



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 02:30 PM UTC

PDB ID : 7KC1 / pdb_00007kc1
EMDB ID : EMD-22804
Title : Cryo-EM structure of SRR2899884.46167H+MEDI8852L fab in complex with Victoria HA
Authors : Gorman, J.; Kwong, P.D.
Deposited on : 2020-10-04
Resolution : 3.41 Å(reported)
Based on initial model : 4O5N

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

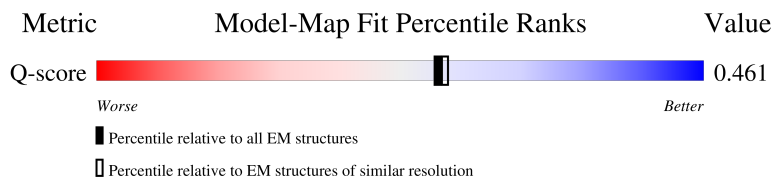
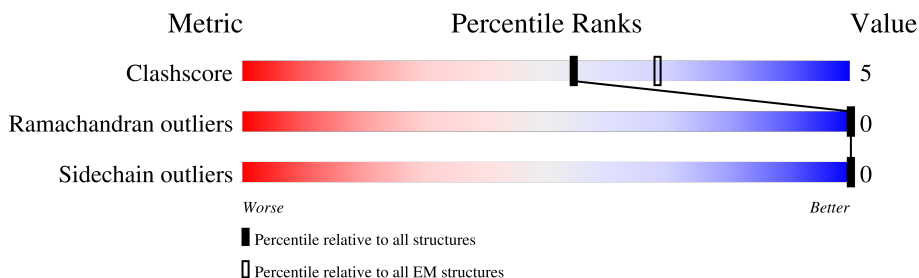
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.41 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.



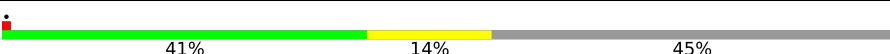
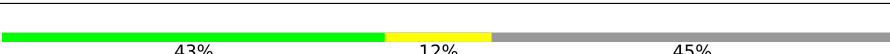
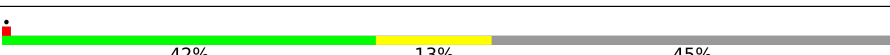
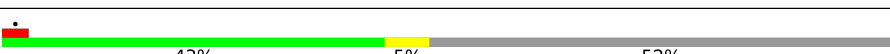
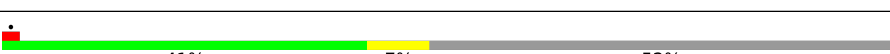
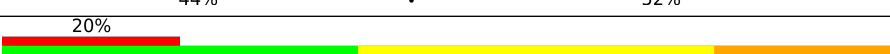
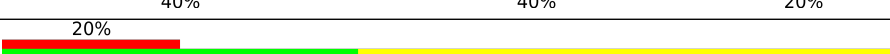
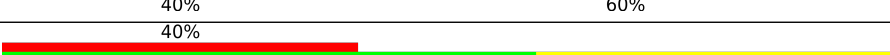
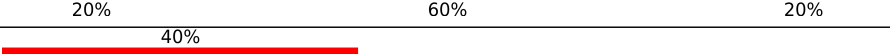
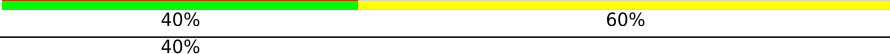
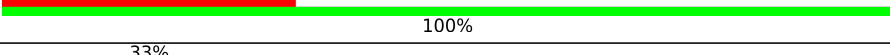
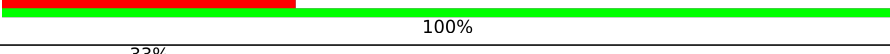
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13997 (2.91 - 3.91)

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	345	 79% 12% 9%
1	C	345	 79% 12% 9%
1	G	345	 78% 13% 9%
2	B	222	 64% 10% 26%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	222	
2	I	222	
3	E	227	
3	H	227	
3	J	227	
4	F	206	
4	K	206	
4	L	206	
5	M	5	
5	N	5	
5	O	5	
5	Q	5	
5	R	5	
5	S	5	
5	U	5	
5	V	5	
5	W	5	
6	P	3	
6	T	3	
6	X	3	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 17463 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	314	Total	C	N	O	S	0	0
			2467	1549	437	469	12		
1	C	314	Total	C	N	O	S	0	0
			2467	1549	437	469	12		
1	G	314	Total	C	N	O	S	0	0
			2467	1549	437	469	12		

- Molecule 2 is a protein called Fusion protein of Hemagglutinin and Envelope glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	164	Total	C	N	O	S	0	0
			1336	827	237	266	6		
2	D	164	Total	C	N	O	S	0	0
			1336	827	237	266	6		
2	I	164	Total	C	N	O	S	0	0
			1336	827	237	266	6		

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	SER	-	linker	UNP A0A2P1E3C0
B	178	GLY	-	linker	UNP A0A2P1E3C0
B	179	ARG	-	linker	UNP A0A2P1E3C0
B	180	LEU	-	linker	UNP A0A2P1E3C0
B	181	VAL	-	linker	UNP A0A2P1E3C0
B	182	PRO	-	linker	UNP A0A2P1E3C0
B	183	ARG	-	linker	UNP A0A2P1E3C0
B	184	GLY	-	linker	UNP A0A2P1E3C0
B	185	SER	-	linker	UNP A0A2P1E3C0
B	186	PRO	-	linker	UNP A0A2P1E3C0
B	187	GLY	-	linker	UNP A0A2P1E3C0
B	188	SER	-	linker	UNP A0A2P1E3C0
B	217	HIS	-	expression tag	UNP M1E1E4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	218	HIS	-	expression tag	UNP M1E1E4
B	219	HIS	-	expression tag	UNP M1E1E4
B	220	HIS	-	expression tag	UNP M1E1E4
B	221	HIS	-	expression tag	UNP M1E1E4
B	222	HIS	-	expression tag	UNP M1E1E4
D	177	SER	-	linker	UNP A0A2P1E3C0
D	178	GLY	-	linker	UNP A0A2P1E3C0
D	179	ARG	-	linker	UNP A0A2P1E3C0
D	180	LEU	-	linker	UNP A0A2P1E3C0
D	181	VAL	-	linker	UNP A0A2P1E3C0
D	182	PRO	-	linker	UNP A0A2P1E3C0
D	183	ARG	-	linker	UNP A0A2P1E3C0
D	184	GLY	-	linker	UNP A0A2P1E3C0
D	185	SER	-	linker	UNP A0A2P1E3C0
D	186	PRO	-	linker	UNP A0A2P1E3C0
D	187	GLY	-	linker	UNP A0A2P1E3C0
D	188	SER	-	linker	UNP A0A2P1E3C0
D	217	HIS	-	expression tag	UNP M1E1E4
D	218	HIS	-	expression tag	UNP M1E1E4
D	219	HIS	-	expression tag	UNP M1E1E4
D	220	HIS	-	expression tag	UNP M1E1E4
D	221	HIS	-	expression tag	UNP M1E1E4
D	222	HIS	-	expression tag	UNP M1E1E4
I	177	SER	-	linker	UNP A0A2P1E3C0
I	178	GLY	-	linker	UNP A0A2P1E3C0
I	179	ARG	-	linker	UNP A0A2P1E3C0
I	180	LEU	-	linker	UNP A0A2P1E3C0
I	181	VAL	-	linker	UNP A0A2P1E3C0
I	182	PRO	-	linker	UNP A0A2P1E3C0
I	183	ARG	-	linker	UNP A0A2P1E3C0
I	184	GLY	-	linker	UNP A0A2P1E3C0
I	185	SER	-	linker	UNP A0A2P1E3C0
I	186	PRO	-	linker	UNP A0A2P1E3C0
I	187	GLY	-	linker	UNP A0A2P1E3C0
I	188	SER	-	linker	UNP A0A2P1E3C0
I	217	HIS	-	expression tag	UNP M1E1E4
I	218	HIS	-	expression tag	UNP M1E1E4
I	219	HIS	-	expression tag	UNP M1E1E4
I	220	HIS	-	expression tag	UNP M1E1E4
I	221	HIS	-	expression tag	UNP M1E1E4
I	222	HIS	-	expression tag	UNP M1E1E4

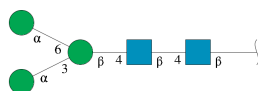
- Molecule 3 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	125	Total	C	N	O	S	0	0
			978	623	165	188	2		
3	E	125	Total	C	N	O	S	0	0
			978	623	165	188	2		
3	J	125	Total	C	N	O	S	0	0
			978	623	165	188	2		

- Molecule 4 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	99	Total	C	N	O	S	0	0
			748	464	129	152	3		
4	F	99	Total	C	N	O	S	0	0
			748	464	129	152	3		
4	K	99	Total	C	N	O	S	0	0
			748	464	129	152	3		

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



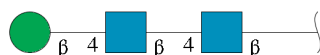
Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	5	Total	C	N	O	0	0
			61	34	2	25		
5	N	5	Total	C	N	O	0	0
			61	34	2	25		
5	O	5	Total	C	N	O	0	0
			61	34	2	25		
5	Q	5	Total	C	N	O	0	0
			61	34	2	25		
5	R	5	Total	C	N	O	0	0
			61	34	2	25		
5	S	5	Total	C	N	O	0	0
			61	34	2	25		
5	U	5	Total	C	N	O	0	0
			61	34	2	25		
5	V	5	Total	C	N	O	0	0
			61	34	2	25		

Continued on next page...

Continued from previous page...

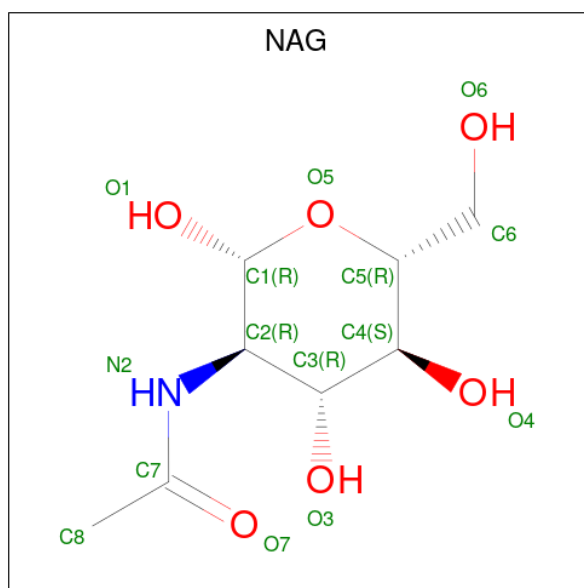
Mol	Chain	Residues	Atoms				AltConf	Trace
5	W	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
6	P	3	Total	C	N	O	0	0
			39	22	2	15		
6	T	3	Total	C	N	O	0	0
			39	22	2	15		
6	X	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

Continued on next page...

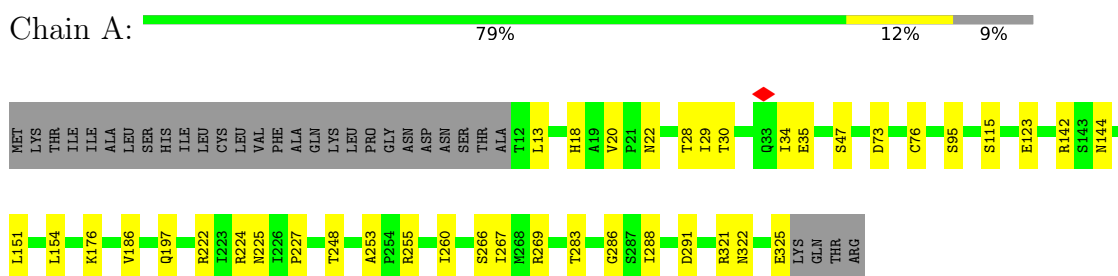
Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total 14	C 8	N 1	O 5	0
7	A	1	Total 14	C 8	N 1	O 5	0
7	B	1	Total 14	C 8	N 1	O 5	0
7	C	1	Total 14	C 8	N 1	O 5	0
7	C	1	Total 14	C 8	N 1	O 5	0
7	C	1	Total 14	C 8	N 1	O 5	0
7	C	1	Total 14	C 8	N 1	O 5	0
7	D	1	Total 14	C 8	N 1	O 5	0
7	G	1	Total 14	C 8	N 1	O 5	0
7	G	1	Total 14	C 8	N 1	O 5	0
7	G	1	Total 14	C 8	N 1	O 5	0
7	G	1	Total 14	C 8	N 1	O 5	0
7	I	1	Total 14	C 8	N 1	O 5	0

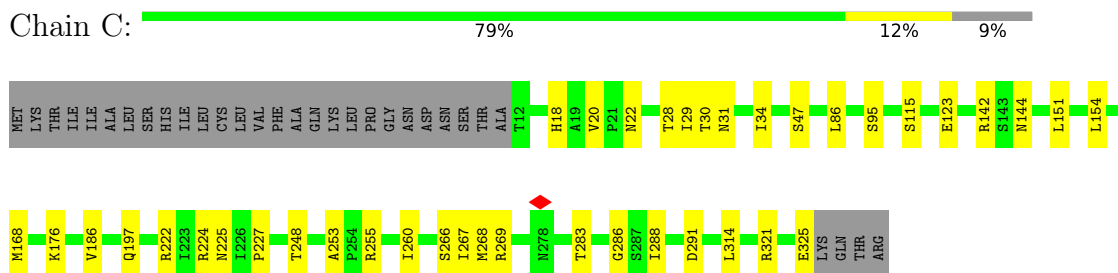
3 Residue-property plots [i](#)

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.

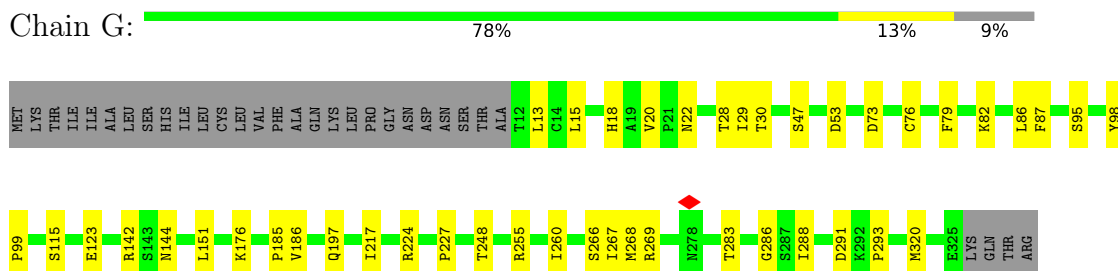
• Molecule 1: Hemagglutinin



• Molecule 1: Hemagglutinin



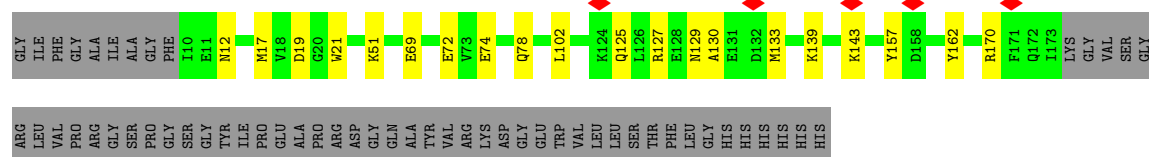
• Molecule 1: Hemagglutinin



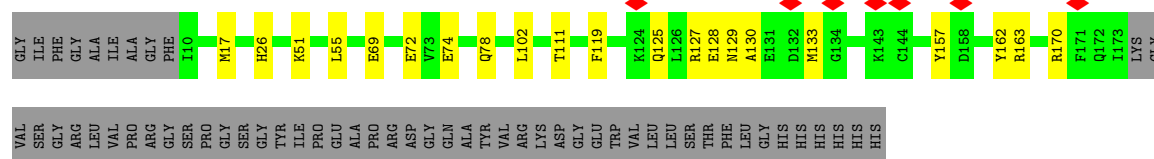
• Molecule 2: Fusion protein of Hemagglutinin and Envelope glycoprotein



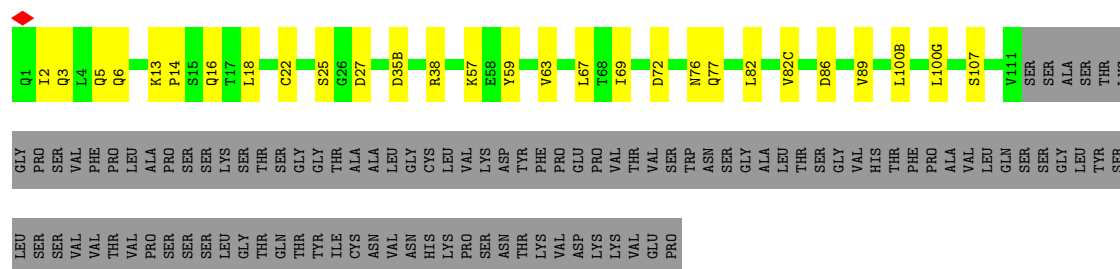
- Molecule 2: Fusion protein of Hemagglutinin and Envelope glycoprotein



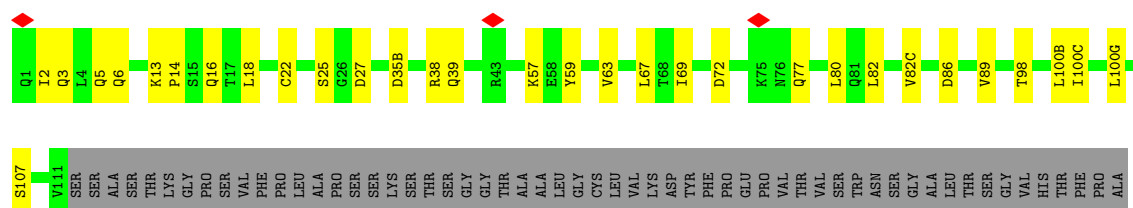
- Molecule 2: Fusion protein of Hemagglutinin and Envelope glycoprotein



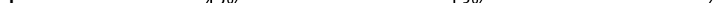
- Molecule 3: Fab heavy chain

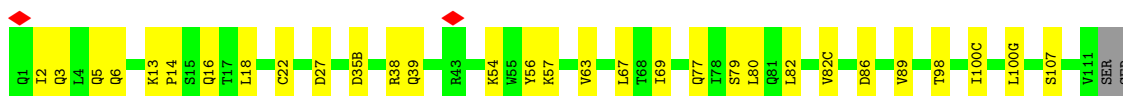


- Molecule 3: Fab heavy chain



- Molecule 3: Fab heavy chain

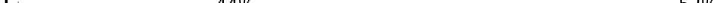
Chain J: 

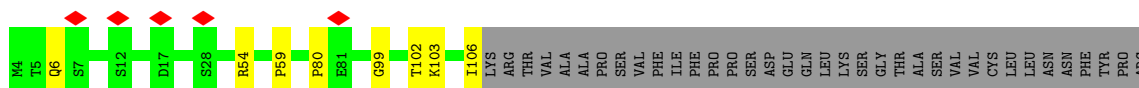


ALA	SER	THR	LYS	GLY	PRO	SER	VAL	PHE	PRO	LEU	ALA	PRO	SER	LYS	SER	THR	SER	GLY	GLY	THR	LYS	ALA	ALA	ALA	LEU	GLY	CYS	VAL	VAL	LYS	ASP	TYR	PHE	GLU	PRO	VAL	THR	VAL	SER	TRP	ASN	SER	GLY	LEU	ALA	THR	GLY	VAL	HIS	PHE	THR	PRO	ALA	VAL	LEU	GLN	SER	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----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

GLY	LEU	TYR	SER	SER	SER	SER	VAL	VAL	THR	THR	VAL	PRO	SER	SER	SER	SER	LEU	GLY	THR	GLN	THR	TYR	ILE	CYS	ASN	ASN	VAL	ASN	ASN	HIS	LYS	PRO	SER	SER	ASN	THR	THR	LYS	VAL	ASP	LYS	LYS	VAL	GLU	PRO
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 4: Fab light chain

Chain L:  44% 52%

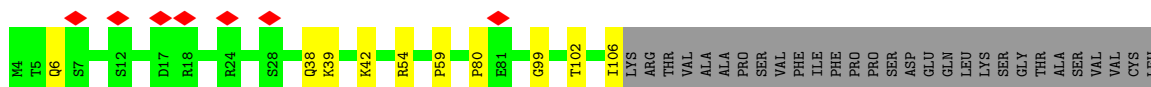


GLU	ALA	LYS	VAL	GLN	TRP	LYS	VAL	ASP	ASN	LEU	GLN	SER	GLY	ASN	SER	GLU	SER	VAL	THR	GLU	GLN	ASP	SER	LYS	SER	SER	THR	THR	TYR	SER	LEU	SER	LYS	HIS	LYS	VAL	TYR	ALA	CYS	GLU	VAL	THR	HIS	GLN	GLY	LEU	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

SER
PRO
VAL
THR
LYS
SER
PHE
ASN
ARG
GLY
GLU

- Molecule 4: Fab light chain

Chain F: 43% 5% 52%



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

VAL
THR
HIS
GLN
GLY
LEU
SER
SER
PRO
VAL
THR
LYS
SER
PHE
ASN
ARG
GLY
GLU

- Molecule 4: Fab light chain

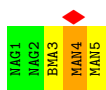
Chain K:



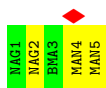
ALA	SER	VAL	VAL	CYS	LEU	LEU	ASN	ASN	ASN	PHE	TYR	PRO	ARG	GLU	GLY	ALA	LYS	VAL	GLN	TRP	LYS	VAL	ASP	ASN	ALA	LEU	GLN	SER	GLY	ASN	SER	GLN	GLU	SER	VAL	THR	GLU	GLN	ASP	SER	LYS	ASP	SER	SER	THR	TYR	SER	LEU	THR	LEU	SER	LYS	ASP	TYR	GLU	LYS	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----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

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

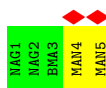
- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



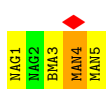
- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



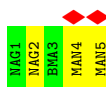
- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

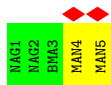


- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



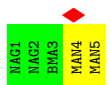
- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S: 



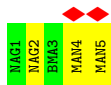
- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U: 



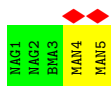
- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V: 



- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W: 



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P: 



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29735	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 ($e^-/\text{\AA}^2$)	71.06	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.764	Depositor
Minimum map value	-0.903	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.071	Depositor
Recommended contour level	0.6	Depositor
Map size ($\text{\AA}$)	377.78403, 377.78403, 377.78403	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07325, 1.07325, 1.07325	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.12	0/2523	0.31	0/3432
1	C	0.12	0/2523	0.32	0/3432
1	G	0.12	0/2523	0.31	0/3432
2	B	0.07	0/1358	0.21	0/1823
2	D	0.08	0/1358	0.22	0/1823
2	I	0.09	0/1358	0.24	0/1823
3	E	0.16	0/1001	0.44	0/1365
3	H	0.13	0/1001	0.38	0/1365
3	J	0.13	0/1001	0.38	0/1365
4	F	0.10	0/764	0.30	0/1034
4	K	0.10	0/764	0.30	0/1034
4	L	0.10	0/764	0.29	0/1034
All	All	0.11	0/16938	0.31	0/22962

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2467	0	2416	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2467	0	2416	24	0
1	G	2467	0	2416	28	0
2	B	1336	0	1265	18	0
2	D	1336	0	1265	17	0
2	I	1336	0	1265	18	0
3	E	978	0	970	19	0
3	H	978	0	970	16	0
3	J	978	0	970	16	0
4	F	748	0	724	6	0
4	K	748	0	724	8	0
4	L	748	0	724	5	0
5	M	61	0	52	1	0
5	N	61	0	52	0	0
5	O	61	0	52	0	0
5	Q	61	0	52	2	0
5	R	61	0	52	0	0
5	S	61	0	52	0	0
5	U	61	0	52	0	0
5	V	61	0	52	0	0
5	W	61	0	52	0	0
6	P	39	0	34	0	0
6	T	39	0	34	0	0
6	X	39	0	34	0	0
7	A	56	0	52	0	0
7	B	14	0	13	0	0
7	C	56	0	52	0	0
7	D	14	0	13	0	0
7	G	56	0	52	0	0
7	I	14	0	13	0	0
All	All	17463	0	16890	176	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 5.

The worst 5 of 176 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:3:GLN:HE22	3:J:5:GLN:HB2	1.56	0.70
3:E:3:GLN:HE22	3:E:5:GLN:HB2	1.58	0.69
2:B:133:MET:SD	2:I:127:ARG:NH1	2.63	0.69
2:I:130:ALA:HA	2:I:170:ARG:HH11	1.59	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:130:ALA:HA	2:B:170:ARG:HH11	1.60	0.66

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	312/345 (90%)	304 (97%)	8 (3%)	0	100	100
1	C	312/345 (90%)	301 (96%)	11 (4%)	0	100	100
1	G	312/345 (90%)	304 (97%)	8 (3%)	0	100	100
2	B	162/222 (73%)	159 (98%)	3 (2%)	0	100	100
2	D	162/222 (73%)	158 (98%)	4 (2%)	0	100	100
2	I	162/222 (73%)	159 (98%)	3 (2%)	0	100	100
3	E	123/227 (54%)	115 (94%)	8 (6%)	0	100	100
3	H	123/227 (54%)	116 (94%)	7 (6%)	0	100	100
3	J	123/227 (54%)	115 (94%)	8 (6%)	0	100	100
4	F	97/206 (47%)	92 (95%)	5 (5%)	0	100	100
4	K	97/206 (47%)	92 (95%)	5 (5%)	0	100	100
4	L	97/206 (47%)	92 (95%)	5 (5%)	0	100	100
All	All	2082/3000 (69%)	2007 (96%)	75 (4%)	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	280/307 (91%)	280 (100%)	0	100	100
1	C	280/307 (91%)	280 (100%)	0	100	100
1	G	280/307 (91%)	280 (100%)	0	100	100
2	B	142/185 (77%)	142 (100%)	0	100	100
2	D	142/185 (77%)	142 (100%)	0	100	100
2	I	142/185 (77%)	142 (100%)	0	100	100
3	E	108/196 (55%)	108 (100%)	0	100	100
3	H	108/196 (55%)	108 (100%)	0	100	100
3	J	108/196 (55%)	108 (100%)	0	100	100
4	F	85/181 (47%)	85 (100%)	0	100	100
4	K	85/181 (47%)	85 (100%)	0	100	100
4	L	85/181 (47%)	85 (100%)	0	100	100
All	All	1845/2607 (71%)	1845 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	49	ASN
2	I	146	ASN
4	K	90	GLN
3	J	3	GLN
2	I	129	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

54 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	M	1	5,1	14,14,15	0.29	0	17,19,21	0.54	0
5	NAG	M	2	5	14,14,15	0.23	0	17,19,21	0.45	0
5	BMA	M	3	5	11,11,12	0.63	0	15,15,17	0.70	0
5	MAN	M	4	5	11,11,12	0.71	0	15,15,17	1.00	2 (13%)
5	MAN	M	5	5	11,11,12	0.70	0	15,15,17	1.01	2 (13%)
5	NAG	N	1	5,1	14,14,15	0.21	0	17,19,21	0.41	0
5	NAG	N	2	5	14,14,15	0.34	0	17,19,21	0.88	1 (5%)
5	BMA	N	3	5	11,11,12	0.64	0	15,15,17	0.72	0
5	MAN	N	4	5	11,11,12	0.72	0	15,15,17	0.92	2 (13%)
5	MAN	N	5	5	11,11,12	0.69	0	15,15,17	1.03	2 (13%)
5	NAG	O	1	5,1	14,14,15	0.19	0	17,19,21	0.48	0
5	NAG	O	2	5	14,14,15	0.25	0	17,19,21	0.58	0
5	BMA	O	3	5	11,11,12	0.64	0	15,15,17	0.69	0
5	MAN	O	4	5	11,11,12	0.70	0	15,15,17	1.01	2 (13%)
5	MAN	O	5	5	11,11,12	0.67	0	15,15,17	0.99	2 (13%)
6	NAG	P	1	6,1	14,14,15	0.23	0	17,19,21	0.45	0
6	NAG	P	2	6	14,14,15	0.26	0	17,19,21	0.43	0
6	BMA	P	3	6	11,11,12	0.63	0	15,15,17	0.78	0
5	NAG	Q	1	5,1	14,14,15	0.28	0	17,19,21	0.54	0
5	NAG	Q	2	5	14,14,15	0.23	0	17,19,21	0.43	0
5	BMA	Q	3	5	11,11,12	0.63	0	15,15,17	0.72	0
5	MAN	Q	4	5	11,11,12	0.71	0	15,15,17	1.00	2 (13%)
5	MAN	Q	5	5	11,11,12	0.71	0	15,15,17	1.02	2 (13%)
5	NAG	R	1	5,1	14,14,15	0.20	0	17,19,21	0.41	0
5	NAG	R	2	5	14,14,15	0.34	0	17,19,21	0.88	1 (5%)
5	BMA	R	3	5	11,11,12	0.65	0	15,15,17	0.72	0
5	MAN	R	4	5	11,11,12	0.72	0	15,15,17	0.93	2 (13%)
5	MAN	R	5	5	11,11,12	0.69	0	15,15,17	1.02	2 (13%)
5	NAG	S	1	5,1	14,14,15	0.18	0	17,19,21	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	S	2	5	14,14,15	0.24	0	17,19,21	0.57	0
5	BMA	S	3	5	11,11,12	0.63	0	15,15,17	0.69	0
5	MAN	S	4	5	11,11,12	0.69	0	15,15,17	1.02	2 (13%)
5	MAN	S	5	5	11,11,12	0.67	0	15,15,17	1.01	2 (13%)
6	NAG	T	1	6,1	14,14,15	0.24	0	17,19,21	0.40	0
6	NAG	T	2	6	14,14,15	0.23	0	17,19,21	0.43	0
6	BMA	T	3	6	11,11,12	0.62	0	15,15,17	0.77	0
5	NAG	U	1	5,1	14,14,15	0.29	0	17,19,21	0.55	0
5	NAG	U	2	5	14,14,15	0.22	0	17,19,21	0.44	0
5	BMA	U	3	5	11,11,12	0.63	0	15,15,17	0.71	0
5	MAN	U	4	5	11,11,12	0.72	0	15,15,17	1.00	2 (13%)
5	MAN	U	5	5	11,11,12	0.70	0	15,15,17	1.01	2 (13%)
5	NAG	V	1	5,1	14,14,15	0.20	0	17,19,21	0.41	0
5	NAG	V	2	5	14,14,15	0.35	0	17,19,21	0.87	1 (5%)
5	BMA	V	3	5	11,11,12	0.64	0	15,15,17	0.72	0
5	MAN	V	4	5	11,11,12	0.71	0	15,15,17	0.92	2 (13%)
5	MAN	V	5	5	11,11,12	0.70	0	15,15,17	1.03	2 (13%)
5	NAG	W	1	5,1	14,14,15	0.19	0	17,19,21	0.48	0
5	NAG	W	2	5	14,14,15	0.24	0	17,19,21	0.57	0
5	BMA	W	3	5	11,11,12	0.64	0	15,15,17	0.69	0
5	MAN	W	4	5	11,11,12	0.69	0	15,15,17	1.02	2 (13%)
5	MAN	W	5	5	11,11,12	0.69	0	15,15,17	1.00	2 (13%)
6	NAG	X	1	6,1	14,14,15	0.24	0	17,19,21	0.44	0
6	NAG	X	2	6	14,14,15	0.24	0	17,19,21	0.44	0
6	BMA	X	3	6	11,11,12	0.63	0	15,15,17	0.78	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	M	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	2/6/23/26	0/1/1/1
5	BMA	M	3	5	-	2/2/19/22	0/1/1/1
5	MAN	M	4	5	-	1/2/19/22	0/1/1/1
5	MAN	M	5	5	-	0/2/19/22	0/1/1/1
5	NAG	N	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	N	2	5	-	4/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BMA	N	3	5	-	0/2/19/22	0/1/1/1
5	MAN	N	4	5	-	0/2/19/22	0/1/1/1
5	MAN	N	5	5	-	0/2/19/22	0/1/1/1
5	NAG	O	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	O	2	5	-	1/6/23/26	0/1/1/1
5	BMA	O	3	5	-	2/2/19/22	0/1/1/1
5	MAN	O	4	5	-	0/2/19/22	0/1/1/1
5	MAN	O	5	5	-	0/2/19/22	0/1/1/1
6	NAG	P	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	P	2	6	-	2/6/23/26	0/1/1/1
6	BMA	P	3	6	-	0/2/19/22	0/1/1/1
5	NAG	Q	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	2/6/23/26	0/1/1/1
5	BMA	Q	3	5	-	2/2/19/22	0/1/1/1
5	MAN	Q	4	5	-	1/2/19/22	0/1/1/1
5	MAN	Q	5	5	-	0/2/19/22	0/1/1/1
5	NAG	R	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	R	2	5	-	4/6/23/26	0/1/1/1
5	BMA	R	3	5	-	0/2/19/22	0/1/1/1
5	MAN	R	4	5	-	0/2/19/22	0/1/1/1
5	MAN	R	5	5	-	0/2/19/22	0/1/1/1
5	NAG	S	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	S	2	5	-	1/6/23/26	0/1/1/1
5	BMA	S	3	5	-	2/2/19/22	0/1/1/1
5	MAN	S	4	5	-	0/2/19/22	0/1/1/1
5	MAN	S	5	5	-	0/2/19/22	0/1/1/1
6	NAG	T	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	T	2	6	-	2/6/23/26	0/1/1/1
6	BMA	T	3	6	-	0/2/19/22	0/1/1/1
5	NAG	U	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	U	2	5	-	2/6/23/26	0/1/1/1
5	BMA	U	3	5	-	2/2/19/22	0/1/1/1
5	MAN	U	4	5	-	1/2/19/22	0/1/1/1
5	MAN	U	5	5	-	0/2/19/22	0/1/1/1
5	NAG	V	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	V	2	5	-	4/6/23/26	0/1/1/1
5	BMA	V	3	5	-	0/2/19/22	0/1/1/1
5	MAN	V	4	5	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MAN	V	5	5	-	0/2/19/22	0/1/1/1
5	NAG	W	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	W	2	5	-	1/6/23/26	0/1/1/1
5	BMA	W	3	5	-	2/2/19/22	0/1/1/1
5	MAN	W	4	5	-	0/2/19/22	0/1/1/1
5	MAN	W	5	5	-	0/2/19/22	0/1/1/1
6	NAG	X	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	X	2	6	-	2/6/23/26	0/1/1/1
6	BMA	X	3	6	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	V	5	MAN	C1-O5-C5	2.72	115.84	112.19
5	N	5	MAN	C1-O5-C5	2.71	115.81	112.19
5	R	5	MAN	C1-O5-C5	2.68	115.77	112.19
5	M	4	MAN	C1-O5-C5	2.62	115.69	112.19
5	Q	4	MAN	C1-O5-C5	2.61	115.69	112.19

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

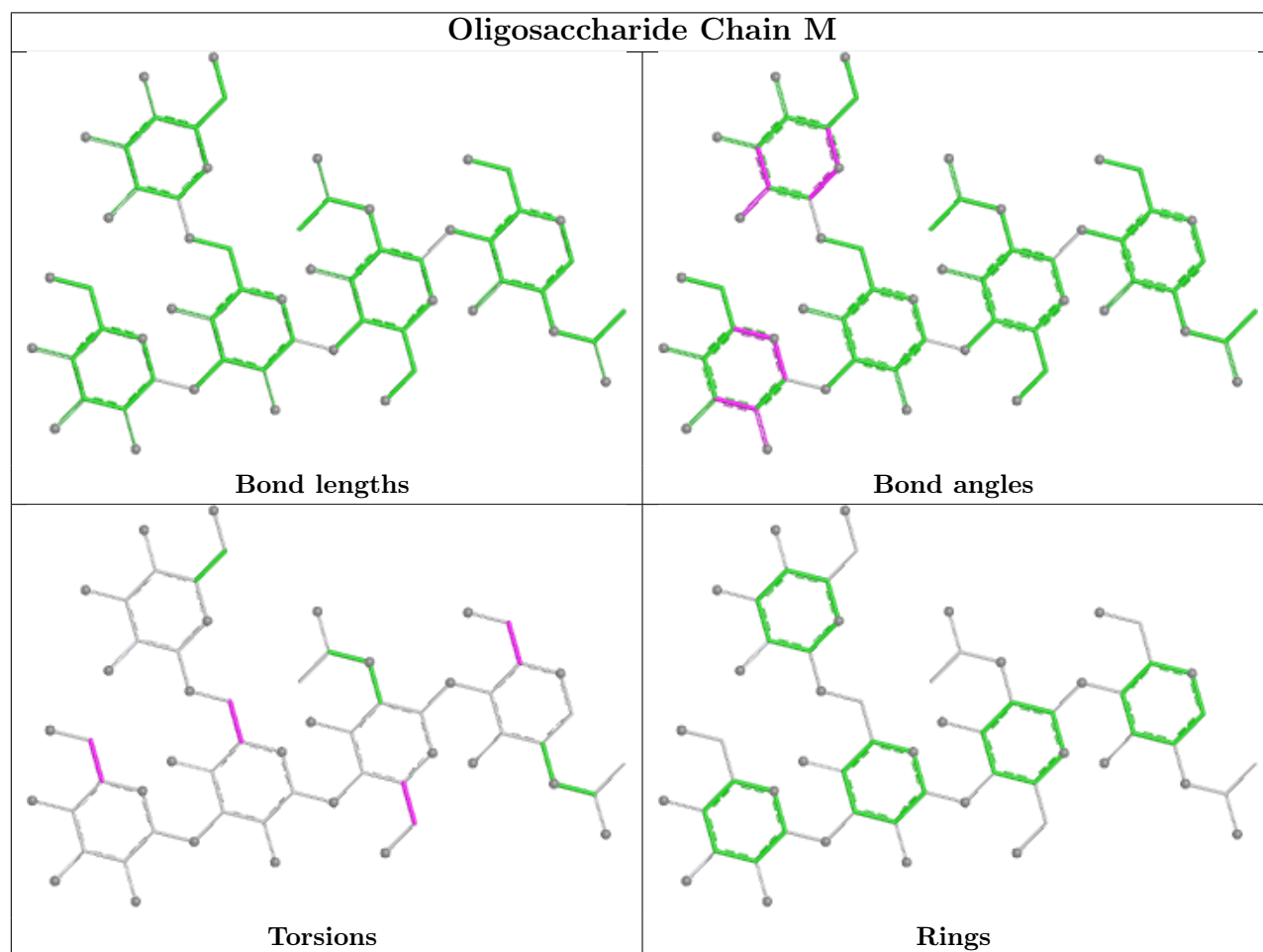
Mol	Chain	Res	Type	Atoms
5	O	3	BMA	C4-C5-C6-O6
5	S	3	BMA	C4-C5-C6-O6
5	W	3	BMA	C4-C5-C6-O6
5	Q	2	NAG	O5-C5-C6-O6
5	S	3	BMA	O5-C5-C6-O6

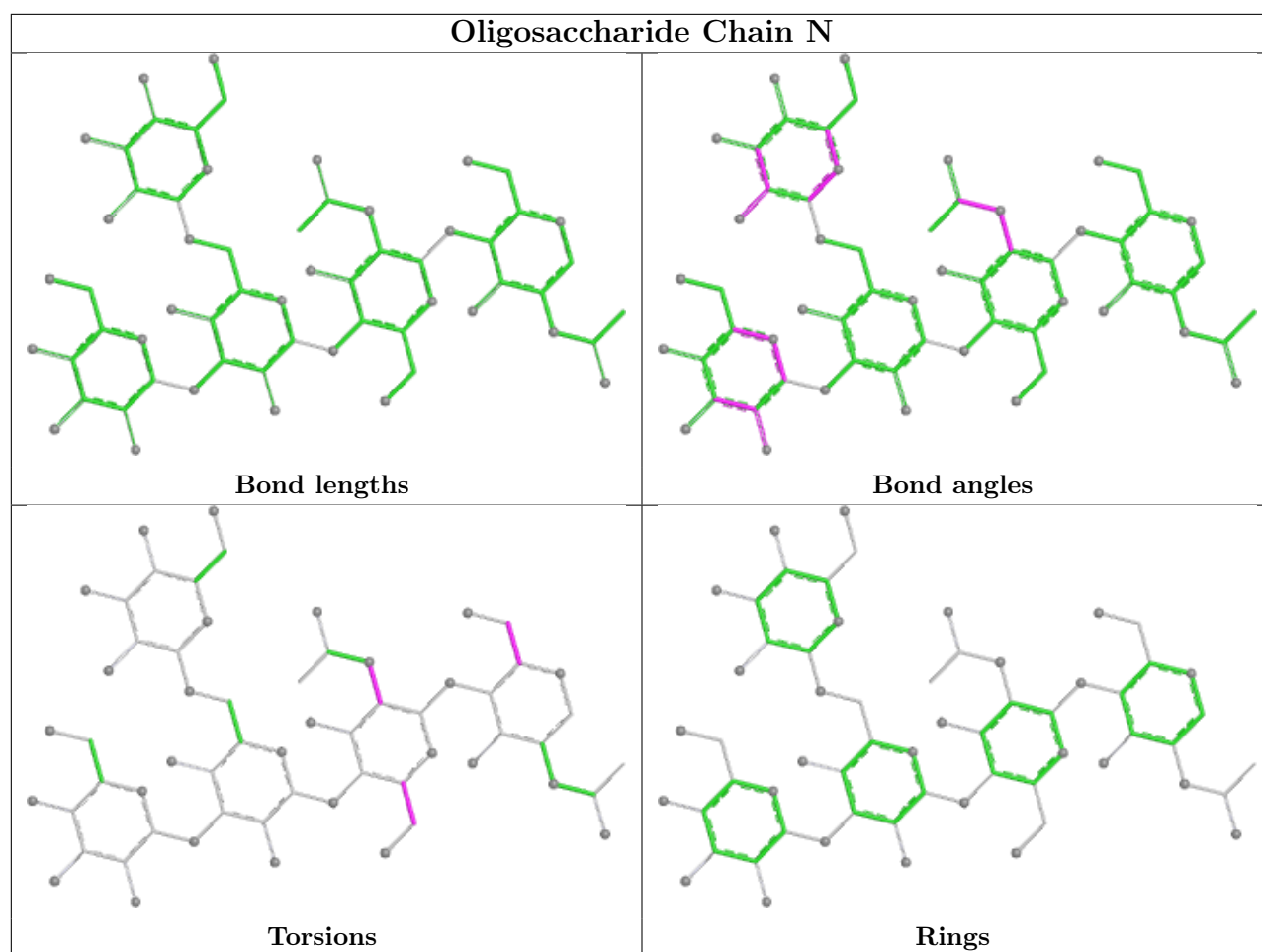
There are no ring outliers.

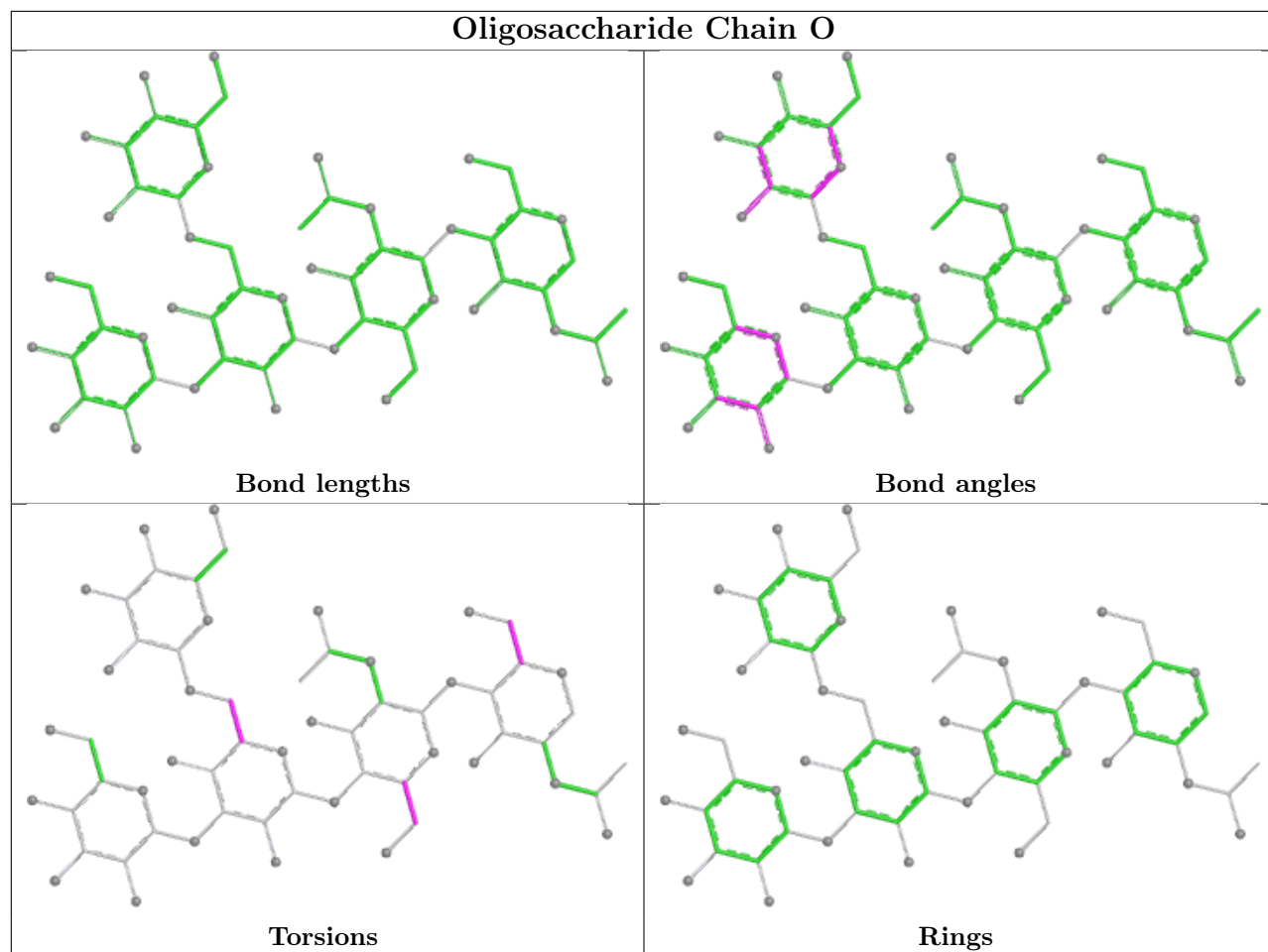
5 monomers are involved in 3 short contacts:

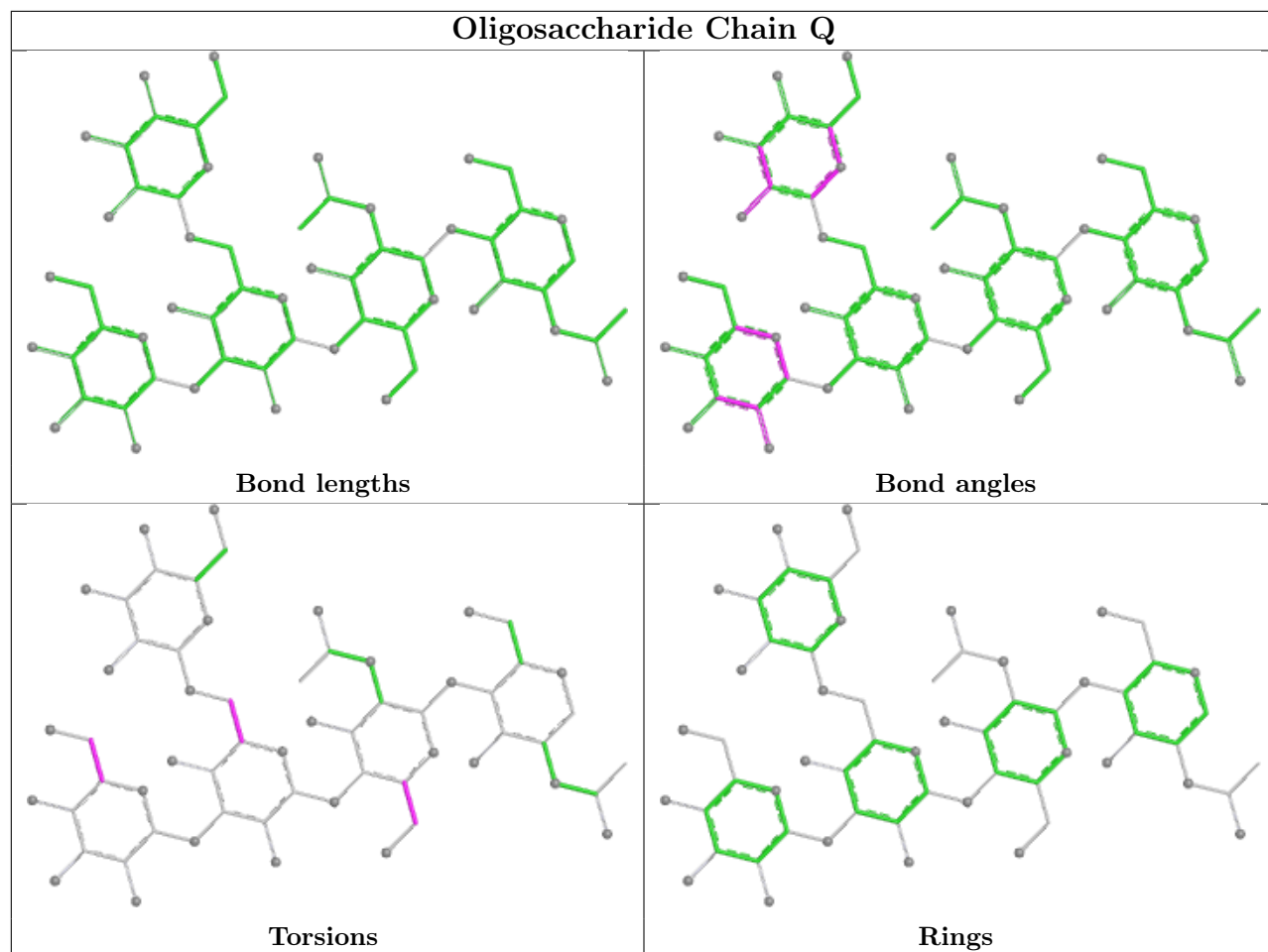
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	Q	1	NAG	1	0
5	Q	3	BMA	1	0
5	M	3	BMA	1	0
5	Q	4	MAN	1	0
5	M	4	MAN	1	0

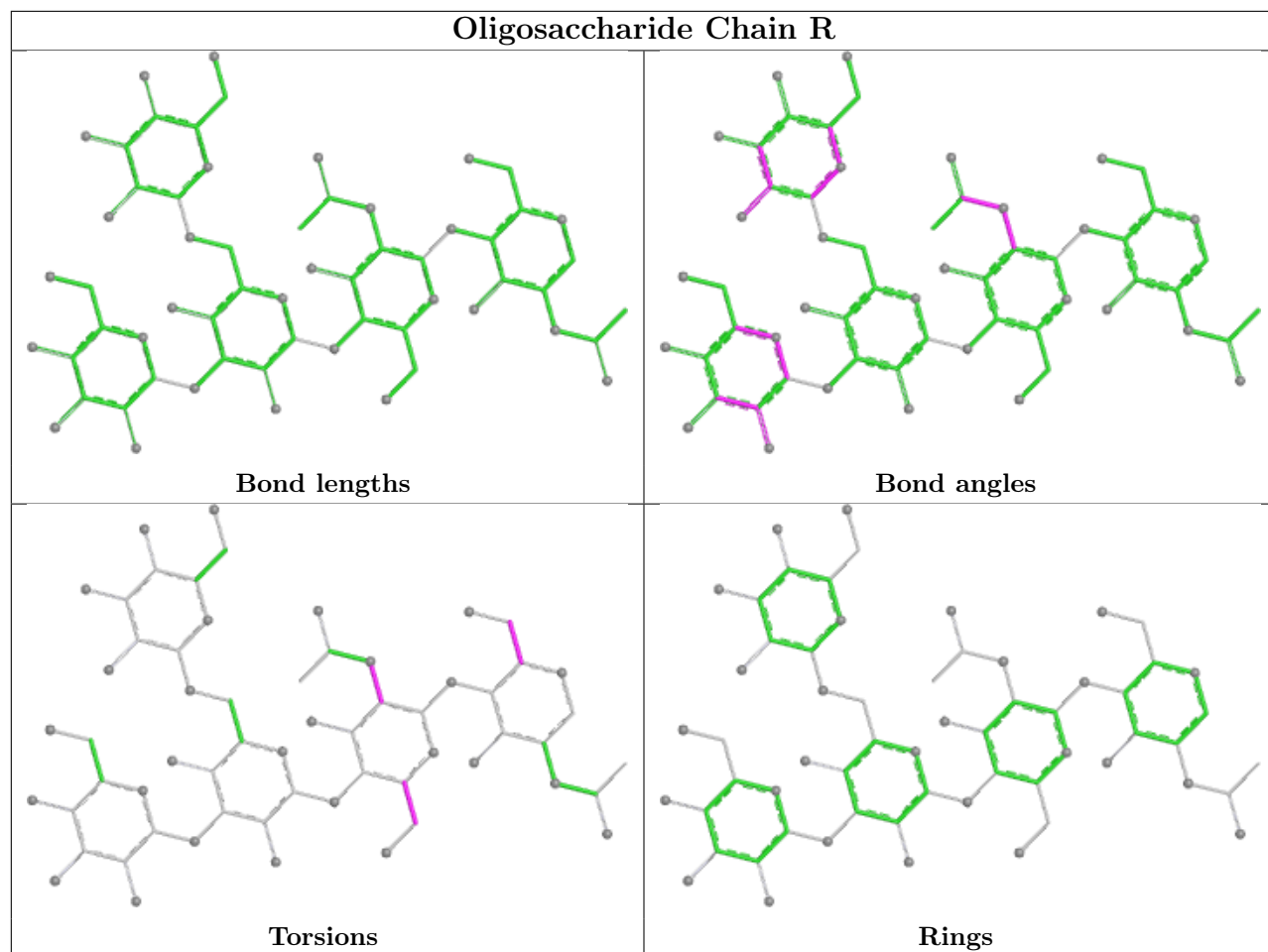
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

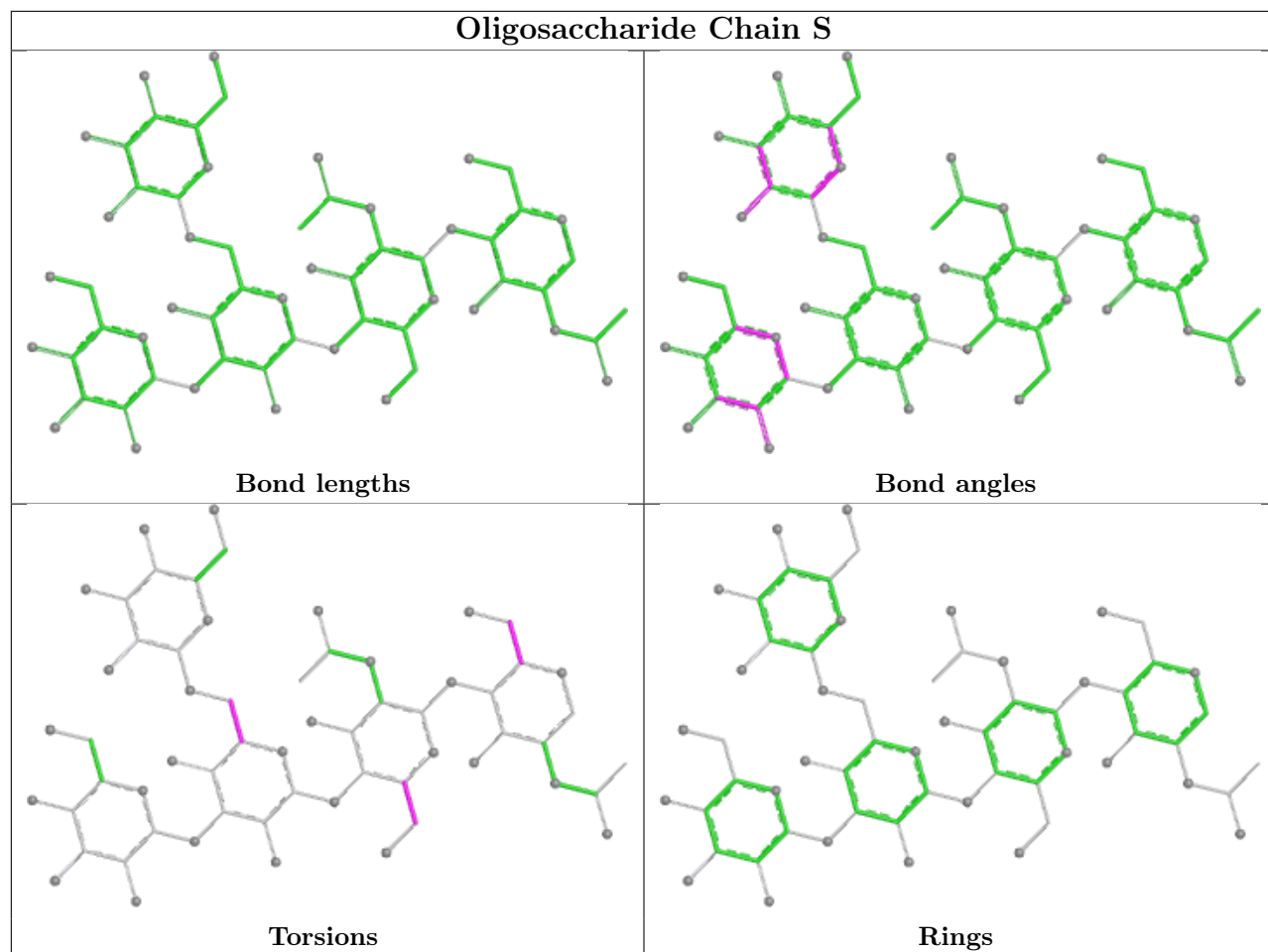


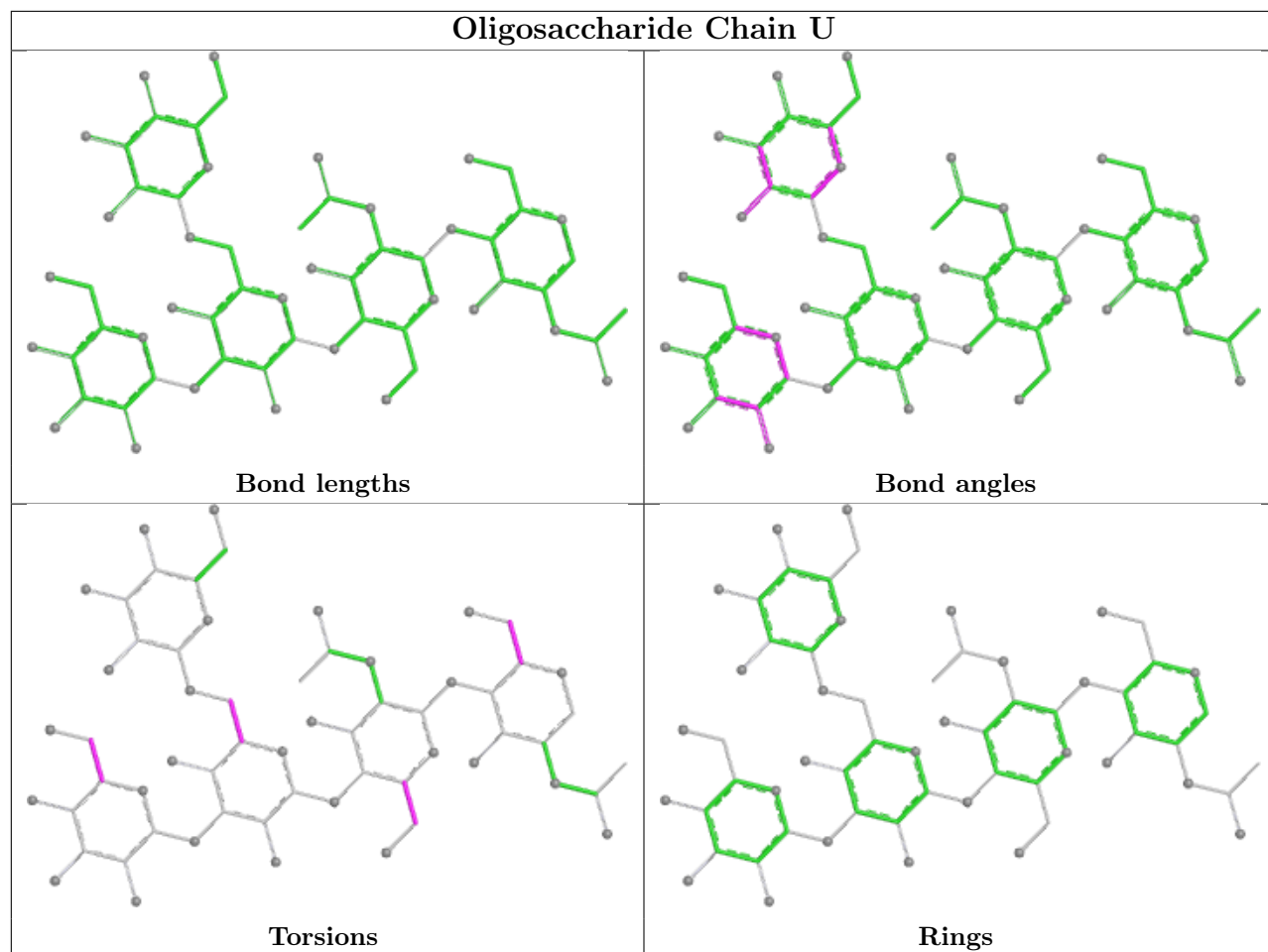


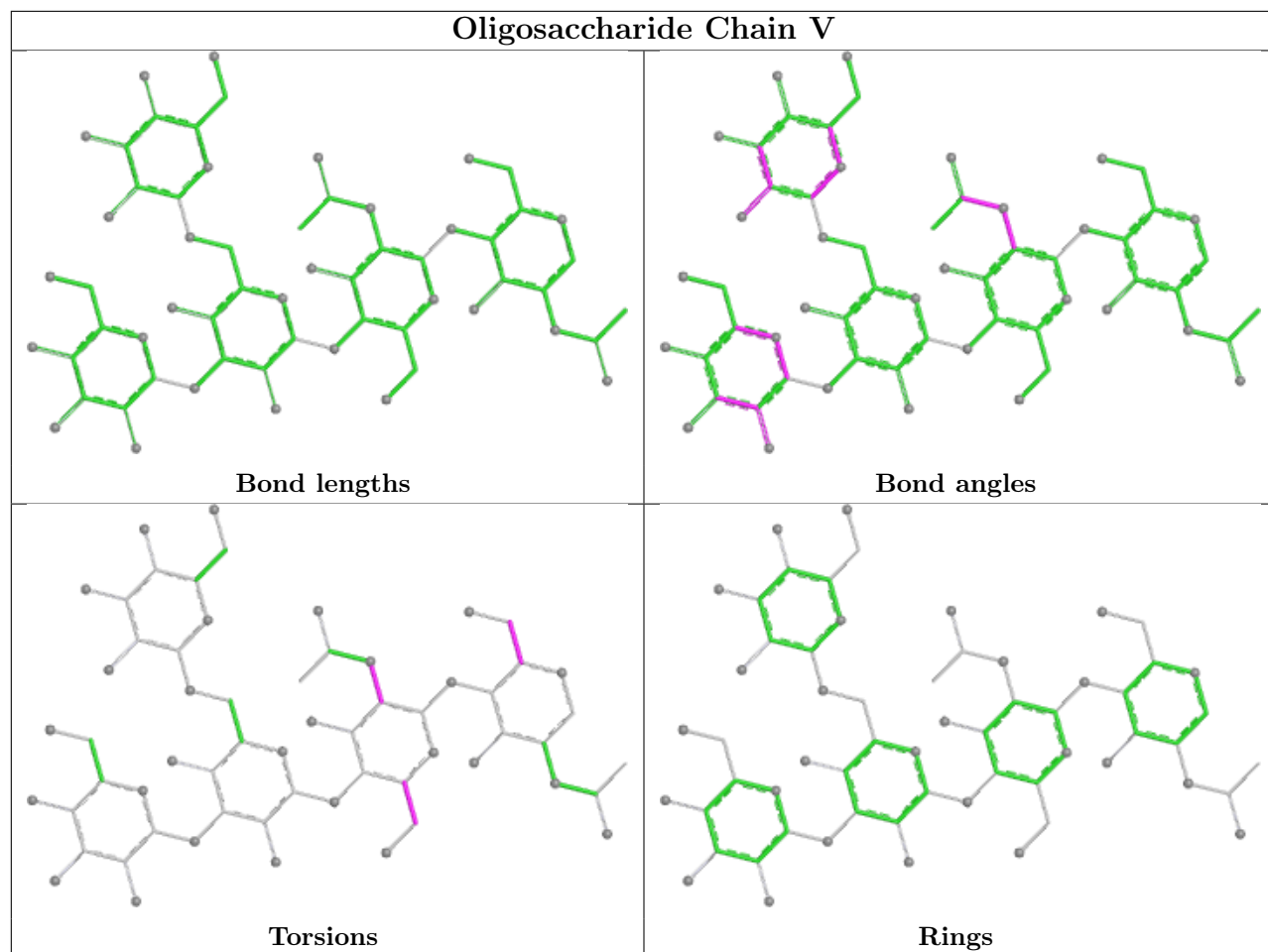


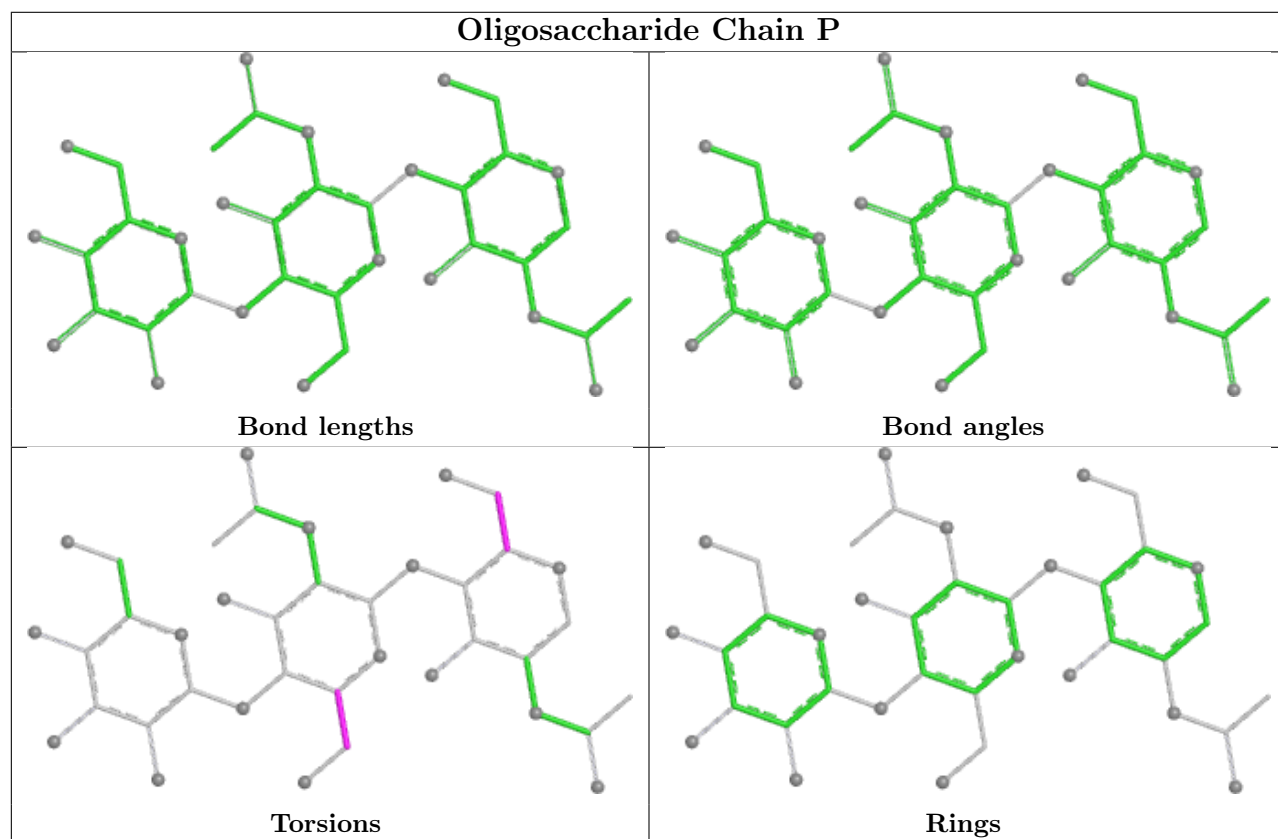
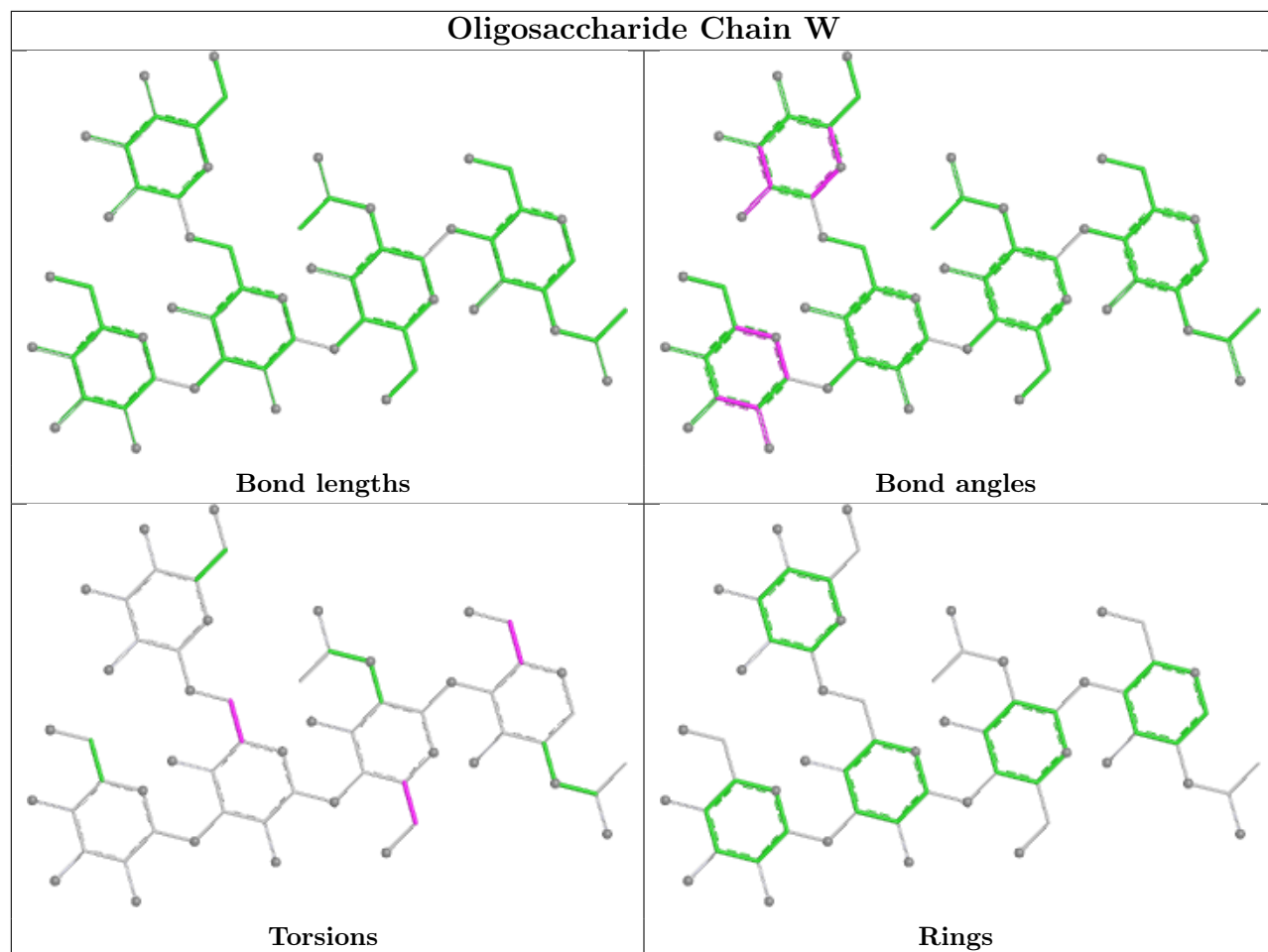


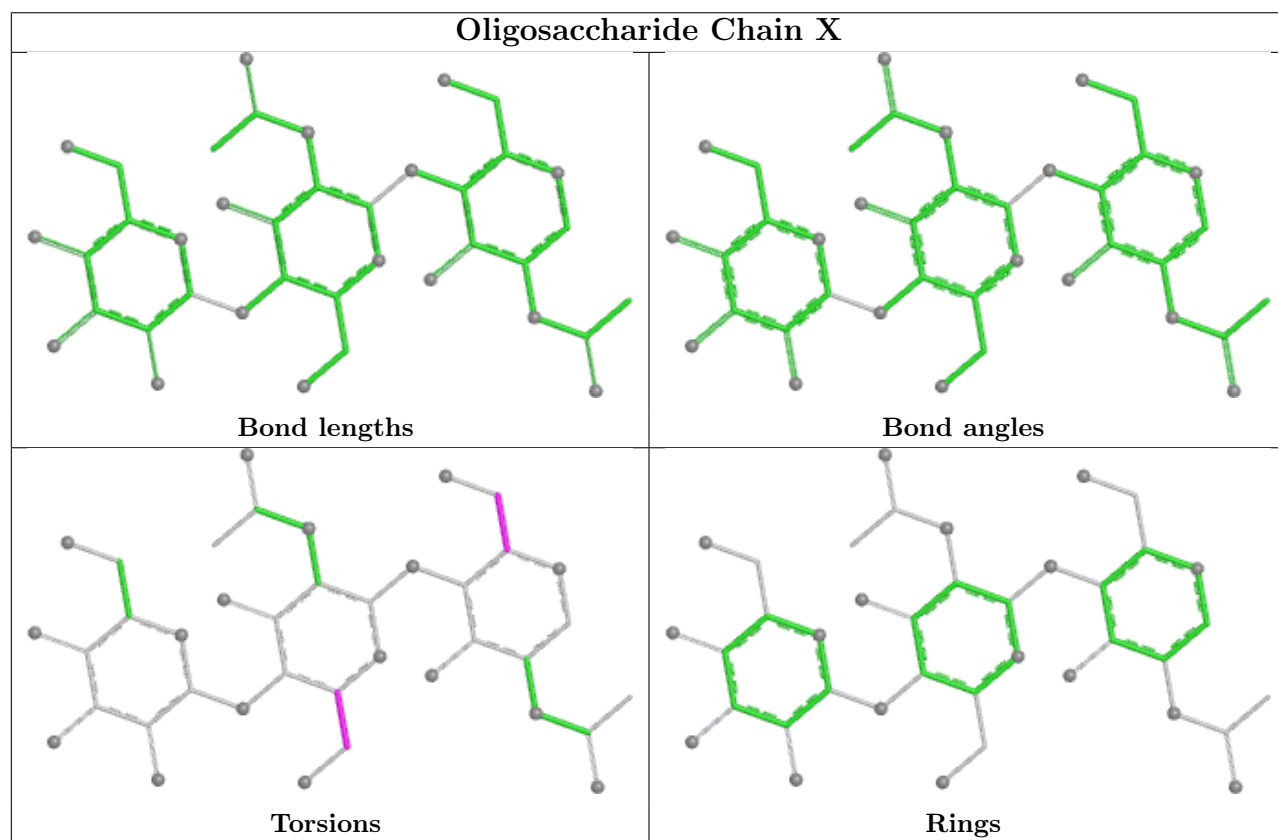
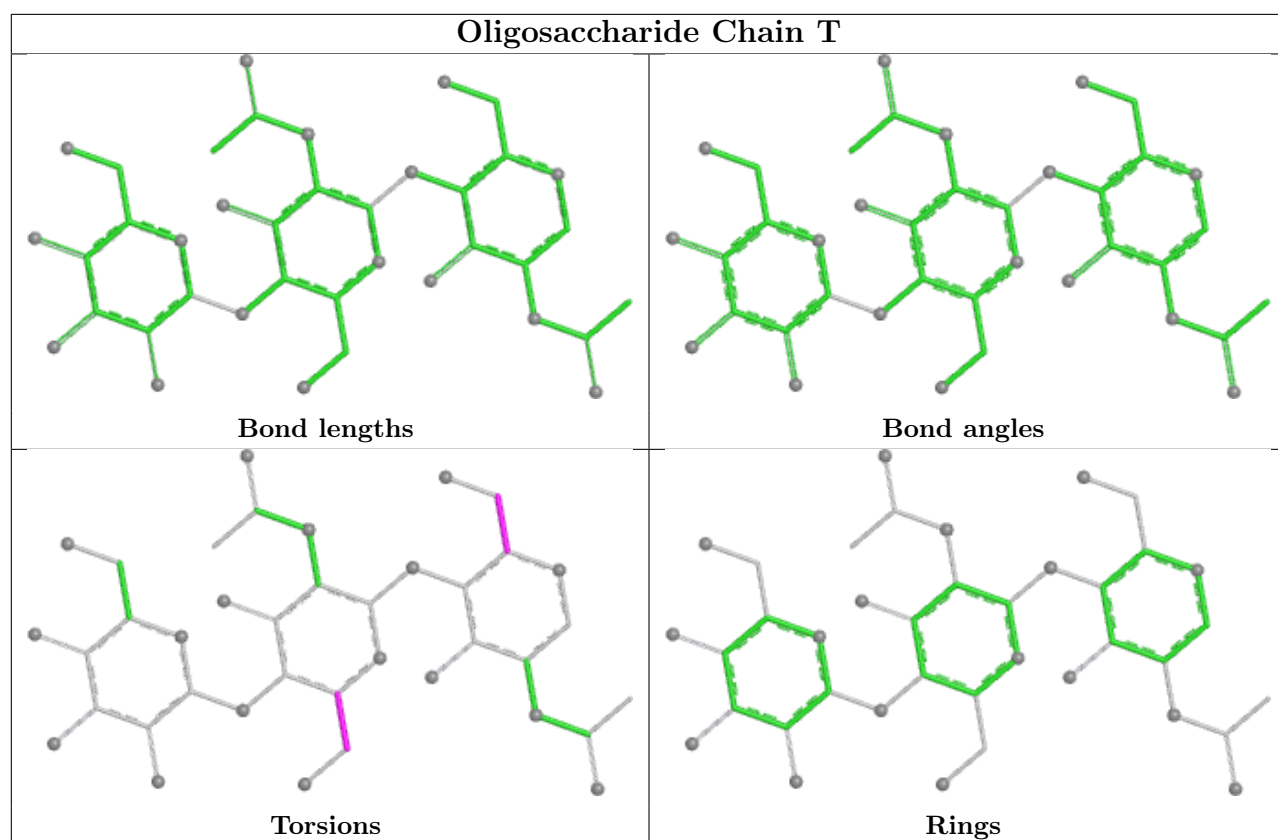












5.6 Ligand geometry

15 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	NAG	B	301	2	14,14,15	0.27	0	17,19,21	0.50	0
7	NAG	A	402	1	14,14,15	0.25	0	17,19,21	0.48	0
7	NAG	I	301	2	14,14,15	0.28	0	17,19,21	0.51	0
7	NAG	C	401	1	14,14,15	0.27	0	17,19,21	0.44	0
7	NAG	C	404	1	14,14,15	0.24	0	17,19,21	0.46	0
7	NAG	D	301	2	14,14,15	0.27	0	17,19,21	0.51	0
7	NAG	C	402	1	14,14,15	0.25	0	17,19,21	0.46	0
7	NAG	A	404	1	14,14,15	0.25	0	17,19,21	0.46	0
7	NAG	G	401	1	14,14,15	0.27	0	17,19,21	0.45	0
7	NAG	G	402	1	14,14,15	0.25	0	17,19,21	0.48	0
7	NAG	G	403	1	14,14,15	0.30	0	17,19,21	0.50	0
7	NAG	A	401	1	14,14,15	0.25	0	17,19,21	0.44	0
7	NAG	C	403	1	14,14,15	0.31	0	17,19,21	0.49	0
7	NAG	A	403	1	14,14,15	0.30	0	17,19,21	0.49	0
7	NAG	G	404	1	14,14,15	0.24	0	17,19,21	0.45	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	B	301	2	-	2/6/23/26	0/1/1/1
7	NAG	A	402	1	-	0/6/23/26	0/1/1/1
7	NAG	I	301	2	-	2/6/23/26	0/1/1/1
7	NAG	C	401	1	-	2/6/23/26	0/1/1/1
7	NAG	C	404	1	-	2/6/23/26	0/1/1/1
7	NAG	D	301	2	-	2/6/23/26	0/1/1/1
7	NAG	C	402	1	-	0/6/23/26	0/1/1/1
7	NAG	A	404	1	-	2/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	G	401	1	-	2/6/23/26	0/1/1/1
7	NAG	G	402	1	-	0/6/23/26	0/1/1/1
7	NAG	G	403	1	-	2/6/23/26	0/1/1/1
7	NAG	A	401	1	-	2/6/23/26	0/1/1/1
7	NAG	C	403	1	-	2/6/23/26	0/1/1/1
7	NAG	A	403	1	-	2/6/23/26	0/1/1/1
7	NAG	G	404	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	401	NAG	O5-C5-C6-O6
7	G	401	NAG	O5-C5-C6-O6
7	A	401	NAG	O5-C5-C6-O6
7	B	301	NAG	O5-C5-C6-O6
7	C	403	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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-22804. These allow visual inspection of the internal detail of the map and identification of artifacts.

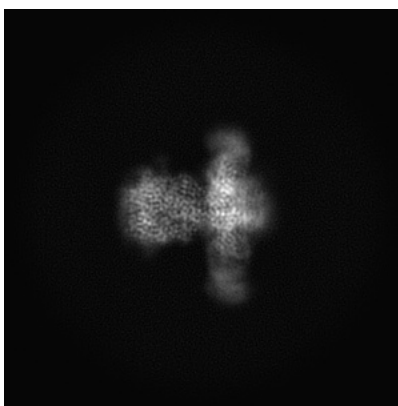
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

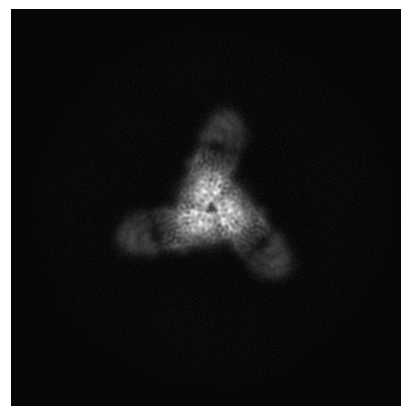
6.1.1 Primary map



X

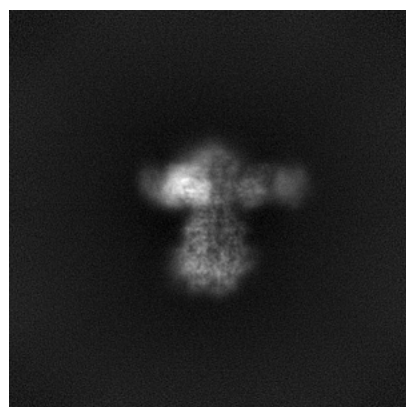


Y

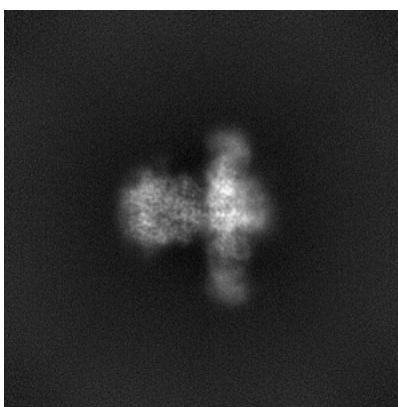


Z

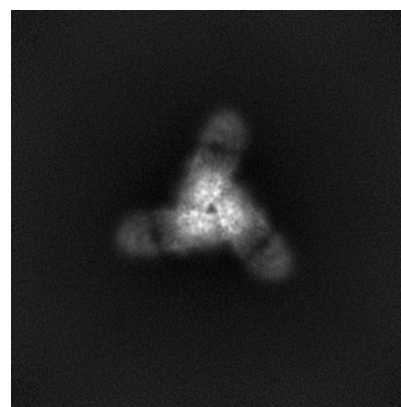
6.1.2 Raw map



X



Y

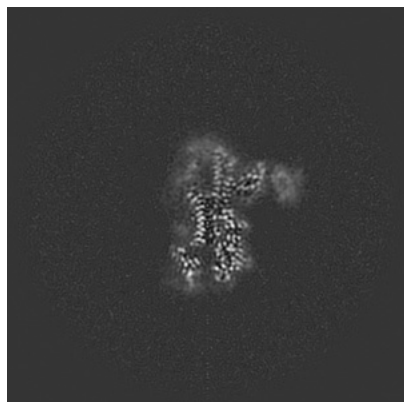


Z

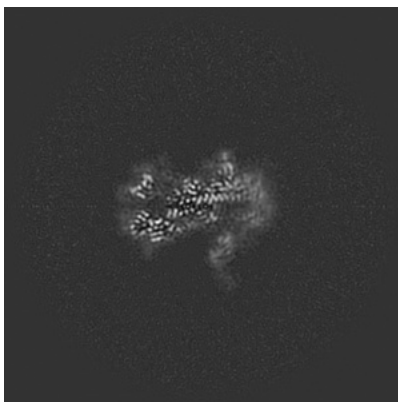
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

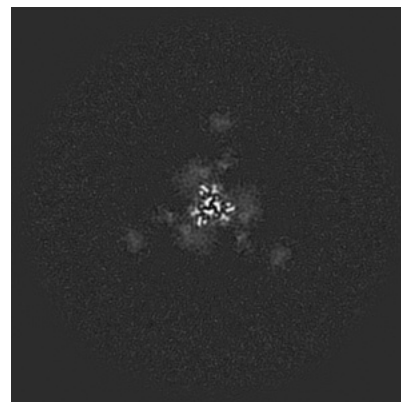
6.2.1 Primary map



X Index: 176

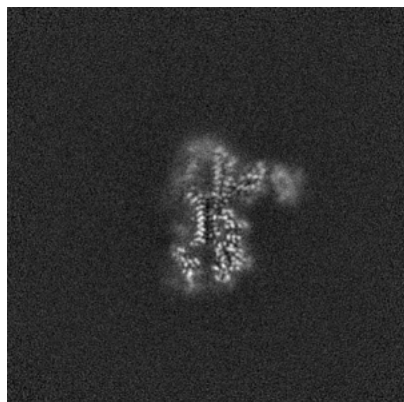


Y Index: 176

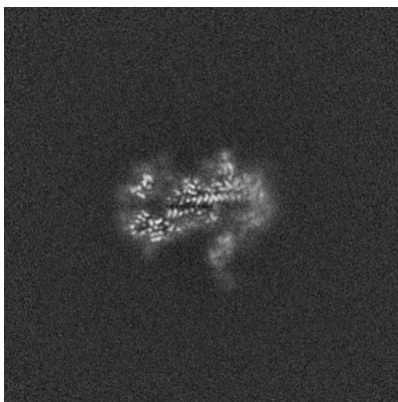


Z Index: 176

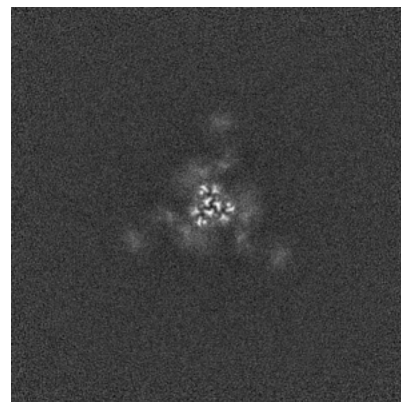
6.2.2 Raw map



X Index: 176



Y Index: 176

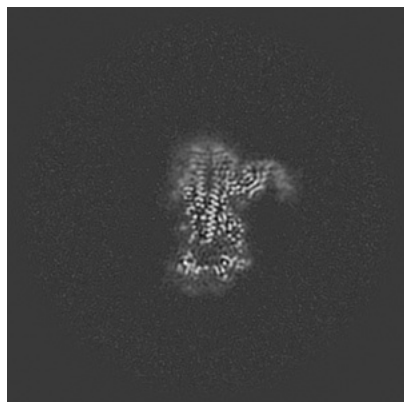


Z Index: 176

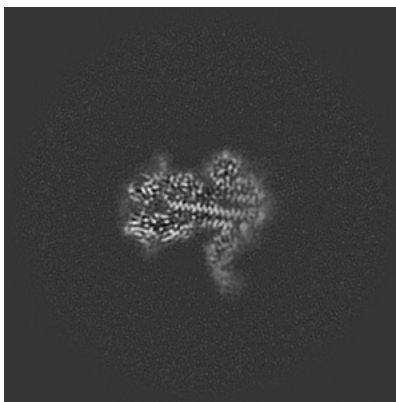
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

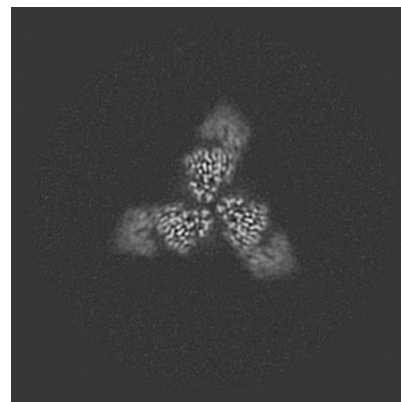
6.3.1 Primary map



X Index: 171

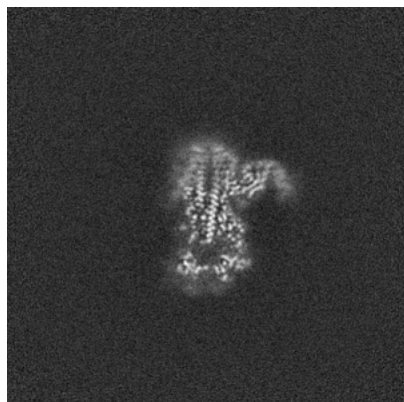


Y Index: 170

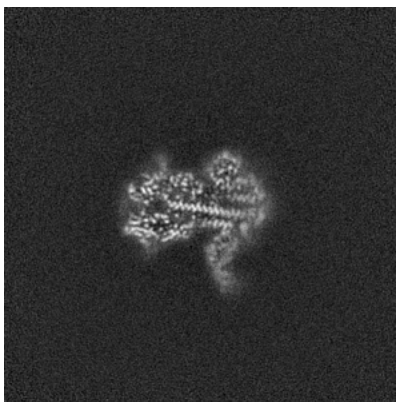


Z Index: 192

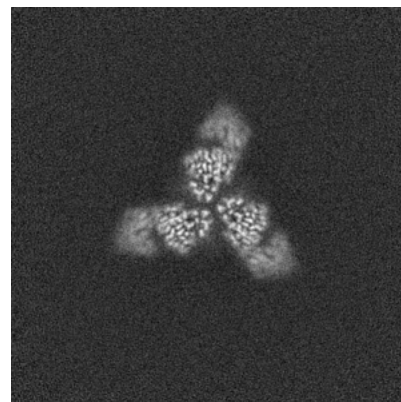
6.3.2 Raw map



X Index: 171



Y Index: 170

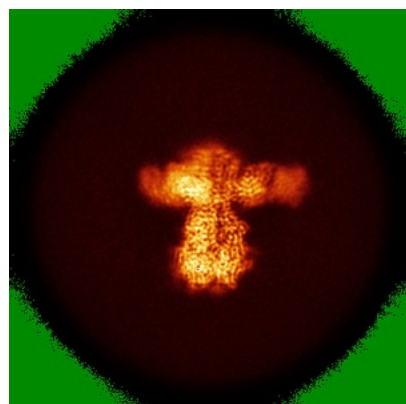


Z Index: 192

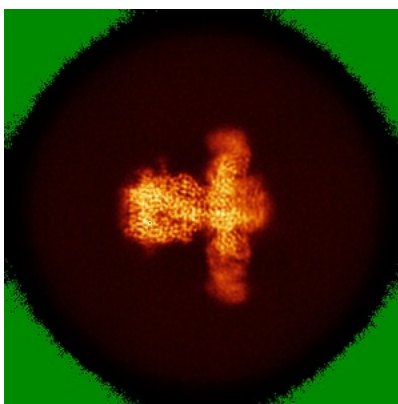
The images above show the largest variance slices of the map in three orthogonal directions.

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

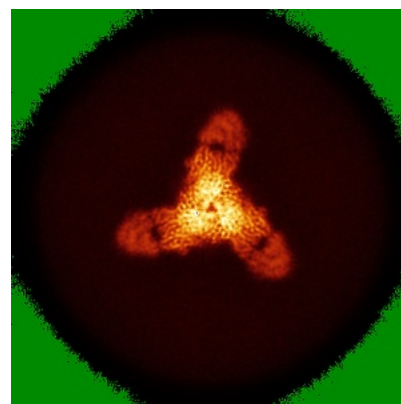
6.4.1 Primary map



X

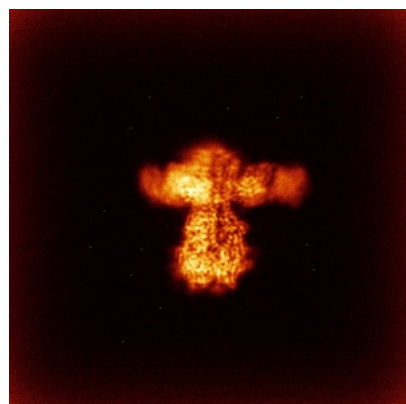


Y

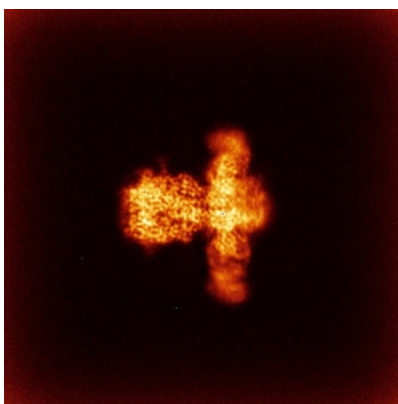


Z

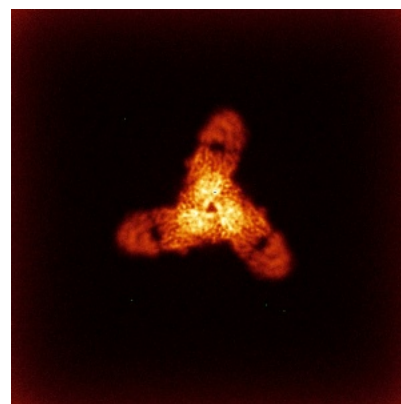
6.4.2 Raw map



X



Y

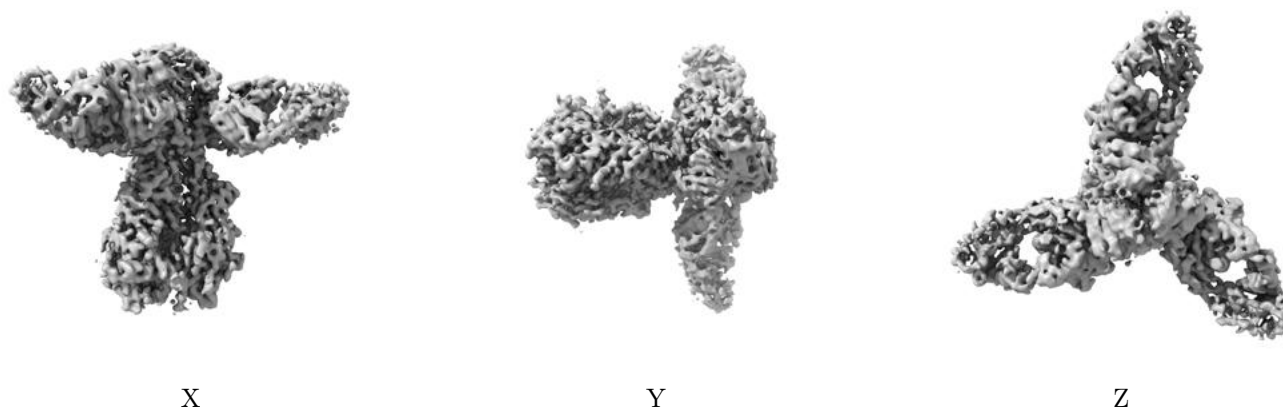


Z

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

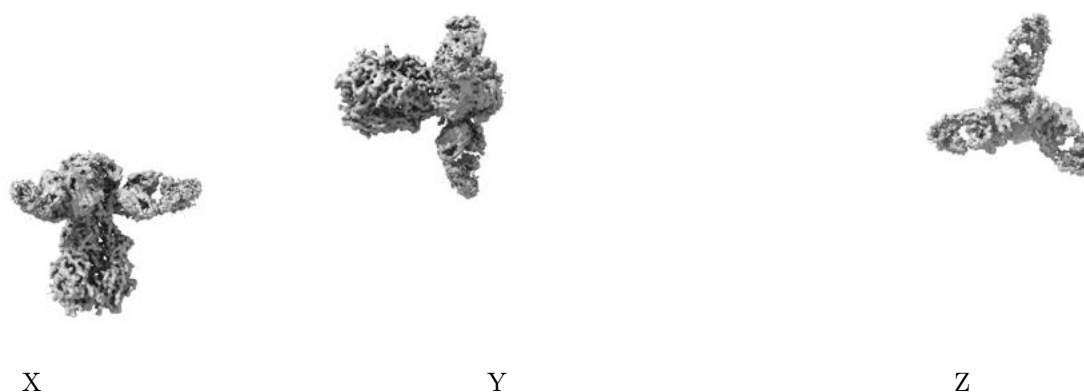
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

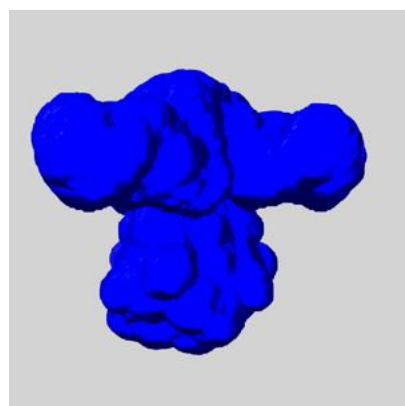
6.6 Mask visualisation [i](#)

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

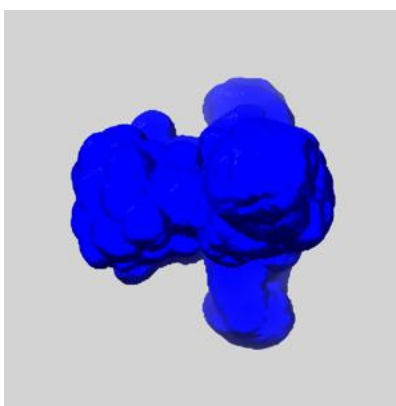
A mask typically either:

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

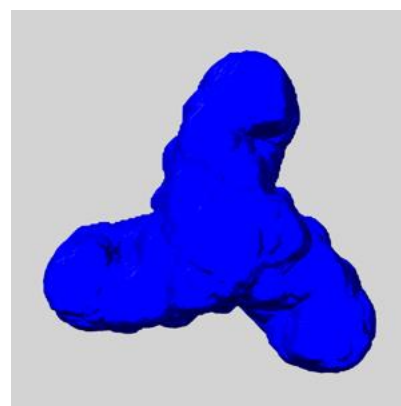
6.6.1 emd_22804_msk_1.map [i](#)



X



Y

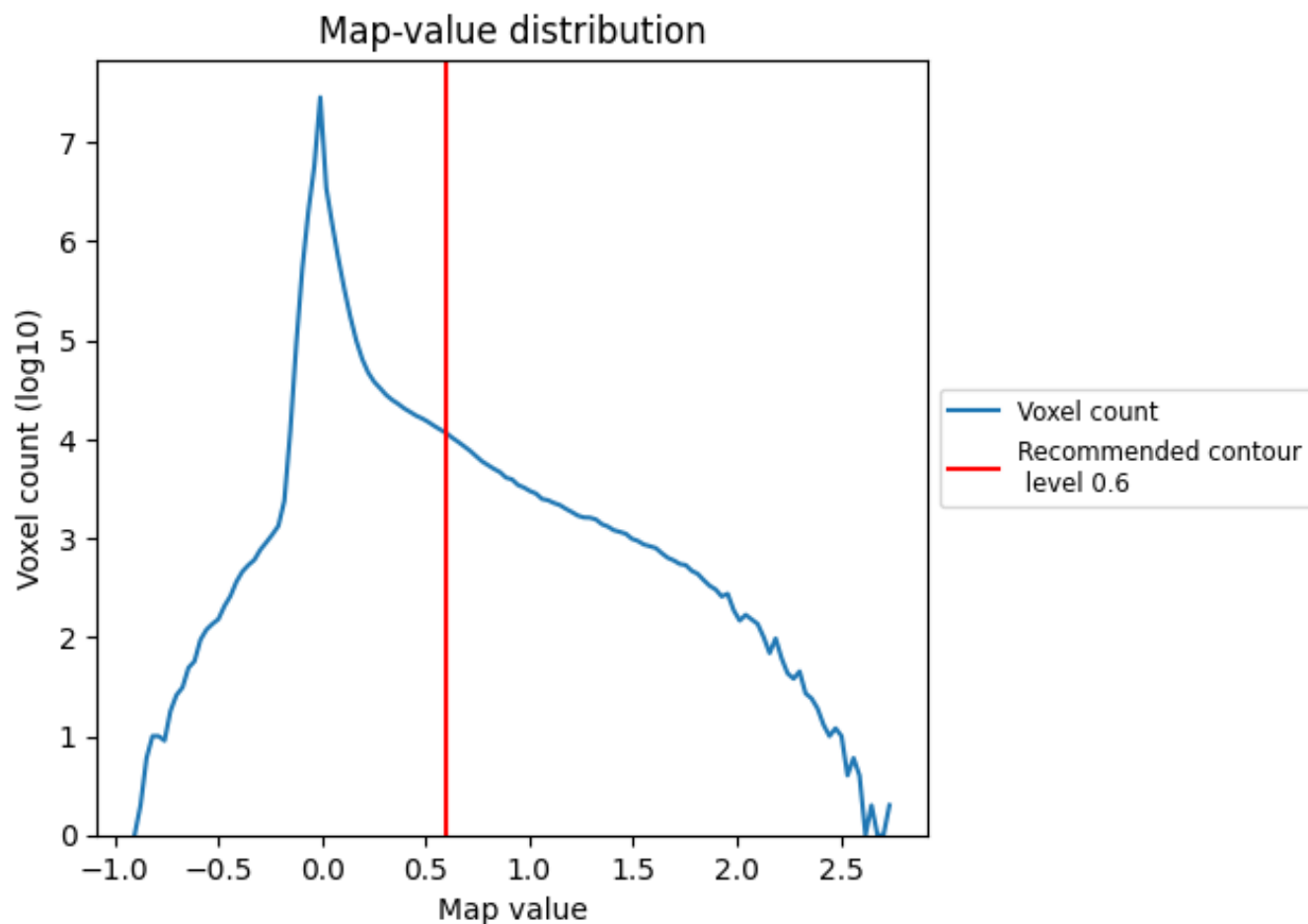


Z

7 Map analysis [i](#)

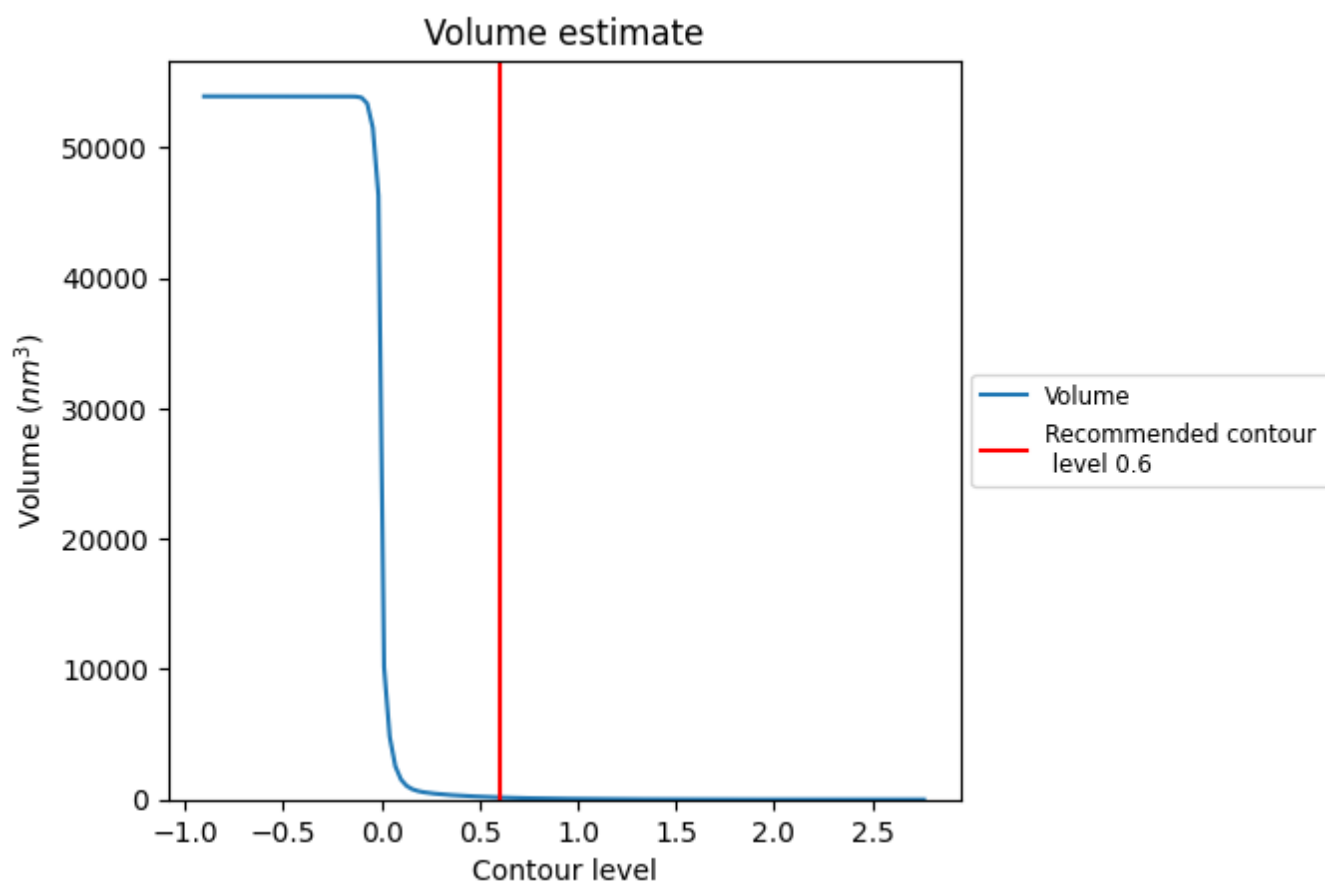
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

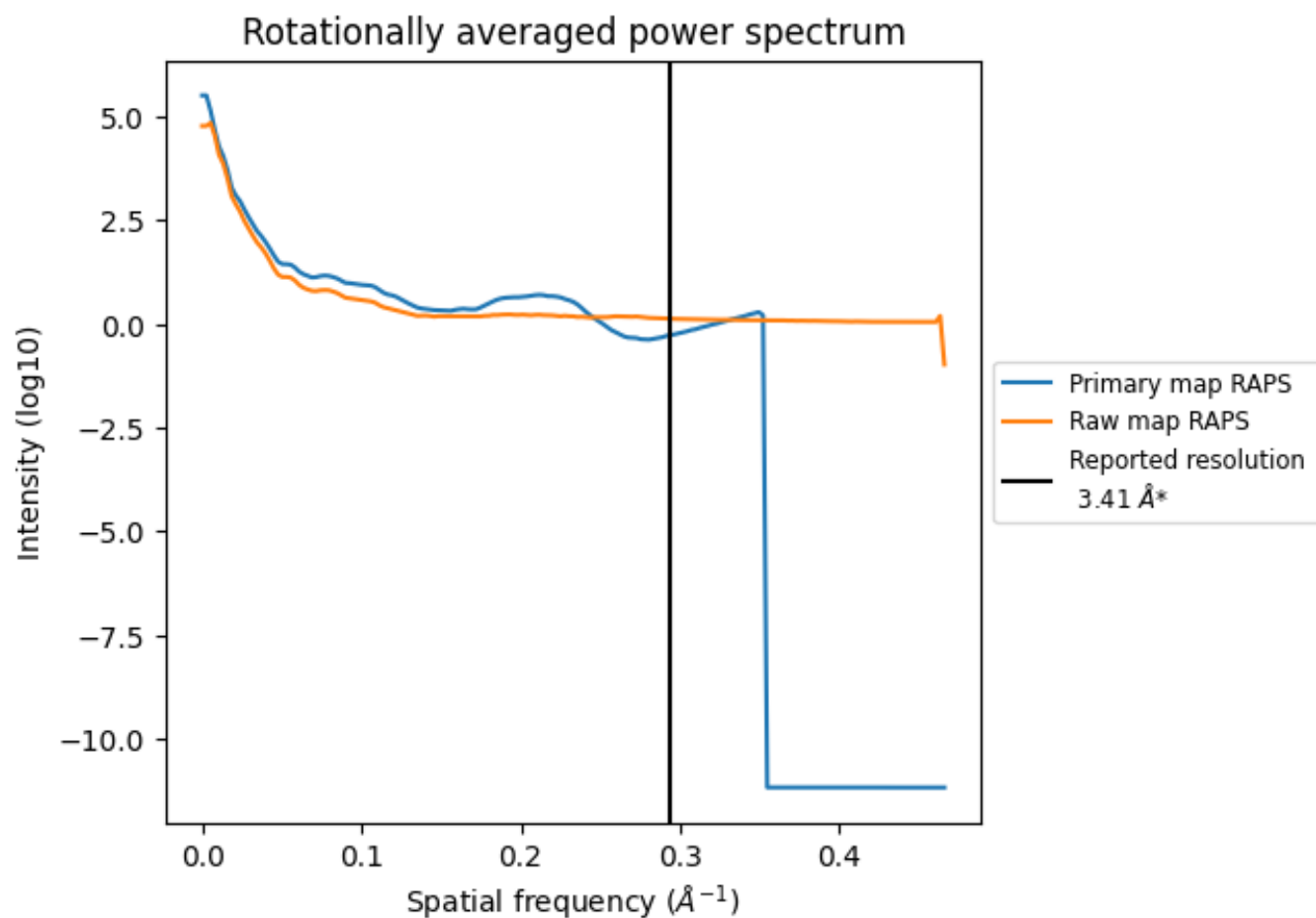
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 163 nm^3 ; this corresponds to an approximate mass of 148 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 ⓘ

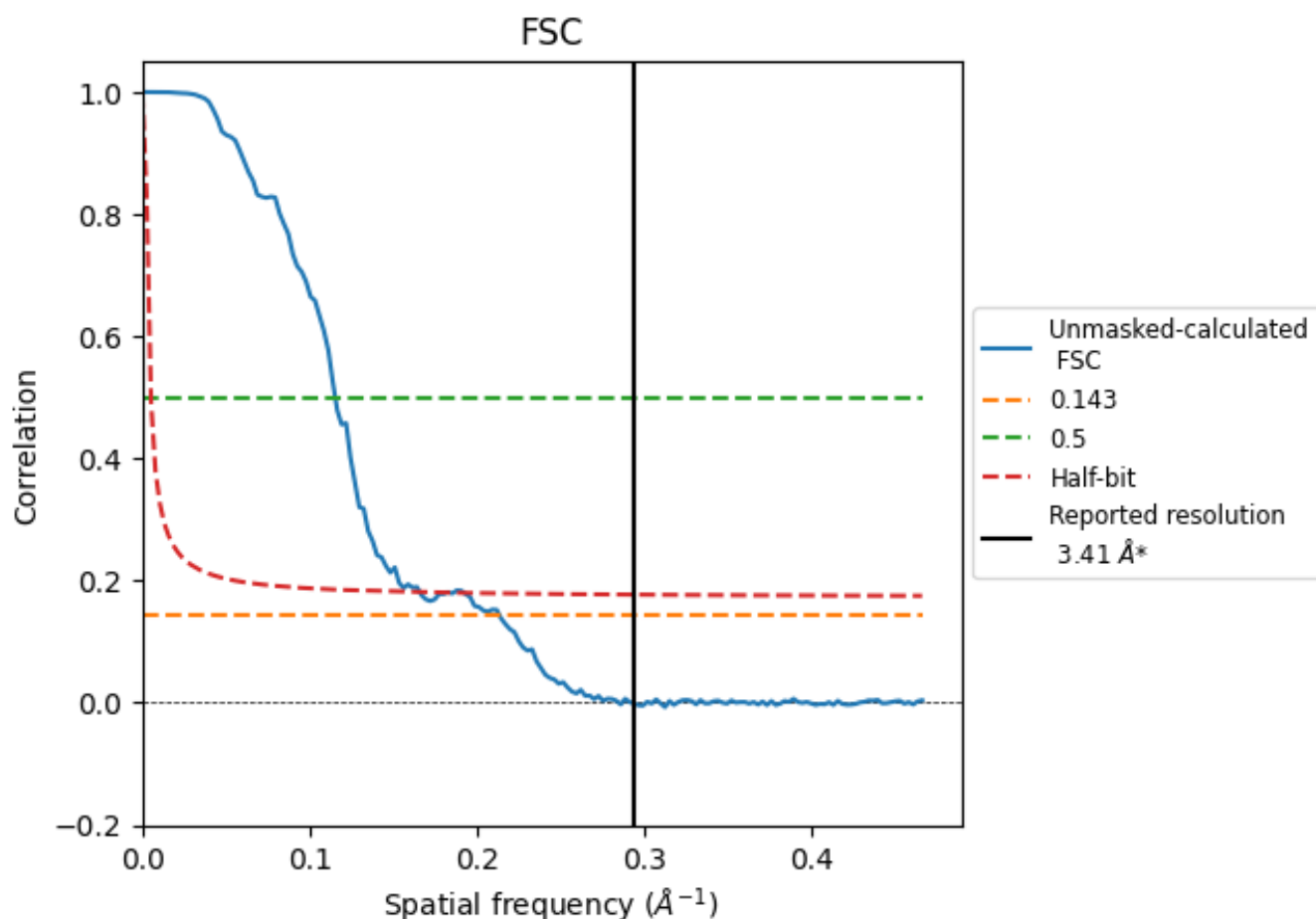


*Reported resolution corresponds to spatial frequency of 0.293 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.293 Å⁻¹

8.2 Resolution estimates [i](#)

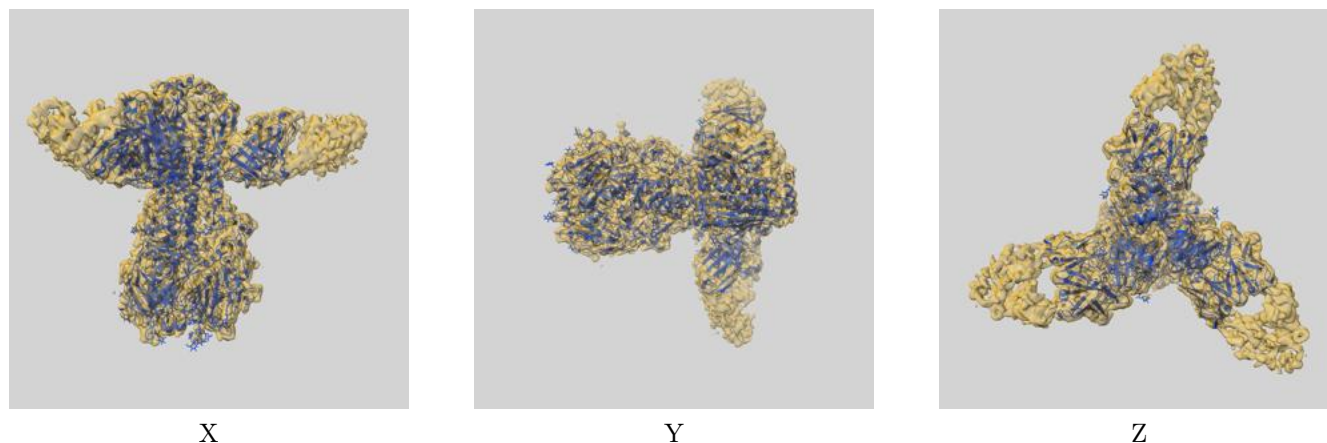
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.41	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.69	8.67	6.03

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.69 differs from the reported value 3.41 by more than 10 %

9 Map-model fit [i](#)

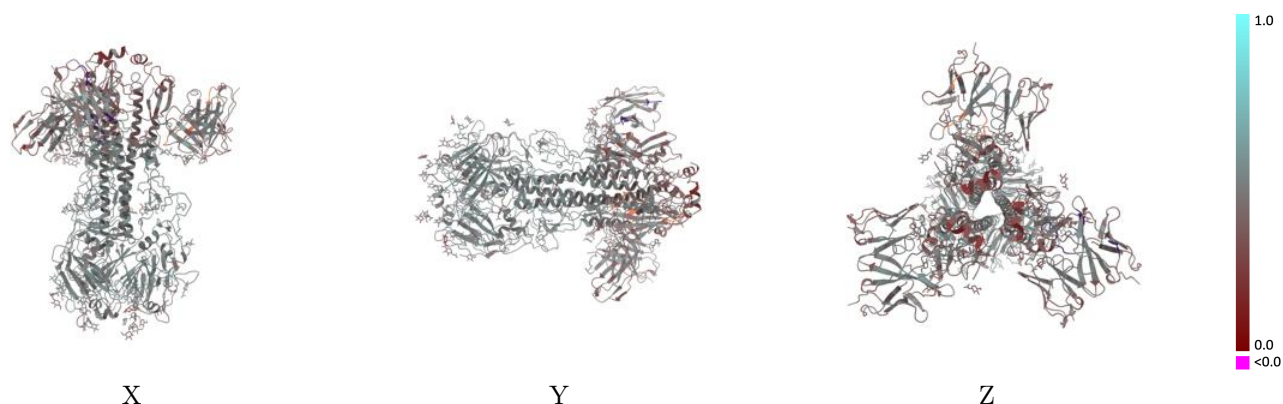
This section contains information regarding the fit between EMDB map EMD-22804 and PDB model 7KC1. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



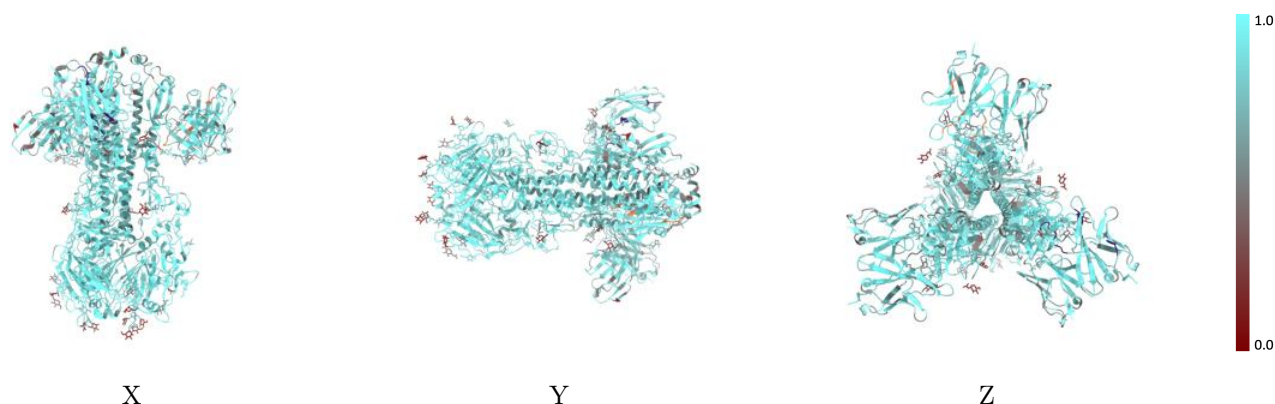
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



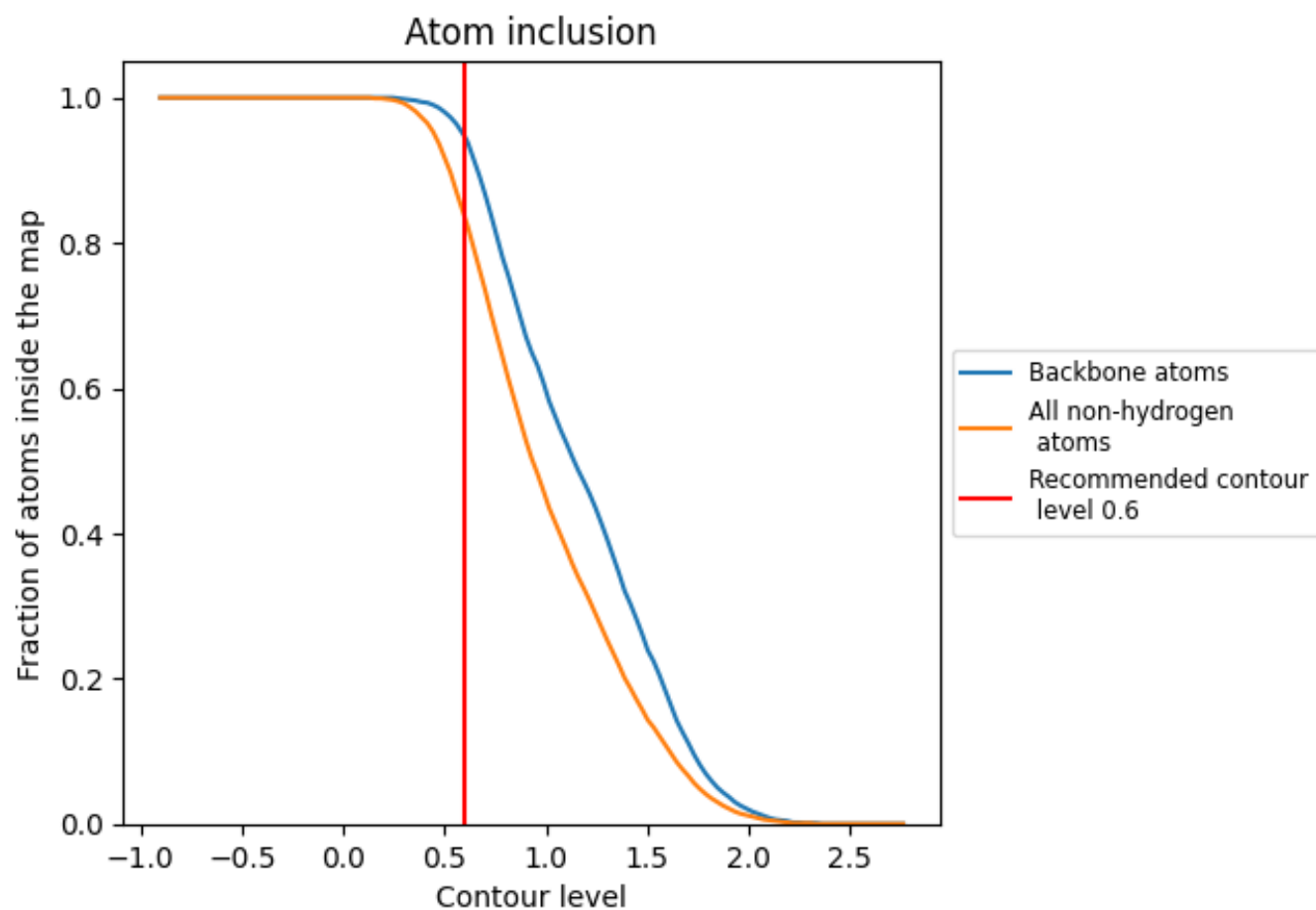
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 84% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8350	 0.4610
A	 0.8920	 0.4960
B	 0.7910	 0.4300
C	 0.8930	 0.4980
D	 0.7920	 0.4260
E	 0.8380	 0.4430
F	 0.7920	 0.4290
G	 0.8950	 0.4990
H	 0.8330	 0.4450
I	 0.7890	 0.4260
J	 0.8320	 0.4400
K	 0.7910	 0.4280
L	 0.7940	 0.4300
M	 0.6560	 0.4500
N	 0.6230	 0.4580
O	 0.5570	 0.4280
P	 0.4870	 0.4690
Q	 0.6890	 0.4410
R	 0.6230	 0.4550
S	 0.5570	 0.4230
T	 0.4870	 0.4740
U	 0.6720	 0.4420
V	 0.6230	 0.4690
W	 0.5570	 0.4350
X	 0.4620	 0.4700

