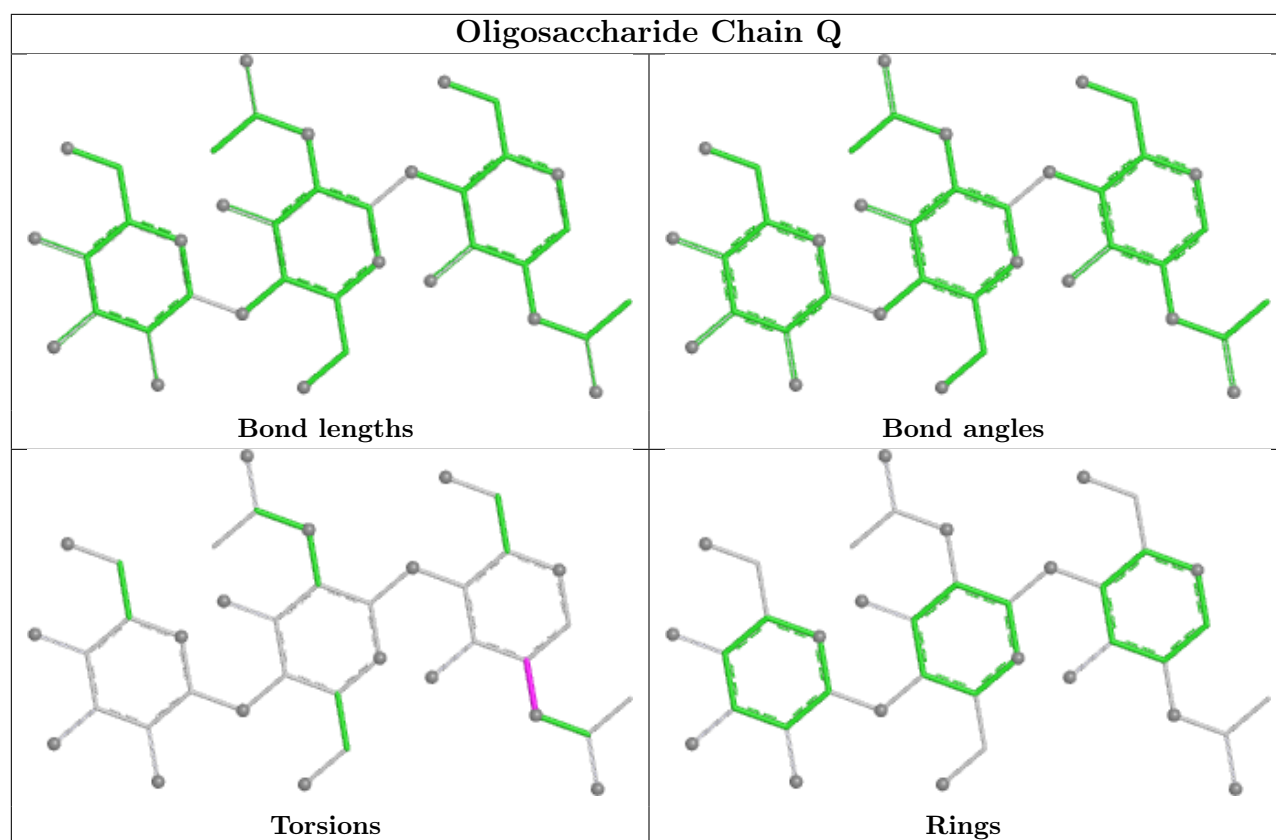


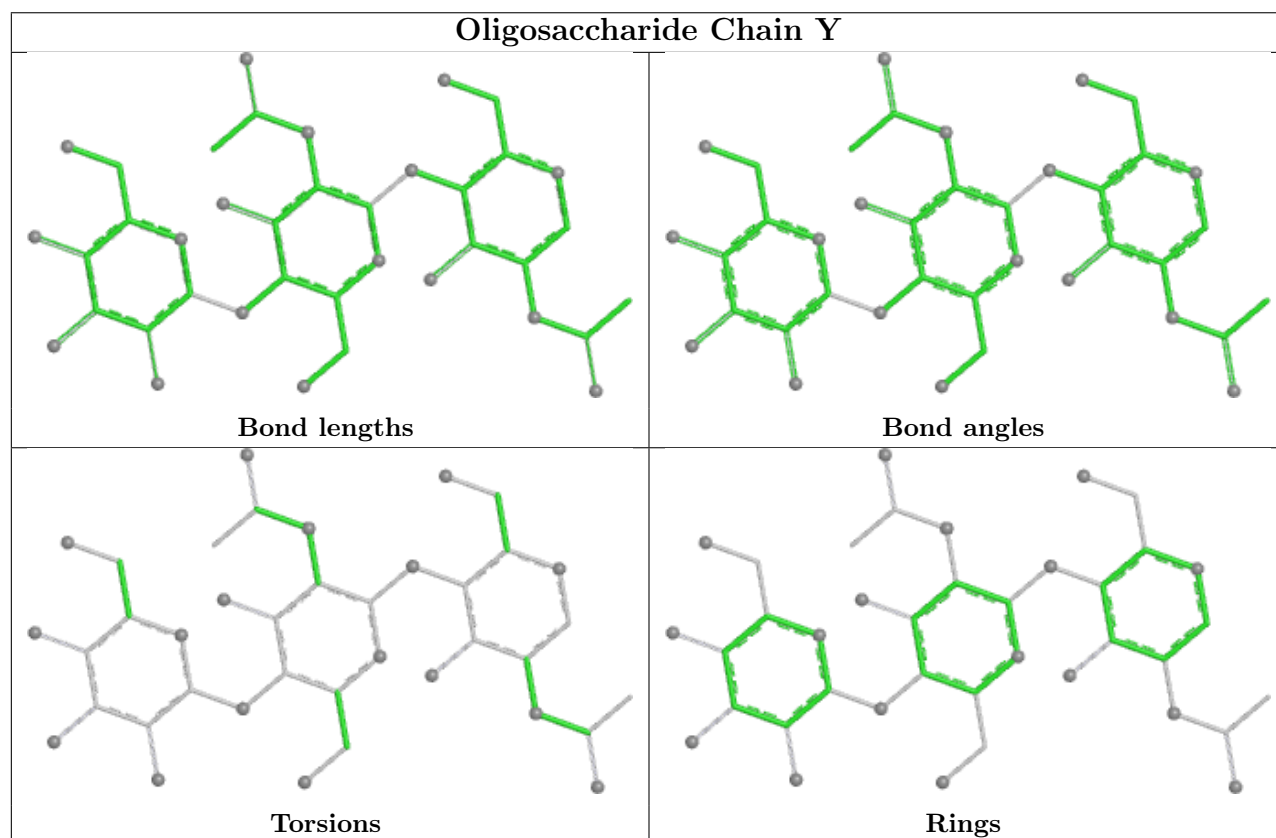
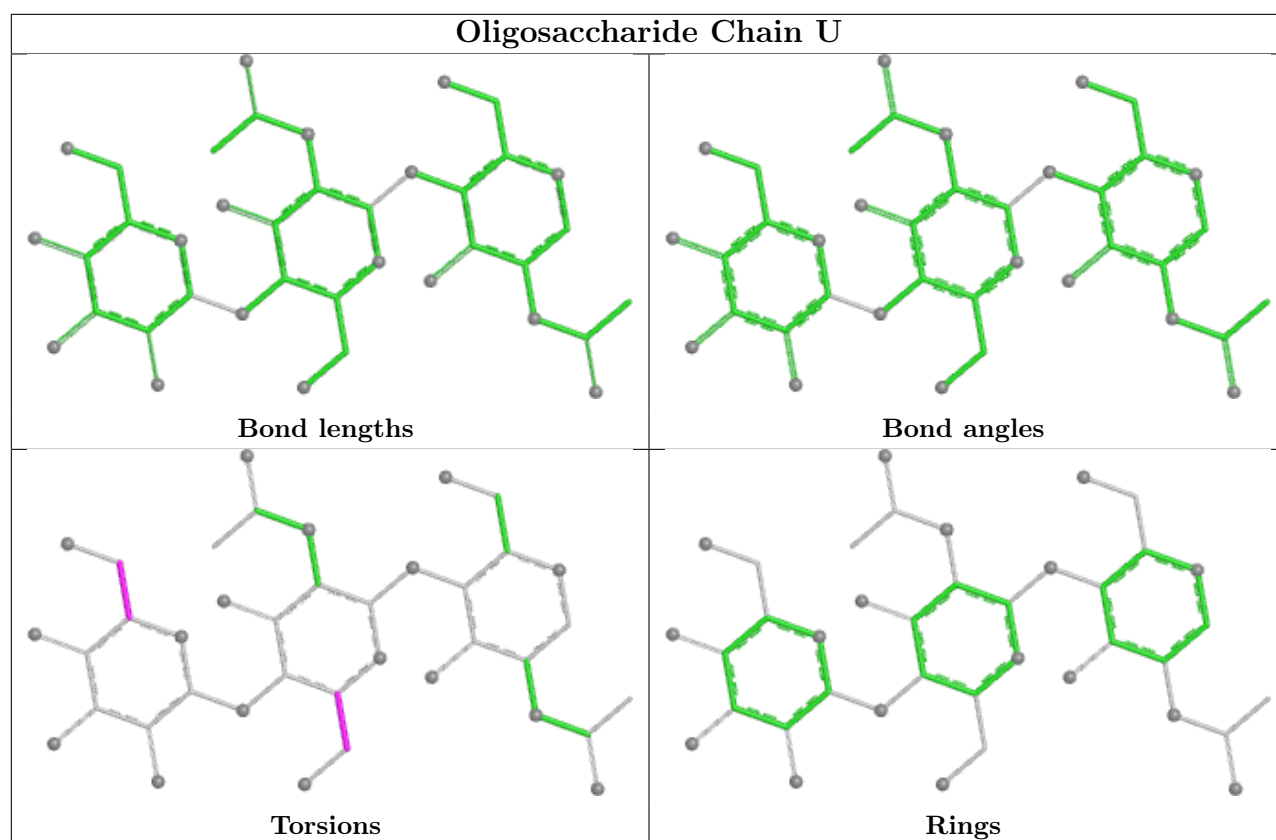


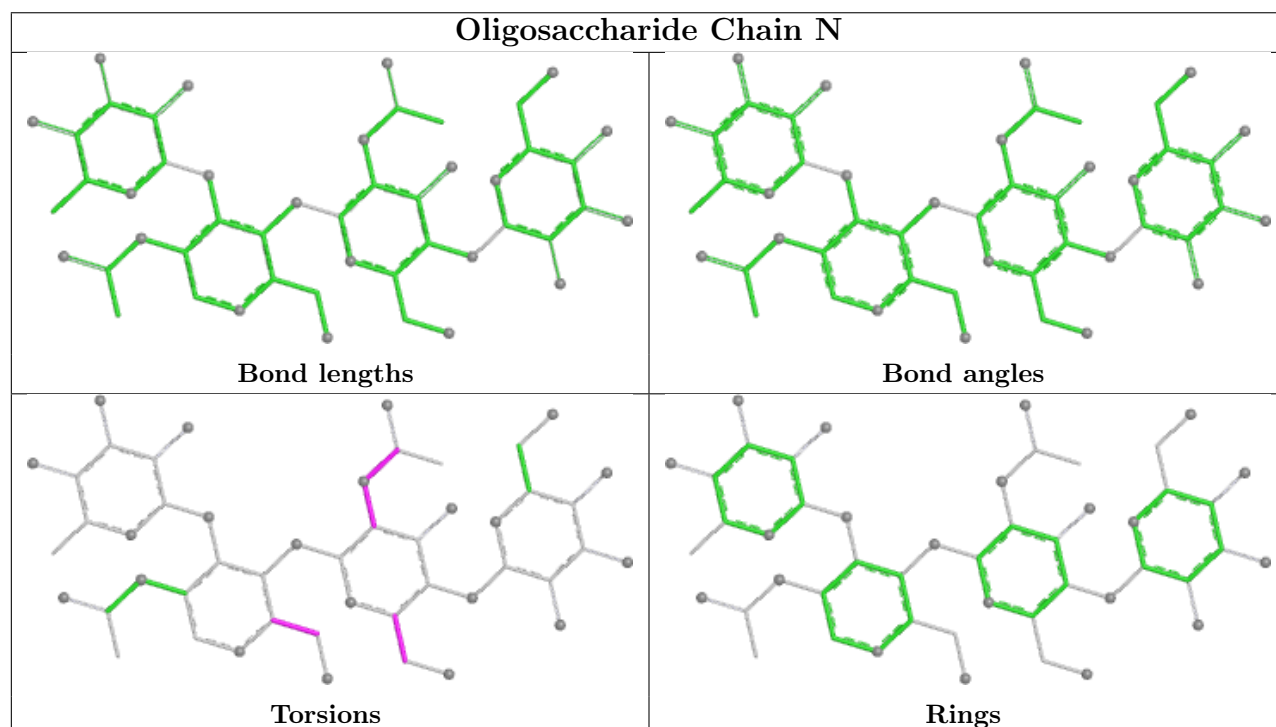
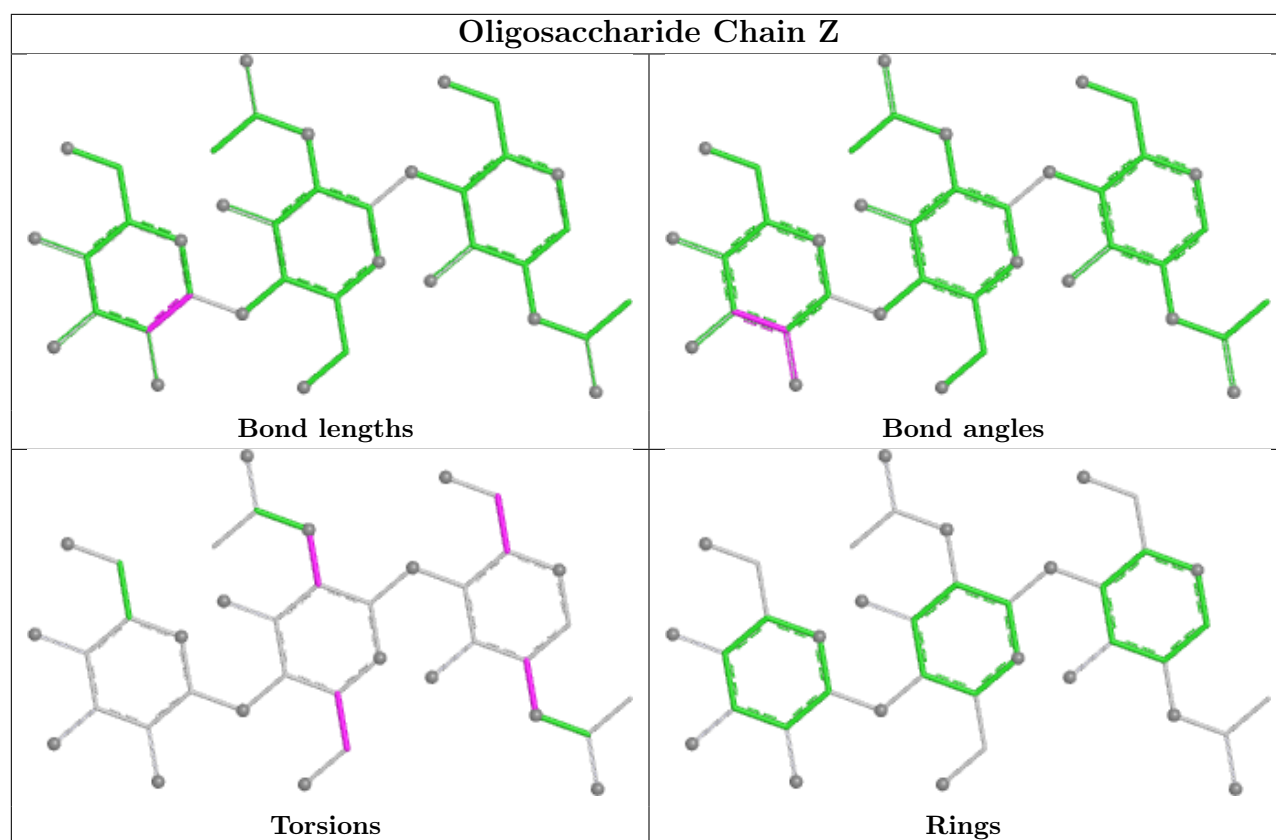


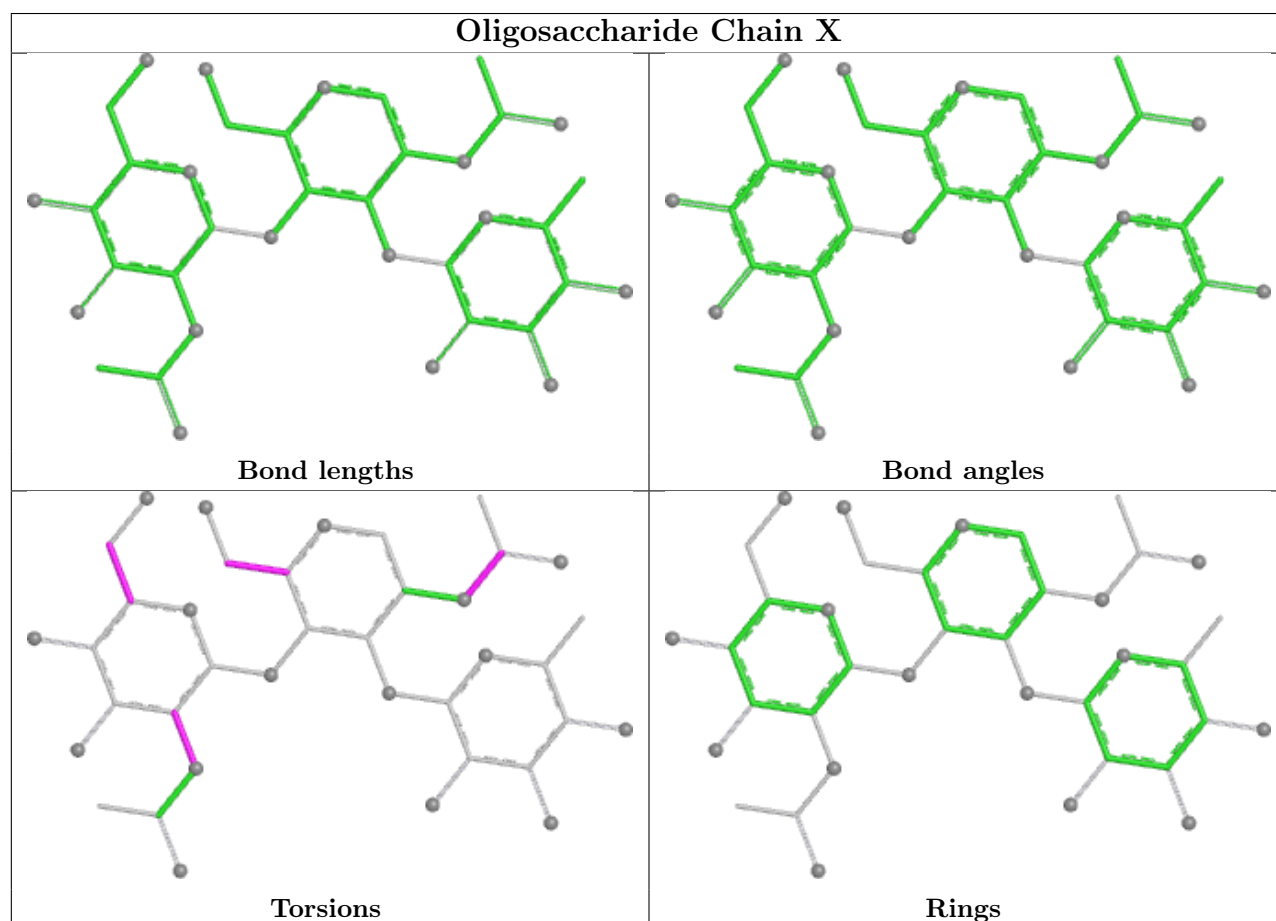
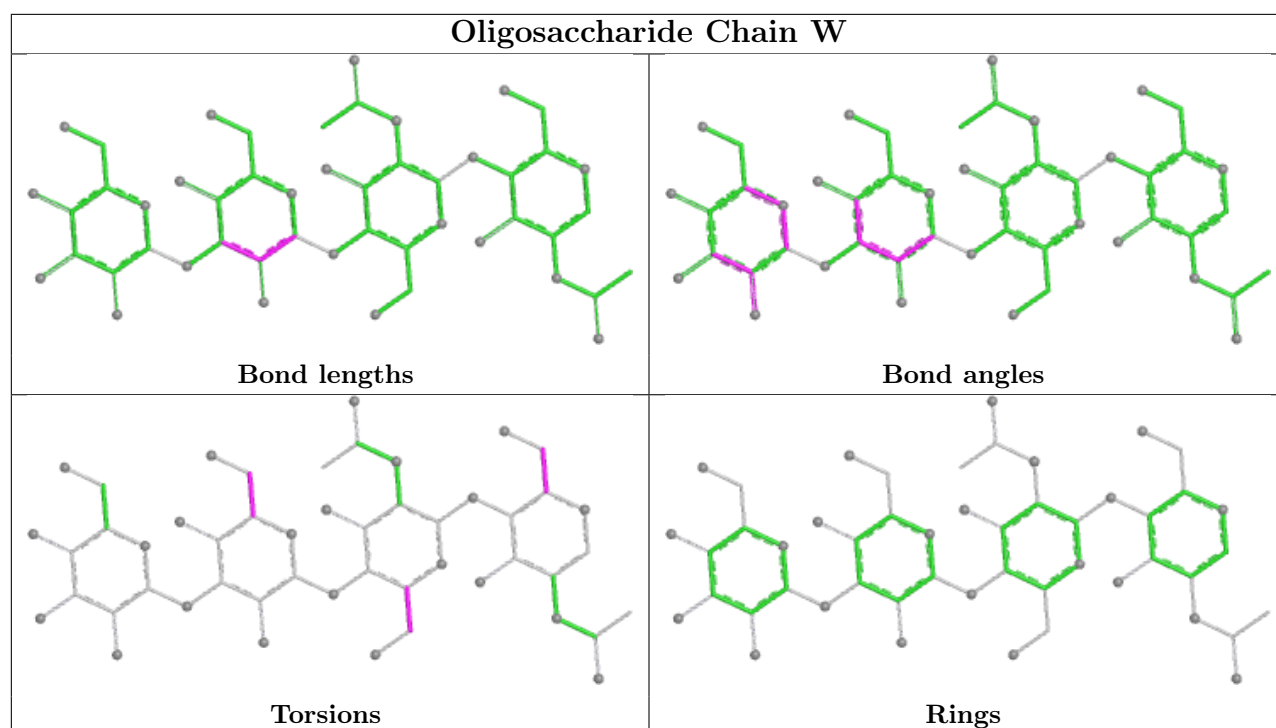












5.6 Ligand geometry

33 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	$\# Z > 2$
10	NAG	B	1311	1	14,14,15	0.25	0	17,19,21	0.56	0
10	NAG	B	1308	1	14,14,15	0.22	0	17,19,21	0.43	0
10	NAG	C	1301	1	14,14,15	0.22	0	17,19,21	0.43	0
10	NAG	A	1311	1	14,14,15	0.22	0	17,19,21	0.42	0
10	NAG	B	1303	1	14,14,15	0.50	0	17,19,21	0.51	0
10	NAG	A	1308	1	14,14,15	0.25	0	17,19,21	0.41	0
10	NAG	B	1302	1	14,14,15	0.22	0	17,19,21	0.42	0
10	NAG	B	1304	1	14,14,15	0.22	0	17,19,21	0.43	0
10	NAG	C	1307	1	14,14,15	0.21	0	17,19,21	0.42	0
10	NAG	A	1303	1	14,14,15	0.22	0	17,19,21	0.41	0
10	NAG	A	1310	1	14,14,15	0.21	0	17,19,21	0.43	0
10	NAG	C	1302	1	14,14,15	0.22	0	17,19,21	0.43	0
10	NAG	C	1308	1	14,14,15	0.24	0	17,19,21	0.40	0
10	NAG	A	1304	1	14,14,15	0.22	0	17,19,21	0.43	0
10	NAG	A	1302	1	14,14,15	0.23	0	17,19,21	0.41	0
10	NAG	C	1305	1	14,14,15	0.23	0	17,19,21	0.43	0
10	NAG	B	1301	1	14,14,15	0.22	0	17,19,21	0.42	0
10	NAG	A	1301	1	14,14,15	0.22	0	17,19,21	0.42	0
10	NAG	B	1306	1	14,14,15	0.21	0	17,19,21	0.41	0
10	NAG	B	1307	1	14,14,15	0.20	0	17,19,21	0.42	0
10	NAG	C	1306	1	14,14,15	0.24	0	17,19,21	0.41	0
10	NAG	A	1307	1	14,14,15	0.21	0	17,19,21	0.41	0
10	NAG	B	1305	1	14,14,15	0.27	0	17,19,21	0.56	0
10	NAG	B	1310	1	14,14,15	0.23	0	17,19,21	0.44	0
10	NAG	C	1303	1	14,14,15	0.22	0	17,19,21	0.43	0
10	NAG	A	1305	1	14,14,15	0.22	0	17,19,21	0.43	0
10	NAG	B	1309	1	14,14,15	0.22	0	17,19,21	0.41	0
10	NAG	C	1310	1	14,14,15	0.22	0	17,19,21	0.42	0
10	NAG	C	1304	1	14,14,15	0.26	0	17,19,21	0.87	1 (5%)
11	AH2	A	1312	-	11,11,11	0.56	0	15,15,15	0.73	0
10	NAG	A	1306	1	14,14,15	0.22	0	17,19,21	0.44	0
10	NAG	A	1309	1	14,14,15	0.21	0	17,19,21	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	NAG	C	1309	1	14,14,15	0.22	0	17,19,21	0.42	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
10	NAG	B	1311	1	-	4/6/23/26	0/1/1/1
10	NAG	B	1308	1	-	4/6/23/26	0/1/1/1
10	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
10	NAG	A	1311	1	-	1/6/23/26	0/1/1/1
10	NAG	B	1303	1	-	4/6/23/26	0/1/1/1
10	NAG	A	1308	1	-	3/6/23/26	0/1/1/1
10	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
10	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
10	NAG	C	1307	1	-	2/6/23/26	0/1/1/1
10	NAG	A	1303	1	-	0/6/23/26	0/1/1/1
10	NAG	A	1310	1	-	2/6/23/26	0/1/1/1
10	NAG	C	1302	1	-	0/6/23/26	0/1/1/1
10	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
10	NAG	A	1304	1	-	1/6/23/26	0/1/1/1
10	NAG	A	1302	1	-	4/6/23/26	0/1/1/1
10	NAG	C	1305	1	-	1/6/23/26	0/1/1/1
10	NAG	B	1301	1	-	1/6/23/26	0/1/1/1
10	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
10	NAG	B	1306	1	-	3/6/23/26	0/1/1/1
10	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
10	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
10	NAG	A	1307	1	-	1/6/23/26	0/1/1/1
10	NAG	B	1305	1	-	6/6/23/26	0/1/1/1
10	NAG	B	1310	1	-	2/6/23/26	0/1/1/1
10	NAG	C	1303	1	-	3/6/23/26	0/1/1/1
10	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
10	NAG	B	1309	1	-	2/6/23/26	0/1/1/1
10	NAG	C	1310	1	-	1/6/23/26	0/1/1/1
10	NAG	C	1304	1	-	6/6/23/26	0/1/1/1
11	AH2	A	1312	-	-	0/2/19/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	NAG	A	1306	1	-	4/6/23/26	0/1/1/1
10	NAG	A	1309	1	-	1/6/23/26	0/1/1/1
10	NAG	C	1309	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	C	1304	NAG	C1-O5-C5	2.79	115.93	112.19

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	1303	NAG	C1-C2-N2-C7
10	B	1304	NAG	C4-C5-C6-O6
10	B	1309	NAG	C4-C5-C6-O6
10	B	1306	NAG	O5-C5-C6-O6
10	C	1304	NAG	C4-C5-C6-O6

There are no ring outliers.

16 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	1311	NAG	4	0
10	B	1308	NAG	2	0
10	C	1301	NAG	2	0
10	B	1303	NAG	1	0
10	A	1308	NAG	2	0
10	A	1303	NAG	1	0
10	C	1308	NAG	2	0
10	A	1304	NAG	1	0
10	A	1302	NAG	1	0
10	A	1301	NAG	2	0
10	B	1306	NAG	1	0
10	B	1307	NAG	2	0
10	C	1306	NAG	1	0
10	B	1305	NAG	4	0
10	A	1305	NAG	1	0
10	C	1304	NAG	6	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.

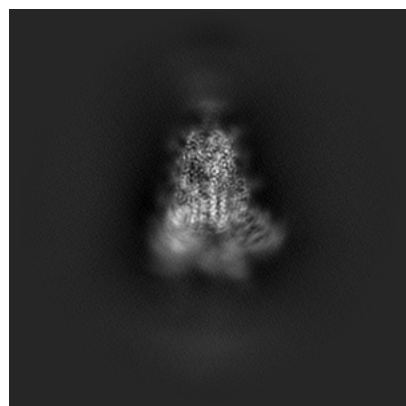
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27073. These allow visual inspection of the internal detail of the map and identification of artifacts.

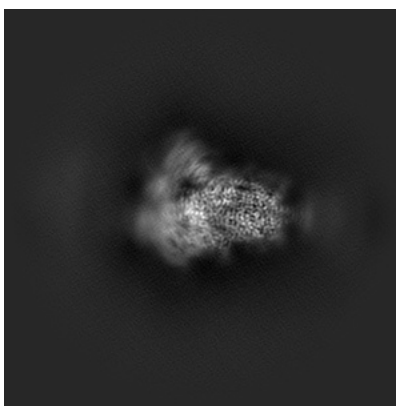
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

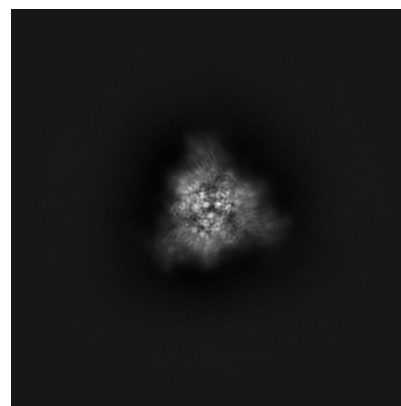
6.1.1 Primary map



X

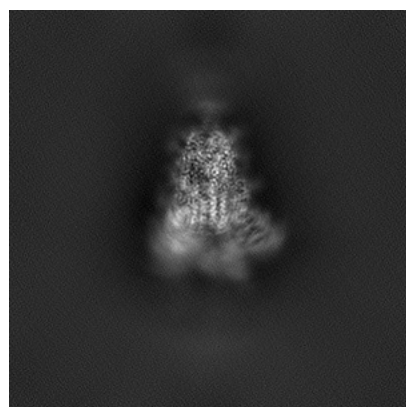


Y

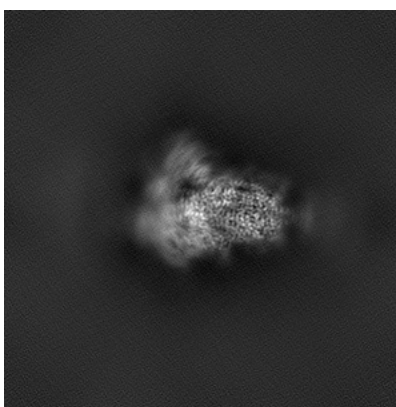


Z

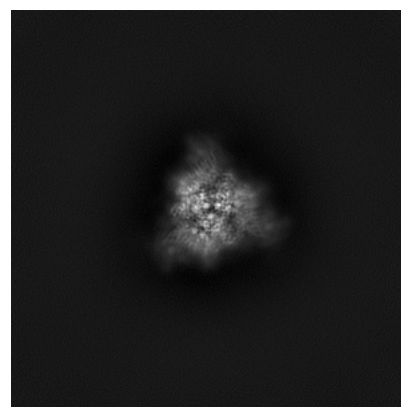
6.1.2 Raw map



X



Y

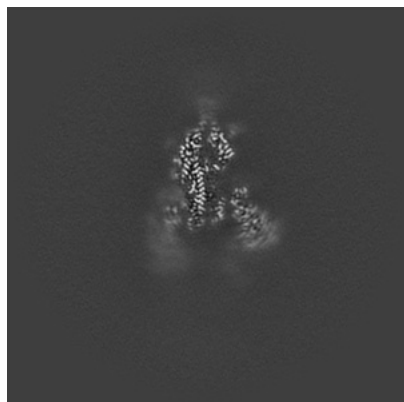


Z

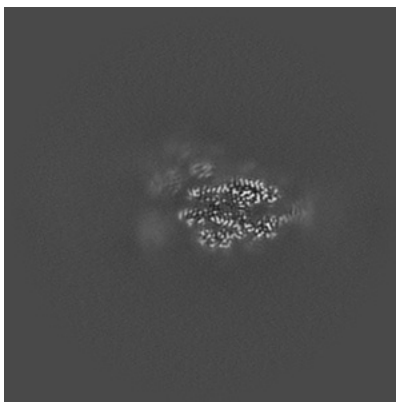
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

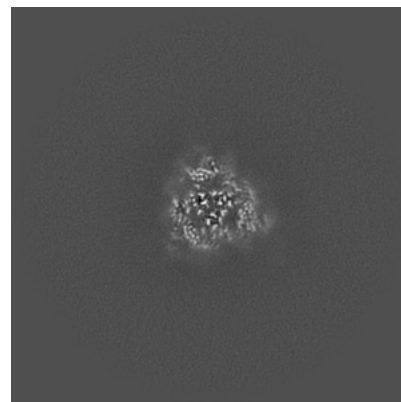
6.2.1 Primary map



X Index: 160

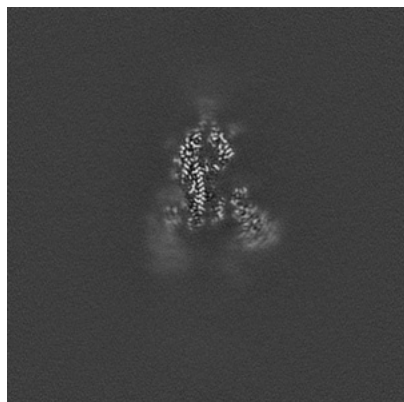


Y Index: 160

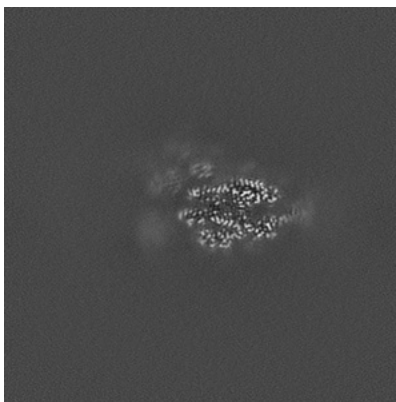


Z Index: 160

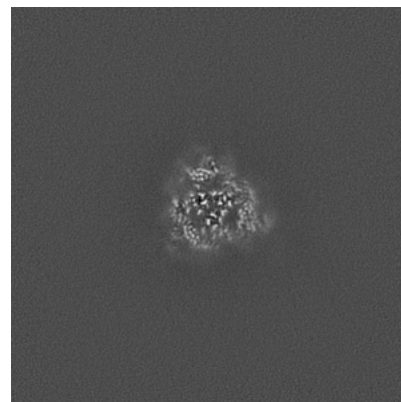
6.2.2 Raw map



X Index: 160



Y Index: 160

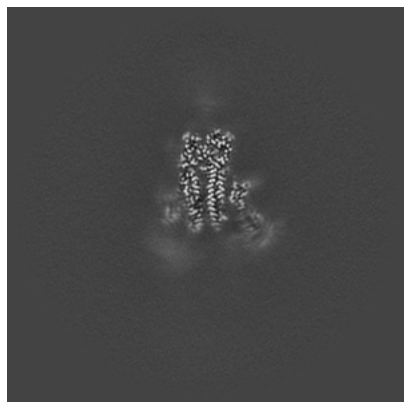


Z Index: 160

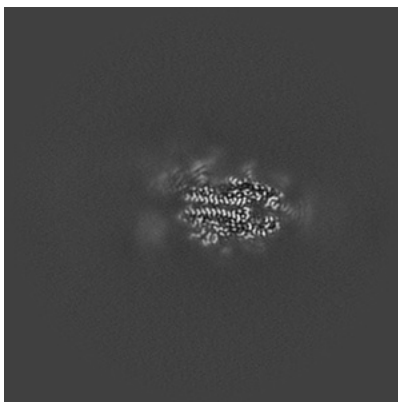
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

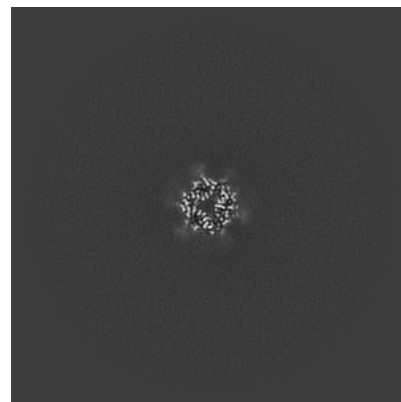
6.3.1 Primary map



X Index: 165

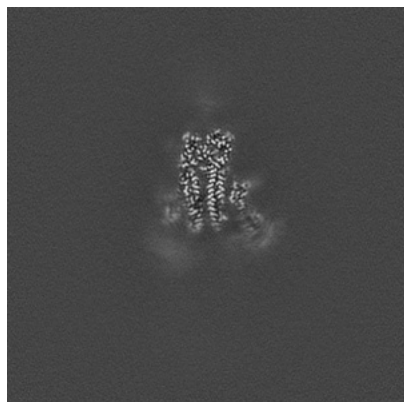


Y Index: 164

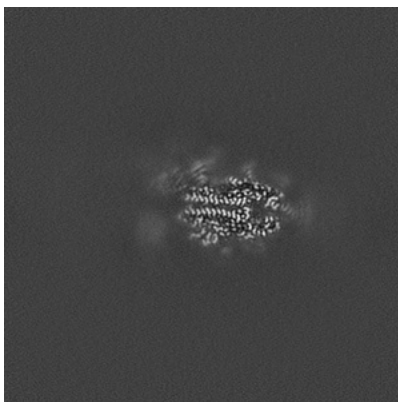


Z Index: 203

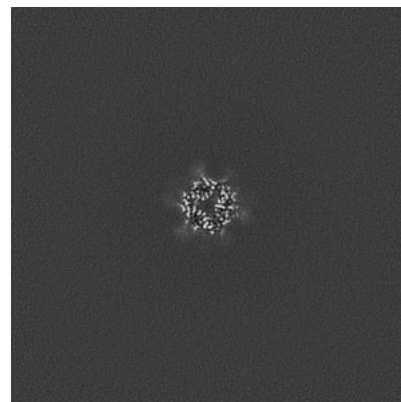
6.3.2 Raw map



X Index: 165



Y Index: 164

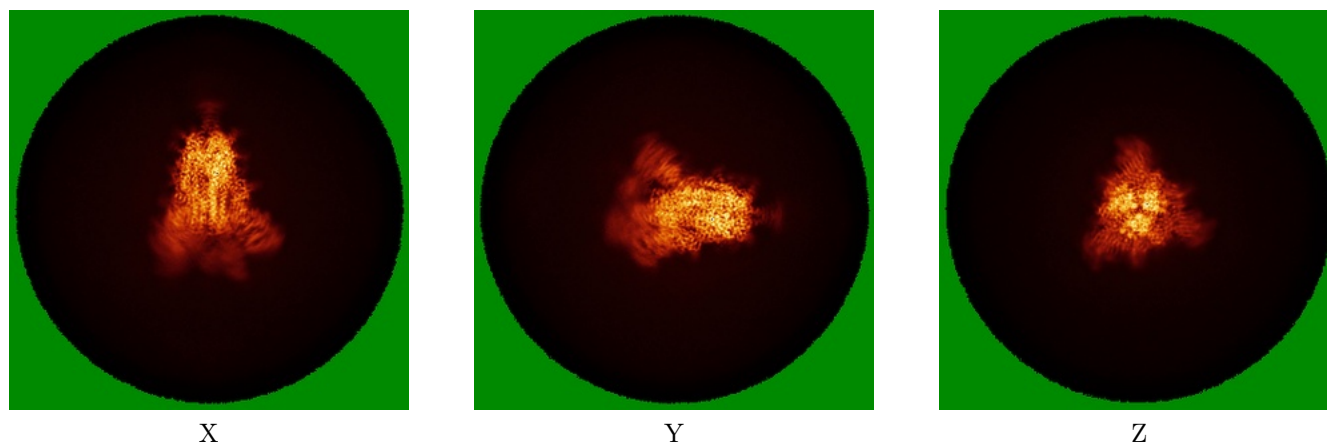


Z Index: 203

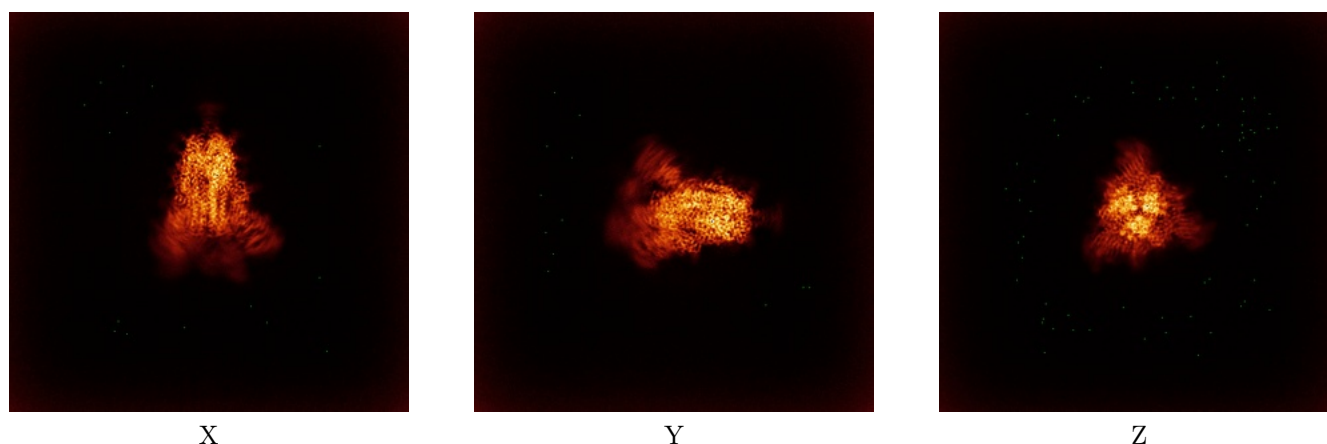
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

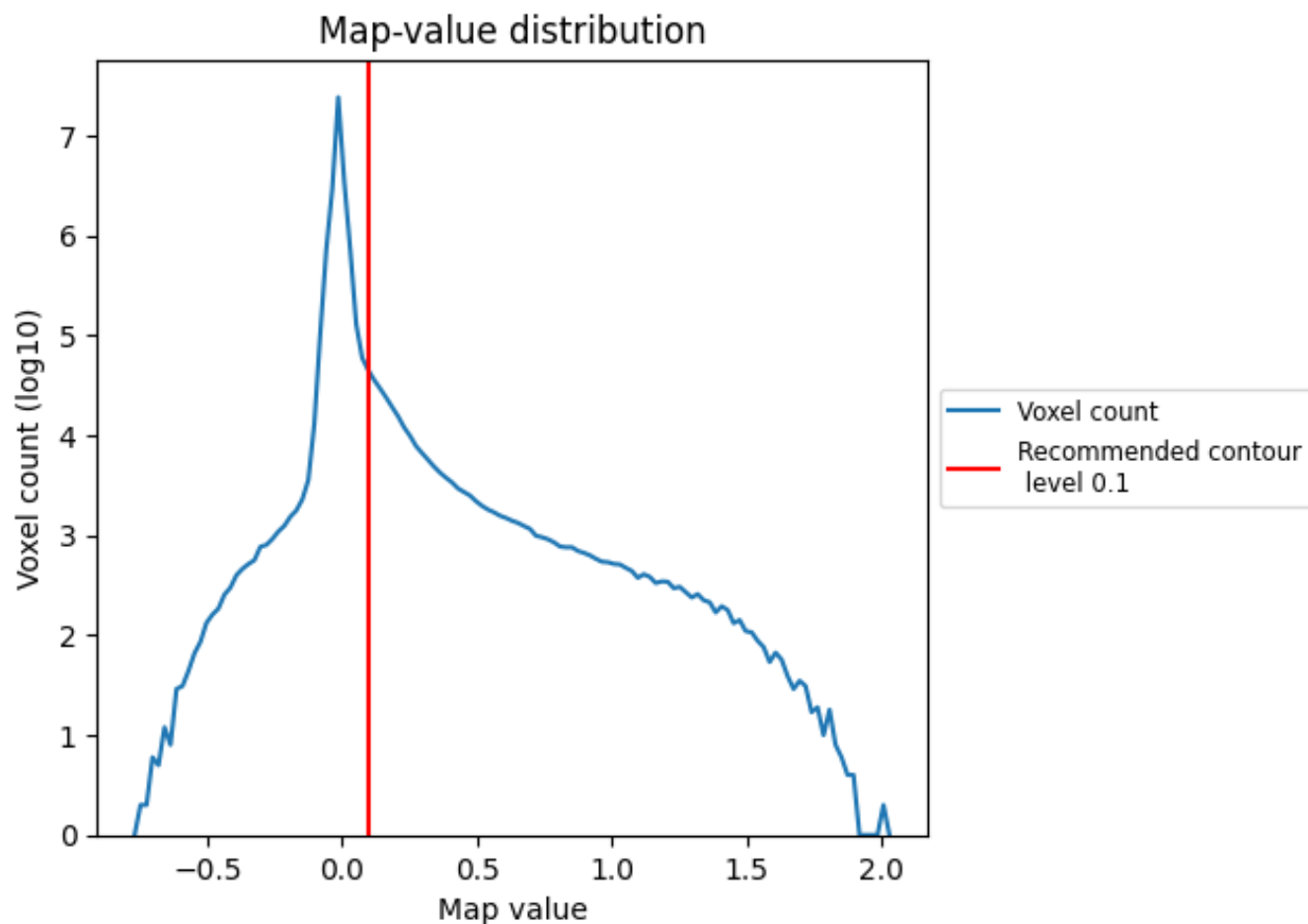
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

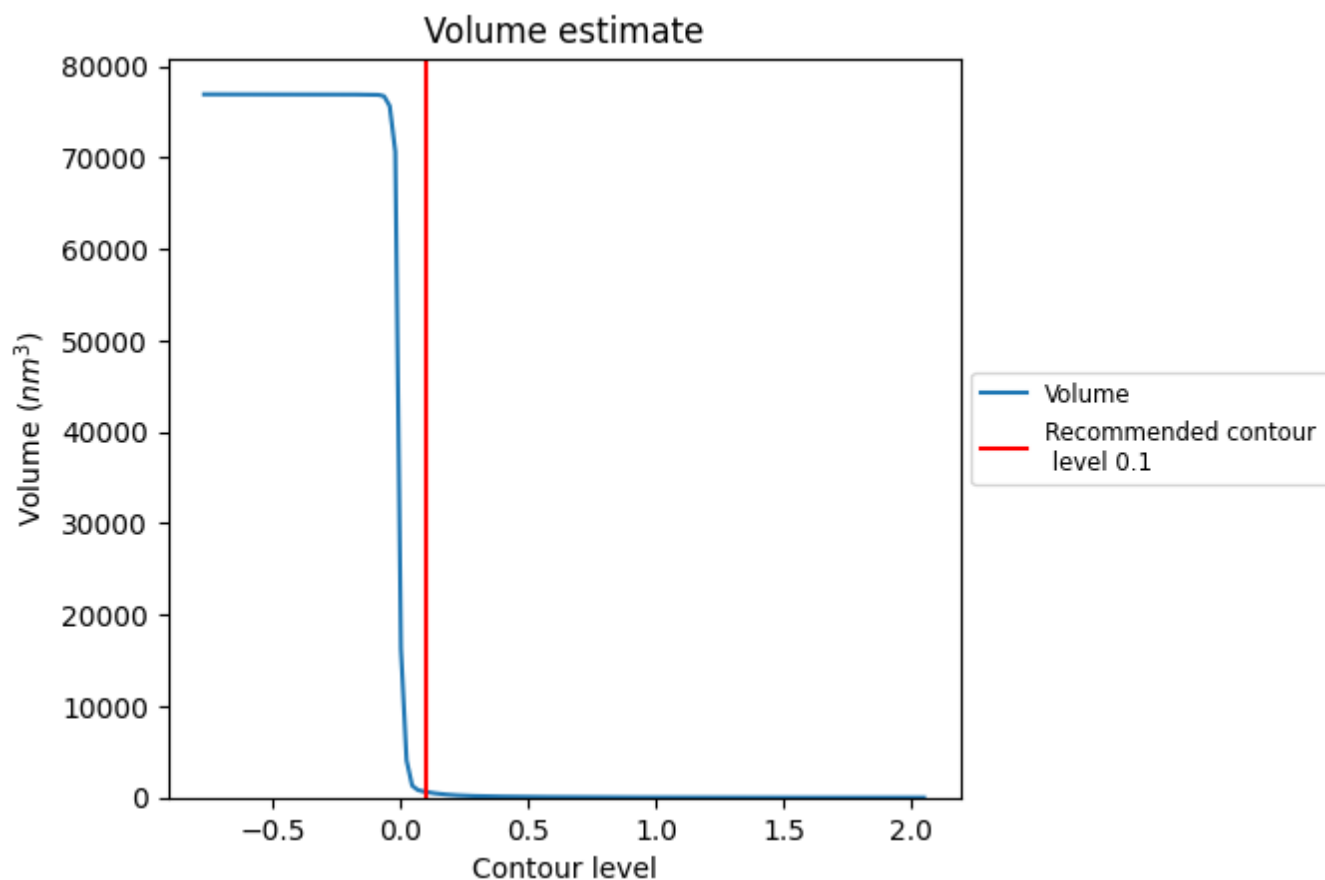
This section contains the results of statistical analysis of the map.

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.

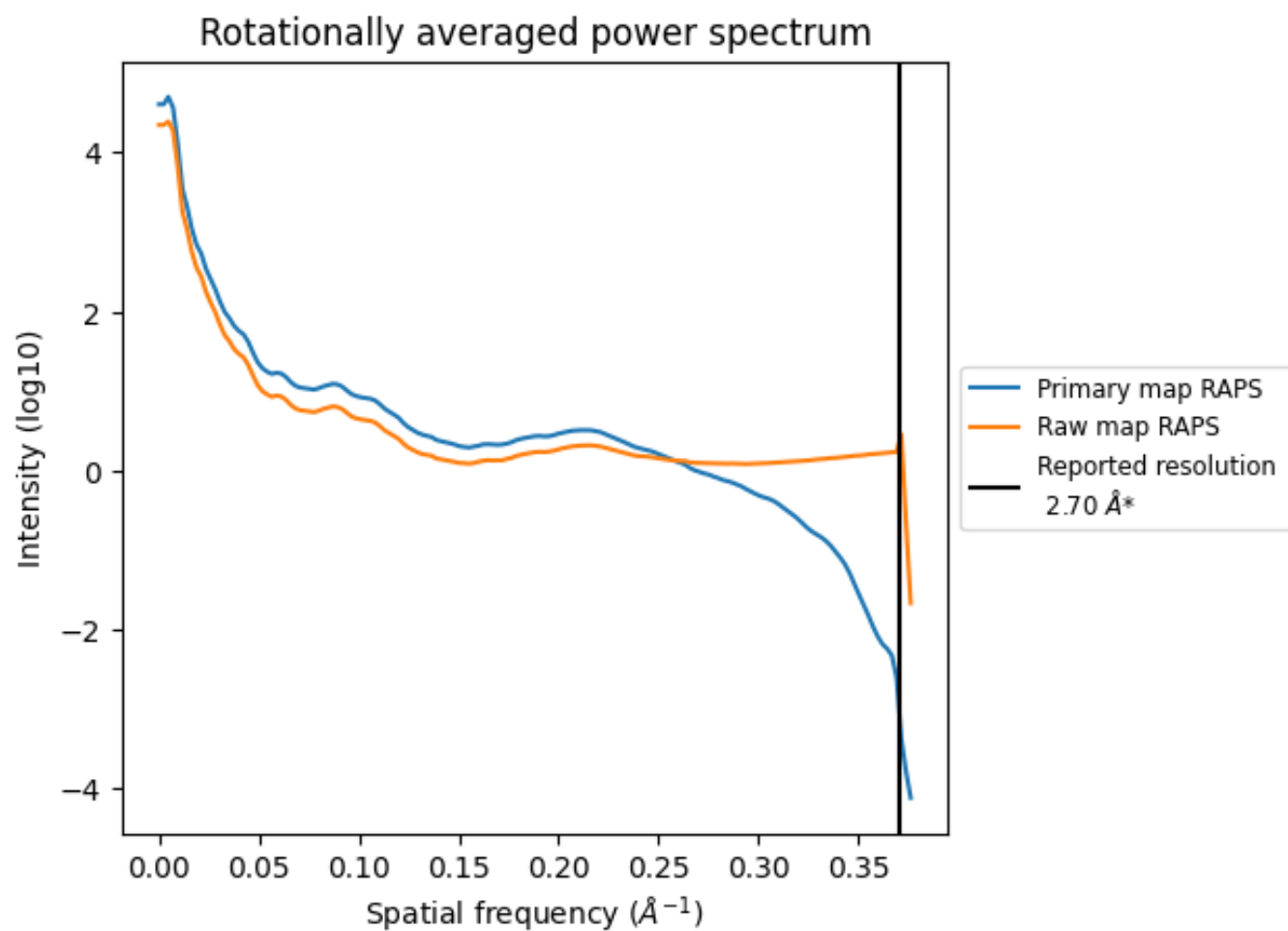
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 614 nm^3 ; this corresponds to an approximate mass of 555 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 ⓘ

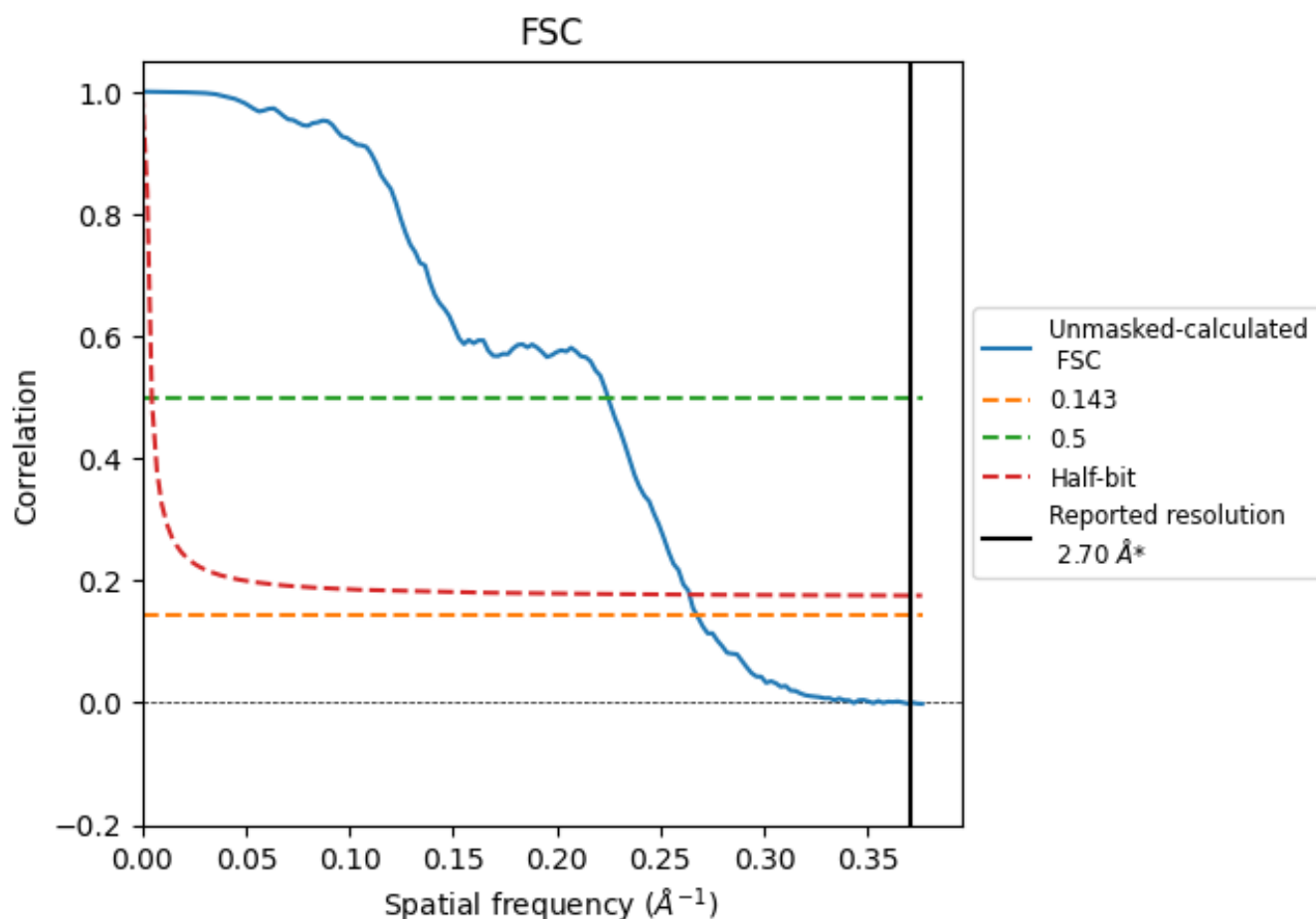


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.74	4.45	3.79

*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 3.74 differs from the reported value 2.7 by more than 10 %

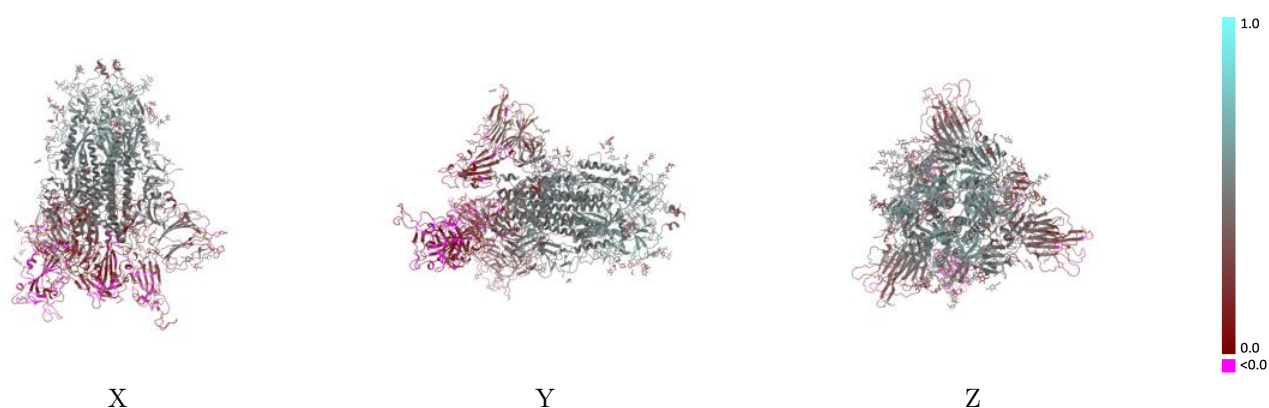
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27073 and PDB model 8CYB. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

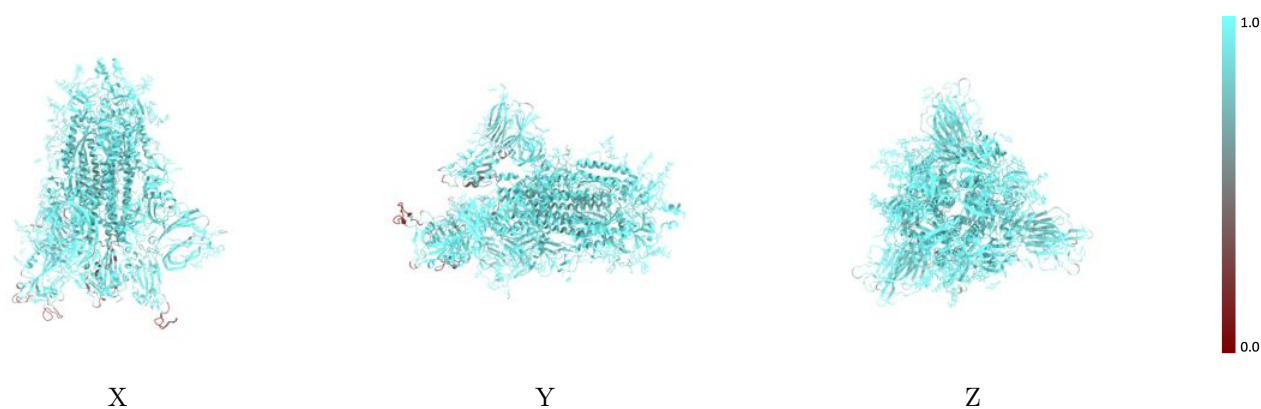
This section was not generated.

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



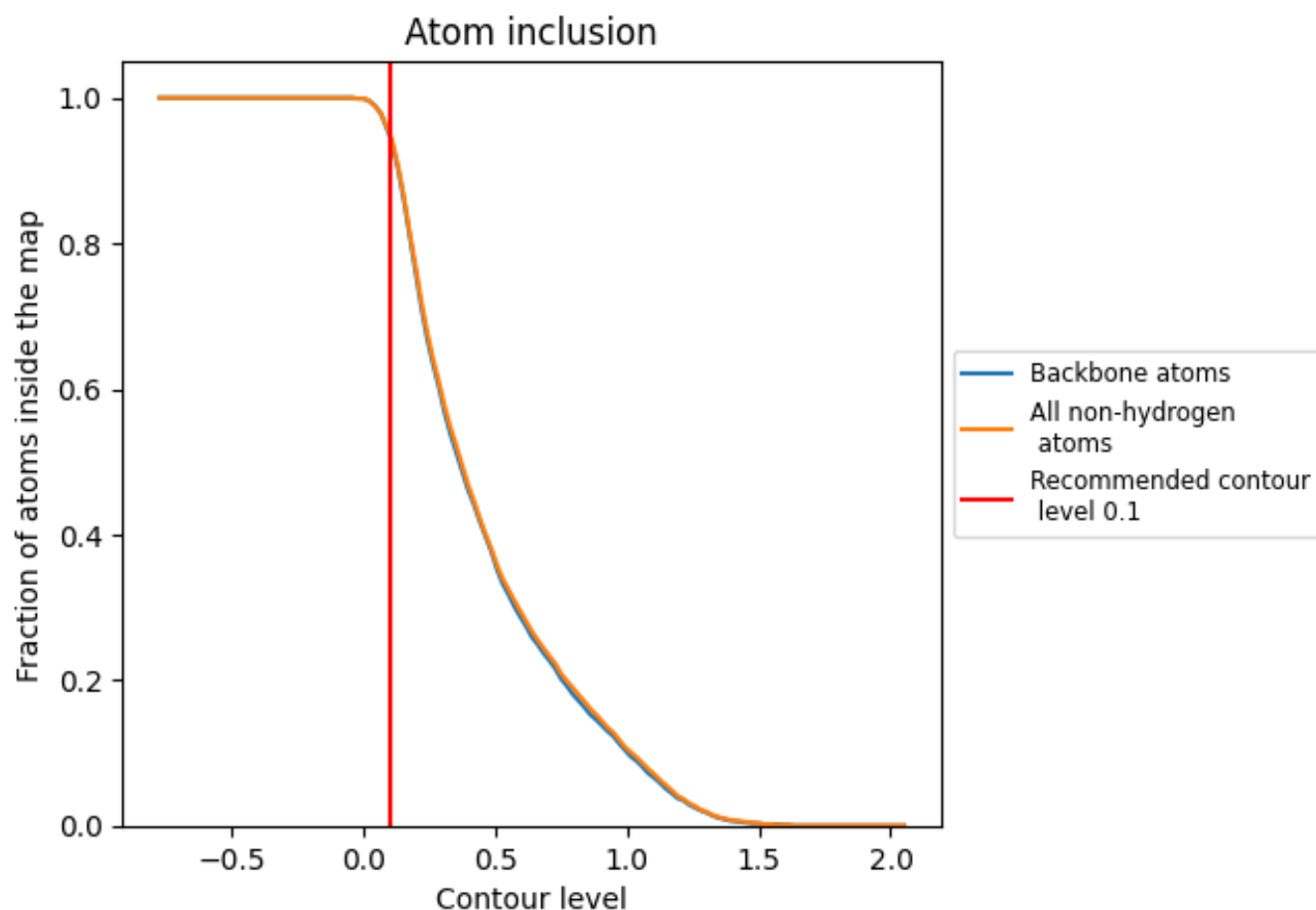
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9530	 0.3530
A	 0.9640	 0.3730
B	 0.9500	 0.3430
C	 0.9610	 0.3780
D	 0.7800	 0.0340
E	 1.0000	 0.3710
F	 1.0000	 0.3650
G	 1.0000	 0.4770
H	 1.0000	 0.3150
I	 0.9290	 0.3230
J	 1.0000	 0.3600
K	 1.0000	 0.4300
L	 1.0000	 0.4330
M	 1.0000	 0.4140
N	 0.9590	 0.2450
O	 1.0000	 0.2950
P	 1.0000	 0.4800
Q	 1.0000	 0.3880
R	 1.0000	 0.2960
S	 1.0000	 0.3690
T	 1.0000	 0.3580
U	 1.0000	 0.3660
V	 1.0000	 0.3780
W	 1.0000	 0.4560
X	 1.0000	 0.2500
Y	 1.0000	 0.4650
Z	 0.9740	 0.3720

