



## Full wwPDB EM Validation Report ⓘ

Apr 29, 2024 – 03:27 PM EDT

PDB ID : 8UT5  
EMDB ID : EMD-42530  
Title : CryoEM structure of A/Michigan/45/2015 H1 in complex with flu HA central stem VH1-18 antibody UCA6\_N55T  
Authors : Huang, J.; Han, J.; Ward, A.B.  
Deposited on : 2023-10-30  
Resolution : 3.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

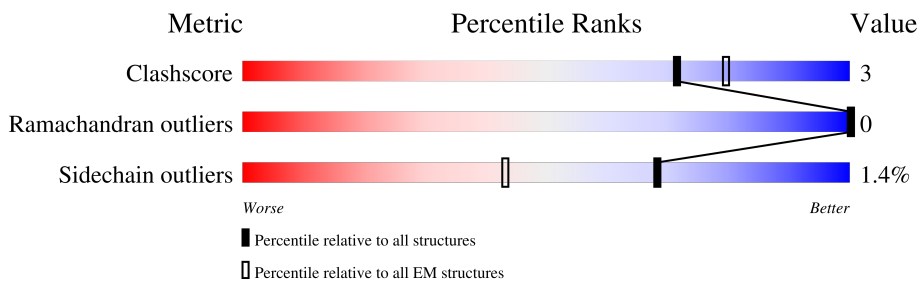
EMDB validation analysis : 0.0.1.dev92  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 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 3.50 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	324	
1	C	324	
1	E	324	
2	B	250	
2	D	250	
2	F	250	
3	G	127	
4	H	109	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13615 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 HA1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	323	2528	1594	437	486	11	0	0
1	C	323	2528	1594	437	486	11	0	0
1	E	323	2528	1594	437	486	11	0	0

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	164	1339	838	230	265	6	0	0
2	D	164	1339	838	230	265	6	0	0
2	F	164	1339	838	230	265	6	0	0

There are 207 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	178	GLY	-	expression tag	UNP A0A6G7M316
B	179	ALA	-	expression tag	UNP A0A6G7M316
B	180	LEU	-	expression tag	UNP A0A6G7M316
B	181	GLU	-	expression tag	UNP A0A6G7M316
B	182	VAL	-	expression tag	UNP A0A6G7M316
B	183	LEU	-	expression tag	UNP A0A6G7M316
B	184	PHE	-	expression tag	UNP A0A6G7M316
B	185	GLN	-	expression tag	UNP A0A6G7M316
B	186	GLY	-	expression tag	UNP A0A6G7M316
B	187	PRO	-	expression tag	UNP A0A6G7M316
B	188	GLY	-	expression tag	UNP A0A6G7M316
B	189	SER	-	expression tag	UNP A0A6G7M316
B	190	HIS	-	expression tag	UNP A0A6G7M316

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Chain	Residue	Modelled	Actual	Comment	Reference
B	191	HIS	-	expression tag	UNP A0A6G7M316
B	192	HIS	-	expression tag	UNP A0A6G7M316
B	193	HIS	-	expression tag	UNP A0A6G7M316
B	194	HIS	-	expression tag	UNP A0A6G7M316
B	195	HIS	-	expression tag	UNP A0A6G7M316
B	196	HIS	-	expression tag	UNP A0A6G7M316
B	197	HIS	-	expression tag	UNP A0A6G7M316
B	198	LEU	-	expression tag	UNP A0A6G7M316
B	199	GLY	-	expression tag	UNP A0A6G7M316
B	200	GLY	-	expression tag	UNP A0A6G7M316
B	201	SER	-	expression tag	UNP A0A6G7M316
B	202	GLY	-	expression tag	UNP A0A6G7M316
B	203	TYR	-	expression tag	UNP A0A6G7M316
B	204	ILE	-	expression tag	UNP A0A6G7M316
B	205	PRO	-	expression tag	UNP A0A6G7M316
B	206	GLU	-	expression tag	UNP A0A6G7M316
B	207	ALA	-	expression tag	UNP A0A6G7M316
B	208	PRO	-	expression tag	UNP A0A6G7M316
B	209	ARG	-	expression tag	UNP A0A6G7M316
B	210	ASP	-	expression tag	UNP A0A6G7M316
B	211	GLY	-	expression tag	UNP A0A6G7M316
B	212	GLN	-	expression tag	UNP A0A6G7M316
B	213	ALA	-	expression tag	UNP A0A6G7M316
B	214	TYR	-	expression tag	UNP A0A6G7M316
B	215	VAL	-	expression tag	UNP A0A6G7M316
B	216	ARG	-	expression tag	UNP A0A6G7M316
B	217	LYS	-	expression tag	UNP A0A6G7M316
B	218	ASP	-	expression tag	UNP A0A6G7M316
B	219	GLY	-	expression tag	UNP A0A6G7M316
B	220	GLU	-	expression tag	UNP A0A6G7M316
B	221	TRP	-	expression tag	UNP A0A6G7M316
B	222	VAL	-	expression tag	UNP A0A6G7M316
B	223	LEU	-	expression tag	UNP A0A6G7M316
B	224	LEU	-	expression tag	UNP A0A6G7M316
B	225	SER	-	expression tag	UNP A0A6G7M316
B	226	THR	-	expression tag	UNP A0A6G7M316
B	227	PHE	-	expression tag	UNP A0A6G7M316
B	228	LEU	-	expression tag	UNP A0A6G7M316
B	229	GLY	-	expression tag	UNP A0A6G7M316
B	230	SER	-	expression tag	UNP A0A6G7M316
B	231	GLY	-	expression tag	UNP A0A6G7M316
B	232	GLY	-	expression tag	UNP A0A6G7M316

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Chain	Residue	Modelled	Actual	Comment	Reference
B	233	GLY	-	expression tag	UNP A0A6G7M316
B	234	LEU	-	expression tag	UNP A0A6G7M316
B	235	ASN	-	expression tag	UNP A0A6G7M316
B	236	ASP	-	expression tag	UNP A0A6G7M316
B	237	ILE	-	expression tag	UNP A0A6G7M316
B	238	PHE	-	expression tag	UNP A0A6G7M316
B	239	GLU	-	expression tag	UNP A0A6G7M316
B	240	ALA	-	expression tag	UNP A0A6G7M316
B	241	GLN	-	expression tag	UNP A0A6G7M316
B	242	LYS	-	expression tag	UNP A0A6G7M316
B	243	ILE	-	expression tag	UNP A0A6G7M316
B	244	GLU	-	expression tag	UNP A0A6G7M316
B	245	TRP	-	expression tag	UNP A0A6G7M316
B	246	HIS	-	expression tag	UNP A0A6G7M316
D	178	GLY	-	expression tag	UNP A0A6G7M316
D	179	ALA	-	expression tag	UNP A0A6G7M316
D	180	LEU	-	expression tag	UNP A0A6G7M316
D	181	GLU	-	expression tag	UNP A0A6G7M316
D	182	VAL	-	expression tag	UNP A0A6G7M316
D	183	LEU	-	expression tag	UNP A0A6G7M316
D	184	PHE	-	expression tag	UNP A0A6G7M316
D	185	GLN	-	expression tag	UNP A0A6G7M316
D	186	GLY	-	expression tag	UNP A0A6G7M316
D	187	PRO	-	expression tag	UNP A0A6G7M316
D	188	GLY	-	expression tag	UNP A0A6G7M316
D	189	SER	-	expression tag	UNP A0A6G7M316
D	190	HIS	-	expression tag	UNP A0A6G7M316
D	191	HIS	-	expression tag	UNP A0A6G7M316
D	192	HIS	-	expression tag	UNP A0A6G7M316
D	193	HIS	-	expression tag	UNP A0A6G7M316
D	194	HIS	-	expression tag	UNP A0A6G7M316
D	195	HIS	-	expression tag	UNP A0A6G7M316
D	196	HIS	-	expression tag	UNP A0A6G7M316
D	197	HIS	-	expression tag	UNP A0A6G7M316
D	198	LEU	-	expression tag	UNP A0A6G7M316
D	199	GLY	-	expression tag	UNP A0A6G7M316
D	200	GLY	-	expression tag	UNP A0A6G7M316
D	201	SER	-	expression tag	UNP A0A6G7M316
D	202	GLY	-	expression tag	UNP A0A6G7M316
D	203	TYR	-	expression tag	UNP A0A6G7M316
D	204	ILE	-	expression tag	UNP A0A6G7M316
D	205	PRO	-	expression tag	UNP A0A6G7M316

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Chain	Residue	Modelled	Actual	Comment	Reference
D	206	GLU	-	expression tag	UNP A0A6G7M316
D	207	ALA	-	expression tag	UNP A0A6G7M316
D	208	PRO	-	expression tag	UNP A0A6G7M316
D	209	ARG	-	expression tag	UNP A0A6G7M316
D	210	ASP	-	expression tag	UNP A0A6G7M316
D	211	GLY	-	expression tag	UNP A0A6G7M316
D	212	GLN	-	expression tag	UNP A0A6G7M316
D	213	ALA	-	expression tag	UNP A0A6G7M316
D	214	TYR	-	expression tag	UNP A0A6G7M316
D	215	VAL	-	expression tag	UNP A0A6G7M316
D	216	ARG	-	expression tag	UNP A0A6G7M316
D	217	LYS	-	expression tag	UNP A0A6G7M316
D	218	ASP	-	expression tag	UNP A0A6G7M316
D	219	GLY	-	expression tag	UNP A0A6G7M316
D	220	GLU	-	expression tag	UNP A0A6G7M316
D	221	TRP	-	expression tag	UNP A0A6G7M316
D	222	VAL	-	expression tag	UNP A0A6G7M316
D	223	LEU	-	expression tag	UNP A0A6G7M316
D	224	LEU	-	expression tag	UNP A0A6G7M316
D	225	SER	-	expression tag	UNP A0A6G7M316
D	226	THR	-	expression tag	UNP A0A6G7M316
D	227	PHE	-	expression tag	UNP A0A6G7M316
D	228	LEU	-	expression tag	UNP A0A6G7M316
D	229	GLY	-	expression tag	UNP A0A6G7M316
D	230	SER	-	expression tag	UNP A0A6G7M316
D	231	GLY	-	expression tag	UNP A0A6G7M316
D	232	GLY	-	expression tag	UNP A0A6G7M316
D	233	GLY	-	expression tag	UNP A0A6G7M316
D	234	LEU	-	expression tag	UNP A0A6G7M316
D	235	ASN	-	expression tag	UNP A0A6G7M316
D	236	ASP	-	expression tag	UNP A0A6G7M316
D	237	ILE	-	expression tag	UNP A0A6G7M316
D	238	PHE	-	expression tag	UNP A0A6G7M316
D	239	GLU	-	expression tag	UNP A0A6G7M316
D	240	ALA	-	expression tag	UNP A0A6G7M316
D	241	GLN	-	expression tag	UNP A0A6G7M316
D	242	LYS	-	expression tag	UNP A0A6G7M316
D	243	ILE	-	expression tag	UNP A0A6G7M316
D	244	GLU	-	expression tag	UNP A0A6G7M316
D	245	TRP	-	expression tag	UNP A0A6G7M316
D	246	HIS	-	expression tag	UNP A0A6G7M316
F	178	GLY	-	expression tag	UNP A0A6G7M316

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Chain	Residue	Modelled	Actual	Comment	Reference
F	179	ALA	-	expression tag	UNP A0A6G7M316
F	180	LEU	-	expression tag	UNP A0A6G7M316
F	181	GLU	-	expression tag	UNP A0A6G7M316
F	182	VAL	-	expression tag	UNP A0A6G7M316
F	183	LEU	-	expression tag	UNP A0A6G7M316
F	184	PHE	-	expression tag	UNP A0A6G7M316
F	185	GLN	-	expression tag	UNP A0A6G7M316
F	186	GLY	-	expression tag	UNP A0A6G7M316
F	187	PRO	-	expression tag	UNP A0A6G7M316
F	188	GLY	-	expression tag	UNP A0A6G7M316
F	189	SER	-	expression tag	UNP A0A6G7M316
F	190	HIS	-	expression tag	UNP A0A6G7M316
F	191	HIS	-	expression tag	UNP A0A6G7M316
F	192	HIS	-	expression tag	UNP A0A6G7M316
F	193	HIS	-	expression tag	UNP A0A6G7M316
F	194	HIS	-	expression tag	UNP A0A6G7M316
F	195	HIS	-	expression tag	UNP A0A6G7M316
F	196	HIS	-	expression tag	UNP A0A6G7M316
F	197	HIS	-	expression tag	UNP A0A6G7M316
F	198	LEU	-	expression tag	UNP A0A6G7M316
F	199	GLY	-	expression tag	UNP A0A6G7M316
F	200	GLY	-	expression tag	UNP A0A6G7M316
F	201	SER	-	expression tag	UNP A0A6G7M316
F	202	GLY	-	expression tag	UNP A0A6G7M316
F	203	TYR	-	expression tag	UNP A0A6G7M316
F	204	ILE	-	expression tag	UNP A0A6G7M316
F	205	PRO	-	expression tag	UNP A0A6G7M316
F	206	GLU	-	expression tag	UNP A0A6G7M316
F	207	ALA	-	expression tag	UNP A0A6G7M316
F	208	PRO	-	expression tag	UNP A0A6G7M316
F	209	ARG	-	expression tag	UNP A0A6G7M316
F	210	ASP	-	expression tag	UNP A0A6G7M316
F	211	GLY	-	expression tag	UNP A0A6G7M316
F	212	GLN	-	expression tag	UNP A0A6G7M316
F	213	ALA	-	expression tag	UNP A0A6G7M316
F	214	TYR	-	expression tag	UNP A0A6G7M316
F	215	VAL	-	expression tag	UNP A0A6G7M316
F	216	ARG	-	expression tag	UNP A0A6G7M316
F	217	LYS	-	expression tag	UNP A0A6G7M316
F	218	ASP	-	expression tag	UNP A0A6G7M316
F	219	GLY	-	expression tag	UNP A0A6G7M316
F	220	GLU	-	expression tag	UNP A0A6G7M316

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Chain	Residue	Modelled	Actual	Comment	Reference
F	221	TRP	-	expression tag	UNP A0A6G7M316
F	222	VAL	-	expression tag	UNP A0A6G7M316
F	223	LEU	-	expression tag	UNP A0A6G7M316
F	224	LEU	-	expression tag	UNP A0A6G7M316
F	225	SER	-	expression tag	UNP A0A6G7M316
F	226	THR	-	expression tag	UNP A0A6G7M316
F	227	PHE	-	expression tag	UNP A0A6G7M316
F	228	LEU	-	expression tag	UNP A0A6G7M316
F	229	GLY	-	expression tag	UNP A0A6G7M316
F	230	SER	-	expression tag	UNP A0A6G7M316
F	231	GLY	-	expression tag	UNP A0A6G7M316
F	232	GLY	-	expression tag	UNP A0A6G7M316
F	233	GLY	-	expression tag	UNP A0A6G7M316
F	234	LEU	-	expression tag	UNP A0A6G7M316
F	235	ASN	-	expression tag	UNP A0A6G7M316
F	236	ASP	-	expression tag	UNP A0A6G7M316
F	237	ILE	-	expression tag	UNP A0A6G7M316
F	238	PHE	-	expression tag	UNP A0A6G7M316
F	239	GLU	-	expression tag	UNP A0A6G7M316
F	240	ALA	-	expression tag	UNP A0A6G7M316
F	241	GLN	-	expression tag	UNP A0A6G7M316
F	242	LYS	-	expression tag	UNP A0A6G7M316
F	243	ILE	-	expression tag	UNP A0A6G7M316
F	244	GLU	-	expression tag	UNP A0A6G7M316
F	245	TRP	-	expression tag	UNP A0A6G7M316
F	246	HIS	-	expression tag	UNP A0A6G7M316

- Molecule 3 is a protein called UCA6\_N55T HC Fv.

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	N	O			S
3	G	125	959	605	159	189	6	0	0

- Molecule 4 is a protein called UCA6\_N55T LC Fv.

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	N	O			S
4	H	107	817	514	140	161	2	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).





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

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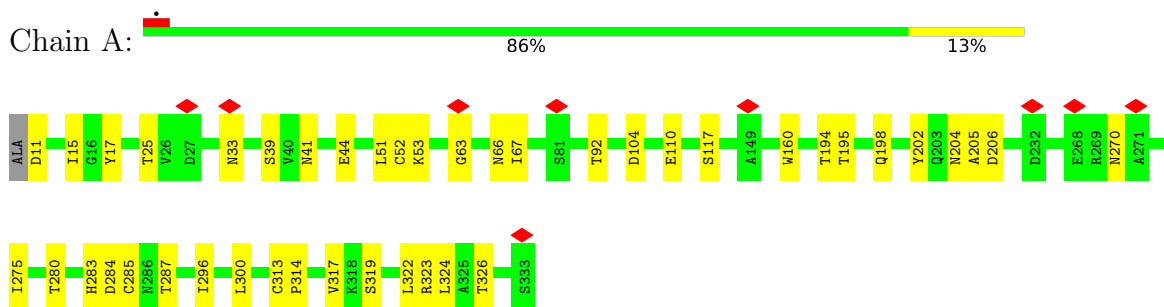
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	E	1	Total 14	8	1	5	0
5	E	1	Total 14	8	1	5	0
5	F	1	Total 14	8	1	5	0

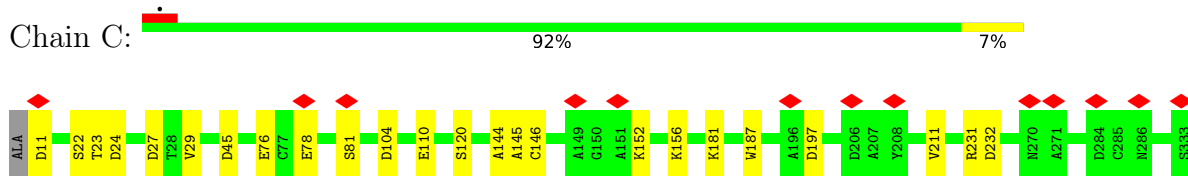
### 3 Residue-property plots

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.

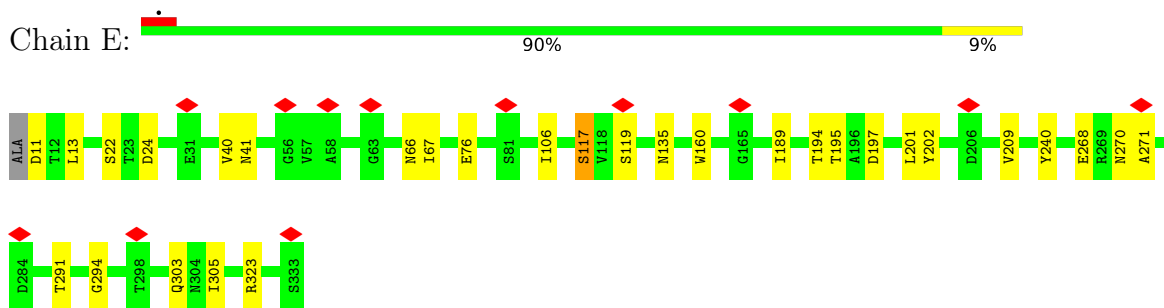
- Molecule 1: Hemagglutinin HA1 chain



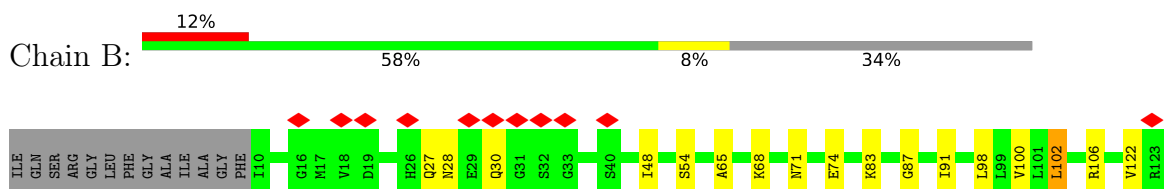
- Molecule 1: Hemagglutinin HA1 chain

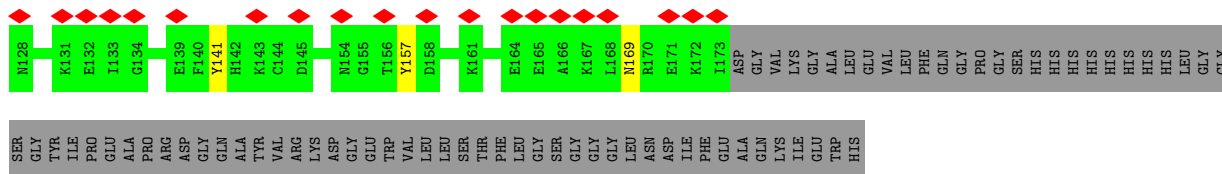


- Molecule 1: Hemagglutinin HA1 chain

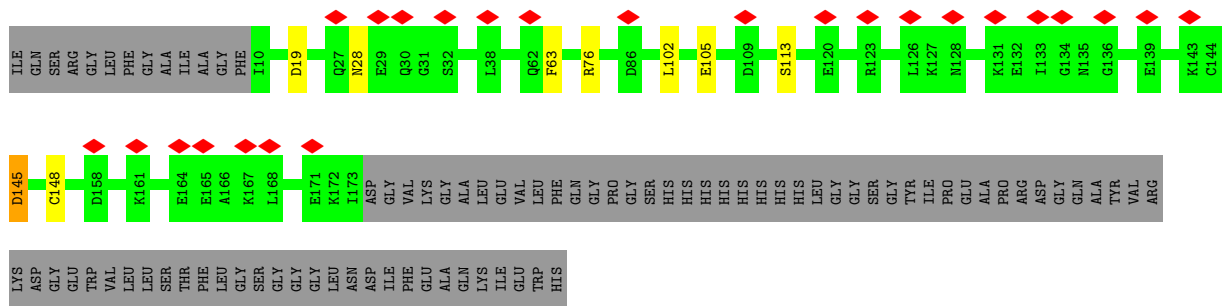


- Molecule 2: Hemagglutinin HA2 chain

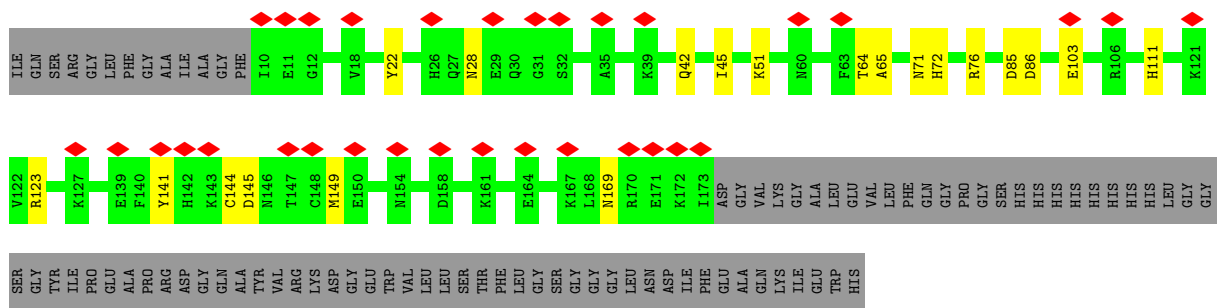




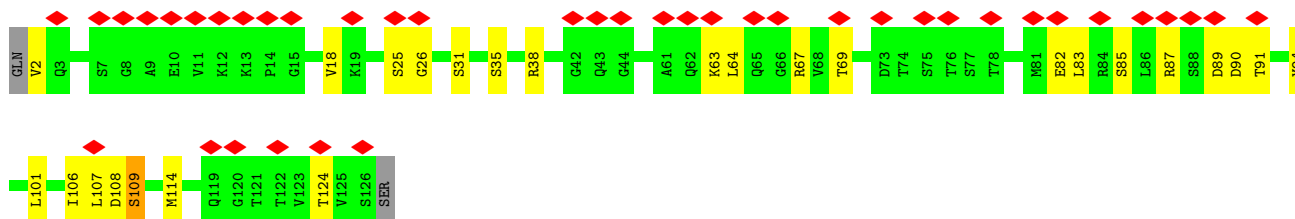
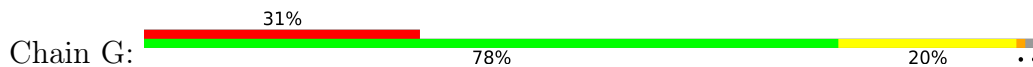
• Molecule 2: Hemagglutinin HA2 chain



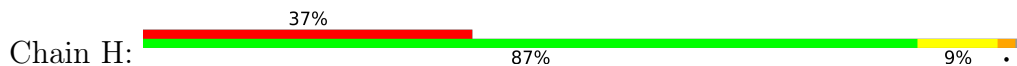
• Molecule 2: Hemagglutinin HA2 chain

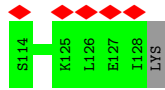
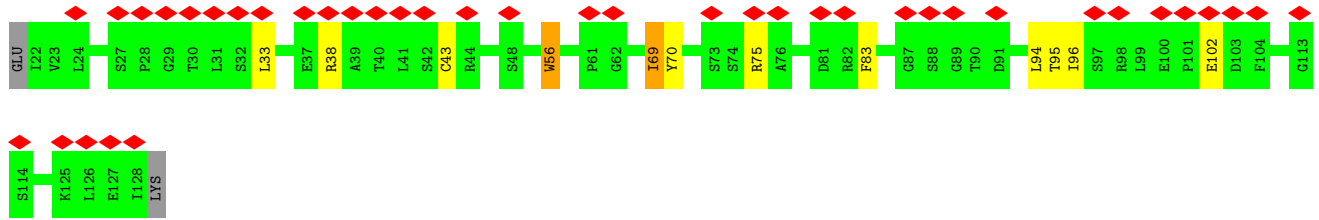


• Molecule 3: UCA6\_N55T HC Fv



• Molecule 4: UCA6\_N55T LC Fv





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	77014	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.491	Depositor
Minimum map value	-0.321	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	278.40002, 278.40002, 278.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7250001, 0.7250001, 0.7250001	Depositor



## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.36	0/2591	0.68	0/3525
1	C	0.35	0/2591	0.68	0/3525
1	E	0.33	0/2591	0.68	0/3525
2	B	0.36	0/1365	0.73	1/1838 (0.1%)
2	D	0.38	0/1365	0.70	1/1838 (0.1%)
2	F	0.37	0/1365	0.68	1/1838 (0.1%)
3	G	0.38	0/979	0.79	0/1332
4	H	0.45	0/837	0.79	2/1137 (0.2%)
All	All	0.36	0/13684	0.70	5/18558 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	145	ASP	CB-CG-OD1	6.60	124.24	118.30
4	H	43	CYS	CA-CB-SG	6.22	125.19	114.00
2	B	102	LEU	CB-CG-CD1	6.00	121.19	111.00
4	H	69	ILE	CG1-CB-CG2	-5.81	98.61	111.40
2	F	145	ASP	CB-CG-OD1	5.09	122.88	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2528	0	2460	26	0
1	C	2528	0	2461	15	0
1	E	2528	0	2461	17	0
2	B	1339	0	1274	12	0
2	D	1339	0	1272	5	0
2	F	1339	0	1272	11	0
3	G	959	0	932	15	0
4	H	817	0	791	5	0
5	A	70	0	65	0	0
5	C	70	0	65	2	0
5	D	14	0	13	0	0
5	E	70	0	65	1	0
5	F	14	0	13	0	0
All	All	13615	0	13144	93	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.

All (93) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:GLU:OE1	1:C:156:LYS:NZ	2.18	0.77
1:A:117:SER:OG	1:A:270:ASN:O	2.04	0.76
1:A:53:LYS:NZ	1:A:284:ASP:OD1	2.22	0.72
1:A:39:SER:OG	1:A:323:ARG:NH1	2.26	0.69
2:F:141:TYR:O	2:F:169:ASN:ND2	2.25	0.68
2:B:83:LYS:NZ	2:F:85:ASP:OD1	2.24	0.67
1:E:291:THR:OG1	1:E:294:GLY:O	2.11	0.65
2:B:28:ASN:OD1	2:B:30:GLN:N	2.29	0.65
1:A:283:HIS:CG	1:A:284:ASP:H	2.16	0.64
1:E:106:ILE:HD12	1:E:240:TYR:CE2	2.35	0.62
3:G:2:VAL:N	3:G:25:SER:O	2.32	0.62
1:E:22:SER:OG	1:E:24:ASP:OD1	2.17	0.62
1:A:198:GLN:NE2	1:A:205:ALA:O	2.33	0.61
1:A:287:THR:OG1	1:A:296:ILE:O	2.17	0.61
3:G:87:ARG:NH2	3:G:90:ASP:OD1	2.33	0.61
1:C:104:ASP:N	1:C:104:ASP:OD1	2.34	0.60
1:E:11:ASP:OD1	2:F:28:ASN:ND2	2.34	0.60
1:E:303:GLN:OE1	1:E:305:ILE:N	2.35	0.59
3:G:38:ARG:NH1	3:G:94:TYR:OH	2.37	0.58
1:E:41:ASN:OD1	1:E:323:ARG:NH2	2.36	0.57
3:G:2:VAL:HG12	3:G:26:GLY:HA3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:VAL:HG12	1:A:319:SER:H	1.69	0.57
2:F:51:LYS:NZ	2:F:103:GLU:OE1	2.19	0.56
2:F:71:ASN:OD1	2:F:72:HIS:N	2.40	0.55
4:H:38:ARG:NH2	4:H:95:THR:OG1	2.40	0.55
1:A:322:LEU:HB3	2:B:100:VAL:HG21	1.90	0.54
1:A:283:HIS:CG	1:A:284:ASP:N	2.75	0.54
3:G:108:ASP:OD1	3:G:109:SER:N	2.42	0.52
1:E:76:GLU:HB2	5:E:405:NAG:H82	1.91	0.52
3:G:91:THR:HG23	3:G:124:THR:HA	1.93	0.51
3:G:35:SER:OG	3:G:114:MET:SD	2.66	0.51
1:A:25:THR:OG1	1:A:33:ASN:OD1	2.21	0.51
3:G:18:VAL:CG1	3:G:83:LEU:HB3	2.40	0.51
1:C:27:ASP:OD1	1:C:27:ASP:N	2.43	0.50
3:G:18:VAL:HG12	3:G:83:LEU:HB3	1.94	0.49
1:E:40:VAL:HG22	3:G:107:LEU:HD11	1.95	0.49
3:G:101:LEU:HG	3:G:106:ILE:HD11	1.93	0.49
1:C:120:SER:OG	1:C:181:LYS:NZ	2.42	0.49
4:H:102:GLU:OE1	4:H:102:GLU:N	2.43	0.49
2:F:64:THR:OG1	2:F:65:ALA:N	2.45	0.49
2:B:141:TYR:O	2:B:169:ASN:ND2	2.46	0.49
1:C:11:ASP:OD2	2:D:28:ASN:ND2	2.45	0.48
2:B:98:LEU:O	2:B:102:LEU:HD12	2.13	0.48
1:A:51:LEU:HG	1:A:280:THR:HG23	1.95	0.48
1:A:104:ASP:N	1:A:104:ASP:OD1	2.44	0.47
3:G:63:LYS:HG3	3:G:64:LEU:HD22	1.96	0.47
2:F:22:TYR:OH	2:F:111:HIS:ND1	2.26	0.47
1:C:146:CYS:HB2	5:C:405:NAG:H81	1.96	0.47
1:A:66:ASN:OD1	1:A:67:ILE:N	2.47	0.46
1:A:67:ILE:HD11	1:A:275:ILE:HD11	1.98	0.46
1:A:110:GLU:OE2	2:D:76:ARG:NH2	2.49	0.46
1:E:13:LEU:HD21	2:F:149:MET:SD	2.56	0.46
2:B:106:ARG:NH1	2:D:105:GLU:OE1	2.49	0.46
1:A:313:CYS:HB3	1:A:314:PRO:CD	2.46	0.46
1:C:110:GLU:OE2	2:F:76:ARG:NE	2.49	0.45
1:C:145:ALA:O	1:C:231:ARG:NH2	2.49	0.45
1:E:66:ASN:OD1	1:E:67:ILE:N	2.47	0.45
4:H:56:TRP:HB2	4:H:69:ILE:HG22	1.97	0.45
3:G:67:ARG:NH2	3:G:85:SER:O	2.50	0.45
2:B:87:GLY:O	2:B:91:ILE:HD12	2.16	0.45
1:C:144:ALA:HB2	1:C:152:LYS:HE3	1.98	0.44
1:A:204:ASN:O	1:A:206:ASP:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:ASP:N	2:B:27:GLN:O	2.51	0.44
1:C:22:SER:OG	1:C:24:ASP:OD1	2.35	0.44
1:E:160:TRP:CZ2	1:E:201:LEU:HD21	2.53	0.44
1:C:76:GLU:CG	5:C:405:NAG:H82	2.48	0.44
1:E:270:ASN:OD1	1:E:271:ALA:N	2.51	0.43
4:H:94:LEU:HG	4:H:96:ILE:HG23	1.99	0.43
1:A:52:CYS:SG	1:A:285:CYS:N	2.92	0.43
1:A:63:GLY:O	1:A:92:THR:OG1	2.30	0.43
2:B:71:ASN:ND2	2:B:74:GLU:OE2	2.51	0.43
2:F:42:GLN:HA	2:F:45:ILE:HG22	2.00	0.43
1:C:187:TRP:CZ2	1:C:211:VAL:HG11	2.54	0.43
1:E:160:TRP:HE1	1:E:202:TYR:HH	1.64	0.43
1:E:194:THR:OG1	1:E:195:THR:N	2.51	0.43
3:G:87:ARG:HE	3:G:89:ASP:HB2	1.82	0.43
2:D:145:ASP:O	2:D:148:CYS:HB3	2.18	0.42
1:C:29:VAL:HG21	2:D:102:LEU:HD23	2.00	0.42
1:A:160:TRP:HE1	1:A:202:TYR:HH	1.66	0.42
2:B:65:ALA:O	2:B:68:LYS:NZ	2.53	0.42
1:A:44:GLU:HG2	1:A:300:LEU:HD12	2.01	0.42
1:E:119:SER:N	1:E:268:GLU:O	2.51	0.42
1:A:41:ASN:O	1:A:300:LEU:HD13	2.20	0.41
1:A:194:THR:HG22	1:A:195:THR:H	1.85	0.41
1:E:117:SER:O	1:E:117:SER:OG	2.38	0.41
2:F:28:ASN:ND2	2:F:144:CYS:O	2.49	0.41
1:A:15:ILE:HD11	2:B:122:VAL:HG21	2.03	0.41
3:G:69:THR:HG22	3:G:82:GLU:HB2	2.03	0.41
1:E:189:ILE:CD1	1:E:209:VAL:HG11	2.51	0.41
4:H:75:ARG:NH1	4:H:83:PHE:O	2.53	0.41
1:C:45:ASP:OD1	1:C:45:ASP:N	2.53	0.40
1:A:326:THR:OG1	2:B:48:ILE:HG21	2.21	0.40
1:C:23:THR:O	1:C:23:THR:HG22	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	321/324 (99%)	315 (98%)	6 (2%)	0	100	100
1	C	321/324 (99%)	315 (98%)	6 (2%)	0	100	100
1	E	321/324 (99%)	311 (97%)	10 (3%)	0	100	100
2	B	162/250 (65%)	160 (99%)	2 (1%)	0	100	100
2	D	162/250 (65%)	159 (98%)	3 (2%)	0	100	100
2	F	162/250 (65%)	160 (99%)	2 (1%)	0	100	100
3	G	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
4	H	105/109 (96%)	103 (98%)	2 (2%)	0	100	100
All	All	1677/1958 (86%)	1644 (98%)	33 (2%)	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	284/284 (100%)	282 (99%)	2 (1%)	84	93
1	C	284/284 (100%)	281 (99%)	3 (1%)	73	88
1	E	284/284 (100%)	281 (99%)	3 (1%)	73	88
2	B	145/209 (69%)	143 (99%)	2 (1%)	67	85
2	D	145/209 (69%)	142 (98%)	3 (2%)	53	79
2	F	145/209 (69%)	143 (99%)	2 (1%)	67	85
3	G	103/105 (98%)	101 (98%)	2 (2%)	57	80
4	H	89/91 (98%)	86 (97%)	3 (3%)	37	68
All	All	1479/1675 (88%)	1459 (99%)	20 (1%)	68	85

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	TYR
1	A	324	LEU
2	B	54	SER
2	B	157	TYR
1	C	81	SER
1	C	197	ASP
1	C	232	ASP
2	D	19	ASP
2	D	63	PHE
2	D	113	SER
1	E	117	SER
1	E	135	ASN
1	E	197	ASP
2	F	86	ASP
2	F	123	ARG
3	G	31	SER
3	G	109	SER
4	H	33	LEU
4	H	56	TRP
4	H	70	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	198	GLN
2	D	111	HIS
2	F	72	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.



## 5.6 Ligand geometry

17 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
5	NAG	A	401	1	14,14,15	0.23	0	17,19,21	0.53	0
5	NAG	C	404	1	14,14,15	0.25	0	17,19,21	0.54	0
5	NAG	A	405	1	14,14,15	0.20	0	17,19,21	0.56	0
5	NAG	E	402	1	14,14,15	0.29	0	17,19,21	0.51	0
5	NAG	A	404	1	14,14,15	0.27	0	17,19,21	0.54	0
5	NAG	A	403	1	14,14,15	0.26	0	17,19,21	0.51	0
5	NAG	C	402	1	14,14,15	0.32	0	17,19,21	0.51	0
5	NAG	D	301	2	14,14,15	0.29	0	17,19,21	0.56	0
5	NAG	E	405	1	14,14,15	0.22	0	17,19,21	0.57	0
5	NAG	C	401	1	14,14,15	0.28	0	17,19,21	0.59	0
5	NAG	E	401	1	14,14,15	0.29	0	17,19,21	0.54	0
5	NAG	C	405	1	14,14,15	0.23	0	17,19,21	0.58	0
5	NAG	F	301	2	14,14,15	0.34	0	17,19,21	0.91	1 (5%)
5	NAG	A	402	1	14,14,15	0.28	0	17,19,21	0.57	0
5	NAG	C	403	1	14,14,15	0.25	0	17,19,21	0.55	0
5	NAG	E	404	1	14,14,15	0.27	0	17,19,21	0.53	0
5	NAG	E	403	1	14,14,15	0.24	0	17,19,21	0.56	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	A	401	1	-	0/6/23/26	0/1/1/1
5	NAG	C	404	1	-	2/6/23/26	0/1/1/1
5	NAG	A	405	1	-	1/6/23/26	0/1/1/1
5	NAG	E	402	1	-	0/6/23/26	0/1/1/1
5	NAG	A	404	1	-	1/6/23/26	0/1/1/1
5	NAG	A	403	1	-	2/6/23/26	0/1/1/1
5	NAG	C	402	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	D	301	2	-	0/6/23/26	0/1/1/1
5	NAG	E	405	1	-	2/6/23/26	0/1/1/1
5	NAG	C	401	1	-	1/6/23/26	0/1/1/1
5	NAG	E	401	1	-	1/6/23/26	0/1/1/1
5	NAG	C	405	1	-	1/6/23/26	0/1/1/1
5	NAG	F	301	2	-	3/6/23/26	0/1/1/1
5	NAG	A	402	1	-	2/6/23/26	0/1/1/1
5	NAG	C	403	1	-	0/6/23/26	0/1/1/1
5	NAG	E	404	1	-	1/6/23/26	0/1/1/1
5	NAG	E	403	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(°)
5	F	301	NAG	C2-N2-C7	2.86	126.98	122.90

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	405	NAG	C4-C5-C6-O6
5	A	402	NAG	O5-C5-C6-O6
5	A	403	NAG	O5-C5-C6-O6
5	E	405	NAG	O5-C5-C6-O6
5	F	301	NAG	C8-C7-N2-C2
5	F	301	NAG	O7-C7-N2-C2
5	A	402	NAG	C4-C5-C6-O6
5	A	403	NAG	C4-C5-C6-O6
5	C	405	NAG	O5-C5-C6-O6
5	C	404	NAG	C4-C5-C6-O6
5	A	405	NAG	O5-C5-C6-O6
5	A	404	NAG	O5-C5-C6-O6
5	E	404	NAG	O5-C5-C6-O6
5	C	401	NAG	O5-C5-C6-O6
5	F	301	NAG	O5-C5-C6-O6
5	E	401	NAG	O5-C5-C6-O6
5	C	404	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	405	NAG	1	0
5	C	405	NAG	2	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.

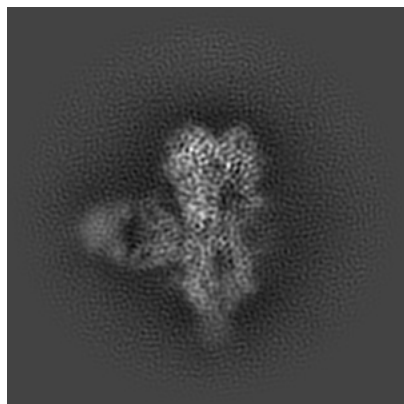
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42530. These allow visual inspection of the internal detail of the map and identification of artifacts.

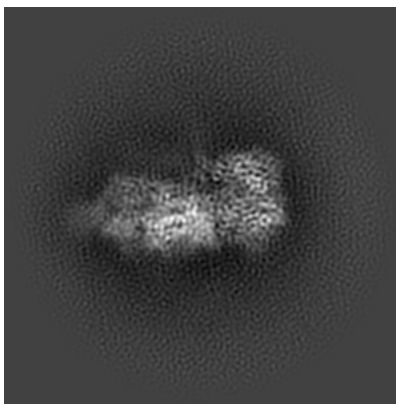
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

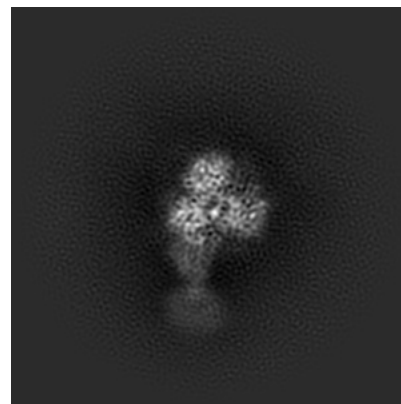
#### 6.1.1 Primary map



X

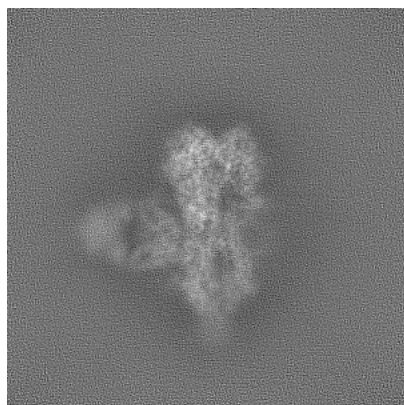


Y

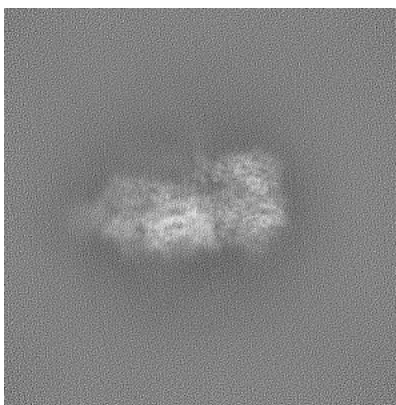


Z

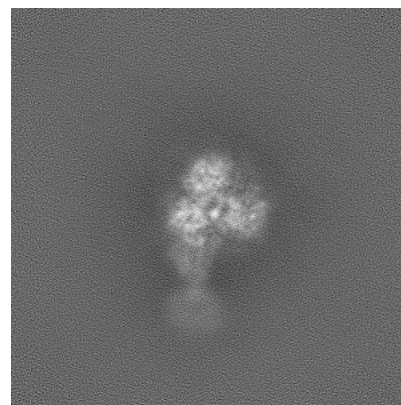
#### 6.1.2 Raw map



X



Y

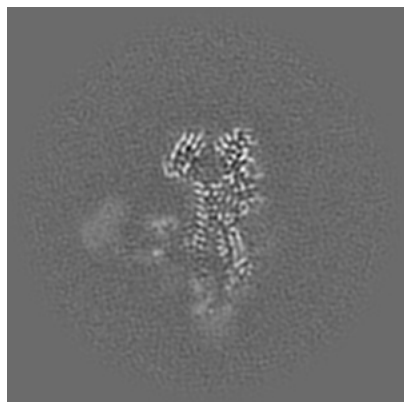


Z

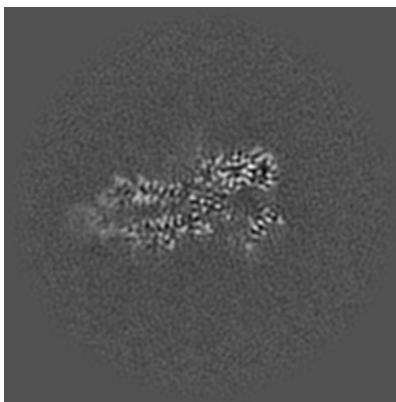
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

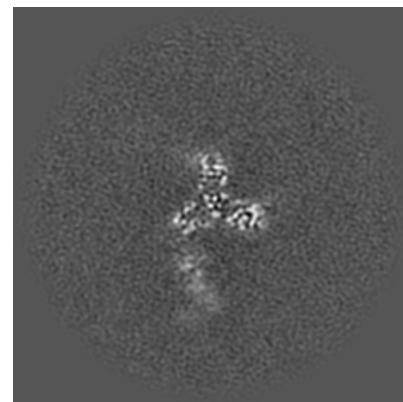
### 6.2.1 Primary map



X Index: 192

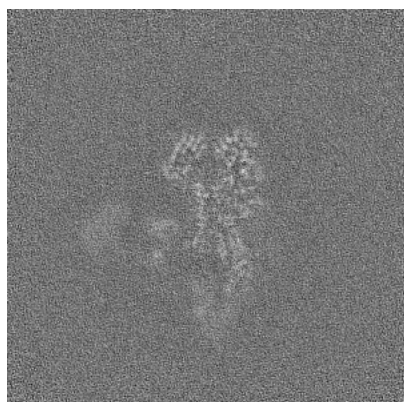


Y Index: 192

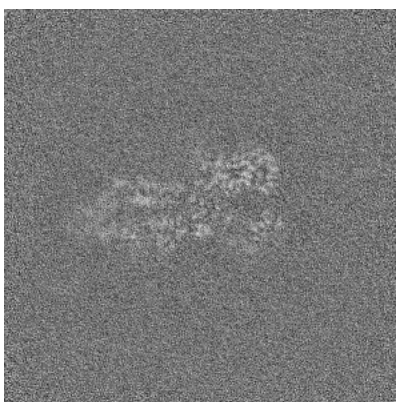


Z Index: 192

### 6.2.2 Raw map



X Index: 192



Y Index: 192



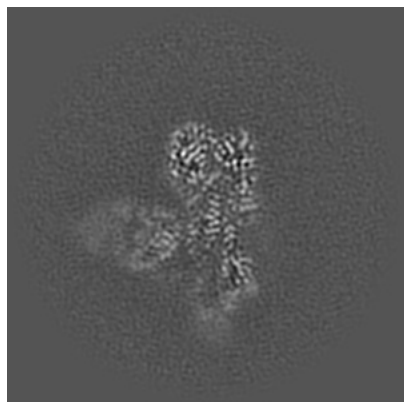
Z Index: 192

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

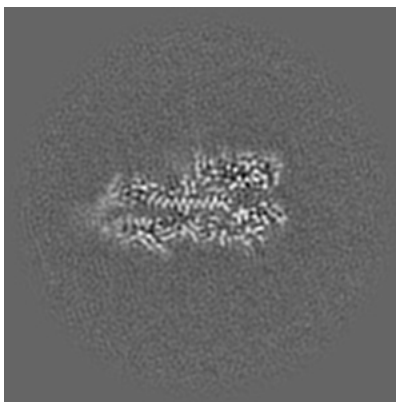


## 6.3 Largest variance slices [i](#)

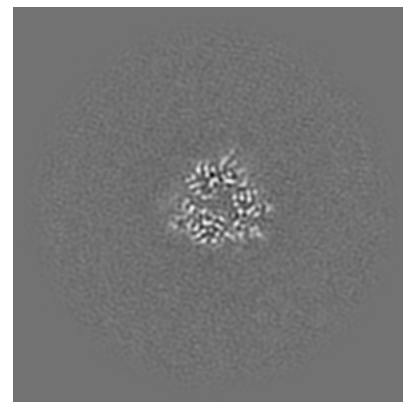
### 6.3.1 Primary map



X Index: 183

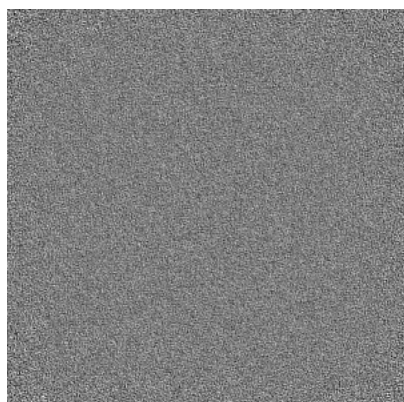


Y Index: 186

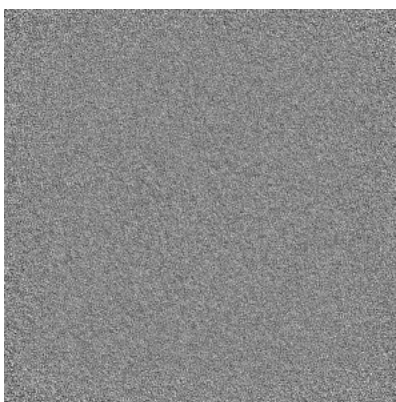


Z Index: 241

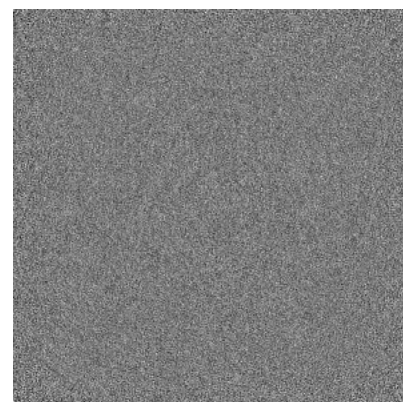
### 6.3.2 Raw map



X Index: 0



Y Index: 0



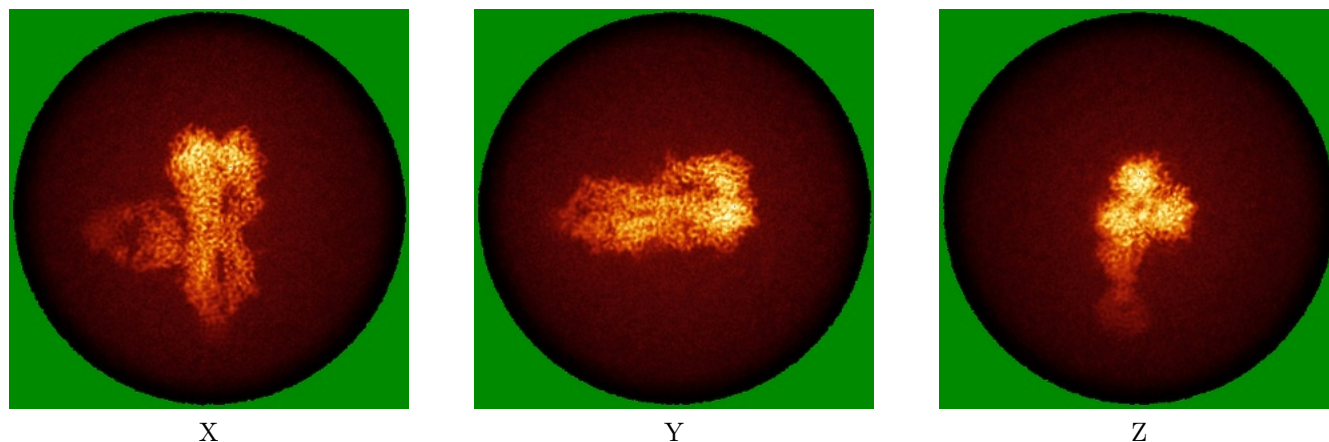
Z Index: 0

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

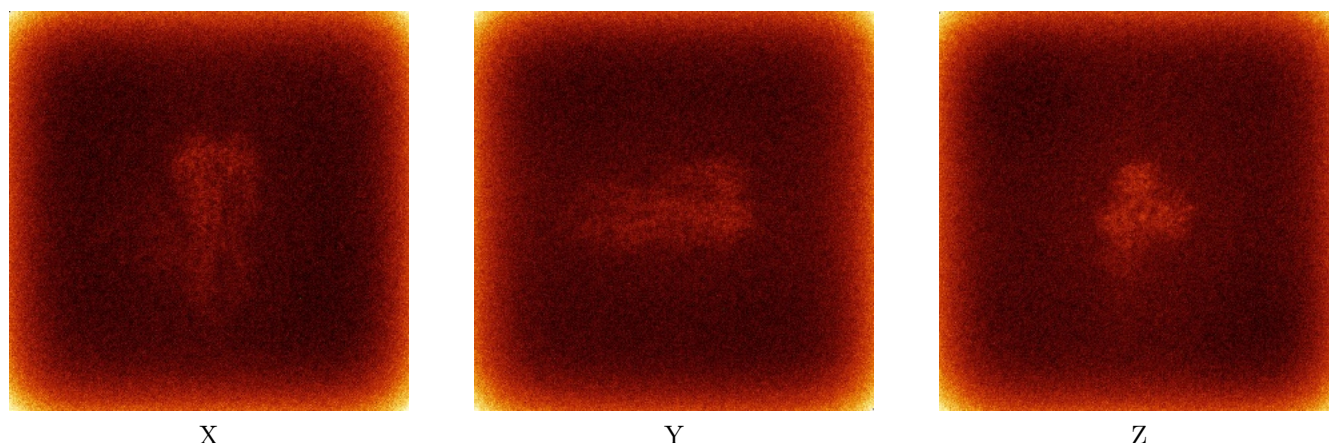


X

Y

Z

### 6.4.2 Raw map



X

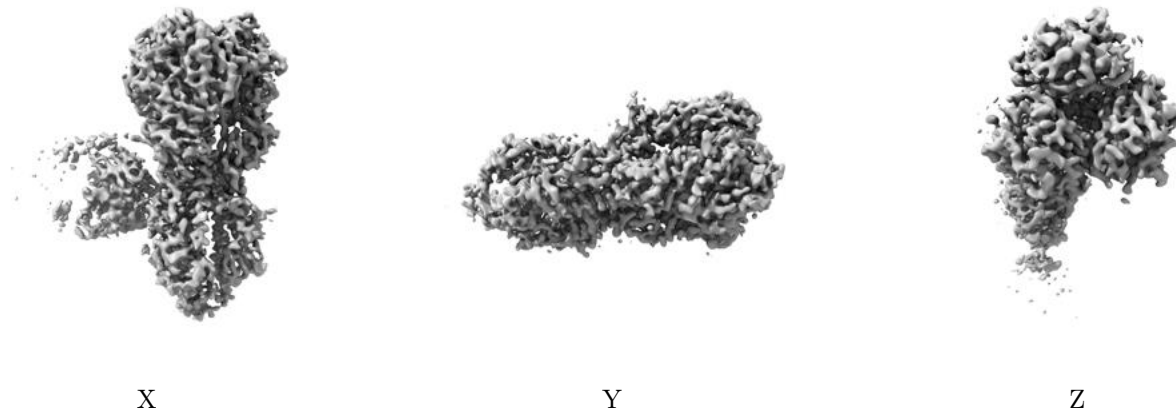
Y

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.

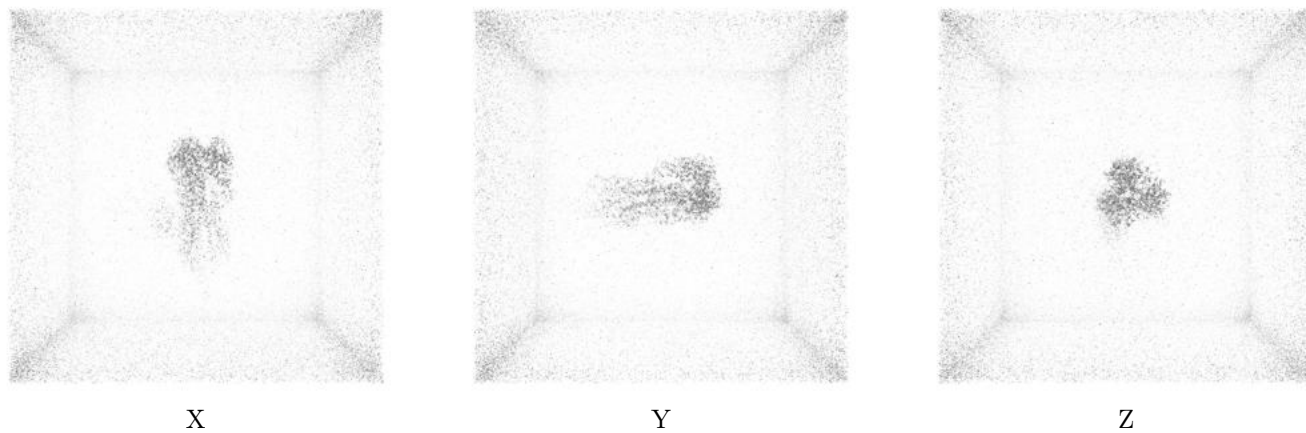
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. 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.

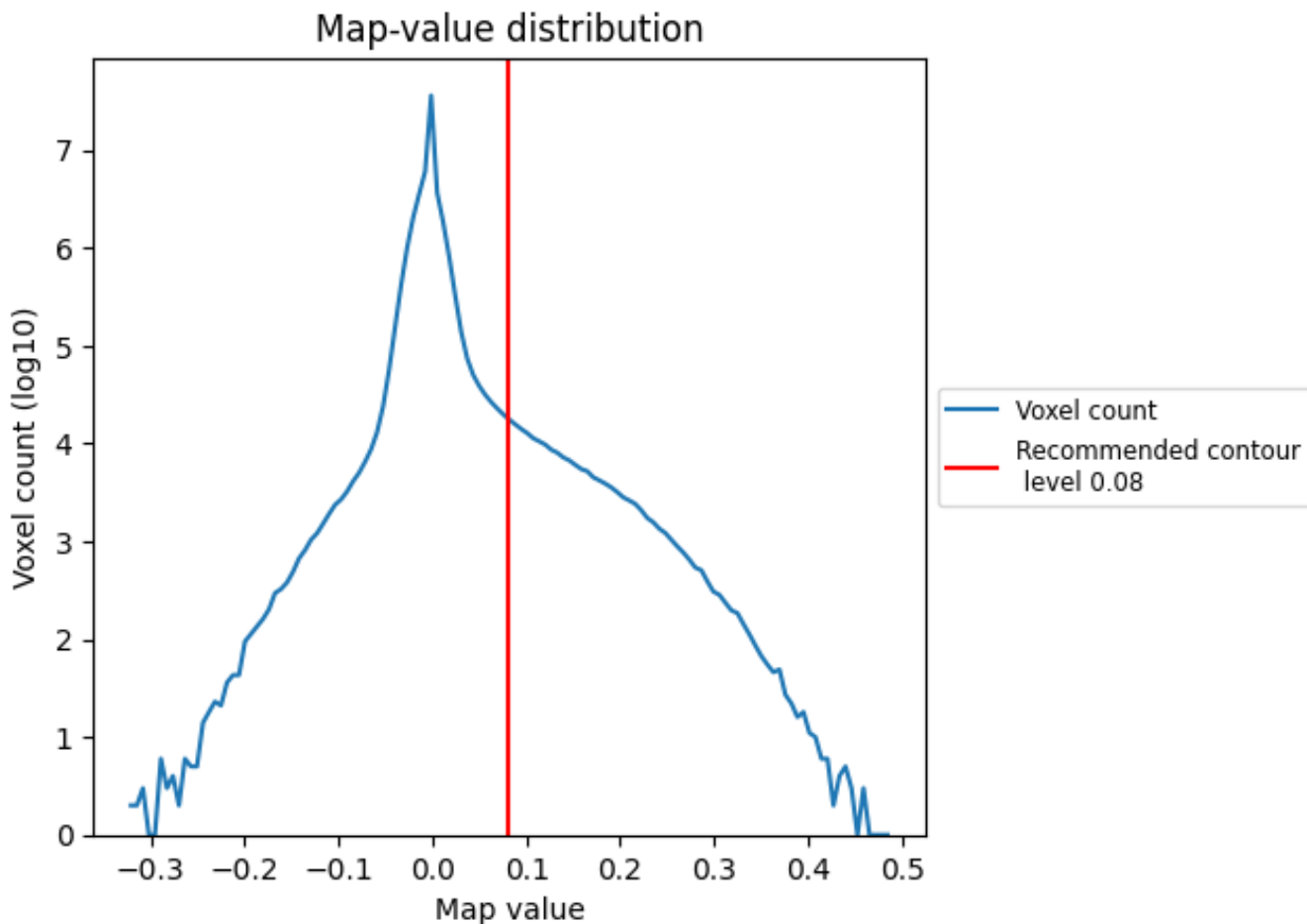
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

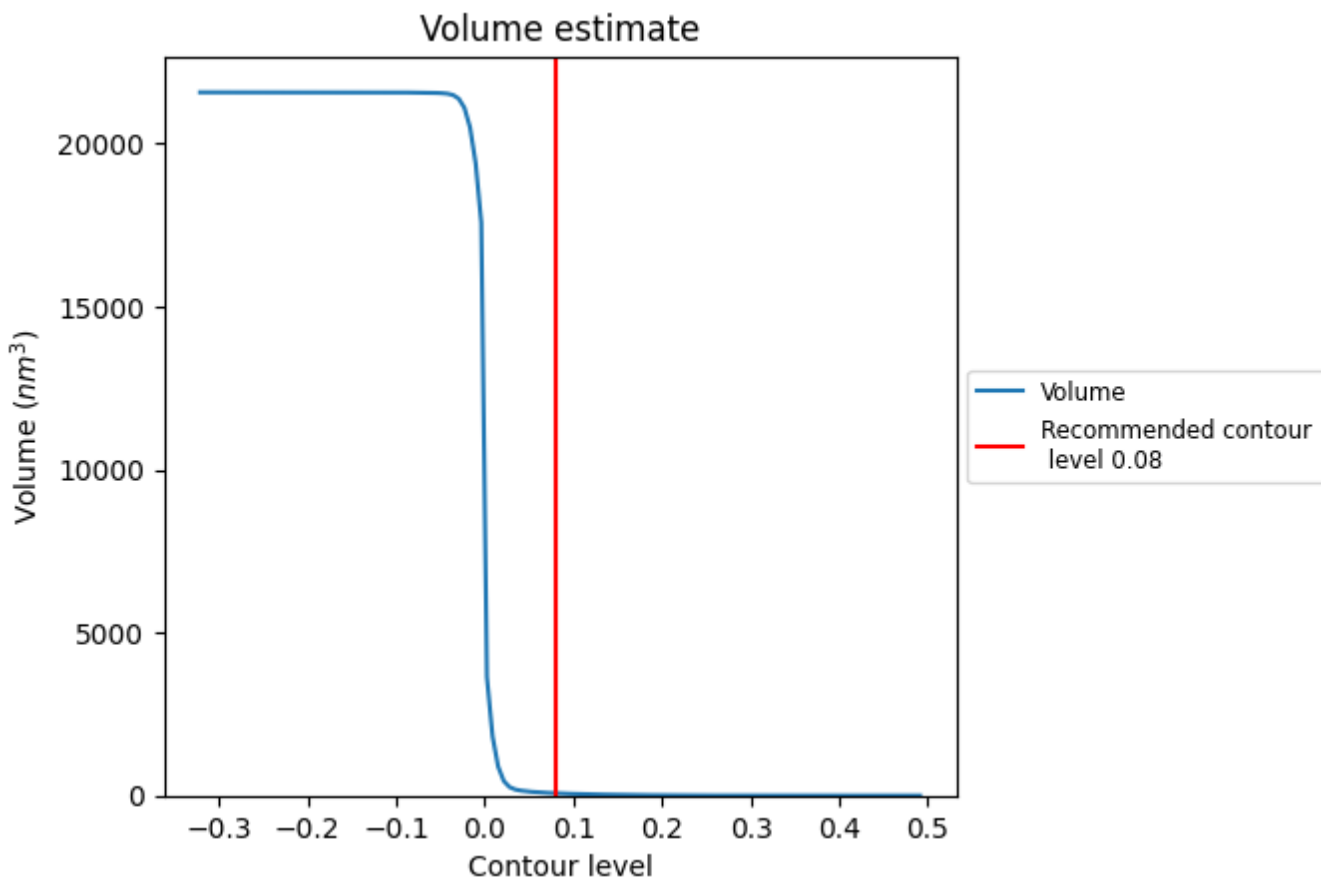
This section contains the results of statistical analysis of the map.

### 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.

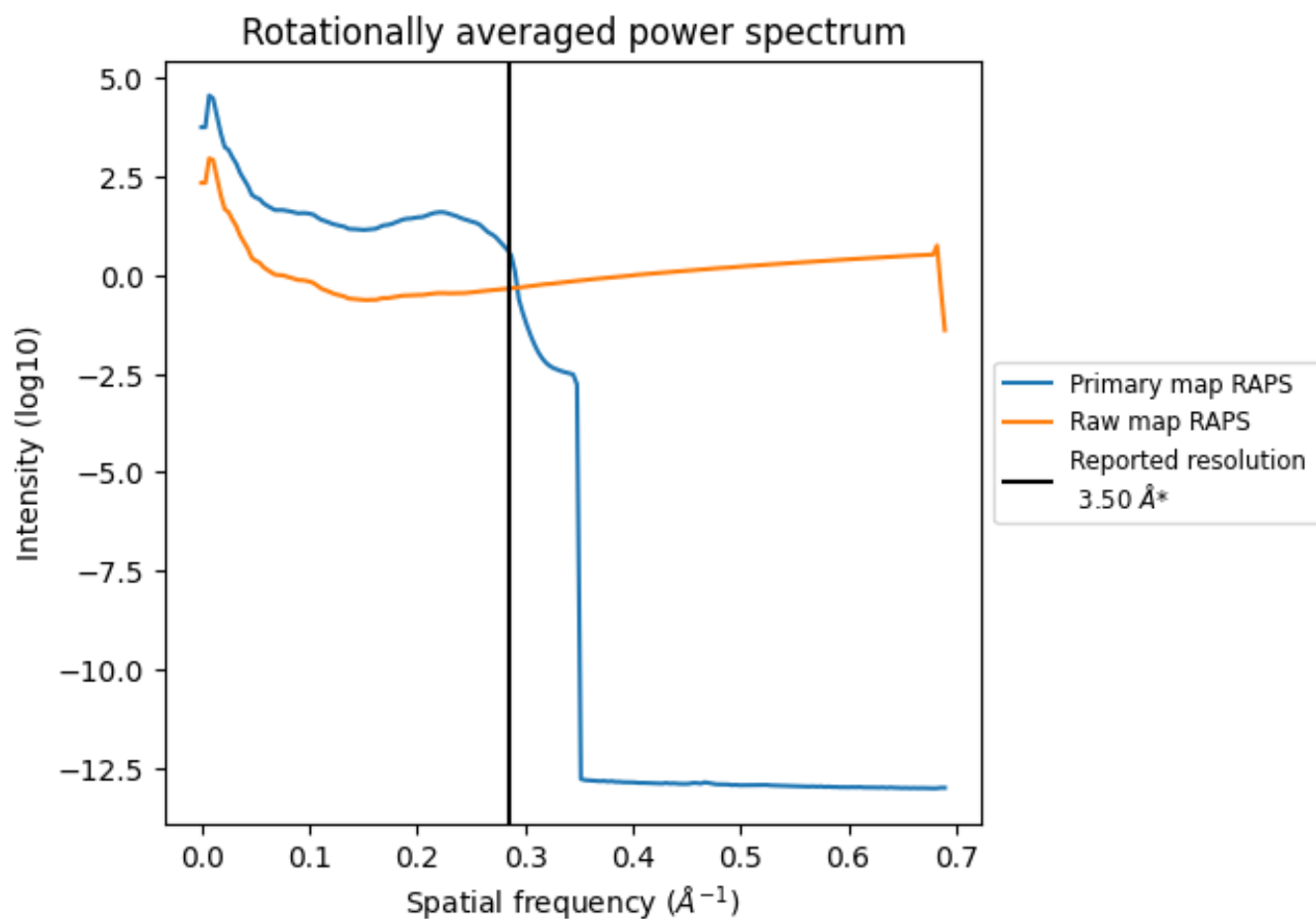
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 71 nm<sup>3</sup>; this corresponds to an approximate mass of 64 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 [i](#)

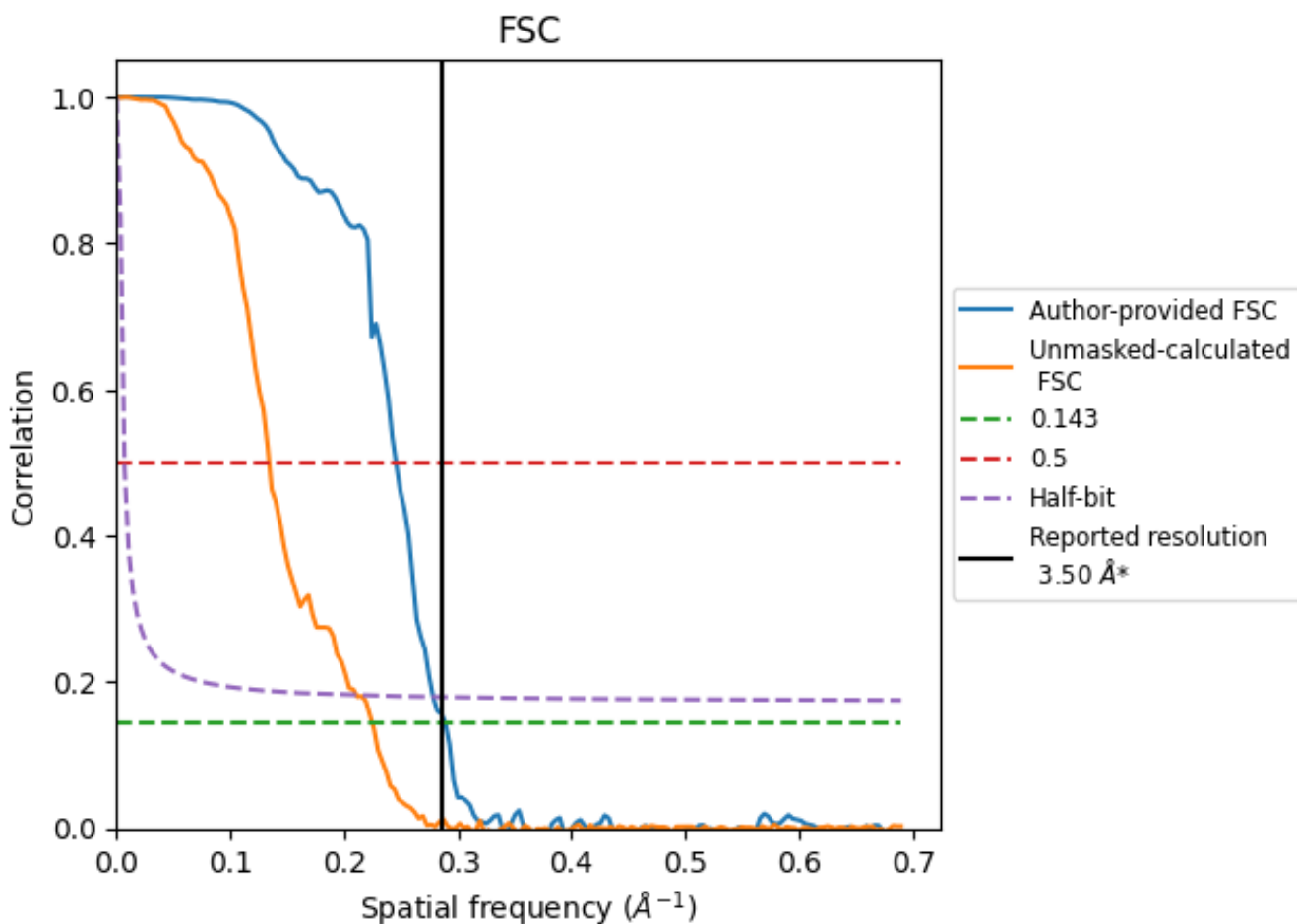


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 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 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.46	4.07	3.59
Unmasked-calculated*	4.45	7.45	4.73

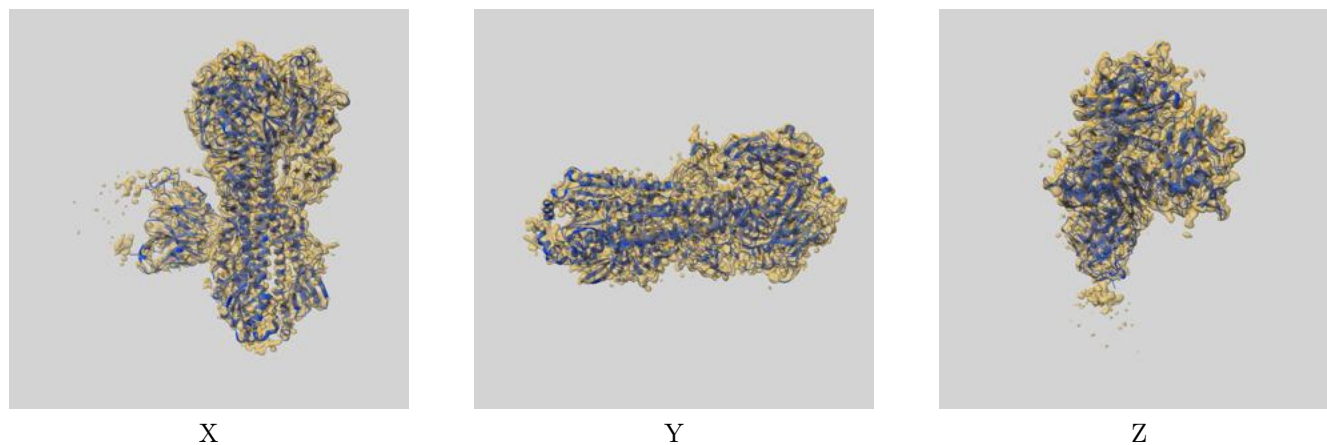
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.45 differs from the reported value 3.5 by more than 10 %



## 9 Map-model fit [i](#)

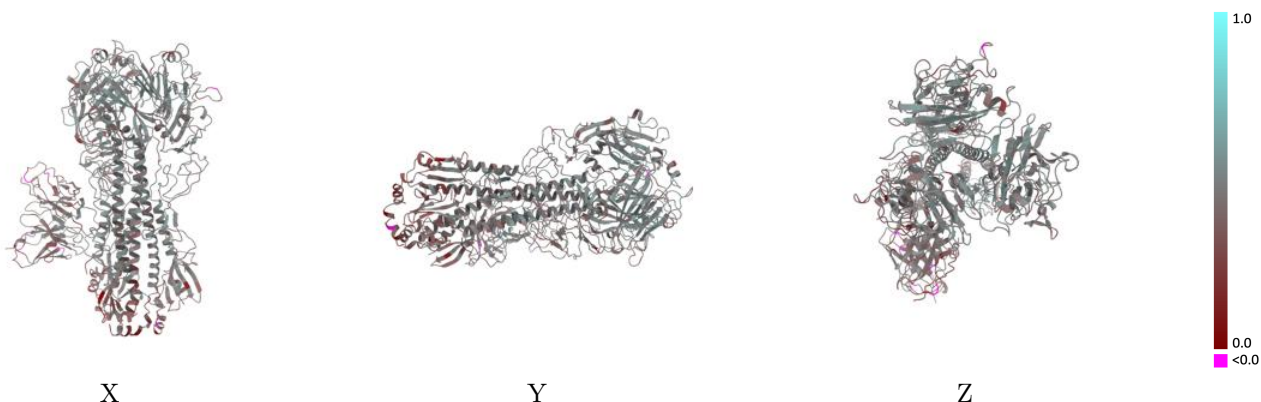
This section contains information regarding the fit between EMDB map EMD-42530 and PDB model 8UT5. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



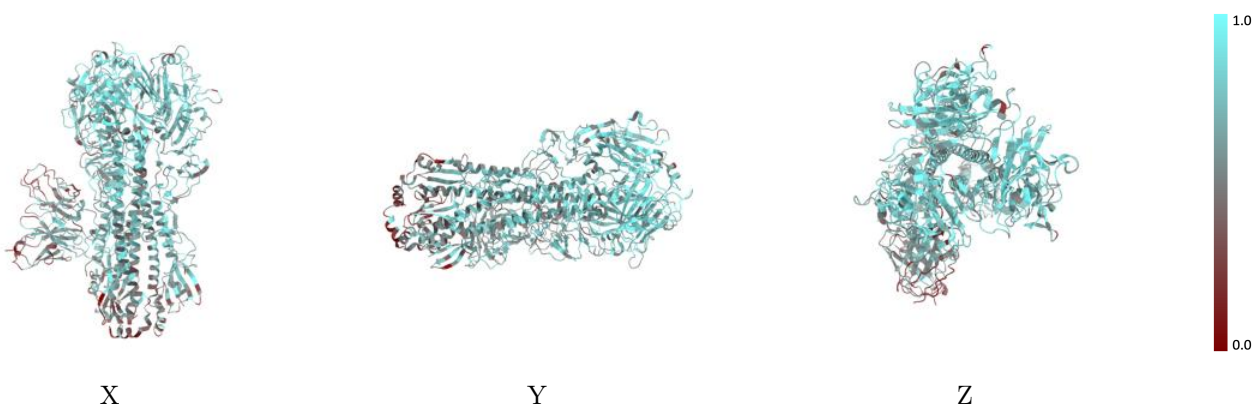
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



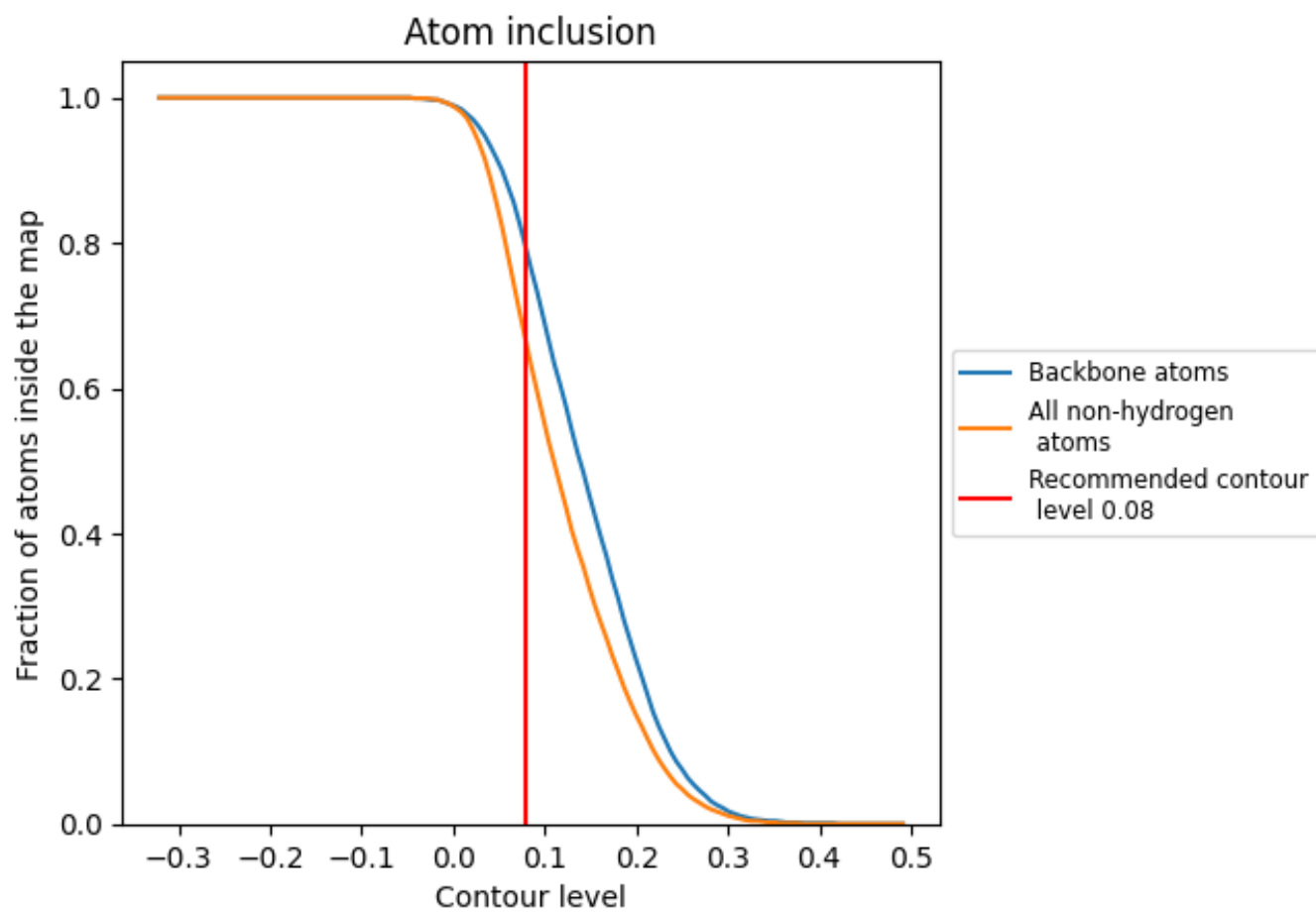
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 66% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6600	 0.4390
A	 0.7270	 0.4710
B	 0.5950	 0.4110
C	 0.7200	 0.4640
D	 0.6130	 0.4270
E	 0.7140	 0.4560
F	 0.6210	 0.4240
G	 0.5350	 0.3840
H	 0.4820	 0.3670

