



## wwPDB EM Validation Summary Report ⓘ

Oct 10, 2022 – 03:55 pm BST

PDB ID : 7Z8K  
EMDB ID : EMD-14555  
Title : Cytoplasmic dynein (A1) bound to BICDR1  
Authors : Chaaban, S.; Carter, A.P.  
Deposited on : 2022-03-17  
Resolution : 4.37 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:

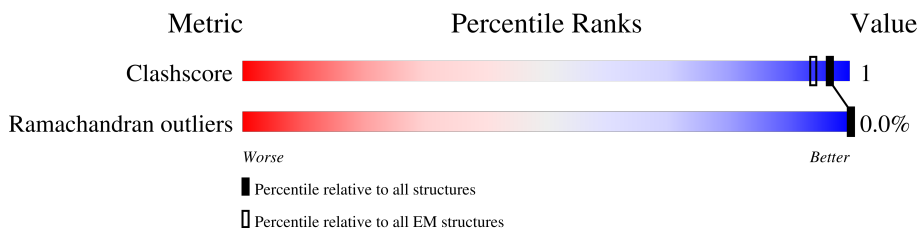
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 4.37 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	e	4646	
1	f	4646	
2	i	492	
3	h	567	
4	W	577	
4	X	577	
4	w	577	
4	x	577	
5	F	376	

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 14474 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 Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	e	854	Total	C	N	O	0	0
			4237	2529	854	854		
1	f	501	Total	C	N	O	0	0
			2488	1486	501	501		

- Molecule 2 is a protein called Cytoplasmic dynein 1 light intermediate chain 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	i	233	Total	C	N	O	0	0
			1160	694	233	233		

- Molecule 3 is a protein called Cytoplasmic dynein 1 intermediate chain 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	h	358	Total	C	N	O	0	0
			1767	1051	358	358		

- Molecule 4 is a protein called BICD family-like cargo adapter 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	X	137	Total	C	N	O	0	0
			683	409	137	137		
4	x	135	Total	C	N	O	0	0
			673	403	135	135		
4	W	165	Total	C	N	O	0	0
			822	492	165	165		
4	w	165	Total	C	N	O	0	0
			822	492	165	165		

- Molecule 5 is a protein called ARP1 actin related protein 1 homolog A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	F	370	1822	1082	370	370	0	0



GI103	P1104	V1105	D1108	V1109	G1110	K1111	V1112	Q1113	S1114	K1115	V1116	M1117	L1118	K1119	V1120	ASP	SER	HIS	TRP	HIS	LYS	GLU	VAL	LEU	SER	LYS	PHE	GLN	GLN	GLN	MET	GLY	GLY	SER	ASN	ASN	THR	GLU	THR	THR	THR	THR						
SER	ASP	ALA	VAL	THR	THR	LYR	GLN	SER	LEU	LYS	ARG	GLN	PHE	GLU	GLY	VAL	GLN	LYS	GLN	ASP	THR	LEU	TYR	GLY	VAL	ARG	GLN	GLY	LEU	THR	VAL	GLU	GLY	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR				
ILE	MET	ARG	GLY	SER	ALA	ILE	GLN	GLN	ALA	ASN	LYS	ILE	ILE	GLY	VAL	GLN	LYS	ARG	THR	THR	THR	GLY	VAL	ARG	GLY	THR	ASP	GLN	THR	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			
GLU	GLY	PHE	GLY	ARG	LEU	LYS	GLN	GLY	ASP	VAL	GLN	ASP	GLY	THR	GLY	VAL	GLN	GLN	THR	THR	GLY	GLY	GLY	THR	GLY	THR	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ILE			
ASP	GLN	MET	LYS	GLN	PRO	TRP	ASP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP			
LYS	SER	GLU	ALA	LEU	ASP	HIS	TRP	ARG	GLN	LYS	ARG	HIS	VAL	ASN	LEU	TRP	LEU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		
LYS	GLN	ILE	ARG	GLU	TRP	ASN	THR	GLY	ASP	VAL	VAL	TRP	GLY	ASN	LEU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
GLU	ASP	LYS	LEU	ILE	MET	ALA	TRP	ARG	GLU	ILE	VAL	VAL	GLY	ALA	LEU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
LYS	SER	PRO	LEU	VAL	ASP	VAL	LEU	GLN	VAL	GLN	ASP	GLY	GLY	LEU	GLY	LEU	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
SER	LYS	ASN	VAL	ALA	LEU	HIS	TRP	PHE	GLY	ALA	ALA	VAL	GLY	ASP	ASN	GLY	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
LEU	VAL	GLU	GLY	MET	ARG	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
THR	ALA	LEU	SER	MET	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
SER	LEU	ILE	SER	LYS	ILE	ASN	ASP	ASN	PRO	LYS	GLN	LEU	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	
LEU	THR	ASP	ARG	CYS	TRP	THR	MET	GLY	TRP	ALA	THR	PRO	THR	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
ILE	PHE	VAL	GLY	CYS	GLN	VAL	GLY	PHE	VAL	GLY	ASP	GLY	ALA	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
LYS	GLN	VAL	LYS	VAL	PRO	ASP	GLY	TRP	VAL	PRO	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
VAL	LEU	ALA	ASN	ILE	PRO	PHE	PRO	PHE	GLN	GLN	GLN	SER	SER	GLN	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
GLU	GLY	ILE	ALA	ASN	LEU	PRO	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
LYS	VAL	CYS	GLN	MET	TRP	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
LEU	GLU	HIS	ILE	PRO	ASP	LEU	ILE	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	









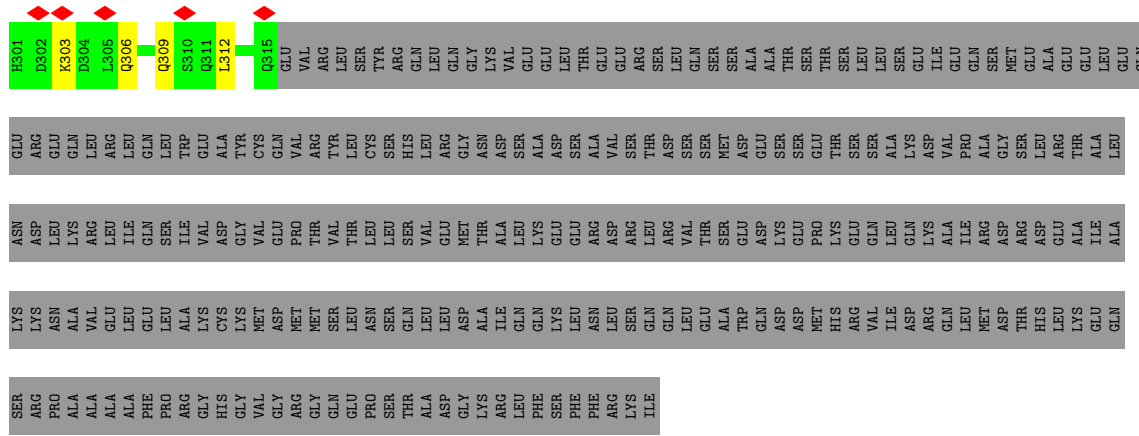




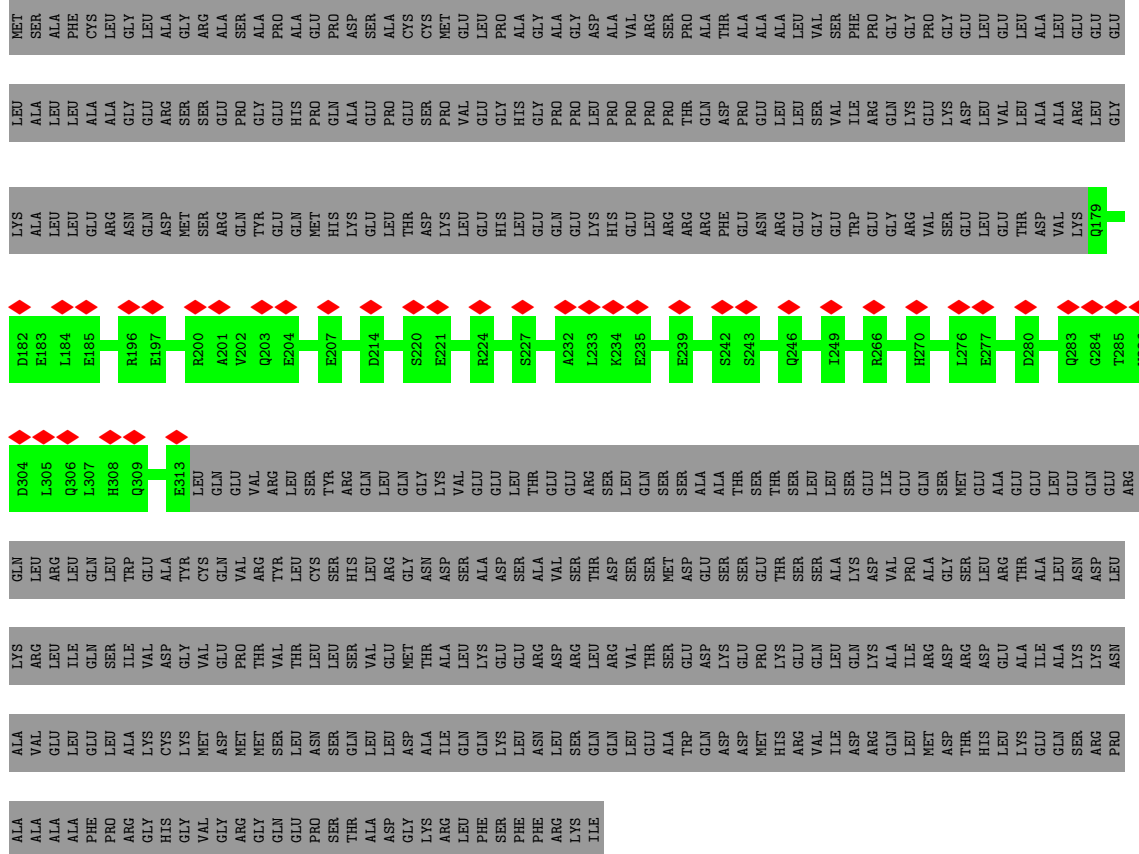




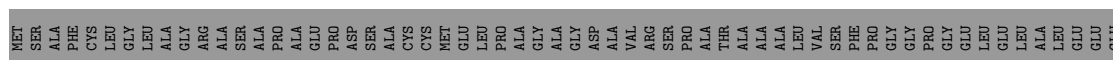


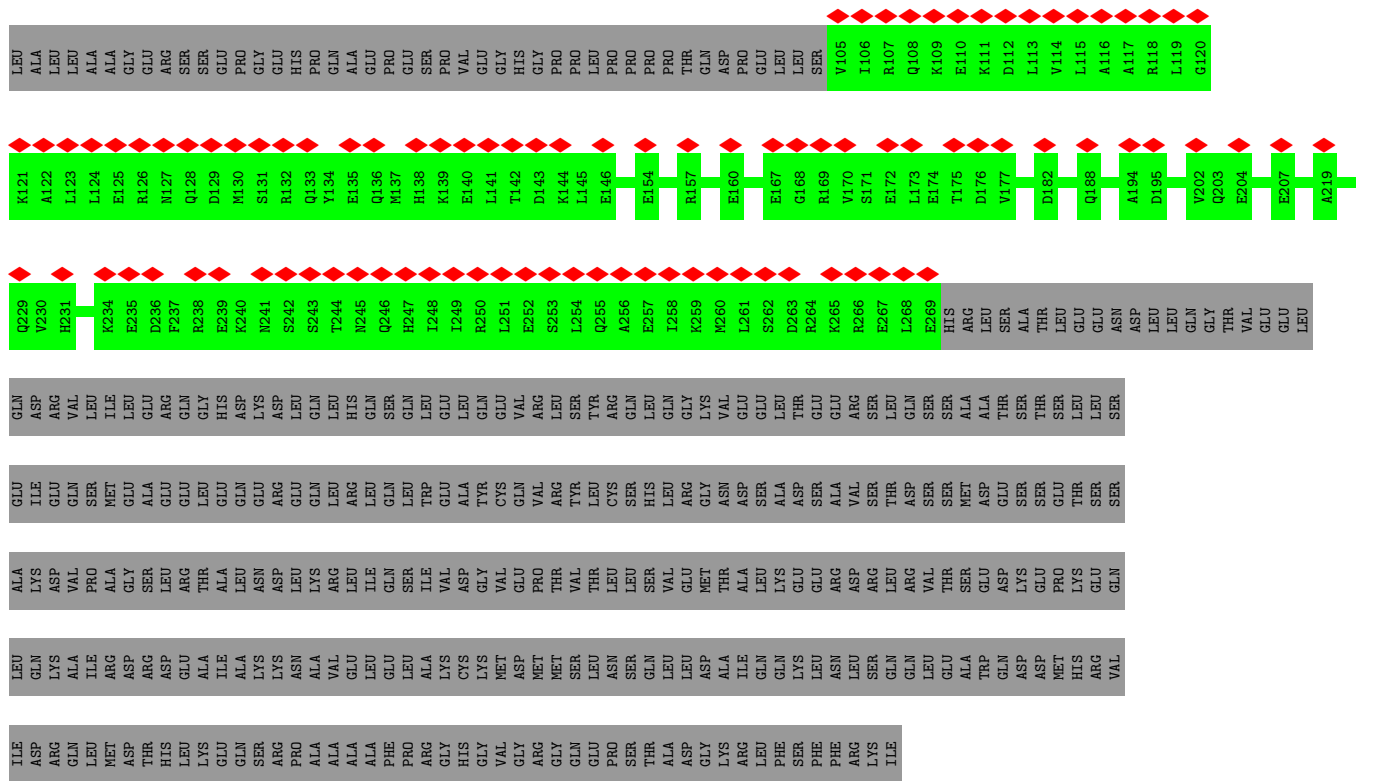


● Molecule 4: BICD family-like cargo adapter 1

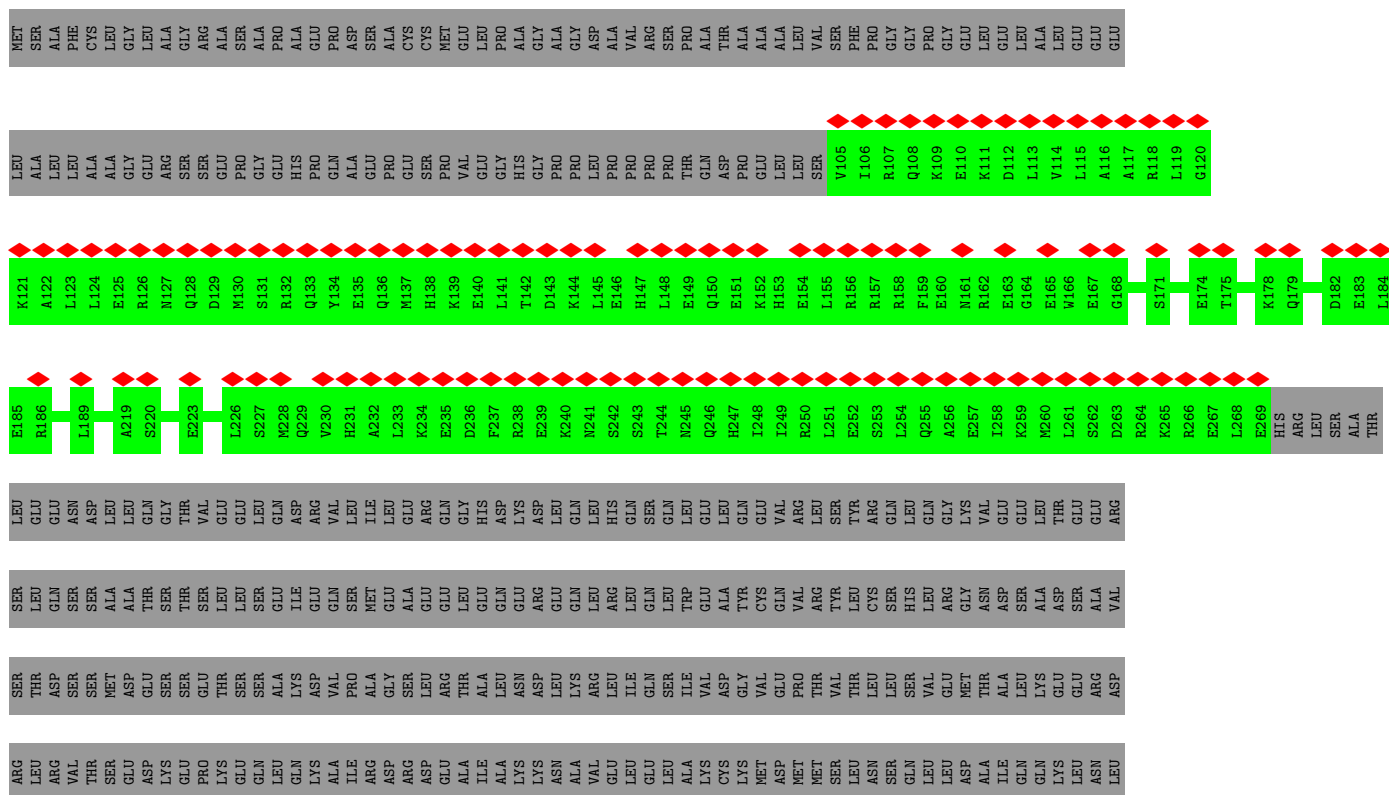


● Molecule 4: BICD family-like cargo adapter 1





• Molecule 4: BICD family-like cargo adapter 1



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

LYS  
ILE

- Molecule 5: ARP1 actin related protein 1 homolog A

Chain F:  98%

MET GLU SER TYR ASP VAL I7 A8 P60 E63 T375 F376



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39644	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 ( $e^-/\text{\AA}^2$ )	53	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.074	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0197	Depositor
Map size (Å)	955.776, 955.776, 955.776	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2445, 1.2445, 1.2445	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	e	0.27	0/4234	0.44	0/5903
1	f	0.27	0/2485	0.44	0/3464
2	i	0.24	0/1158	0.46	0/1615
3	h	0.25	0/1766	0.52	0/2457
4	W	0.23	0/821	0.39	0/1146
4	X	0.27	0/682	0.44	0/952
4	w	0.23	0/821	0.35	0/1146
4	x	0.24	0/672	0.40	0/938
5	F	0.27	0/1821	0.48	0/2531
All	All	0.26	0/14460	0.45	0/20152

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	e	4237	0	1866	0	0
1	f	2488	0	1103	0	0
2	i	1160	0	504	0	0
3	h	1767	0	799	0	0
4	W	822	0	356	0	0
4	X	683	0	293	2	0
4	w	822	0	356	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	x	673	0	289	0	0
5	F	1822	0	820	1	0
All	All	14474	0	6386	3	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 1.

All (3) 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)
5:F:60:PRO:O	5:F:63:GLU:N	2.43	0.51
4:X:309:GLN:O	4:X:312:LEU:N	3.39	0.45
4:X:303:LYS:O	4:X:306:GLN:N	3.44	0.44

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	e	848/4646 (18%)	829 (98%)	18 (2%)	1 (0%)	51	85
1	f	495/4646 (11%)	484 (98%)	11 (2%)	0	100	100
2	i	229/492 (46%)	217 (95%)	12 (5%)	0	100	100
3	h	356/567 (63%)	346 (97%)	10 (3%)	0	100	100
4	W	163/577 (28%)	163 (100%)	0	0	100	100
4	X	135/577 (23%)	135 (100%)	0	0	100	100
4	w	163/577 (28%)	163 (100%)	0	0	100	100
4	x	133/577 (23%)	133 (100%)	0	0	100	100
5	F	368/376 (98%)	361 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2890/13035 (22%)	2831 (98%)	58 (2%)	1 (0%)	100 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	e	973	PRO

### 5.3.2 Protein sidechains [i](#)

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

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

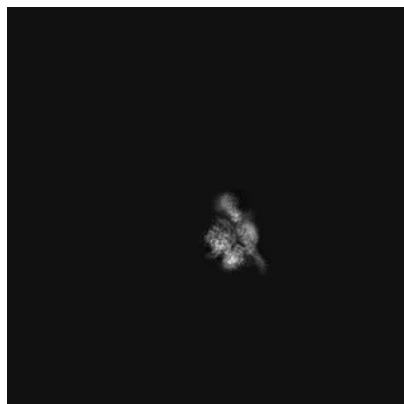
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14555. These allow visual inspection of the internal detail of the map and identification of artifacts.

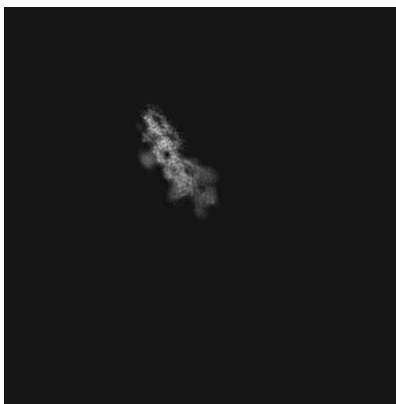
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

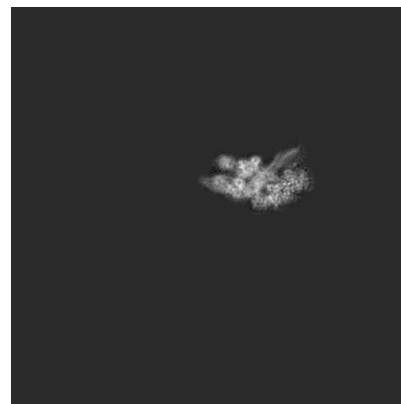
#### 6.1.1 Primary map



X

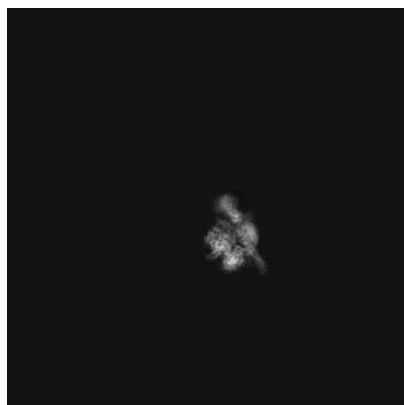


Y

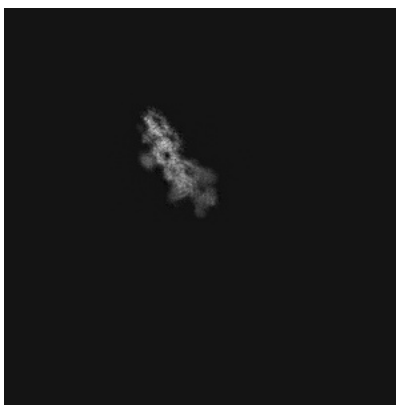


Z

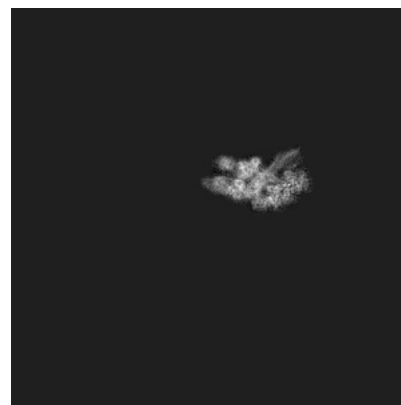
#### 6.1.2 Raw map



X



Y



Z

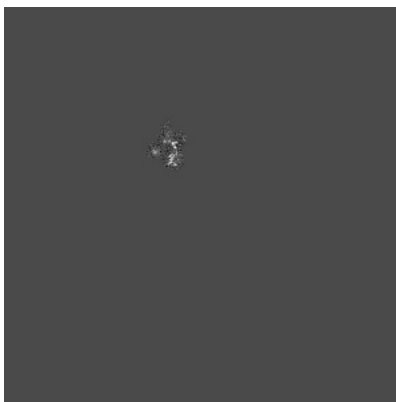
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 384

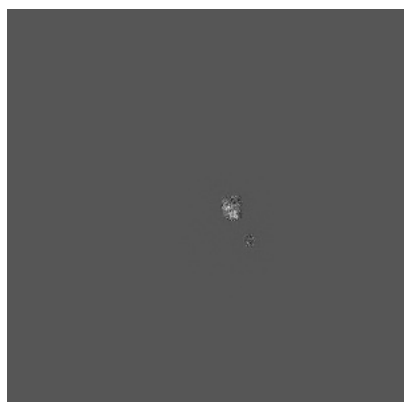


Y Index: 384

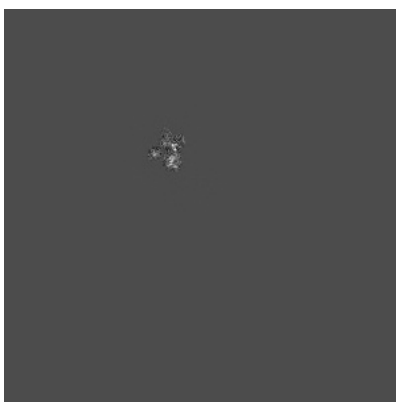


Z Index: 384

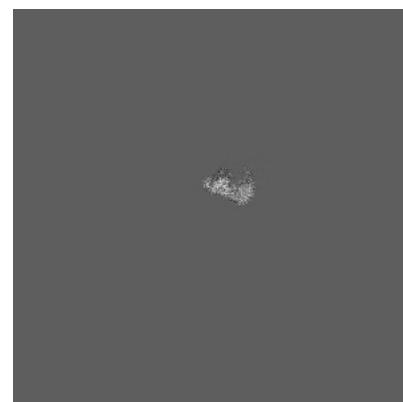
### 6.2.2 Raw map



X Index: 384



Y Index: 384

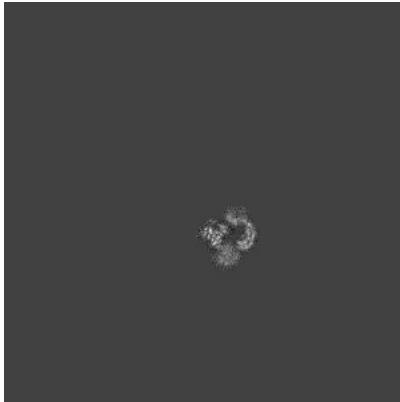


Z Index: 384

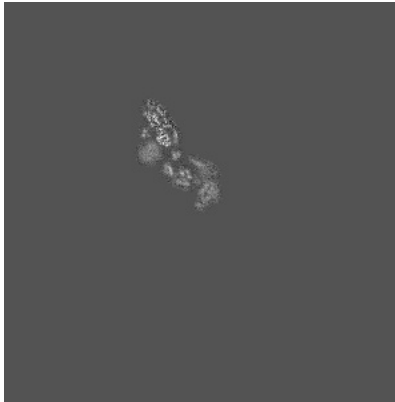
The images above show central slices of the map in three orthogonal directions.

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

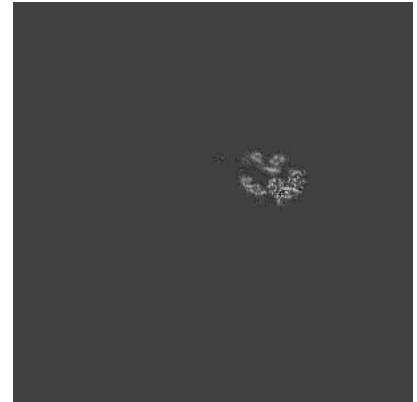
### 6.3.1 Primary map



X Index: 472

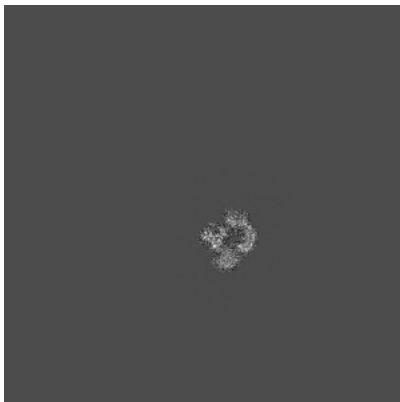


Y Index: 423

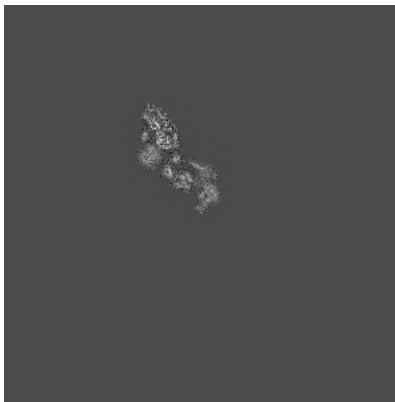


Z Index: 309

### 6.3.2 Raw map



X Index: 471



Y Index: 422



Z Index: 309

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

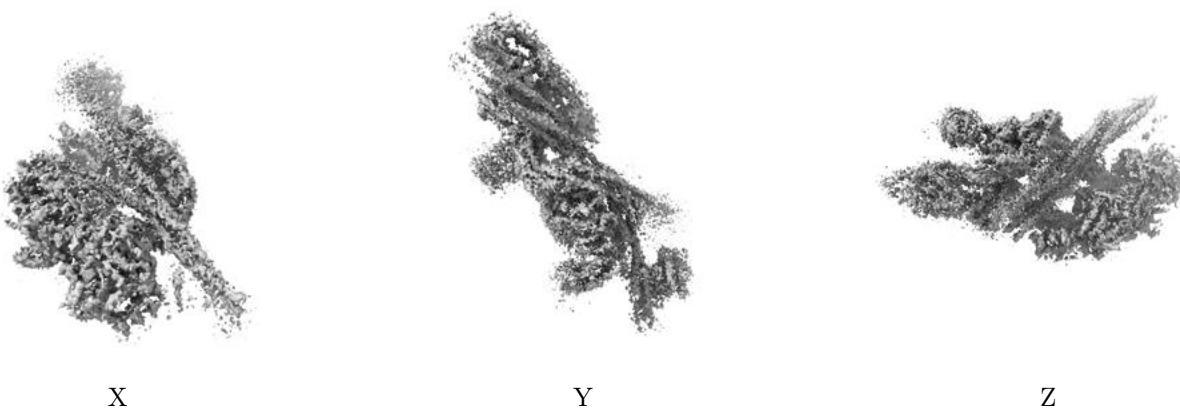
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0197. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.



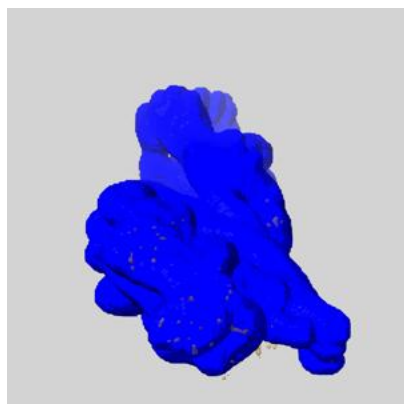
## 6.5 Mask visualisation [i](#)

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

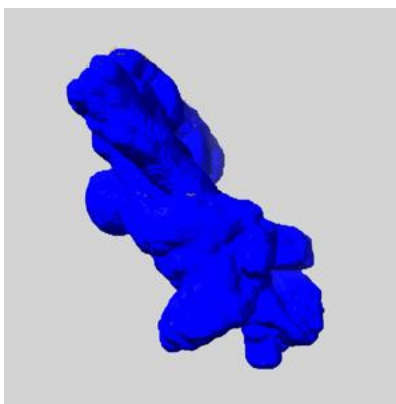
A mask typically either:

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

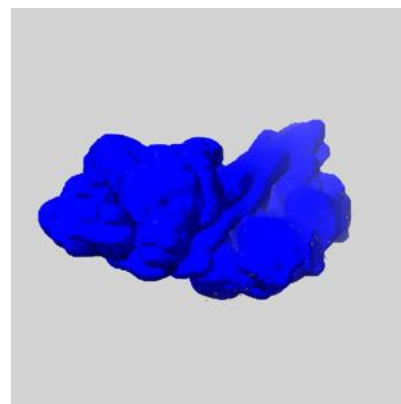
### 6.5.1 emd\_14555\_msk\_1.map [i](#)



X



Y

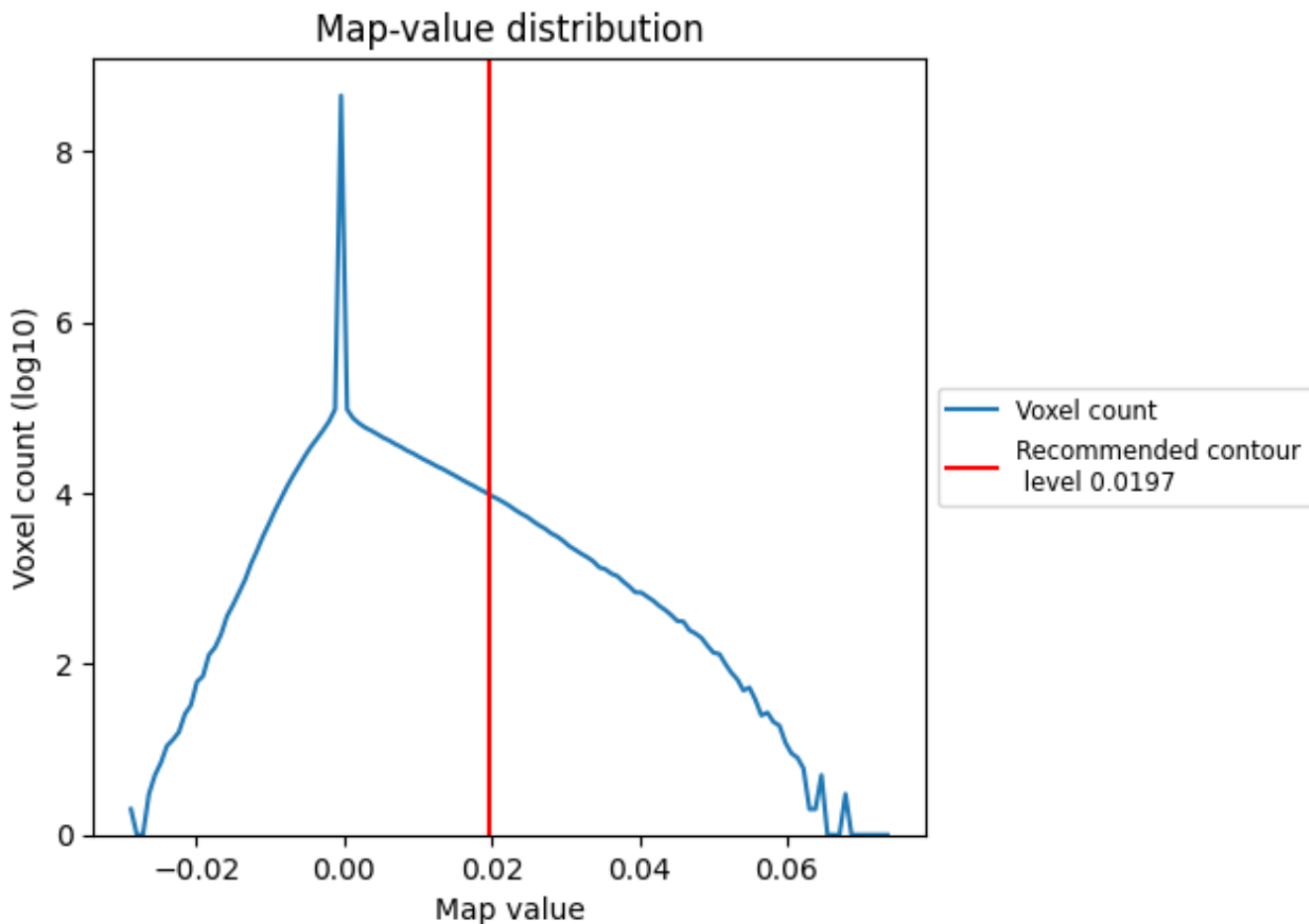


Z

## 7 Map analysis [i](#)

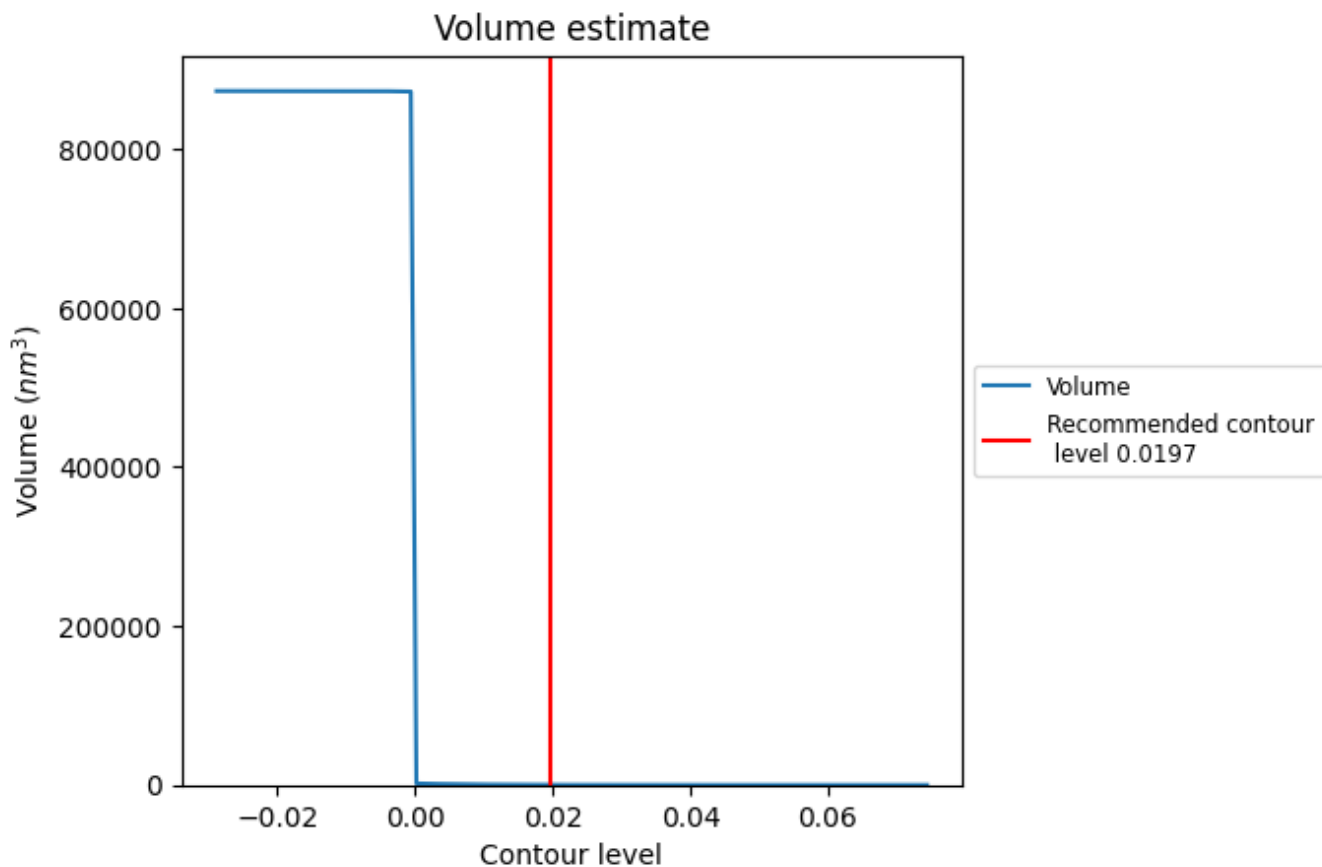
This section contains the results of statistical analysis of the map.

### 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.

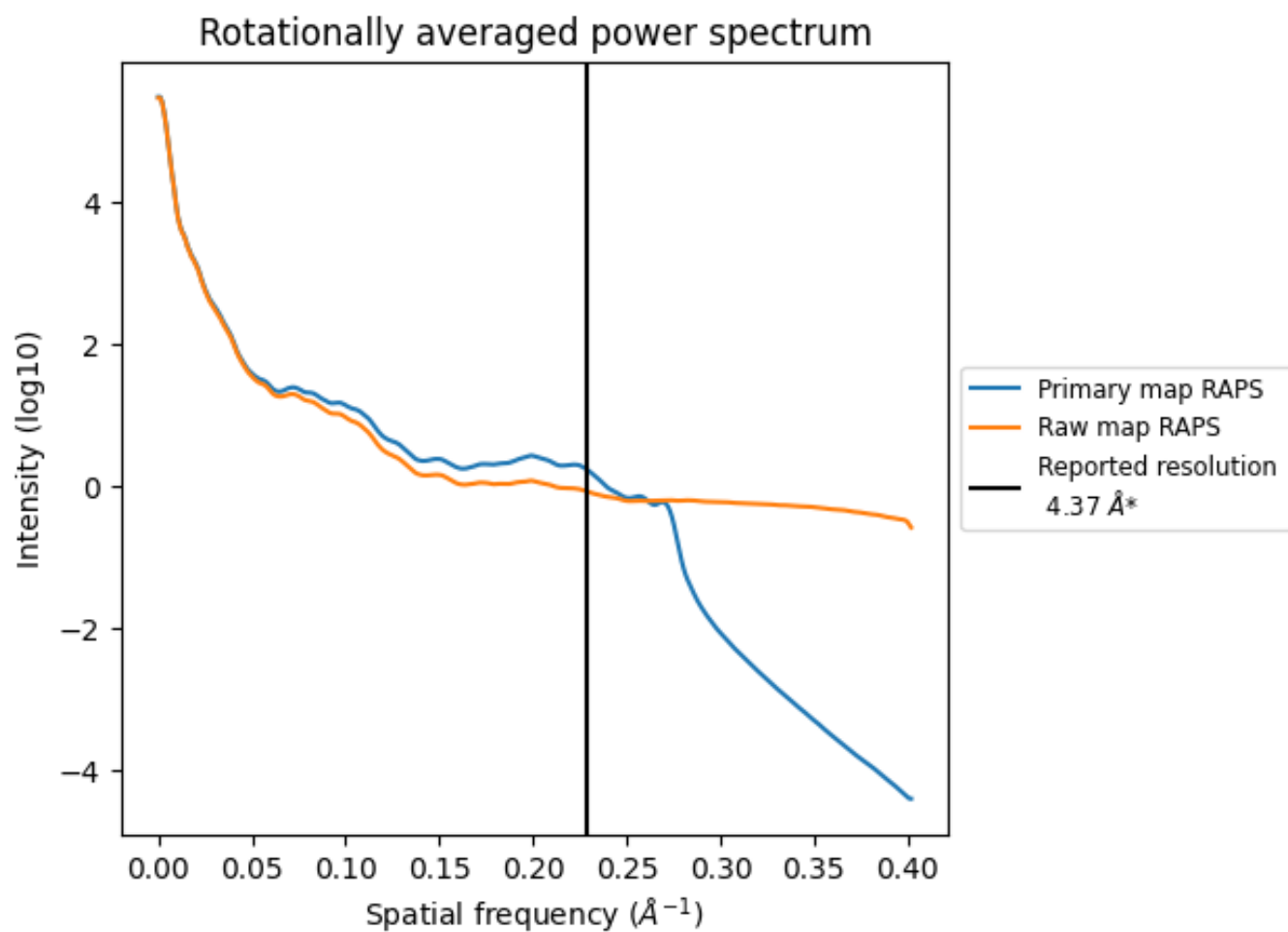
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 189 nm<sup>3</sup>; this corresponds to an approximate mass of 171 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

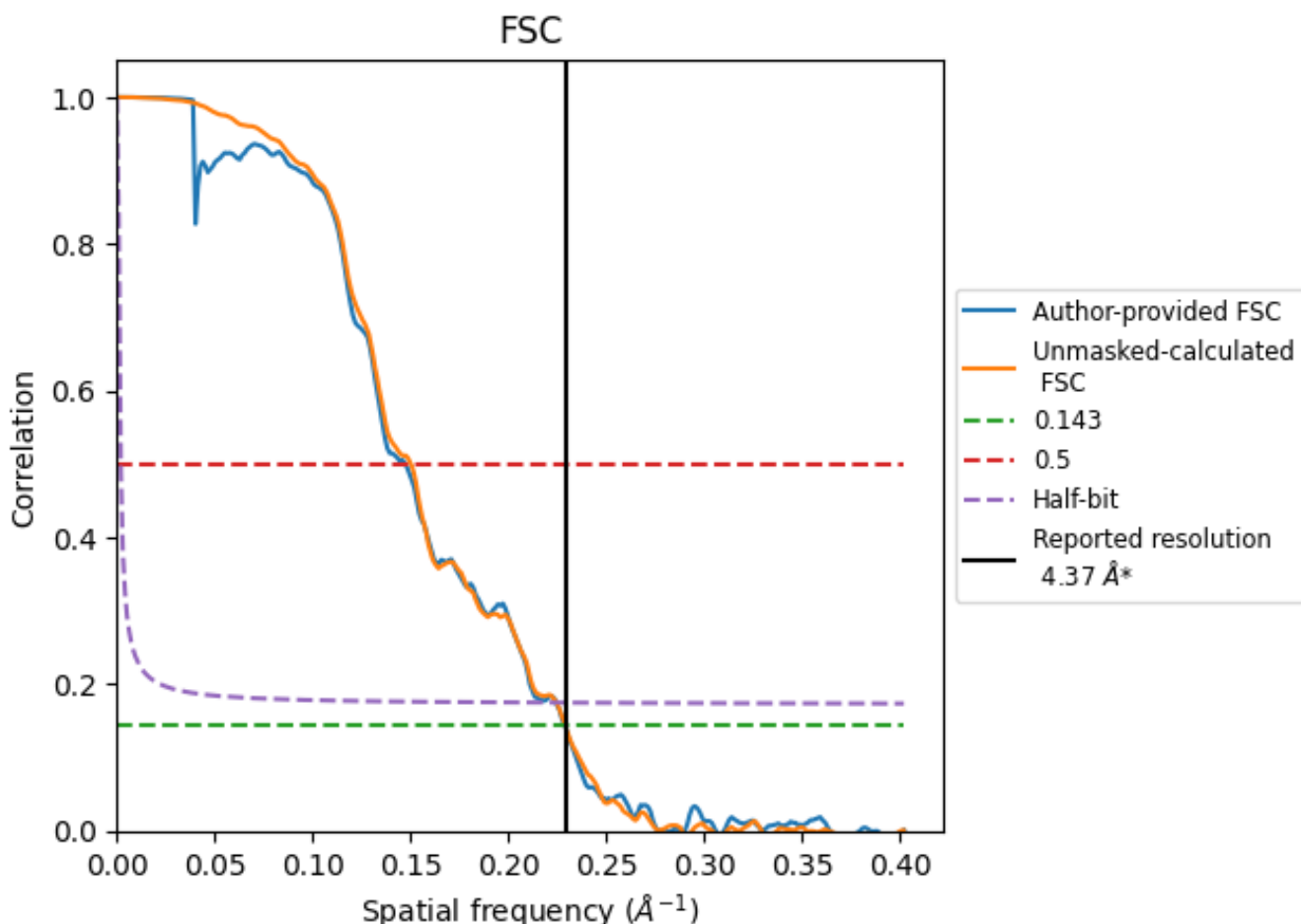


\*Reported resolution corresponds to spatial frequency of 0.229 Å<sup>-1</sup>

## 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 0.229 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

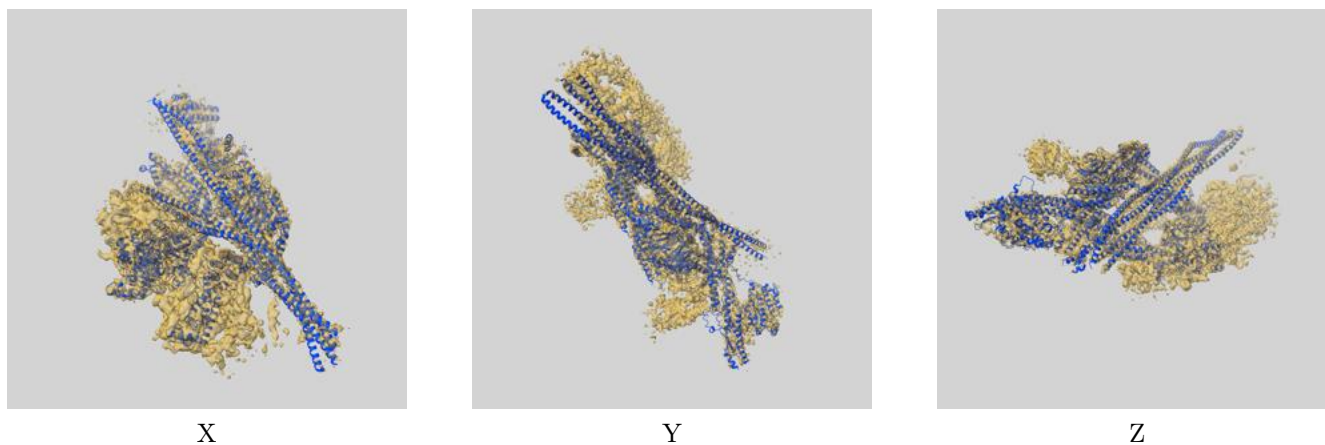
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.37	-	-
Author-provided FSC curve	4.37	6.79	4.46
Unmasked-calculated*	4.37	6.67	4.45

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

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

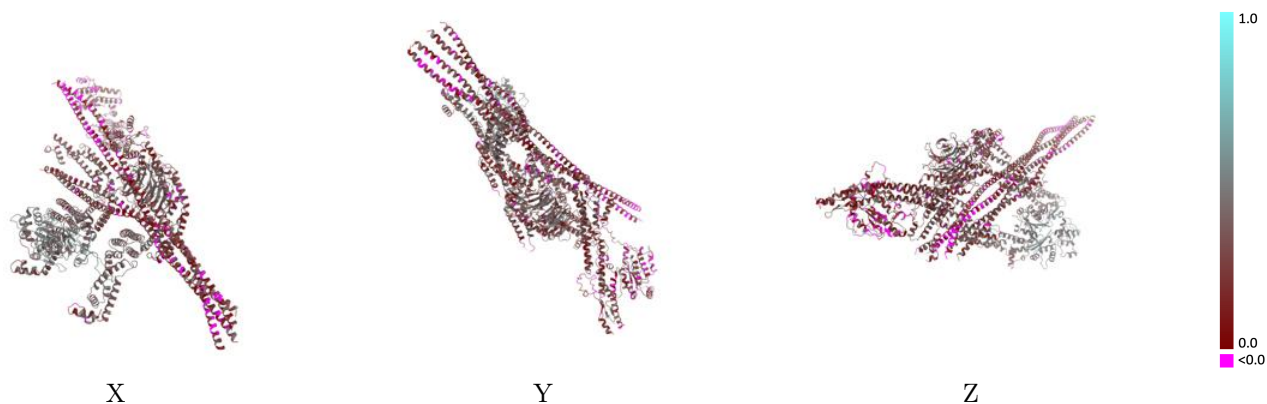
This section contains information regarding the fit between EMDB map EMD-14555 and PDB model 7Z8K. Per-residue inclusion information can be found in section 3 on page 5.

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



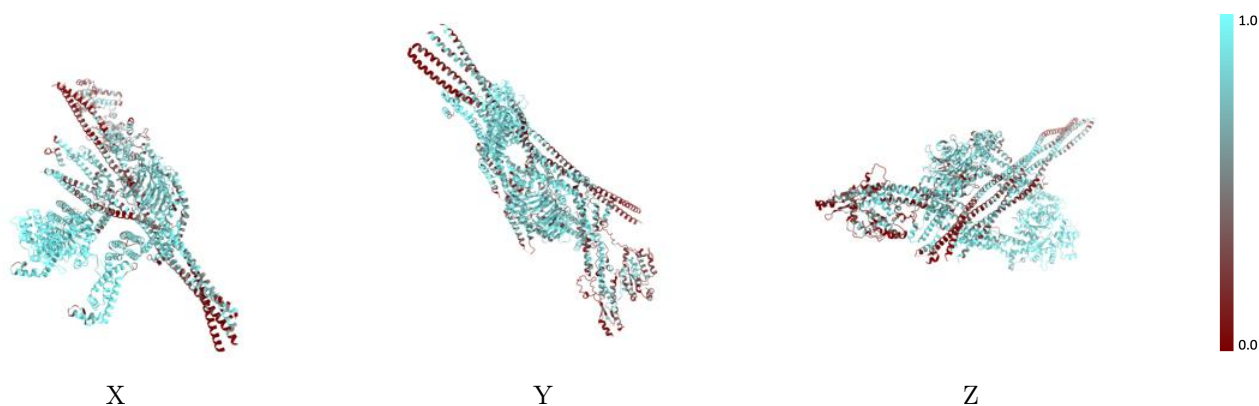
The images above show the 3D surface view of the map at the recommended contour level 0.0197 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

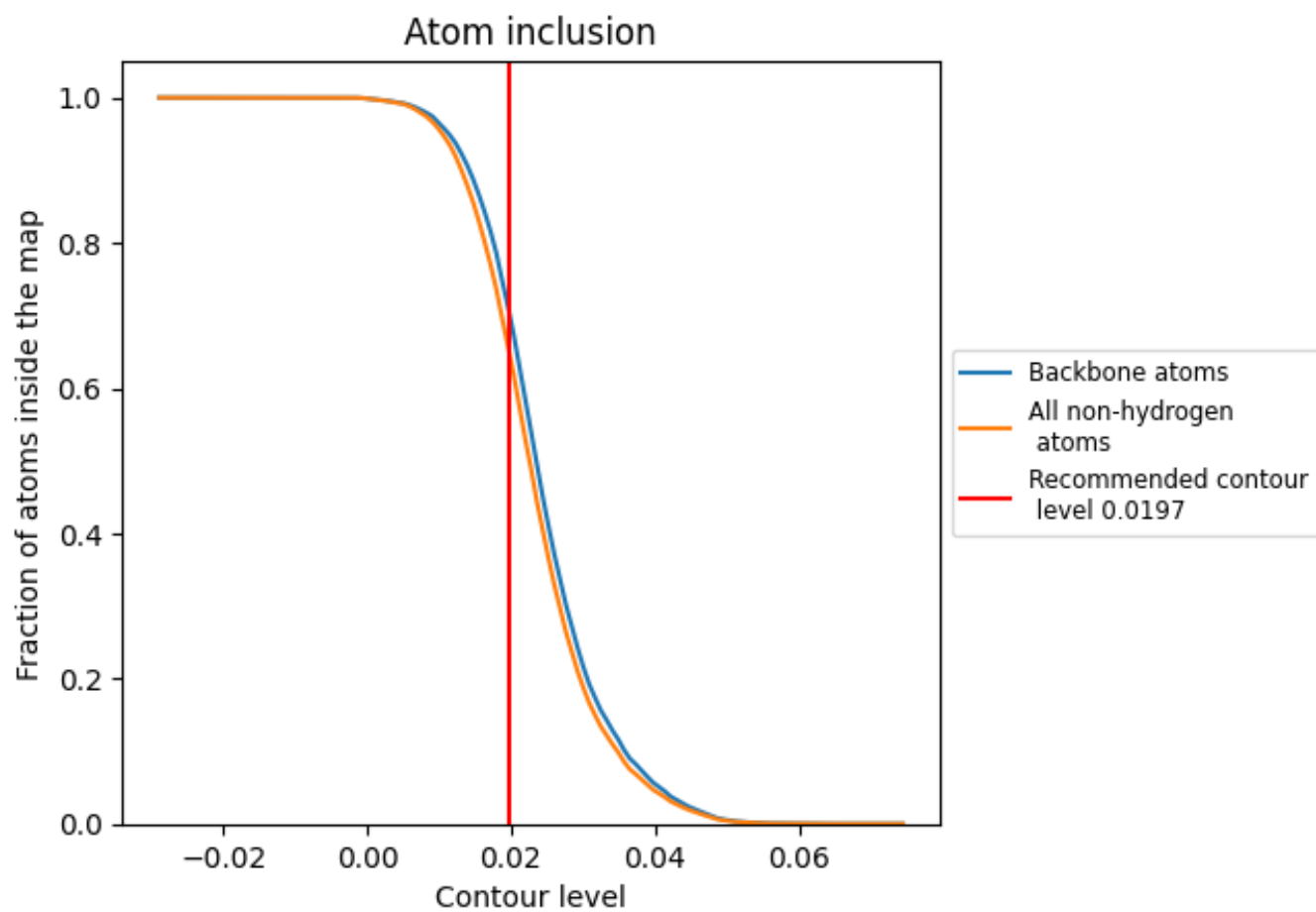
## 9.3 Atom inclusion mapped to coordinate model [\(i\)](#)



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 (0.0197).























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.0197) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6524	 0.2900
F	 0.9358	 0.4740
W	 0.4148	 0.1720
X	 0.5827	 0.2300
e	 0.6372	 0.2800
f	 0.7745	 0.3150
h	 0.7136	 0.3290
i	 0.3612	 0.1930
w	 0.3358	 0.1190
x	 0.6181	 0.2330

