



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 07:53 am BST

PDB ID : 8Q6T
EMDB ID : EMD-18198
Title : Helical reconstruction of the relaxed thick filament from FIB milled left ventricular mouse myofibrils
Authors : Tamborrini, D.; Raunser, S.
Deposited on : 2023-08-14
Resolution : 18.00 Å(reported)
Based on initial model : .

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.dev113
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

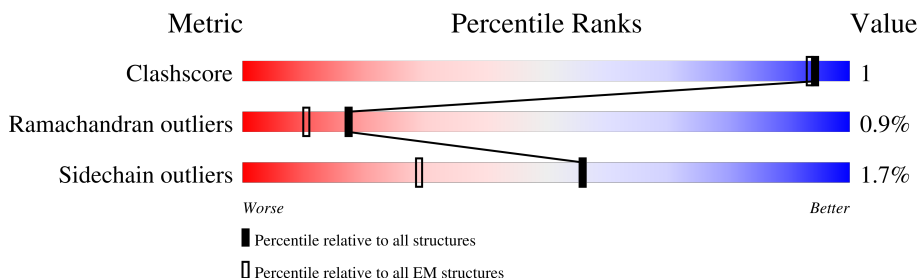
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 18.00 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)
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 ≥ 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	1935	<div> <div>14%</div> <div>95%</div> <div>.</div> </div>
1	B	1935	<div> <div>9%</div> <div>94%</div> <div>5%</div> </div>
1	H	1935	<div> <div>10%</div> <div>94%</div> <div>5%</div> </div>
1	N	1935	<div> <div>8%</div> <div>95%</div> <div>.</div> </div>
1	O	1935	<div> <div>7%</div> <div>94%</div> <div>5%</div> </div>
1	Q	1935	<div> <div>7%</div> <div>94%</div> <div>5%</div> </div>
2	C	152	<div> <div>42%</div> <div>93%</div> <div>7%</div> <div>.</div> </div>
2	D	152	<div> <div>12%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	J	152	
2	K	152	
2	R	152	
2	S	152	
3	E	160	
3	F	160	
3	L	160	
3	M	160	
3	T	160	
3	U	160	
4	G	400	
4	V	400	
5	I	1079	
5	P	1079	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 131418 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 Myosin-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1926	Total	C	N	O	S	0	0
			15571	9670	2761	3076	64		
1	B	1926	Total	C	N	O	S	0	0
			15571	9670	2761	3076	64		
1	H	1930	Total	C	N	O	S	0	0
			15600	9690	2765	3080	65		
1	N	1930	Total	C	N	O	S	0	0
			15600	9690	2765	3080	65		
1	O	1926	Total	C	N	O	S	0	0
			15571	9670	2761	3076	64		
1	Q	1926	Total	C	N	O	S	0	0
			15571	9670	2761	3076	64		

- Molecule 2 is a protein called Myosin light chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	152	Total	C	N	O	S	0	0
			1206	758	200	239	9		
2	D	152	Total	C	N	O	S	0	0
			1206	758	200	239	9		
2	J	152	Total	C	N	O	S	0	0
			1206	758	200	239	9		
2	K	152	Total	C	N	O	S	0	0
			1206	758	200	239	9		
2	R	152	Total	C	N	O	S	0	0
			1206	758	200	239	9		
2	S	152	Total	C	N	O	S	0	0
			1206	758	200	239	9		

- Molecule 3 is a protein called Myosin regulatory light chain 2, ventricular/cardiac muscle isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	160	Total	C	N	O	S	0	0
			1283	811	211	255	6		
3	F	160	Total	C	N	O	S	0	0
			1283	811	211	255	6		
3	L	160	Total	C	N	O	S	0	0
			1283	811	211	255	6		
3	M	160	Total	C	N	O	S	0	0
			1283	811	211	255	6		
3	T	160	Total	C	N	O	S	0	0
			1283	811	211	255	6		
3	U	160	Total	C	N	O	S	0	0
			1283	811	211	255	6		

- Molecule 4 is a protein called Myosin binding protein C, cardiac.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	400	Total	C	N	O	S	0	0
			3151	2002	556	579	14		
4	V	400	Total	C	N	O	S	0	0
			3151	2002	556	579	14		

- Molecule 5 is a protein called Titin.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	1079	Total	C	N	O	S	0	0
			8349	5261	1424	1637	27		
5	P	1079	Total	C	N	O	S	0	0
			8349	5261	1424	1637	27		

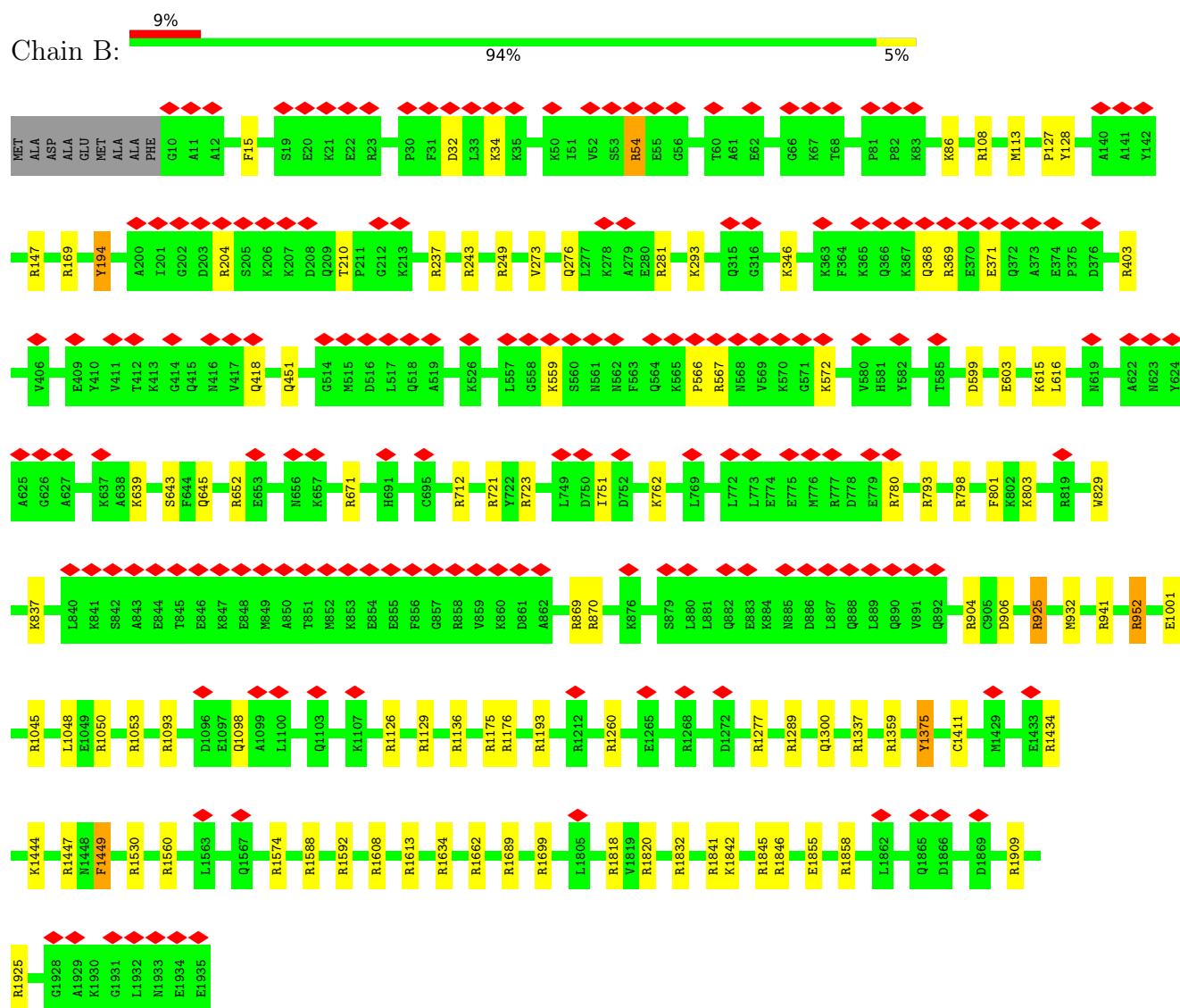
3 Residue-property plots [i](#)

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

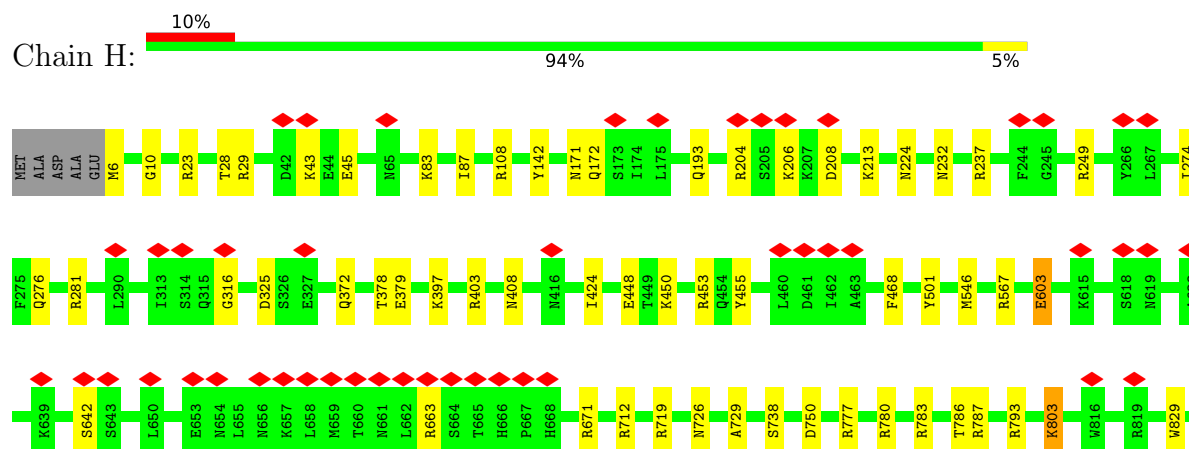
• Molecule 1: Myosin-7



- Molecule 1: Myosin-7

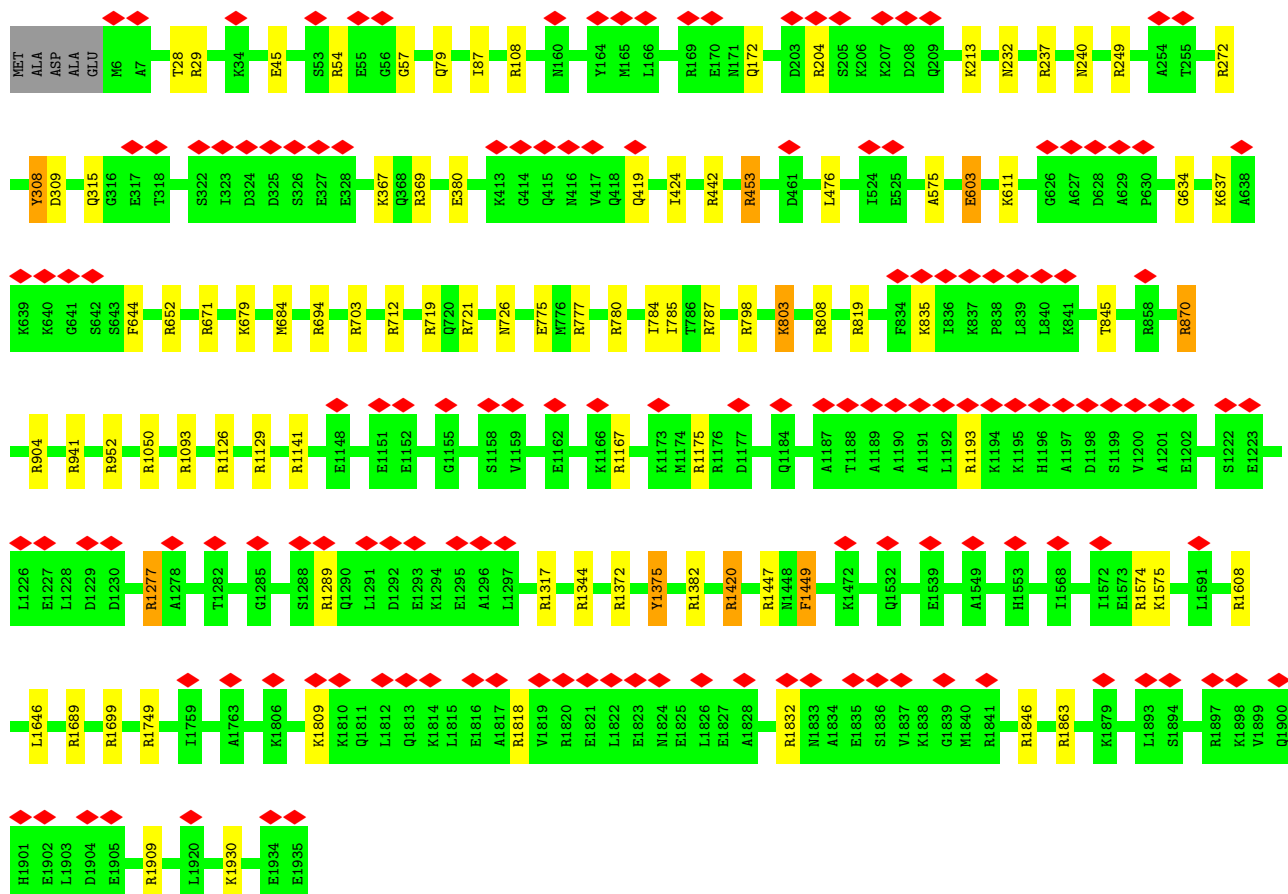


- Molecule 1: Myosin-7

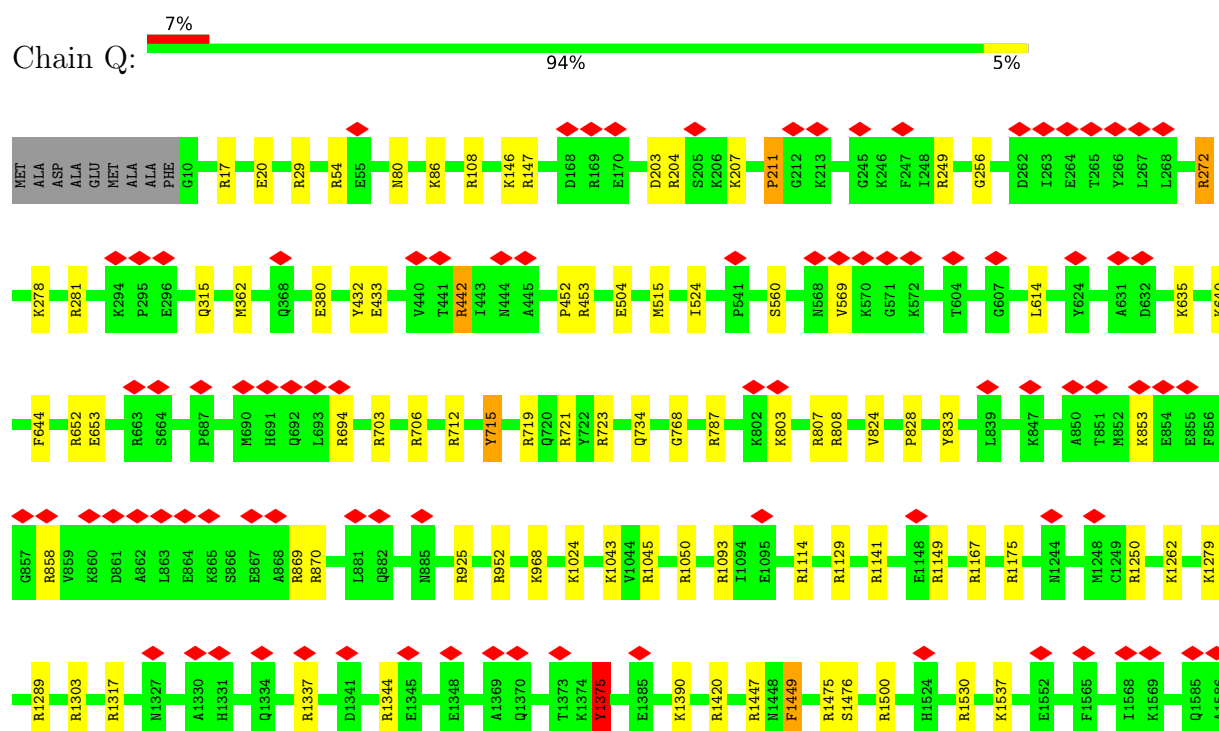
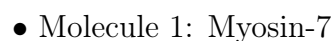


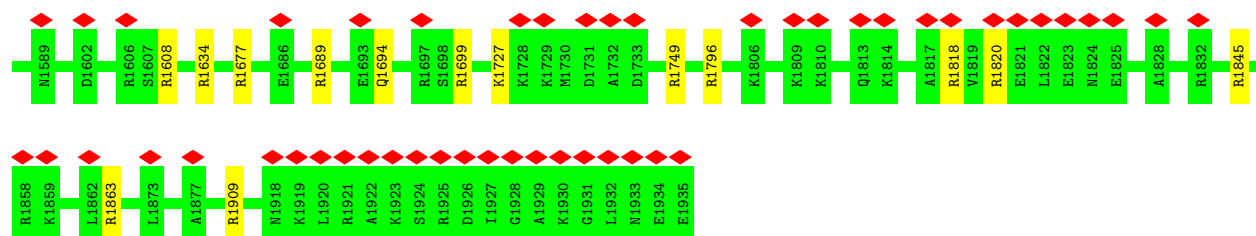


• Molecule 1: Myosin-7

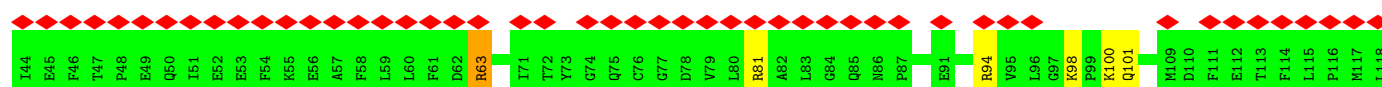
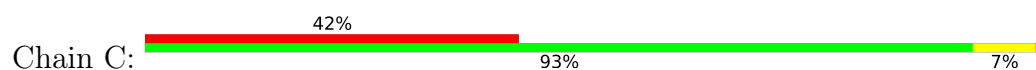


• Molecule 1: Myosin-7

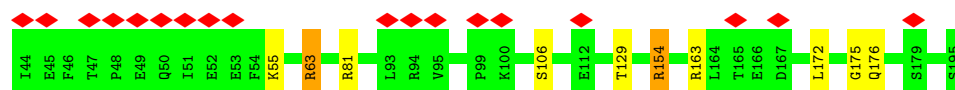




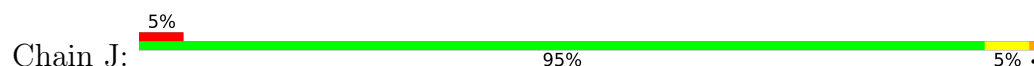
• Molecule 2: Myosin light chain 3



• Molecule 2: Myosin light chain 3



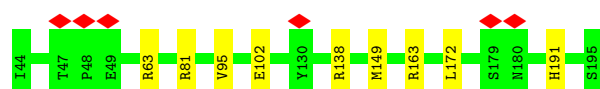
• Molecule 2: Myosin light chain 3



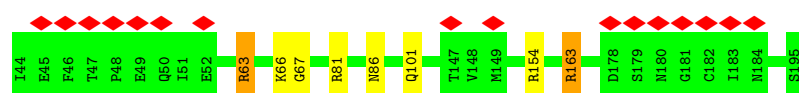
• Molecule 2: Myosin light chain 3



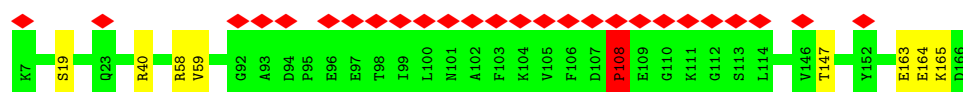
• Molecule 2: Myosin light chain 3



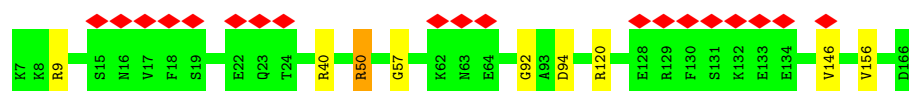
• Molecule 2: Myosin light chain 3



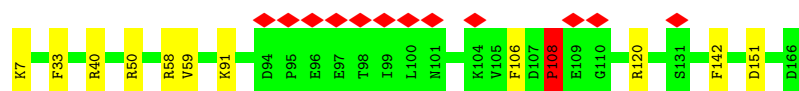
- Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform



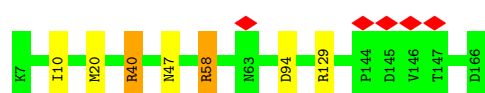
- Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform



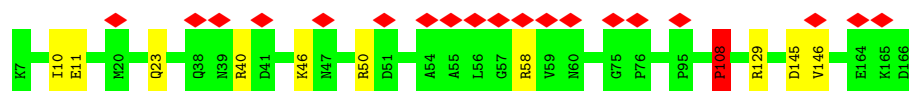
- Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform



- Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform



- Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform



- Molecule 3: Myosin regulatory light chain 2, ventricular/cardiac muscle isoform





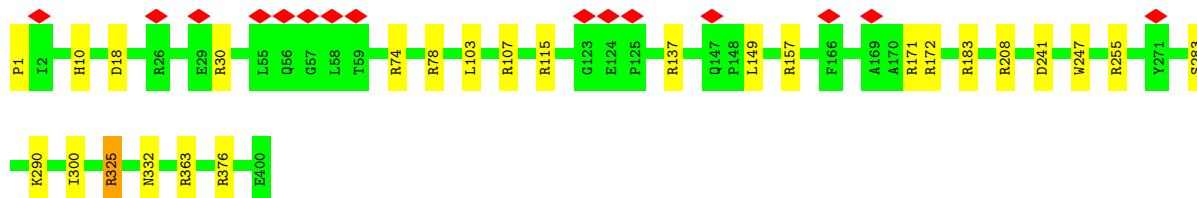
- Molecule 4: Myosin binding protein C, cardiac

Chain G: 96%



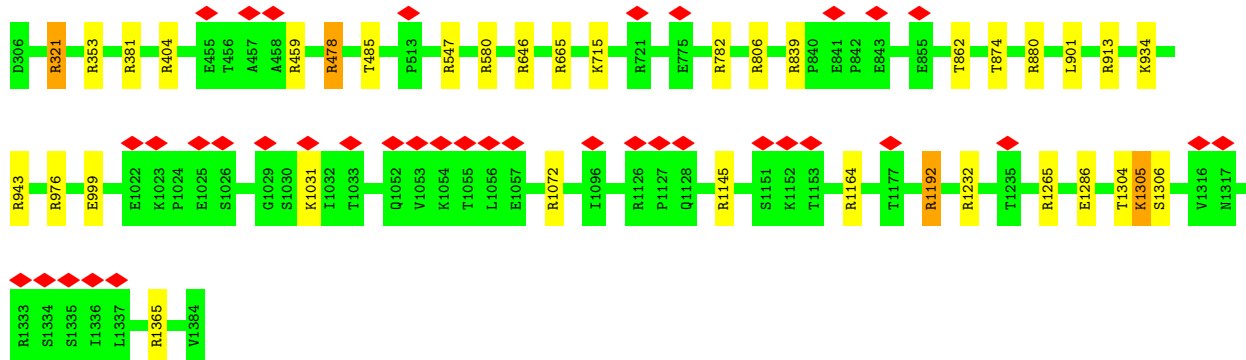
- Molecule 4: Myosin binding protein C, cardiac

Chain V: 94% 6%



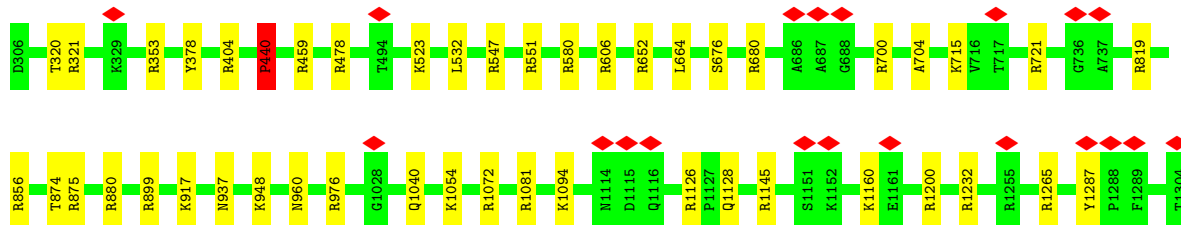
- Molecule 5: Titin

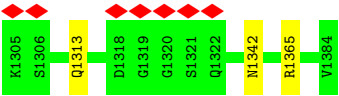
Chain I: 97%



- Molecule 5: Titin

Chain P: 95%





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	HELICAL, twist=0°, rise=430 Å, axial sym=C3	Depositor
Number of subtomograms used	1589	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 ($e^-/\text{\AA}^2$)	140	Depositor
Minimum defocus (nm)	3000	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	13.522	Depositor
Minimum map value	0.000	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.387	Depositor
Recommended contour level	2.41	Depositor
Map size (Å)	2168.76, 2168.76, 2168.76	wwPDB
Map dimensions	372, 372, 372	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	5.83, 5.83, 5.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1.24	13/15751 (0.1%)	0.95	66/21093 (0.3%)
1	B	1.14	13/15751 (0.1%)	0.97	69/21093 (0.3%)
1	H	1.24	13/15781 (0.1%)	0.95	64/21133 (0.3%)
1	N	1.24	13/15781 (0.1%)	0.94	65/21133 (0.3%)
1	O	1.14	12/15751 (0.1%)	0.97	81/21093 (0.4%)
1	Q	1.14	12/15751 (0.1%)	0.95	69/21093 (0.3%)
2	C	0.70	0/1225	0.97	5/1643 (0.3%)
2	D	0.71	0/1225	0.98	4/1643 (0.2%)
2	J	0.71	0/1225	0.93	2/1643 (0.1%)
2	K	0.72	0/1225	0.98	5/1643 (0.3%)
2	R	0.71	0/1225	0.94	4/1643 (0.2%)
2	S	0.72	0/1225	0.95	3/1643 (0.2%)
3	E	1.69	5/1306 (0.4%)	0.94	1/1752 (0.1%)
3	F	0.74	0/1306	0.99	4/1752 (0.2%)
3	L	1.70	5/1306 (0.4%)	0.93	2/1752 (0.1%)
3	M	0.74	0/1306	0.95	3/1752 (0.2%)
3	T	1.70	5/1306 (0.4%)	0.93	4/1752 (0.2%)
3	U	0.73	0/1306	0.96	2/1752 (0.1%)
4	G	0.72	0/3233	1.01	11/4398 (0.3%)
4	V	0.72	0/3233	1.02	15/4398 (0.3%)
5	I	0.70	0/8525	0.96	23/11602 (0.2%)
5	P	0.70	0/8525	0.98	28/11602 (0.2%)
All	All	1.11	91/133268 (0.1%)	0.96	530/179008 (0.3%)

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
1	A	0	1
1	B	0	2
1	H	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	0	1
1	Q	0	5
2	S	0	1
3	L	0	1
5	I	0	1
5	P	0	1
All	All	0	15

The worst 5 of 91 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	1375	TYR	CD2-CE2	75.26	2.52	1.39
1	O	1375	TYR	CD2-CE2	75.22	2.52	1.39
1	A	1375	TYR	CD2-CE2	75.14	2.52	1.39
1	B	1375	TYR	CD2-CE2	75.09	2.52	1.39
1	N	1375	TYR	CD2-CE2	75.08	2.52	1.39

The worst 5 of 530 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	1375	TYR	CG-CD2-CE2	-12.56	111.25	121.30
1	O	1375	TYR	CG-CD2-CE2	-12.49	111.31	121.30
1	A	1375	TYR	CG-CD2-CE2	-12.47	111.32	121.30
1	B	1375	TYR	CG-CD2-CE2	-12.47	111.33	121.30
1	N	1375	TYR	CG-CD2-CE2	-12.43	111.36	121.30

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1375	TYR	Sidechain
1	B	194	TYR	Sidechain
1	B	925	ARG	Sidechain
1	H	1375	TYR	Sidechain
1	H	1608	ARG	Sidechain

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	15571	0	15684	85	0
1	B	15571	0	15684	52	0
1	H	15600	0	15711	83	0
1	N	15600	0	15712	87	0
1	O	15571	0	15683	57	0
1	Q	15571	0	15684	54	0
2	C	1206	0	1182	0	0
2	D	1206	0	1182	0	0
2	J	1206	0	1182	0	0
2	K	1206	0	1182	0	0
2	R	1206	0	1182	0	0
2	S	1206	0	1182	0	0
3	E	1283	0	1245	37	0
3	F	1283	0	1245	0	0
3	L	1283	0	1245	35	0
3	M	1283	0	1245	0	0
3	T	1283	0	1245	38	0
3	U	1283	0	1245	0	0
4	G	3151	0	3155	0	0
4	V	3151	0	3155	0	0
5	I	8349	0	8362	0	0
5	P	8349	0	8362	0	0
All	All	131418	0	131754	282	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.

The worst 5 of 282 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:A:1375:TYR:CE2	1:B:1375:TYR:CE2	2.12	1.38
1:A:1375:TYR:CD2	1:B:1375:TYR:CE2	2.12	1.38
1:A:1449:PHE:CD1	1:B:1449:PHE:CD2	2.12	1.38
1:A:1375:TYR:CE2	1:B:1375:TYR:CD2	2.12	1.38
1:A:1375:TYR:CD2	1:B:1375:TYR:CD2	2.12	1.38

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1924/1935 (99%)	1836 (95%)	75 (4%)	13 (1%)	19	57
1	B	1924/1935 (99%)	1810 (94%)	98 (5%)	16 (1%)	16	55
1	H	1928/1935 (100%)	1834 (95%)	78 (4%)	16 (1%)	16	55
1	N	1928/1935 (100%)	1854 (96%)	62 (3%)	12 (1%)	22	60
1	O	1924/1935 (99%)	1825 (95%)	86 (4%)	13 (1%)	19	57
1	Q	1924/1935 (99%)	1827 (95%)	81 (4%)	16 (1%)	16	55
2	C	150/152 (99%)	140 (93%)	6 (4%)	4 (3%)	4	25
2	D	150/152 (99%)	138 (92%)	8 (5%)	4 (3%)	4	25
2	J	150/152 (99%)	138 (92%)	10 (7%)	2 (1%)	10	43
2	K	150/152 (99%)	138 (92%)	12 (8%)	0	100	100
2	R	150/152 (99%)	133 (89%)	16 (11%)	1 (1%)	19	57
2	S	150/152 (99%)	136 (91%)	11 (7%)	3 (2%)	6	32
3	E	158/160 (99%)	139 (88%)	14 (9%)	5 (3%)	3	21
3	F	158/160 (99%)	134 (85%)	19 (12%)	5 (3%)	3	21
3	L	158/160 (99%)	141 (89%)	14 (9%)	3 (2%)	6	32
3	M	158/160 (99%)	137 (87%)	19 (12%)	2 (1%)	10	43
3	T	158/160 (99%)	138 (87%)	17 (11%)	3 (2%)	6	32
3	U	158/160 (99%)	139 (88%)	13 (8%)	6 (4%)	2	19
4	G	398/400 (100%)	371 (93%)	25 (6%)	2 (0%)	25	64
4	V	398/400 (100%)	376 (94%)	15 (4%)	7 (2%)	7	35
5	I	1077/1079 (100%)	1036 (96%)	35 (3%)	6 (1%)	22	60
5	P	1077/1079 (100%)	1035 (96%)	40 (4%)	2 (0%)	44	78
All	All	16350/16440 (100%)	15455 (94%)	754 (5%)	141 (1%)	17	52

5 of 141 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	605	VAL
1	B	451	GLN
3	E	163	GLU
3	F	92	GLY
1	N	575	ALA

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	1688/1693 (100%)	1665 (99%)	23 (1%)	62	75
1	B	1688/1693 (100%)	1659 (98%)	29 (2%)	56	72
1	H	1690/1693 (100%)	1656 (98%)	34 (2%)	50	68
1	N	1690/1693 (100%)	1660 (98%)	30 (2%)	54	71
1	O	1688/1693 (100%)	1670 (99%)	18 (1%)	70	80
1	Q	1688/1693 (100%)	1661 (98%)	27 (2%)	58	73
2	C	131/131 (100%)	128 (98%)	3 (2%)	45	64
2	D	131/131 (100%)	127 (97%)	4 (3%)	35	54
2	J	131/131 (100%)	126 (96%)	5 (4%)	28	49
2	K	131/131 (100%)	125 (95%)	6 (5%)	23	44
2	R	131/131 (100%)	127 (97%)	4 (3%)	35	54
2	S	131/131 (100%)	128 (98%)	3 (2%)	45	64
3	E	139/139 (100%)	136 (98%)	3 (2%)	47	65
3	F	139/139 (100%)	138 (99%)	1 (1%)	81	87
3	L	139/139 (100%)	133 (96%)	6 (4%)	25	46
3	M	139/139 (100%)	135 (97%)	4 (3%)	37	56
3	T	139/139 (100%)	137 (99%)	2 (1%)	62	75
3	U	139/139 (100%)	134 (96%)	5 (4%)	30	50
4	G	344/344 (100%)	341 (99%)	3 (1%)	75	83
4	V	344/344 (100%)	339 (98%)	5 (2%)	60	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	I	928/928 (100%)	918 (99%)	10 (1%)	70	80
5	P	928/928 (100%)	907 (98%)	21 (2%)	45	64
All	All	14296/14322 (100%)	14050 (98%)	246 (2%)	56	72

5 of 246 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	51	ILE
1	Q	1262	LYS
1	N	419	GLN
1	Q	1024	LYS
3	U	33	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	104	ASN
1	H	1720	ASN
1	H	1833	ASN
1	O	1486	ASN

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 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.

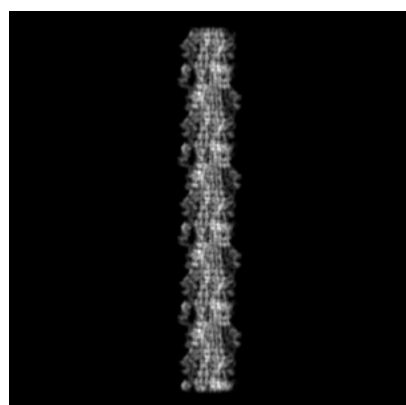
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18198. These allow visual inspection of the internal detail of the map and identification of artifacts.

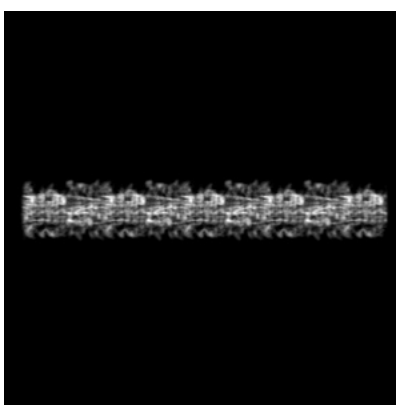
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

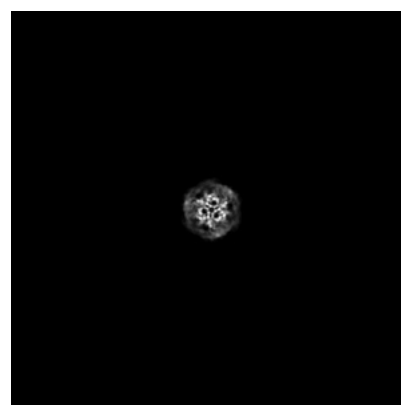
6.1.1 Primary map



X



Y

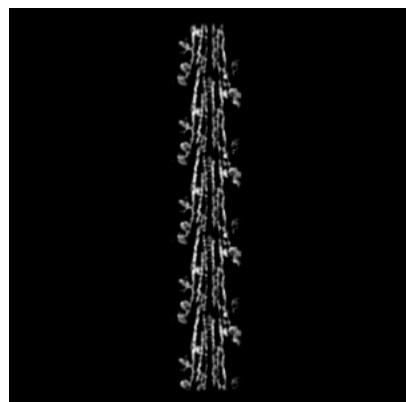


Z

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

6.2 Central slices [i](#)

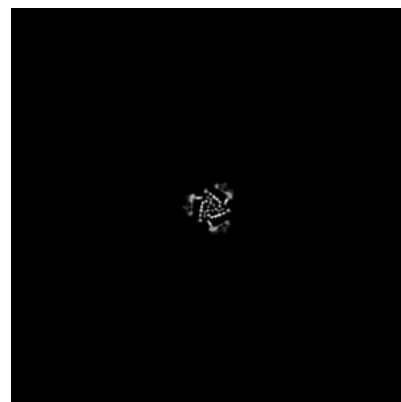
6.2.1 Primary map



X Index: 186



Y Index: 186



Z Index: 186

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: 183



Y Index: 193

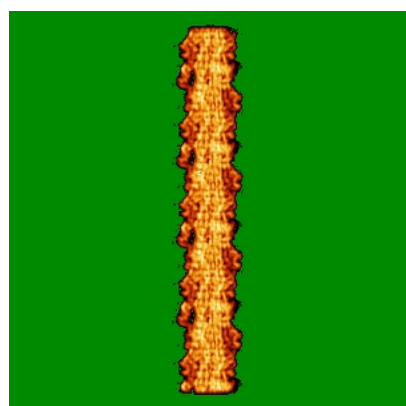


Z Index: 172

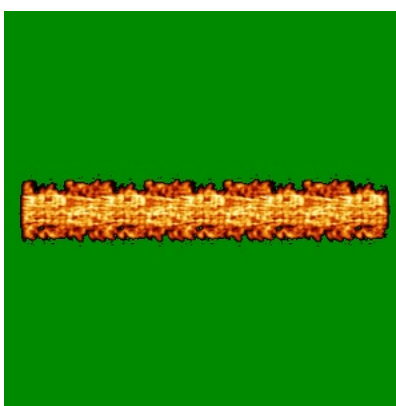
The images above show the largest variance slices of the map in three orthogonal directions.

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

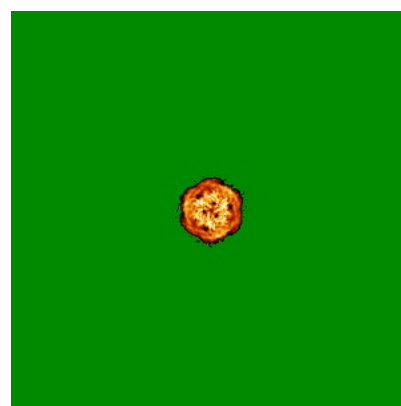
6.4.1 Primary map



X



Y

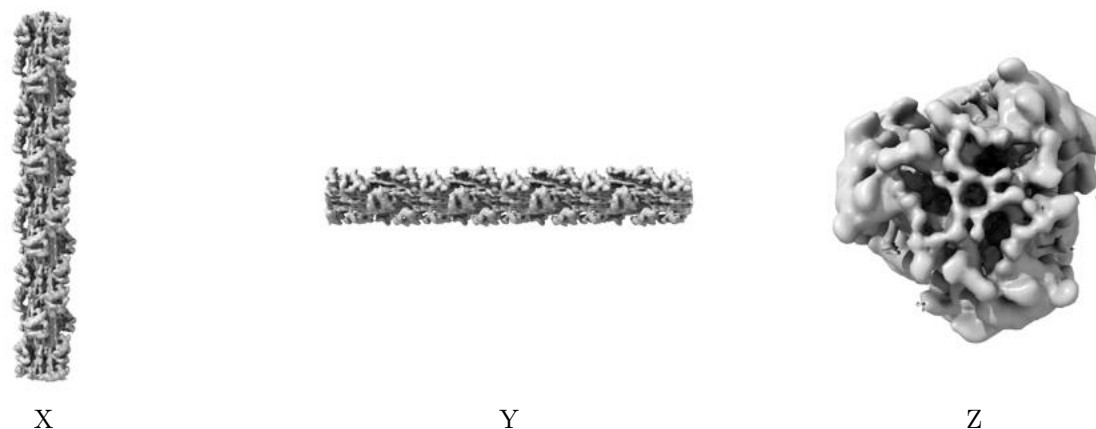


Z

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

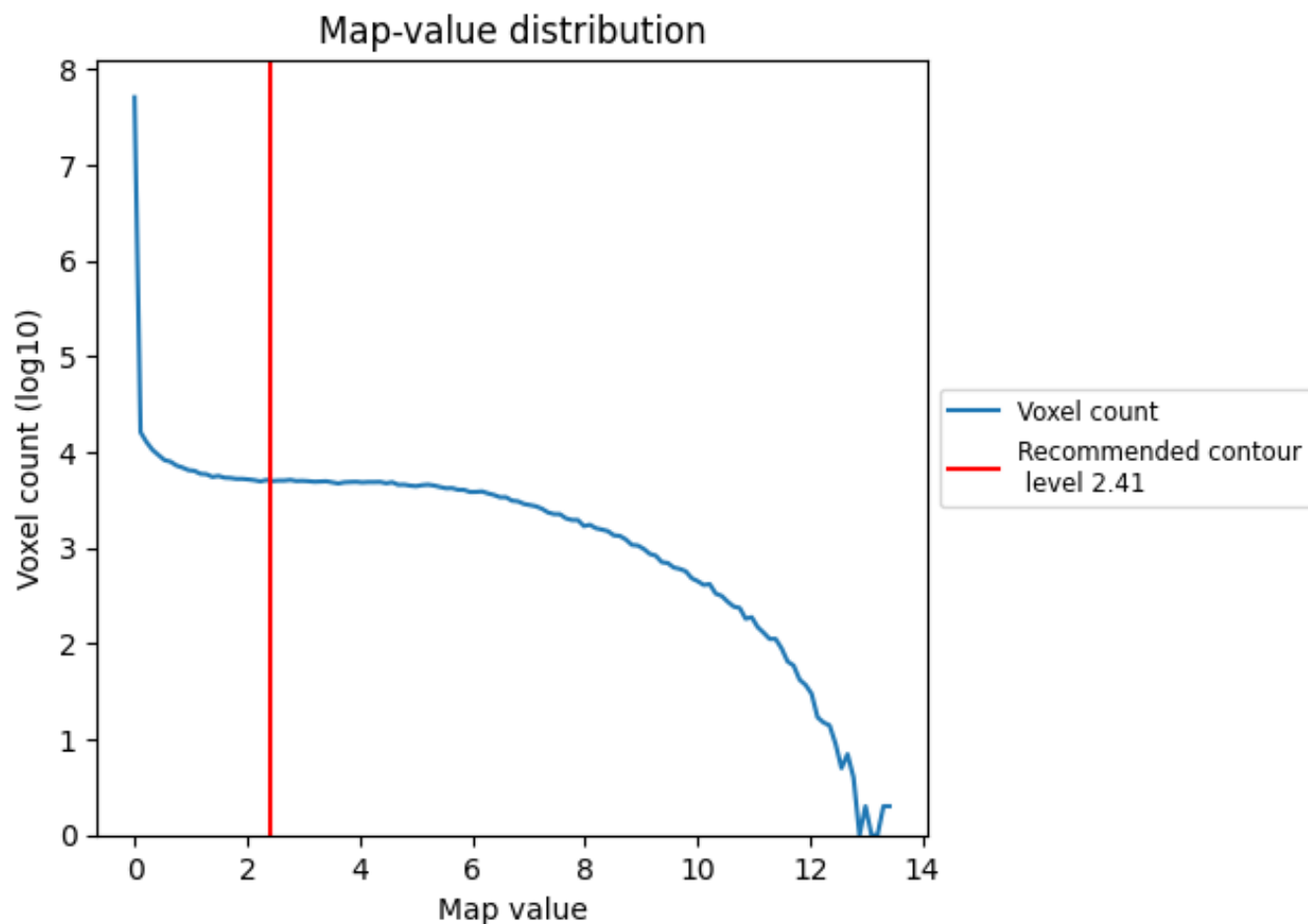
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

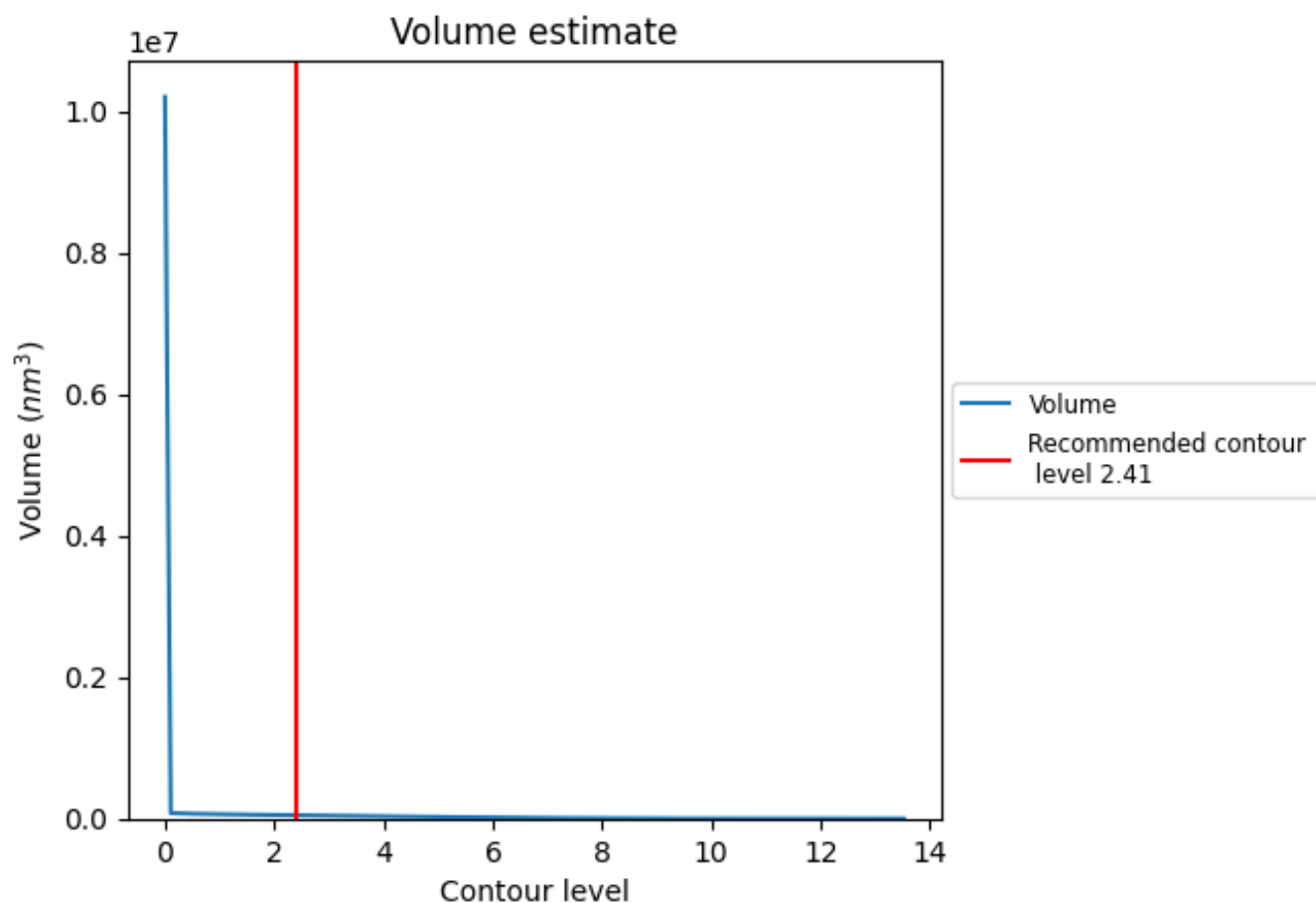
This section contains the results of statistical analysis of the map.

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.

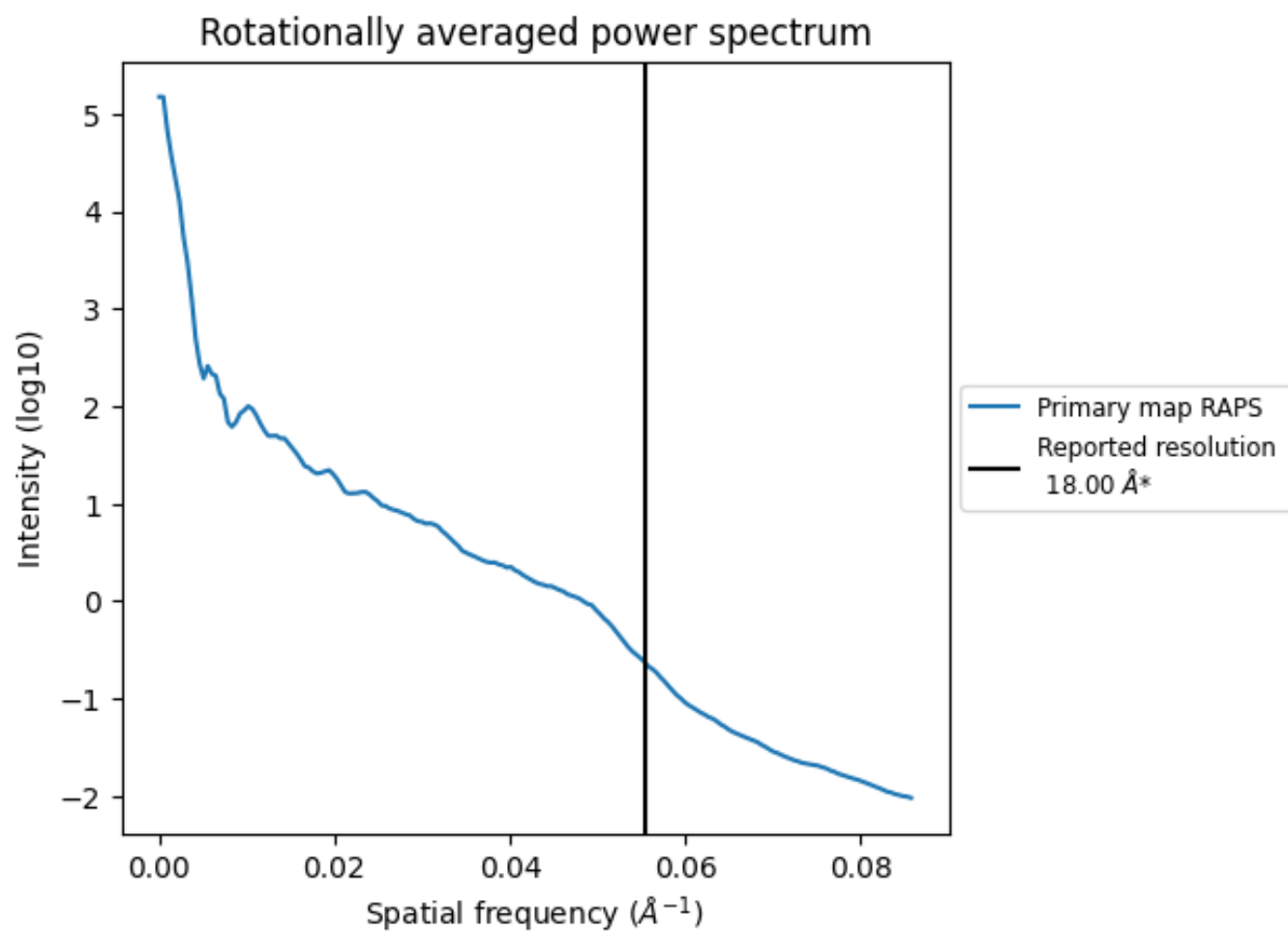
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 47100 nm³; this corresponds to an approximate mass of 42547 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 0.056 Å⁻¹

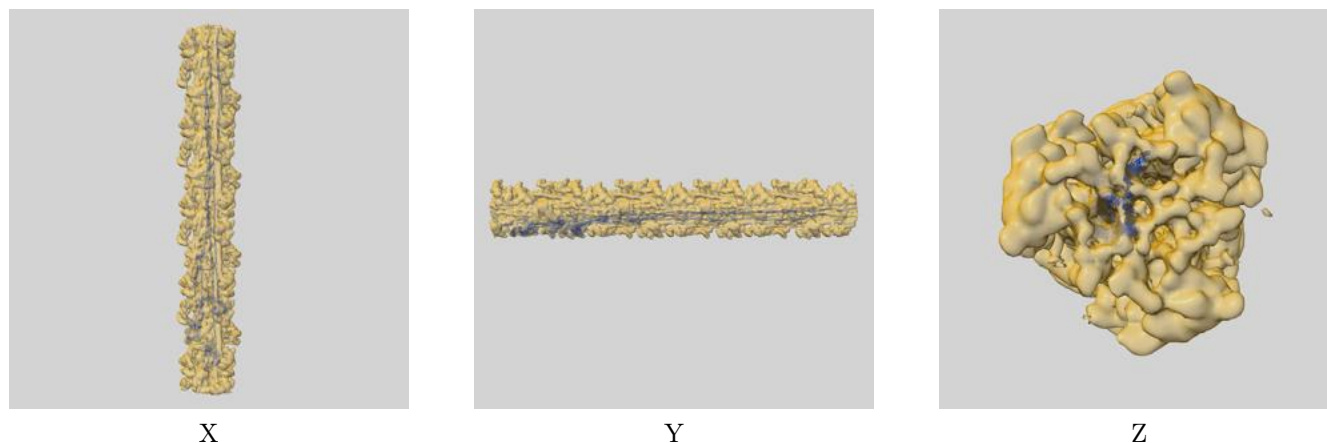
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

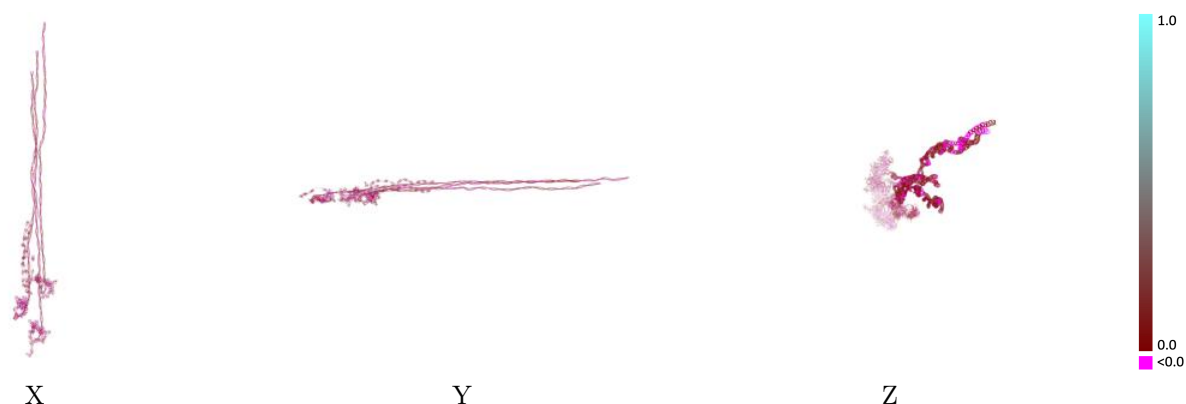
This section contains information regarding the fit between EMDB map EMD-18198 and PDB model 8Q6T. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 2.41 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](#)



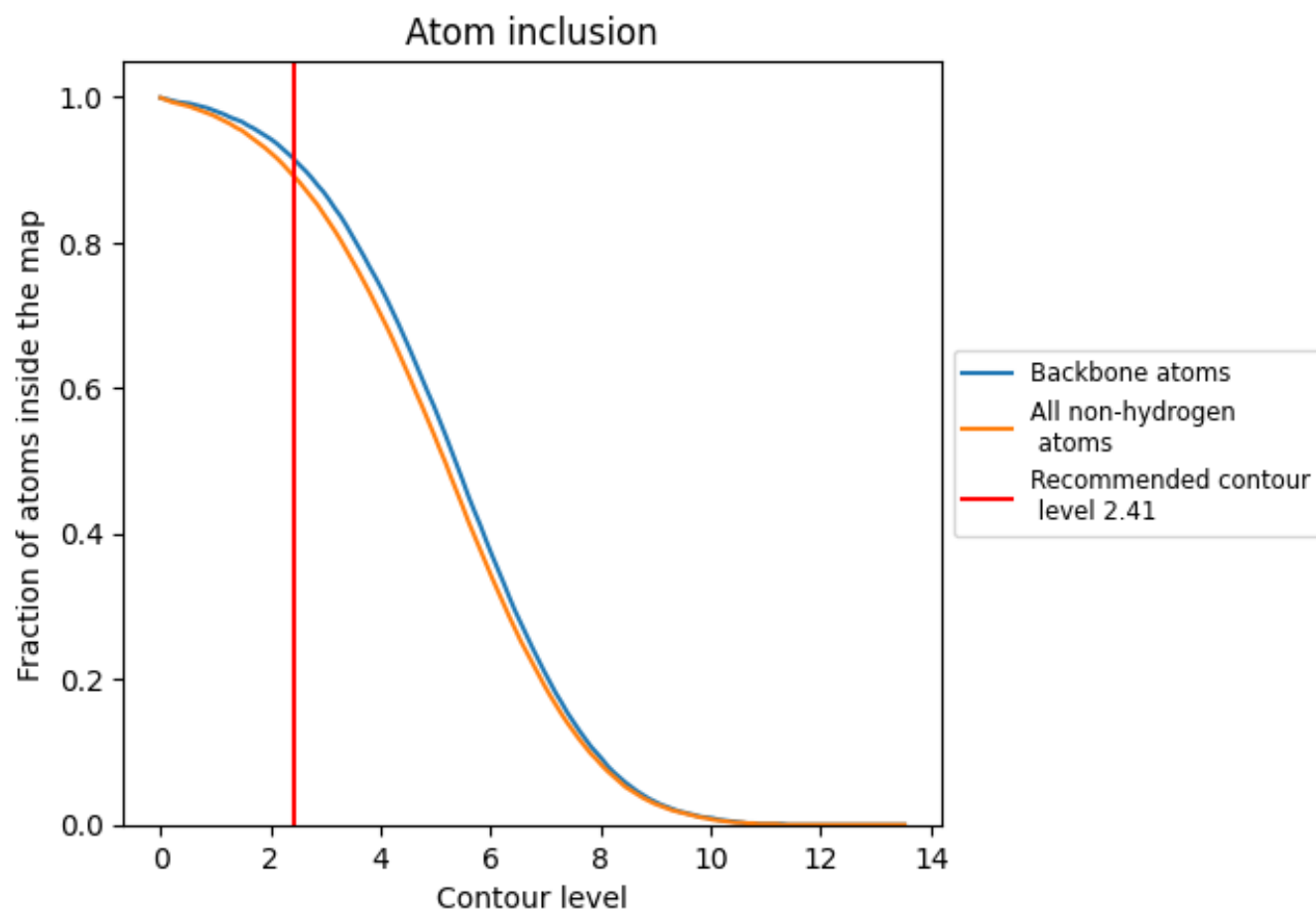
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.41).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 89% 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 (2.41) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8920	 0.0560
A	 0.8380	 0.0430
B	 0.8820	 0.0610
C	 0.5730	 0.0040
D	 0.8670	 0.0470
E	 0.8080	 0.0530
F	 0.8500	 0.0420
G	 0.9600	 0.0610
H	 0.8710	 0.0520
I	 0.9420	 0.0690
J	 0.9500	 0.0670
K	 0.9330	 0.0530
L	 0.8900	 0.0650
M	 0.9450	 0.0550
N	 0.9010	 0.0600
O	 0.8910	 0.0610
P	 0.9560	 0.0590
Q	 0.9050	 0.0550
R	 0.9400	 0.0650
S	 0.8980	 0.0550
T	 0.8570	 0.0360
U	 0.9690	 0.0660
V	 0.9470	 0.0550

