



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:25 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 Full wwPDB EM Validation 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

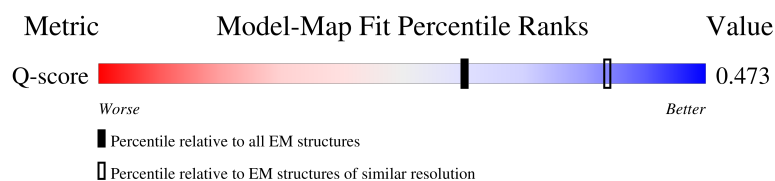
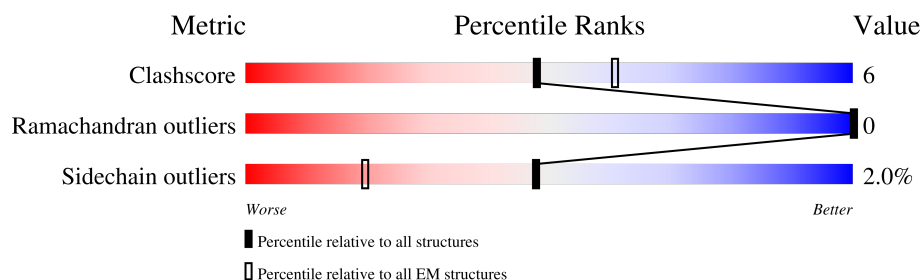
1 Overall quality at a glance

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.



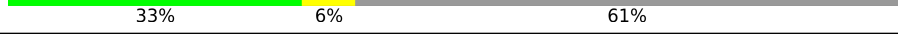
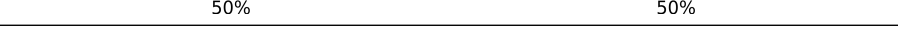
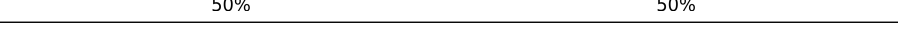
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	
1	B	409	
1	C	409	
1	D	409	

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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.

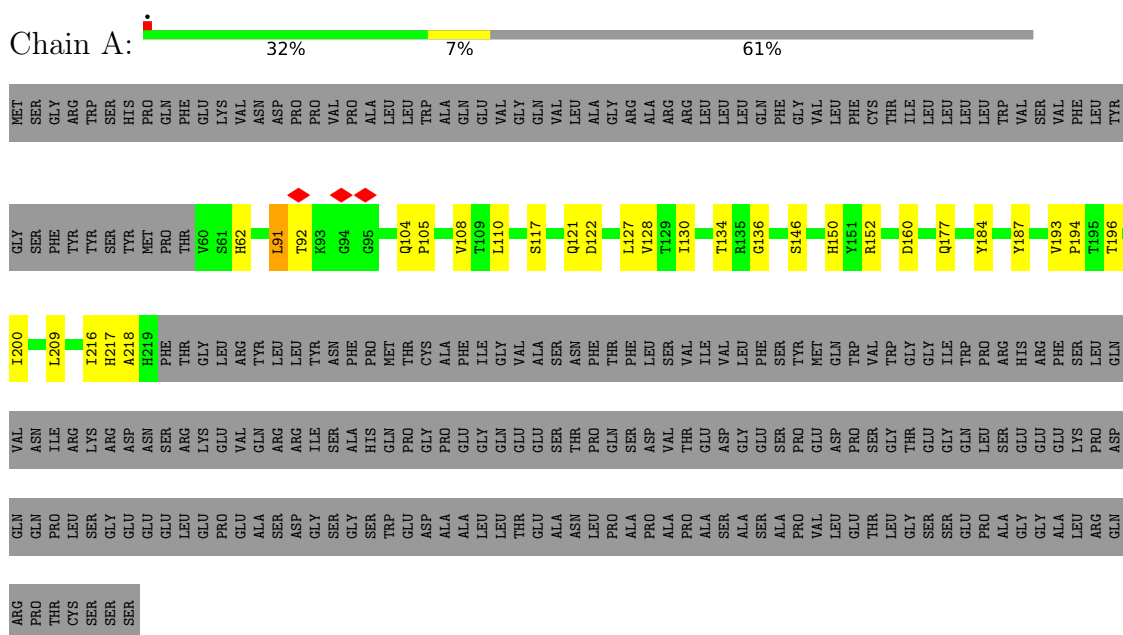


Mol	Chain	Residues	Atoms				AltConf	Trace
2	L	2	Total	C	N	O	0	0
			28	16	2	10		
2	M	2	Total	C	N	O	0	0
			28	16	2	10		
2	N	2	Total	C	N	O	0	0
			28	16	2	10		
2	O	2	Total	C	N	O	0	0
			28	16	2	10		
2	P	2	Total	C	N	O	0	0
			28	16	2	10		
2	Q	2	Total	C	N	O	0	0
			28	16	2	10		
2	R	2	Total	C	N	O	0	0
			28	16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

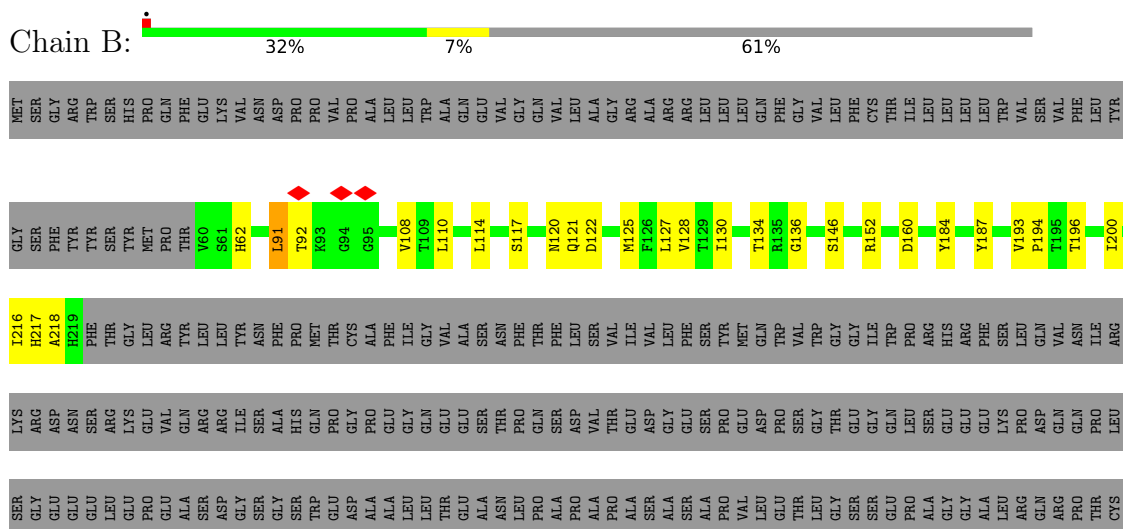
3 Residue-property plots [i](#)

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



CYS	SER	SER	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
LEU	ARG	LYS	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

● Molecule 1: Seipin



PRO	GLU	GLU	GLU	ASP	GLY	GLY	GLY	GLY	GLY	GLU	GLU	GLU	GLU	LEU	LEU	THR	GLU	GLU	GLU	ALA	ALA	PRO	PRO	PRO	PRO	PRO	ALA	ALA	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY</
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------

● Molecule 1: Seipin



MET	SER	GLY	ARG	TRP	SER	HIS	PRO	GLN	PHE	GLU	LYS	VAL	ASN	ASP	PRO	PRO	VAL	PRO	ALA	LEU	LEU	TRP	GLN	VAL	LEU	ALA	GLY	GLY	GLN	VAL	LEU	ALA	ARG	ARG	ARG	LEU	LEU	LEU	GLN	PHE	GLY	VAL	LEU	PHE	CYS	THR	ILE	LEU	LEU	LEU	TRP	VAL	SER	VAL	PHE	LEU	TYR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
GLY	SER	PHE	TYR	TYR	SER	TYR	MET	PRO	THR	V60	S61	H62	L91	T92	K93	G94	G95	V108	L110	L114	S117	N120	Q121	D122	L123	L127	V128	T129	I130	T134	R135	G136	S146	H150	Y151	R152	D160	Q177	Y184	Y187	T196	I200																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											

[illegible]

- Molecule 1: Seipin

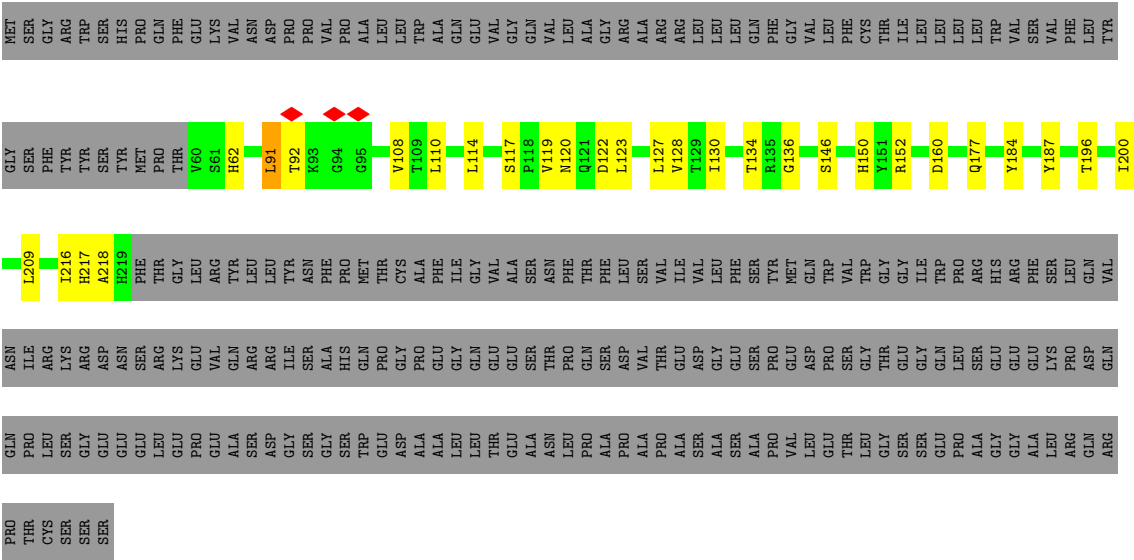
[illegible]

- Molecule 1: Seipin

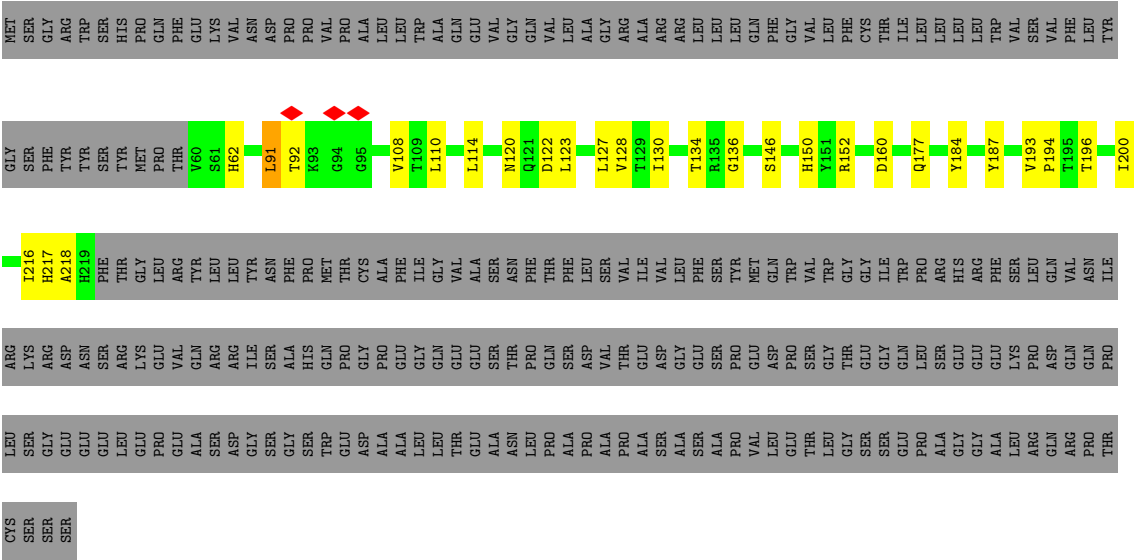
[illegible]

- Molecule 1: Seipin

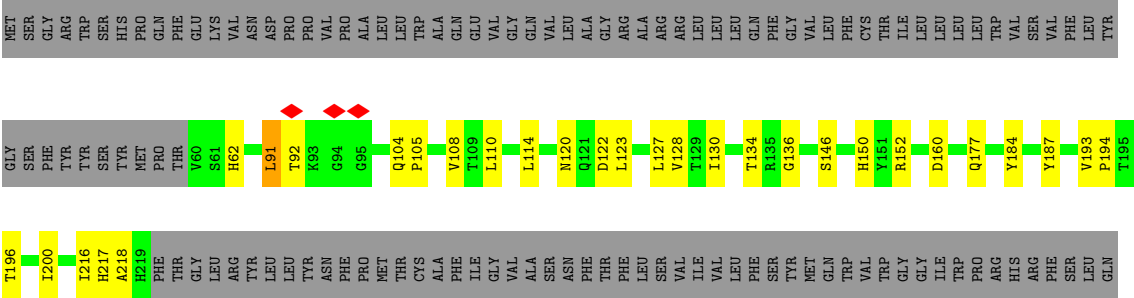




● Molecule 1: Seipin



● Molecule 1: Seipin



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

Chain O:  50% 50%



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

Chain P:  50% 50%



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

Chain Q:  50% 50%



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

Chain R:  50% 50%



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

Chain S:  50% 50%



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

Chain T:  50% 50%



- 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:  50% 50%



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.

All (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
1	D	122	ASP	N-CA-C	8.82	120.51	111.07
1	E	122	ASP	N-CA-C	8.53	120.20	111.07
1	I	122	ASP	N-CA-C	8.35	120.00	111.07
1	H	122	ASP	N-CA-C	8.32	119.97	111.07
1	K	122	ASP	N-CA-C	8.16	119.81	111.07
1	J	122	ASP	N-CA-C	7.88	119.51	111.07
1	B	117	SER	CA-C-N	-6.48	111.78	118.85
1	B	117	SER	C-N-CA	-6.48	111.78	118.85

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	117	SER	CA-C-N	-6.46	111.80	118.85
1	F	117	SER	C-N-CA	-6.46	111.80	118.85
1	A	117	SER	CA-C-N	-6.35	111.93	118.85
1	A	117	SER	C-N-CA	-6.35	111.93	118.85
1	C	117	SER	CA-C-N	-6.23	112.06	118.85
1	C	117	SER	C-N-CA	-6.23	112.06	118.85
1	D	117	SER	CA-C-N	-6.17	112.13	118.85
1	D	117	SER	C-N-CA	-6.17	112.13	118.85
1	G	117	SER	CA-C-N	-5.34	113.03	118.85
1	G	117	SER	C-N-CA	-5.34	113.03	118.85
1	I	122	ASP	CA-C-N	5.09	129.36	121.26
1	I	122	ASP	C-N-CA	5.09	129.36	121.26
1	K	119	VAL	CB-CA-C	-5.04	105.33	112.14
1	H	119	VAL	CB-CA-C	-5.01	105.38	112.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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.

All (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
1:C:184:TYR:HB3	1:C:187:TYR:HB2	1.81	0.62
1:G:184:TYR:HB3	1:G:187:TYR:HB2	1.80	0.62
1:J:184:TYR:HB3	1:J:187:TYR:HB2	1.81	0.62
1:B:184:TYR:HB3	1:B:187:TYR:HB2	1.81	0.62
1:F:184:TYR:HB3	1:F:187:TYR:HB2	1.81	0.61
1:A:184:TYR:HB3	1:A:187:TYR:HB2	1.81	0.61
1:J:114:LEU:HD22	1:J:120:ASN:HD21	1.68	0.58
1:G:152:ARG:NH2	1:G:160:ASP:OD2	2.37	0.58
1:F:152:ARG:NH2	1:F:160:ASP:OD2	2.37	0.58
1:H:152:ARG:NH2	1:H:160:ASP:OD2	2.37	0.58
1:K:114:LEU:HD22	1:K:120:ASN:HD21	1.69	0.58
1:E:152:ARG:NH2	1:E:160:ASP:OD2	2.37	0.58
1:H:114:LEU:HD22	1:H:120:ASN:HD21	1.69	0.58
1:I:152:ARG:NH2	1:I:160:ASP:OD2	2.37	0.58
1:D:152:ARG:NH2	1:D:160:ASP:OD2	2.37	0.57
1:A:152:ARG:NH2	1:A:160:ASP:OD2	2.37	0.57
1:J:152:ARG:NH2	1:J:160:ASP:OD2	2.37	0.57
1:K:152:ARG:NH2	1:K:160:ASP:OD2	2.37	0.57
1:C:152:ARG:NH2	1:C:160:ASP:OD2	2.37	0.57
1:B:152:ARG:NH2	1:B:160:ASP:OD2	2.37	0.56
1:I:114:LEU:HD22	1:I:120:ASN:HD21	1.71	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:91:LEU:HD13	1:G:92:THR:H	1.72	0.55
1:J:91:LEU:HD13	1:J:92:THR:H	1.72	0.55
1:F:91:LEU:HD13	1:F:92:THR:H	1.72	0.55
1:A:91:LEU:HD13	1:A:92:THR:H	1.72	0.55
1:H:91:LEU:HD13	1:H:92:THR:H	1.72	0.55
1:B:91:LEU:HD13	1:B:92:THR:H	1.72	0.55
1:C:91:LEU:HD13	1:C:92:THR:H	1.72	0.55
1:K:91:LEU:HD13	1:K:92:THR:H	1.72	0.54
1:E:91:LEU:HD13	1:E:92:THR:H	1.72	0.54
1:D:91:LEU:HD13	1:D:92:THR:H	1.72	0.54
1:I:91:LEU:HD13	1:I:92:THR:H	1.72	0.53
1:A:108:VAL:HG22	1:A:184:TYR:HB2	1.90	0.53
1:B:108:VAL:HG22	1:B:184:TYR:HB2	1.90	0.53
1:G:108:VAL:HG22	1:G:184:TYR:HB2	1.90	0.53
1:H:108:VAL:HG22	1:H:184:TYR:HB2	1.90	0.53
1:C:108:VAL:HG22	1:C:184:TYR:HB2	1.90	0.53
1:E:114:LEU:HD22	1:E:120:ASN:HD21	1.71	0.53
1:K:108:VAL:HG22	1:K:184:TYR:HB2	1.90	0.53
1:F:108:VAL:HG22	1:F:184:TYR:HB2	1.90	0.53
1:D:134:THR:O	1:D:196:THR:OG1	2.24	0.53
1:K:108:VAL:HG12	1:K:216:ILE:HG22	1.91	0.52
1:E:108:VAL:HG22	1:E:184:TYR:HB2	1.90	0.52
1:A:108:VAL:HG12	1:A:216:ILE:HG22	1.91	0.52
1:J:108:VAL:HG12	1:J:216:ILE:HG22	1.91	0.52
1:D:108:VAL:HG22	1:D:184:TYR:HB2	1.90	0.52
1:J:108:VAL:HG22	1:J:184:TYR:HB2	1.90	0.52
1:I:108:VAL:HG22	1:I:184:TYR:HB2	1.90	0.52
1:B:108:VAL:HG12	1:B:216:ILE:HG22	1.91	0.52
1:E:134:THR:O	1:E:196:THR:OG1	2.23	0.52
1:I:108:VAL:HG12	1:I:216:ILE:HG22	1.91	0.52
1:C:108:VAL:HG12	1:C:216:ILE:HG22	1.91	0.51
1:E:108:VAL:HG12	1:E:216:ILE:HG22	1.91	0.51
1:H:108:VAL:HG12	1:H:216:ILE:HG22	1.91	0.51
1:A:134:THR:O	1:A:196:THR:OG1	2.24	0.51
1:F:108:VAL:HG12	1:F:216:ILE:HG22	1.91	0.51
1:D:108:VAL:HG12	1:D:216:ILE:HG22	1.91	0.51
1:G:108:VAL:HG12	1:G:216:ILE:HG22	1.91	0.51
1:G:130:ILE:HG13	1:G:200:ILE:HG22	1.93	0.51
1:I:130:ILE:HG13	1:I:200:ILE:HG22	1.93	0.51
1:B:130:ILE:HG13	1:B:200:ILE:HG22	1.93	0.50
1:E:130:ILE:HG13	1:E:200:ILE:HG22	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:134:THR:O	1:I:196:THR:OG1	2.23	0.50
1:A:130:ILE:HG13	1:A:200:ILE:HG22	1.93	0.50
1:C:130:ILE:HG13	1:C:200:ILE:HG22	1.93	0.50
1:K:130:ILE:HG13	1:K:200:ILE:HG22	1.93	0.50
1:D:130:ILE:HG13	1:D:200:ILE:HG22	1.93	0.49
1:H:130:ILE:HG13	1:H:200:ILE:HG22	1.93	0.49
1:F:114:LEU:HD22	1:F:120:ASN:HD21	1.78	0.49
1:F:130:ILE:HG13	1:F:200:ILE:HG22	1.93	0.49
1:B:110:LEU:HD11	1:B:200:ILE:HD13	1.94	0.49
1:J:130:ILE:HG13	1:J:200:ILE:HG22	1.93	0.49
1:A:110:LEU:HD11	1:A:200:ILE:HD13	1.94	0.48
1:H:110:LEU:HD11	1:H:200:ILE:HD13	1.94	0.48
1:K:110:LEU:HD11	1:K:200:ILE:HD13	1.94	0.48
1:B:134:THR:O	1:B:196:THR:OG1	2.23	0.48
1:C:110:LEU:HD11	1:C:200:ILE:HD13	1.94	0.48
1:I:110:LEU:HD11	1:I:200:ILE:HD13	1.94	0.48
1:J:134:THR:O	1:J:196:THR:OG1	2.23	0.48
1:G:110:LEU:HD11	1:G:200:ILE:HD13	1.94	0.48
1:G:134:THR:O	1:G:196:THR:OG1	2.23	0.48
1:E:110:LEU:HD11	1:E:200:ILE:HD13	1.94	0.48
1:F:110:LEU:HD11	1:F:200:ILE:HD13	1.94	0.48
1:J:110:LEU:HD11	1:J:200:ILE:HD13	1.94	0.48
1:D:110:LEU:HD11	1:D:200:ILE:HD13	1.94	0.47
1:J:120:ASN:O	1:J:123:LEU:HG	2.15	0.47
1:F:134:THR:O	1:F:196:THR:OG1	2.24	0.46
1:B:114:LEU:HD22	1:B:120:ASN:HD21	1.81	0.45
1:G:136:GLY:HA2	2:R:2:NAG:H4	1.99	0.45
1:E:136:GLY:HA2	2:P:2:NAG:H4	1.99	0.45
1:H:136:GLY:HA2	2:S:2:NAG:H4	1.99	0.45
1:D:136:GLY:HA2	2:O:2:NAG:H4	1.99	0.45
1:F:136:GLY:HA2	2:Q:2:NAG:H4	1.99	0.45
1:H:134:THR:O	1:H:196:THR:OG1	2.24	0.45
1:I:136:GLY:HA2	2:T:2:NAG:H4	1.99	0.45
1:C:150:HIS:O	1:C:177:GLN:NE2	2.50	0.45
1:C:136:GLY:HA2	2:N:2:NAG:H4	1.99	0.44
1:C:134:THR:O	1:C:196:THR:OG1	2.24	0.44
1:H:150:HIS:O	1:H:177:GLN:NE2	2.50	0.44
1:J:136:GLY:HA2	2:U:2:NAG:H4	1.99	0.44
1:K:136:GLY:HA2	2:V:2:NAG:H4	1.99	0.44
1:H:120:ASN:O	1:H:123:LEU:HG	2.18	0.44
1:K:134:THR:O	1:K:196:THR:OG1	2.23	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:GLN:HA	1:A:105:PRO:HD3	1.90	0.44
1:A:136:GLY:HA2	2:L:2:NAG:H4	1.99	0.44
1:B:136:GLY:HA2	2:M:2:NAG:H4	1.99	0.44
1:D:150:HIS:O	1:D:177:GLN:NE2	2.50	0.43
1:I:150:HIS:O	1:I:177:GLN:NE2	2.50	0.43
1:F:193:VAL:HA	1:F:194:PRO:HD3	1.90	0.43
1:J:150:HIS:O	1:J:177:GLN:NE2	2.50	0.42
1:A:193:VAL:HA	1:A:194:PRO:HD3	1.90	0.42
1:E:120:ASN:O	1:E:123:LEU:HG	2.19	0.42
1:J:193:VAL:HA	1:J:194:PRO:HD3	1.90	0.42
1:A:209:LEU:H	1:K:125:MET:HE2	1.85	0.42
1:E:150:HIS:O	1:E:177:GLN:NE2	2.50	0.42
1:B:62:HIS:CE1	1:B:216:ILE:HD11	2.55	0.42
1:I:62:HIS:CE1	1:I:216:ILE:HD11	2.55	0.41
1:H:62:HIS:CE1	1:H:216:ILE:HD11	2.55	0.41
1:G:62:HIS:CE1	1:G:216:ILE:HD11	2.56	0.41
1:J:62:HIS:CE1	1:J:216:ILE:HD11	2.55	0.41
1:E:62:HIS:CE1	1:E:216:ILE:HD11	2.55	0.41
1:E:217:HIS:ND1	1:E:218:ALA:O	2.53	0.41
1:I:120:ASN:O	1:I:123:LEU:HG	2.20	0.41
1:K:150:HIS:O	1:K:177:GLN:NE2	2.49	0.41
1:D:62:HIS:CE1	1:D:216:ILE:HD11	2.55	0.41
1:D:217:HIS:ND1	1:D:218:ALA:O	2.53	0.41
1:F:150:HIS:O	1:F:177:GLN:NE2	2.50	0.41
1:F:217:HIS:ND1	1:F:218:ALA:O	2.53	0.41
1:A:62:HIS:CE1	1:A:216:ILE:HD11	2.55	0.41
1:C:62:HIS:CE1	1:C:216:ILE:HD11	2.55	0.41
1:C:114:LEU:HD22	1:C:120:ASN:HD21	1.86	0.41
1:G:125:MET:HE2	1:H:209:LEU:H	1.86	0.41
1:G:217:HIS:ND1	1:G:218:ALA:O	2.53	0.41
1:K:62:HIS:CE1	1:K:216:ILE:HD11	2.55	0.41
1:C:217:HIS:ND1	1:C:218:ALA:O	2.53	0.41
1:A:127:LEU:HA	1:A:146:SER:HA	2.03	0.41
1:B:193:VAL:HA	1:B:194:PRO:HD3	1.90	0.41
1:B:217:HIS:ND1	1:B:218:ALA:O	2.53	0.41
1:H:217:HIS:ND1	1:H:218:ALA:O	2.53	0.41
1:I:217:HIS:ND1	1:I:218:ALA:O	2.53	0.41
1:J:104:GLN:HA	1:J:105:PRO:HD3	1.90	0.41
1:J:127:LEU:HA	1:J:146:SER:HA	2.03	0.41
1:J:217:HIS:ND1	1:J:218:ALA:O	2.53	0.41
1:A:217:HIS:ND1	1:A:218:ALA:O	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:MET:HE2	1:C:209:LEU:H	1.86	0.41
1:C:127:LEU:HA	1:C:146:SER:HA	2.03	0.41
1:K:217:HIS:ND1	1:K:218:ALA:O	2.53	0.41
1:B:127:LEU:HA	1:B:146:SER:HA	2.03	0.40
1:H:127:LEU:HA	1:H:146:SER:HA	2.03	0.40
1:I:127:LEU:HA	1:I:146:SER:HA	2.03	0.40
1:F:62:HIS:CE1	1:F:216:ILE:HD11	2.56	0.40
1:I:193:VAL:HA	1:I:194:PRO:HD3	1.90	0.40
1:A:150:HIS:O	1:A:177:GLN:NE2	2.50	0.40
1:K:127:LEU:HA	1:K:146:SER:HA	2.03	0.40
1:E:127:LEU:HA	1:E:146:SER:HA	2.03	0.40
1:G:150:HIS:O	1:G:177:GLN:NE2	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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
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

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	LEU
1	A	121	GLN
1	A	128	VAL
1	B	91	LEU
1	B	121	GLN
1	B	128	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	91	LEU
1	C	121	GLN
1	C	128	VAL
1	D	91	LEU
1	D	121	GLN
1	D	128	VAL
1	E	91	LEU
1	E	117	SER
1	E	128	VAL
1	F	91	LEU
1	F	121	GLN
1	F	128	VAL
1	G	91	LEU
1	G	121	GLN
1	G	128	VAL
1	H	91	LEU
1	H	117	SER
1	H	128	VAL
1	I	91	LEU
1	I	128	VAL
1	J	91	LEU
1	J	128	VAL
1	K	91	LEU
1	K	128	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	HIS
1	A	120	ASN
1	B	67	HIS
1	C	67	HIS
1	D	67	HIS
1	E	67	HIS
1	F	67	HIS
1	G	67	HIS
1	H	67	HIS
1	I	67	HIS
1	J	67	HIS
1	K	67	HIS
1	K	120	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
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.

All (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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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
2	L	1	NAG	C1-O5-C5	6.51	120.92	112.19
2	R	1	NAG	C1-O5-C5	6.50	120.90	112.19
2	T	1	NAG	C1-O5-C5	6.49	120.89	112.19
2	S	1	NAG	C1-O5-C5	6.49	120.88	112.19
2	V	1	NAG	C1-O5-C5	6.49	120.88	112.19
2	Q	1	NAG	C1-O5-C5	6.46	120.84	112.19
2	S	2	NAG	C1-O5-C5	2.37	115.36	112.19
2	P	2	NAG	C1-O5-C5	2.37	115.36	112.19
2	R	2	NAG	C1-O5-C5	2.37	115.36	112.19
2	M	2	NAG	C1-O5-C5	2.36	115.35	112.19
2	L	2	NAG	C1-O5-C5	2.35	115.34	112.19
2	Q	2	NAG	C1-O5-C5	2.35	115.33	112.19
2	U	2	NAG	C1-O5-C5	2.35	115.33	112.19
2	T	2	NAG	C1-O5-C5	2.35	115.33	112.19
2	V	2	NAG	C1-O5-C5	2.34	115.32	112.19
2	N	2	NAG	C1-O5-C5	2.34	115.32	112.19
2	O	2	NAG	C1-O5-C5	2.33	115.30	112.19

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	2	NAG	O5-C5-C6-O6
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
2	S	2	NAG	O5-C5-C6-O6
2	T	2	NAG	O5-C5-C6-O6
2	U	2	NAG	O5-C5-C6-O6
2	N	2	NAG	O5-C5-C6-O6
2	P	2	NAG	O5-C5-C6-O6
2	V	2	NAG	O5-C5-C6-O6

There are no ring outliers.

11 monomers are involved in 11 short contacts:

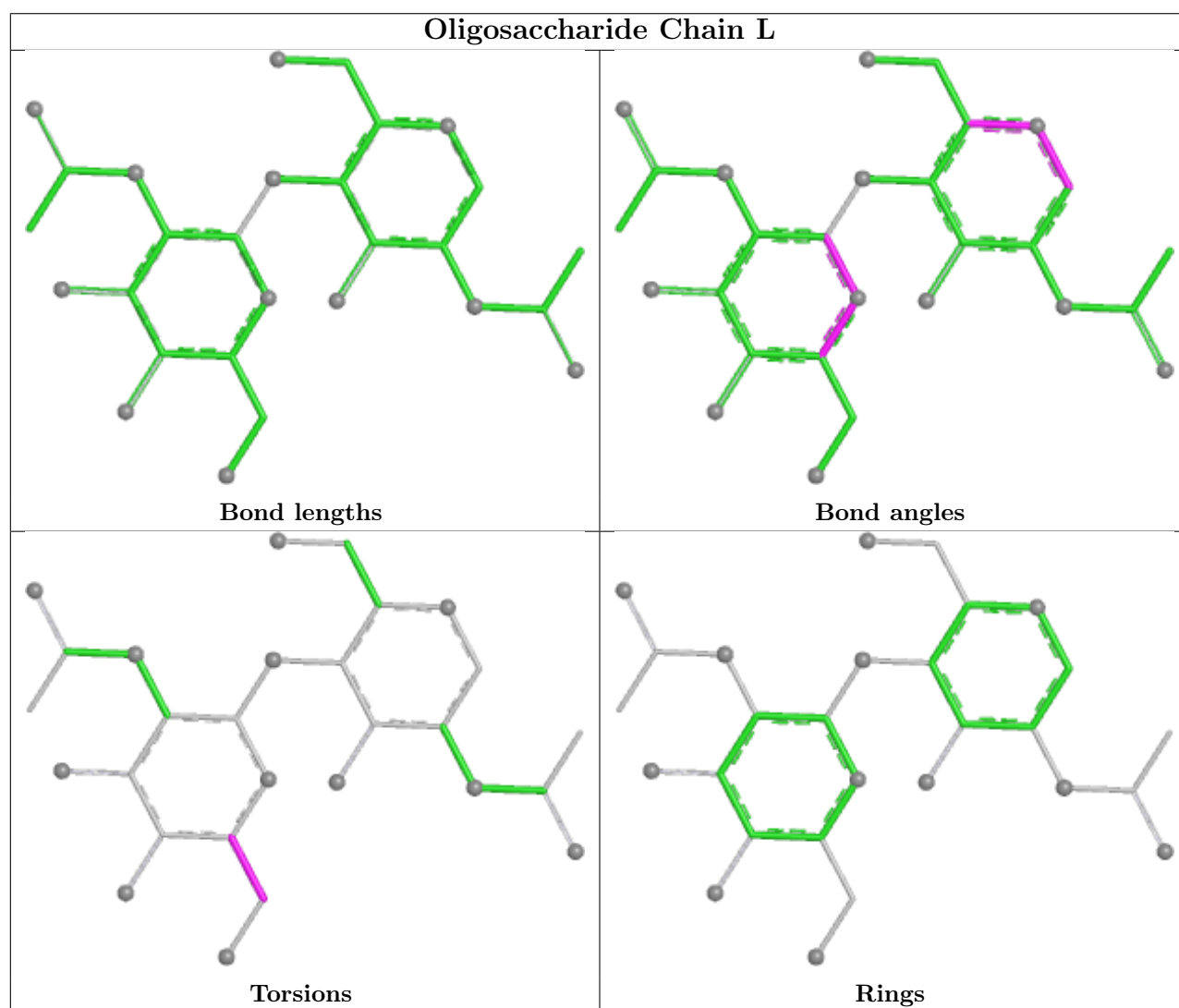
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	2	NAG	1	0

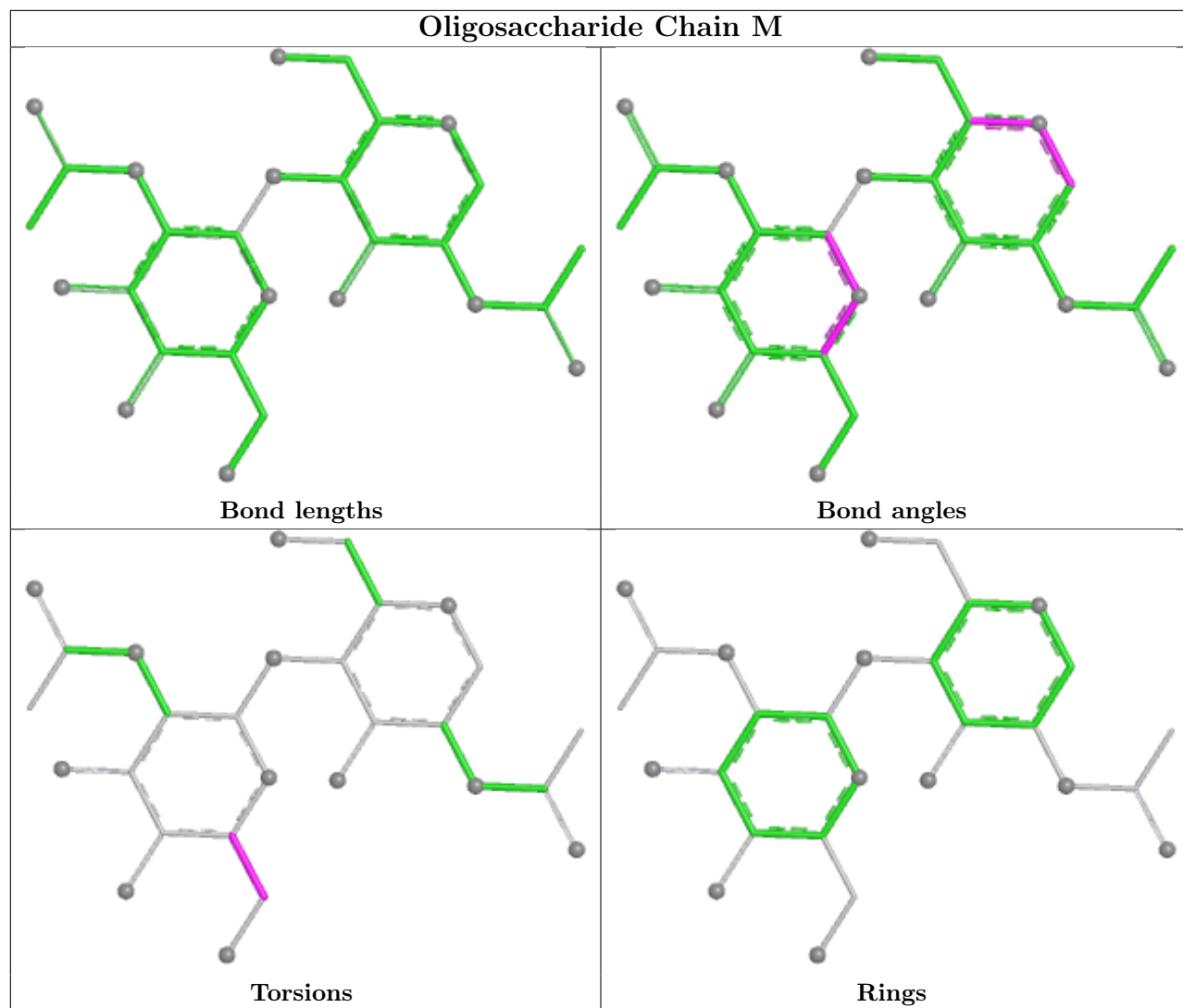
Continued on next page...

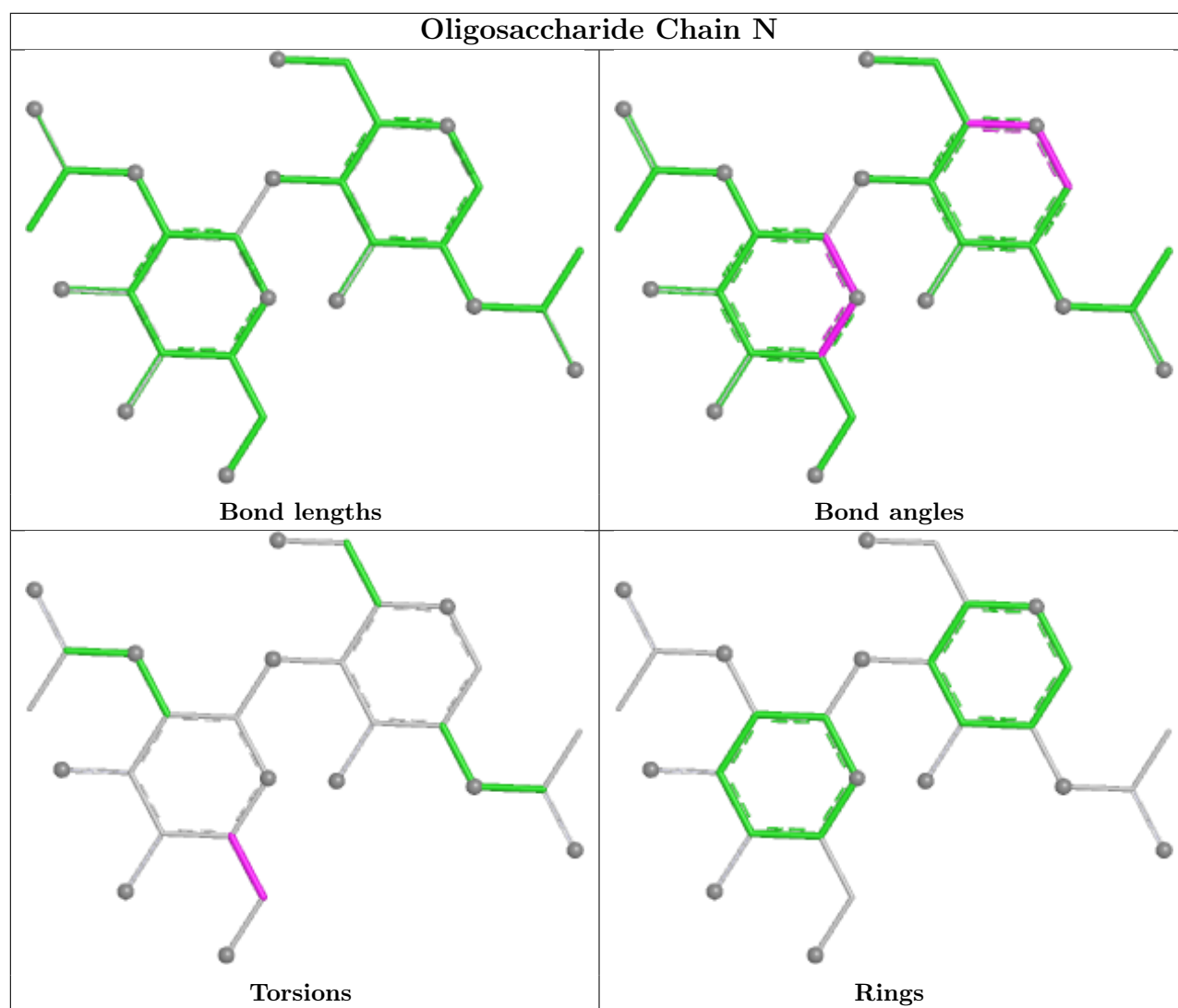
Continued from previous page...

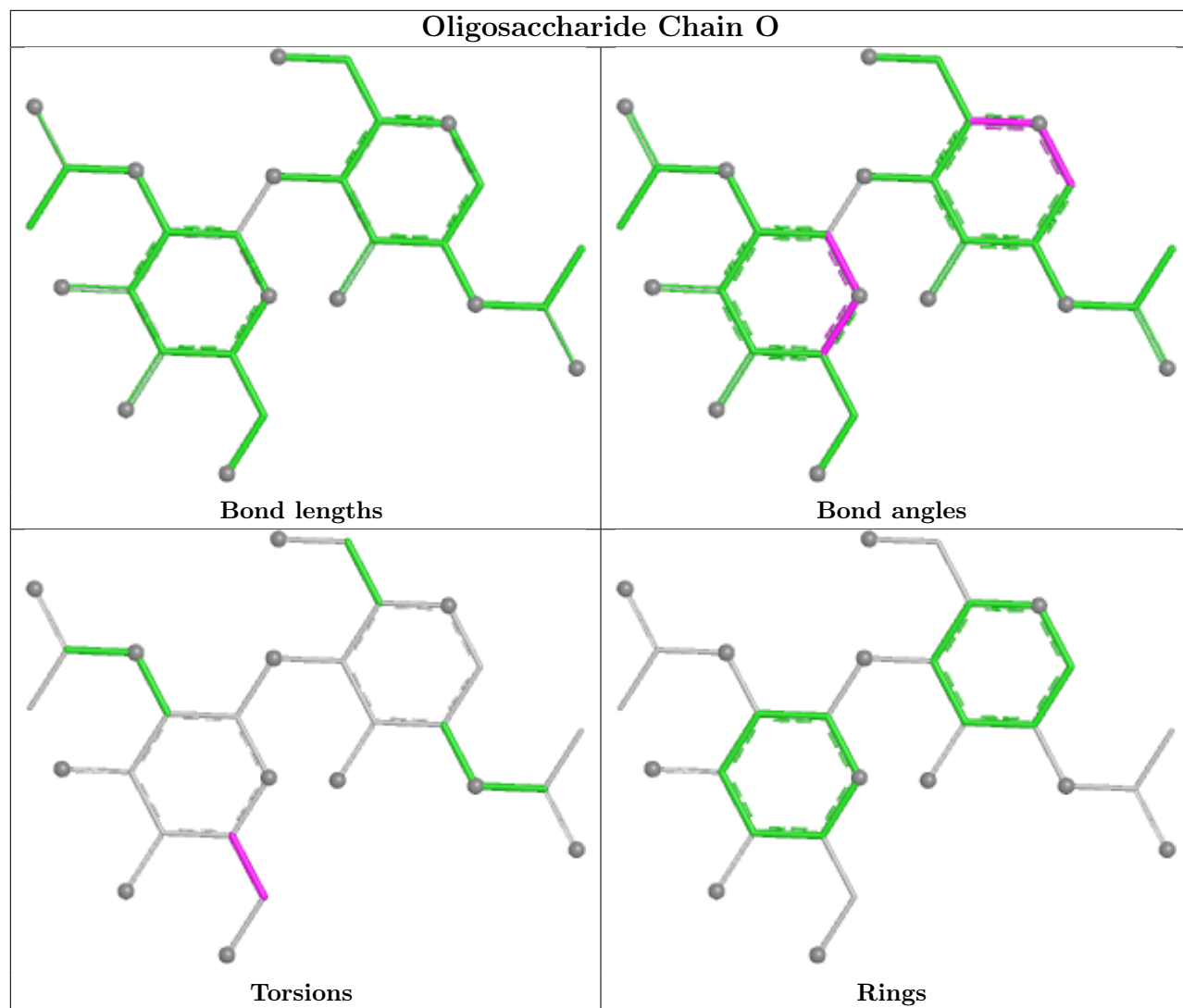
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	T	2	NAG	1	0
2	R	2	NAG	1	0
2	Q	2	NAG	1	0
2	S	2	NAG	1	0
2	P	2	NAG	1	0
2	U	2	NAG	1	0
2	N	2	NAG	1	0
2	V	2	NAG	1	0
2	M	2	NAG	1	0
2	L	2	NAG	1	0

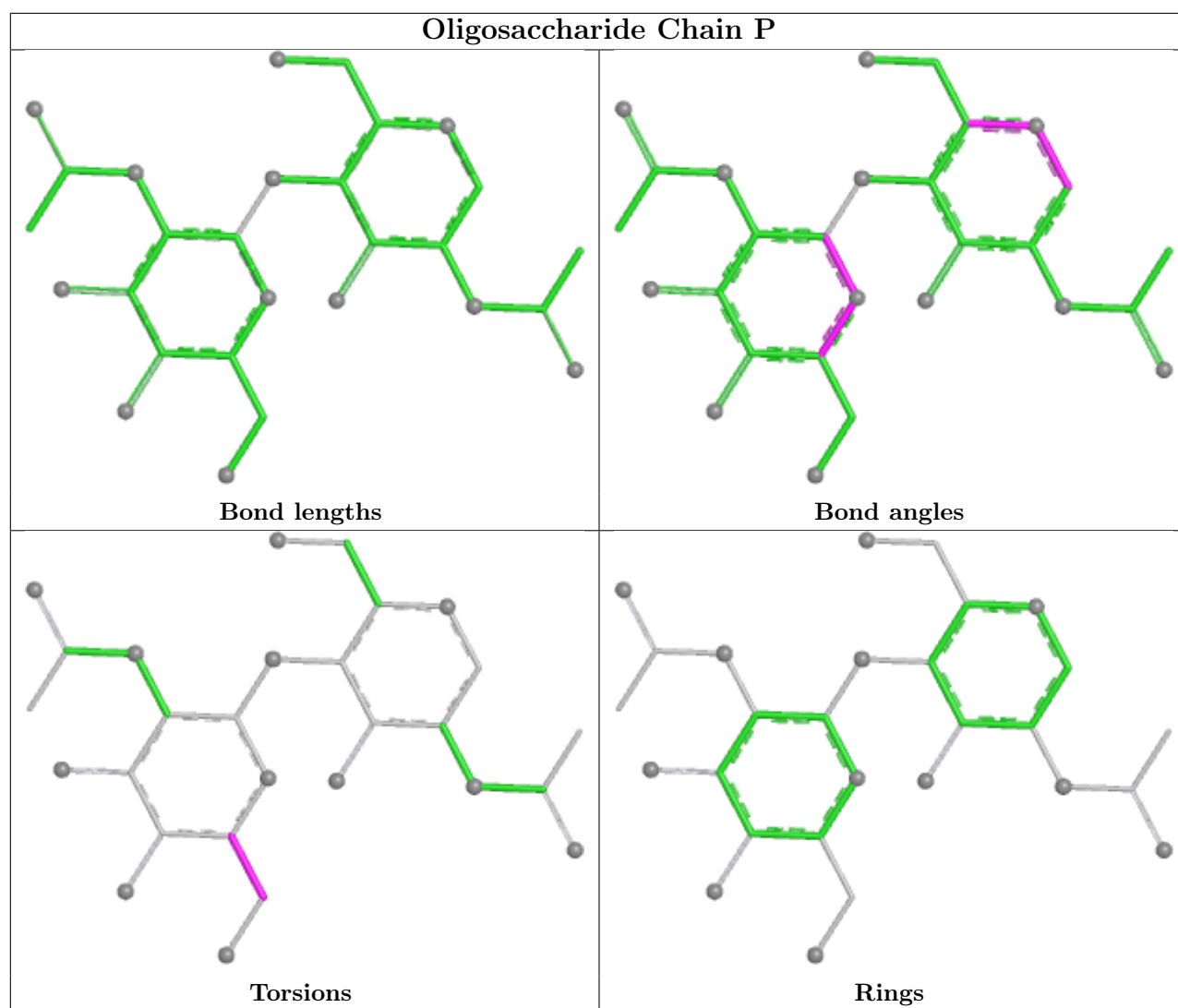
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

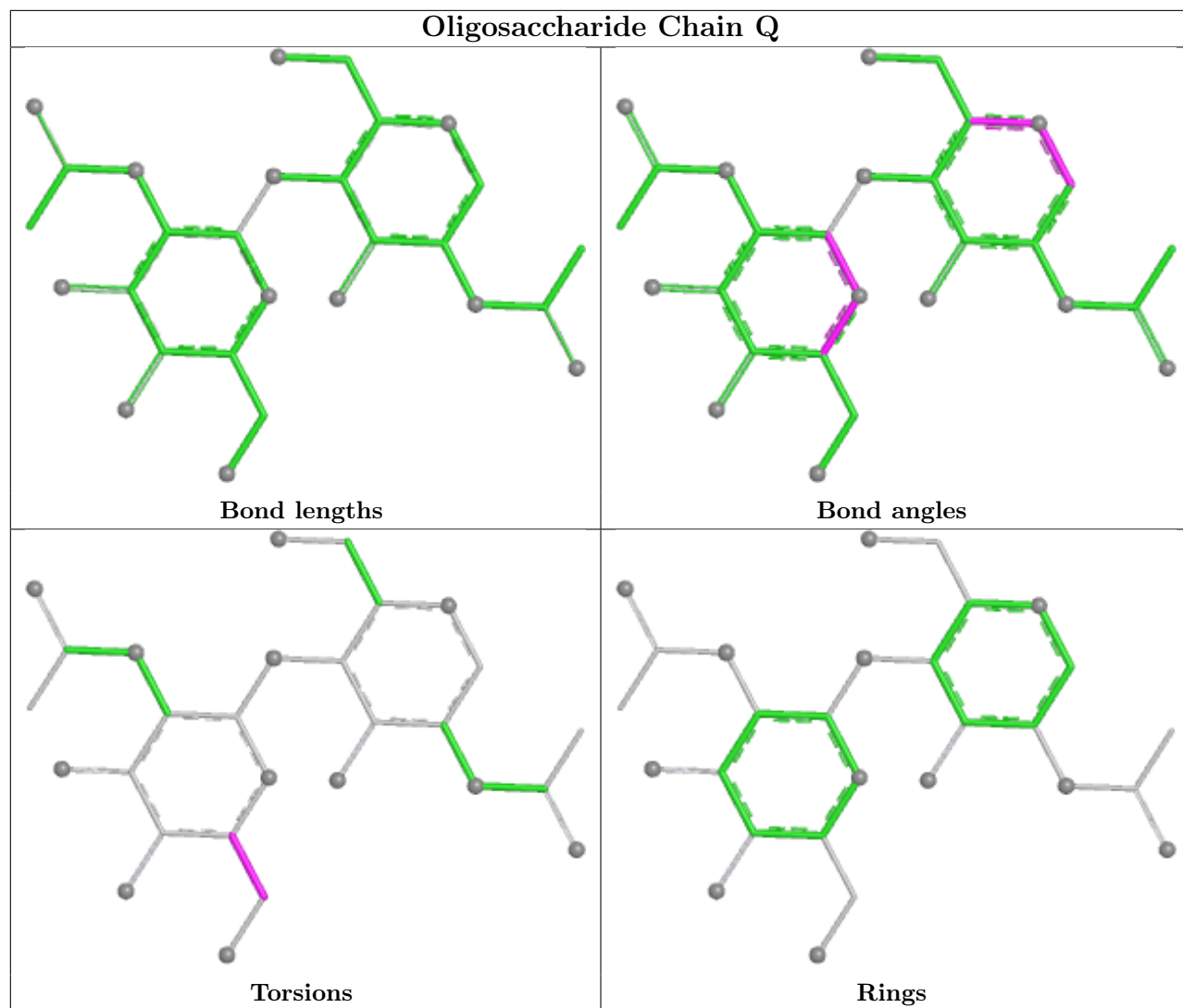


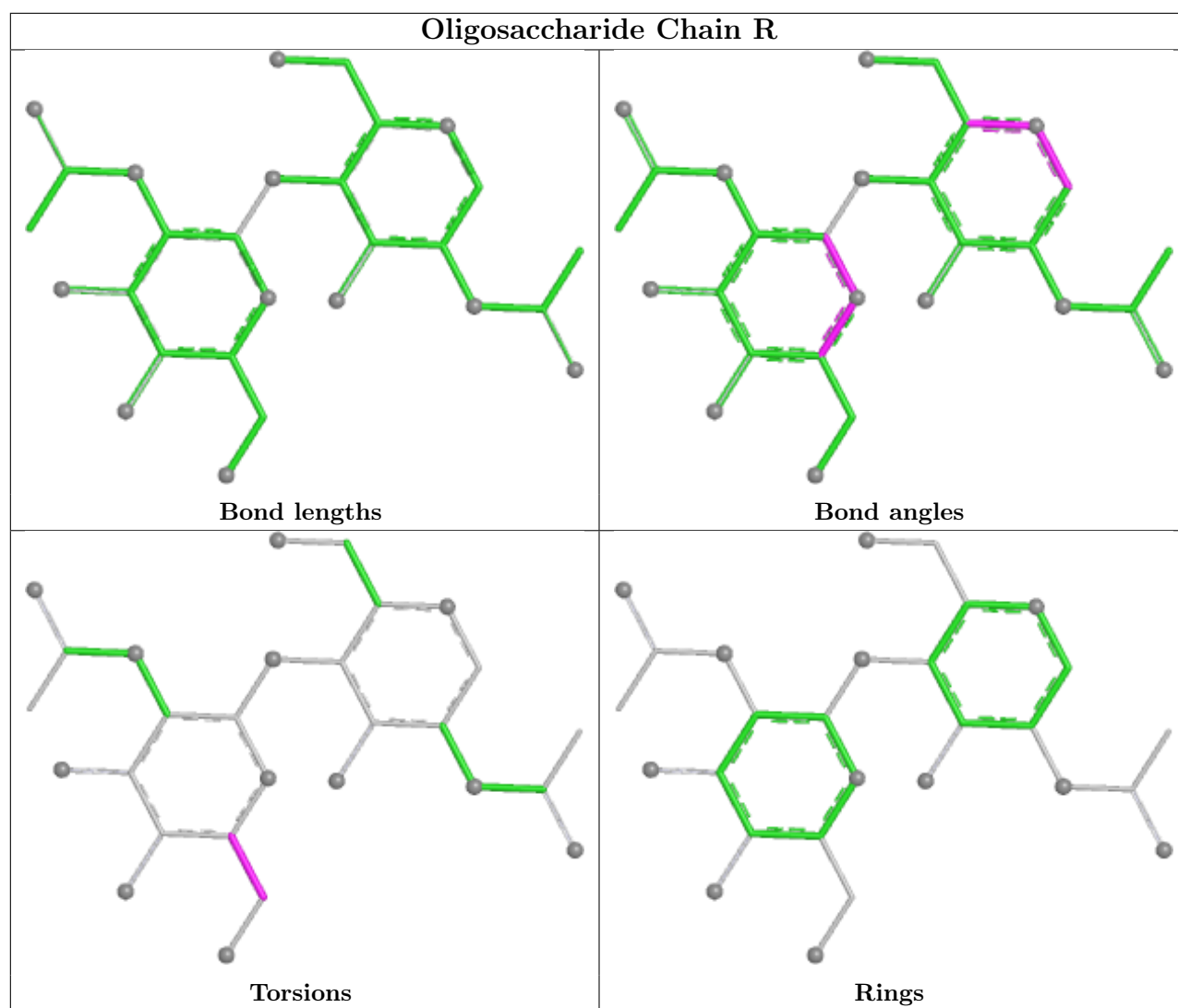


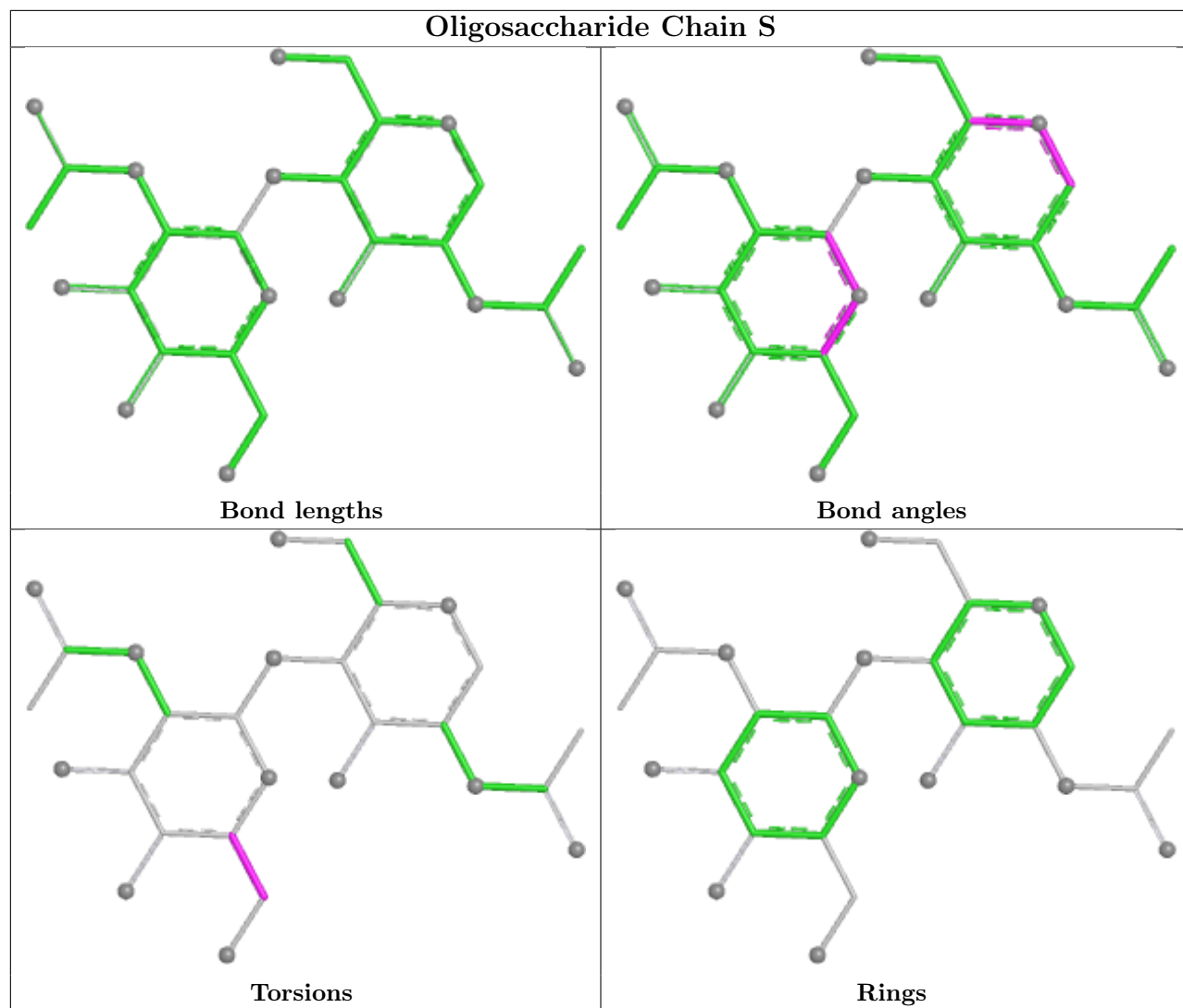


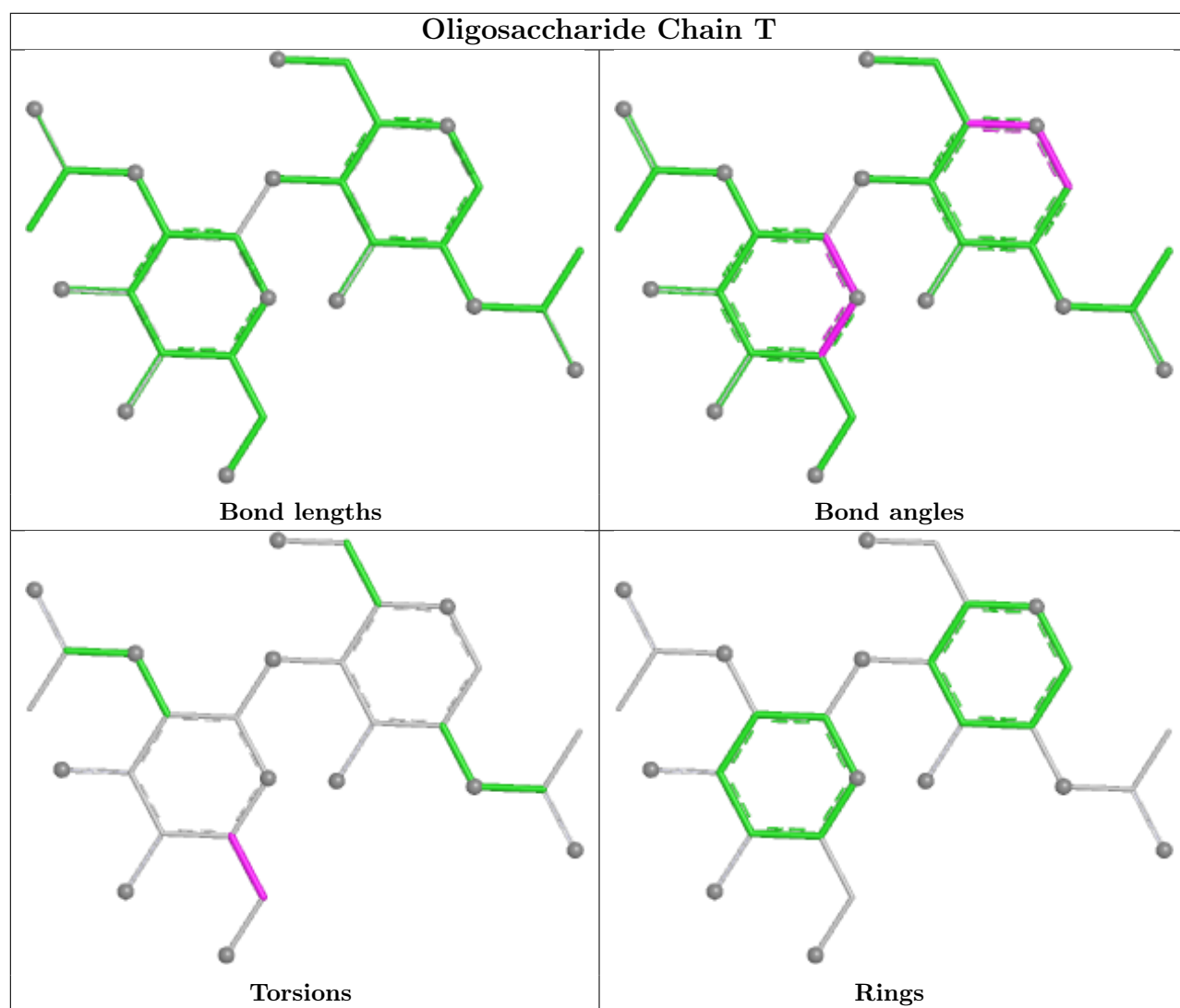


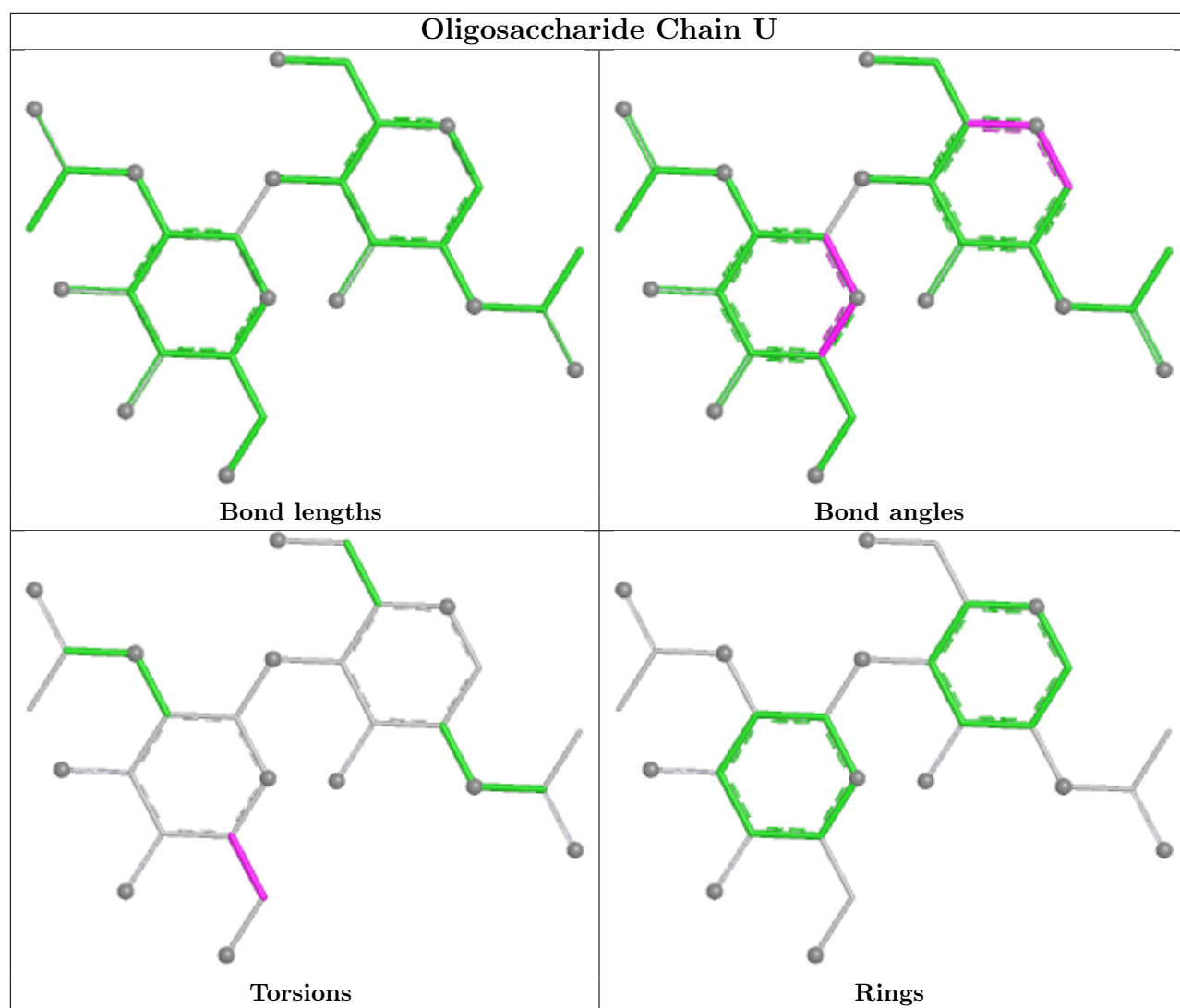


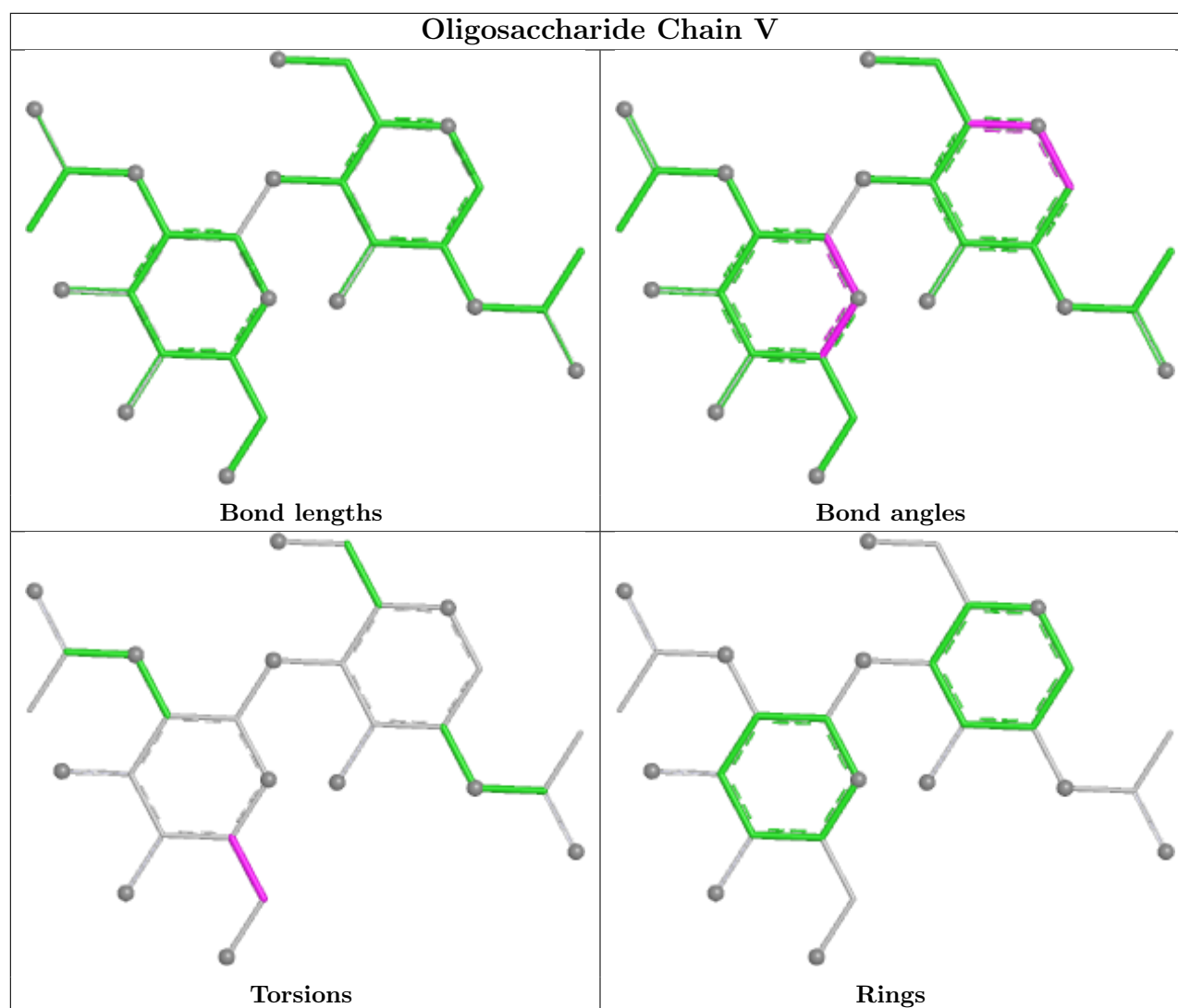












5.6 Ligand geometry [i](#)

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.

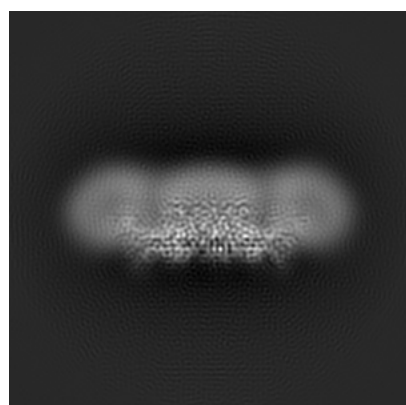
6 Map visualisation [i](#)

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.

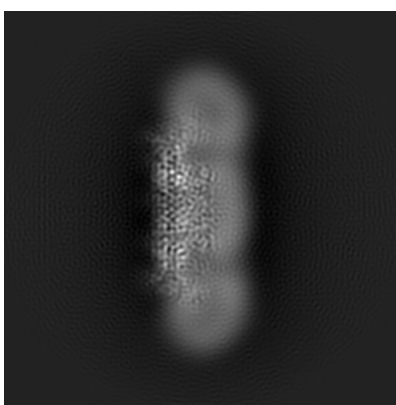
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

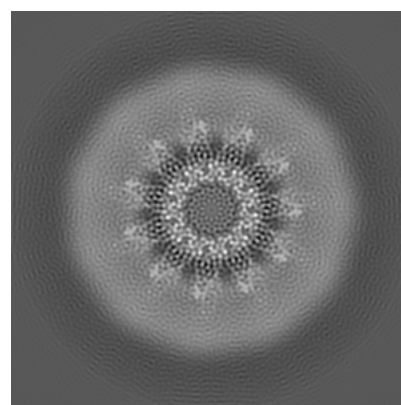
6.1.1 Primary map



X



Y

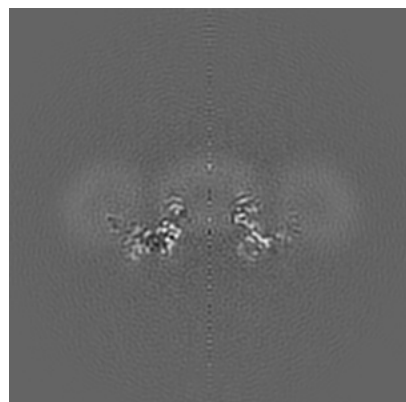


Z

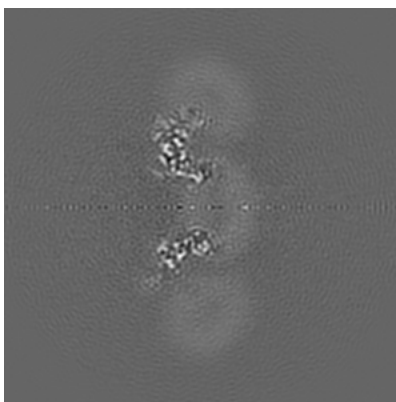
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

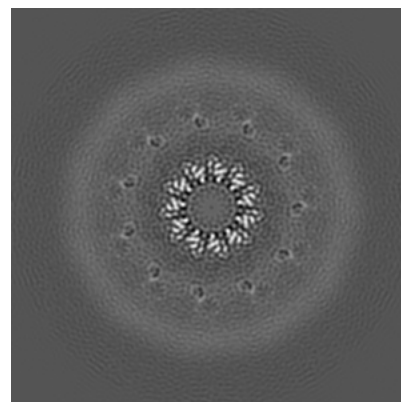
6.2.1 Primary map



X Index: 180



Y Index: 180

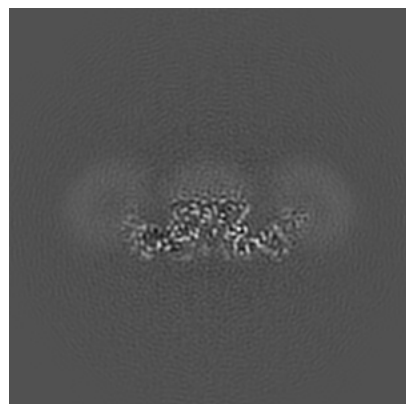


Z Index: 180

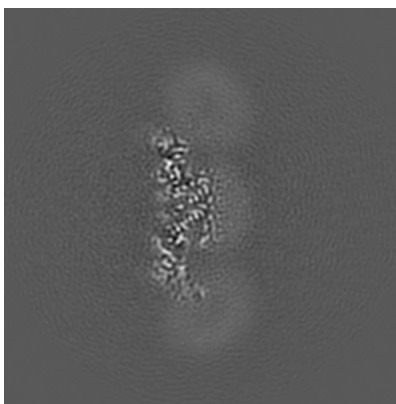
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

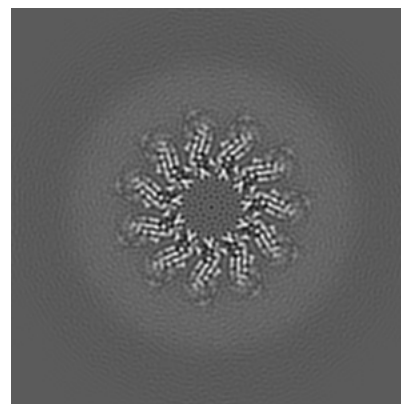
6.3.1 Primary map



X Index: 207



Y Index: 153

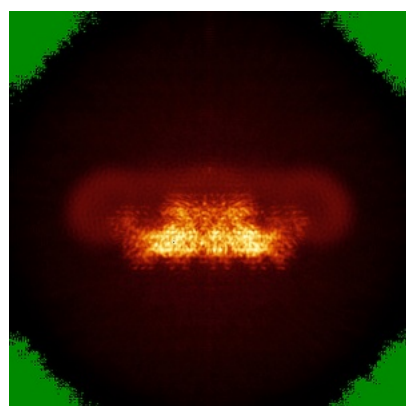


Z Index: 156

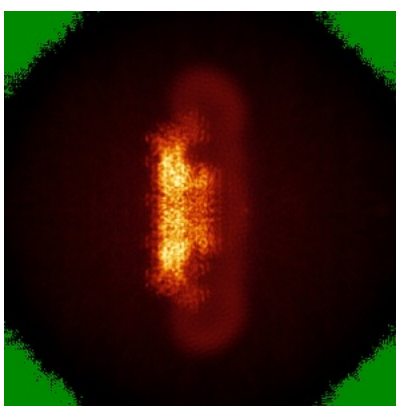
The images above show the largest variance slices of the map in three orthogonal directions.

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

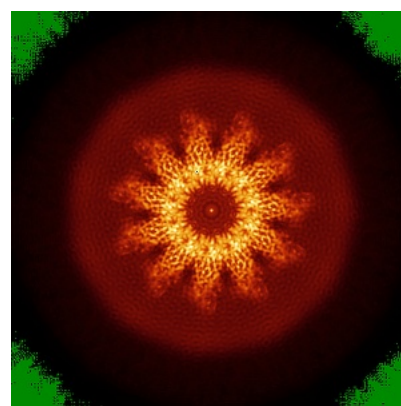
6.4.1 Primary map



X



Y

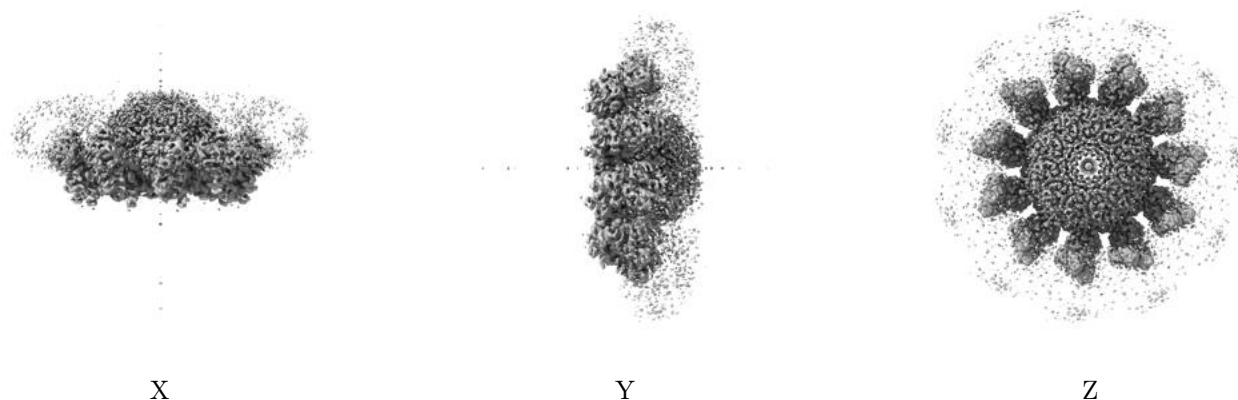


Z

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.

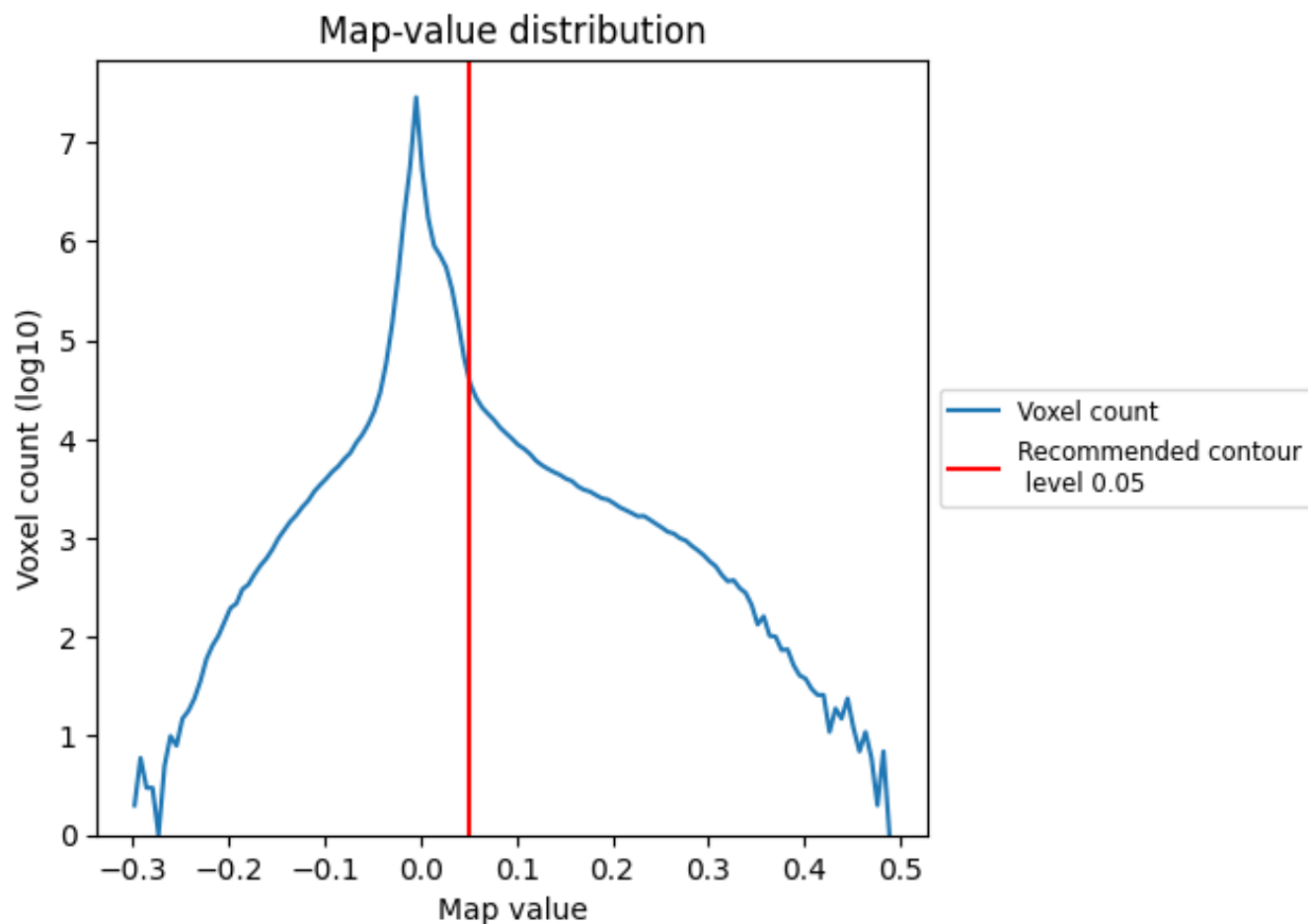
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

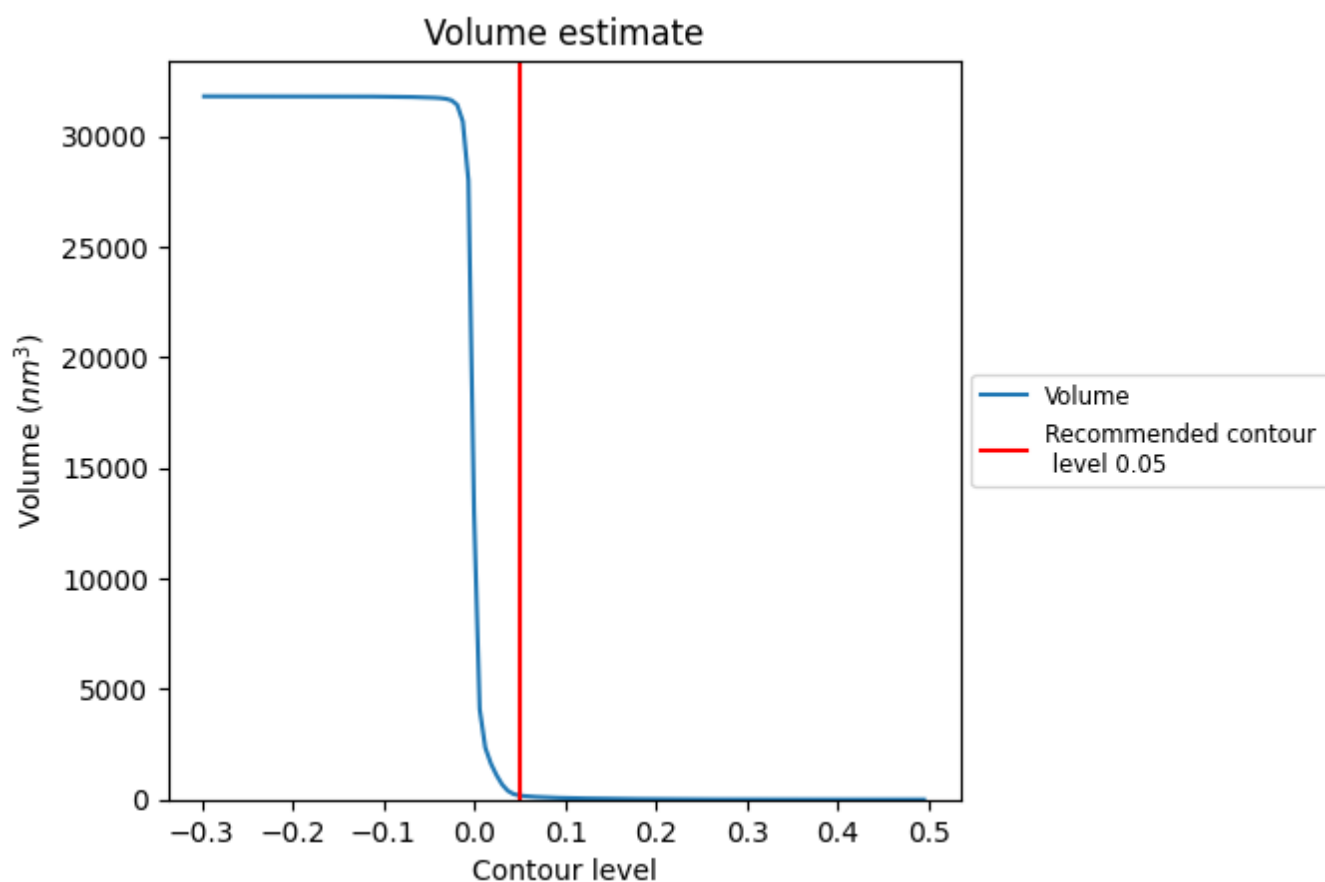
This section contains the results of statistical analysis of the map.

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.

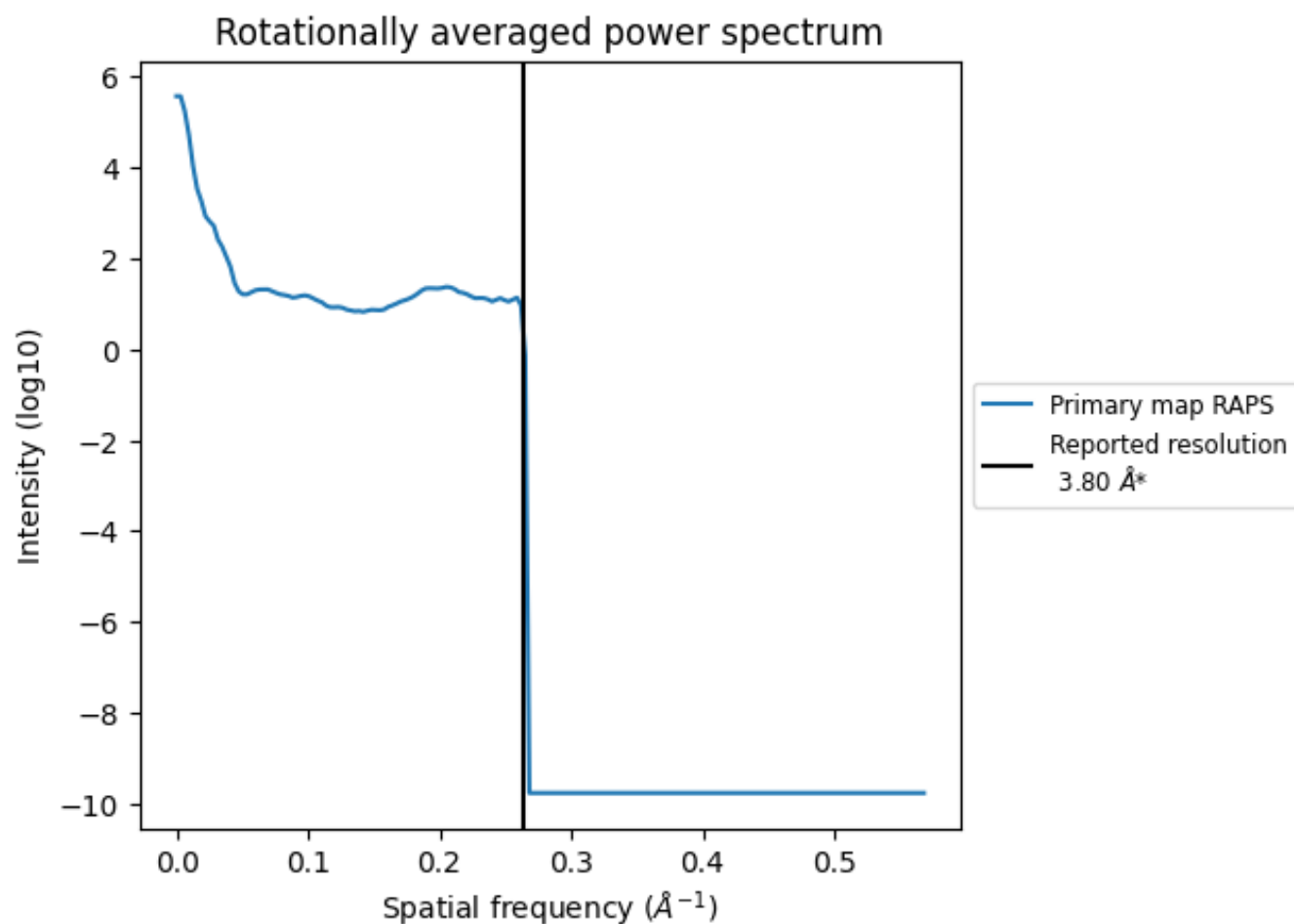
7.2 Volume estimate [i](#)



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

8 Fourier-Shell correlation ⓘ

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

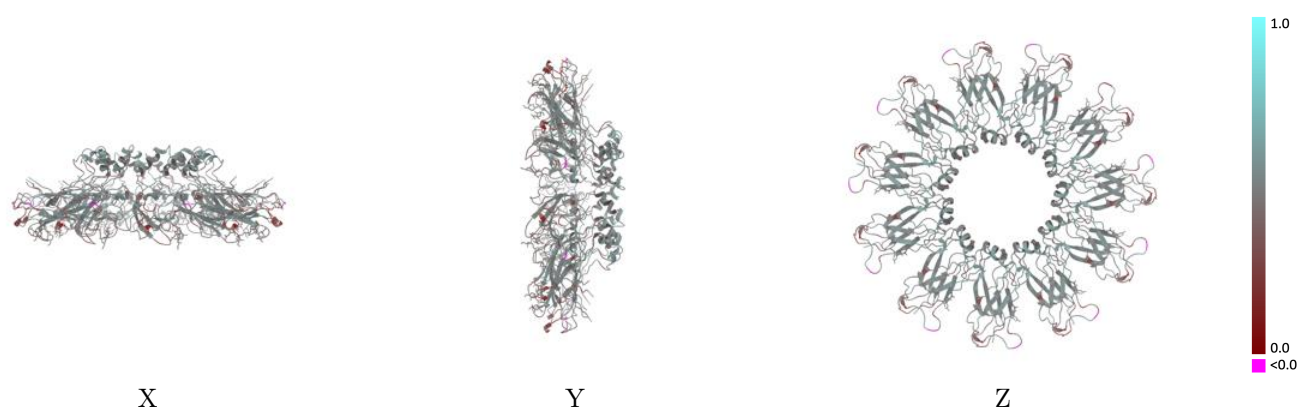
9 Map-model fit [i](#)

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](#)

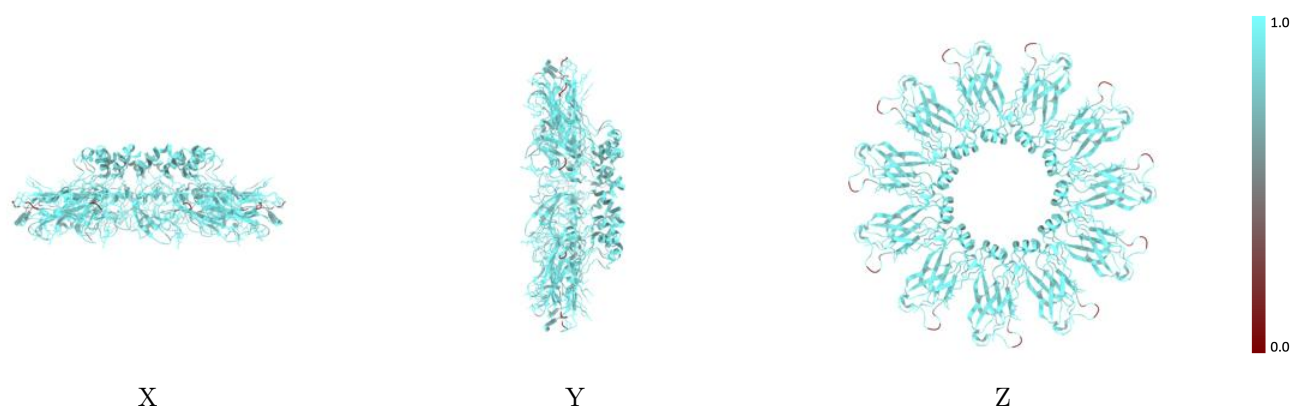
This section was not generated.

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



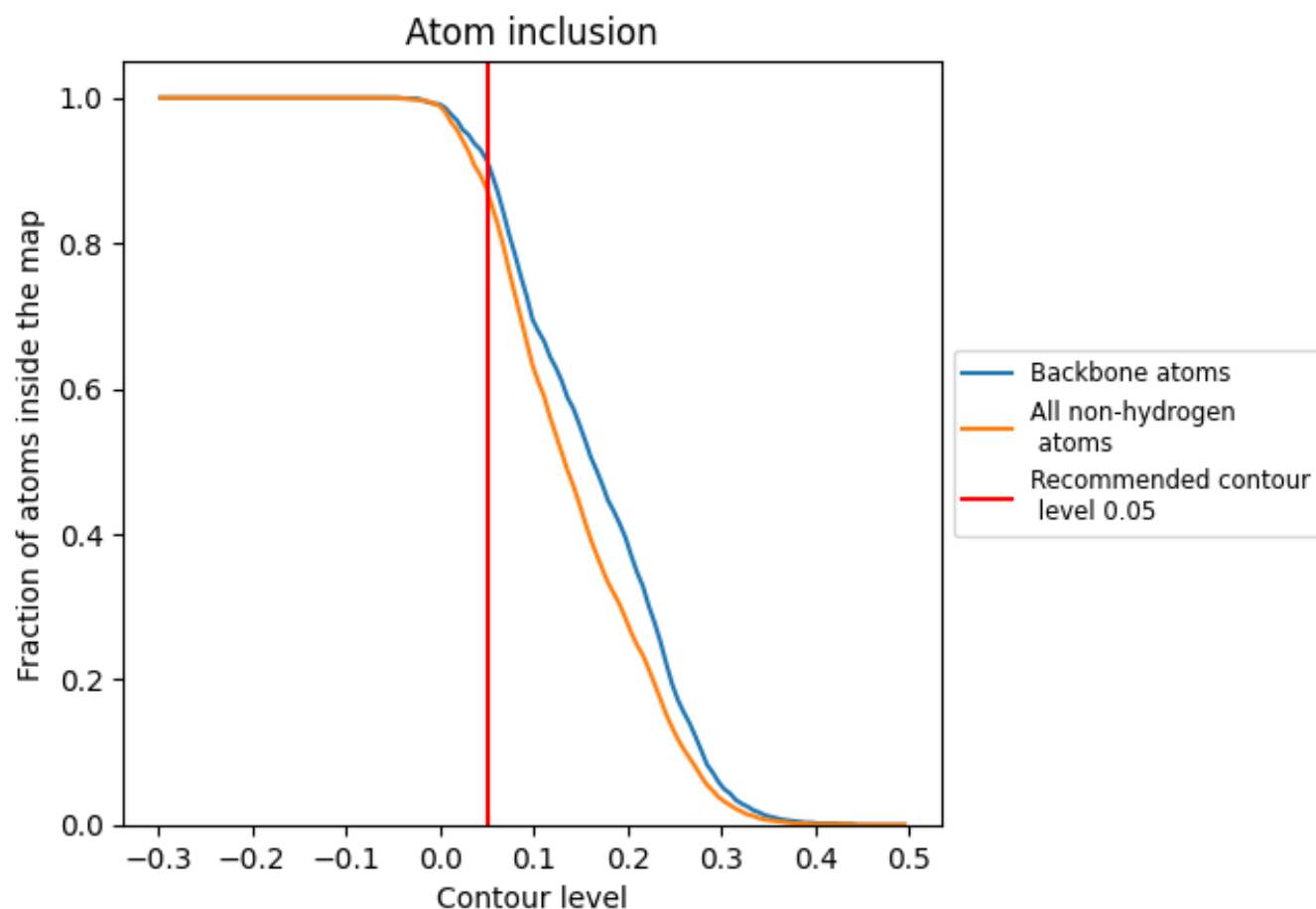
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

