



## Full wwPDB EM Validation Report ⓘ

Mar 5, 2024 – 12:38 AM JST

PDB ID : 8W9Z  
EMDB ID : EMD-37386  
Title : The cryo-EM structure of the Nicotiana tabacum PEP-PAP  
Authors : Wu, X.X.; Zhang, Y.  
Deposited on : 2023-09-06  
Resolution : 3.00 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:

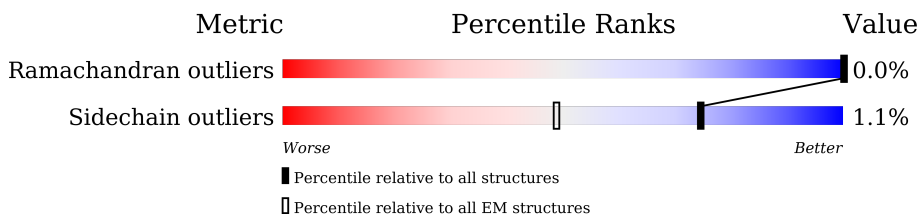
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 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 3.00 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)
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	337	
1	a	337	
2	B	1070	
3	C	688	
4	c	1388	
5	D	892	
6	E	860	
7	F	682	
8	G	266	

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Mol	Chain	Length	Quality of chain
9	H	531	 49% 51%
10	I	486	 77% 23%
11	i	648	 58% 41%
12	J	507	 82% 17%
13	K	331	 64% 35%
14	L	303	 75% 23%
15	M	178	 65% 35%
15	m	178	 61% 39%
16	N	770	 69% 30%
17	O	167	 52% 47%
18	P	143	 73% 27%

## 2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 60525 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	293	Total	C	N	O	S	0	0
			2202	1397	382	411	12		
1	a	318	Total	C	N	O	S	0	0
			2441	1555	424	452	10		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	909	Total	C	N	O	S	0	0
			6820	4328	1216	1253	23		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	592	Total	C	N	O	S	0	0
			4431	2832	783	799	17		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta”.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	c	1174	Total	C	N	O	S	0	0
			8086	5072	1482	1503	29		

- Molecule 5 is a protein called PAP1(pTAC3).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	645	Total	C	N	O	S	0	0
			5088	3228	878	956	26		

- Molecule 6 is a protein called Pentatricopeptide repeat-containing protein At1g74850, chloroplastic-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	700	4534	2823	822	866	23	0	0

- Molecule 7 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	544	4233	2678	756	780	19	0	0

- Molecule 8 is a protein called superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	218	1727	1122	291	309	5	0	0

- Molecule 9 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	260	2110	1338	371	393	8	0	0

- Molecule 10 is a protein called Fructokinase-like 1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	374	2897	1856	512	517	12	0	0

- Molecule 11 is a protein called Fructokinase-like 2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	i	383	2983	1902	508	557	16	0	0

- Molecule 12 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 14-like isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	J	422	3368	2157	578	612	21	0	0

- Molecule 13 is a protein called PAP8(pTAC6).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	214	Total	C	N	O	S	0	0
			1779	1127	307	337	8		

- Molecule 14 is a protein called superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	234	Total	C	N	O	S	0	0
			1475	943	261	270	1		

- Molecule 15 is a protein called Thioredoxin-like protein CITRX1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	116	Total	C	N	O	S	0	0
			935	598	150	180	7		
15	m	109	Total	C	N	O	S	0	0
			851	545	135	164	7		

- Molecule 16 is a protein called UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	537	Total	C	N	O	S	0	0
			2982	1814	579	583	6		

- Molecule 17 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 7-like isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	88	Total	C	N	O	S	0	0
			692	434	124	131	3		

- Molecule 18 is a protein called PAP13(pTAC18).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	105	Total	C	N	O	S	0	0
			887	576	148	158	5		

- Molecule 19 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	B	1	Total	Zn	0
			1	1	

- Molecule 20 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
20	C	1	Total 1	Mg 1	0

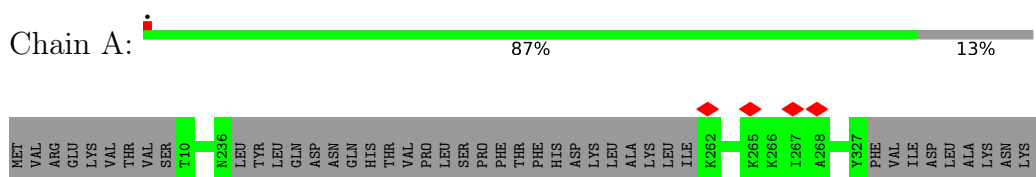
- Molecule 21 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		AltConf
21	G	1	Total 1	Fe 1	0
21	L	1	Total 1	Fe 1	0

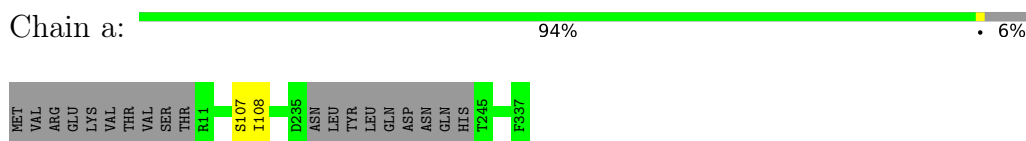
### 3 Residue-property plots [i](#)

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.

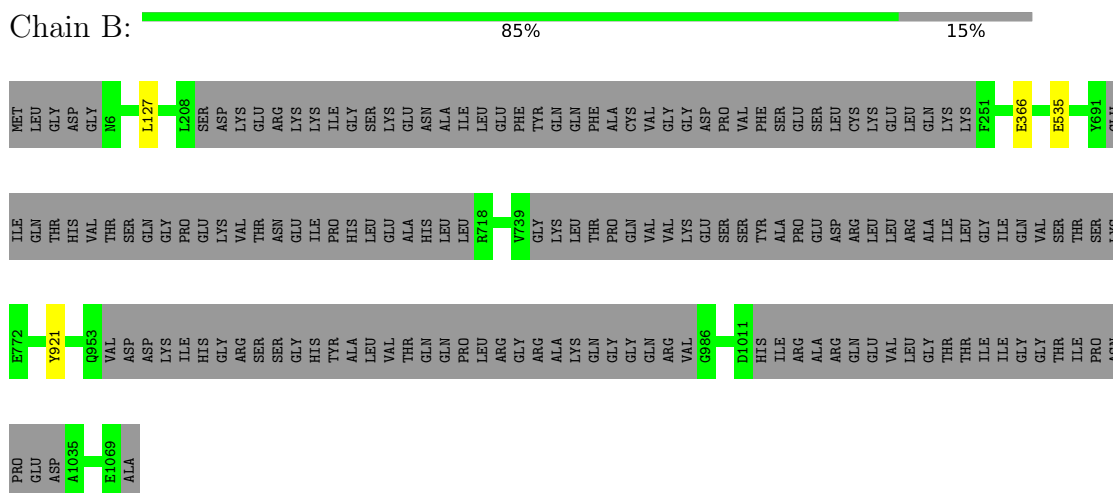
- Molecule 1: DNA-directed RNA polymerase subunit alpha



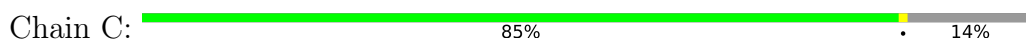
- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 2: DNA-directed RNA polymerase subunit beta



- Molecule 3: DNA-directed RNA polymerase subunit gamma

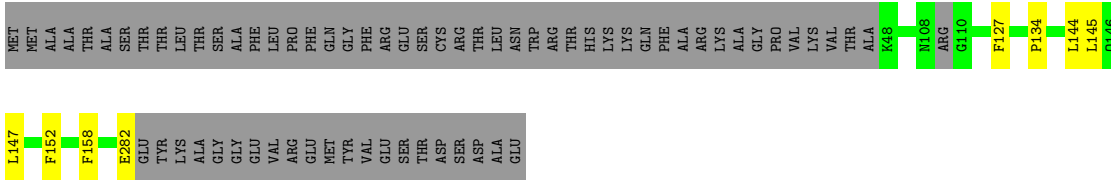




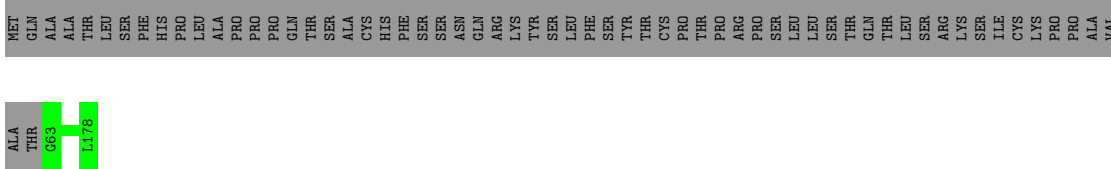




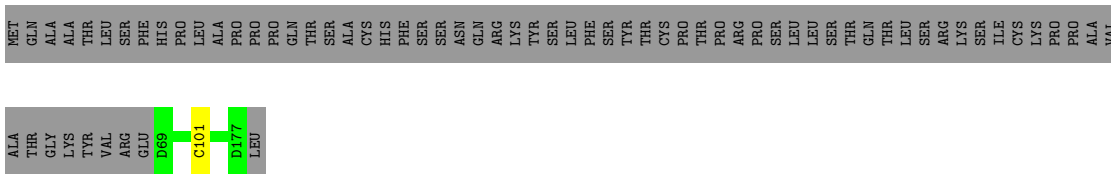




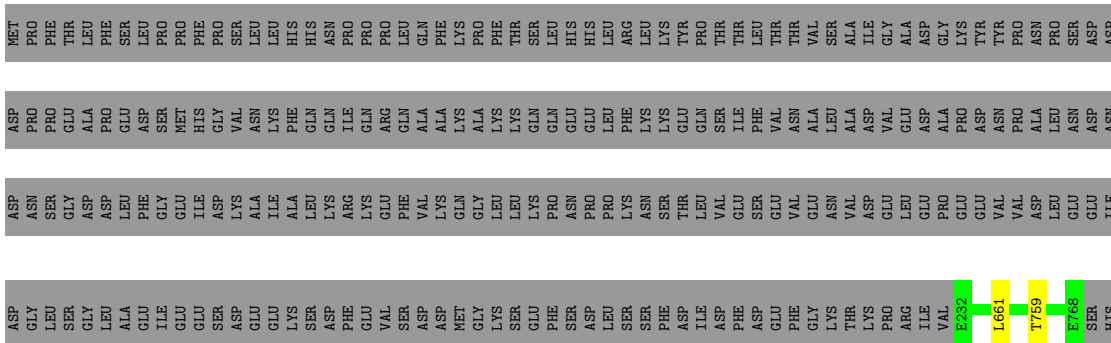
- Molecule 15: Thioredoxin-like protein CITRX1, chloroplastic



- Molecule 15: Thioredoxin-like protein CITRX1, chloroplastic



- Molecule 16: UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase-like



- Molecule 17: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 7-like isoform X1



- Molecule 18: PAP13(pTAC18)

Chain P:  73% 27%

MET	ALA	SER	PHE	ILE	THR	MET	PRO	ALA	LEU	SER	TYR	LEU	SER	THR	ASN	THR	SER	SER	LEU	GLU	ARG	THR	ASN	PHE	ARG	PRO	SER	SER	ARG	GLY	TYR	GLN	GLY	VAL	ARG	ALA	H38	D142	SER
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	410910	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.856	Depositor
Minimum map value	-0.729	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.050	Depositor
Recommended contour level	0.1	Depositor
Map size ( $\text{\AA}$ )	440.0, 440.0, 440.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, FE

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	0.29	0/2237	0.44	0/3034
1	a	0.31	0/2487	0.44	0/3374
2	B	0.27	0/6945	0.43	0/9418
3	C	0.25	0/4518	0.42	0/6148
4	c	0.32	0/8213	0.46	0/11205
5	D	0.29	0/5191	0.43	0/7029
6	E	0.38	0/4604	0.49	0/6285
7	F	0.33	0/4339	0.45	0/5885
8	G	0.41	0/1777	0.46	0/2417
9	H	0.28	0/2167	0.40	0/2942
10	I	0.34	0/2970	0.42	0/4026
11	i	0.33	0/3056	0.44	0/4141
12	J	0.30	0/3454	0.42	0/4689
13	K	0.26	0/1824	0.41	0/2468
14	L	0.69	0/1514	0.76	1/2100 (0.0%)
15	M	0.45	0/951	0.52	0/1286
15	m	0.41	0/865	0.55	0/1175
16	N	0.23	0/3011	0.41	0/4163
17	O	0.24	0/702	0.36	0/945
18	P	0.24	0/915	0.42	0/1241
All	All	0.32	0/61740	0.45	1/83971 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	L	152	PHE	N-CA-C	-6.93	92.30	111.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	289/337 (86%)	277 (96%)	12 (4%)	0	100	100
1	a	314/337 (93%)	303 (96%)	11 (4%)	0	100	100
2	B	897/1070 (84%)	862 (96%)	35 (4%)	0	100	100
3	C	584/688 (85%)	555 (95%)	29 (5%)	0	100	100
4	c	1160/1388 (84%)	1124 (97%)	36 (3%)	0	100	100
5	D	639/892 (72%)	620 (97%)	19 (3%)	0	100	100
6	E	698/860 (81%)	680 (97%)	18 (3%)	0	100	100
7	F	542/682 (80%)	529 (98%)	13 (2%)	0	100	100
8	G	216/266 (81%)	211 (98%)	5 (2%)	0	100	100
9	H	258/531 (49%)	254 (98%)	4 (2%)	0	100	100
10	I	372/486 (76%)	349 (94%)	23 (6%)	0	100	100
11	i	381/648 (59%)	365 (96%)	16 (4%)	0	100	100
12	J	420/507 (83%)	404 (96%)	16 (4%)	0	100	100
13	K	212/331 (64%)	207 (98%)	5 (2%)	0	100	100
14	L	230/303 (76%)	220 (96%)	9 (4%)	1 (0%)	34	72
15	M	114/178 (64%)	112 (98%)	2 (2%)	0	100	100
15	m	107/178 (60%)	100 (94%)	7 (6%)	0	100	100
16	N	535/770 (70%)	521 (97%)	14 (3%)	0	100	100
17	O	86/167 (52%)	84 (98%)	2 (2%)	0	100	100
18	P	103/143 (72%)	99 (96%)	4 (4%)	0	100	100
All	All	8157/10762 (76%)	7876 (97%)	280 (3%)	1 (0%)	100	100



All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	L	134	PRO

### 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	223/308 (72%)	223 (100%)	0	100	100
1	a	257/308 (83%)	255 (99%)	2 (1%)	81	93
2	B	667/924 (72%)	663 (99%)	4 (1%)	86	95
3	C	429/612 (70%)	424 (99%)	5 (1%)	71	90
4	c	679/1238 (55%)	671 (99%)	8 (1%)	71	90
5	D	528/770 (69%)	521 (99%)	7 (1%)	69	89
6	E	300/741 (40%)	294 (98%)	6 (2%)	55	83
7	F	395/615 (64%)	393 (100%)	2 (0%)	88	96
8	G	172/232 (74%)	170 (99%)	2 (1%)	71	90
9	H	212/472 (45%)	210 (99%)	2 (1%)	78	92
10	I	287/437 (66%)	286 (100%)	1 (0%)	92	97
11	i	316/567 (56%)	310 (98%)	6 (2%)	57	84
12	J	352/449 (78%)	346 (98%)	6 (2%)	60	85
13	K	199/300 (66%)	197 (99%)	2 (1%)	76	91
14	L	83/258 (32%)	77 (93%)	6 (7%)	14	45
15	M	103/160 (64%)	103 (100%)	0	100	100
15	m	92/160 (58%)	91 (99%)	1 (1%)	73	90
16	N	95/659 (14%)	93 (98%)	2 (2%)	53	82
17	O	69/144 (48%)	68 (99%)	1 (1%)	67	88
18	P	91/129 (70%)	91 (100%)	0	100	100
All	All	5549/9483 (58%)	5486 (99%)	63 (1%)	74	90

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	107	SER
1	a	108	ILE
2	B	127	LEU
2	B	366	GLU
2	B	535	GLU
2	B	921	TYR
3	C	114	ILE
3	C	172	GLU
3	C	257	LEU
3	C	301	GLU
3	C	521	PHE
4	c	94	VAL
4	c	102	GLU
4	c	103	ILE
4	c	350	GLU
4	c	1128	THR
4	c	1129	LEU
4	c	1292	GLU
4	c	1293	THR
5	D	383	LEU
5	D	406	ARG
5	D	602	LEU
5	D	740	VAL
5	D	762	TRP
5	D	804	CYS
5	D	821	LEU
6	E	502	LEU
6	E	568	CYS
6	E	634	ILE
6	E	697	GLU
6	E	704	LEU
6	E	757	ILE
7	F	206	ASP
7	F	594	ILE
8	G	135	GLU
8	G	174	LEU
9	H	238	TRP
9	H	354	THR
10	I	443	LEU
11	i	531	VAL
11	i	539	HIS
11	i	558	THR
11	i	584	HIS

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Mol	Chain	Res	Type
11	i	587	THR
11	i	638	GLU
12	J	116	ILE
12	J	119	ARG
12	J	245	GLN
12	J	278	CYS
12	J	400	HIS
12	J	402	SER
13	K	173	THR
13	K	298	ASP
14	L	127	PHE
14	L	144	LEU
14	L	145	LEU
14	L	147	LEU
14	L	158	PHE
14	L	282	GLU
15	m	101	CYS
16	N	661	LEU
16	N	759	THR
17	O	83	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (132) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	150	GLN
1	A	196	GLN
1	A	221	ASN
1	A	276	GLN
1	A	285	ASN
1	a	41	GLN
1	a	150	GLN
1	a	191	ASN
1	a	196	GLN
1	a	231	HIS
2	B	16	ASN
2	B	58	GLN
2	B	124	ASN
2	B	128	GLN
2	B	276	GLN
2	B	322	GLN
2	B	372	HIS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	386	GLN
2	B	503	GLN
2	B	522	GLN
2	B	551	GLN
2	B	621	HIS
2	B	622	GLN
2	B	625	GLN
2	B	636	GLN
2	B	666	ASN
2	B	810	GLN
2	B	910	GLN
2	B	934	ASN
2	B	938	GLN
3	C	110	GLN
3	C	209	GLN
3	C	300	ASN
3	C	311	ASN
3	C	331	GLN
3	C	449	GLN
3	C	453	GLN
3	C	455	HIS
3	C	471	GLN
3	C	474	GLN
3	C	513	GLN
3	C	523	HIS
3	C	560	ASN
4	c	11	ASN
4	c	29	HIS
4	c	41	GLN
4	c	73	GLN
4	c	77	GLN
4	c	90	ASN
4	c	145	GLN
4	c	376	HIS
4	c	397	ASN
4	c	497	GLN
4	c	924	GLN
4	c	1001	ASN
4	c	1019	GLN
4	c	1042	ASN
4	c	1051	ASN
4	c	1090	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	c	1095	GLN
4	c	1151	GLN
4	c	1196	GLN
4	c	1207	GLN
4	c	1212	GLN
5	D	175	GLN
5	D	194	ASN
5	D	420	GLN
5	D	882	GLN
6	E	464	GLN
6	E	491	ASN
6	E	534	GLN
6	E	579	GLN
6	E	612	HIS
6	E	643	ASN
6	E	711	HIS
6	E	727	ASN
6	E	792	GLN
7	F	81	ASN
7	F	128	ASN
7	F	148	GLN
7	F	196	HIS
7	F	251	GLN
7	F	278	GLN
7	F	288	HIS
7	F	317	HIS
7	F	318	HIS
7	F	518	HIS
7	F	591	ASN
8	G	92	GLN
8	G	96	ASN
8	G	151	GLN
8	G	226	ASN
8	G	253	GLN
9	H	195	GLN
9	H	216	HIS
9	H	247	GLN
9	H	271	GLN
9	H	300	GLN
9	H	320	GLN
9	H	332	GLN
9	H	353	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
9	H	399	GLN
10	I	139	GLN
10	I	142	GLN
10	I	193	GLN
10	I	200	ASN
10	I	317	GLN
10	I	346	GLN
10	I	440	GLN
11	i	287	GLN
11	i	354	GLN
11	i	361	ASN
11	i	363	ASN
11	i	607	GLN
12	J	180	ASN
12	J	243	GLN
12	J	244	GLN
12	J	254	ASN
12	J	281	GLN
12	J	313	GLN
12	J	381	HIS
12	J	496	GLN
13	K	121	GLN
13	K	313	GLN
15	m	176	ASN
16	N	691	HIS
17	O	61	GLN
17	O	77	HIS
17	O	85	ASN
17	O	99	GLN
18	P	104	GLN

### 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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.

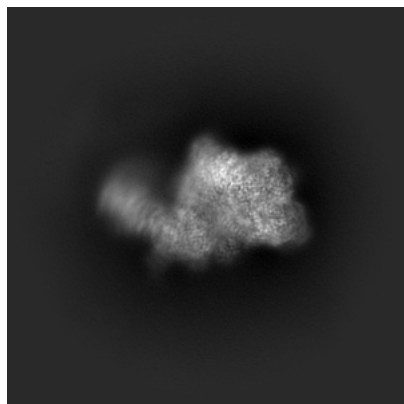
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37386. These allow visual inspection of the internal detail of the map and identification of artifacts.

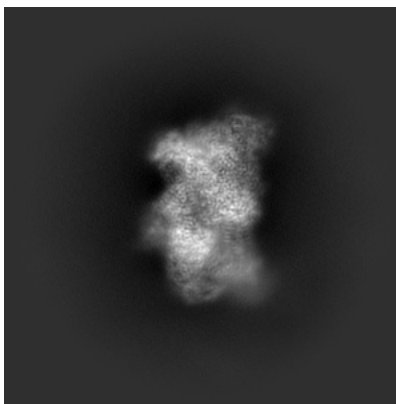
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

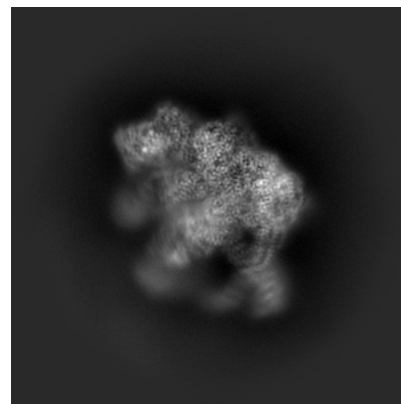
#### 6.1.1 Primary map



X

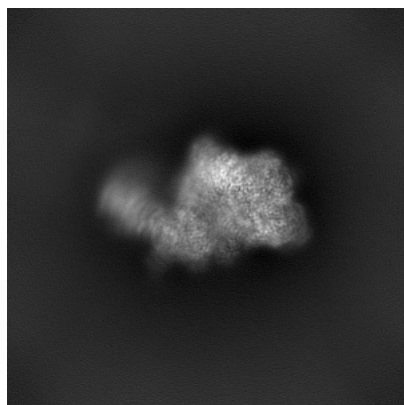


Y

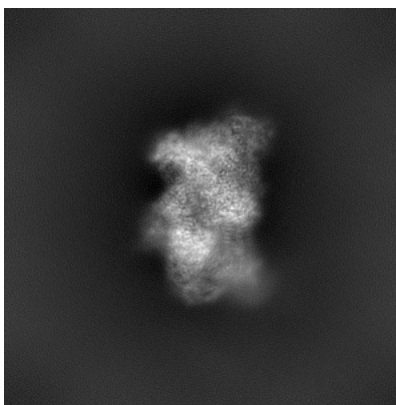


Z

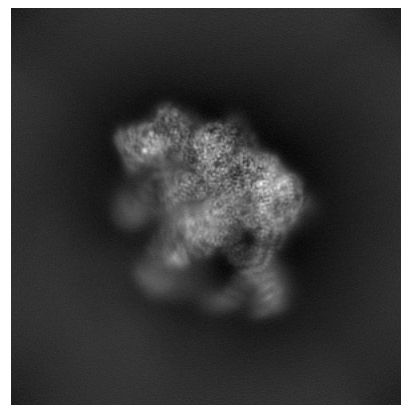
#### 6.1.2 Raw map



X



Y



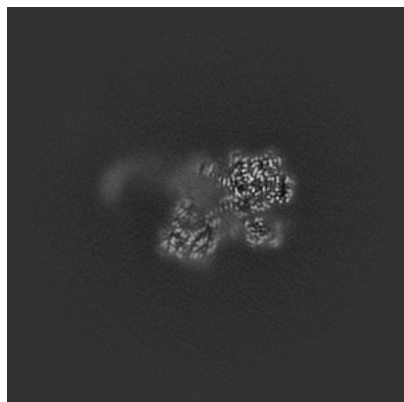
Z

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

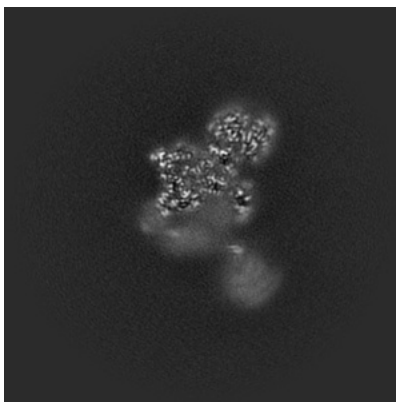


## 6.2 Central slices [i](#)

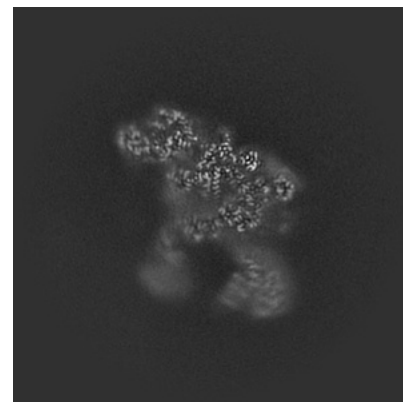
### 6.2.1 Primary map



X Index: 200

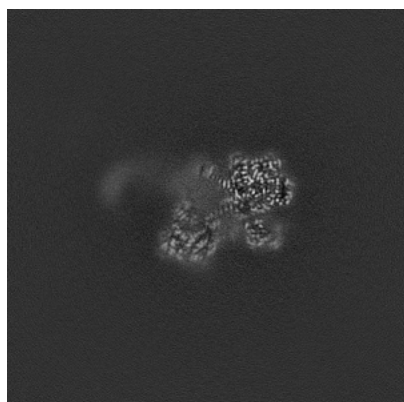


Y Index: 200

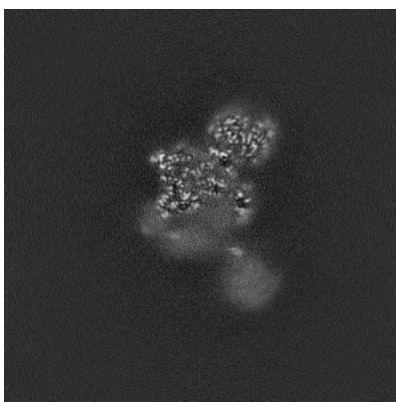


Z Index: 200

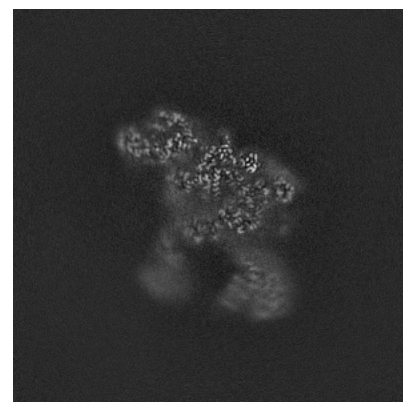
### 6.2.2 Raw map



X Index: 200



Y Index: 200

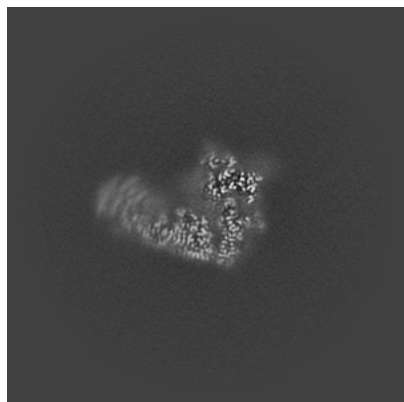


Z Index: 200

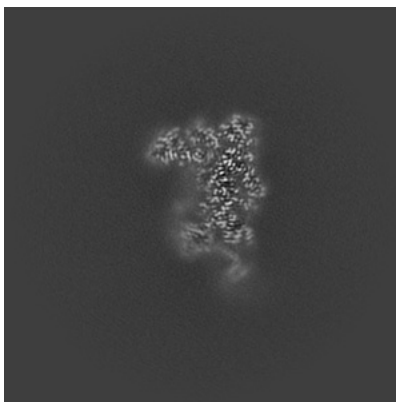
The images above show central slices of the map in three orthogonal directions.

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

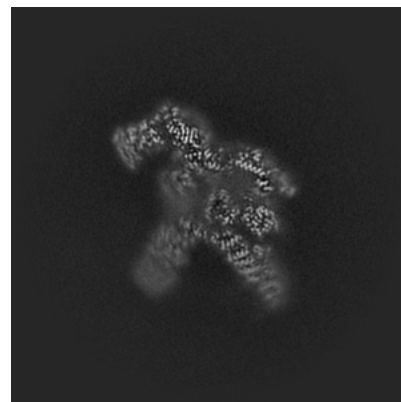
### 6.3.1 Primary map



X Index: 250

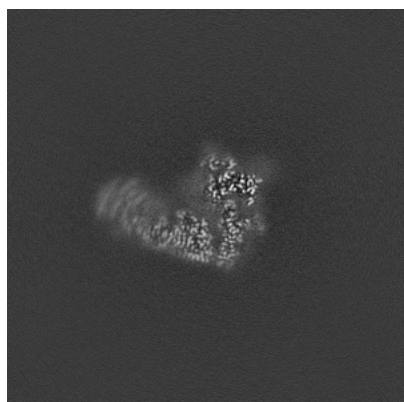


Y Index: 223

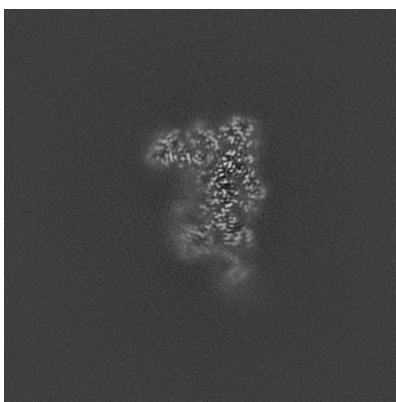


Z Index: 184

### 6.3.2 Raw map



X Index: 250



Y Index: 223

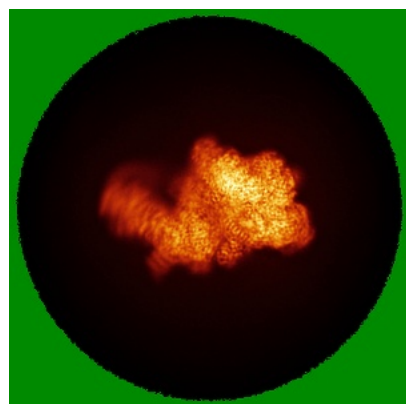


Z Index: 184

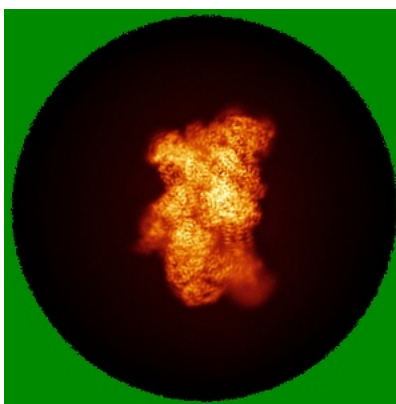
The images above show the largest variance slices of the map in three orthogonal directions.

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

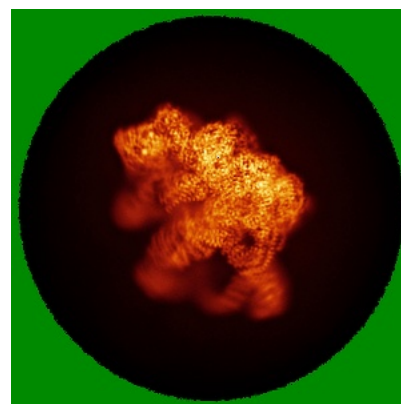
### 6.4.1 Primary map



X

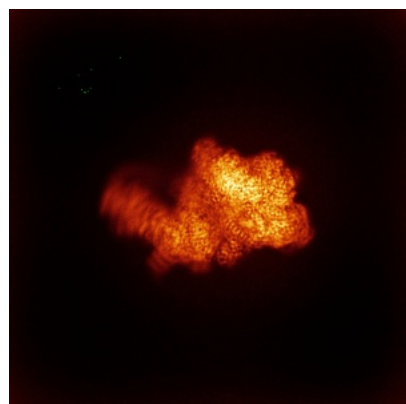


Y

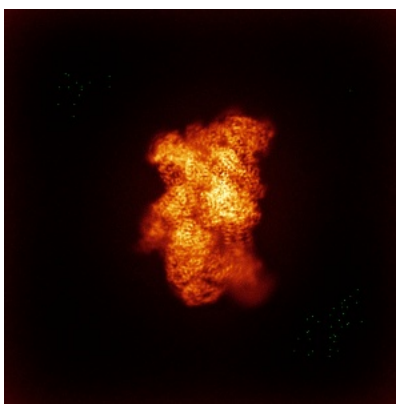


Z

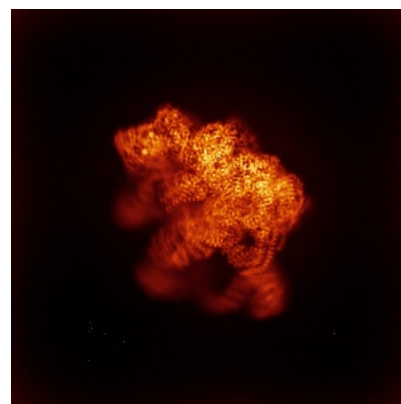
### 6.4.2 Raw map



X



Y

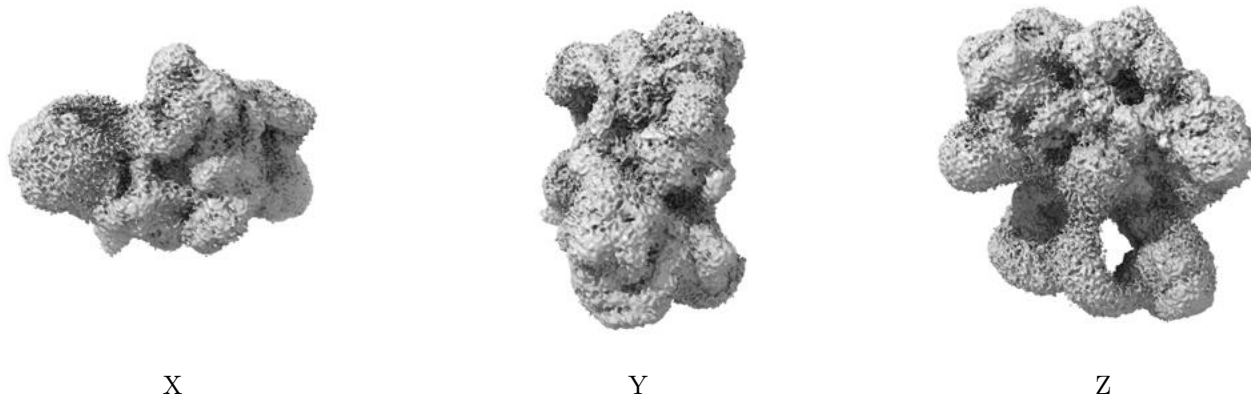


Z

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.

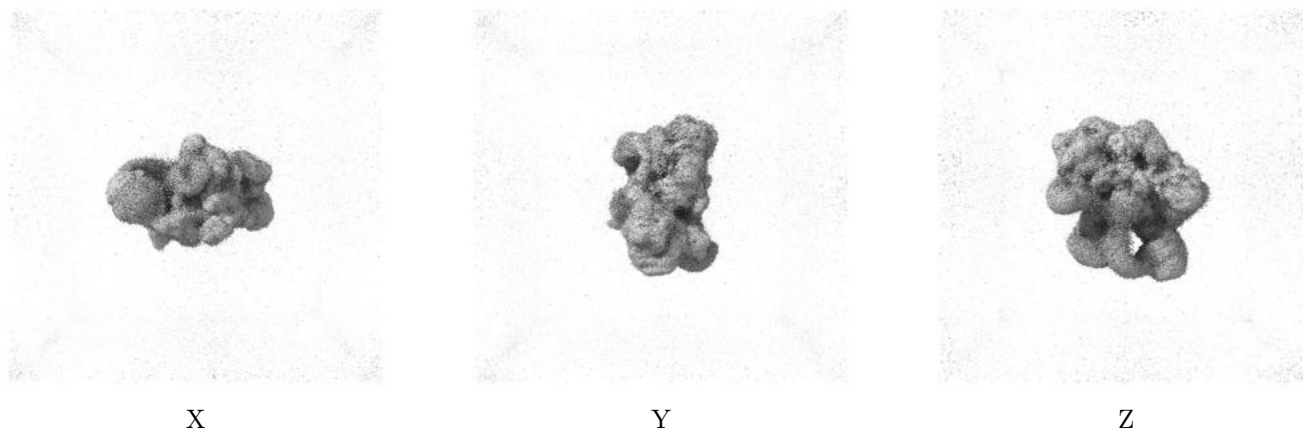
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

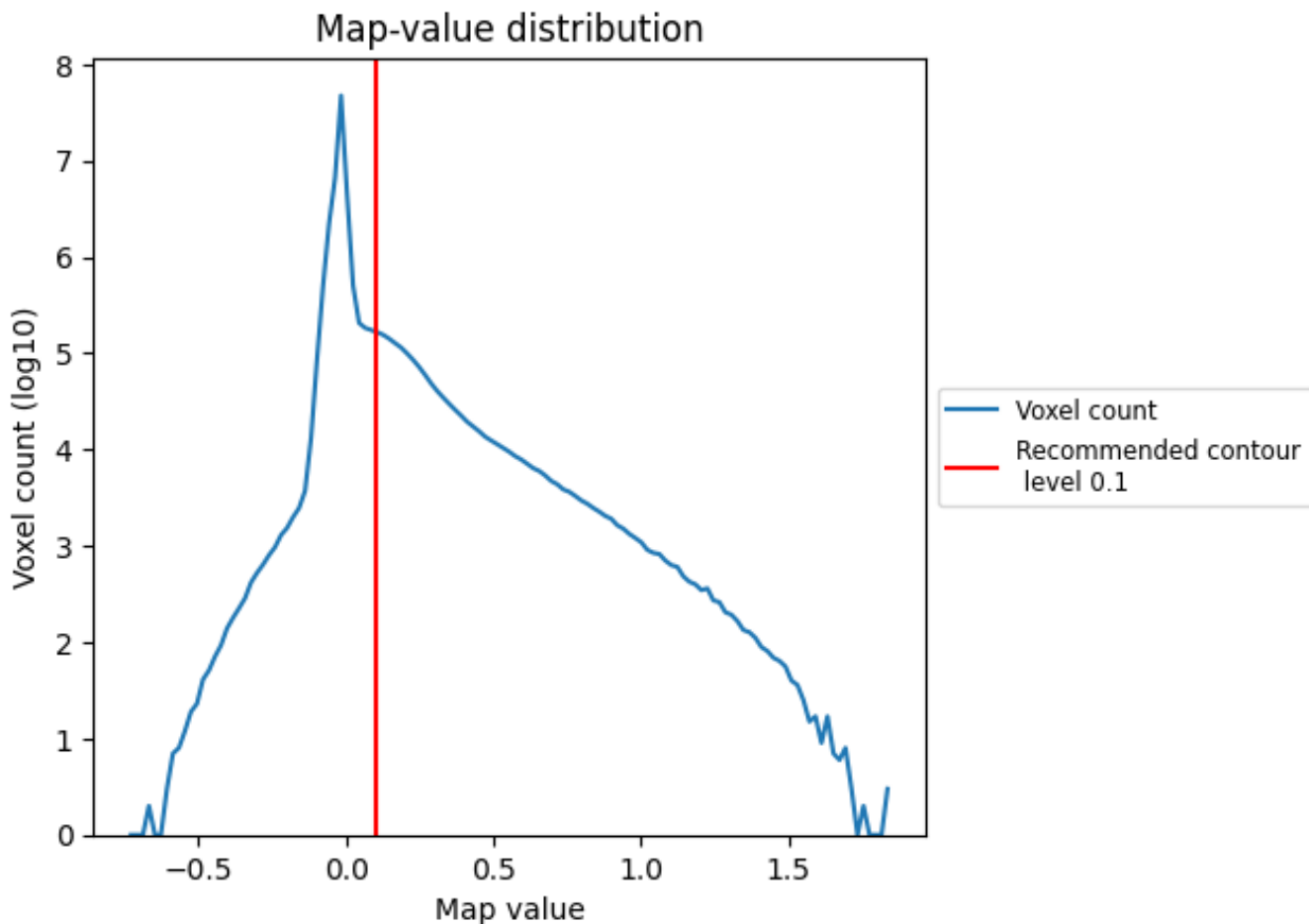
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

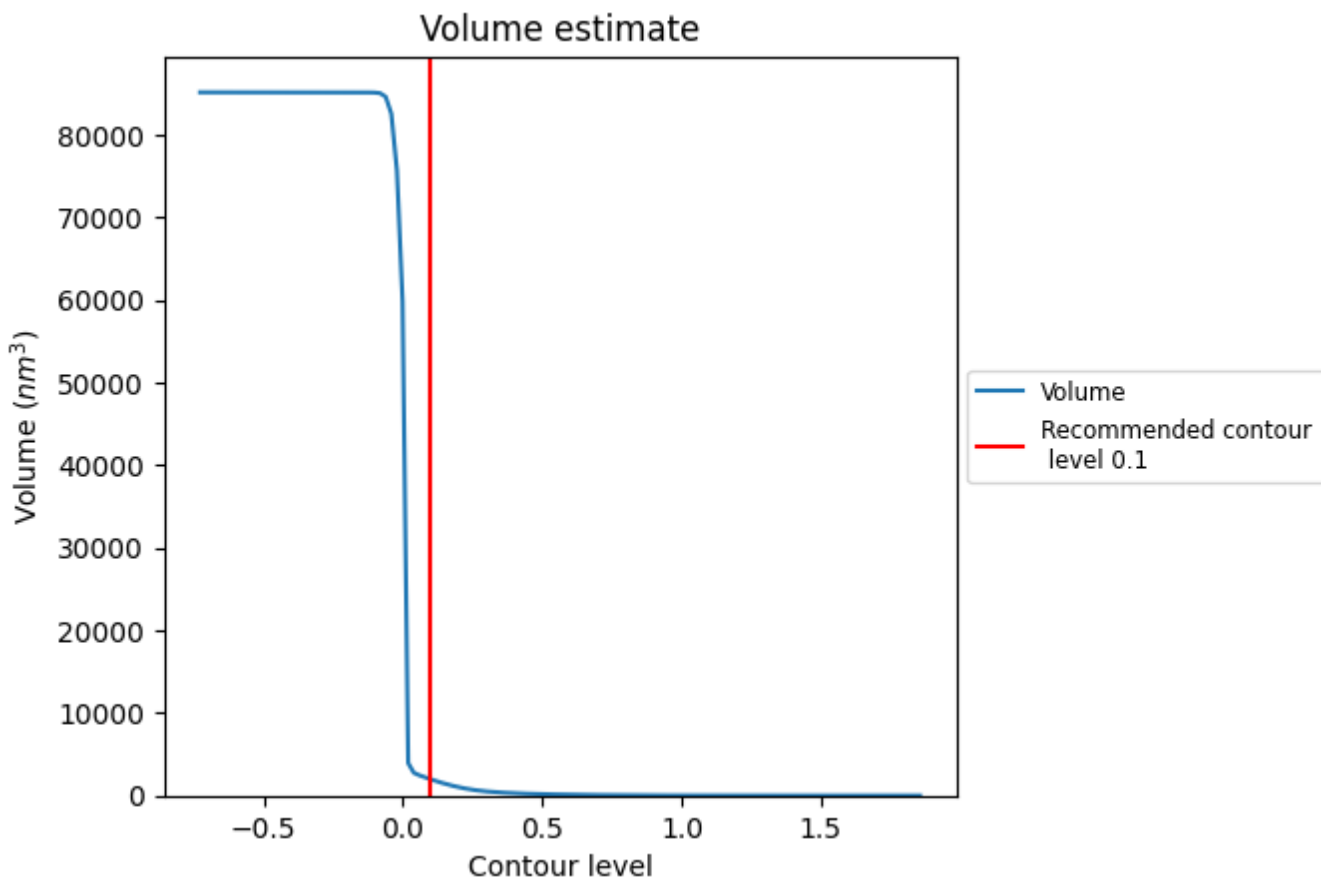
This section contains the results of statistical analysis of the map.

### 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.

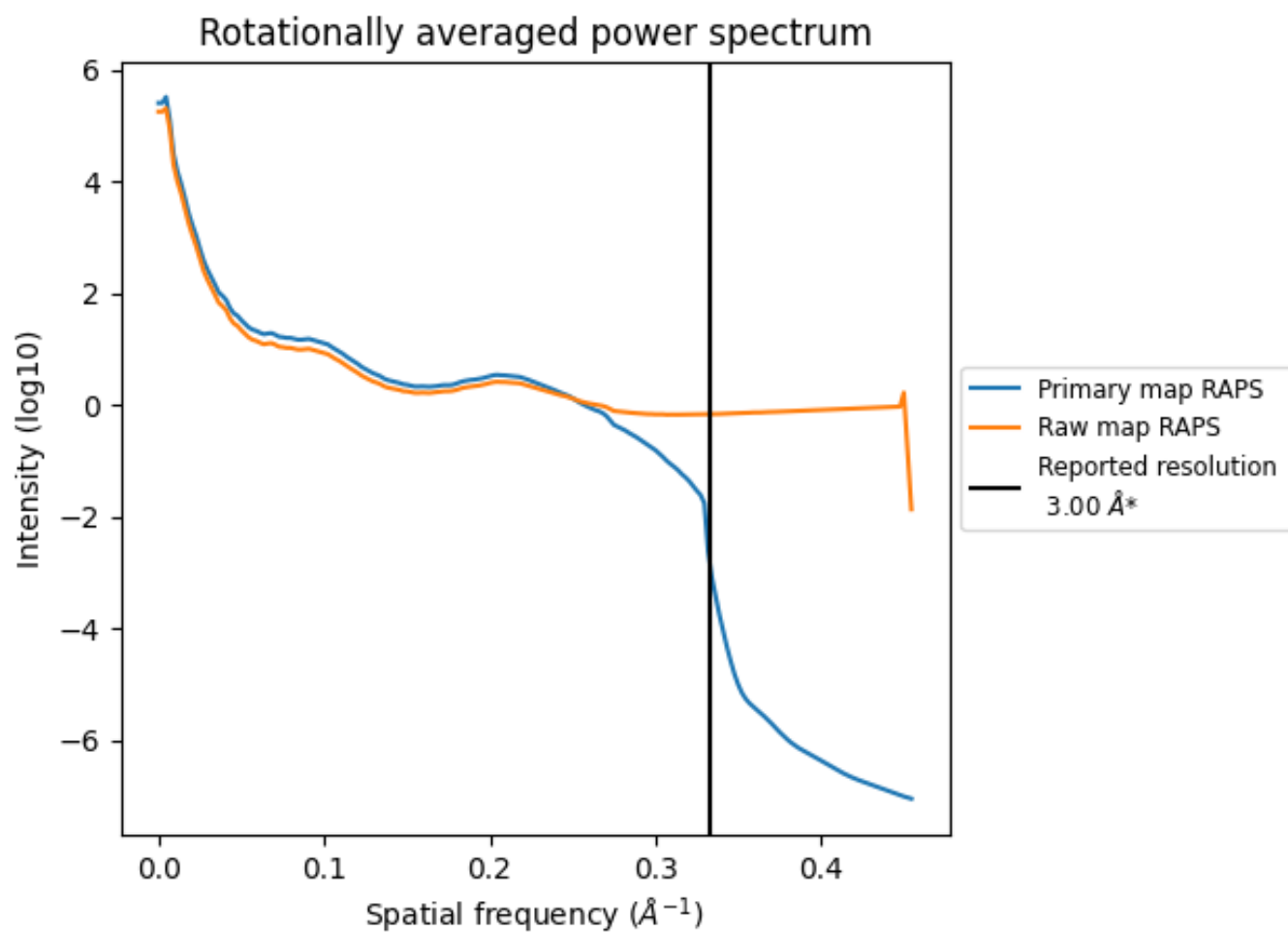
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1962  $\text{nm}^3$ ; this corresponds to an approximate mass of 1772 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

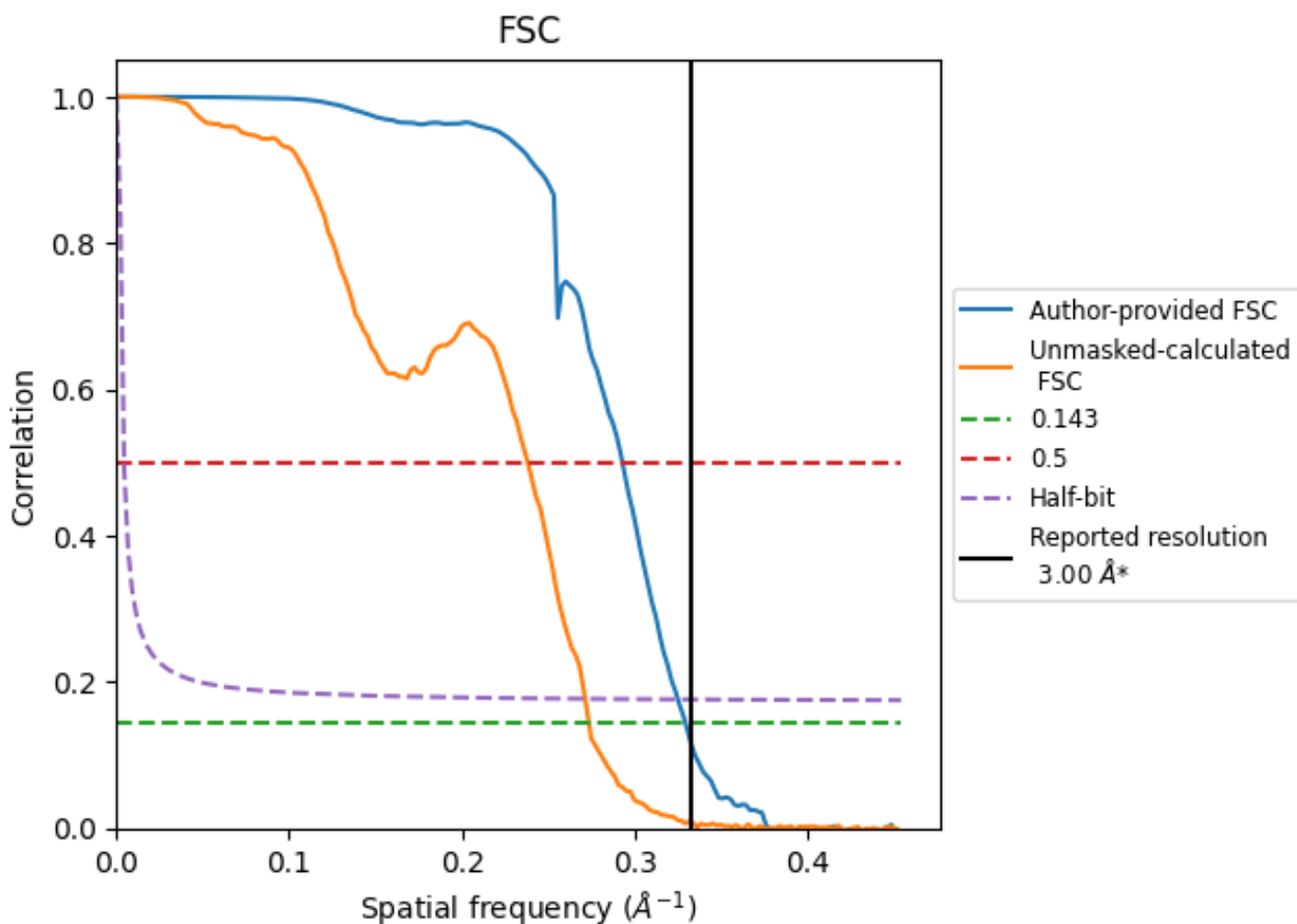


\*Reported resolution corresponds to spatial frequency of  $0.333 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.333 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

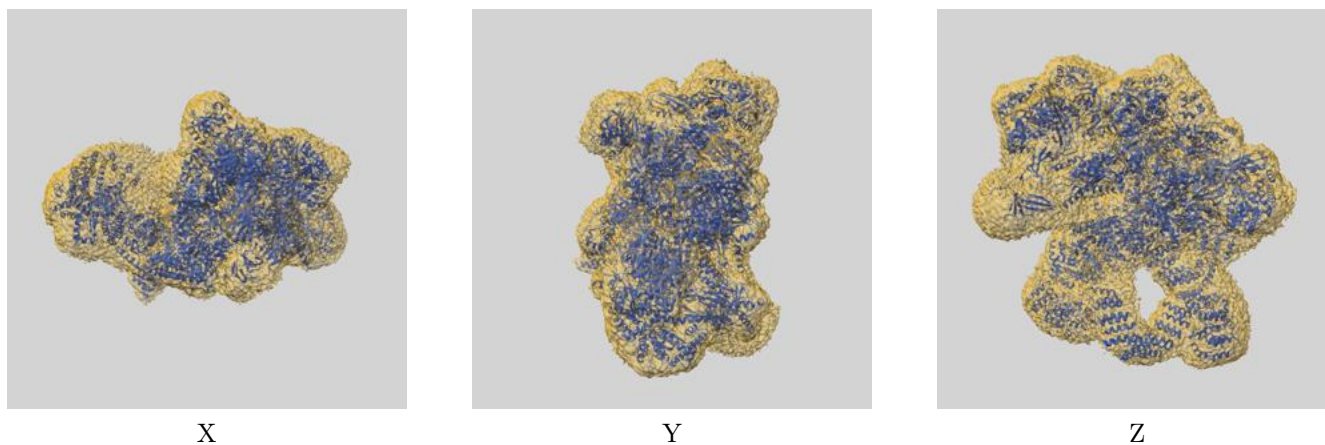
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.03	3.41	3.08
Unmasked-calculated*	3.65	4.20	3.68

\*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 3.65 differs from the reported value 3.0 by more than 10 %

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

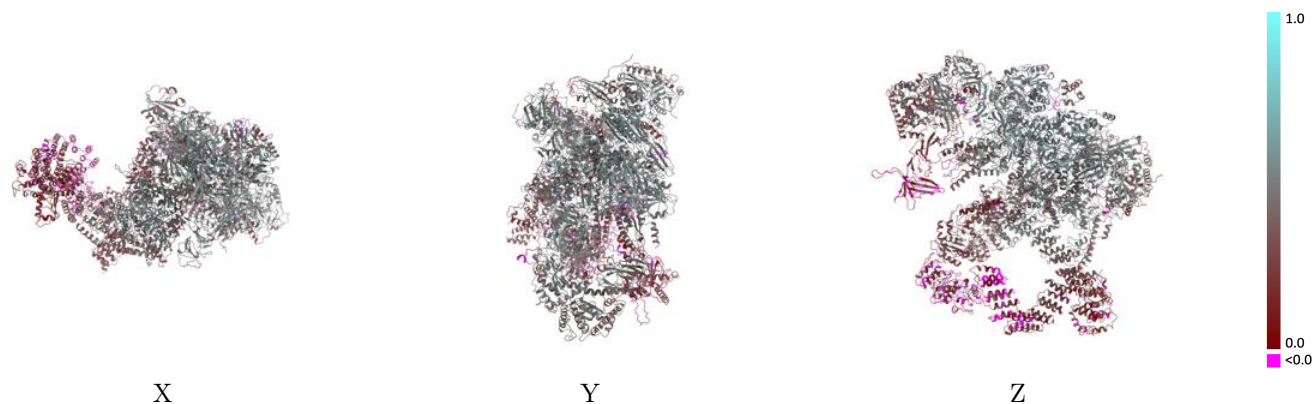
This section contains information regarding the fit between EMDB map EMD-37386 and PDB model 8W9Z. Per-residue inclusion information can be found in section 3 on page 8.

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



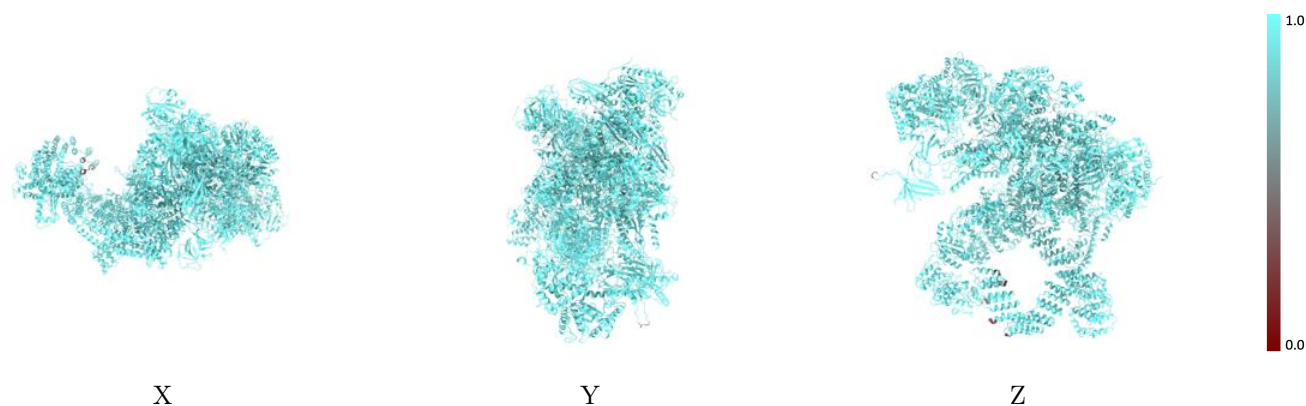
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



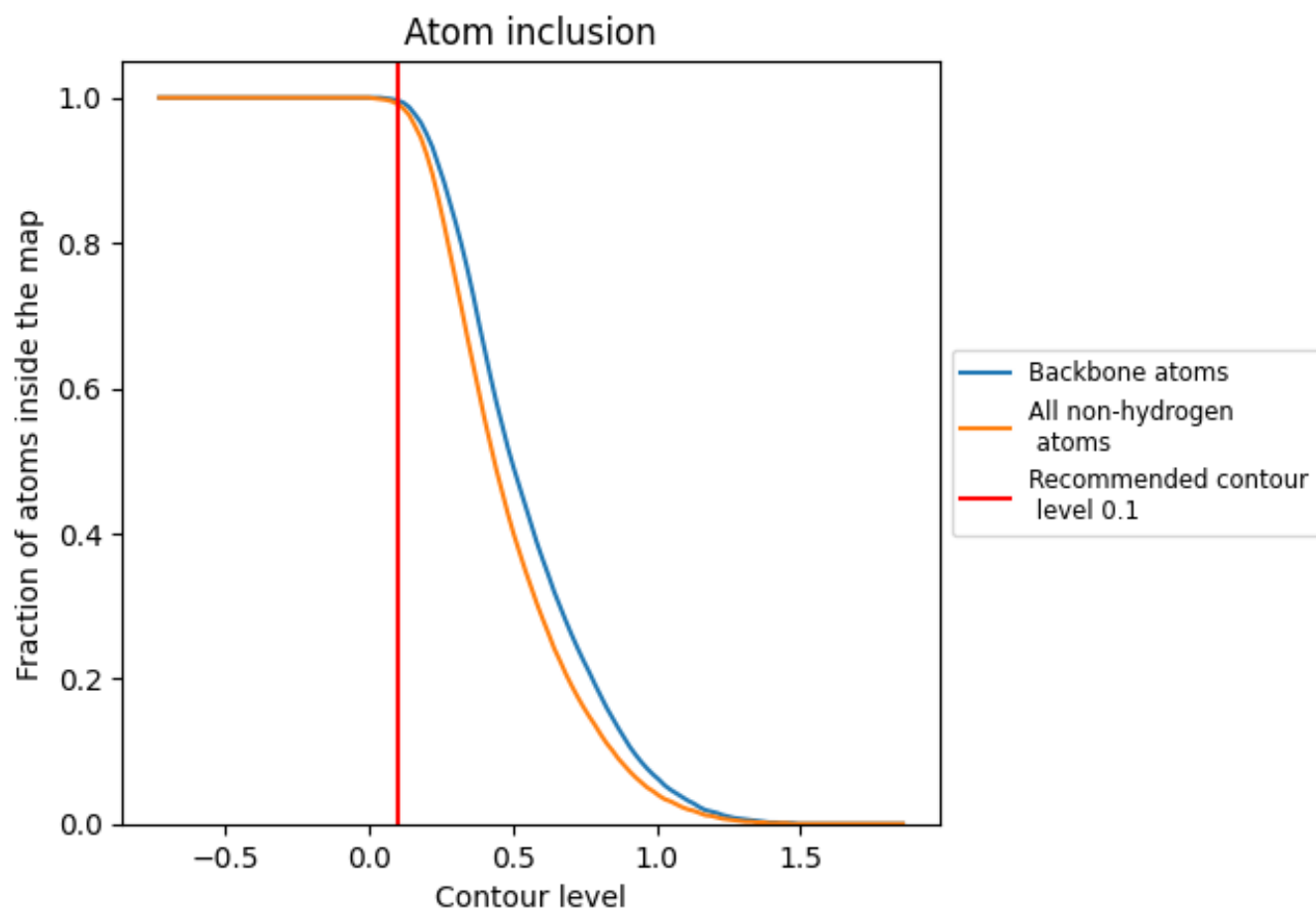
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).











































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9910	 0.4050
A	 0.9810	 0.4340
B	 0.9900	 0.4720
C	 0.9950	 0.3800
D	 0.9950	 0.3680
E	 0.9750	 0.1700
F	 0.9960	 0.4270
G	 0.9940	 0.4700
H	 0.9920	 0.5000
I	 0.9930	 0.5180
J	 0.9940	 0.4570
K	 0.9910	 0.4560
L	 1.0000	 0.4250
M	 0.9900	 0.5070
N	 1.0000	 0.1620
O	 0.9930	 0.4450
P	 0.9930	 0.4410
a	 0.9910	 0.4690
c	 0.9910	 0.4090
i	 0.9950	 0.4700
m	 0.9950	 0.4400

