



## wwPDB EM Validation Summary Report ⓘ

Jun 8, 2026 – 04:24 PM EDT

PDB ID : 9OKL / pdb\_00009okl  
EMDB ID : EMD-70568  
Title : Structure of the Bombyx mori apo-bmCCAN  
Authors : Yatskevich, S.; Ciferri, C.  
Deposited on : 2025-05-10  
Resolution : 3.00 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:

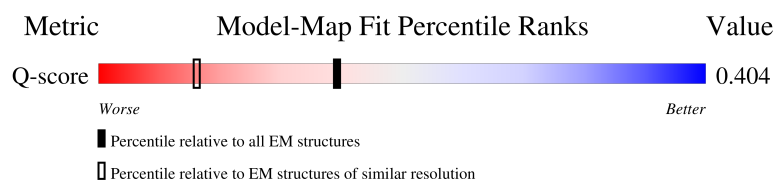
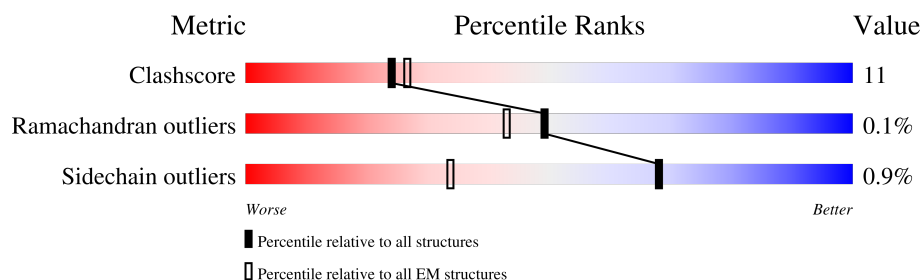
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

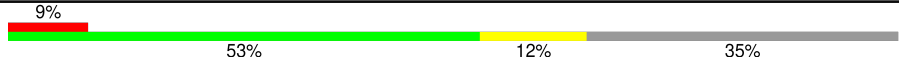
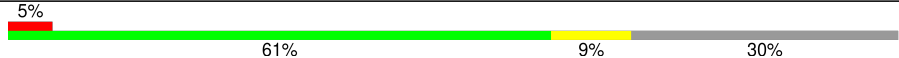


The reported resolution of this entry is 3.00 Å.

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.





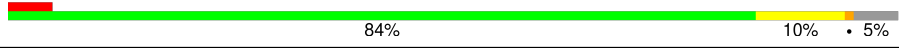



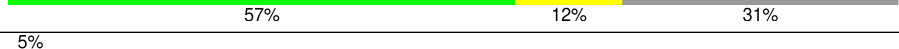
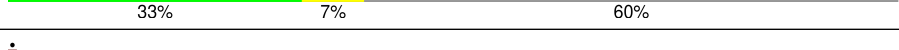
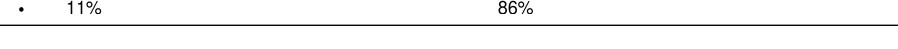
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 ( 2.50 - 3.50 )

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	108	
2	B	82	
3	C	71	
4	D	81	

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Mol	Chain	Length	Quality of chain
5	H	239	 77%18%5%
6	I	661	 66%15%19%
7	K	219	 84%10%5%
8	L	302	 65%14%21%
9	M	180	 80%11%9%
10	N	328	 81%16%
11	O	325	 57%12%31%
12	P	638	 33%7%60%
13	T	1016	 11%86%

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 39509 atoms, of which 18862 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 CS-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	70	Total	C	H	N	O	0	0
			1108	342	558	99	109		

- Molecule 2 is a protein called CS-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	57	Total	C	H	N	O S	0	0
			907	282	459	74	91 1		

- Molecule 3 is a protein called SFRICE\_007223.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	55	Total	C	H	N	O S	0	0
			880	270	441	78	87 4		

- Molecule 4 is a protein called CS-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	71	Total	C	H	N	O S	0	0
			1050	357	481	103	108 1		

- Molecule 5 is a protein called bm-CENPH.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	228	Total	C	H	N	O S	0	0
			3517	1170	1666	326	345 10		

- Molecule 6 is a protein called Centromere protein I.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	534	Total	C	H	N	O S	0	0
			8726	2815	4397	721	774 19		

- Molecule 7 is a protein called bmCENP-K.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	K	208	Total	C	H	N	O	S	0	0
			3282	1025	1639	272	337	9		

- Molecule 8 is a protein called Centromere protein L.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	L	239	Total	C	H	N	O	S	0	0
			3880	1237	1974	309	353	7		

- Molecule 9 is a protein called Centromere protein M.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	M	163	Total	C	H	N	O	S	0	0
			2626	818	1340	225	240	3		

- Molecule 10 is a protein called bmCENP-N.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	N	319	Total	C	H	N	O	S	0	0
			5105	1604	2583	440	465	13		

- Molecule 11 is a protein called Centromere protein O.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	O	224	Total	C	H	N	O	S	0	0
			3317	1163	1487	320	335	12		

- Molecule 12 is a protein called bmCENP-P.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	P	255	Total	C	H	N	O	S	0	0
			3868	1290	1837	343	387	11		

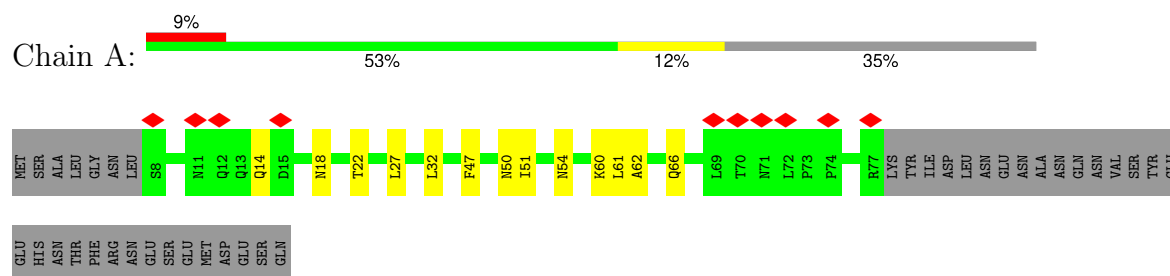
- Molecule 13 is a protein called bmCENP-T.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	146	Total	C	N	O	S	0	0
			1243	803	220	216	4		

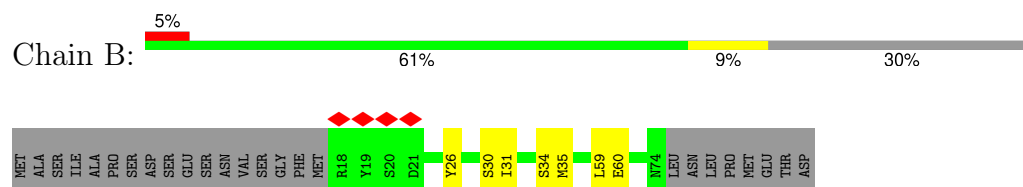
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

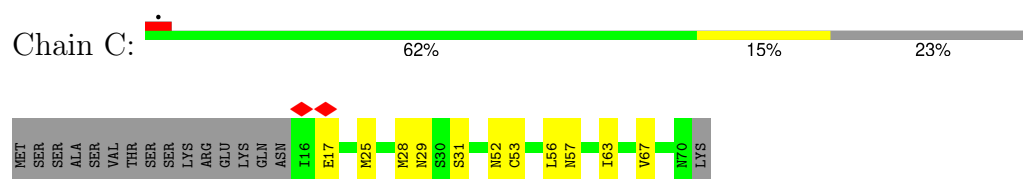
#### • Molecule 1: CS-1



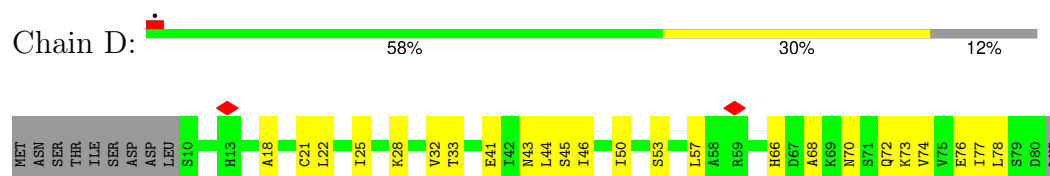
#### • Molecule 2: CS-2



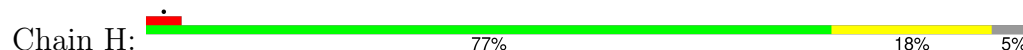
#### • Molecule 3: SFRICE\_007223

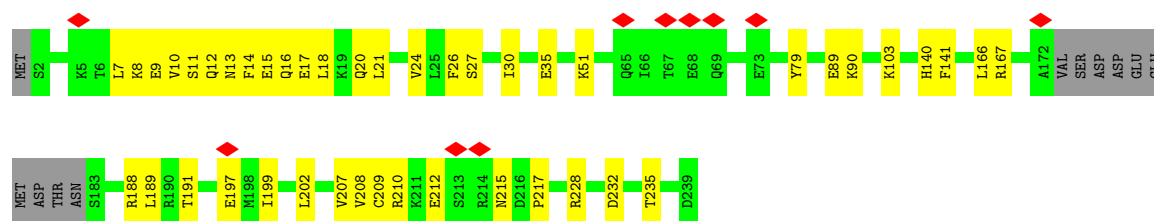


#### • Molecule 4: CS-4



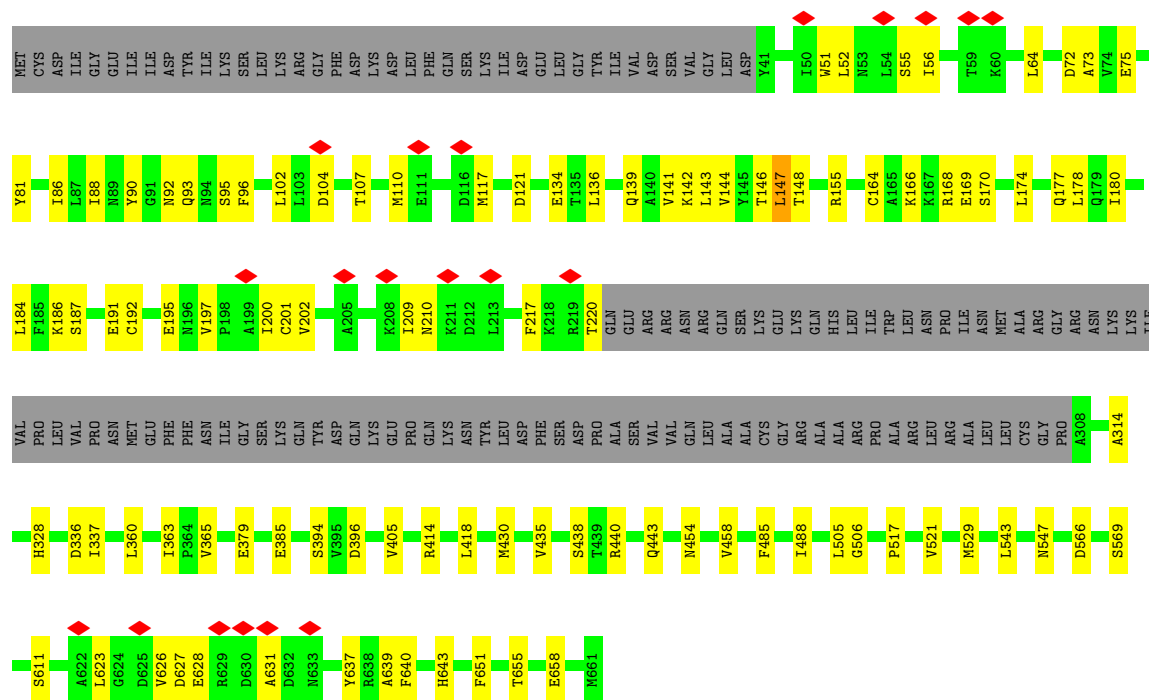
#### • Molecule 5: bm-CENPH





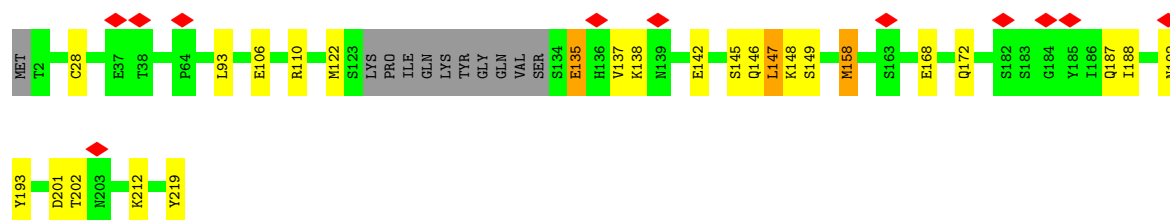
• Molecule 6: Centromere protein I

Chain I: 66% 15% 19%



• Molecule 7: bmCENP-K

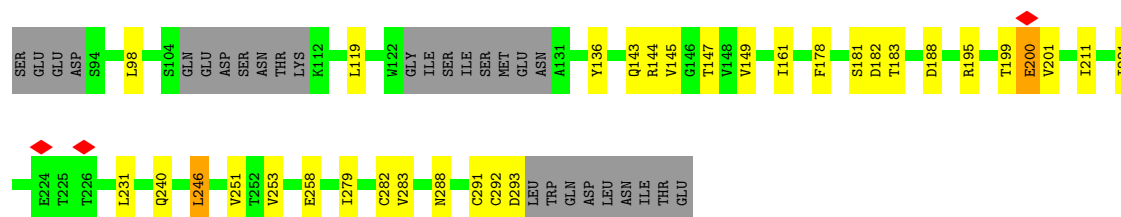
Chain K: 5% 84% 10% 5%



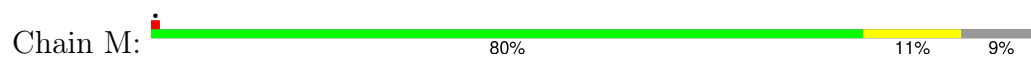
• Molecule 8: Centromere protein L

Chain L: 65% 14% 21%

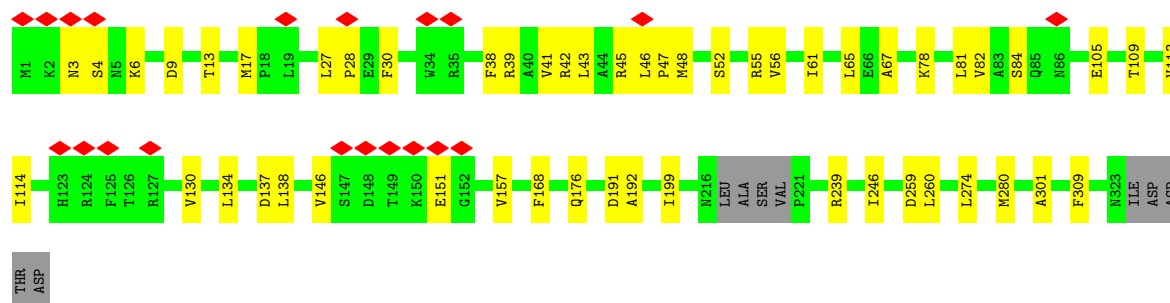
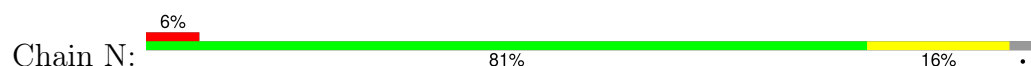




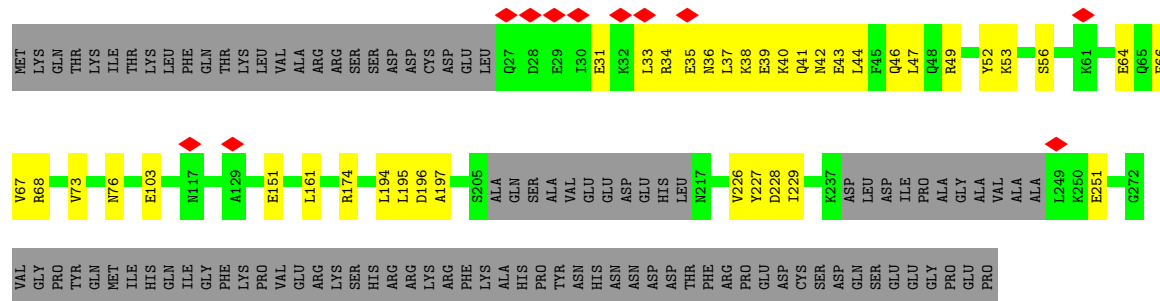
• Molecule 9: Centromere protein M



• Molecule 10: bmCENP-N



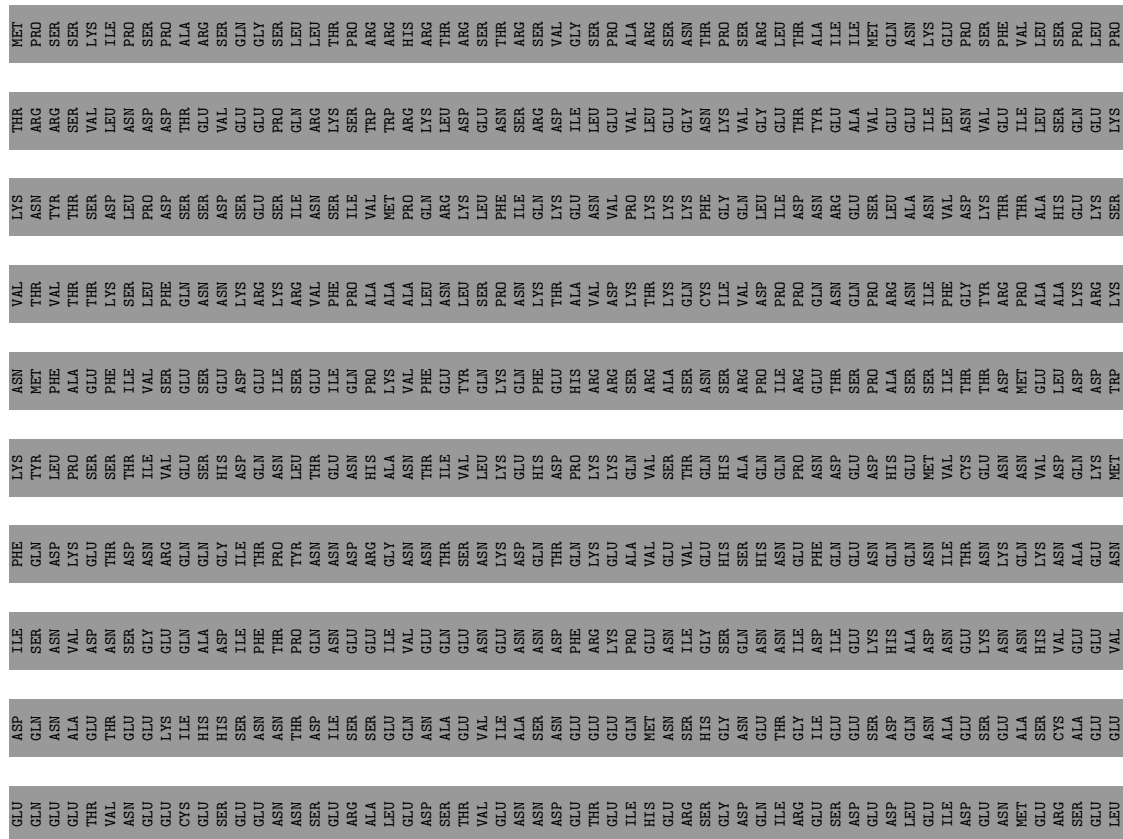
• Molecule 11: Centromere protein O



• Molecule 12: bmCENP-P







D965	T905	PHE	GLY	PRO	GLY
I966	T906	ASN	TRP	GLU	ASN
K967	K907	PHE	ASP	ALA	GLU
K968	R908	LYS	SER	ILE	SER
T969	L909	VAL	HIS	HIS	ASN
H970	Y910	PRO	ARG	HIS	ALA
F971	K911	ALA	THR	ASP	SER
D972	Y912	LYS	THR	LYS	ASN
F973	L913	PRO	ARG	ASN	ASP
Y974	E914	LEU	LYS	GLU	GLU
Q975	D915	PHE	THR	THR	HIS
F976	K916	ALA	LEU	SER	LEU
F977	L917	ARG	GLN	ASP	LEU
H978	E918	HIS	THR	PHE	THR
	P919	SER	THR	ASN	SER
	K920	THR	ASN	GLY	ASP
	Y921	LYS	HIS	GLY	ASP
	D922	PRO	LYS	GLY	ASN
	Y923	VAL	ILE	ASP	ASN
	K924	GLN	PHE	ASN	ASP
A925	R926	ASN	THR	THR	GLU
R926	V927	LYS	PRO	THR	PRO
R927	R928	ASN	ARG	ARG	GLU
R928	A929	LYS	LYS	LEU	ASN
A929	E930	VAL	GLN	ARG	SER
K931	K931	ARG	LEU	LYS	SER
L932	L932	ALA	THR	THR	ALA
V933	V933	GLU	ARG	LYS	GLY
E934	E934	THR	THR	ALA	ALA
T935	T935	ILE	ILE	VAL	ASP
I936	I936	SER	MET	ILE	ASP
Y937	Y937	MET	GLU	MET	ILE
H938	H938	PRO	LYS	LEU	ASN
F939	F939	LEU	LYS	SER	ASN
T940	T940	ASP	ALA	ILE	ASP
K941	K941	LEU	LYS	ARG	ASN
E942	E942	PRO	GLN	PRO	SER
V943	V943	PRO	THR	SER	PRO
K944	K944	GLU	ALA	LEU	ASN
K945	K945	LEU	LEU	PRO	THR
H946	H946	LEU	VAL	ASN	ASP
E947	E947	ASP	ASP	VAL	LEU
V948	V948	MET	ALA	ASP	ASN
A949	A949	MET	LYS	GLU	ASN
P950	P950	K890	ILE	THR	ASN
N951	N951	Y891	GLU	ALA	GLU
D952	D952	K892	SER	ILE	SER
A953	A953	P893	THR	MET	ILE
V954	V954	P894	LYS	THR	THR
D955	D955	K895	MET	ASP	ASP
V956	V956	R896	PRO	GLY	ARG
L957	L957	Y897	GLN	THR	SER
K958	K958	Q898	ASN	ASN	THR
H959	H959	P899	LYS	VAL	VAL
E960	E960	K900	GLN	SER	SER
M961	M961	N901	CYS	THR	GLU
A962	A962	A902	LYS	GLU	LYS
R963	R963	S903	GLN	ILE	VAL
L964	L964	W904	ASN	PRO	GLY
			GLU	SER	LEU

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	265941	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.027	Depositor
Minimum map value	-0.822	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0514	Depositor
Map size (Å)	341.066, 346.932, 343.58	wwPDB
Map dimensions	407, 414, 410	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.838, 0.838, 0.83799994	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	A	0.09	0/554	0.20	0/750
2	B	0.10	0/453	0.25	0/613
3	C	0.10	0/440	0.18	0/591
4	D	0.11	0/573	0.22	0/768
5	H	0.12	0/1872	0.24	0/2508
6	I	0.10	0/4433	0.22	0/6015
7	K	0.11	0/1662	0.22	0/2243
8	L	0.10	0/1935	0.26	0/2614
9	M	0.12	0/1302	0.24	0/1764
10	N	0.12	0/2571	0.25	0/3483
11	O	0.10	0/1858	0.23	0/2490
12	P	0.09	0/2067	0.22	0/2803
13	T	0.09	0/1271	0.22	0/1705
All	All	0.11	0/20991	0.23	0/28347

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	550	558	566	8	0
2	B	448	459	458	9	0
3	C	439	441	449	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	569	481	605	24	0
5	H	1851	1666	1938	48	0
6	I	4329	4397	4395	69	0
7	K	1643	1639	1646	20	0
8	L	1906	1974	1969	29	0
9	M	1286	1340	1348	15	0
10	N	2522	2583	2592	48	0
11	O	1830	1487	1866	52	0
12	P	2031	1837	2067	52	0
13	T	1243	0	1284	157	0
All	All	20647	18862	21183	452	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 452 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)
13:T:917:LEU:HD13	13:T:928:ARG:HB3	1.33	1.10
13:T:978:HIS:HA	13:T:986:ARG:HD3	1.43	0.98
13:T:947:GLU:HG2	13:T:948:VAL:HG23	1.42	0.97
13:T:916:LYS:HD3	13:T:966:ILE:HA	1.44	0.96
13:T:900:LYS:H	13:T:900:LYS:HD2	1.32	0.93

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	68/108 (63%)	67 (98%)	1 (2%)	0	100	100
2	B	55/82 (67%)	55 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	53/71 (75%)	53 (100%)	0	0	100	100
4	D	69/81 (85%)	68 (99%)	1 (1%)	0	100	100
5	H	224/239 (94%)	220 (98%)	4 (2%)	0	100	100
6	I	530/661 (80%)	520 (98%)	10 (2%)	0	100	100
7	K	204/219 (93%)	203 (100%)	1 (0%)	0	100	100
8	L	229/302 (76%)	220 (96%)	7 (3%)	2 (1%)	14	48
9	M	161/180 (89%)	160 (99%)	1 (1%)	0	100	100
10	N	315/328 (96%)	302 (96%)	13 (4%)	0	100	100
11	O	218/325 (67%)	209 (96%)	9 (4%)	0	100	100
12	P	251/638 (39%)	247 (98%)	4 (2%)	0	100	100
13	T	142/1016 (14%)	137 (96%)	5 (4%)	0	100	100
All	All	2519/4250 (59%)	2461 (98%)	56 (2%)	2 (0%)	49	80

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	L	200	GLU
8	L	201	VAL

### 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	62/97 (64%)	60 (97%)	2 (3%)	34	67
2	B	53/75 (71%)	53 (100%)	0	100	100
3	C	51/66 (77%)	51 (100%)	0	100	100
4	D	66/76 (87%)	63 (96%)	3 (4%)	24	59
5	H	206/217 (95%)	206 (100%)	0	100	100
6	I	473/584 (81%)	471 (100%)	2 (0%)	84	90
7	K	188/198 (95%)	182 (97%)	6 (3%)	34	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	L	218/277 (79%)	215 (99%)	3 (1%)	59	80
9	M	147/161 (91%)	147 (100%)	0	100	100
10	N	282/290 (97%)	280 (99%)	2 (1%)	76	86
11	O	206/295 (70%)	206 (100%)	0	100	100
12	P	231/579 (40%)	231 (100%)	0	100	100
13	T	138/942 (15%)	135 (98%)	3 (2%)	45	74
All	All	2321/3857 (60%)	2300 (99%)	21 (1%)	68	85

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	L	144	ARG
10	N	274	LEU
13	T	977	PHE
13	T	890	LYS
10	N	137	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
11	O	76	ASN
11	O	217	ASN
11	O	176	GLN
11	O	252	GLN
6	I	93	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



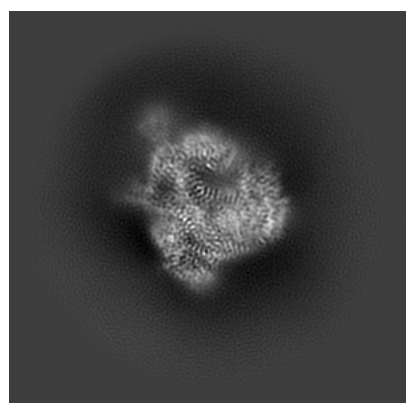
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70568. These allow visual inspection of the internal detail of the map and identification of artifacts.

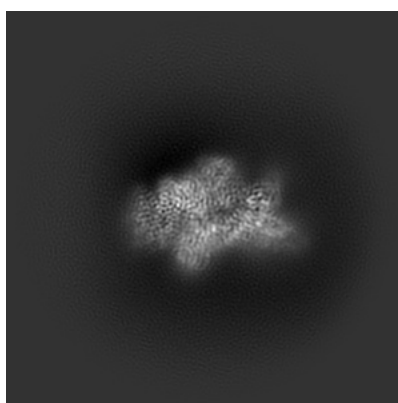
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

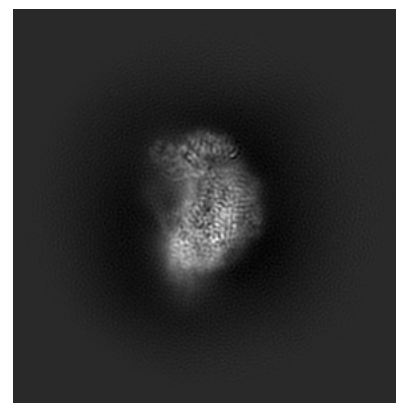
#### 6.1.1 Primary map



X



Y

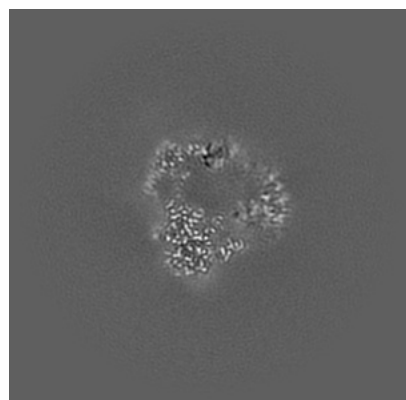


Z

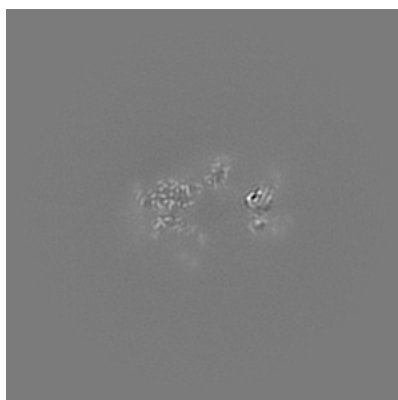
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

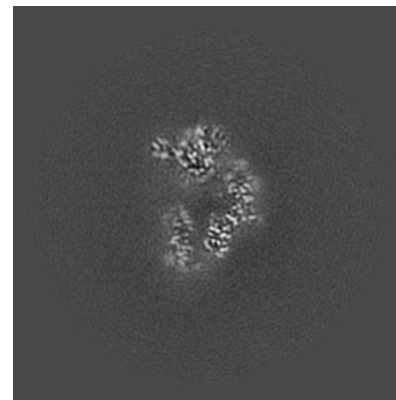
#### 6.2.1 Primary map



X Index: 203



Y Index: 207

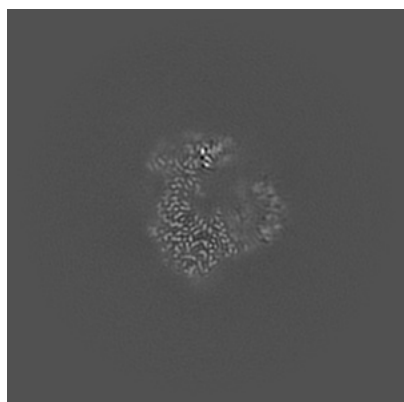


Z Index: 205

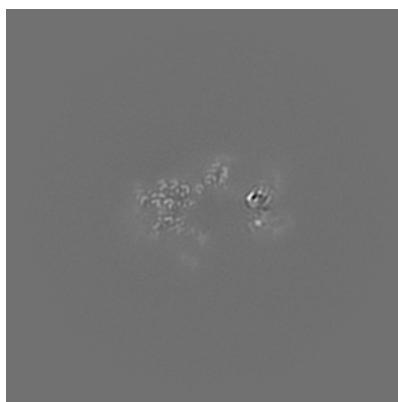
The images above show central slices of the map in three orthogonal directions.

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

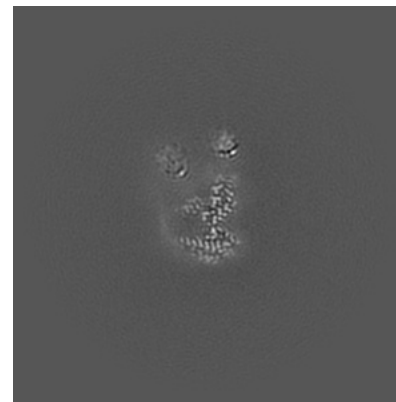
### 6.3.1 Primary map



X Index: 211



Y Index: 206

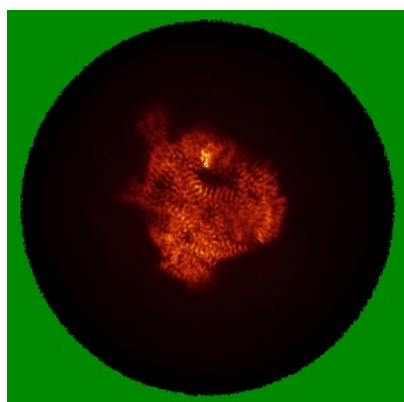


Z Index: 176

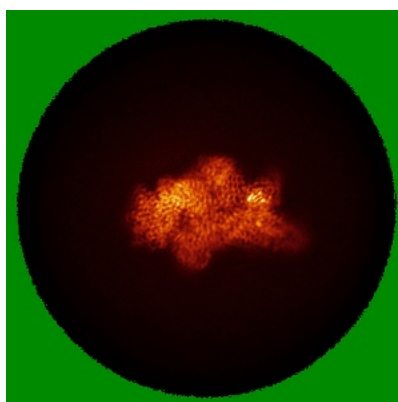
The images above show the largest variance slices of the map in three orthogonal directions.

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

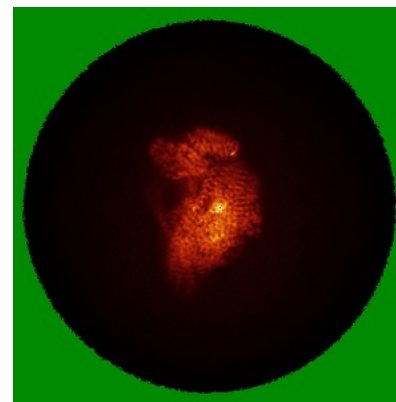
### 6.4.1 Primary map



X



Y

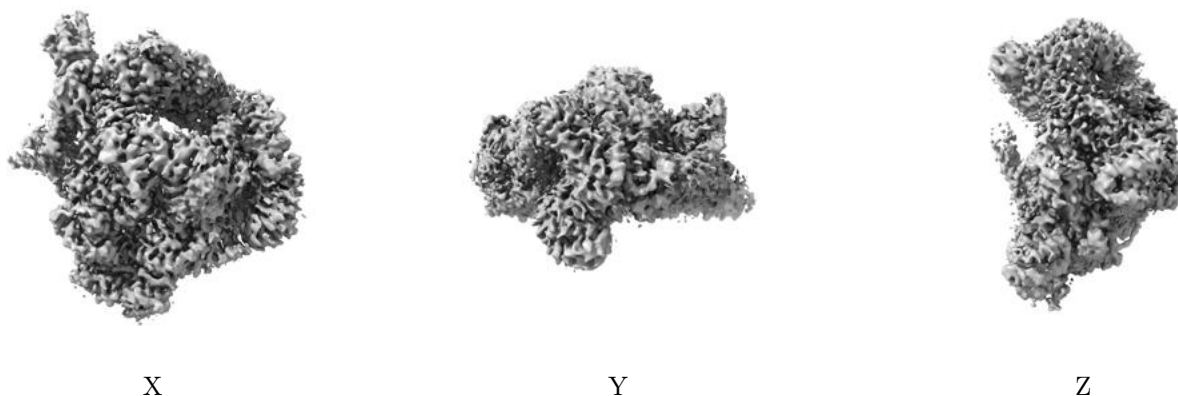


Z

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 0.0514. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

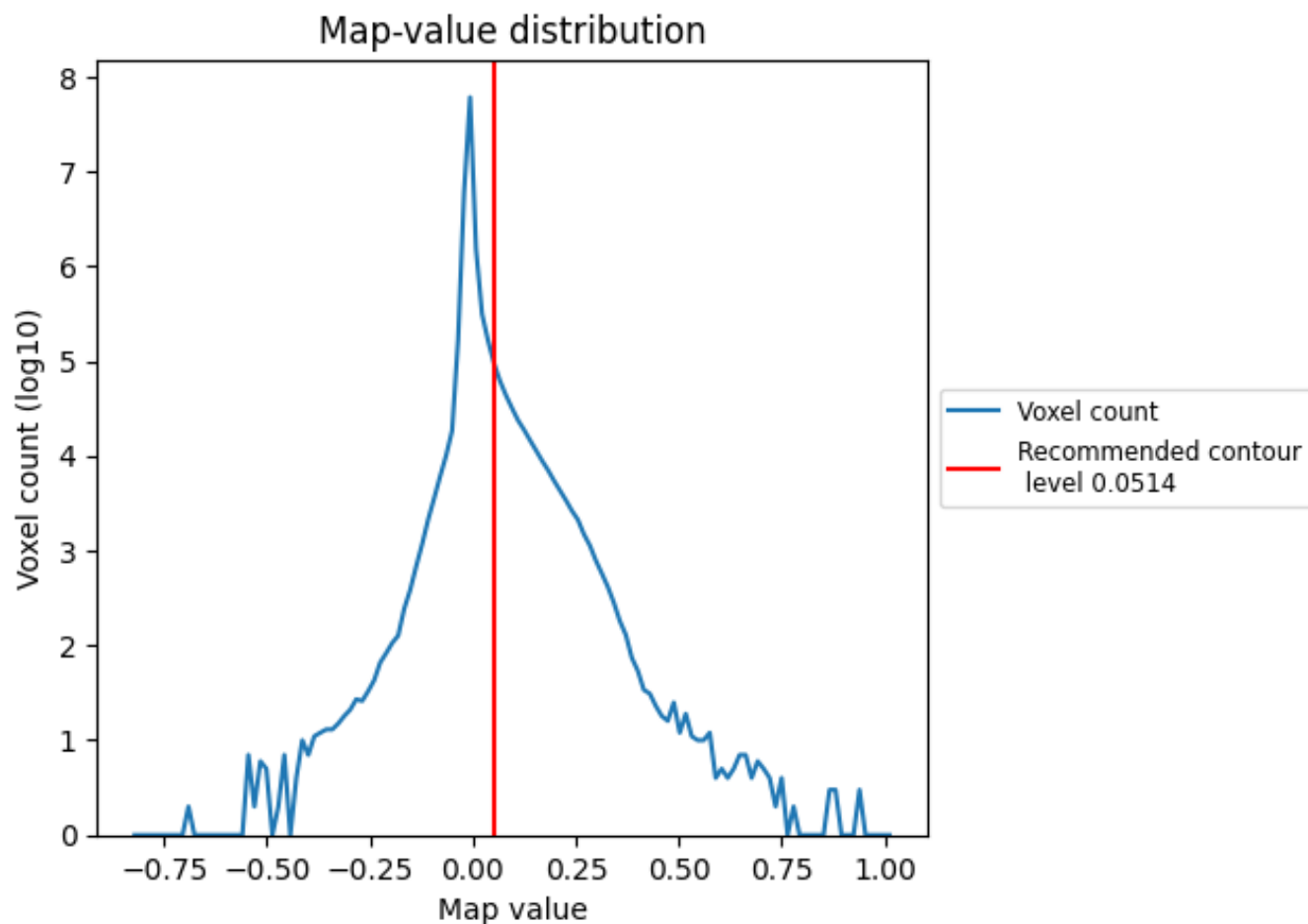
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

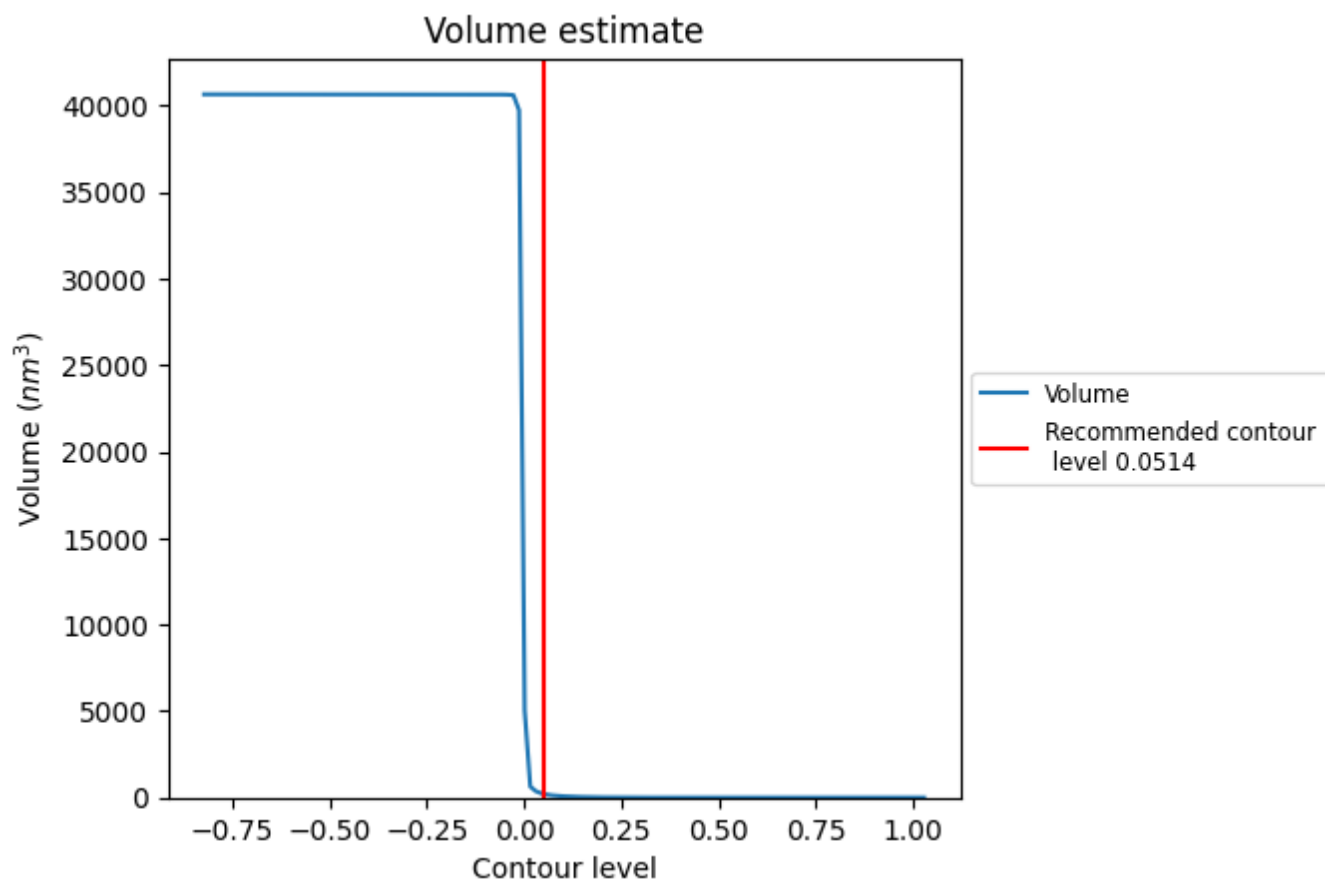
This section contains the results of statistical analysis of the map.

### 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 206 nm<sup>3</sup>; this corresponds to an approximate mass of 186 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

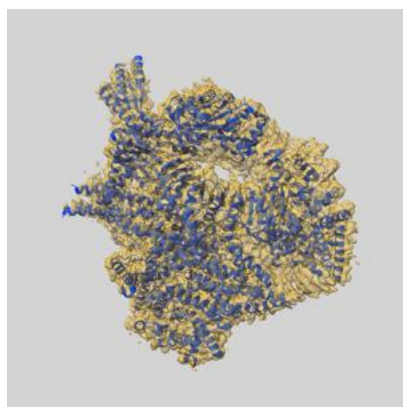
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

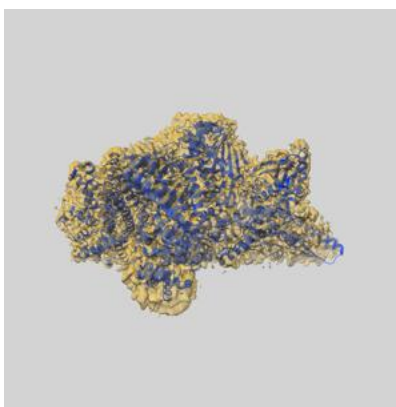
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-70568 and PDB model 9OKL. Per-residue inclusion information can be found in section [3](#) on page [6](#).

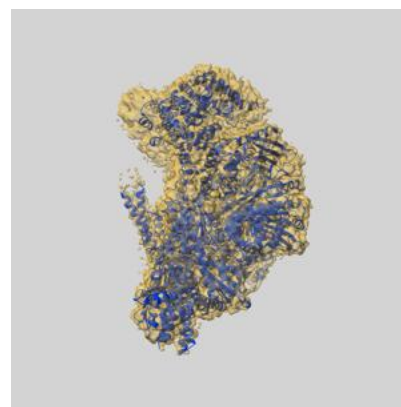
### 9.1 Map-model overlay [i](#)



X



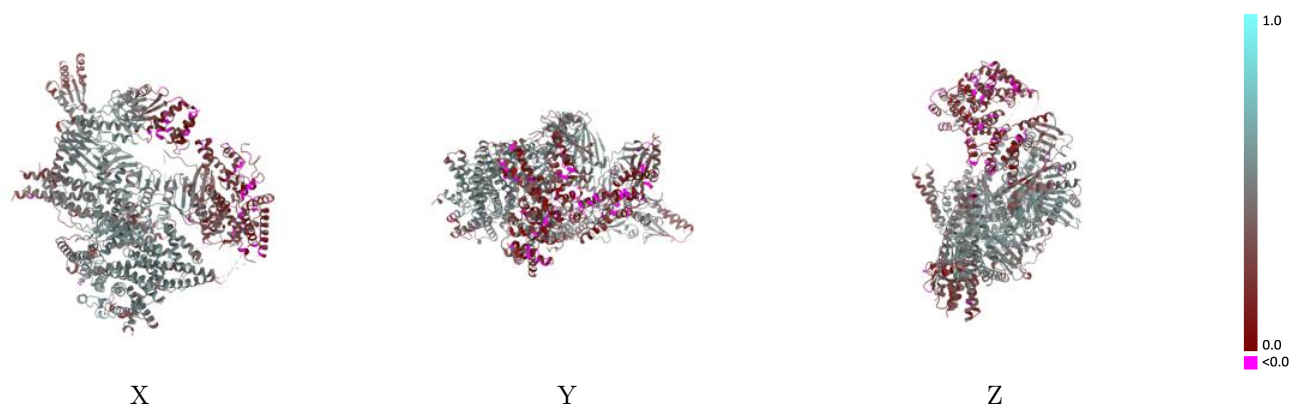
Y



Z

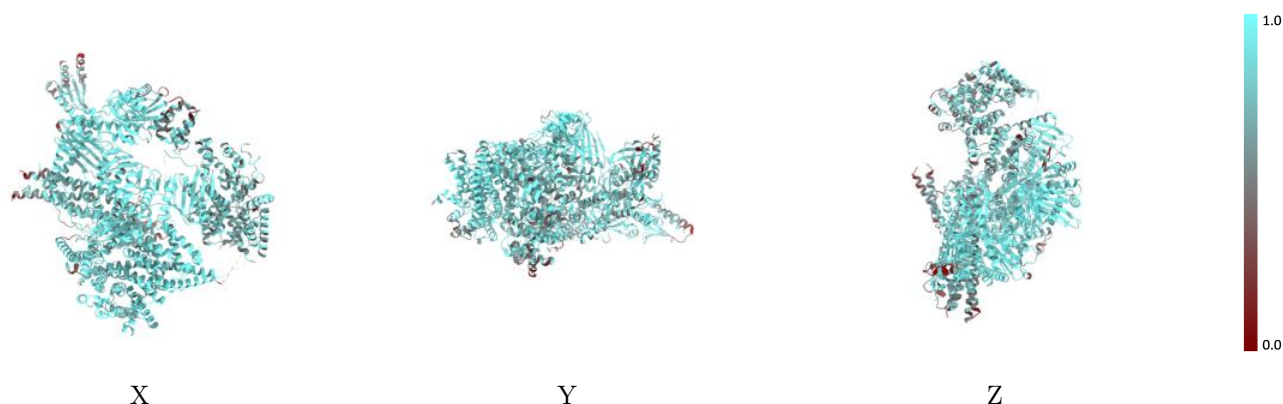
The images above show the 3D surface view of the map at the recommended contour level 0.0514 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

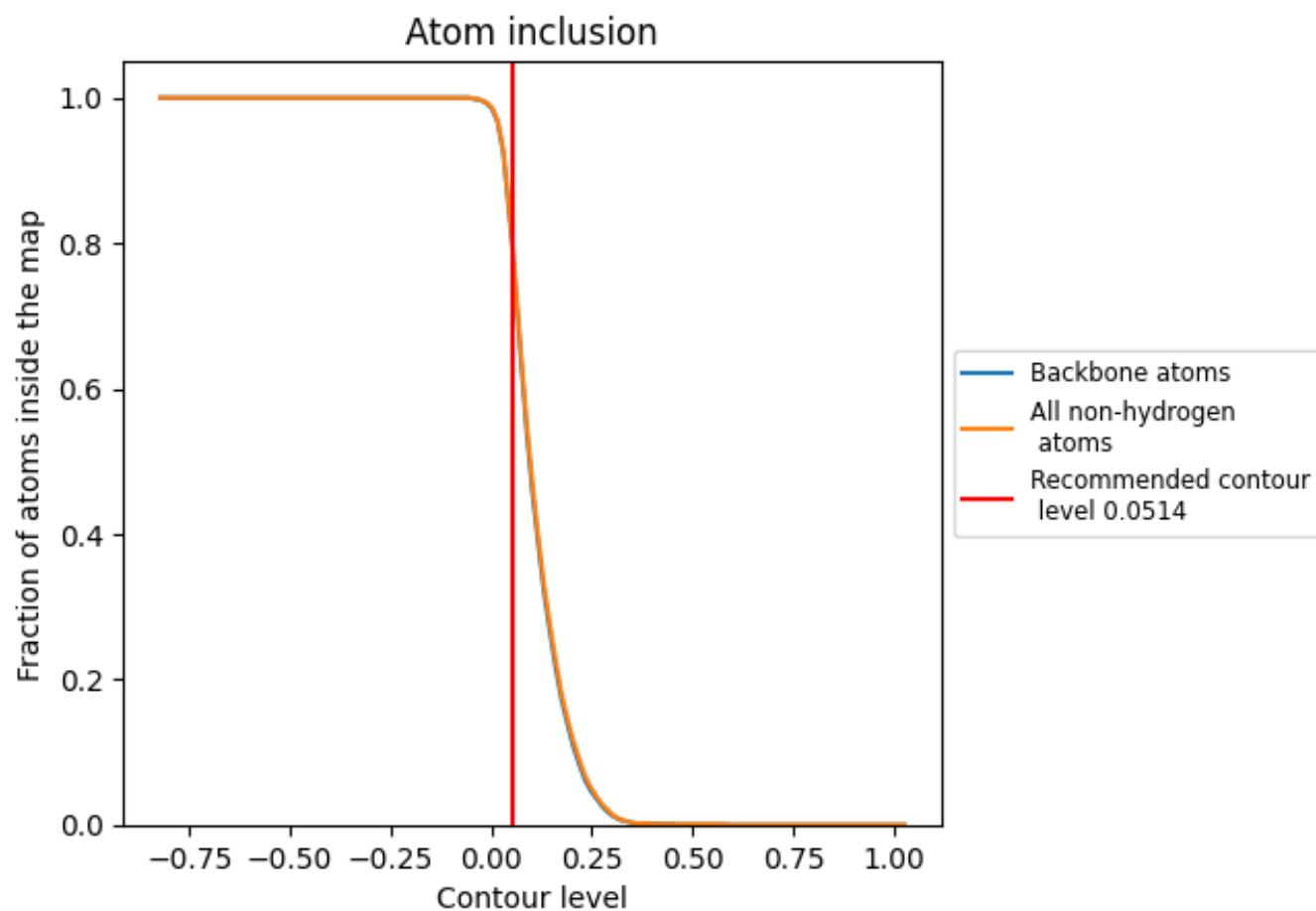
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.0514).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 81% 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 (0.0514) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8070	<div></div> 0.4040
A	<div></div> 0.6790	<div></div> 0.4010
B	<div></div> 0.7760	<div></div> 0.4560
C	<div></div> 0.8060	<div></div> 0.4600
D	<div></div> 0.7960	<div></div> 0.4450
H	<div></div> 0.8100	<div></div> 0.4020
I	<div></div> 0.8390	<div></div> 0.4050
K	<div></div> 0.8000	<div></div> 0.3310
L	<div></div> 0.8800	<div></div> 0.4490
M	<div></div> 0.9130	<div></div> 0.5320
N	<div></div> 0.8010	<div></div> 0.3720
O	<div></div> 0.8450	<div></div> 0.4520
P	<div></div> 0.7500	<div></div> 0.4140
T	<div></div> 0.7190	<div></div> 0.2230

1.0

0.0

<0.0