



## wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 07:49 PM EDT

PDB ID : 8TOF  
EMDB ID : EMD-41449  
Title : Rpd3S bound to an H3K36Cme3 modified nucleosome  
Authors : Markert, J.W.; Vos, S.M.; Farnung, L.  
Deposited on : 2023-08-03  
Resolution : 2.80 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

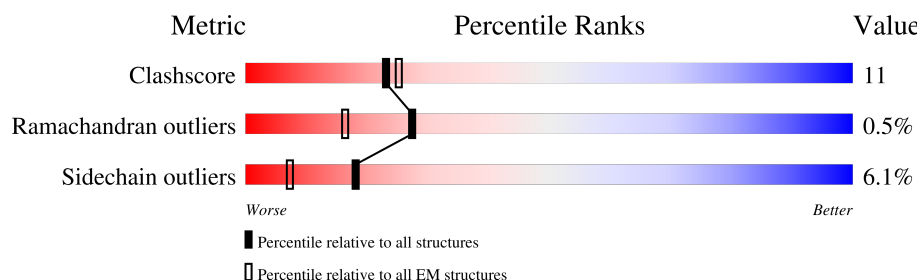
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.80 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1536	
2	B	433	
3	D	401	
3	E	401	
4	F	684	
4	G	684	
5	H	5	
6	N	206	

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Mol	Chain	Length	Quality of chain
7	T	215	
8	a	136	
8	e	136	
9	b	103	
9	f	103	
10	c	130	
10	g	130	
11	d	123	
11	h	123	
12	x	7	

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 29102 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 Transcriptional regulatory protein SIN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	545	Total	C	N	O	S	0	0
			4572	2936	774	848	14		

- Molecule 2 is a protein called Histone deacetylase RPD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	385	Total	C	N	O	S	0	0
			3057	1948	513	571	25		

- Molecule 3 is a protein called Chromatin modification-related protein EAF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	289	Total	C	N	O	S	0	0
			2356	1513	387	443	13		
3	E	253	Total	C	N	O	S	0	0
			2080	1345	342	380	13		

- Molecule 4 is a protein called Transcriptional regulatory protein RCO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	89	Total	C	N	O	S	0	0
			724	463	121	131	9		
4	G	369	Total	C	N	O	S	0	0
			3010	1905	516	571	18		

- Molecule 5 is a protein called Rco1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	5	Total	C	N	O	0	0
			31	18	8	5		

- Molecule 6 is a DNA chain called DNA (176-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	176	Total	C	N	O	P	0	0
			3623	1719	651	1077	176		

- Molecule 7 is a DNA chain called DNA (176-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	176	Total	C	N	O	P	0	0
			3593	1702	680	1035	176		

- Molecule 8 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a	101	Total	C	N	O	S	0	0
			836	528	161	143	4		
8	e	101	Total	C	N	O	S	0	0
			836	528	161	143	4		

- Molecule 9 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b	81	Total	C	N	O	S	0	0
			646	407	126	112	1		
9	f	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

- Molecule 10 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	c	103	Total	C	N	O	0	0
			795	501	155	139		
10	g	105	Total	C	N	O	0	0
			809	510	158	141		

- Molecule 11 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	d	95	Total	C	N	O	S	0	0
			745	469	134	140	2		
11	h	93	Total	C	N	O	S	0	0
			726	457	130	137	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	0	MET	-	initiating methionine	UNP P02281
d	29	THR	SER	engineered mutation	UNP P02281
h	0	MET	-	initiating methionine	UNP P02281
h	29	THR	SER	engineered mutation	UNP P02281

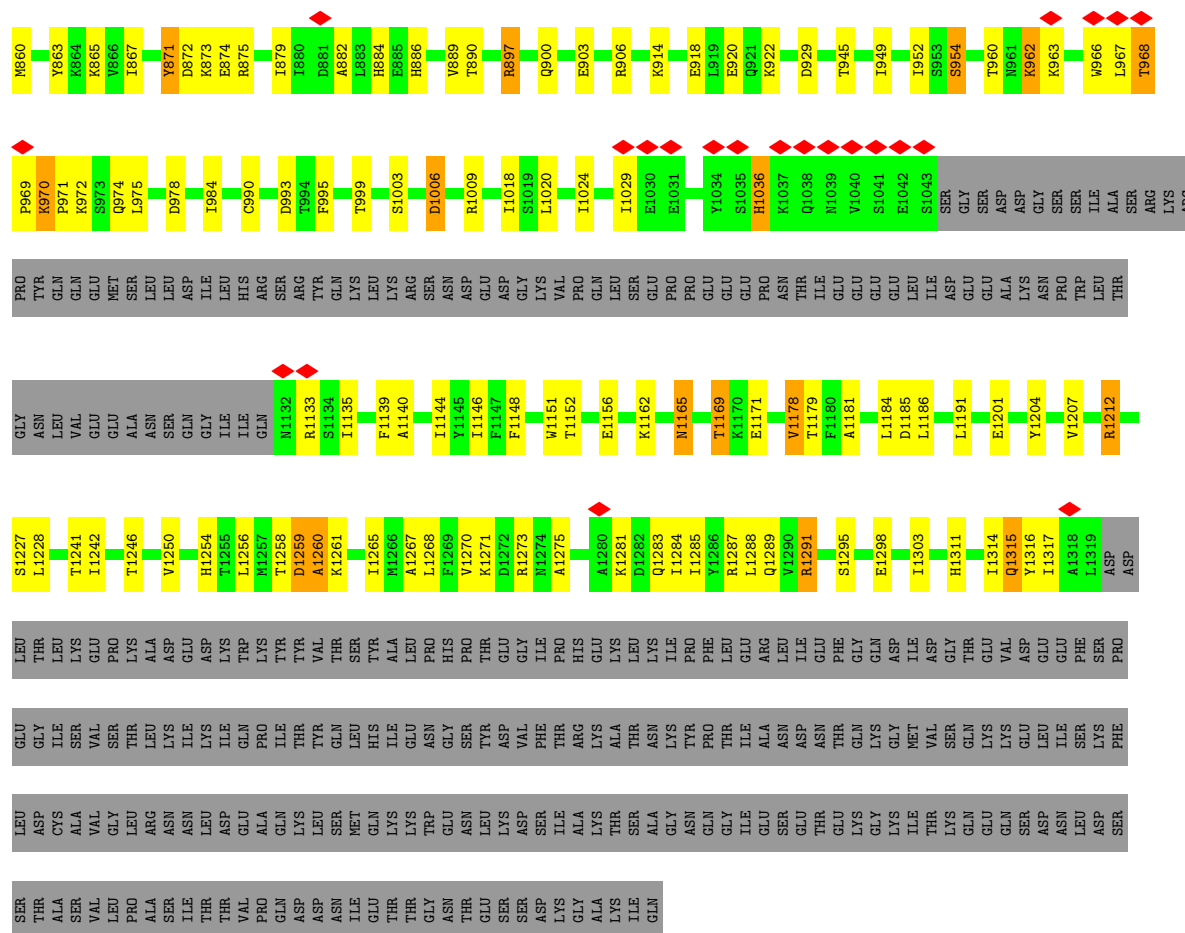
- Molecule 12 is a protein called histone N-terminal tail.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	x	7	Total	C	N	O	0	0
			39	24	8	7		

- Molecule 13 is ZINC ION (three-letter code: ZN) (formula: Zn).

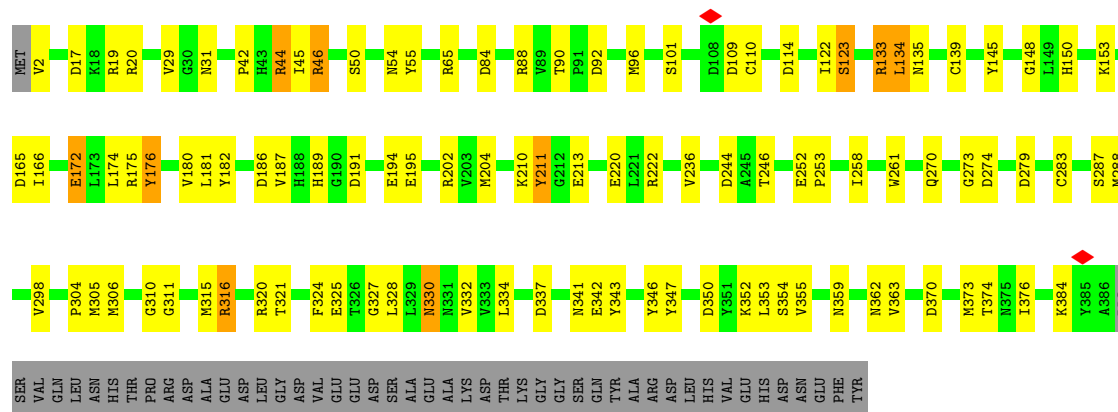
Mol	Chain	Residues	Atoms		AltConf
13	B	1	Total	Zn	0
			1	1	
13	G	4	Total	Zn	0
			4	4	





### • Molecule 2: Histone deacetylase RPD3

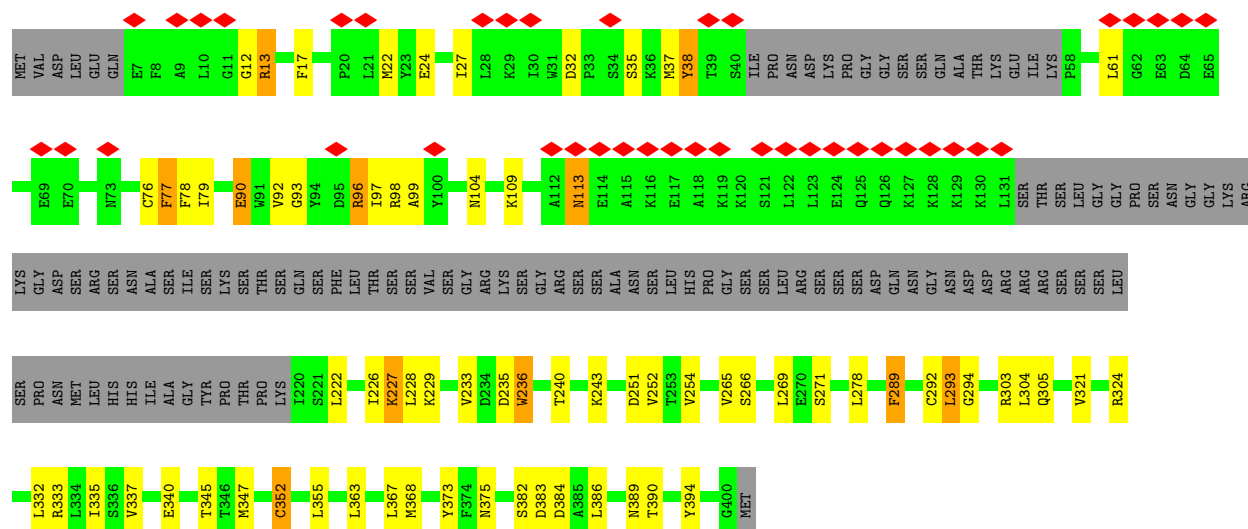
Chain B:  65% 22% 11%



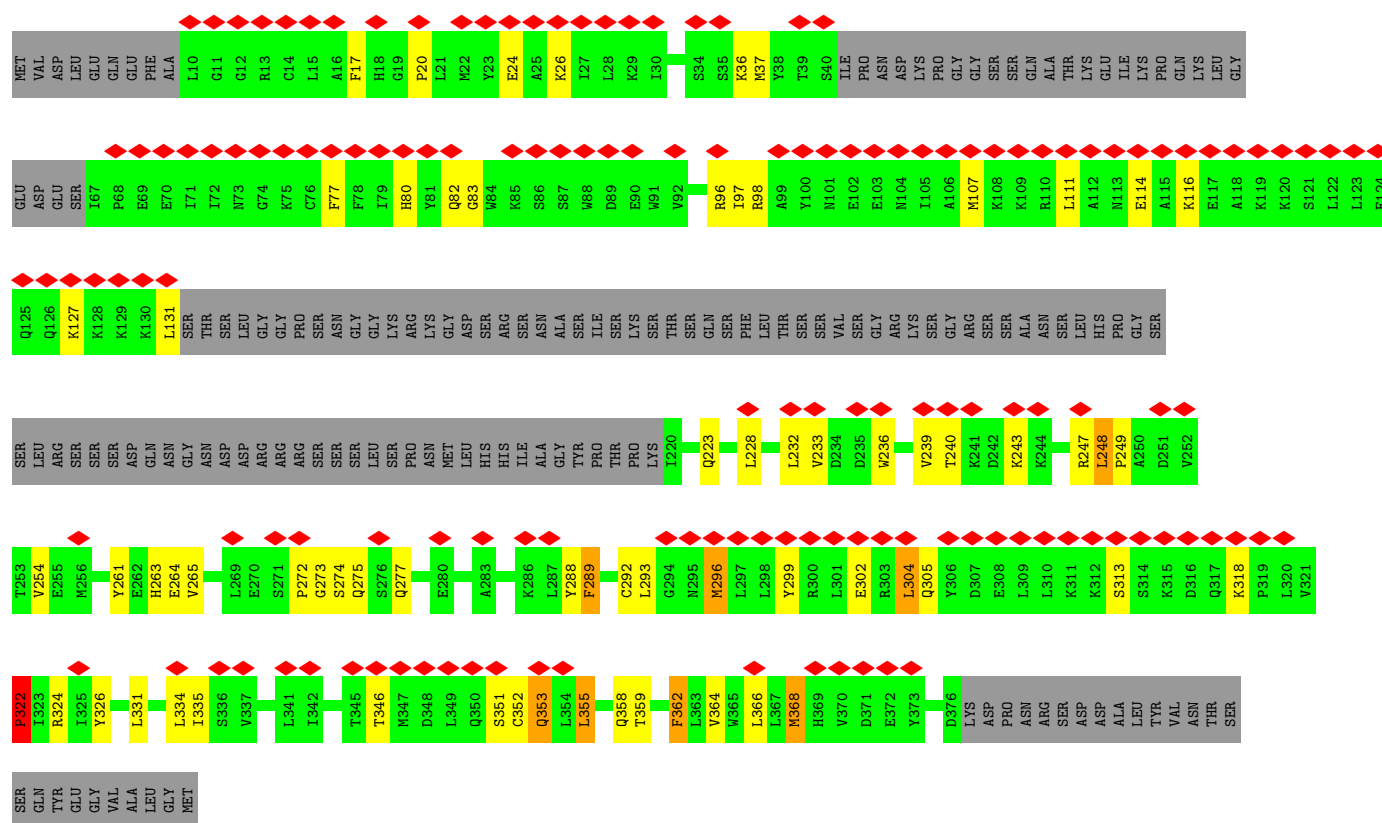
### • Molecule 3: Chromatin modification-related protein EAF3

Chain D:  10% 54% 15% 28%

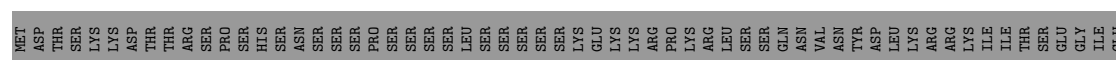




• Molecule 3: Chromatin modification-related protein EAF3



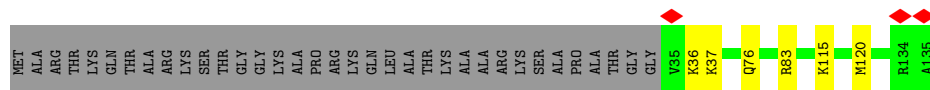
• Molecule 4: Transcriptional regulatory protein RCO1



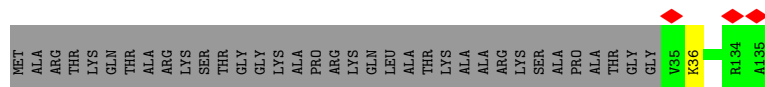





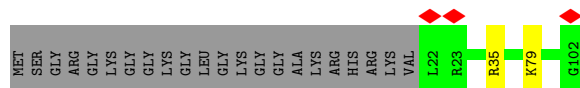
## • Molecule 8: Histone H3

Chain a:  70% 26%

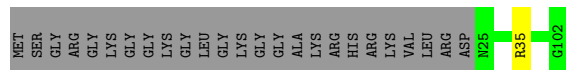
## • Molecule 8: Histone H3

Chain e:  74% 26%


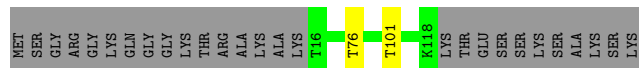
## • Molecule 9: Histone H4

Chain b:  77% 21%


## • Molecule 9: Histone H4

Chain f:  75% 24%

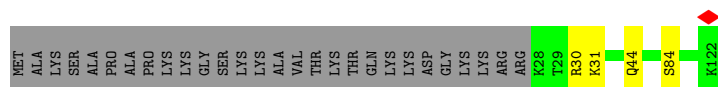
## • Molecule 10: Histone H2A

Chain c:  78% 21%

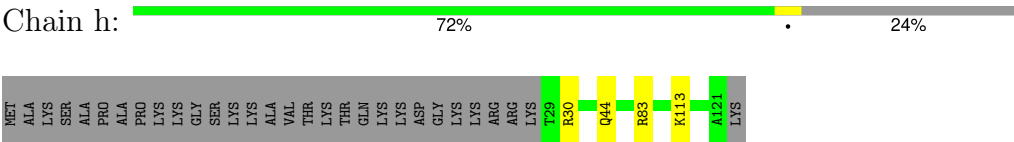
## • Molecule 10: Histone H2A

Chain g:  80% 19%

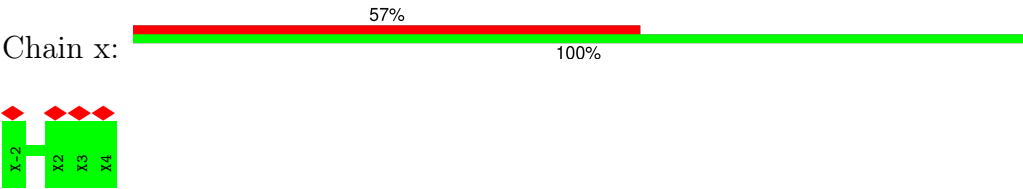
## • Molecule 11: Histone H2B 1.1

Chain d:  74% 23%

● Molecule 11: Histone H2B 1.1



● Molecule 12: histone N-terminal tail



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	484141	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 ( $e^-/\text{\AA}^2$ )	51.1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2250	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.614	Depositor
Minimum map value	-0.278	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.07768	Depositor
Map size (Å)	369.90002, 369.90002, 369.90002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	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: ZN, ML3

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	0/4675	0.51	0/6301
2	B	0.37	0/3137	0.52	0/4246
3	D	0.29	0/2403	0.50	0/3236
3	E	0.43	1/2122 (0.0%)	0.73	4/2856 (0.1%)
4	F	1.14	3/740 (0.4%)	1.08	6/991 (0.6%)
4	G	0.30	0/3077	0.53	1/4145 (0.0%)
5	H	0.21	0/10	1.06	0/11
6	N	0.81	0/4060	1.31	0/6272
7	T	0.88	0/4034	1.20	0/6216
8	a	0.32	0/835	0.56	0/1118
8	e	0.33	0/835	0.57	0/1118
9	b	0.33	0/653	0.56	0/873
9	f	0.34	0/626	0.56	0/837
10	c	0.32	0/805	0.55	0/1088
10	g	0.31	0/819	0.54	0/1106
11	d	0.34	0/756	0.48	0/1015
11	h	0.33	0/737	0.48	0/993
12	x	0.24	0/8	0.43	0/8
All	All	0.55	4/30332 (0.0%)	0.84	11/42430 (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
2	B	0	1
3	E	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	279	PRO	CB-CG	22.34	2.61	1.50
4	F	279	PRO	CG-CD	-18.41	0.89	1.50
3	E	322	PRO	CG-CD	-14.70	1.02	1.50
4	F	279	PRO	N-CD	5.40	1.55	1.47

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	279	PRO	CB-CG-CD	-25.12	8.51	106.50
3	E	322	PRO	N-CD-CG	-20.66	72.22	103.20
3	E	322	PRO	CA-CB-CG	-16.07	73.46	104.00
4	F	279	PRO	N-CA-CB	-10.45	90.77	103.30
4	G	403	PRO	CA-N-CD	-9.59	98.07	111.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	46	ARG	Sidechain
3	E	248	LEU	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.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4572	0	4534	118	0
2	B	3057	0	2934	74	0
3	D	2356	0	2377	54	0
3	E	2080	0	2126	50	0
4	F	724	0	701	30	0
4	G	3010	0	2952	110	0
5	H	31	0	19	0	0
6	N	3623	0	1986	105	0
7	T	3593	0	1965	84	0
8	a	836	0	883	0	0
8	e	836	0	883	0	0
9	b	646	0	687	0	0
9	f	619	0	659	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	c	795	0	846	0	0
10	g	809	0	864	0	0
11	d	745	0	773	0	0
11	h	726	0	747	0	0
12	x	39	0	22	0	0
13	B	1	0	0	0	0
13	G	4	0	0	0	0
All	All	29102	0	25958	535	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 11.

The worst 5 of 535 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)
4:F:279:PRO:N	4:F:279:PRO:CG	1.82	1.42
6:N:38:DG:C2	7:T:-37:DG:N2	1.90	1.38
6:N:59:DA:C2	7:T:-58:DG:N2	2.01	1.27
6:N:73:DA:C2	7:T:-72:DA:C2	2.24	1.25
4:F:279:PRO:CD	4:F:279:PRO:HG2	1.66	1.16

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	A	539/1536 (35%)	478 (89%)	57 (11%)	4 (1%)	19 48
2	B	383/433 (88%)	348 (91%)	32 (8%)	3 (1%)	16 44
3	D	283/401 (71%)	272 (96%)	10 (4%)	1 (0%)	30 61
3	E	247/401 (62%)	238 (96%)	9 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	F	85/684 (12%)	83 (98%)	2 (2%)	0	100	100
4	G	357/684 (52%)	301 (84%)	52 (15%)	4 (1%)	12	37
5	H	1/5 (20%)	1 (100%)	0	0	100	100
8	a	98/136 (72%)	96 (98%)	1 (1%)	1 (1%)	13	39
8	e	98/136 (72%)	97 (99%)	1 (1%)	0	100	100
9	b	79/103 (77%)	79 (100%)	0	0	100	100
9	f	76/103 (74%)	75 (99%)	1 (1%)	0	100	100
10	c	101/130 (78%)	100 (99%)	1 (1%)	0	100	100
10	g	103/130 (79%)	100 (97%)	3 (3%)	0	100	100
11	d	93/123 (76%)	90 (97%)	3 (3%)	0	100	100
11	h	91/123 (74%)	90 (99%)	1 (1%)	0	100	100
12	x	1/7 (14%)	1 (100%)	0	0	100	100
All	All	2635/5135 (51%)	2449 (93%)	173 (7%)	13 (0%)	27	56

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	970	LYS
1	A	1260	ALA
2	B	316	ARG
4	G	102	ILE
4	G	394	SER

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	508/1391 (36%)	472 (93%)	36 (7%)	12	35
2	B	326/367 (89%)	312 (96%)	14 (4%)	25	57
3	D	263/359 (73%)	244 (93%)	19 (7%)	12	34
3	E	233/359 (65%)	214 (92%)	19 (8%)	9	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	F	85/653 (13%)	77 (91%)	8 (9%)	7	23
4	G	349/653 (53%)	318 (91%)	31 (9%)	8	25
5	H	1/1 (100%)	1 (100%)	0	100	100
8	a	87/110 (79%)	83 (95%)	4 (5%)	23	55
8	e	87/110 (79%)	87 (100%)	0	100	100
9	b	66/79 (84%)	64 (97%)	2 (3%)	36	70
9	f	63/79 (80%)	62 (98%)	1 (2%)	58	85
10	c	82/102 (80%)	80 (98%)	2 (2%)	44	77
10	g	83/102 (81%)	82 (99%)	1 (1%)	67	89
11	d	81/103 (79%)	77 (95%)	4 (5%)	21	52
11	h	79/103 (77%)	75 (95%)	4 (5%)	20	51
12	x	1/1 (100%)	1 (100%)	0	100	100
All	All	2394/4572 (52%)	2249 (94%)	145 (6%)	18	43

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	G	417	CYS
11	h	83	ARG
4	G	476	LYS
8	a	120	MET
2	B	330	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
8	a	39	HIS
9	b	75	HIS
9	f	75	HIS
1	A	1252	HIS
2	B	291	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	ML3	a	36	8	10,11,12	2.57	1 (10%)	11,14,16	1.10	1 (9%)
8	ML3	e	36	8	10,11,12	2.57	1 (10%)	11,14,16	1.52	2 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	ML3	a	36	8	-	3/8/10/12	-
8	ML3	e	36	8	-	3/8/10/12	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	a	36	ML3	CA-N	-7.56	1.26	1.48
8	e	36	ML3	CA-N	-7.53	1.27	1.48

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	e	36	ML3	CB-CA-C	-3.75	100.63	110.80
8	a	36	ML3	CB-CA-C	-2.75	103.34	110.80
8	e	36	ML3	CB-SG-CD	2.62	110.04	102.26

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	a	36	ML3	N-CA-CB-SG
8	a	36	ML3	C-CA-CB-SG
8	e	36	ML3	N-CA-CB-SG
8	e	36	ML3	C-CA-CB-SG
8	e	36	ML3	SG-CD-CE-NZ

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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.

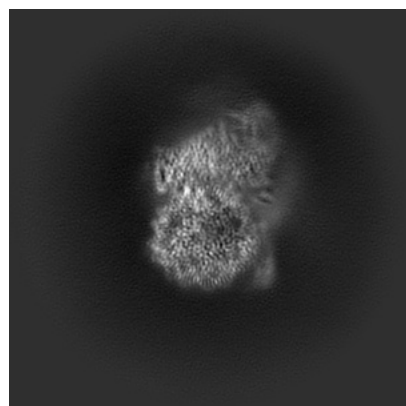
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41449. These allow visual inspection of the internal detail of the map and identification of artifacts.

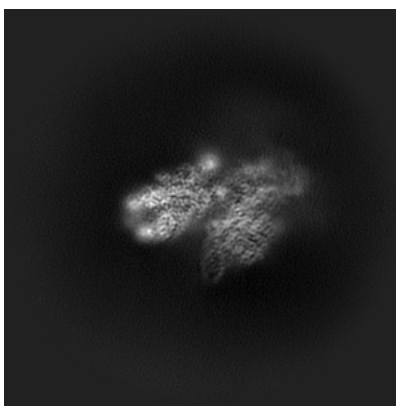
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

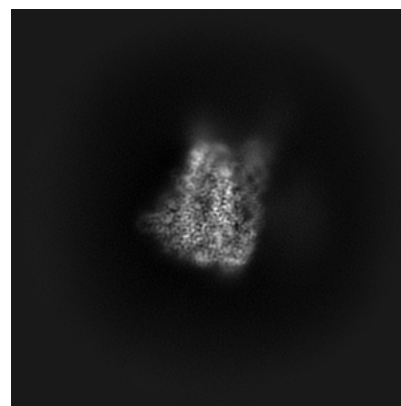
#### 6.1.1 Primary map



X

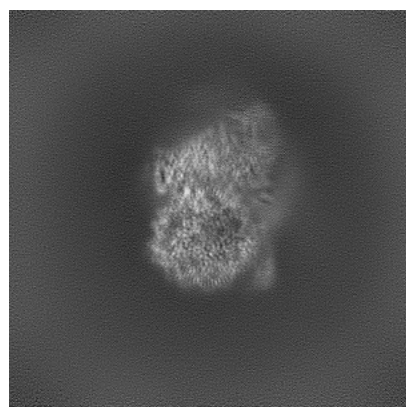


Y

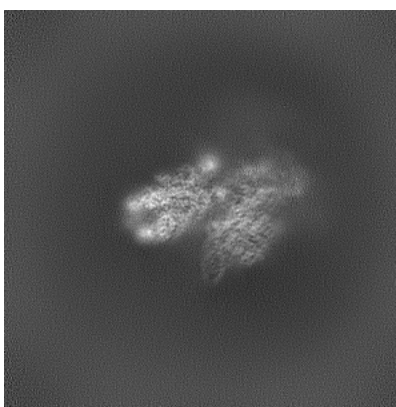


Z

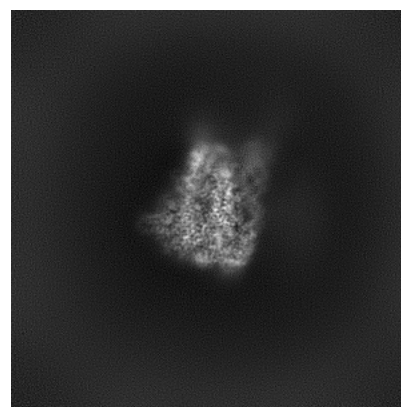
#### 6.1.2 Raw map



X



Y

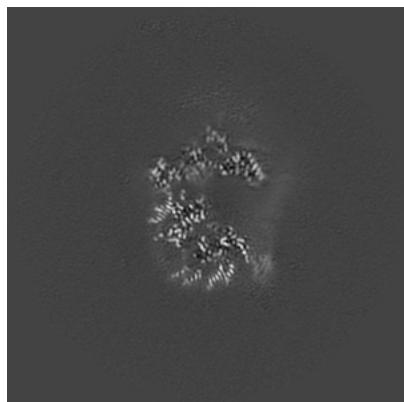


Z

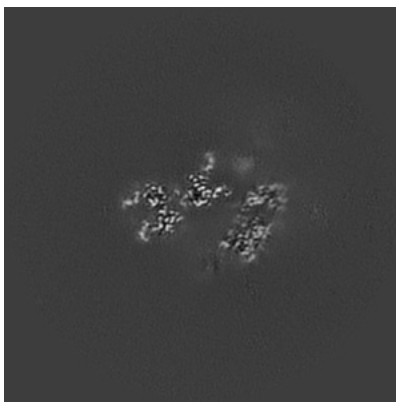
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

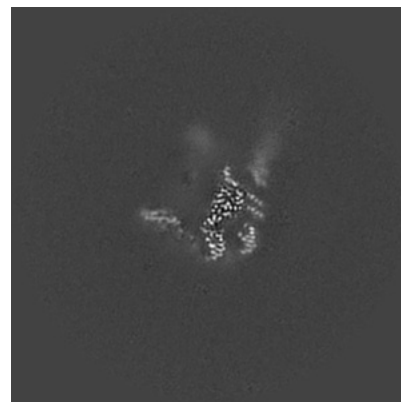
### 6.2.1 Primary map



X Index: 225

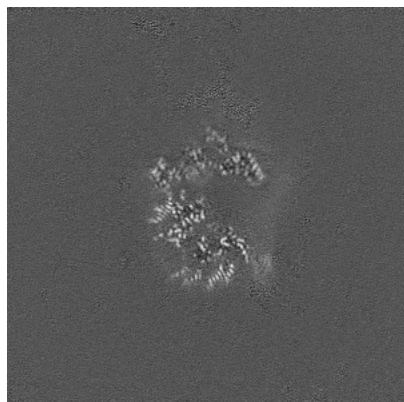


Y Index: 225

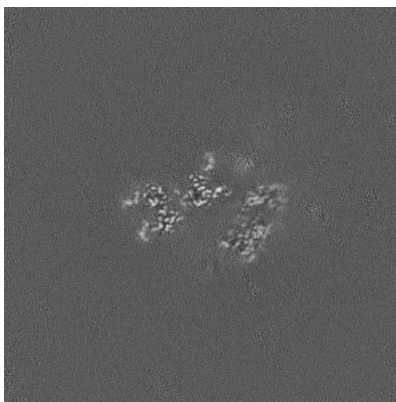


Z Index: 225

### 6.2.2 Raw map



X Index: 225



Y Index: 225



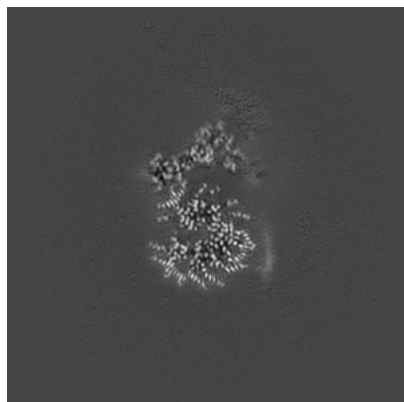
Z Index: 225

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

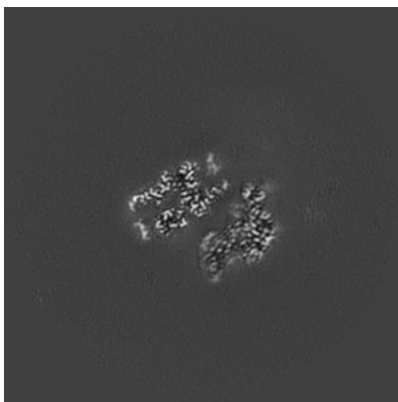


## 6.3 Largest variance slices [i](#)

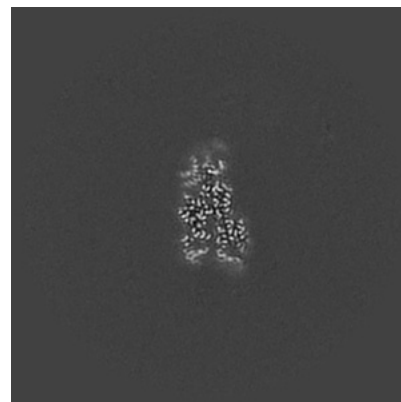
### 6.3.1 Primary map



X Index: 234

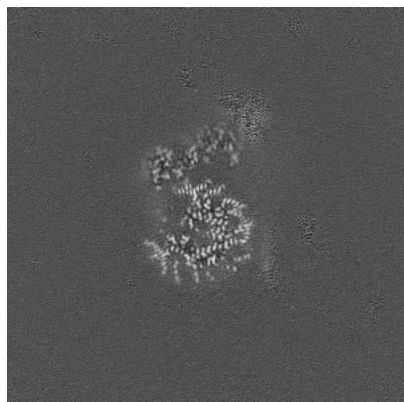


Y Index: 208

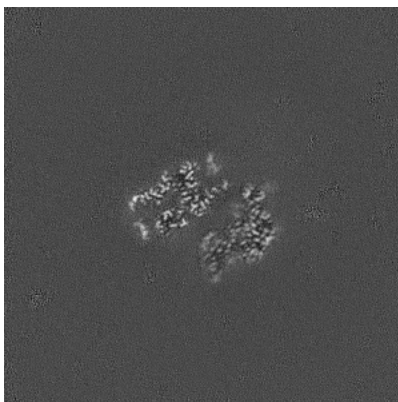


Z Index: 178

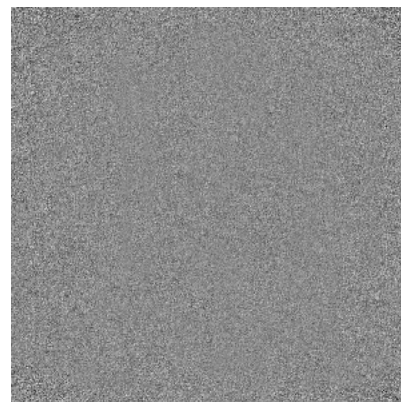
### 6.3.2 Raw map



X Index: 241



Y Index: 208



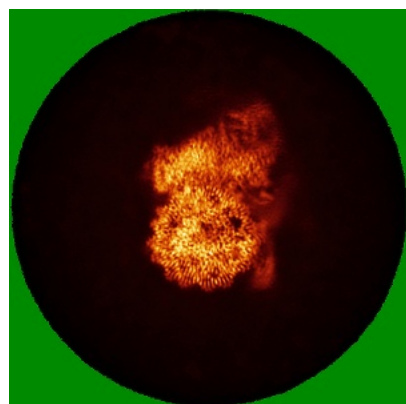
Z Index: 0

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

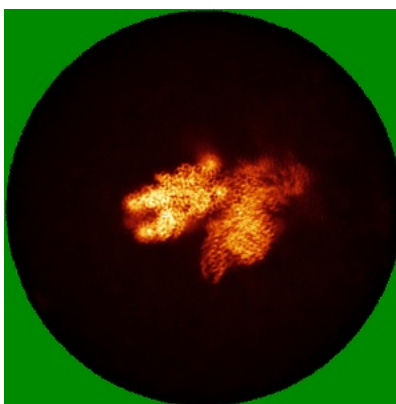


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

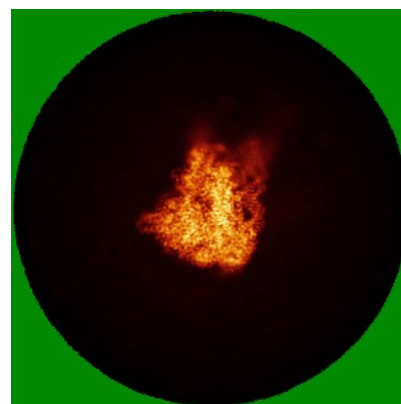
### 6.4.1 Primary map



X

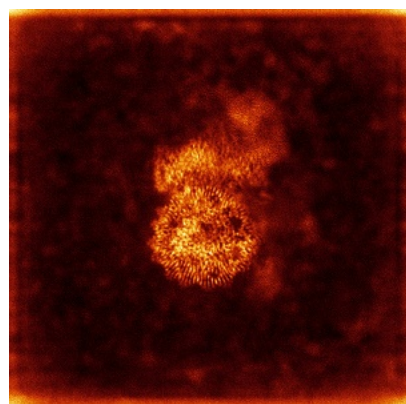


Y

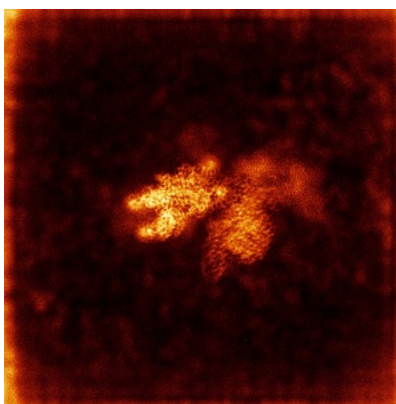


Z

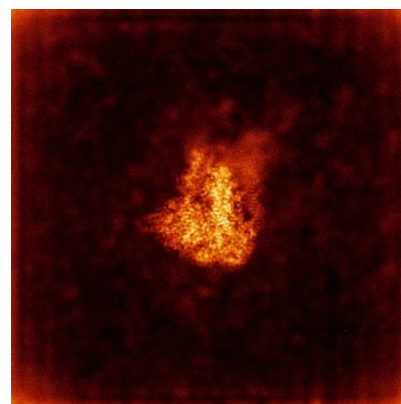
### 6.4.2 Raw map



X



Y



Z

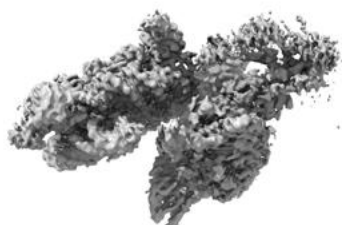
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

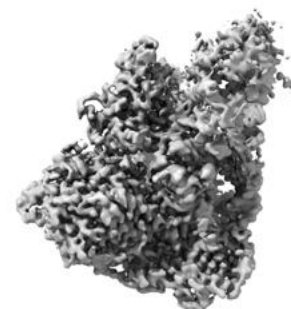
### 6.5.1 Primary map



X



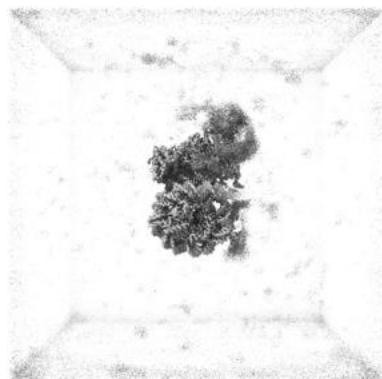
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07768. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

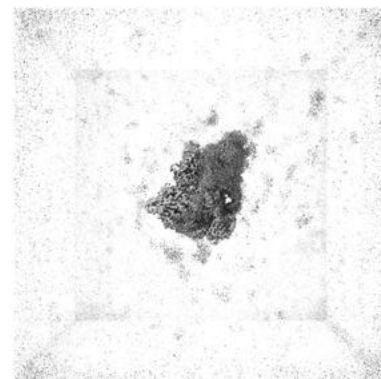
### 6.5.2 Raw map



X



Y



Z

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.

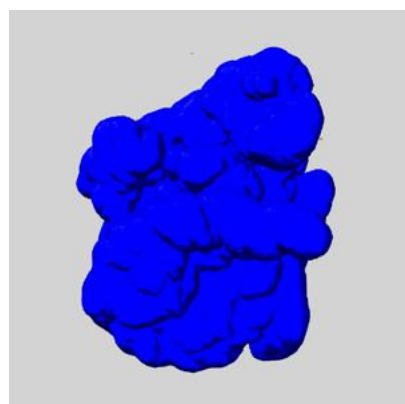
## 6.6 Mask visualisation [i](#)

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

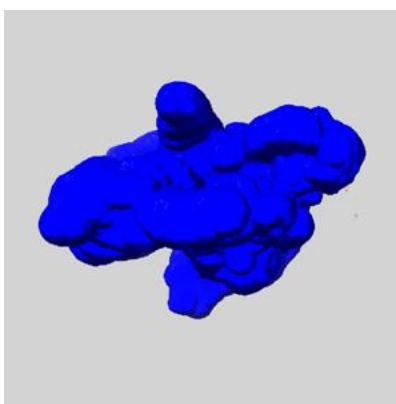
A mask typically either:

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

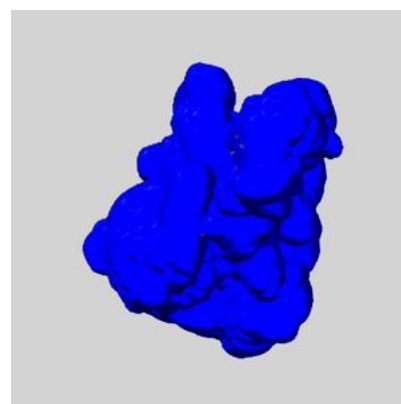
### 6.6.1 emd\_41449\_msk\_1.map [i](#)



X



Y

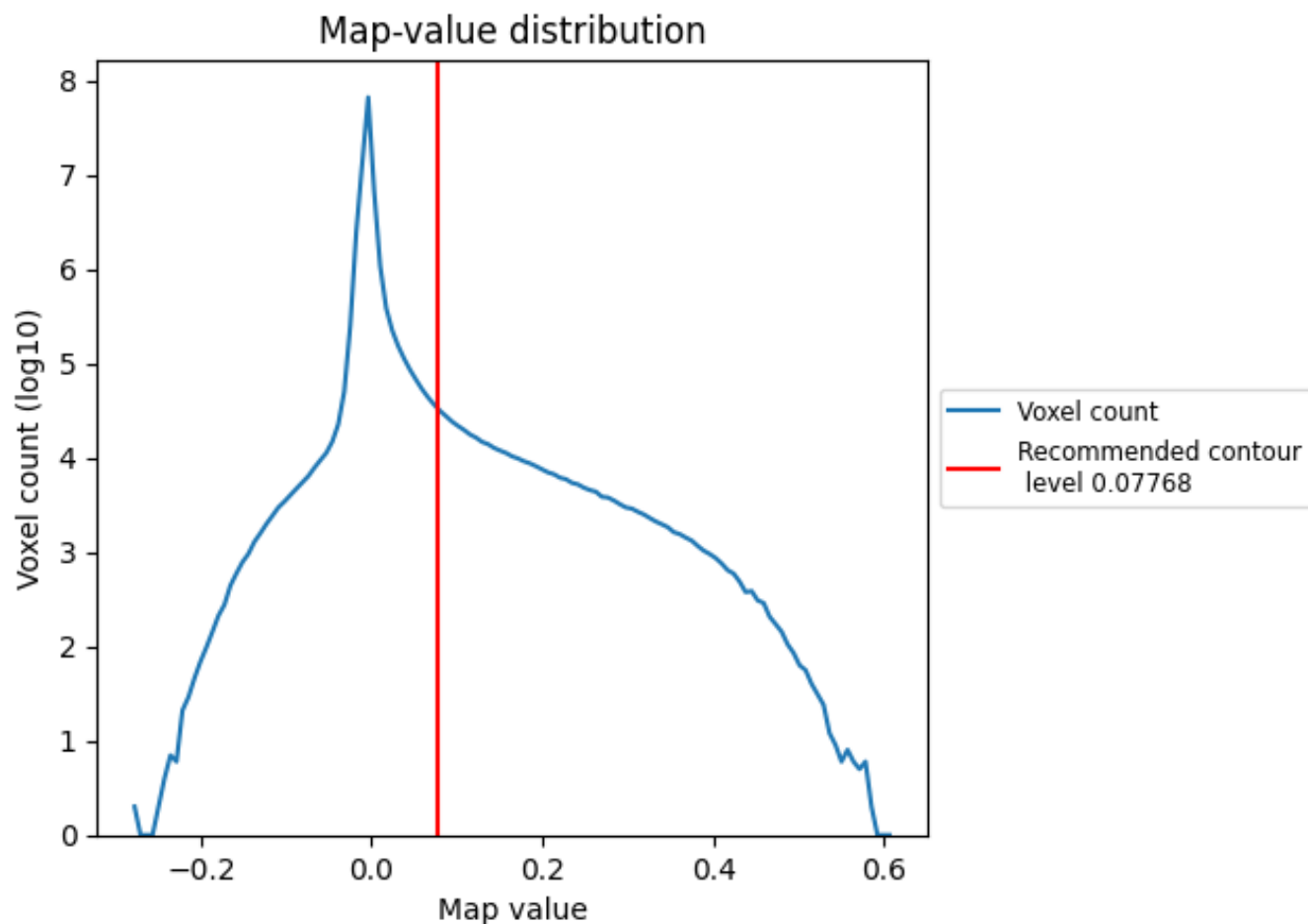


Z

## 7 Map analysis [i](#)

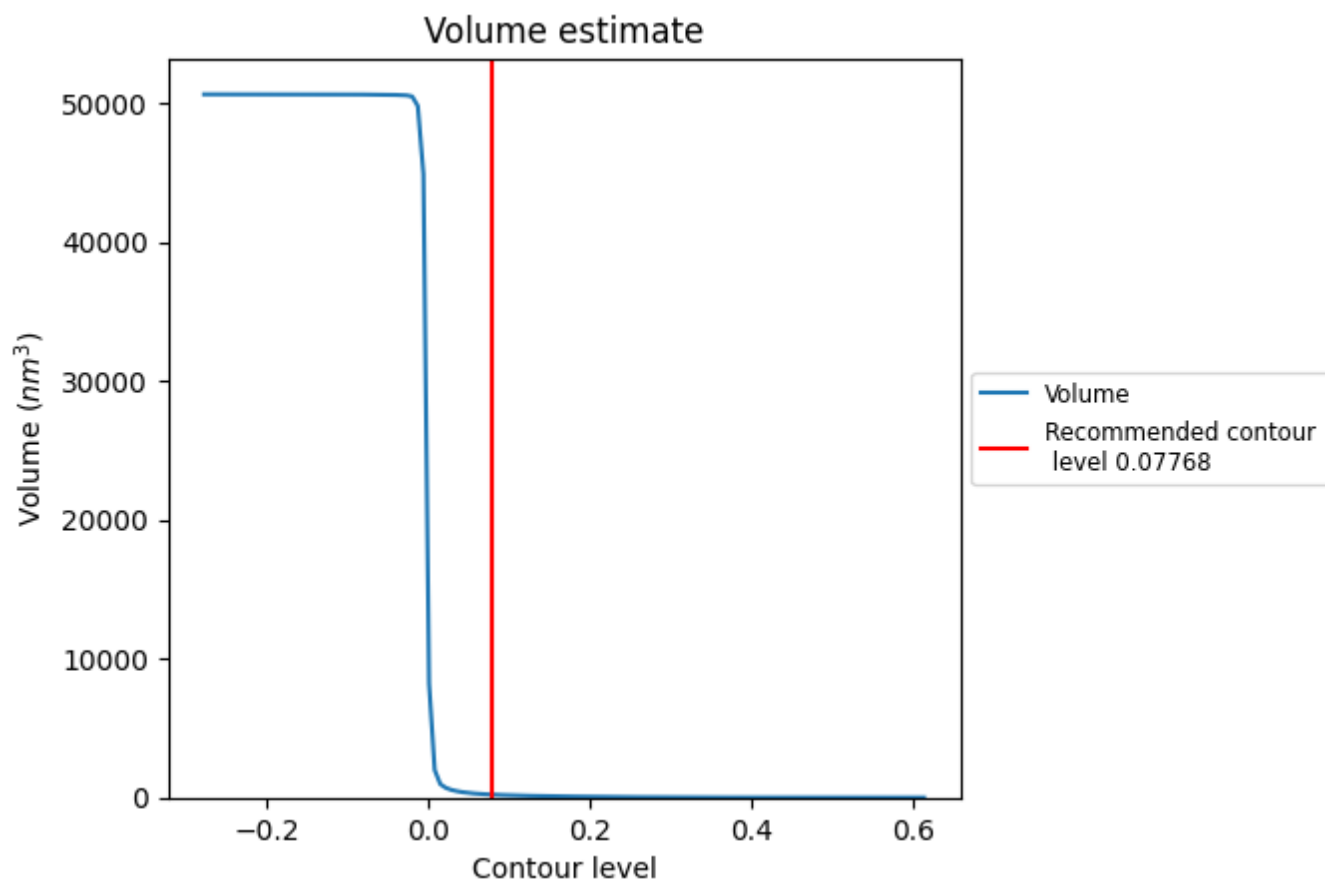
This section contains the results of statistical analysis of the map.

### 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.

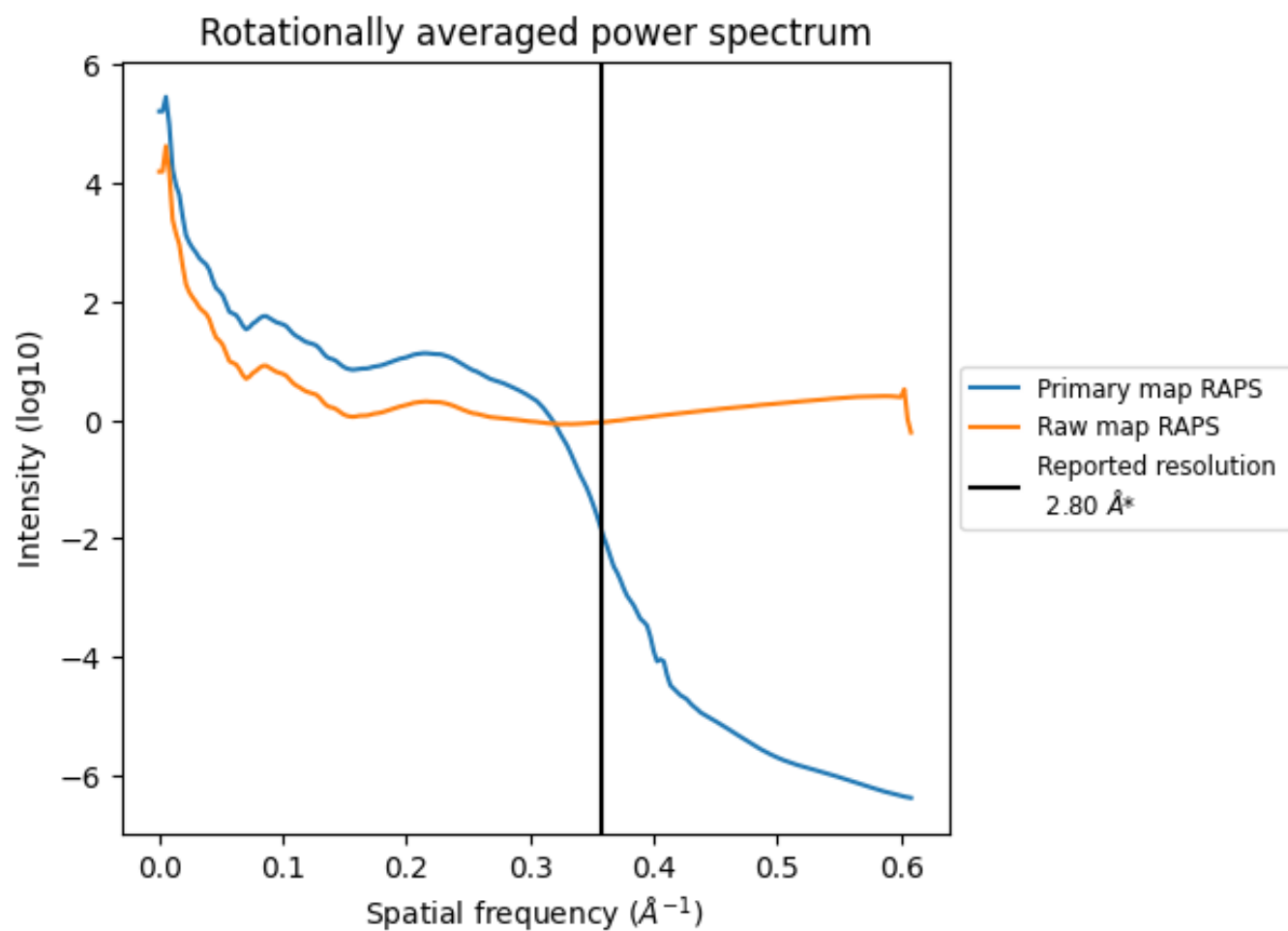
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 215 nm<sup>3</sup>; this corresponds to an approximate mass of 194 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 ⓘ

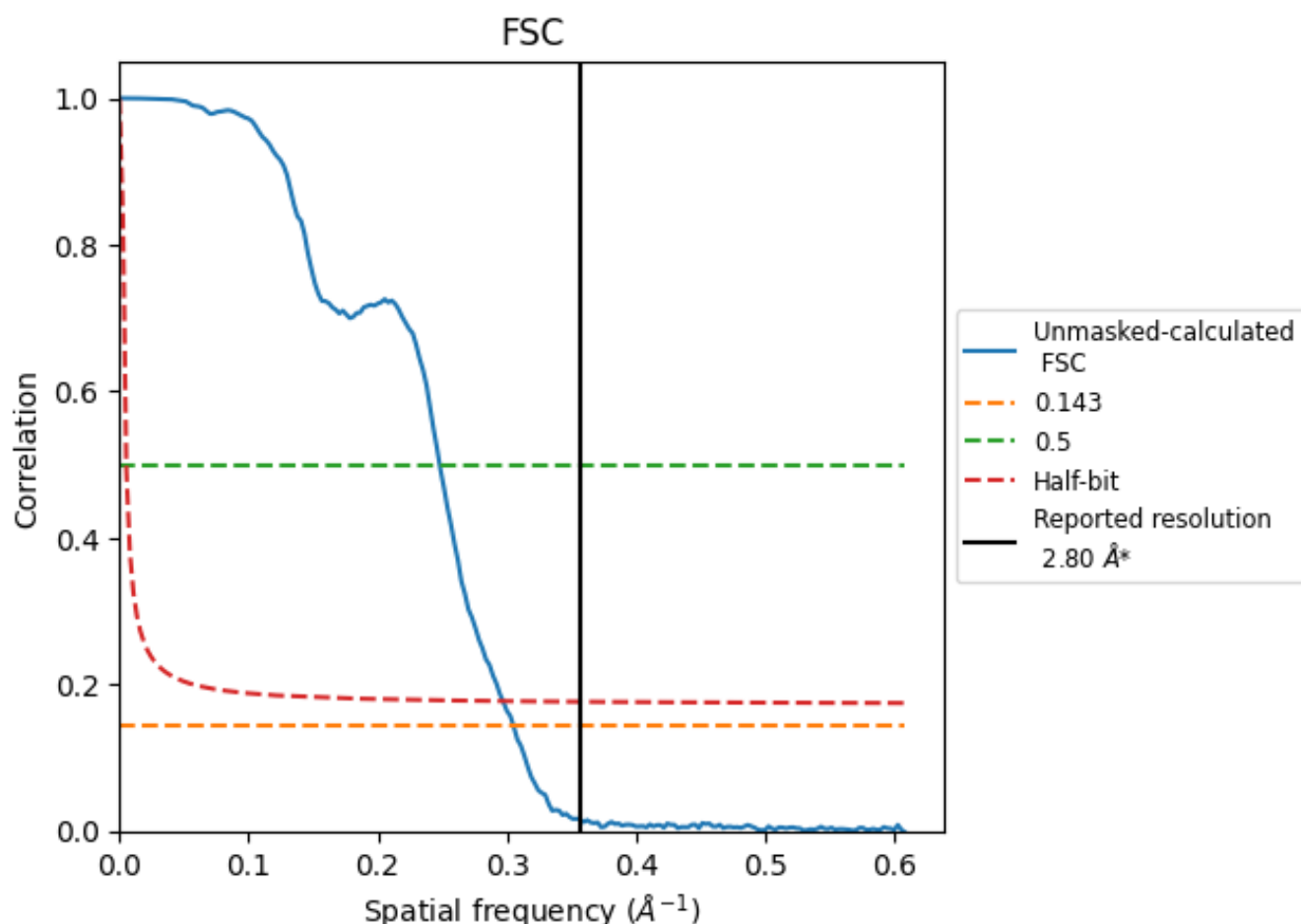


\*Reported resolution corresponds to spatial frequency of 0.357 Å<sup>-1</sup>

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.357  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.28	4.03	3.37

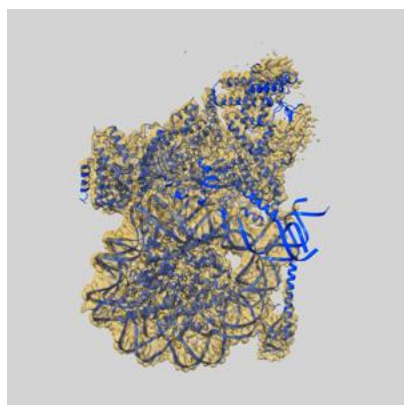
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.28 differs from the reported value 2.8 by more than 10 %



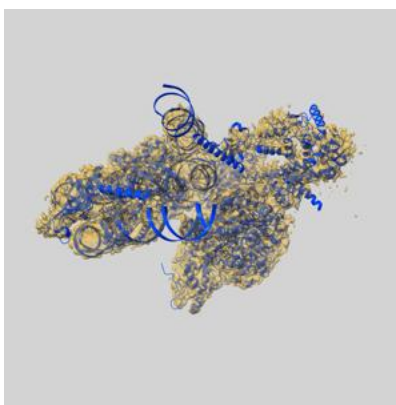
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41449 and PDB model 8TOF. Per-residue inclusion information can be found in section [3](#) on page [7](#).

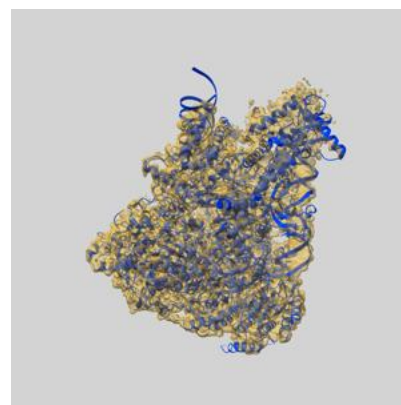
### 9.1 Map-model overlay [i](#)



X



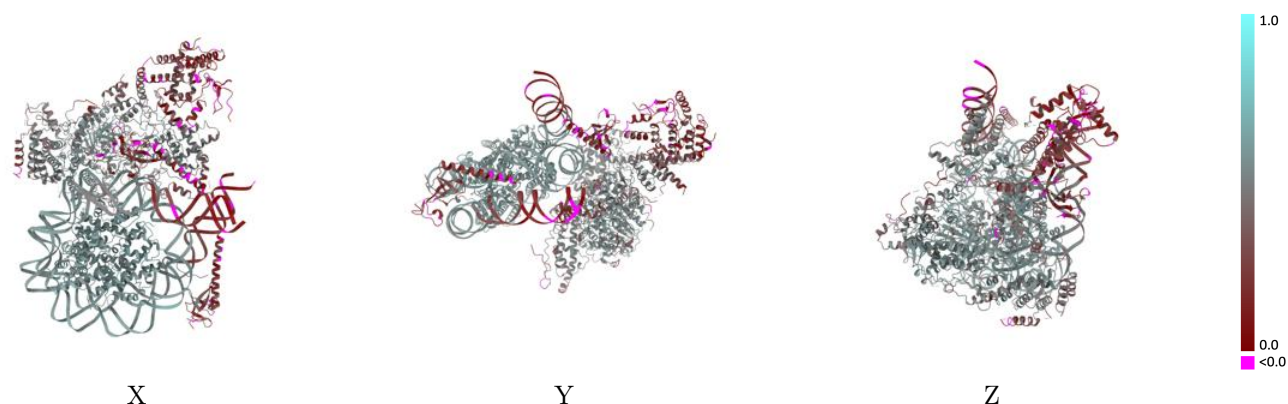
Y



Z

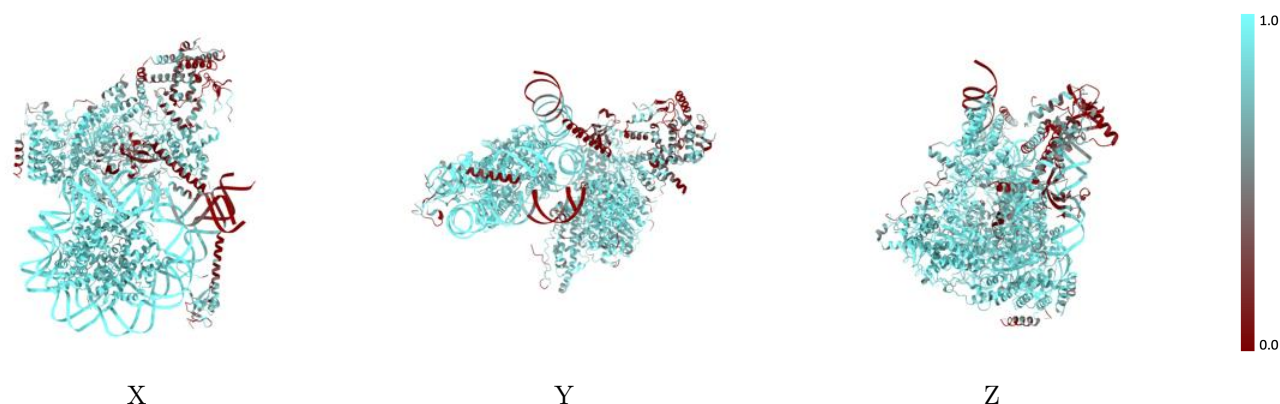
The images above show the 3D surface view of the map at the recommended contour level 0.07768 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



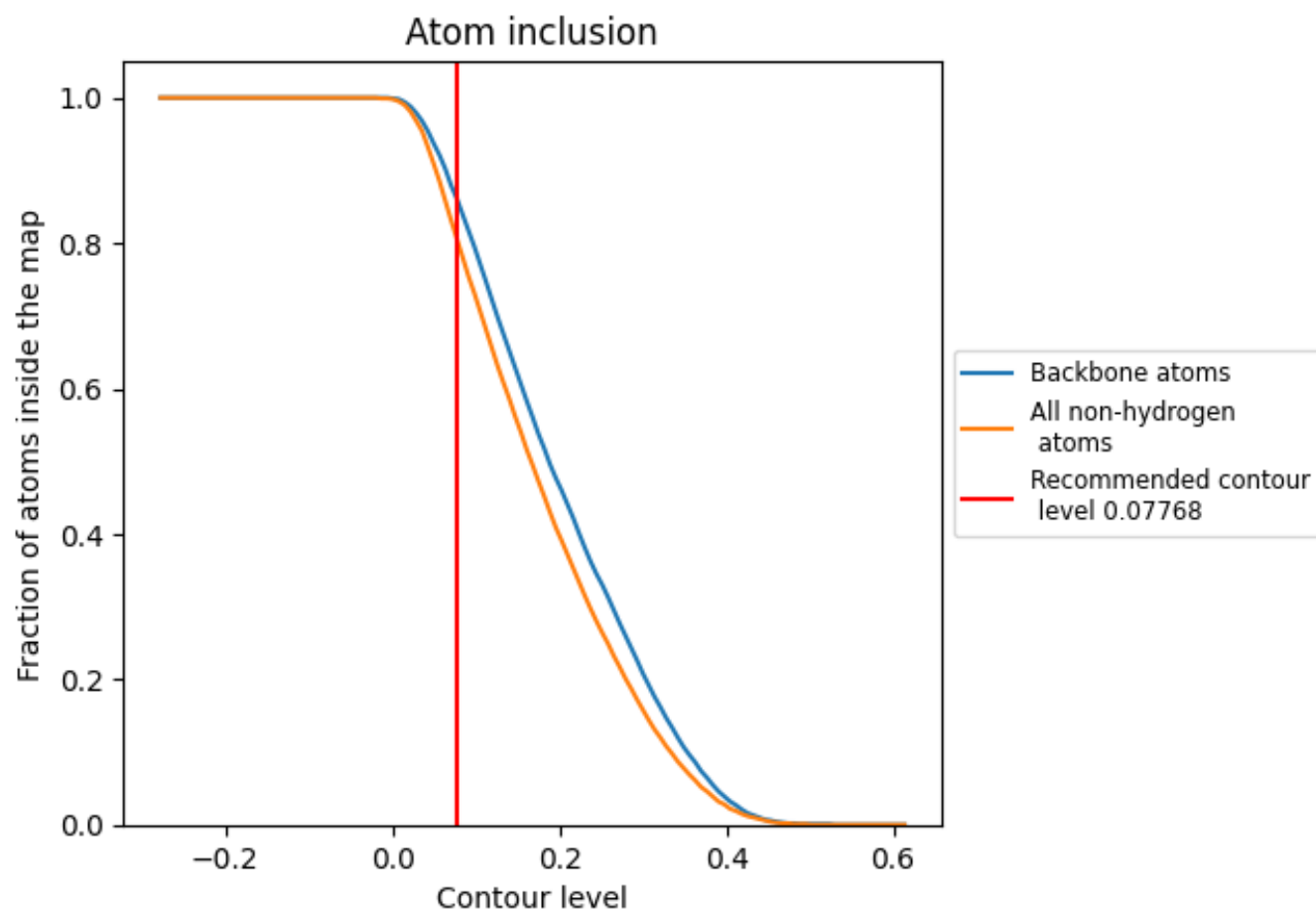
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07768).







































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.07768) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8050	 0.4640
A	 0.8090	 0.4690
B	 0.9270	 0.5460
D	 0.7460	 0.4060
E	 0.3420	 0.2070
F	 0.3550	 0.1550
G	 0.7130	 0.4160
H	 0.6550	 0.5430
N	 0.8750	 0.4780
T	 0.8620	 0.4700
a	 0.9290	 0.5780
b	 0.9310	 0.5850
c	 0.9680	 0.5890
d	 0.9410	 0.5660
e	 0.9500	 0.5780
f	 0.9770	 0.5940
g	 0.9630	 0.5870
h	 0.9620	 0.5740
x	 0.4360	 0.4010

