



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:06 PM UTC

PDB ID : 6E5P / pdb_00006e5p
EMDB ID : EMD-8981
Title : Backbone model based on cryo-EM map at 8.5 Å of domain-swapped, glycan-reactive, neutralizing antibody 2G12 bound to HIV-1 Env BG505 DS-SOSIP, which was also bound to CD4-binding site antibody VRC03
Authors : Acharya, P.; Kwong, P.D.
Deposited on : 2018-07-21
Resolution : 8.80 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:

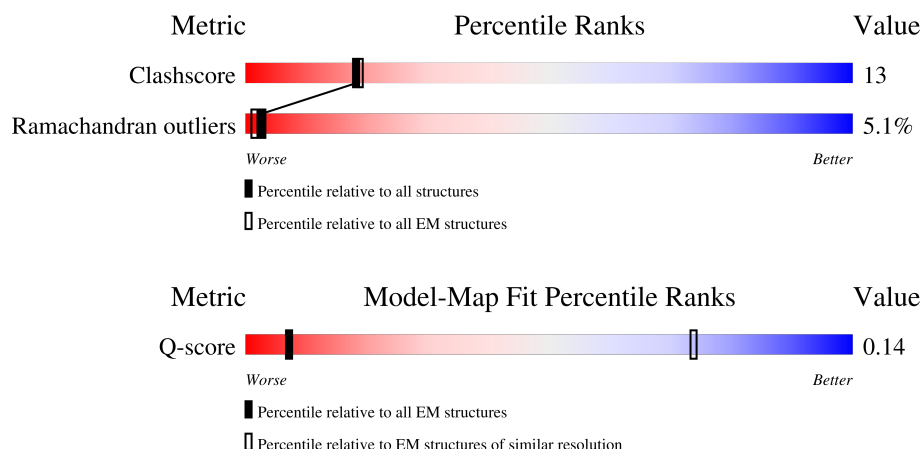
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 8.80 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	-
Q-score	-	25397	265 (8.30 - 9.30)

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	1	212	67% 28% 5%
1	4	212	68% 26% 5%
1	K	212	66% 29% 6%
1	L	212	67% 29%
1	Q	212	66% 29% 5%

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Mol	Chain	Length	Quality of chain
1	T	212	
2	2	225	
2	3	225	
2	H	225	
2	M	225	
2	R	225	
2	S	225	
3	A	474	
3	C	474	
3	E	474	
4	B	170	
4	D	170	
4	F	170	
5	I	227	
5	O	227	
5	V	227	
6	J	208	
6	P	208	
6	W	208	
7	G	2	
7	N	2	
7	Y	2	
7	g	2	
7	h	2	
7	i	2	

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Mol	Chain	Length	Quality of chain
7	k	2	100%
7	l	2	50%
7	o	2	100%
8	U	6	33% 50% 33% 17%
8	j	6	33% 50% 33% 17%
8	m	6	17% 50% 33% 17%
9	X	7	29% 71%
9	Z	7	29% 71%
9	b	7	29% 71%
9	d	7	29% 71%
9	f	7	29% 71%
9	n	7	29% 71%
10	a	4	75% 25%
10	c	4	75% 25%
10	e	4	75% 25%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	MAN	G	1	-	-	X	-
7	MAN	N	1	-	-	X	-
7	MAN	N	2	X	-	-	-
7	MAN	Y	1	-	-	X	-
7	MAN	Y	2	X	-	-	-
7	MAN	g	1	-	-	X	-
7	MAN	g	2	X	-	-	-
7	MAN	h	1	-	-	X	-
7	MAN	i	1	-	-	X	-
7	MAN	i	2	X	-	-	-
7	MAN	k	1	-	-	X	-
7	MAN	l	1	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	MAN	l	2	X	-	-	-
7	MAN	o	1	-	-	X	-
7	MAN	o	2	X	-	-	-
9	MAN	X	7	-	-	X	-
9	MAN	Z	4	-	-	X	-
9	MAN	Z	5	-	-	X	-
9	MAN	Z	7	-	-	X	-
9	MAN	b	4	-	-	X	-
9	MAN	b	5	-	-	X	-
9	MAN	b	7	-	-	X	-
9	MAN	d	5	-	-	X	-
9	MAN	d	7	-	-	X	-
9	MAN	f	7	-	-	X	-
9	MAN	n	7	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 21252 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 2G12 Light chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	212	Total	C	N	O	0	0
			848	424	212	212		
1	4	212	Total	C	N	O	0	0
			848	424	212	212		
1	K	212	Total	C	N	O	0	0
			848	424	212	212		
1	L	212	Total	C	N	O	0	0
			848	424	212	212		
1	Q	212	Total	C	N	O	0	0
			848	424	212	212		
1	T	212	Total	C	N	O	0	0
			848	424	212	212		

- Molecule 2 is a protein called 2G12 heavy chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	2	225	Total	C	N	O	0	0
			900	450	225	225		
2	3	225	Total	C	N	O	0	0
			900	450	225	225		
2	H	225	Total	C	N	O	0	0
			900	450	225	225		
2	M	225	Total	C	N	O	0	0
			900	450	225	225		
2	R	225	Total	C	N	O	0	0
			900	450	225	225		
2	S	225	Total	C	N	O	0	0
			900	450	225	225		

- Molecule 3 is a protein called Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	A	453	Total	C	N	O	0	0
			1812	906	453	453		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	453	Total	C	N	O	0	0
			1812	906	453	453		
3	E	453	Total	C	N	O	0	0
			1812	906	453	453		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	CYS	ILE	conflict	UNP Q2N0S6
A	332	ASN	THR	conflict	UNP Q2N0S6
A	433	CYS	ALA	conflict	UNP Q2N0S6
A	501	CYS	ALA	conflict	UNP Q2N0S6
C	201	CYS	ILE	conflict	UNP Q2N0S6
C	332	ASN	THR	conflict	UNP Q2N0S6
C	433	CYS	ALA	conflict	UNP Q2N0S6
C	501	CYS	ALA	conflict	UNP Q2N0S6
E	201	CYS	ILE	conflict	UNP Q2N0S6
E	332	ASN	THR	conflict	UNP Q2N0S6
E	433	CYS	ALA	conflict	UNP Q2N0S6
E	501	CYS	ALA	conflict	UNP Q2N0S6

- Molecule 4 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	B	126	Total	C	N	O	0	0
			504	252	126	126		
4	D	126	Total	C	N	O	0	0
			504	252	126	126		
4	F	126	Total	C	N	O	0	0
			504	252	126	126		

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	559	PRO	ILE	conflict	UNP Q2N0S9
B	605	CYS	THR	conflict	UNP Q2N0S9
B	665	GLY	-	expression tag	UNP Q2N0S9
B	666	SER	-	expression tag	UNP Q2N0S9
B	667	ALA	-	expression tag	UNP Q2N0S9
B	668	PRO	-	expression tag	UNP Q2N0S9
B	669	THR	-	expression tag	UNP Q2N0S9
B	670	LYS	-	expression tag	UNP Q2N0S9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	671	ALA	-	expression tag	UNP Q2N0S9
B	672	LYS	-	expression tag	UNP Q2N0S9
B	673	ARG	-	expression tag	UNP Q2N0S9
B	674	ARG	-	expression tag	UNP Q2N0S9
B	675	VAL	-	expression tag	UNP Q2N0S9
B	676	VAL	-	expression tag	UNP Q2N0S9
B	677	GLN	-	expression tag	UNP Q2N0S9
B	678	ARG	-	expression tag	UNP Q2N0S9
B	679	GLU	-	expression tag	UNP Q2N0S9
B	680	LYS	-	expression tag	UNP Q2N0S9
B	681	ARG	-	expression tag	UNP Q2N0S9
D	559	PRO	ILE	conflict	UNP Q2N0S9
D	605	CYS	THR	conflict	UNP Q2N0S9
D	665	GLY	-	expression tag	UNP Q2N0S9
D	666	SER	-	expression tag	UNP Q2N0S9
D	667	ALA	-	expression tag	UNP Q2N0S9
D	668	PRO	-	expression tag	UNP Q2N0S9
D	669	THR	-	expression tag	UNP Q2N0S9
D	670	LYS	-	expression tag	UNP Q2N0S9
D	671	ALA	-	expression tag	UNP Q2N0S9
D	672	LYS	-	expression tag	UNP Q2N0S9
D	673	ARG	-	expression tag	UNP Q2N0S9
D	674	ARG	-	expression tag	UNP Q2N0S9
D	675	VAL	-	expression tag	UNP Q2N0S9
D	676	VAL	-	expression tag	UNP Q2N0S9
D	677	GLN	-	expression tag	UNP Q2N0S9
D	678	ARG	-	expression tag	UNP Q2N0S9
D	679	GLU	-	expression tag	UNP Q2N0S9
D	680	LYS	-	expression tag	UNP Q2N0S9
D	681	ARG	-	expression tag	UNP Q2N0S9
F	559	PRO	ILE	conflict	UNP Q2N0S9
F	605	CYS	THR	conflict	UNP Q2N0S9
F	665	GLY	-	expression tag	UNP Q2N0S9
F	666	SER	-	expression tag	UNP Q2N0S9
F	667	ALA	-	expression tag	UNP Q2N0S9
F	668	PRO	-	expression tag	UNP Q2N0S9
F	669	THR	-	expression tag	UNP Q2N0S9
F	670	LYS	-	expression tag	UNP Q2N0S9
F	671	ALA	-	expression tag	UNP Q2N0S9
F	672	LYS	-	expression tag	UNP Q2N0S9
F	673	ARG	-	expression tag	UNP Q2N0S9
F	674	ARG	-	expression tag	UNP Q2N0S9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	675	VAL	-	expression tag	UNP Q2N0S9
F	676	VAL	-	expression tag	UNP Q2N0S9
F	677	GLN	-	expression tag	UNP Q2N0S9
F	678	ARG	-	expression tag	UNP Q2N0S9
F	679	GLU	-	expression tag	UNP Q2N0S9
F	680	LYS	-	expression tag	UNP Q2N0S9
F	681	ARG	-	expression tag	UNP Q2N0S9

- Molecule 5 is a protein called VRC03 heavy chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	I	128	Total	C	N	O	0	0
			512	256	128	128		
5	O	128	Total	C	N	O	0	0
			512	256	128	128		
5	V	128	Total	C	N	O	0	0
			512	256	128	128		

- Molecule 6 is a protein called VRC03 Light chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	J	101	Total	C	N	O	0	0
			404	202	101	101		
6	P	101	Total	C	N	O	0	0
			404	202	101	101		
6	W	101	Total	C	N	O	0	0
			404	202	101	101		

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose.



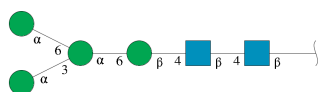
Mol	Chain	Residues	Atoms			AltConf	Trace
7	G	2	Total	C	O	0	0
			22	12	10		
7	N	2	Total	C	O	0	0
			22	12	10		
7	Y	2	Total	C	O	0	0
			22	12	10		

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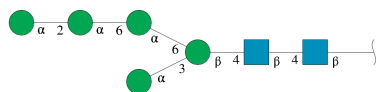
Mol	Chain	Residues	Atoms			AltConf	Trace
7	g	2	Total	C	O	0	0
			22	12	10		
7	h	2	Total	C	O	0	0
			22	12	10		
7	i	2	Total	C	O	0	0
			22	12	10		
7	k	2	Total	C	O	0	0
			22	12	10		
7	l	2	Total	C	O	0	0
			22	12	10		
7	o	2	Total	C	O	0	0
			22	12	10		

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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	U	6	Total	C	N	O	0	0
			72	40	2	30		
8	j	6	Total	C	N	O	0	0
			72	40	2	30		
8	m	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 9 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[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	X	7	Total	C	N	O	0	0
			84	46	2	36		

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Mol	Chain	Residues	Atoms				AltConf	Trace
9	Z	7	Total	C	N	O	0	0
			84	46	2	36		
9	b	7	Total	C	N	O	0	0
			84	46	2	36		
9	d	7	Total	C	N	O	0	0
			84	46	2	36		
9	f	7	Total	C	N	O	0	0
			84	46	2	36		
9	n	7	Total	C	N	O	0	0
			84	46	2	36		

- Molecule 10 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.

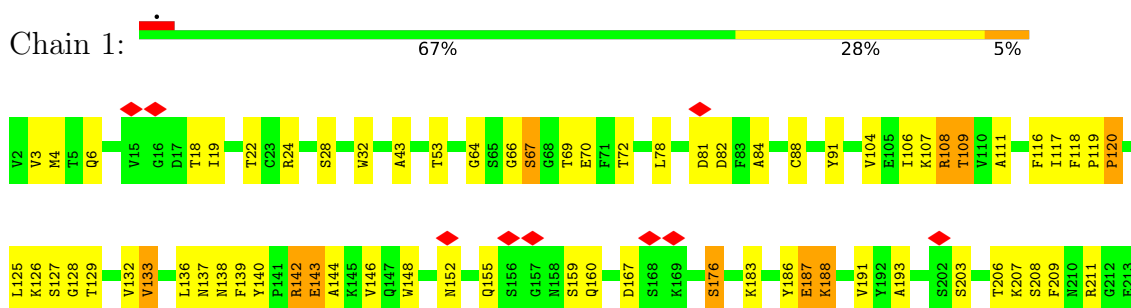


Mol	Chain	Residues	Atoms				AltConf	Trace
10	a	4	Total	C	N	O	0	0
			50	28	2	20		
10	c	4	Total	C	N	O	0	0
			50	28	2	20		
10	e	4	Total	C	N	O	0	0
			50	28	2	20		

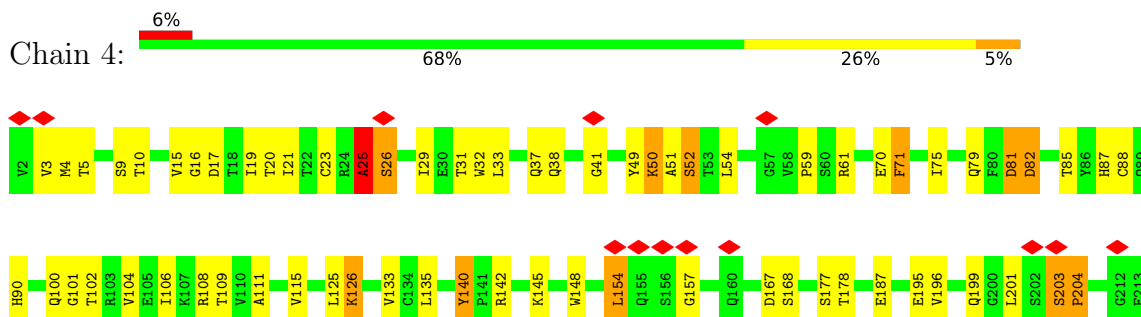
3 Residue-property plots

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.

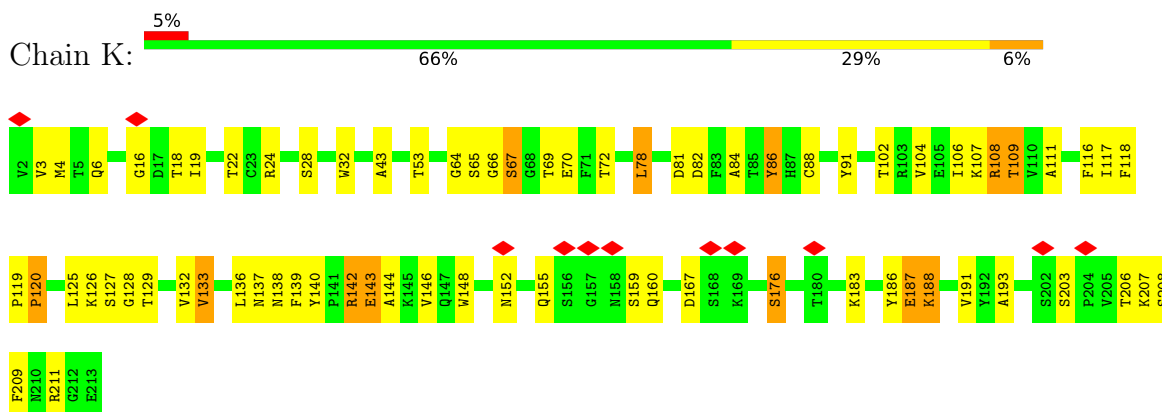
- Molecule 1: 2G12 Light chain



- Molecule 1: 2G12 Light chain

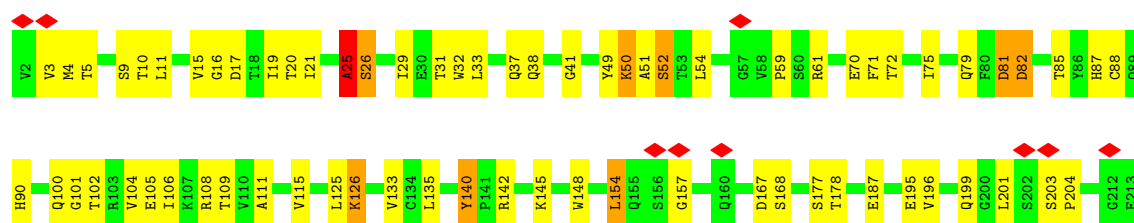


- Molecule 1: 2G12 Light chain



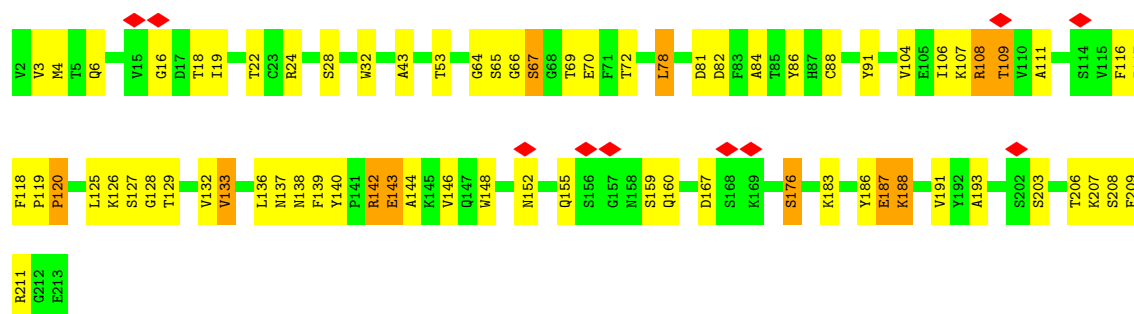
- Molecule 1: 2G12 Light chain

Chain L: 



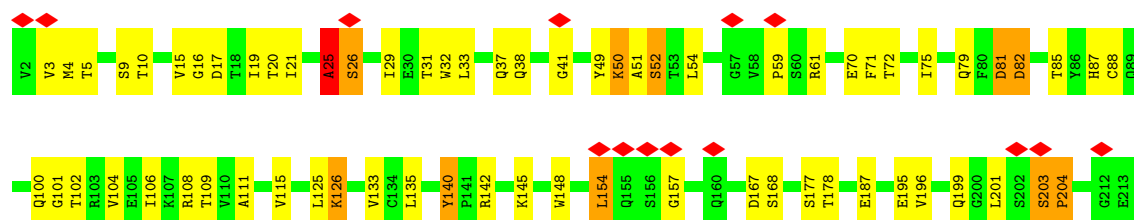
• Molecule 1: 2G12 Light chain

Chain Q: 

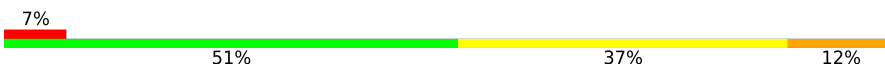


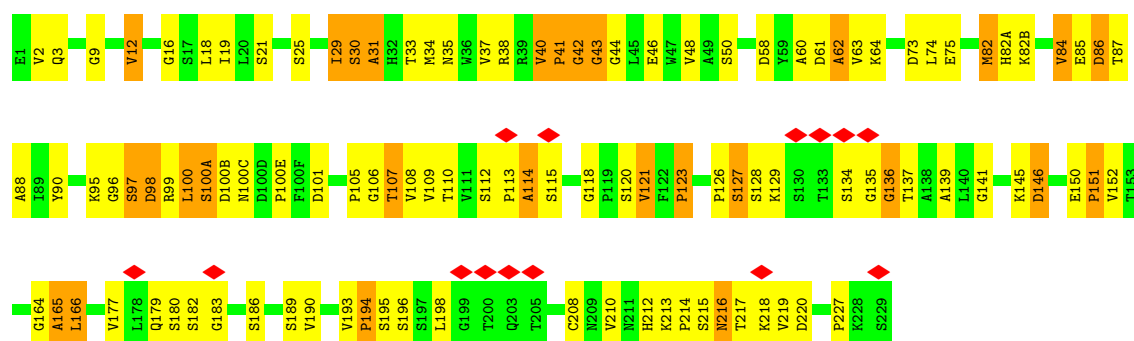
• Molecule 1: 2G12 Light chain

Chain T: 

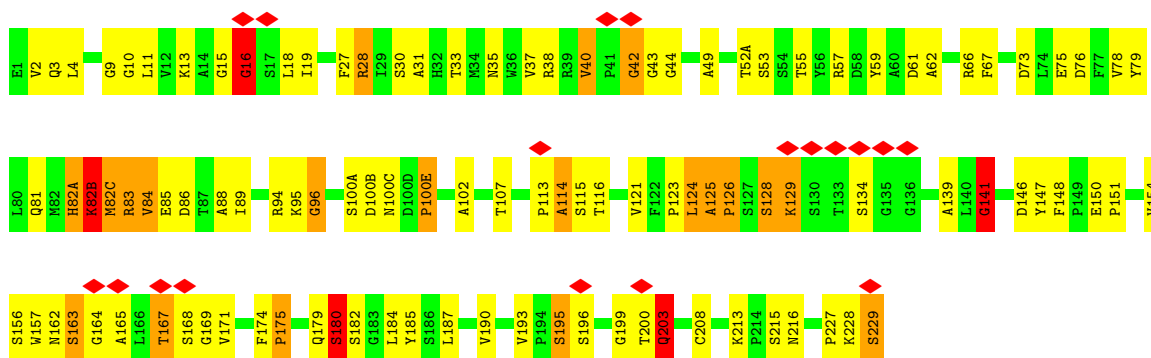


• Molecule 2: 2G12 heavy chain

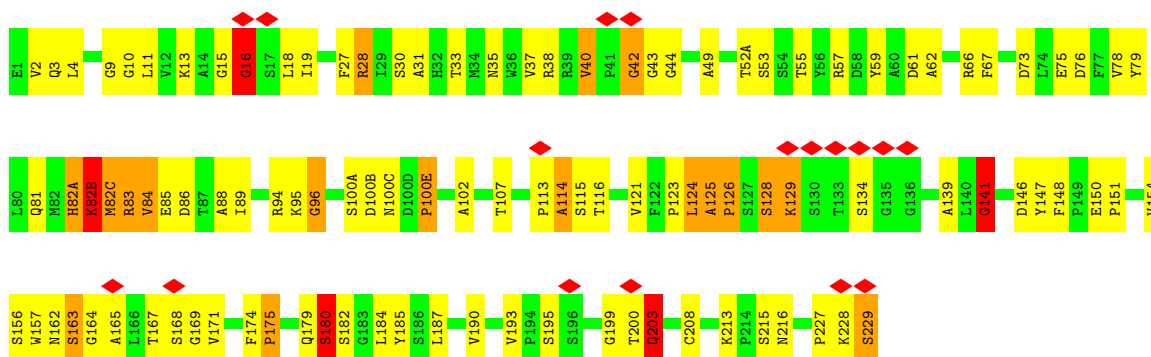
Chain 2: 



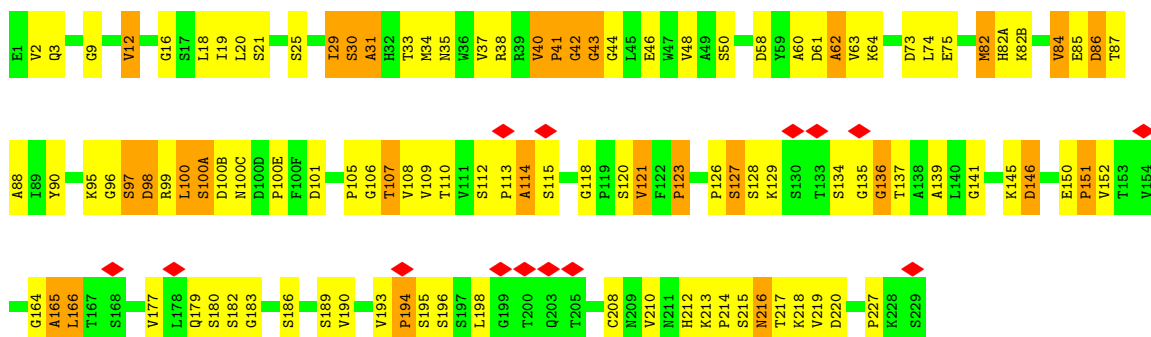
• Molecule 2: 2G12 heavy chain



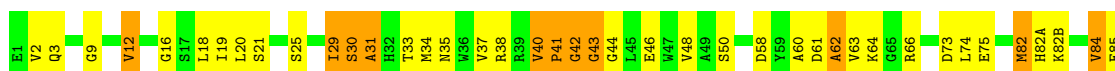
• Molecule 2: 2G12 heavy chain



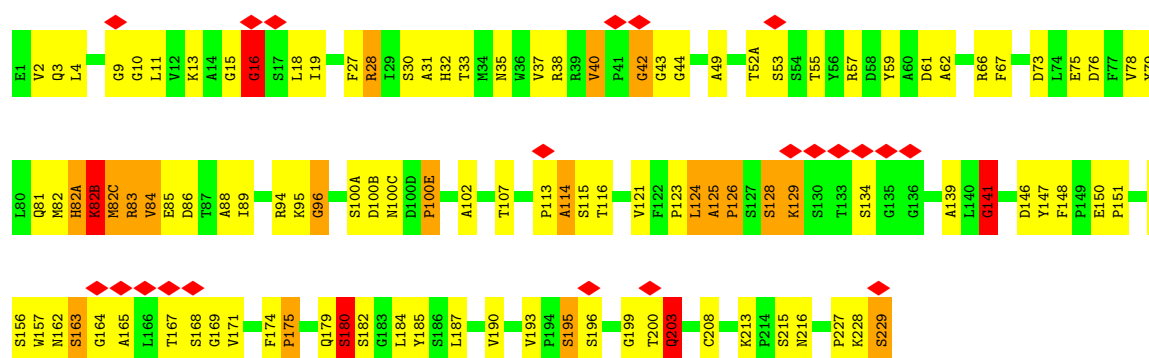
• Molecule 2: 2G12 heavy chain



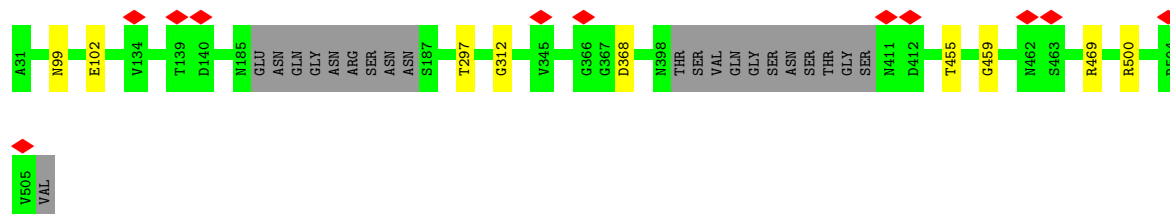
• Molecule 2: 2G12 heavy chain



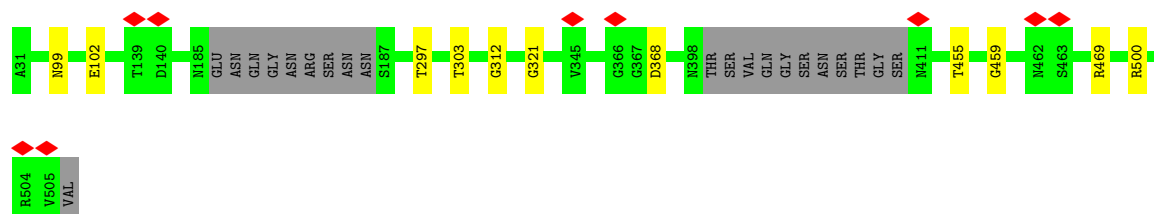
- Molecule 2: 2G12 heavy chain



- Molecule 3: Envelope glycoprotein gp120

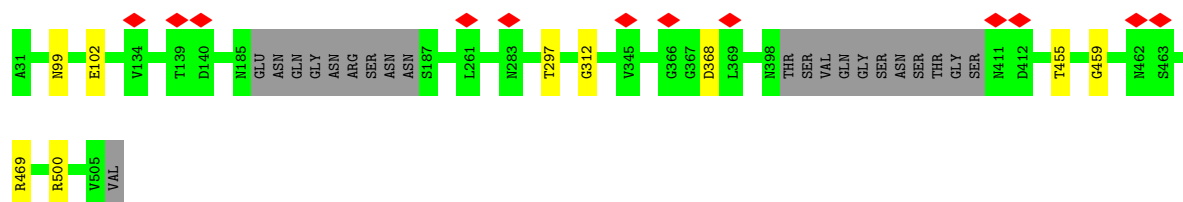


- Molecule 3: Envelope glycoprotein gp120

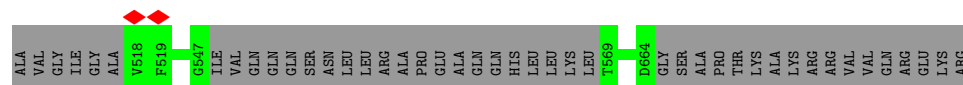


- Molecule 3: Envelope glycoprotein gp120

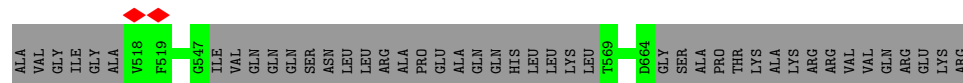
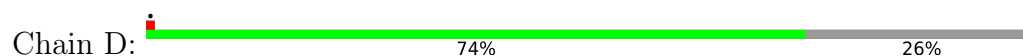




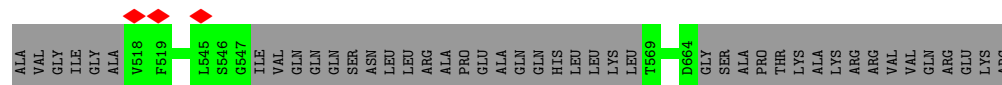
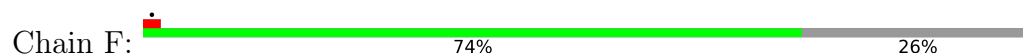
- Molecule 4: Envelope glycoprotein gp160



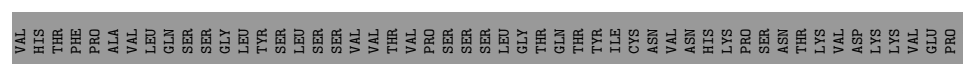
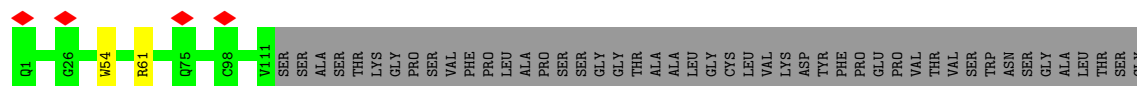
- Molecule 4: Envelope glycoprotein gp160



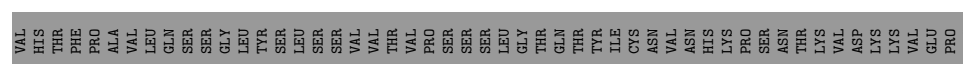
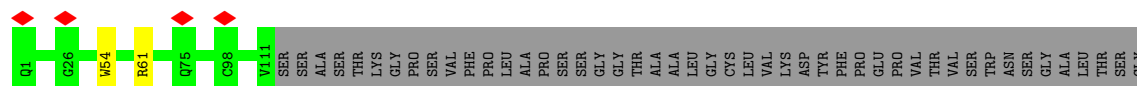
- Molecule 4: Envelope glycoprotein gp160



- Molecule 5: VRC03 heavy chain

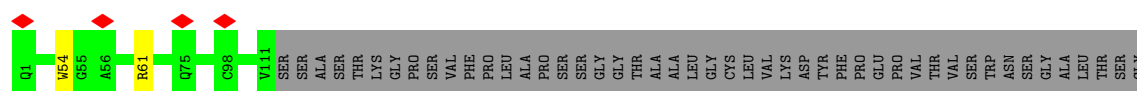


- Molecule 5: VRC03 heavy chain



- Molecule 5: VRC03 heavy chain

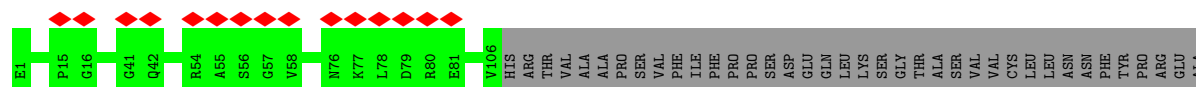
Chain V:  56% 44%



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

- Molecule 6: VRC03 Light chain

Chain J:  7% 49% 51%

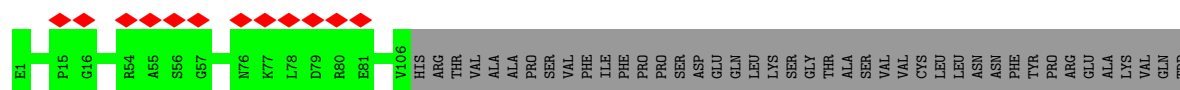


LYS VAL GLN TRP LYS VAL ASP ASN ALA LEU SER SER GLY ASN GLN VAL THR GLU GLN ASP SER LYS ASP HIS ARG THR VAL ALA SER SER THR LEU SER SER THR LEU PHE LEU SER PHE PRO ASP TYR ASP GLU GLN LYS HIS VAL LYS SER GLY THR ALA CYS GLU VAL THR HIS GLN LEU ASN PHE TYR PRO ARG GLU PRO

VAL THR LYS SER PHE ASN ARG GLY GLU

- Molecule 6: VRC03 Light chain

Chain P:  6% 49% 51%

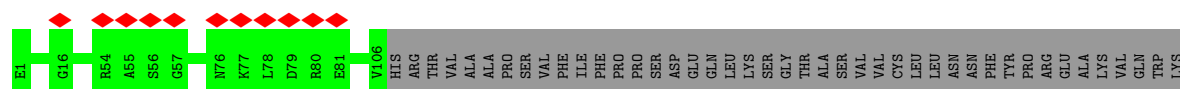


LYS VAL ASP ASN ALA LEU SER SER GLN VAL THR GLU GLN ASP SER LYS ASP HIS ARG THR VAL ALA SER SER THR LEU SER SER THR LEU PHE LEU SER PHE PRO ASP TYR ASP GLU GLN LYS HIS VAL LYS SER GLY THR ALA CYS VAL THR HIS GLN LEU ASN PHE TYR PRO ARG GLU PRO

PHE ASN ARG GLY GLU

- Molecule 6: VRC03 Light chain

Chain W:  5% 49% 51%



VAL ASP ASN ALA LEU GLN SER SER GLY ASN GLN VAL THR GLU GLN ASP SER LYS ASP HIS ARG THR VAL ALA SER SER THR LEU SER SER THR LEU PHE LEU SER SER THR LEU PHE PRO ASP TYR ASP GLU GLN LYS HIS VAL LYS SER GLY THR ALA CYS VAL THR HIS GLN LEU ASN PHE TYR PRO ARG GLU PRO

ASN ARG GLY GLU

- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain G:  100%



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain N:



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain Y:



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain g:



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain h:



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain i:



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain k:



- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain l:



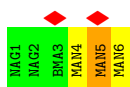
- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose

Chain o:  100%



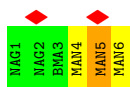
- Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:  33% 50% 33% 17%



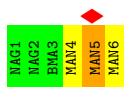
- Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j:  33% 50% 33% 17%



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

Chain m:  17% 50% 33% 17%



- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:  29% 29% 71%



- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z: 



- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b: 



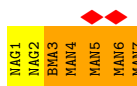
- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d: 



- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f: 



- Molecule 9: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain n: 



- Molecule 10: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a: 



- Molecule 10: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:



- Molecule 10: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain e:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	5245	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 ($e^-/\text{\AA}^2$)	63.84	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.203	Depositor
Minimum map value	-0.294	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.125	Depositor
Recommended contour level	0.734	Depositor
Map size (Å)	420.9024, 420.9024, 420.9024	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0961, 1.0961, 1.0961	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1	1.95	25/847 (3.0%)	2.23	38/1057 (3.6%)
1	4	2.18	27/847 (3.2%)	2.42	45/1057 (4.3%)
1	K	1.95	26/847 (3.1%)	2.23	38/1057 (3.6%)
1	L	2.18	28/847 (3.3%)	2.42	45/1057 (4.3%)
1	Q	1.95	26/847 (3.1%)	2.23	38/1057 (3.6%)
1	T	2.18	28/847 (3.3%)	2.42	45/1057 (4.3%)
2	2	1.92	19/899 (2.1%)	2.44	58/1122 (5.2%)
2	3	2.17	33/899 (3.7%)	2.42	71/1122 (6.3%)
2	H	2.16	32/899 (3.6%)	2.42	69/1122 (6.1%)
2	M	1.92	20/899 (2.2%)	2.44	58/1122 (5.2%)
2	R	1.93	20/899 (2.2%)	2.44	59/1122 (5.3%)
2	S	2.17	34/899 (3.8%)	2.42	69/1122 (6.1%)
3	A	0.39	0/1809	1.03	1/2256 (0.0%)
3	C	0.39	0/1809	1.03	1/2256 (0.0%)
3	E	0.39	0/1809	1.03	1/2256 (0.0%)
4	B	0.38	0/502	1.00	0/624
4	D	0.38	0/502	1.00	0/624
4	F	0.38	0/502	1.00	0/624
5	I	0.46	0/511	0.86	0/637
5	O	0.46	0/511	0.86	0/637
5	V	0.46	0/511	0.86	0/637
6	J	0.51	0/403	0.88	0/502
6	P	0.52	0/403	0.88	0/502
6	W	0.51	0/403	0.87	0/502
All	All	1.51	318/20151 (1.6%)	1.85	636/25131 (2.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1
1	4	0	1
1	K	0	1
1	L	0	1
1	Q	0	1
1	T	0	1
2	2	0	9
2	3	0	4
2	H	0	4
2	M	0	9
2	R	0	9
2	S	0	4
All	All	0	45

The worst 5 of 318 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	123	PRO	C-O	14.11	1.42	1.24
2	H	123	PRO	C-O	14.11	1.42	1.24
2	3	123	PRO	C-O	14.06	1.42	1.24
2	2	44	GLY	N-CA	10.54	1.58	1.45
2	M	44	GLY	N-CA	10.49	1.58	1.45

The worst 5 of 636 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	96	GLY	N-CA-C	16.34	138.55	111.27
2	M	96	GLY	N-CA-C	16.33	138.54	111.27
2	R	96	GLY	N-CA-C	16.32	138.52	111.27
1	Q	133	VAL	N-CA-C	12.66	127.60	108.23
1	1	133	VAL	N-CA-C	12.65	127.58	108.23

There are no chirality outliers.

5 of 45 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	19	ILE	Peptide
2	2	40	VAL	Peptide
2	2	42	GLY	Peptide
2	2	88	ALA	Peptide
2	2	97	SER	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	1	848	0	230	9	0
1	4	848	0	230	9	0
1	K	848	0	230	11	0
1	L	848	0	230	8	0
1	Q	848	0	230	11	0
1	T	848	0	230	8	0
2	2	900	0	256	25	0
2	3	900	0	256	32	0
2	H	900	0	256	31	0
2	M	900	0	256	24	0
2	R	900	0	256	25	0
2	S	900	0	256	32	0
3	A	1812	0	482	12	0
3	C	1812	0	482	13	0
3	E	1812	0	482	11	0
4	B	504	0	143	0	0
4	D	504	0	143	0	0
4	F	504	0	143	0	0
5	I	512	0	147	9	0
5	O	512	0	147	10	0
5	V	512	0	147	10	0
6	J	404	0	121	0	0
6	P	404	0	121	0	0
6	W	404	0	121	0	0
7	G	22	0	19	8	0
7	N	22	0	17	7	0
7	Y	22	0	17	8	0
7	g	22	0	17	8	0
7	h	22	0	19	8	0
7	i	22	0	17	8	0
7	k	22	0	19	8	0
7	l	22	0	17	7	0
7	o	22	0	17	8	0
8	U	72	0	61	1	0
8	j	72	0	61	1	0
8	m	72	0	61	1	0
9	X	84	0	72	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	Z	84	0	72	19	0
9	b	84	0	72	20	0
9	d	84	0	72	18	0
9	f	84	0	72	13	0
9	n	84	0	72	14	0
10	a	50	0	43	4	0
10	c	50	0	43	4	0
10	e	50	0	43	4	0
All	All	21252	0	6498	367	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 13.

The worst 5 of 367 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:C:459:GLY:CA	5:O:61:ARG:H	1.25	1.50
3:A:459:GLY:HA3	5:V:61:ARG:CA	1.44	1.47
3:C:459:GLY:HA3	5:O:61:ARG:CA	1.44	1.47
3:A:459:GLY:CA	5:V:61:ARG:H	1.25	1.46
3:E:459:GLY:CA	5:I:61:ARG:H	1.25	1.46

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	1	210/212 (99%)	158 (75%)	39 (19%)	13 (6%)	1	13
1	4	210/212 (99%)	177 (84%)	24 (11%)	9 (4%)	2	17
1	K	210/212 (99%)	158 (75%)	39 (19%)	13 (6%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	210/212 (99%)	177 (84%)	24 (11%)	9 (4%)	2	17
1	Q	210/212 (99%)	158 (75%)	39 (19%)	13 (6%)	1	13
1	T	210/212 (99%)	177 (84%)	24 (11%)	9 (4%)	2	17
2	2	223/225 (99%)	157 (70%)	28 (13%)	38 (17%)	0	2
2	3	223/225 (99%)	160 (72%)	40 (18%)	23 (10%)	0	6
2	H	223/225 (99%)	159 (71%)	41 (18%)	23 (10%)	0	6
2	M	223/225 (99%)	157 (70%)	28 (13%)	38 (17%)	0	2
2	R	223/225 (99%)	157 (70%)	28 (13%)	38 (17%)	0	2
2	S	223/225 (99%)	159 (71%)	41 (18%)	23 (10%)	0	6
3	A	447/474 (94%)	406 (91%)	39 (9%)	2 (0%)	30	67
3	C	447/474 (94%)	406 (91%)	39 (9%)	2 (0%)	30	67
3	E	447/474 (94%)	406 (91%)	39 (9%)	2 (0%)	30	67
4	B	122/170 (72%)	109 (89%)	13 (11%)	0	100	100
4	D	122/170 (72%)	109 (89%)	13 (11%)	0	100	100
4	F	122/170 (72%)	109 (89%)	13 (11%)	0	100	100
5	I	126/227 (56%)	124 (98%)	2 (2%)	0	100	100
5	O	126/227 (56%)	125 (99%)	1 (1%)	0	100	100
5	V	126/227 (56%)	123 (98%)	3 (2%)	0	100	100
6	J	99/208 (48%)	96 (97%)	3 (3%)	0	100	100
6	P	99/208 (48%)	96 (97%)	3 (3%)	0	100	100
6	W	99/208 (48%)	96 (97%)	3 (3%)	0	100	100
All	All	4980/5859 (85%)	4159 (84%)	566 (11%)	255 (5%)	3	15

5 of 255 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	152	ASN
1	1	176	SER
1	1	187	GLU
2	2	16	GLY
2	2	30	SER

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

90 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	MAN	G	1	7	11,11,12	1.57	3 (27%)	15,15,17	3.27	9 (60%)
7	MAN	G	2	7	11,11,12	1.20	1 (9%)	15,15,17	3.14	6 (40%)
7	MAN	N	1	7	11,11,12	1.27	2 (18%)	15,15,17	3.88	10 (66%)
7	MAN	N	2	7	11,11,12	1.33	2 (18%)	15,15,17	3.00	7 (46%)
8	NAG	U	1	8	14,14,15	0.31	0	17,19,21	0.46	0
8	NAG	U	2	8	14,14,15	0.36	0	17,19,21	0.67	0
8	BMA	U	3	8	11,11,12	0.63	0	15,15,17	0.82	0
8	MAN	U	4	8	11,11,12	0.73	0	15,15,17	1.00	2 (13%)
8	MAN	U	5	8	11,11,12	0.75	1 (9%)	15,15,17	1.04	2 (13%)
8	MAN	U	6	8	11,11,12	0.66	0	15,15,17	1.00	2 (13%)
9	NAG	X	1	9	15,15,15	1.22	1 (6%)	21,21,21	2.66	9 (42%)
9	NAG	X	2	9	14,14,15	0.92	0	17,19,21	2.21	5 (29%)
9	BMA	X	3	9	11,11,12	1.18	0	15,15,17	2.84	8 (53%)
9	MAN	X	4	9	11,11,12	0.92	0	15,15,17	2.28	5 (33%)
9	MAN	X	5	9	11,11,12	1.80	2 (18%)	15,15,17	3.39	10 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	MAN	X	6	9	11,11,12	2.12	5 (45%)	15,15,17	2.61	4 (26%)
9	MAN	X	7	9	11,11,12	1.47	2 (18%)	15,15,17	2.01	5 (33%)
7	MAN	Y	1	7	11,11,12	1.27	2 (18%)	15,15,17	3.88	10 (66%)
7	MAN	Y	2	7	11,11,12	1.32	2 (18%)	15,15,17	3.01	7 (46%)
9	NAG	Z	1	9	15,15,15	1.22	1 (6%)	21,21,21	2.67	9 (42%)
9	NAG	Z	2	9	14,14,15	0.92	0	17,19,21	2.22	5 (29%)
9	BMA	Z	3	9	11,11,12	1.19	0	15,15,17	2.84	8 (53%)
9	MAN	Z	4	9	11,11,12	0.93	0	15,15,17	2.27	5 (33%)
9	MAN	Z	5	9	11,11,12	1.81	3 (27%)	15,15,17	3.40	10 (66%)
9	MAN	Z	6	9	11,11,12	2.12	5 (45%)	15,15,17	2.60	4 (26%)
9	MAN	Z	7	9	11,11,12	1.47	2 (18%)	15,15,17	1.99	5 (33%)
10	NAG	a	1	10	14,14,15	1.65	4 (28%)	17,19,21	2.94	8 (47%)
10	NAG	a	2	10	14,14,15	1.00	1 (7%)	17,19,21	2.70	8 (47%)
10	BMA	a	3	10	11,11,12	1.33	2 (18%)	15,15,17	2.60	7 (46%)
10	MAN	a	4	10	11,11,12	1.08	1 (9%)	15,15,17	2.40	6 (40%)
9	NAG	b	1	9	15,15,15	1.23	1 (6%)	21,21,21	2.66	9 (42%)
9	NAG	b	2	9	14,14,15	0.92	0	17,19,21	2.21	5 (29%)
9	BMA	b	3	9	11,11,12	1.19	0	15,15,17	2.84	8 (53%)
9	MAN	b	4	9	11,11,12	0.93	0	15,15,17	2.28	5 (33%)
9	MAN	b	5	9	11,11,12	1.81	3 (27%)	15,15,17	3.40	10 (66%)
9	MAN	b	6	9	11,11,12	2.12	5 (45%)	15,15,17	2.60	4 (26%)
9	MAN	b	7	9	11,11,12	1.47	2 (18%)	15,15,17	1.99	5 (33%)
10	NAG	c	1	10	14,14,15	1.65	4 (28%)	17,19,21	2.94	8 (47%)
10	NAG	c	2	10	14,14,15	1.01	1 (7%)	17,19,21	2.70	8 (47%)
10	BMA	c	3	10	11,11,12	1.33	2 (18%)	15,15,17	2.59	7 (46%)
10	MAN	c	4	10	11,11,12	1.08	1 (9%)	15,15,17	2.39	6 (40%)
9	NAG	d	1	9	15,15,15	1.22	1 (6%)	21,21,21	2.66	9 (42%)
9	NAG	d	2	9	14,14,15	0.92	0	17,19,21	2.21	5 (29%)
9	BMA	d	3	9	11,11,12	1.19	0	15,15,17	2.84	7 (46%)
9	MAN	d	4	9	11,11,12	0.92	0	15,15,17	2.28	5 (33%)
9	MAN	d	5	9	11,11,12	1.81	3 (27%)	15,15,17	3.40	10 (66%)
9	MAN	d	6	9	11,11,12	2.12	5 (45%)	15,15,17	2.60	4 (26%)
9	MAN	d	7	9	11,11,12	1.47	2 (18%)	15,15,17	1.99	5 (33%)
10	NAG	e	1	10	14,14,15	1.65	4 (28%)	17,19,21	2.94	8 (47%)
10	NAG	e	2	10	14,14,15	1.01	1 (7%)	17,19,21	2.71	8 (47%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	BMA	e	3	10	11,11,12	1.33	2 (18%)	15,15,17	2.60	7 (46%)
10	MAN	e	4	10	11,11,12	1.08	1 (9%)	15,15,17	2.39	6 (40%)
9	NAG	f	1	9	15,15,15	1.22	1 (6%)	21,21,21	2.66	9 (42%)
9	NAG	f	2	9	14,14,15	0.92	0	17,19,21	2.21	5 (29%)
9	BMA	f	3	9	11,11,12	1.18	0	15,15,17	2.84	7 (46%)
9	MAN	f	4	9	11,11,12	0.92	0	15,15,17	2.27	5 (33%)
9	MAN	f	5	9	11,11,12	1.80	3 (27%)	15,15,17	3.39	10 (66%)
9	MAN	f	6	9	11,11,12	2.13	5 (45%)	15,15,17	2.61	4 (26%)
9	MAN	f	7	9	11,11,12	1.47	2 (18%)	15,15,17	2.00	5 (33%)
7	MAN	g	1	7	11,11,12	1.28	2 (18%)	15,15,17	3.87	10 (66%)
7	MAN	g	2	7	11,11,12	1.32	2 (18%)	15,15,17	3.00	7 (46%)
7	MAN	h	1	7	11,11,12	1.57	3 (27%)	15,15,17	3.27	9 (60%)
7	MAN	h	2	7	11,11,12	1.21	1 (9%)	15,15,17	3.14	6 (40%)
7	MAN	i	1	7	11,11,12	1.28	2 (18%)	15,15,17	3.88	10 (66%)
7	MAN	i	2	7	11,11,12	1.32	2 (18%)	15,15,17	3.00	7 (46%)
8	NAG	j	1	8	14,14,15	0.31	0	17,19,21	0.47	0
8	NAG	j	2	8	14,14,15	0.37	0	17,19,21	0.66	0
8	BMA	j	3	8	11,11,12	0.63	0	15,15,17	0.83	0
8	MAN	j	4	8	11,11,12	0.72	0	15,15,17	0.99	2 (13%)
8	MAN	j	5	8	11,11,12	0.76	1 (9%)	15,15,17	1.04	1 (6%)
8	MAN	j	6	8	11,11,12	0.66	0	15,15,17	1.01	2 (13%)
7	MAN	k	1	7	11,11,12	1.57	3 (27%)	15,15,17	3.27	9 (60%)
7	MAN	k	2	7	11,11,12	1.21	1 (9%)	15,15,17	3.15	6 (40%)
7	MAN	l	1	7	11,11,12	1.28	2 (18%)	15,15,17	3.87	10 (66%)
7	MAN	l	2	7	11,11,12	1.30	2 (18%)	15,15,17	3.01	7 (46%)
8	NAG	m	1	8	14,14,15	0.31	0	17,19,21	0.47	0
8	NAG	m	2	8	14,14,15	0.38	0	17,19,21	0.67	0
8	BMA	m	3	8	11,11,12	0.63	0	15,15,17	0.83	0
8	MAN	m	4	8	11,11,12	0.72	0	15,15,17	1.00	2 (13%)
8	MAN	m	5	8	11,11,12	0.77	1 (9%)	15,15,17	1.04	1 (6%)
8	MAN	m	6	8	11,11,12	0.66	0	15,15,17	1.01	2 (13%)
9	NAG	n	1	9	15,15,15	1.22	1 (6%)	21,21,21	2.66	9 (42%)
9	NAG	n	2	9	14,14,15	0.92	0	17,19,21	2.21	5 (29%)
9	BMA	n	3	9	11,11,12	1.19	0	15,15,17	2.85	7 (46%)
9	MAN	n	4	9	11,11,12	0.92	0	15,15,17	2.27	5 (33%)
9	MAN	n	5	9	11,11,12	1.79	3 (27%)	15,15,17	3.40	10 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	MAN	n	6	9	11,11,12	2.13	5 (45%)	15,15,17	2.60	4 (26%)
9	MAN	n	7	9	11,11,12	1.46	2 (18%)	15,15,17	2.01	5 (33%)
7	MAN	o	1	7	11,11,12	1.27	2 (18%)	15,15,17	3.87	10 (66%)
7	MAN	o	2	7	11,11,12	1.32	2 (18%)	15,15,17	3.00	7 (46%)

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	MAN	G	1	7	-	1/2/19/22	0/1/1/1
7	MAN	G	2	7	-	1/2/19/22	0/1/1/1
7	MAN	N	1	7	-	1/2/19/22	0/1/1/1
7	MAN	N	2	7	1/1/4/5	2/2/19/22	0/1/1/1
8	NAG	U	1	8	-	2/6/23/26	0/1/1/1
8	NAG	U	2	8	-	4/6/23/26	0/1/1/1
8	BMA	U	3	8	-	0/2/19/22	0/1/1/1
8	MAN	U	4	8	-	2/2/19/22	0/1/1/1
8	MAN	U	5	8	-	1/2/19/22	0/1/1/1
8	MAN	U	6	8	-	0/2/19/22	0/1/1/1
9	NAG	X	1	9	-	4/6/26/26	0/1/1/1
9	NAG	X	2	9	-	2/6/23/26	0/1/1/1
9	BMA	X	3	9	-	2/2/19/22	0/1/1/1
9	MAN	X	4	9	-	2/2/19/22	0/1/1/1
9	MAN	X	5	9	-	2/2/19/22	0/1/1/1
9	MAN	X	6	9	-	0/2/19/22	0/1/1/1
9	MAN	X	7	9	-	2/2/19/22	0/1/1/1
7	MAN	Y	1	7	-	1/2/19/22	0/1/1/1
7	MAN	Y	2	7	1/1/4/5	2/2/19/22	0/1/1/1
9	NAG	Z	1	9	-	4/6/26/26	0/1/1/1
9	NAG	Z	2	9	-	2/6/23/26	0/1/1/1
9	BMA	Z	3	9	-	2/2/19/22	0/1/1/1
9	MAN	Z	4	9	-	2/2/19/22	0/1/1/1
9	MAN	Z	5	9	-	2/2/19/22	0/1/1/1
9	MAN	Z	6	9	-	0/2/19/22	0/1/1/1
9	MAN	Z	7	9	-	2/2/19/22	0/1/1/1
10	NAG	a	1	10	-	1/6/23/26	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	i	1	7	-	1/2/19/22	0/1/1/1
7	MAN	i	2	7	1/1/4/5	2/2/19/22	0/1/1/1
8	NAG	j	1	8	-	2/6/23/26	0/1/1/1
8	NAG	j	2	8	-	4/6/23/26	0/1/1/1
8	BMA	j	3	8	-	0/2/19/22	0/1/1/1
8	MAN	j	4	8	-	2/2/19/22	0/1/1/1
8	MAN	j	5	8	-	1/2/19/22	0/1/1/1
8	MAN	j	6	8	-	0/2/19/22	0/1/1/1
7	MAN	k	1	7	-	1/2/19/22	0/1/1/1
7	MAN	k	2	7	-	1/2/19/22	0/1/1/1
7	MAN	l	1	7	-	1/2/19/22	0/1/1/1
7	MAN	l	2	7	1/1/4/5	2/2/19/22	0/1/1/1
8	NAG	m	1	8	-	2/6/23/26	0/1/1/1
8	NAG	m	2	8	-	4/6/23/26	0/1/1/1
8	BMA	m	3	8	-	0/2/19/22	0/1/1/1
8	MAN	m	4	8	-	2/2/19/22	0/1/1/1
8	MAN	m	5	8	-	1/2/19/22	0/1/1/1
8	MAN	m	6	8	-	0/2/19/22	0/1/1/1
9	NAG	n	1	9	-	4/6/26/26	0/1/1/1
9	NAG	n	2	9	-	2/6/23/26	0/1/1/1
9	BMA	n	3	9	-	2/2/19/22	0/1/1/1
9	MAN	n	4	9	-	2/2/19/22	0/1/1/1
9	MAN	n	5	9	-	2/2/19/22	0/1/1/1
9	MAN	n	6	9	-	0/2/19/22	0/1/1/1
9	MAN	n	7	9	-	2/2/19/22	0/1/1/1
7	MAN	o	1	7	-	1/2/19/22	0/1/1/1
7	MAN	o	2	7	1/1/4/5	2/2/19/22	0/1/1/1

The worst 5 of 128 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	c	1	NAG	C1-C2	4.01	1.57	1.52
10	e	1	NAG	C1-C2	3.97	1.57	1.52
10	a	1	NAG	C1-C2	3.97	1.57	1.52
9	f	5	MAN	C4-C5	3.66	1.60	1.53
9	X	5	MAN	C4-C5	3.66	1.60	1.53

The worst 5 of 523 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	1	MAN	O2-C2-C3	-7.76	94.07	110.15
7	h	1	MAN	O2-C2-C3	-7.76	94.07	110.15
7	k	1	MAN	O2-C2-C3	-7.75	94.10	110.15
7	Y	2	MAN	C1-C2-C3	-7.66	98.49	109.64
7	N	2	MAN	C1-C2-C3	-7.64	98.52	109.64

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	N	2	MAN	C1
7	Y	2	MAN	C1
7	g	2	MAN	C1
7	i	2	MAN	C1
7	l	2	MAN	C1

5 of 156 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	X	1	NAG	C8-C7-N2-C2
9	X	1	NAG	O7-C7-N2-C2
9	Z	1	NAG	C8-C7-N2-C2
9	Z	1	NAG	O7-C7-N2-C2
9	b	1	NAG	C8-C7-N2-C2

There are no ring outliers.

51 monomers are involved in 127 short contacts:

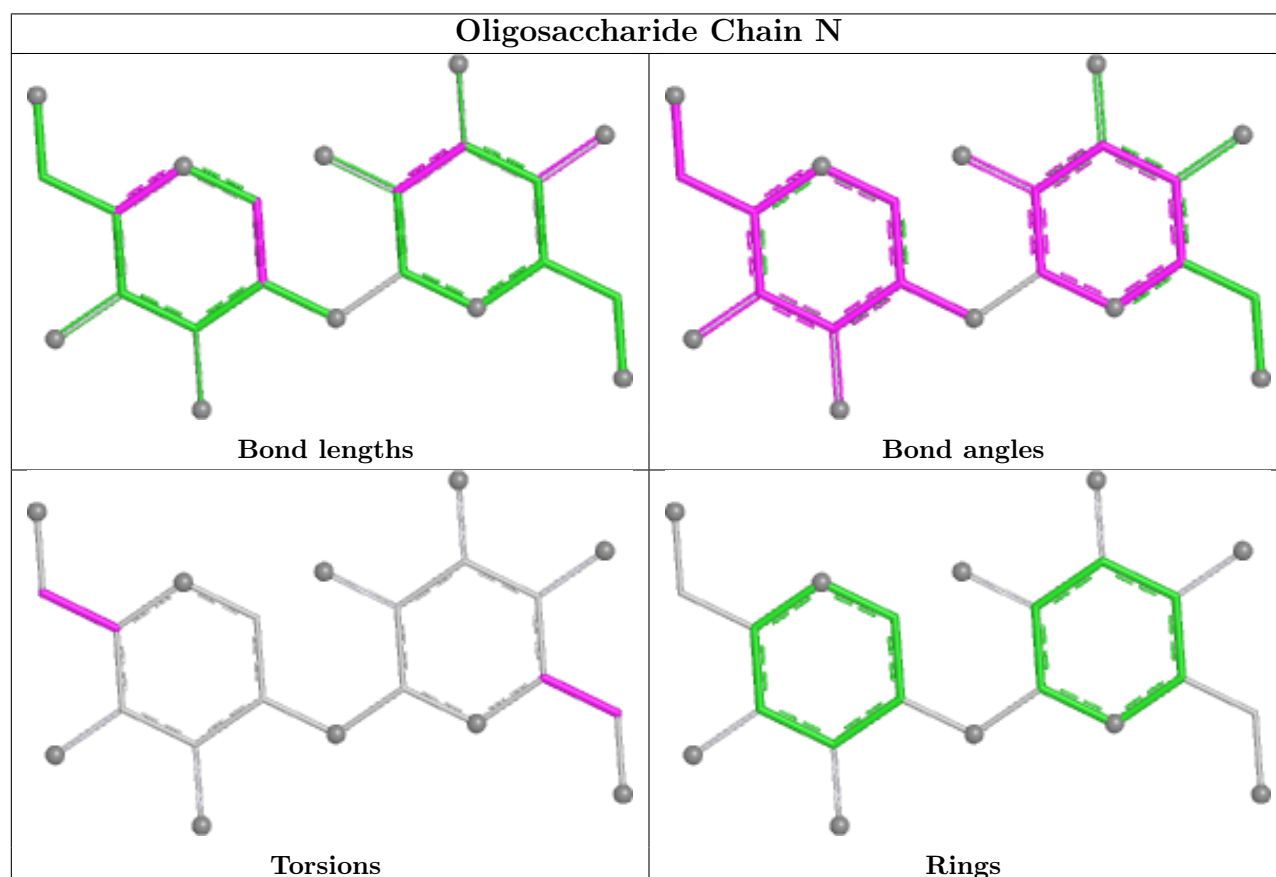
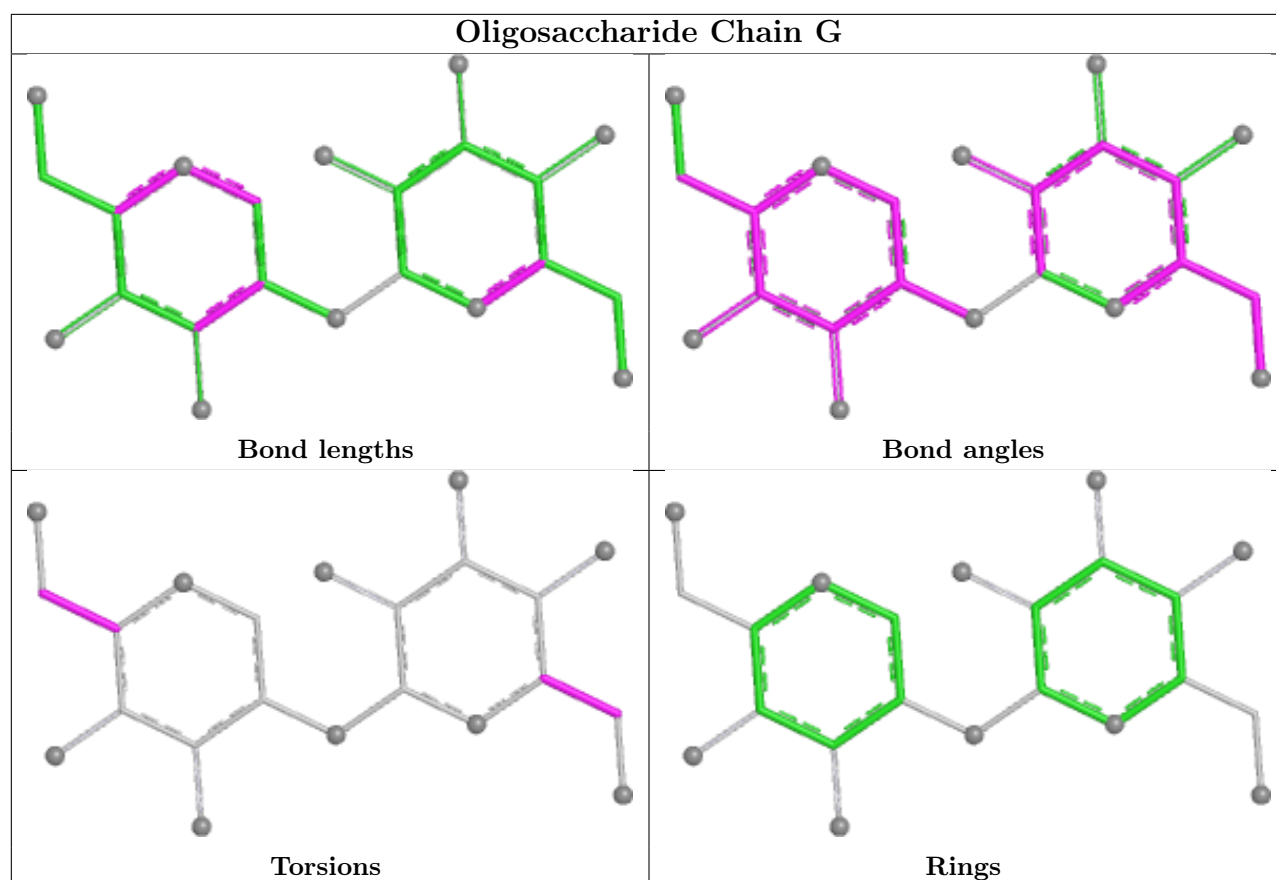
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	Z	5	MAN	7	0
9	X	3	BMA	4	0
7	i	1	MAN	8	0
7	k	2	MAN	3	0
9	b	3	BMA	5	0
9	n	4	MAN	5	0
7	Y	1	MAN	7	0
7	o	2	MAN	1	0
7	o	1	MAN	7	0
9	Z	3	BMA	5	0
9	b	5	MAN	7	0
9	n	5	MAN	3	0
9	f	7	MAN	7	0
9	f	4	MAN	4	0
10	a	4	MAN	4	0

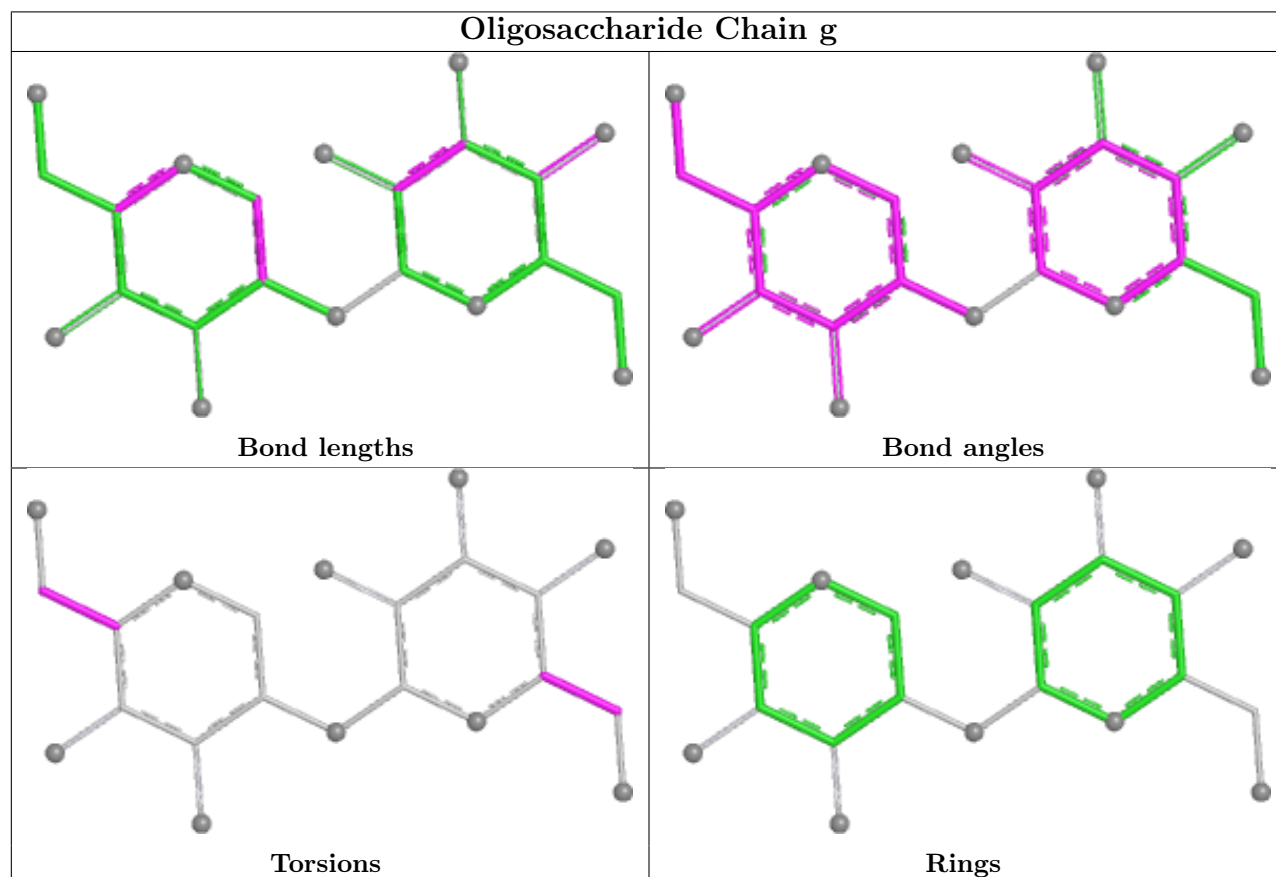
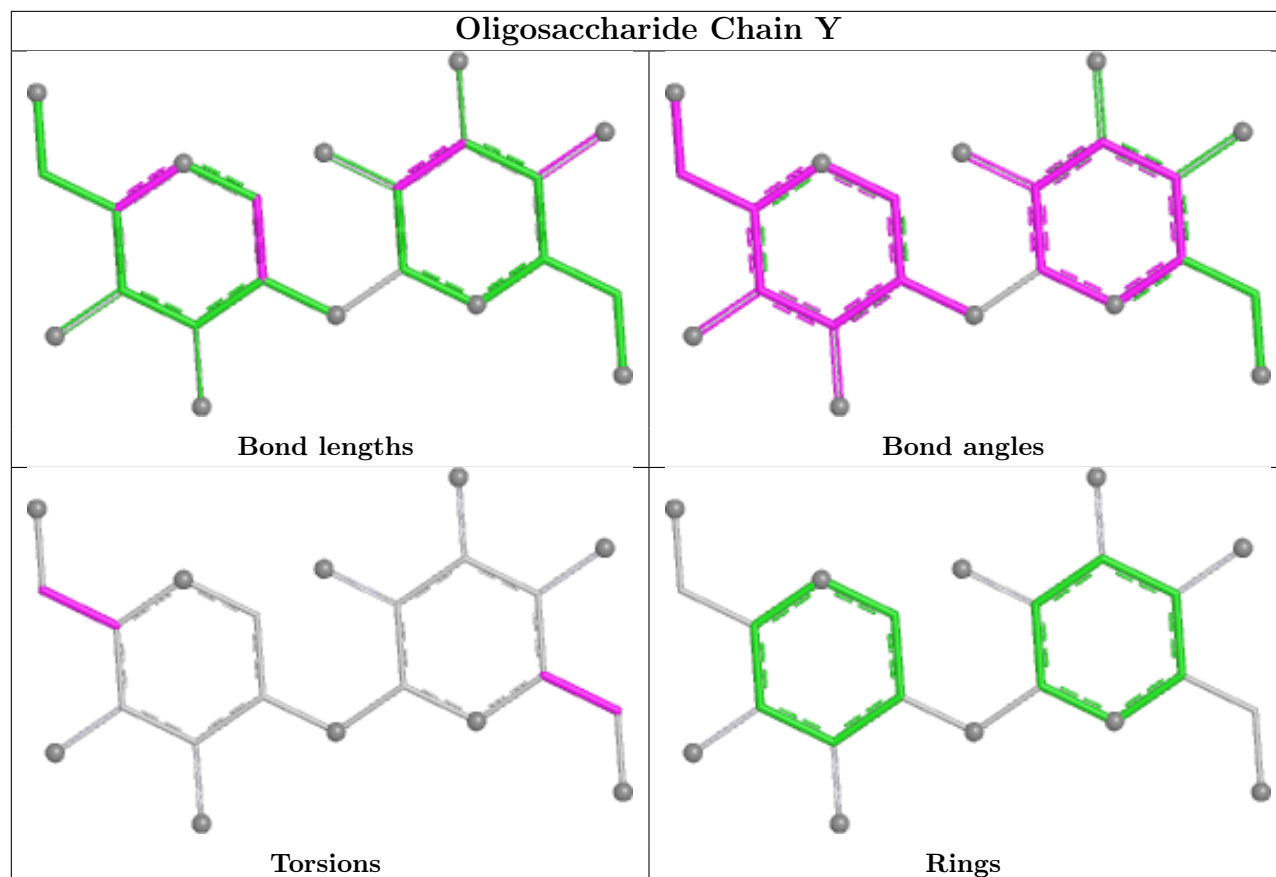
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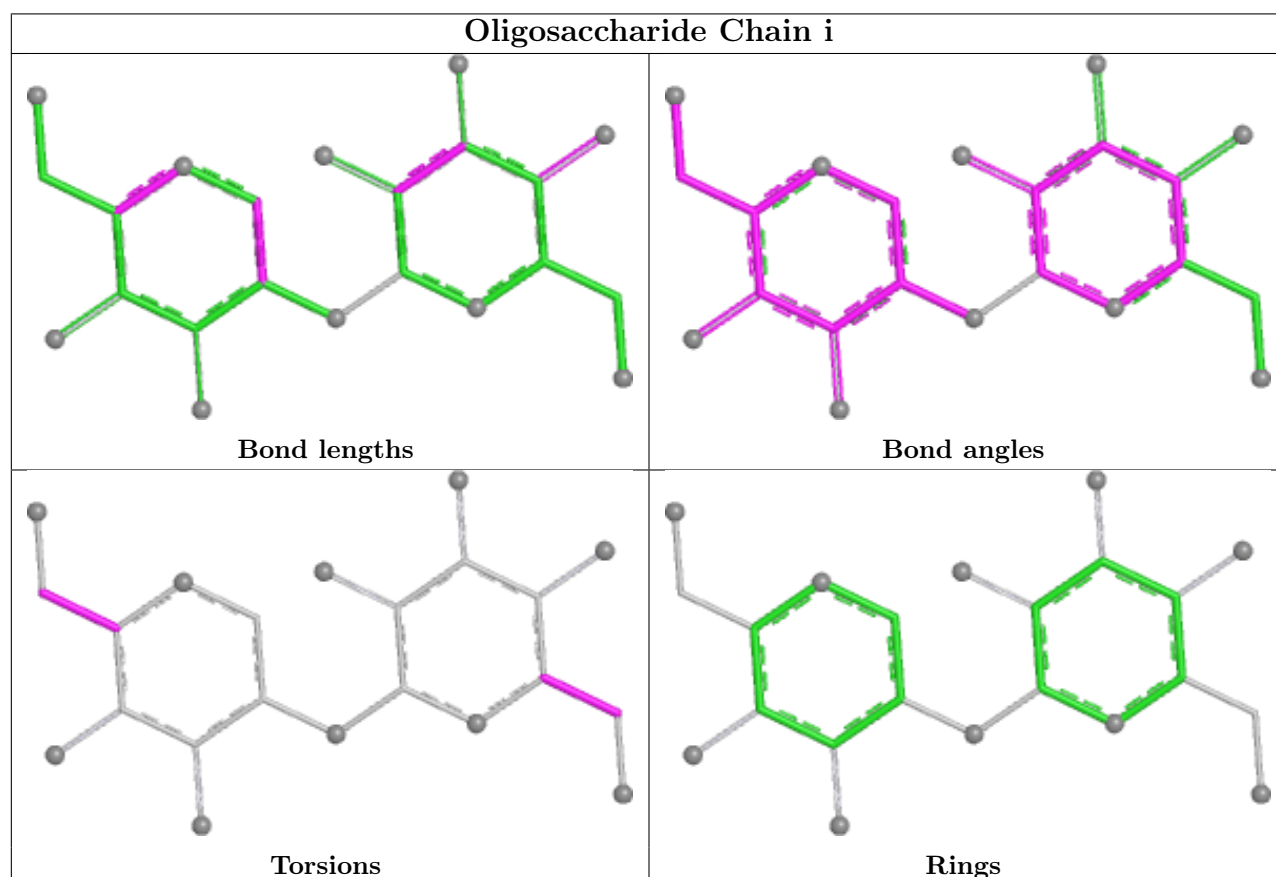
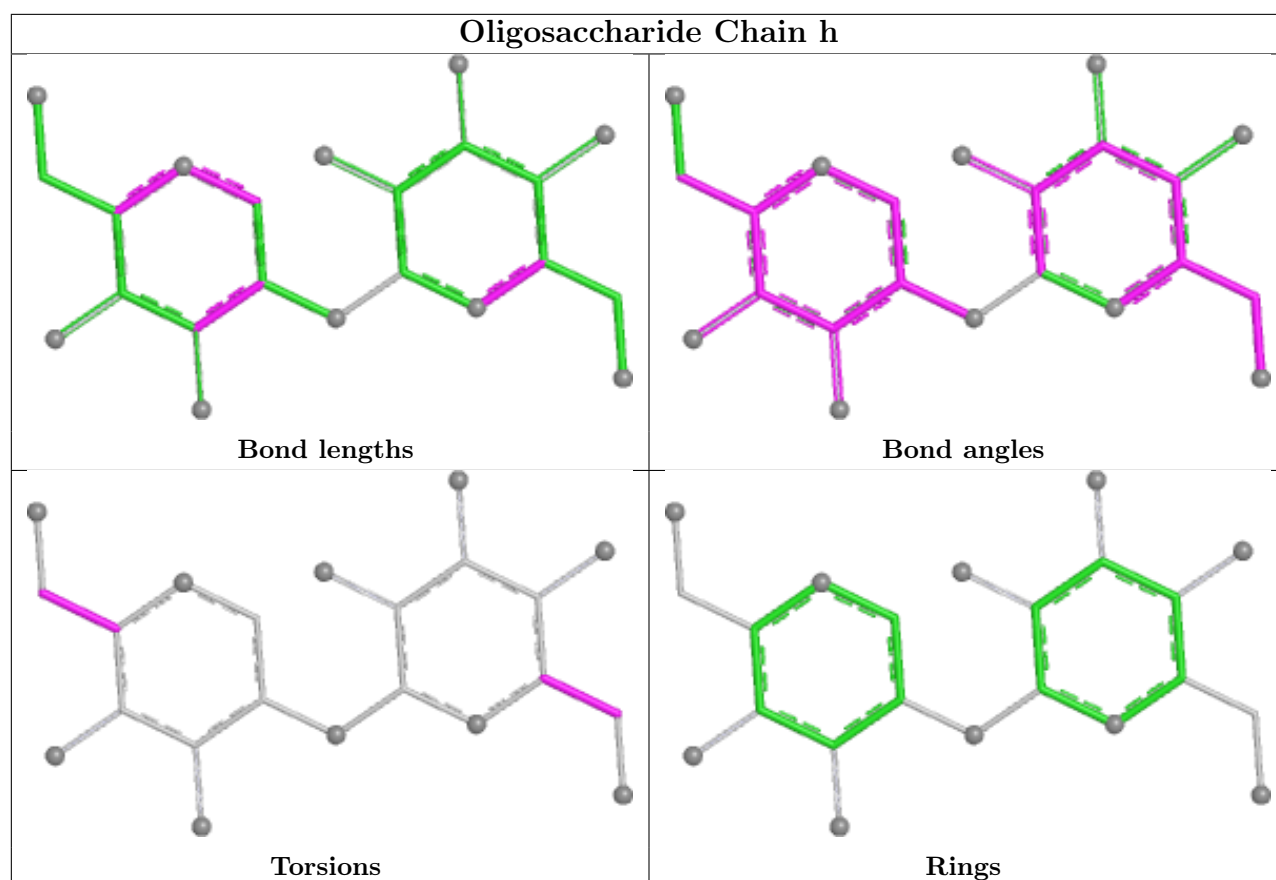
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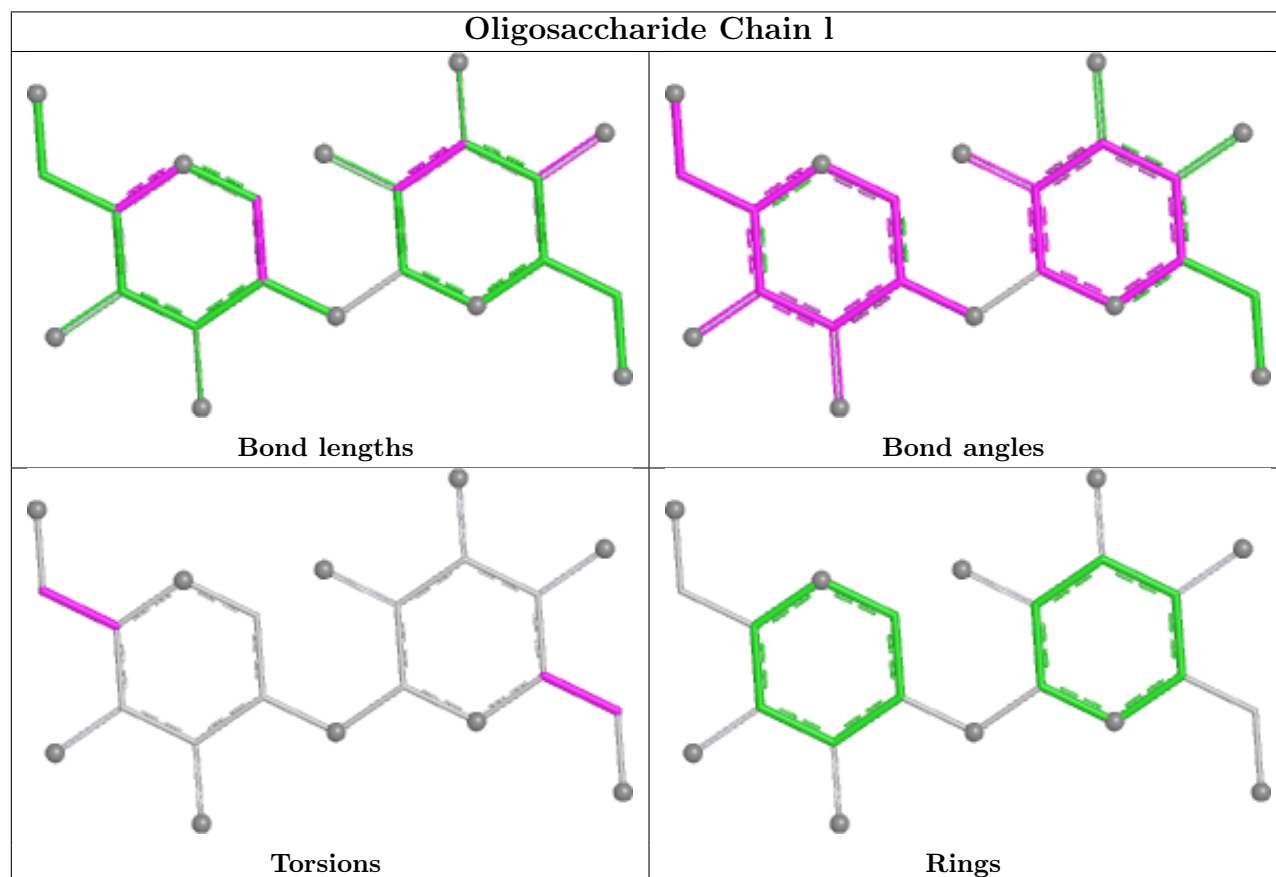
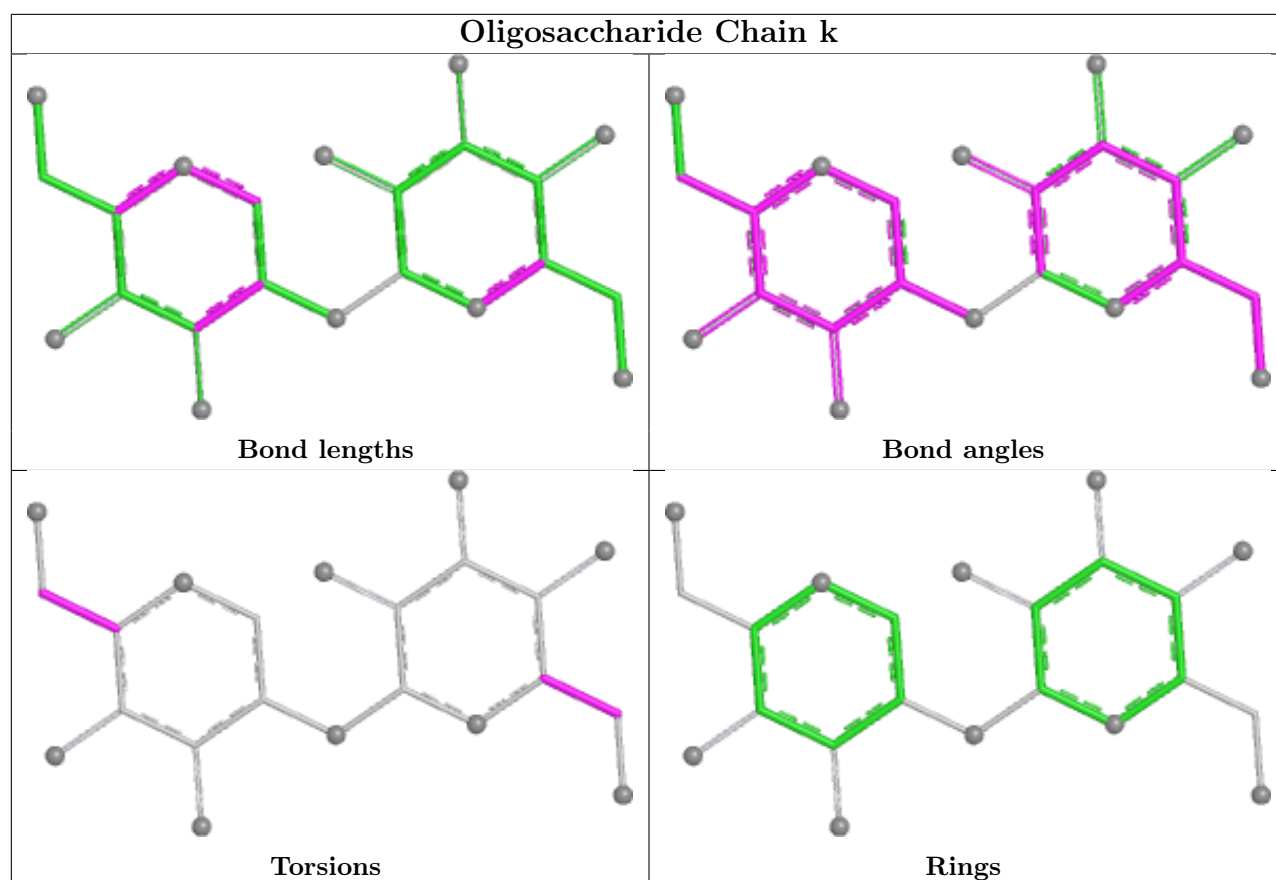
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	f	6	MAN	2	0
7	G	2	MAN	3	0
7	h	1	MAN	8	0
9	b	7	MAN	8	0
9	d	3	BMA	4	0
7	k	1	MAN	8	0
7	g	2	MAN	1	0
9	X	5	MAN	2	0
7	N	1	MAN	7	0
7	g	1	MAN	7	0
9	Z	4	MAN	6	0
8	U	5	MAN	1	0
9	f	5	MAN	3	0
10	e	4	MAN	4	0
7	h	2	MAN	3	0
8	j	5	MAN	1	0
9	X	7	MAN	7	0
9	n	3	BMA	4	0
9	f	3	BMA	3	0
9	d	4	MAN	5	0
9	Z	6	MAN	2	0
7	l	1	MAN	7	0
9	d	6	MAN	2	0
9	d	7	MAN	7	0
9	X	6	MAN	2	0
10	c	4	MAN	4	0
8	m	5	MAN	1	0
9	d	5	MAN	7	0
7	Y	2	MAN	1	0
9	Z	7	MAN	7	0
9	b	4	MAN	6	0
9	n	6	MAN	2	0
9	n	7	MAN	7	0
7	G	1	MAN	8	0
9	X	4	MAN	4	0
9	b	6	MAN	2	0

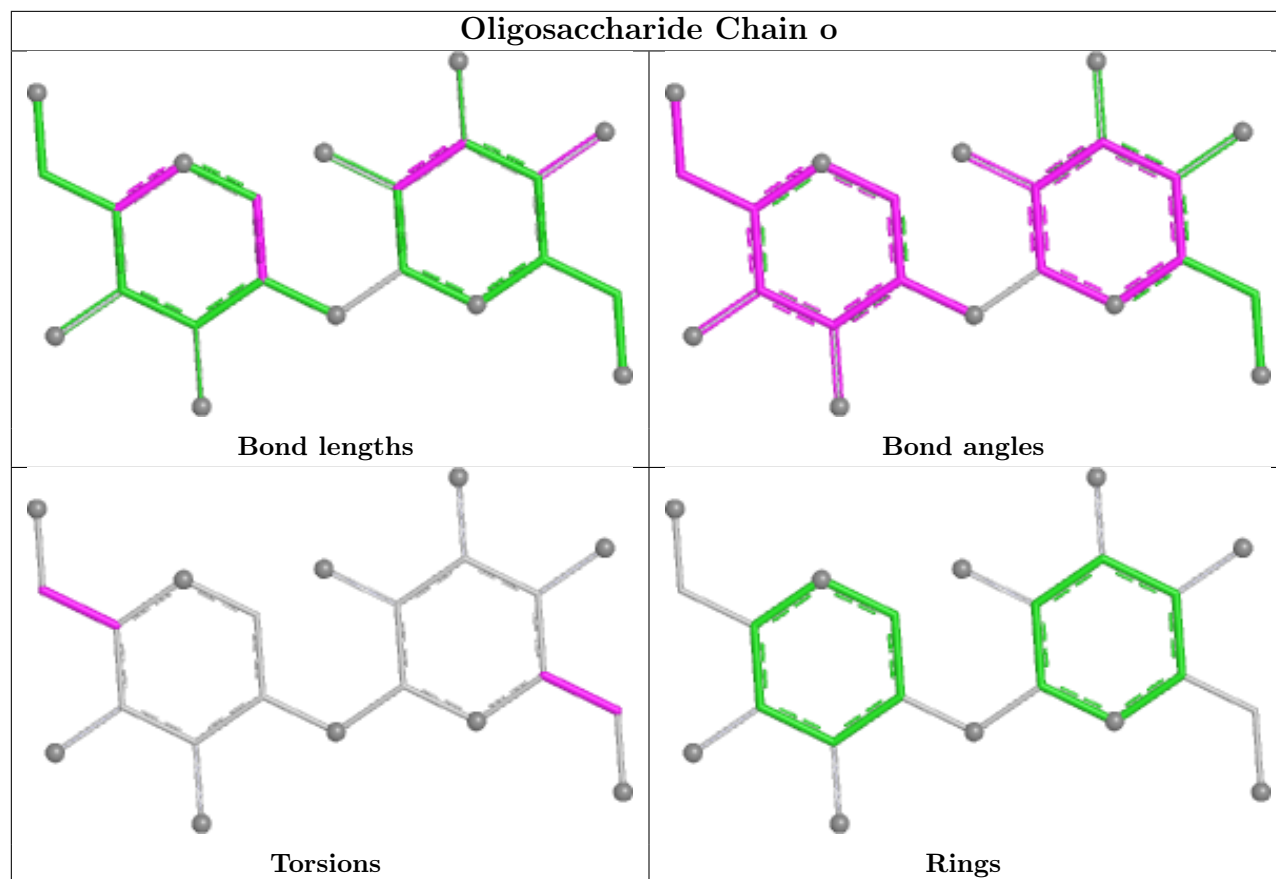
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

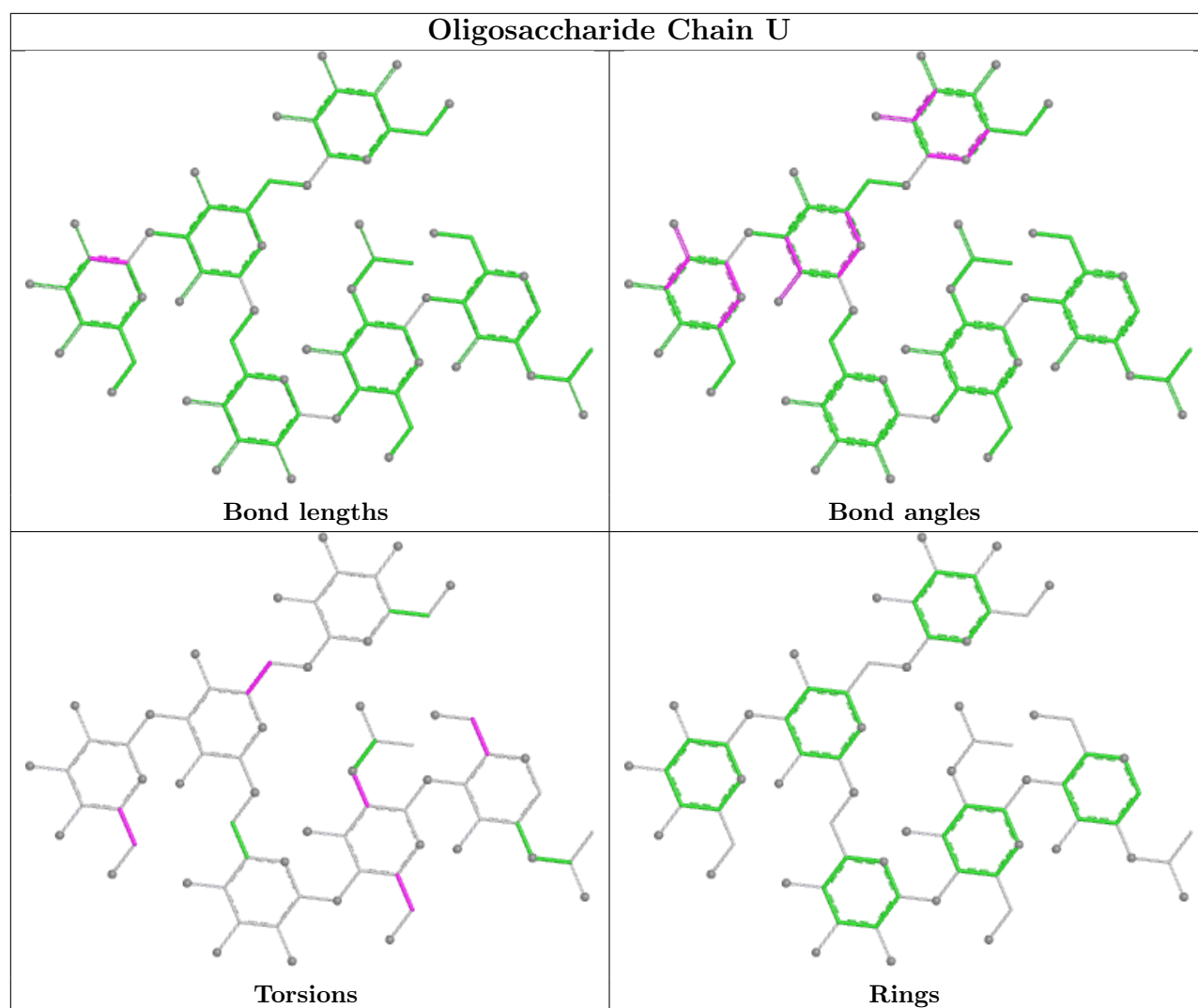


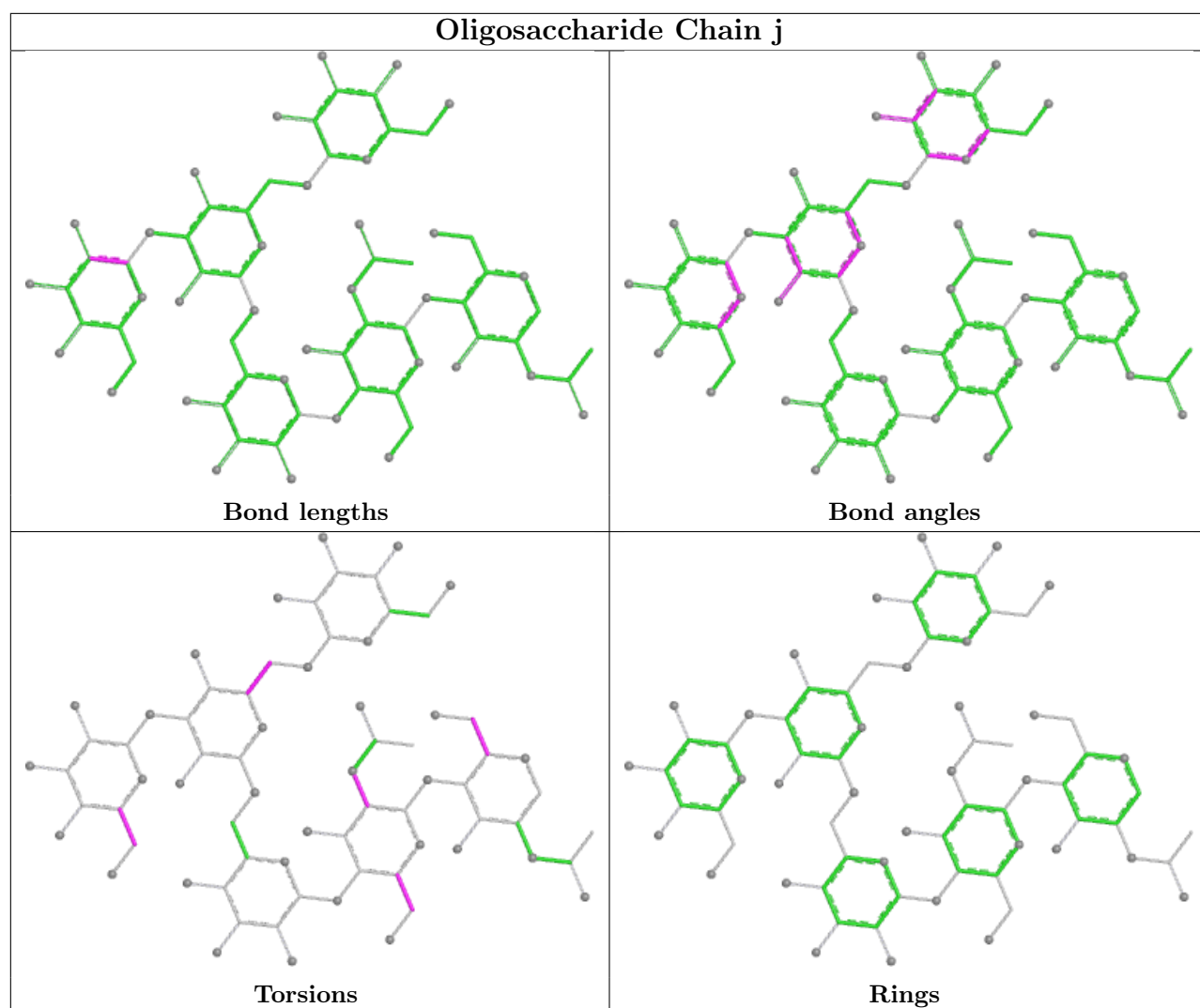


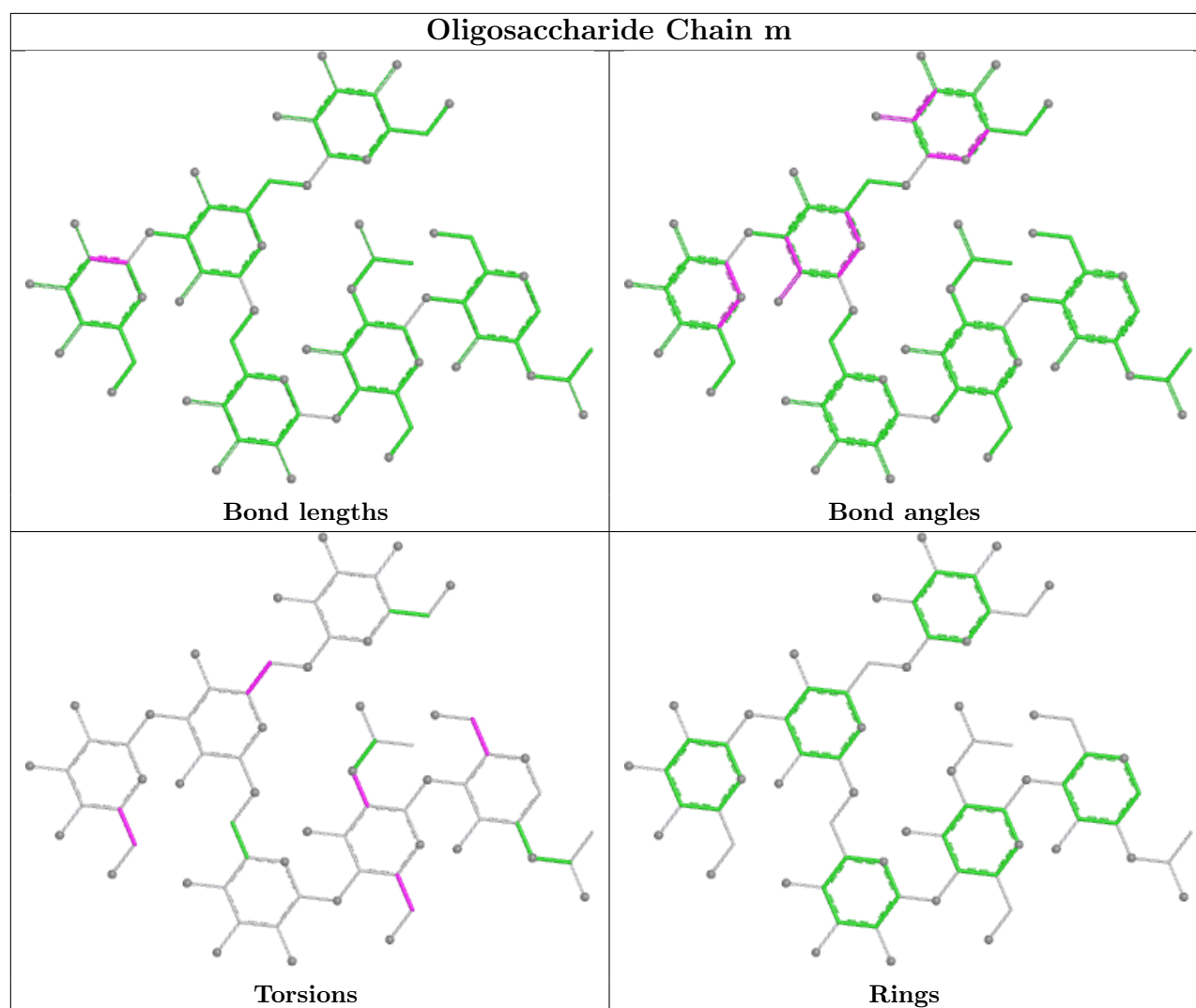


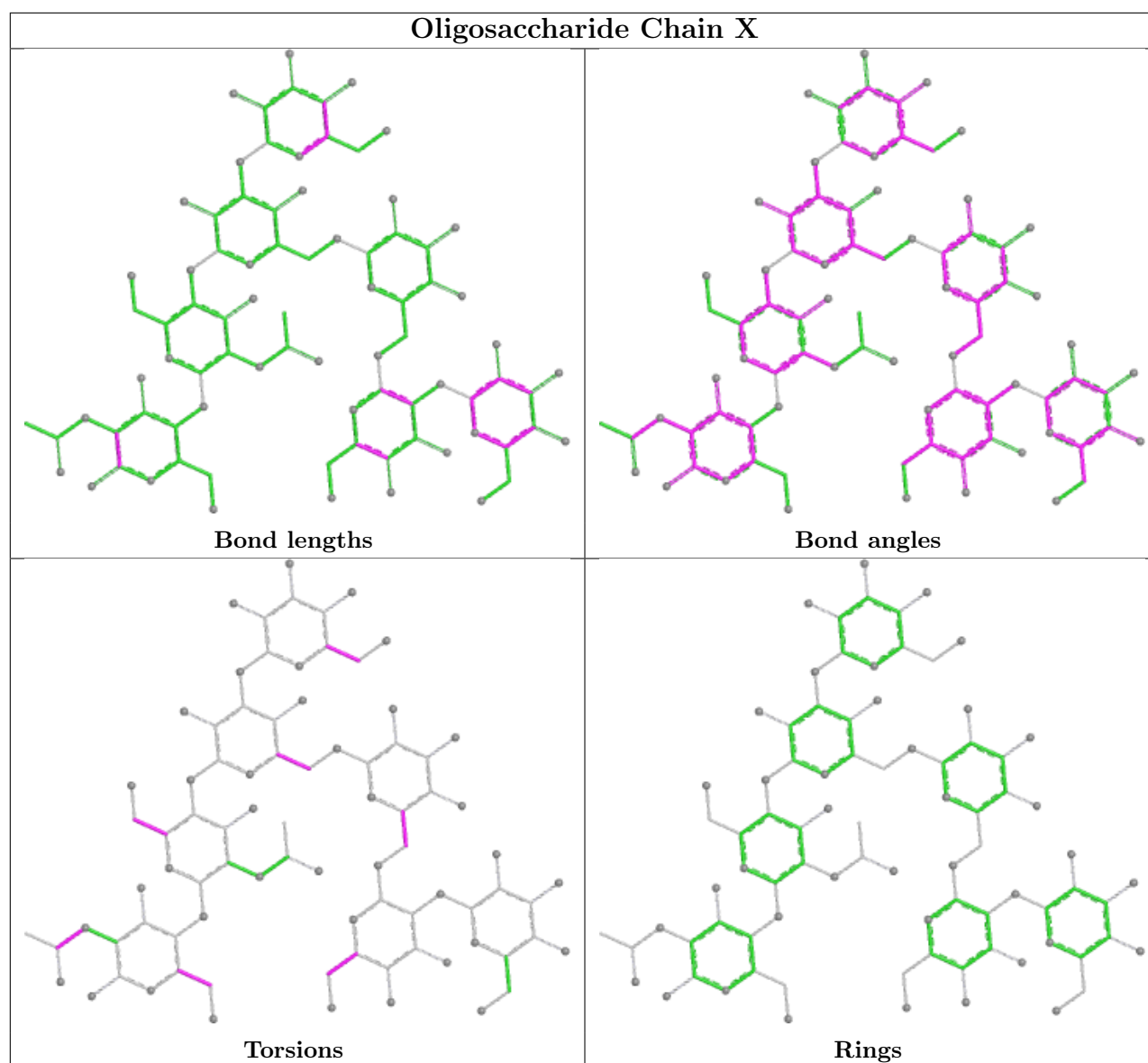


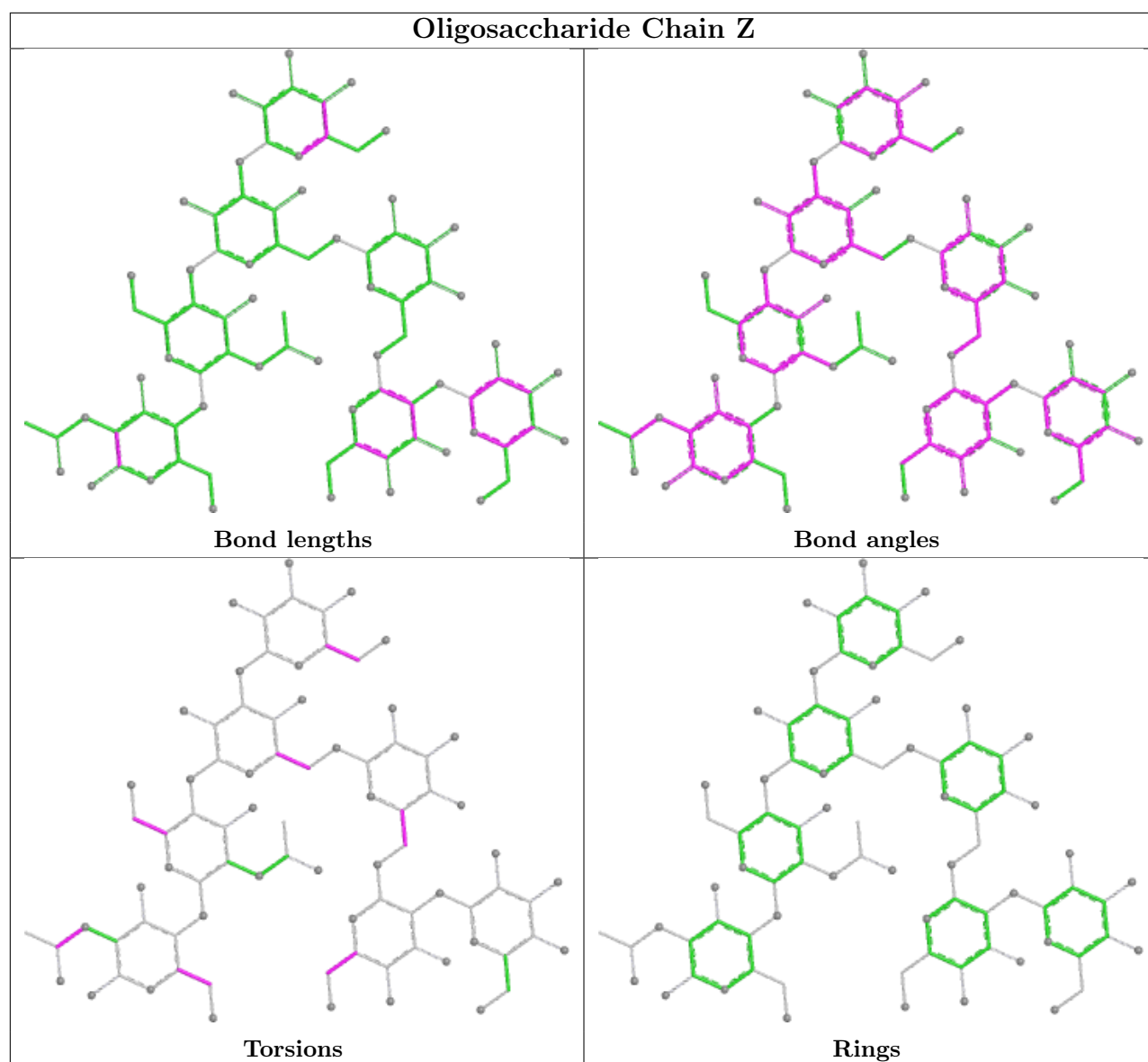


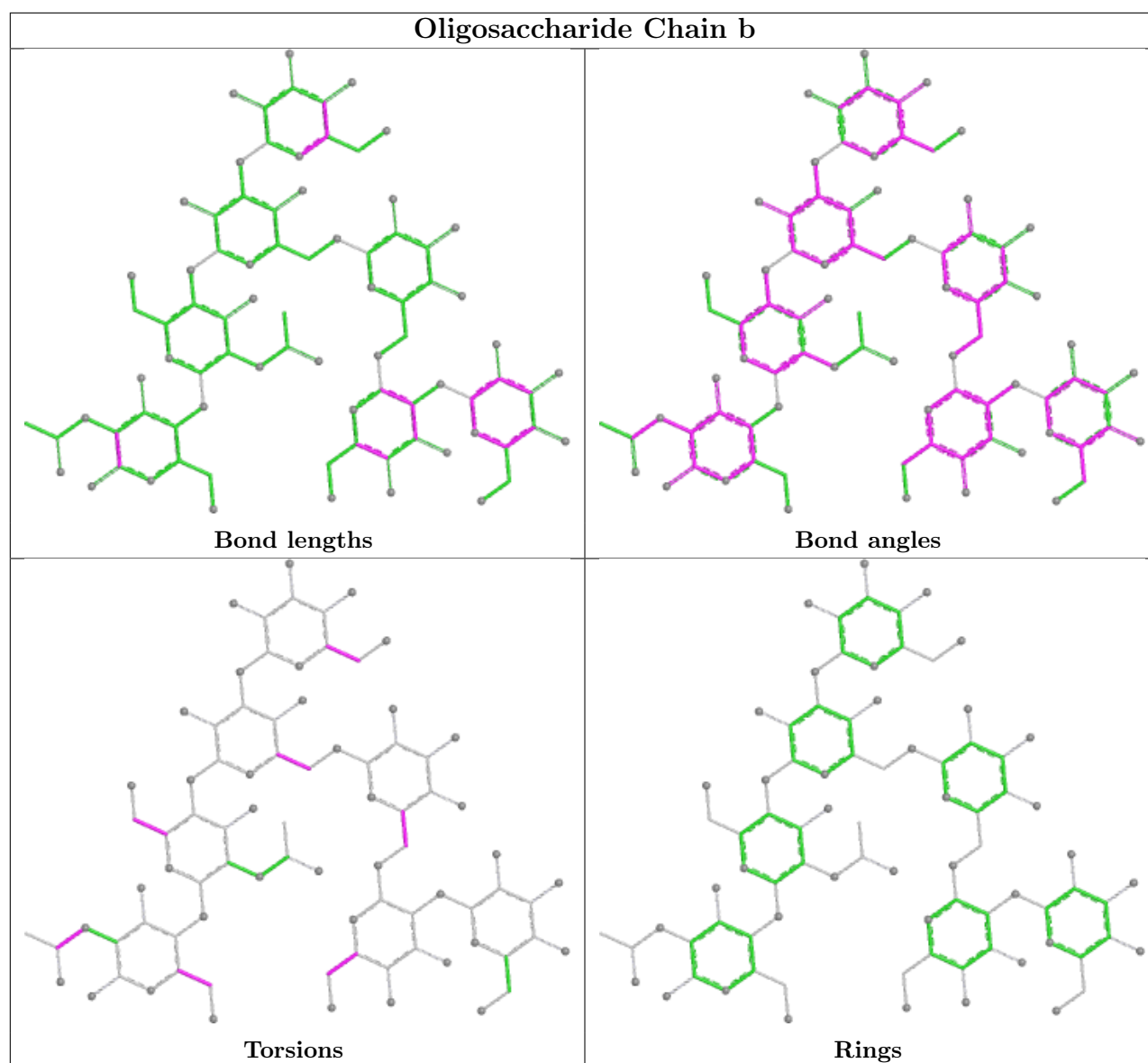


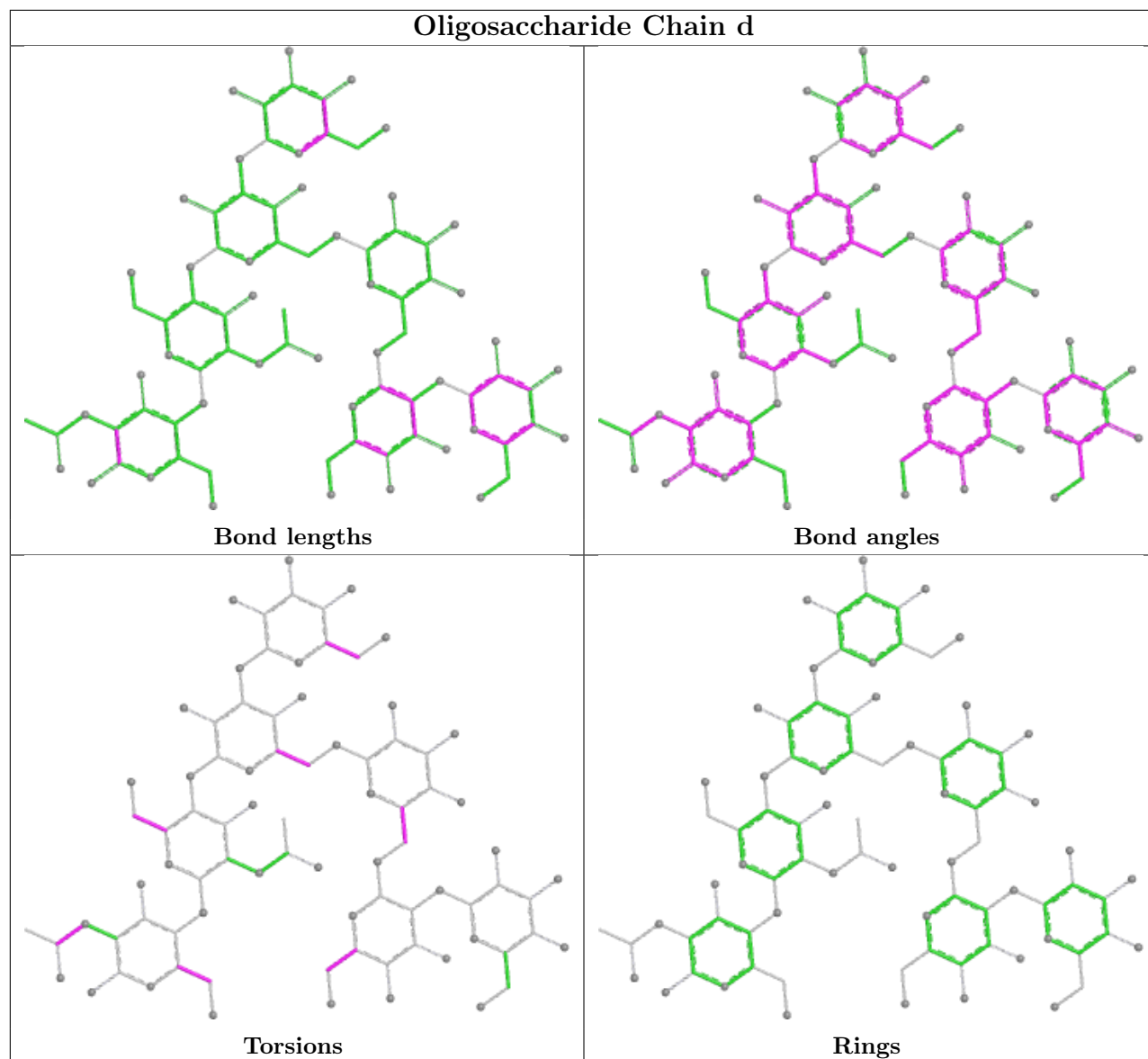


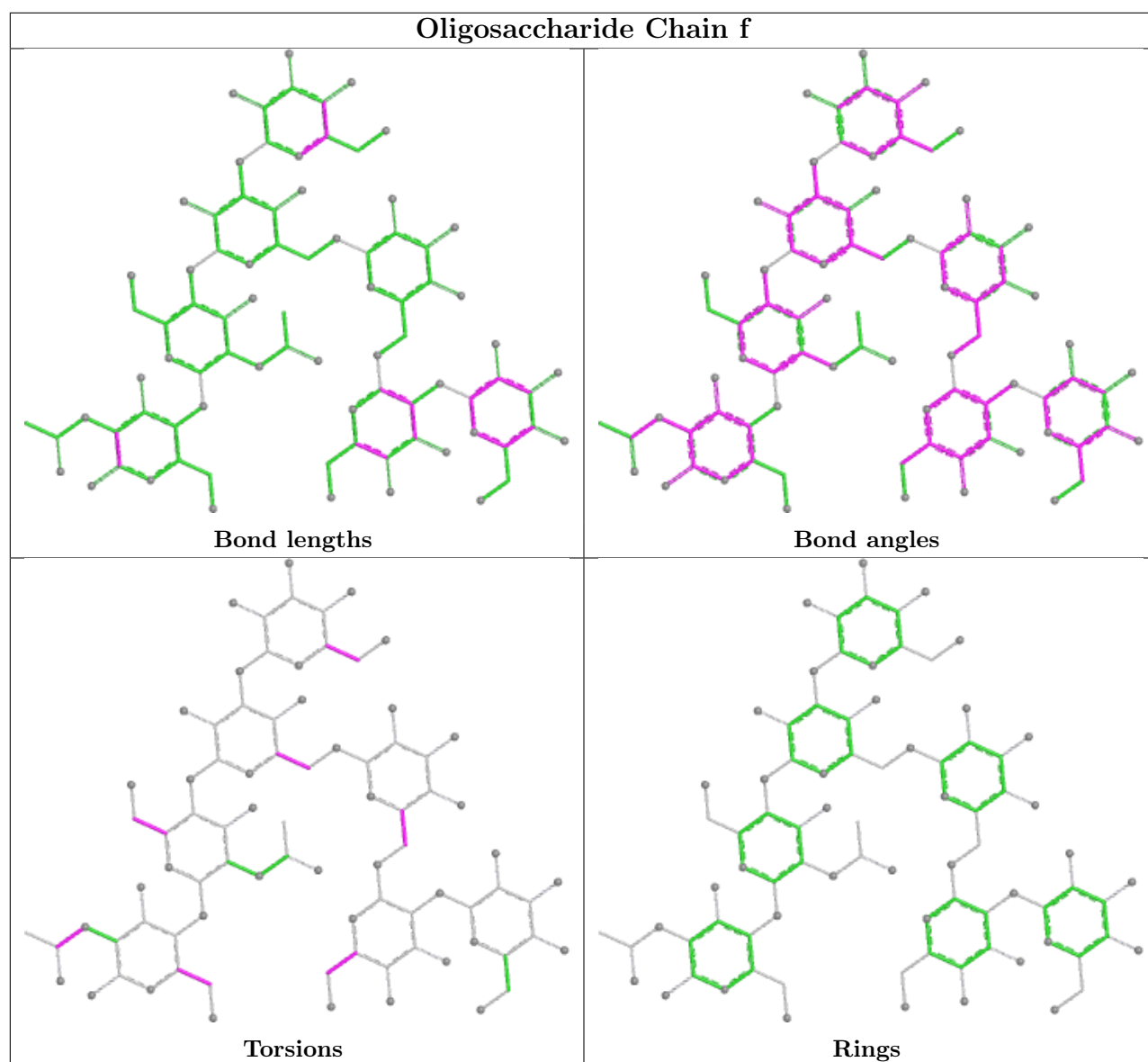


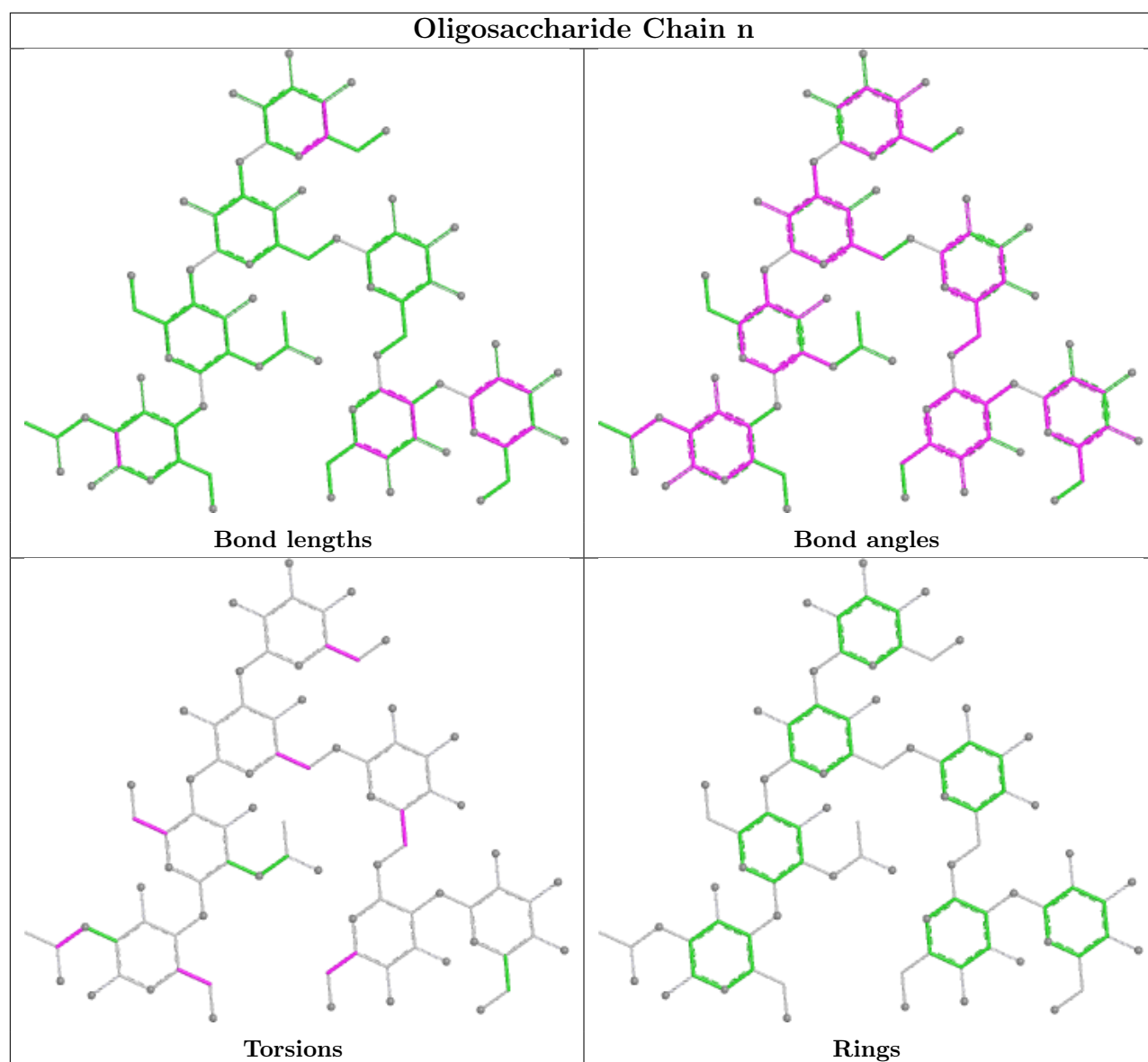


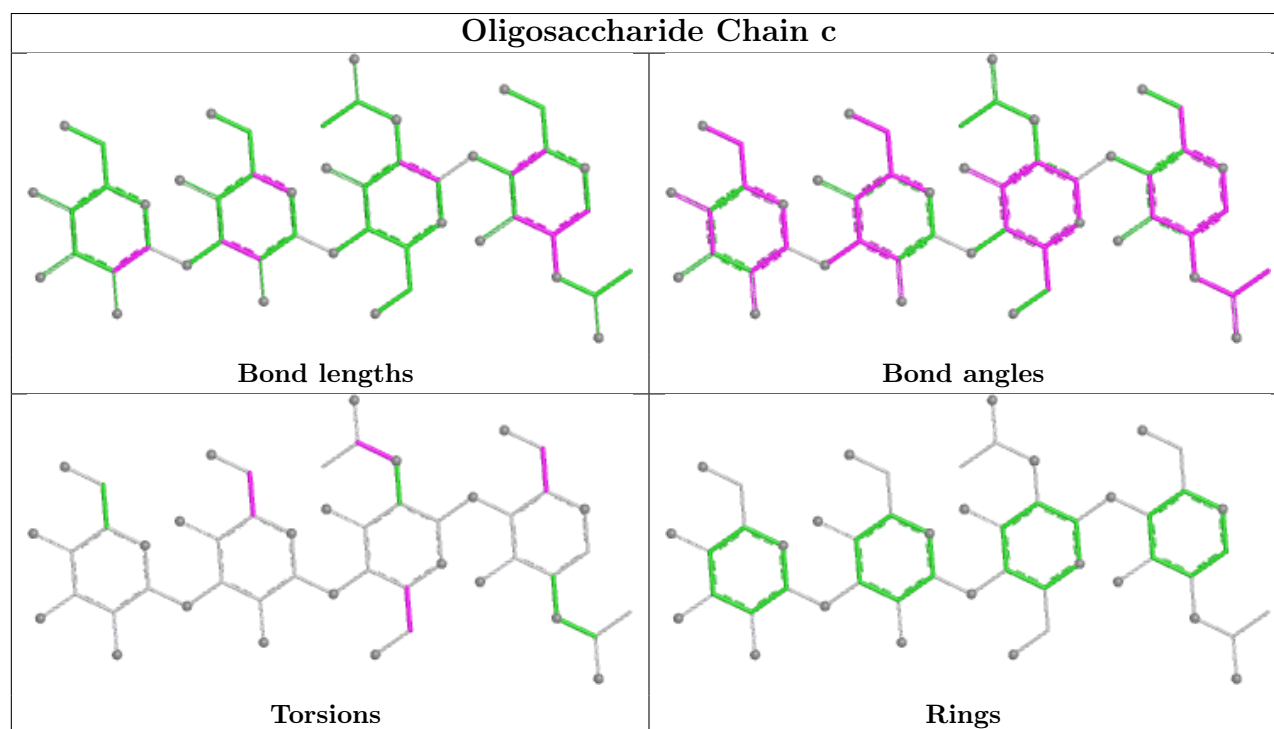
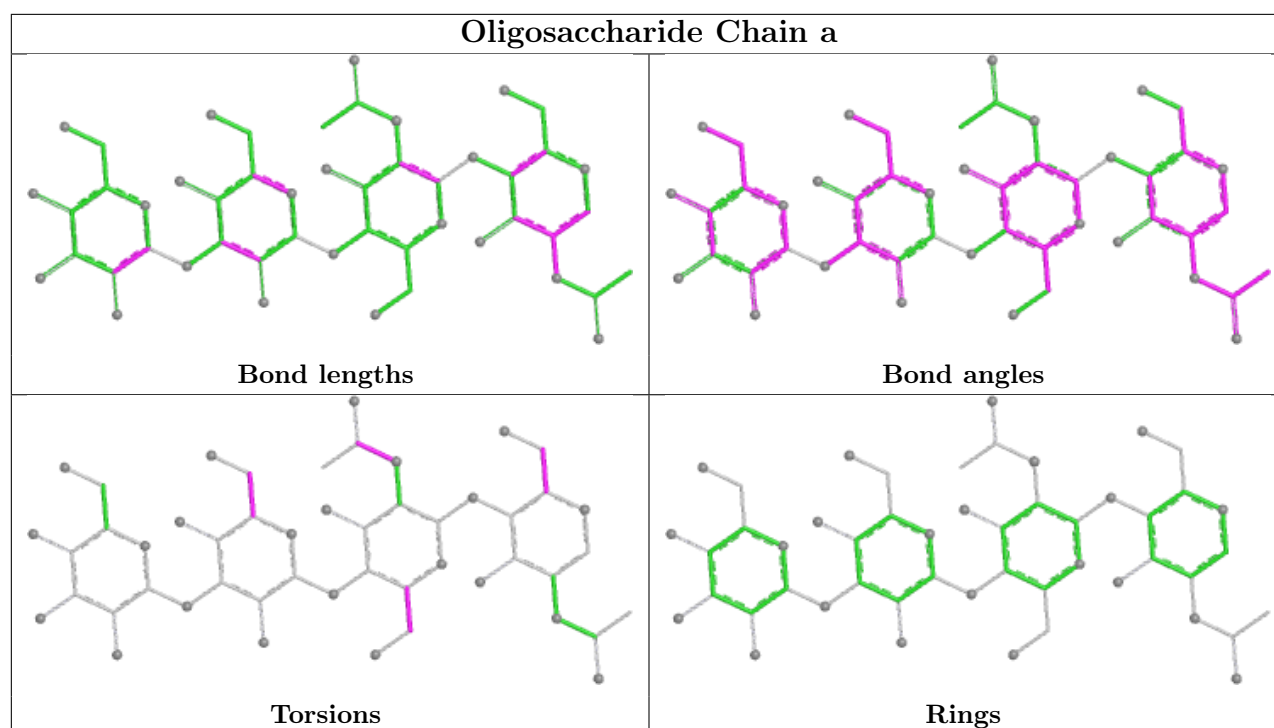


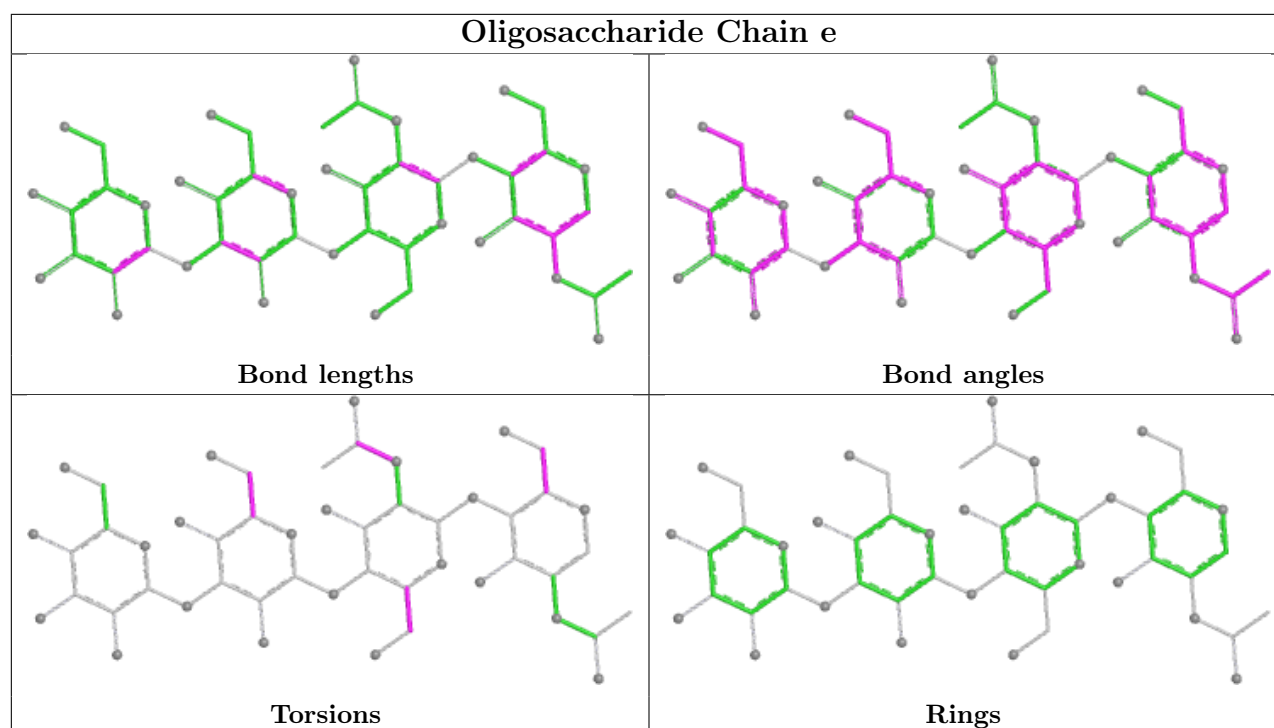












5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

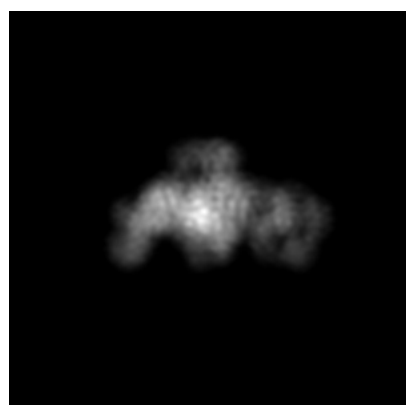
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8981. These allow visual inspection of the internal detail of the map and identification of artifacts.

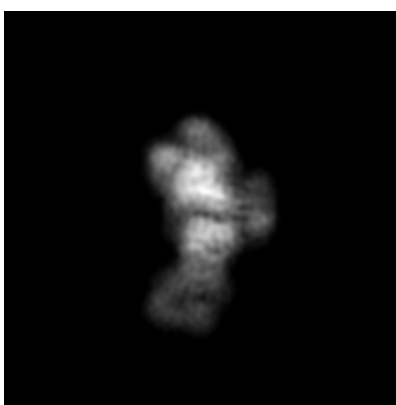
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

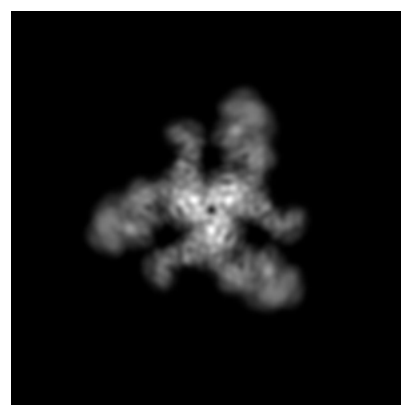
6.1.1 Primary map



X



Y

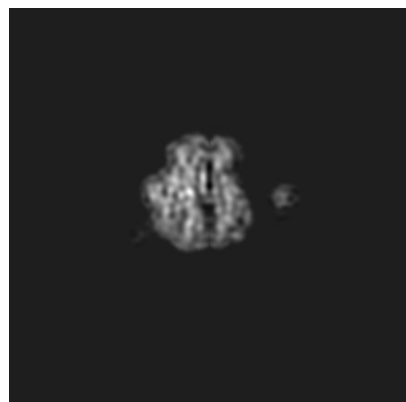


Z

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

6.2 Central slices [i](#)

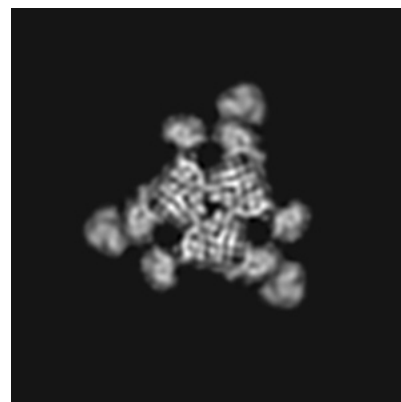
6.2.1 Primary map



X Index: 192



Y Index: 192



Z Index: 192

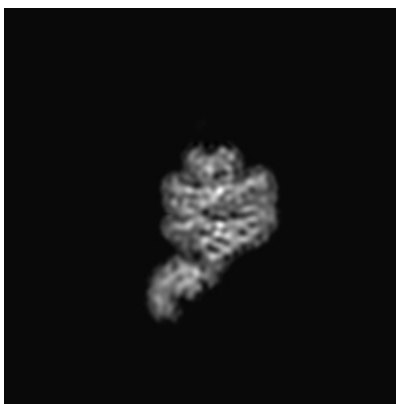
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 211



Y Index: 202

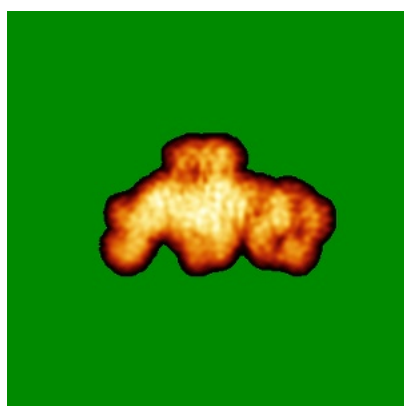


Z Index: 188

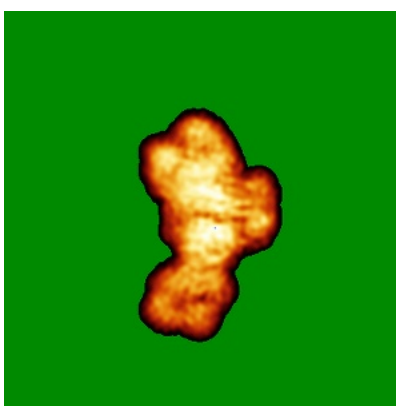
The images above show the largest variance slices of the map in three orthogonal directions.

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

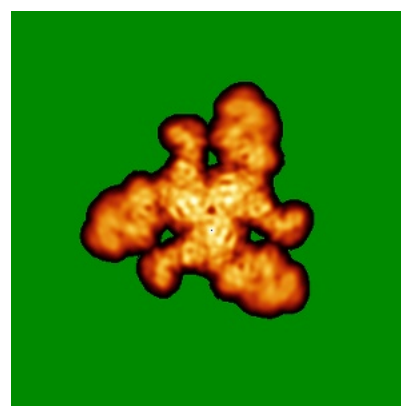
6.4.1 Primary map



X



Y

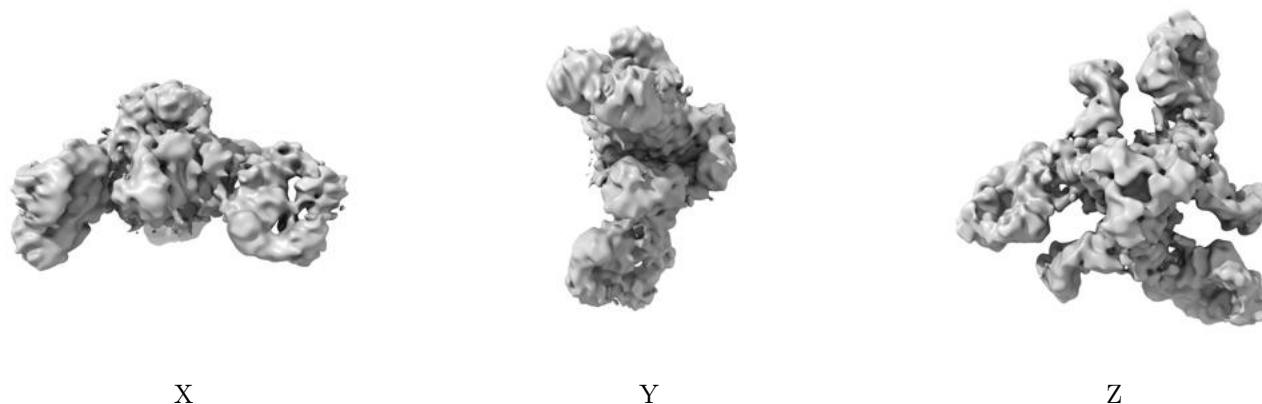


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.734. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

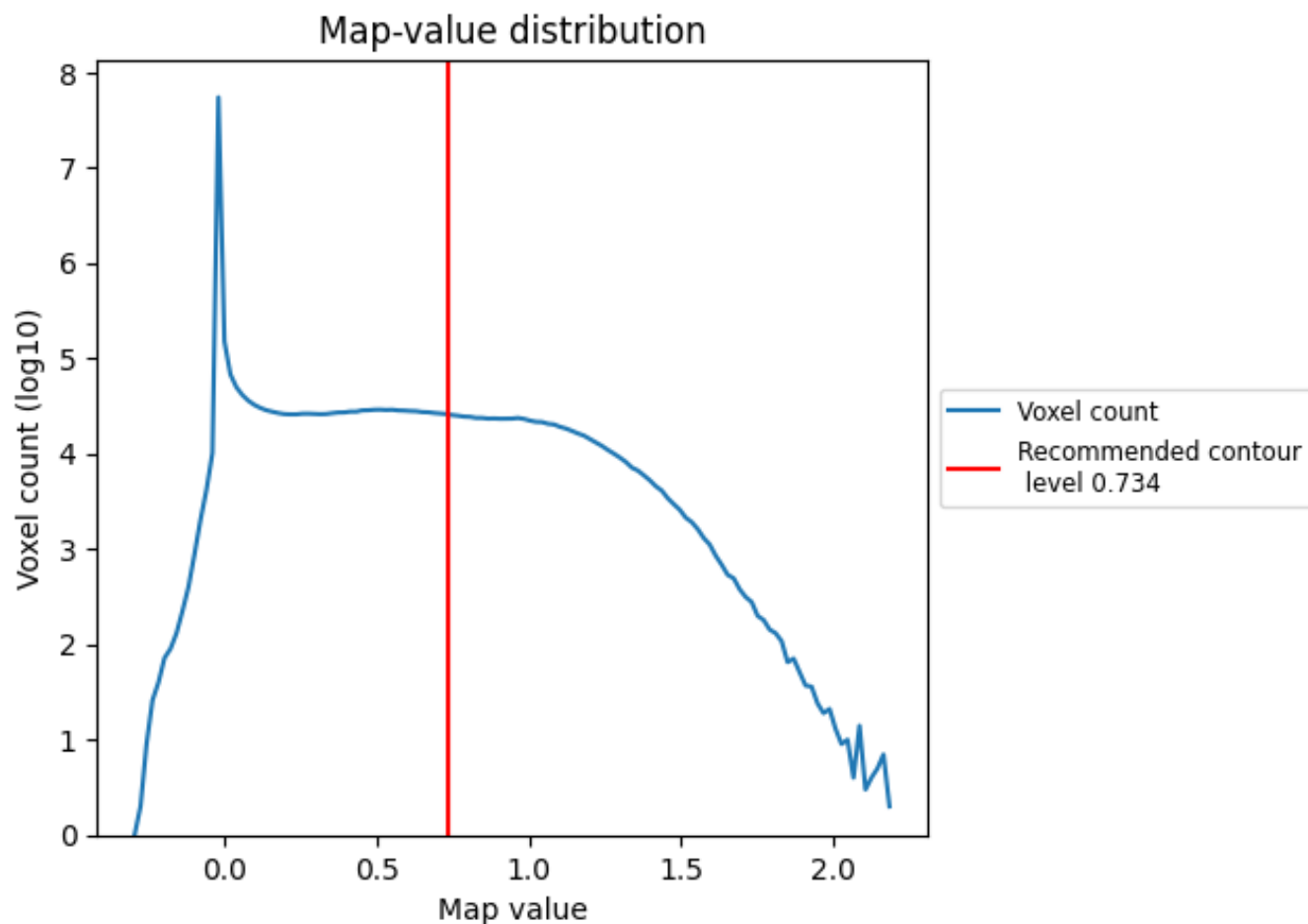
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

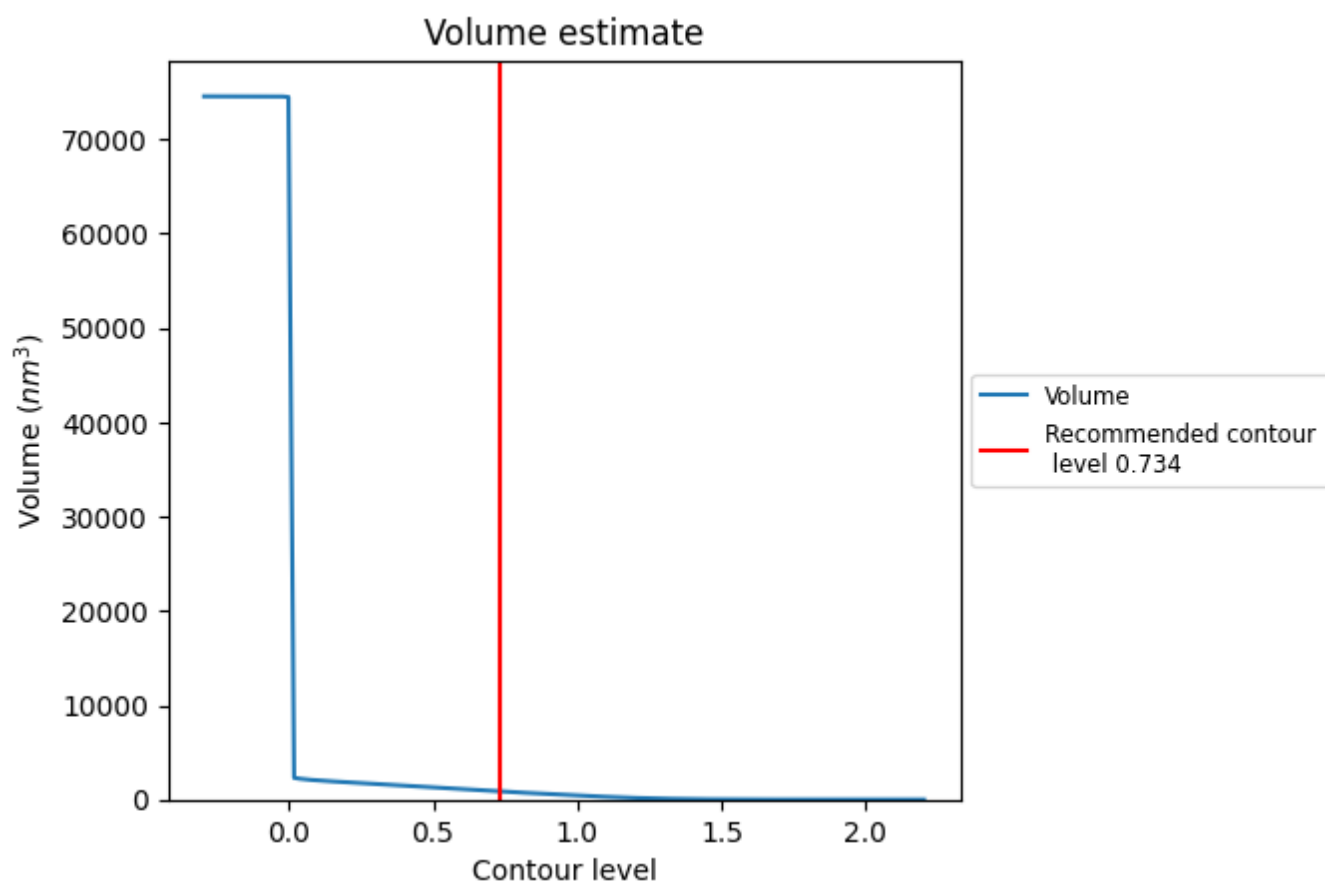
This section contains the results of statistical analysis of the map.

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.

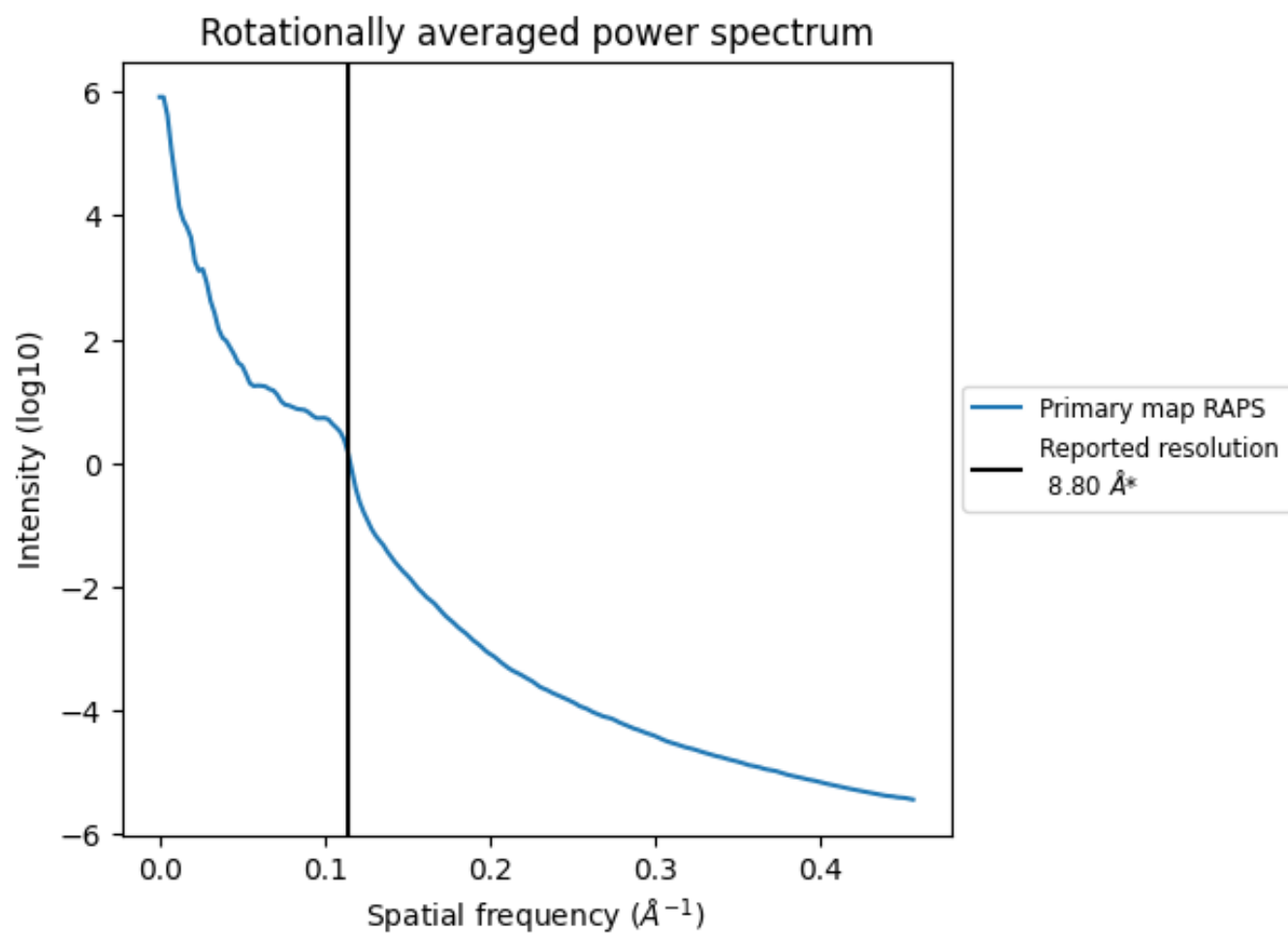
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 861 nm³; this corresponds to an approximate mass of 778 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 ⓘ

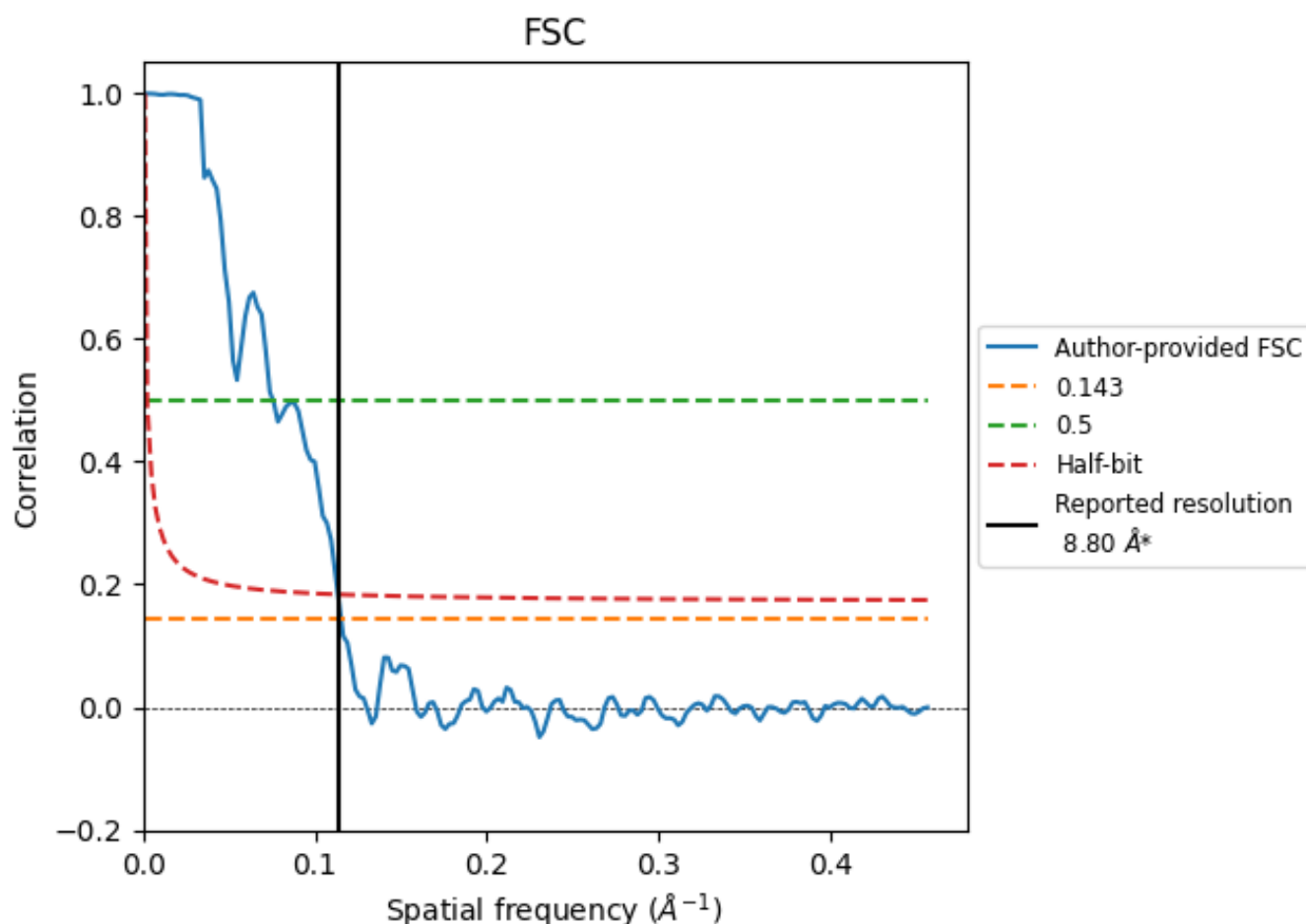


*Reported resolution corresponds to spatial frequency of 0.114 Å⁻¹

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 0.114 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.80	-	-
Author-provided FSC curve	8.68	13.23	8.83
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8981 and PDB model 6E5P. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

This section was not generated.

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

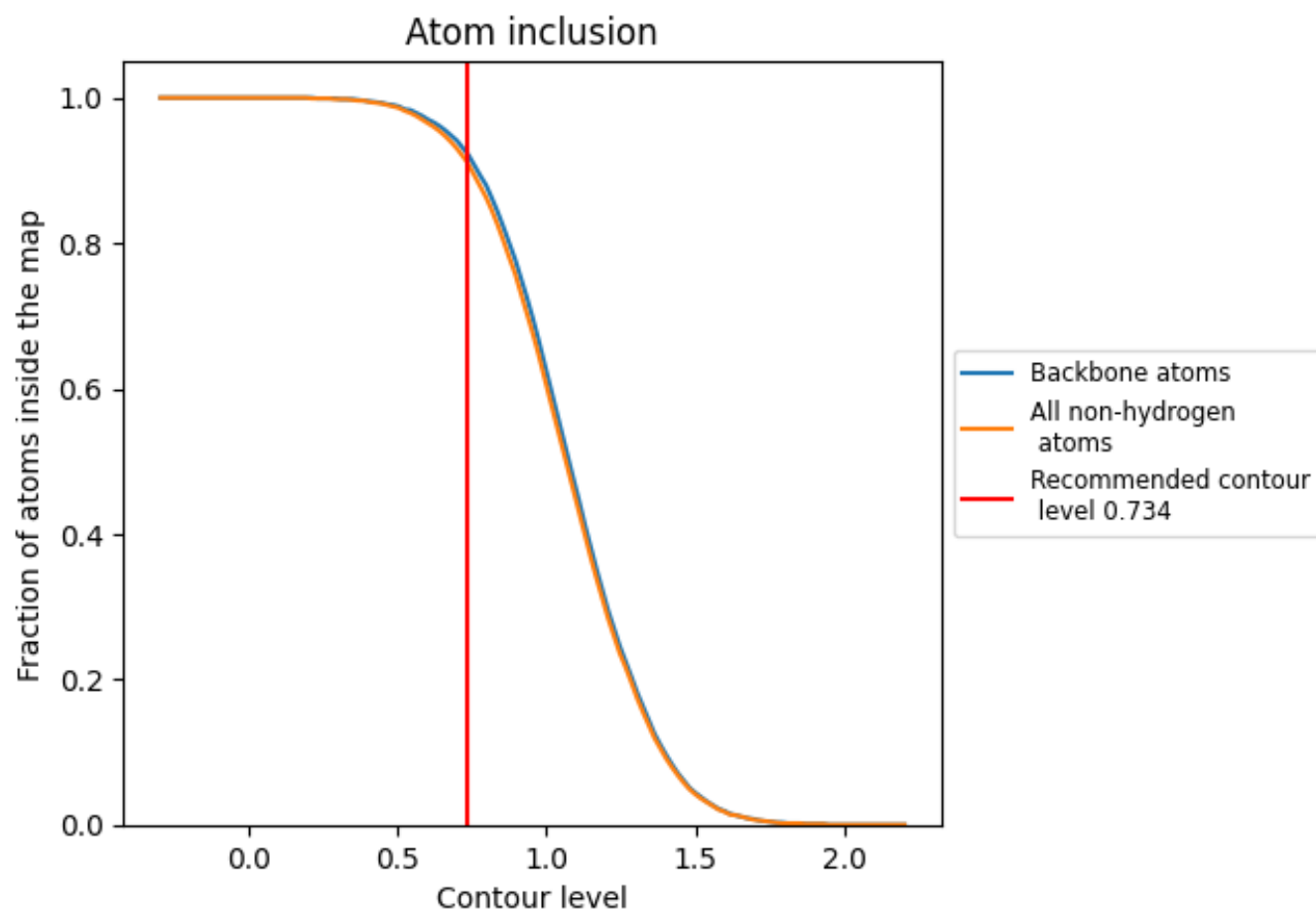


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (0.734) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9120	 0.1400
1	 0.9280	 0.1350
2	 0.8900	 0.1290
3	 0.8910	 0.1210
4	 0.9120	 0.1170
A	 0.9650	 0.1770
B	 0.9540	 0.1830
C	 0.9650	 0.1730
D	 0.9520	 0.1920
E	 0.9600	 0.1690
F	 0.9480	 0.1790
G	 0.9090	 0.0740
H	 0.9010	 0.1270
I	 0.9280	 0.1320
J	 0.8440	 0.0520
K	 0.9300	 0.1350
L	 0.9240	 0.1230
M	 0.8930	 0.1400
N	 0.7730	 0.1640
O	 0.9380	 0.1360
P	 0.8610	 0.0750
Q	 0.9240	 0.1430
R	 0.8920	 0.1310
S	 0.8830	 0.1200
T	 0.9120	 0.1060
U	 0.5420	 0.0340
V	 0.9380	 0.1380
W	 0.8640	 0.0690
X	 0.5480	 0.2050
Y	 0.9550	 0.2170
Z	 0.7140	 0.0910
a	 0.8000	 0.1850
b	 0.6790	 0.0940
c	 0.8000	 0.1990
d	 0.7020	 0.0960



Continued on next page...

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Chain	Atom inclusion	Q-score
e	 0.8000	 0.1750
f	 0.5710	 0.1800
g	 0.9550	 0.1940
h	 0.9090	 0.0520
i	 0.5910	 0.2480
j	 0.5560	 0.0460
k	 0.9090	 0.1050
l	 0.6360	 0.1800
m	 0.5690	 0.0470
n	 0.5590	 0.1810
o	 0.9090	 0.2140