



wwPDB EM Validation Summary Report ⓘ

Nov 23, 2022 – 02:12 AM EST

PDB ID : 7TKP
EMDB ID : EMD-25977
Title : Yeast ATP synthase State 3catalytic(b) with 10 mM ATP backbone model
Authors : Guo, H.; Rubinstein, J.L.
Deposited on : 2022-01-17
Resolution : 4.60 Å(reported)
Based on initial model : 2HLD

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.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) : 2.31.3

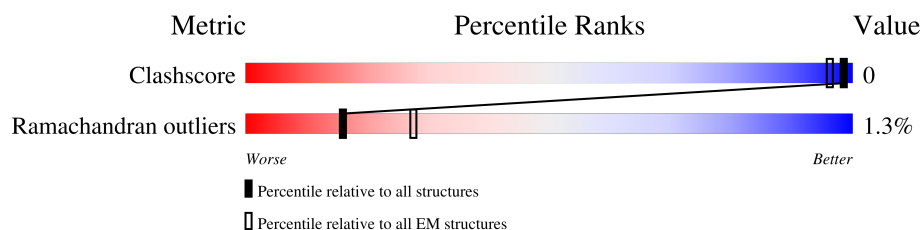
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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.



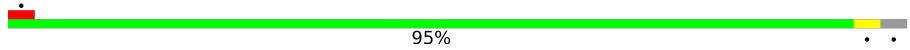
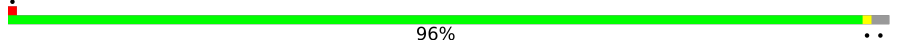
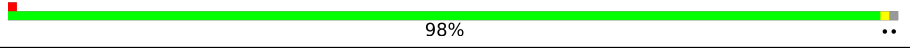
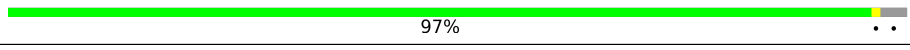
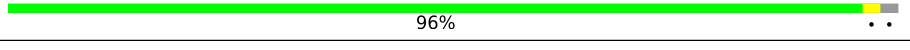
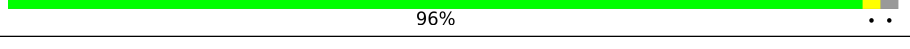
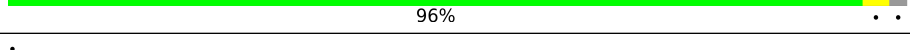
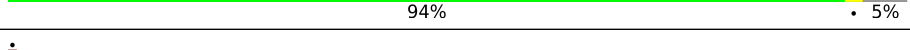
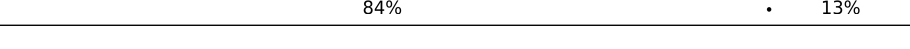
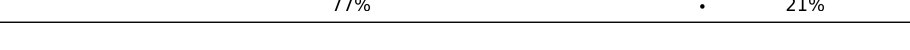
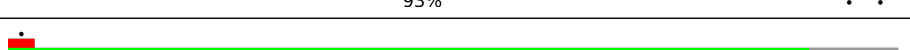



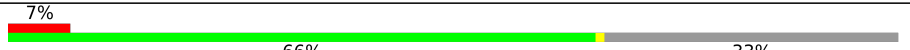



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023

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	0	76	99% .
1	1	76	96% ..
1	2	76	99% .
1	3	76	95% ..
1	4	76	95% ..
1	5	76	95% ..
1	6	76	95% ..
1	7	76	93% ..
1	8	76	96% ..

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Mol	Chain	Length	Quality of chain
1	9	76	 95%
2	A	510	 96%
2	B	510	 98%
2	C	510	 97%
3	D	478	 96%
3	E	478	 96%
3	F	478	 96%
4	G	278	 94% 5%
5	H	138	 84% 13%
6	I	61	 77% 21%
7	O	195	 93%
8	T	249	 90% 10%
9	U	209	 74% 26%
10	V	173	 12% 98%
11	W	95	 17% 84% 5% 11%
12	X	92	 7% 66% 33%
13	Y	59	 7% 61% 37%
14	Z	48	 98%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 20228 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 ATP synthase subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	75	Total	C	N	O	0	0
			300	150	75	75		
1	1	75	Total	C	N	O	0	0
			300	150	75	75		
1	2	75	Total	C	N	O	0	0
			300	150	75	75		
1	3	74	Total	C	N	O	0	0
			296	148	74	74		
1	4	75	Total	C	N	O	0	0
			300	150	75	75		
1	5	75	Total	C	N	O	0	0
			300	150	75	75		
1	6	74	Total	C	N	O	0	0
			296	148	74	74		
1	7	73	Total	C	N	O	0	0
			292	146	73	73		
1	8	75	Total	C	N	O	0	0
			300	150	75	75		
1	9	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 2 is a protein called ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A	499	Total	C	N	O	0	0
			1996	998	499	499		
2	B	507	Total	C	N	O	0	0
			2028	1014	507	507		
2	C	496	Total	C	N	O	0	0
			1984	992	496	496		

- Molecule 3 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	468	Total	C	N	O	0	0
			1872	936	468	468		
3	E	469	Total	C	N	O	0	0
			1876	938	469	469		
3	F	470	Total	C	N	O	0	0
			1880	940	470	470		

- Molecule 4 is a protein called ATP synthase subunit gamma.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	265	Total	C	N	O	0	0
			1060	530	265	265		

- Molecule 5 is a protein called ATP synthase subunit delta.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	120	Total	C	N	O	0	0
			480	240	120	120		

- Molecule 6 is a protein called ATP synthase subunit epsilon.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	48	Total	C	N	O	0	0
			193	96	48	49		

- Molecule 7 is a protein called ATP synthase subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	187	Total	C	N	O	0	0
			748	374	187	187		

- Molecule 8 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	T	224	Total	C	N	O	0	0
			897	448	224	225		

- Molecule 9 is a protein called ATP synthase subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	155	Total	C	N	O	0	0
			620	310	155	155		

- Molecule 10 is a protein called ATP synthase subunit d.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	V	171	Total	C	N	O	0	0
			685	342	171	172		

- Molecule 11 is a protein called ATP synthase subunit f.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	W	85	Total	C	N	O	0	0
			340	170	85	85		

- Molecule 12 is a protein called ATP synthase subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	X	62	Total	C	N	O	0	0
			248	124	62	62		

- Molecule 13 is a protein called ATP synthase subunit J.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Y	37	Total	C	N	O	0	0
			148	74	37	37		

- Molecule 14 is a protein called ATP synthase protein 8.

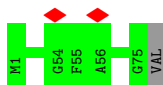
Mol	Chain	Residues	Atoms				AltConf	Trace
14	Z	48	Total	C	N	O	0	0
			193	96	48	49		

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.

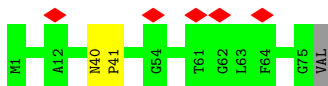
- Molecule 1: ATP synthase subunit 9

Chain 0:  99%



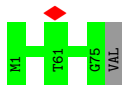
- Molecule 1: ATP synthase subunit 9

Chain 1:  96%



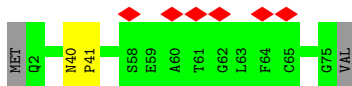
- Molecule 1: ATP synthase subunit 9

Chain 2:  99%



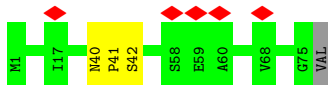
- Molecule 1: ATP synthase subunit 9

Chain 3:  95%

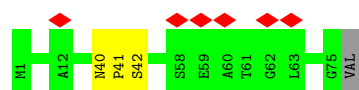


- Molecule 1: ATP synthase subunit 9

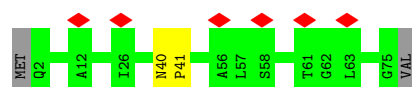
Chain 4:  95%



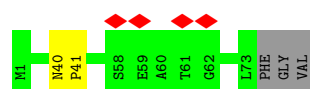
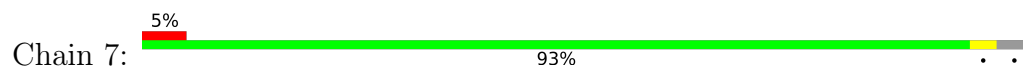
- Molecule 1: ATP synthase subunit 9



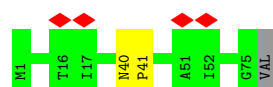
- Molecule 1: ATP synthase subunit 9



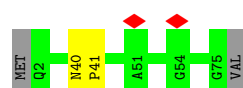
- Molecule 1: ATP synthase subunit 9



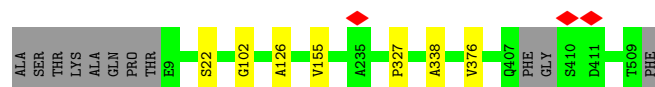
- Molecule 1: ATP synthase subunit 9



- Molecule 1: ATP synthase subunit 9



- Molecule 2: ATP synthase subunit alpha



- Molecule 2: ATP synthase subunit alpha





- Molecule 2: ATP synthase subunit alpha

Chain C: 97%



- Molecule 3: ATP synthase subunit beta

Chain D: 96%



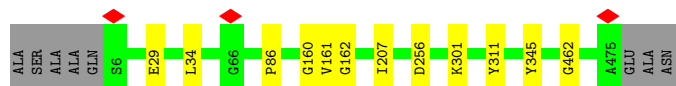
- Molecule 3: ATP synthase subunit beta

Chain E: 96%



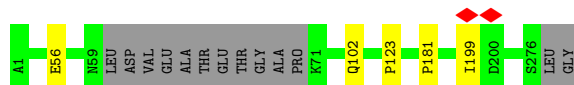
- Molecule 3: ATP synthase subunit beta

Chain F: 96%



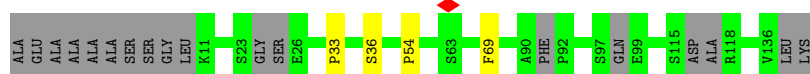
- Molecule 4: ATP synthase subunit gamma

Chain G: 94%



- Molecule 5: ATP synthase subunit delta

Chain H: 84%



- Molecule 6: ATP synthase subunit epsilon

Sequence logo for the 18th position. The y-axis represents information content in bits, ranging from 0 to 1. The x-axis shows amino acids: SER, ALA, TRP, ARG, LYS, ALA, GLY, I8, S23, SER, LEU, LYS, T27, A42, N49, GLY, THR, ALA, A53, K61. The 'I8' position has a high peak for 'I' (Ile) at approximately 0.8 bits. The 'A42' position has a high peak for 'A' (Ala) at approximately 0.8 bits. The 'T27' position has a high peak for 'T' (Thr) at approximately 0.8 bits. The 'S23' position has a high peak for 'S' (Ser) at approximately 0.8 bits. The 'N49' position has a high peak for 'N' (Asn) at approximately 0.8 bits. The 'A53' position has a high peak for 'A' (Ala) at approximately 0.8 bits. The 'K61' position has a high peak for 'K' (Lys) at approximately 0.8 bits. The 'SER' position has a high peak for 'S' (Ser) at approximately 0.8 bits. The 'LEU' position has a high peak for 'L' (Leu) at approximately 0.8 bits. The 'LYS' position has a high peak for 'Y' (Lys) at approximately 0.8 bits. The 'THR' position has a high peak for 'R' (Thr) at approximately 0.8 bits. The 'GLY' position has a high peak for 'G' (Gly) at approximately 0.8 bits. The 'ALA' position has a high peak for 'A' (Ala) at approximately 0.8 bits. The 'TRP' position has a high peak for 'W' (Trp) at approximately 0.8 bits. The 'ARG' position has a high peak for 'R' (Arg) at approximately 0.8 bits. The 'LYS' position has a high peak for 'Y' (Lys) at approximately 0.8 bits. The 'SER' position has a high peak for 'S' (Ser) at approximately 0.8 bits. The 'ALA' position has a high peak for 'A' (Ala) at approximately 0.8 bits. The 'GLY' position has a high peak for 'G' (Gly) at approximately 0.8 bits. The 'I8' position has a high peak for 'I' (Ile) at approximately 0.8 bits. The 'S23' position has a high peak for 'S' (Ser) at approximately 0.8 bits. The 'SER' position has a high peak for 'S' (Ser) at approximately 0.8 bits. The 'LEU' position has a high peak for 'L' (Leu) at approximately 0.8 bits. The 'LYS' position has a high peak for 'Y' (Lys) at approximately 0.8 bits. The 'T27' position has a high peak for 'T' (Thr) at approximately 0.8 bits. The 'A42' position has a high peak for 'A' (Ala) at approximately 0.8 bits. The 'N49' position has a high peak for 'N' (Asn) at approximately 0.8 bits. The 'GLY' position has a high peak for 'G' (Gly) at approximately 0.8 bits. The 'THR' position has a high peak for 'R' (Thr) at approximately 0.8 bits. The 'ALA' position has a high peak for 'A' (Ala) at approximately 0.8 bits. The 'A53' position has a high peak for 'A' (Ala) at approximately 0.8 bits. The 'K61' position has a high peak for 'K' (Lys) at approximately 0.8 bits.










- | | | | | | | | | |
|-----|----|-----|-----|------------|-----|-----|------|------------|
| ALA | P7 | V10 | P51 | H55
L56 | A61 | G83 | D193 | SER
ILE |
|-----|----|-----|-----|------------|-----|-----|------|------------|

- SER
 PRO
 LEU
 ASP
 GLN
 PHE
 GLU
 ILE
 ARG
 THR
 LEU
 PHE
 GLY
 LEU
 GLN
 SER
 PHE
 PHE
 ILE
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 P147
 V207
 F208
 G209
 F210
 V211
 P212
 L213
 H245

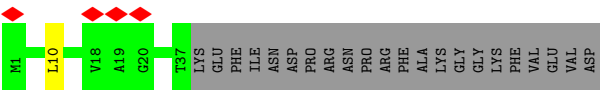
- MET SER SER SER THR PRO PRO GLU LYS GLN THR ASP PRO PRO LYS ALA LYS ALA ASN ASN ILE ILE ASN ALA ILE ILE PRO PRO GLY ASN ASN ILE LEU LEU THR LYS THR THR GLY VAL LEU LEU THR THR SER SER ALA ALA ALA VAL ILE ILE SER ASN ASN GLU LEU THR TYR TYR VAL ILE ILE M53 664 K207 LEU LYS

-
- Figure 1 shows a schematic representation of the 17 amino acid residues of the protein. The residues are arranged in a horizontal bar, with their three-letter codes (SER, LEU, A3, K4, S5, A6, A6, A7, N8, K9, L19, T22, G23, S24, N36, D37, T51, K63, N64, T65, F130, D131, D159, V160, P161, N169, V172, M173) and their corresponding amino acid symbols (S, L, A, K, S, A, A, A, N, K, L, T, G, S, N, D, T, K, N, T, F, D, D, V, P, N, V, M) shown below them. Red diamonds are placed above each residue label.

-

-  **M1**
 **P13**
 **S19**
 **Q35**
 **E41**
 **G46**
 **A49**
 **V58**
 **H62**
 VAL
 ALA
 LYS
 GLU
 GLU
 SER
 GLU
 GLU
 GLY
 GLU
 SER
 SER
 GLU
 PRO
 ILE
 LEU
 GLU
 ASP
 ASP
 TRP
 LEU
 VAL
 LEU
 ASP
 ASP
 ALA
 ALA
 GLU
 GLU
 THR
 LYS
 GLU
 SER
 HIS

● Molecule 13: ATP synthase subunit J



● Molecule 14: ATP synthase protein 8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	16774	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	103896	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.256	Depositor
Minimum map value	-0.706	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.120	Depositor
Recommended contour level	0.66	Depositor
Map size (Å)	344.96, 344.96, 344.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3475, 1.3475, 1.3475	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	0	0.74	0/299	0.69	0/372
1	1	0.73	0/299	0.66	0/372
1	2	0.76	0/299	0.67	0/372
1	3	0.75	0/295	0.68	0/367
1	4	0.73	0/299	0.72	0/372
1	5	0.73	0/299	0.75	0/372
1	6	0.73	0/295	0.70	0/367
1	7	0.74	0/291	0.67	0/362
1	8	0.74	0/299	0.72	0/372
1	9	0.73	0/295	0.67	0/367
2	A	0.91	0/1994	0.91	0/2489
2	B	0.92	0/2027	0.90	1/2532 (0.0%)
2	C	0.92	0/1982	0.93	1/2474 (0.0%)
3	D	0.92	0/1871	0.97	1/2337 (0.0%)
3	E	0.93	0/1875	0.94	2/2342 (0.1%)
3	F	0.92	0/1879	0.96	3/2347 (0.1%)
4	G	0.85	0/1058	0.82	1/1319 (0.1%)
5	H	0.88	0/475	1.11	1/585 (0.2%)
6	I	0.78	0/190	0.95	0/231
7	O	0.89	0/747	0.94	0/932
8	T	0.78	0/896	0.74	0/1117
9	U	0.72	0/619	0.58	0/772
10	V	0.76	0/684	0.80	0/852
11	W	0.75	0/339	0.86	0/422
12	X	0.80	0/247	0.94	0/307
13	Y	0.73	0/147	0.78	0/182
14	Z	0.76	0/192	0.72	0/237
All	All	0.87	0/20192	0.88	10/25172 (0.0%)

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	1	0	1
1	3	0	1
1	4	0	1
1	5	0	1
1	6	0	1
1	7	0	1
1	8	0	1
1	9	0	1
3	E	0	2
3	F	0	1
5	H	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	29	GLU	C-N-CA	6.06	136.84	121.70
3	F	345	TYR	N-CA-C	-5.48	96.22	111.00
3	F	311	TYR	N-CA-C	-5.38	96.49	111.00
4	G	102	GLN	N-CA-C	-5.21	96.94	111.00
3	D	305	THR	N-CA-C	-5.14	97.13	111.00

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	40	ASN	Peptide
1	3	40	ASN	Peptide
1	4	40	ASN	Peptide
1	5	40	ASN	Peptide
1	6	40	ASN	Peptide

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.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	300	0	95	0	0
1	1	300	0	95	0	0
1	2	300	0	95	0	0
1	3	296	0	91	0	0
1	4	300	0	95	0	0
1	5	300	0	95	0	0
1	6	296	0	91	0	0
1	7	292	0	91	0	0
1	8	300	0	95	0	0
1	9	296	0	91	0	0
2	A	1996	0	570	1	0
2	B	2028	0	580	0	0
2	C	1984	0	567	0	0
3	D	1872	0	537	0	0
3	E	1876	0	537	0	0
3	F	1880	0	538	1	0
4	G	1060	0	277	0	0
5	H	480	0	122	0	0
6	I	193	0	43	0	0
7	O	748	0	205	0	0
8	T	897	0	248	0	0
9	U	620	0	158	0	0
10	V	685	0	173	0	0
11	W	340	0	92	0	0
12	X	248	0	61	0	0
13	Y	148	0	40	0	0
14	Z	193	0	49	0	0
All	All	20228	0	5731	2	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 (2) 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:A:102:GLY:HA3	2:A:126:ALA:H	1.72	0.53
3:F:160:GLY:C	3:F:162:GLY:H	2.22	0.42

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	0	73/76 (96%)	72 (99%)	1 (1%)	0	100	100
1	1	73/76 (96%)	71 (97%)	1 (1%)	1 (1%)	11	47
1	2	73/76 (96%)	72 (99%)	1 (1%)	0	100	100
1	3	72/76 (95%)	69 (96%)	2 (3%)	1 (1%)	11	47
1	4	73/76 (96%)	70 (96%)	1 (1%)	2 (3%)	5	34
1	5	73/76 (96%)	70 (96%)	1 (1%)	2 (3%)	5	34
1	6	72/76 (95%)	70 (97%)	1 (1%)	1 (1%)	11	47
1	7	71/76 (93%)	69 (97%)	1 (1%)	1 (1%)	11	47
1	8	73/76 (96%)	70 (96%)	2 (3%)	1 (1%)	11	47
1	9	72/76 (95%)	70 (97%)	1 (1%)	1 (1%)	11	47
2	A	495/510 (97%)	470 (95%)	20 (4%)	5 (1%)	15	54
2	B	505/510 (99%)	480 (95%)	19 (4%)	6 (1%)	13	50
2	C	492/510 (96%)	474 (96%)	16 (3%)	2 (0%)	34	72
3	D	466/478 (98%)	439 (94%)	20 (4%)	7 (2%)	10	46
3	E	467/478 (98%)	439 (94%)	23 (5%)	5 (1%)	14	52
3	F	468/478 (98%)	438 (94%)	24 (5%)	6 (1%)	12	48
4	G	261/278 (94%)	249 (95%)	8 (3%)	4 (2%)	10	46
5	H	110/138 (80%)	105 (96%)	3 (3%)	2 (2%)	8	42
6	I	42/61 (69%)	38 (90%)	3 (7%)	1 (2%)	6	36
7	O	185/195 (95%)	169 (91%)	10 (5%)	6 (3%)	4	30
8	T	222/249 (89%)	211 (95%)	11 (5%)	0	100	100
9	U	153/209 (73%)	152 (99%)	1 (1%)	0	100	100
10	V	169/173 (98%)	152 (90%)	15 (9%)	2 (1%)	13	50
11	W	83/95 (87%)	68 (82%)	10 (12%)	5 (6%)	1	19
12	X	60/92 (65%)	53 (88%)	6 (10%)	1 (2%)	9	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	Y	35/59 (59%)	32 (91%)	2 (6%)	1 (3%)	4	32
14	Z	46/48 (96%)	40 (87%)	5 (11%)	1 (2%)	6	37
All	All	4984/5321 (94%)	4712 (94%)	208 (4%)	64 (1%)	16	48

5 of 64 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	41	PRO
1	3	41	PRO
1	4	41	PRO
1	5	41	PRO
1	6	41	PRO

5.3.2 Protein sidechains [i](#)

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

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 ⓘ

There are no chain breaks in this entry.

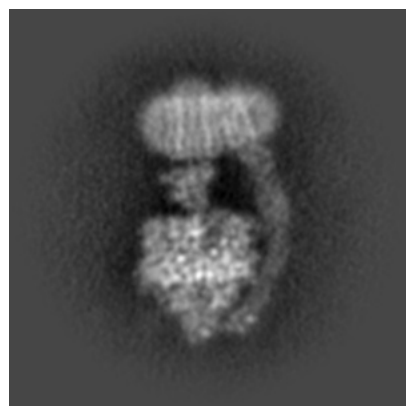
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25977. These allow visual inspection of the internal detail of the map and identification of artifacts.

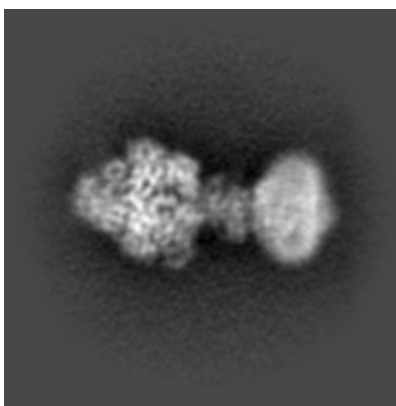
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

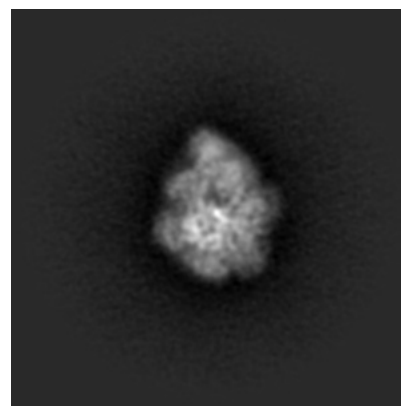
6.1.1 Primary map



X

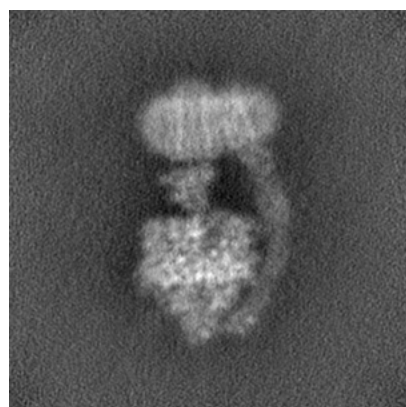


Y

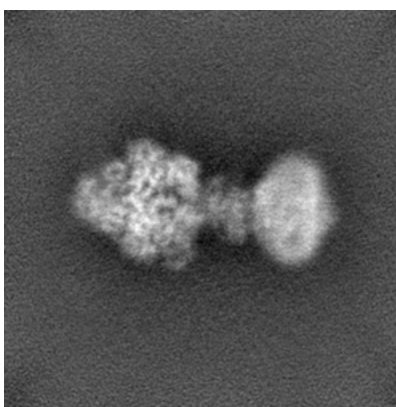


Z

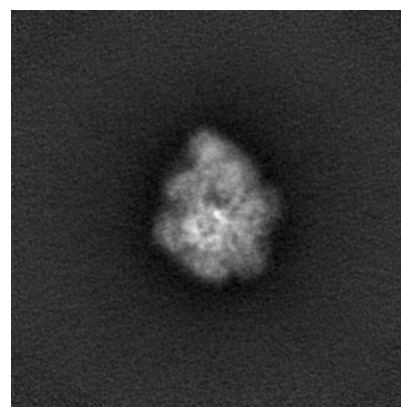
6.1.2 Raw map



X



Y

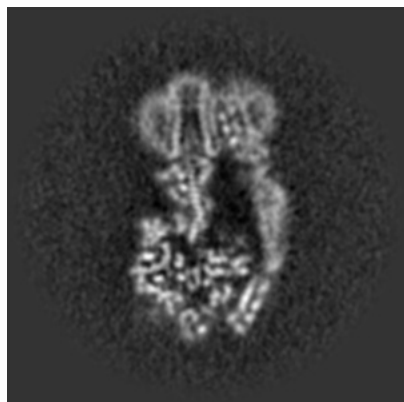


Z

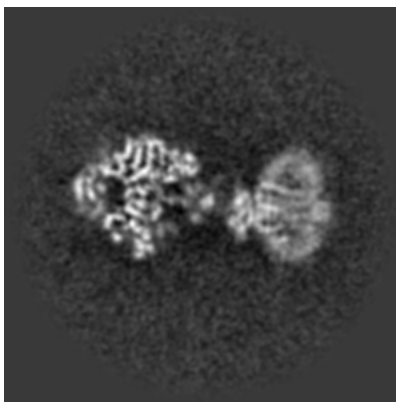
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

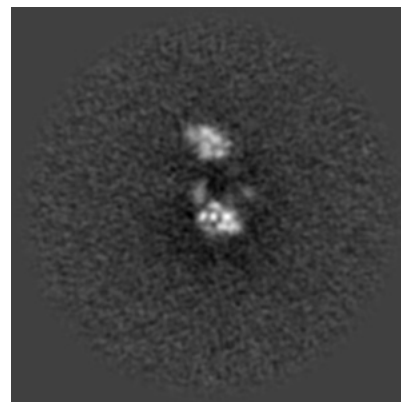
6.2.1 Primary map



X Index: 128

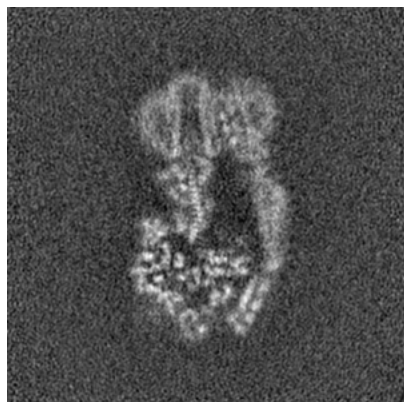


Y Index: 128

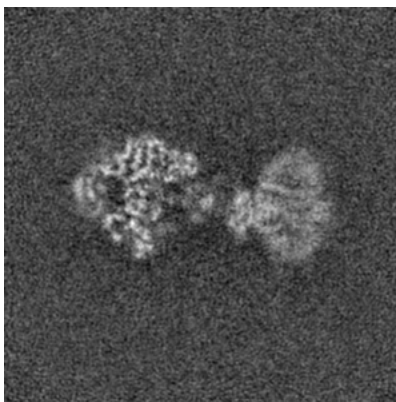


Z Index: 128

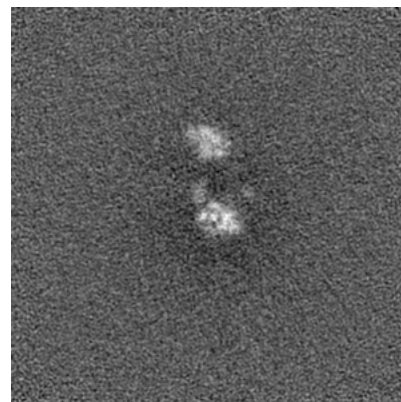
6.2.2 Raw map



X Index: 128



Y Index: 128

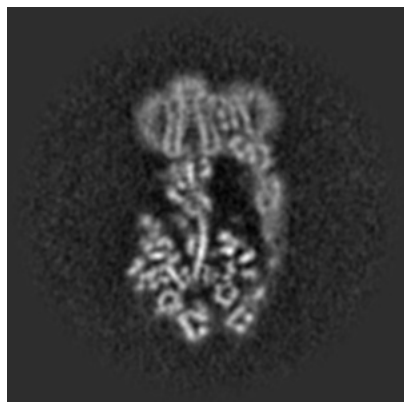


Z Index: 128

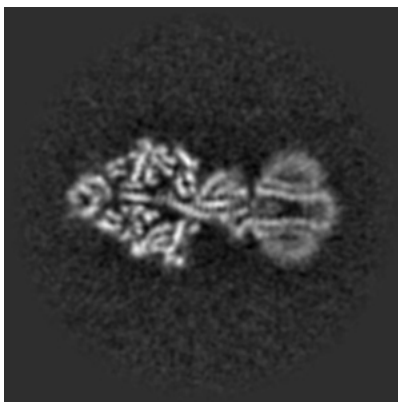
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

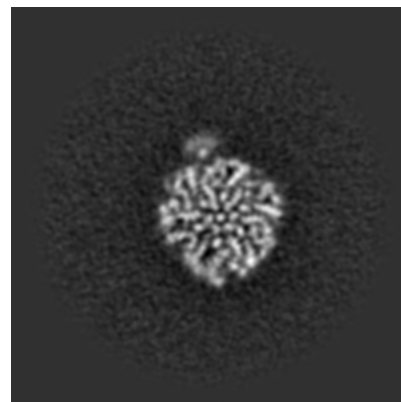
6.3.1 Primary map



X Index: 132

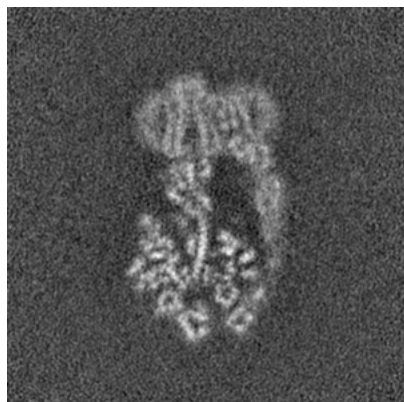


Y Index: 120

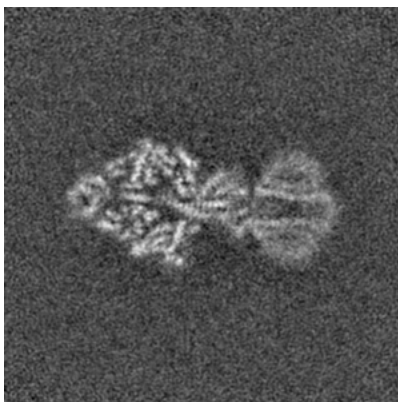


Z Index: 86

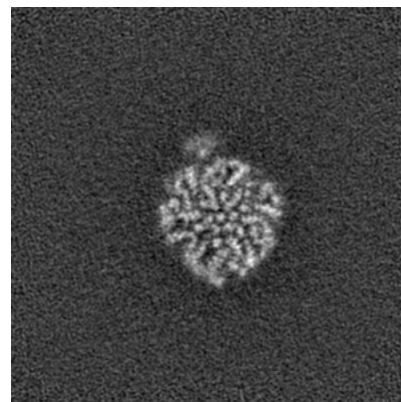
6.3.2 Raw map



X Index: 132



Y Index: 120

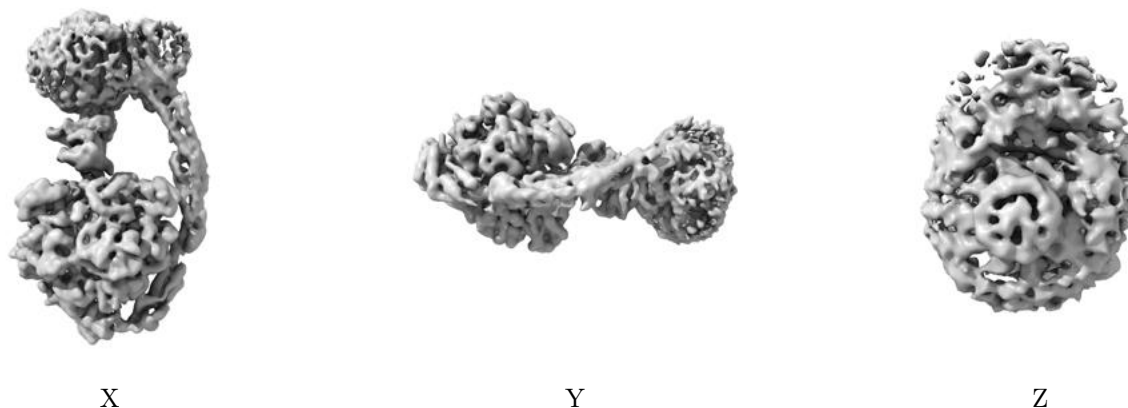


Z Index: 86

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

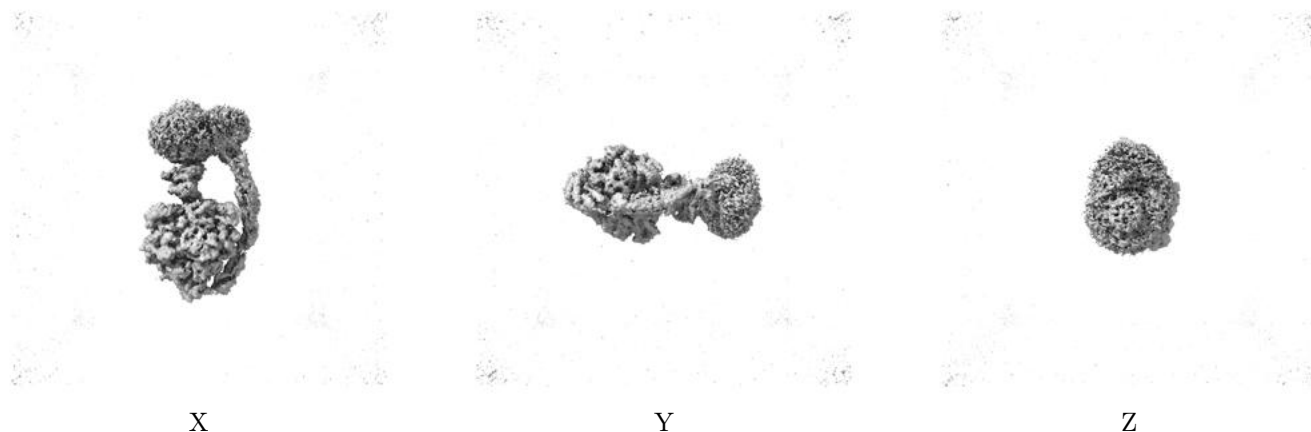
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.66. 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.

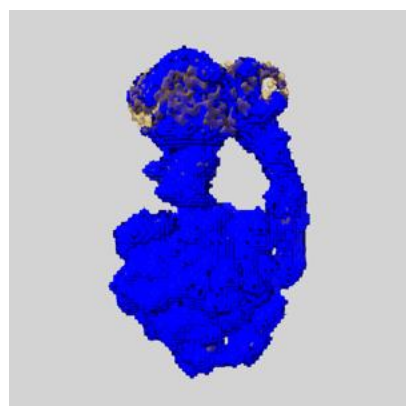
6.5 Mask visualisation [i](#)

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

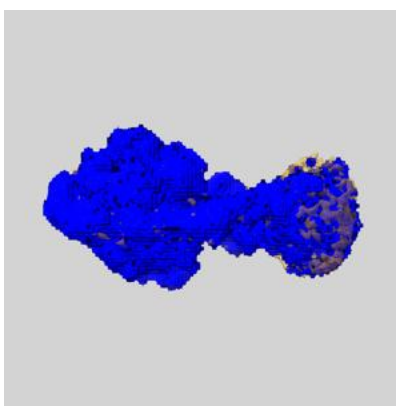
A mask typically either:

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

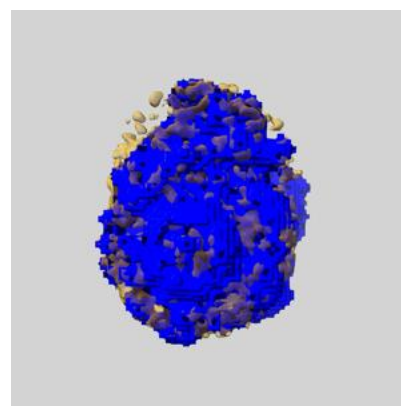
6.5.1 emd_25977_msk_1.map [i](#)



X



Y

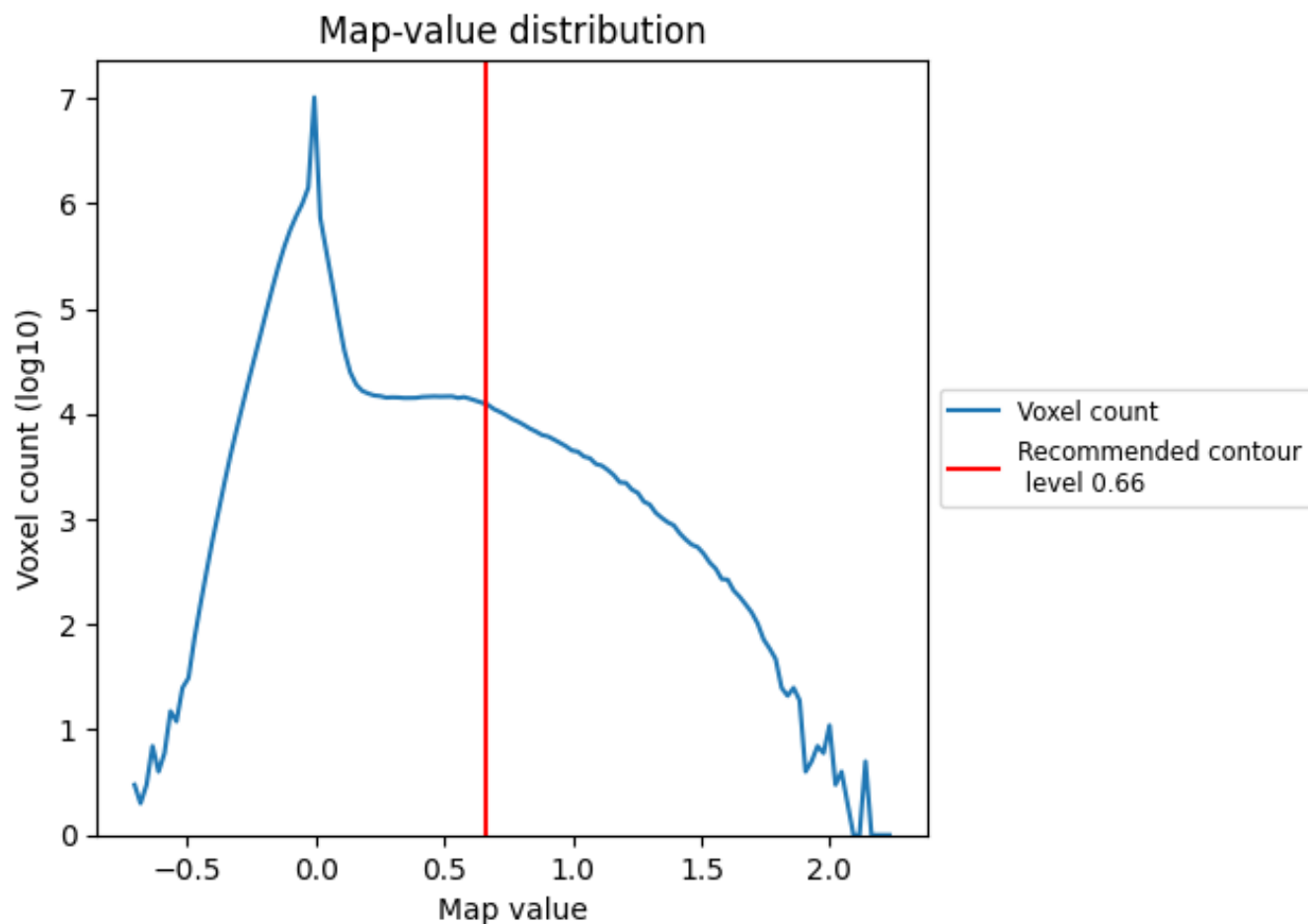


Z

7 Map analysis [i](#)

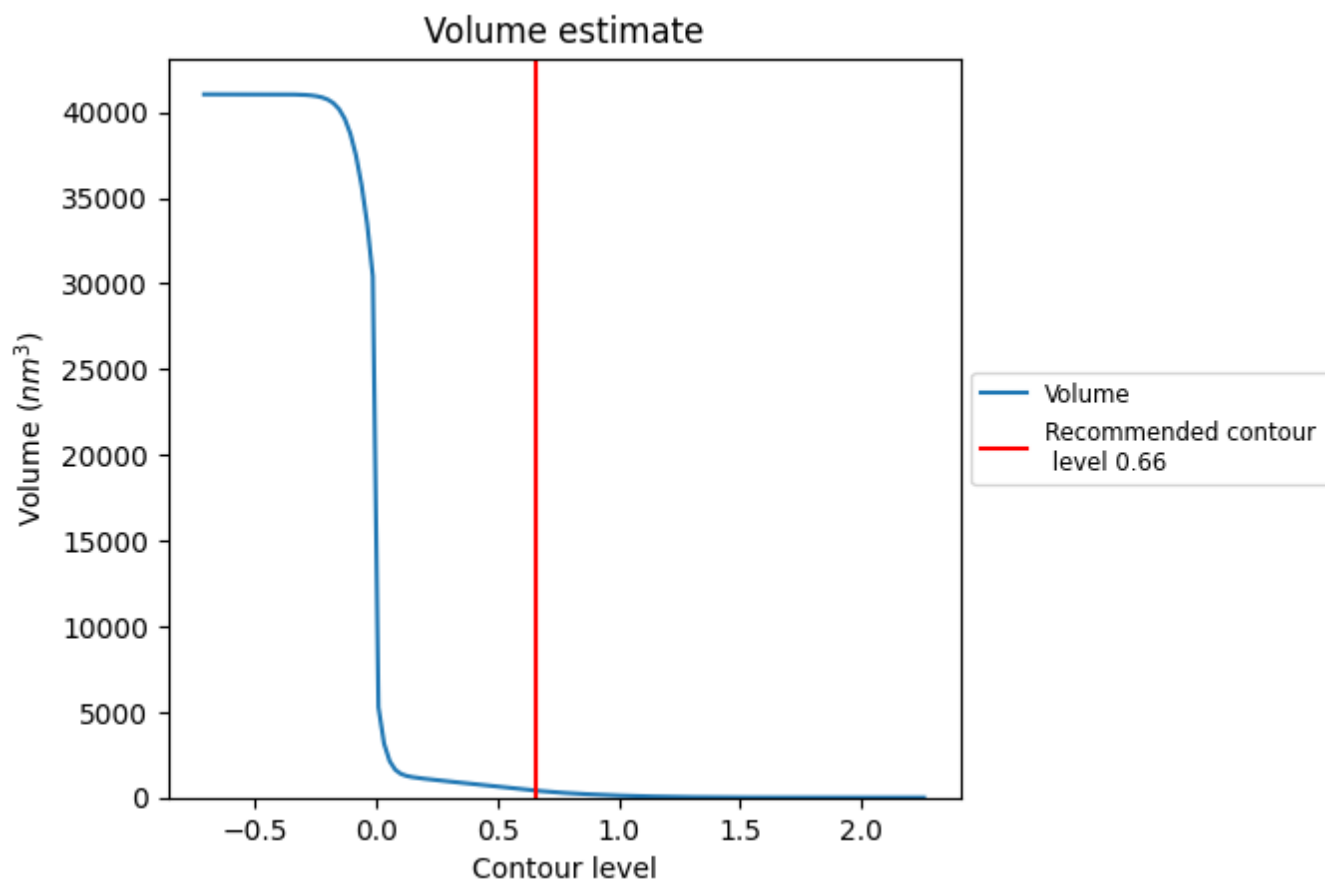
This section contains the results of statistical analysis of the map.

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.

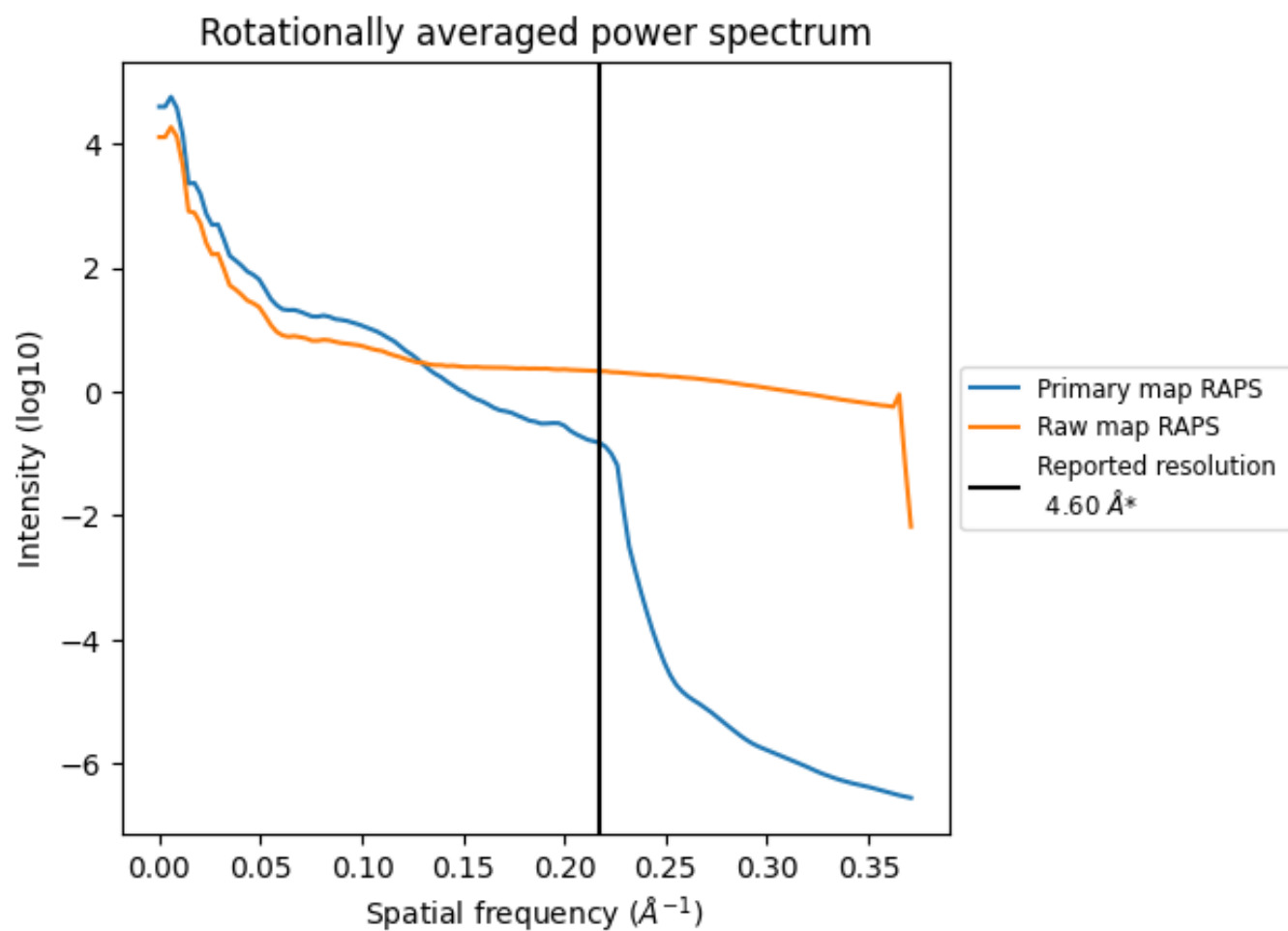
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 405 nm³; this corresponds to an approximate mass of 366 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 ⓘ

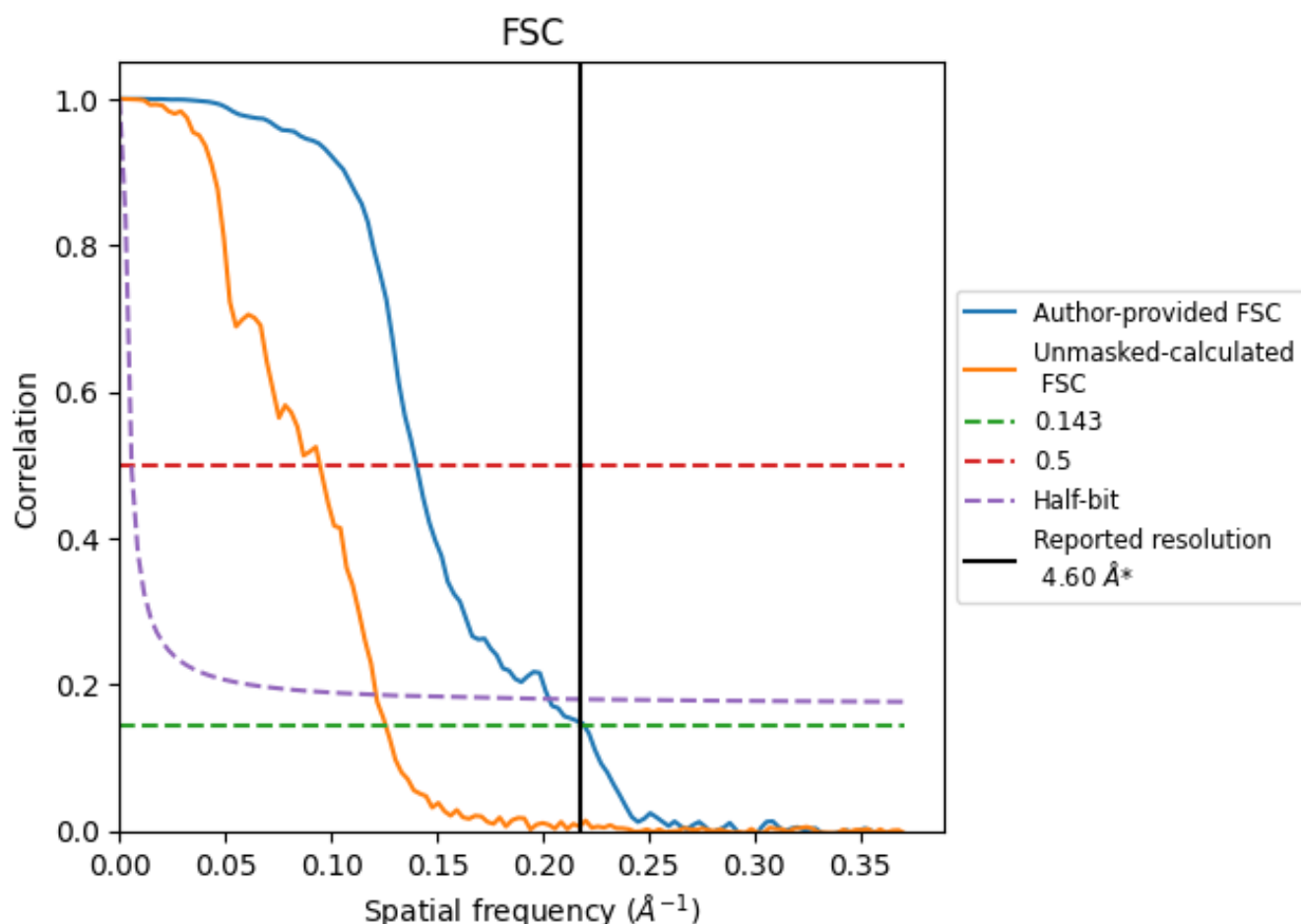


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 \AA^{-1}

8.2 Resolution estimates [i](#)

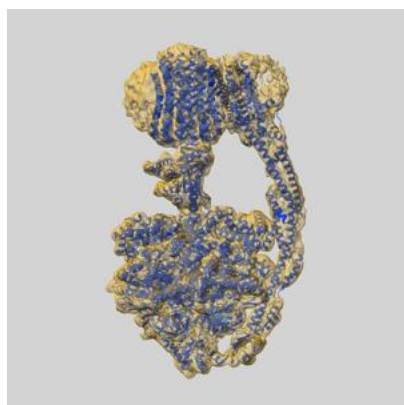
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.55	7.13	4.93
Unmasked-calculated*	7.95	10.57	8.25

*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 7.95 differs from the reported value 4.6 by more than 10 %

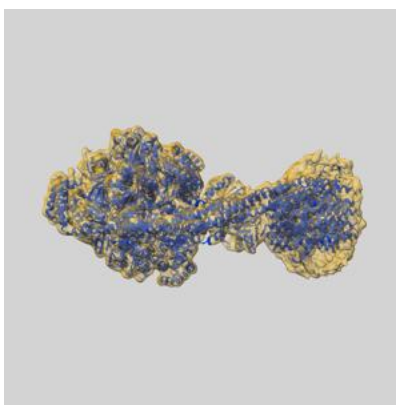
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25977 and PDB model 7TKP. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

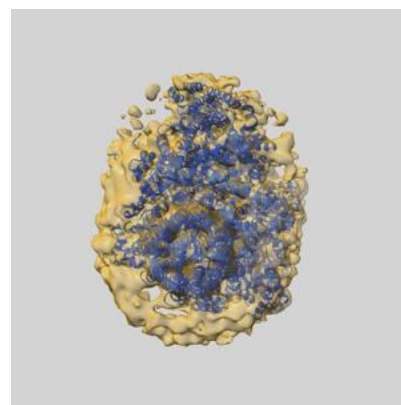
9.1 Map-model overlay [i](#)



X



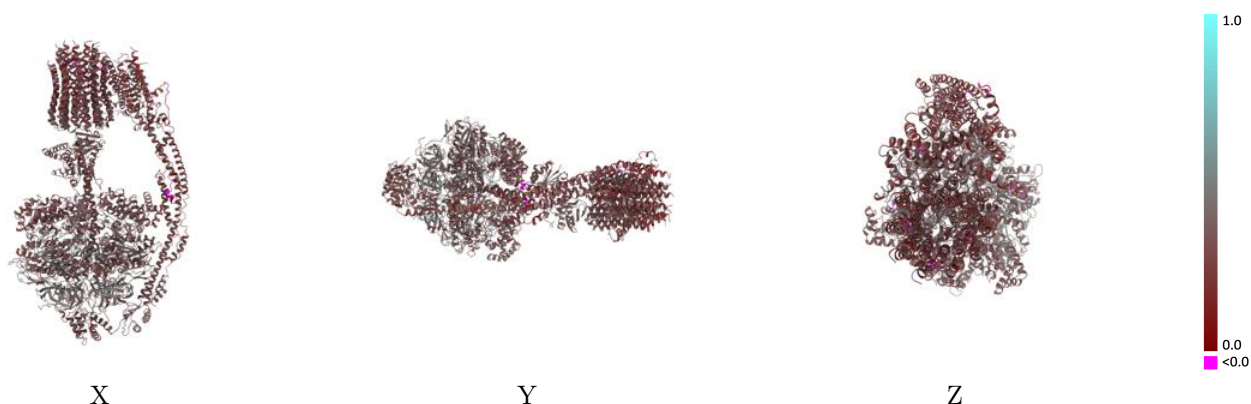
Y



Z

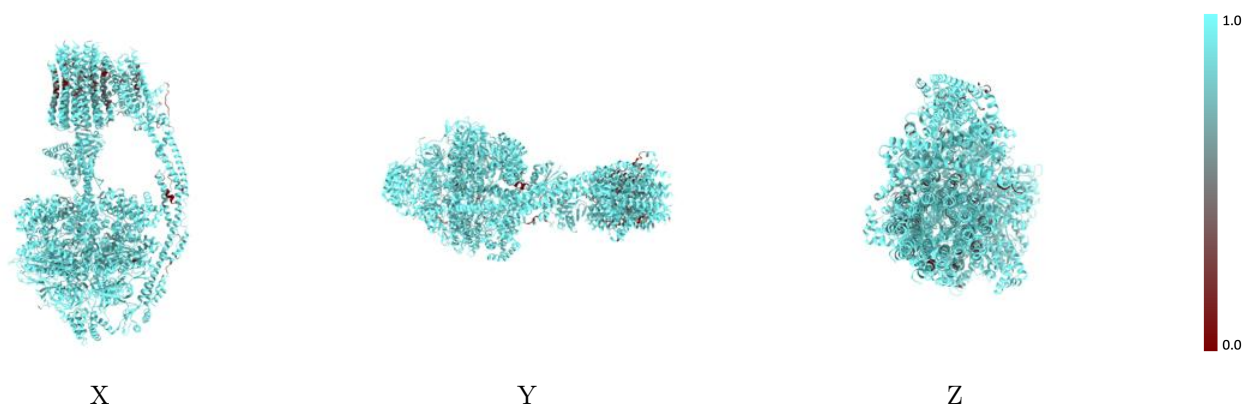
The images above show the 3D surface view of the map at the recommended contour level 0.66 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



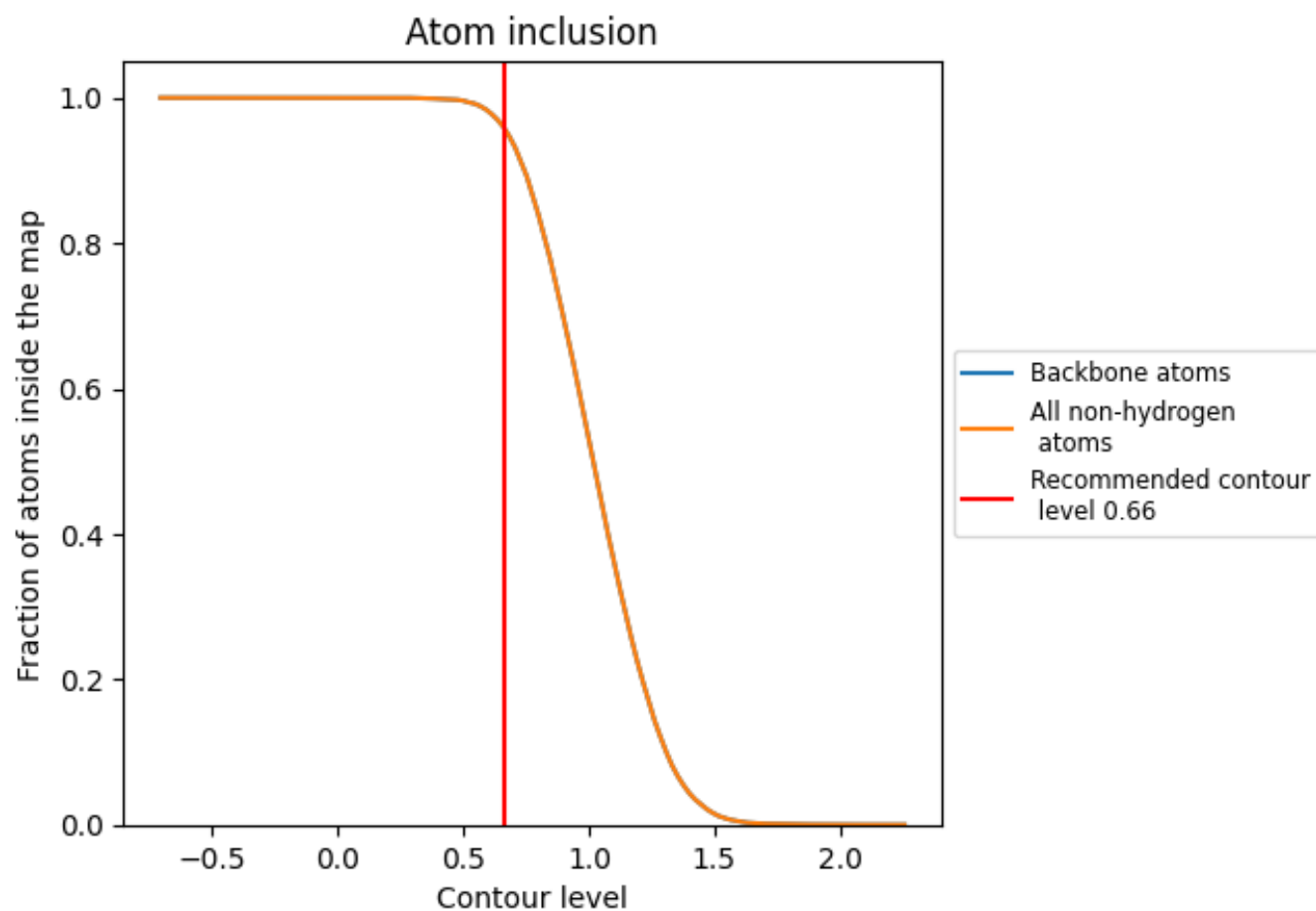
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.66).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.66) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9595	 0.3350
0	 0.8933	 0.2800
1	 0.8600	 0.2640
2	 0.9600	 0.2770
3	 0.8885	 0.2730
4	 0.9000	 0.2760
5	 0.8733	 0.2780
6	 0.9088	 0.2690
7	 0.9110	 0.2730
8	 0.8667	 0.2820
9	 0.9189	 0.2810
A	 0.9805	 0.3660
B	 0.9827	 0.3640
C	 0.9899	 0.3680
D	 0.9861	 0.3650
E	 0.9941	 0.3800
F	 0.9878	 0.3710
G	 0.9792	 0.3330
H	 0.9750	 0.3320
I	 0.9793	 0.3350
O	 0.9947	 0.3350
T	 0.9320	 0.2830
U	 0.9855	 0.2920
V	 0.8496	 0.2430
W	 0.7824	 0.2030
X	 0.8347	 0.3170
Y	 0.8108	 0.2430
Z	 0.9845	 0.2690

