



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:22 PM UTC

PDB ID : 6DS5 / pdb_00006ds5
EMDB ID : EMD-8909
Title : Cryo EM structure of human SEIPIN
Authors : Yan, R.H.; Qian, H.W.; Yan, N.; Yang, H.Y.
Deposited on : 2018-06-13
Resolution : 3.80 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

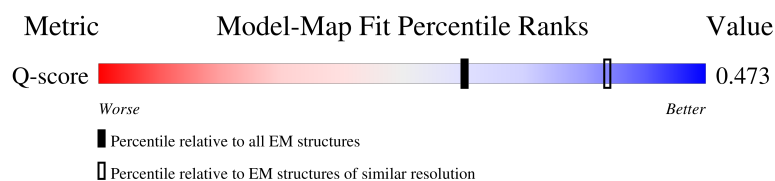
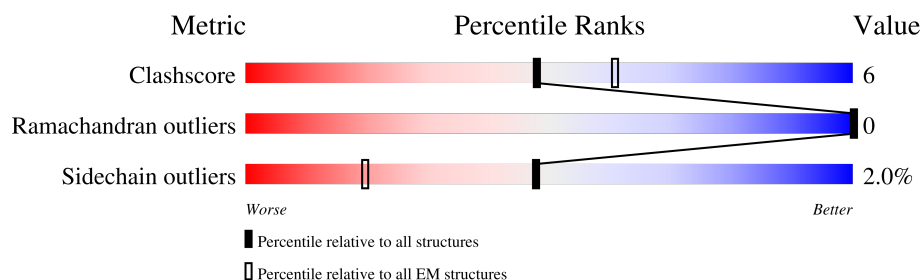
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



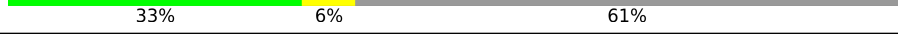
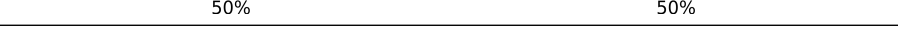
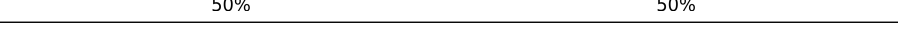
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	A	409	 32% 7% 61%
1	B	409	 32% 7% 61%
1	C	409	 32% 7% 61%
1	D	409	 33% 5% 61%

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Mol	Chain	Length	Quality of chain
1	E	409	
1	F	409	
1	G	409	
1	H	409	
1	I	409	
1	J	409	
1	K	409	
2	L	2	
2	M	2	
2	N	2	
2	O	2	
2	P	2	
2	Q	2	
2	R	2	
2	S	2	
2	T	2	
2	U	2	
2	V	2	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13970 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 Seipin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	B	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	C	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	D	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	E	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	F	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	G	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	H	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	I	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	J	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		
1	K	160	Total	C	N	O	S	0	0
			1242	790	210	236	6		

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP Q96G97
A	-9	SER	-	expression tag	UNP Q96G97
A	-8	GLY	-	expression tag	UNP Q96G97
A	-7	ARG	-	expression tag	UNP Q96G97
A	-6	TRP	-	expression tag	UNP Q96G97
A	-5	SER	-	expression tag	UNP Q96G97
A	-4	HIS	-	expression tag	UNP Q96G97
A	-3	PRO	-	expression tag	UNP Q96G97

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLN	-	expression tag	UNP Q96G97
A	-1	PHE	-	expression tag	UNP Q96G97
A	0	GLU	-	expression tag	UNP Q96G97
A	1	LYS	-	expression tag	UNP Q96G97
B	-10	MET	-	initiating methionine	UNP Q96G97
B	-9	SER	-	expression tag	UNP Q96G97
B	-8	GLY	-	expression tag	UNP Q96G97
B	-7	ARG	-	expression tag	UNP Q96G97
B	-6	TRP	-	expression tag	UNP Q96G97
B	-5	SER	-	expression tag	UNP Q96G97
B	-4	HIS	-	expression tag	UNP Q96G97
B	-3	PRO	-	expression tag	UNP Q96G97
B	-2	GLN	-	expression tag	UNP Q96G97
B	-1	PHE	-	expression tag	UNP Q96G97
B	0	GLU	-	expression tag	UNP Q96G97
B	1	LYS	-	expression tag	UNP Q96G97
C	-10	MET	-	initiating methionine	UNP Q96G97
C	-9	SER	-	expression tag	UNP Q96G97
C	-8	GLY	-	expression tag	UNP Q96G97
C	-7	ARG	-	expression tag	UNP Q96G97
C	-6	TRP	-	expression tag	UNP Q96G97
C	-5	SER	-	expression tag	UNP Q96G97
C	-4	HIS	-	expression tag	UNP Q96G97
C	-3	PRO	-	expression tag	UNP Q96G97
C	-2	GLN	-	expression tag	UNP Q96G97
C	-1	PHE	-	expression tag	UNP Q96G97
C	0	GLU	-	expression tag	UNP Q96G97
C	1	LYS	-	expression tag	UNP Q96G97
D	-10	MET	-	initiating methionine	UNP Q96G97
D	-9	SER	-	expression tag	UNP Q96G97
D	-8	GLY	-	expression tag	UNP Q96G97
D	-7	ARG	-	expression tag	UNP Q96G97
D	-6	TRP	-	expression tag	UNP Q96G97
D	-5	SER	-	expression tag	UNP Q96G97
D	-4	HIS	-	expression tag	UNP Q96G97
D	-3	PRO	-	expression tag	UNP Q96G97
D	-2	GLN	-	expression tag	UNP Q96G97
D	-1	PHE	-	expression tag	UNP Q96G97
D	0	GLU	-	expression tag	UNP Q96G97
D	1	LYS	-	expression tag	UNP Q96G97
E	-10	MET	-	initiating methionine	UNP Q96G97
E	-9	SER	-	expression tag	UNP Q96G97

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-8	GLY	-	expression tag	UNP Q96G97
E	-7	ARG	-	expression tag	UNP Q96G97
E	-6	TRP	-	expression tag	UNP Q96G97
E	-5	SER	-	expression tag	UNP Q96G97
E	-4	HIS	-	expression tag	UNP Q96G97
E	-3	PRO	-	expression tag	UNP Q96G97
E	-2	GLN	-	expression tag	UNP Q96G97
E	-1	PHE	-	expression tag	UNP Q96G97
E	0	GLU	-	expression tag	UNP Q96G97
E	1	LYS	-	expression tag	UNP Q96G97
F	-10	MET	-	initiating methionine	UNP Q96G97
F	-9	SER	-	expression tag	UNP Q96G97
F	-8	GLY	-	expression tag	UNP Q96G97
F	-7	ARG	-	expression tag	UNP Q96G97
F	-6	TRP	-	expression tag	UNP Q96G97
F	-5	SER	-	expression tag	UNP Q96G97
F	-4	HIS	-	expression tag	UNP Q96G97
F	-3	PRO	-	expression tag	UNP Q96G97
F	-2	GLN	-	expression tag	UNP Q96G97
F	-1	PHE	-	expression tag	UNP Q96G97
F	0	GLU	-	expression tag	UNP Q96G97
F	1	LYS	-	expression tag	UNP Q96G97
G	-10	MET	-	initiating methionine	UNP Q96G97
G	-9	SER	-	expression tag	UNP Q96G97
G	-8	GLY	-	expression tag	UNP Q96G97
G	-7	ARG	-	expression tag	UNP Q96G97
G	-6	TRP	-	expression tag	UNP Q96G97
G	-5	SER	-	expression tag	UNP Q96G97
G	-4	HIS	-	expression tag	UNP Q96G97
G	-3	PRO	-	expression tag	UNP Q96G97
G	-2	GLN	-	expression tag	UNP Q96G97
G	-1	PHE	-	expression tag	UNP Q96G97
G	0	GLU	-	expression tag	UNP Q96G97
G	1	LYS	-	expression tag	UNP Q96G97
H	-10	MET	-	initiating methionine	UNP Q96G97
H	-9	SER	-	expression tag	UNP Q96G97
H	-8	GLY	-	expression tag	UNP Q96G97
H	-7	ARG	-	expression tag	UNP Q96G97
H	-6	TRP	-	expression tag	UNP Q96G97
H	-5	SER	-	expression tag	UNP Q96G97
H	-4	HIS	-	expression tag	UNP Q96G97
H	-3	PRO	-	expression tag	UNP Q96G97

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-2	GLN	-	expression tag	UNP Q96G97
H	-1	PHE	-	expression tag	UNP Q96G97
H	0	GLU	-	expression tag	UNP Q96G97
H	1	LYS	-	expression tag	UNP Q96G97
I	-10	MET	-	initiating methionine	UNP Q96G97
I	-9	SER	-	expression tag	UNP Q96G97
I	-8	GLY	-	expression tag	UNP Q96G97
I	-7	ARG	-	expression tag	UNP Q96G97
I	-6	TRP	-	expression tag	UNP Q96G97
I	-5	SER	-	expression tag	UNP Q96G97
I	-4	HIS	-	expression tag	UNP Q96G97
I	-3	PRO	-	expression tag	UNP Q96G97
I	-2	GLN	-	expression tag	UNP Q96G97
I	-1	PHE	-	expression tag	UNP Q96G97
I	0	GLU	-	expression tag	UNP Q96G97
I	1	LYS	-	expression tag	UNP Q96G97
J	-10	MET	-	initiating methionine	UNP Q96G97
J	-9	SER	-	expression tag	UNP Q96G97
J	-8	GLY	-	expression tag	UNP Q96G97
J	-7	ARG	-	expression tag	UNP Q96G97
J	-6	TRP	-	expression tag	UNP Q96G97
J	-5	SER	-	expression tag	UNP Q96G97
J	-4	HIS	-	expression tag	UNP Q96G97
J	-3	PRO	-	expression tag	UNP Q96G97
J	-2	GLN	-	expression tag	UNP Q96G97
J	-1	PHE	-	expression tag	UNP Q96G97
J	0	GLU	-	expression tag	UNP Q96G97
J	1	LYS	-	expression tag	UNP Q96G97
K	-10	MET	-	initiating methionine	UNP Q96G97
K	-9	SER	-	expression tag	UNP Q96G97
K	-8	GLY	-	expression tag	UNP Q96G97
K	-7	ARG	-	expression tag	UNP Q96G97
K	-6	TRP	-	expression tag	UNP Q96G97
K	-5	SER	-	expression tag	UNP Q96G97
K	-4	HIS	-	expression tag	UNP Q96G97
K	-3	PRO	-	expression tag	UNP Q96G97
K	-2	GLN	-	expression tag	UNP Q96G97
K	-1	PHE	-	expression tag	UNP Q96G97
K	0	GLU	-	expression tag	UNP Q96G97
K	1	LYS	-	expression tag	UNP Q96G97

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

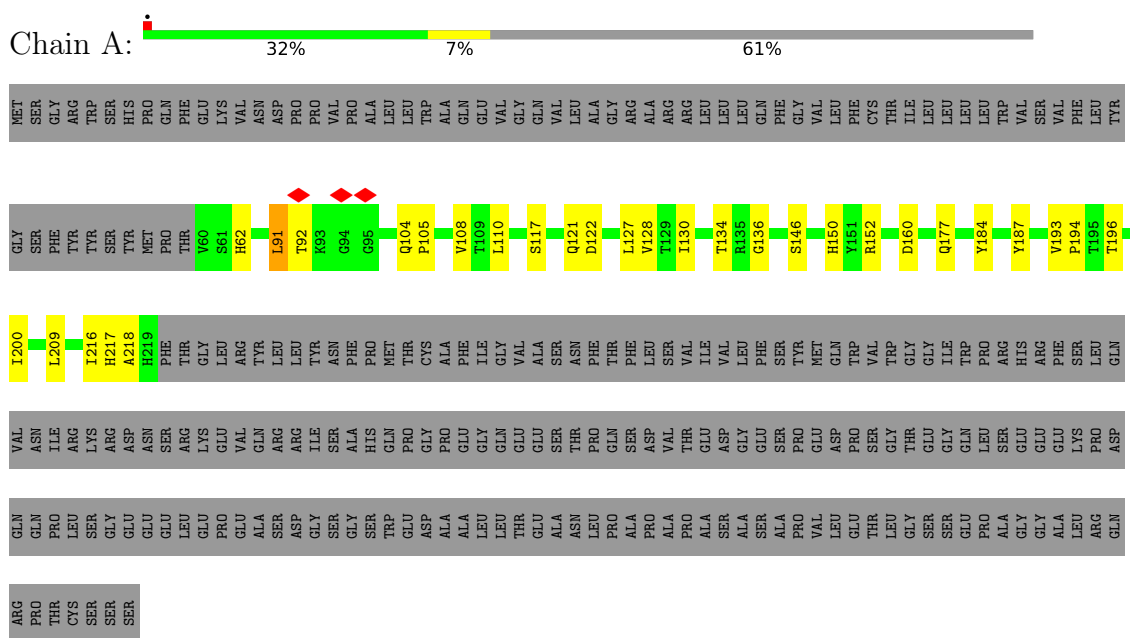


Mol	Chain	Residues	Atoms				AltConf	Trace
2	L	2	Total	C	N	O	0	0
			28	16	2	10		
2	M	2	Total	C	N	O	0	0
			28	16	2	10		
2	N	2	Total	C	N	O	0	0
			28	16	2	10		
2	O	2	Total	C	N	O	0	0
			28	16	2	10		
2	P	2	Total	C	N	O	0	0
			28	16	2	10		
2	Q	2	Total	C	N	O	0	0
			28	16	2	10		
2	R	2	Total	C	N	O	0	0
			28	16	2	10		
2	S	2	Total	C	N	O	0	0
			28	16	2	10		
2	T	2	Total	C	N	O	0	0
			28	16	2	10		
2	U	2	Total	C	N	O	0	0
			28	16	2	10		
2	V	2	Total	C	N	O	0	0
			28	16	2	10		

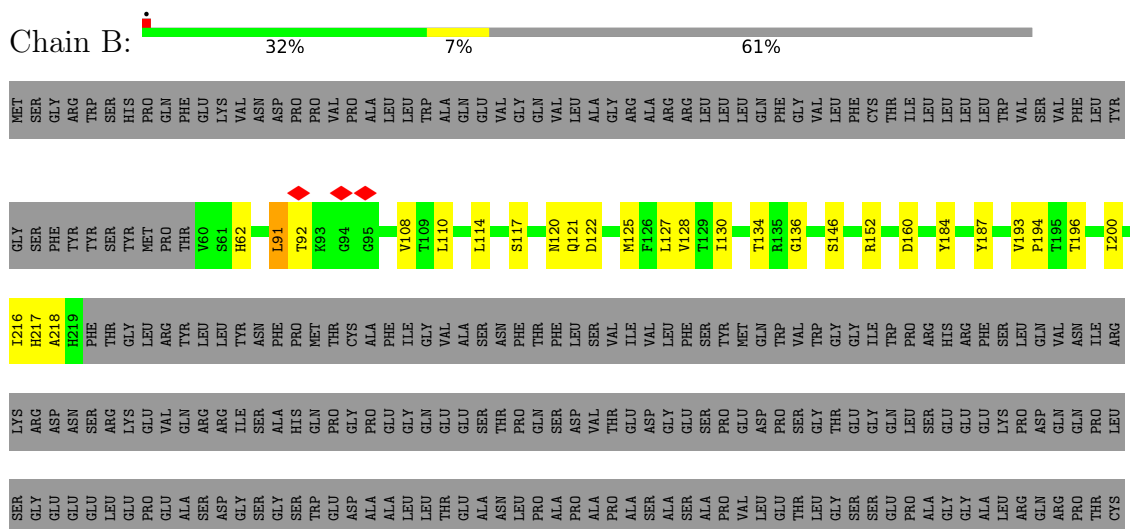
3 Residue-property plots [i](#)

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: Seipin

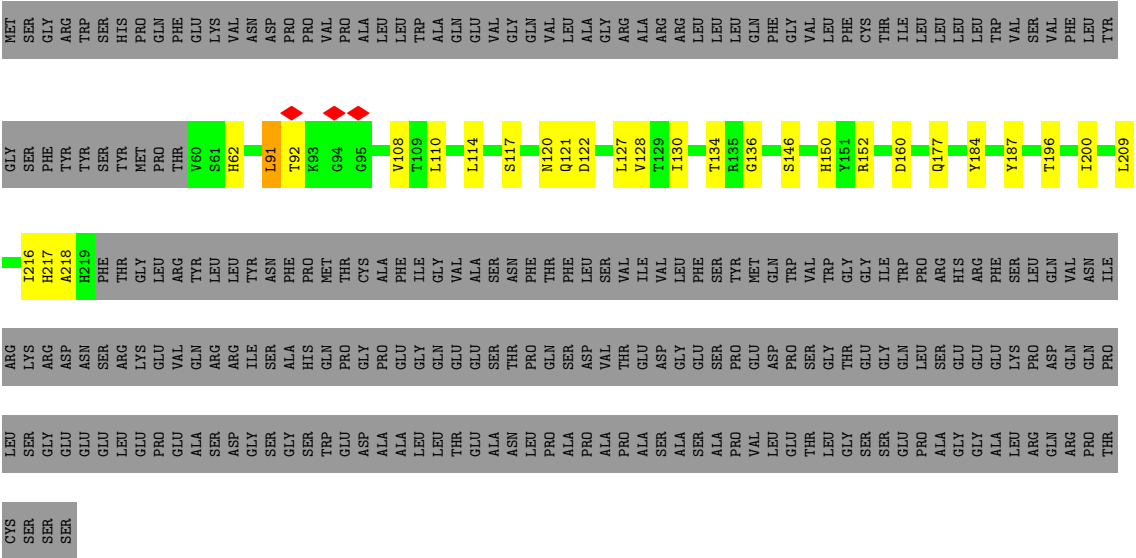


• Molecule 1: Seipin

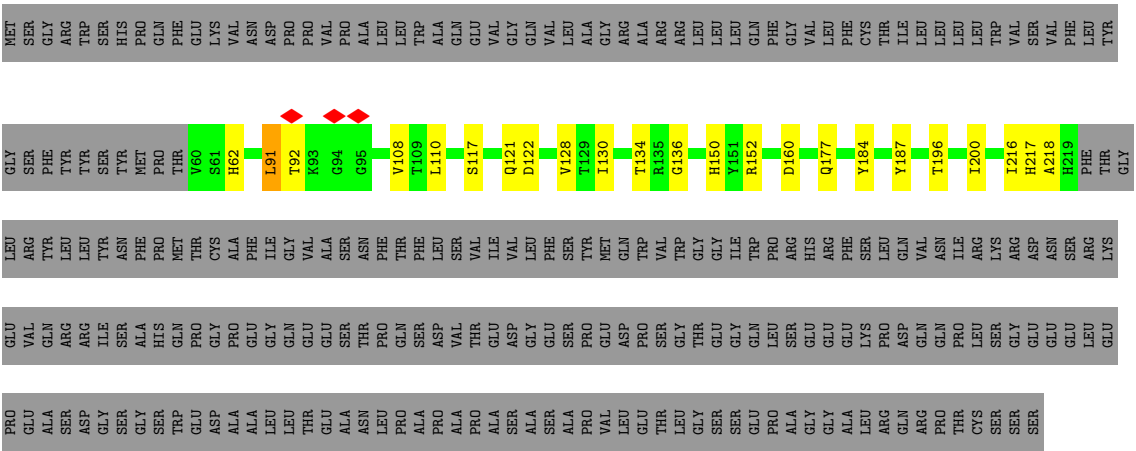


SER
SER
SER

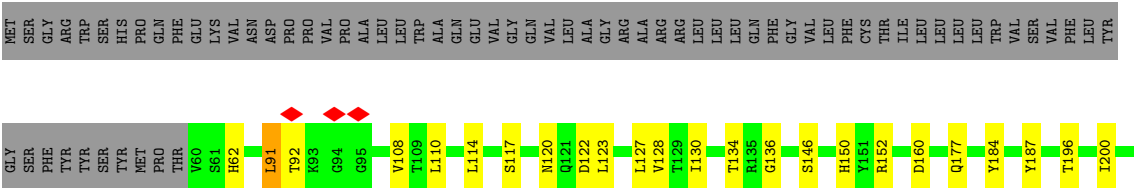
● Molecule 1: Seipin



● Molecule 1: Seipin



● Molecule 1: Seipin



SER SER SER	I216 H217 H218 H219 PHE THR GLY LEU ARG TYR LEU ARG LEU LEU TYR ASN PHE PRO MET THR CYS ALA PHE ILE GLY VAL ALA SER SER ASN PHE THR PHE LEU SER SER VAL ILE VAL LEU PHE SER TYR MET GLN TRP VAL TRP GLY GLY ILE TRP PRO ARG HIS ARG PHE SER LEU GLN VAL ASN PRO ILE ARG																																																									
	LYS	ARG	ASP	ASN	SER	ARG	LYS	GLY	VAL	GLN	ARG	ARG	GLY	ILE	SER	GLY	ASP	GLY	THR	PRO	GLY	ALA	GLY	GLY	THR	GLY	THR	ASN	PRO	GLN	ASP	ALA	VAL	THR	GLY	ASP	GLY	SER	PRO	VAL	GLY	THR	GLY	GLY	GLN	TRP	LEU	GLY	GLY	VAL	ASP	GLN	PRO	THR	LEU			
	GLY	GLY	GLU	GLU	GLU	GLU	GLY	LEU	PRO	GLY	ALA	SER	ARG	ASP	GLY	SER	GLY	THR	GLY	VAL	ALA	ALA	LEU	LEU	THR	GLY	ALA	ASN	ASN	PRO	GLN	ALA	ASP	PRO	ALA	PRO	PRO	GLY	ALA	VAL	THR	GLY	THR	SER	SER	GLY	GLY	GLN	TRP	LEU	GLY	GLY	VAL	ASP	GLN	PRO	THR	CYS

• Molecule 1: Seipin



SER	SER	GLY	GLY	ASP	ARG	GLY	H217	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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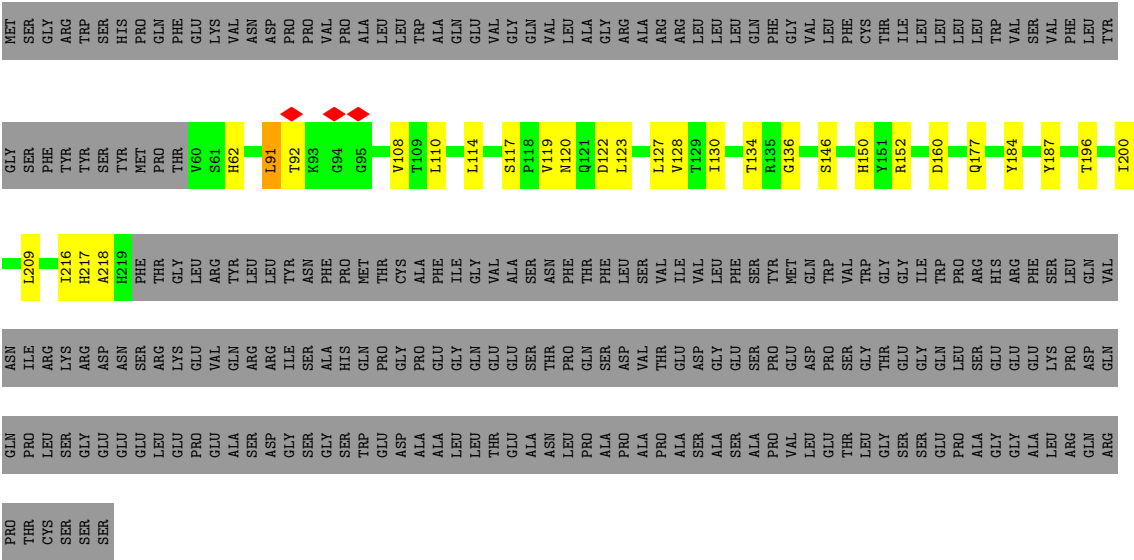
• Molecule 1: Seipin



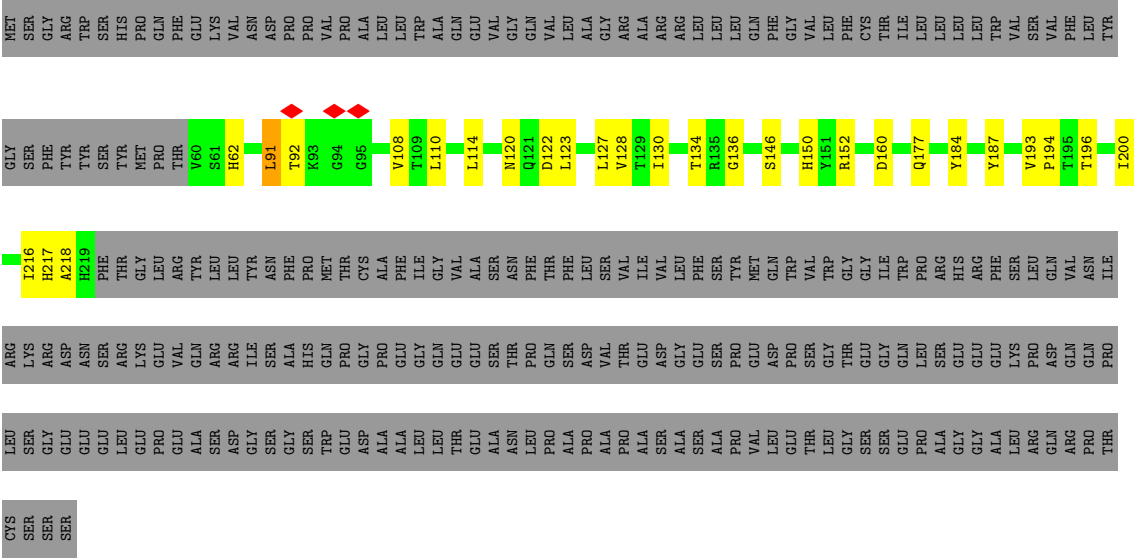
LEU	GLY	LYS	THR	GLY	SER	MET
PRO	GLY	GLY	LEU	PHE	GLY	GLY
GLY	VAL	ARG	ARG	TYR	TYR	ARG
ALA	GLN	TYR	TYR	LEU	SER	SER
SER	ARG	LEU	LEU	LEU	TYR	HIS
ASP	ILE	LEU	TYR	ASN	MET	PRO
GLY	SER	ASN	PHE	THR	PRO	GLN
SER	ALA	PHE	PRO	THR	GLY	PHE
GLY	HIS	GLY	GLY	GLY	V60	LEU
SER	GLN	GLN	PRO	MET	S61	GLN
TRP	PRO	PRO	THR	THR	H62	VAL
ASP	GLY	CYS	ALA	CYS	L91	ASP
ALA	PRO	ALA	PHE	ALA	T92	ASN
ALA	GLY	GLY	ILE	ILE	K93	PRO
LEU	GLY	GLN	GLY	VAL	G94	VAL
LEU	THR	GLY	VAL	ALA	G95	PRO
GLY	GLY	GLY	ALA	SER		ALA
ALA	ASN	THR	ASN	ASN	V108	LEU
LEU	PRO	GLN	PHE	PHE	T109	LEU
PRO	GLN	THR	THR	THR	L110	TRP
ALA	ASP	ASP	PHE	PHE		ALA
PRO	ASP	LEU	LEU	LEU	S117	GLN
ALA	VAL	VAL	SER	SER		VAL
PRO	THR	THR	VAL	VAL	Q121	GLY
ALA	GLY	ILE	ILE	ILE	D122	GLN
SER	ASP	ASP	VAL	VAL		VAL
ALA	GLY	LEU	LEU	LEU	M125	LEU
SER	GLY	PHE	PHE	PHE		ALA
ALA	SER	SER	SER	SER	V128	GLY
PRO	PRO	THR	TYR	TYR	T129	ARG
VAL	VAL	GLY	MET	MET	I130	ALA
LEU	ASP	GLN	GLN	GLN		ARG
GLY	PRO	TRP	TRP	TRP	T134	ARG
THR	PRO	VAL	VAL	VAL	R135	LEU
LEU	GLY	GLY	TRP	TRP	G136	LEU
GLY	THR	THR	GLY	GLY		LEU
SER	SER	GLY	GLY	GLY	H150	GLN
SER	GLY	ILE	ILE	ILE	Y151	PHE
GLY	GLN	TRP	TRP	TRP	R152	GLY
PRO	LEU	PRO	PRO	PRO		VAL
ALA	SER	GLY	HIS	ARG	D160	LEU
GLY	GLY	GLY	ARG	ARG		PHE
GLY	ALA	GLY	PHE	PHE	Q177	CYS
LEU	LEU	LYS	SER	SER	Y184	THR
ARG	PRO	PRO	LEU	LEU		ILE
GLN	ASP	ASN	GLN	GLN	Y187	LEU
ARG	GLN	GLN	VAL	VAL		LEU
PRO	PRO	GLN	ASN	ASN	T196	LEU
THR	PRO	PRO	ILE	ILE		TRP
CYS	CYS	LEU	ARG	ARG	I200	VAL
SER	SER	LYS	LYS	LYS		SER
SER	GLY	ARG	ARG	ARG	I216	VAL
SER	GLY	GLY	ASP	ASP	H217	PHE
SER	GLY	ASN	ASN	ASN	A218	LEU
SER	GLY	SER	SER	SER	H219	TVR

• Molecule 1: Seipin

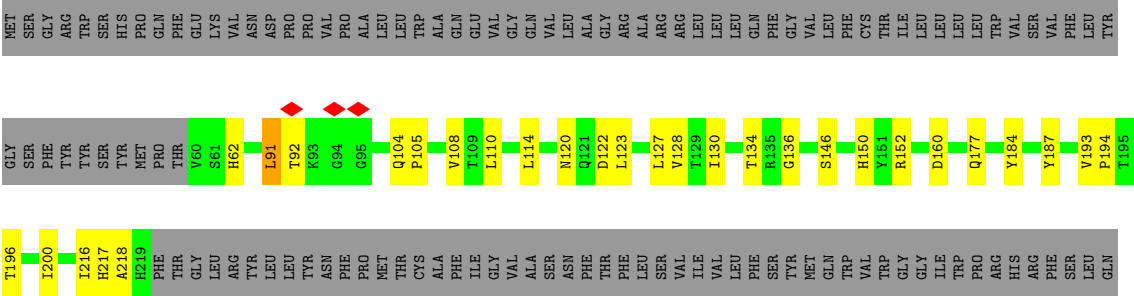


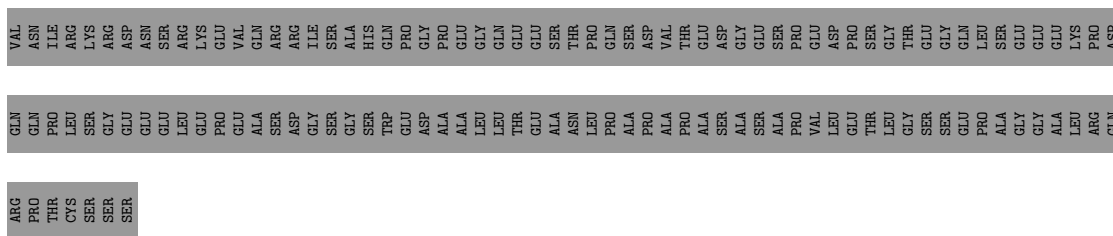


• Molecule 1: Seipin

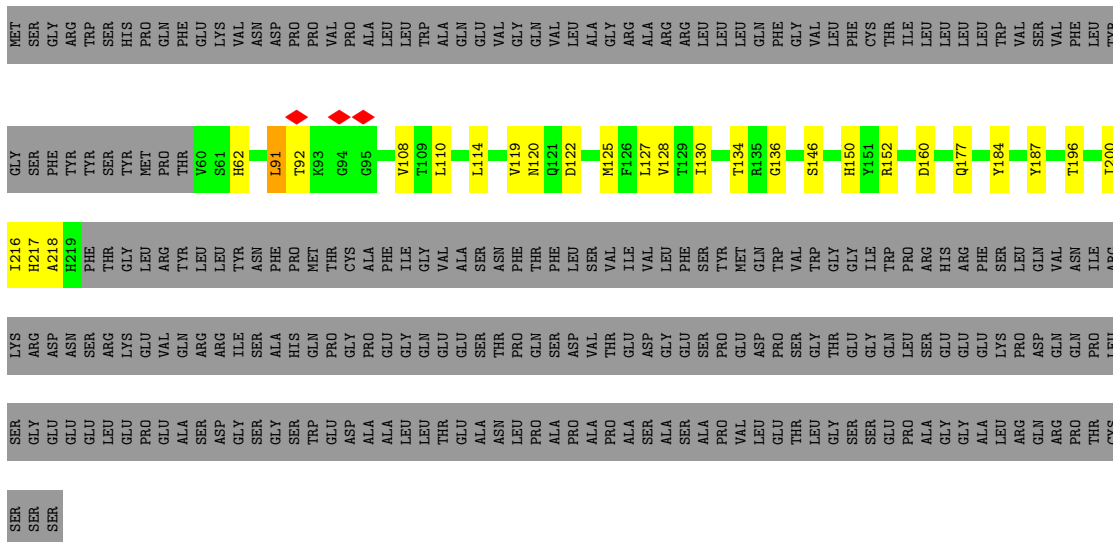


• Molecule 1: Seipin





- Molecule 1: Seipin



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



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



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



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

Chain O:  50% 50%

MAG1
MAG2

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

Chain P:  50% 50%

MAG1
MAG2

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

Chain Q:  50% 50%

MAG1
MAG2

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

Chain R:  50% 50%

MAG1
MAG2

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

Chain S:  50% 50%

MAG1
MAG2

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

Chain T:  50% 50%

MAG1
MAG2

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

Chain U:  50% 50%



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

Chain V:
The bar is a horizontal line divided into two equal halves. The left half is yellow and labeled '50%' below it. The right half is orange and labeled '50%' below it.



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	99281	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.495	Depositor
Minimum map value	-0.298	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	316.8, 316.8, 316.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.88, 0.88, 0.88	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.48	0/1269	0.80	3/1725 (0.2%)
1	B	0.48	0/1269	0.81	3/1725 (0.2%)
1	C	0.48	0/1269	0.81	3/1725 (0.2%)
1	D	0.48	0/1269	0.80	3/1725 (0.2%)
1	E	0.48	0/1269	0.77	1/1725 (0.1%)
1	F	0.48	0/1269	0.81	3/1725 (0.2%)
1	G	0.48	0/1269	0.80	3/1725 (0.2%)
1	H	0.48	0/1269	0.77	2/1725 (0.1%)
1	I	0.48	0/1269	0.78	3/1725 (0.2%)
1	J	0.47	0/1269	0.77	1/1725 (0.1%)
1	K	0.48	0/1269	0.78	2/1725 (0.1%)
All	All	0.48	0/13959	0.79	27/18975 (0.1%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	G	122	ASP	N-CA-C	9.23	120.94	111.07
1	C	122	ASP	N-CA-C	9.15	120.86	111.07
1	F	122	ASP	N-CA-C	9.12	120.83	111.07
1	B	122	ASP	N-CA-C	9.01	120.70	111.07
1	A	122	ASP	N-CA-C	8.94	120.64	111.07

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1242	0	1197	16	0
1	B	1242	0	1197	15	0
1	C	1242	0	1197	15	0
1	D	1242	0	1197	12	0
1	E	1242	0	1197	15	0
1	F	1242	0	1197	14	0
1	G	1242	0	1197	13	0
1	H	1242	0	1197	16	0
1	I	1242	0	1197	16	0
1	J	1242	0	1197	17	0
1	K	1242	0	1197	15	0
2	L	28	0	25	1	0
2	M	28	0	25	1	0
2	N	28	0	25	1	0
2	O	28	0	25	1	0
2	P	28	0	25	1	0
2	Q	28	0	25	1	0
2	R	28	0	25	1	0
2	S	28	0	25	1	0
2	T	28	0	25	1	0
2	U	28	0	25	1	0
2	V	28	0	25	1	0
All	All	13970	0	13442	161	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 6.

The worst 5 of 161 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:184:TYR:HB3	1:I:187:TYR:HB2	1.81	0.63
1:H:184:TYR:HB3	1:H:187:TYR:HB2	1.81	0.62
1:K:184:TYR:HB3	1:K:187:TYR:HB2	1.81	0.62
1:D:184:TYR:HB3	1:D:187:TYR:HB2	1.81	0.62
1:E:184:TYR:HB3	1:E:187:TYR:HB2	1.81	0.62

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	B	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	C	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	D	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	E	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	F	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	G	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	H	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	I	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	J	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
1	K	158/409 (39%)	136 (86%)	22 (14%)	0	100	100
All	All	1738/4499 (39%)	1496 (86%)	242 (14%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	136/356 (38%)	133 (98%)	3 (2%)	45	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	136/356 (38%)	133 (98%)	3 (2%)	45	63
1	C	136/356 (38%)	133 (98%)	3 (2%)	45	63
1	D	136/356 (38%)	133 (98%)	3 (2%)	45	63
1	E	136/356 (38%)	133 (98%)	3 (2%)	45	63
1	F	136/356 (38%)	133 (98%)	3 (2%)	45	63
1	G	136/356 (38%)	133 (98%)	3 (2%)	45	63
1	H	136/356 (38%)	133 (98%)	3 (2%)	45	63
1	I	136/356 (38%)	134 (98%)	2 (2%)	57	69
1	J	136/356 (38%)	134 (98%)	2 (2%)	57	69
1	K	136/356 (38%)	134 (98%)	2 (2%)	57	69
All	All	1496/3916 (38%)	1466 (98%)	30 (2%)	48	65

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	128	VAL
1	J	128	VAL
1	F	128	VAL
1	K	128	VAL
1	I	91	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	67	HIS
1	H	67	HIS
1	K	120	ASN
1	J	67	HIS
1	K	67	HIS

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 ⓘ

22 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	$\# Z > 2$
2	NAG	L	1	2,1	14,14,15	0.46	0	17,19,21	1.72	1 (5%)
2	NAG	L	2	2	14,14,15	0.48	0	17,19,21	0.71	1 (5%)
2	NAG	M	1	2,1	14,14,15	0.46	0	17,19,21	1.73	1 (5%)
2	NAG	M	2	2	14,14,15	0.48	0	17,19,21	0.72	1 (5%)
2	NAG	N	1	2,1	14,14,15	0.46	0	17,19,21	1.72	1 (5%)
2	NAG	N	2	2	14,14,15	0.49	0	17,19,21	0.71	1 (5%)
2	NAG	O	1	2,1	14,14,15	0.46	0	17,19,21	1.73	1 (5%)
2	NAG	O	2	2	14,14,15	0.49	0	17,19,21	0.71	1 (5%)
2	NAG	P	1	2,1	14,14,15	0.47	0	17,19,21	1.72	1 (5%)
2	NAG	P	2	2	14,14,15	0.48	0	17,19,21	0.72	1 (5%)
2	NAG	Q	1	2,1	14,14,15	0.47	0	17,19,21	1.71	1 (5%)
2	NAG	Q	2	2	14,14,15	0.49	0	17,19,21	0.72	1 (5%)
2	NAG	R	1	2,1	14,14,15	0.48	0	17,19,21	1.72	1 (5%)
2	NAG	R	2	2	14,14,15	0.47	0	17,19,21	0.72	1 (5%)
2	NAG	S	1	2,1	14,14,15	0.47	0	17,19,21	1.72	1 (5%)
2	NAG	S	2	2	14,14,15	0.48	0	17,19,21	0.72	1 (5%)
2	NAG	T	1	2,1	14,14,15	0.48	0	17,19,21	1.72	1 (5%)
2	NAG	T	2	2	14,14,15	0.48	0	17,19,21	0.72	1 (5%)
2	NAG	U	1	2,1	14,14,15	0.46	0	17,19,21	1.72	1 (5%)
2	NAG	U	2	2	14,14,15	0.49	0	17,19,21	0.72	1 (5%)
2	NAG	V	1	2,1	14,14,15	0.47	0	17,19,21	1.72	1 (5%)
2	NAG	V	2	2	14,14,15	0.48	0	17,19,21	0.72	1 (5%)

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
2	NAG	L	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	L	2	2	-	1/6/23/26	0/1/1/1
2	NAG	M	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	M	2	2	-	1/6/23/26	0/1/1/1
2	NAG	N	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	N	2	2	-	1/6/23/26	0/1/1/1
2	NAG	O	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	O	2	2	-	1/6/23/26	0/1/1/1
2	NAG	P	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	P	2	2	-	1/6/23/26	0/1/1/1
2	NAG	Q	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	Q	2	2	-	1/6/23/26	0/1/1/1
2	NAG	R	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	R	2	2	-	1/6/23/26	0/1/1/1
2	NAG	S	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	S	2	2	-	1/6/23/26	0/1/1/1
2	NAG	T	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	T	2	2	-	1/6/23/26	0/1/1/1
2	NAG	U	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	U	2	2	-	1/6/23/26	0/1/1/1
2	NAG	V	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	V	2	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	1	NAG	C1-O5-C5	6.54	120.95	112.19
2	M	1	NAG	C1-O5-C5	6.53	120.93	112.19
2	N	1	NAG	C1-O5-C5	6.52	120.92	112.19
2	U	1	NAG	C1-O5-C5	6.52	120.92	112.19
2	P	1	NAG	C1-O5-C5	6.51	120.92	112.19

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

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

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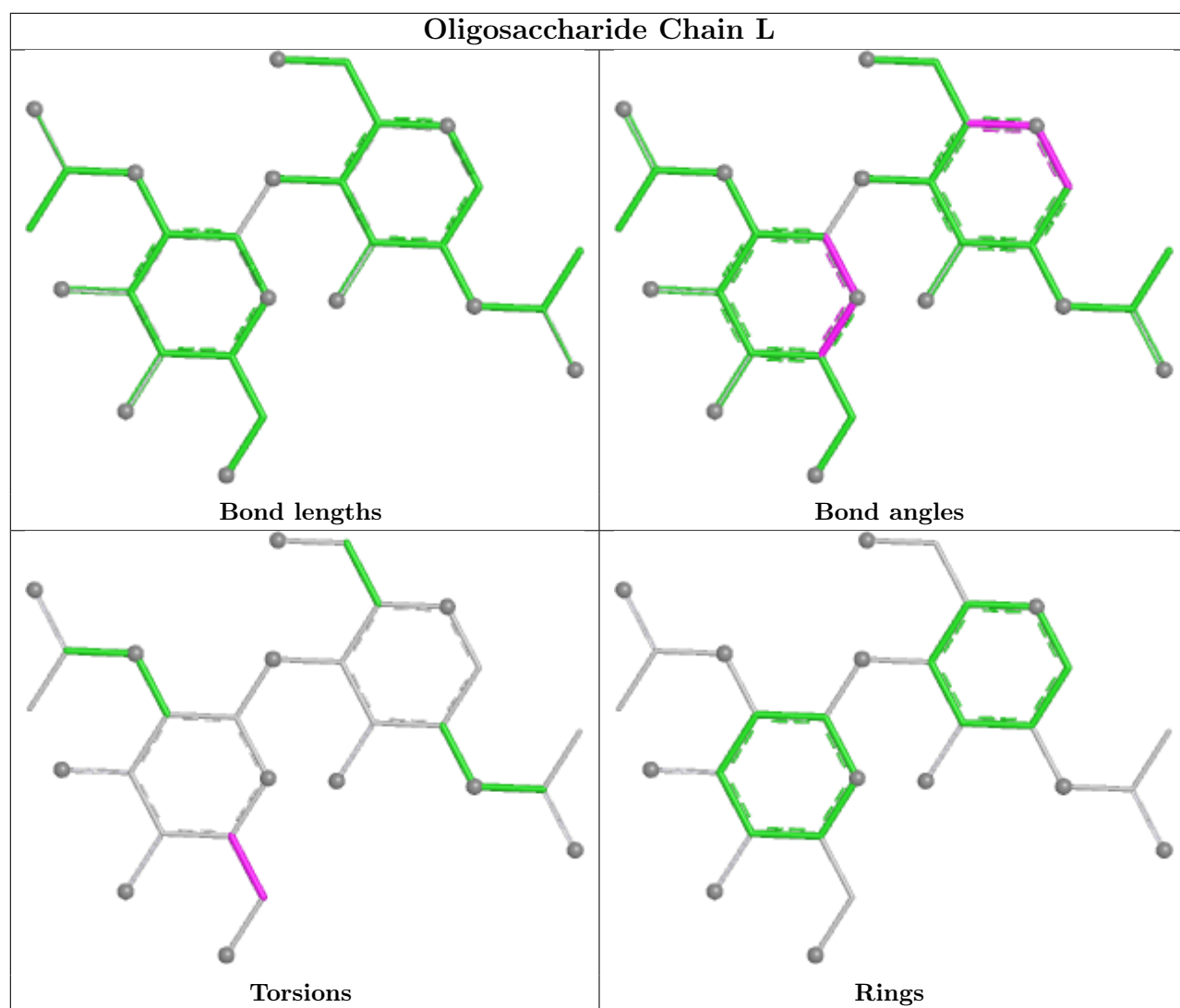
Mol	Chain	Res	Type	Atoms
2	M	2	NAG	O5-C5-C6-O6
2	O	2	NAG	O5-C5-C6-O6
2	Q	2	NAG	O5-C5-C6-O6
2	R	2	NAG	O5-C5-C6-O6

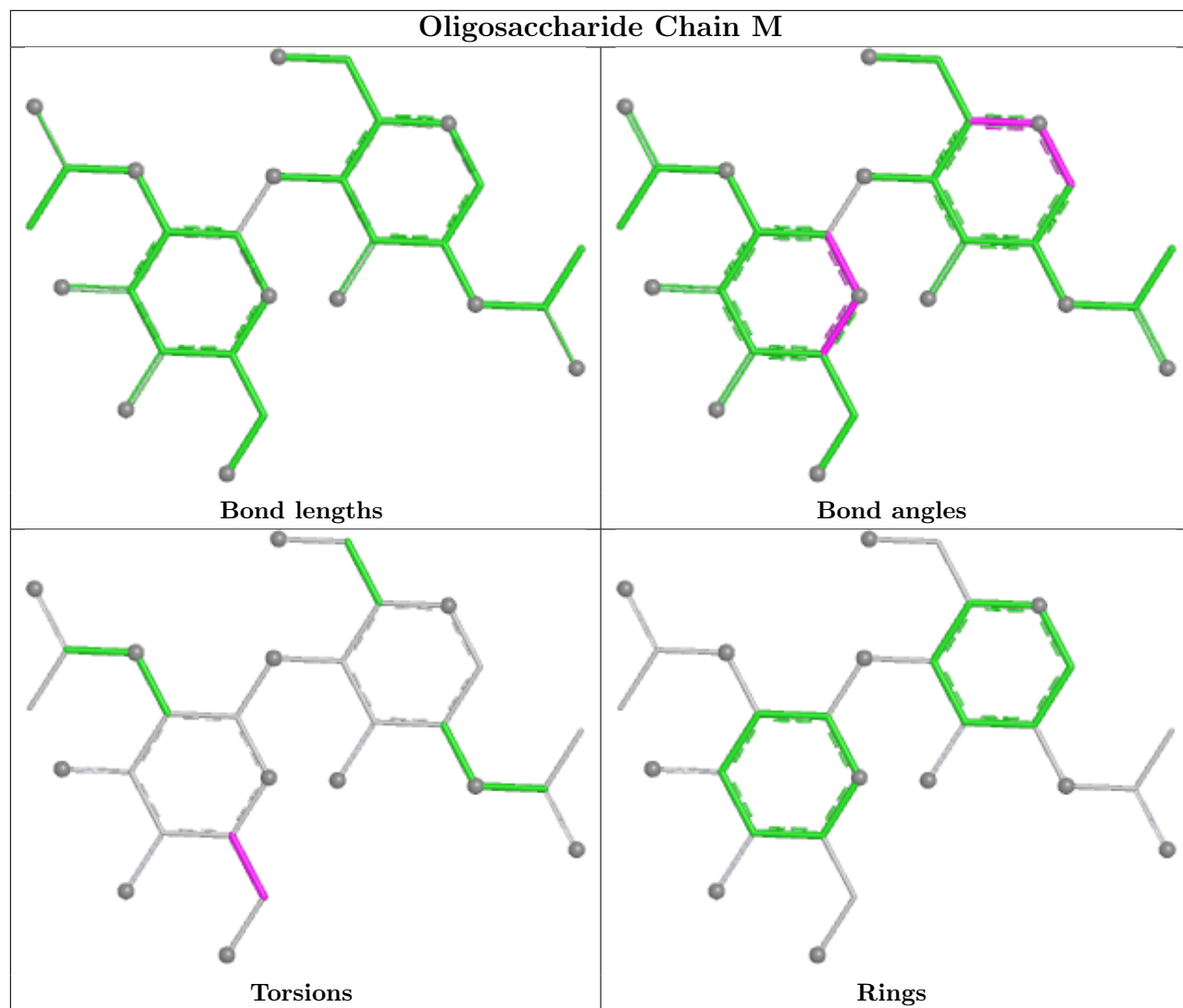
There are no ring outliers.

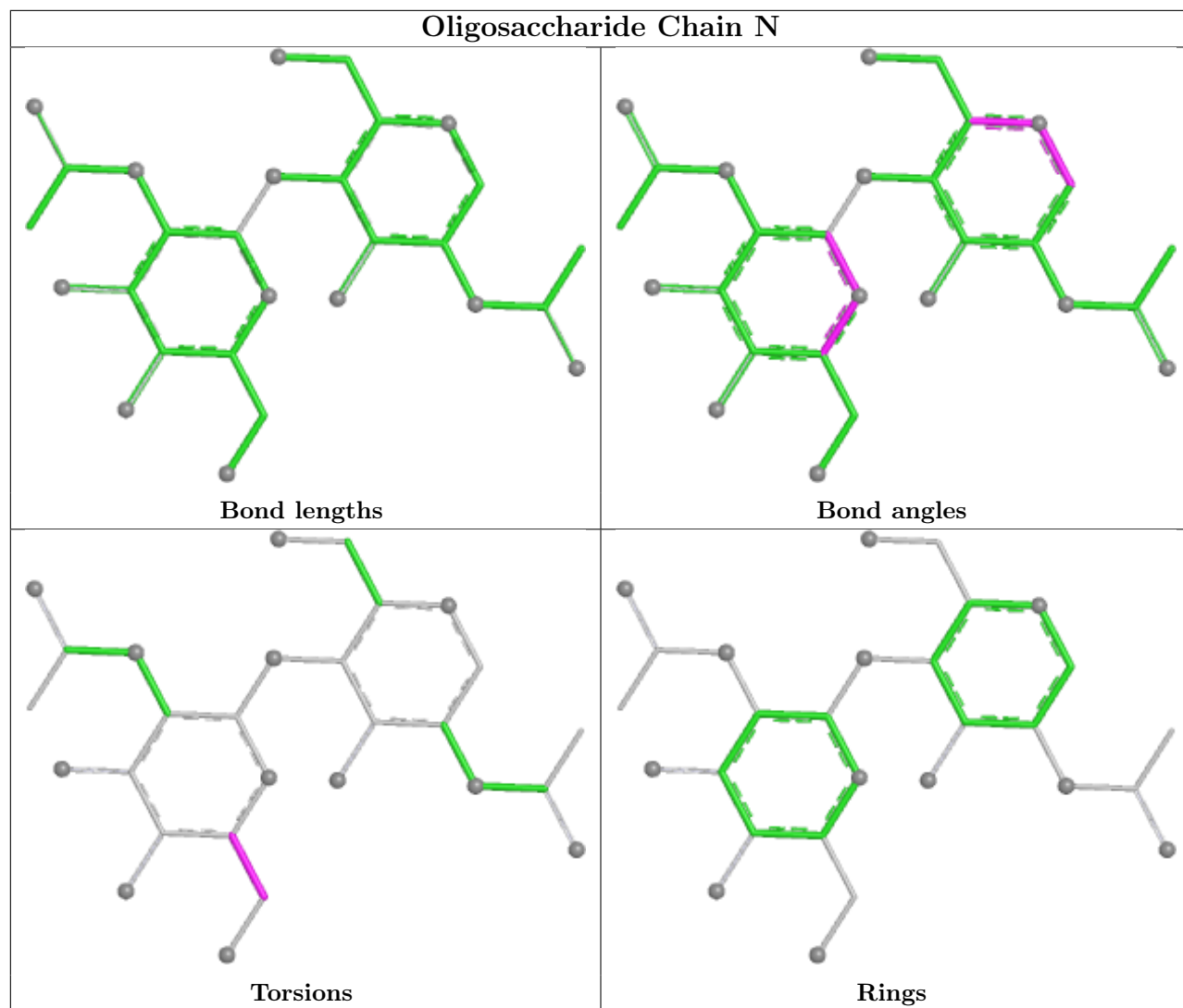
11 monomers are involved in 11 short contacts:

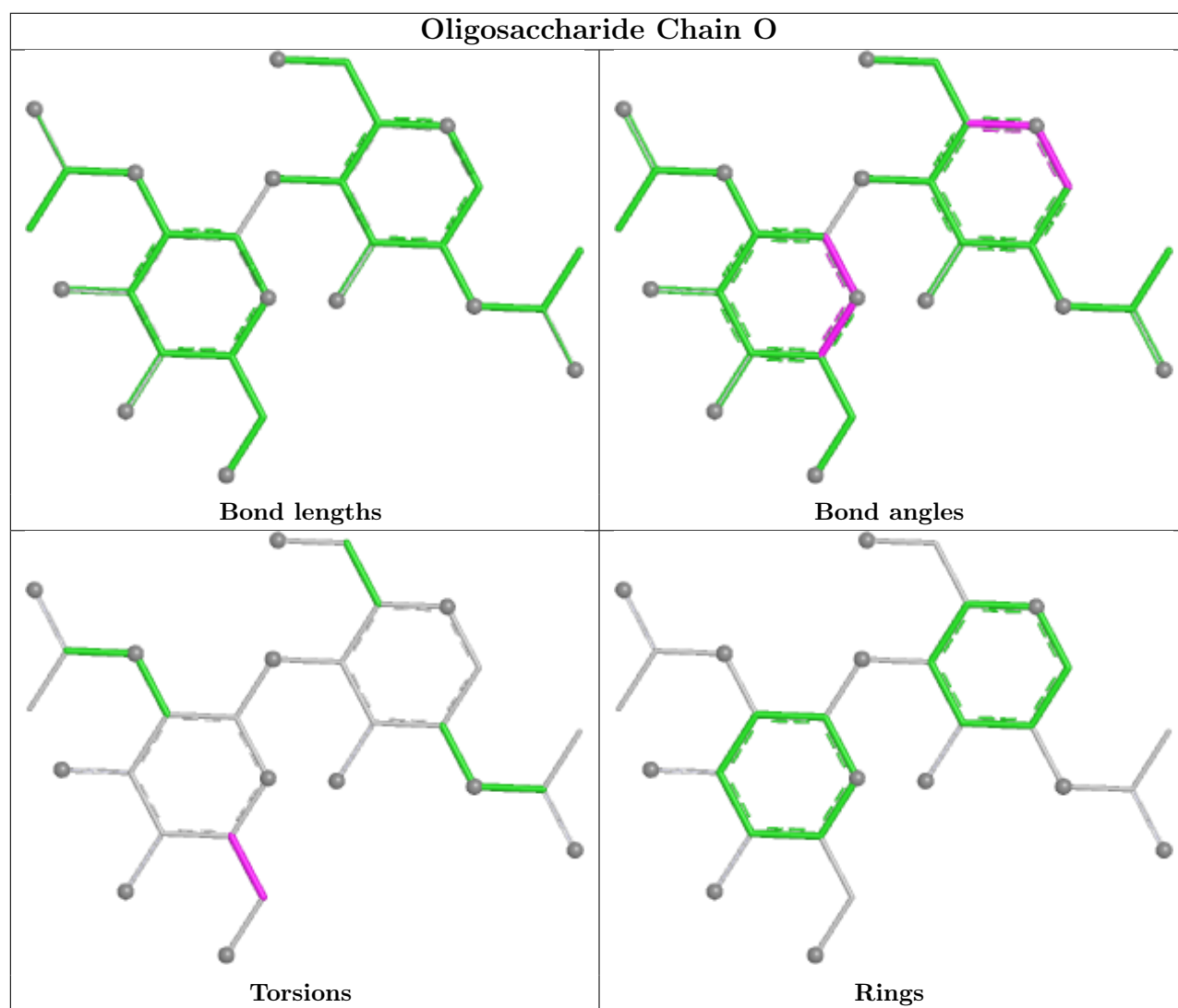
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	2	NAG	1	0
2	T	2	NAG	1	0
2	R	2	NAG	1	0
2	Q	2	NAG	1	0
2	S	2	NAG	1	0
2	P	2	NAG	1	0
2	U	2	NAG	1	0
2	N	2	NAG	1	0
2	V	2	NAG	1	0
2	M	2	NAG	1	0
2	L	2	NAG	1	0

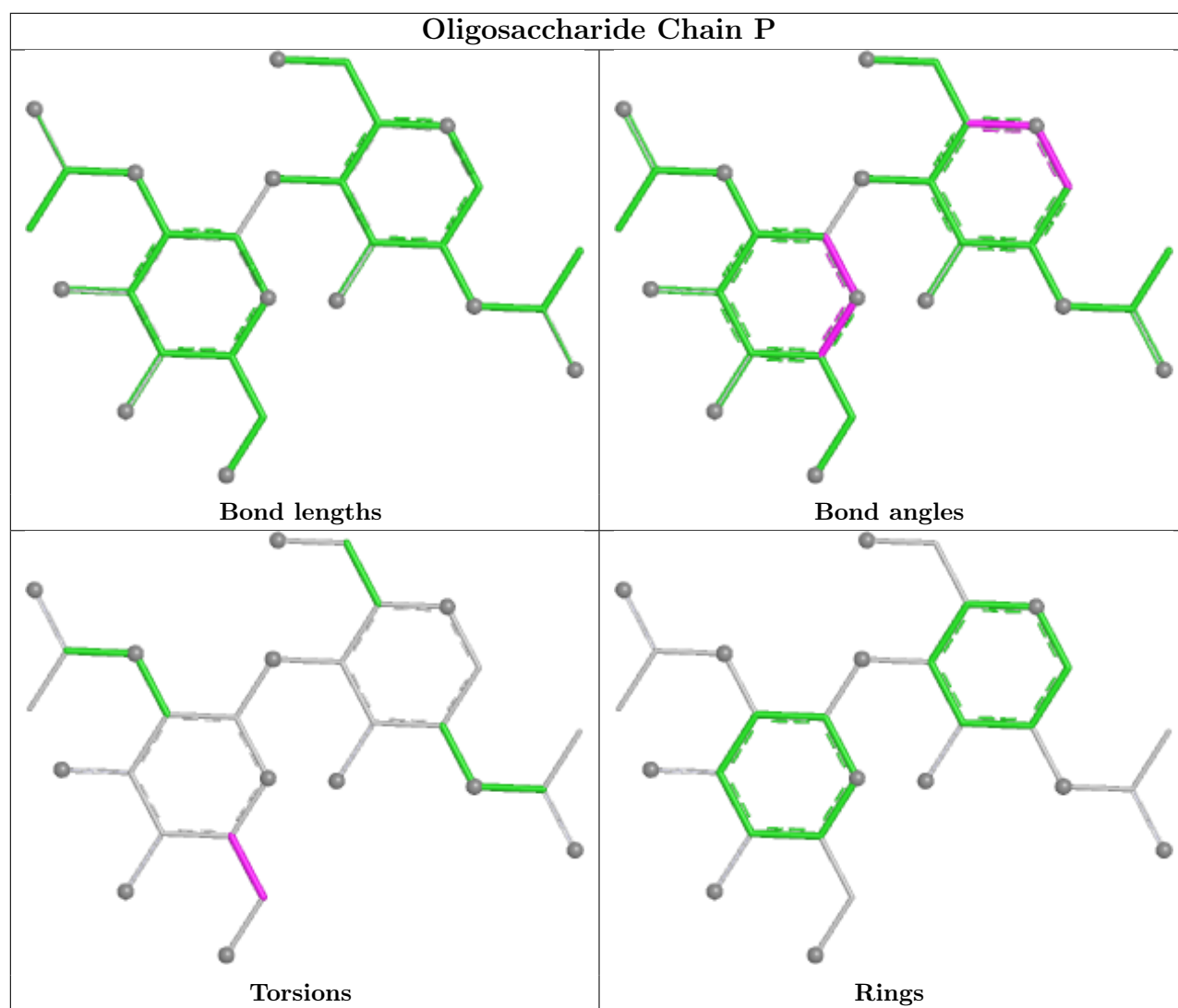
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

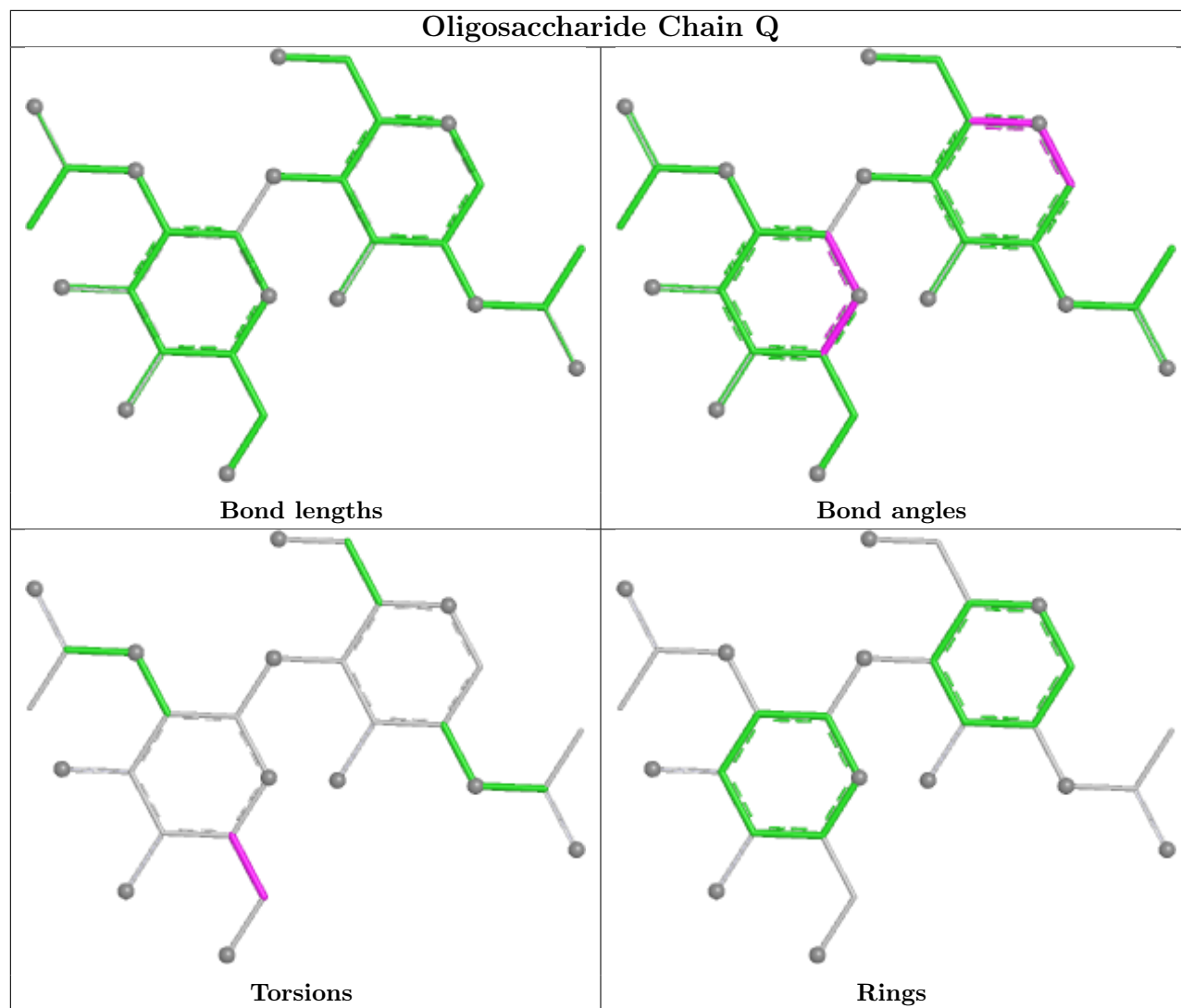


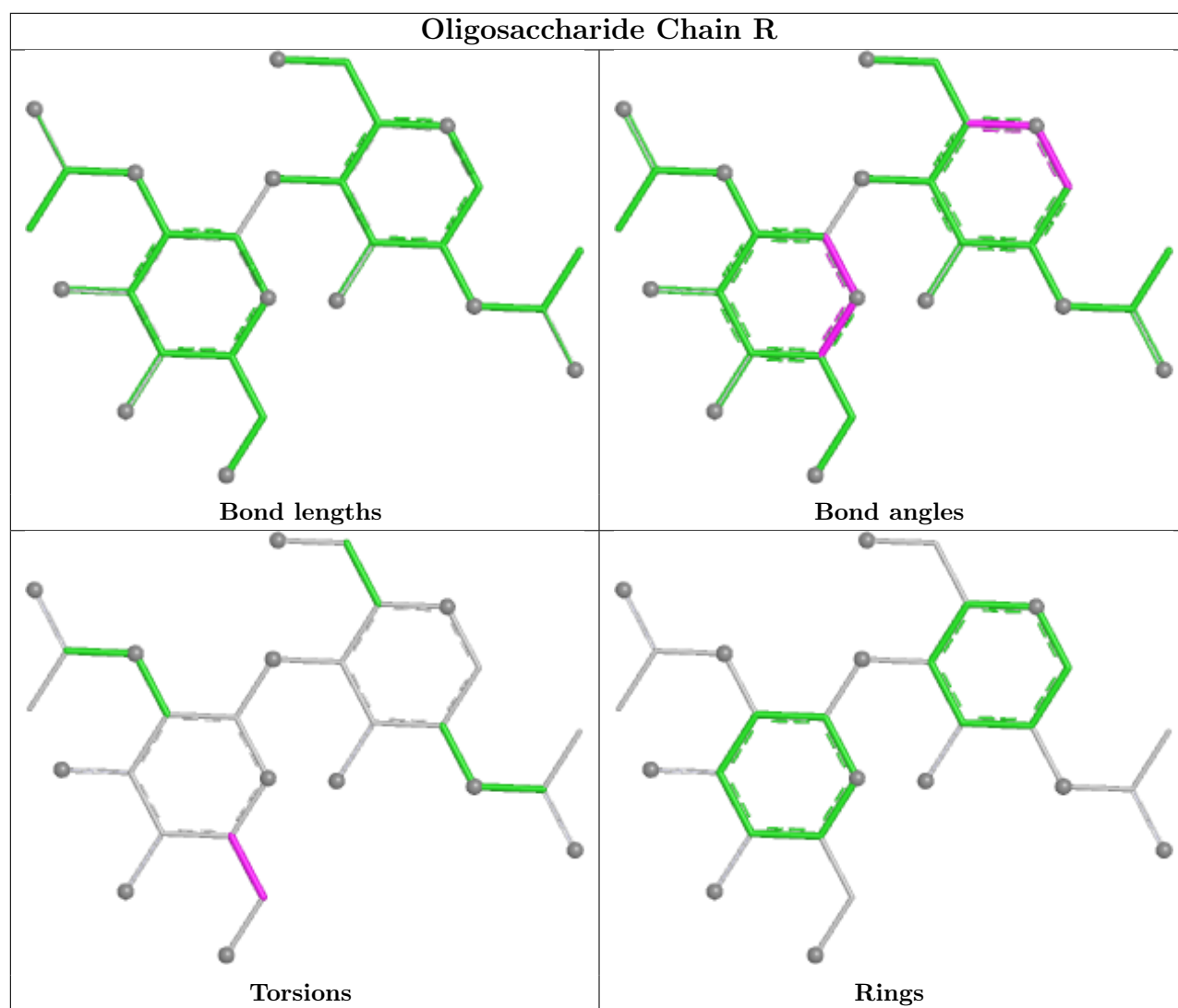


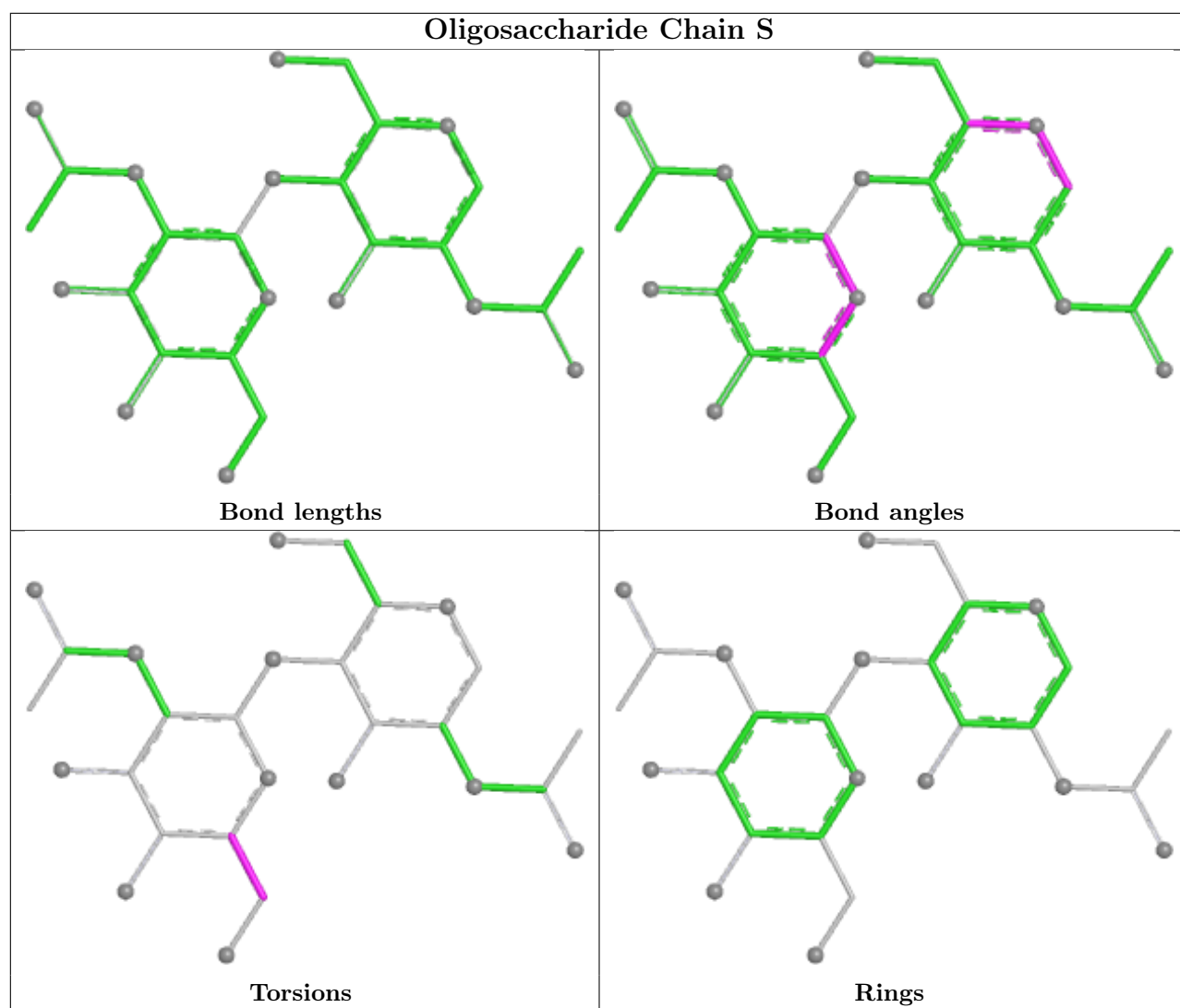


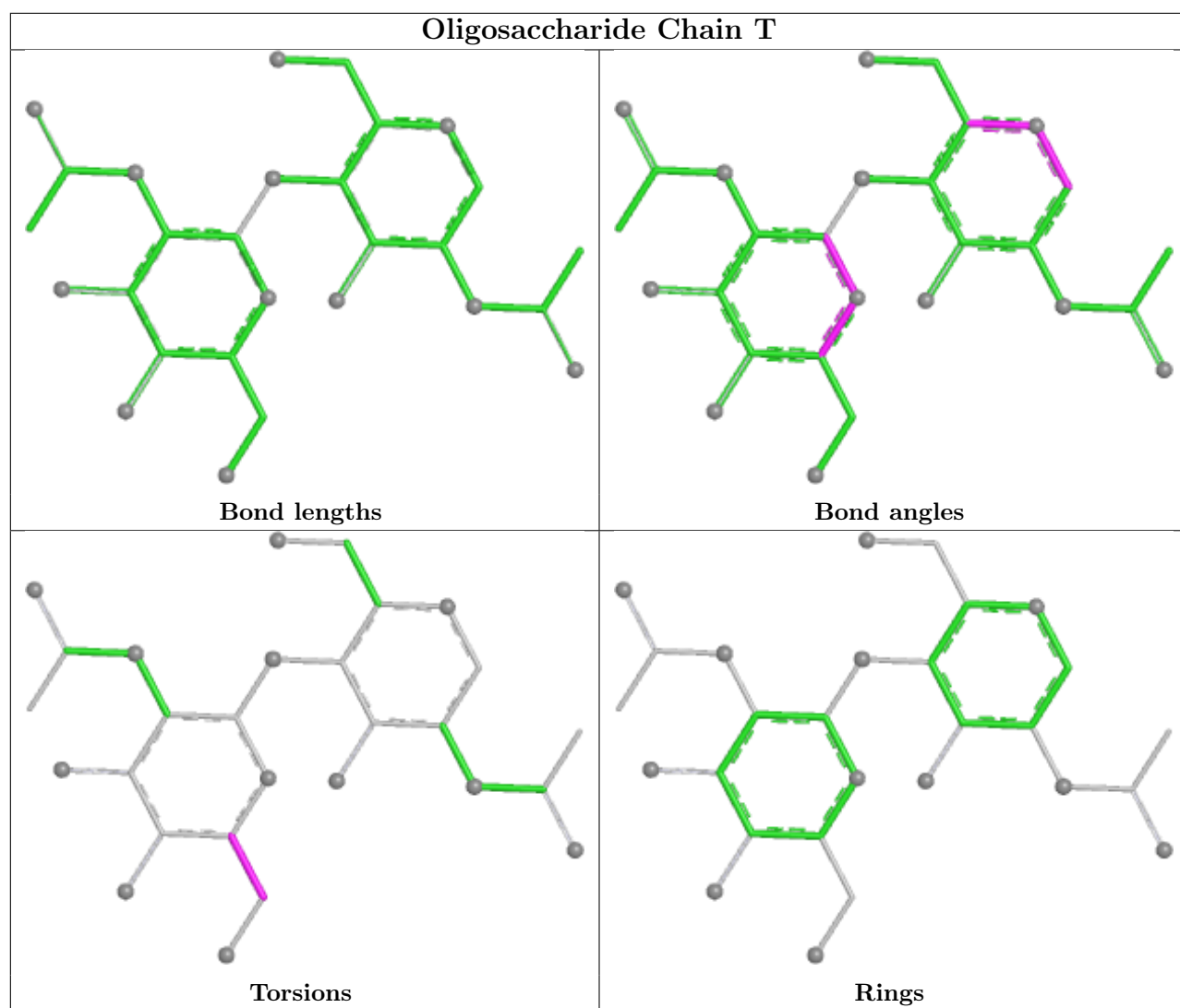


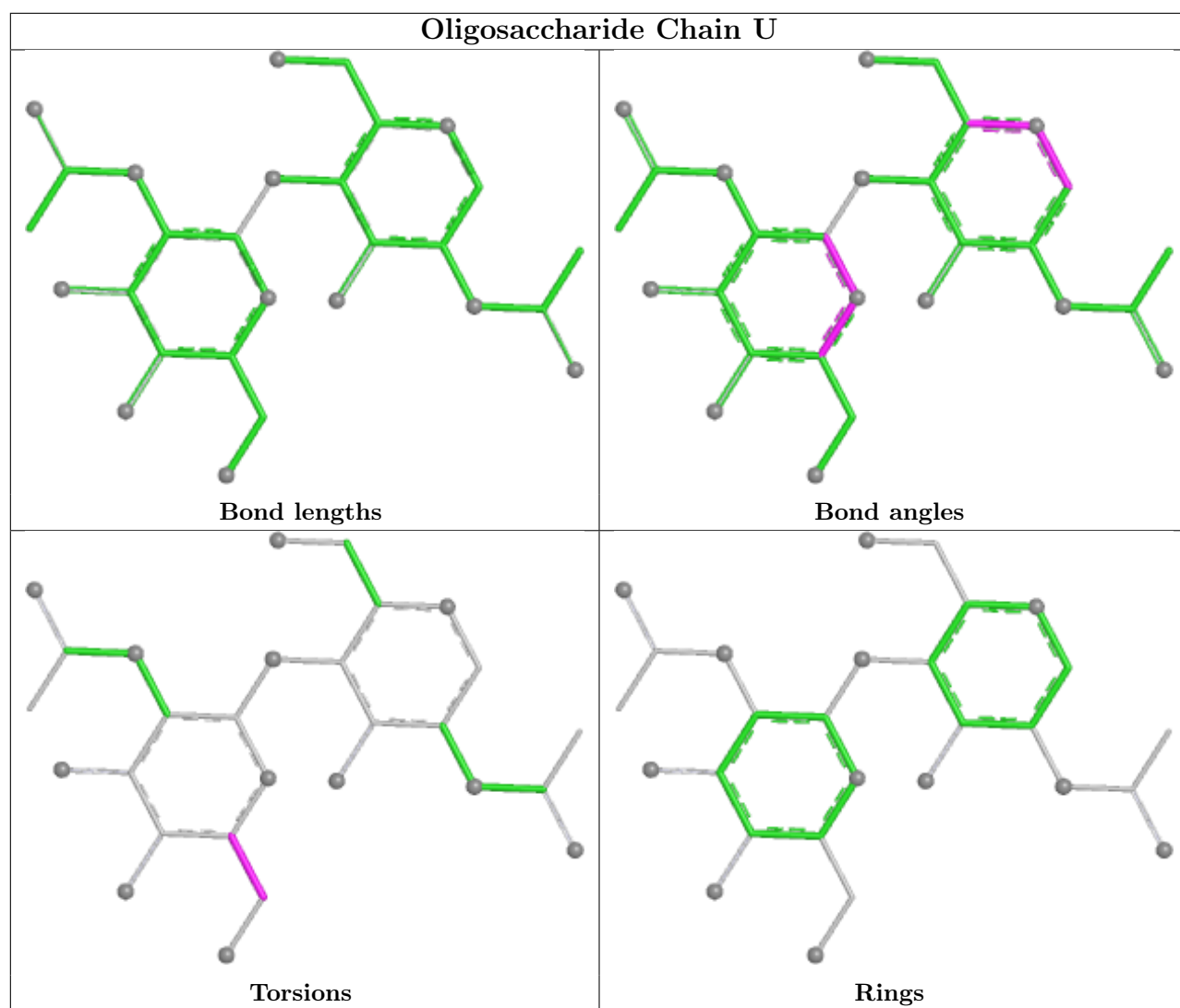


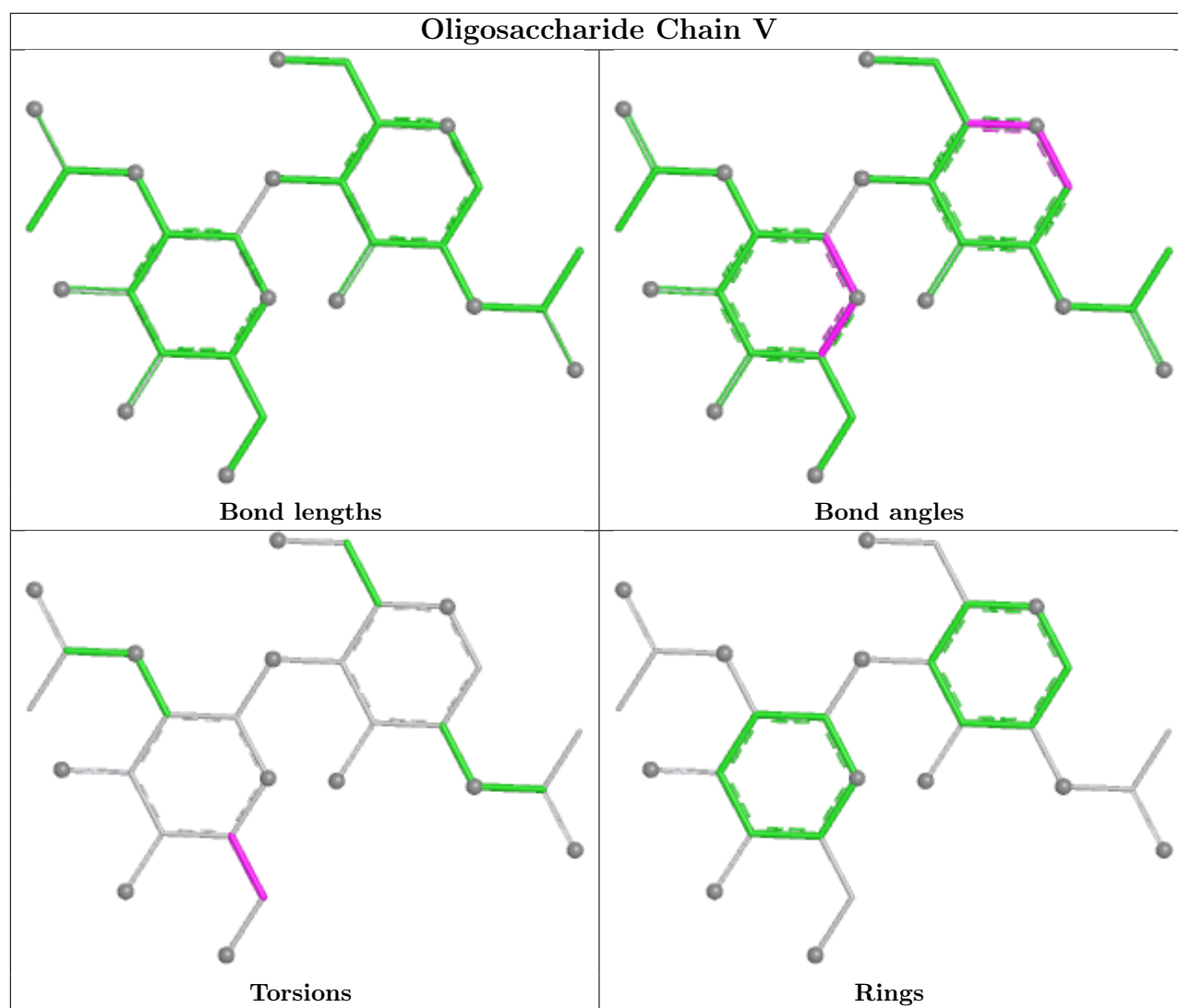












5.6 Ligand geometry [i](#)

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.

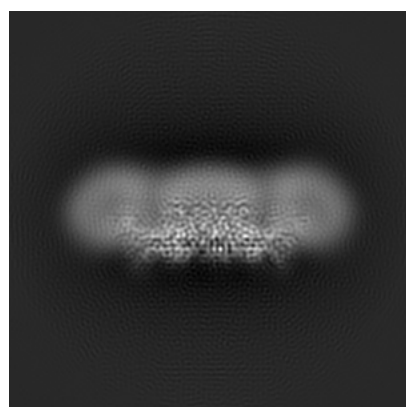
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8909. These allow visual inspection of the internal detail of the map and identification of artifacts.

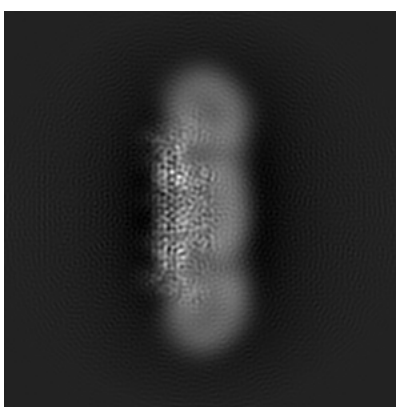
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

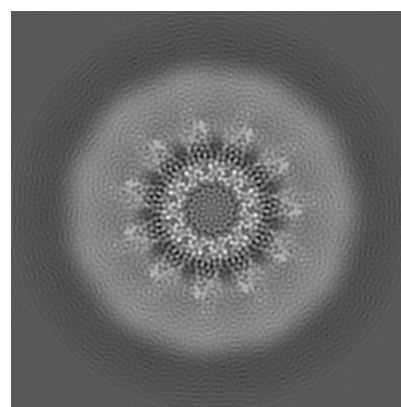
6.1.1 Primary map



X



Y

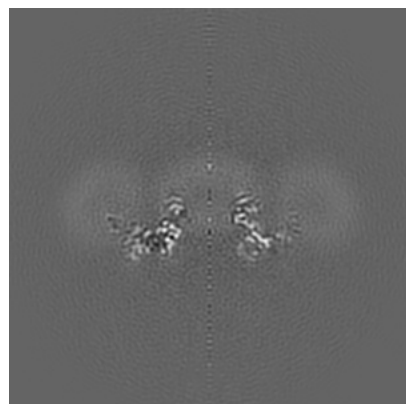


Z

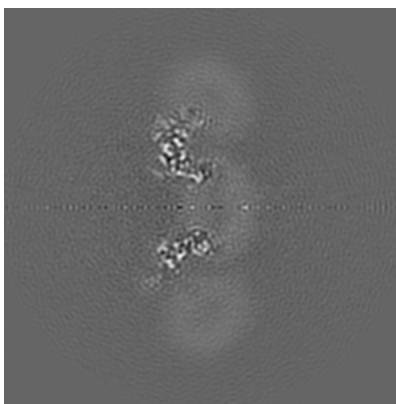
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

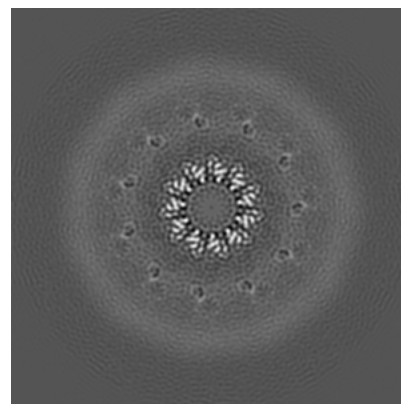
6.2.1 Primary map



X Index: 180



Y Index: 180

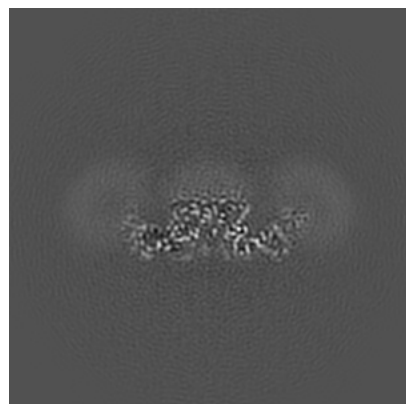


Z Index: 180

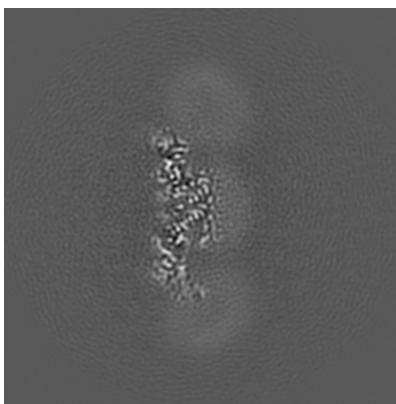
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

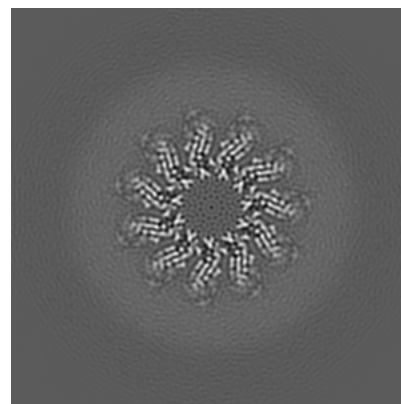
6.3.1 Primary map



X Index: 207



Y Index: 153

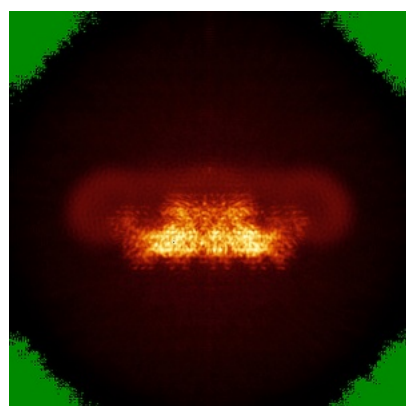


Z Index: 156

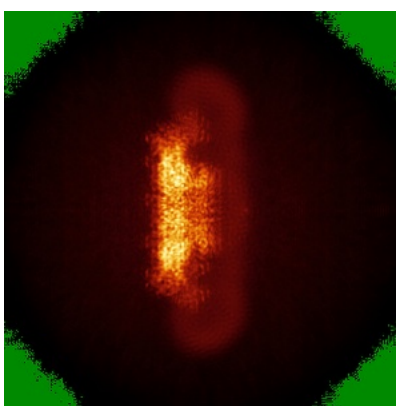
The images above show the largest variance slices of the map in three orthogonal directions.

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

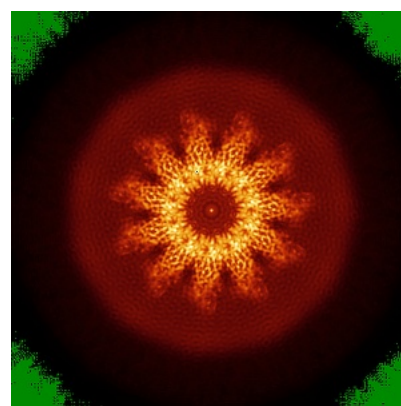
6.4.1 Primary map



X



Y

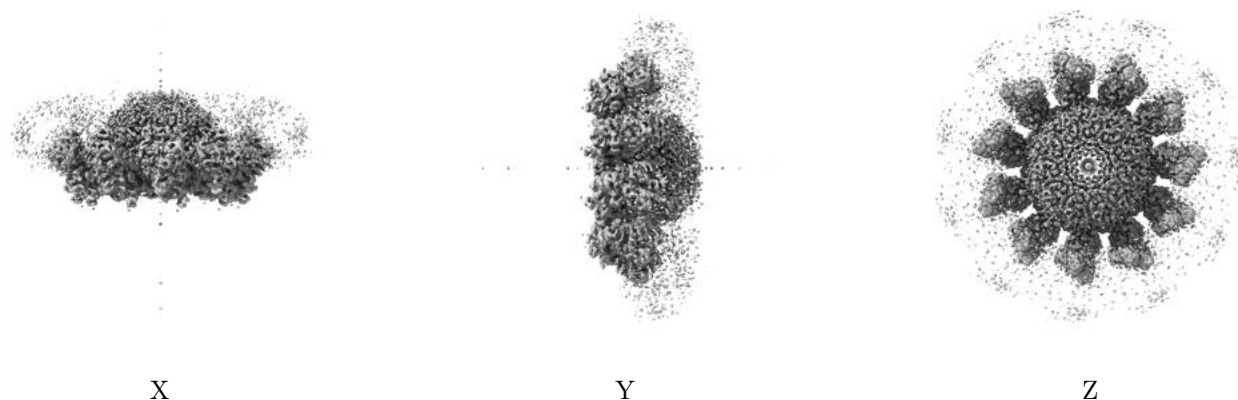


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

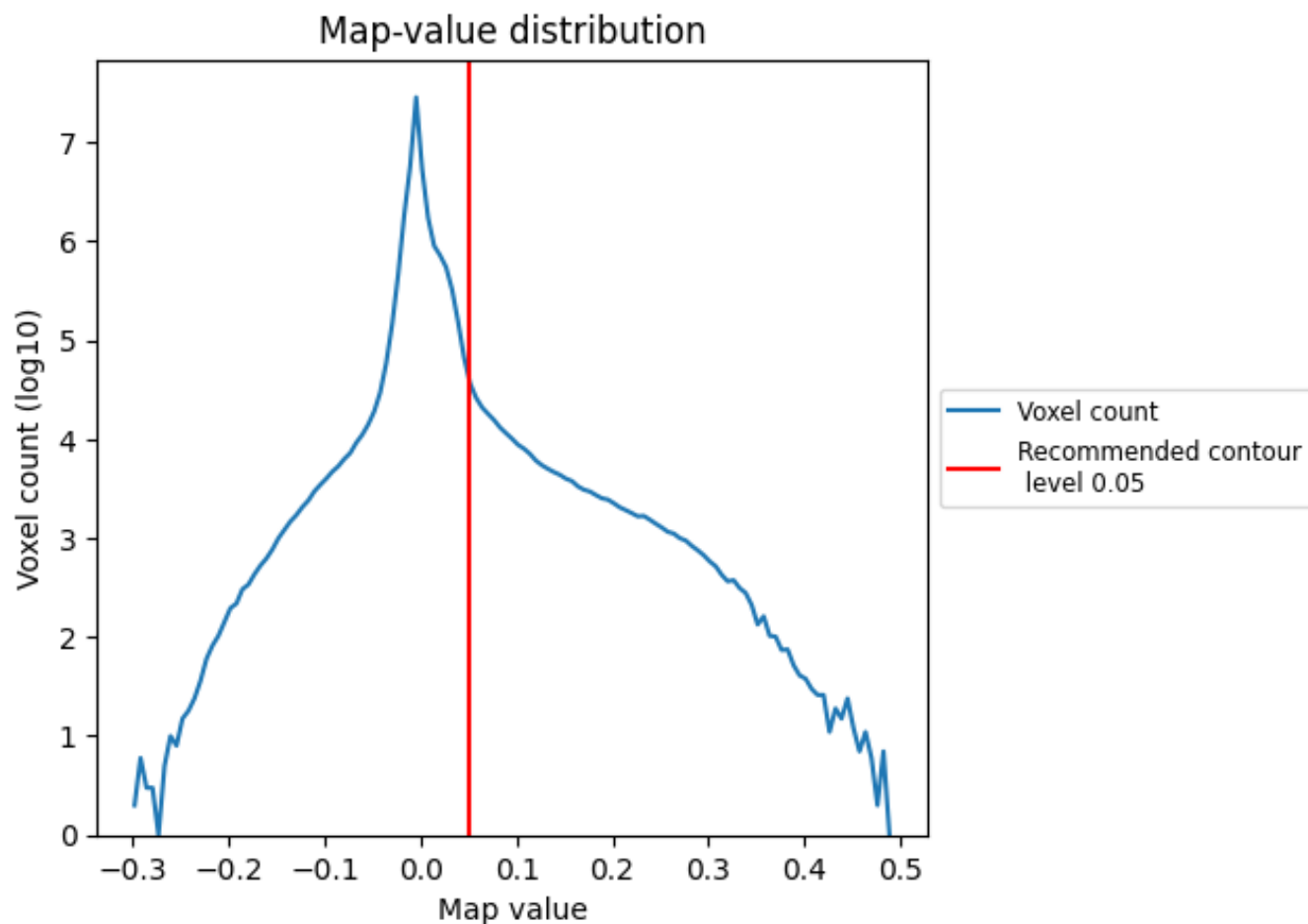
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

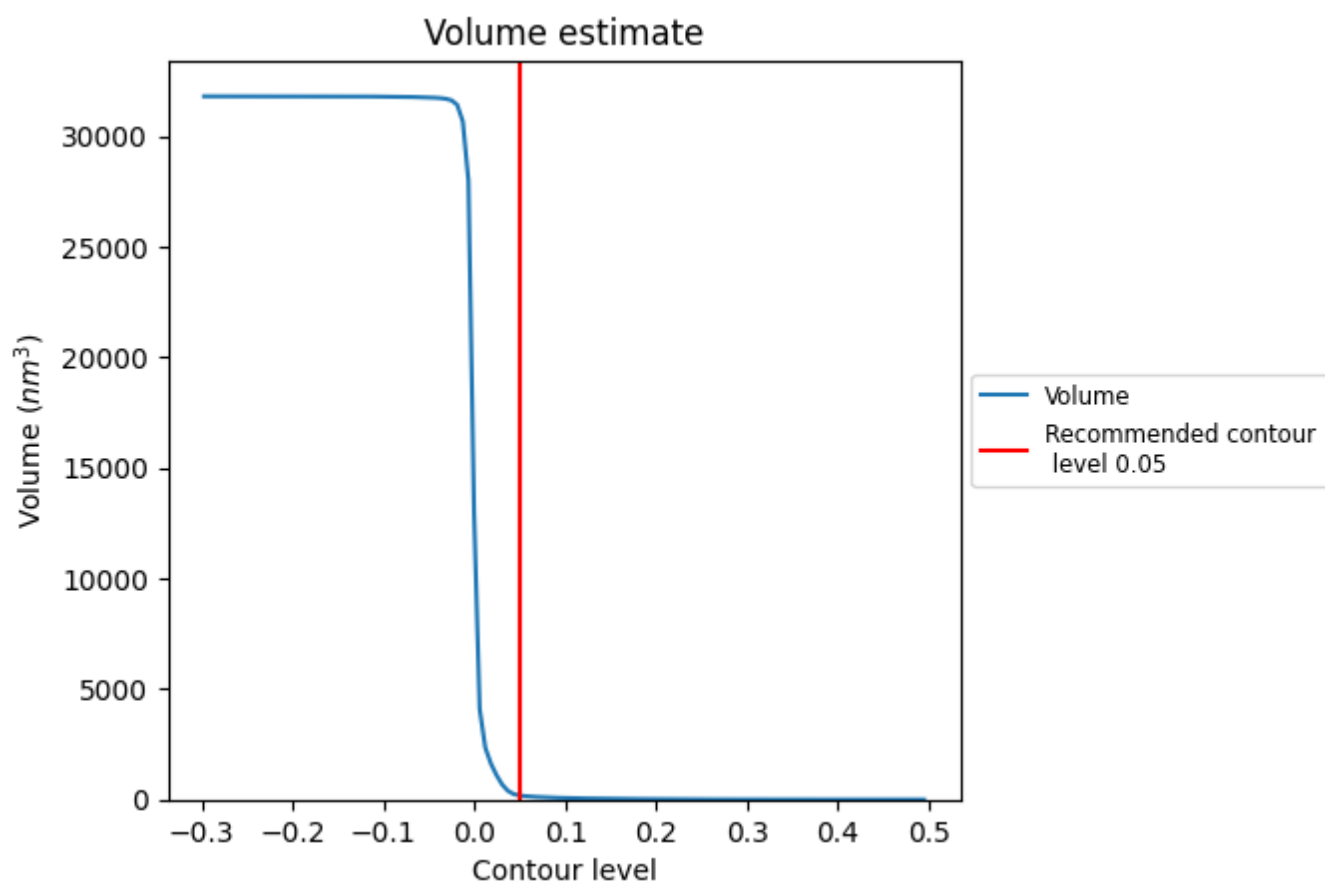
This section contains the results of statistical analysis of the map.

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.

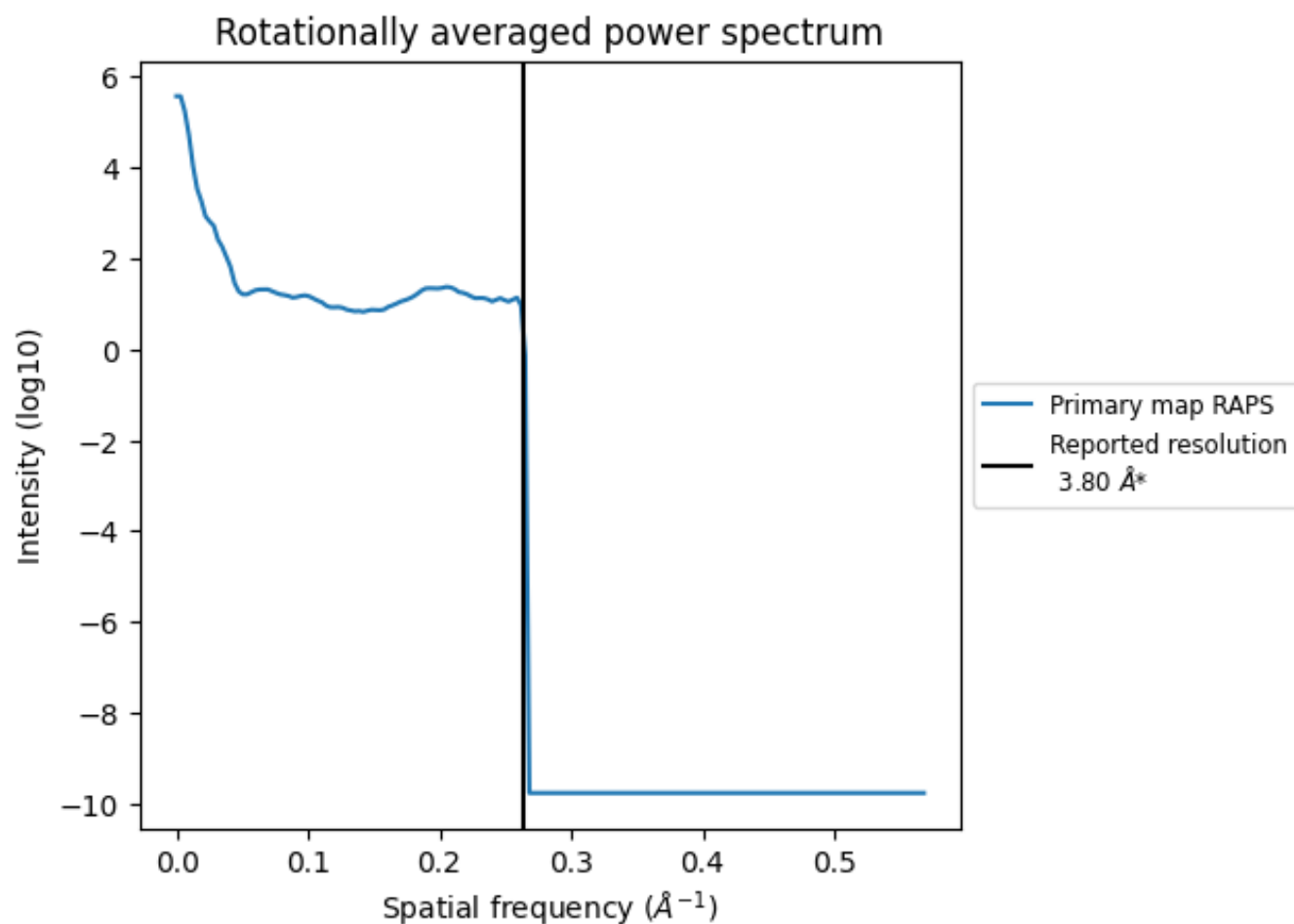
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 183 nm^3 ; this corresponds to an approximate mass of 165 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 0.263 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

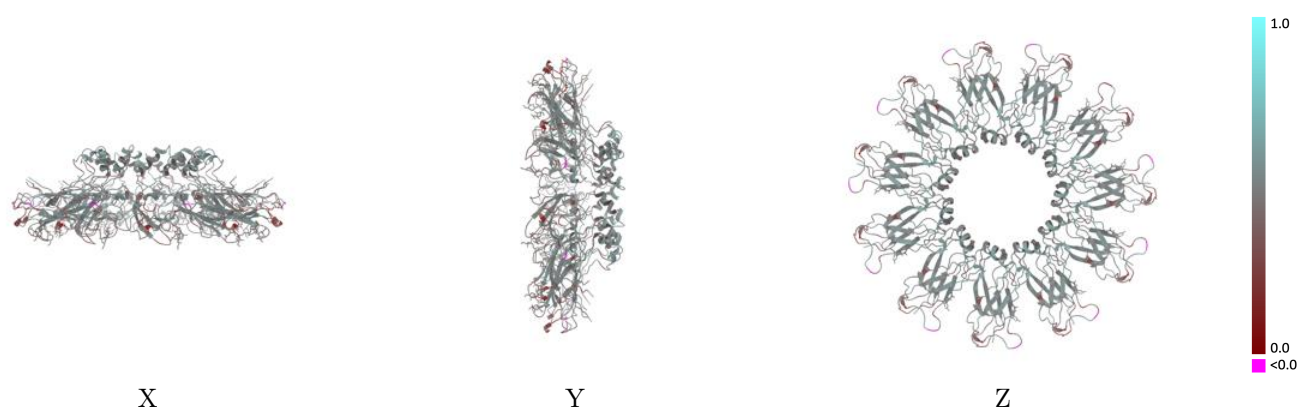
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8909 and PDB model 6DS5. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

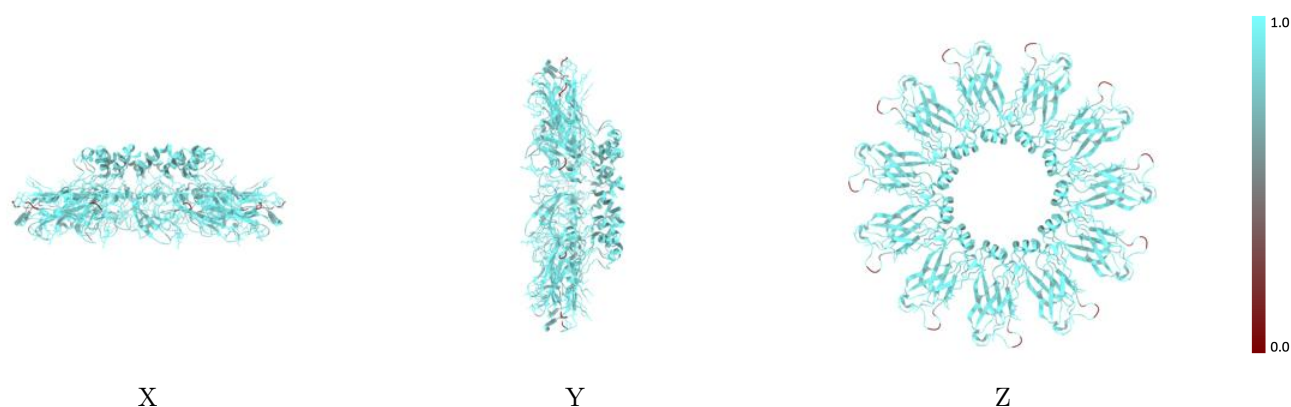
This section was not generated.

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



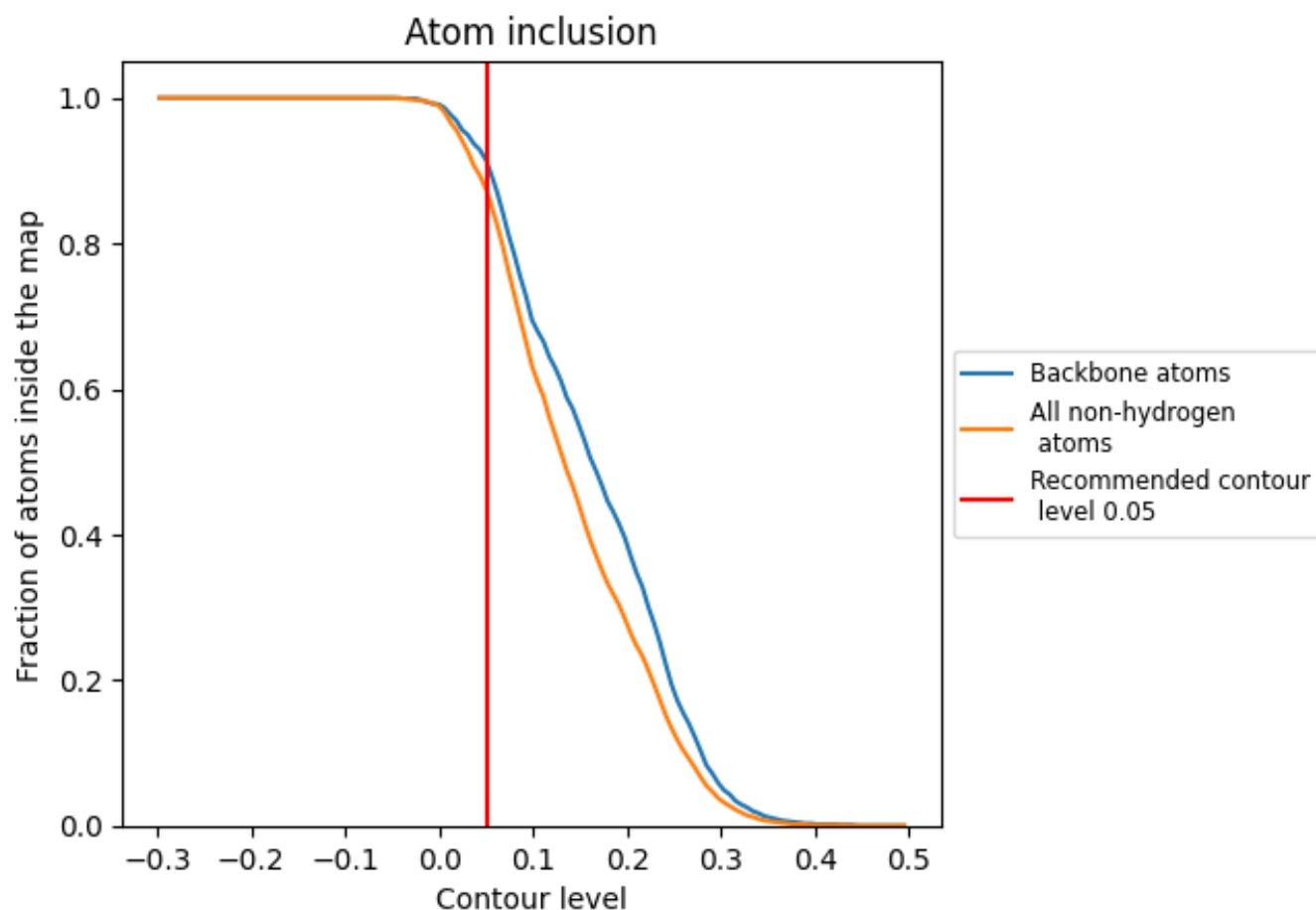
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 87% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.4730
A	 0.8690	 0.4730
B	 0.8720	 0.4730
C	 0.8720	 0.4730
D	 0.8720	 0.4750
E	 0.8710	 0.4720
F	 0.8760	 0.4740
G	 0.8700	 0.4730
H	 0.8740	 0.4730
I	 0.8710	 0.4740
J	 0.8750	 0.4720
K	 0.8740	 0.4730
L	 0.9640	 0.4420
M	 0.9640	 0.4540
N	 0.9640	 0.4550
O	 0.9640	 0.4440
P	 0.9640	 0.4570
Q	 0.9640	 0.4500
R	 0.9640	 0.4550
S	 0.9640	 0.4620
T	 0.9640	 0.4480
U	 0.9640	 0.4440
V	 0.9640	 0.4440

