



wwPDB EM Validation Summary Report ⓘ

Oct 26, 2024 – 10:31 PM EDT

PDB ID : 6UM5
EMDB ID : EMD-20817
Title : Cryo-EM structure of HIV-1 neutralizing antibody DH270 UCA3 in complex with CH848 10.17DT Env
Authors : Acharya, P.; Henderson, R.C.; Saunders, K.O.; Haynes, B.F.
Deposited on : 2019-10-09
Resolution : 4.20 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

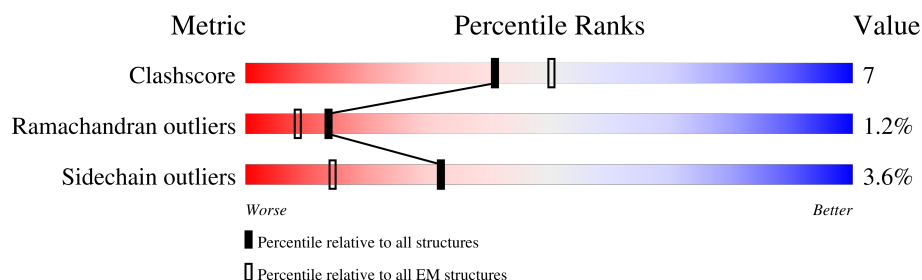
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.



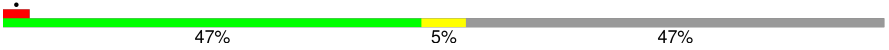
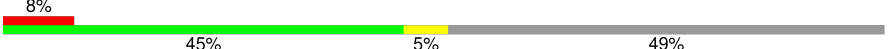
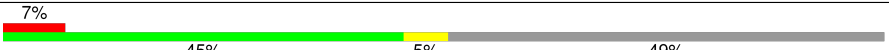
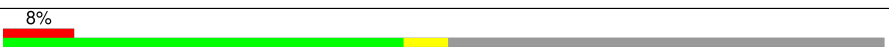
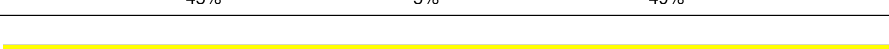

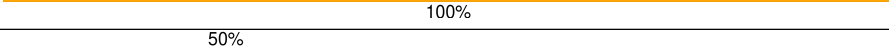

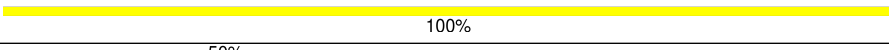
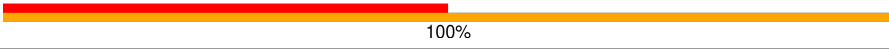

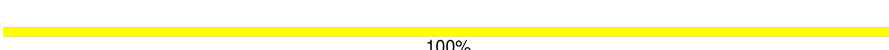
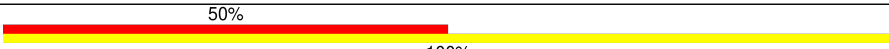
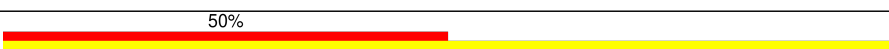
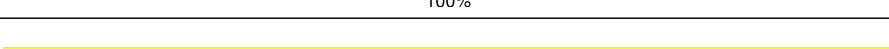
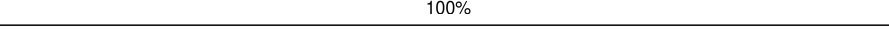

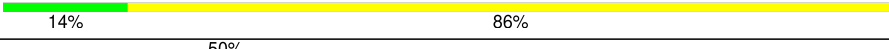


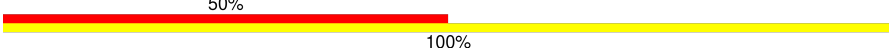
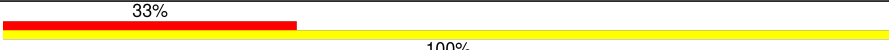

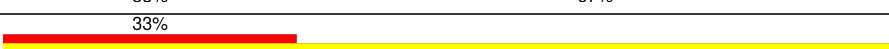
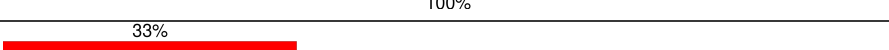
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	462	
1	E	462	
1	I	462	
2	B	153	
2	F	153	
2	J	153	
3	C	238	
3	G	238	

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Mol	Chain	Length	Quality of chain
3	K	238	
4	D	216	
4	H	216	
4	L	216	
5	M	2	
5	Q	2	
5	S	2	
5	T	2	
5	X	2	
5	Z	2	
5	a	2	
5	e	2	
5	g	2	
6	N	7	
6	U	7	
6	b	7	
7	O	4	
7	V	4	
7	c	4	
8	P	3	
8	R	3	
8	W	3	
8	Y	3	
8	d	3	
8	f	3	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 20562 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 CH848 10.17 DT gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	462	Total	C	N	O	S	0	0
			3615	2263	625	698	29		
1	E	462	Total	C	N	O	S	0	0
			3615	2263	625	698	29		
1	I	462	Total	C	N	O	S	0	0
			3615	2263	625	698	29		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLU	-	expression tag	UNP A0A1W6IPB2
A	33	ASN	-	expression tag	UNP A0A1W6IPB2
A	133	ASP	ASN	conflict	UNP A0A1W6IPB2
A	138	THR	ASN	conflict	UNP A0A1W6IPB2
A	200	CYS	ALA	conflict	UNP A0A1W6IPB2
A	433	CYS	ALA	conflict	UNP A0A1W6IPB2
A	490	LYS	GLU	conflict	UNP A0A1W6IPB2
A	492	GLU	GLN	conflict	UNP A0A1W6IPB2
A	496	VAL	ILE	conflict	UNP A0A1W6IPB2
A	500	ARG	GLY	conflict	UNP A0A1W6IPB2
A	501	CYS	ALA	conflict	UNP A0A1W6IPB2
E	32	GLU	-	expression tag	UNP A0A1W6IPB2
E	33	ASN	-	expression tag	UNP A0A1W6IPB2
E	133	ASP	ASN	conflict	UNP A0A1W6IPB2
E	138	THR	ASN	conflict	UNP A0A1W6IPB2
E	200	CYS	ALA	conflict	UNP A0A1W6IPB2
E	433	CYS	ALA	conflict	UNP A0A1W6IPB2
E	490	LYS	GLU	conflict	UNP A0A1W6IPB2
E	492	GLU	GLN	conflict	UNP A0A1W6IPB2
E	496	VAL	ILE	conflict	UNP A0A1W6IPB2
E	500	ARG	GLY	conflict	UNP A0A1W6IPB2
E	501	CYS	ALA	conflict	UNP A0A1W6IPB2
I	32	GLU	-	expression tag	UNP A0A1W6IPB2
I	33	ASN	-	expression tag	UNP A0A1W6IPB2

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Chain	Residue	Modelled	Actual	Comment	Reference
I	133	ASP	ASN	conflict	UNP A0A1W6IPB2
I	138	THR	ASN	conflict	UNP A0A1W6IPB2
I	200	CYS	ALA	conflict	UNP A0A1W6IPB2
I	433	CYS	ALA	conflict	UNP A0A1W6IPB2
I	490	LYS	GLU	conflict	UNP A0A1W6IPB2
I	492	GLU	GLN	conflict	UNP A0A1W6IPB2
I	496	VAL	ILE	conflict	UNP A0A1W6IPB2
I	500	ARG	GLY	conflict	UNP A0A1W6IPB2
I	501	CYS	ALA	conflict	UNP A0A1W6IPB2

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	131	Total	C	N	O	S	0	0
			1030	652	177	195	6		
2	F	131	Total	C	N	O	S	0	0
			1030	652	177	195	6		
2	J	131	Total	C	N	O	S	0	0
			1030	652	177	195	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	605	CYS	THR	conflict	UNP Q2N0S7
F	605	CYS	THR	conflict	UNP Q2N0S7
J	605	CYS	THR	conflict	UNP Q2N0S7

- Molecule 3 is a protein called DH270 UCA3 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	126	Total	C	N	O	S	0	0
			989	627	168	188	6		
3	G	126	Total	C	N	O	S	0	0
			989	627	168	188	6		
3	K	126	Total	C	N	O	S	0	0
			989	627	168	188	6		

- Molecule 4 is a protein called DH270 UCA3 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	110	Total	C	N	O	S	0	0
			796	492	133	167	4		

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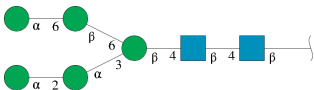
Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	110	Total	C	N	O	S	0	0
			796	492	133	167	4		
4	L	110	Total	C	N	O	S	0	0
			796	492	133	167	4		

- Molecule 5 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
5	M	2	Total	C	N	O	0	0
			28	16	2	10		
5	Q	2	Total	C	N	O	0	0
			28	16	2	10		
5	S	2	Total	C	N	O	0	0
			28	16	2	10		
5	T	2	Total	C	N	O	0	0
			28	16	2	10		
5	X	2	Total	C	N	O	0	0
			28	16	2	10		
5	Z	2	Total	C	N	O	0	0
			28	16	2	10		
5	a	2	Total	C	N	O	0	0
			28	16	2	10		
5	e	2	Total	C	N	O	0	0
			28	16	2	10		
5	g	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)-beta-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.



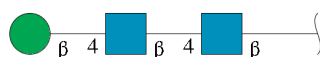
Mol	Chain	Residues	Atoms				AltConf	Trace
6	N	7	Total	C	N	O	0	0
			83	46	2	35		
6	U	7	Total	C	N	O	0	0
			83	46	2	35		
6	b	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



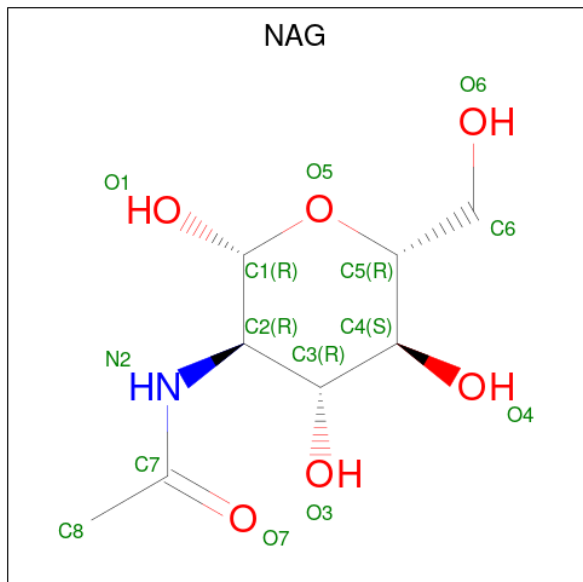
Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	4	Total	C	N	O	0	0
			53	30	3	20		
7	V	4	Total	C	N	O	0	0
			53	30	3	20		
7	c	4	Total	C	N	O	0	0
			53	30	3	20		

- Molecule 8 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
8	P	3	Total	C	N	O	0	0
			39	22	2	15		
8	R	3	Total	C	N	O	0	0
			39	22	2	15		
8	W	3	Total	C	N	O	0	0
			39	22	2	15		
8	Y	3	Total	C	N	O	0	0
			39	22	2	15		
8	d	3	Total	C	N	O	0	0
			39	22	2	15		
8	f	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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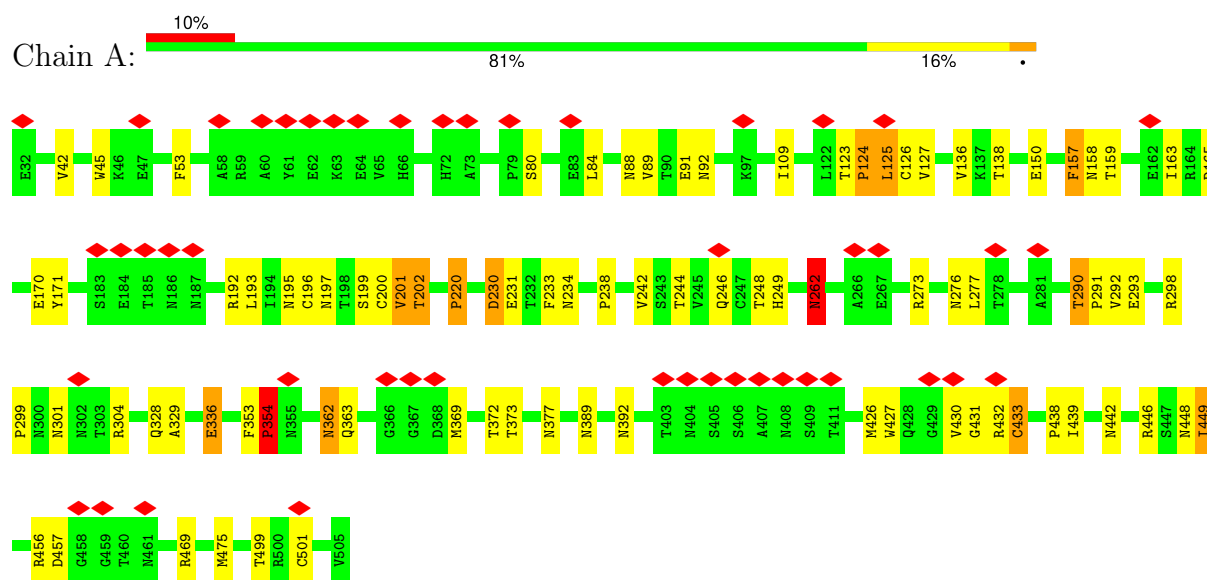
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Mol	Chain	Residues	Atoms				AltConf
9	E	1	Total 14	C 8	N 1	O 5	0
9	E	1	Total 14	C 8	N 1	O 5	0
9	E	1	Total 14	C 8	N 1	O 5	0
9	E	1	Total 14	C 8	N 1	O 5	0
9	E	1	Total 14	C 8	N 1	O 5	0
9	E	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0
9	I	1	Total 14	C 8	N 1	O 5	0

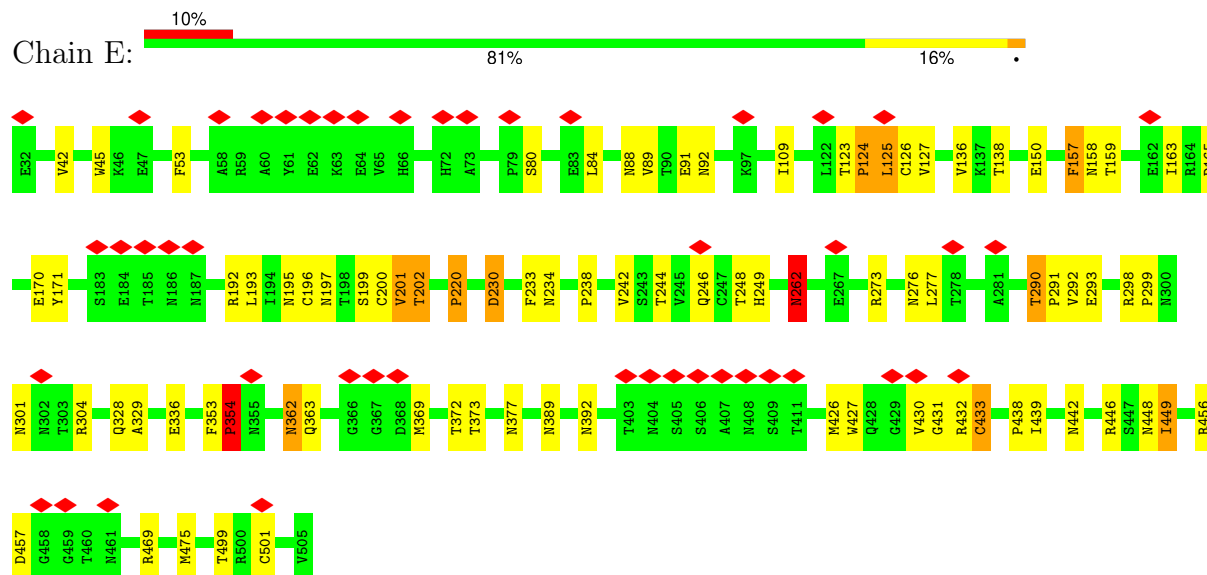
3 Residue-property plots

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.

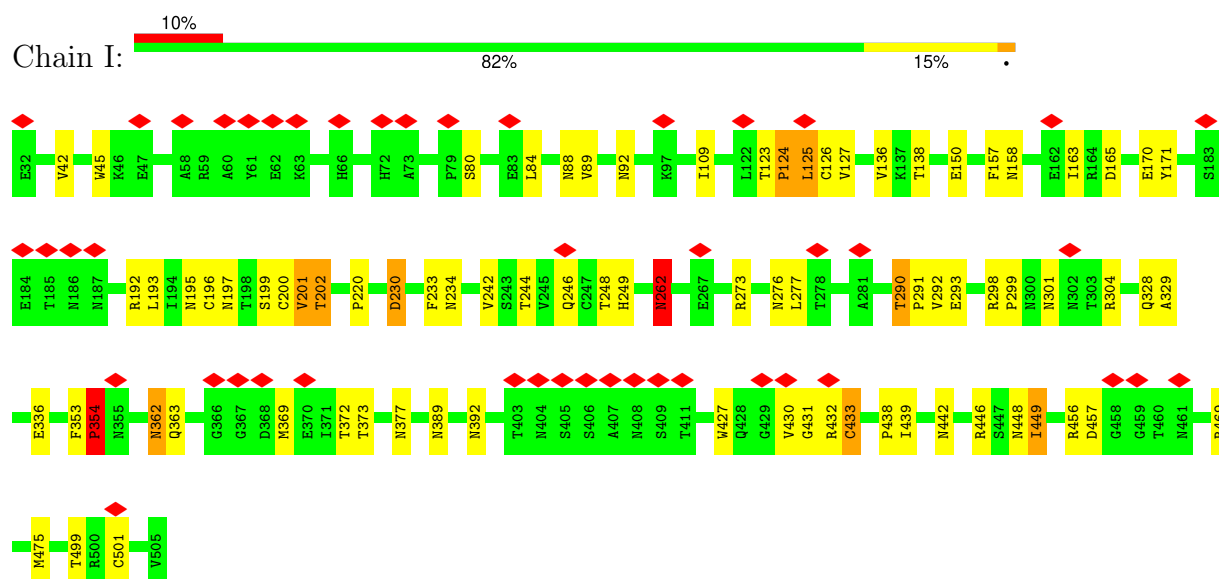
- Molecule 1: CH848 10.17 DT gp120



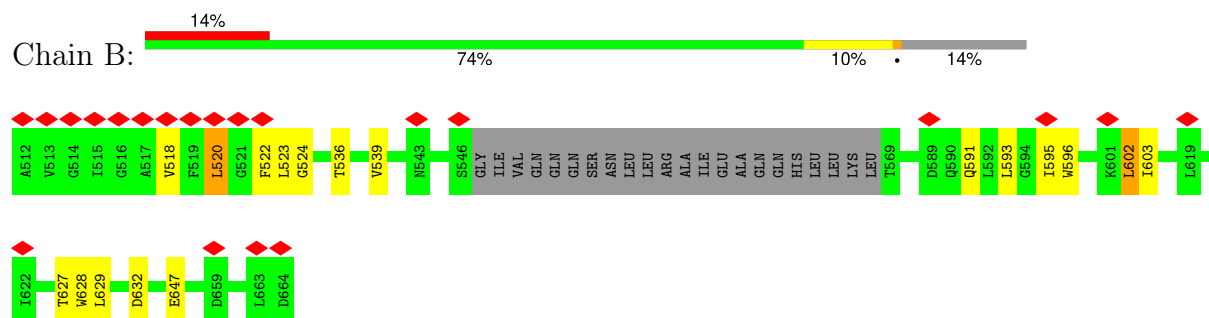
- Molecule 1: CH848 10.17 DT gp120



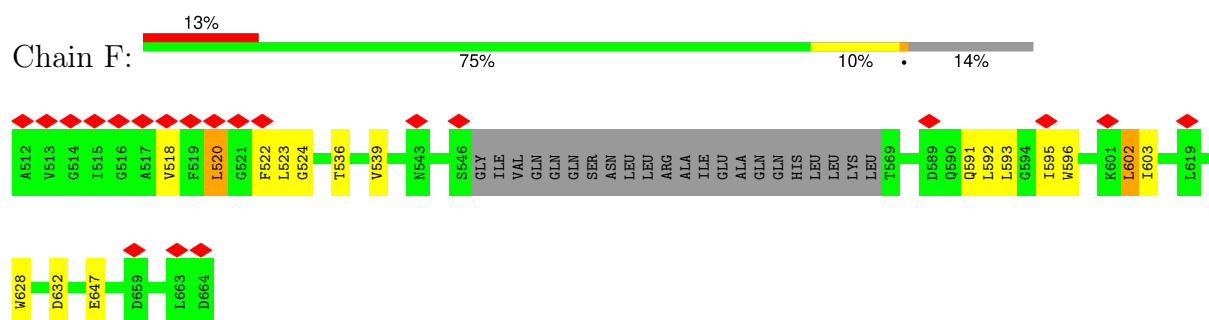
- Molecule 1: CH848 10.17 DT gp120



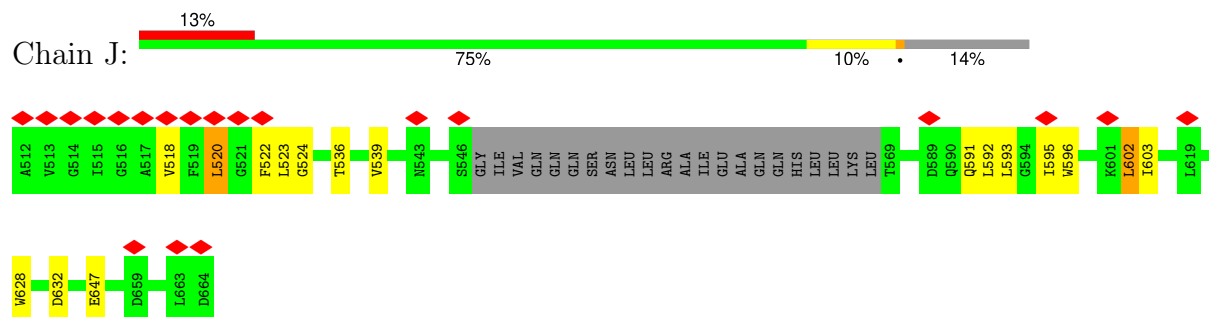
• Molecule 2: Envelope glycoprotein gp160



• Molecule 2: Envelope glycoprotein gp160



• Molecule 2: Envelope glycoprotein gp160



Chain C:

Position	Conservation (bits)	Most Conserved Residue
1	0.24	GLY
2	0.24	GLY
3	0.24	LEU
4	0.24	VAL
5	0.24	LYS
6	0.24	ASP
7	0.24	THR
8	0.24	PHE
9	0.24	PRO
10	0.24	ASP
11	0.12	GLU
12	0.12	LYS
13	0.12	ARG
14	0.12	VAL
15	0.12	GLU
16	0.08	PRO
17	0.08	LYS
18	0.08	SER
19	0.08	CYS
20	0.08	ASP
21	0.08	LYS
22	0.08	HIS
23	0.08	HIS
24	0.08	HIS
25	0.08	HIS
26	0.08	HIS
27	0.08	HIS

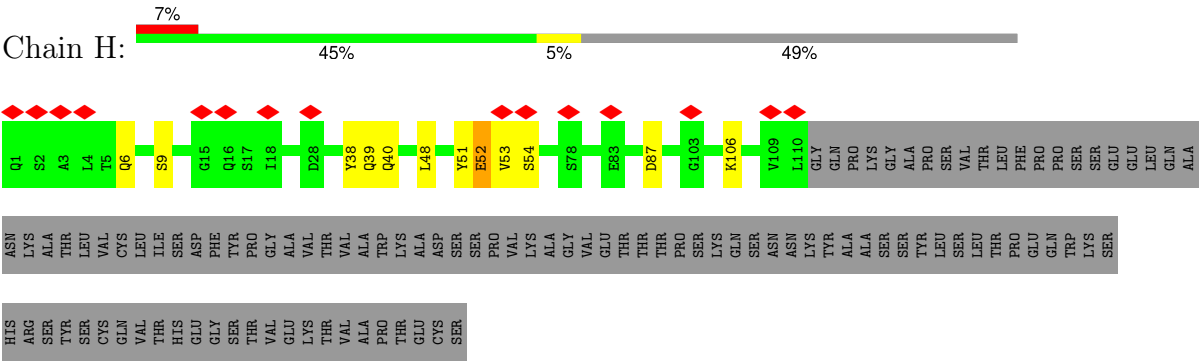
[illegible]

Chain K:

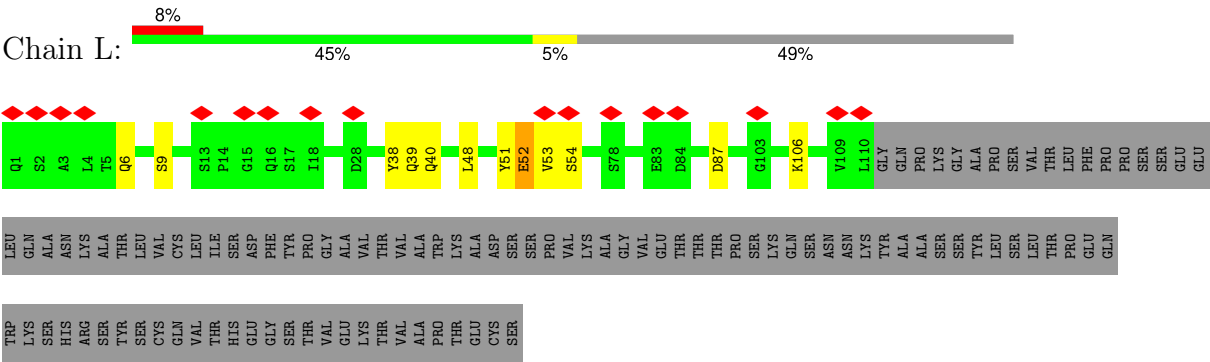
Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Conservation (%)	47	47	47	47	47	47	47	47	47	47	5	47	47	47	47	47	47	47	47	47
Sequence Logo (bits)	1.00	0.95	0.90	0.85	0.80	0.75	0.70	0.65	0.60	0.55	0.05	0.50	0.45	0.40	0.35	0.30	0.25	0.20	0.15	0.10

[illegible]

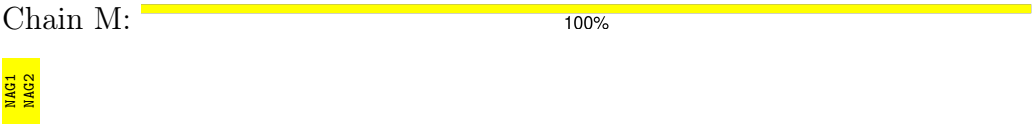
• Molecule 4: DH270 UCA3 Fab Light Chain



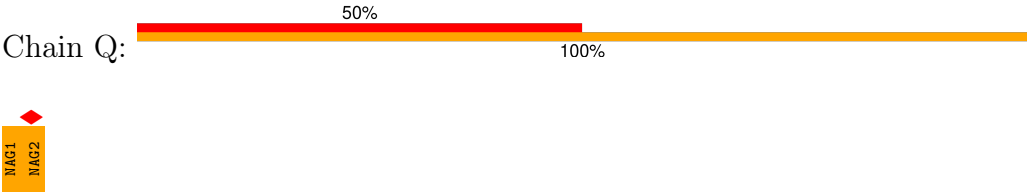
• Molecule 4: DH270 UCA3 Fab Light Chain



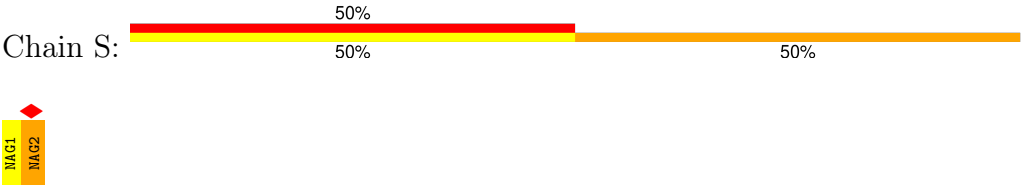
• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:  100%

MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:  50%
 100%

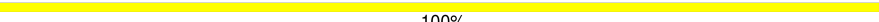
MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:  50%
 50%

MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:  100%

MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain e:  50%
 100%

MAG1
MAG2

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:  50%
 100%

MAG1
MAG2

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

Chain N:  100%

MAG1
MAG2
BMA3
MAN4
MAN5
BMA6
MAN7

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

Chain U:  14% 86%

MAG1
MAG2
BMA3
MAN4
MAN5
BMA6
MAN7

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

Chain b:  14% 86%


MAG1
MAG2
BMA3
MAN4
MAN5
BMA6
MAN7

- Molecule 7: 2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain O:  50% 100%

MAG1
MAG2
BMA3
MAG4

- Molecule 7: 2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain V:  50% 75% 25%

MAG1
MAG2
BMA3
MAG4

- Molecule 7: 2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)- β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain c:  50% 100%



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



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



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



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



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



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



MAG1
MAG2
EM13

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	22093	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.085	Depositor
Minimum map value	-0.945	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	345.6, 345.6, 345.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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, BMA, MAN

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	0.57	3/3692 (0.1%)	0.75	9/5024 (0.2%)
1	E	0.57	3/3692 (0.1%)	0.75	9/5024 (0.2%)
1	I	0.57	3/3692 (0.1%)	0.75	9/5024 (0.2%)
2	B	0.41	0/1048	0.51	0/1422
2	F	0.41	0/1048	0.52	0/1422
2	J	0.41	0/1048	0.52	0/1422
3	C	0.42	0/1017	0.50	0/1381
3	G	0.42	0/1017	0.51	0/1381
3	K	0.42	0/1017	0.50	0/1381
4	D	0.36	0/811	0.50	0/1100
4	H	0.36	0/811	0.50	0/1100
4	L	0.36	0/811	0.50	0/1100
All	All	0.50	9/19704 (0.0%)	0.65	27/26781 (0.1%)

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
4	D	0	1
4	H	0	1
4	L	0	1
All	All	0	3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	354	PRO	N-CA	13.79	1.70	1.47
1	A	354	PRO	N-CA	13.78	1.70	1.47
1	E	354	PRO	N-CA	13.74	1.70	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	353	PHE	C-N	6.03	1.45	1.34
1	A	353	PHE	C-N	5.99	1.45	1.34

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	249	HIS	CB-CA-C	-11.28	87.84	110.40
1	E	249	HIS	CB-CA-C	-11.28	87.85	110.40
1	A	249	HIS	CB-CA-C	-11.27	87.86	110.40
1	E	197	ASN	CB-CA-C	-9.58	91.24	110.40
1	A	197	ASN	CB-CA-C	-9.57	91.26	110.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	52	GLU	Peptide
4	H	52	GLU	Peptide
4	L	52	GLU	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3615	0	3521	50	0
1	E	3615	0	3521	47	0
1	I	3615	0	3521	44	0
2	B	1030	0	1011	14	0
2	F	1030	0	1011	12	0
2	J	1030	0	1011	13	0
3	C	989	0	935	6	0
3	G	989	0	935	5	0
3	K	989	0	935	8	0
4	D	796	0	772	6	0
4	H	796	0	772	5	0
4	L	796	0	772	6	0
5	M	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	Q	28	0	25	3	0
5	S	28	0	25	2	0
5	T	28	0	25	0	0
5	X	28	0	25	3	0
5	Z	28	0	25	2	0
5	a	28	0	25	0	0
5	e	28	0	25	0	0
5	g	28	0	25	0	0
6	N	83	0	70	1	0
6	U	83	0	70	0	0
6	b	83	0	70	0	0
7	O	53	0	46	0	0
7	V	53	0	46	1	0
7	c	53	0	46	0	0
8	P	39	0	34	0	0
8	R	39	0	34	4	0
8	W	39	0	34	0	0
8	Y	39	0	34	5	0
8	d	39	0	34	0	0
8	f	39	0	34	0	0
9	A	126	0	117	15	0
9	E	126	0	117	16	0
9	I	126	0	117	14	0
All	All	20562	0	19845	262	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 262 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:I:354:PRO:N	1:I:354:PRO:CA	1.70	1.43
1:E:354:PRO:CA	1:E:354:PRO:N	1.70	1.42
1:A:354:PRO:N	1:A:354:PRO:CA	1.70	1.39
4:L:52:GLU:O	4:L:54:SER:N	2.09	0.86
4:H:52:GLU:O	4:H:54:SER:N	2.09	0.85

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	460/462 (100%)	414 (90%)	37 (8%)	9 (2%)	6	34
1	E	460/462 (100%)	414 (90%)	37 (8%)	9 (2%)	6	34
1	I	460/462 (100%)	414 (90%)	37 (8%)	9 (2%)	6	34
2	B	127/153 (83%)	120 (94%)	7 (6%)	0	100	100
2	F	127/153 (83%)	120 (94%)	7 (6%)	0	100	100
2	J	127/153 (83%)	120 (94%)	7 (6%)	0	100	100
3	C	124/238 (52%)	121 (98%)	3 (2%)	0	100	100
3	G	124/238 (52%)	121 (98%)	3 (2%)	0	100	100
3	K	124/238 (52%)	121 (98%)	3 (2%)	0	100	100
4	D	108/216 (50%)	105 (97%)	2 (2%)	1 (1%)	14	50
4	H	108/216 (50%)	105 (97%)	2 (2%)	1 (1%)	14	50
4	L	108/216 (50%)	105 (97%)	2 (2%)	1 (1%)	14	50
All	All	2457/3207 (77%)	2280 (93%)	147 (6%)	30 (1%)	14	44

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	VAL
1	A	124	PRO
1	A	201	VAL
1	A	449	ILE
4	D	53	VAL

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	412/412 (100%)	395 (96%)	17 (4%)	26	49
1	E	412/412 (100%)	395 (96%)	17 (4%)	26	49
1	I	412/412 (100%)	395 (96%)	17 (4%)	26	49
2	B	110/129 (85%)	106 (96%)	4 (4%)	30	52
2	F	110/129 (85%)	106 (96%)	4 (4%)	30	52
2	J	110/129 (85%)	106 (96%)	4 (4%)	30	52
3	C	103/200 (52%)	100 (97%)	3 (3%)	37	58
3	G	103/200 (52%)	100 (97%)	3 (3%)	37	58
3	K	103/200 (52%)	100 (97%)	3 (3%)	37	58
4	D	90/181 (50%)	88 (98%)	2 (2%)	47	65
4	H	90/181 (50%)	88 (98%)	2 (2%)	47	65
4	L	90/181 (50%)	88 (98%)	2 (2%)	47	65
All	All	2145/2766 (78%)	2067 (96%)	78 (4%)	32	52

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	196	CYS
2	J	602	LEU
1	I	262	ASN
1	I	392	ASN
3	K	89	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	203	GLN
2	J	591	GLN
2	J	540	GLN
3	K	39	GLN
4	D	40	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

69 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$
5	NAG	M	1	5,1	14,14,15	0.70	1 (7%)	17,19,21	0.73	0
5	NAG	M	2	5	14,14,15	0.85	1 (7%)	17,19,21	0.51	0
6	NAG	N	1	1,6	14,14,15	0.71	1 (7%)	17,19,21	0.50	0
6	NAG	N	2	6	14,14,15	0.38	0	17,19,21	0.58	0
6	BMA	N	3	6	11,11,12	1.03	1 (9%)	15,15,17	0.82	1 (6%)
6	MAN	N	4	6	11,11,12	0.81	1 (9%)	15,15,17	1.10	2 (13%)
6	MAN	N	5	6	11,11,12	0.91	0	15,15,17	1.10	1 (6%)
6	BMA	N	6	6	11,11,12	0.98	0	15,15,17	1.07	1 (6%)
6	MAN	N	7	6	11,11,12	0.73	0	15,15,17	0.97	2 (13%)
7	NAG	O	1	1,7	14,14,15	2.06	6 (42%)	17,19,21	3.01	7 (41%)
7	NAG	O	2	7	14,14,15	0.87	0	17,19,21	2.74	7 (41%)
7	BMA	O	3	7	11,11,12	0.70	0	15,15,17	1.77	3 (20%)
7	NAG	O	4	7	14,14,15	0.54	0	17,19,21	1.82	6 (35%)
8	NAG	P	1	8,1	14,14,15	1.93	5 (35%)	17,19,21	2.94	9 (52%)
8	NAG	P	2	8	14,14,15	0.51	0	17,19,21	2.40	7 (41%)
8	BMA	P	3	8	11,11,12	0.67	0	15,15,17	2.03	5 (33%)
5	NAG	Q	1	5,1	14,14,15	1.94	4 (28%)	17,19,21	2.54	7 (41%)
5	NAG	Q	2	5	14,14,15	0.99	2 (14%)	17,19,21	1.98	5 (29%)
8	NAG	R	1	8,1	14,14,15	0.85	1 (7%)	17,19,21	1.79	4 (23%)
8	NAG	R	2	8	14,14,15	0.84	0	17,19,21	2.03	5 (29%)
8	BMA	R	3	8	11,11,12	0.47	0	15,15,17	1.30	3 (20%)
5	NAG	S	1	5,1	14,14,15	1.40	2 (14%)	17,19,21	1.75	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	S	2	5	14,14,15	0.70	1 (7%)	17,19,21	2.27	7 (41%)
5	NAG	T	1	5,1	14,14,15	0.70	1 (7%)	17,19,21	0.73	0
5	NAG	T	2	5	14,14,15	0.85	1 (7%)	17,19,21	0.51	0
6	NAG	U	1	1,6	14,14,15	0.71	1 (7%)	17,19,21	0.49	0
6	NAG	U	2	6	14,14,15	0.37	0	17,19,21	0.57	0
6	BMA	U	3	6	11,11,12	1.03	1 (9%)	15,15,17	0.82	1 (6%)
6	MAN	U	4	6	11,11,12	0.80	1 (9%)	15,15,17	1.10	2 (13%)
6	MAN	U	5	6	11,11,12	0.92	0	15,15,17	1.10	1 (6%)
6	BMA	U	6	6	11,11,12	0.99	0	15,15,17	1.06	1 (6%)
6	MAN	U	7	6	11,11,12	0.74	0	15,15,17	0.97	2 (13%)
7	NAG	V	1	1,7	14,14,15	2.06	6 (42%)	17,19,21	3.00	7 (41%)
7	NAG	V	2	7	14,14,15	0.86	0	17,19,21	2.74	7 (41%)
7	BMA	V	3	7	11,11,12	0.70	0	15,15,17	1.77	3 (20%)
7	NAG	V	4	7	14,14,15	0.54	0	17,19,21	1.82	6 (35%)
8	NAG	W	1	8,1	14,14,15	1.93	5 (35%)	17,19,21	2.94	9 (52%)
8	NAG	W	2	8	14,14,15	0.51	0	17,19,21	2.40	7 (41%)
8	BMA	W	3	8	11,11,12	0.67	0	15,15,17	2.03	5 (33%)
5	NAG	X	1	5,1	14,14,15	1.94	4 (28%)	17,19,21	2.54	7 (41%)
5	NAG	X	2	5	14,14,15	0.99	2 (14%)	17,19,21	1.98	5 (29%)
8	NAG	Y	1	8,1	14,14,15	0.85	1 (7%)	17,19,21	1.79	4 (23%)
8	NAG	Y	2	8	14,14,15	0.84	0	17,19,21	2.03	5 (29%)
8	BMA	Y	3	8	11,11,12	0.49	0	15,15,17	1.29	3 (20%)
5	NAG	Z	1	5,1	14,14,15	1.40	2 (14%)	17,19,21	1.75	5 (29%)
5	NAG	Z	2	5	14,14,15	0.71	1 (7%)	17,19,21	2.27	7 (41%)
5	NAG	a	1	5,1	14,14,15	0.71	1 (7%)	17,19,21	0.74	0
5	NAG	a	2	5	14,14,15	0.85	1 (7%)	17,19,21	0.51	0
6	NAG	b	1	1,6	14,14,15	0.71	1 (7%)	17,19,21	0.50	0
6	NAG	b	2	6	14,14,15	0.37	0	17,19,21	0.58	0
6	BMA	b	3	6	11,11,12	1.03	1 (9%)	15,15,17	0.82	1 (6%)
6	MAN	b	4	6	11,11,12	0.81	1 (9%)	15,15,17	1.10	2 (13%)
6	MAN	b	5	6	11,11,12	0.91	0	15,15,17	1.10	1 (6%)
6	BMA	b	6	6	11,11,12	0.98	0	15,15,17	1.07	1 (6%)
6	MAN	b	7	6	11,11,12	0.74	0	15,15,17	0.97	2 (13%)
7	NAG	c	1	1,7	14,14,15	2.06	6 (42%)	17,19,21	3.00	7 (41%)
7	NAG	c	2	7	14,14,15	0.86	0	17,19,21	2.75	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	BMA	c	3	7	11,11,12	0.70	0	15,15,17	1.77	3 (20%)
7	NAG	c	4	7	14,14,15	0.54	0	17,19,21	1.81	6 (35%)
8	NAG	d	1	8,1	14,14,15	1.92	5 (35%)	17,19,21	2.94	9 (52%)
8	NAG	d	2	8	14,14,15	0.51	0	17,19,21	2.41	7 (41%)
8	BMA	d	3	8	11,11,12	0.67	0	15,15,17	2.03	5 (33%)
5	NAG	e	1	5,1	14,14,15	1.94	4 (28%)	17,19,21	2.54	7 (41%)
5	NAG	e	2	5	14,14,15	0.99	2 (14%)	17,19,21	1.98	5 (29%)
8	NAG	f	1	8,1	14,14,15	0.84	0	17,19,21	1.79	4 (23%)
8	NAG	f	2	8	14,14,15	0.83	0	17,19,21	2.03	5 (29%)
8	BMA	f	3	8	11,11,12	0.49	0	15,15,17	1.29	2 (13%)
5	NAG	g	1	5,1	14,14,15	1.40	2 (14%)	17,19,21	1.75	5 (29%)
5	NAG	g	2	5	14,14,15	0.71	1 (7%)	17,19,21	2.27	7 (41%)

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	M	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	2/6/23/26	0/1/1/1
6	NAG	N	1	1,6	-	4/6/23/26	0/1/1/1
6	NAG	N	2	6	-	4/6/23/26	0/1/1/1
6	BMA	N	3	6	-	2/2/19/22	0/1/1/1
6	MAN	N	4	6	-	2/2/19/22	0/1/1/1
6	MAN	N	5	6	-	1/2/19/22	0/1/1/1
6	BMA	N	6	6	-	2/2/19/22	0/1/1/1
6	MAN	N	7	6	-	2/2/19/22	0/1/1/1
7	NAG	O	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	O	2	7	-	2/6/23/26	0/1/1/1
7	BMA	O	3	7	-	0/2/19/22	0/1/1/1
7	NAG	O	4	7	-	1/6/23/26	0/1/1/1
8	NAG	P	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	P	2	8	-	0/6/23/26	0/1/1/1
8	BMA	P	3	8	-	1/2/19/22	0/1/1/1
5	NAG	Q	1	5,1	-	5/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	R	1	8,1	-	4/6/23/26	0/1/1/1
8	NAG	R	2	8	-	2/6/23/26	0/1/1/1
8	BMA	R	3	8	-	0/2/19/22	0/1/1/1
5	NAG	S	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	S	2	5	-	2/6/23/26	0/1/1/1
5	NAG	T	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	T	2	5	-	2/6/23/26	0/1/1/1
6	NAG	U	1	1,6	-	4/6/23/26	0/1/1/1
6	NAG	U	2	6	-	4/6/23/26	0/1/1/1
6	BMA	U	3	6	-	2/2/19/22	0/1/1/1
6	MAN	U	4	6	-	2/2/19/22	0/1/1/1
6	MAN	U	5	6	-	1/2/19/22	0/1/1/1
6	BMA	U	6	6	-	2/2/19/22	0/1/1/1
6	MAN	U	7	6	-	2/2/19/22	0/1/1/1
7	NAG	V	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	V	2	7	-	2/6/23/26	0/1/1/1
7	BMA	V	3	7	-	0/2/19/22	0/1/1/1
7	NAG	V	4	7	-	1/6/23/26	0/1/1/1
8	NAG	W	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	W	2	8	-	0/6/23/26	0/1/1/1
8	BMA	W	3	8	-	1/2/19/22	0/1/1/1
5	NAG	X	1	5,1	-	5/6/23/26	0/1/1/1
5	NAG	X	2	5	-	3/6/23/26	0/1/1/1
8	NAG	Y	1	8,1	-	4/6/23/26	0/1/1/1
8	NAG	Y	2	8	-	2/6/23/26	0/1/1/1
8	BMA	Y	3	8	-	0/2/19/22	0/1/1/1
5	NAG	Z	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	Z	2	5	-	2/6/23/26	0/1/1/1
5	NAG	a	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	a	2	5	-	2/6/23/26	0/1/1/1
6	NAG	b	1	1,6	-	4/6/23/26	0/1/1/1
6	NAG	b	2	6	-	4/6/23/26	0/1/1/1
6	BMA	b	3	6	-	2/2/19/22	0/1/1/1
6	MAN	b	4	6	-	2/2/19/22	0/1/1/1
6	MAN	b	5	6	-	1/2/19/22	0/1/1/1
6	BMA	b	6	6	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	b	7	6	-	2/2/19/22	0/1/1/1
7	NAG	c	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	c	2	7	-	2/6/23/26	0/1/1/1
7	BMA	c	3	7	-	0/2/19/22	0/1/1/1
7	NAG	c	4	7	-	1/6/23/26	0/1/1/1
8	NAG	d	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	d	2	8	-	0/6/23/26	0/1/1/1
8	BMA	d	3	8	-	1/2/19/22	0/1/1/1
5	NAG	e	1	5,1	-	5/6/23/26	0/1/1/1
5	NAG	e	2	5	-	3/6/23/26	0/1/1/1
8	NAG	f	1	8,1	-	4/6/23/26	0/1/1/1
8	NAG	f	2	8	-	2/6/23/26	0/1/1/1
8	BMA	f	3	8	-	0/2/19/22	0/1/1/1
5	NAG	g	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	g	2	5	-	2/6/23/26	0/1/1/1

The worst 5 of 77 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	e	1	NAG	O5-C1	-5.37	1.34	1.43
5	Q	1	NAG	O5-C1	-5.37	1.34	1.43
5	X	1	NAG	O5-C1	-5.36	1.34	1.43
8	W	1	NAG	O5-C1	-3.90	1.37	1.43
8	d	1	NAG	O5-C1	-3.88	1.37	1.43

The worst 5 of 260 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	V	1	NAG	O5-C1-C2	-6.55	101.15	111.29
7	O	1	NAG	O5-C1-C2	-6.54	101.17	111.29
7	c	1	NAG	O5-C1-C2	-6.54	101.17	111.29
7	c	2	NAG	O5-C1-C2	-5.98	102.04	111.29
7	V	2	NAG	O5-C1-C2	-5.98	102.04	111.29

There are no chirality outliers.

5 of 138 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	Q	1	NAG	C1-C2-N2-C7

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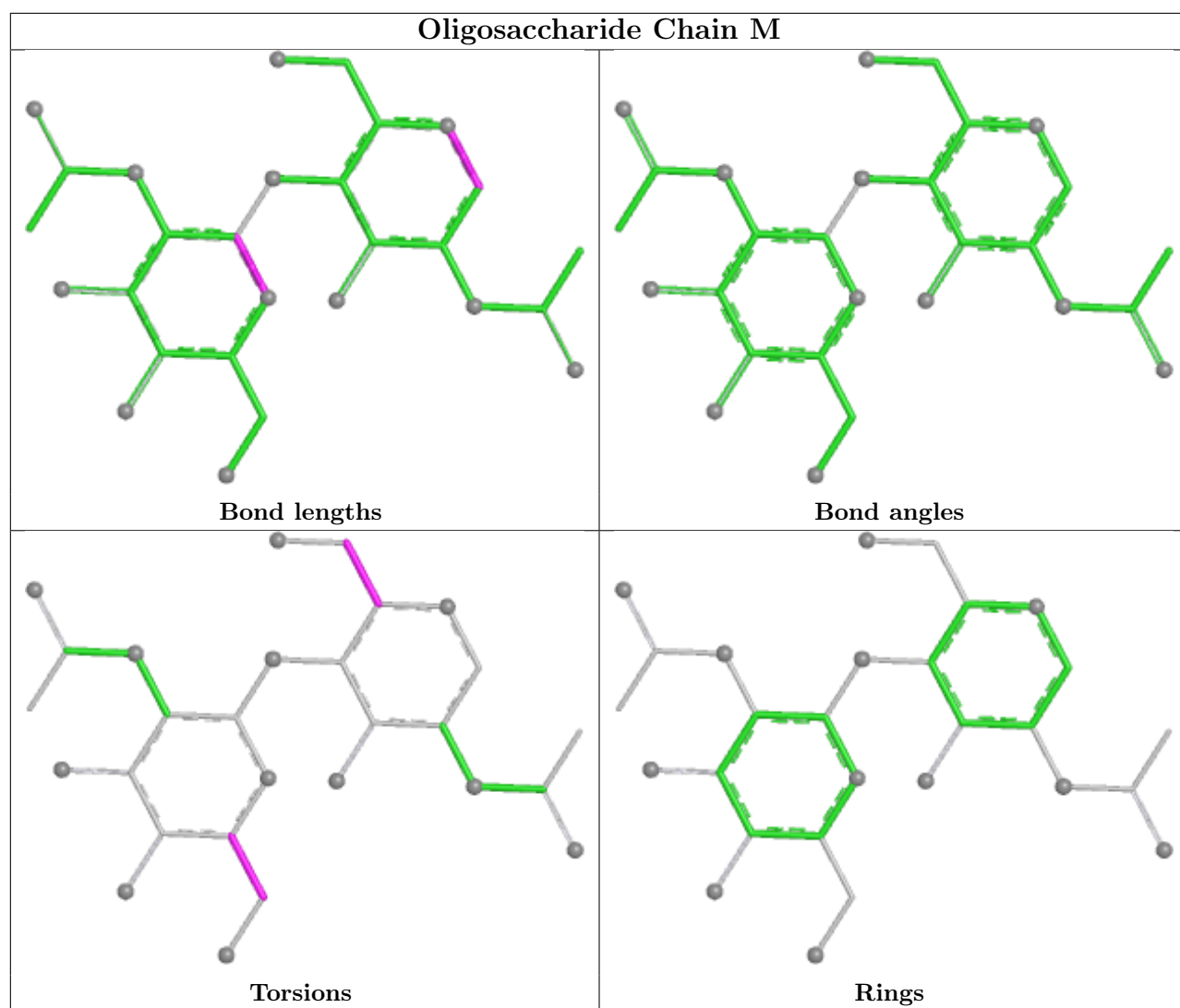
Mol	Chain	Res	Type	Atoms
5	Q	1	NAG	C8-C7-N2-C2
5	Q	1	NAG	O7-C7-N2-C2
5	X	1	NAG	C1-C2-N2-C7
5	X	1	NAG	C8-C7-N2-C2

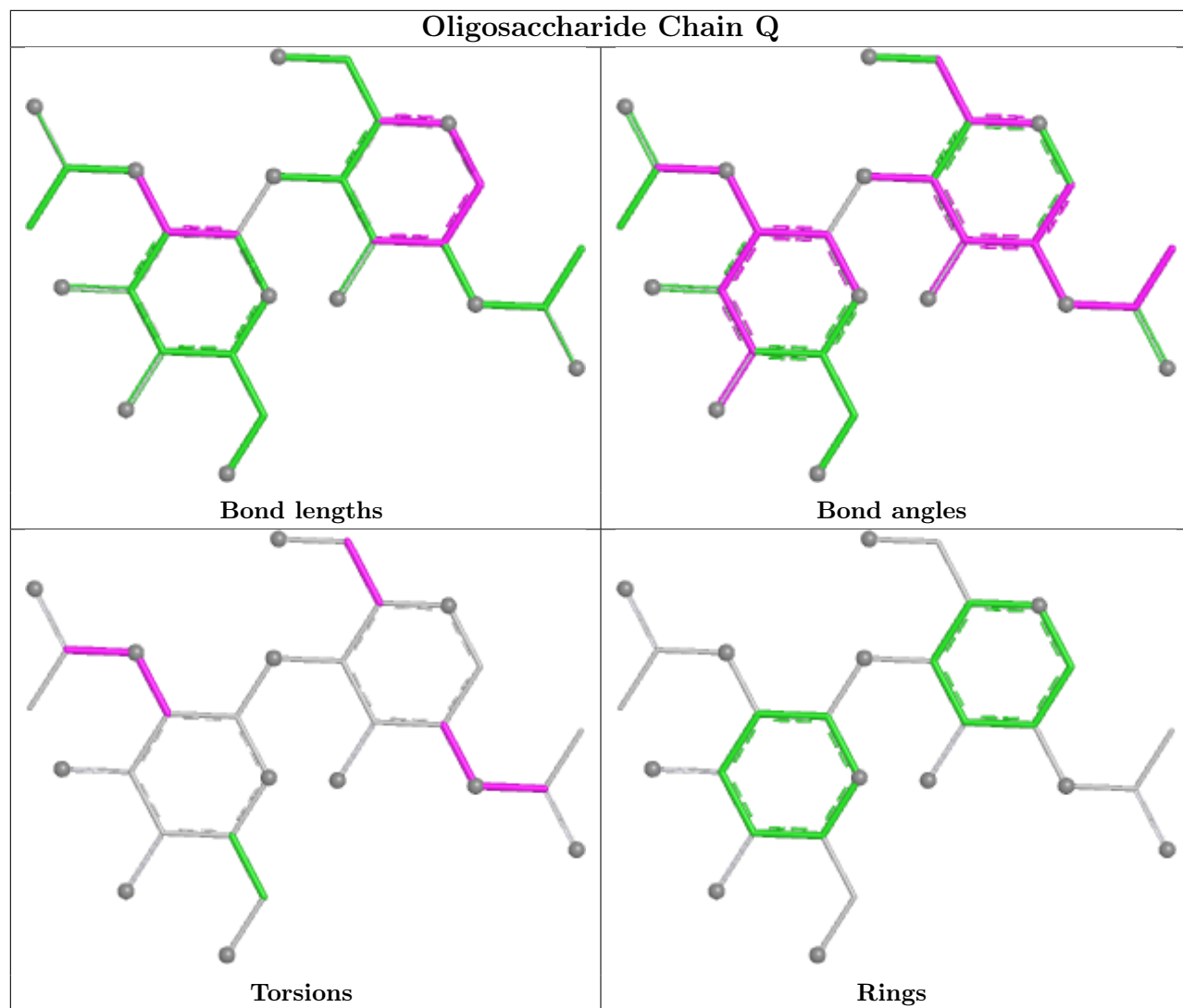
There are no ring outliers.

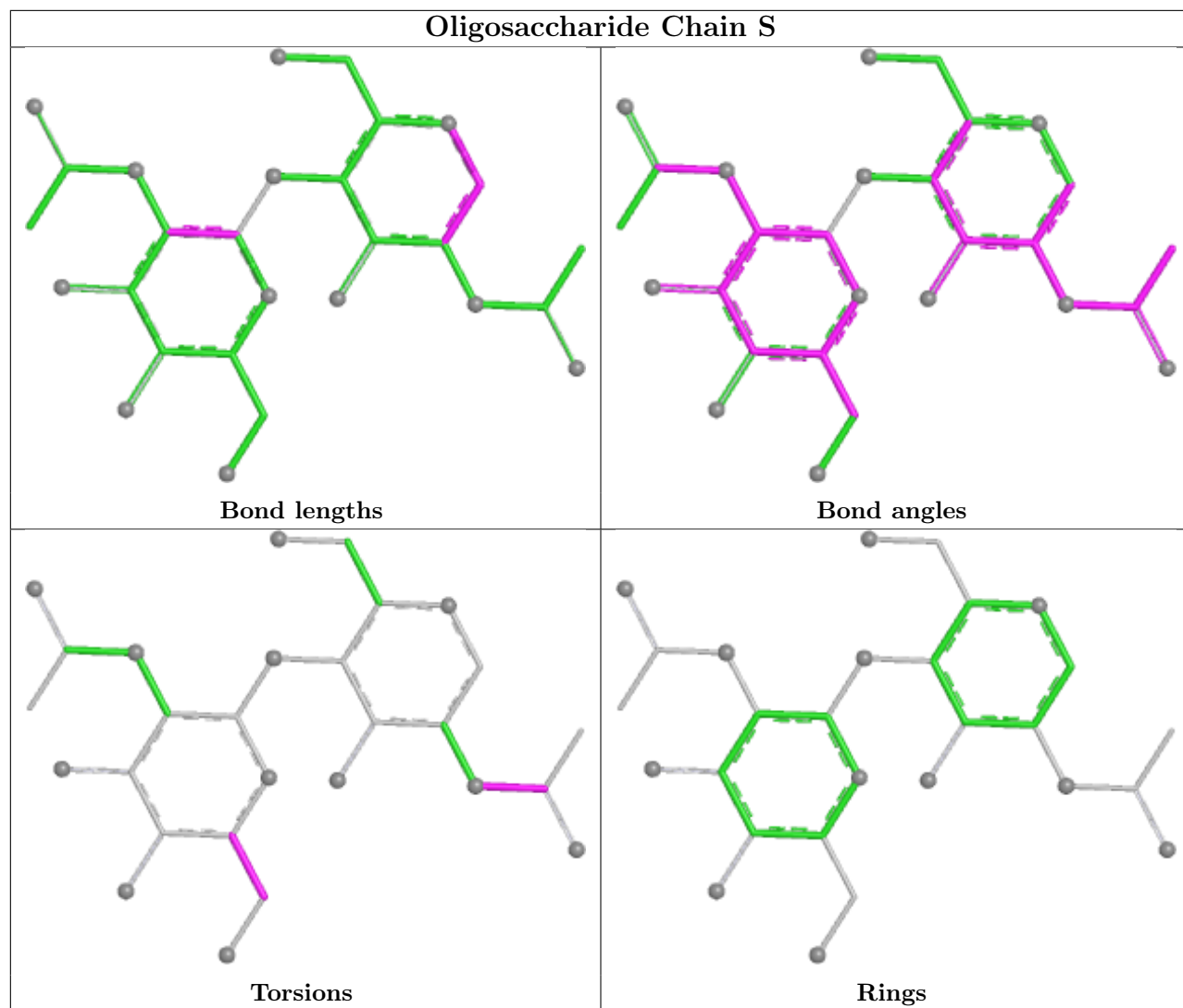
12 monomers are involved in 21 short contacts:

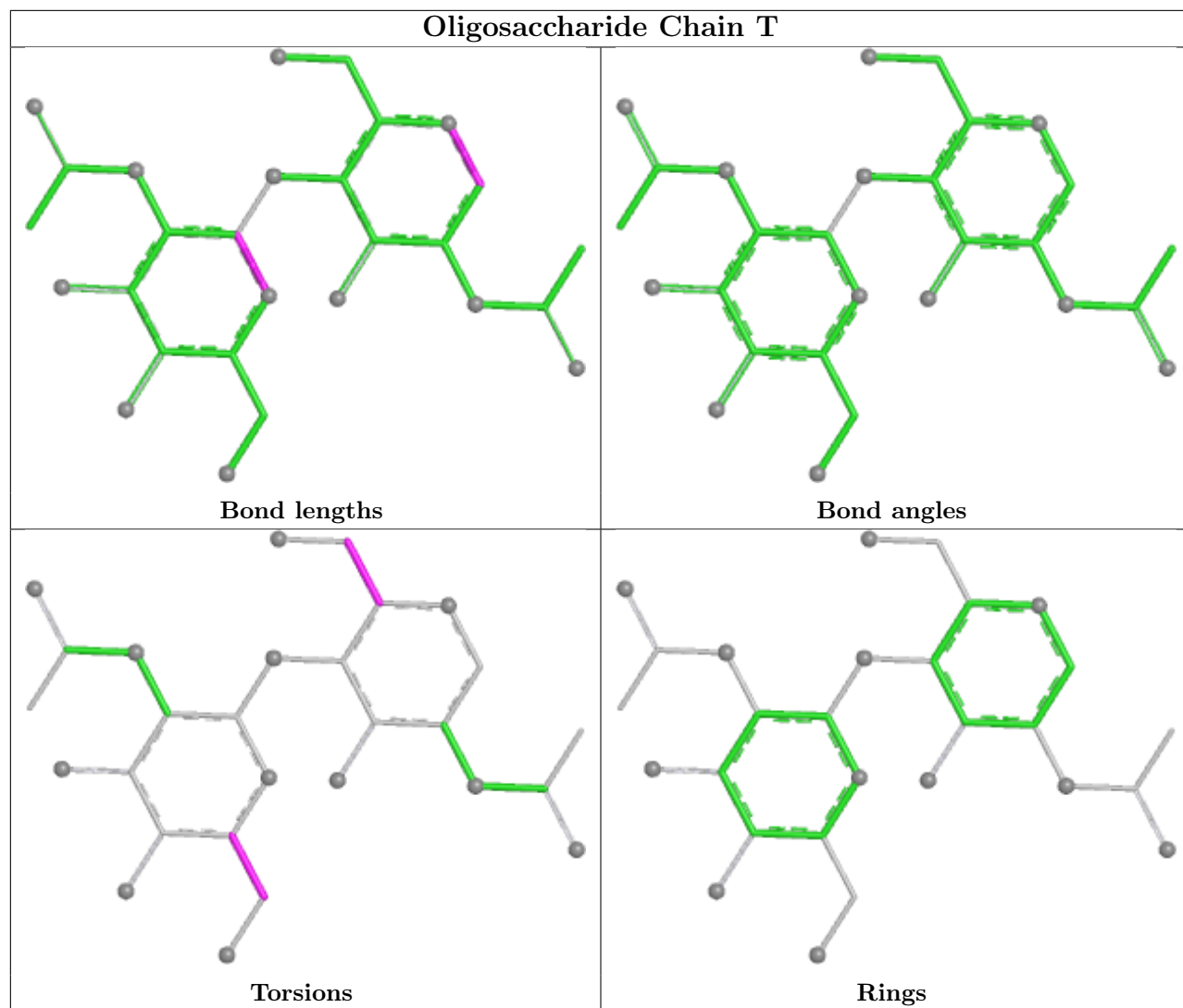
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	N	2	NAG	1	0
5	Q	1	NAG	1	0
8	Y	1	NAG	4	0
8	Y	2	NAG	2	0
5	Z	2	NAG	2	0
7	V	2	NAG	1	0
8	R	1	NAG	3	0
5	S	2	NAG	2	0
5	X	1	NAG	1	0
8	R	2	NAG	2	0
5	X	2	NAG	2	0
5	Q	2	NAG	2	0

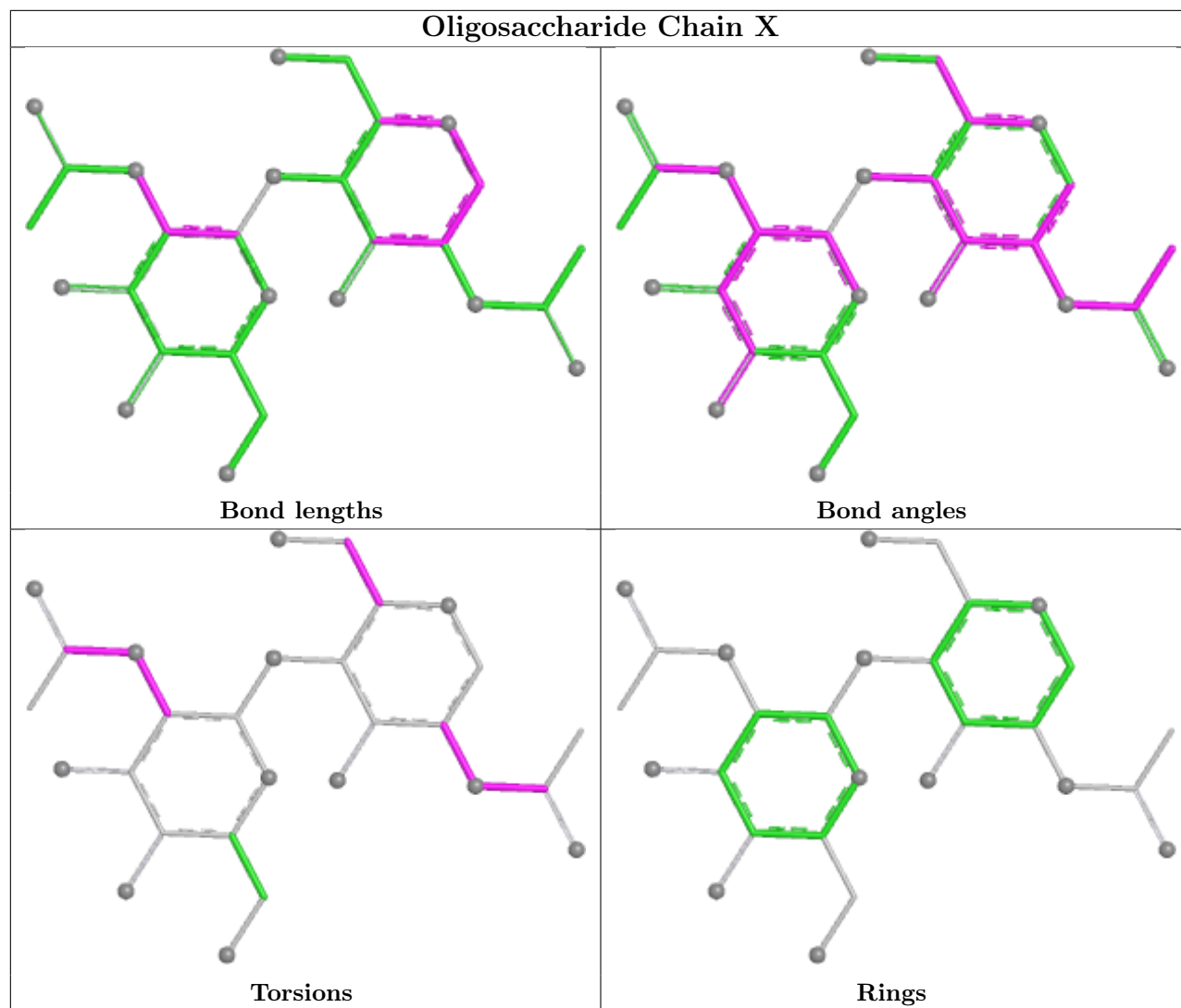
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

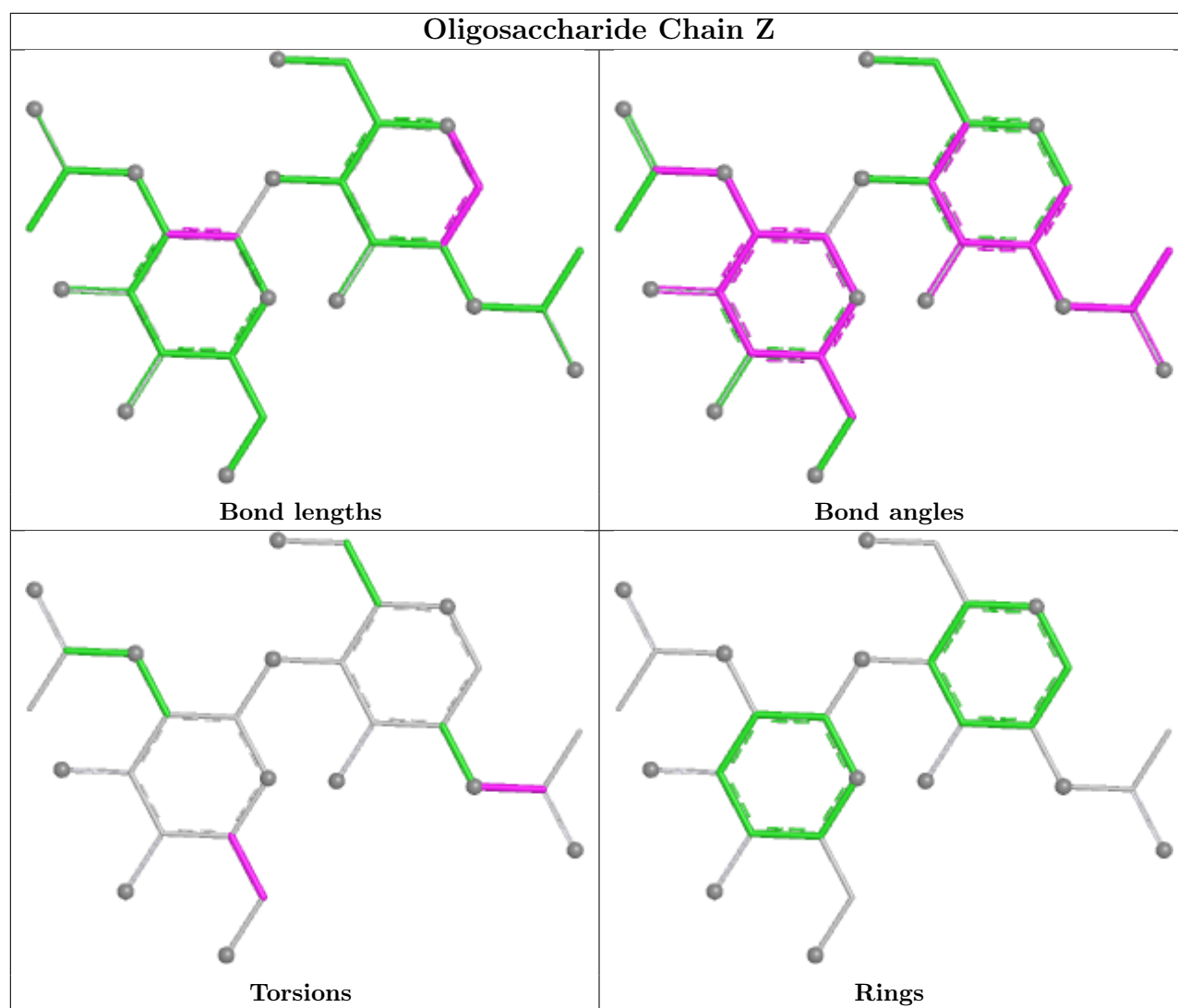


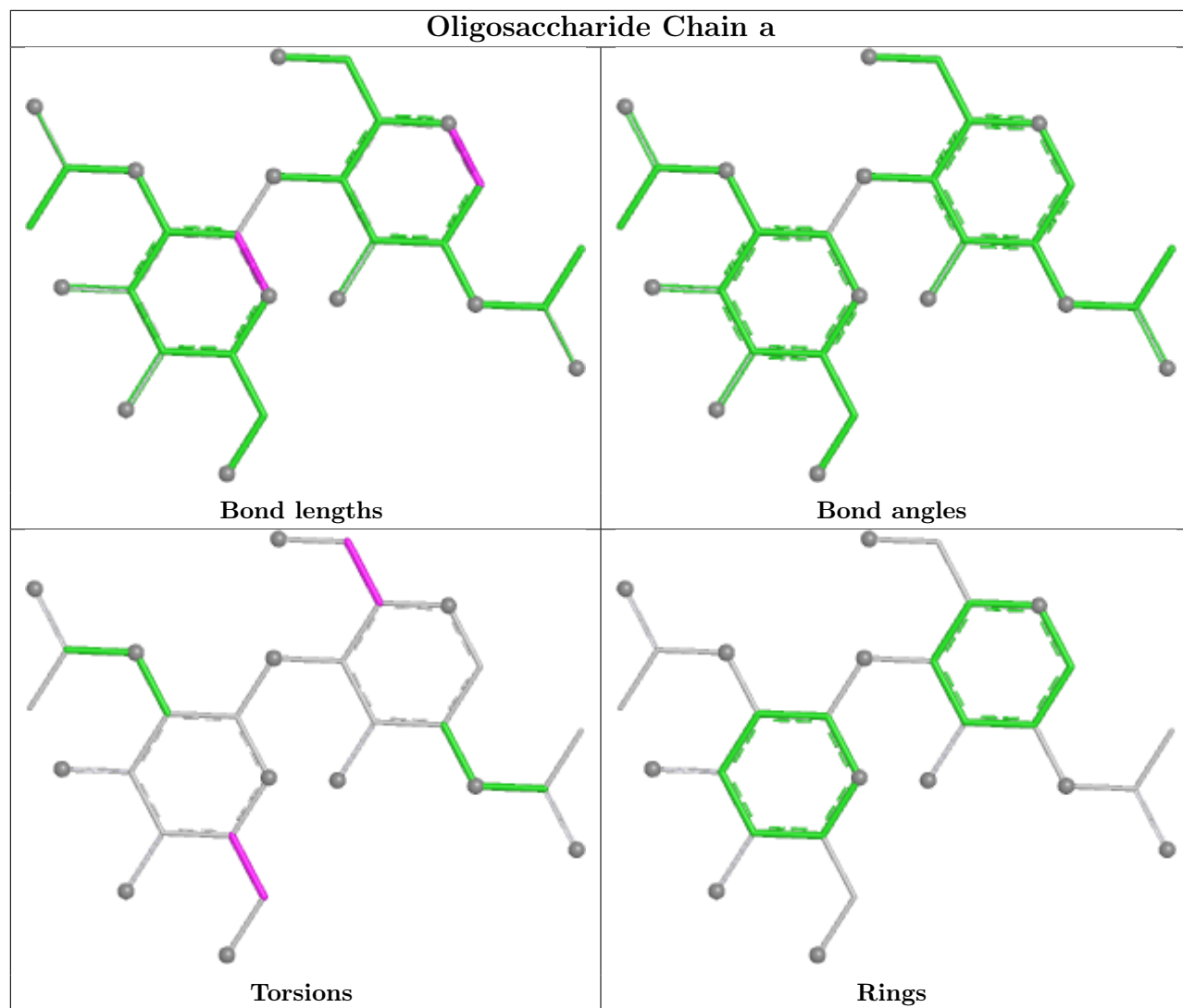


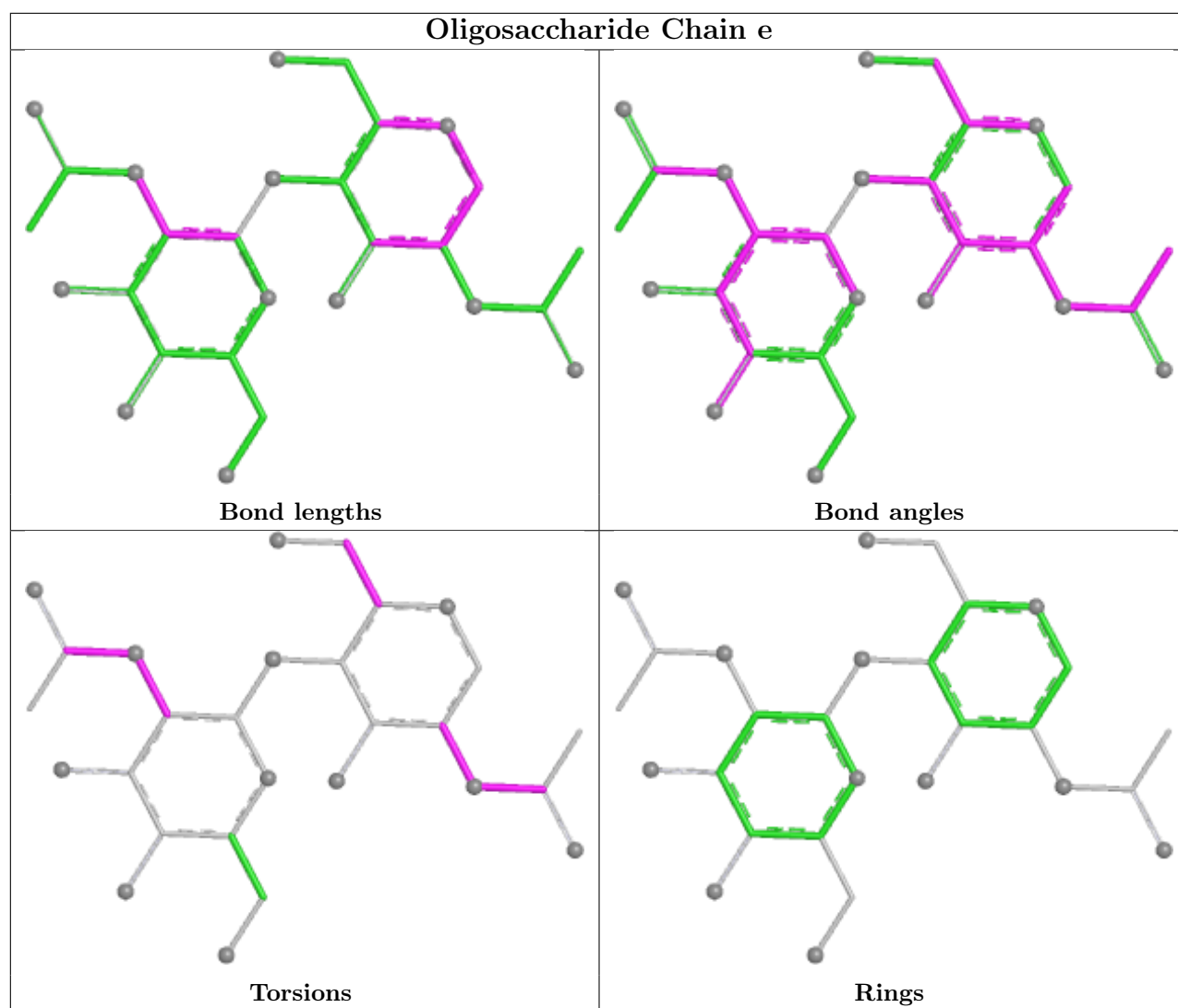


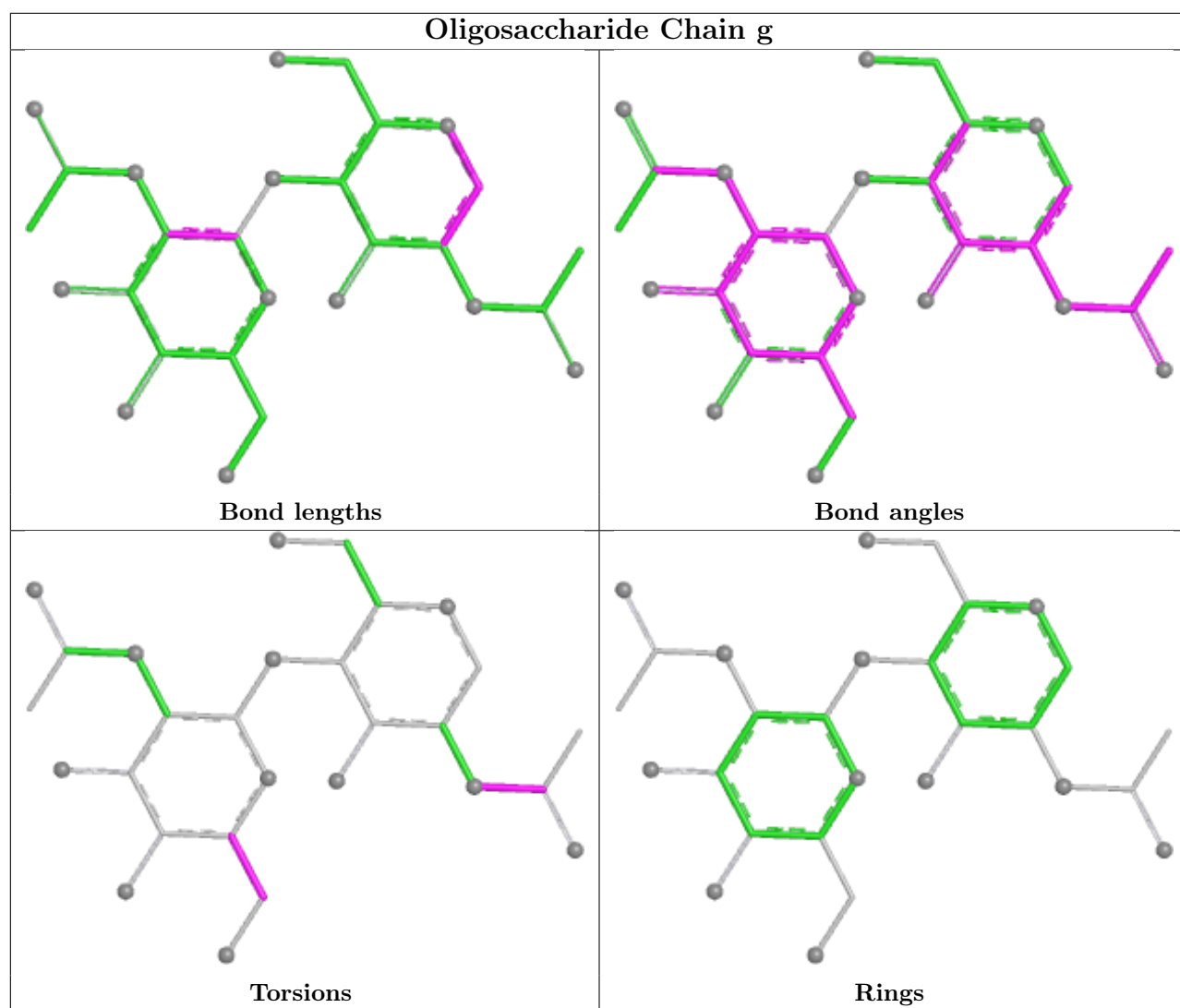


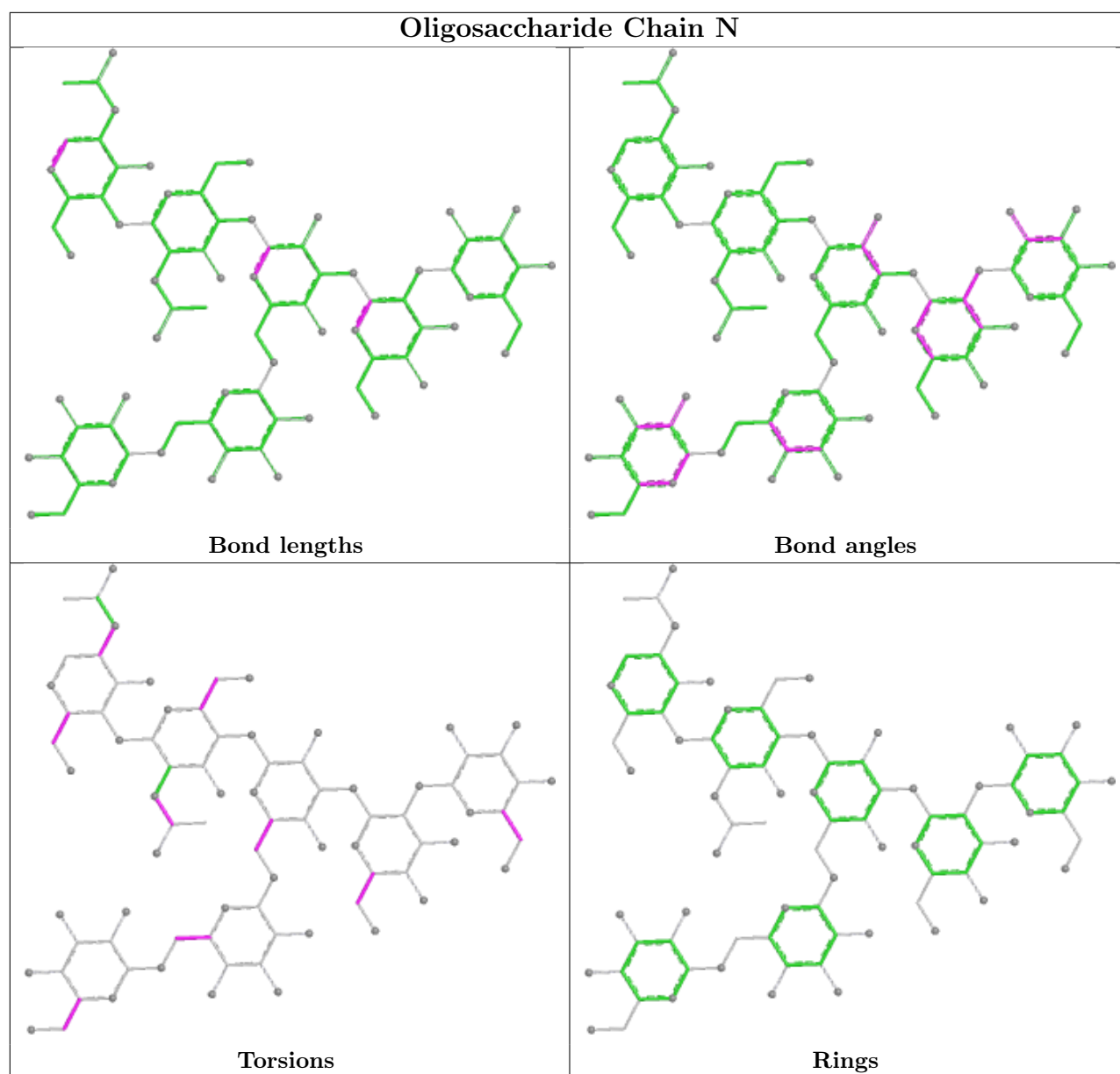


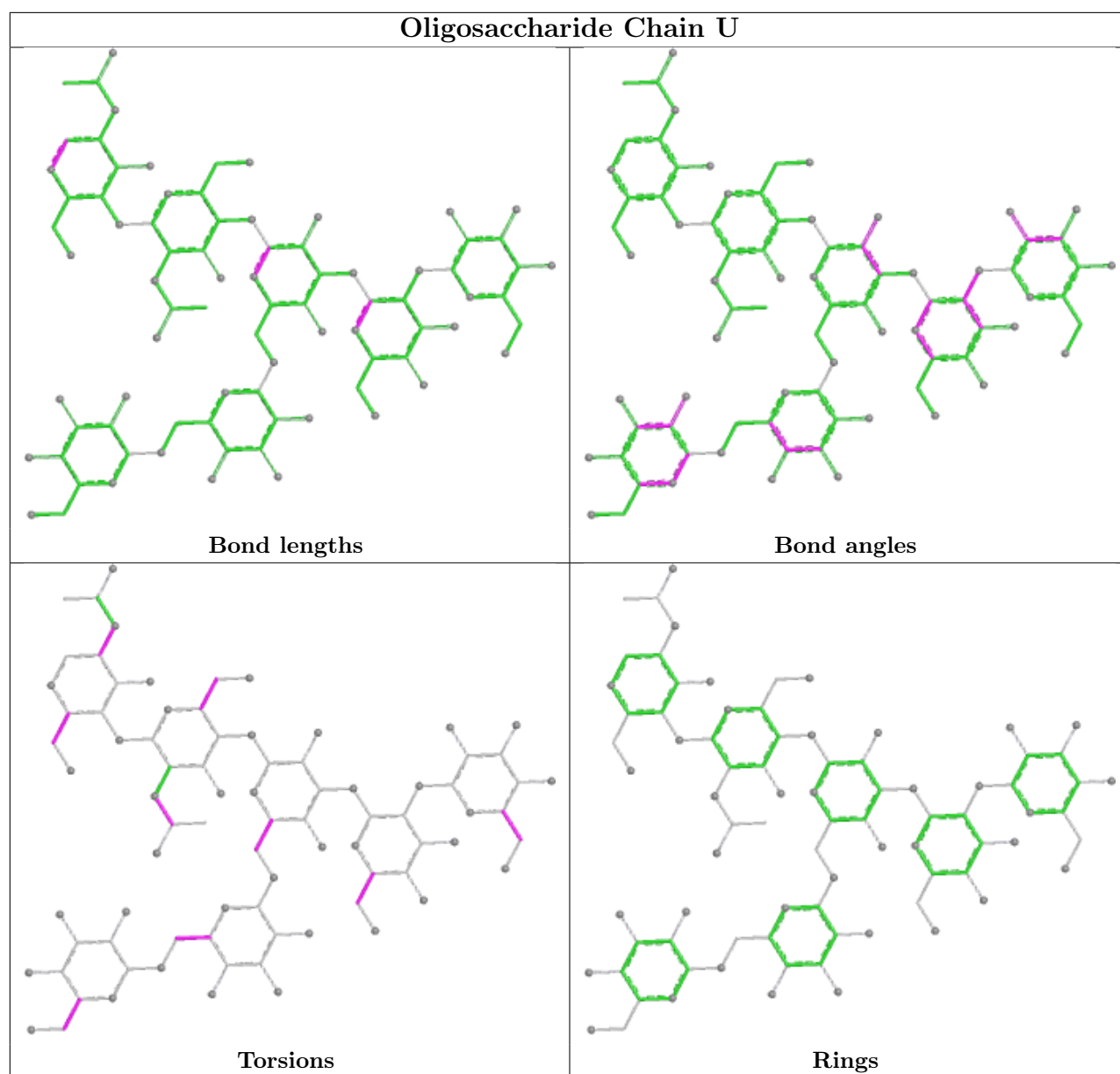


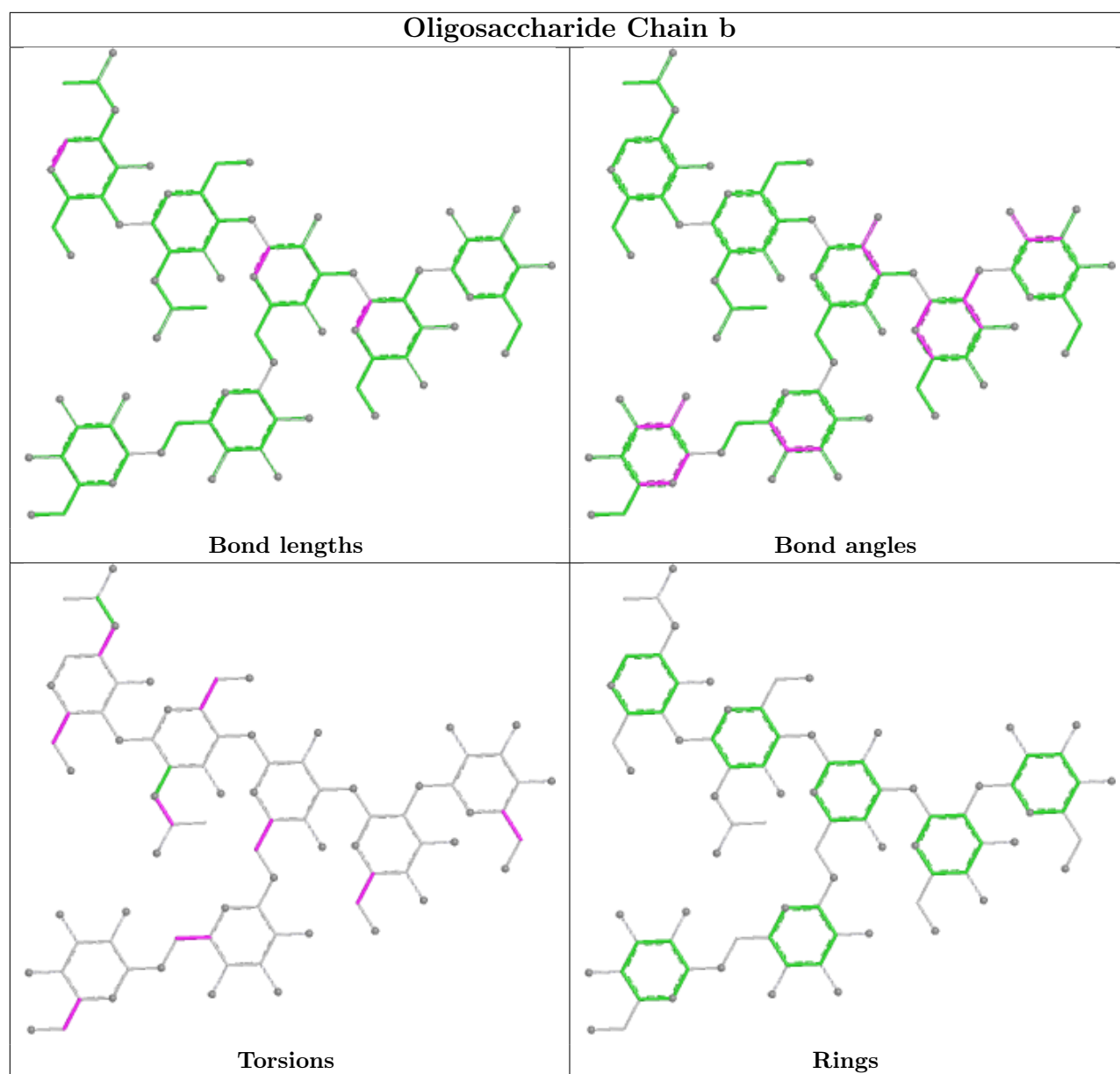


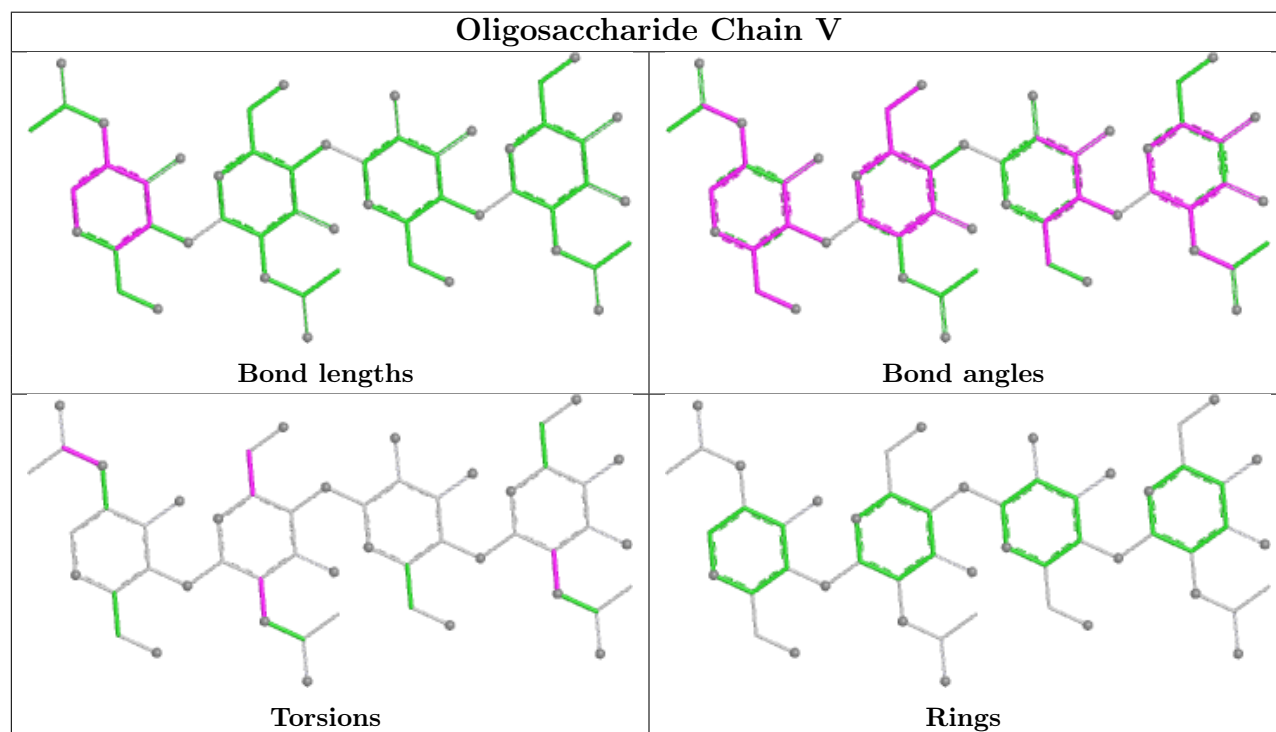
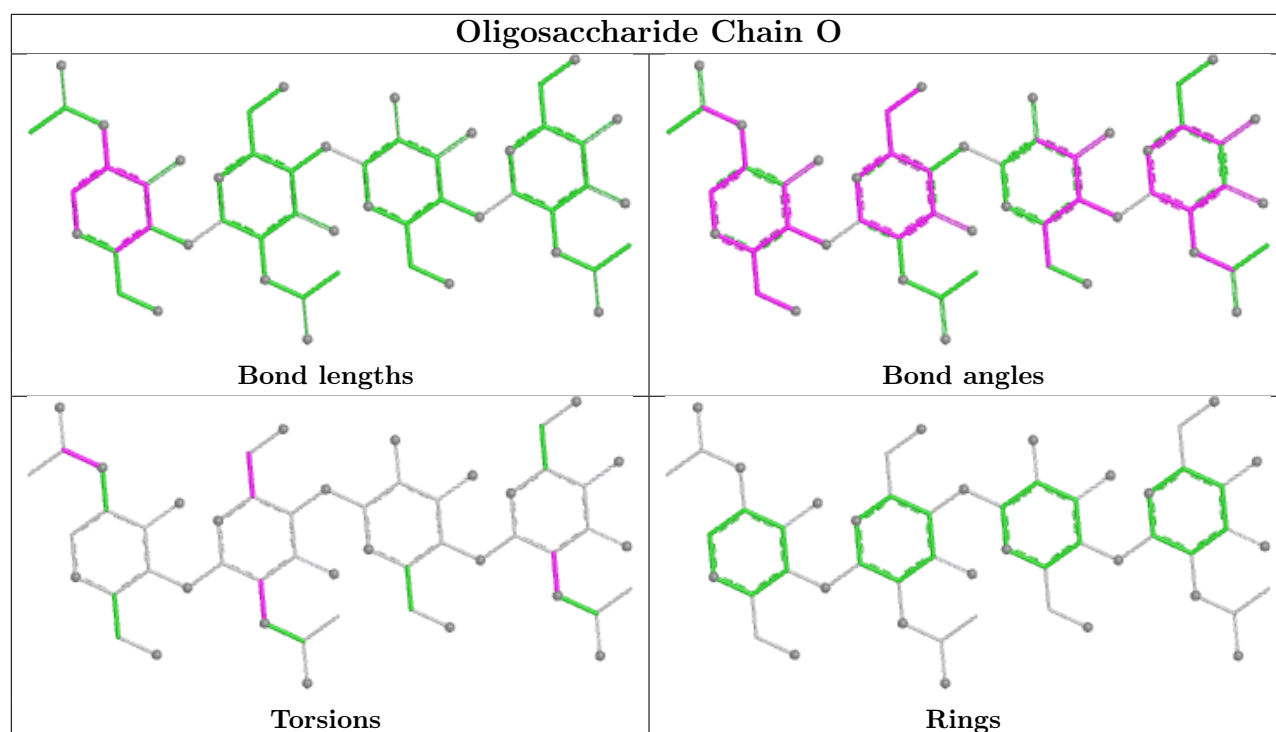


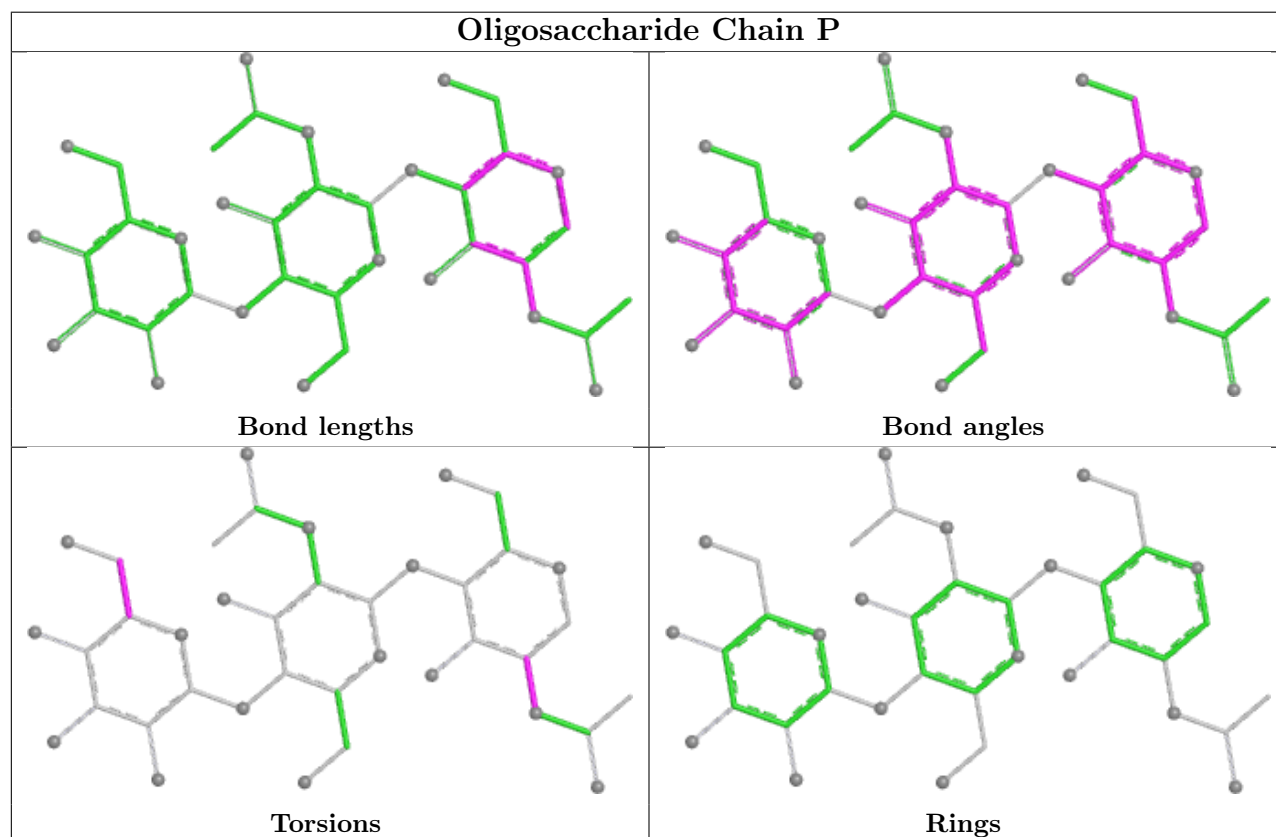
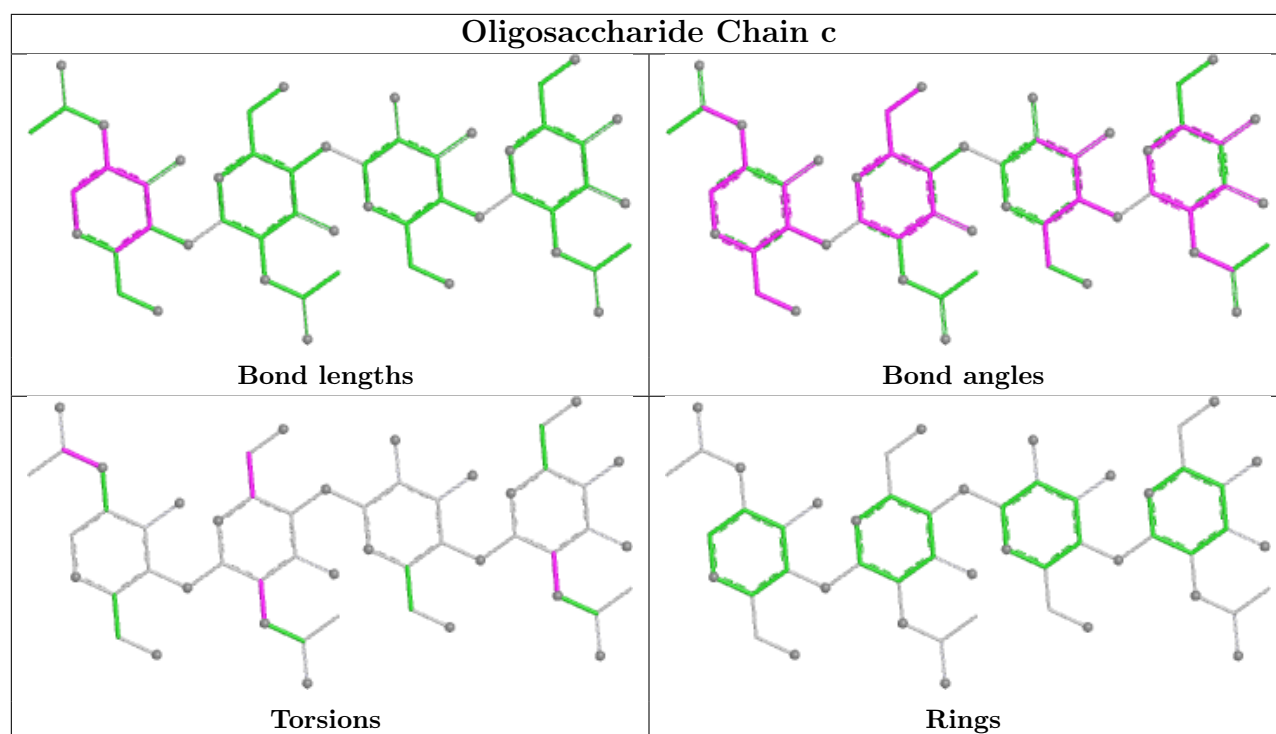


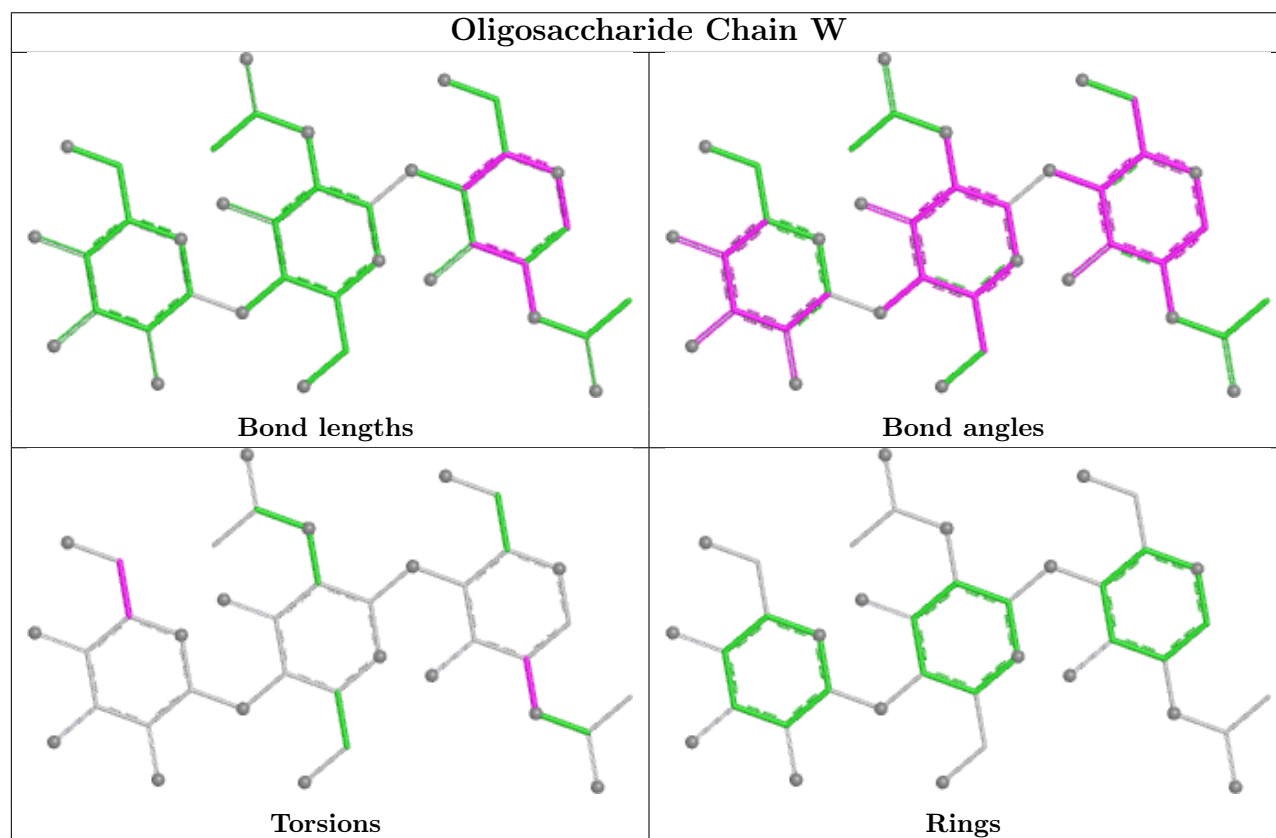
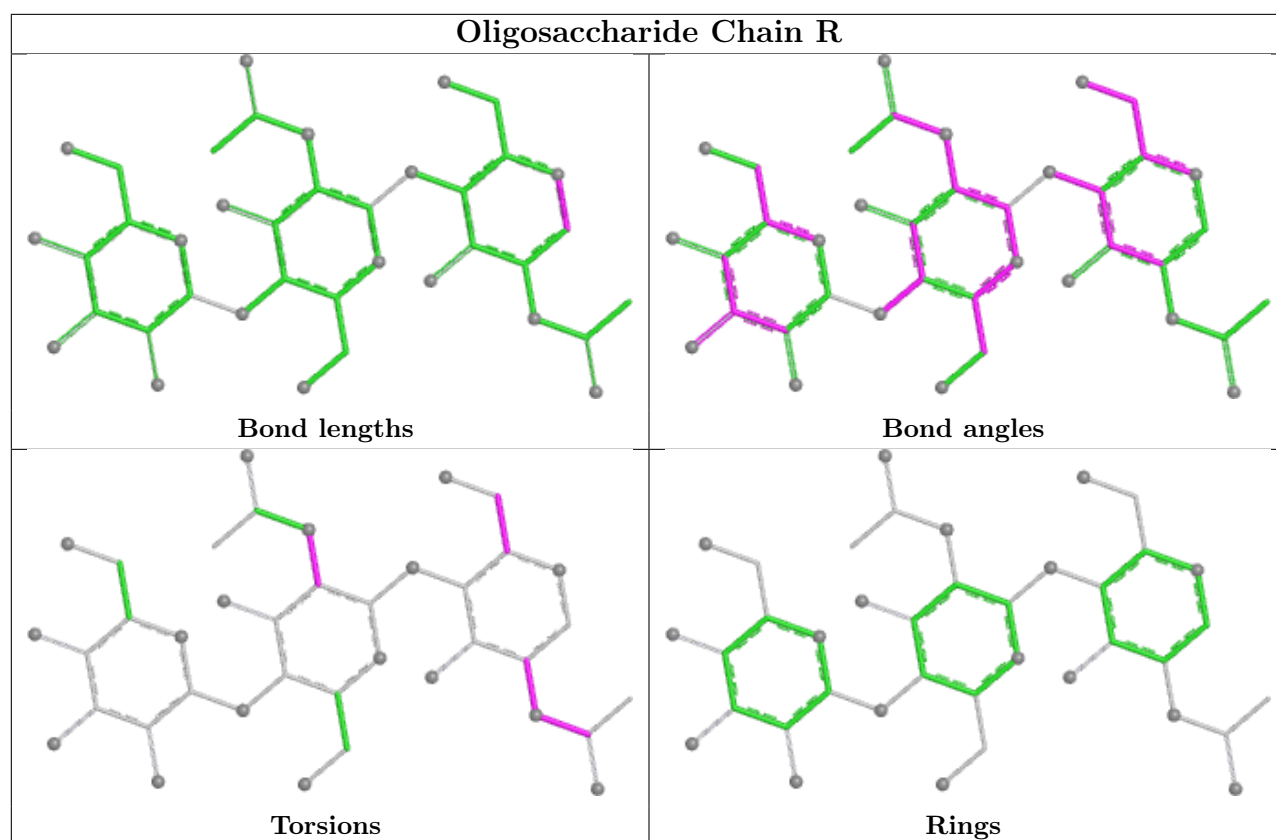


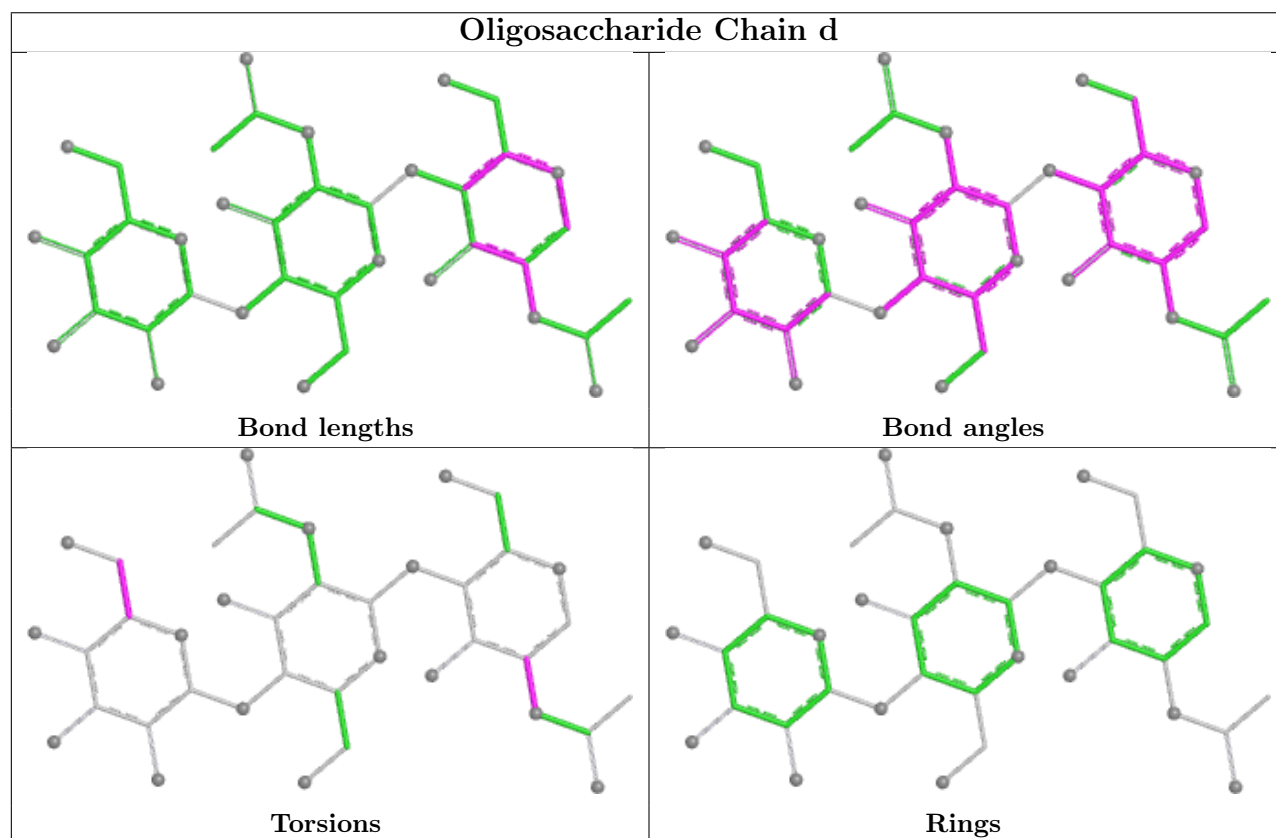
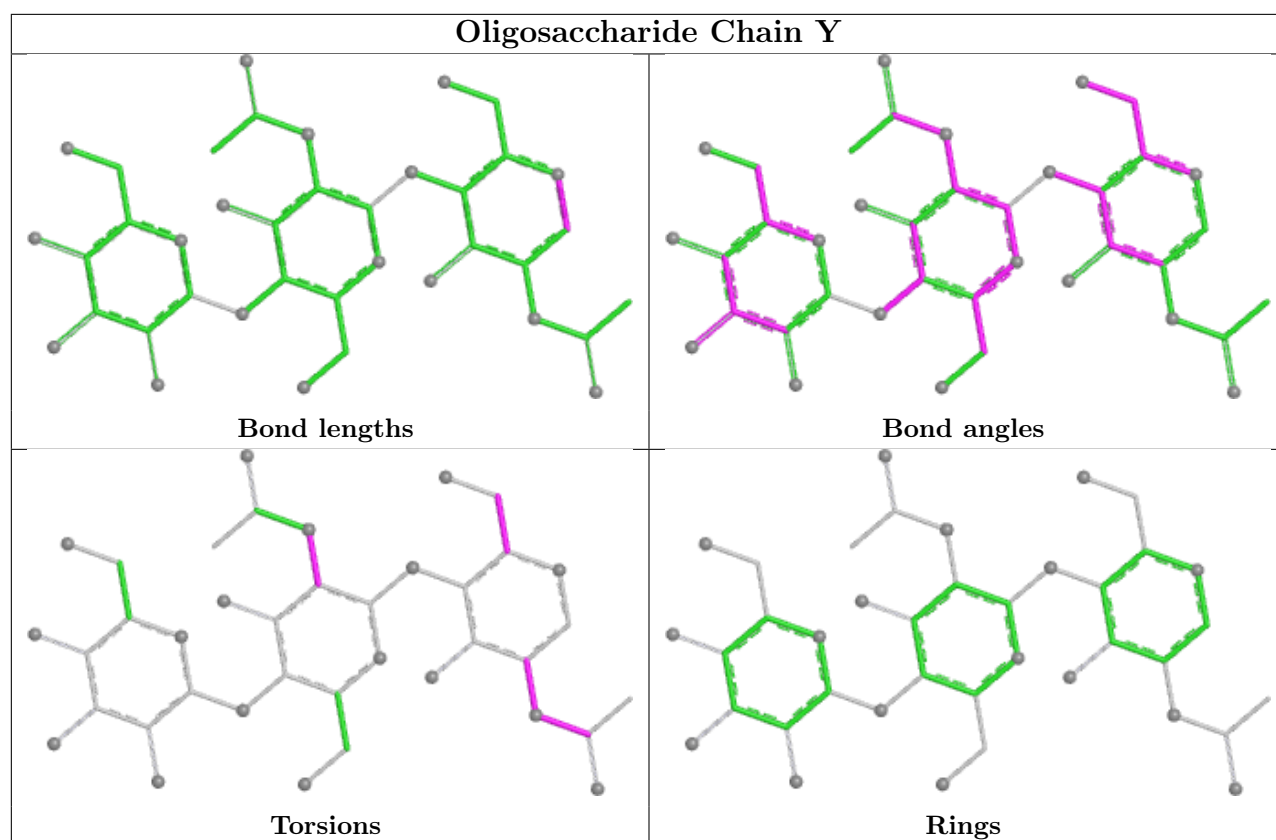


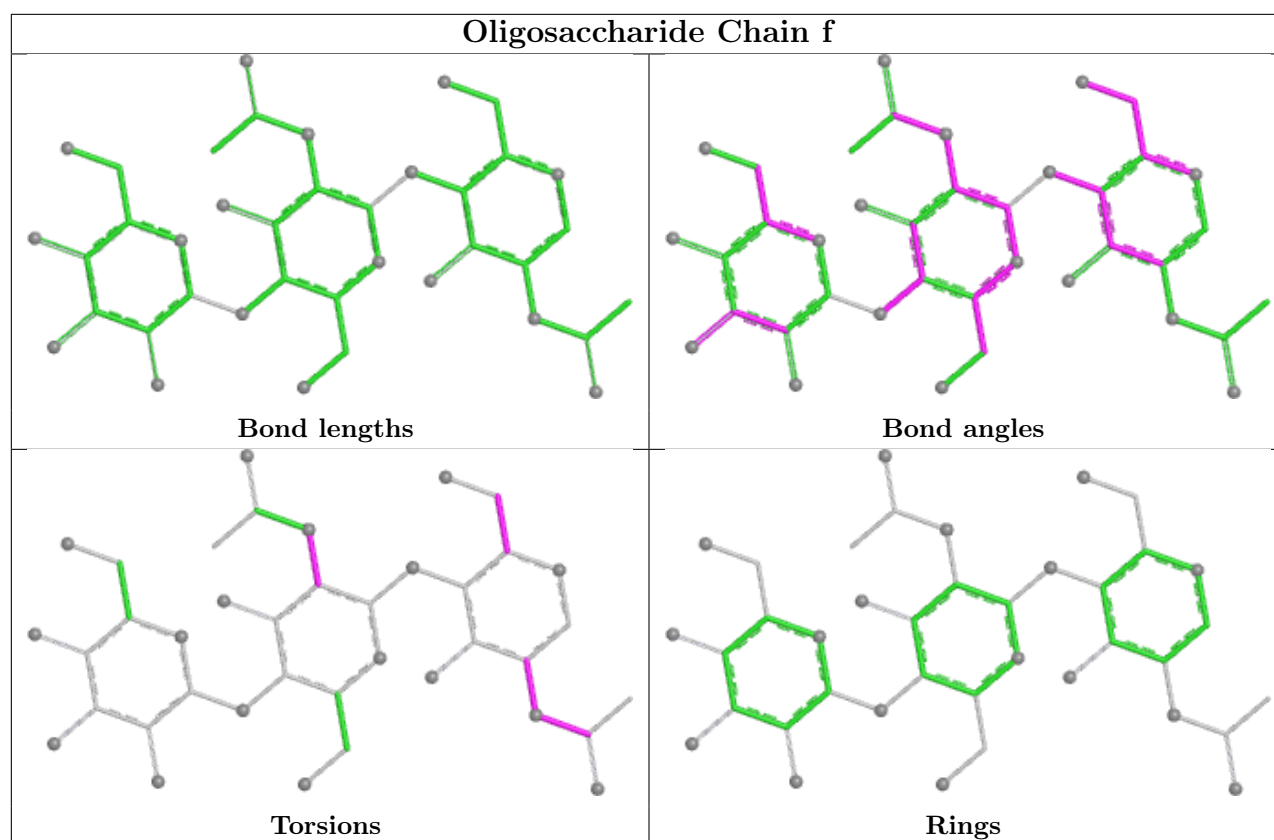












5.6 Ligand geometry [i](#)

27 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
9	NAG	E	630	1	14,14,15	0.88	1 (7%)	17,19,21	2.22	7 (41%)
9	NAG	A	622	1	14,14,15	1.43	4 (28%)	17,19,21	2.28	7 (41%)
9	NAG	I	632	1	14,14,15	1.12	1 (7%)	17,19,21	2.61	6 (35%)
9	NAG	E	626	1	14,14,15	0.84	0	17,19,21	2.39	6 (35%)
9	NAG	I	619	1	14,14,15	1.36	3 (21%)	17,19,21	1.90	6 (35%)
9	NAG	E	619	1	14,14,15	1.36	3 (21%)	17,19,21	1.89	6 (35%)
9	NAG	I	626	1	14,14,15	0.84	0	17,19,21	2.40	6 (35%)
9	NAG	I	622	1	14,14,15	1.43	4 (28%)	17,19,21	2.28	7 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	I	631	1	14,14,15	1.15	1 (7%)	17,19,21	1.71	6 (35%)
9	NAG	A	618	1	14,14,15	1.58	4 (28%)	17,19,21	2.50	6 (35%)
9	NAG	E	632	1	14,14,15	1.11	1 (7%)	17,19,21	2.61	6 (35%)
9	NAG	A	619	1	14,14,15	1.36	3 (21%)	17,19,21	1.89	6 (35%)
9	NAG	E	618	1	14,14,15	1.57	4 (28%)	17,19,21	2.50	6 (35%)
9	NAG	A	632	1	14,14,15	1.12	1 (7%)	17,19,21	2.61	6 (35%)
9	NAG	A	626	1	14,14,15	0.85	0	17,19,21	2.39	6 (35%)
9	NAG	I	617	1	14,14,15	2.82	9 (64%)	17,19,21	3.04	9 (52%)
9	NAG	E	617	1	14,14,15	2.81	9 (64%)	17,19,21	3.04	9 (52%)
9	NAG	I	630	1	14,14,15	0.88	1 (7%)	17,19,21	2.22	7 (41%)
9	NAG	E	631	1	14,14,15	1.15	1 (7%)	17,19,21	1.71	6 (35%)
9	NAG	A	627	1	14,14,15	1.19	3 (21%)	17,19,21	1.78	4 (23%)
9	NAG	I	618	1	14,14,15	1.57	4 (28%)	17,19,21	2.50	6 (35%)
9	NAG	A	631	1	14,14,15	1.15	1 (7%)	17,19,21	1.71	6 (35%)
9	NAG	A	617	1	14,14,15	2.82	9 (64%)	17,19,21	3.04	9 (52%)
9	NAG	I	627	1	14,14,15	1.20	3 (21%)	17,19,21	1.77	4 (23%)
9	NAG	E	627	1	14,14,15	1.18	3 (21%)	17,19,21	1.78	5 (29%)
9	NAG	A	630	1	14,14,15	0.88	1 (7%)	17,19,21	2.22	7 (41%)
9	NAG	E	622	1	14,14,15	1.43	4 (28%)	17,19,21	2.27	7 (41%)

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
9	NAG	E	630	1	-	4/6/23/26	0/1/1/1
9	NAG	A	622	1	-	4/6/23/26	0/1/1/1
9	NAG	I	632	1	-	1/6/23/26	0/1/1/1
9	NAG	E	626	1	-	5/6/23/26	0/1/1/1
9	NAG	I	619	1	-	5/6/23/26	0/1/1/1
9	NAG	E	619	1	-	5/6/23/26	0/1/1/1
9	NAG	I	626	1	-	5/6/23/26	0/1/1/1
9	NAG	I	622	1	-	4/6/23/26	0/1/1/1
9	NAG	I	631	1	-	4/6/23/26	0/1/1/1
9	NAG	A	618	1	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	E	632	1	-	1/6/23/26	0/1/1/1
9	NAG	A	619	1	-	5/6/23/26	0/1/1/1
9	NAG	E	618	1	-	3/6/23/26	0/1/1/1
9	NAG	A	632	1	-	1/6/23/26	0/1/1/1
9	NAG	A	626	1	-	5/6/23/26	0/1/1/1
9	NAG	I	617	1	-	4/6/23/26	0/1/1/1
9	NAG	E	617	1	-	4/6/23/26	0/1/1/1
9	NAG	I	630	1	-	4/6/23/26	0/1/1/1
9	NAG	E	631	1	-	4/6/23/26	0/1/1/1
9	NAG	A	627	1	-	3/6/23/26	0/1/1/1
9	NAG	I	618	1	-	3/6/23/26	0/1/1/1
9	NAG	A	631	1	-	4/6/23/26	0/1/1/1
9	NAG	A	617	1	-	4/6/23/26	0/1/1/1
9	NAG	I	627	1	-	3/6/23/26	0/1/1/1
9	NAG	E	627	1	-	3/6/23/26	0/1/1/1
9	NAG	A	630	1	-	4/6/23/26	0/1/1/1
9	NAG	E	622	1	-	4/6/23/26	0/1/1/1

The worst 5 of 78 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	E	617	NAG	O5-C1	-4.42	1.36	1.43
9	I	617	NAG	O5-C1	-4.42	1.36	1.43
9	A	617	NAG	O5-C1	-4.41	1.36	1.43
9	I	617	NAG	C1-C2	-4.01	1.46	1.52
9	A	617	NAG	C1-C2	-4.01	1.46	1.52

The worst 5 of 172 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	632	NAG	O5-C1-C2	-6.28	101.57	111.29
9	A	632	NAG	O5-C1-C2	-6.28	101.58	111.29
9	E	632	NAG	O5-C1-C2	-6.28	101.58	111.29
9	E	630	NAG	C2-N2-C7	-5.84	115.08	122.90
9	A	630	NAG	C2-N2-C7	-5.83	115.08	122.90

There are no chirality outliers.

5 of 99 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	617	NAG	O7-C7-N2-C2
9	A	618	NAG	C1-C2-N2-C7
9	A	619	NAG	C1-C2-N2-C7
9	A	622	NAG	C3-C2-N2-C7
9	A	622	NAG	C8-C7-N2-C2

There are no ring outliers.

24 monomers are involved in 45 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	630	NAG	3	0
9	A	622	NAG	2	0
9	I	632	NAG	1	0
9	E	626	NAG	1	0
9	I	619	NAG	1	0
9	E	619	NAG	3	0
9	I	626	NAG	1	0
9	I	622	NAG	3	0
9	I	631	NAG	3	0
9	E	632	NAG	1	0
9	A	619	NAG	2	0
9	A	632	NAG	1	0
9	A	626	NAG	1	0
9	I	617	NAG	1	0
9	E	617	NAG	1	0
9	I	630	NAG	3	0
9	E	631	NAG	4	0
9	A	627	NAG	2	0
9	A	631	NAG	3	0
9	A	617	NAG	1	0
9	I	627	NAG	1	0
9	E	627	NAG	1	0
9	A	630	NAG	3	0
9	E	622	NAG	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

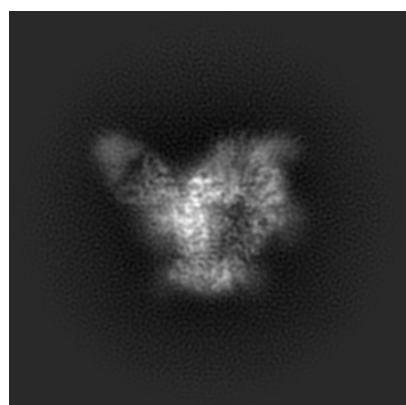
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20817. These allow visual inspection of the internal detail of the map and identification of artifacts.

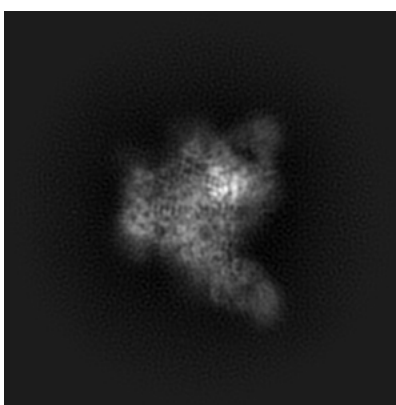
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

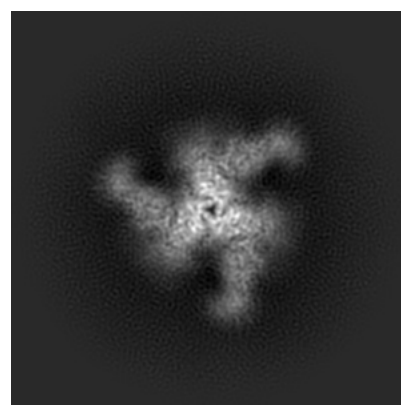
6.1.1 Primary map



X



Y

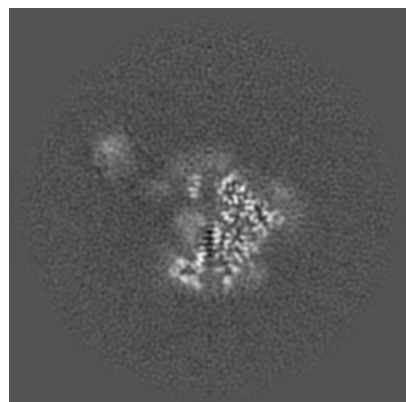


Z

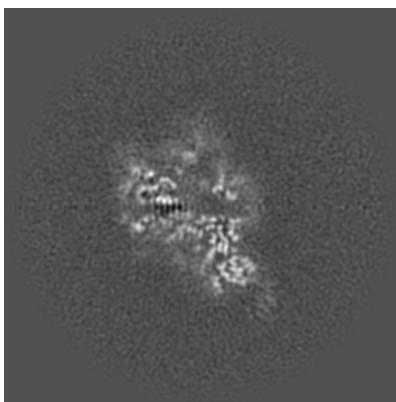
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

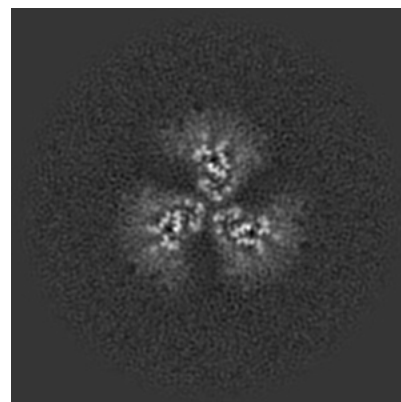
6.2.1 Primary map



X Index: 160



Y Index: 160

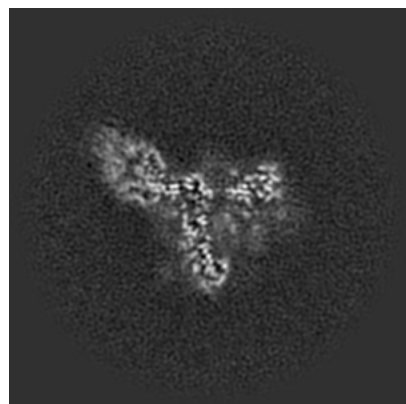


Z Index: 160

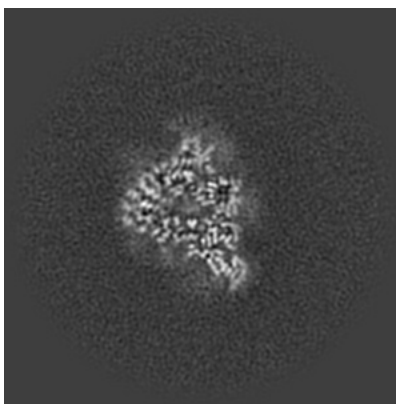
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

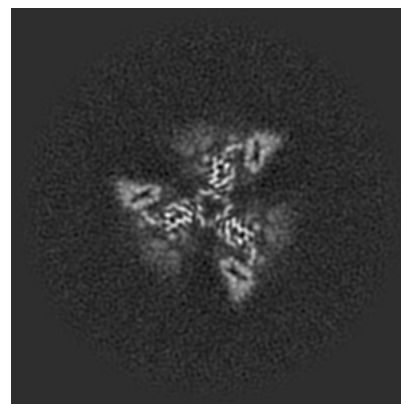
6.3.1 Primary map



X Index: 176



Y Index: 150

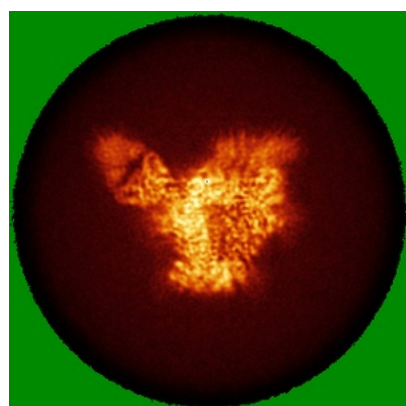


Z Index: 168

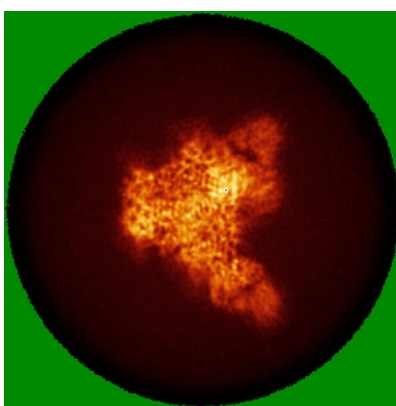
The images above show the largest variance slices of the map in three orthogonal directions.

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

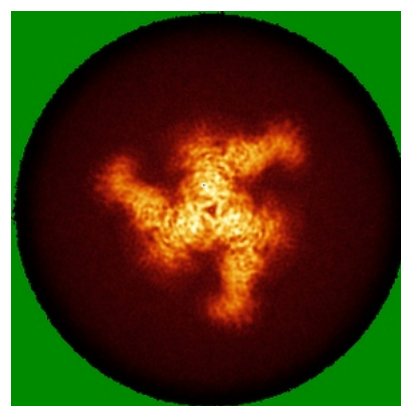
6.4.1 Primary map



X



Y

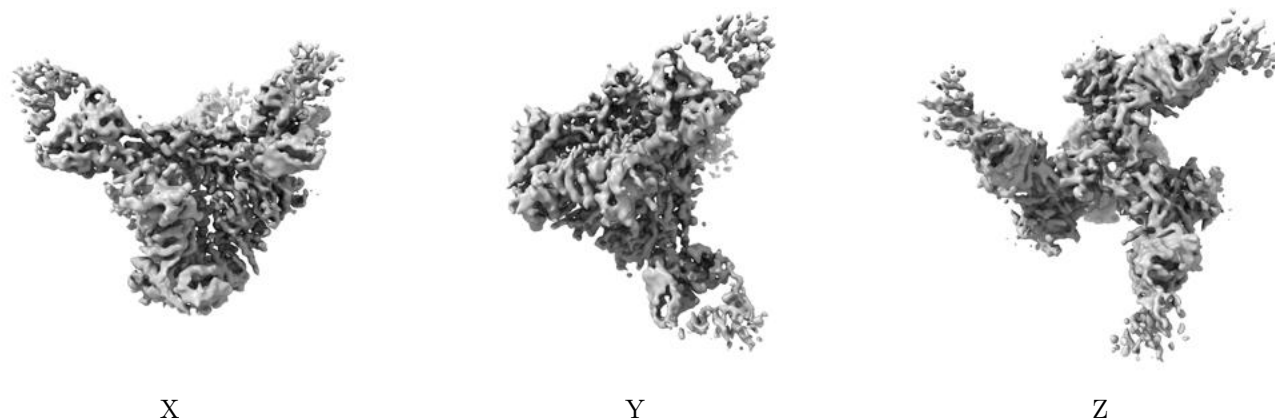


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

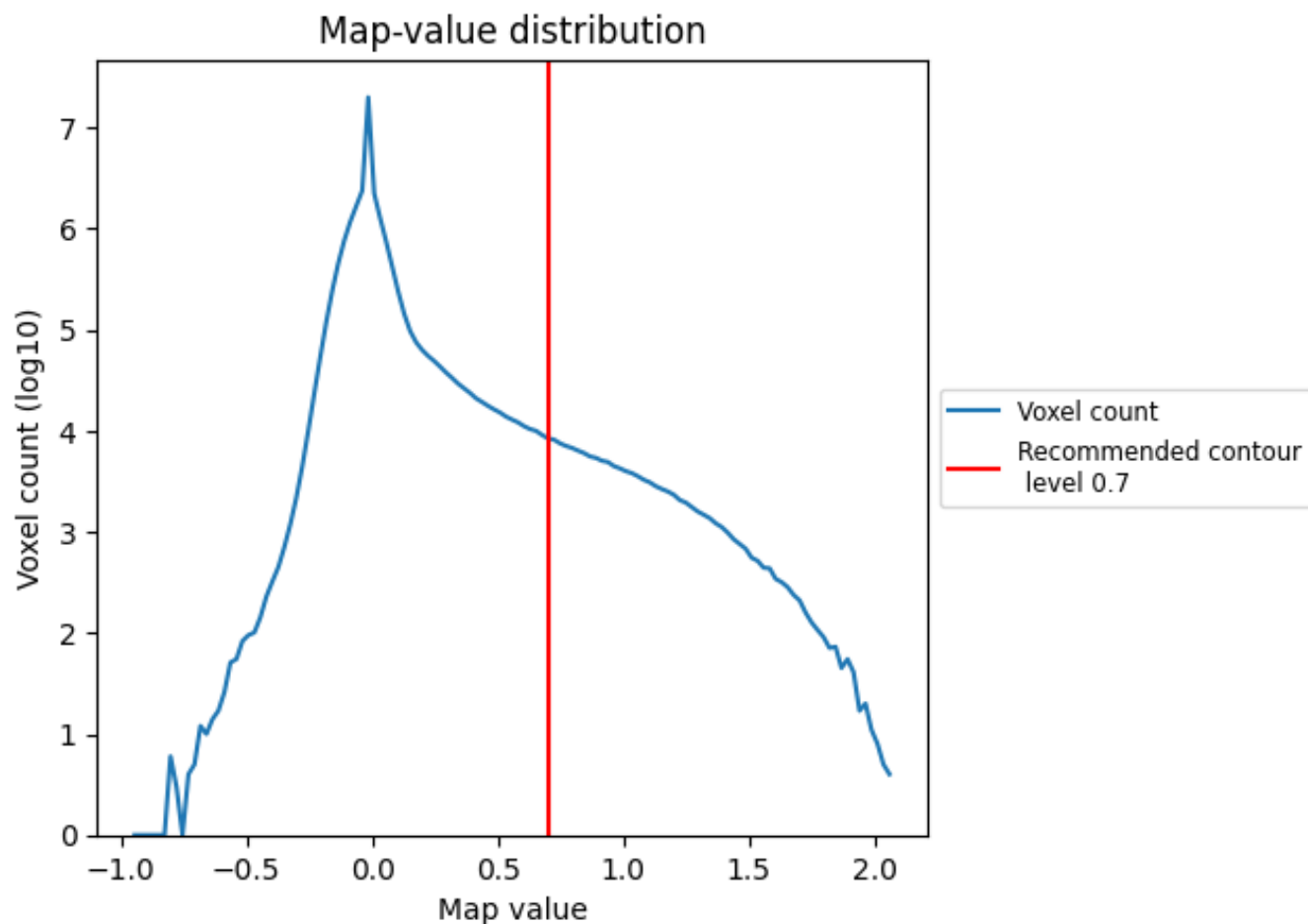
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

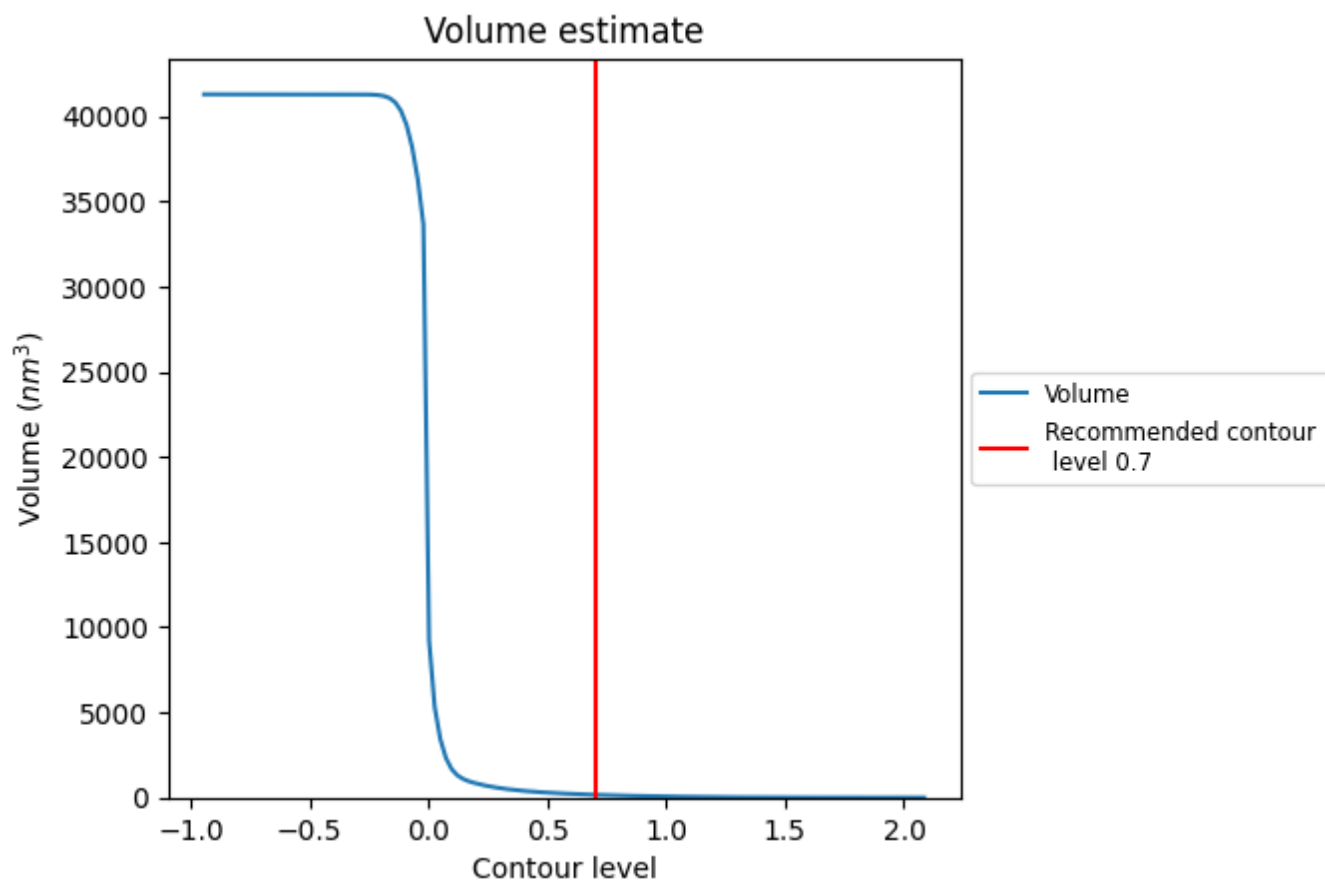
This section contains the results of statistical analysis of the map.

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.

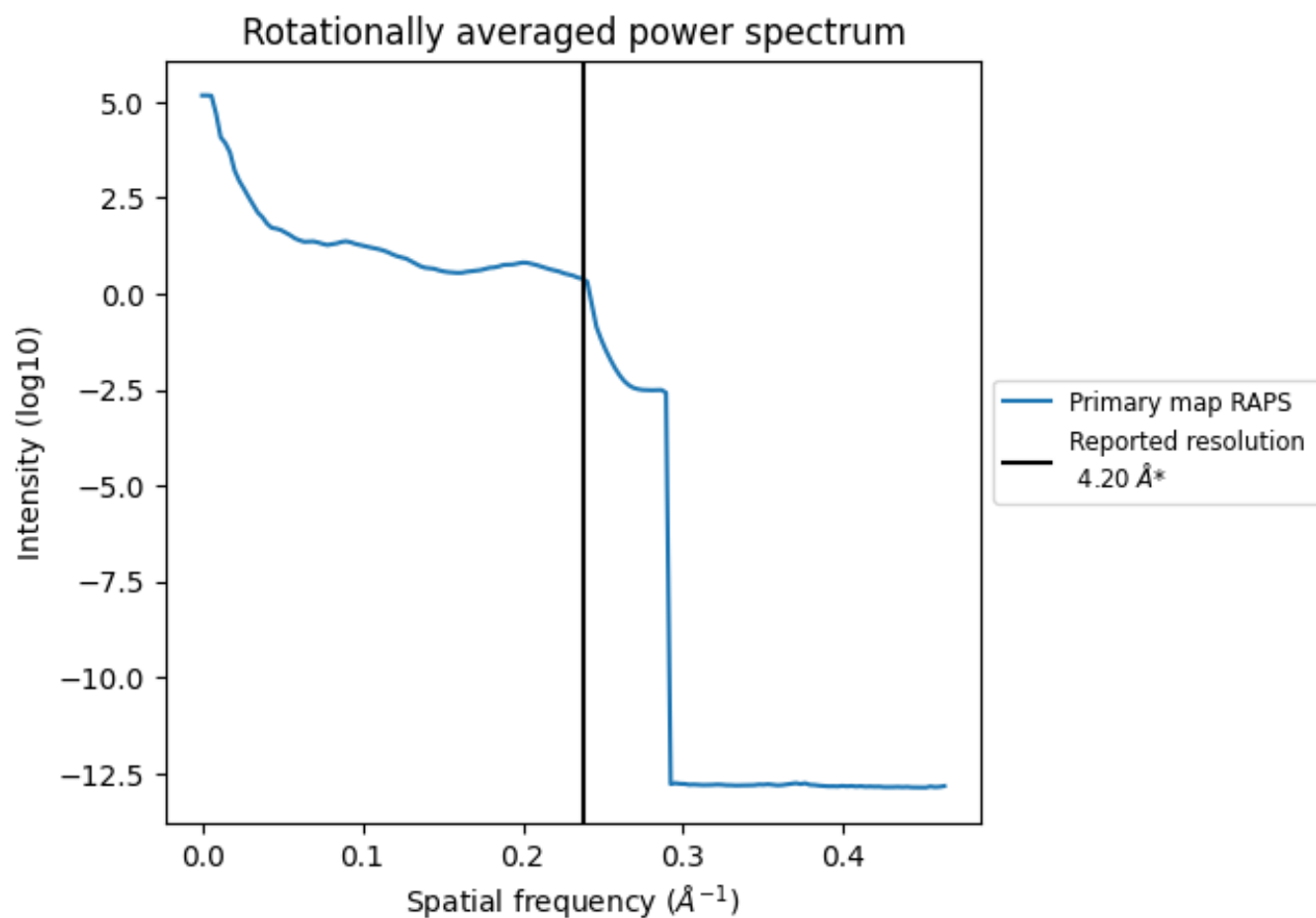
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 162 nm³; this corresponds to an approximate mass of 146 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 0.238 Å⁻¹

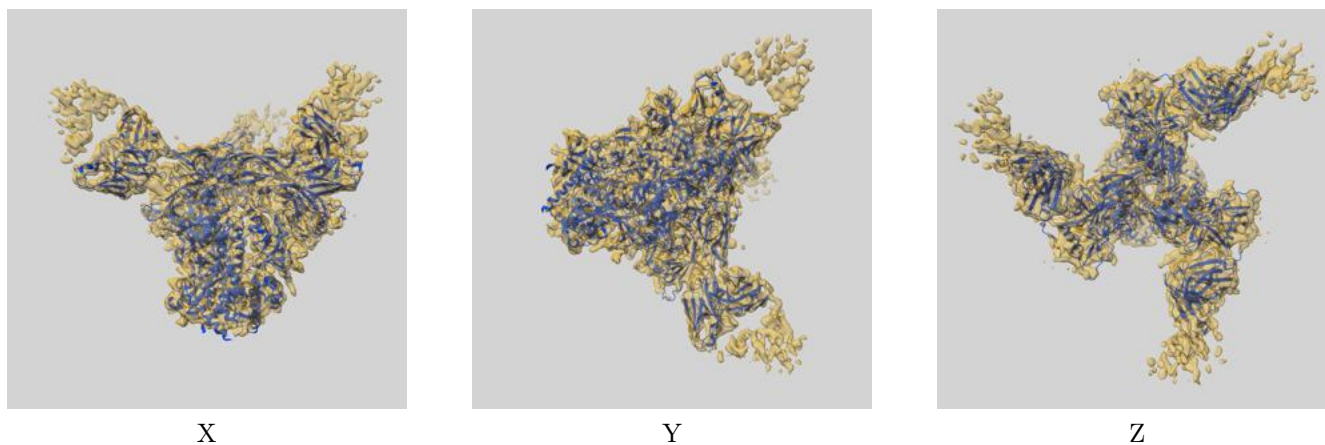
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

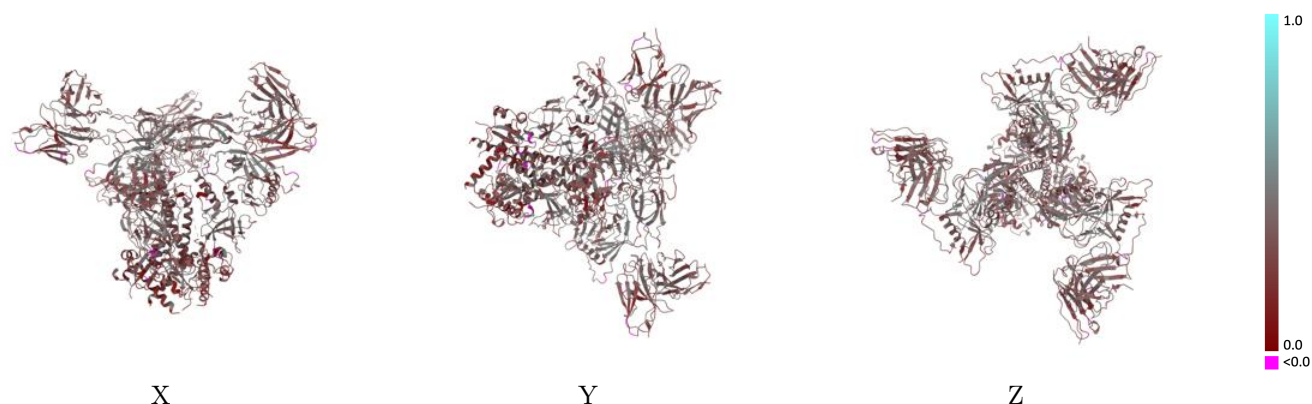
This section contains information regarding the fit between EMDB map EMD-20817 and PDB model 6UM5. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



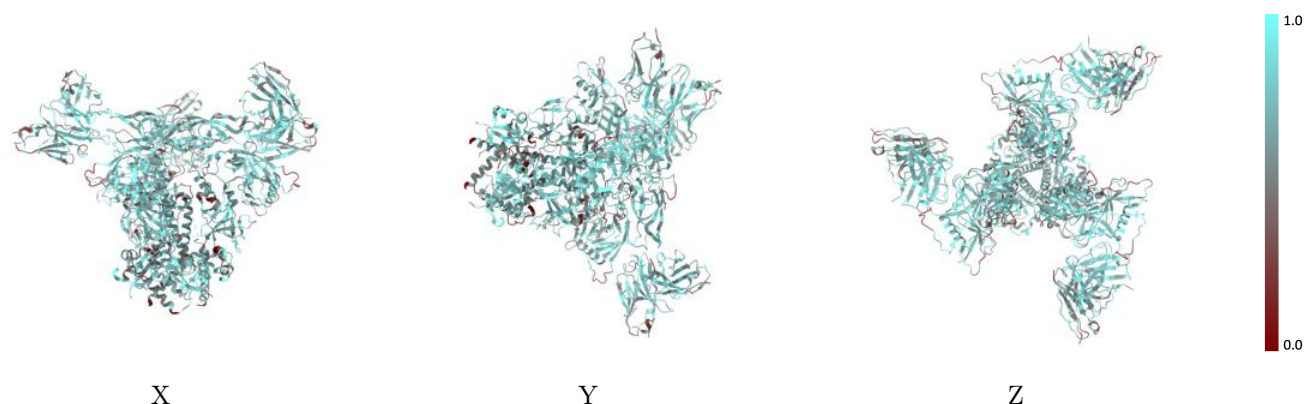
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



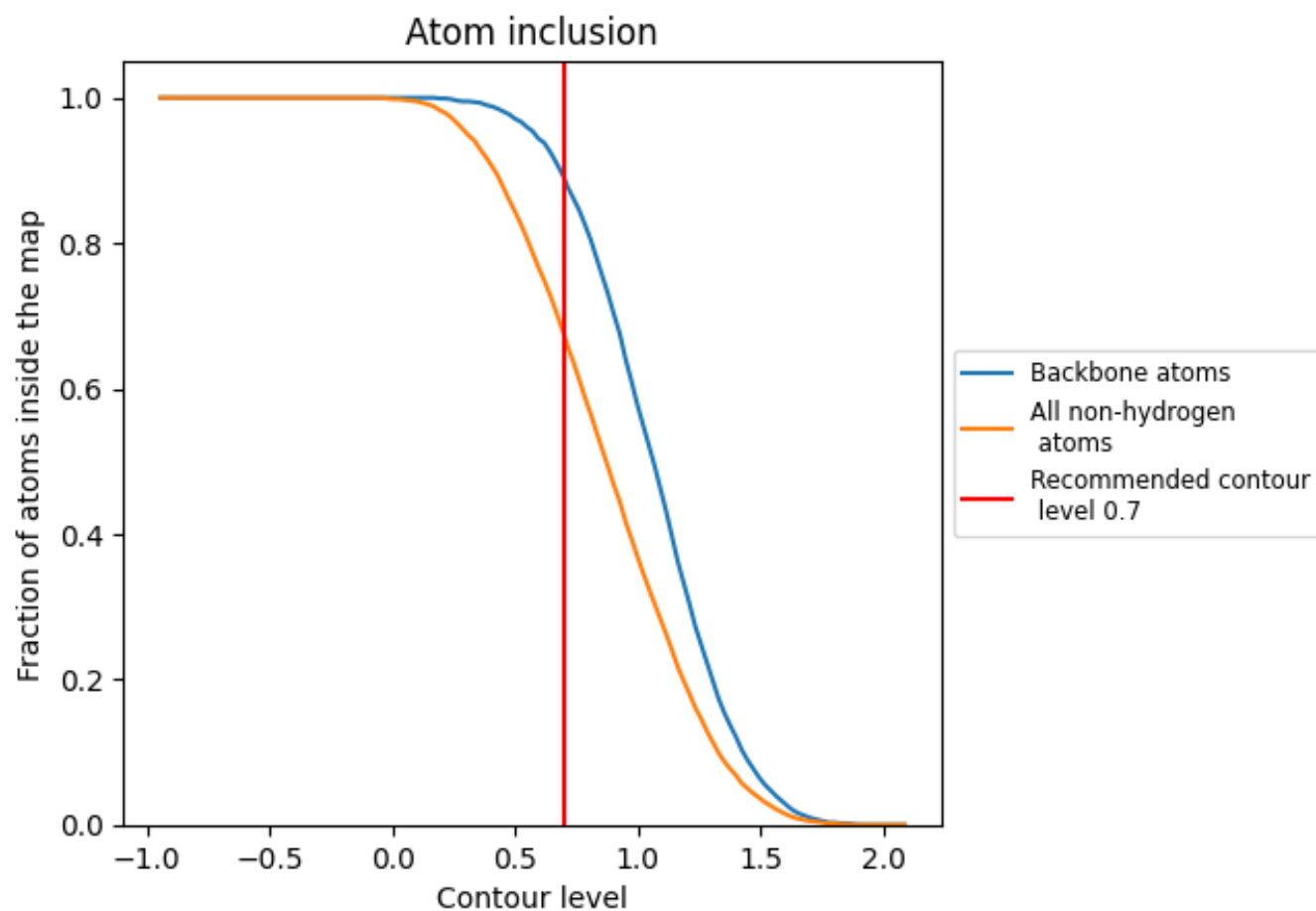
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7).





































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 67% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6720	 0.3470
A	 0.6860	 0.3620
B	 0.6380	 0.2830
C	 0.7310	 0.3540
D	 0.6150	 0.3100
E	 0.6880	 0.3630
F	 0.6340	 0.2800
G	 0.7310	 0.3550
H	 0.6140	 0.3120
I	 0.6870	 0.3630
J	 0.6350	 0.2830
K	 0.7310	 0.3550
L	 0.6150	 0.3160
M	 0.6430	 0.4240
N	 0.7710	 0.4500
O	 0.4910	 0.4570
P	 0.4360	 0.3860
Q	 0.4640	 0.4140
R	 0.5640	 0.4500
S	 0.2860	 0.4390
T	 0.6430	 0.4360
U	 0.7710	 0.4410
V	 0.4910	 0.4670
W	 0.4360	 0.3930
X	 0.4640	 0.4000
Y	 0.5640	 0.4430
Z	 0.2860	 0.4290
a	 0.6430	 0.4330
b	 0.7830	 0.4530
c	 0.4910	 0.4560
d	 0.4620	 0.3860
e	 0.4640	 0.4170
f	 0.5380	 0.4400
g	 0.2860	 0.4480

