



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 01:08 AM UTC

PDB ID : 9Q5V / pdb_00009q5v
EMDB ID : EMD-72242
Title : Structure of the Measles virus Fusion glycoprotein ectodomain in complex with two neutralizing antibodies mAb77 and Y10F
Authors : Zyla, D.; Niemeyer, G.; Porotto, M.; Saphire, E.O.
Deposited on : 2025-08-21
Resolution : 2.82 Å (reported)
Based on initial models : ., 8UUT

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:

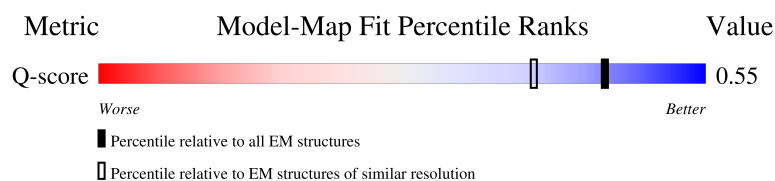
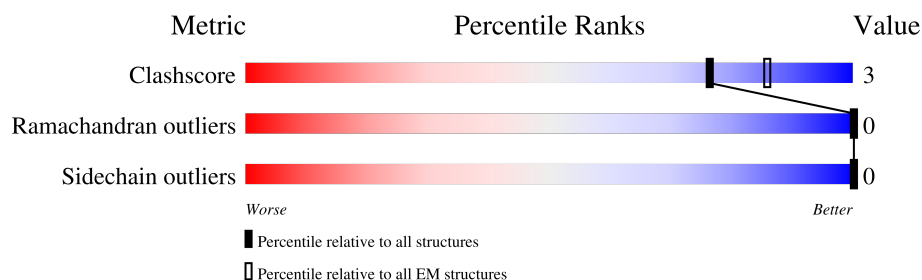
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 2.82 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.






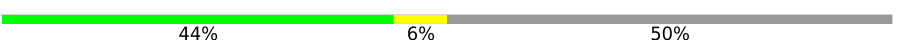

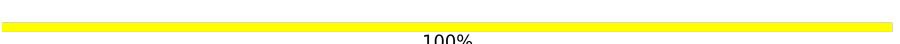

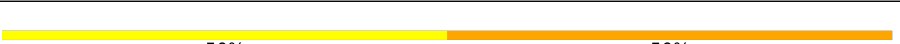
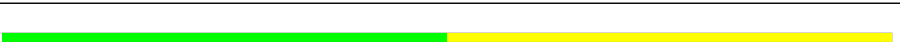
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11795 (2.32 - 3.32)

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	532	
1	B	532	
1	C	532	
1	D	532	

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Mol	Chain	Length	Quality of chain
1	E	532	
1	F	532	
2	G	232	
3	I	478	
4	J	214	
5	K	460	
6	H	2	
6	L	2	
6	M	2	
6	N	2	
6	O	2	
6	P	2	
6	Q	2	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14049 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 Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	81	Total	C	N	O	S	0	0
			637	400	120	113	4		
1	B	372	Total	C	N	O	S	0	0
			2800	1767	473	546	14		
1	C	81	Total	C	N	O	S	0	0
			637	400	120	113	4		
1	D	372	Total	C	N	O	S	0	0
			2800	1767	473	546	14		
1	E	81	Total	C	N	O	S	0	0
			637	400	120	113	4		
1	F	372	Total	C	N	O	S	0	0
			2800	1767	473	546	14		

There are 234 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	170	GLY	GLU	conflict	UNP Q786F3
A	455	GLY	GLU	conflict	UNP Q786F3
A	496	GLY	-	expression tag	UNP Q786F3
A	497	VAL	-	expression tag	UNP Q786F3
A	498	ASP	-	expression tag	UNP Q786F3
A	499	ASP	-	expression tag	UNP Q786F3
A	500	ASP	-	expression tag	UNP Q786F3
A	501	ASP	-	expression tag	UNP Q786F3
A	502	LYS	-	expression tag	UNP Q786F3
A	503	ALA	-	expression tag	UNP Q786F3
A	504	GLY	-	expression tag	UNP Q786F3
A	505	TRP	-	expression tag	UNP Q786F3
A	506	SER	-	expression tag	UNP Q786F3
A	507	HIS	-	expression tag	UNP Q786F3
A	508	PRO	-	expression tag	UNP Q786F3
A	509	GLN	-	expression tag	UNP Q786F3
A	510	PHE	-	expression tag	UNP Q786F3
A	511	GLU	-	expression tag	UNP Q786F3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	512	LYS	-	expression tag	UNP Q786F3
A	513	GLY	-	expression tag	UNP Q786F3
A	514	GLY	-	expression tag	UNP Q786F3
A	515	GLY	-	expression tag	UNP Q786F3
A	516	SER	-	expression tag	UNP Q786F3
A	517	GLY	-	expression tag	UNP Q786F3
A	518	GLY	-	expression tag	UNP Q786F3
A	519	GLY	-	expression tag	UNP Q786F3
A	520	SER	-	expression tag	UNP Q786F3
A	521	GLY	-	expression tag	UNP Q786F3
A	522	GLY	-	expression tag	UNP Q786F3
A	523	GLY	-	expression tag	UNP Q786F3
A	524	SER	-	expression tag	UNP Q786F3
A	525	TRP	-	expression tag	UNP Q786F3
A	526	SER	-	expression tag	UNP Q786F3
A	527	HIS	-	expression tag	UNP Q786F3
A	528	PRO	-	expression tag	UNP Q786F3
A	529	GLN	-	expression tag	UNP Q786F3
A	530	PHE	-	expression tag	UNP Q786F3
A	531	GLU	-	expression tag	UNP Q786F3
A	532	LYS	-	expression tag	UNP Q786F3
B	170	GLY	GLU	conflict	UNP Q786F3
B	455	GLY	GLU	conflict	UNP Q786F3
B	496	GLY	-	expression tag	UNP Q786F3
B	497	VAL	-	expression tag	UNP Q786F3
B	498	ASP	-	expression tag	UNP Q786F3
B	499	ASP	-	expression tag	UNP Q786F3
B	500	ASP	-	expression tag	UNP Q786F3
B	501	ASP	-	expression tag	UNP Q786F3
B	502	LYS	-	expression tag	UNP Q786F3
B	503	ALA	-	expression tag	UNP Q786F3
B	504	GLY	-	expression tag	UNP Q786F3
B	505	TRP	-	expression tag	UNP Q786F3
B	506	SER	-	expression tag	UNP Q786F3
B	507	HIS	-	expression tag	UNP Q786F3
B	508	PRO	-	expression tag	UNP Q786F3
B	509	GLN	-	expression tag	UNP Q786F3
B	510	PHE	-	expression tag	UNP Q786F3
B	511	GLU	-	expression tag	UNP Q786F3
B	512	LYS	-	expression tag	UNP Q786F3
B	513	GLY	-	expression tag	UNP Q786F3
B	514	GLY	-	expression tag	UNP Q786F3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	515	GLY	-	expression tag	UNP Q786F3
B	516	SER	-	expression tag	UNP Q786F3
B	517	GLY	-	expression tag	UNP Q786F3
B	518	GLY	-	expression tag	UNP Q786F3
B	519	GLY	-	expression tag	UNP Q786F3
B	520	SER	-	expression tag	UNP Q786F3
B	521	GLY	-	expression tag	UNP Q786F3
B	522	GLY	-	expression tag	UNP Q786F3
B	523	GLY	-	expression tag	UNP Q786F3
B	524	SER	-	expression tag	UNP Q786F3
B	525	TRP	-	expression tag	UNP Q786F3
B	526	SER	-	expression tag	UNP Q786F3
B	527	HIS	-	expression tag	UNP Q786F3
B	528	PRO	-	expression tag	UNP Q786F3
B	529	GLN	-	expression tag	UNP Q786F3
B	530	PHE	-	expression tag	UNP Q786F3
B	531	GLU	-	expression tag	UNP Q786F3
B	532	LYS	-	expression tag	UNP Q786F3
C	170	GLY	GLU	conflict	UNP Q786F3
C	455	GLY	GLU	conflict	UNP Q786F3
C	496	GLY	-	expression tag	UNP Q786F3
C	497	VAL	-	expression tag	UNP Q786F3
C	498	ASP	-	expression tag	UNP Q786F3
C	499	ASP	-	expression tag	UNP Q786F3
C	500	ASP	-	expression tag	UNP Q786F3
C	501	ASP	-	expression tag	UNP Q786F3
C	502	LYS	-	expression tag	UNP Q786F3
C	503	ALA	-	expression tag	UNP Q786F3
C	504	GLY	-	expression tag	UNP Q786F3
C	505	TRP	-	expression tag	UNP Q786F3
C	506	SER	-	expression tag	UNP Q786F3
C	507	HIS	-	expression tag	UNP Q786F3
C	508	PRO	-	expression tag	UNP Q786F3
C	509	GLN	-	expression tag	UNP Q786F3
C	510	PHE	-	expression tag	UNP Q786F3
C	511	GLU	-	expression tag	UNP Q786F3
C	512	LYS	-	expression tag	UNP Q786F3
C	513	GLY	-	expression tag	UNP Q786F3
C	514	GLY	-	expression tag	UNP Q786F3
C	515	GLY	-	expression tag	UNP Q786F3
C	516	SER	-	expression tag	UNP Q786F3
C	517	GLY	-	expression tag	UNP Q786F3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	518	GLY	-	expression tag	UNP Q786F3
C	519	GLY	-	expression tag	UNP Q786F3
C	520	SER	-	expression tag	UNP Q786F3
C	521	GLY	-	expression tag	UNP Q786F3
C	522	GLY	-	expression tag	UNP Q786F3
C	523	GLY	-	expression tag	UNP Q786F3
C	524	SER	-	expression tag	UNP Q786F3
C	525	TRP	-	expression tag	UNP Q786F3
C	526	SER	-	expression tag	UNP Q786F3
C	527	HIS	-	expression tag	UNP Q786F3
C	528	PRO	-	expression tag	UNP Q786F3
C	529	GLN	-	expression tag	UNP Q786F3
C	530	PHE	-	expression tag	UNP Q786F3
C	531	GLU	-	expression tag	UNP Q786F3
C	532	LYS	-	expression tag	UNP Q786F3
D	170	GLY	GLU	conflict	UNP Q786F3
D	455	GLY	GLU	conflict	UNP Q786F3
D	496	GLY	-	expression tag	UNP Q786F3
D	497	VAL	-	expression tag	UNP Q786F3
D	498	ASP	-	expression tag	UNP Q786F3
D	499	ASP	-	expression tag	UNP Q786F3
D	500	ASP	-	expression tag	UNP Q786F3
D	501	ASP	-	expression tag	UNP Q786F3
D	502	LYS	-	expression tag	UNP Q786F3
D	503	ALA	-	expression tag	UNP Q786F3
D	504	GLY	-	expression tag	UNP Q786F3
D	505	TRP	-	expression tag	UNP Q786F3
D	506	SER	-	expression tag	UNP Q786F3
D	507	HIS	-	expression tag	UNP Q786F3
D	508	PRO	-	expression tag	UNP Q786F3
D	509	GLN	-	expression tag	UNP Q786F3
D	510	PHE	-	expression tag	UNP Q786F3
D	511	GLU	-	expression tag	UNP Q786F3
D	512	LYS	-	expression tag	UNP Q786F3
D	513	GLY	-	expression tag	UNP Q786F3
D	514	GLY	-	expression tag	UNP Q786F3
D	515	GLY	-	expression tag	UNP Q786F3
D	516	SER	-	expression tag	UNP Q786F3
D	517	GLY	-	expression tag	UNP Q786F3
D	518	GLY	-	expression tag	UNP Q786F3
D	519	GLY	-	expression tag	UNP Q786F3
D	520	SER	-	expression tag	UNP Q786F3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	521	GLY	-	expression tag	UNP Q786F3
D	522	GLY	-	expression tag	UNP Q786F3
D	523	GLY	-	expression tag	UNP Q786F3
D	524	SER	-	expression tag	UNP Q786F3
D	525	TRP	-	expression tag	UNP Q786F3
D	526	SER	-	expression tag	UNP Q786F3
D	527	HIS	-	expression tag	UNP Q786F3
D	528	PRO	-	expression tag	UNP Q786F3
D	529	GLN	-	expression tag	UNP Q786F3
D	530	PHE	-	expression tag	UNP Q786F3
D	531	GLU	-	expression tag	UNP Q786F3
D	532	LYS	-	expression tag	UNP Q786F3
E	170	GLY	GLU	conflict	UNP Q786F3
E	455	GLY	GLU	conflict	UNP Q786F3
E	496	GLY	-	expression tag	UNP Q786F3
E	497	VAL	-	expression tag	UNP Q786F3
E	498	ASP	-	expression tag	UNP Q786F3
E	499	ASP	-	expression tag	UNP Q786F3
E	500	ASP	-	expression tag	UNP Q786F3
E	501	ASP	-	expression tag	UNP Q786F3
E	502	LYS	-	expression tag	UNP Q786F3
E	503	ALA	-	expression tag	UNP Q786F3
E	504	GLY	-	expression tag	UNP Q786F3
E	505	TRP	-	expression tag	UNP Q786F3
E	506	SER	-	expression tag	UNP Q786F3
E	507	HIS	-	expression tag	UNP Q786F3
E	508	PRO	-	expression tag	UNP Q786F3
E	509	GLN	-	expression tag	UNP Q786F3
E	510	PHE	-	expression tag	UNP Q786F3
E	511	GLU	-	expression tag	UNP Q786F3
E	512	LYS	-	expression tag	UNP Q786F3
E	513	GLY	-	expression tag	UNP Q786F3
E	514	GLY	-	expression tag	UNP Q786F3
E	515	GLY	-	expression tag	UNP Q786F3
E	516	SER	-	expression tag	UNP Q786F3
E	517	GLY	-	expression tag	UNP Q786F3
E	518	GLY	-	expression tag	UNP Q786F3
E	519	GLY	-	expression tag	UNP Q786F3
E	520	SER	-	expression tag	UNP Q786F3
E	521	GLY	-	expression tag	UNP Q786F3
E	522	GLY	-	expression tag	UNP Q786F3
E	523	GLY	-	expression tag	UNP Q786F3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	524	SER	-	expression tag	UNP Q786F3
E	525	TRP	-	expression tag	UNP Q786F3
E	526	SER	-	expression tag	UNP Q786F3
E	527	HIS	-	expression tag	UNP Q786F3
E	528	PRO	-	expression tag	UNP Q786F3
E	529	GLN	-	expression tag	UNP Q786F3
E	530	PHE	-	expression tag	UNP Q786F3
E	531	GLU	-	expression tag	UNP Q786F3
E	532	LYS	-	expression tag	UNP Q786F3
F	170	GLY	GLU	conflict	UNP Q786F3
F	455	GLY	GLU	conflict	UNP Q786F3
F	496	GLY	-	expression tag	UNP Q786F3
F	497	VAL	-	expression tag	UNP Q786F3
F	498	ASP	-	expression tag	UNP Q786F3
F	499	ASP	-	expression tag	UNP Q786F3
F	500	ASP	-	expression tag	UNP Q786F3
F	501	ASP	-	expression tag	UNP Q786F3
F	502	LYS	-	expression tag	UNP Q786F3
F	503	ALA	-	expression tag	UNP Q786F3
F	504	GLY	-	expression tag	UNP Q786F3
F	505	TRP	-	expression tag	UNP Q786F3
F	506	SER	-	expression tag	UNP Q786F3
F	507	HIS	-	expression tag	UNP Q786F3
F	508	PRO	-	expression tag	UNP Q786F3
F	509	GLN	-	expression tag	UNP Q786F3
F	510	PHE	-	expression tag	UNP Q786F3
F	511	GLU	-	expression tag	UNP Q786F3
F	512	LYS	-	expression tag	UNP Q786F3
F	513	GLY	-	expression tag	UNP Q786F3
F	514	GLY	-	expression tag	UNP Q786F3
F	515	GLY	-	expression tag	UNP Q786F3
F	516	SER	-	expression tag	UNP Q786F3
F	517	GLY	-	expression tag	UNP Q786F3
F	518	GLY	-	expression tag	UNP Q786F3
F	519	GLY	-	expression tag	UNP Q786F3
F	520	SER	-	expression tag	UNP Q786F3
F	521	GLY	-	expression tag	UNP Q786F3
F	522	GLY	-	expression tag	UNP Q786F3
F	523	GLY	-	expression tag	UNP Q786F3
F	524	SER	-	expression tag	UNP Q786F3
F	525	TRP	-	expression tag	UNP Q786F3
F	526	SER	-	expression tag	UNP Q786F3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	527	HIS	-	expression tag	UNP Q786F3
F	528	PRO	-	expression tag	UNP Q786F3
F	529	GLN	-	expression tag	UNP Q786F3
F	530	PHE	-	expression tag	UNP Q786F3
F	531	GLU	-	expression tag	UNP Q786F3
F	532	LYS	-	expression tag	UNP Q786F3

- Molecule 2 is a protein called Y10F light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	106	Total	C	N	O	S	0	0
			801	506	133	158	4		

- Molecule 3 is a protein called Y10F heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	120	Total	C	N	O	S	0	0
			932	592	154	182	4		

- Molecule 4 is a protein called mAb77 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	107	Total	C	N	O	S	0	0
			828	523	134	168	3		

- Molecule 5 is a protein called mAb77 heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	119	Total	C	N	O	S	0	0
			953	614	152	184	3		

- Molecule 6 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
6	H	2	Total	C	N	O	0	0
			28	16	2	10		

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

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

Chain E: 14% 85%

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

- Molecule 1: Fusion glycoprotein F0

Chain F:  65% 5% 30%

[illegible]

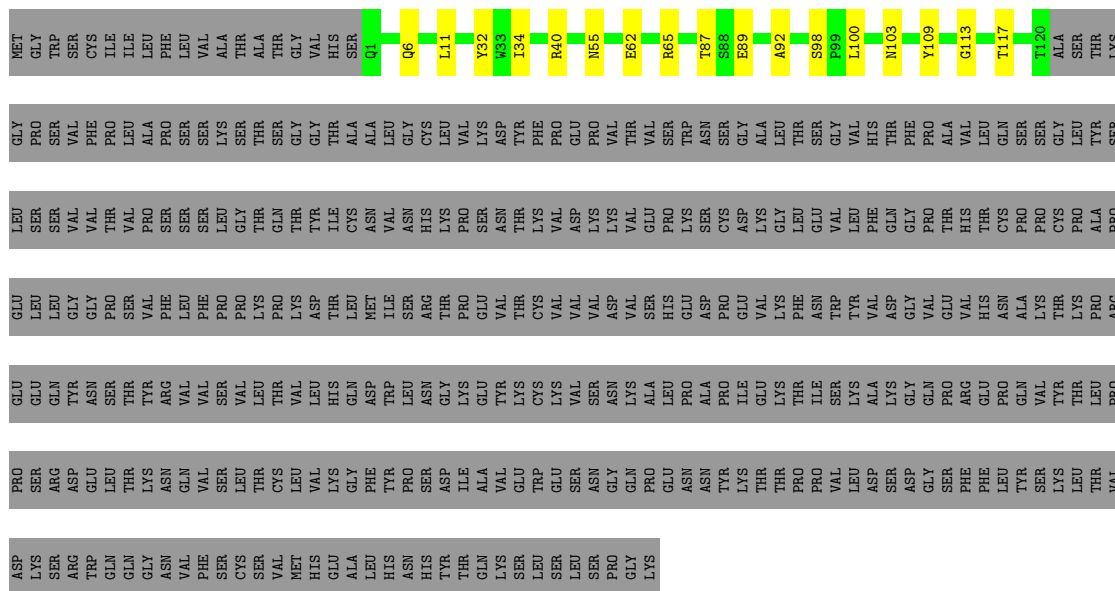
- Molecule 2: Y10F light chain

Chain G:  42% 0 54%

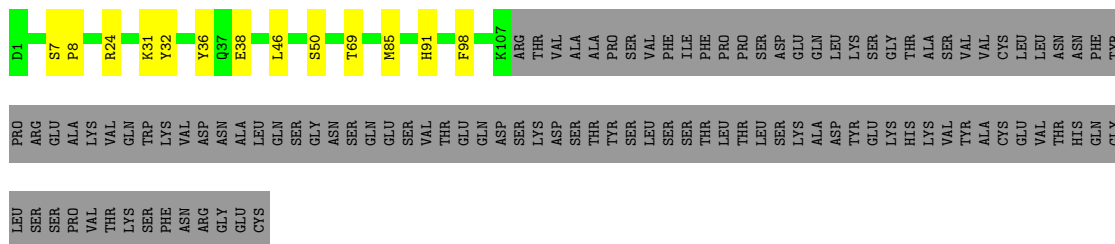
VAL	TYR	VAL	SER	MET
ALA	ALA	VAL	VAL	GLY
CYS	CYS	TRP	SER	TRP
GLU	GLU	CYS	LEU	CYS
VAL	VAL	LEU	LEU	ILE
THR	THR	ASN	ASN	ILE
HIS	HIS	ASN	LEU	LEU
GLN	GLN	PHE	PHE	PHE
GLY	GLY	TRP	TRP	LEU
LEU	LEU	ARG	ARG	VAL
SER	SER	GLU	GLU	ALA
PRO	PRO	ALA	ALA	THR
VAL	VAL	LYS	LYS	THR
THR	THR	VAL	VAL	GLY
LYS	LYS	GLN	GLN	VAL
SER	SER	TRP	TRP	HIS
PHE	PHE	LYS	LYS	SER
ASN	ASN	VAL	VAL	Q0
ARG	ARG	ASP	ASP	Q0
GLY	GLY	ALA	ALA	L3
GLU	GLU	LEU	LEU	S4
CYS	CYS	GLN	GLN	Q5
		SER	SER	Q31
		GLY	GLY	Q68
		ASN	ASN	Q88
		SER	SER	N92
		GLN	GLN	P93
		GLU	GLU	Y94
		SER	SER	T95
		VAL	VAL	
		THR	THR	
		GLU	GLU	T100
		GLN	GLN	
		ASP	ASP	K105
		SER	SER	ARG
		LYS	LYS	THR
		ASP	ASP	VAL
		SER	SER	ALA
		THR	THR	ALA
		TYR	TYR	PRO
		SER	SER	SER
		LEU	LEU	VAL
		SER	SER	PHE
		SER	SER	ILE
		THR	THR	PHE
		LEU	LEU	PRO
		THR	THR	PRO
		LEU	LEU	SER
		SER	SER	ASP
		LYS	LYS	GLU
		ALA	ALA	GLN
		ASP	ASP	LEU
		TYR	TYR	LYS
		GLU	GLU	GLY
		LYS	LYS	THR
		HIS	HIS	ALA
		LYS	LYS	THR

- Molecule 3: Y10F heavy chain

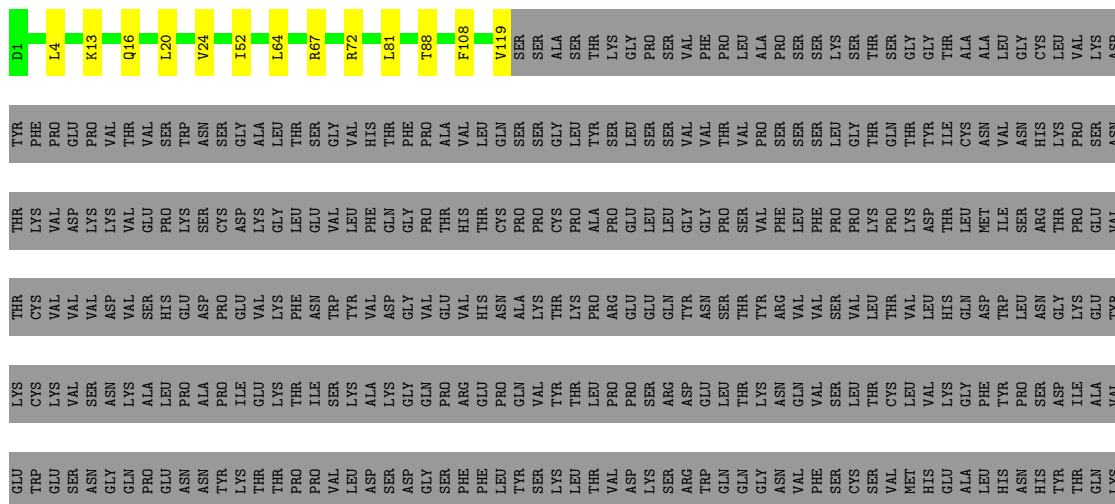
Chain I:  22% . 75%



- Molecule 4: mAb77 light chain



- Molecule 5: mAb77 heavy chain



SER
LEU
SER
LEU
SER
PRO
GLY
LYS

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

Chain H:  100%

NAG1
NAG2

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

Chain L:  100%

NAG1
NAG2

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

Chain M:  50%  50%

NAG1
NAG2

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

Chain N:  50%  50%

NAG1
NAG2

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

Chain O:  50%  50%

NAG1
NAG2

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

Chain P:  50%  50%

NAG1
NAG2

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

Chain Q:

100%

MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	221000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.861	Depositor
Minimum map value	-0.536	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.0321	Depositor
Map size (Å)	409.26, 409.26, 409.26	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.077, 1.077, 1.077	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: 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	0.11	0/645	0.23	0/873
1	B	0.10	0/2841	0.23	0/3859
1	C	0.11	0/645	0.25	0/873
1	D	0.10	0/2841	0.23	0/3859
1	E	0.11	0/645	0.27	0/873
1	F	0.11	0/2841	0.23	0/3859
2	G	0.12	0/823	0.30	0/1122
3	I	0.12	0/956	0.31	0/1300
4	J	0.09	0/846	0.26	0/1145
5	K	0.09	0/982	0.25	0/1344
All	All	0.11	0/14065	0.25	0/19107

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	637	0	671	9	0
1	B	2800	0	2830	18	0
1	C	637	0	671	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2800	0	2832	18	0
1	E	637	0	671	6	0
1	F	2800	0	2830	18	0
2	G	801	0	773	5	0
3	I	932	0	893	10	0
4	J	828	0	805	8	0
5	K	953	0	910	7	0
6	H	28	0	25	0	0
6	L	28	0	25	0	0
6	M	28	0	25	0	0
6	N	28	0	25	1	0
6	O	28	0	25	1	0
6	P	28	0	25	0	0
6	Q	28	0	25	1	0
7	A	14	0	13	1	0
7	C	14	0	13	0	0
All	All	14049	0	14087	84	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 3.

The worst 5 of 84 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:I:6:GLN:HG3	3:I:113:GLY:H	1.44	0.80
1:E:66:ASN:HD21	6:O:1:NAG:H82	1.52	0.75
1:C:69:THR:HG22	1:D:199:GLY:HA2	1.76	0.67
1:D:441:VAL:HB	1:D:446:ILE:HD11	1.77	0.67
1:A:69:THR:HG21	1:B:202:LEU:HD23	1.77	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	79/532 (15%)	77 (98%)	2 (2%)	0	100	100
1	B	370/532 (70%)	364 (98%)	6 (2%)	0	100	100
1	C	79/532 (15%)	78 (99%)	1 (1%)	0	100	100
1	D	370/532 (70%)	363 (98%)	7 (2%)	0	100	100
1	E	79/532 (15%)	75 (95%)	4 (5%)	0	100	100
1	F	370/532 (70%)	364 (98%)	6 (2%)	0	100	100
2	G	104/232 (45%)	100 (96%)	4 (4%)	0	100	100
3	I	118/478 (25%)	109 (92%)	9 (8%)	0	100	100
4	J	105/214 (49%)	98 (93%)	7 (7%)	0	100	100
5	K	117/460 (25%)	114 (97%)	3 (3%)	0	100	100
All	All	1791/4576 (39%)	1742 (97%)	49 (3%)	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	73/442 (16%)	73 (100%)	0	100	100
1	B	308/442 (70%)	308 (100%)	0	100	100
1	C	73/442 (16%)	73 (100%)	0	100	100
1	D	308/442 (70%)	308 (100%)	0	100	100
1	E	73/442 (16%)	73 (100%)	0	100	100
1	F	308/442 (70%)	308 (100%)	0	100	100
2	G	88/200 (44%)	88 (100%)	0	100	100
3	I	99/420 (24%)	99 (100%)	0	100	100
4	J	92/188 (49%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	K	106/414 (26%)	106 (100%)	0	100	100
All	All	1528/3874 (39%)	1528 (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. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	383	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

14 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	$\# Z > 2$
6	NAG	H	1	1,6	14,14,15	0.75	0	17,19,21	1.00	1 (5%)
6	NAG	H	2	6	14,14,15	0.71	0	17,19,21	1.24	1 (5%)
6	NAG	L	1	1,6	14,14,15	0.81	0	17,19,21	1.54	3 (17%)
6	NAG	L	2	6	14,14,15	0.79	0	17,19,21	0.99	1 (5%)
6	NAG	M	1	1,6	14,14,15	0.72	0	17,19,21	1.41	2 (11%)
6	NAG	M	2	6	14,14,15	0.75	0	17,19,21	0.89	0
6	NAG	N	1	1,6	14,14,15	0.75	0	17,19,21	2.44	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	N	2	6	14,14,15	0.71	0	17,19,21	0.89	0
6	NAG	O	1	1,6	14,14,15	0.66	0	17,19,21	0.97	1 (5%)
6	NAG	O	2	6	14,14,15	0.71	0	17,19,21	0.90	1 (5%)
6	NAG	P	1	1,6	14,14,15	0.79	0	17,19,21	1.26	1 (5%)
6	NAG	P	2	6	14,14,15	0.73	0	17,19,21	0.93	0
6	NAG	Q	1	1,6	14,14,15	0.82	0	17,19,21	1.39	3 (17%)
6	NAG	Q	2	6	14,14,15	0.71	0	17,19,21	0.81	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
6	NAG	H	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	H	2	6	-	2/6/23/26	0/1/1/1
6	NAG	L	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	L	2	6	-	0/6/23/26	0/1/1/1
6	NAG	M	1	1,6	-	3/6/23/26	0/1/1/1
6	NAG	M	2	6	-	0/6/23/26	0/1/1/1
6	NAG	N	1	1,6	-	3/6/23/26	0/1/1/1
6	NAG	N	2	6	-	1/6/23/26	0/1/1/1
6	NAG	O	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	O	2	6	-	2/6/23/26	0/1/1/1
6	NAG	P	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	P	2	6	-	2/6/23/26	0/1/1/1
6	NAG	Q	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	Q	2	6	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	N	1	NAG	C2-N2-C7	8.88	134.80	122.90
6	P	1	NAG	C1-O5-C5	3.73	117.18	112.19
6	H	2	NAG	C2-N2-C7	3.39	127.44	122.90
6	L	1	NAG	C4-C3-C2	3.36	115.94	111.02
6	M	1	NAG	C2-N2-C7	3.31	127.34	122.90

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

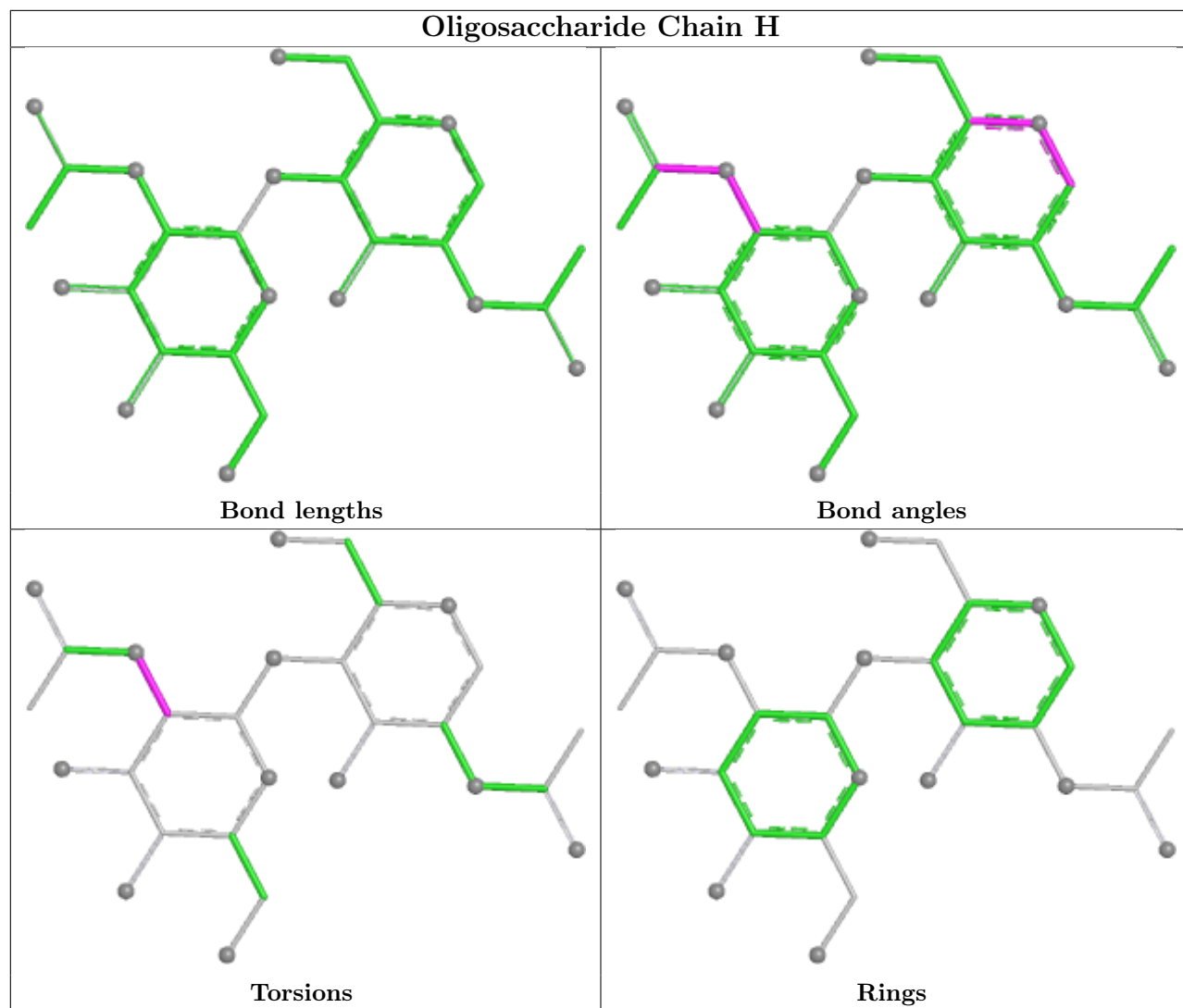
Mol	Chain	Res	Type	Atoms
6	M	1	NAG	O5-C5-C6-O6
6	N	1	NAG	C8-C7-N2-C2
6	N	1	NAG	O7-C7-N2-C2
6	O	2	NAG	C8-C7-N2-C2
6	O	2	NAG	O7-C7-N2-C2

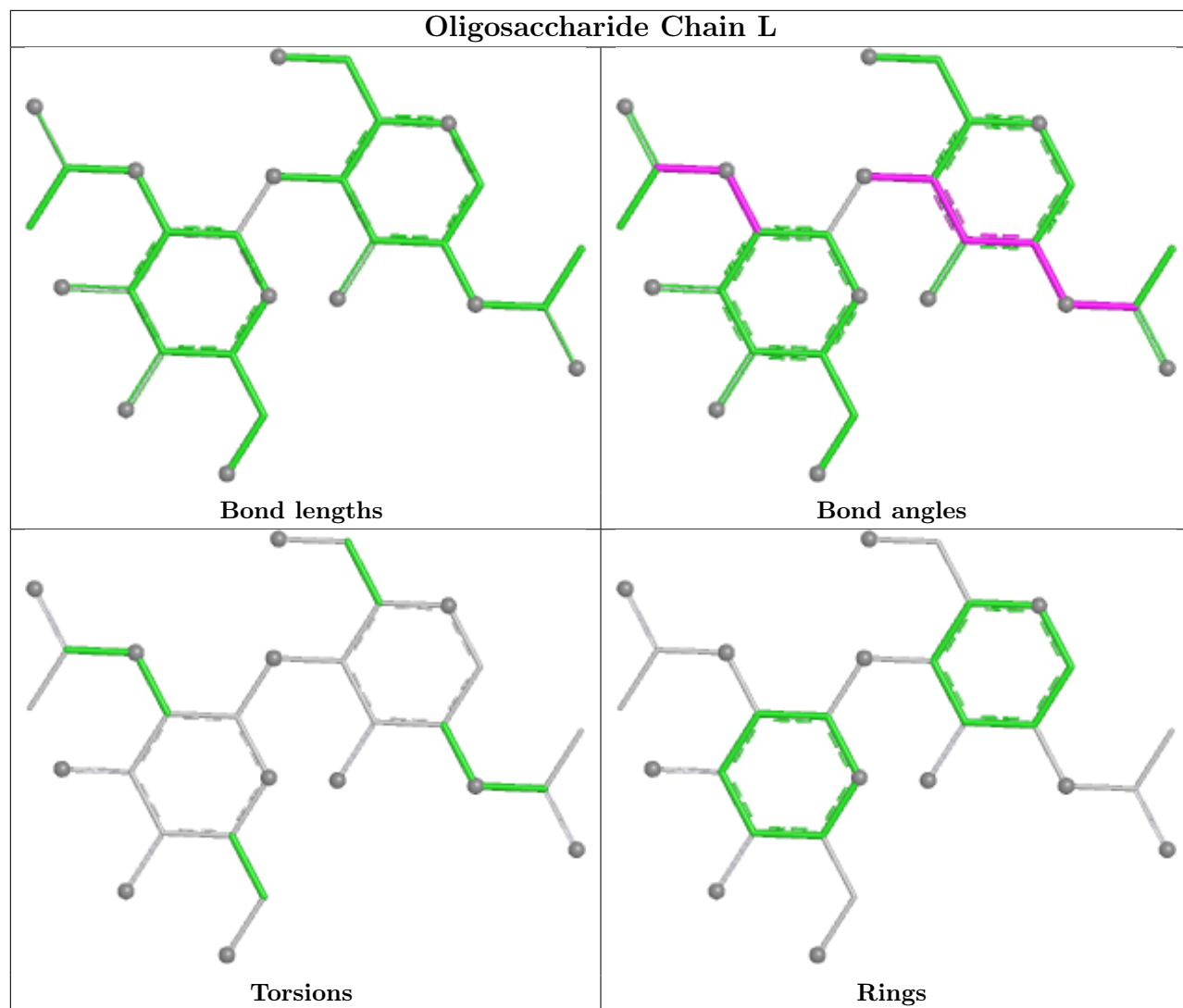
There are no ring outliers.

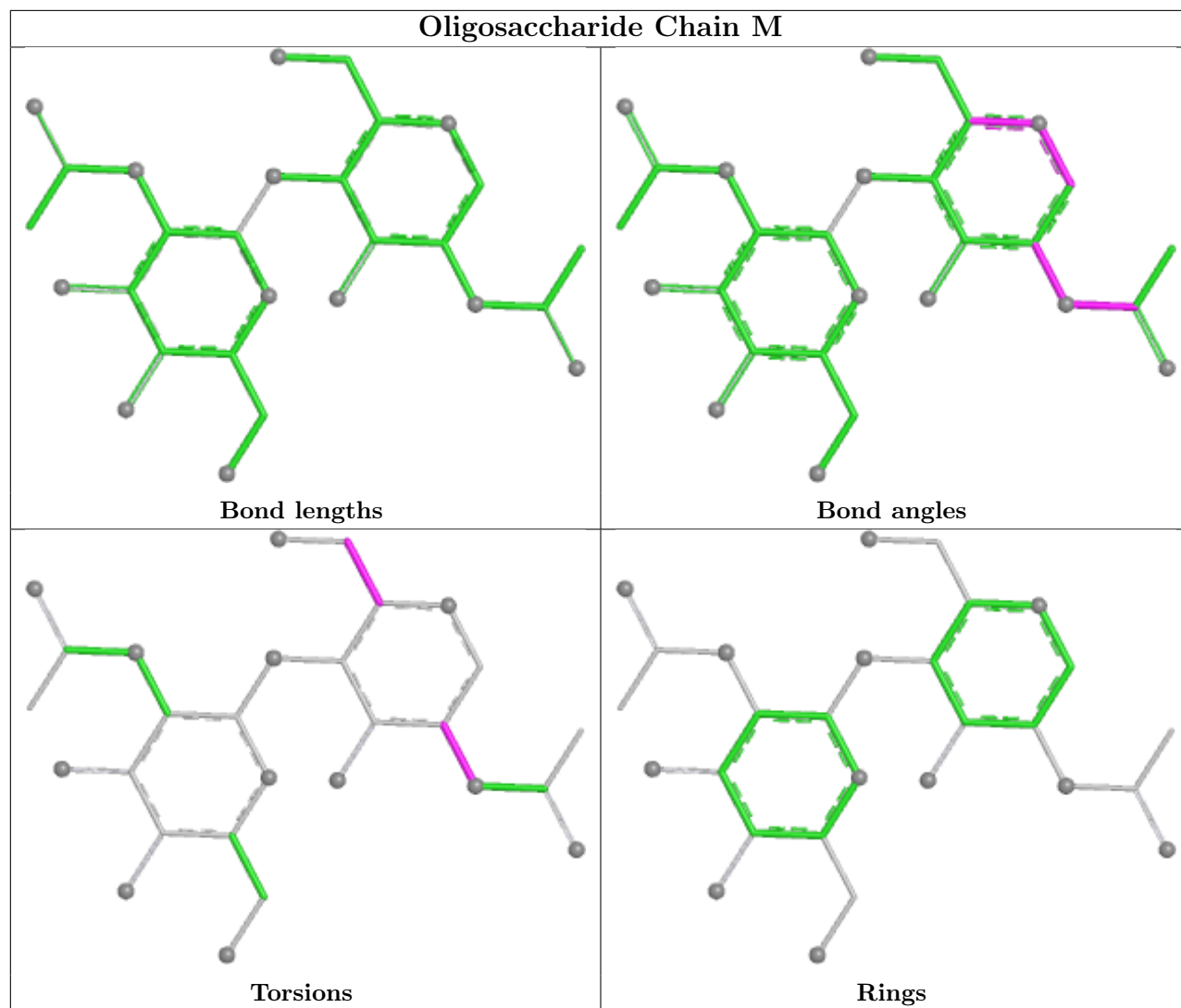
3 monomers are involved in 3 short contacts:

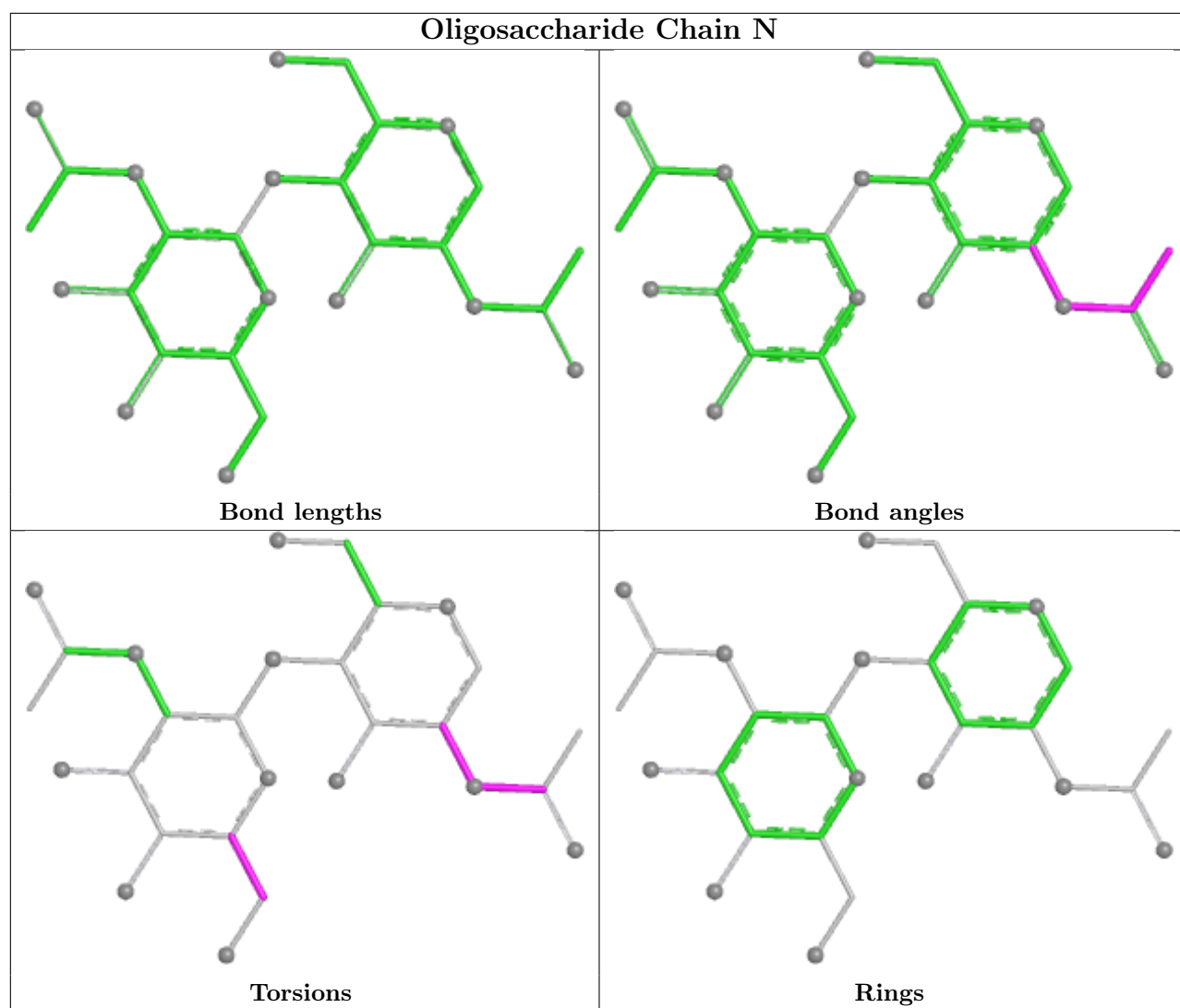
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	N	1	NAG	1	0
6	O	1	NAG	1	0
6	Q	2	NAG	1	0

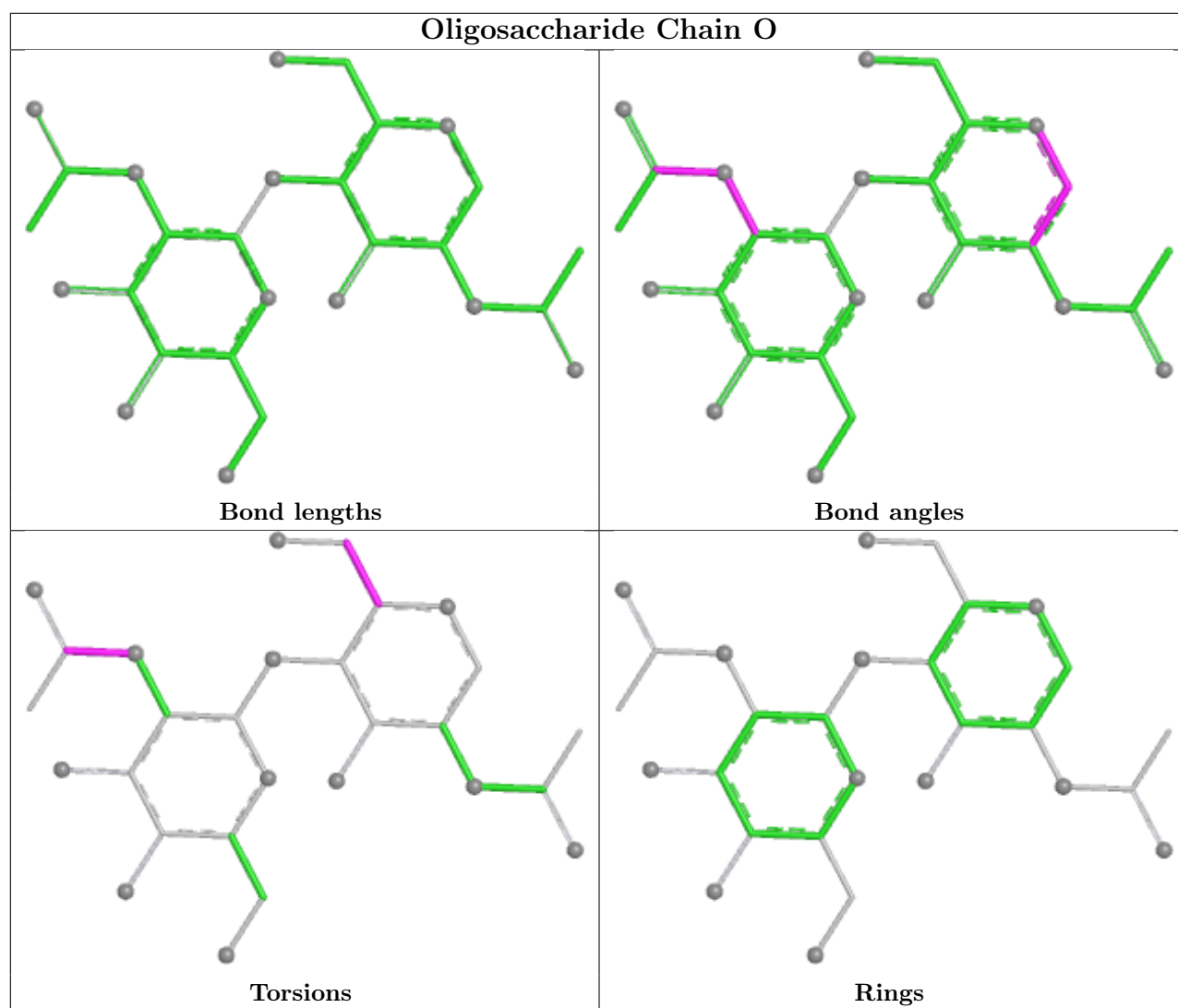
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

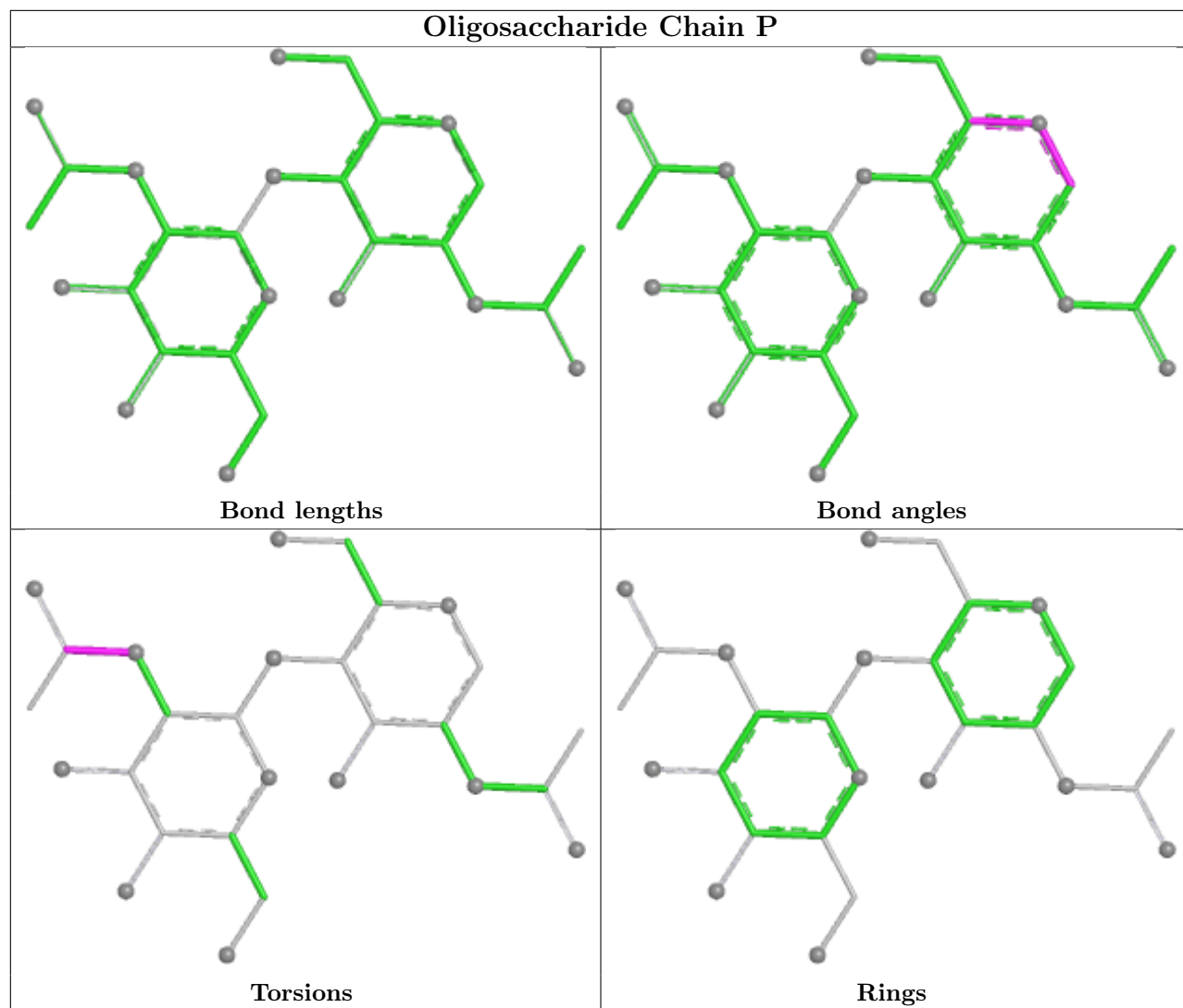


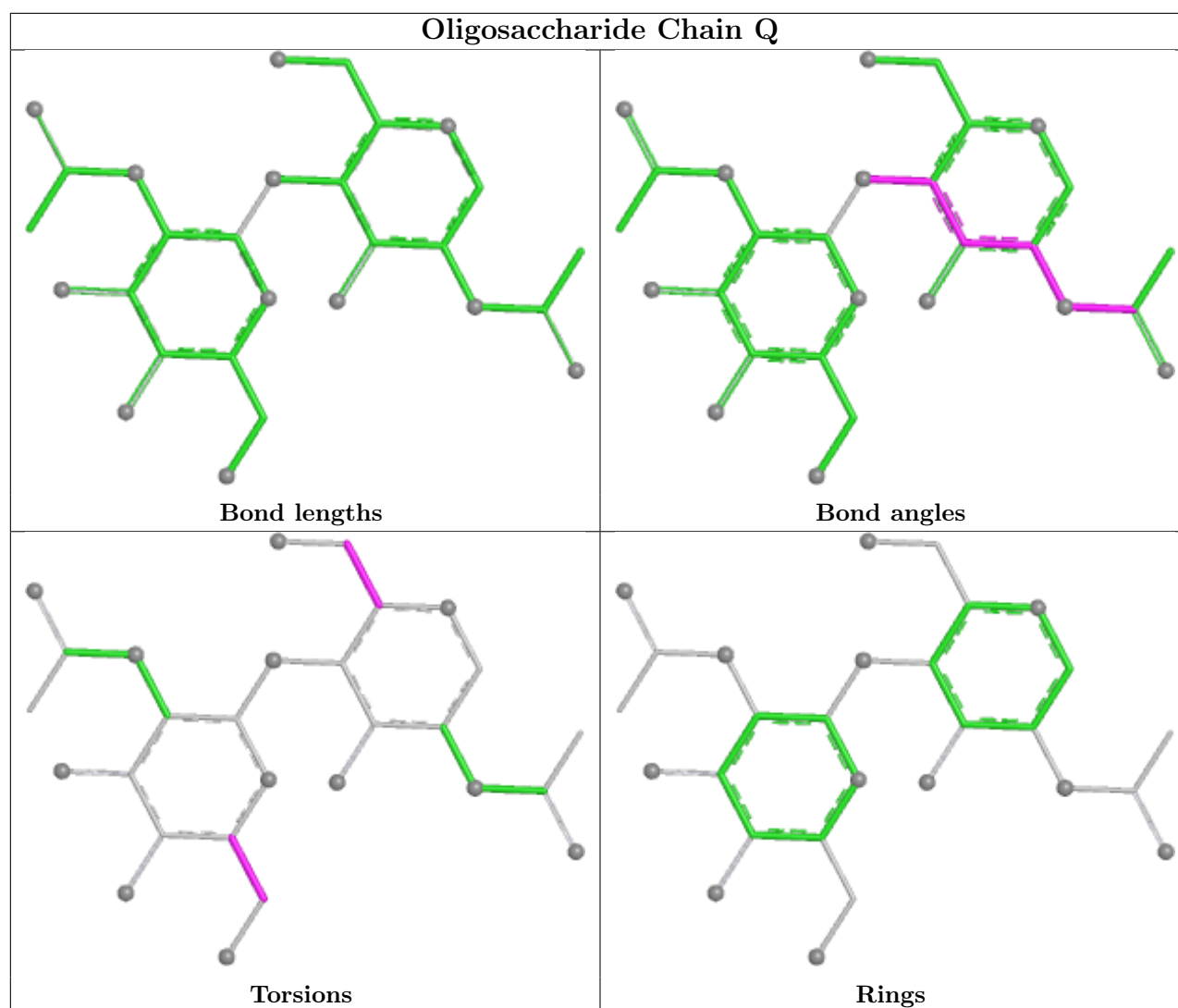












5.6 Ligand geometry [i](#)

2 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	A	601	1	14,14,15	0.76	0	17,19,21	1.12	1 (5%)
7	NAG	C	601	1	14,14,15	0.74	0	17,19,21	0.81	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	A	601	1	-	2/6/23/26	0/1/1/1
7	NAG	C	601	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	601	NAG	C2-N2-C7	3.22	127.22	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	601	NAG	C1-C2-N2-C7
7	A	601	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	601	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

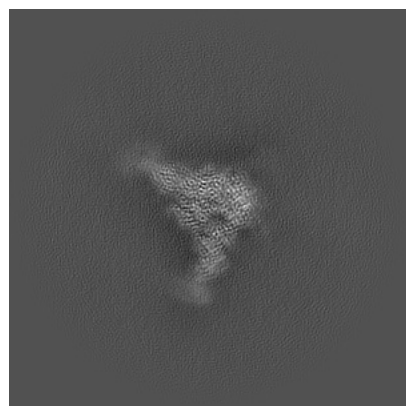
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72242. These allow visual inspection of the internal detail of the map and identification of artifacts.

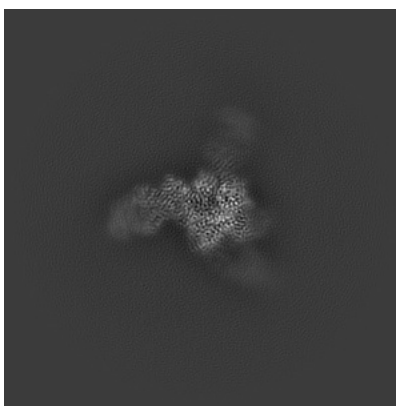
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

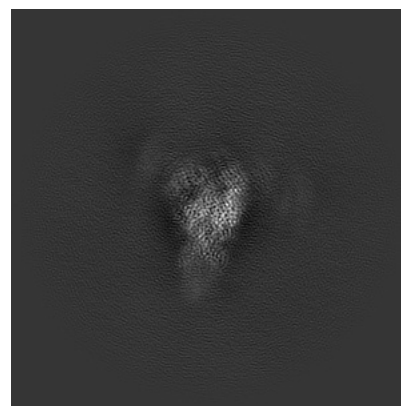
6.1.1 Primary map



X

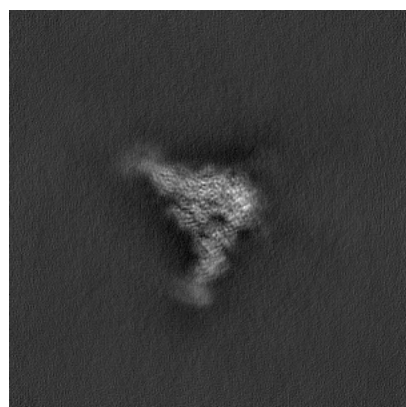


Y

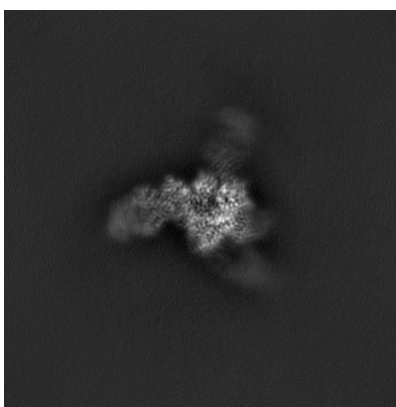


Z

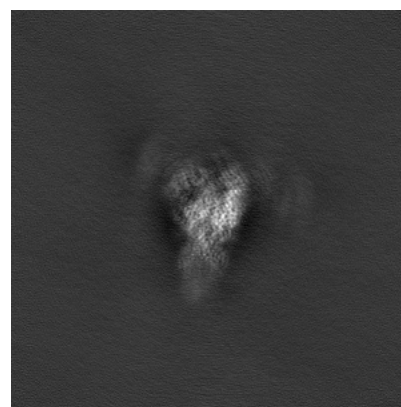
6.1.2 Raw map



X



Y

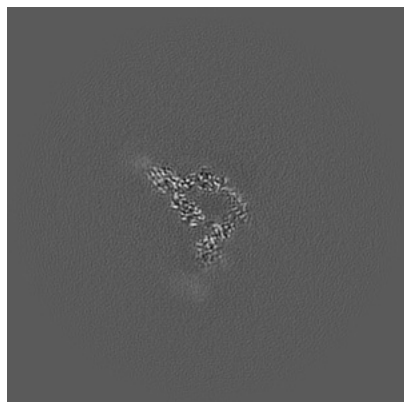


Z

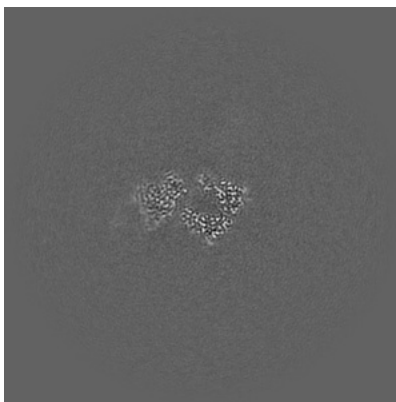
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

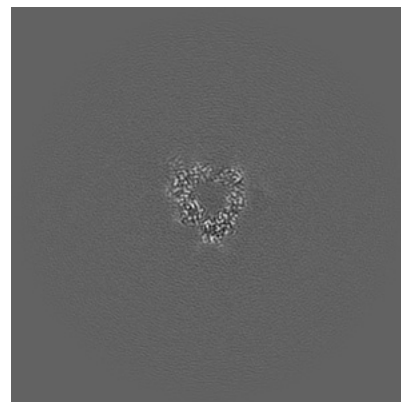
6.2.1 Primary map



X Index: 190

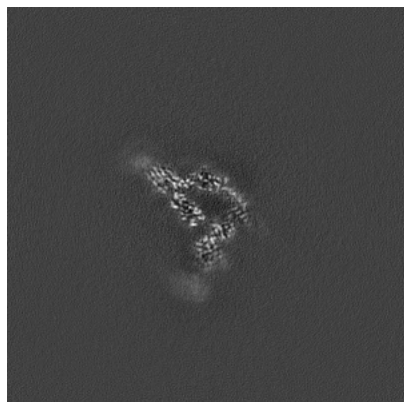


Y Index: 190

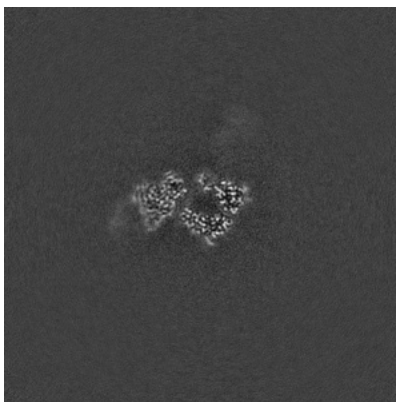


Z Index: 190

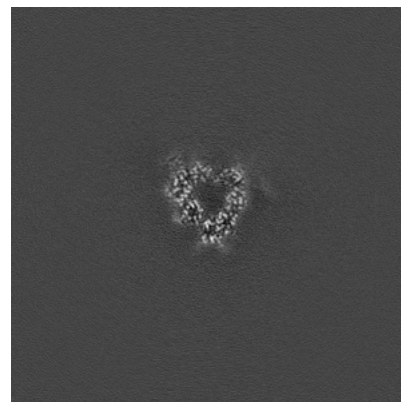
6.2.2 Raw map



X Index: 190



Y Index: 190

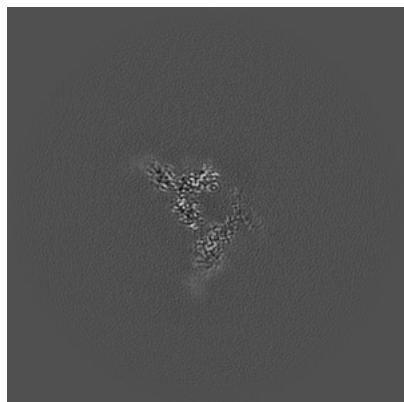


Z Index: 190

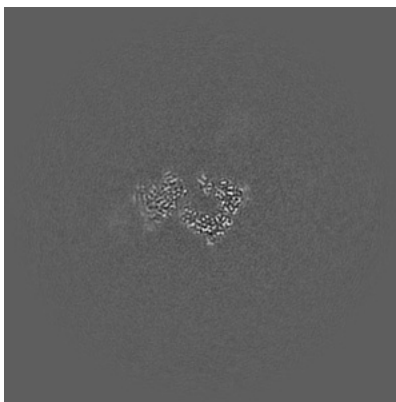
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

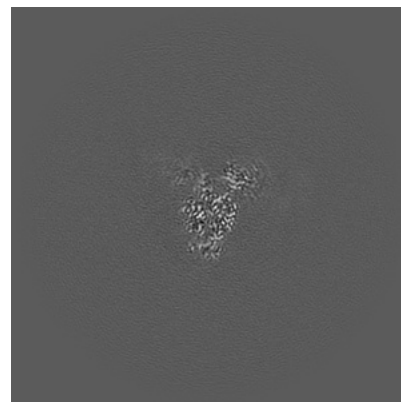
6.3.1 Primary map



X Index: 195

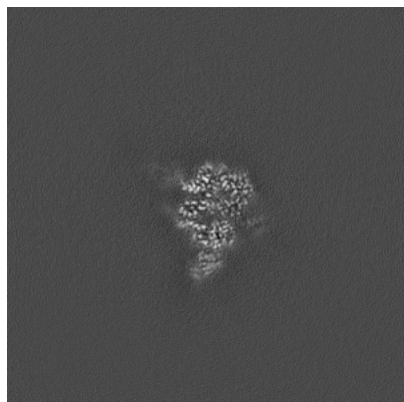


Y Index: 189

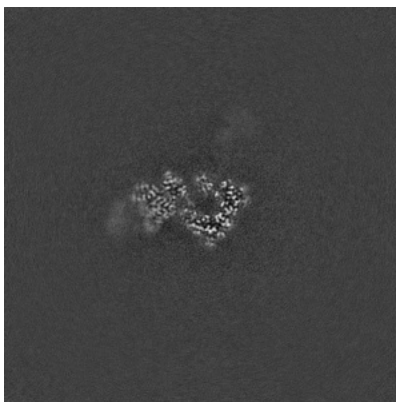


Z Index: 208

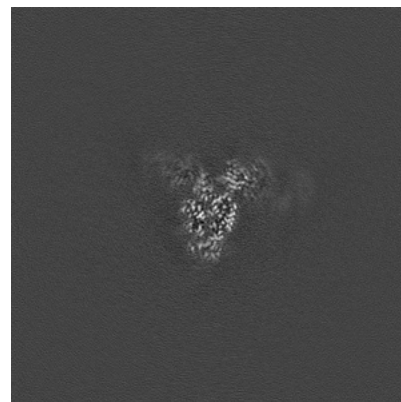
6.3.2 Raw map



X Index: 208



Y Index: 188

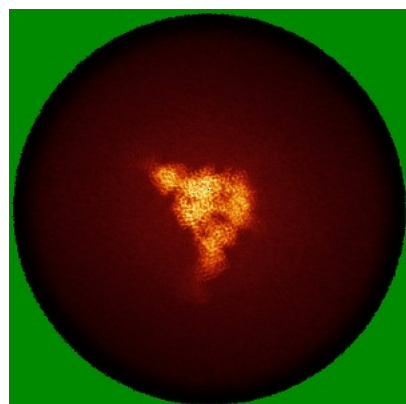


Z Index: 208

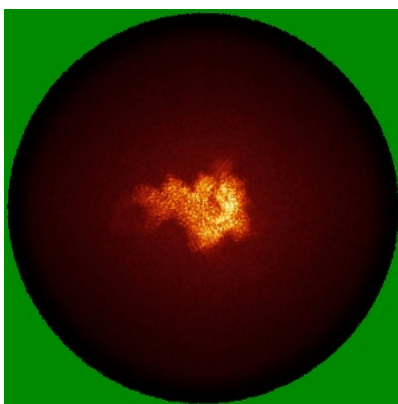
The images above show the largest variance slices of the map in three orthogonal directions.

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

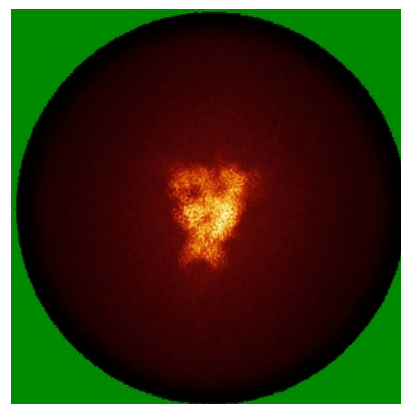
6.4.1 Primary map



X

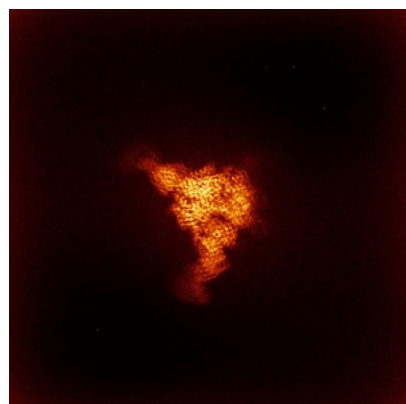


Y

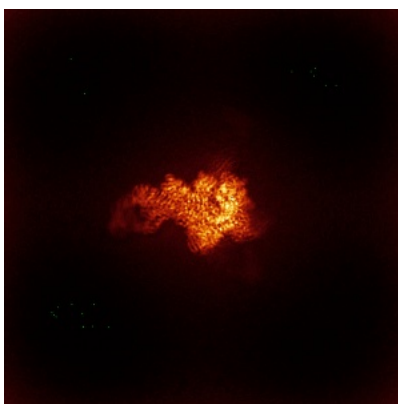


Z

6.4.2 Raw map



X



Y

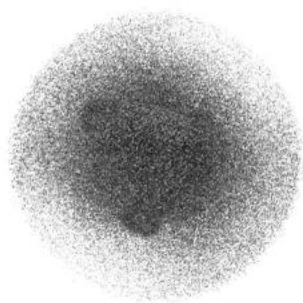


Z

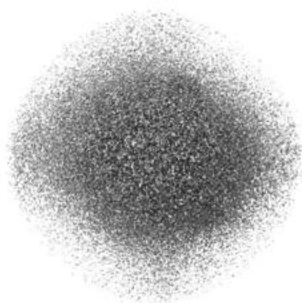
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

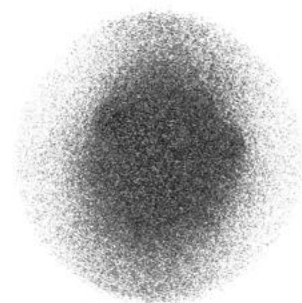
6.5.1 Primary map



X



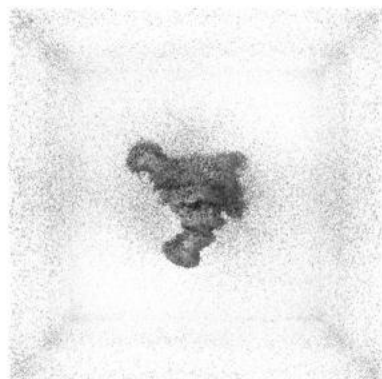
Y



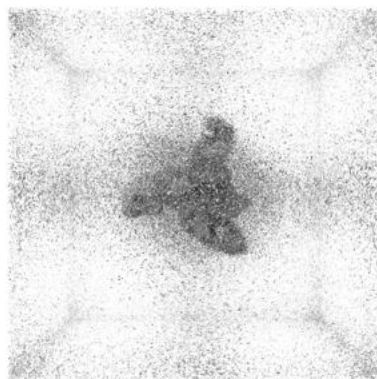
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0321. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

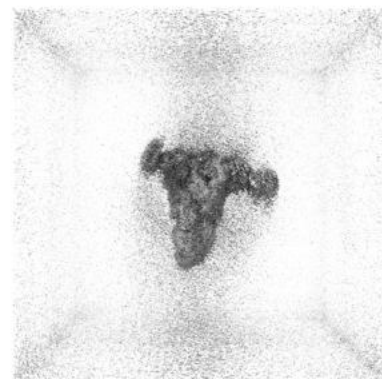
6.5.2 Raw map



X



Y



Z

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.

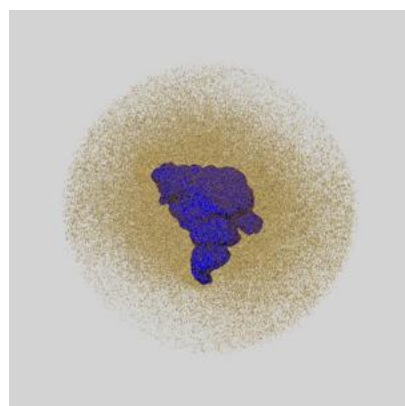
6.6 Mask visualisation [i](#)

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

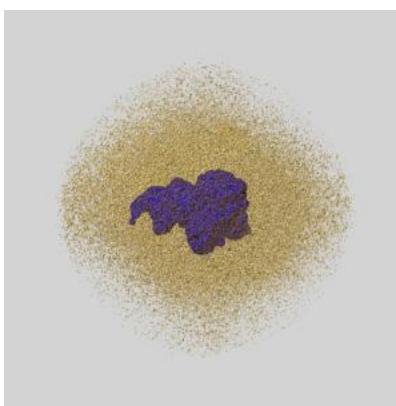
A mask typically either:

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

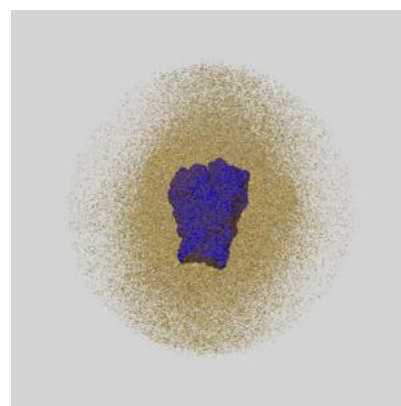
6.6.1 emd_72242_msk_1.map [i](#)



X



Y

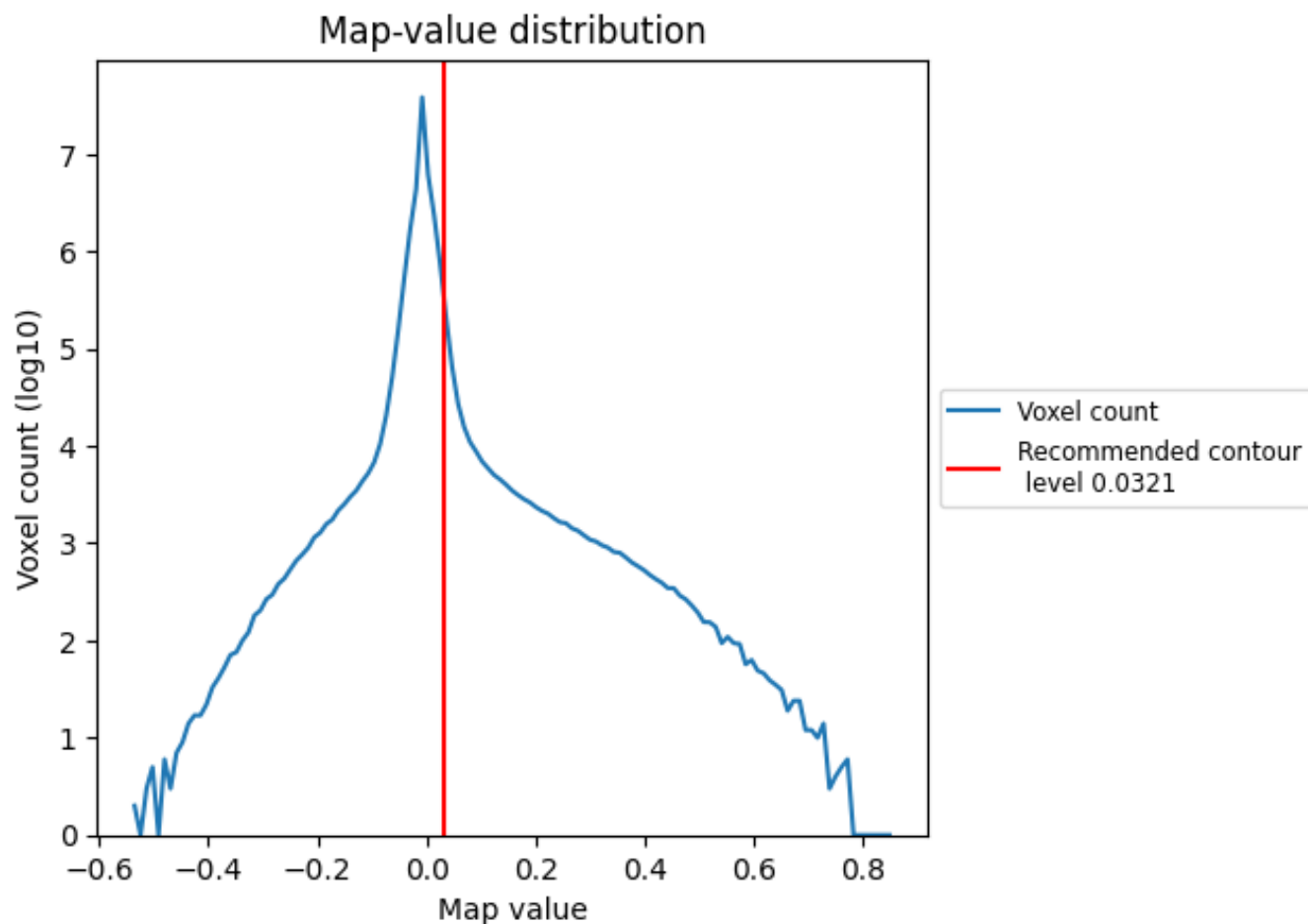


Z

7 Map analysis [i](#)

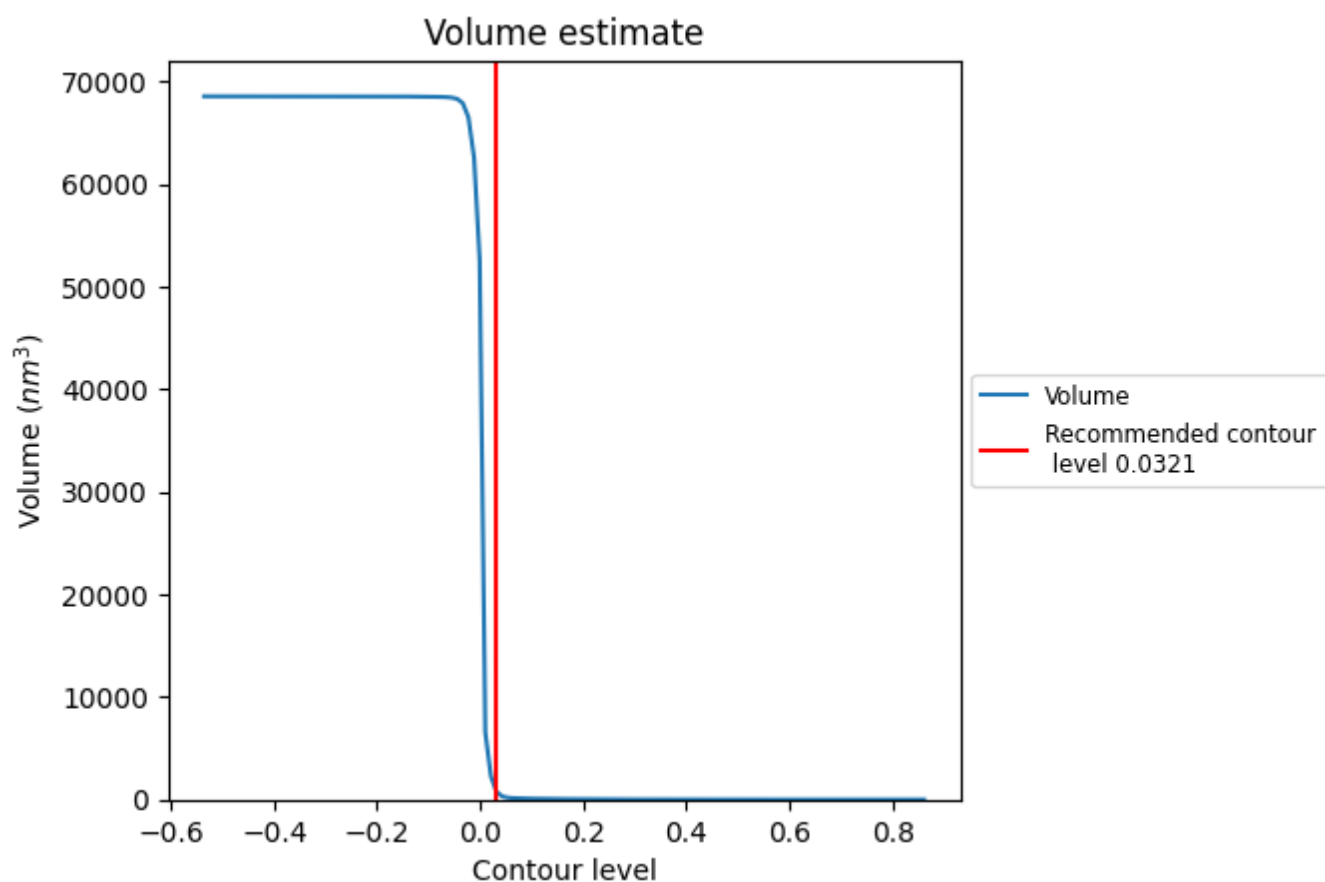
This section contains the results of statistical analysis of the map.

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.

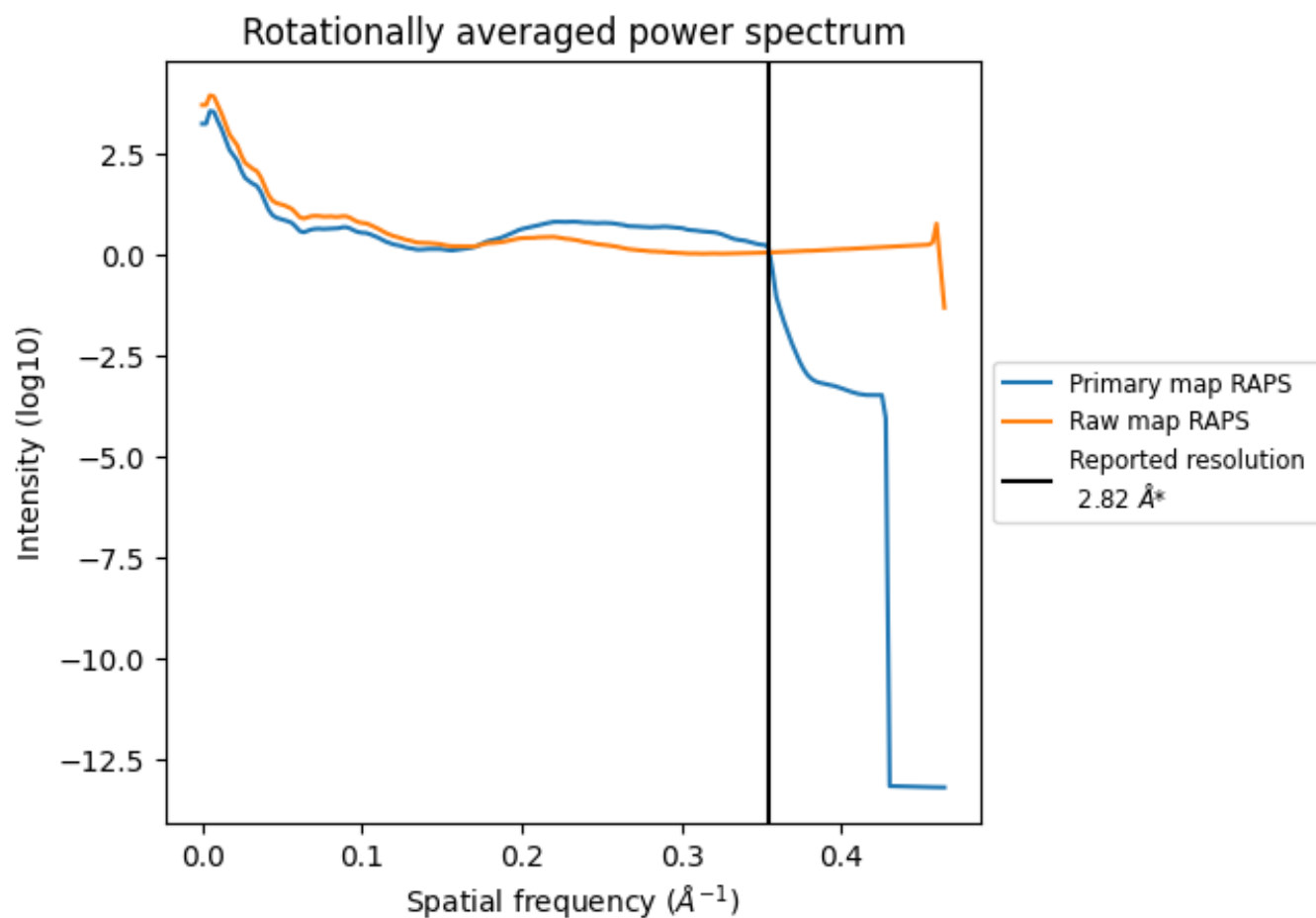
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 744 nm^3 ; this corresponds to an approximate mass of 672 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 ⓘ

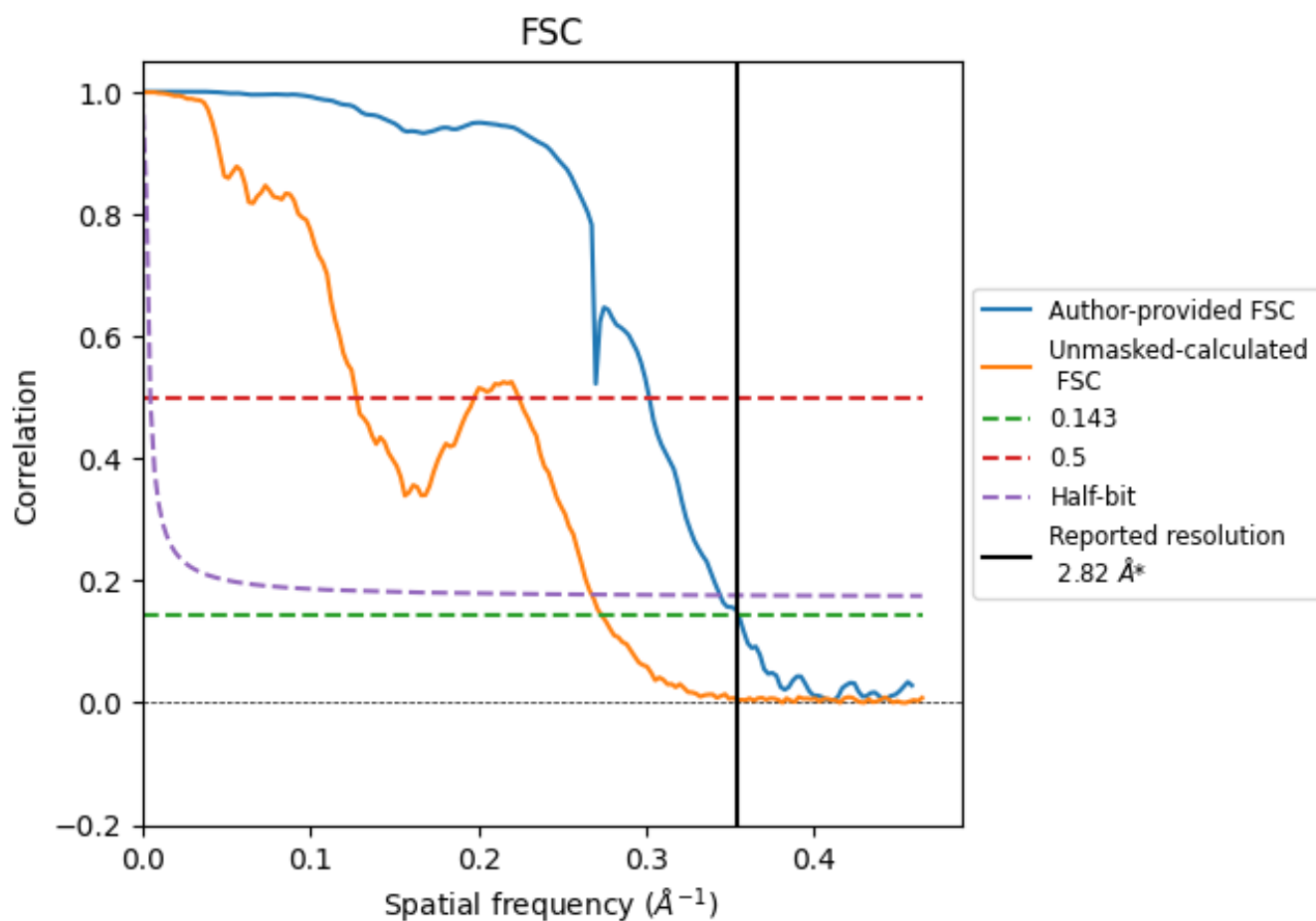


*Reported resolution corresponds to spatial frequency of 0.355 \AA^{-1}

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 0.355 Å⁻¹

8.2 Resolution estimates [i](#)

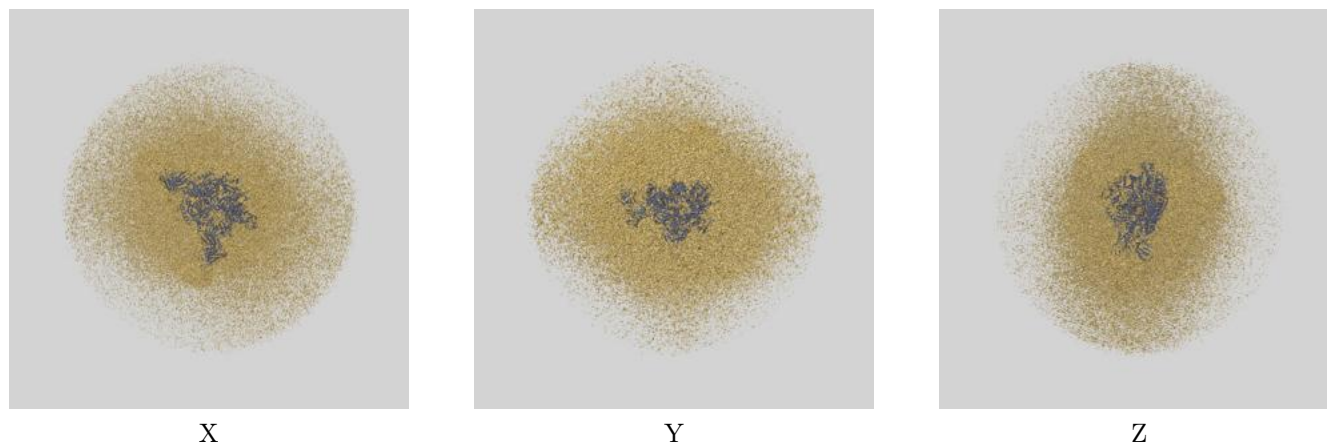
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.82	-	-
Author-provided FSC curve	2.82	3.31	2.91
Unmasked-calculated*	3.66	7.84	3.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.66 differs from the reported value 2.82 by more than 10 %

9 Map-model fit [i](#)

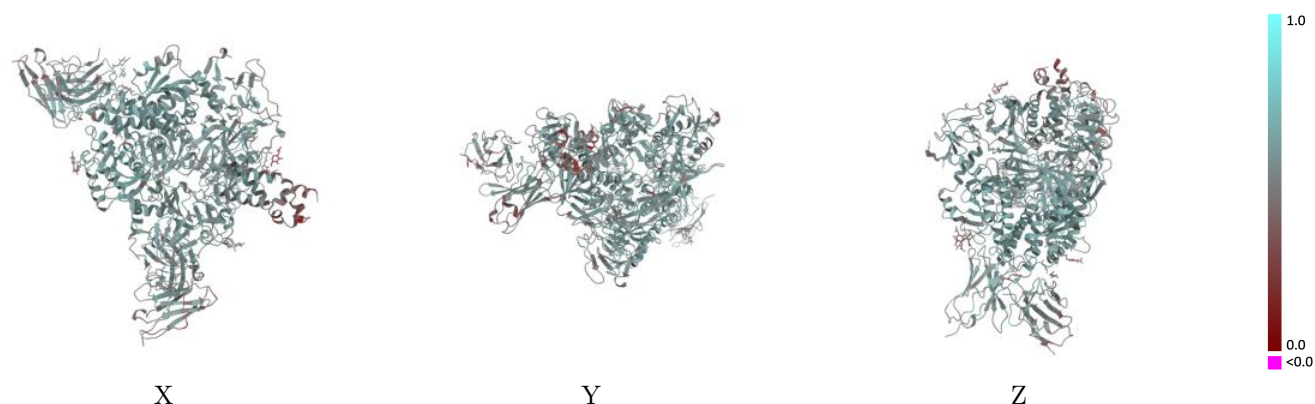
This section contains information regarding the fit between EMDB map EMD-72242 and PDB model 9Q5V. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



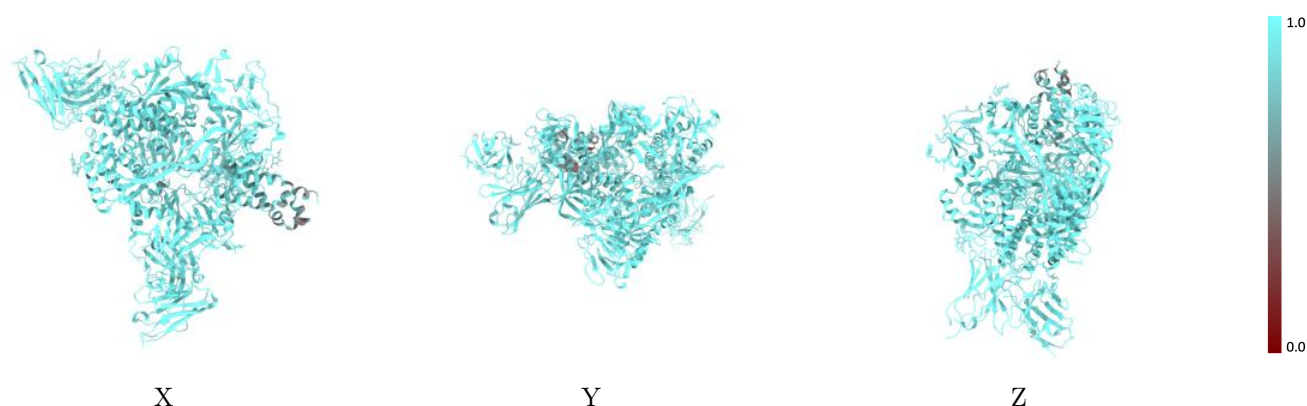
The images above show the 3D surface view of the map at the recommended contour level 0.0321 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



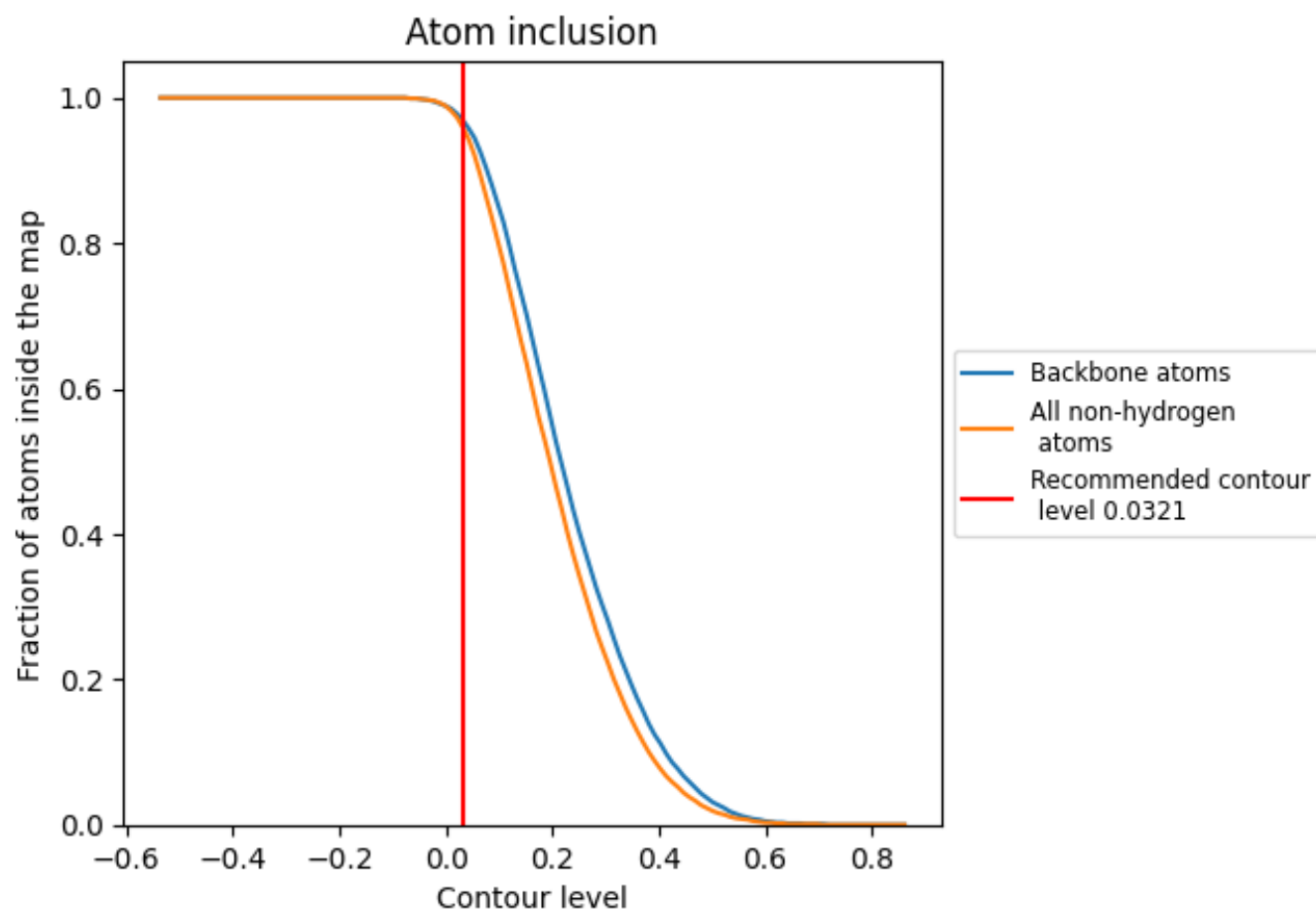
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0321).





































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (0.0321) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9590	 0.5500
A	 0.9870	 0.5790
B	 0.9560	 0.5560
C	 0.9830	 0.5720
D	 0.9550	 0.5600
E	 0.9860	 0.5800
F	 0.9620	 0.5660
G	 0.9520	 0.5170
H	 0.8570	 0.3370
I	 0.9620	 0.5470
J	 0.9360	 0.4840
K	 0.9600	 0.5160
L	 0.8930	 0.4690
M	 0.8930	 0.3760
N	 1.0000	 0.5450
O	 0.8570	 0.2880
P	 0.8210	 0.4000
Q	 1.0000	 0.5050

