



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 08:09 PM UTC

PDB ID : 7TIJ / pdb_00007tij
EMDB ID : EMD-25911
Title : Cardiac F-actin decorated with regulatory M-domain of cardiac myosin binding protein C
Authors : Risi, C.M.; Galkin, V.E.
Deposited on : 2022-01-13
Resolution : 8.00 Å (reported)
Based on initial models : 5K6P, 3MFP

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.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

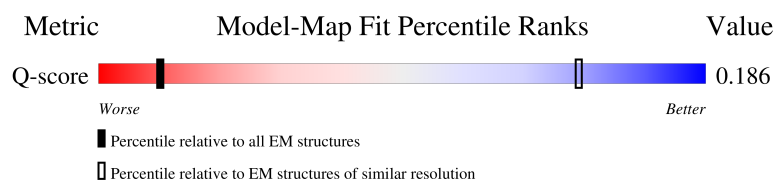
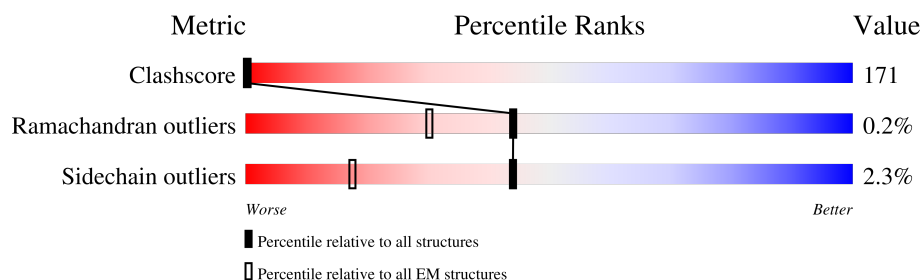
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.00 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	361 (7.50 - 8.50)

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 ≥ 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	375	 7% 89% .
1	B	375	 7% 89% .
1	C	375	 6% 90% .
1	D	375	 6% 89% .

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Mol	Chain	Length	Quality of chain
1	E	375	8%88%
1	F	375	8%88%
2	G	220	5%14%82%
2	H	220	5%14%82%
2	I	220	5%14%82%
2	J	220	5%13%82%
2	K	220	5%14%82%
2	L	220	5%14%82%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 21588 atoms, of which 2016 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 cardiac actin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	375	Total	C	N	O	S	0	0
			2932	1854	493	565	20		
1	B	375	Total	C	N	O	S	0	0
			2932	1854	493	565	20		
1	C	375	Total	C	N	O	S	0	0
			2932	1854	493	565	20		
1	D	375	Total	C	N	O	S	0	0
			2932	1854	493	565	20		
1	E	375	Total	C	N	O	S	0	0
			2932	1854	493	565	20		
1	F	375	Total	C	N	O	S	0	0
			2932	1854	493	565	20		

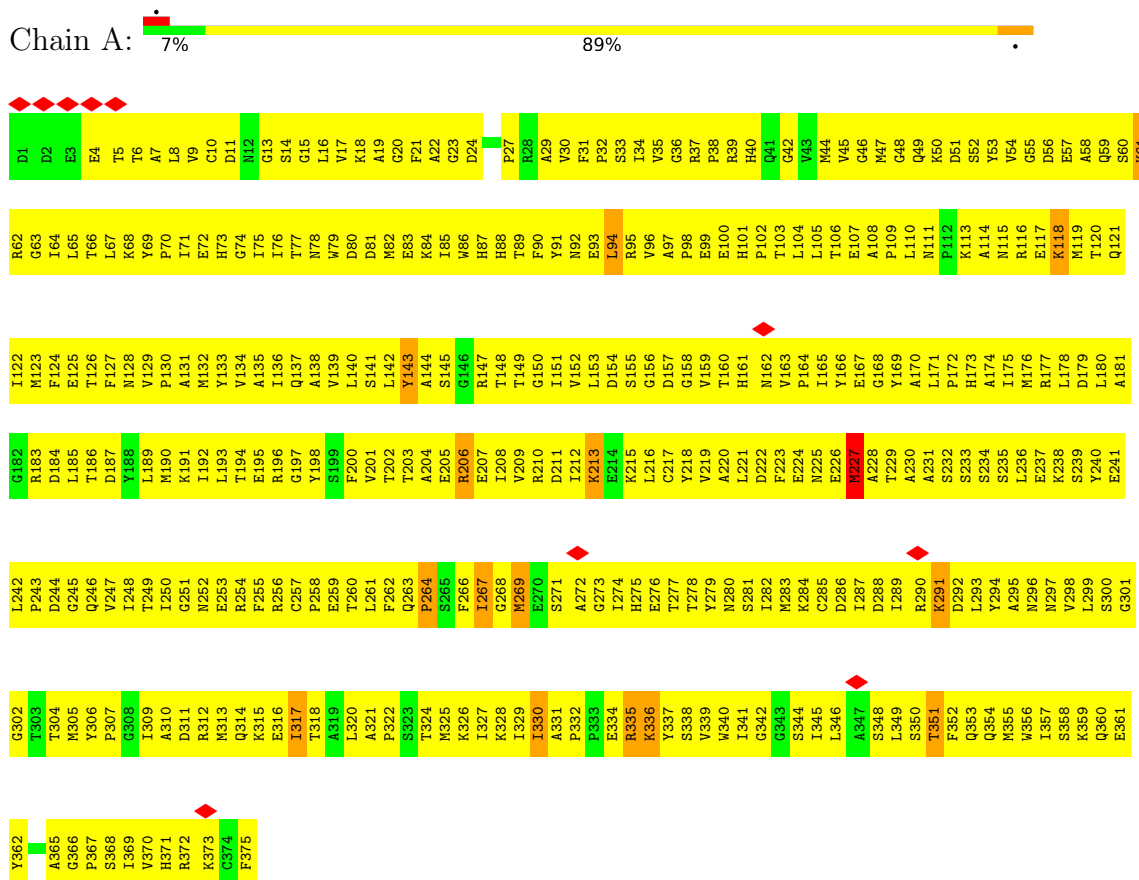
- Molecule 2 is a protein called Myosin-binding protein C, cardiac-type.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	G	39	Total 666	C 209	H 336	N 62	O 57	S 2	0	0
2	H	39	Total 666	C 209	H 336	N 62	O 57	S 2	0	0
2	I	39	Total 666	C 209	H 336	N 62	O 57	S 2	0	0
2	J	39	Total 666	C 209	H 336	N 62	O 57	S 2	0	0
2	K	39	Total 666	C 209	H 336	N 62	O 57	S 2	0	0
2	L	39	Total 666	C 209	H 336	N 62	O 57	S 2	0	0

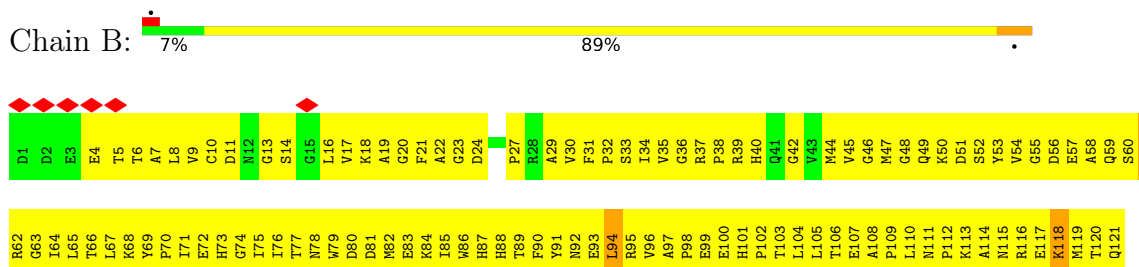
3 Residue-property plots

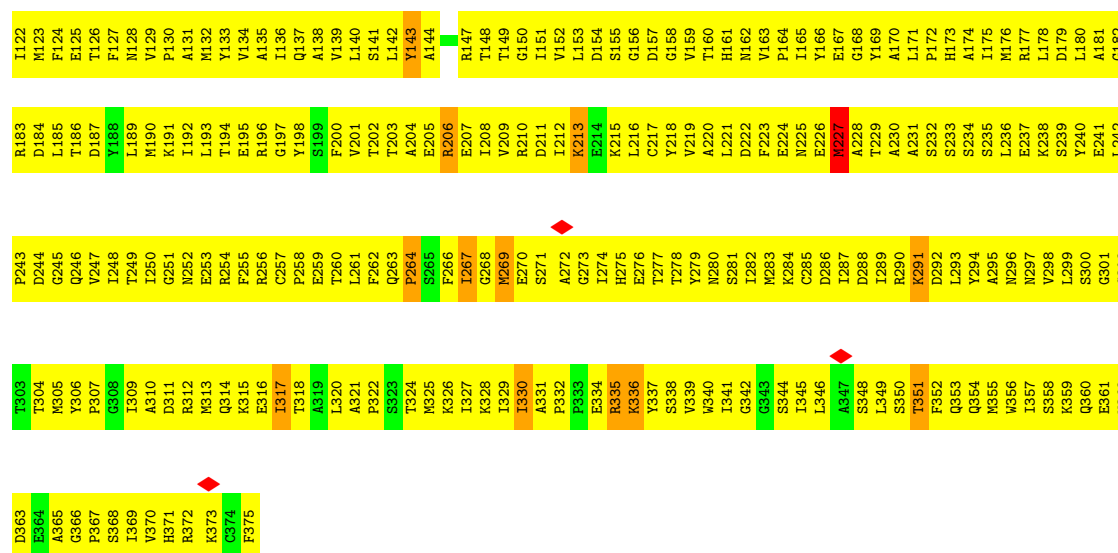
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: cardiac actin

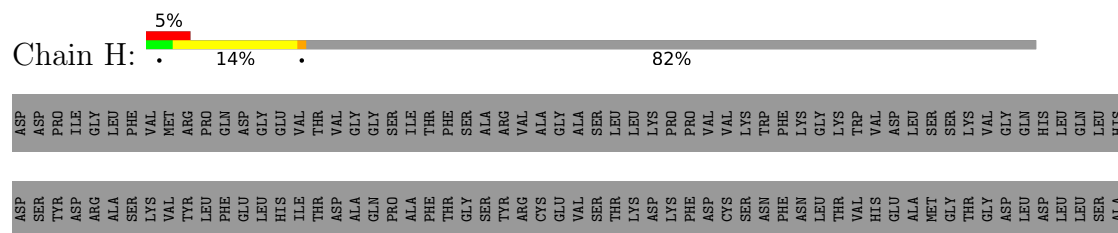


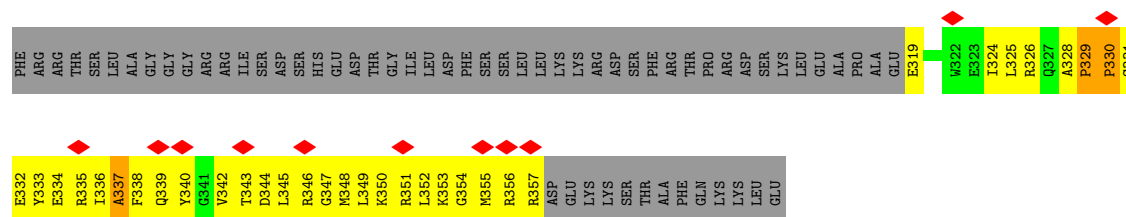
• Molecule 1: cardiac actin





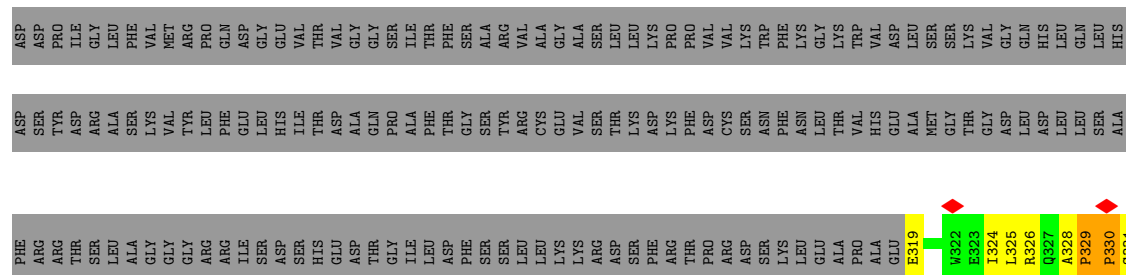






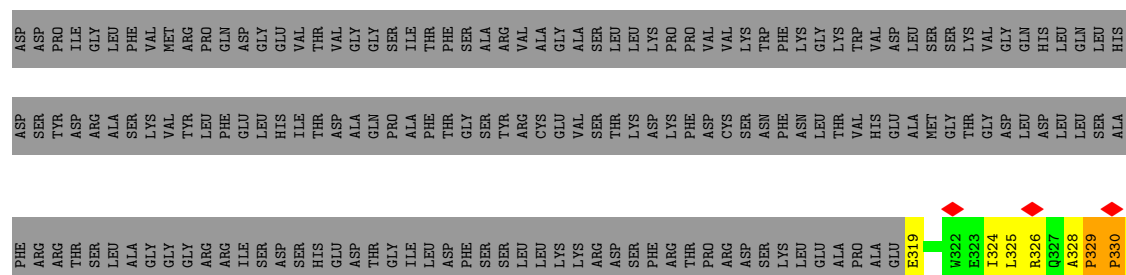
• Molecule 2: Myosin-binding protein C, cardiac-type

Chain I: 14% 82%



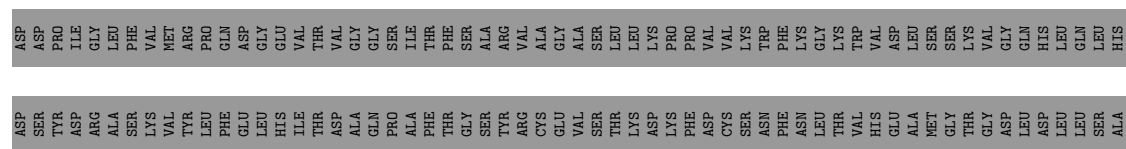
• Molecule 2: Myosin-binding protein C, cardiac-type

Chain J: 5% 13% 82%



• Molecule 2: Myosin-binding protein C, cardiac-type

Chain K: 14% 82%



PHE	ARG	ARG	THR	SER	LEU	ALA	GLY	GLY	ARG	ARG	ILE	SER	ASP	SER	HIS	GLU	ASP	THR	GLY	ILE	LEU	LEU	ASP	PHE	SER	SER	LEU	LEU	LYS	LYS	ARG	ASP	PHE	ARG	THR	PRO	ARG	ASP	SER	LYS	LEU	GLU	ALA	PRO	ALA	ALA	GLU	E319	W322	E323	I324	L325	R326	Q327	A328	P329	P330	S331
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E332	Y333	E334	R335	I336	A337	F338	Q339	Y340	G341	V342	T343	D344	L345	R346	G347	M348	L349	K350	R351	L352	K353	G354	M355	R356	R357	ASP	GLU	GLY	LYS	LYS	SER	THR	ALA	PHE	GLN	LYS	LYS	LEU	GLU
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• Molecule 2: Myosin-binding protein C, cardiac-type



ASP	ASP	PRO	TYR	ILE	GLY	LEU	PHE	VAL	MET	TYR	ARG	PRO	GLN	ASP	GLY	GLY	ILE	THR	PHE	THR	SER	GLY	ALA	ARG	VAL	ALA	GLY	VAL	SER	LEU	LYS	LEU	LYS	PRO	PRO	VAL	VAL	LYS	TRP	PHE	LYS	GLY	LEU	LYS	THR	ASP	LEU	SER	SER	LYS	VAL	GLY	HIS	LEU	GLN	LEU	LEU	HIS
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ASP	SER	ASP	TYR	ASP	ARG	ALA	SER	LYS	VAL	VAL	TYR	LEU	PHE	GLU	LEU	HIS	THR	THR	ASP	GLN	ALA	ASP	GLY	PRO	VAL	GLY	THR	LYS	ASP	THR	LYS	ASP	PHE	ASP	CYS	ASN	ASN	LEU	THR	VAL	HIS	GLU	ASP	ALA	ALA	MET	GLY	THR	ASP	GLY	LEU	LEU	ALA
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PHE	ARG	ARG	THR	SER	LEU	ALA	GLY	GLY	ARG	ARG	ILE	SER	ASP	SER	HIS	GLU	ASP	THR	GLY	ILE	LEU	LEU	PHE	SER	SER	LEU	LEU	LYS	LYS	ARG	ASP	SER	THR	PHE	ARG	THR	PRO	ARG	ASP	LYS	LYS	LEU	GLU	ALA	PRO	ALA	GLU	E319	W322	E323	I324	L325	R326	Q327	A328	P329	P330	S331
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E332	Y333	E334	R335	I336	A337	F338	Q339	Y340	G341	V342	T343	D344	L345	R346	G347	M348	L349	K350	R351	L352	K353	G354	M355	R356	R357	ASP	GLU	GLY	LYS	LYS	SER	THR	ALA	PHE	GLN	LYS	LYS	LEU	GLU
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4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-166.7°, rise=27.4 Å, axial sym=C1	Depositor
Number of segments used	15244	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 ($e^-/\text{\AA}^2$)	34	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	9.867	Depositor
Minimum map value	-3.931	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.673	Depositor
Map size (Å)	87.425, 103.565, 255.55	wwPDB
Map dimensions	65, 77, 190	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.345, 1.345, 1.345	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	0.25	0/2995	0.73	14/4057 (0.3%)
1	B	0.25	0/2995	0.74	14/4057 (0.3%)
1	C	0.25	0/2995	0.74	14/4057 (0.3%)
1	D	0.26	0/2995	0.74	14/4057 (0.3%)
1	E	0.26	0/2995	0.74	14/4057 (0.3%)
1	F	0.26	0/2995	0.74	14/4057 (0.3%)
2	G	0.44	0/336	1.06	3/449 (0.7%)
2	H	0.44	0/336	1.06	3/449 (0.7%)
2	I	0.44	0/336	1.06	3/449 (0.7%)
2	J	0.44	0/336	1.06	3/449 (0.7%)
2	K	0.44	0/336	1.06	3/449 (0.7%)
2	L	0.44	0/336	1.06	3/449 (0.7%)
All	All	0.28	0/19986	0.77	102/27036 (0.4%)

There are no bond length outliers.

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	337	ALA	N-CA-C	-9.71	99.75	111.69
2	I	337	ALA	N-CA-C	-9.71	99.75	111.69
2	H	337	ALA	N-CA-C	-9.70	99.76	111.69
2	J	337	ALA	N-CA-C	-9.68	99.78	111.69
2	G	337	ALA	N-CA-C	-9.67	99.79	111.69

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	2932	0	2894	1081	0
1	B	2932	0	2894	1098	0
1	C	2932	0	2894	1136	0
1	D	2932	0	2894	1134	0
1	E	2932	0	2894	1094	0
1	F	2932	0	2894	1068	0
2	G	330	336	335	85	0
2	H	330	336	335	84	0
2	I	330	336	335	91	0
2	J	330	336	335	84	0
2	K	330	336	335	89	0
2	L	330	336	335	88	0
All	All	19572	2016	19374	6671	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 171.

The worst 5 of 6671 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)
1:E:152:VAL:HG12	1:E:163:VAL:HB	1.22	1.20
1:F:299:LEU:HD21	1:F:304:THR:HG21	1.20	1.19
1:C:203:THR:HA	1:C:206:ARG:HD3	1.23	1.18
1:D:299:LEU:HD21	1:D:304:THR:HG21	1.20	1.18
1:D:141:SER:HB3	1:D:339:VAL:HG12	1.26	1.18

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	373/375 (100%)	301 (81%)	72 (19%)	0	100	100
1	B	373/375 (100%)	301 (81%)	72 (19%)	0	100	100
1	C	373/375 (100%)	301 (81%)	72 (19%)	0	100	100
1	D	373/375 (100%)	301 (81%)	72 (19%)	0	100	100
1	E	373/375 (100%)	301 (81%)	72 (19%)	0	100	100
1	F	373/375 (100%)	301 (81%)	72 (19%)	0	100	100
2	G	37/220 (17%)	26 (70%)	10 (27%)	1 (3%)	4	25
2	H	37/220 (17%)	26 (70%)	10 (27%)	1 (3%)	4	25
2	I	37/220 (17%)	26 (70%)	10 (27%)	1 (3%)	4	25
2	J	37/220 (17%)	26 (70%)	10 (27%)	1 (3%)	4	25
2	K	37/220 (17%)	26 (70%)	10 (27%)	1 (3%)	4	25
2	L	37/220 (17%)	26 (70%)	10 (27%)	1 (3%)	4	25
All	All	2460/3570 (69%)	1962 (80%)	492 (20%)	6 (0%)	44	78

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	330	PRO
2	H	330	PRO
2	I	330	PRO
2	J	330	PRO
2	K	330	PRO

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	318/318 (100%)	310 (98%)	8 (2%)	42	63
1	B	318/318 (100%)	310 (98%)	8 (2%)	42	63
1	C	318/318 (100%)	310 (98%)	8 (2%)	42	63
1	D	318/318 (100%)	310 (98%)	8 (2%)	42	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	318/318 (100%)	310 (98%)	8 (2%)	42	63
1	F	318/318 (100%)	310 (98%)	8 (2%)	42	63
2	G	34/189 (18%)	34 (100%)	0	100	100
2	H	34/189 (18%)	34 (100%)	0	100	100
2	I	34/189 (18%)	34 (100%)	0	100	100
2	J	34/189 (18%)	34 (100%)	0	100	100
2	K	34/189 (18%)	34 (100%)	0	100	100
2	L	34/189 (18%)	34 (100%)	0	100	100
All	All	2112/3042 (69%)	2064 (98%)	48 (2%)	44	64

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	213	LYS
1	E	206	ARG
1	D	227	MET
1	E	61	LYS
1	E	227	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	88	HIS
1	F	173	HIS
1	C	88	HIS
1	C	40	HIS
1	F	296	ASN

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 [i](#)

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.

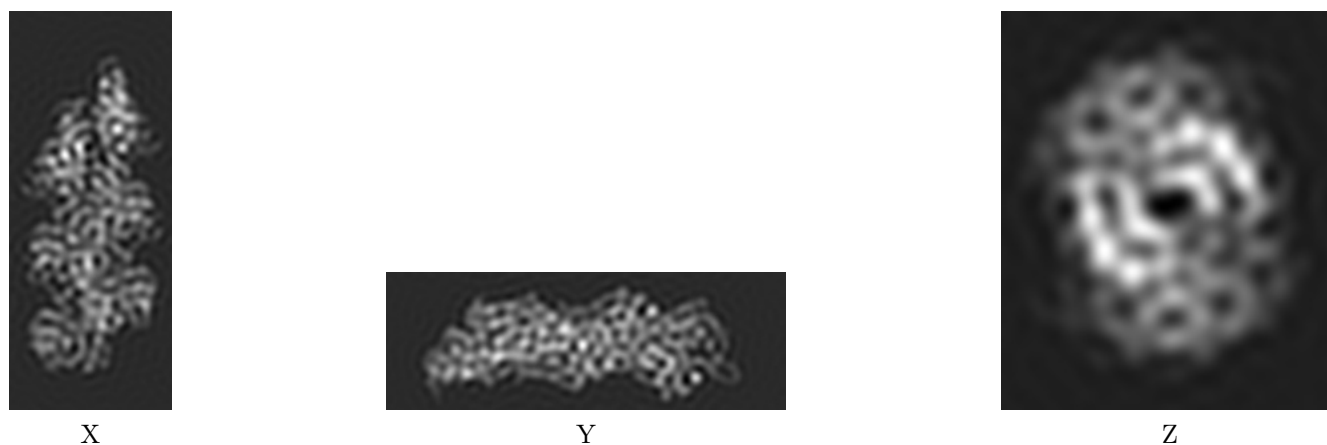
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25911. 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



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

6.2 Central slices [i](#)

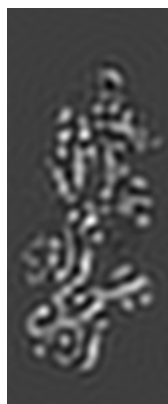
6.2.1 Primary map



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: 25



Y Index: 44

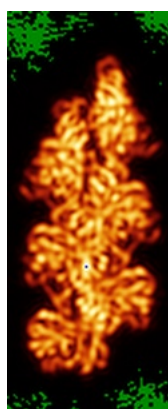


Z Index: 72

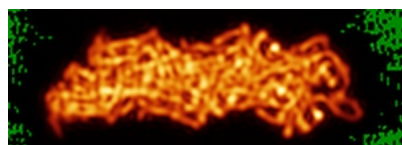
The images above show the largest variance slices of the map in three orthogonal directions.

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

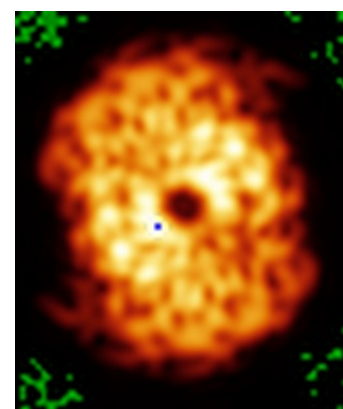
6.4.1 Primary map



X



Y

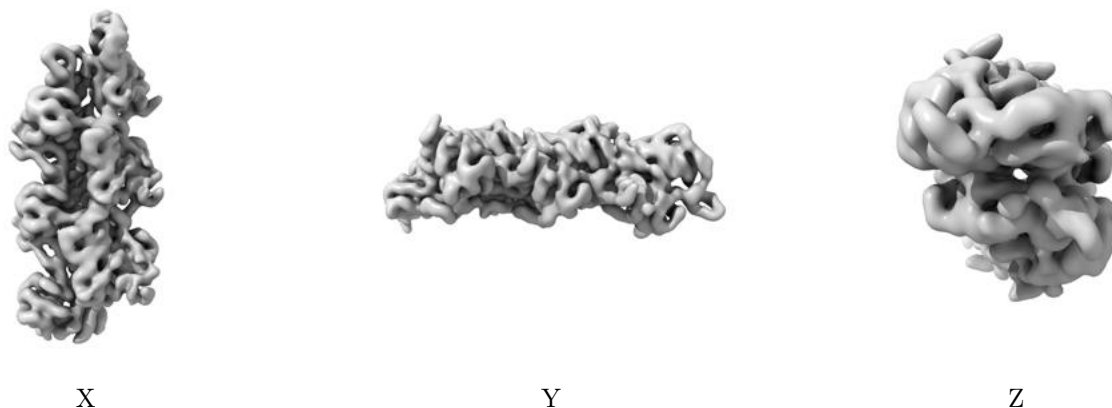


Z

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

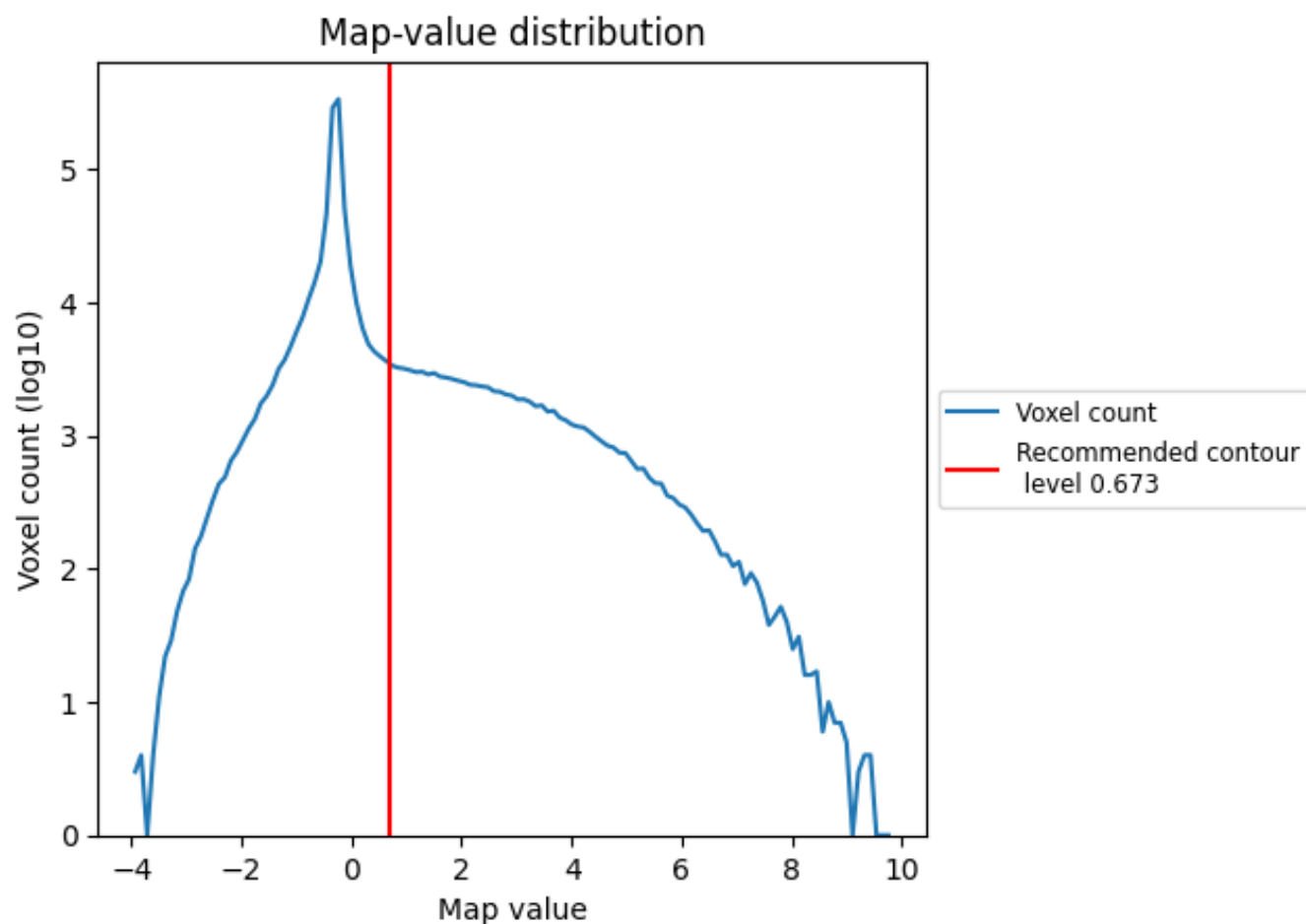
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

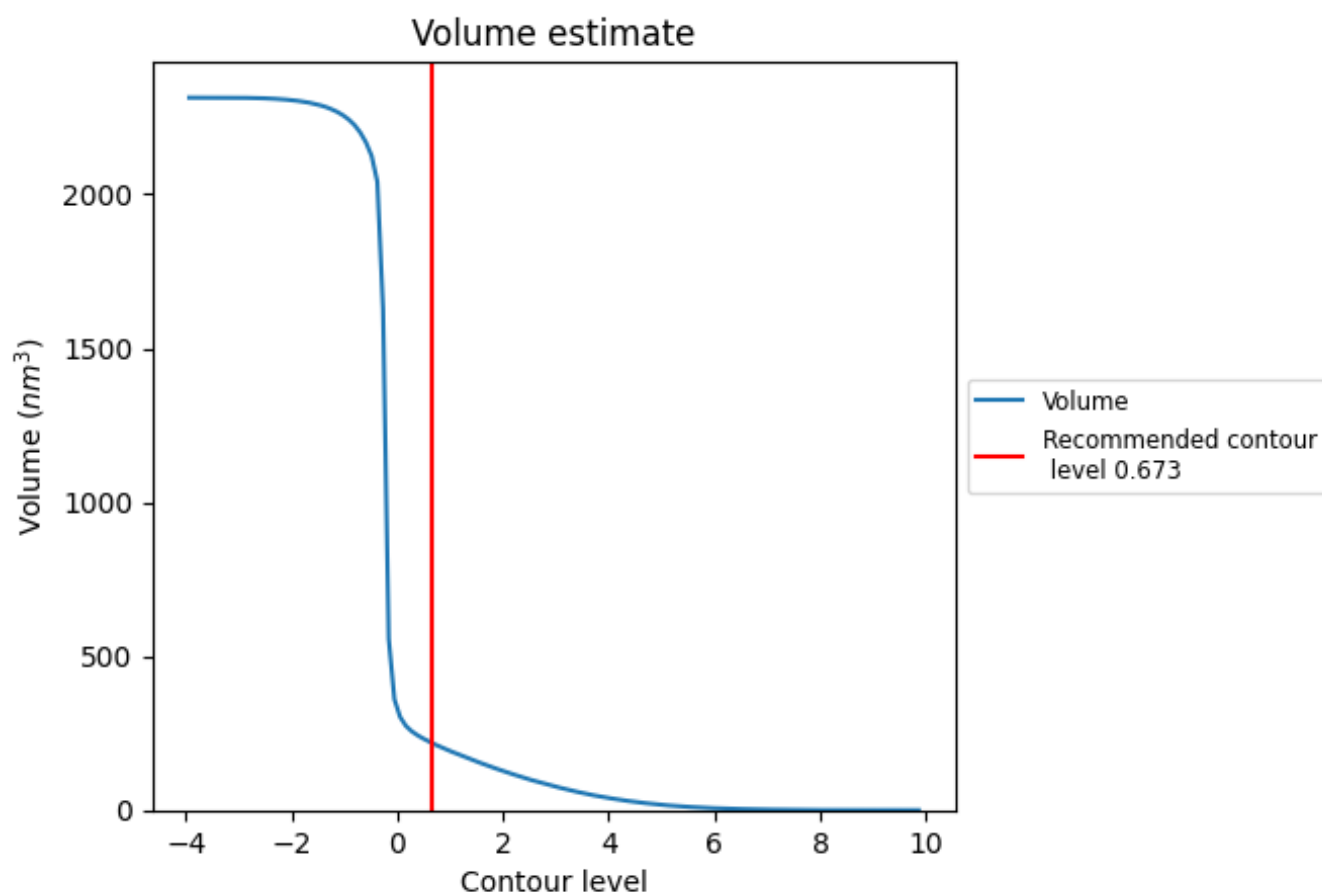
This section contains the results of statistical analysis of the map.

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 217 nm^3 ; this corresponds to an approximate mass of 196 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.

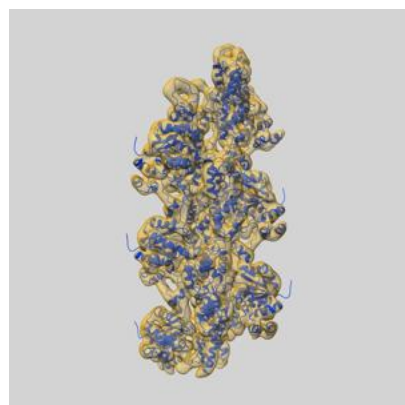
8 Fourier-Shell correlation

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

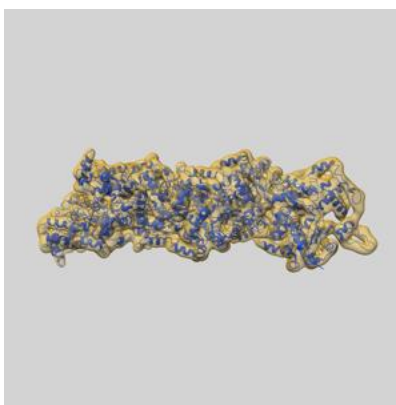
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25911 and PDB model 7TIJ. Per-residue inclusion information can be found in section 3 on page 5.

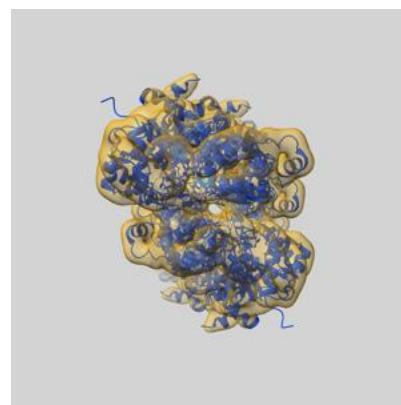
9.1 Map-model overlay [i](#)



X



Y



Z

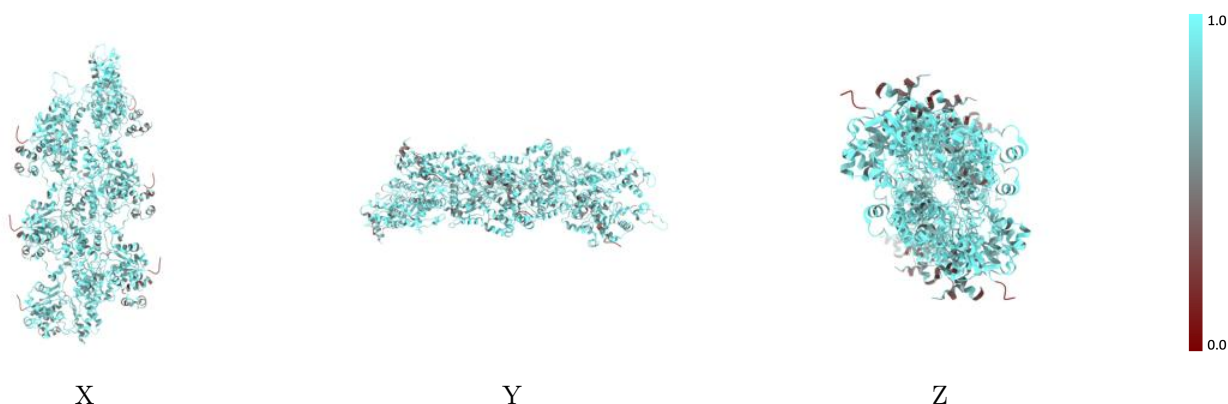
The images above show the 3D surface view of the map at the recommended contour level 0.673 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



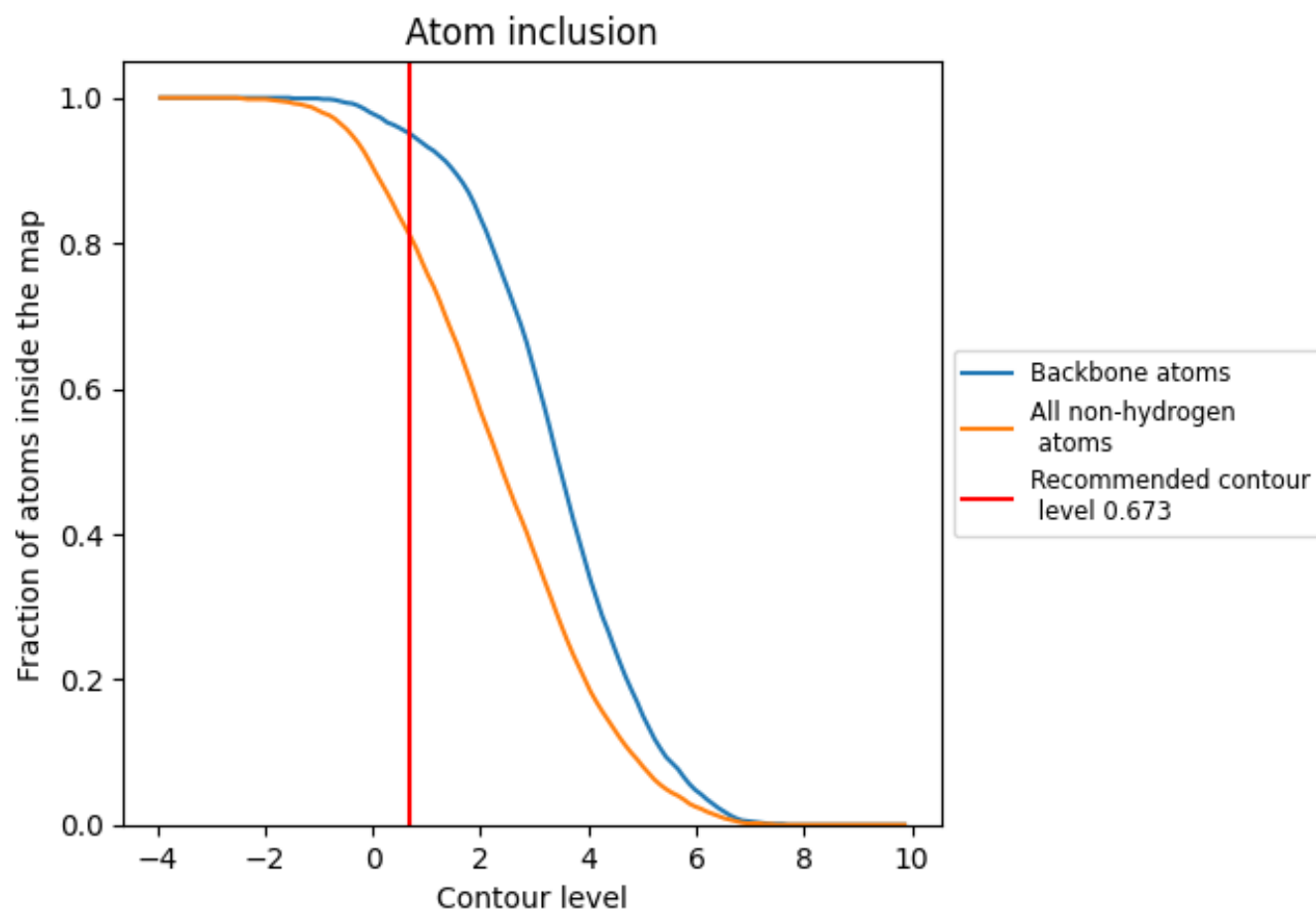
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.673).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.673) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8130	 0.1860
A	 0.8230	 0.1950
B	 0.8270	 0.1940
C	 0.8290	 0.1950
D	 0.8300	 0.1950
E	 0.8300	 0.1940
F	 0.8270	 0.1950
G	 0.5780	 0.1100
H	 0.5650	 0.0990
I	 0.5750	 0.1050
J	 0.5620	 0.1030
K	 0.5910	 0.1060
L	 0.5810	 0.1060

