



wwPDB EM Validation Summary Report ⓘ

May 18, 2026 – 12:54 PM EDT

PDB ID : 9YIG / pdb_00009yig
EMDB ID : EMD-72989
Title : V634-136 Fab in complex with HIV-1 Env 5MUT-3fill SOSIP
Authors : Gristick, H.B.; Gavor, E.; Bjorkman, P.J.
Deposited on : 2025-10-01
Resolution : 3.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

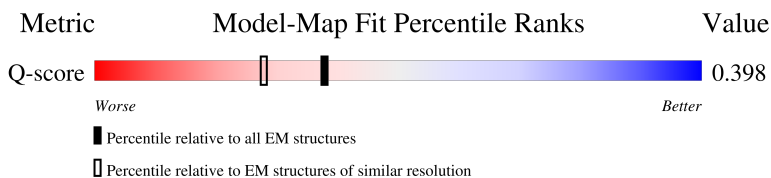
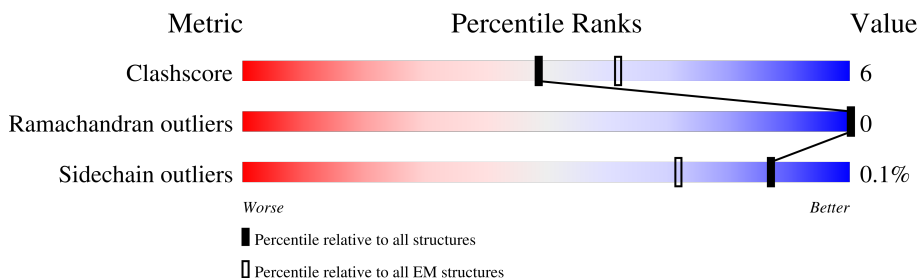
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	153	 63% 16% 21%
1	B	153	 65% 14% 21%
1	C	153	 66% 13% 21%
2	E	479	 77% 14% 9%

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Mol	Chain	Length	Quality of chain
2	F	479	 78%13%9%
2	G	479	 77%14%9%
3	H	129	 10%81%17%.
3	J	129	 11%81%16%.
3	M	129	 10%81%16%.
4	K	112	 12%85%15%
4	L	112	 16%86%14%
4	N	112	 13%84%16%
5	D	4	 100%
5	O	4	 100%
5	Q	4	 100%
6	I	5	 60%40%
6	P	5	 60%40%
6	R	5	 60%40%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 19747 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 Transmembrane protein gp41.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	121	Total	C	N	O	S	0	0
			956	600	165	185	6		
1	B	121	Total	C	N	O	S	0	0
			956	600	165	185	6		
1	C	121	Total	C	N	O	S	0	0
			956	600	165	185	6		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	519	SER	PHE	conflict	UNP Q2N0S6
A	559	PRO	ILE	conflict	UNP Q2N0S6
A	561	PRO	ALA	conflict	UNP Q2N0S6
A	568	ASP	LEU	conflict	UNP Q2N0S6
A	570	HIS	VAL	conflict	UNP Q2N0S6
A	585	HIS	ARG	conflict	UNP Q2N0S6
A	605	CYS	THR	conflict	UNP Q2N0S6
B	519	SER	PHE	conflict	UNP Q2N0S6
B	559	PRO	ILE	conflict	UNP Q2N0S6
B	561	PRO	ALA	conflict	UNP Q2N0S6
B	568	ASP	LEU	conflict	UNP Q2N0S6
B	570	HIS	VAL	conflict	UNP Q2N0S6
B	585	HIS	ARG	conflict	UNP Q2N0S6
B	605	CYS	THR	conflict	UNP Q2N0S6
C	519	SER	PHE	conflict	UNP Q2N0S6
C	559	PRO	ILE	conflict	UNP Q2N0S6
C	561	PRO	ALA	conflict	UNP Q2N0S6
C	568	ASP	LEU	conflict	UNP Q2N0S6
C	570	HIS	VAL	conflict	UNP Q2N0S6
C	585	HIS	ARG	conflict	UNP Q2N0S6
C	605	CYS	THR	conflict	UNP Q2N0S6

- Molecule 2 is a protein called Envelope glycoprotein gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	437	Total 3453	C 2170	N 609	O 645	S 29	0	0
2	F	437	Total 3453	C 2170	N 609	O 645	S 29	0	0
2	G	436	Total 3445	C 2166	N 607	O 643	S 29	0	0

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	106	GLU	THR	conflict	UNP Q2N0S6
E	134	TYR	VAL	conflict	UNP Q2N0S6
E	136	PRO	ASN	conflict	UNP Q2N0S6
E	138	LEU	ILE	conflict	UNP Q2N0S6
E	140	ASN	ASP	conflict	UNP Q2N0S6
E	201	CYS	ILE	conflict	UNP Q2N0S6
E	230	ASN	ASP	conflict	UNP Q2N0S6
E	232	THR	LYS	conflict	UNP Q2N0S6
E	241	ASN	SER	conflict	UNP Q2N0S6
E	271	ILE	MET	conflict	UNP Q2N0S6
E	288	LEU	PHE	conflict	UNP Q2N0S6
E	304	VAL	ARG	conflict	UNP Q2N0S6
E	319	TYR	ALA	conflict	UNP Q2N0S6
E	332	ASN	THR	conflict	UNP Q2N0S6
E	344	ASN	LYS	conflict	UNP Q2N0S6
E	346	SER	VAL	conflict	UNP Q2N0S6
E	363	GLN	ASN	conflict	UNP Q2N0S6
E	433	CYS	ALA	conflict	UNP Q2N0S6
E	501	CYS	ALA	conflict	UNP Q2N0S6
E	509	ARG	GLU	conflict	UNP Q2N0S6
E	510	ARG	LYS	conflict	UNP Q2N0S6
E	512	ARG	ALA	conflict	UNP Q2N0S6
E	513	ARG	VAL	conflict	UNP Q2N0S6
F	106	GLU	THR	conflict	UNP Q2N0S6
F	134	TYR	VAL	conflict	UNP Q2N0S6
F	136	PRO	ASN	conflict	UNP Q2N0S6
F	138	LEU	ILE	conflict	UNP Q2N0S6
F	140	ASN	ASP	conflict	UNP Q2N0S6
F	201	CYS	ILE	conflict	UNP Q2N0S6
F	230	ASN	ASP	conflict	UNP Q2N0S6
F	232	THR	LYS	conflict	UNP Q2N0S6
F	241	ASN	SER	conflict	UNP Q2N0S6
F	271	ILE	MET	conflict	UNP Q2N0S6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	288	LEU	PHE	conflict	UNP Q2N0S6
F	304	VAL	ARG	conflict	UNP Q2N0S6
F	319	TYR	ALA	conflict	UNP Q2N0S6
F	332	ASN	THR	conflict	UNP Q2N0S6
F	344	ASN	LYS	conflict	UNP Q2N0S6
F	346	SER	VAL	conflict	UNP Q2N0S6
F	363	GLN	ASN	conflict	UNP Q2N0S6
F	433	CYS	ALA	conflict	UNP Q2N0S6
F	501	CYS	ALA	conflict	UNP Q2N0S6
F	509	ARG	GLU	conflict	UNP Q2N0S6
F	510	ARG	LYS	conflict	UNP Q2N0S6
F	512	ARG	ALA	conflict	UNP Q2N0S6
F	513	ARG	VAL	conflict	UNP Q2N0S6
G	106	GLU	THR	conflict	UNP Q2N0S6
G	134	TYR	VAL	conflict	UNP Q2N0S6
G	136	PRO	ASN	conflict	UNP Q2N0S6
G	138	LEU	ILE	conflict	UNP Q2N0S6
G	140	ASN	ASP	conflict	UNP Q2N0S6
G	201	CYS	ILE	conflict	UNP Q2N0S6
G	230	ASN	ASP	conflict	UNP Q2N0S6
G	232	THR	LYS	conflict	UNP Q2N0S6
G	241	ASN	SER	conflict	UNP Q2N0S6
G	271	ILE	MET	conflict	UNP Q2N0S6
G	288	LEU	PHE	conflict	UNP Q2N0S6
G	304	VAL	ARG	conflict	UNP Q2N0S6
G	319	TYR	ALA	conflict	UNP Q2N0S6
G	332	ASN	THR	conflict	UNP Q2N0S6
G	344	ASN	LYS	conflict	UNP Q2N0S6
G	346	SER	VAL	conflict	UNP Q2N0S6
G	363	GLN	ASN	conflict	UNP Q2N0S6
G	433	CYS	ALA	conflict	UNP Q2N0S6
G	501	CYS	ALA	conflict	UNP Q2N0S6
G	509	ARG	GLU	conflict	UNP Q2N0S6
G	510	ARG	LYS	conflict	UNP Q2N0S6
G	512	ARG	ALA	conflict	UNP Q2N0S6
G	513	ARG	VAL	conflict	UNP Q2N0S6

- Molecule 3 is a protein called V634-136 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	126	Total	C	N	O	S	0	0
			980	625	160	193	2		

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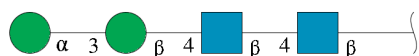
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	126	Total	C	N	O	S	0	0
			980	625	160	193	2		
3	M	126	Total	C	N	O	S	0	0
			980	625	160	193	2		

- Molecule 4 is a protein called V634-136 Fab light chain.

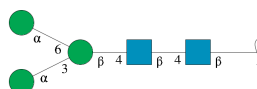
Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	112	Total	C	N	O	S	0	0
			861	541	150	166	4		
4	L	112	Total	C	N	O	S	0	0
			861	541	150	166	4		
4	N	112	Total	C	N	O	S	0	0
			861	541	150	166	4		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
5	D	4	Total	C	N	O	0	0
			50	28	2	20		
5	O	4	Total	C	N	O	0	0
			50	28	2	20		
5	Q	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 6 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.



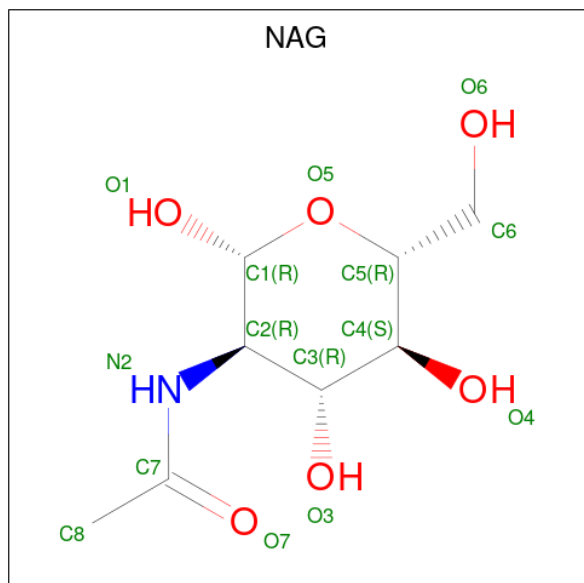
Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	5	Total	C	N	O	0	0
			61	34	2	25		

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

- 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	B	1	Total	C	N	O	0
			14	8	1	5	
7	C	1	Total	C	N	O	0
			14	8	1	5	
7	E	1	Total	C	N	O	0
			14	8	1	5	
7	E	1	Total	C	N	O	0
			14	8	1	5	
7	E	1	Total	C	N	O	0
			14	8	1	5	
7	E	1	Total	C	N	O	0
			14	8	1	5	
7	E	1	Total	C	N	O	0
			14	8	1	5	

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

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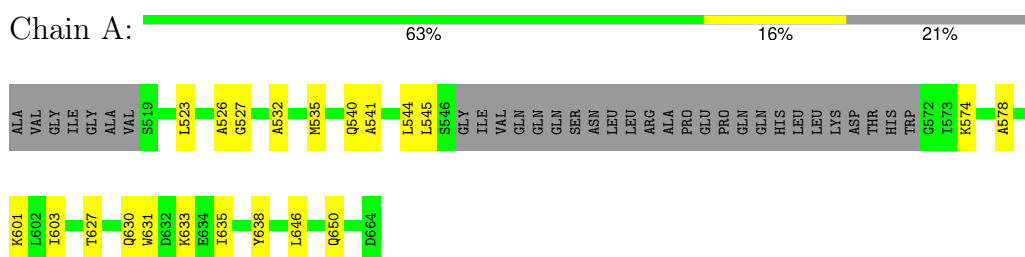
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Mol	Chain	Residues	Atoms				AltConf
7	F	1	Total	C	N	O	0
			14	8	1	5	
7	F	1	Total	C	N	O	0
			14	8	1	5	
7	F	1	Total	C	N	O	0
			14	8	1	5	
7	G	1	Total	C	N	O	0
			14	8	1	5	
7	G	1	Total	C	N	O	0
			14	8	1	5	
7	G	1	Total	C	N	O	0
			14	8	1	5	
7	G	1	Total	C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

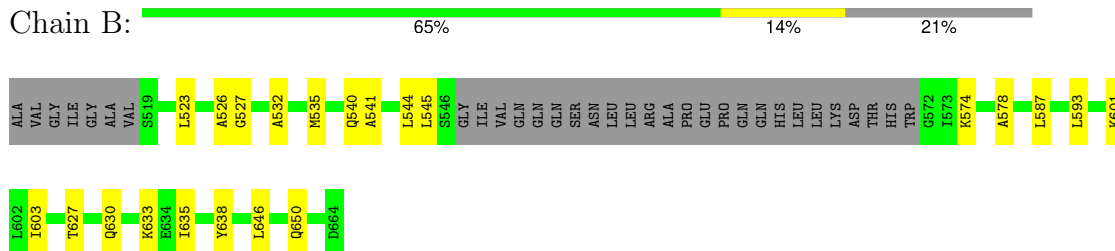
3 Residue-property plots [i](#)

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.

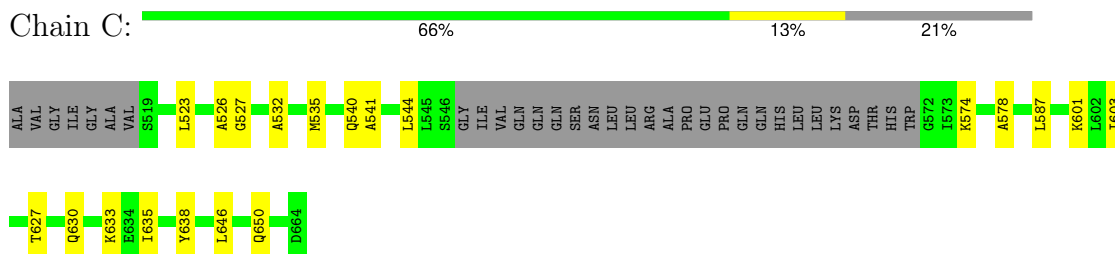
- Molecule 1: Transmembrane protein gp41



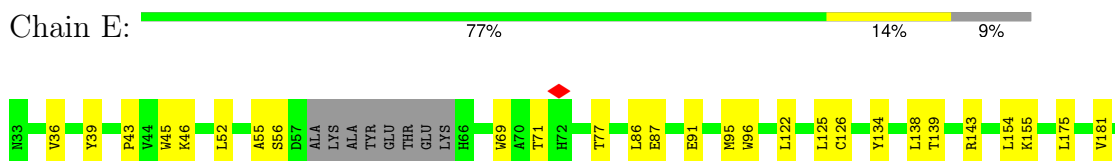
- Molecule 1: Transmembrane protein gp41



- Molecule 1: Transmembrane protein gp41



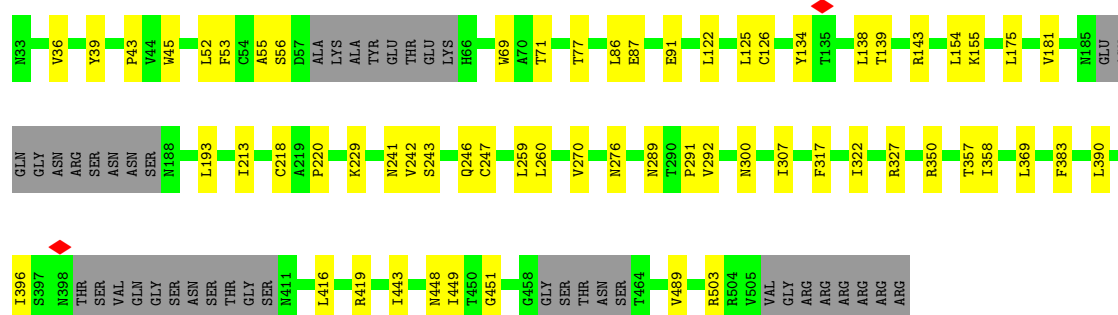
- Molecule 2: Envelope glycoprotein gp120





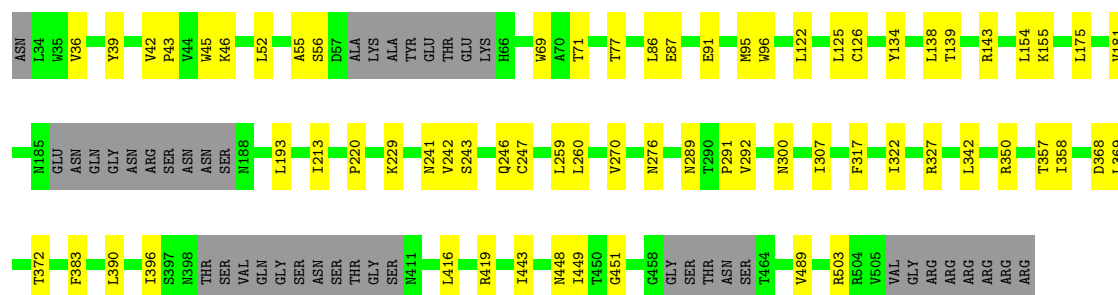
- Molecule 2: Envelope glycoprotein gp120

Chain F: 78% 13% 9%



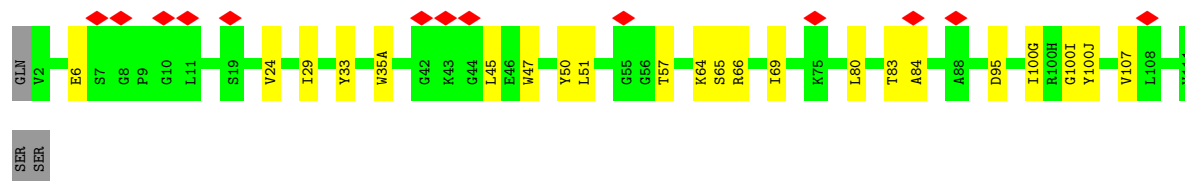
- Molecule 2: Envelope glycoprotein gp120

Chain G: 77% 14% 9%



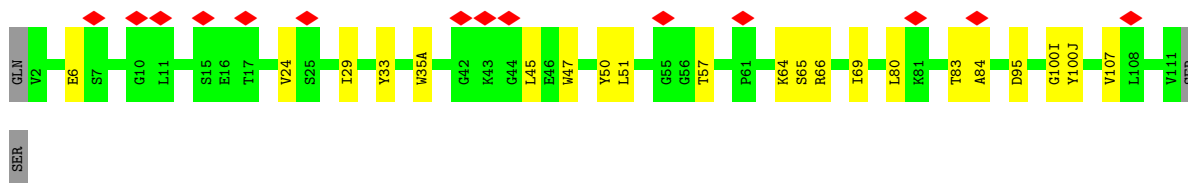
- Molecule 3: V634-136 Fab heavy chain

Chain H: 10% 81% 17%

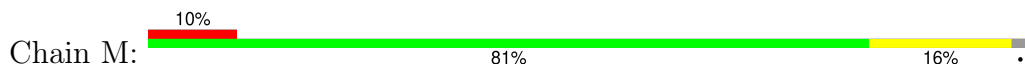


- Molecule 3: V634-136 Fab heavy chain

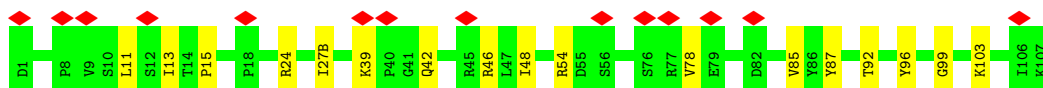
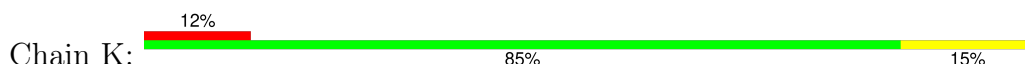
Chain J: 11% 81% 16%



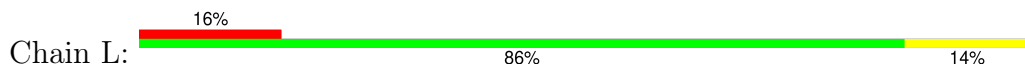
- Molecule 3: V634-136 Fab heavy chain



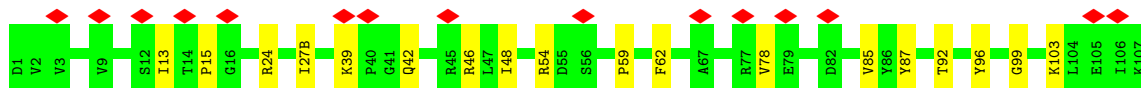
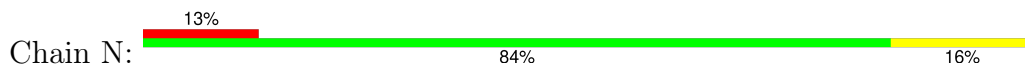
- Molecule 4: V634-136 Fab light chain



- Molecule 4: V634-136 Fab light chain



- Molecule 4: V634-136 Fab light chain



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



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





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

Chain Q:  100%



- Molecule 6: 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 I:  60% 40%



- Molecule 6: 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 P:  60% 40%



- Molecule 6: 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 R:  60% 40%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37282	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.530	Depositor
Minimum map value	-0.292	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.0331	Depositor
Map size (Å)	313.2, 313.2, 313.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87, 0.87, 0.87	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, BMA, MAN

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	0.08	0/972	0.22	0/1317
1	B	0.08	0/972	0.22	0/1317
1	C	0.08	0/972	0.22	0/1317
2	E	0.10	0/3526	0.26	0/4791
2	F	0.10	0/3526	0.26	0/4791
2	G	0.10	0/3518	0.26	0/4780
3	H	0.10	0/1007	0.32	0/1374
3	J	0.10	0/1007	0.32	0/1374
3	M	0.10	0/1007	0.32	0/1374
4	K	0.09	0/883	0.28	0/1200
4	L	0.09	0/883	0.28	0/1200
4	N	0.09	0/883	0.30	0/1200
All	All	0.10	0/19156	0.27	0/26035

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	956	0	929	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	956	0	929	17	0
1	C	956	0	929	16	0
2	E	3453	0	3373	45	0
2	F	3453	0	3373	41	0
2	G	3445	0	3367	45	0
3	H	980	0	936	19	0
3	J	980	0	936	17	0
3	M	980	0	936	17	0
4	K	861	0	849	12	0
4	L	861	0	849	11	0
4	N	861	0	849	12	0
5	D	50	0	43	0	0
5	O	50	0	43	0	0
5	Q	50	0	43	0	0
6	I	61	0	52	0	0
6	P	61	0	52	0	0
6	R	61	0	52	0	0
7	A	14	0	13	0	0
7	B	14	0	13	0	0
7	C	14	0	13	0	0
7	E	210	0	195	2	0
7	F	210	0	195	2	0
7	G	210	0	195	2	0
All	All	19747	0	19164	227	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 227 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)
2:E:69:TRP:HE1	2:E:213:ILE:H	1.25	0.84
2:G:69:TRP:HE1	2:G:213:ILE:H	1.25	0.82
2:F:69:TRP:HE1	2:F:213:ILE:H	1.25	0.81
2:E:327:ARG:NH2	3:M:33:TYR:HE1	1.81	0.78
2:F:327:ARG:NH2	3:J:33:TYR:HE1	1.81	0.78

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	117/153 (76%)	114 (97%)	3 (3%)	0	100	100
1	B	117/153 (76%)	114 (97%)	3 (3%)	0	100	100
1	C	117/153 (76%)	114 (97%)	3 (3%)	0	100	100
2	E	427/479 (89%)	423 (99%)	4 (1%)	0	100	100
2	F	427/479 (89%)	423 (99%)	4 (1%)	0	100	100
2	G	426/479 (89%)	421 (99%)	5 (1%)	0	100	100
3	H	124/129 (96%)	116 (94%)	8 (6%)	0	100	100
3	J	124/129 (96%)	116 (94%)	8 (6%)	0	100	100
3	M	124/129 (96%)	116 (94%)	8 (6%)	0	100	100
4	K	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
4	L	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
4	N	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
All	All	2333/2619 (89%)	2281 (98%)	52 (2%)	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	104/130 (80%)	104 (100%)	0	100	100
1	B	104/130 (80%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	104/130 (80%)	104 (100%)	0	100	100
2	E	394/429 (92%)	393 (100%)	1 (0%)	86	84
2	F	394/429 (92%)	393 (100%)	1 (0%)	86	84
2	G	393/429 (92%)	392 (100%)	1 (0%)	86	84
3	H	108/111 (97%)	108 (100%)	0	100	100
3	J	108/111 (97%)	108 (100%)	0	100	100
3	M	108/111 (97%)	108 (100%)	0	100	100
4	K	97/97 (100%)	97 (100%)	0	100	100
4	L	97/97 (100%)	97 (100%)	0	100	100
4	N	97/97 (100%)	97 (100%)	0	100	100
All	All	2108/2301 (92%)	2105 (100%)	3 (0%)	87	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	126	CYS
2	F	126	CYS
2	G	126	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	440	GLN
4	K	27(D)	HIS
2	E	103	GLN
1	C	652	GLN
4	L	27(D)	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

27 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	D	1	5,2	14,14,15	0.29	0	17,19,21	0.65	0
5	NAG	D	2	5	14,14,15	0.31	0	17,19,21	0.68	0
5	BMA	D	3	5	11,11,12	0.32	0	15,15,17	0.94	0
5	MAN	D	4	5	11,11,12	0.30	0	15,15,17	0.86	0
6	NAG	I	1	6,2	14,14,15	0.37	0	17,19,21	1.17	2 (11%)
6	NAG	I	2	6	14,14,15	0.32	0	17,19,21	0.76	1 (5%)
6	BMA	I	3	6	11,11,12	0.26	0	15,15,17	0.81	0
6	MAN	I	4	6	11,11,12	0.25	0	15,15,17	0.69	0
6	MAN	I	5	6	11,11,12	0.23	0	15,15,17	0.64	0
5	NAG	O	1	5,2	14,14,15	0.30	0	17,19,21	0.65	0
5	NAG	O	2	5	14,14,15	0.31	0	17,19,21	0.68	0
5	BMA	O	3	5	11,11,12	0.31	0	15,15,17	0.94	0
5	MAN	O	4	5	11,11,12	0.29	0	15,15,17	0.85	0
6	NAG	P	1	6,2	14,14,15	0.35	0	17,19,21	1.18	2 (11%)
6	NAG	P	2	6	14,14,15	0.32	0	17,19,21	0.75	1 (5%)
6	BMA	P	3	6	11,11,12	0.26	0	15,15,17	0.81	0
6	MAN	P	4	6	11,11,12	0.26	0	15,15,17	0.70	0
6	MAN	P	5	6	11,11,12	0.24	0	15,15,17	0.65	0
5	NAG	Q	1	5,2	14,14,15	0.30	0	17,19,21	0.66	0
5	NAG	Q	2	5	14,14,15	0.31	0	17,19,21	0.69	0
5	BMA	Q	3	5	11,11,12	0.31	0	15,15,17	0.95	0
5	MAN	Q	4	5	11,11,12	0.30	0	15,15,17	0.85	0
6	NAG	R	1	6,2	14,14,15	0.35	0	17,19,21	1.18	2 (11%)
6	NAG	R	2	6	14,14,15	0.32	0	17,19,21	0.76	1 (5%)
6	BMA	R	3	6	11,11,12	0.26	0	15,15,17	0.81	0
6	MAN	R	4	6	11,11,12	0.25	0	15,15,17	0.69	0
6	MAN	R	5	6	11,11,12	0.24	0	15,15,17	0.64	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	D	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	D	2	5	-	0/6/23/26	0/1/1/1
5	BMA	D	3	5	-	0/2/19/22	0/1/1/1
5	MAN	D	4	5	-	0/2/19/22	0/1/1/1
6	NAG	I	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	0/6/23/26	0/1/1/1
6	BMA	I	3	6	-	2/2/19/22	0/1/1/1
6	MAN	I	4	6	-	0/2/19/22	0/1/1/1
6	MAN	I	5	6	-	0/2/19/22	0/1/1/1
5	NAG	O	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	O	2	5	-	0/6/23/26	0/1/1/1
5	BMA	O	3	5	-	0/2/19/22	0/1/1/1
5	MAN	O	4	5	-	0/2/19/22	0/1/1/1
6	NAG	P	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	P	2	6	-	0/6/23/26	0/1/1/1
6	BMA	P	3	6	-	2/2/19/22	0/1/1/1
6	MAN	P	4	6	-	0/2/19/22	0/1/1/1
6	MAN	P	5	6	-	0/2/19/22	0/1/1/1
5	NAG	Q	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	0/6/23/26	0/1/1/1
5	BMA	Q	3	5	-	0/2/19/22	0/1/1/1
5	MAN	Q	4	5	-	0/2/19/22	0/1/1/1
6	NAG	R	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	R	2	6	-	0/6/23/26	0/1/1/1
6	BMA	R	3	6	-	2/2/19/22	0/1/1/1
6	MAN	R	4	6	-	0/2/19/22	0/1/1/1
6	MAN	R	5	6	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	P	1	NAG	O4-C4-C5	-2.58	102.98	109.32
6	R	1	NAG	O4-C4-C5	-2.57	103.01	109.32
6	I	1	NAG	O4-C4-C5	-2.56	103.02	109.32
6	P	1	NAG	C1-O5-C5	-2.11	109.36	112.19
6	R	1	NAG	C1-O5-C5	-2.09	109.38	112.19

There are no chirality outliers.

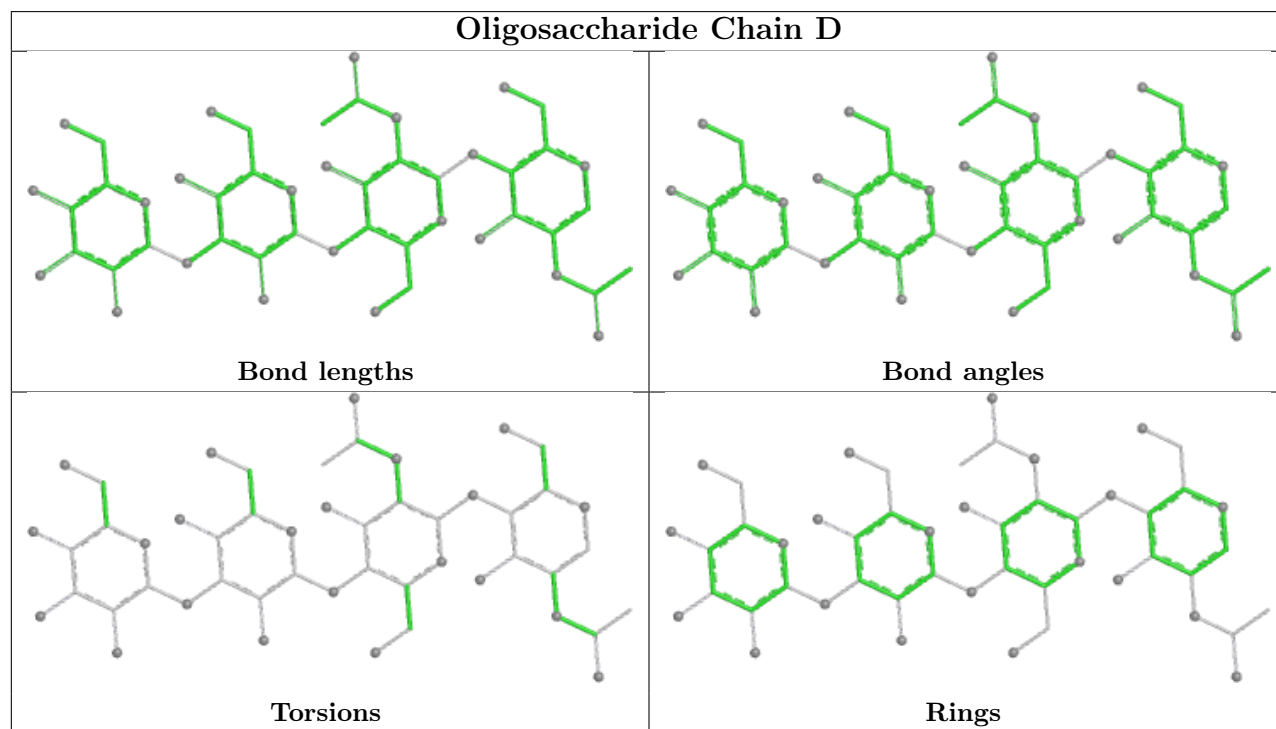
5 of 6 torsion outliers are listed below:

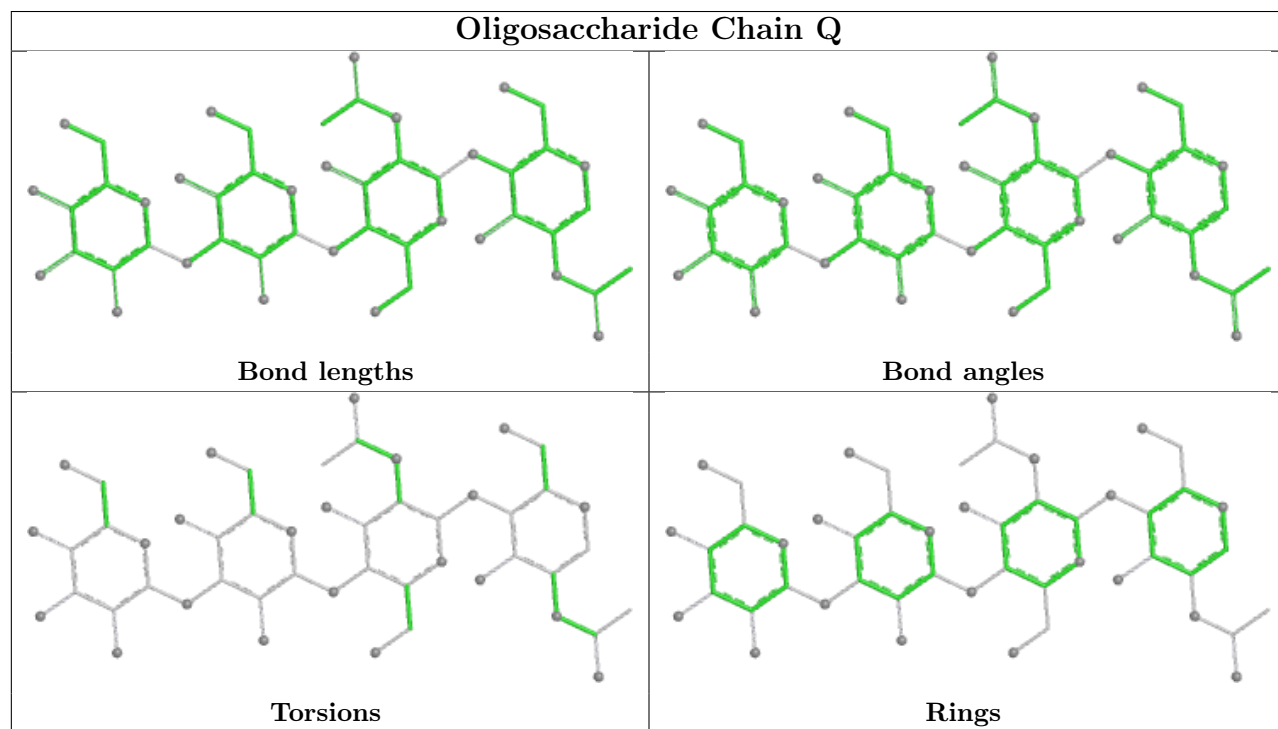
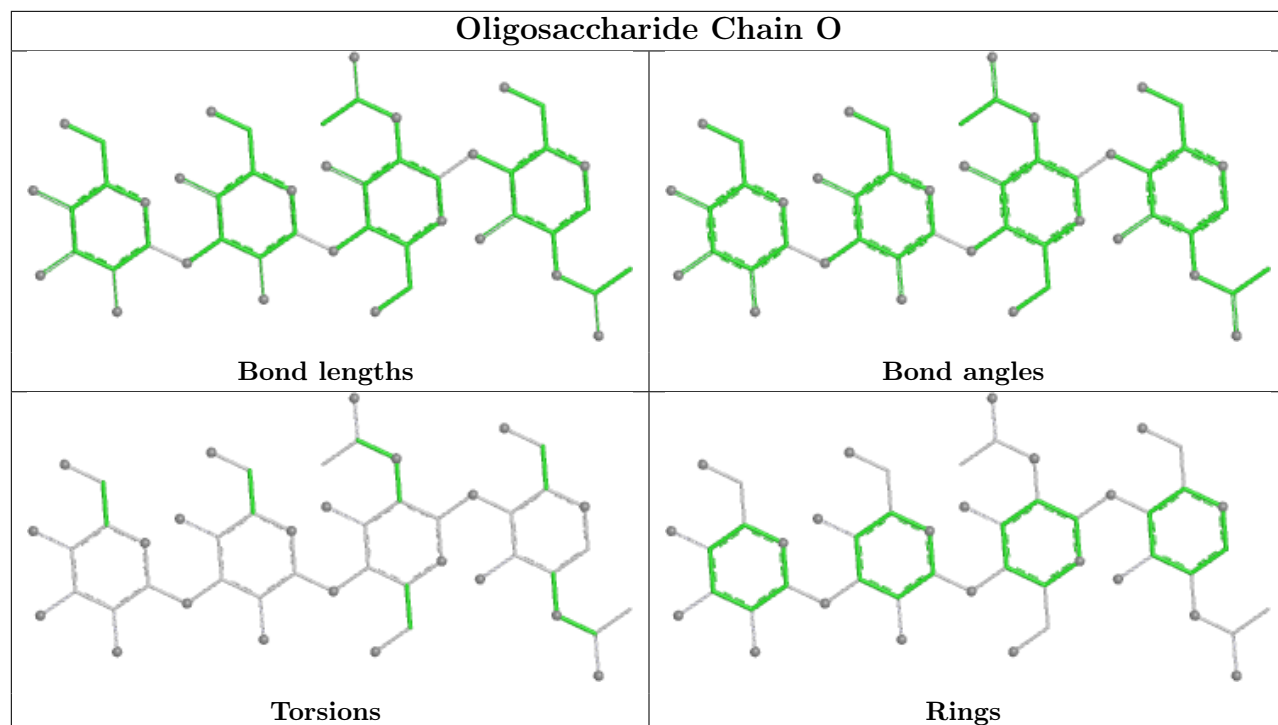
Mol	Chain	Res	Type	Atoms
6	I	3	BMA	C4-C5-C6-O6
6	P	3	BMA	C4-C5-C6-O6
6	R	3	BMA	C4-C5-C6-O6
6	I	3	BMA	O5-C5-C6-O6
6	P	3	BMA	O5-C5-C6-O6

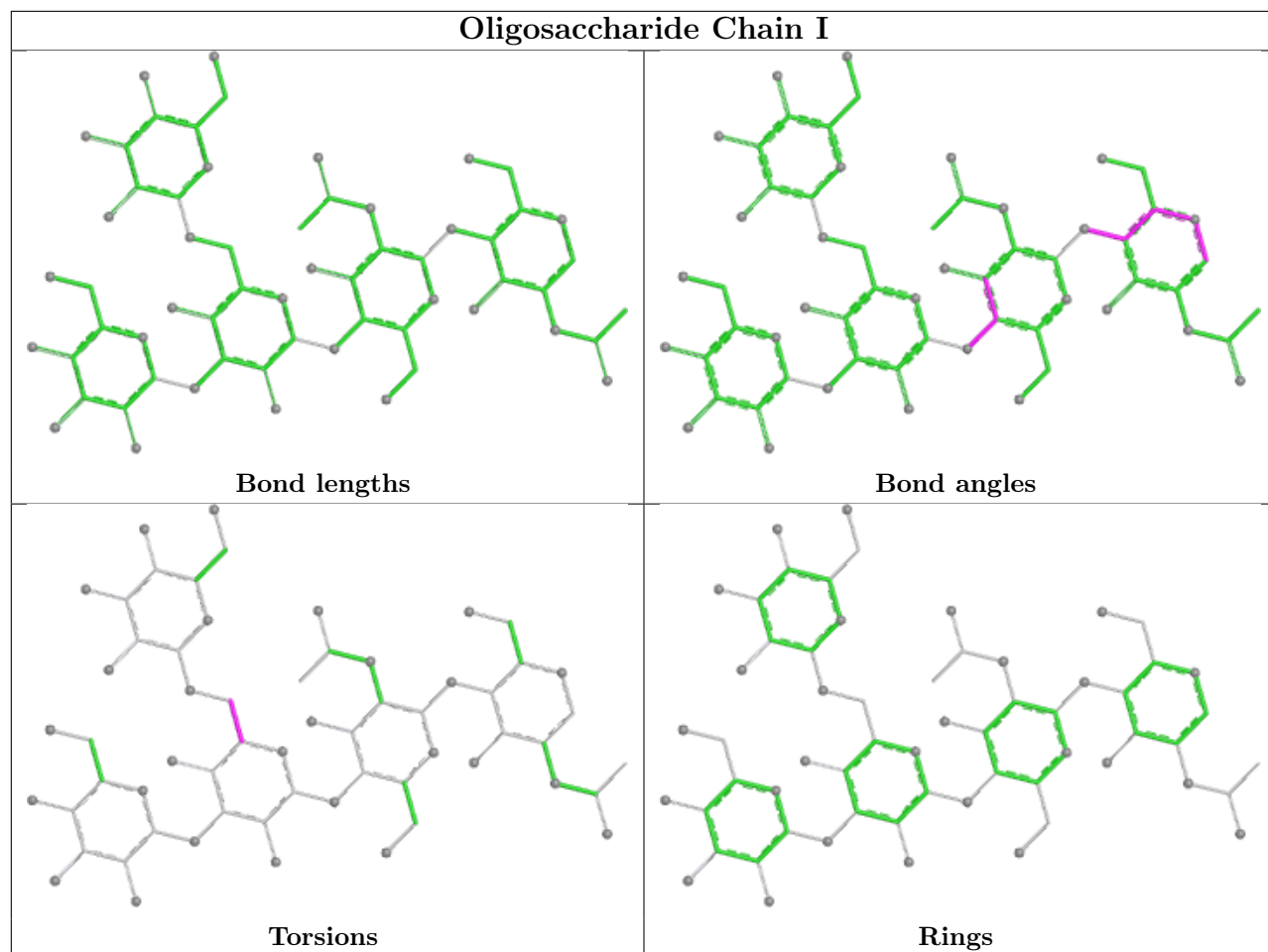
There are no ring outliers.

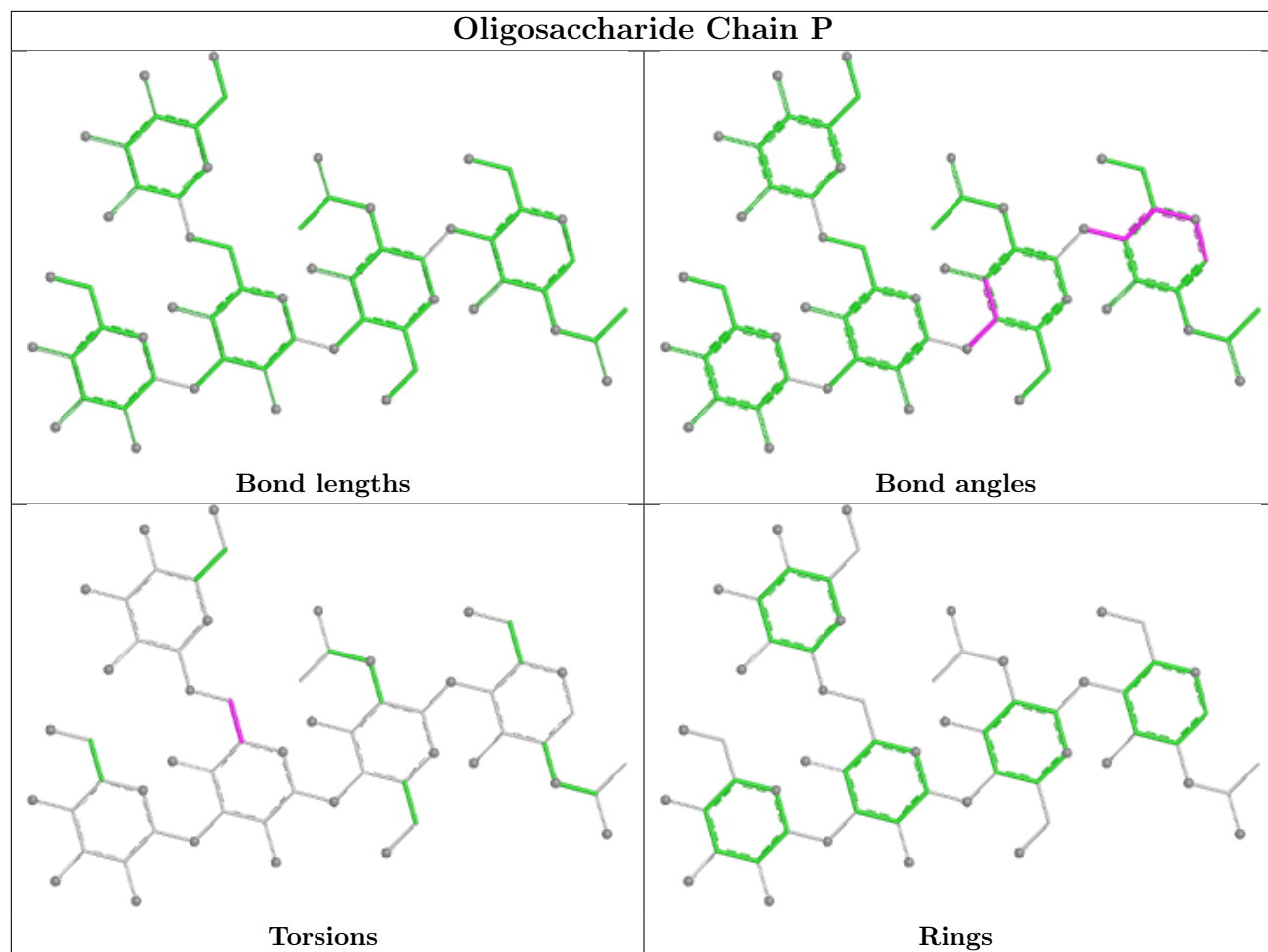
No monomer is involved in short contacts.

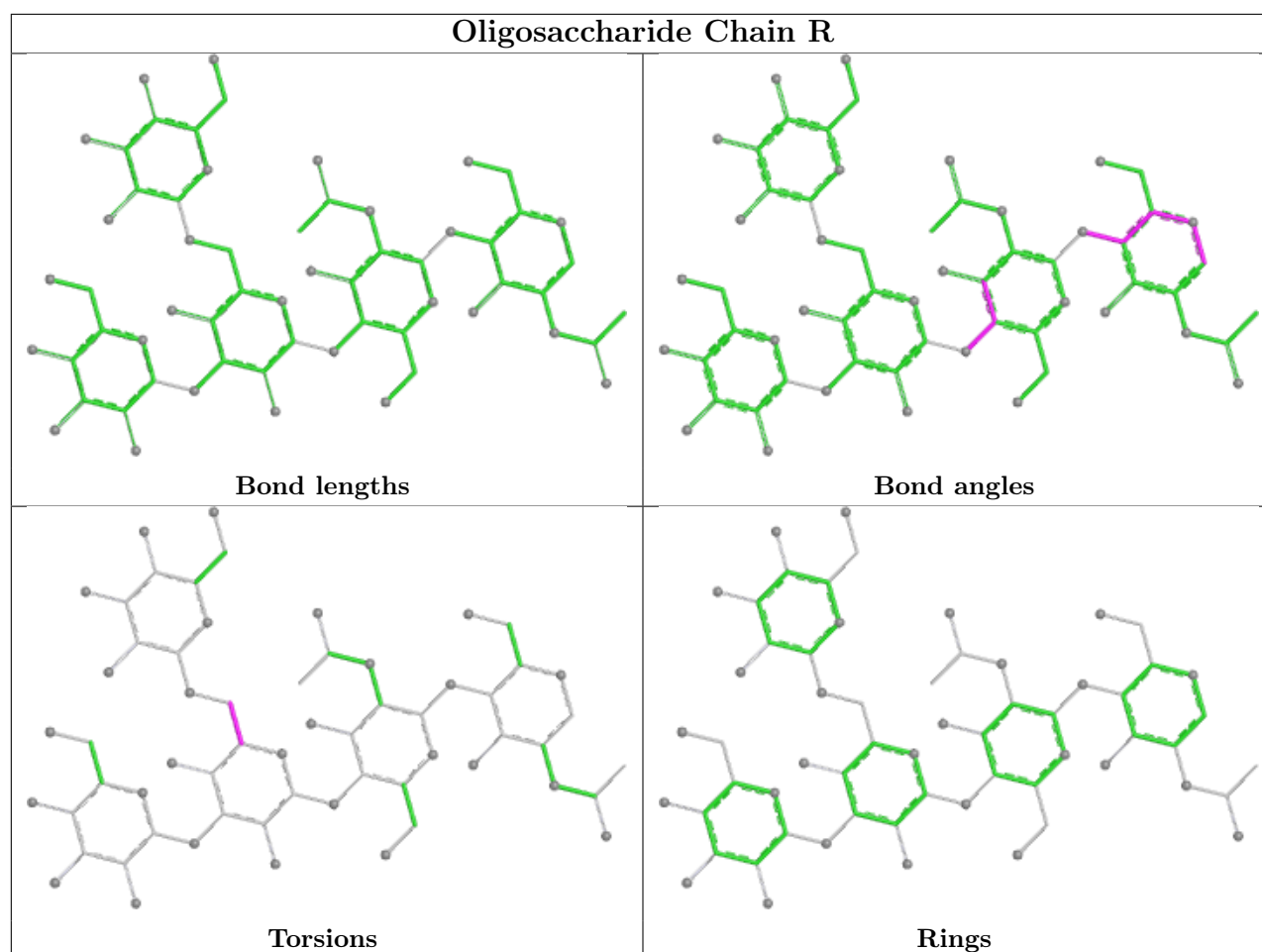
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

48 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	E	609	2	14,14,15	0.30	0	17,19,21	0.66	0
7	NAG	G	601	2	14,14,15	0.30	0	17,19,21	0.58	0
7	NAG	E	603	2	14,14,15	0.31	0	17,19,21	0.67	0
7	NAG	E	606	2	14,14,15	0.31	0	17,19,21	0.59	0
7	NAG	F	610	2	14,14,15	0.28	0	17,19,21	0.68	0
7	NAG	E	605	2	14,14,15	0.29	0	17,19,21	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	E	604	2	14,14,15	0.30	0	17,19,21	0.68	0
7	NAG	G	609	2	14,14,15	0.30	0	17,19,21	0.66	0
7	NAG	E	608	2	14,14,15	0.29	0	17,19,21	0.66	0
7	NAG	F	604	2	14,14,15	0.30	0	17,19,21	0.69	0
7	NAG	F	614	2	14,14,15	0.27	0	17,19,21	0.67	0
7	NAG	G	611	2	14,14,15	0.26	0	17,19,21	0.96	1 (5%)
7	NAG	F	605	2	14,14,15	0.29	0	17,19,21	0.68	0
7	NAG	G	612	2	14,14,15	0.36	0	17,19,21	0.89	1 (5%)
7	NAG	G	615	2	14,14,15	0.27	0	17,19,21	0.55	0
7	NAG	E	612	2	14,14,15	0.36	0	17,19,21	0.88	1 (5%)
7	NAG	G	613	2	14,14,15	0.30	0	17,19,21	0.56	0
7	NAG	E	607	2	14,14,15	0.27	0	17,19,21	0.76	0
7	NAG	E	611	2	14,14,15	0.27	0	17,19,21	0.95	1 (5%)
7	NAG	F	608	2	14,14,15	0.30	0	17,19,21	0.67	0
7	NAG	F	606	2	14,14,15	0.33	0	17,19,21	0.59	0
7	NAG	F	609	2	14,14,15	0.30	0	17,19,21	0.66	0
7	NAG	C	701	1	14,14,15	0.29	0	17,19,21	0.60	0
7	NAG	G	607	2	14,14,15	0.28	0	17,19,21	0.76	0
7	NAG	E	602	2	14,14,15	0.37	0	17,19,21	0.81	0
7	NAG	F	612	2	14,14,15	0.37	0	17,19,21	0.89	1 (5%)
7	NAG	E	613	2	14,14,15	0.30	0	17,19,21	0.55	0
7	NAG	E	610	2	14,14,15	0.29	0	17,19,21	0.68	0
7	NAG	E	615	2	14,14,15	0.28	0	17,19,21	0.55	0
7	NAG	F	611	2	14,14,15	0.27	0	17,19,21	0.95	1 (5%)
7	NAG	G	602	2	14,14,15	0.37	0	17,19,21	0.80	0
7	NAG	F	613	2	14,14,15	0.30	0	17,19,21	0.56	0
7	NAG	G	608	2	14,14,15	0.30	0	17,19,21	0.66	0
7	NAG	G	603	2	14,14,15	0.31	0	17,19,21	0.68	0
7	NAG	G	610	2	14,14,15	0.28	0	17,19,21	0.68	0
7	NAG	A	701	1	14,14,15	0.28	0	17,19,21	0.59	0
7	NAG	E	614	2	14,14,15	0.29	0	17,19,21	0.67	0
7	NAG	F	601	2	14,14,15	0.31	0	17,19,21	0.58	0
7	NAG	F	602	2	14,14,15	0.37	0	17,19,21	0.81	0
7	NAG	G	614	2	14,14,15	0.30	0	17,19,21	0.67	0
7	NAG	F	607	2	14,14,15	0.27	0	17,19,21	0.76	0
7	NAG	G	606	2	14,14,15	0.31	0	17,19,21	0.59	0
7	NAG	F	603	2	14,14,15	0.31	0	17,19,21	0.68	0
7	NAG	B	701	1	14,14,15	0.29	0	17,19,21	0.60	0
7	NAG	F	615	2	14,14,15	0.28	0	17,19,21	0.55	0
7	NAG	G	604	2	14,14,15	0.30	0	17,19,21	0.69	0
7	NAG	E	601	2	14,14,15	0.29	0	17,19,21	0.58	0
7	NAG	G	605	2	14,14,15	0.29	0	17,19,21	0.69	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	E	609	2	-	0/6/23/26	0/1/1/1
7	NAG	G	601	2	-	4/6/23/26	0/1/1/1
7	NAG	E	603	2	-	0/6/23/26	0/1/1/1
7	NAG	E	606	2	-	0/6/23/26	0/1/1/1
7	NAG	F	610	2	-	0/6/23/26	0/1/1/1
7	NAG	E	605	2	-	1/6/23/26	0/1/1/1
7	NAG	E	604	2	-	0/6/23/26	0/1/1/1
7	NAG	G	609	2	-	0/6/23/26	0/1/1/1
7	NAG	E	608	2	-	0/6/23/26	0/1/1/1
7	NAG	F	604	2	-	0/6/23/26	0/1/1/1
7	NAG	F	614	2	-	0/6/23/26	0/1/1/1
7	NAG	G	611	2	-	3/6/23/26	0/1/1/1
7	NAG	F	605	2	-	1/6/23/26	0/1/1/1
7	NAG	G	612	2	-	0/6/23/26	0/1/1/1
7	NAG	G	615	2	-	2/6/23/26	0/1/1/1
7	NAG	E	612	2	-	0/6/23/26	0/1/1/1
7	NAG	G	613	2	-	0/6/23/26	0/1/1/1
7	NAG	E	607	2	-	0/6/23/26	0/1/1/1
7	NAG	E	611	2	-	3/6/23/26	0/1/1/1
7	NAG	F	608	2	-	0/6/23/26	0/1/1/1
7	NAG	F	606	2	-	0/6/23/26	0/1/1/1
7	NAG	F	609	2	-	0/6/23/26	0/1/1/1
7	NAG	C	701	1	-	0/6/23/26	0/1/1/1
7	NAG	G	607	2	-	0/6/23/26	0/1/1/1
7	NAG	E	602	2	-	0/6/23/26	0/1/1/1
7	NAG	F	612	2	-	0/6/23/26	0/1/1/1
7	NAG	E	613	2	-	0/6/23/26	0/1/1/1
7	NAG	E	610	2	-	0/6/23/26	0/1/1/1
7	NAG	E	615	2	-	2/6/23/26	0/1/1/1
7	NAG	F	611	2	-	3/6/23/26	0/1/1/1
7	NAG	G	602	2	-	0/6/23/26	0/1/1/1
7	NAG	F	613	2	-	0/6/23/26	0/1/1/1
7	NAG	G	608	2	-	0/6/23/26	0/1/1/1
7	NAG	G	603	2	-	0/6/23/26	0/1/1/1
7	NAG	G	610	2	-	0/6/23/26	0/1/1/1
7	NAG	A	701	1	-	0/6/23/26	0/1/1/1
7	NAG	E	614	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	F	601	2	-	4/6/23/26	0/1/1/1
7	NAG	F	602	2	-	0/6/23/26	0/1/1/1
7	NAG	G	614	2	-	0/6/23/26	0/1/1/1
7	NAG	F	607	2	-	0/6/23/26	0/1/1/1
7	NAG	G	606	2	-	0/6/23/26	0/1/1/1
7	NAG	F	603	2	-	0/6/23/26	0/1/1/1
7	NAG	B	701	1	-	0/6/23/26	0/1/1/1
7	NAG	F	615	2	-	2/6/23/26	0/1/1/1
7	NAG	G	604	2	-	0/6/23/26	0/1/1/1
7	NAG	E	601	2	-	4/6/23/26	0/1/1/1
7	NAG	G	605	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	612	NAG	C1-O5-C5	2.47	115.49	112.19
7	G	612	NAG	C1-O5-C5	2.45	115.47	112.19
7	E	612	NAG	C1-O5-C5	2.43	115.44	112.19
7	E	611	NAG	C2-N2-C7	2.17	125.80	122.90
7	G	611	NAG	C2-N2-C7	2.14	125.76	122.90

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	E	601	NAG	C8-C7-N2-C2
7	E	601	NAG	O7-C7-N2-C2
7	E	615	NAG	C8-C7-N2-C2
7	E	615	NAG	O7-C7-N2-C2
7	F	601	NAG	C8-C7-N2-C2

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	603	NAG	1	0
7	E	608	NAG	1	0
7	F	608	NAG	1	0
7	G	608	NAG	1	0

Continued on next page...

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	G	603	NAG	1	0
7	F	603	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.

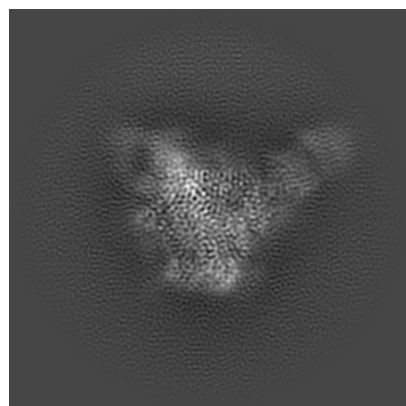
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72989. These allow visual inspection of the internal detail of the map and identification of artifacts.

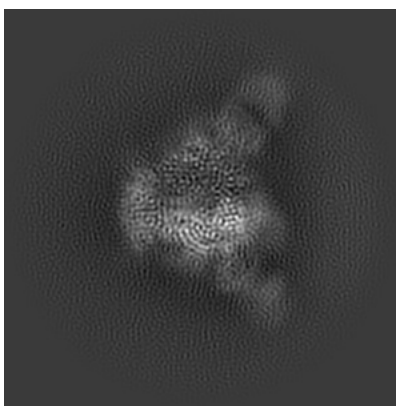
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

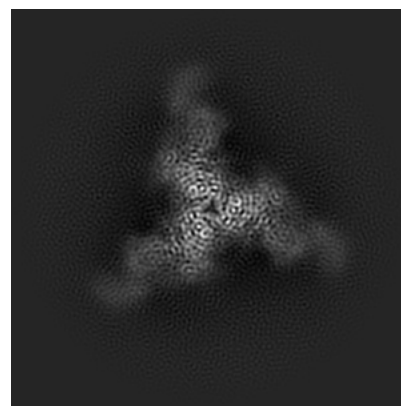
6.1.1 Primary map



X

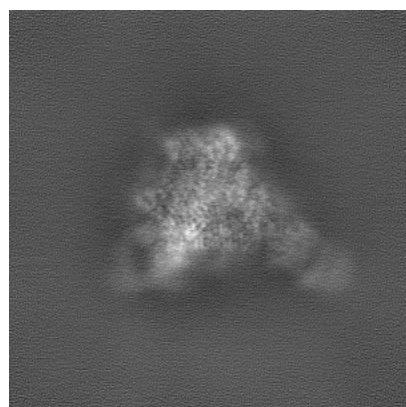


Y

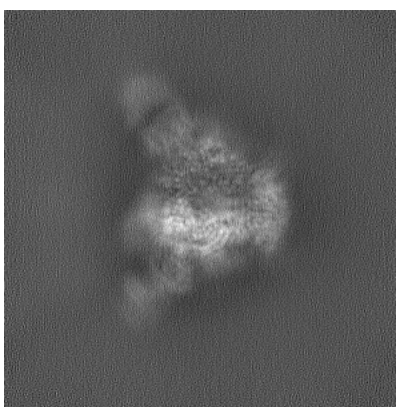


Z

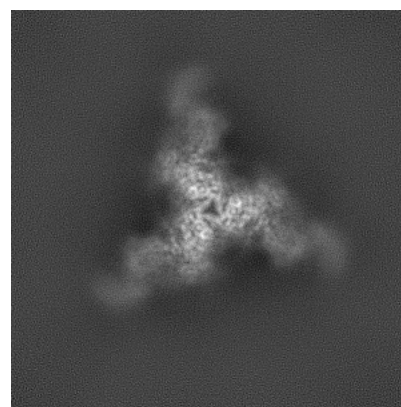
6.1.2 Raw map



X



Y

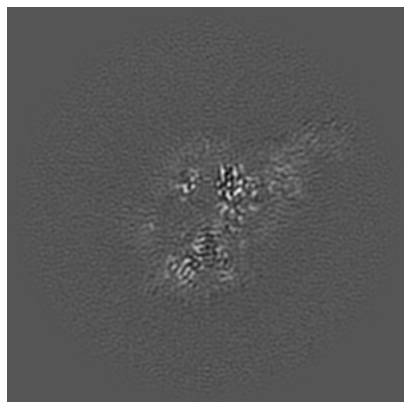


Z

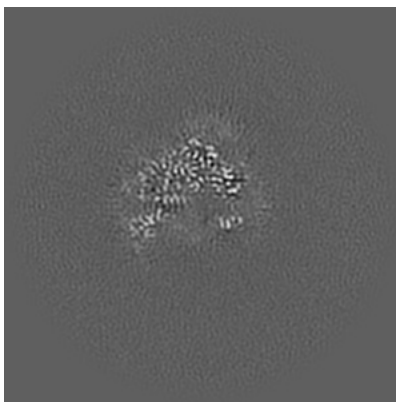
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

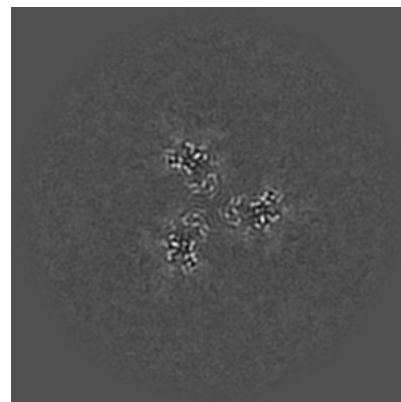
6.2.1 Primary map



X Index: 180

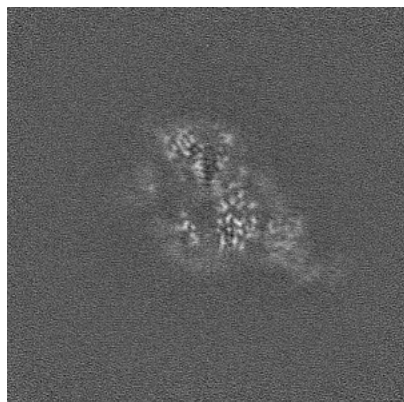


Y Index: 180

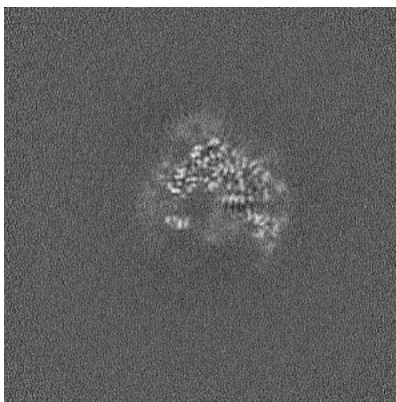


Z Index: 180

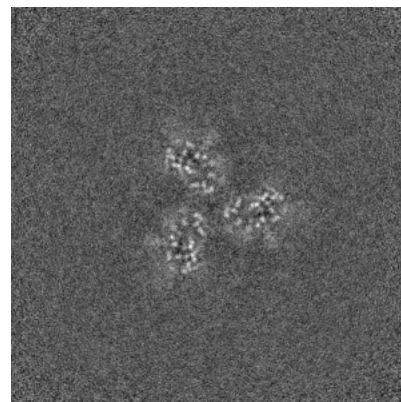
6.2.2 Raw map



X Index: 180



Y Index: 180

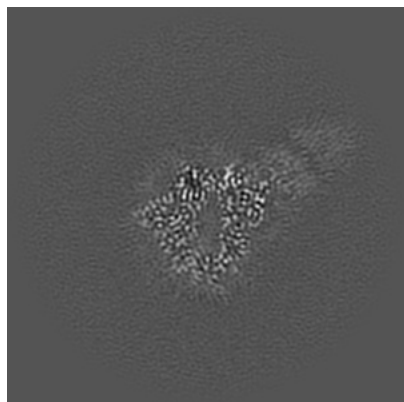


Z Index: 180

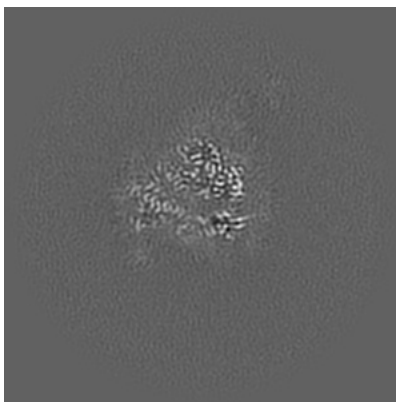
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

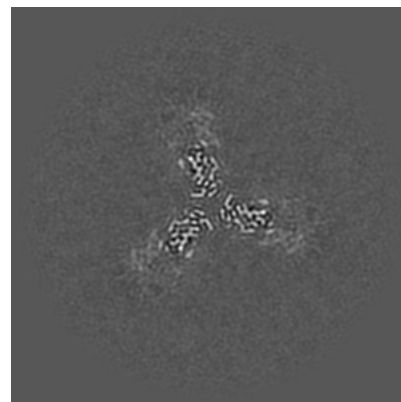
6.3.1 Primary map



X Index: 166

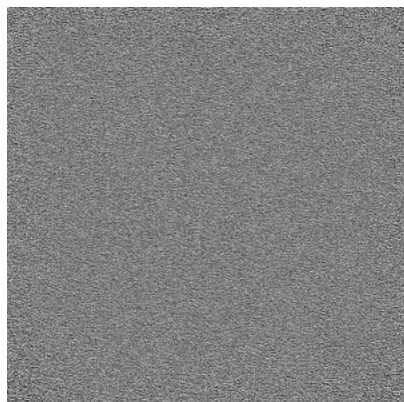


Y Index: 173

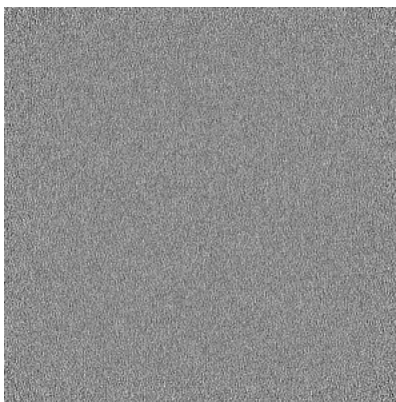


Z Index: 193

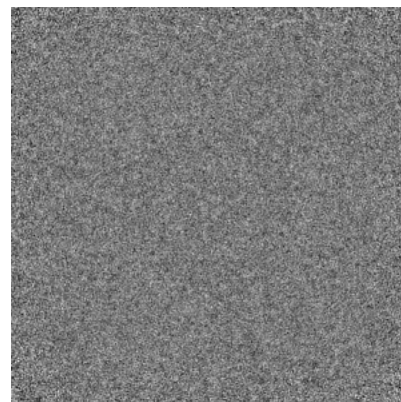
6.3.2 Raw map



X Index: 0



Y Index: 0

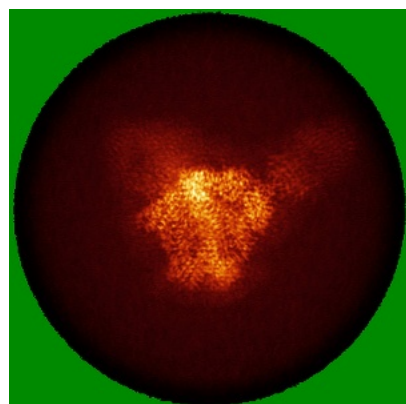


Z Index: 0

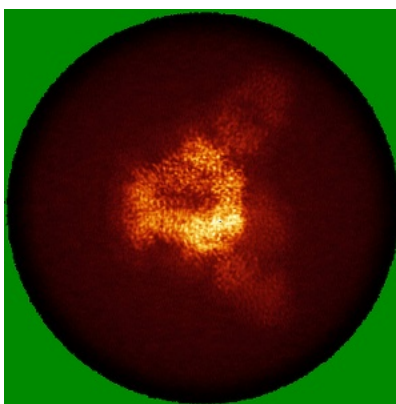
The images above show the largest variance slices of the map in three orthogonal directions.

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

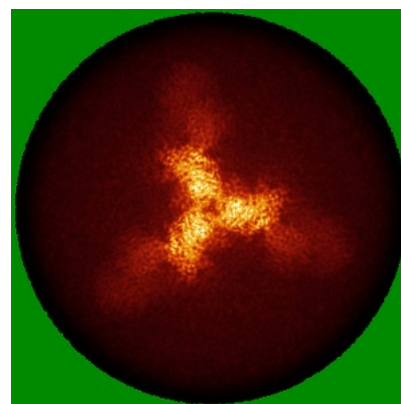
6.4.1 Primary map



X

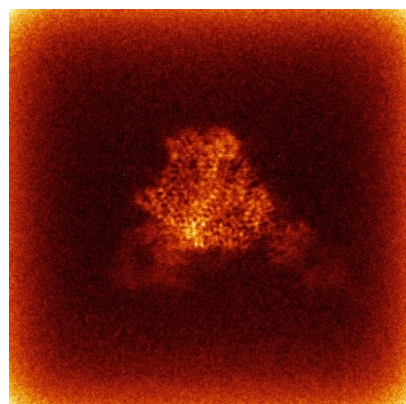


Y

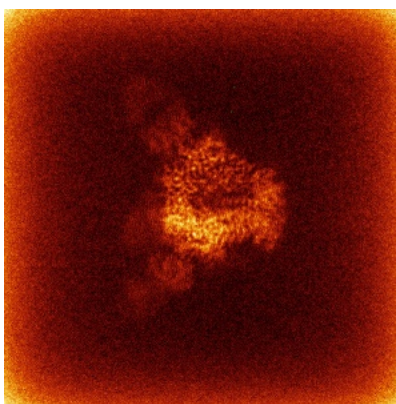


Z

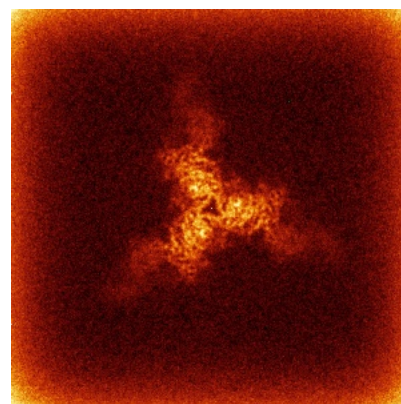
6.4.2 Raw map



X



Y

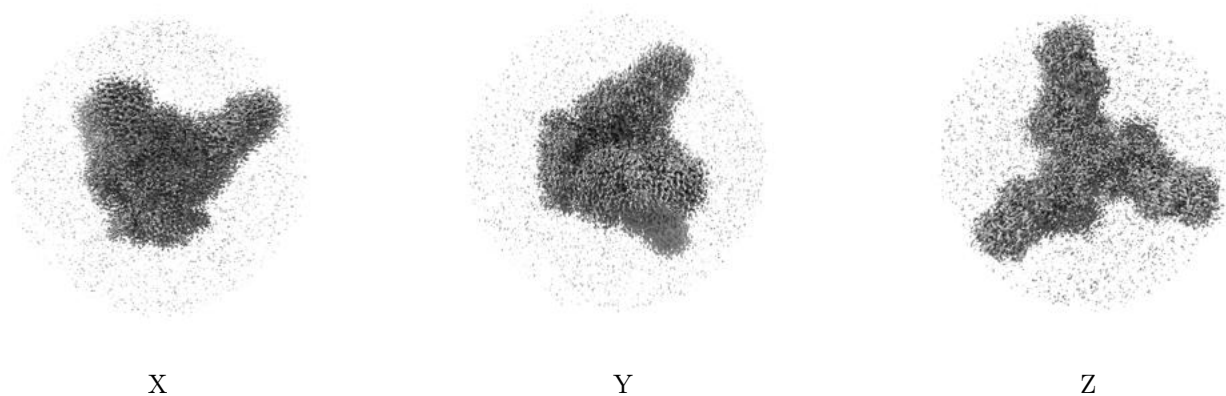


Z

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.

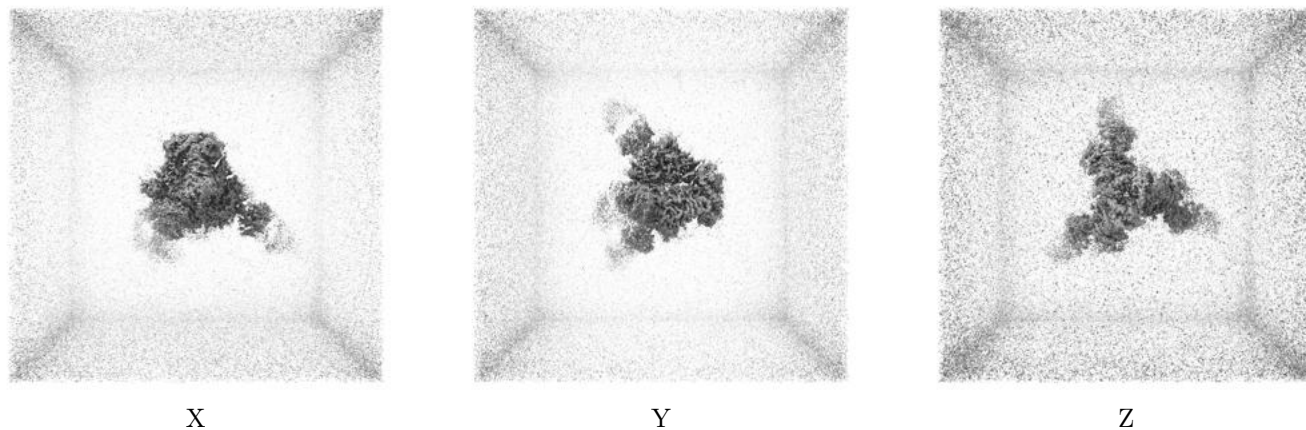
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0331. 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.

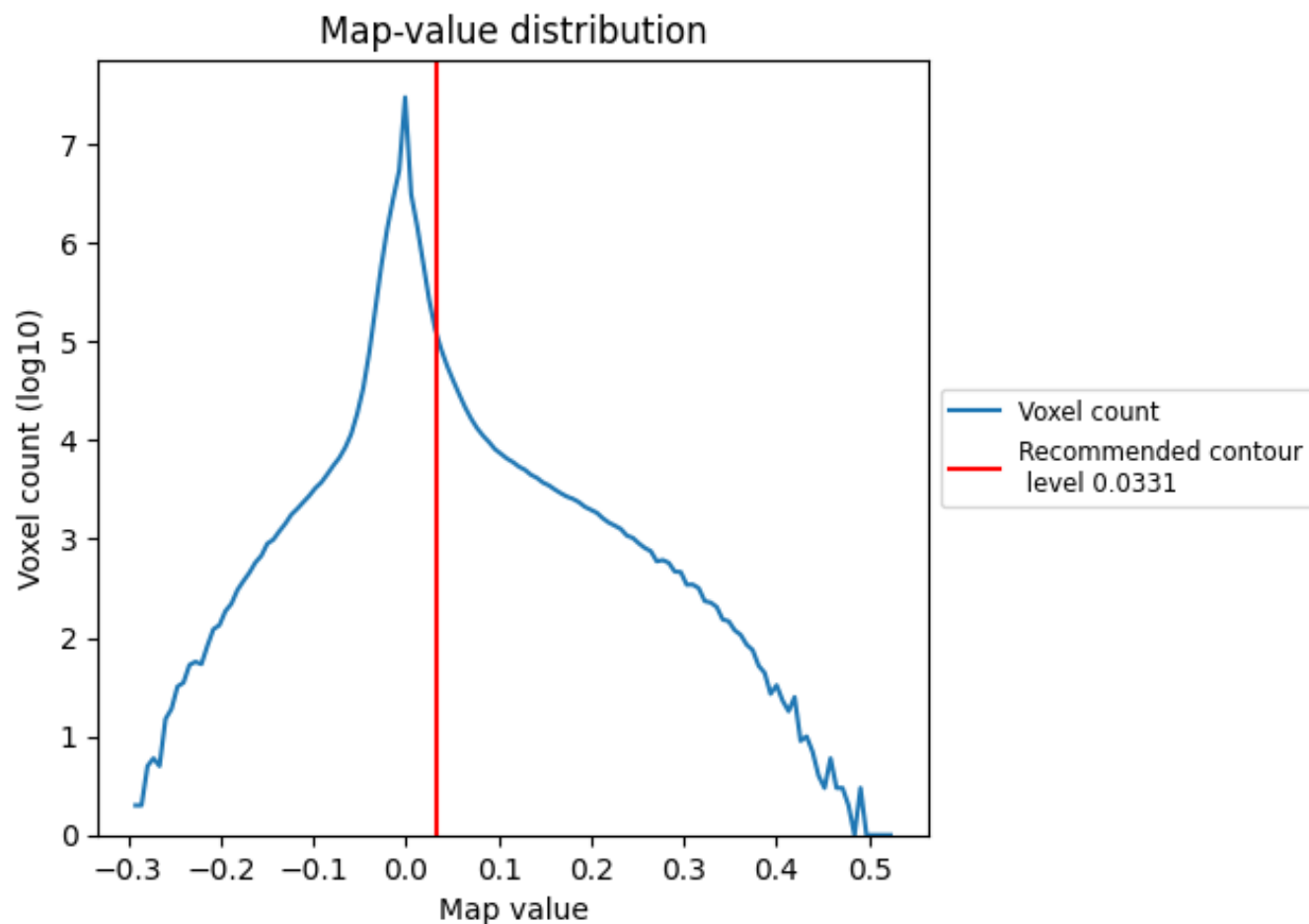
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

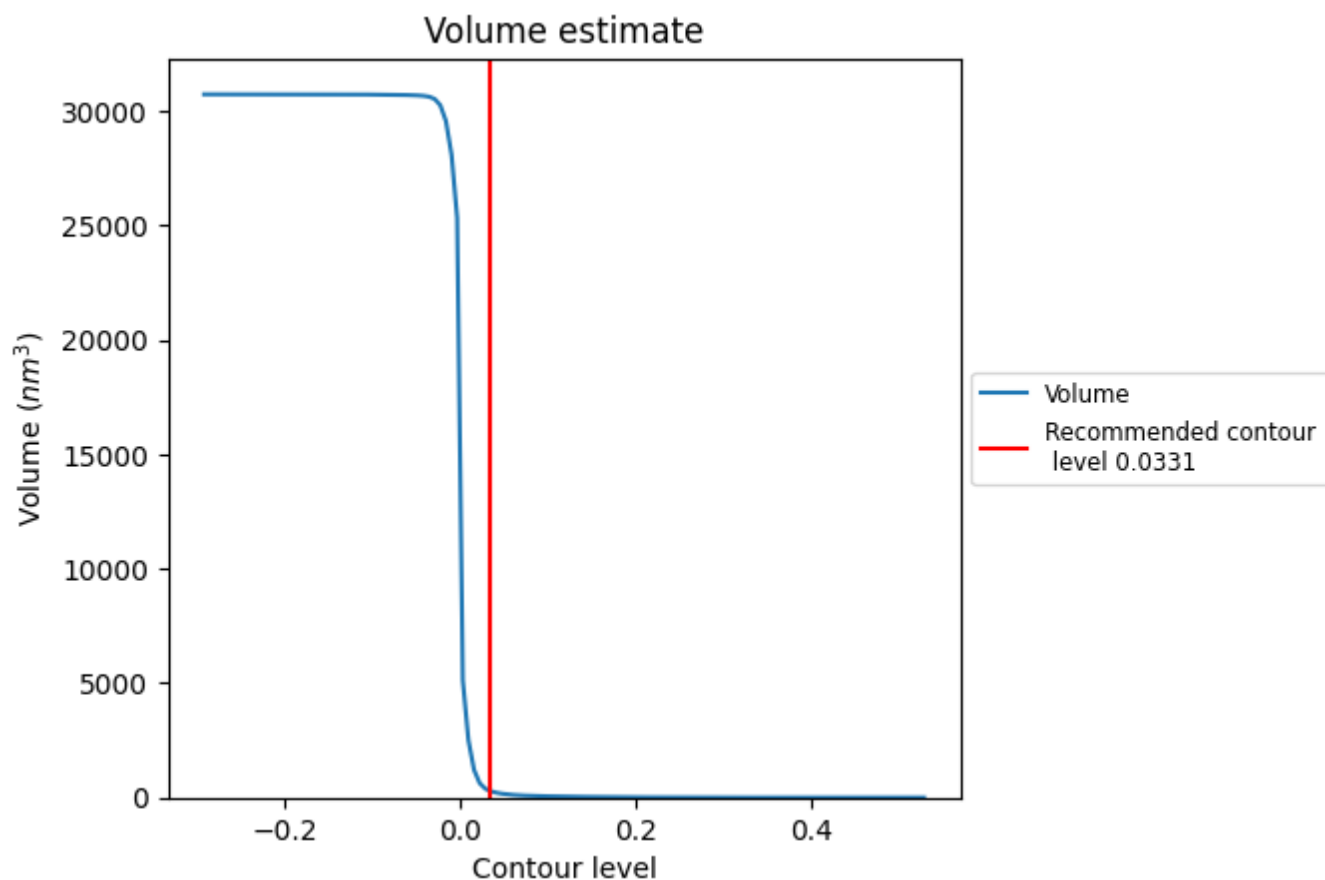
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

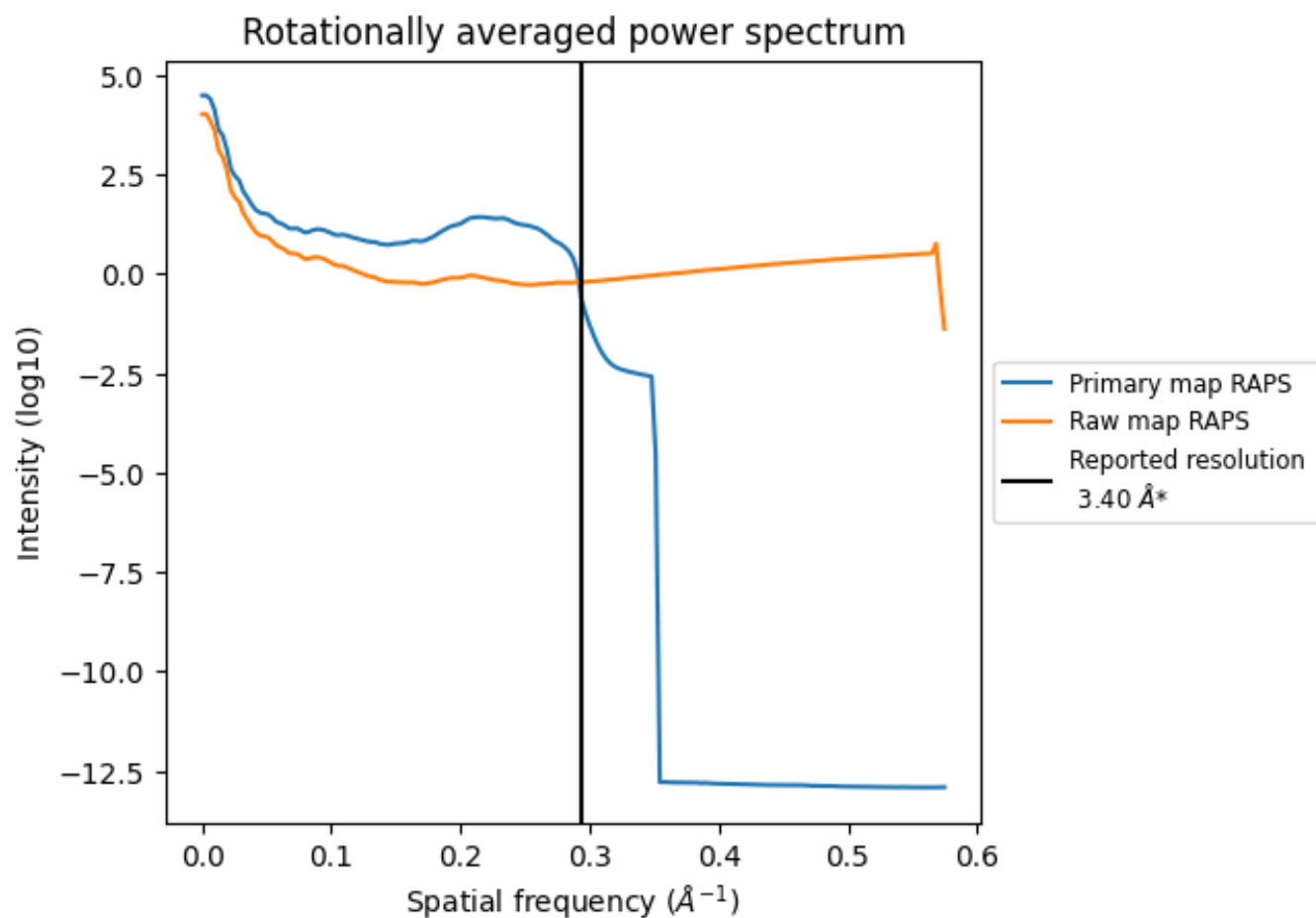
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 315 nm³; this corresponds to an approximate mass of 284 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 ⓘ

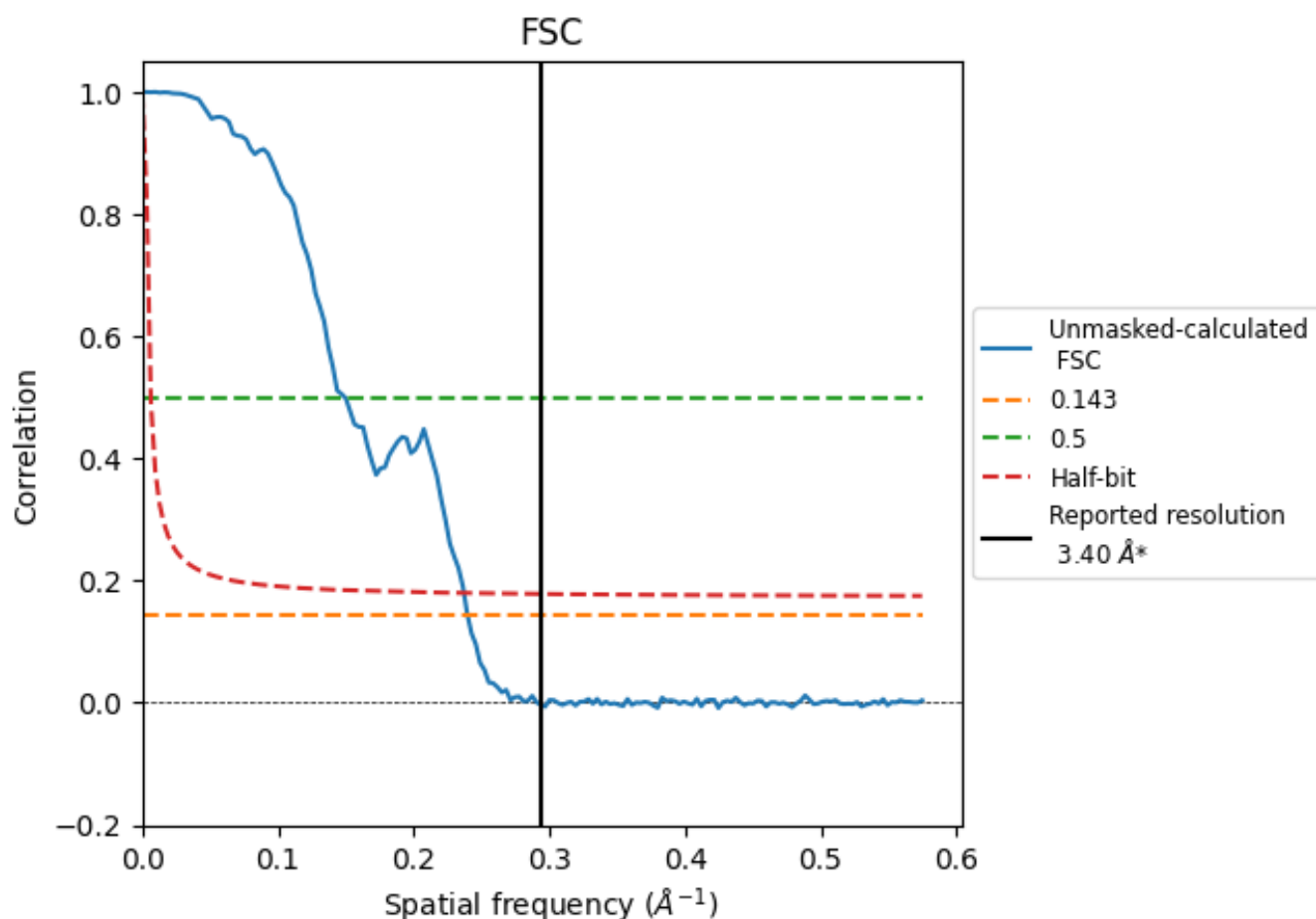


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

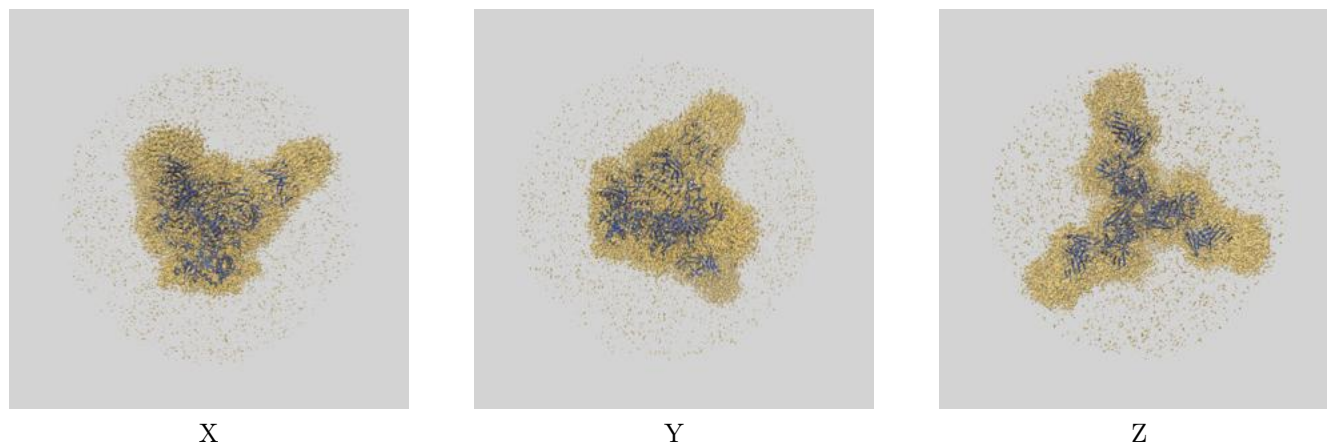
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.17	6.70	4.22

*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 4.17 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

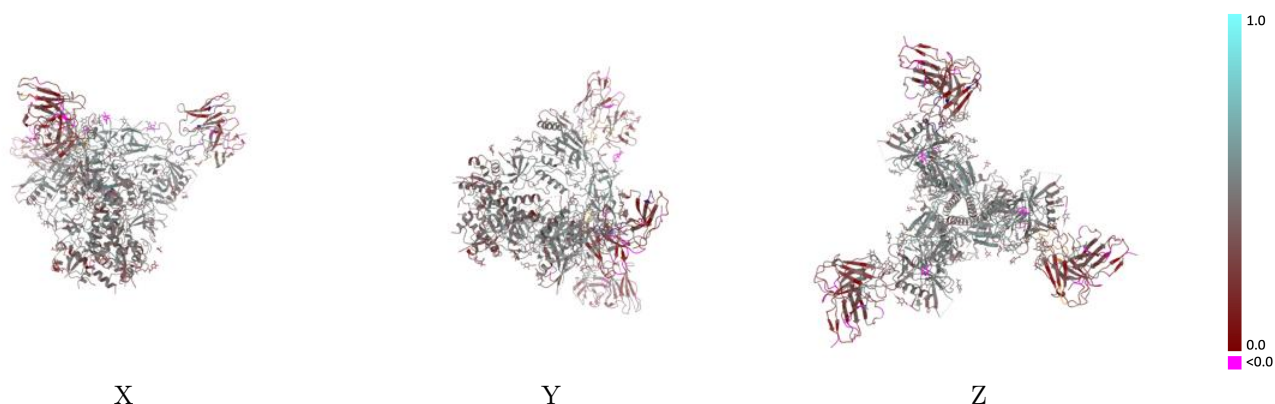
This section contains information regarding the fit between EMDB map EMD-72989 and PDB model 9YIG. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



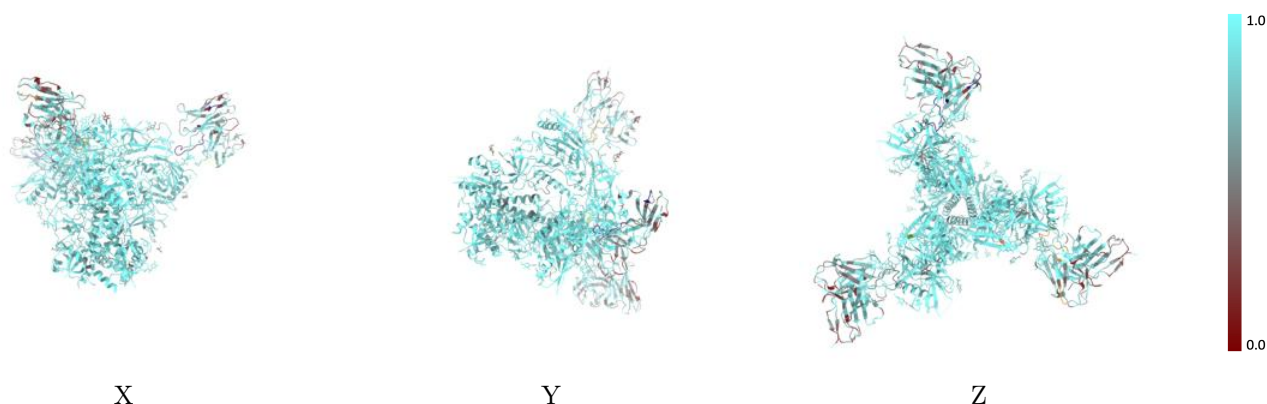
The images above show the 3D surface view of the map at the recommended contour level 0.0331 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



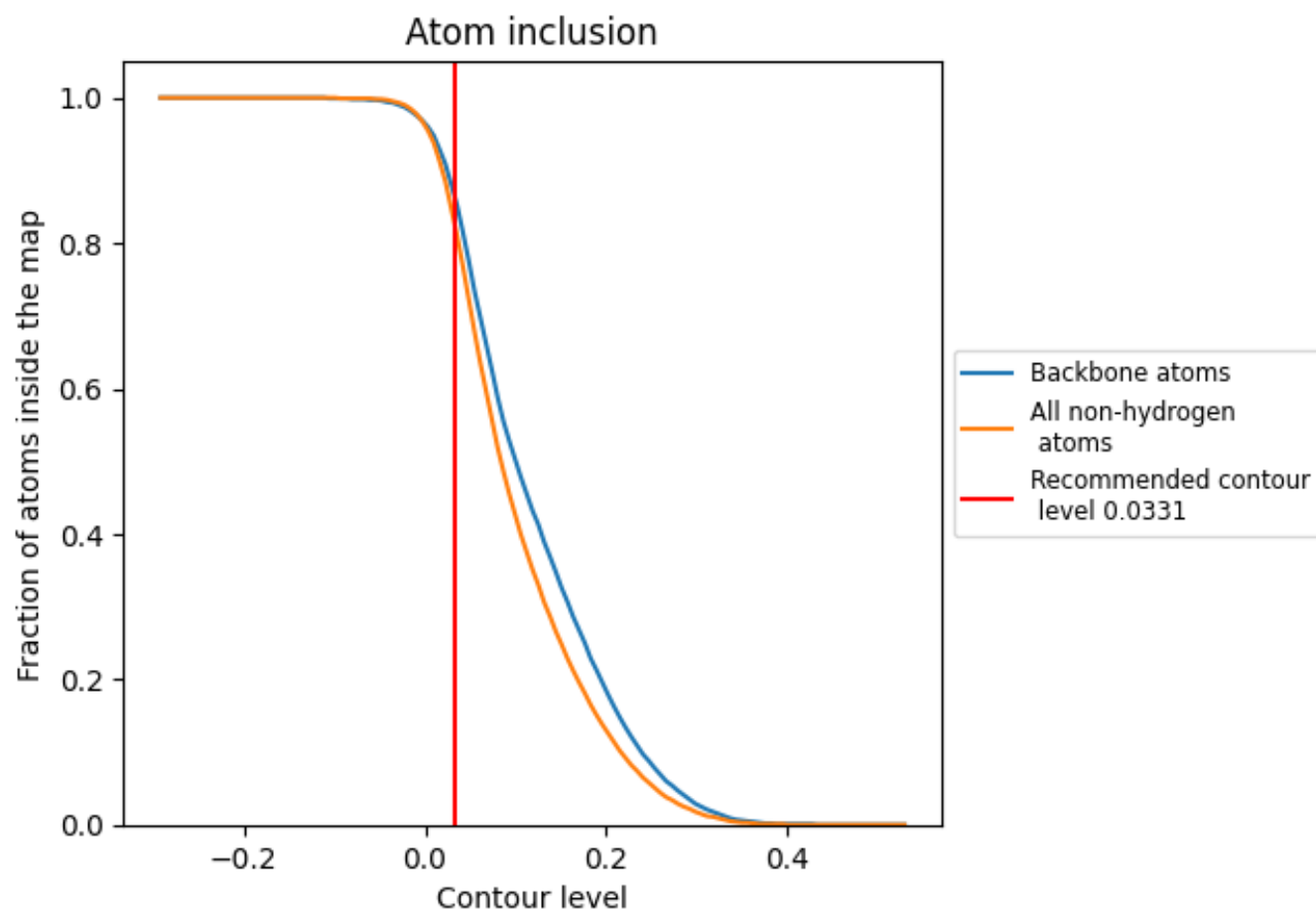
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0331).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% 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 (0.0331) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8250	 0.3980
A	 0.8510	 0.4000
B	 0.8560	 0.3990
C	 0.8570	 0.3900
D	 0.9000	 0.4320
E	 0.8800	 0.4560
F	 0.8800	 0.4560
G	 0.8820	 0.4500
H	 0.7030	 0.3070
I	 0.9020	 0.4330
J	 0.6950	 0.2980
K	 0.6970	 0.2710
L	 0.6820	 0.2610
M	 0.7000	 0.2970
N	 0.6810	 0.2710
O	 0.8800	 0.4230
P	 0.8850	 0.4280
Q	 0.9600	 0.4420
R	 0.9020	 0.4320

