



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 08:09 PM UTC

PDB ID : 9OGT / pdb_00009ogt
EMDB ID : EMD-70475
Title : HIV-1 Env BG505 SOSIP.664-His in complex with PGT122 and 3BNC117 Fabs
Authors : Andrade, T.G.; Ozorowski, G.; Ward, A.B.
Deposited on : 2025-05-01
Resolution : 3.00 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

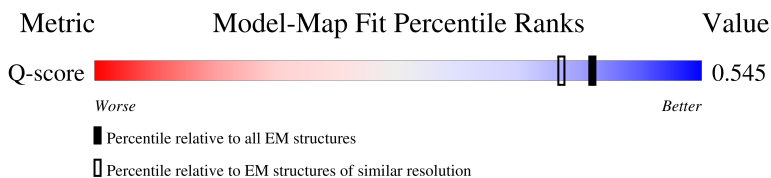
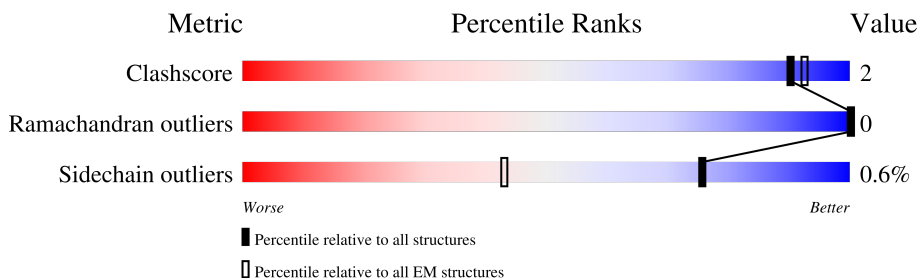
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

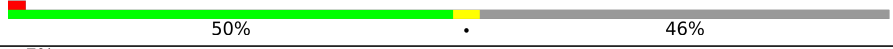
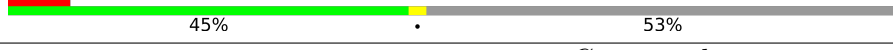
The reported resolution of this entry is 3.00 Å.

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	14081 (2.50 - 3.50)

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	H	226	
1	K	226	
1	P	226	
2	L	206	

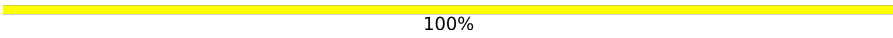
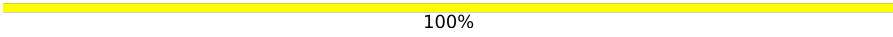
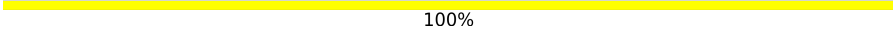
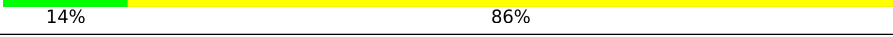
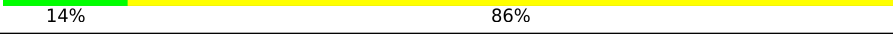
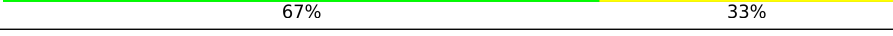
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Mol	Chain	Length	Quality of chain
2	N	206	
2	R	206	
3	G	235	
3	J	235	
3	O	235	
4	I	211	
4	M	211	
4	Q	211	
5	A	516	
5	C	516	
5	E	516	
6	B	169	
6	D	169	
6	F	169	
7	S	2	
7	V	2	
7	X	2	
7	Z	2	
7	c	2	
7	e	2	
7	g	2	
7	j	2	
7	l	2	
8	T	5	
8	a	5	

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Mol	Chain	Length	Quality of chain
8	h	5	
9	U	4	
9	b	4	
9	i	4	
10	W	7	
10	d	7	
10	k	7	
11	Y	3	
11	f	3	
11	m	3	

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 25401 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 3BNC117 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	121	Total	C	N	O	S	0	0
			985	626	177	179	3		
1	K	121	Total	C	N	O	S	0	0
			985	626	177	179	3		
1	P	121	Total	C	N	O	S	0	0
			985	626	177	179	3		

- Molecule 2 is a protein called 3BNC117 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	97	Total	C	N	O	S	0	0
			775	489	136	147	3		
2	N	97	Total	C	N	O	S	0	0
			775	489	136	147	3		
2	R	97	Total	C	N	O	S	0	0
			775	489	136	147	3		

- Molecule 3 is a protein called PGT122 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	132	Total	C	N	O	S	0	0
			1047	669	180	195	3		
3	J	132	Total	C	N	O	S	0	0
			1047	669	180	195	3		
3	O	132	Total	C	N	O	S	0	0
			1047	669	180	195	3		

- Molecule 4 is a protein called PGT122 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	106	Total	C	N	O	S	0	0
			811	507	140	162	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	106	Total	C	N	O	S	0	0
			811	507	140	162	2		
4	Q	106	Total	C	N	O	S	0	0
			811	507	140	162	2		

- Molecule 5 is a protein called HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	428	Total	C	N	O	S	0	0
			3376	2127	596	625	28		
5	C	428	Total	C	N	O	S	0	0
			3376	2127	596	625	28		
5	E	428	Total	C	N	O	S	0	0
			3376	2127	596	625	28		

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	MET	-	expression tag	UNP Q2N0S6
A	-3	ASP	-	expression tag	UNP Q2N0S6
A	-2	ALA	-	expression tag	UNP Q2N0S6
A	-1	MET	-	expression tag	UNP Q2N0S6
A	0	LYS	-	expression tag	UNP Q2N0S6
A	1	ARG	-	expression tag	UNP Q2N0S6
A	2	GLY	-	expression tag	UNP Q2N0S6
A	3	LEU	-	expression tag	UNP Q2N0S6
A	4	CYS	-	expression tag	UNP Q2N0S6
A	5	CYS	-	expression tag	UNP Q2N0S6
A	6	VAL	-	expression tag	UNP Q2N0S6
A	7	LEU	-	expression tag	UNP Q2N0S6
A	8	LEU	-	expression tag	UNP Q2N0S6
A	9	LEU	-	expression tag	UNP Q2N0S6
A	10	CYS	-	expression tag	UNP Q2N0S6
A	11	GLY	-	expression tag	UNP Q2N0S6
A	12	ALA	-	expression tag	UNP Q2N0S6
A	13	VAL	-	expression tag	UNP Q2N0S6
A	14	PHE	-	expression tag	UNP Q2N0S6
A	15	VAL	-	expression tag	UNP Q2N0S6
A	16	SER	-	expression tag	UNP Q2N0S6
A	17	PRO	-	expression tag	UNP Q2N0S6
A	18	SER	-	expression tag	UNP Q2N0S6
A	19	GLN	-	expression tag	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	20	GLU	-	expression tag	UNP Q2N0S6
A	21	ILE	-	expression tag	UNP Q2N0S6
A	22	HIS	-	expression tag	UNP Q2N0S6
A	23	ALA	-	expression tag	UNP Q2N0S6
A	24	ARG	-	expression tag	UNP Q2N0S6
A	25	PHE	-	expression tag	UNP Q2N0S6
A	26	ARG	-	expression tag	UNP Q2N0S6
A	27	ARG	-	expression tag	UNP Q2N0S6
A	28	GLY	-	expression tag	UNP Q2N0S6
A	29	ALA	-	expression tag	UNP Q2N0S6
A	30	ARG	-	expression tag	UNP Q2N0S6
A	332	ASN	THR	engineered mutation	UNP Q2N0S6
A	501	CYS	ALA	engineered mutation	UNP Q2N0S6
A	509	ARG	-	expression tag	UNP Q2N0S6
A	510	ARG	-	expression tag	UNP Q2N0S6
A	511	ARG	-	expression tag	UNP Q2N0S6
A	512	ARG	-	expression tag	UNP Q2N0S6
A	513	ARG	-	expression tag	UNP Q2N0S6
C	-4	MET	-	expression tag	UNP Q2N0S6
C	-3	ASP	-	expression tag	UNP Q2N0S6
C	-2	ALA	-	expression tag	UNP Q2N0S6
C	-1	MET	-	expression tag	UNP Q2N0S6
C	0	LYS	-	expression tag	UNP Q2N0S6
C	1	ARG	-	expression tag	UNP Q2N0S6
C	2	GLY	-	expression tag	UNP Q2N0S6
C	3	LEU	-	expression tag	UNP Q2N0S6
C	4	CYS	-	expression tag	UNP Q2N0S6
C	5	CYS	-	expression tag	UNP Q2N0S6
C	6	VAL	-	expression tag	UNP Q2N0S6
C	7	LEU	-	expression tag	UNP Q2N0S6
C	8	LEU	-	expression tag	UNP Q2N0S6
C	9	LEU	-	expression tag	UNP Q2N0S6
C	10	CYS	-	expression tag	UNP Q2N0S6
C	11	GLY	-	expression tag	UNP Q2N0S6
C	12	ALA	-	expression tag	UNP Q2N0S6
C	13	VAL	-	expression tag	UNP Q2N0S6
C	14	PHE	-	expression tag	UNP Q2N0S6
C	15	VAL	-	expression tag	UNP Q2N0S6
C	16	SER	-	expression tag	UNP Q2N0S6
C	17	PRO	-	expression tag	UNP Q2N0S6
C	18	SER	-	expression tag	UNP Q2N0S6
C	19	GLN	-	expression tag	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	20	GLU	-	expression tag	UNP Q2N0S6
C	21	ILE	-	expression tag	UNP Q2N0S6
C	22	HIS	-	expression tag	UNP Q2N0S6
C	23	ALA	-	expression tag	UNP Q2N0S6
C	24	ARG	-	expression tag	UNP Q2N0S6
C	25	PHE	-	expression tag	UNP Q2N0S6
C	26	ARG	-	expression tag	UNP Q2N0S6
C	27	ARG	-	expression tag	UNP Q2N0S6
C	28	GLY	-	expression tag	UNP Q2N0S6
C	29	ALA	-	expression tag	UNP Q2N0S6
C	30	ARG	-	expression tag	UNP Q2N0S6
C	332	ASN	THR	engineered mutation	UNP Q2N0S6
C	501	CYS	ALA	engineered mutation	UNP Q2N0S6
C	509	ARG	-	expression tag	UNP Q2N0S6
C	510	ARG	-	expression tag	UNP Q2N0S6
C	511	ARG	-	expression tag	UNP Q2N0S6
C	512	ARG	-	expression tag	UNP Q2N0S6
C	513	ARG	-	expression tag	UNP Q2N0S6
E	-4	MET	-	expression tag	UNP Q2N0S6
E	-3	ASP	-	expression tag	UNP Q2N0S6
E	-2	ALA	-	expression tag	UNP Q2N0S6
E	-1	MET	-	expression tag	UNP Q2N0S6
E	0	LYS	-	expression tag	UNP Q2N0S6
E	1	ARG	-	expression tag	UNP Q2N0S6
E	2	GLY	-	expression tag	UNP Q2N0S6
E	3	LEU	-	expression tag	UNP Q2N0S6
E	4	CYS	-	expression tag	UNP Q2N0S6
E	5	CYS	-	expression tag	UNP Q2N0S6
E	6	VAL	-	expression tag	UNP Q2N0S6
E	7	LEU	-	expression tag	UNP Q2N0S6
E	8	LEU	-	expression tag	UNP Q2N0S6
E	9	LEU	-	expression tag	UNP Q2N0S6
E	10	CYS	-	expression tag	UNP Q2N0S6
E	11	GLY	-	expression tag	UNP Q2N0S6
E	12	ALA	-	expression tag	UNP Q2N0S6
E	13	VAL	-	expression tag	UNP Q2N0S6
E	14	PHE	-	expression tag	UNP Q2N0S6
E	15	VAL	-	expression tag	UNP Q2N0S6
E	16	SER	-	expression tag	UNP Q2N0S6
E	17	PRO	-	expression tag	UNP Q2N0S6
E	18	SER	-	expression tag	UNP Q2N0S6
E	19	GLN	-	expression tag	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	20	GLU	-	expression tag	UNP Q2N0S6
E	21	ILE	-	expression tag	UNP Q2N0S6
E	22	HIS	-	expression tag	UNP Q2N0S6
E	23	ALA	-	expression tag	UNP Q2N0S6
E	24	ARG	-	expression tag	UNP Q2N0S6
E	25	PHE	-	expression tag	UNP Q2N0S6
E	26	ARG	-	expression tag	UNP Q2N0S6
E	27	ARG	-	expression tag	UNP Q2N0S6
E	28	GLY	-	expression tag	UNP Q2N0S6
E	29	ALA	-	expression tag	UNP Q2N0S6
E	30	ARG	-	expression tag	UNP Q2N0S6
E	332	ASN	THR	engineered mutation	UNP Q2N0S6
E	501	CYS	ALA	engineered mutation	UNP Q2N0S6
E	509	ARG	-	expression tag	UNP Q2N0S6
E	510	ARG	-	expression tag	UNP Q2N0S6
E	511	ARG	-	expression tag	UNP Q2N0S6
E	512	ARG	-	expression tag	UNP Q2N0S6
E	513	ARG	-	expression tag	UNP Q2N0S6

- Molecule 6 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	126	Total	C	N	O	S	0	0
			1013	641	177	189	6		
6	D	126	Total	C	N	O	S	0	0
			1013	641	177	189	6		
6	F	126	Total	C	N	O	S	0	0
			1013	641	177	189	6		

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	engineered mutation	UNP A0A6H1VYE7
B	605	CYS	THR	engineered mutation	UNP A0A6H1VYE7
B	665	GLY	-	expression tag	UNP A0A6H1VYE7
B	666	SER	-	expression tag	UNP A0A6H1VYE7
B	667	GLY	-	expression tag	UNP A0A6H1VYE7
B	668	SER	-	expression tag	UNP A0A6H1VYE7
B	669	GLY	-	expression tag	UNP A0A6H1VYE7
B	670	GLY	-	expression tag	UNP A0A6H1VYE7
B	671	SER	-	expression tag	UNP A0A6H1VYE7
B	672	GLY	-	expression tag	UNP A0A6H1VYE7

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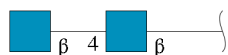
Chain	Residue	Modelled	Actual	Comment	Reference
B	673	HIS	-	expression tag	UNP A0A6H1VYE7
B	674	HIS	-	expression tag	UNP A0A6H1VYE7
B	675	HIS	-	expression tag	UNP A0A6H1VYE7
B	676	HIS	-	expression tag	UNP A0A6H1VYE7
B	677	HIS	-	expression tag	UNP A0A6H1VYE7
B	678	HIS	-	expression tag	UNP A0A6H1VYE7
B	679	HIS	-	expression tag	UNP A0A6H1VYE7
B	680	HIS	-	expression tag	UNP A0A6H1VYE7
D	559	PRO	ILE	engineered mutation	UNP A0A6H1VYE7
D	605	CYS	THR	engineered mutation	UNP A0A6H1VYE7
D	665	GLY	-	expression tag	UNP A0A6H1VYE7
D	666	SER	-	expression tag	UNP A0A6H1VYE7
D	667	GLY	-	expression tag	UNP A0A6H1VYE7
D	668	SER	-	expression tag	UNP A0A6H1VYE7
D	669	GLY	-	expression tag	UNP A0A6H1VYE7
D	670	GLY	-	expression tag	UNP A0A6H1VYE7
D	671	SER	-	expression tag	UNP A0A6H1VYE7
D	672	GLY	-	expression tag	UNP A0A6H1VYE7
D	673	HIS	-	expression tag	UNP A0A6H1VYE7
D	674	HIS	-	expression tag	UNP A0A6H1VYE7
D	675	HIS	-	expression tag	UNP A0A6H1VYE7
D	676	HIS	-	expression tag	UNP A0A6H1VYE7
D	677	HIS	-	expression tag	UNP A0A6H1VYE7
D	678	HIS	-	expression tag	UNP A0A6H1VYE7
D	679	HIS	-	expression tag	UNP A0A6H1VYE7
D	680	HIS	-	expression tag	UNP A0A6H1VYE7
F	559	PRO	ILE	engineered mutation	UNP A0A6H1VYE7
F	605	CYS	THR	engineered mutation	UNP A0A6H1VYE7
F	665	GLY	-	expression tag	UNP A0A6H1VYE7
F	666	SER	-	expression tag	UNP A0A6H1VYE7
F	667	GLY	-	expression tag	UNP A0A6H1VYE7
F	668	SER	-	expression tag	UNP A0A6H1VYE7
F	669	GLY	-	expression tag	UNP A0A6H1VYE7
F	670	GLY	-	expression tag	UNP A0A6H1VYE7
F	671	SER	-	expression tag	UNP A0A6H1VYE7
F	672	GLY	-	expression tag	UNP A0A6H1VYE7
F	673	HIS	-	expression tag	UNP A0A6H1VYE7
F	674	HIS	-	expression tag	UNP A0A6H1VYE7
F	675	HIS	-	expression tag	UNP A0A6H1VYE7
F	676	HIS	-	expression tag	UNP A0A6H1VYE7
F	677	HIS	-	expression tag	UNP A0A6H1VYE7
F	678	HIS	-	expression tag	UNP A0A6H1VYE7

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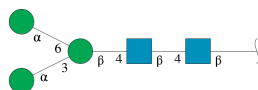
Chain	Residue	Modelled	Actual	Comment	Reference
F	679	HIS	-	expression tag	UNP A0A6H1VYE7
F	680	HIS	-	expression tag	UNP A0A6H1VYE7

- Molecule 7 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
7	S	2	Total	C	N	O	0	0
			28	16	2	10		
7	V	2	Total	C	N	O	0	0
			28	16	2	10		
7	X	2	Total	C	N	O	0	0
			28	16	2	10		
7	Z	2	Total	C	N	O	0	0
			28	16	2	10		
7	c	2	Total	C	N	O	0	0
			28	16	2	10		
7	e	2	Total	C	N	O	0	0
			28	16	2	10		
7	g	2	Total	C	N	O	0	0
			28	16	2	10		
7	j	2	Total	C	N	O	0	0
			28	16	2	10		
7	l	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 8 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
8	T	5	Total	C	N	O	0	0
			61	34	2	25		

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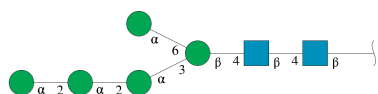
Mol	Chain	Residues	Atoms				AltConf	Trace
8	a	5	Total	C	N	O	0	0
			61	34	2	25		
8	h	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 9 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.



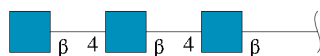
Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	4	Total	C	N	O	0	0
			50	28	2	20		
9	b	4	Total	C	N	O	0	0
			50	28	2	20		
9	i	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-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.



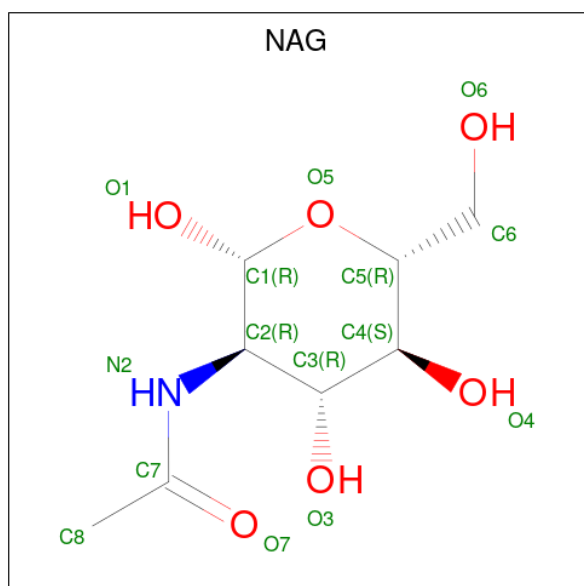
Mol	Chain	Residues	Atoms				AltConf	Trace
10	W	7	Total	C	N	O	0	0
			83	46	2	35		
10	d	7	Total	C	N	O	0	0
			83	46	2	35		
10	k	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 11 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
11	Y	3	Total	C	N	O	0	0
			42	24	3	15		
11	f	3	Total	C	N	O	0	0
			42	24	3	15		
11	m	3	Total	C	N	O	0	0
			42	24	3	15		

- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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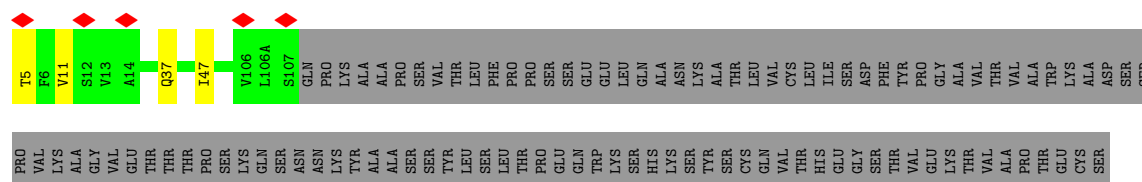
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Mol	Chain	Residues	Atoms				AltConf
12	A	1	Total 14	C 8	N 1	O 5	0
12	A	1	Total 14	C 8	N 1	O 5	0
12	A	1	Total 14	C 8	N 1	O 5	0
12	A	1	Total 14	C 8	N 1	O 5	0
12	C	1	Total 14	C 8	N 1	O 5	0
12	C	1	Total 14	C 8	N 1	O 5	0
12	C	1	Total 14	C 8	N 1	O 5	0
12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

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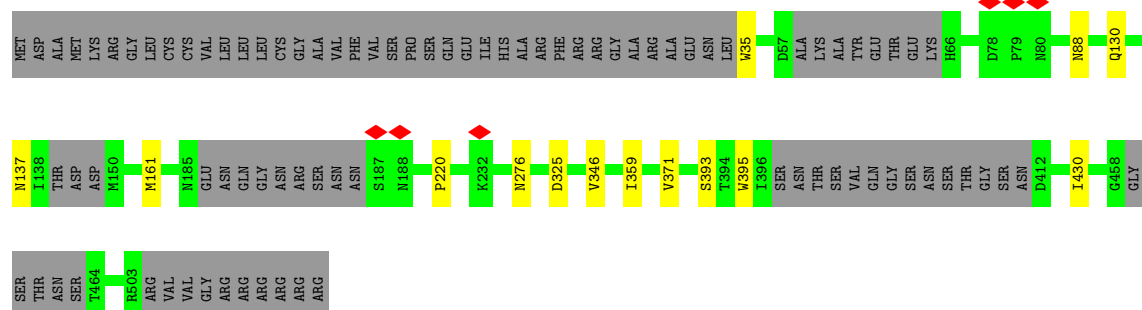
Continued from previous page...

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



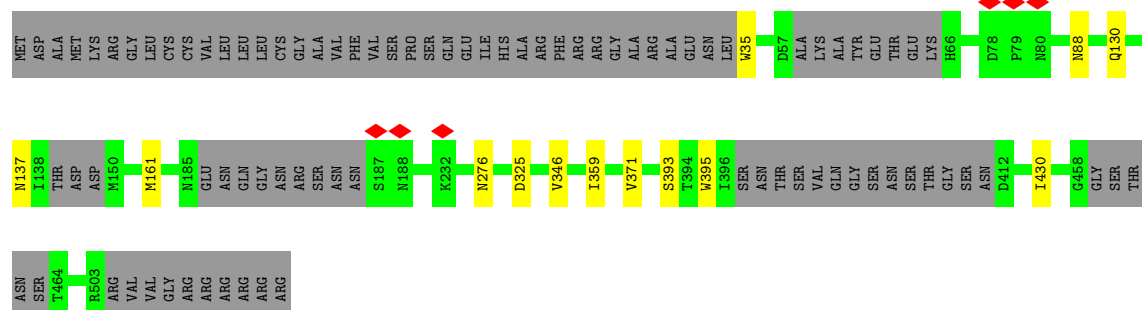
• Molecule 5: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120

Chain A: 80% 17%



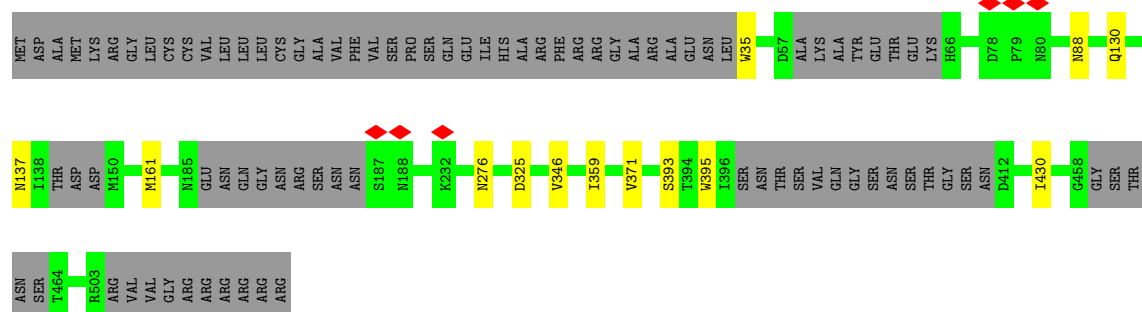
• Molecule 5: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120

Chain C: 80% 17%

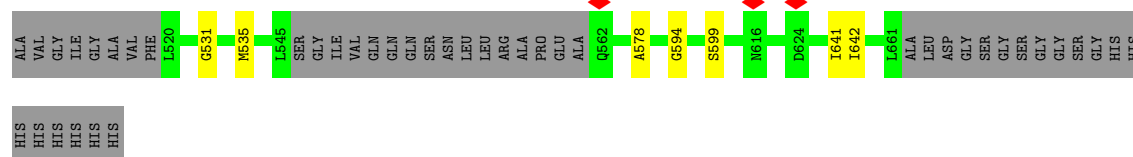


• Molecule 5: HIV-1 Envelope Glycoprotein BG505 SOSIP.664 gp120

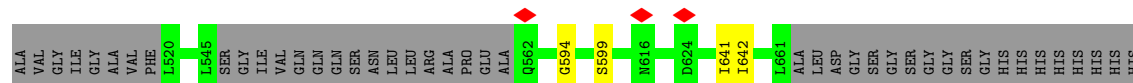
Chain E: 80% 17%



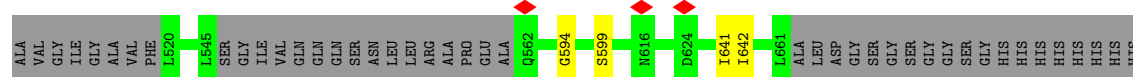
• Molecule 6: Envelope glycoprotein gp160



- Molecule 6: Envelope glycoprotein gp160



- Molecule 6: Envelope glycoprotein gp160



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



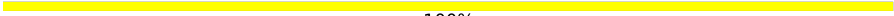
- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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

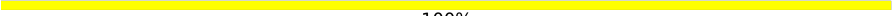


- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:  100%

NAG1
NAG2

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

Chain c:  100%

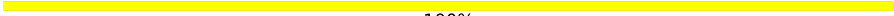
NAG1
NAG2

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

Chain e:  100%

NAG1
NAG2

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

Chain g:  100%

NAG1
NAG2

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

Chain j:  100%

NAG1
NAG2

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

Chain l:  100%

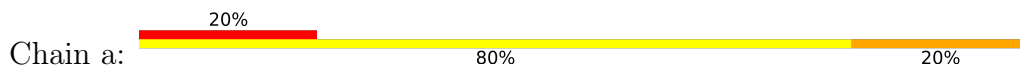
NAG1
NAG2

- Molecule 8: 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

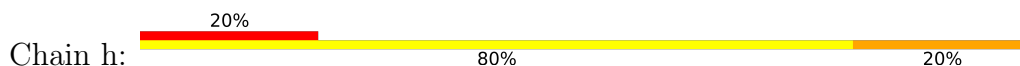
Chain T:  20% 80% 20%



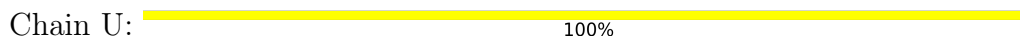
- Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 8: 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



- Molecule 9: 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



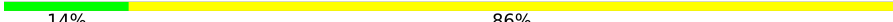
- Molecule 9: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 9: 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



- Molecule 10: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-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 W:  14% 86%

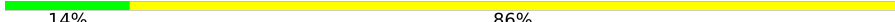


- Molecule 10: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain d:  14% 86%



- Molecule 10: α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-2)- α -D-mannopyranose-(1-3)-[α -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 k:  14% 86%



- Molecule 11: 2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain Y:  67% 33%



- Molecule 11: 2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain f:  67% 33%



- Molecule 11: 2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain m:  67% 33%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	181660	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	190000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.848	Depositor
Minimum map value	-0.508	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	406.0, 406.0, 406.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.725, 0.725, 0.725	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: BMA, MAN, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	H	0.22	0/1017	0.45	0/1386
1	K	0.22	0/1017	0.45	0/1386
1	P	0.22	0/1017	0.45	0/1386
2	L	0.21	0/792	0.46	0/1075
2	N	0.21	0/792	0.46	0/1075
2	R	0.21	0/792	0.46	0/1075
3	G	0.22	0/1076	0.49	0/1465
3	J	0.22	0/1076	0.49	0/1465
3	O	0.22	0/1076	0.49	0/1465
4	I	0.19	0/832	0.43	0/1138
4	M	0.19	0/832	0.43	0/1138
4	Q	0.19	0/832	0.43	0/1138
5	A	0.23	0/3446	0.49	0/4675
5	C	0.23	0/3446	0.49	0/4675
5	E	0.23	0/3446	0.49	0/4675
6	B	0.22	0/1031	0.51	0/1397
6	D	0.23	0/1031	0.51	0/1397
6	F	0.23	0/1031	0.51	0/1397
All	All	0.22	0/24582	0.48	0/33408

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	985	0	919	6	0
1	K	985	0	919	6	0
1	P	985	0	919	6	0
2	L	775	0	757	3	0
2	N	775	0	757	3	0
2	R	775	0	757	3	0
3	G	1047	0	1026	9	0
3	J	1047	0	1026	8	0
3	O	1047	0	1026	7	0
4	I	811	0	766	4	0
4	M	811	0	766	4	0
4	Q	811	0	766	4	0
5	A	3376	0	3321	8	0
5	C	3376	0	3321	7	0
5	E	3376	0	3321	7	0
6	B	1013	0	1001	4	0
6	D	1013	0	1001	2	0
6	F	1013	0	1001	2	0
7	S	28	0	25	0	0
7	V	28	0	25	0	0
7	X	28	0	25	0	0
7	Z	28	0	25	0	0
7	c	28	0	25	0	0
7	e	28	0	25	0	0
7	g	28	0	25	0	0
7	j	28	0	25	0	0
7	l	28	0	25	0	0
8	T	61	0	52	1	0
8	a	61	0	52	1	0
8	h	61	0	52	1	0
9	U	50	0	43	0	0
9	b	50	0	43	0	0
9	i	50	0	43	0	0
10	W	83	0	70	1	0
10	d	83	0	70	1	0
10	k	83	0	70	1	0
11	Y	42	0	37	0	0
11	f	42	0	37	0	0
11	m	42	0	37	0	0
12	A	140	0	130	3	0
12	C	140	0	130	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	E	140	0	130	3	0
All	All	25401	0	24591	83	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 2.

The worst 5 of 83 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)
3:J:30:ARG:HB3	3:J:73:LYS:HE2	1.24	1.16
3:G:30:ARG:HB3	3:G:73:LYS:HE2	1.24	1.13
3:O:30:ARG:HB3	3:O:73:LYS:HE2	1.24	1.10
3:O:7:SER:OG	3:O:21:THR:HG22	1.72	0.89
3:G:7:SER:OG	3:G:21:THR:HG22	1.72	0.89

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	H	119/226 (53%)	113 (95%)	6 (5%)	0	100	100
1	K	119/226 (53%)	113 (95%)	6 (5%)	0	100	100
1	P	119/226 (53%)	113 (95%)	6 (5%)	0	100	100
2	L	95/206 (46%)	83 (87%)	12 (13%)	0	100	100
2	N	95/206 (46%)	83 (87%)	12 (13%)	0	100	100
2	R	95/206 (46%)	83 (87%)	12 (13%)	0	100	100
3	G	130/235 (55%)	126 (97%)	4 (3%)	0	100	100
3	J	130/235 (55%)	125 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	O	130/235 (55%)	126 (97%)	4 (3%)	0	100	100
4	I	104/211 (49%)	99 (95%)	5 (5%)	0	100	100
4	M	104/211 (49%)	99 (95%)	5 (5%)	0	100	100
4	Q	104/211 (49%)	99 (95%)	5 (5%)	0	100	100
5	A	416/516 (81%)	393 (94%)	23 (6%)	0	100	100
5	C	416/516 (81%)	393 (94%)	23 (6%)	0	100	100
5	E	416/516 (81%)	393 (94%)	23 (6%)	0	100	100
6	B	122/169 (72%)	117 (96%)	5 (4%)	0	100	100
6	D	122/169 (72%)	117 (96%)	5 (4%)	0	100	100
6	F	122/169 (72%)	117 (96%)	5 (4%)	0	100	100
All	All	2958/4689 (63%)	2792 (94%)	166 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	H	102/193 (53%)	101 (99%)	1 (1%)	68	84
1	K	102/193 (53%)	101 (99%)	1 (1%)	68	84
1	P	102/193 (53%)	101 (99%)	1 (1%)	68	84
2	L	85/183 (46%)	85 (100%)	0	100	100
2	N	85/183 (46%)	85 (100%)	0	100	100
2	R	85/183 (46%)	85 (100%)	0	100	100
3	G	116/205 (57%)	116 (100%)	0	100	100
3	J	116/205 (57%)	116 (100%)	0	100	100
3	O	116/205 (57%)	116 (100%)	0	100	100
4	I	89/180 (49%)	89 (100%)	0	100	100
4	M	89/180 (49%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Q	89/180 (49%)	89 (100%)	0	100	100
5	A	383/456 (84%)	379 (99%)	4 (1%)	68	84
5	C	383/456 (84%)	379 (99%)	4 (1%)	68	84
5	E	383/456 (84%)	379 (99%)	4 (1%)	68	84
6	B	110/140 (79%)	110 (100%)	0	100	100
6	D	110/140 (79%)	110 (100%)	0	100	100
6	F	110/140 (79%)	110 (100%)	0	100	100
All	All	2655/4071 (65%)	2640 (99%)	15 (1%)	76	88

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	C	88	ASN
5	E	276	ASN
5	C	276	ASN
5	E	325	ASP
5	E	35	TRP

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

Mol	Chain	Res	Type
5	C	440	GLN
1	P	35	HIS
6	F	564	HIS
6	D	653	GLN
2	R	38	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 ⓘ

75 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$
7	NAG	S	1	7,5	14,14,15	0.74	0	17,19,21	1.62	1 (5%)
7	NAG	S	2	7	14,14,15	0.68	0	17,19,21	1.54	2 (11%)
8	NAG	T	1	8,5	14,14,15	0.78	0	17,19,21	1.89	3 (17%)
8	NAG	T	2	8	14,14,15	0.74	0	17,19,21	0.97	1 (5%)
8	BMA	T	3	8	11,11,12	0.77	0	15,15,17	3.06	4 (26%)
8	MAN	T	4	8	11,11,12	0.68	0	15,15,17	1.41	1 (6%)
8	MAN	T	5	8	11,11,12	0.68	0	15,15,17	1.13	1 (6%)
9	NAG	U	1	9,5	14,14,15	0.74	0	17,19,21	1.05	1 (5%)
9	NAG	U	2	9	14,14,15	0.68	0	17,19,21	1.59	2 (11%)
9	BMA	U	3	9	11,11,12	0.79	0	15,15,17	2.53	6 (40%)
9	MAN	U	4	9	11,11,12	0.69	0	15,15,17	1.17	1 (6%)
7	NAG	V	1	7,5	14,14,15	0.76	0	17,19,21	1.82	4 (23%)
7	NAG	V	2	7	14,14,15	0.75	0	17,19,21	1.04	1 (5%)
10	NAG	W	1	10,5	14,14,15	0.39	0	17,19,21	0.67	0
10	NAG	W	2	10	14,14,15	0.40	0	17,19,21	0.75	0
10	BMA	W	3	10	11,11,12	0.89	0	15,15,17	2.21	6 (40%)
10	MAN	W	4	10	11,11,12	0.73	0	15,15,17	1.03	1 (6%)
10	MAN	W	5	10	11,11,12	0.74	0	15,15,17	1.12	1 (6%)
10	MAN	W	6	10	11,11,12	0.79	1 (9%)	15,15,17	0.95	1 (6%)
10	MAN	W	7	10	11,11,12	0.73	0	15,15,17	1.05	1 (6%)
7	NAG	X	1	7,5	14,14,15	0.85	0	17,19,21	0.89	0
7	NAG	X	2	7	14,14,15	0.72	0	17,19,21	0.91	0
11	NAG	Y	1	11,5	14,14,15	0.72	0	17,19,21	1.01	1 (5%)
11	NAG	Y	2	11	14,14,15	0.70	0	17,19,21	1.04	0
11	NAG	Y	3	11	14,14,15	0.73	0	17,19,21	0.87	0
7	NAG	Z	1	7,5	14,14,15	0.74	0	17,19,21	1.62	1 (5%)
7	NAG	Z	2	7	14,14,15	0.67	0	17,19,21	1.54	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	a	1	8,5	14,14,15	0.79	0	17,19,21	1.89	3 (17%)
8	NAG	a	2	8	14,14,15	0.74	0	17,19,21	0.97	1 (5%)
8	BMA	a	3	8	11,11,12	0.77	0	15,15,17	3.06	4 (26%)
8	MAN	a	4	8	11,11,12	0.67	0	15,15,17	1.41	1 (6%)
8	MAN	a	5	8	11,11,12	0.68	0	15,15,17	1.13	1 (6%)
9	NAG	b	1	9,5	14,14,15	0.73	0	17,19,21	1.05	1 (5%)
9	NAG	b	2	9	14,14,15	0.67	0	17,19,21	1.59	2 (11%)
9	BMA	b	3	9	11,11,12	0.79	0	15,15,17	2.53	6 (40%)
9	MAN	b	4	9	11,11,12	0.69	0	15,15,17	1.17	1 (6%)
7	NAG	c	1	7,5	14,14,15	0.76	0	17,19,21	1.82	4 (23%)
7	NAG	c	2	7	14,14,15	0.75	0	17,19,21	1.05	1 (5%)
10	NAG	d	1	10,5	14,14,15	0.39	0	17,19,21	0.67	0
10	NAG	d	2	10	14,14,15	0.39	0	17,19,21	0.75	0
10	BMA	d	3	10	11,11,12	0.89	0	15,15,17	2.22	6 (40%)
10	MAN	d	4	10	11,11,12	0.73	0	15,15,17	1.03	1 (6%)
10	MAN	d	5	10	11,11,12	0.74	0	15,15,17	1.13	1 (6%)
10	MAN	d	6	10	11,11,12	0.79	0	15,15,17	0.95	1 (6%)
10	MAN	d	7	10	11,11,12	0.73	0	15,15,17	1.05	1 (6%)
7	NAG	e	1	7,5	14,14,15	0.85	0	17,19,21	0.90	0
7	NAG	e	2	7	14,14,15	0.72	0	17,19,21	0.91	0
11	NAG	f	1	11,5	14,14,15	0.73	0	17,19,21	1.02	1 (5%)
11	NAG	f	2	11	14,14,15	0.69	0	17,19,21	1.04	0
11	NAG	f	3	11	14,14,15	0.71	0	17,19,21	0.87	0
7	NAG	g	1	7,5	14,14,15	0.74	0	17,19,21	1.62	1 (5%)
7	NAG	g	2	7	14,14,15	0.67	0	17,19,21	1.54	2 (11%)
8	NAG	h	1	8,5	14,14,15	0.78	0	17,19,21	1.89	3 (17%)
8	NAG	h	2	8	14,14,15	0.74	0	17,19,21	0.97	1 (5%)
8	BMA	h	3	8	11,11,12	0.78	0	15,15,17	3.06	4 (26%)
8	MAN	h	4	8	11,11,12	0.68	0	15,15,17	1.42	1 (6%)
8	MAN	h	5	8	11,11,12	0.69	0	15,15,17	1.13	1 (6%)
9	NAG	i	1	9,5	14,14,15	0.73	0	17,19,21	1.05	1 (5%)
9	NAG	i	2	9	14,14,15	0.68	0	17,19,21	1.59	2 (11%)
9	BMA	i	3	9	11,11,12	0.78	0	15,15,17	2.53	6 (40%)
9	MAN	i	4	9	11,11,12	0.70	0	15,15,17	1.17	1 (6%)
7	NAG	j	1	7,5	14,14,15	0.77	0	17,19,21	1.82	4 (23%)
7	NAG	j	2	7	14,14,15	0.74	0	17,19,21	1.04	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	NAG	k	1	10,5	14,14,15	0.40	0	17,19,21	0.67	0
10	NAG	k	2	10	14,14,15	0.39	0	17,19,21	0.75	0
10	BMA	k	3	10	11,11,12	0.89	0	15,15,17	2.21	6 (40%)
10	MAN	k	4	10	11,11,12	0.73	0	15,15,17	1.03	1 (6%)
10	MAN	k	5	10	11,11,12	0.74	0	15,15,17	1.13	1 (6%)
10	MAN	k	6	10	11,11,12	0.79	1 (9%)	15,15,17	0.95	1 (6%)
10	MAN	k	7	10	11,11,12	0.73	0	15,15,17	1.05	1 (6%)
7	NAG	l	1	7,5	14,14,15	0.85	0	17,19,21	0.90	0
7	NAG	l	2	7	14,14,15	0.73	0	17,19,21	0.91	0
11	NAG	m	1	11,5	14,14,15	0.73	0	17,19,21	1.01	1 (5%)
11	NAG	m	2	11	14,14,15	0.70	0	17,19,21	1.04	0
11	NAG	m	3	11	14,14,15	0.73	0	17,19,21	0.87	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
7	NAG	S	1	7,5	-	2/6/23/26	0/1/1/1
7	NAG	S	2	7	-	2/6/23/26	0/1/1/1
8	NAG	T	1	8,5	-	2/6/23/26	0/1/1/1
8	NAG	T	2	8	-	0/6/23/26	0/1/1/1
8	BMA	T	3	8	-	2/2/19/22	0/1/1/1
8	MAN	T	4	8	-	2/2/19/22	0/1/1/1
8	MAN	T	5	8	-	0/2/19/22	0/1/1/1
9	NAG	U	1	9,5	-	0/6/23/26	0/1/1/1
9	NAG	U	2	9	-	4/6/23/26	0/1/1/1
9	BMA	U	3	9	-	0/2/19/22	0/1/1/1
9	MAN	U	4	9	-	0/2/19/22	0/1/1/1
7	NAG	V	1	7,5	-	2/6/23/26	0/1/1/1
7	NAG	V	2	7	-	0/6/23/26	0/1/1/1
10	NAG	W	1	10,5	-	2/6/23/26	0/1/1/1
10	NAG	W	2	10	-	2/6/23/26	0/1/1/1
10	BMA	W	3	10	-	0/2/19/22	0/1/1/1
10	MAN	W	4	10	-	1/2/19/22	0/1/1/1
10	MAN	W	5	10	-	2/2/19/22	0/1/1/1
10	MAN	W	6	10	-	2/2/19/22	0/1/1/1
10	MAN	W	7	10	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	X	1	7,5	-	0/6/23/26	0/1/1/1
7	NAG	X	2	7	-	0/6/23/26	0/1/1/1
11	NAG	Y	1	11,5	-	0/6/23/26	0/1/1/1
11	NAG	Y	2	11	-	0/6/23/26	0/1/1/1
11	NAG	Y	3	11	-	0/6/23/26	0/1/1/1
7	NAG	Z	1	7,5	-	2/6/23/26	0/1/1/1
7	NAG	Z	2	7	-	2/6/23/26	0/1/1/1
8	NAG	a	1	8,5	-	2/6/23/26	0/1/1/1
8	NAG	a	2	8	-	0/6/23/26	0/1/1/1
8	BMA	a	3	8	-	2/2/19/22	0/1/1/1
8	MAN	a	4	8	-	2/2/19/22	0/1/1/1
8	MAN	a	5	8	-	0/2/19/22	0/1/1/1
9	NAG	b	1	9,5	-	0/6/23/26	0/1/1/1
9	NAG	b	2	9	-	4/6/23/26	0/1/1/1
9	BMA	b	3	9	-	0/2/19/22	0/1/1/1
9	MAN	b	4	9	-	0/2/19/22	0/1/1/1
7	NAG	c	1	7,5	-	2/6/23/26	0/1/1/1
7	NAG	c	2	7	-	0/6/23/26	0/1/1/1
10	NAG	d	1	10,5	-	2/6/23/26	0/1/1/1
10	NAG	d	2	10	-	2/6/23/26	0/1/1/1
10	BMA	d	3	10	-	0/2/19/22	0/1/1/1
10	MAN	d	4	10	-	1/2/19/22	0/1/1/1
10	MAN	d	5	10	-	2/2/19/22	0/1/1/1
10	MAN	d	6	10	-	2/2/19/22	0/1/1/1
10	MAN	d	7	10	-	0/2/19/22	0/1/1/1
7	NAG	e	1	7,5	-	0/6/23/26	0/1/1/1
7	NAG	e	2	7	-	0/6/23/26	0/1/1/1
11	NAG	f	1	11,5	-	0/6/23/26	0/1/1/1
11	NAG	f	2	11	-	0/6/23/26	0/1/1/1
11	NAG	f	3	11	-	0/6/23/26	0/1/1/1
7	NAG	g	1	7,5	-	2/6/23/26	0/1/1/1
7	NAG	g	2	7	-	2/6/23/26	0/1/1/1
8	NAG	h	1	8,5	-	2/6/23/26	0/1/1/1
8	NAG	h	2	8	-	0/6/23/26	0/1/1/1
8	BMA	h	3	8	-	2/2/19/22	0/1/1/1
8	MAN	h	4	8	-	2/2/19/22	0/1/1/1
8	MAN	h	5	8	-	0/2/19/22	0/1/1/1
9	NAG	i	1	9,5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	i	2	9	-	4/6/23/26	0/1/1/1
9	BMA	i	3	9	-	0/2/19/22	0/1/1/1
9	MAN	i	4	9	-	0/2/19/22	0/1/1/1
7	NAG	j	1	7,5	-	2/6/23/26	0/1/1/1
7	NAG	j	2	7	-	0/6/23/26	0/1/1/1
10	NAG	k	1	10,5	-	2/6/23/26	0/1/1/1
10	NAG	k	2	10	-	2/6/23/26	0/1/1/1
10	BMA	k	3	10	-	0/2/19/22	0/1/1/1
10	MAN	k	4	10	-	1/2/19/22	0/1/1/1
10	MAN	k	5	10	-	2/2/19/22	0/1/1/1
10	MAN	k	6	10	-	2/2/19/22	0/1/1/1
10	MAN	k	7	10	-	0/2/19/22	0/1/1/1
7	NAG	l	1	7,5	-	0/6/23/26	0/1/1/1
7	NAG	l	2	7	-	0/6/23/26	0/1/1/1
11	NAG	m	1	11,5	-	0/6/23/26	0/1/1/1
11	NAG	m	2	11	-	0/6/23/26	0/1/1/1
11	NAG	m	3	11	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	W	6	MAN	O5-C1	-2.02	1.40	1.43
10	k	6	MAN	O5-C1	-2.02	1.40	1.43

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	a	3	BMA	C1-O5-C5	10.20	125.86	112.19
8	h	3	BMA	C1-O5-C5	10.19	125.84	112.19
8	T	3	BMA	C1-O5-C5	10.17	125.82	112.19
9	U	3	BMA	C1-O5-C5	7.26	121.92	112.19
9	i	3	BMA	C1-O5-C5	7.25	121.90	112.19

There are no chirality outliers.

5 of 75 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	W	6	MAN	O5-C5-C6-O6
10	d	6	MAN	O5-C5-C6-O6
10	k	6	MAN	O5-C5-C6-O6

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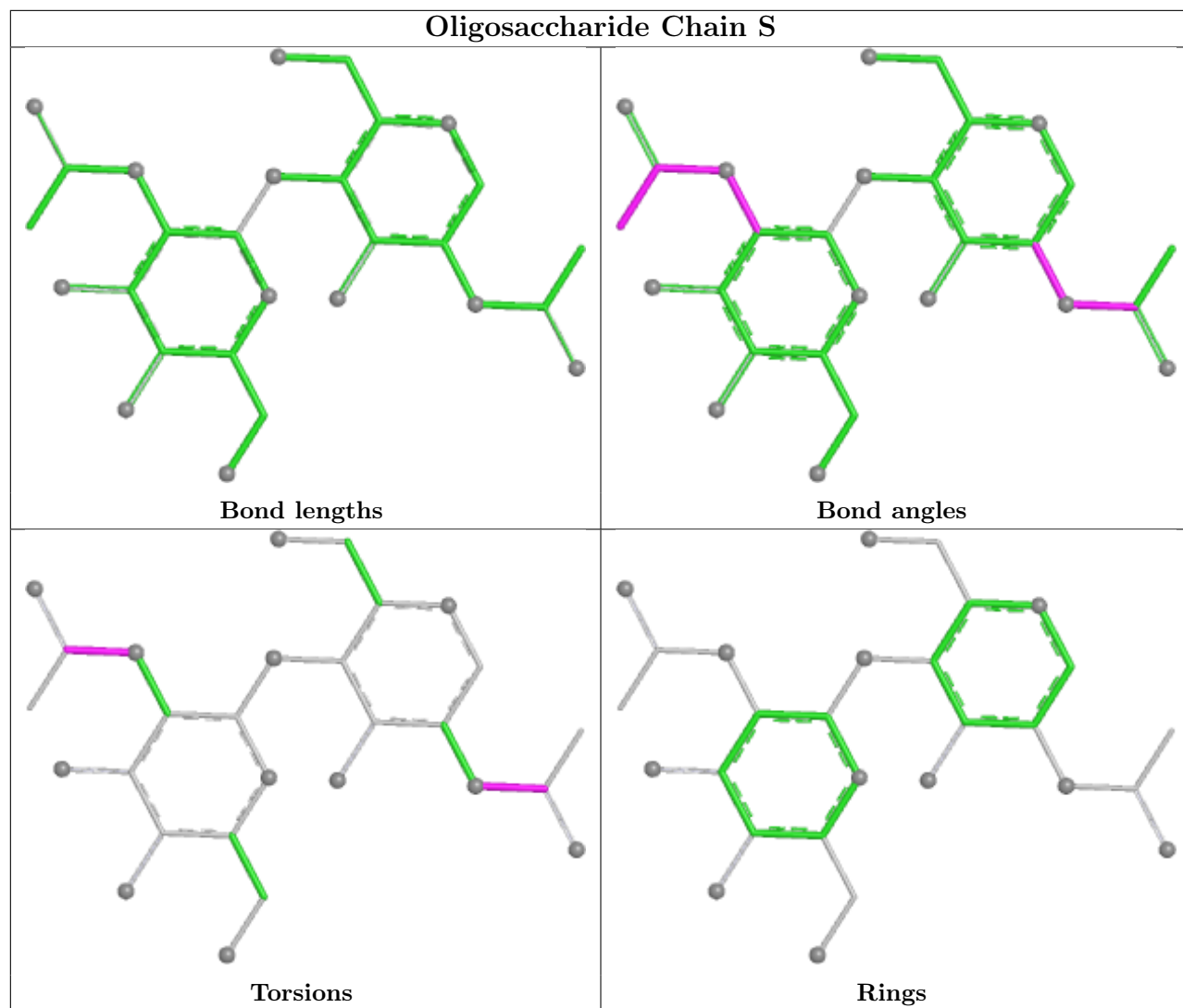
Mol	Chain	Res	Type	Atoms
8	T	3	BMA	C4-C5-C6-O6
8	a	3	BMA	C4-C5-C6-O6

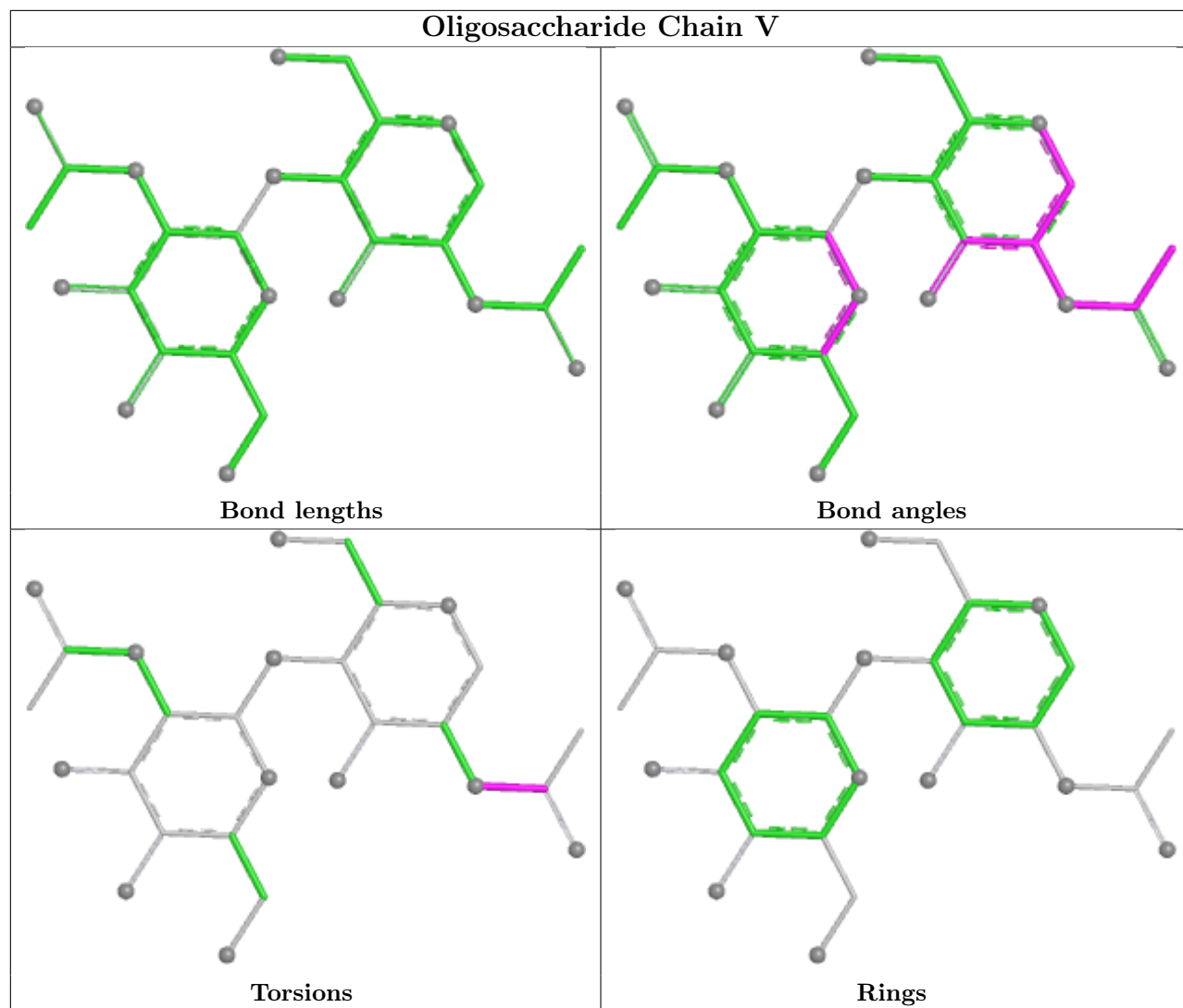
There are no ring outliers.

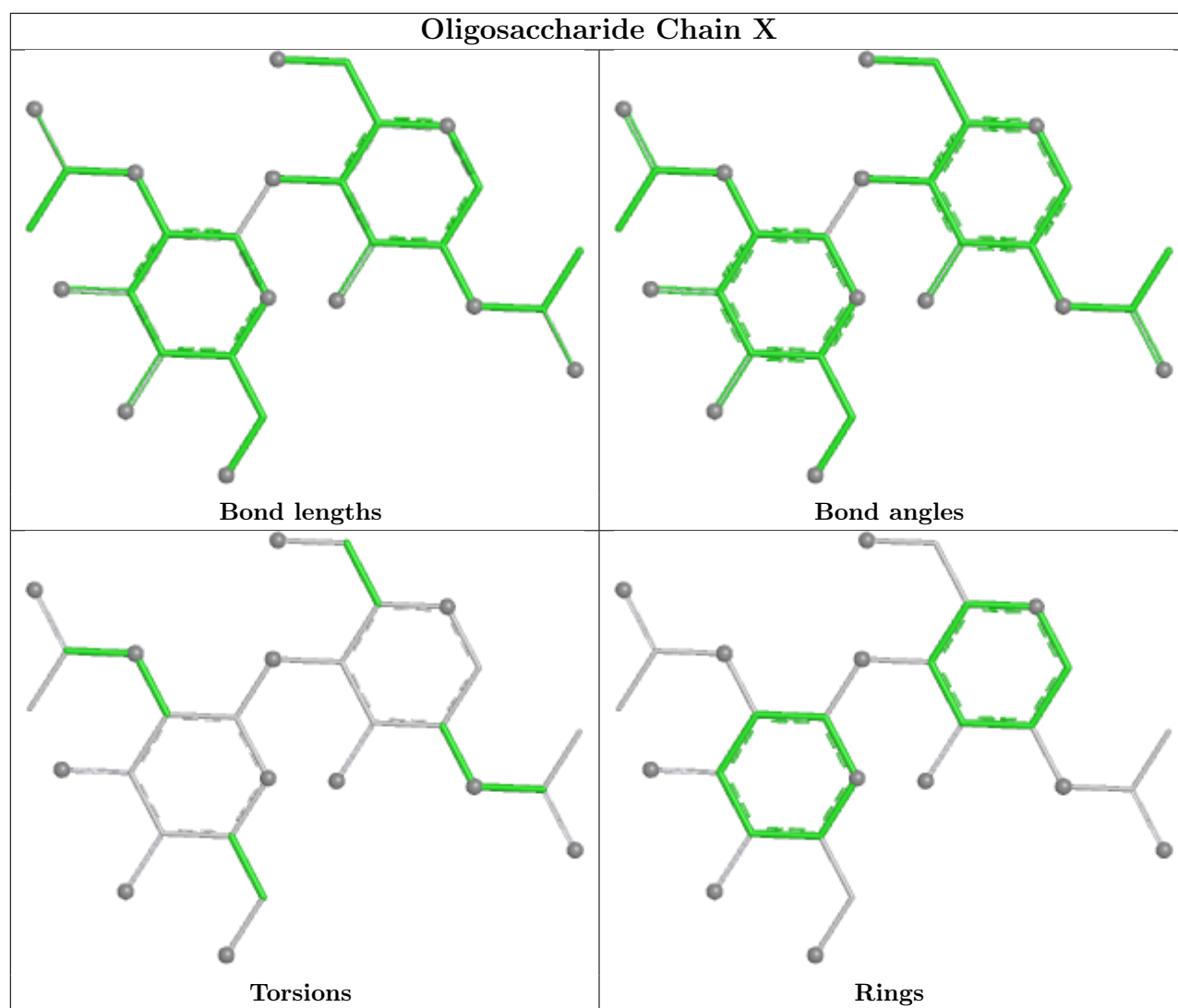
6 monomers are involved in 6 short contacts:

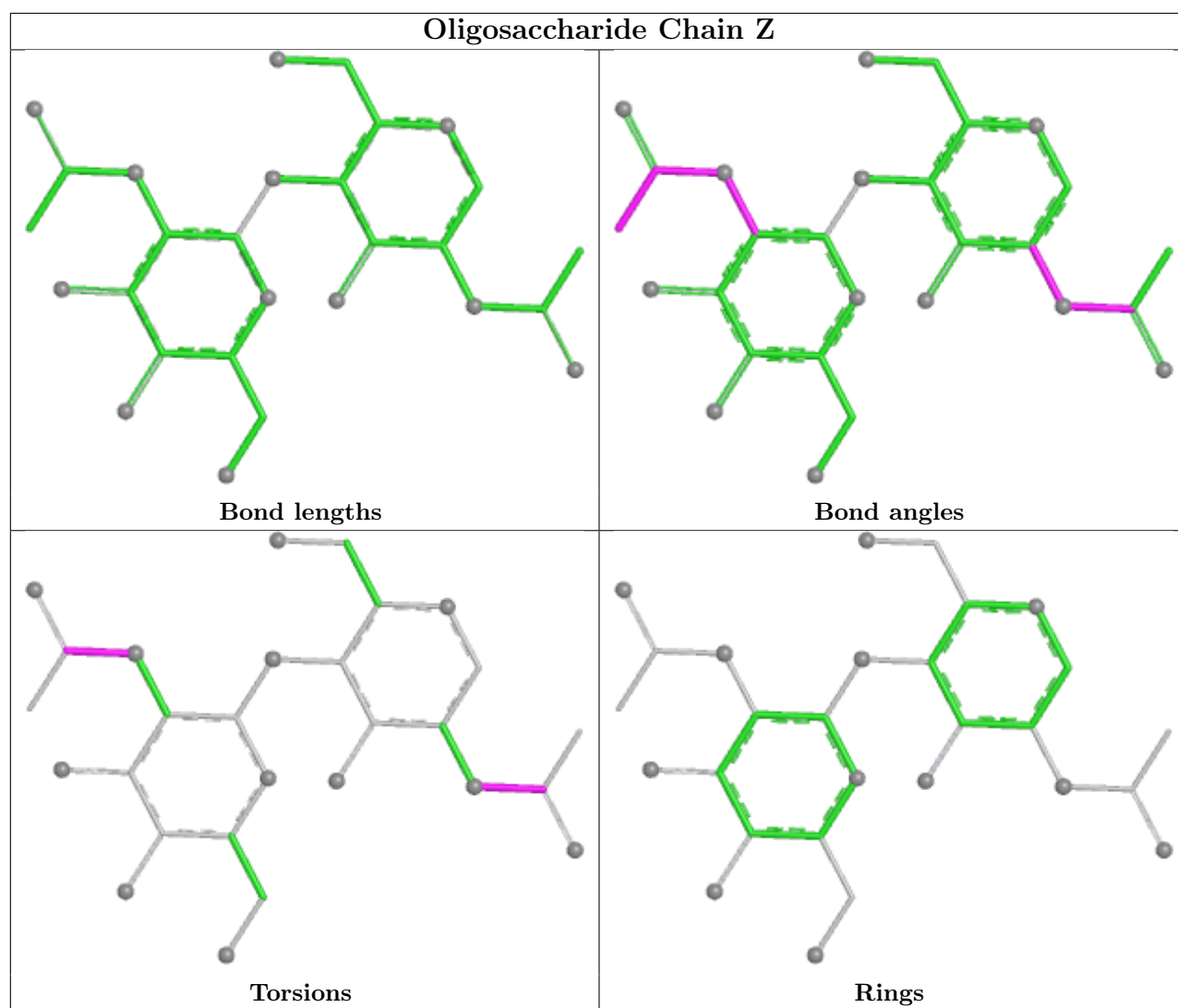
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	a	1	NAG	1	0
10	W	2	NAG	1	0
8	h	1	NAG	1	0
8	T	1	NAG	1	0
10	d	2	NAG	1	0
10	k	2	NAG	1	0

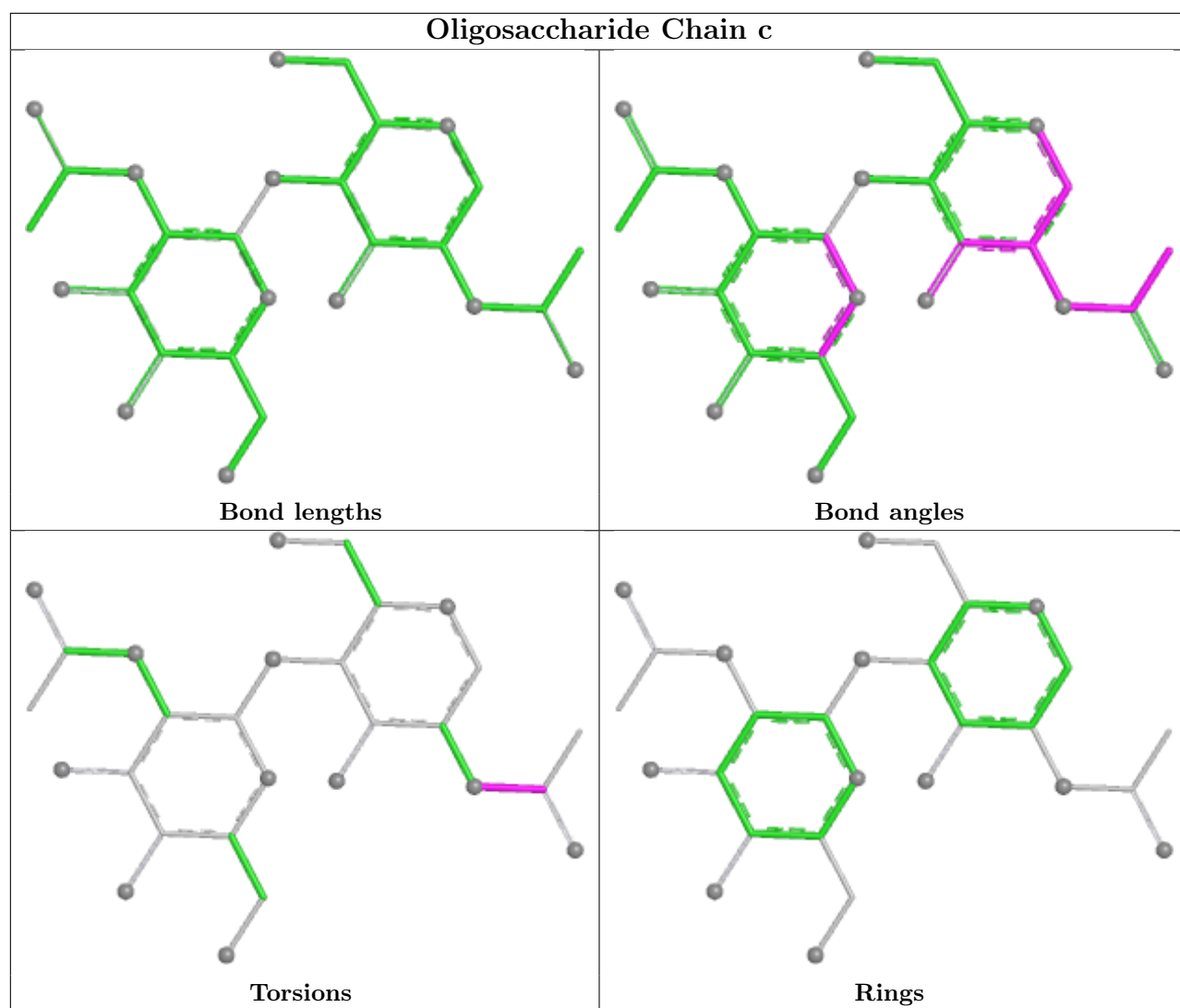
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

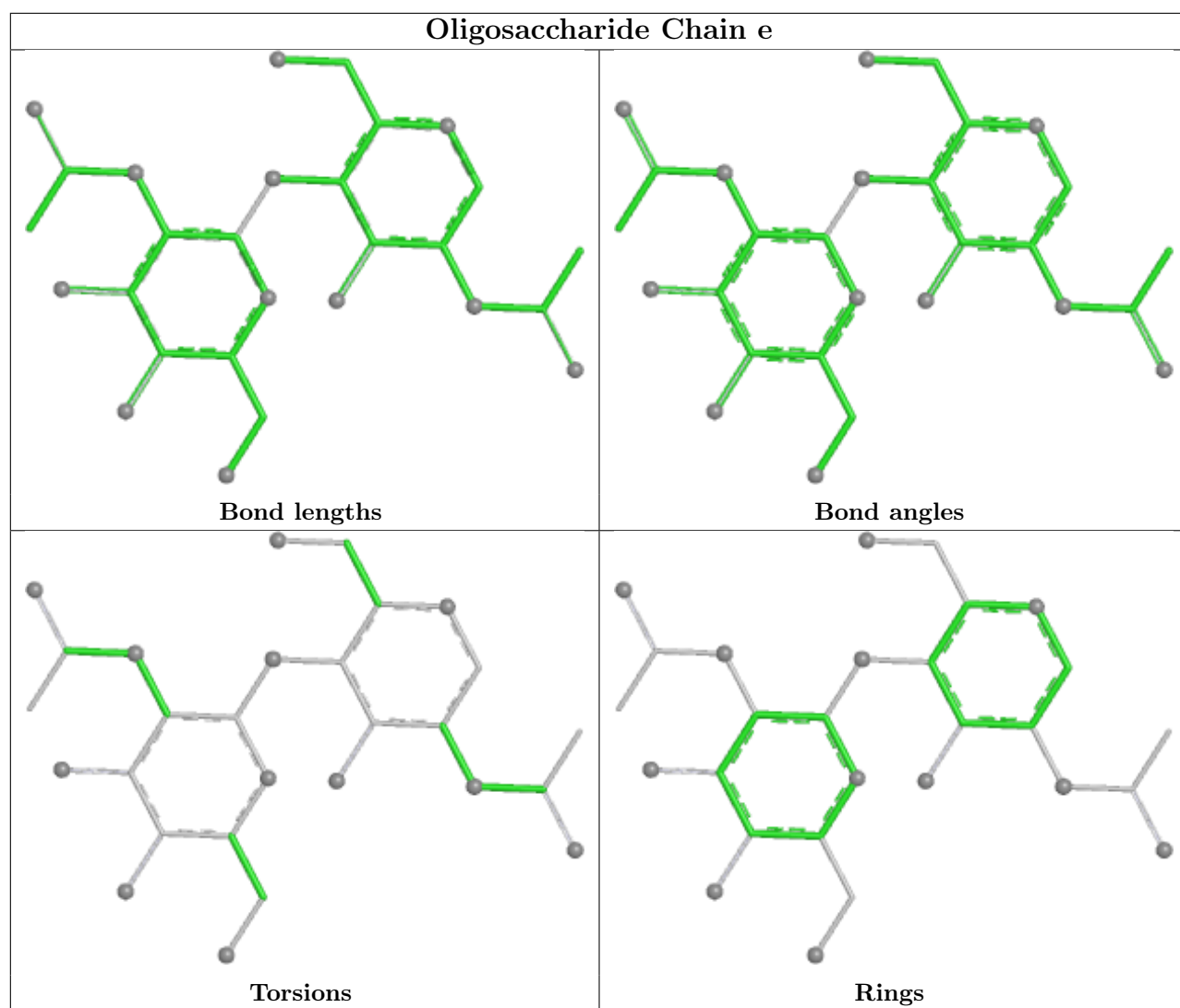


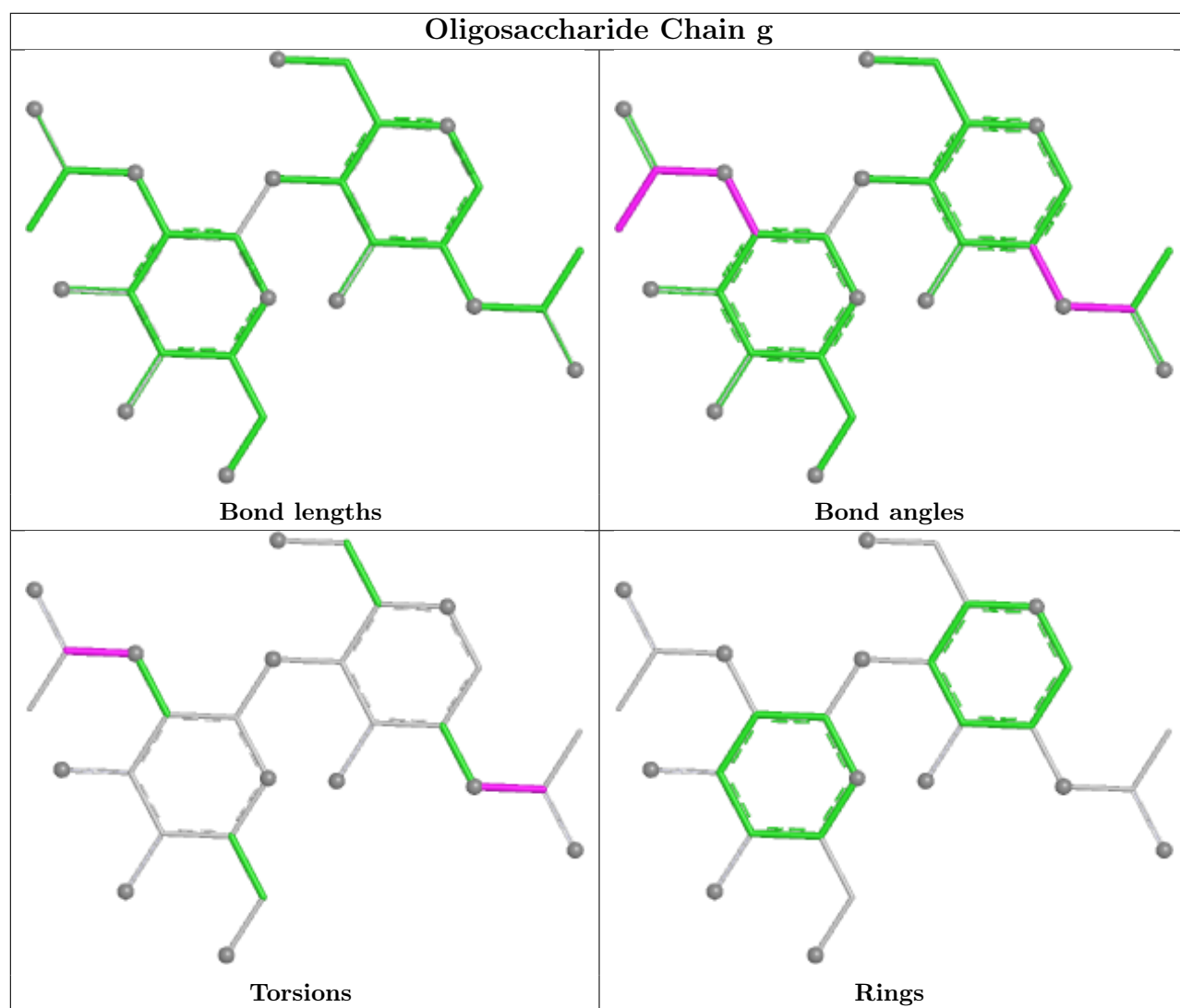


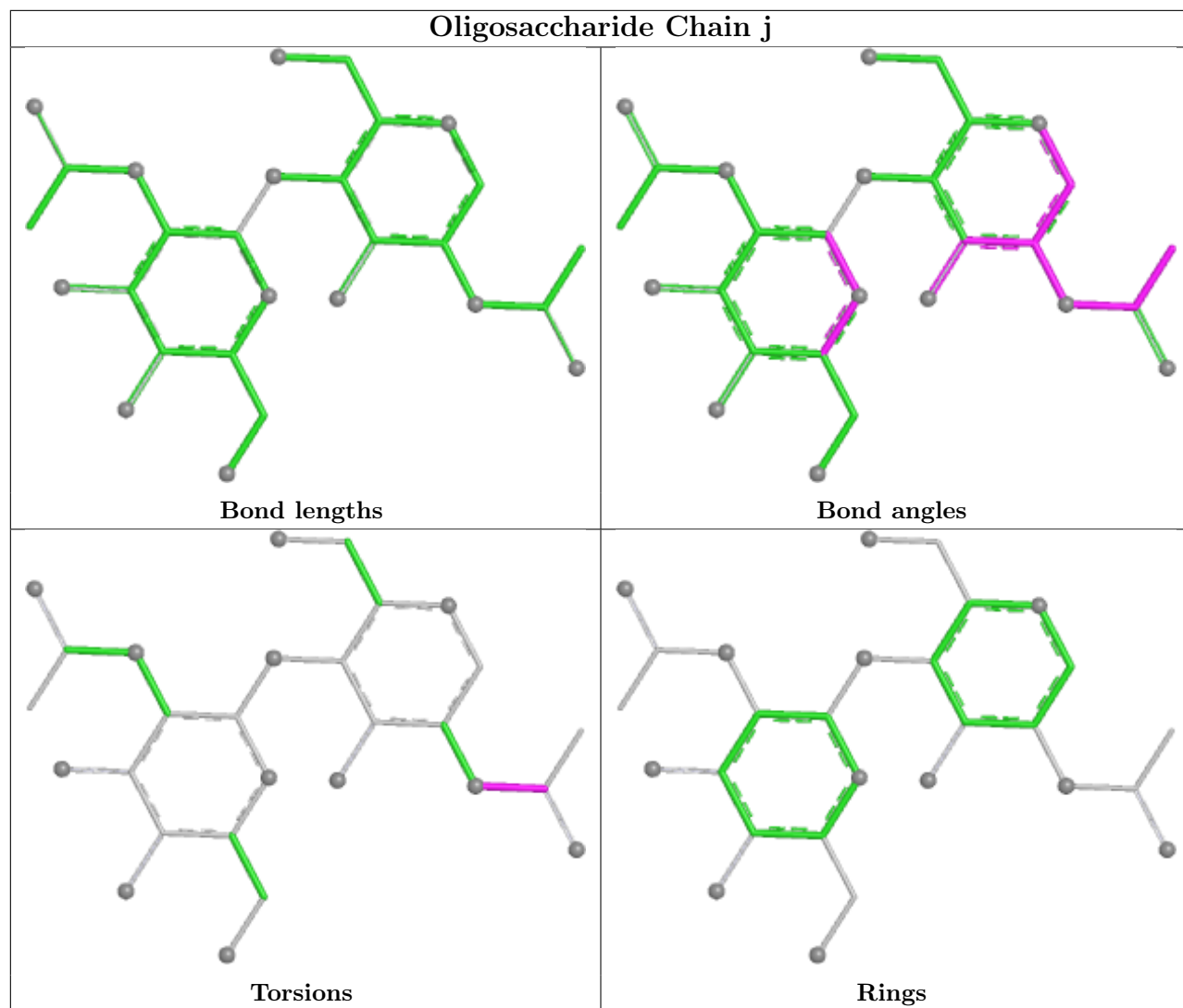


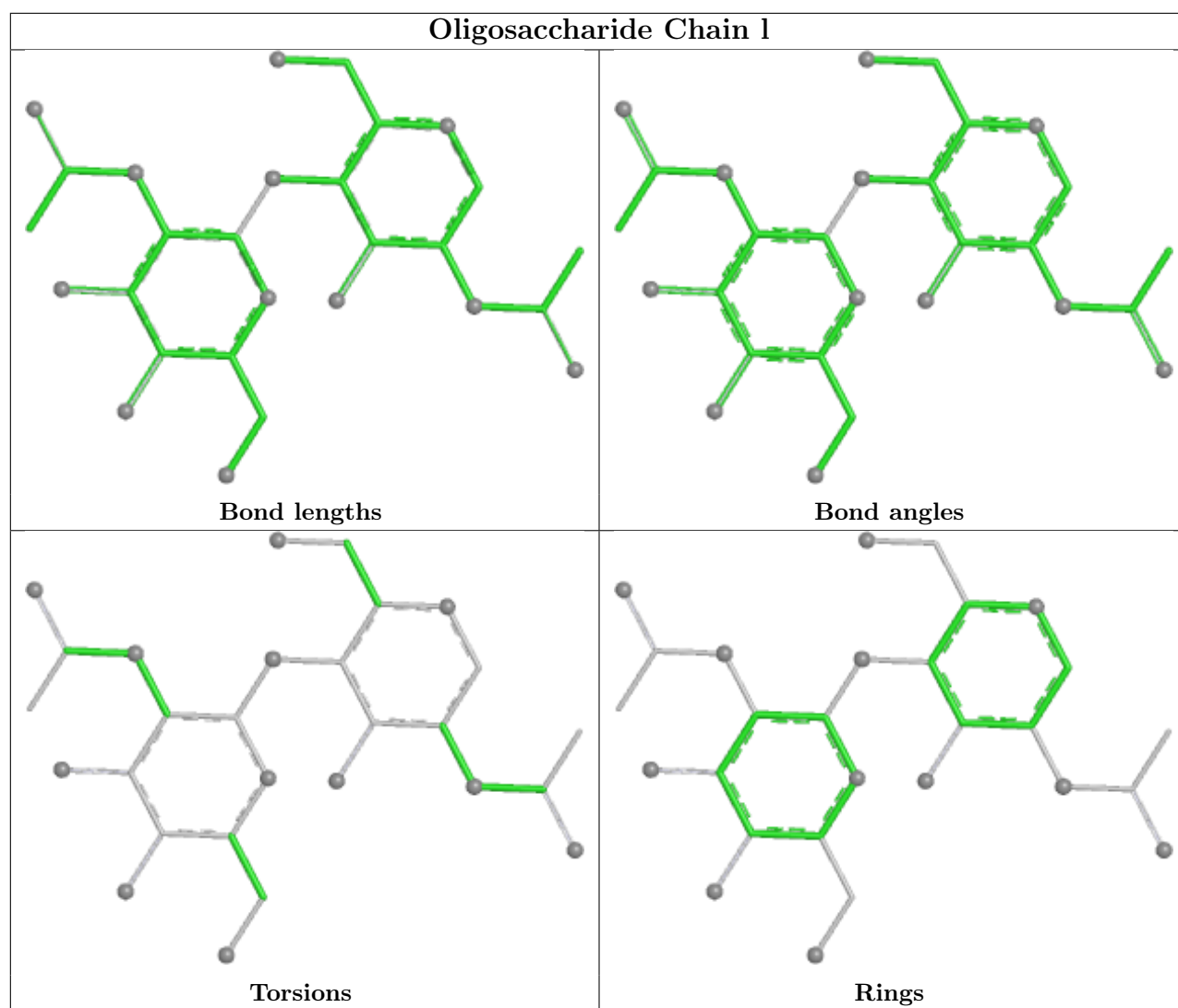


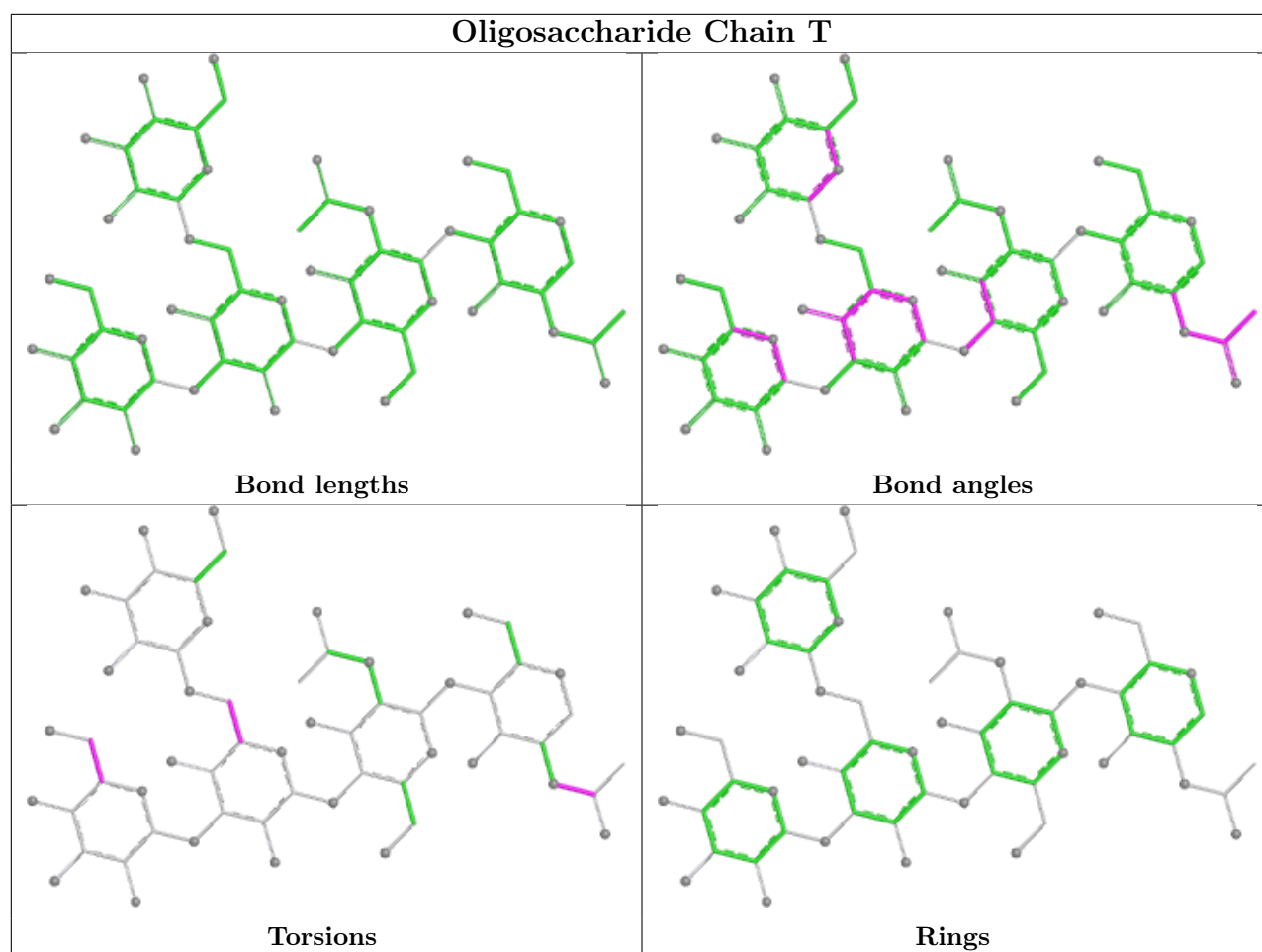


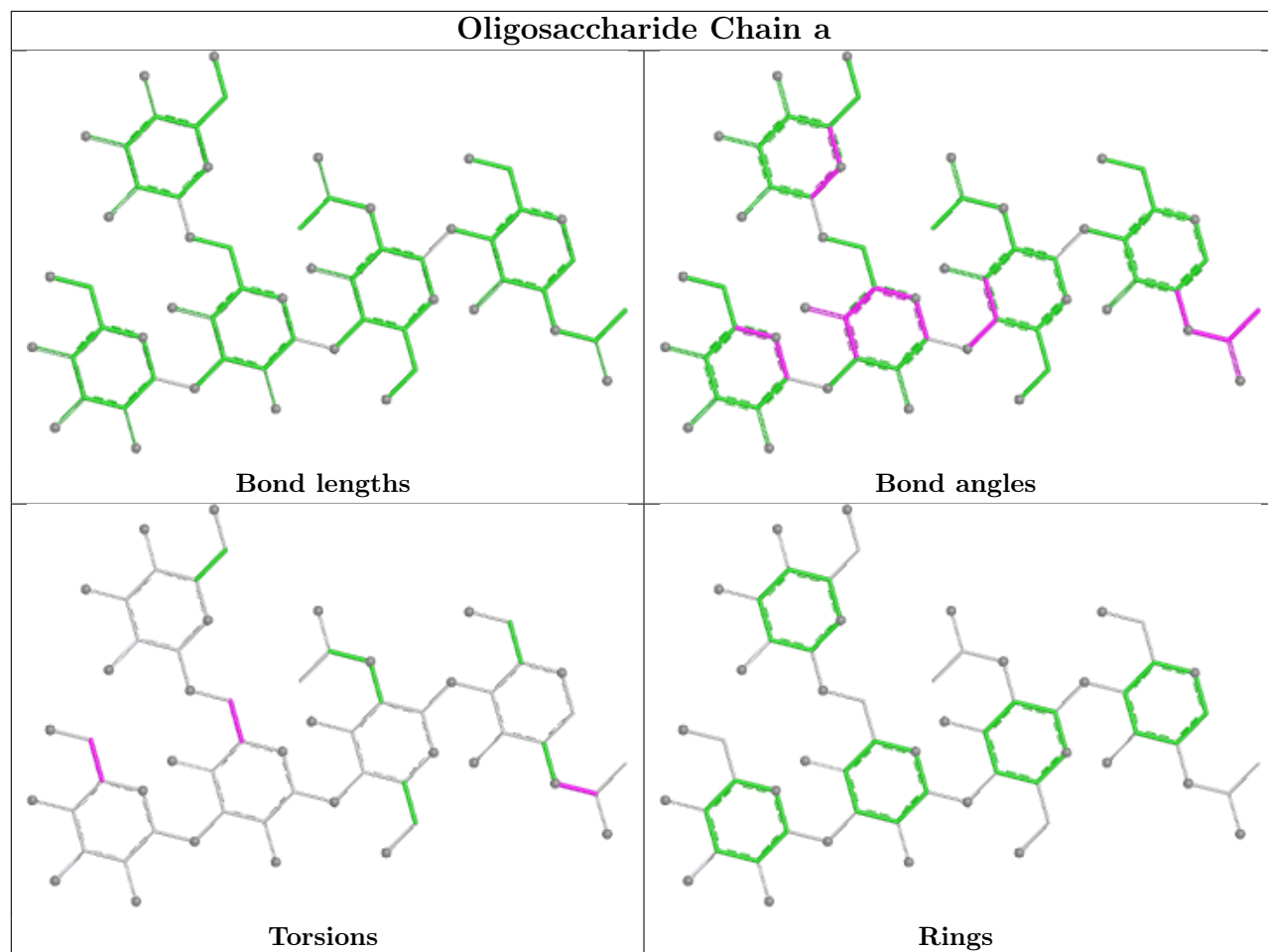


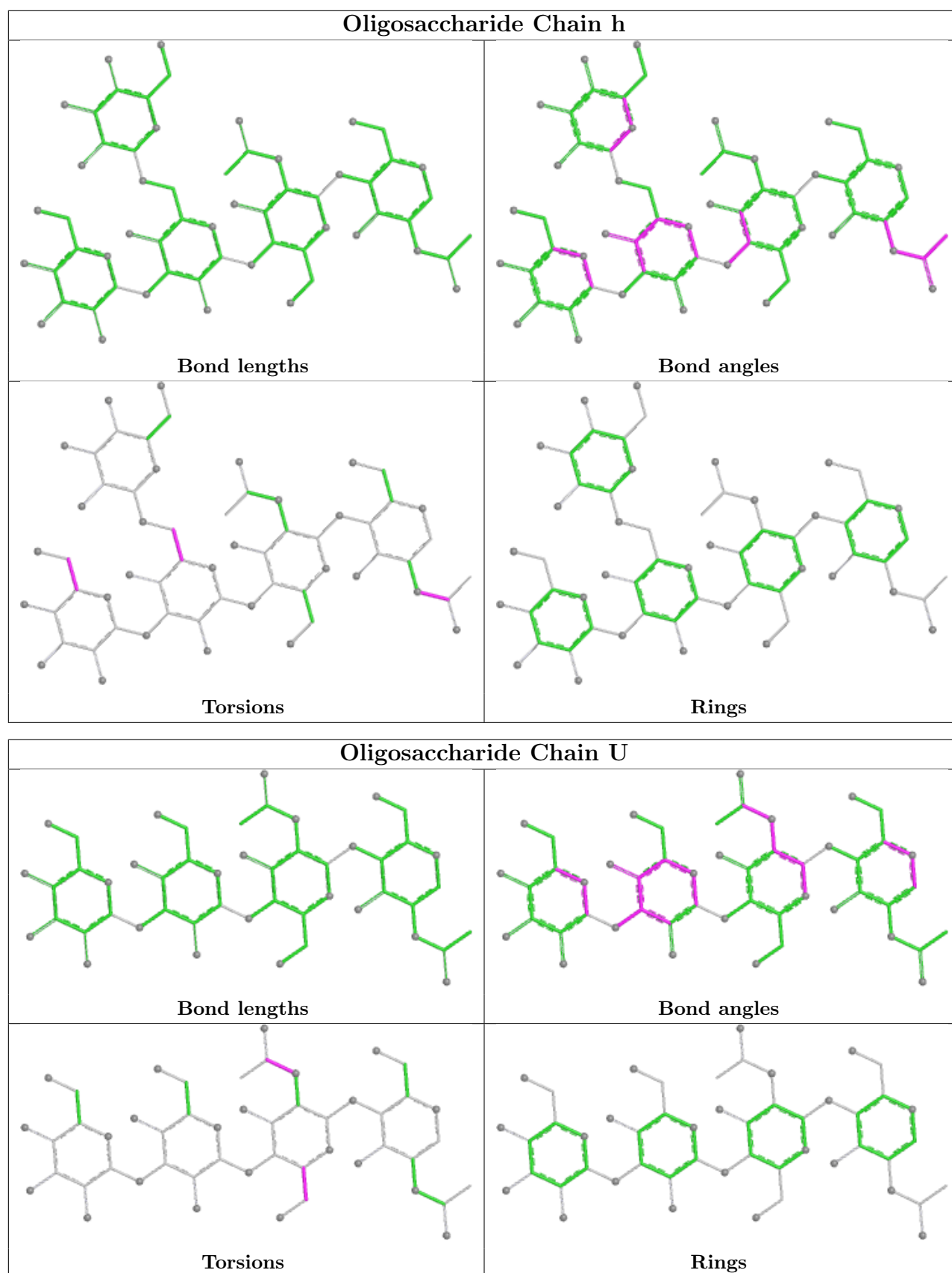


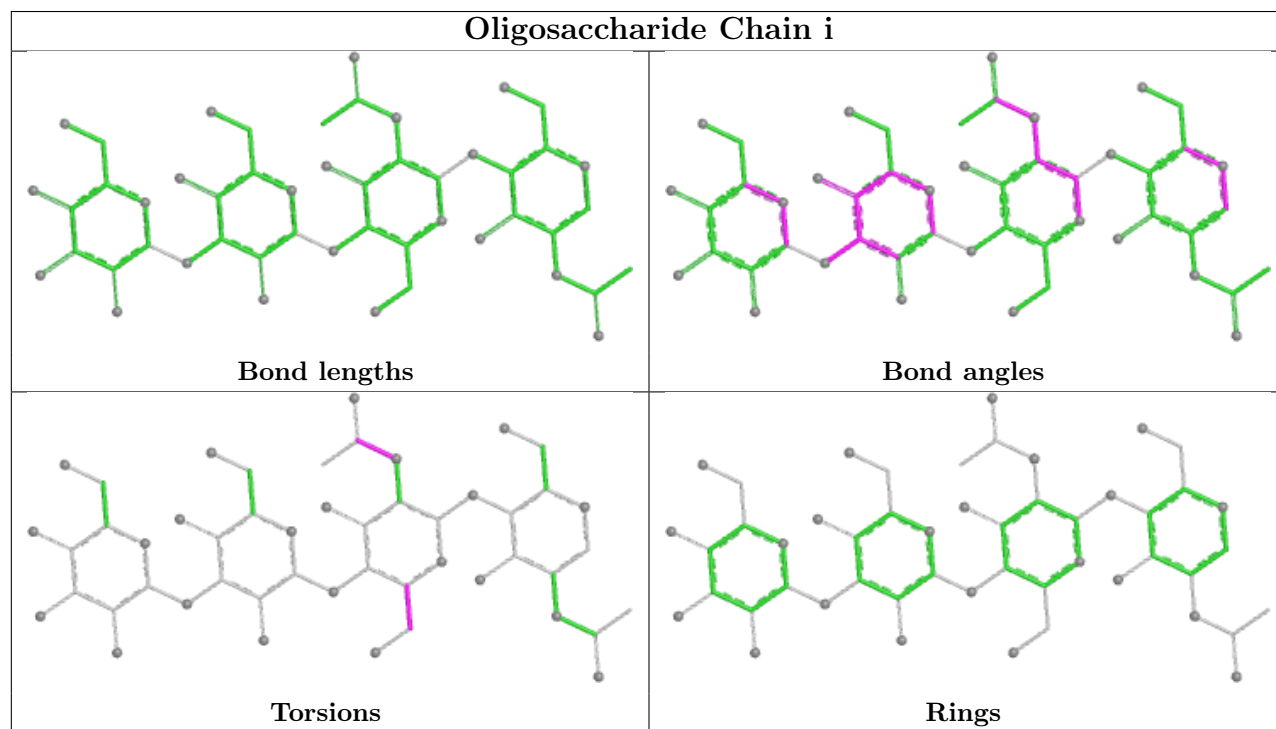
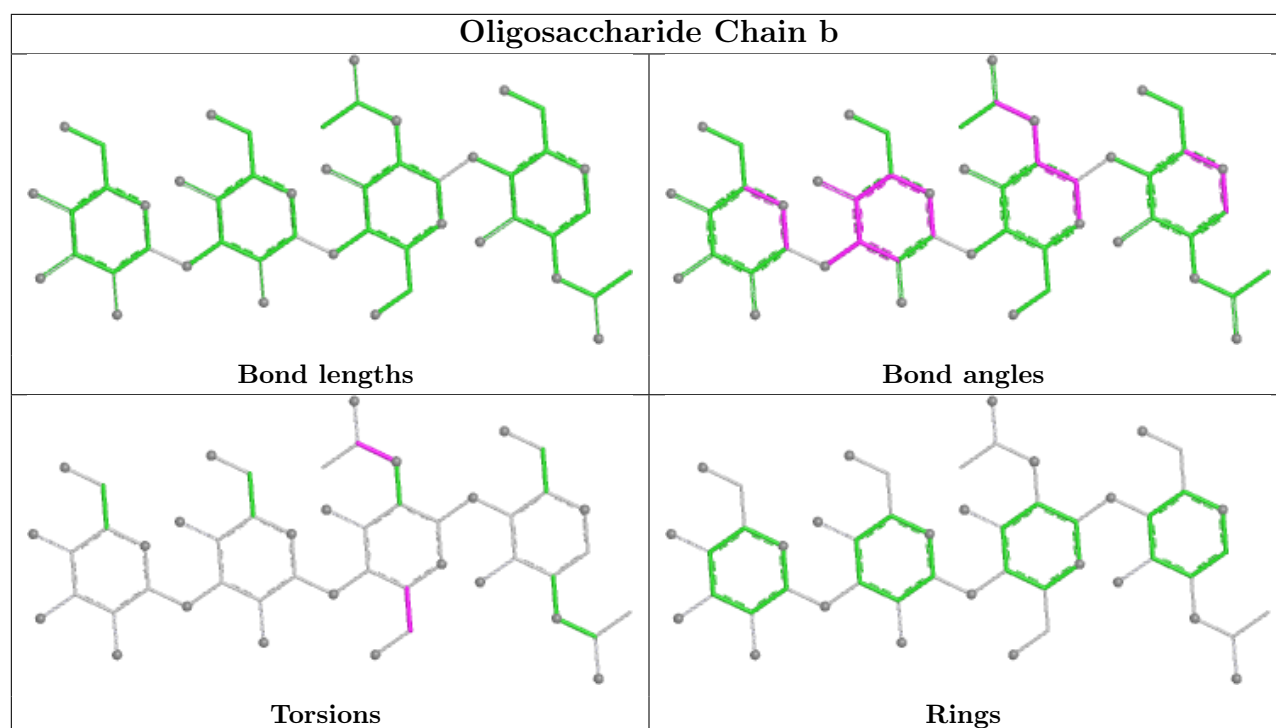


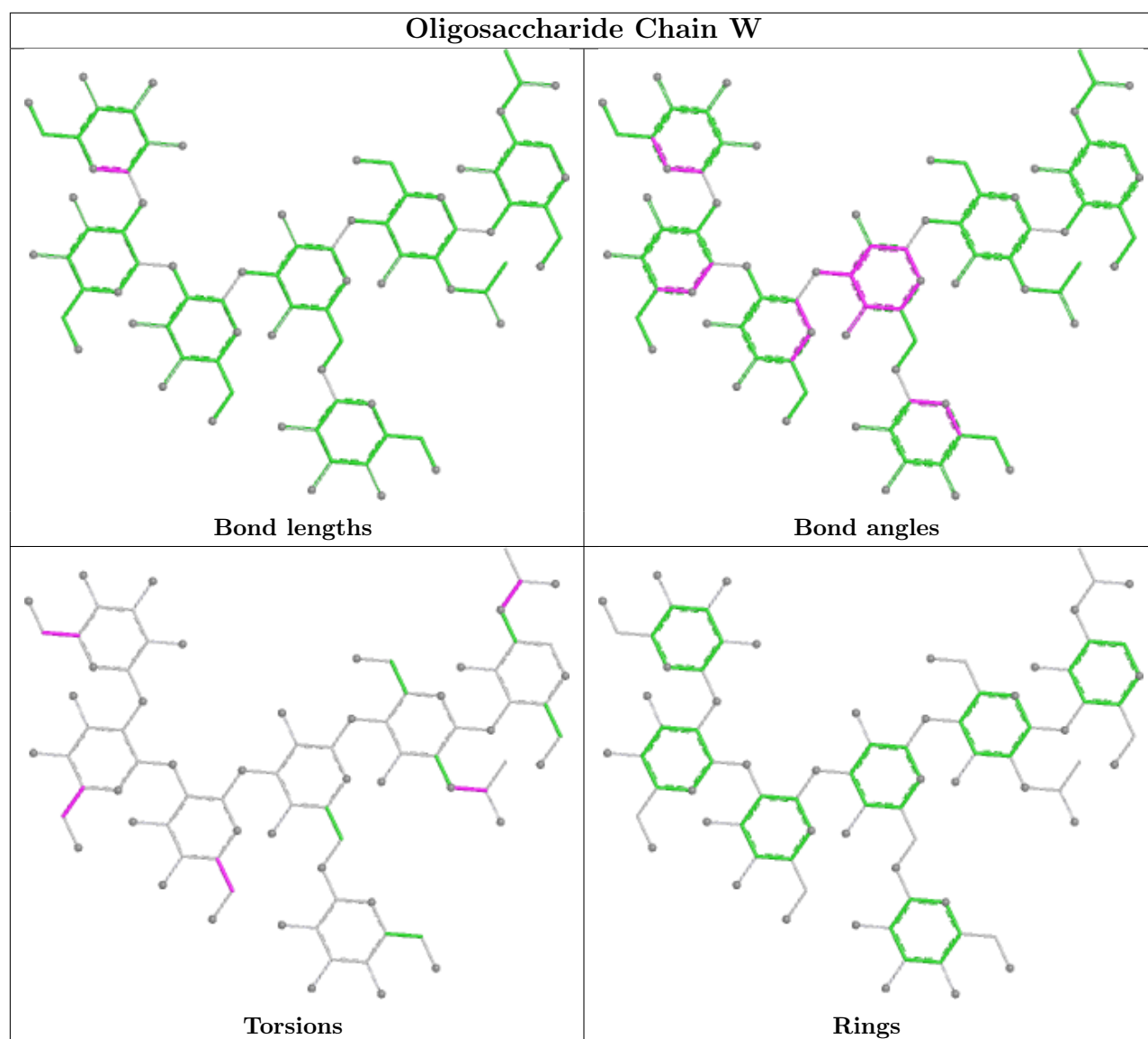


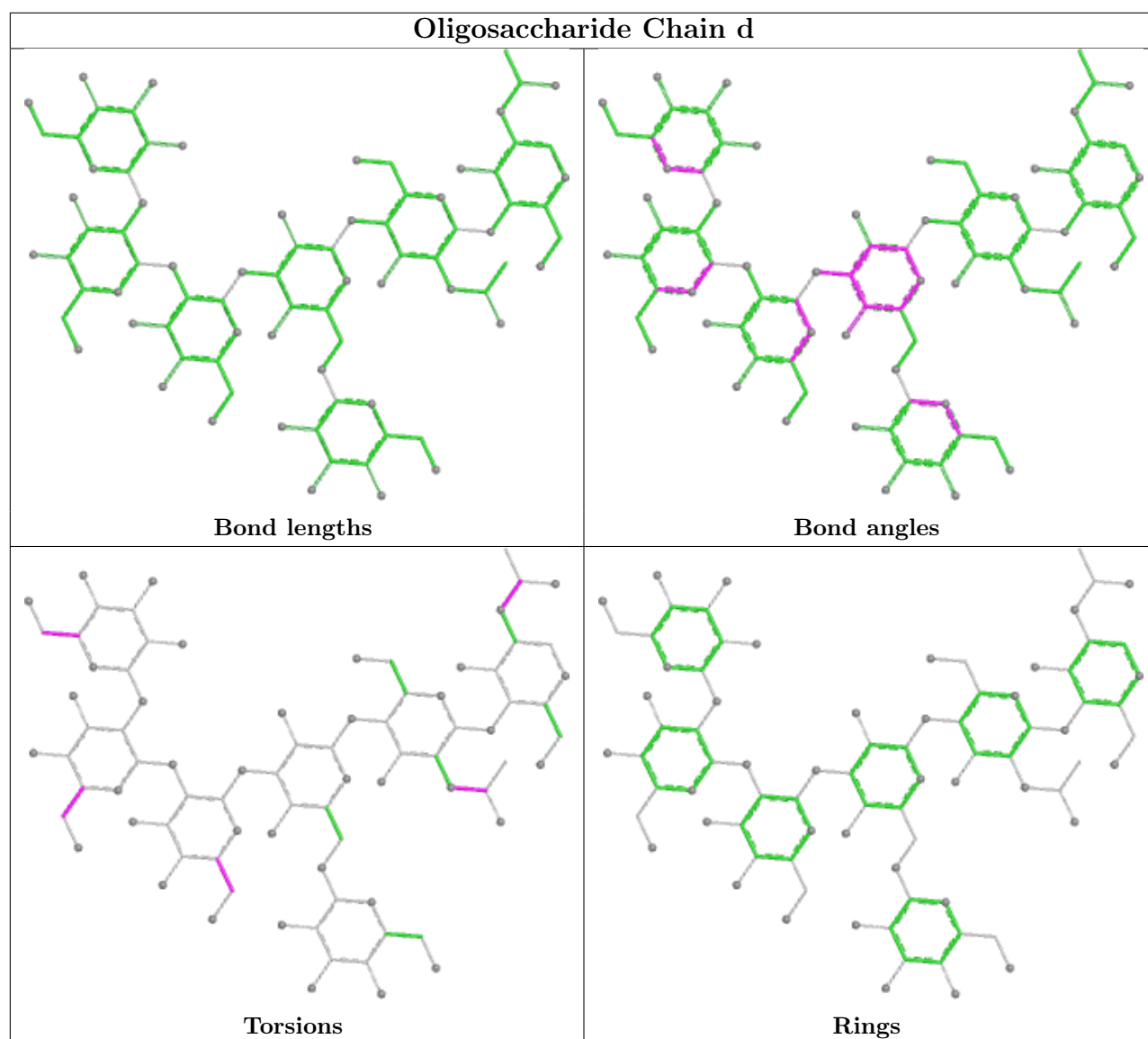


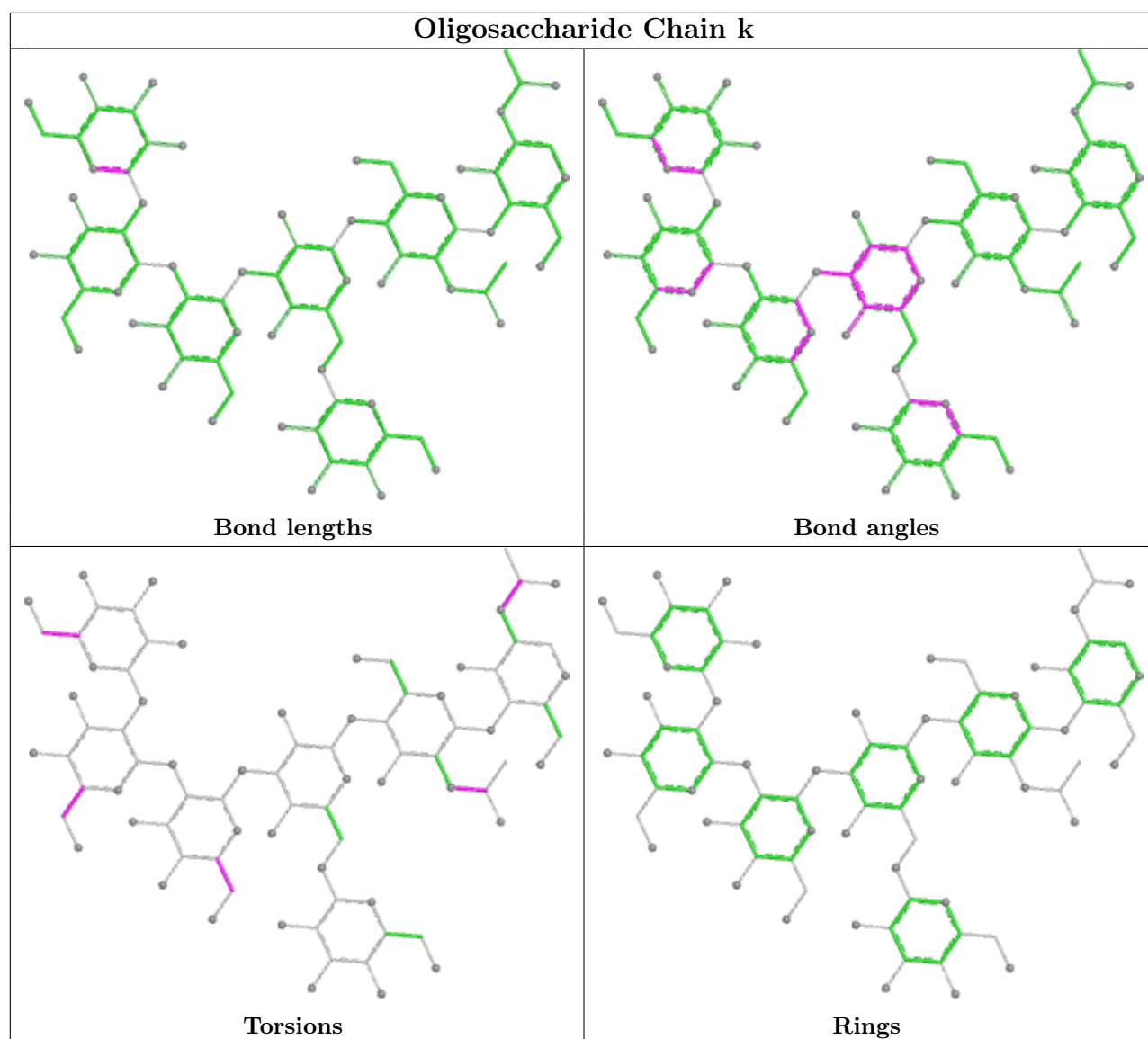


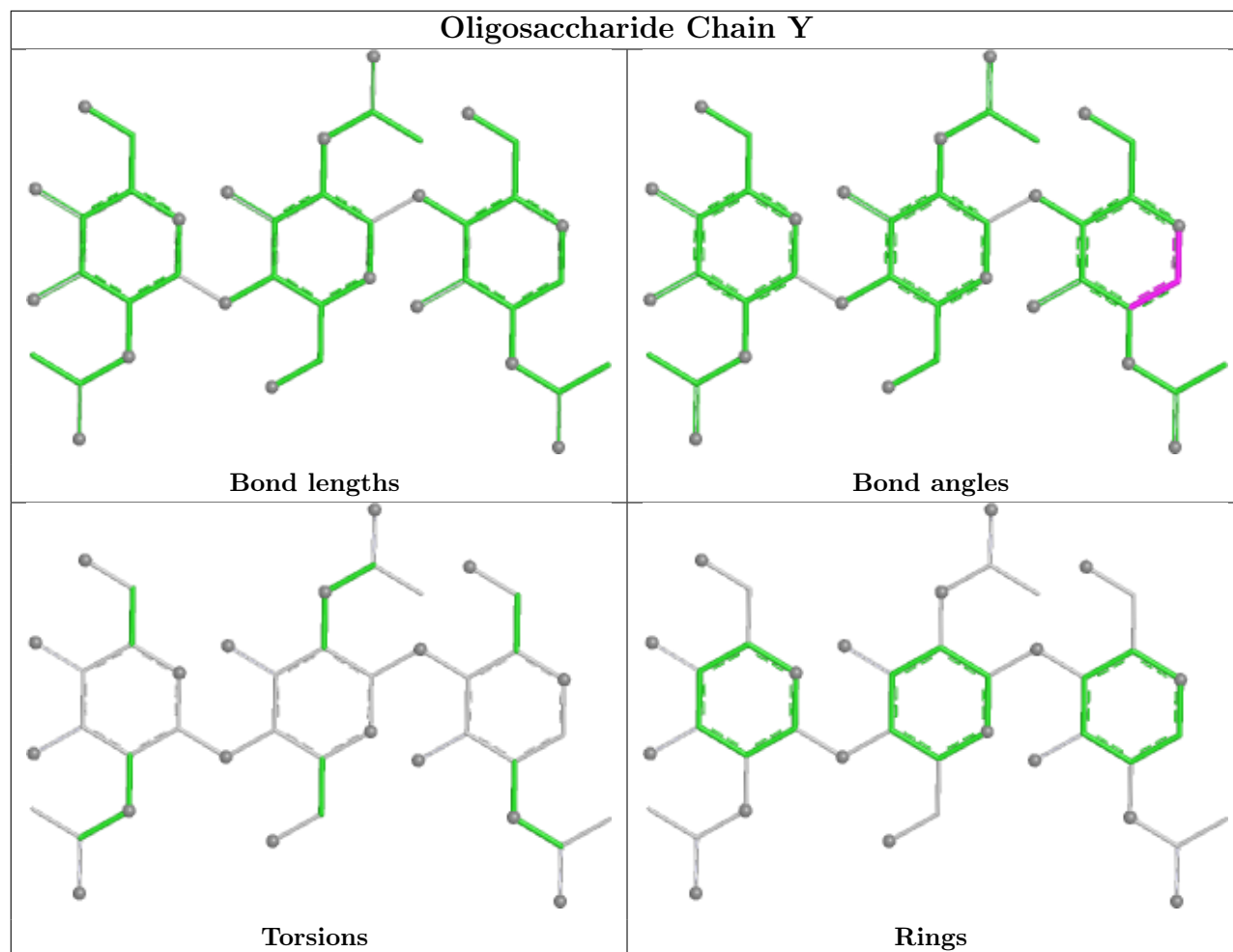


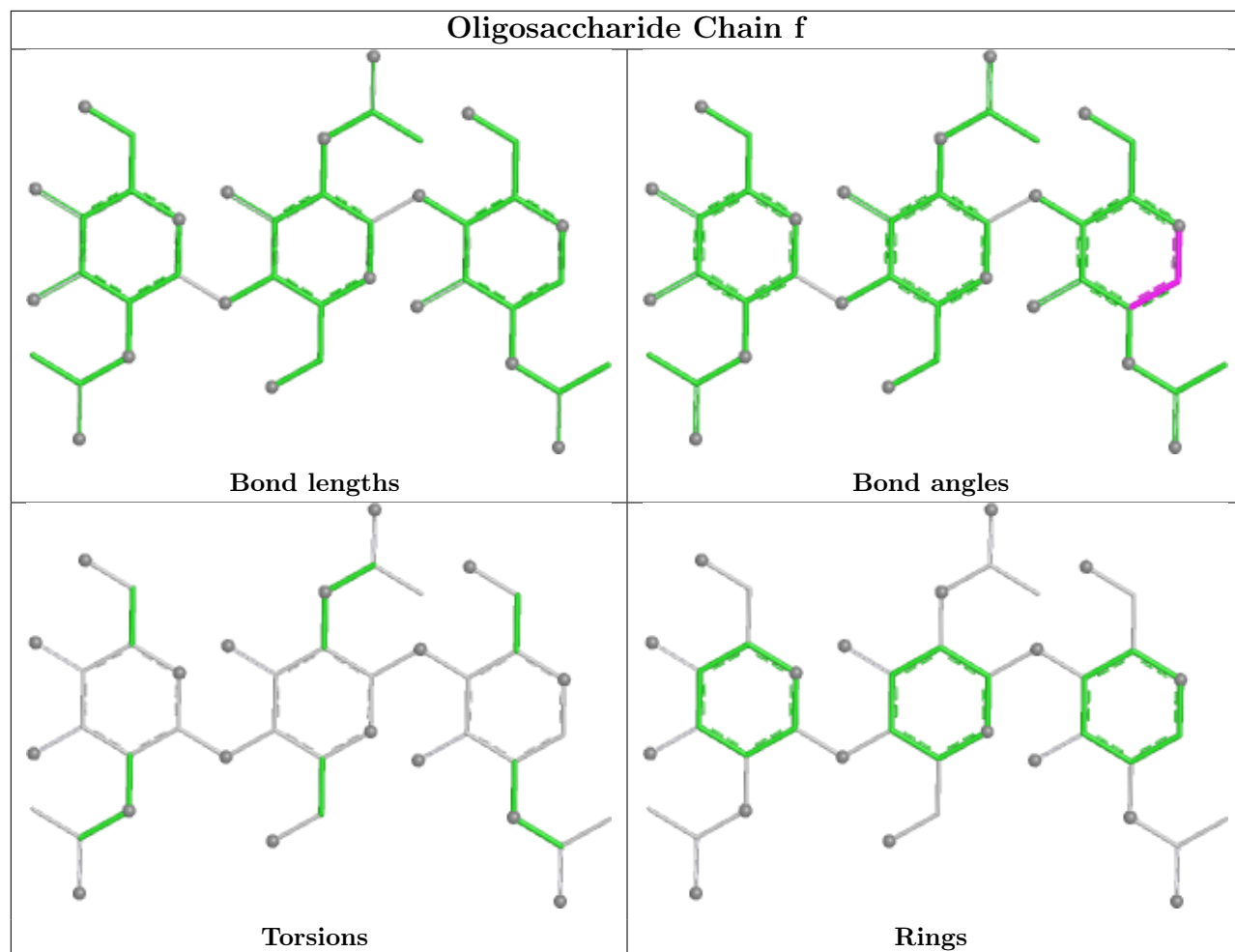


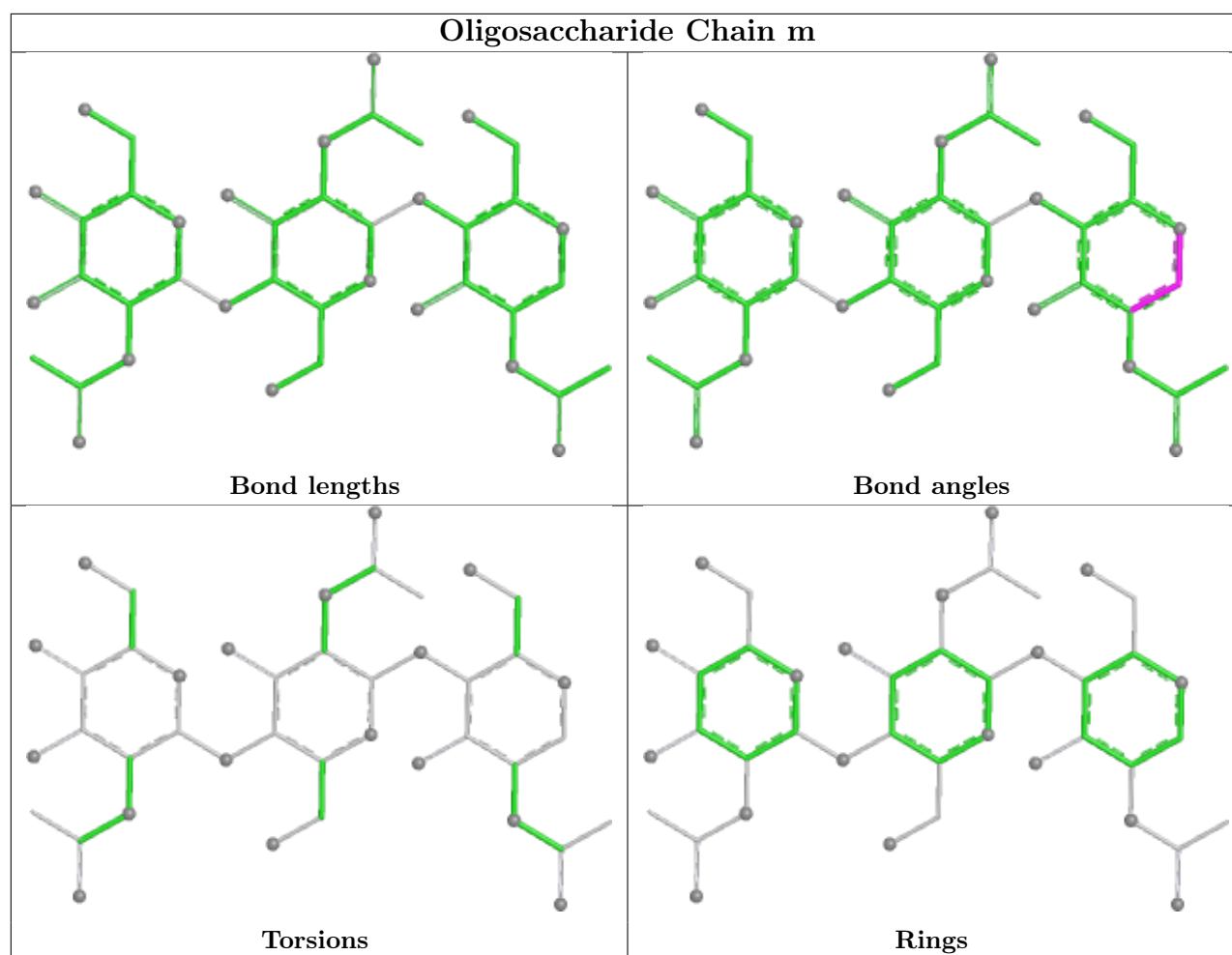












5.6 Ligand geometry [i](#)

30 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	$\# Z > 2$
12	NAG	A	604	5	14,14,15	0.74	0	17,19,21	1.20	1 (5%)
12	NAG	A	610	5	14,14,15	0.81	0	17,19,21	1.34	2 (11%)
12	NAG	C	608	5	14,14,15	0.65	0	17,19,21	1.98	3 (17%)
12	NAG	E	607	5	14,14,15	0.72	0	17,19,21	0.92	0
12	NAG	A	609	5	14,14,15	0.77	0	17,19,21	1.72	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	NAG	C	604	5	14,14,15	0.74	0	17,19,21	1.20	1 (5%)
12	NAG	C	601	5	14,14,15	0.76	0	17,19,21	0.83	0
12	NAG	C	607	5	14,14,15	0.72	0	17,19,21	0.92	0
12	NAG	A	601	5	14,14,15	0.76	0	17,19,21	0.83	0
12	NAG	A	606	5	14,14,15	0.73	0	17,19,21	1.72	3 (17%)
12	NAG	C	602	5	14,14,15	0.73	0	17,19,21	1.06	1 (5%)
12	NAG	E	603	5	14,14,15	0.70	0	17,19,21	0.98	0
12	NAG	C	605	5	14,14,15	0.73	0	17,19,21	1.27	1 (5%)
12	NAG	E	602	5	14,14,15	0.73	0	17,19,21	1.05	1 (5%)
12	NAG	C	610	5	14,14,15	0.82	0	17,19,21	1.34	2 (11%)
12	NAG	A	603	5	14,14,15	0.70	0	17,19,21	0.98	0
12	NAG	E	608	5	14,14,15	0.64	0	17,19,21	1.98	3 (17%)
12	NAG	C	609	5	14,14,15	0.77	0	17,19,21	1.72	1 (5%)
12	NAG	E	605	5	14,14,15	0.73	0	17,19,21	1.26	1 (5%)
12	NAG	A	602	5	14,14,15	0.73	0	17,19,21	1.06	1 (5%)
12	NAG	E	606	5	14,14,15	0.73	0	17,19,21	1.72	3 (17%)
12	NAG	A	608	5	14,14,15	0.64	0	17,19,21	1.98	3 (17%)
12	NAG	E	610	5	14,14,15	0.81	0	17,19,21	1.34	2 (11%)
12	NAG	C	606	5	14,14,15	0.73	0	17,19,21	1.73	3 (17%)
12	NAG	E	609	5	14,14,15	0.77	0	17,19,21	1.72	1 (5%)
12	NAG	A	605	5	14,14,15	0.73	0	17,19,21	1.27	1 (5%)
12	NAG	A	607	5	14,14,15	0.72	0	17,19,21	0.92	0
12	NAG	C	603	5	14,14,15	0.70	0	17,19,21	0.98	0
12	NAG	E	604	5	14,14,15	0.74	0	17,19,21	1.21	1 (5%)
12	NAG	E	601	5	14,14,15	0.76	0	17,19,21	0.83	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
12	NAG	A	604	5	-	2/6/23/26	0/1/1/1
12	NAG	A	610	5	-	1/6/23/26	0/1/1/1
12	NAG	C	608	5	-	2/6/23/26	0/1/1/1
12	NAG	E	607	5	-	2/6/23/26	0/1/1/1
12	NAG	A	609	5	-	0/6/23/26	0/1/1/1
12	NAG	C	604	5	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	NAG	C	601	5	-	0/6/23/26	0/1/1/1
12	NAG	C	607	5	-	2/6/23/26	0/1/1/1
12	NAG	A	601	5	-	0/6/23/26	0/1/1/1
12	NAG	A	606	5	-	2/6/23/26	0/1/1/1
12	NAG	C	602	5	-	0/6/23/26	0/1/1/1
12	NAG	E	603	5	-	1/6/23/26	0/1/1/1
12	NAG	C	605	5	-	1/6/23/26	0/1/1/1
12	NAG	E	602	5	-	0/6/23/26	0/1/1/1
12	NAG	C	610	5	-	1/6/23/26	0/1/1/1
12	NAG	A	603	5	-	1/6/23/26	0/1/1/1
12	NAG	E	608	5	-	2/6/23/26	0/1/1/1
12	NAG	C	609	5	-	0/6/23/26	0/1/1/1
12	NAG	E	605	5	-	1/6/23/26	0/1/1/1
12	NAG	A	602	5	-	0/6/23/26	0/1/1/1
12	NAG	E	606	5	-	2/6/23/26	0/1/1/1
12	NAG	A	608	5	-	2/6/23/26	0/1/1/1
12	NAG	E	610	5	-	1/6/23/26	0/1/1/1
12	NAG	C	606	5	-	2/6/23/26	0/1/1/1
12	NAG	E	609	5	-	0/6/23/26	0/1/1/1
12	NAG	A	605	5	-	1/6/23/26	0/1/1/1
12	NAG	A	607	5	-	2/6/23/26	0/1/1/1
12	NAG	C	603	5	-	1/6/23/26	0/1/1/1
12	NAG	E	604	5	-	2/6/23/26	0/1/1/1
12	NAG	E	601	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	E	609	NAG	C1-O5-C5	5.98	120.20	112.19
12	A	609	NAG	C1-O5-C5	5.97	120.19	112.19
12	C	609	NAG	C1-O5-C5	5.97	120.19	112.19
12	C	606	NAG	C2-N2-C7	5.47	130.23	122.90
12	E	606	NAG	C2-N2-C7	5.44	130.20	122.90

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	607	NAG	C1-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
12	C	607	NAG	C1-C2-N2-C7
12	E	607	NAG	C1-C2-N2-C7
12	A	606	NAG	C8-C7-N2-C2
12	A	606	NAG	O7-C7-N2-C2

There are no ring outliers.

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	604	NAG	2	0
12	C	604	NAG	2	0
12	E	603	NAG	1	0
12	A	603	NAG	1	0
12	C	603	NAG	1	0
12	E	604	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.

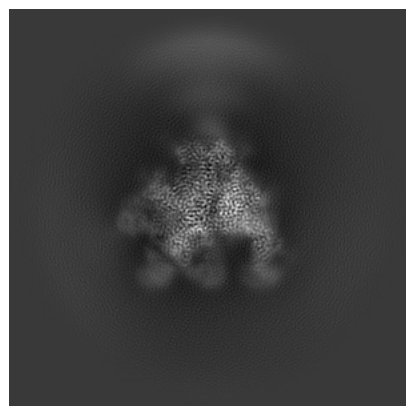
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70475. These allow visual inspection of the internal detail of the map and identification of artifacts.

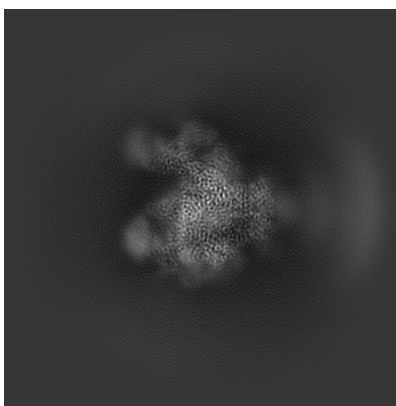
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

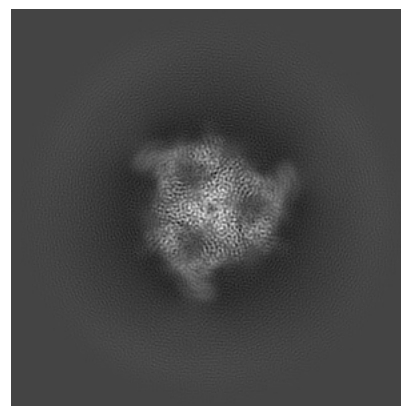
6.1.1 Primary map



X

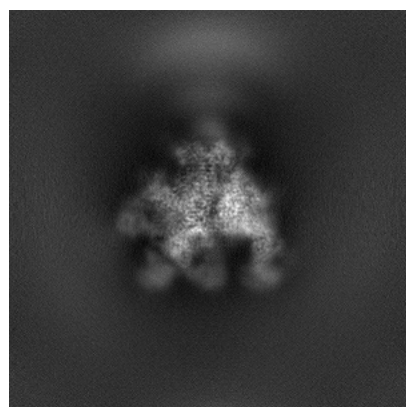


Y

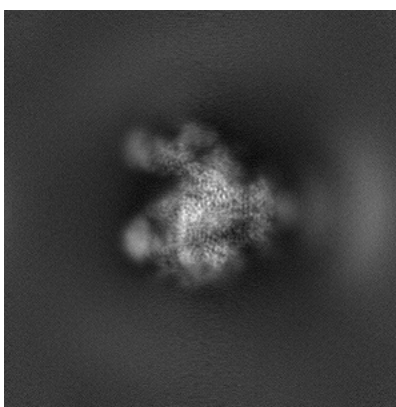


Z

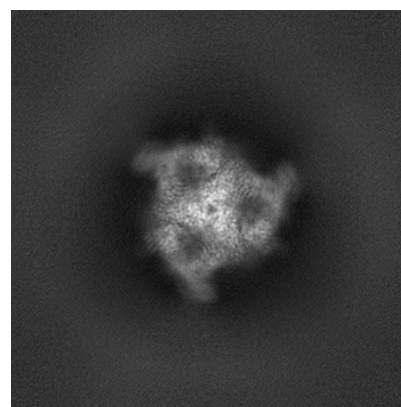
6.1.2 Raw map



X



Y

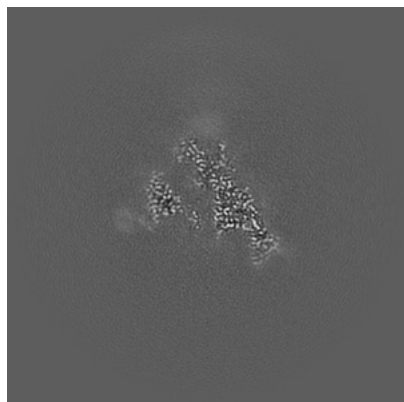


Z

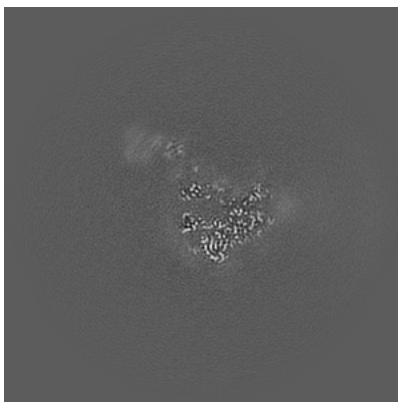
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

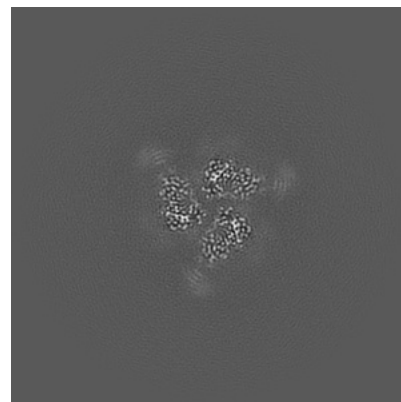
6.2.1 Primary map



X Index: 280

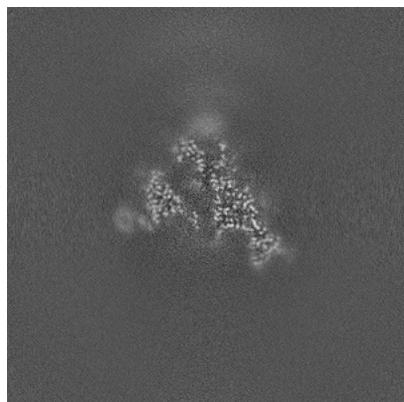


Y Index: 280

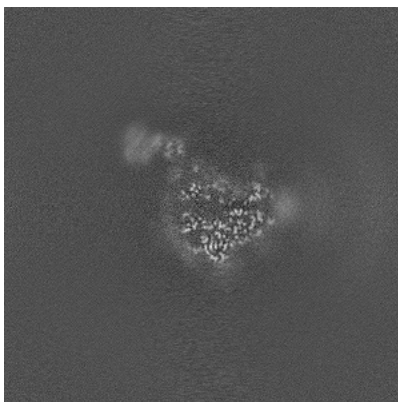


Z Index: 280

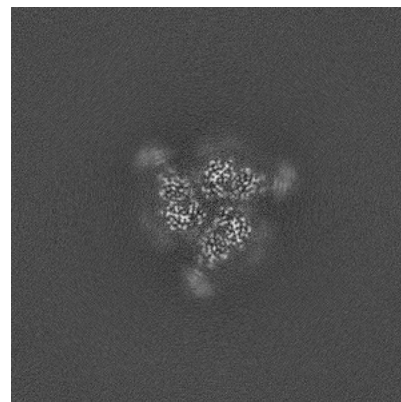
6.2.2 Raw map



X Index: 280



Y Index: 280

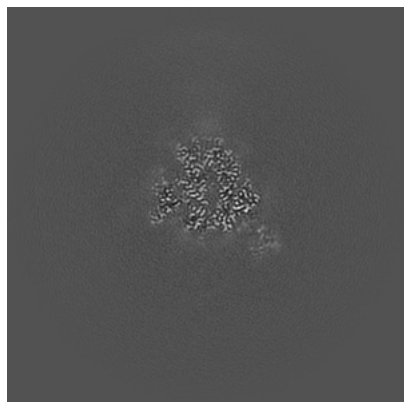


Z Index: 280

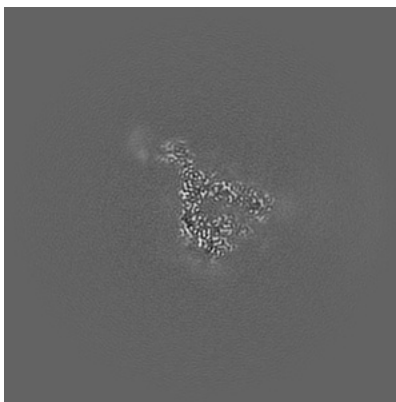
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

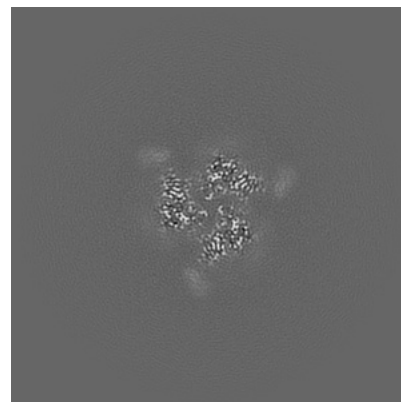
6.3.1 Primary map



X Index: 292

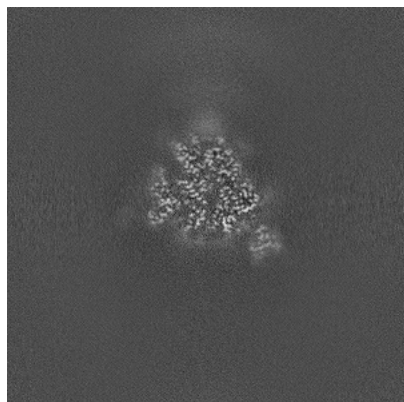


Y Index: 264

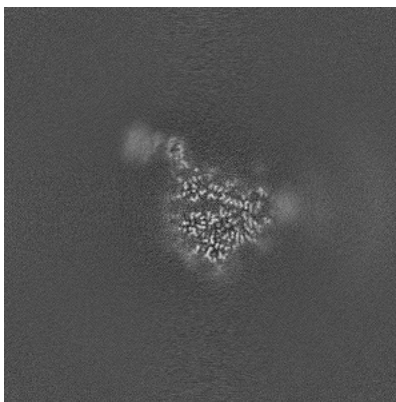


Z Index: 286

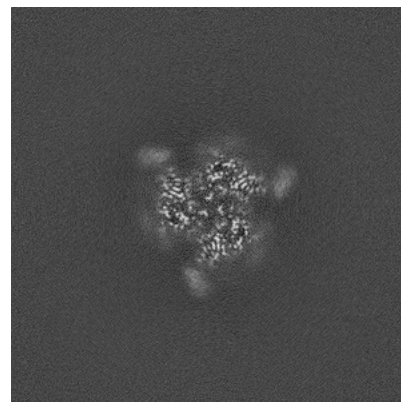
6.3.2 Raw map



X Index: 291



Y Index: 273

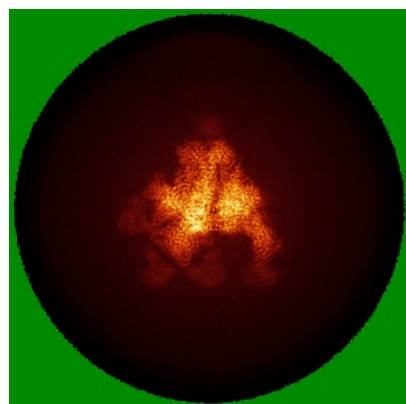


Z Index: 286

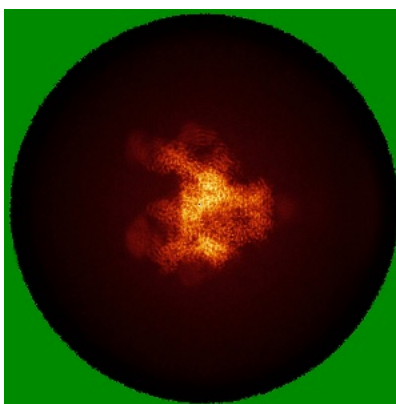
The images above show the largest variance slices of the map in three orthogonal directions.

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

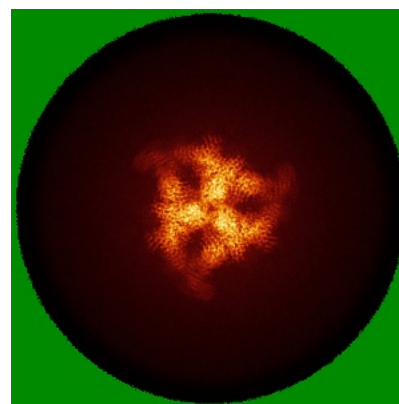
6.4.1 Primary map



X

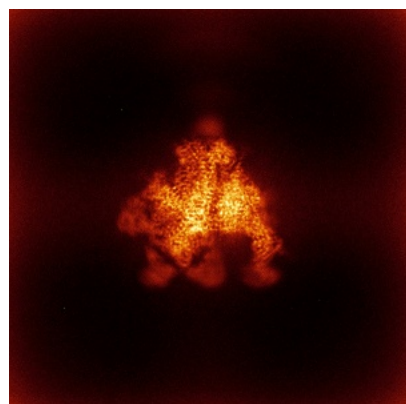


Y

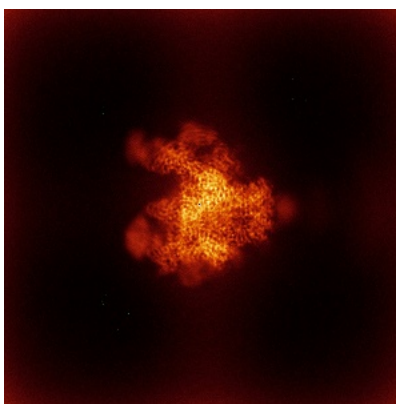


Z

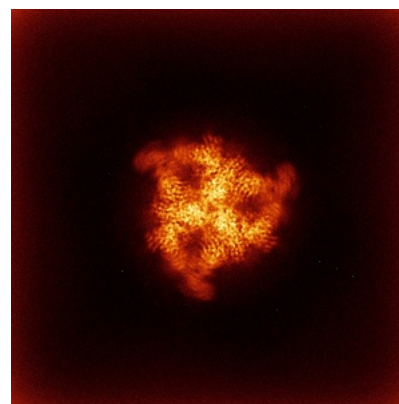
6.4.2 Raw map



X



Y



Z

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

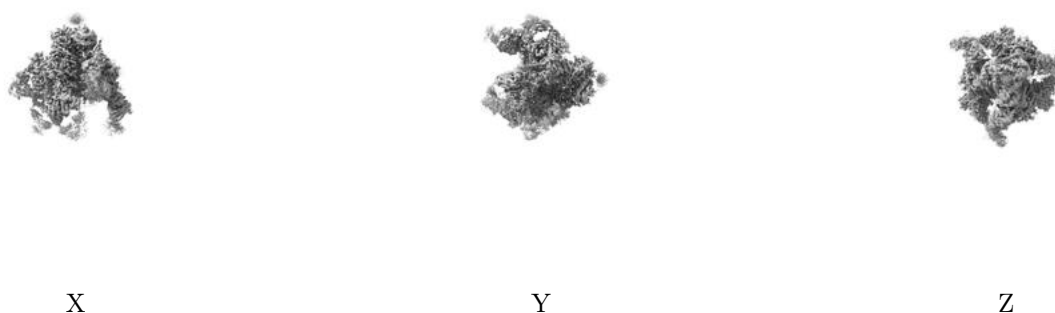
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

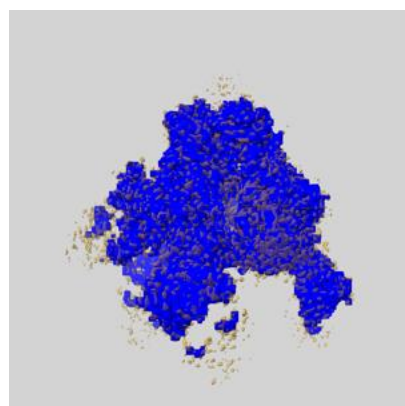
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

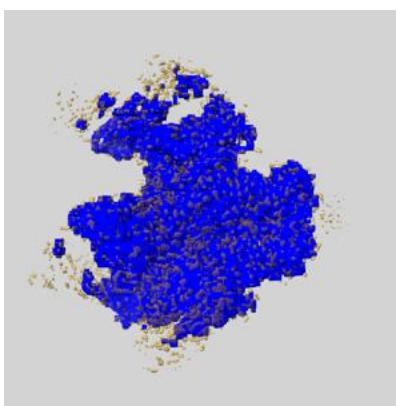
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

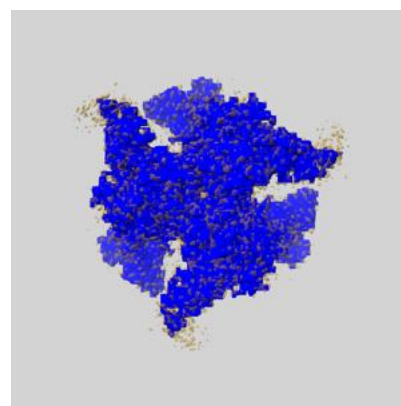
6.6.1 emd_70475_msk_1.map [i](#)



X



Y

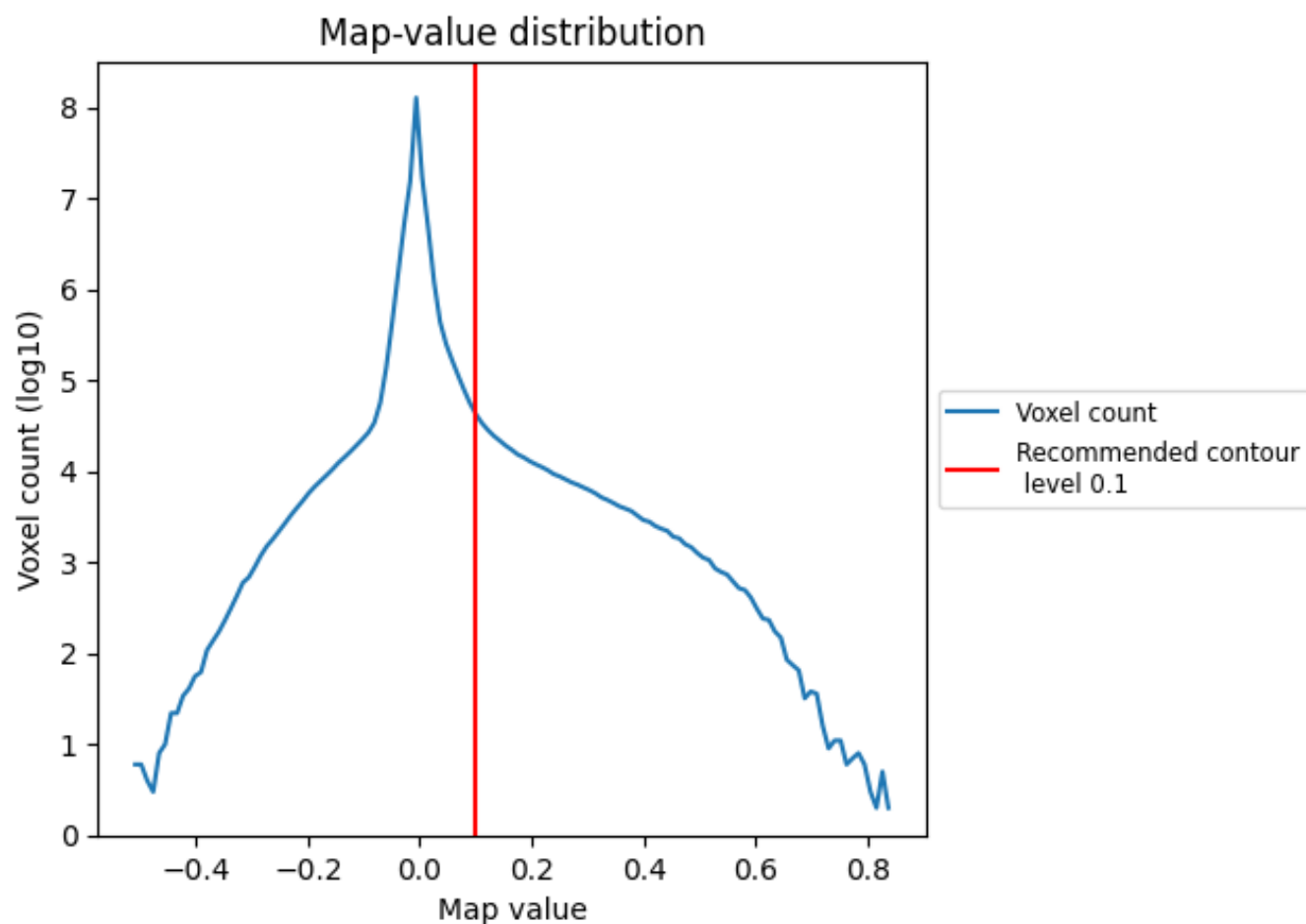


Z

7 Map analysis [i](#)

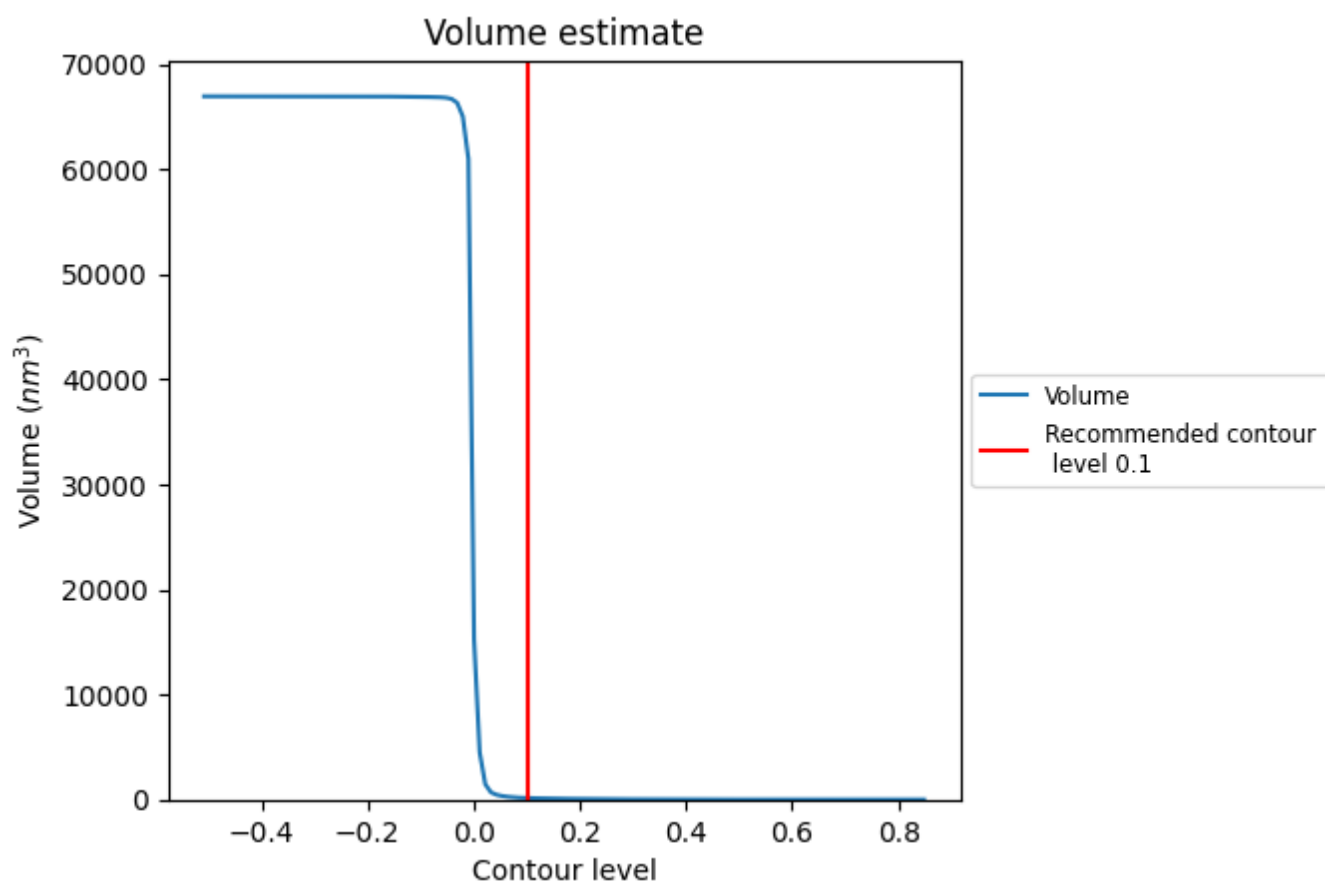
This section contains the results of statistical analysis of the map.

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.

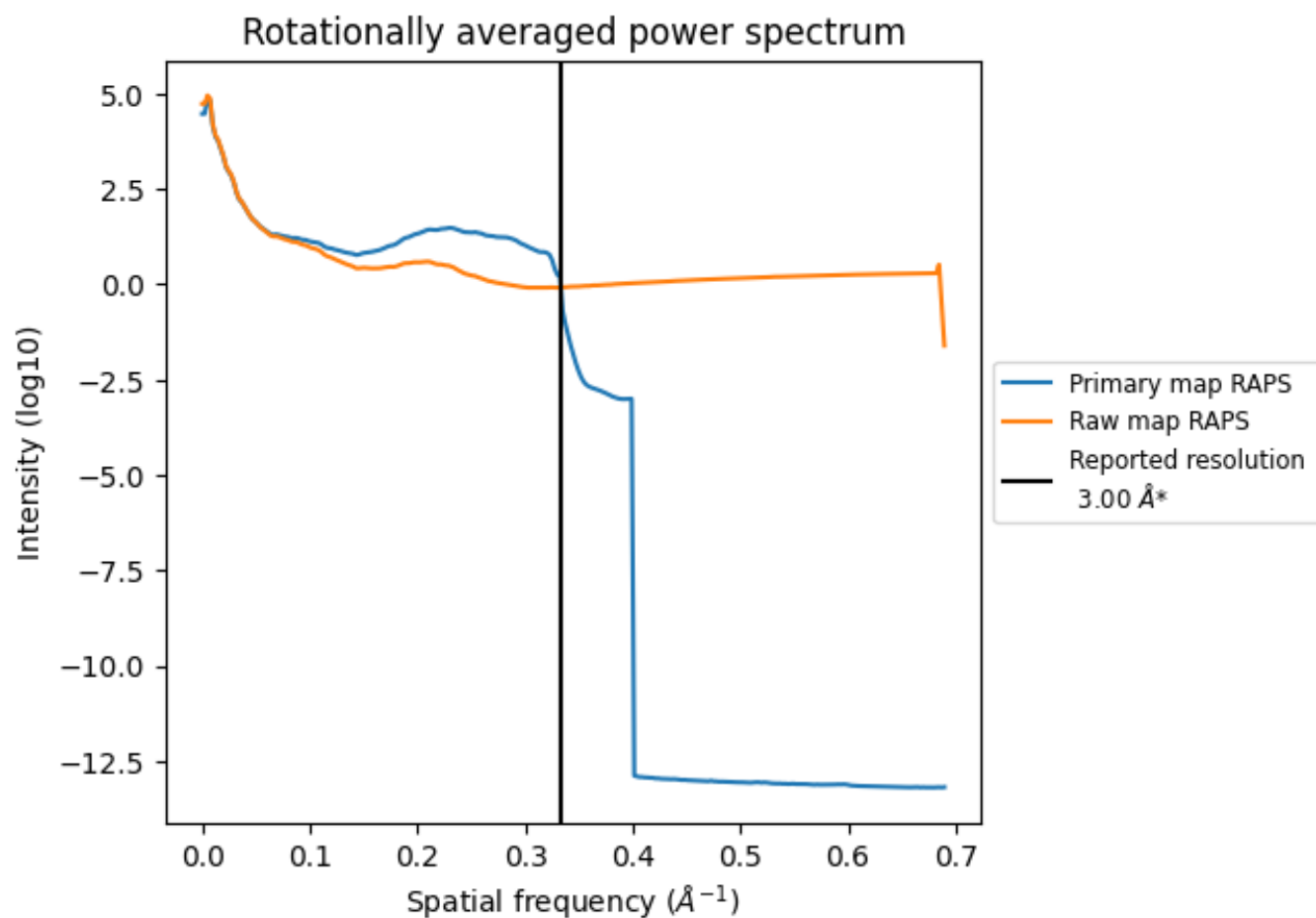
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 147 nm³; this corresponds to an approximate mass of 133 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 ⓘ

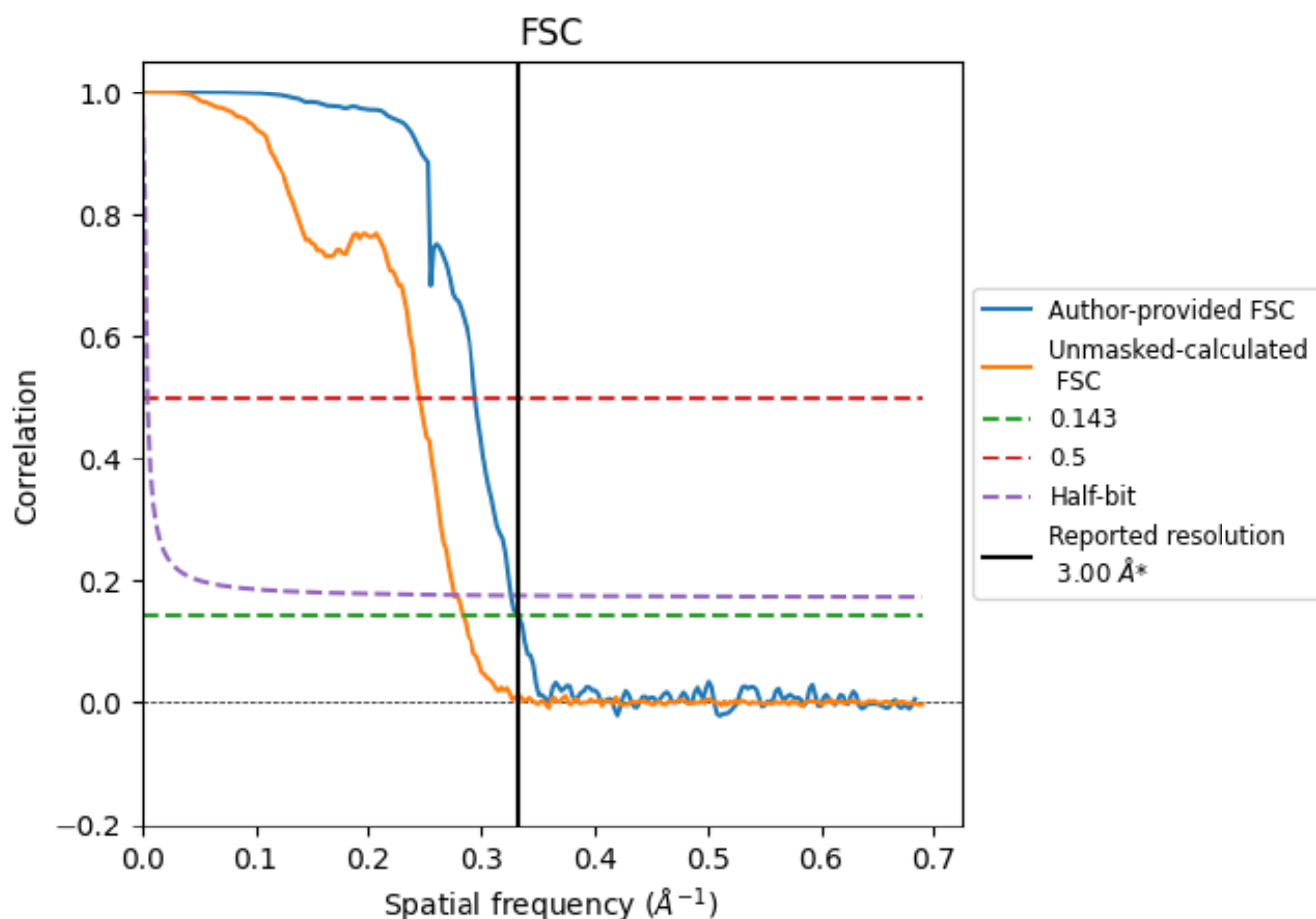


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

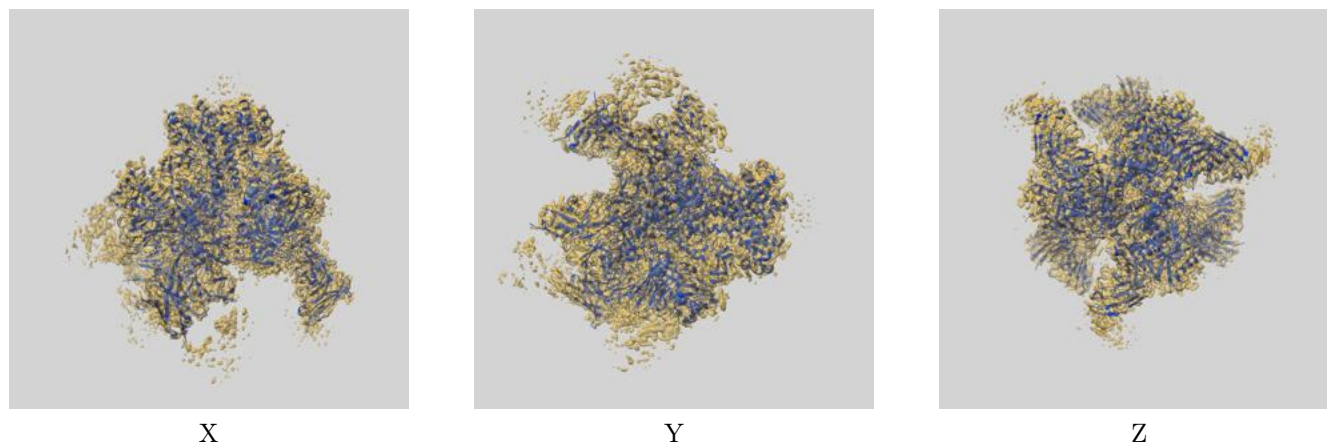
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.01	3.40	3.07
Unmasked-calculated*	3.53	4.08	3.63

*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 3.53 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

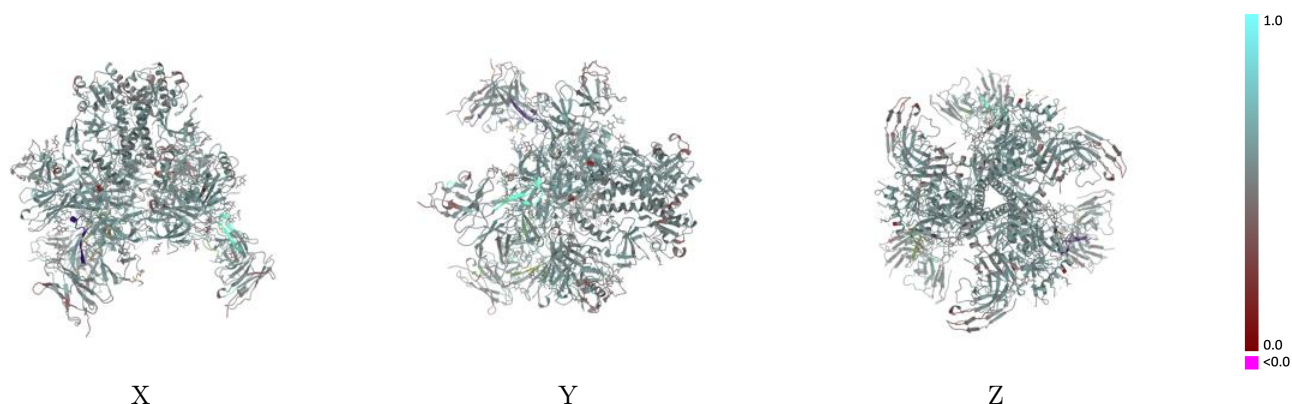
This section contains information regarding the fit between EMDB map EMD-70475 and PDB model 9OGT. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



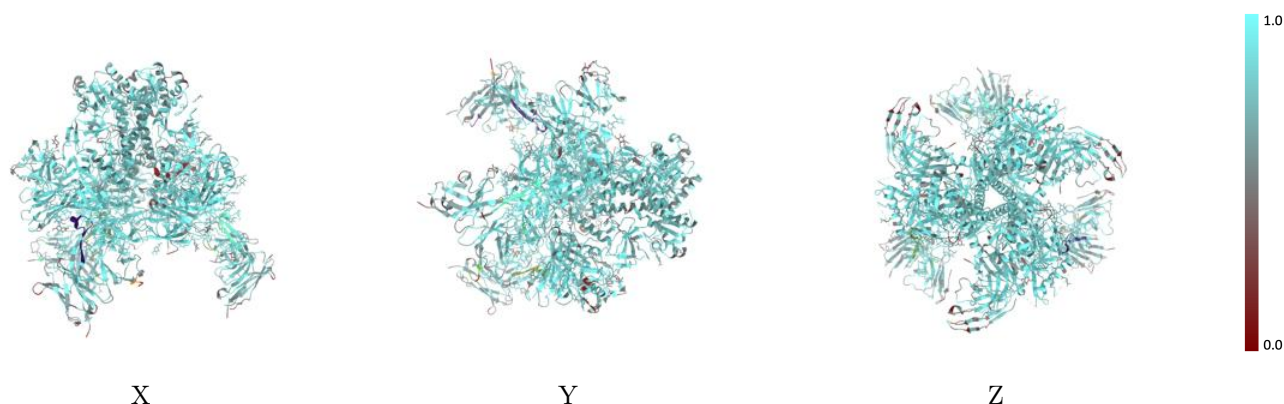
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



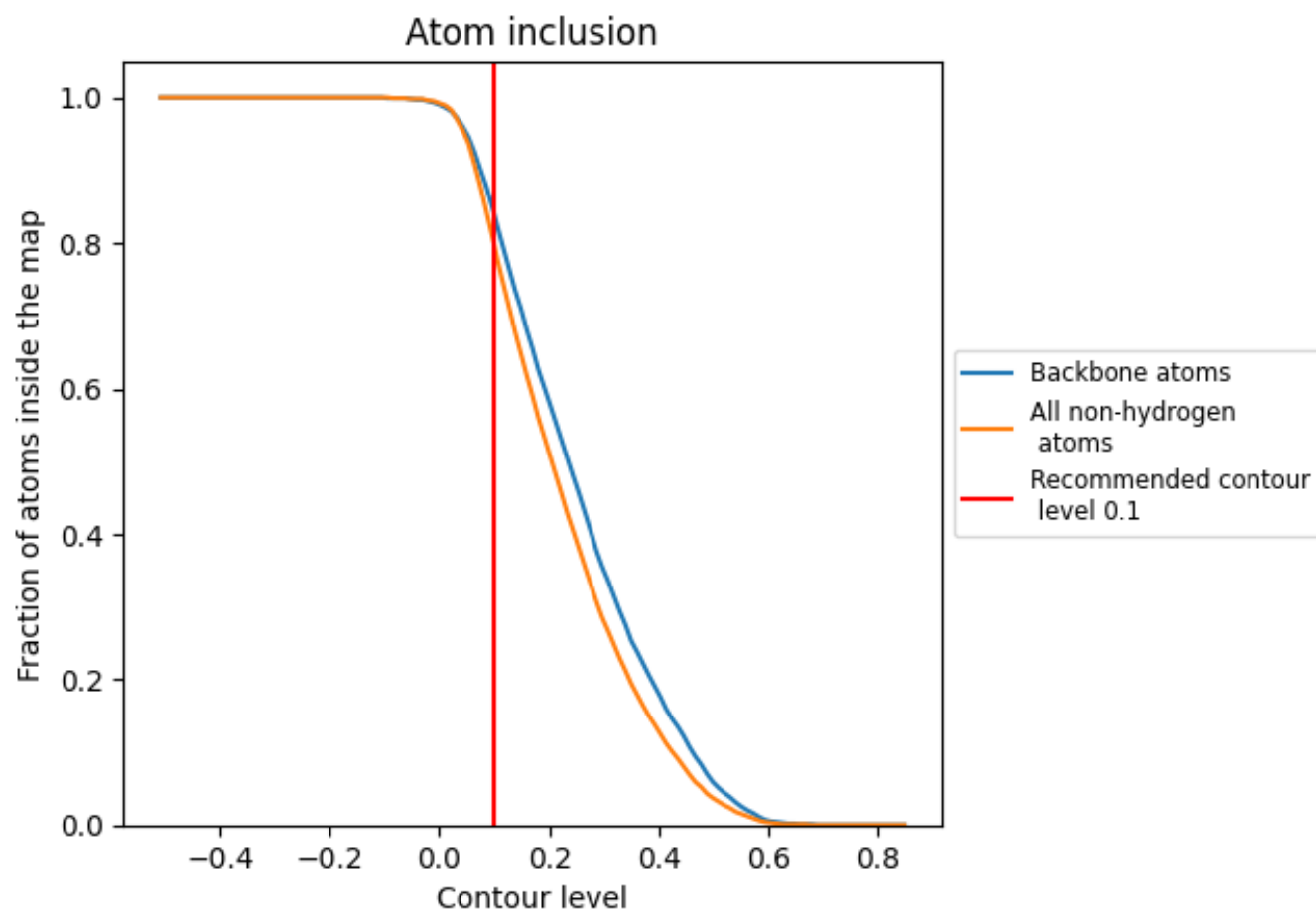
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7990	 0.5450
A	 0.8590	 0.5730
B	 0.7700	 0.5330
C	 0.8560	 0.5740
D	 0.7660	 0.5280
E	 0.8570	 0.5740
F	 0.7690	 0.5290
G	 0.7290	 0.5170
H	 0.8220	 0.5530
I	 0.7620	 0.5440
J	 0.7300	 0.5170
K	 0.8200	 0.5520
L	 0.6800	 0.4720
M	 0.7680	 0.5440
N	 0.6770	 0.4720
O	 0.7280	 0.5170
P	 0.8190	 0.5510
Q	 0.7580	 0.5440
R	 0.6810	 0.4780
S	 0.8570	 0.5780
T	 0.7050	 0.4970
U	 0.7600	 0.5050
V	 0.7500	 0.5250
W	 0.8550	 0.5320
X	 0.8930	 0.5840
Y	 0.7140	 0.4960
Z	 0.8570	 0.5670
a	 0.6720	 0.5040
b	 0.7600	 0.5040
c	 0.7500	 0.4940
d	 0.8550	 0.5290
e	 0.8930	 0.5840
f	 0.7140	 0.4910
g	 0.8570	 0.5770
h	 0.6890	 0.4990



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Chain	Atom inclusion	Q-score
i	 0.7600	 0.4970
j	 0.7500	 0.5120
k	 0.8680	 0.5310
l	 0.8930	 0.5780
m	 0.7140	 0.4940