



Full wwPDB EM Validation Report ⓘ

Nov 16, 2022 – 10:49 AM EST

PDB ID : 7KQE
EMDB ID : EMD-22997
Title : SARS-CoV-2 spike glycoprotein:Fab 3D11 complex
Authors : Asarnow, D.; Charles, C.; Cheng, Y.
Deposited on : 2020-11-15
Resolution : 2.88 Å (reported)
Based on initial model : 7A94

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

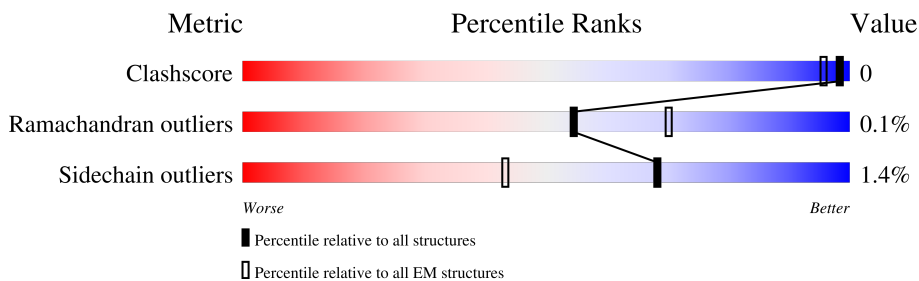
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 2.88 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 ≥ 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	H	448	
1	I	448	
1	J	448	
2	L	216	
2	M	216	
2	N	216	
3	A	1208	
3	B	1208	

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Mol	Chain	Length	Quality of chain
3	C	1208	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '5%', a large green segment in the middle labeled '85%', and a grey segment on the right labeled '12%'. A small black dot is visible on the green segment near the right edge.</p>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 68370 atoms, of which 33744 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 Fab 3D11 heavy chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	H	211	3187	1026	1580	271	306	4	0	0
1	J	211	3187	1026	1580	271	306	4	0	0
1	I	211	3187	1026	1580	271	306	4	0	0

- Molecule 2 is a protein called Fab 3D11 light chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	L	212	3117	990	1526	266	330	5	0	0
2	M	212	3117	990	1526	266	330	5	0	0
2	N	212	3117	990	1526	266	330	5	0	0

- Molecule 3 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	A	1066	16486	5324	8142	1394	1588	38	0	0
3	B	1066	16486	5324	8142	1394	1588	38	0	0
3	C	1066	16486	5324	8142	1394	1588	38	0	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	conflict	UNP P0DTC2
A	683	SER	ARG	conflict	UNP P0DTC2
A	685	SER	ARG	conflict	UNP P0DTC2

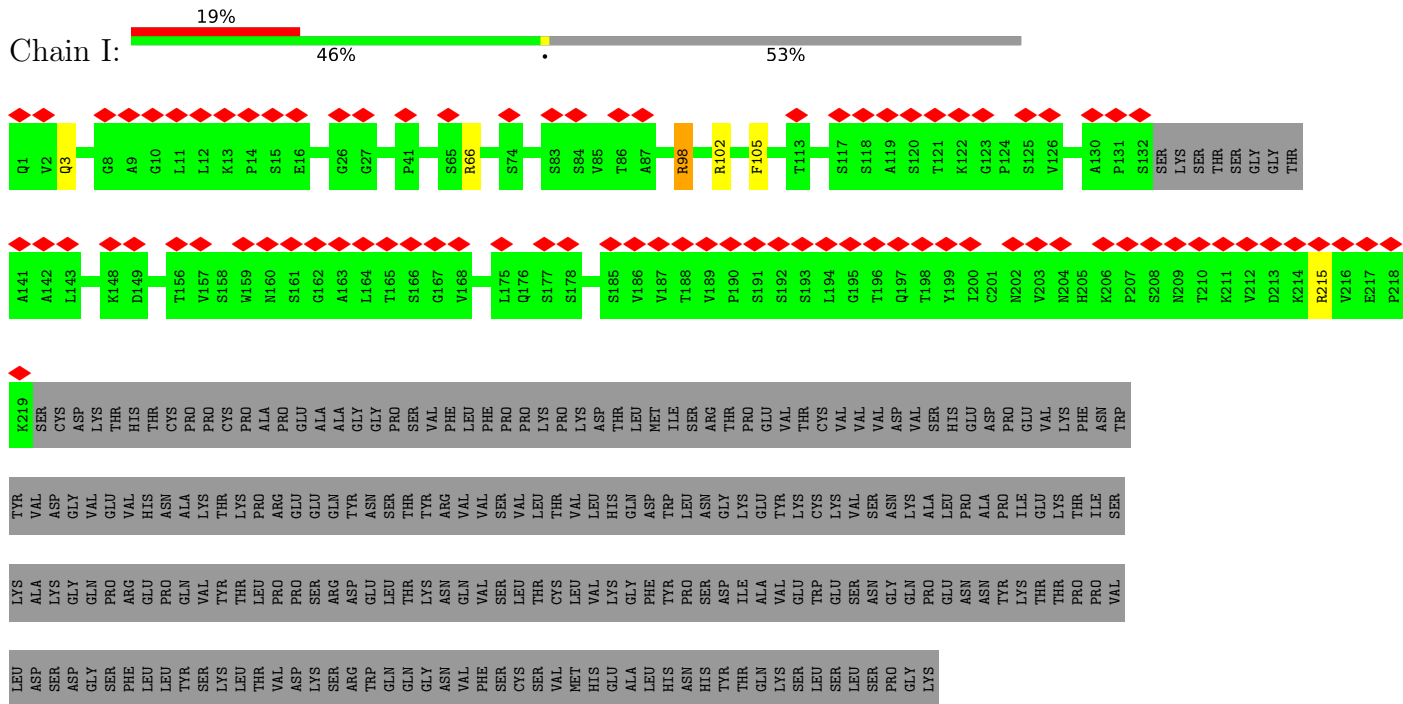
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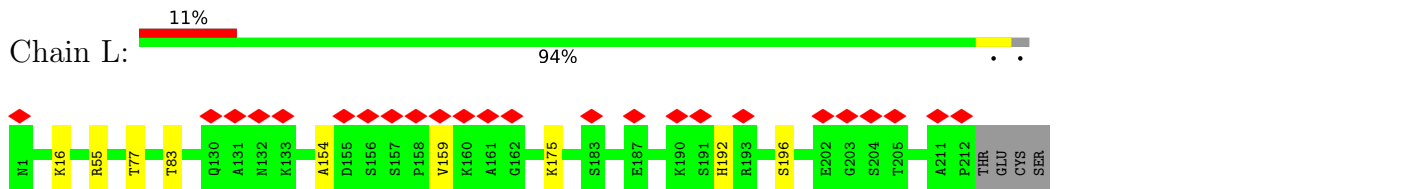
Chain	Residue	Modelled	Actual	Comment	Reference
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
B	682	GLY	ARG	conflict	UNP P0DTC2
B	683	SER	ARG	conflict	UNP P0DTC2
B	685	SER	ARG	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
C	682	GLY	ARG	conflict	UNP P0DTC2
C	683	SER	ARG	conflict	UNP P0DTC2
C	685	SER	ARG	conflict	UNP P0DTC2
C	986	PRO	LYS	conflict	UNP P0DTC2
C	987	PRO	VAL	conflict	UNP P0DTC2

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

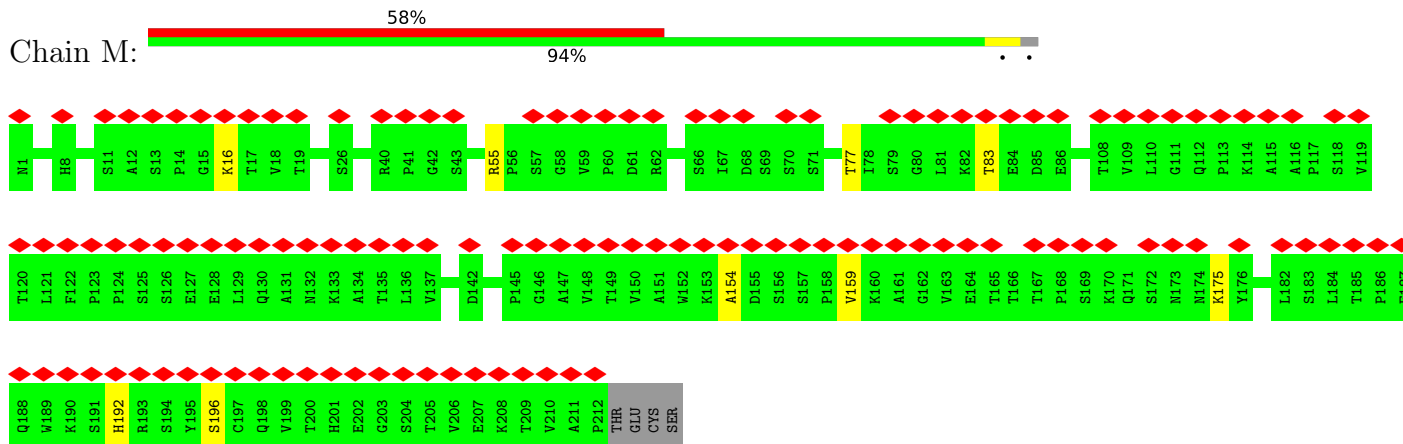
- Molecule 1: Fab 3D11 heavy chain



- Molecule 2: Fab 3D11 light chain



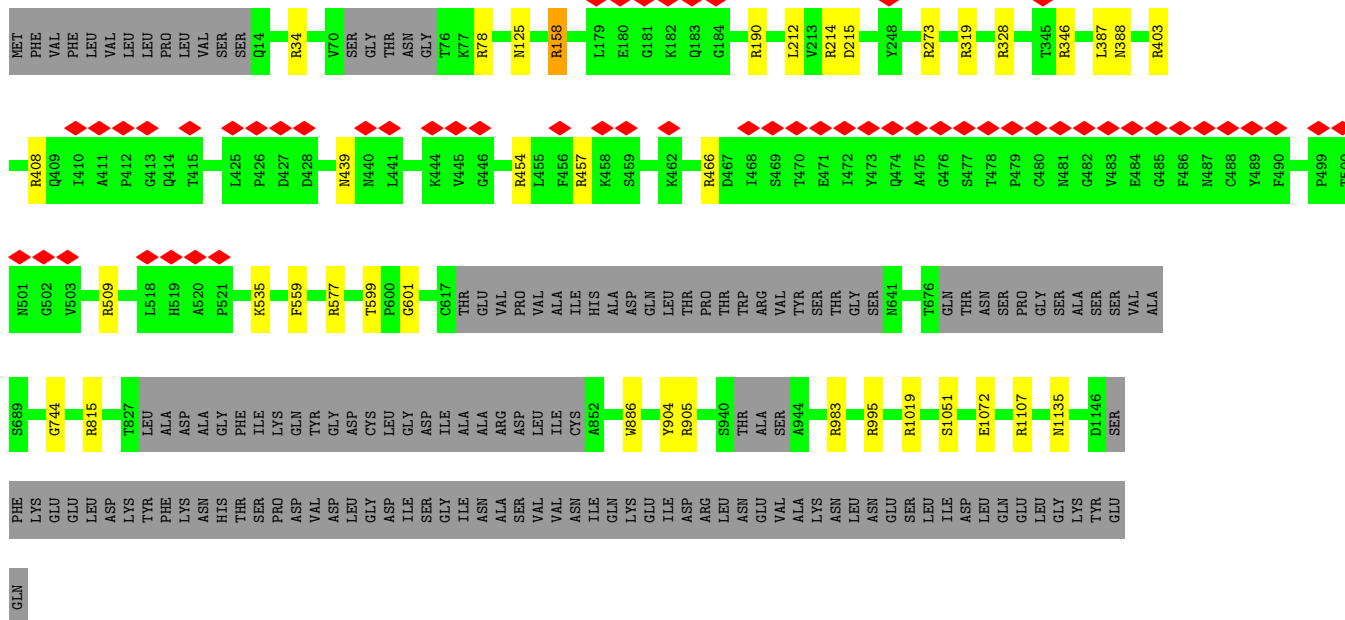
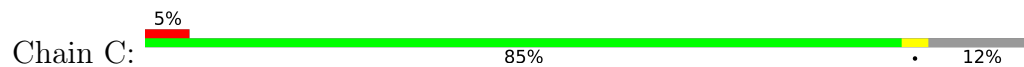
- Molecule 2: Fab 3D11 light chain



- Molecule 2: Fab 3D11 light chain

LEU
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GLN
GLU
LEU
GLY
LYS
TYR
GLU
GLN

Molecule 3: Spike glycoprotein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	197150	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	67.7	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.291	Depositor
Minimum map value	-0.777	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.086	Depositor
Recommended contour level	0.5	Depositor
Map size (\AA)	427.52, 427.52, 427.52	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.4250666, 1.4250666, 1.4250666	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	H	0.63	0/1652	1.03	4/2258 (0.2%)
1	I	0.63	0/1652	1.03	4/2258 (0.2%)
1	J	0.63	0/1652	1.03	4/2258 (0.2%)
2	L	0.61	0/1630	0.97	1/2228 (0.0%)
2	M	0.61	0/1630	0.97	1/2228 (0.0%)
2	N	0.61	0/1630	0.97	1/2228 (0.0%)
3	A	0.64	0/8538	0.95	20/11618 (0.2%)
3	B	0.64	0/8538	0.94	19/11618 (0.2%)
3	C	0.65	0/8538	0.96	25/11618 (0.2%)
All	All	0.64	0/35460	0.96	79/48312 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1
1	I	0	1
1	J	0	1
3	A	0	3
3	B	0	2
All	All	0	8

There are no bond length outliers.

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	66	ARG	NE-CZ-NH1	8.59	124.59	120.30
1	J	66	ARG	NE-CZ-NH1	8.55	124.58	120.30
1	H	66	ARG	NE-CZ-NH1	8.44	124.52	120.30
3	B	995	ARG	NE-CZ-NH1	8.14	124.37	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	509	ARG	NE-CZ-NH1	8.10	124.35	120.30
3	C	995	ARG	NE-CZ-NH1	8.01	124.30	120.30
3	B	509	ARG	NE-CZ-NH1	7.94	124.27	120.30
1	J	215	ARG	NE-CZ-NH1	7.81	124.20	120.30
1	H	215	ARG	NE-CZ-NH1	7.74	124.17	120.30
1	I	215	ARG	NE-CZ-NH1	7.71	124.16	120.30
3	A	995	ARG	NE-CZ-NH1	7.64	124.12	120.30
3	A	34	ARG	NE-CZ-NH1	7.62	124.11	120.30
3	C	34	ARG	NE-CZ-NH1	7.44	124.02	120.30
3	B	457	ARG	NE-CZ-NH1	7.13	123.87	120.30
3	A	457	ARG	NE-CZ-NH1	7.11	123.86	120.30
3	C	1107	ARG	NE-CZ-NH1	7.10	123.85	120.30
3	B	403	ARG	NE-CZ-NH1	7.09	123.85	120.30
3	C	457	ARG	NE-CZ-NH1	7.07	123.83	120.30
3	A	403	ARG	NE-CZ-NH1	7.06	123.83	120.30
3	C	403	ARG	NE-CZ-NH1	7.04	123.82	120.30
3	A	815	ARG	NE-CZ-NH1	7.04	123.82	120.30
3	A	577	ARG	NE-CZ-NH1	7.01	123.81	120.30
3	C	190	ARG	NE-CZ-NH1	6.98	123.79	120.30
3	C	1019	ARG	NE-CZ-NH1	6.91	123.76	120.30
3	B	1039	ARG	NE-CZ-NH1	6.86	123.73	120.30
3	B	983	ARG	NE-CZ-NH1	6.80	123.70	120.30
3	B	1019	ARG	NE-CZ-NH1	6.79	123.69	120.30
3	C	273	ARG	NE-CZ-NH1	6.66	123.63	120.30
3	A	904	TYR	CB-CG-CD2	-6.59	117.05	121.00
3	B	273	ARG	NE-CZ-NH1	6.36	123.48	120.30
3	C	904	TYR	CB-CG-CD2	-6.34	117.20	121.00
2	N	55	ARG	NE-CZ-NH1	6.32	123.46	120.30
2	M	55	ARG	NE-CZ-NH1	6.29	123.44	120.30
2	L	55	ARG	NE-CZ-NH1	6.24	123.42	120.30
3	B	904	TYR	CB-CG-CD2	-6.14	117.32	121.00
3	C	346	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	I	102	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	J	102	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	H	102	ARG	NE-CZ-NH1	5.99	123.30	120.30
3	C	158	ARG	NE-CZ-NH1	5.94	123.27	120.30
3	A	44	ARG	NE-CZ-NH1	5.84	123.22	120.30
3	B	454	ARG	NE-CZ-NH1	5.76	123.18	120.30
3	C	454	ARG	NE-CZ-NH1	5.76	123.18	120.30
3	A	21	ARG	NE-CZ-NH2	-5.75	117.42	120.30
3	A	815	ARG	NE-CZ-NH2	-5.73	117.44	120.30
3	A	246	ARG	NE-CZ-NH1	5.70	123.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1039	ARG	NE-CZ-NH2	-5.70	117.45	120.30
3	C	983	ARG	NE-CZ-NH1	5.70	123.15	120.30
3	A	454	ARG	NE-CZ-NH1	5.68	123.14	120.30
3	B	78	ARG	NE-CZ-NH1	5.60	123.10	120.30
3	C	815	ARG	NE-CZ-NH2	-5.57	117.52	120.30
3	C	214	ARG	NE-CZ-NH1	5.56	123.08	120.30
3	A	509	ARG	NE-CZ-NH1	5.53	123.07	120.30
3	B	346	ARG	NE-CZ-NH1	5.52	123.06	120.30
3	B	246	ARG	NE-CZ-NH2	-5.52	117.54	120.30
3	C	815	ARG	NE-CZ-NH1	5.49	123.05	120.30
3	C	577	ARG	NE-CZ-NH1	5.47	123.03	120.30
3	C	319	ARG	NE-CZ-NH1	5.45	123.03	120.30
3	C	466	ARG	NE-CZ-NH1	5.37	122.98	120.30
3	B	559	PHE	CB-CG-CD2	-5.32	117.08	120.80
3	A	466	ARG	NE-CZ-NH1	5.31	122.95	120.30
3	B	646	ARG	NE-CZ-NH1	5.31	122.95	120.30
3	A	78	ARG	NE-CZ-NH1	5.31	122.95	120.30
3	A	1019	ARG	NE-CZ-NH1	5.30	122.95	120.30
3	B	466	ARG	NE-CZ-NH1	5.29	122.94	120.30
3	B	145	TYR	CB-CG-CD2	-5.28	117.83	121.00
3	C	78	ARG	NE-CZ-NH1	5.26	122.93	120.30
3	B	408	ARG	NE-CZ-NH1	5.24	122.92	120.30
3	C	559	PHE	CB-CG-CD2	-5.22	117.15	120.80
3	C	408	ARG	NE-CZ-NH1	5.17	122.89	120.30
3	A	408	ARG	NE-CZ-NH1	5.13	122.86	120.30
3	C	905	ARG	NE-CZ-NH1	5.13	122.86	120.30
3	B	815	ARG	NE-CZ-NH1	5.11	122.86	120.30
1	J	215	ARG	NE-CZ-NH2	-5.11	117.75	120.30
3	A	214	ARG	NE-CZ-NH1	5.09	122.85	120.30
1	I	215	ARG	NE-CZ-NH2	-5.05	117.77	120.30
3	C	328	ARG	NE-CZ-NH2	5.03	122.82	120.30
1	H	215	ARG	NE-CZ-NH2	-5.03	117.79	120.30
3	A	328	ARG	NE-CZ-NH1	5.01	122.81	120.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	246	ARG	Sidechain
3	A	655	HIS	Sidechain
3	A	79	PHE	Sidechain
3	B	246	ARG	Sidechain

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Mol	Chain	Res	Type	Group
3	B	660	TYR	Sidechain
1	H	98	ARG	Sidechain
1	I	98	ARG	Sidechain
1	J	98	ARG	Sidechain

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	H	1607	1580	1579	1	0
1	I	1607	1580	1579	1	0
1	J	1607	1580	1579	1	0
2	L	1591	1526	1526	2	0
2	M	1591	1526	1526	2	0
2	N	1591	1526	1526	2	0
3	A	8344	8142	8136	1	0
3	B	8344	8142	8136	3	0
3	C	8344	8142	8136	1	0
All	All	34626	33744	33723	14	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 0.

All (14) 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:M:154:ALA:HB3	2:M:159:VAL:HG21	1.89	0.54
2:N:154:ALA:HB3	2:N:159:VAL:HG21	1.89	0.53
2:L:154:ALA:HB3	2:L:159:VAL:HG21	1.89	0.53
3:C:599:THR:HG22	3:C:601:GLY:H	1.77	0.50
1:J:98:ARG:HD3	1:J:105:PHE:CE1	2.47	0.50
1:H:98:ARG:HD3	1:H:105:PHE:CE1	2.47	0.49
1:I:98:ARG:HD3	1:I:105:PHE:CE1	2.47	0.49
2:M:154:ALA:HB1	2:M:192:HIS:CG	2.48	0.49
2:N:154:ALA:HB1	2:N:192:HIS:CG	2.48	0.49
3:B:69:HIS:CE1	3:B:77:LYS:HG2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:154:ALA:HB1	2:L:192:HIS:CG	2.48	0.48
3:A:1083:HIS:CE1	3:A:1137:VAL:H	2.33	0.47
3:B:590:CYS:HA	3:B:592:PHE:CZ	2.55	0.41
3:B:227:VAL:HG22	3:B:228:ASP:H	1.86	0.40

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	H	207/448 (46%)	194 (94%)	13 (6%)	0	100	100
1	I	207/448 (46%)	194 (94%)	13 (6%)	0	100	100
1	J	207/448 (46%)	194 (94%)	13 (6%)	0	100	100
2	L	210/216 (97%)	201 (96%)	9 (4%)	0	100	100
2	M	210/216 (97%)	201 (96%)	9 (4%)	0	100	100
2	N	210/216 (97%)	201 (96%)	9 (4%)	0	100	100
3	A	1054/1208 (87%)	978 (93%)	74 (7%)	2 (0%)	47	76
3	B	1054/1208 (87%)	986 (94%)	67 (6%)	1 (0%)	51	80
3	C	1054/1208 (87%)	981 (93%)	71 (7%)	2 (0%)	47	76
All	All	4413/5616 (79%)	4130 (94%)	278 (6%)	5 (0%)	54	80

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	158	ARG
3	A	158	ARG
3	B	744	GLY
3	A	594	GLY
3	C	744	GLY

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	H	180/396 (46%)	179 (99%)	1 (1%)	86	95
1	I	180/396 (46%)	179 (99%)	1 (1%)	86	95
1	J	180/396 (46%)	179 (99%)	1 (1%)	86	95
2	L	182/186 (98%)	177 (97%)	5 (3%)	44	75
2	M	182/186 (98%)	177 (97%)	5 (3%)	44	75
2	N	182/186 (98%)	177 (97%)	5 (3%)	44	75
3	A	932/1053 (88%)	918 (98%)	14 (2%)	65	86
3	B	932/1053 (88%)	920 (99%)	12 (1%)	69	88
3	C	932/1053 (88%)	921 (99%)	11 (1%)	71	89
All	All	3882/4905 (79%)	3827 (99%)	55 (1%)	68	87

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	3	GLN
2	L	16	LYS
2	L	77	THR
2	L	83	THR
2	L	175	LYS
2	L	196	SER
3	A	61	ASN
3	A	211	ASN
3	A	212	LEU
3	A	215	ASP
3	A	282	ASN
3	A	387	LEU
3	A	388	ASN
3	A	439	ASN
3	A	557	LYS
3	A	617	CYS
3	A	703	ASN
3	A	973	ILE

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Mol	Chain	Res	Type
3	A	1051	SER
3	A	1072	GLU
3	B	97	LYS
3	B	175	PHE
3	B	387	LEU
3	B	439	ASN
3	B	544	ASN
3	B	703	ASN
3	B	878	LEU
3	B	977	LEU
3	B	1004	LEU
3	B	1051	SER
3	B	1072	GLU
3	B	1116	THR
3	C	125	ASN
3	C	212	LEU
3	C	215	ASP
3	C	387	LEU
3	C	388	ASN
3	C	439	ASN
3	C	535	LYS
3	C	886	TRP
3	C	1051	SER
3	C	1072	GLU
3	C	1135	ASN
1	J	3	GLN
2	M	16	LYS
2	M	77	THR
2	M	83	THR
2	M	175	LYS
2	M	196	SER
1	I	3	GLN
2	N	16	LYS
2	N	77	THR
2	N	83	THR
2	N	175	LYS
2	N	196	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	354	ASN

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Mol	Chain	Res	Type
3	B	354	ASN
3	B	787	GLN
3	B	925	ASN
3	C	354	ASN

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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

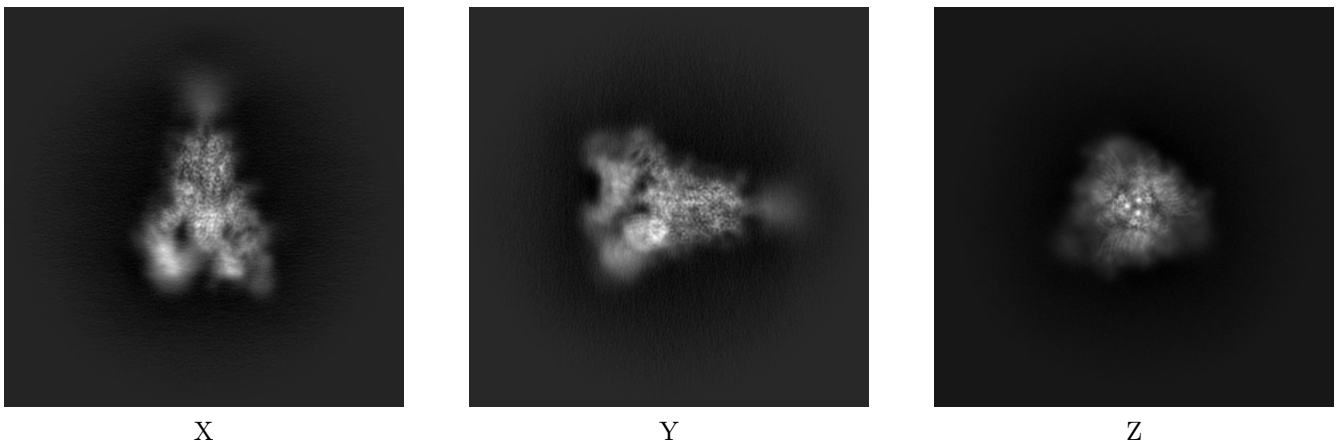
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22997. These allow visual inspection of the internal detail of the map and identification of artifacts.

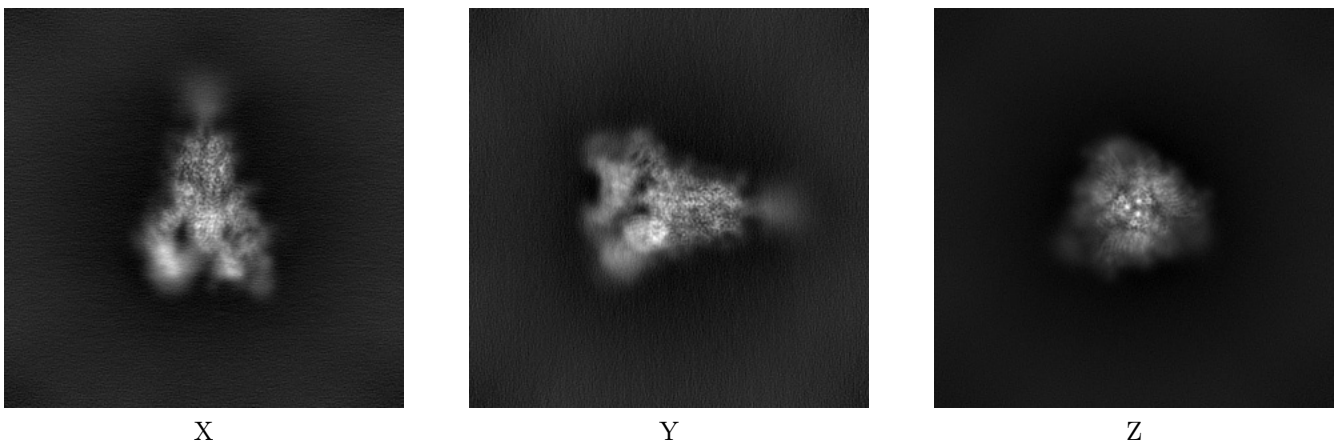
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



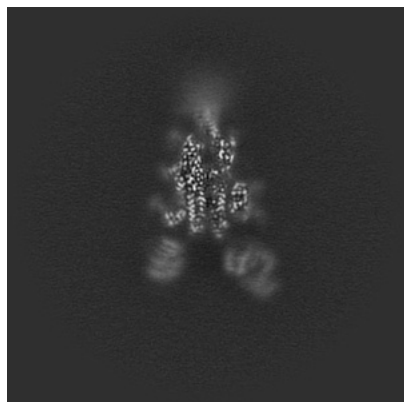
6.1.2 Raw map



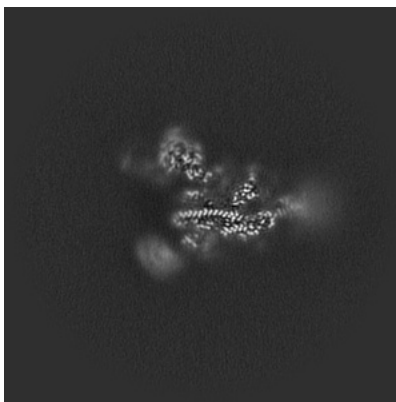
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

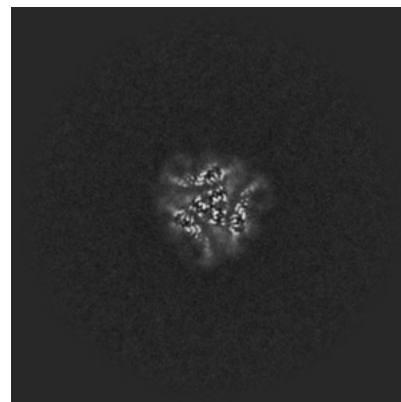
6.2.1 Primary map



X Index: 150

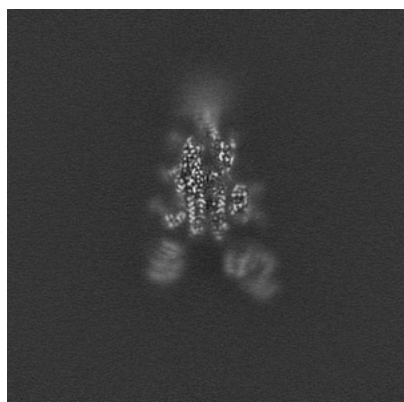


Y Index: 150

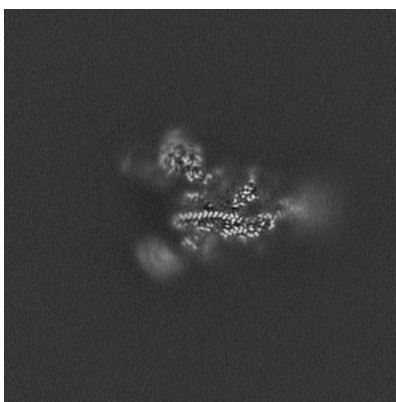


Z Index: 150

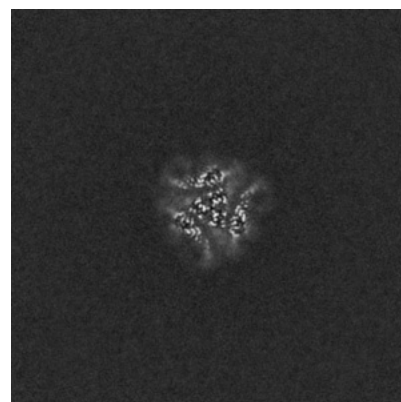
6.2.2 Raw map



X Index: 150



Y Index: 150



Z Index: 150

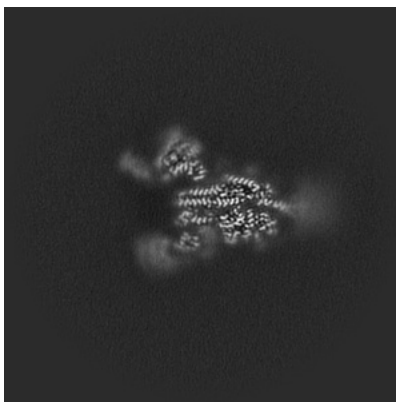
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

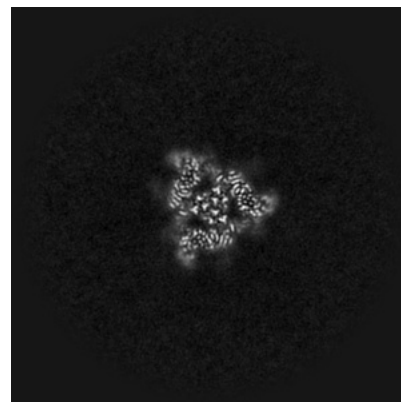
6.3.1 Primary map



X Index: 153

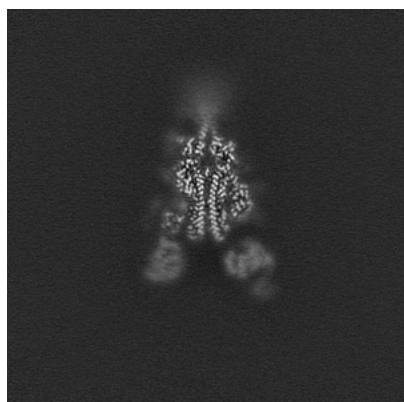


Y Index: 155

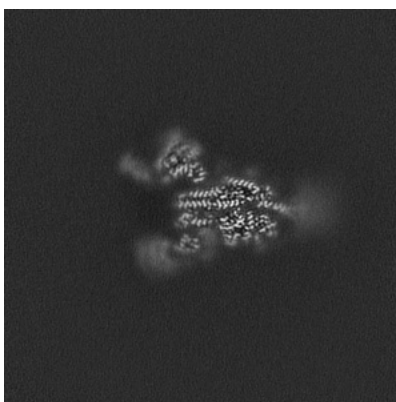


Z Index: 143

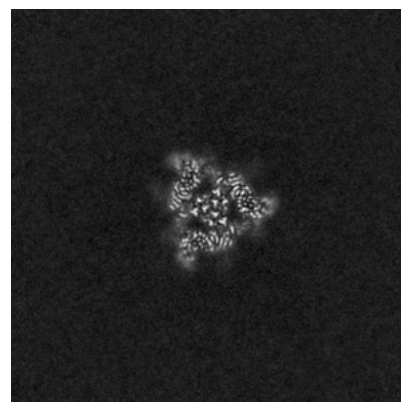
6.3.2 Raw map



X Index: 153



Y Index: 155

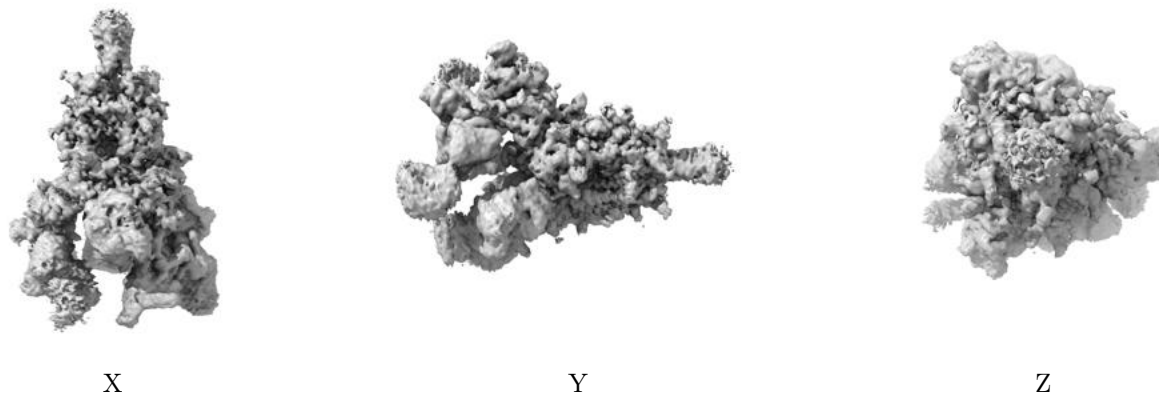


Z Index: 143

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

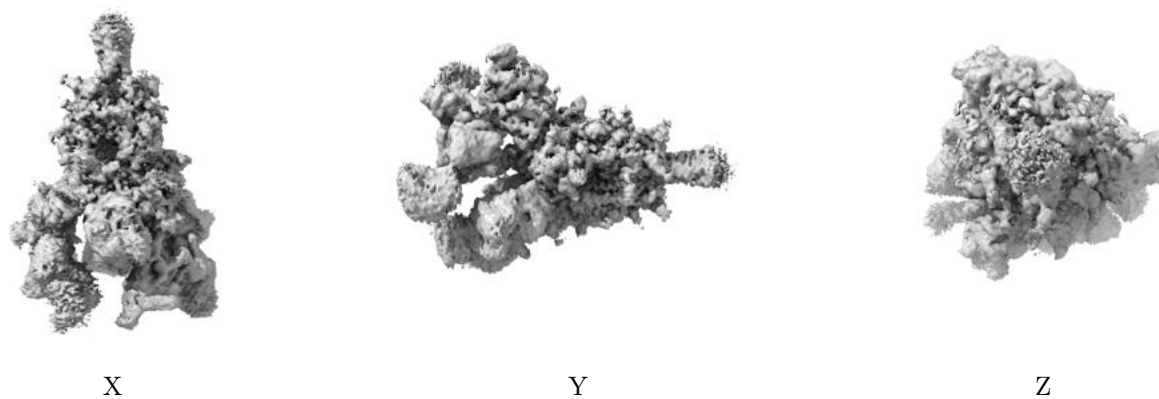
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

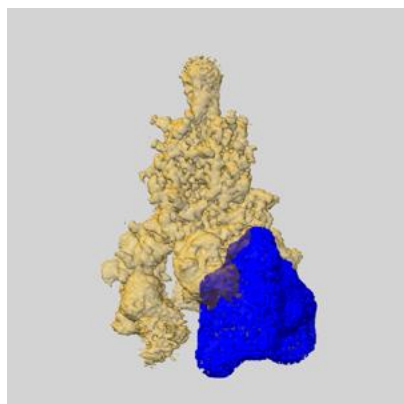
6.5 Mask visualisation [i](#)

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

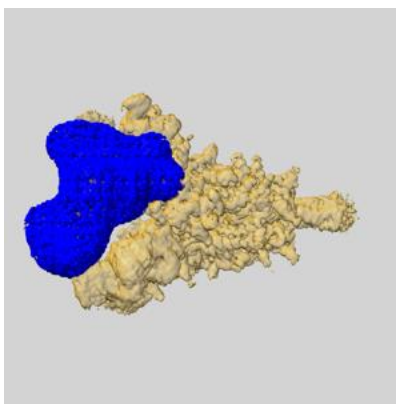
A mask typically either:

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

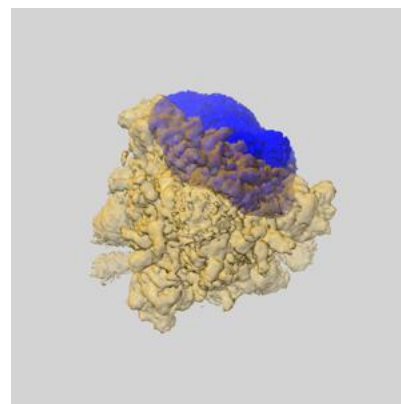
6.5.1 emd_22997_msk_1.map [i](#)



X



Y

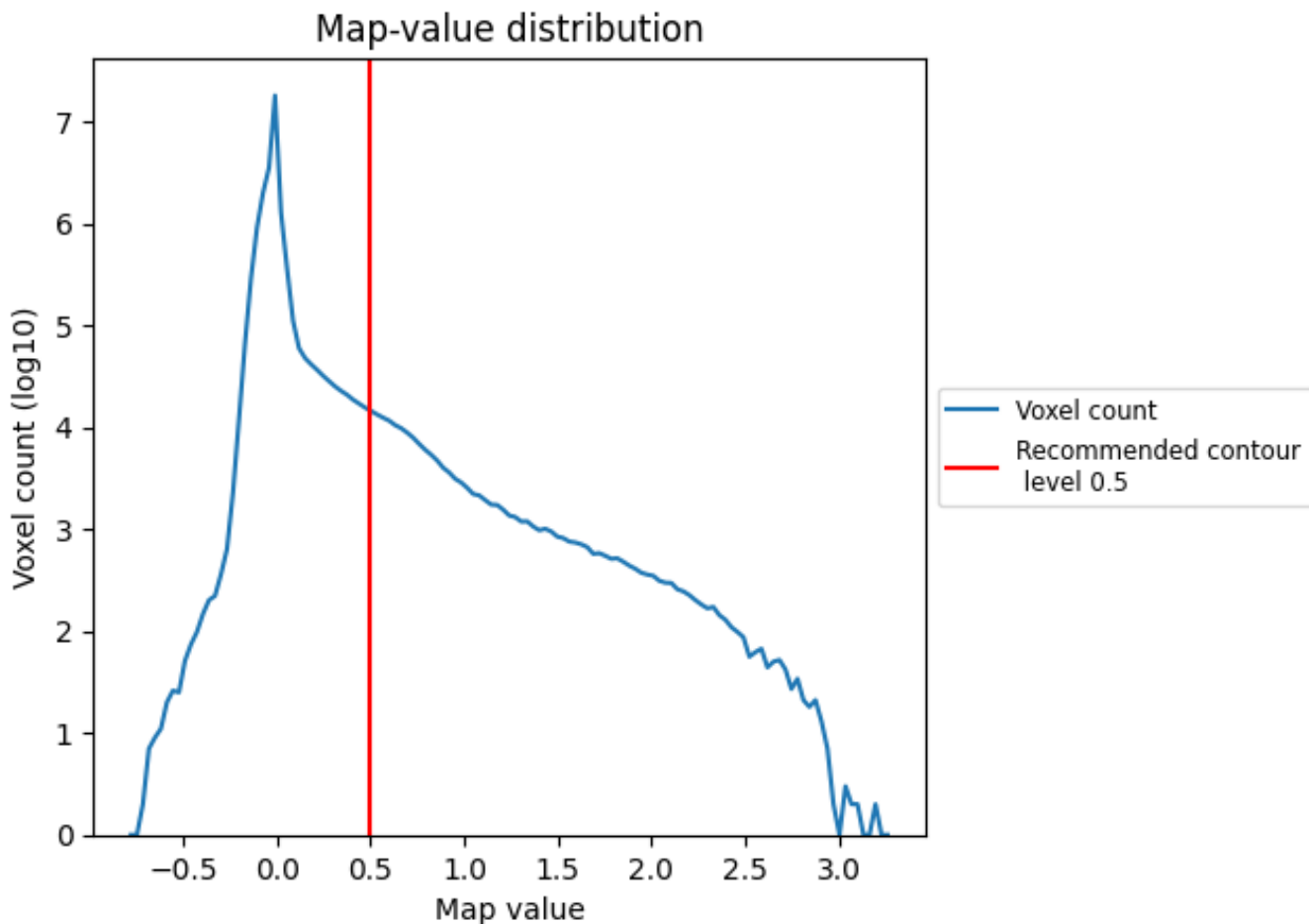


Z

7 Map analysis [i](#)

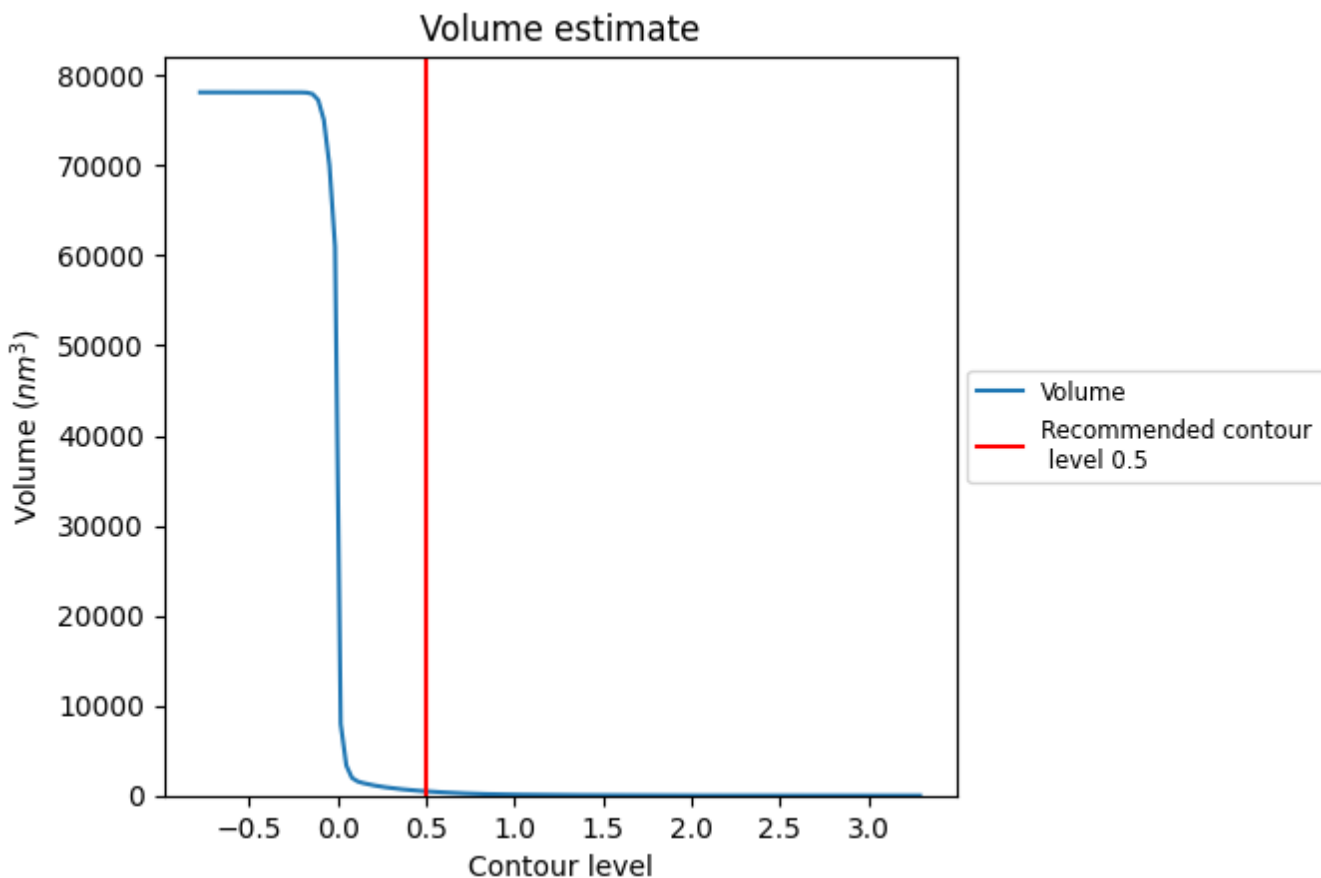
This section contains the results of statistical analysis of the map.

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.

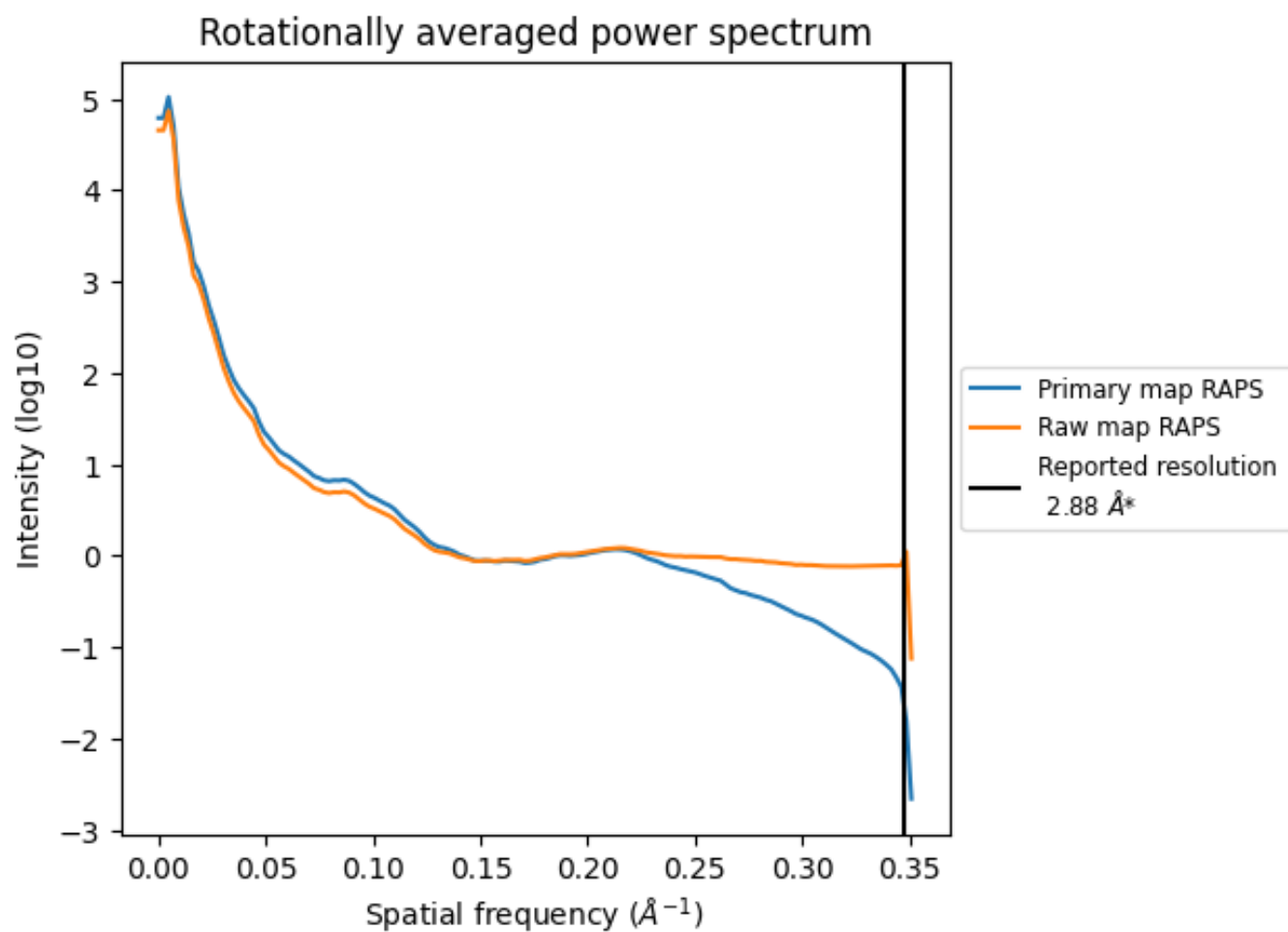
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 473 nm^3 ; this corresponds to an approximate mass of 427 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

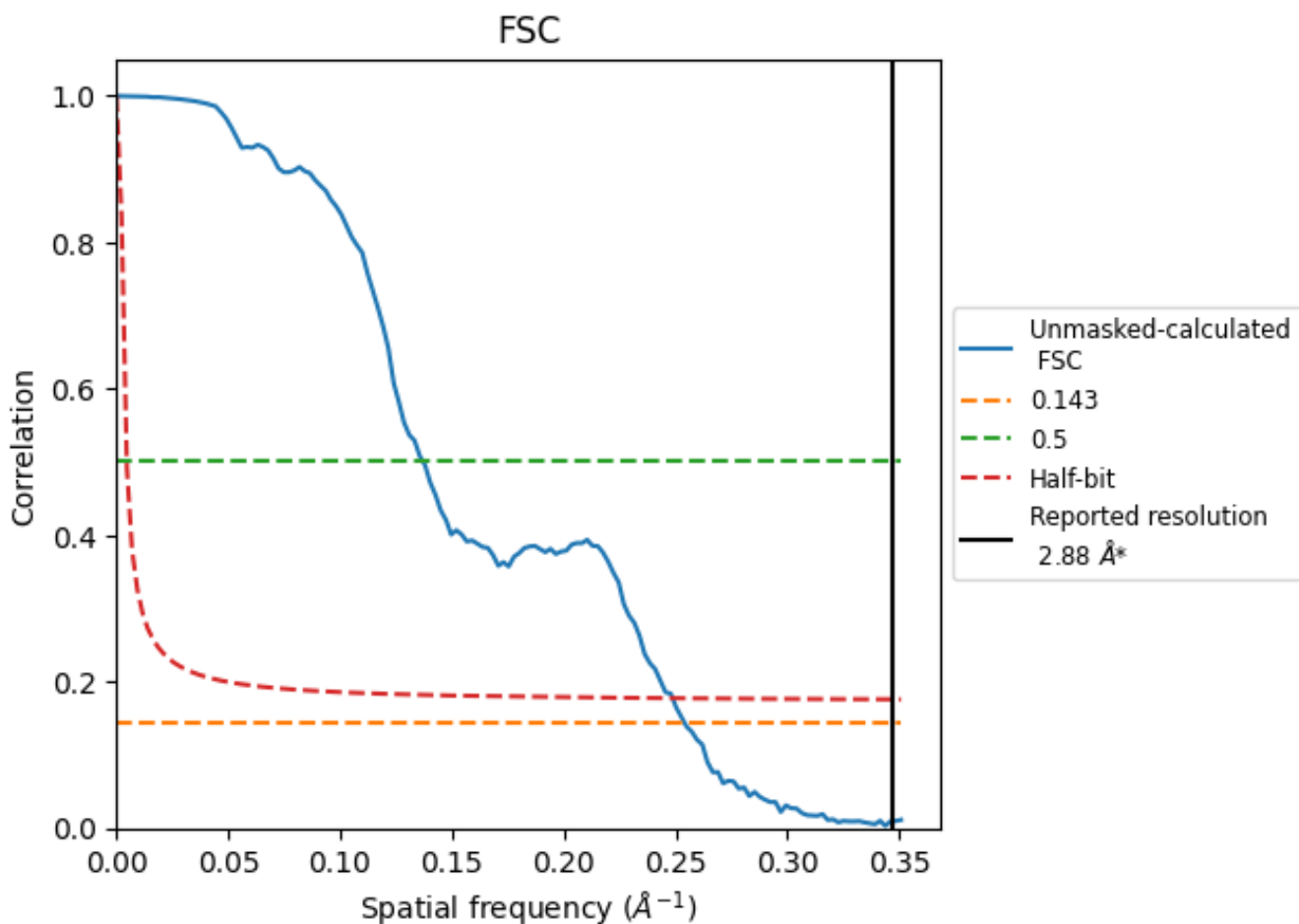


*Reported resolution corresponds to spatial frequency of 0.347 Å⁻¹

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 0.347 Å⁻¹

8.2 Resolution estimates [i](#)

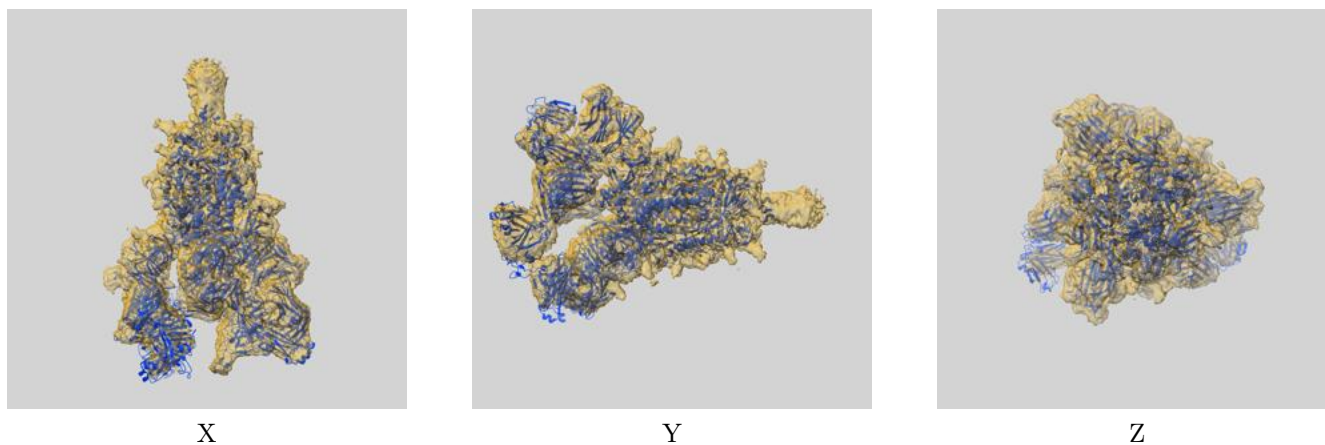
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.88	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.94	7.29	4.02

*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 3.94 differs from the reported value 2.88 by more than 10 %

9 Map-model fit [i](#)

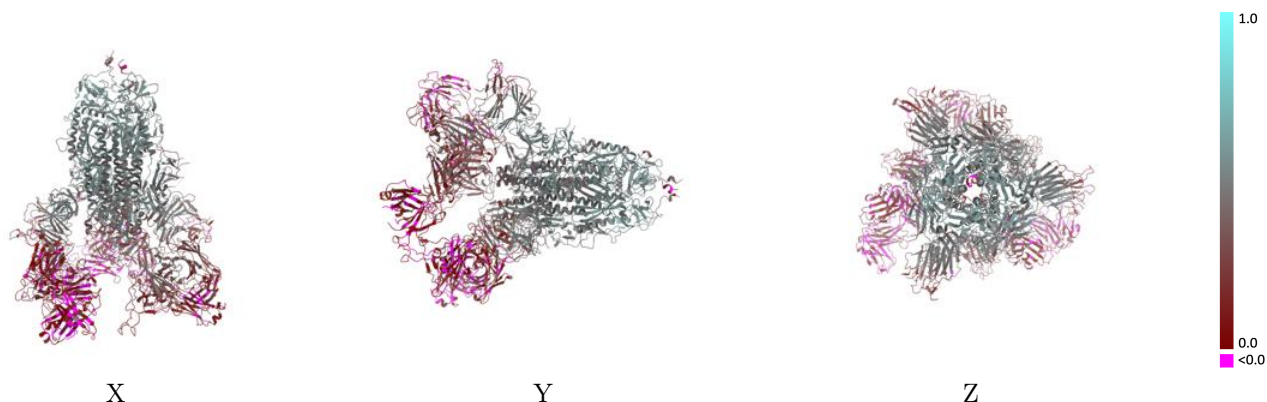
This section contains information regarding the fit between EMDB map EMD-22997 and PDB model 7KQE. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



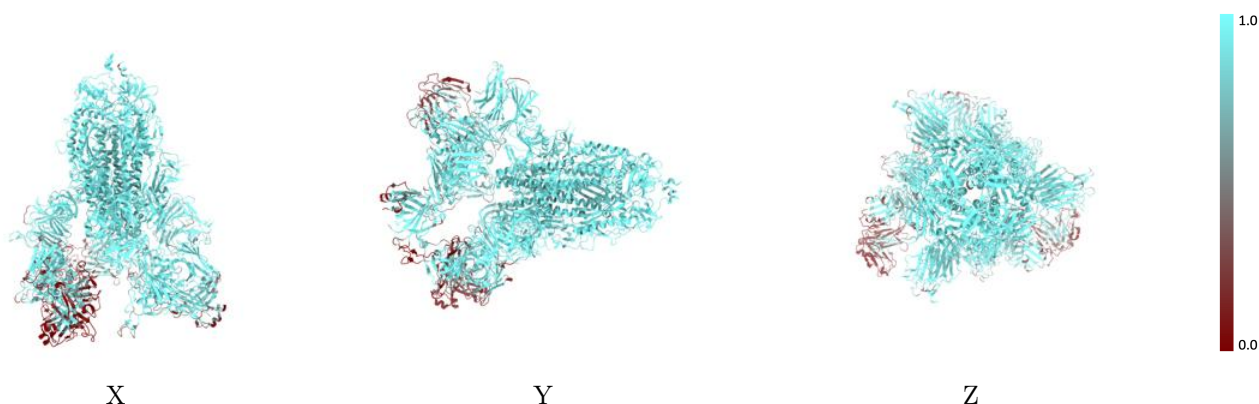
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



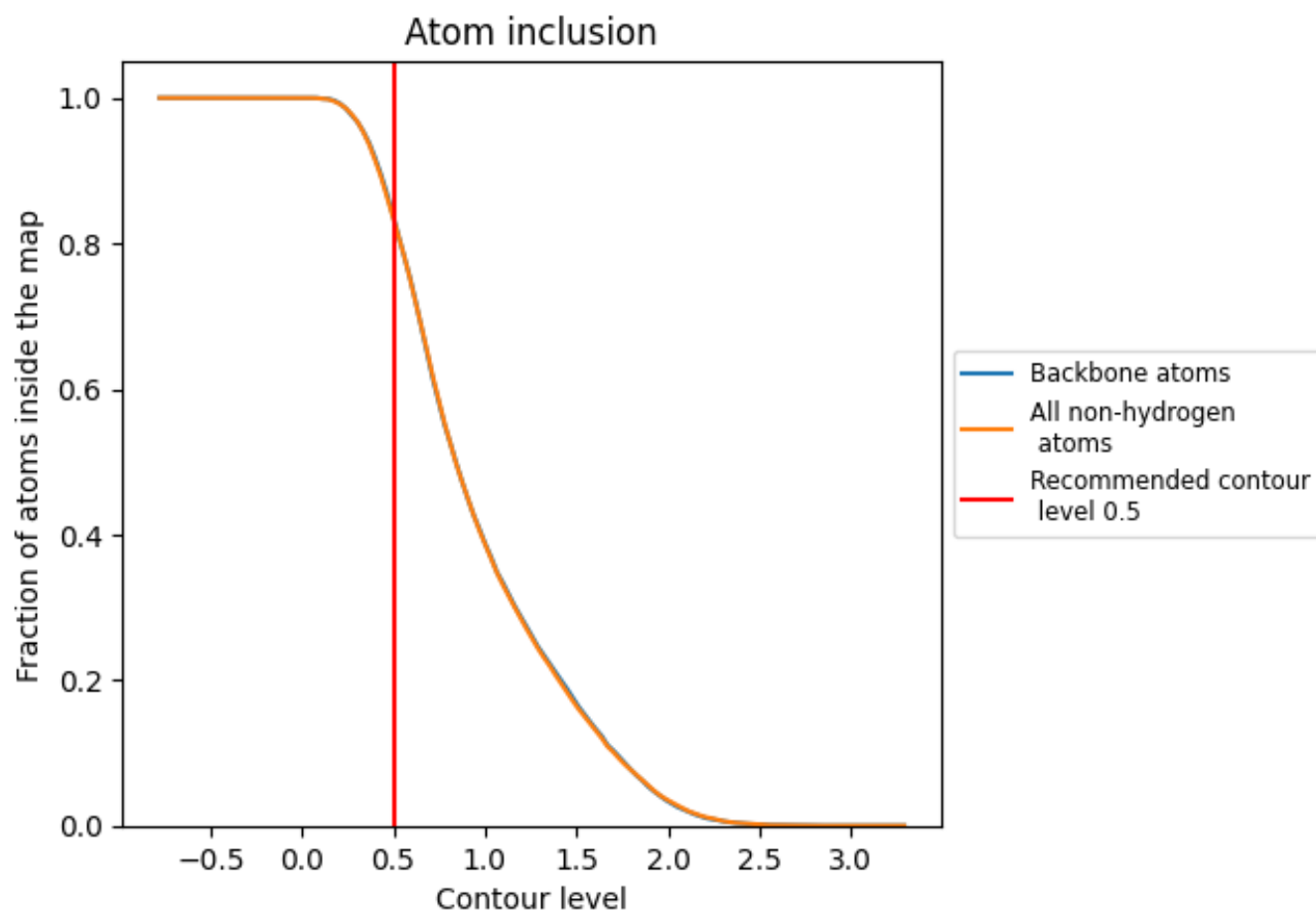
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).





















9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8346	 0.3330
A	 0.9407	 0.4140
B	 0.9222	 0.4280
C	 0.9052	 0.3910
H	 0.8701	 0.2130
I	 0.5887	 0.1110
J	 0.4449	 0.0740
L	 0.8376	 0.2130
M	 0.3994	 0.0480
N	 0.5242	 0.1120

