



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:40 AM UTC

PDB ID : 8SYF / pdb_00008syf
EMDB ID : EMD-29646
Title : Homology model of Acto-HMM complex in ADP-state. Chicken smooth muscle HMM and chicken pectoralis actin
Authors : Hojjatian, A.; Taylor, D.W.; Daneshparvar, N.; Trybus, K.M.; Taylor, K.A.
Deposited on : 2023-05-25
Resolution : 19.00 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

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

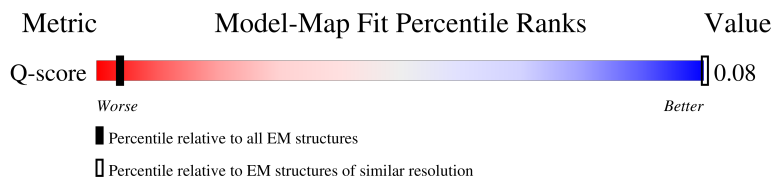
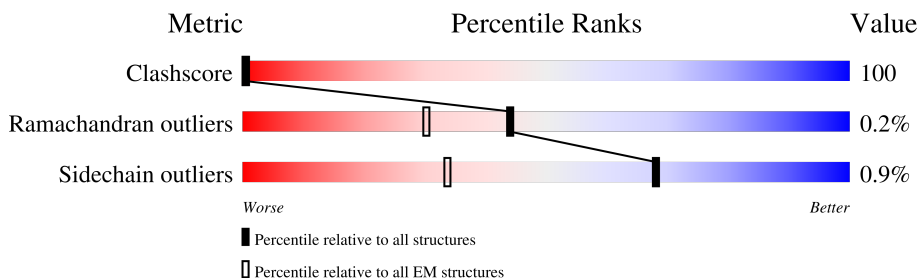
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 19.00 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.



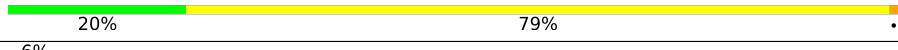
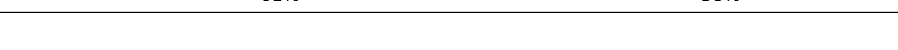
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	17 (18.70 - 19.50)

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	843	
1	B	843	
2	C	375	
2	D	375	

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Mol	Chain	Length	Quality of chain
3	E	148	
3	H	148	
4	F	143	
4	G	143	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 23456 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, heavy chain 11, smooth muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	800	Total	C	N	O	S	0	0
			6474	4129	1118	1195	32		
1	B	800	Total	C	N	O	S	0	0
			6474	4129	1118	1195	32		

- Molecule 2 is a protein called Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	375	Total	C	N	O	S	0	0
			2933	1854	493	565	21		
2	D	375	Total	C	N	O	S	0	0
			2933	1854	493	565	21		

- Molecule 3 is a protein called Myosin light polypeptide 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	148	Total	C	N	O	S	0	0
			1160	720	193	236	11		
3	H	148	Total	C	N	O	S	0	0
			1160	720	193	236	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	65	ASN	LYS	conflict	UNP P02607
H	65	ASN	LYS	conflict	UNP P02607

- Molecule 4 is a protein called Myosin regulatory light chain 2, smooth muscle major isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	143	Total	C	N	O	S	0	0
			1161	727	189	235	10		

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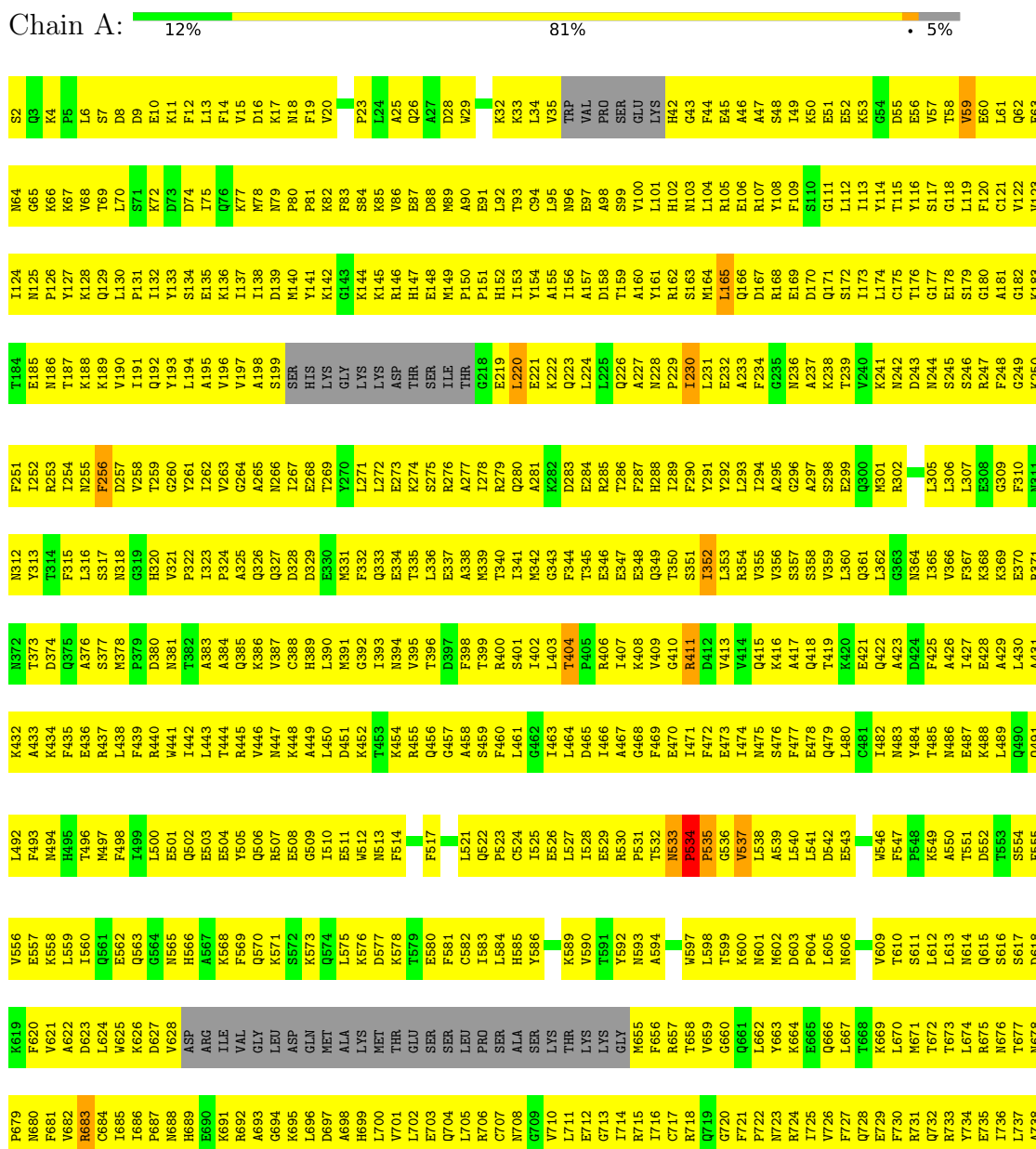
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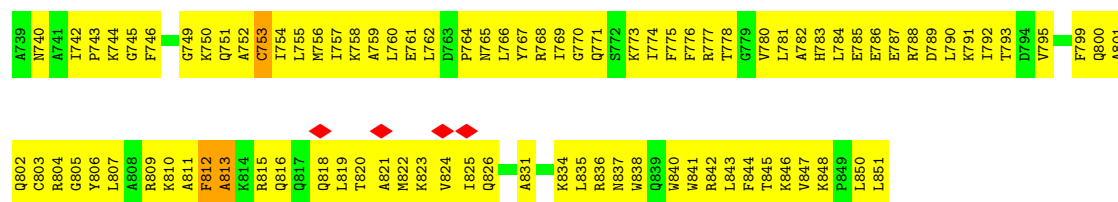
Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	143	Total	C	N	O	S	0	0
			1161	727	189	235	10		

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.

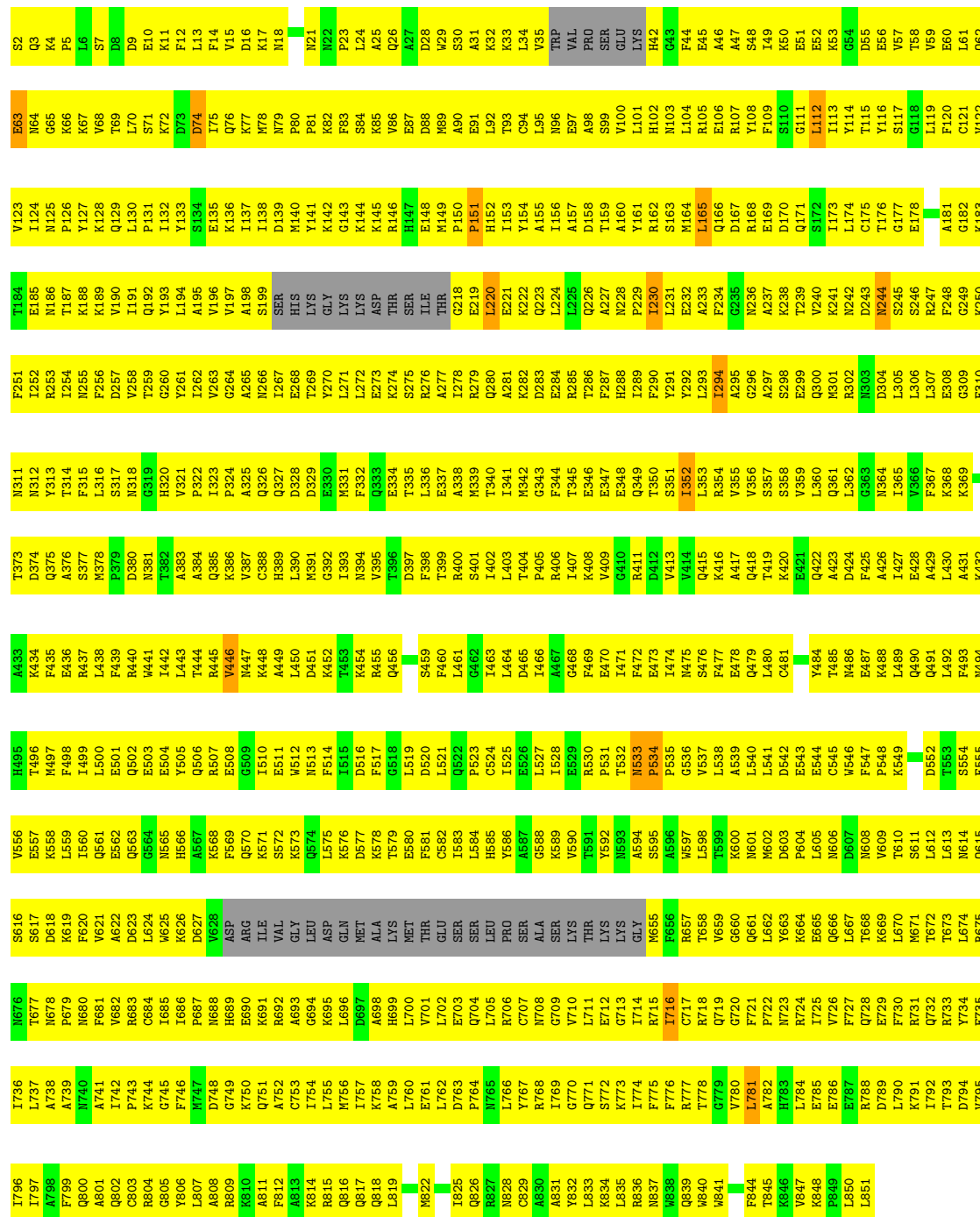
- Molecule 1: Myosin, heavy chain 11, smooth muscle



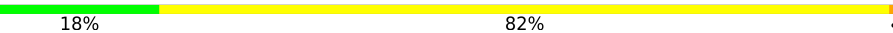


• Molecule 1: Myosin, heavy chain 11, smooth muscle

Chain B: 10% 83% 5%



- Molecule 2: Actin, alpha skeletal muscle

Chain C:  18% 82%

K315	E316	I317	T318	A319	L320	A321						M325	K326	I327	E328	L329	I330	A331	P332	P333	E334	R335	K336	Y337	S338	V339	K340	I341	G342	G343	S344	S345	S346	T347	F348	G349	S350	T351	F352	Q353	Q354	M355	Q356	E357	L358	K359	G360	I361	H362	V363	P364	M365	T366	F367	C368	D369	E370	L371	S372	R373	C374	F375		
T349	L250	G251	N252	E253	R254	F255	R256	C257	P258	E259	T260	L261	F262	Q263	S264	S265	F266						T274	H275	E276	T277	T278	Y279	N280	S281	R282	M283	K284	L285	C286	D287	D288	L289	R290	F291	K292	L293	Y294	A295	N296	N297	V298	M299	G300	G301	G302	T303	T304	M305	Y306	H307	R308	K309	R310	D311	R312	M313	Q314	
G182	R183	D184	L185	Y188		L189	M190	K191	I192	E193	T194	L195	R196	G197	Y198	S199	F200	V201	T202	T203	A204	E205	R206	E207	T208	V209	R210	D211	K212	K213	E214	L215	L216	C217	Y218	V219	A220	F223		N224	N225	E226	P227	A228	T229	S233		L236	E237	K238	S239	Y240	E241	L242	Q246	F247	L248							
D1	E2	D3	E4	T5	T6	A7	L8	V9	C10	D11	N12	G13	S14	G15	L16	V17	N18	K19	A20	G21	D22	E23	G24	D25	A26	P27	R28	F29	A30	F31	P32	S33	L34	V35	G36	R37	P38	R39	H40	Q41	G42	V43	M44	V45	G46	M47						K50	D51	S52	Y53	V54	N55	G56	D57	E58	Q59	S60	T61	K61
R62	G63	I64	L65	T66	L67	K68	V69	P70	I71	E72	N73	H74	G75	I76	T77	N78	V79	D80	A81	G82	L83	E84	T85	R86	H87	R88	T89	F90	Y91	N92	E93	L94	R95	V96	A97	P98	E99	E100	H101	P102	T103	L104	L105	T106	A107	A108	P109	L110	N111	P112	Y113	A114	N115	R116	E117	K118	M119	T120	Q121					
T122	M123	F124	E125	T126	L127	M128	V129	P130	C131	M132	H133	G134	A135	I136	Q137	V138	L139	L140	S141	L142	Y143	A144	S145	G146	R147	T148	D149	I150	V151	V152	L153	L154	S155	C156	D157	G158	V159	T160	H161	M162	V163	P164	I165	Y166	E167	G168	Y169	A170	L171	P172	H173	A174	I175	M176	R177	L178	D179	L180	A181					
G182	R183	D184	L185	Y188		L189	M190	K191	I192	E193	T194	L195	R196	G197	Y198	S199	F200	V201	T202	T203	A204	E205	R206	E207	T208	V209	R210	D211	K212	K213	E214	L215	L216	C217	Y218	V219	A220	F223		N224	N225	E226	P227	A228	T229	S233		L236	E237	K238	S239	Y240	E241	L242	Q246	F247	L248							
T249	L250	G251	N252	E253	R254	F255	R256	C257	P258	E259	T260	L261	F262	Q263	S264	S265	F266						T274	H275	E276	T277	T278	Y279	N280	S281	R282	M283	K284	L285	C286	D287	D288	L289	R290	F291	K292	L293	Y294	A295	N296	N297	V298	M299	G300	G301	G302	T303	T304	M305	Y306	H307	R308	K309	R310	D311	R312	M313	Q314	
K315	E316	I317	T318	A319	L320	A321						M325	K326	I327	E328	L329	I330	A331	P332	P333	E334	R335	K336	Y337	S338	V339	K340	I341	G342	G343	S344	S345	S346	T347	F348	G349	S350	T351	F352	Q353	Q354	M355	Q356	E357	L358	K359	G360	I361	H362	V363	P364	M365	T366	F367	C368	D369	E370	L371	S372	R373	C374	F375		

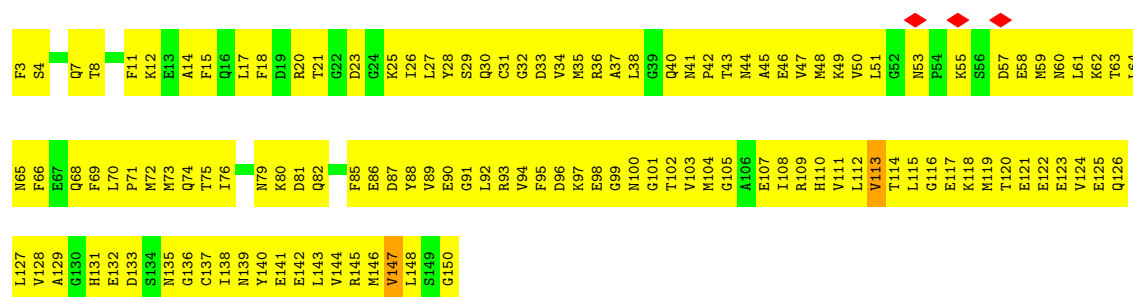
- Molecule 2: Actin, alpha skeletal muscle

Chain D:  14% 85%

K373 C374 F375	R312 M313 Q314 K315 E316 I317 T318	V247 I248 T249 L250 G251 N252 E253 R254 F255 R256 C257 P258	G182 R183 D184 L185 Y188 L189 M190 K191 C192 P193 E194 L195	Q121 T122 M123 F124 E125 T126 L127 M128 V129 P130 C131 M132 H133 G134 A135 I136 Q137 V138 L139 L140 S141 L142 Y143 A144 S145	K61	R62	G63	I64	L65	T66	L67	K68	V69	P70	I71	E72	N73	H74	G75	L76	V77	N78	K79	A80	G81	D82	E83	L84	T85	R86	H87	R88	T89	F90	Y91	N92	E93	L94	R95	V96	A97	P98	E99	E100	H101	P102	T103	L104	L105	T106	A107	A108	P109	L110	N111	P112	Y113	A114	N115	R116	E117	K118	M119	T120																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
					G186	R187	D188	L189	Y190	L191	M192	K193	C194	P195	E196	L197	R198	G199	T200	V201	T202	T203	A204	E205	R206	E207	T208	V209	R210	D211	K212	K213	E214	L215	L216	C217	Y218	V219	A220	F221	N222	E223	E224	E225	E226	E227	P164	M227	A228	T229	S230	L231	E232	K233	S234	L235	E236	K237	S238	Y239	Y240	E241	L242	Q243	F244	L245	R246	C247	P248	H249	T250	V251	P252	R253	F254	R255	C256	P257	E258	T259	T260	L261	F262	Q263	S264	F265	H266	G267	Y268	S269	V270	T271	T272	Y273	N274	R275	H276	E277	V278	K279	L280	S281	R282	M283	K284	L285	C286	D287	D288	L289	R290	F291	K292	D293	L294	Y295	A296	N297	N298	V299	G300	G301	G302	T303	T304	M305	Y306	H307	R308	K309	R310	D311	R312	M313	Q314																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
					A321	M325	K326	I327	E328	L329	I330	A331	P332	P333	E334	R335	K336	Y337	S338	V339	K340	I341	G342	G343	L344	S345	S346	T347	F348	G349	S350	T351	F352	Q353	Q354	M355	Q356	E357	G358	P359	I360	H361	G362	P363	E364	A365	G366	P367	I368	H369	V370	H371	R372	C373	F374																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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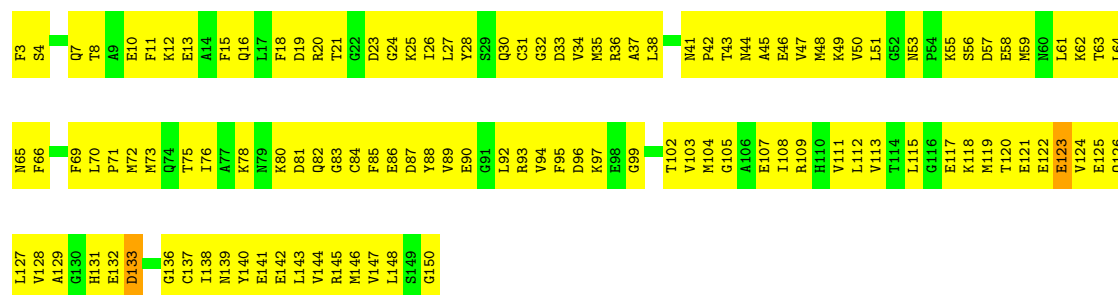
- Molecule 3: Myosin light polypeptide 6

Chain E:  15% 84%



• Molecule 3: Myosin light polypeptide 6

Chain H: 20% 79%



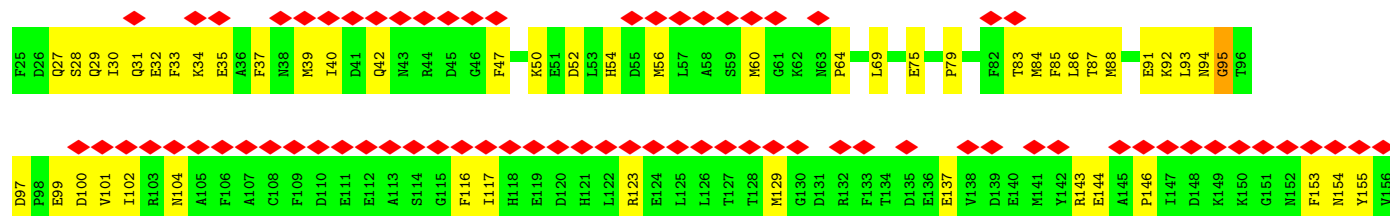
• Molecule 4: Myosin regulatory light chain 2, smooth muscle major isoform

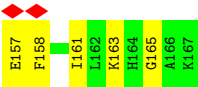
Chain F: 6% 40% 60%



• Molecule 4: Myosin regulatory light chain 2, smooth muscle major isoform

Chain G: 52% 61% 38%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17394	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29.6	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-64 (8k x 8k)	Depositor
Maximum map value	0.261	Depositor
Minimum map value	-0.127	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.0472	Depositor
Map size ($\text{\AA}$)	537.6, 537.6, 537.6	wwPDB
Map dimensions	210, 210, 210	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.56, 2.56, 2.56	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	0.42	0/6595	0.71	2/8886 (0.0%)
1	B	0.42	0/6595	0.71	8/8886 (0.1%)
2	C	0.38	0/2996	0.64	0/4058
2	D	0.40	1/2996 (0.0%)	0.65	1/4058 (0.0%)
3	E	0.32	0/1175	0.68	1/1575 (0.1%)
3	H	0.29	0/1175	0.57	0/1575
4	F	0.19	0/1185	0.50	0/1589
4	G	0.17	0/1185	0.47	1/1589 (0.1%)
All	All	0.38	1/23902 (0.0%)	0.67	13/32216 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
2	C	0	1
2	D	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	170	ALA	C-N	5.63	1.42	1.33

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	63	GLU	N-CA-C	-7.08	105.83	114.75
4	G	95	GLY	N-CA-C	-5.97	107.98	115.08
1	B	244	ASN	N-CA-C	-5.95	105.84	112.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	126	THR	N-CA-C	-5.92	106.68	114.31
1	A	220	LEU	CA-CB-CG	-5.89	95.68	116.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	533	ASN	Peptide
1	A	534	PRO	Peptide
1	A	683	ARG	Peptide
1	B	533	ASN	Peptide
2	C	356	TRP	Peptide

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	6474	0	6518	1468	0
1	B	6474	0	6518	1506	0
2	C	2933	0	2894	655	0
2	D	2933	0	2894	642	0
3	E	1160	0	1119	284	0
3	H	1160	0	1119	203	0
4	F	1161	0	1076	104	0
4	G	1161	0	1076	62	0
All	All	23456	0	23214	4678	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 100.

The worst 5 of 4678 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:B:2:SER:N	1:B:141:TYR:HH	1.38	1.22
1:B:446:VAL:O	1:B:450:LEU:HB2	1.45	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:154:ASP:O	2:C:160:THR:HA	1.46	1.14
3:E:32:GLY:HA2	3:E:72:MET:HE1	1.39	1.05
1:A:61:LEU:O	1:A:65:GLY:N	1.91	1.03

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	792/843 (94%)	655 (83%)	132 (17%)	5 (1%)	21	59
1	B	792/843 (94%)	653 (82%)	138 (17%)	1 (0%)	48	83
2	C	373/375 (100%)	319 (86%)	54 (14%)	0	100	100
2	D	373/375 (100%)	313 (84%)	60 (16%)	0	100	100
3	E	146/148 (99%)	120 (82%)	26 (18%)	0	100	100
3	H	146/148 (99%)	129 (88%)	17 (12%)	0	100	100
4	F	141/143 (99%)	133 (94%)	8 (6%)	0	100	100
4	G	141/143 (99%)	128 (91%)	13 (9%)	0	100	100
All	All	2904/3018 (96%)	2450 (84%)	448 (15%)	6 (0%)	44	78

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	812	PHE
1	B	534	PRO
1	A	813	ALA
1	A	535	PRO
1	A	537	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	703/741 (95%)	696 (99%)	7 (1%)	68	78
1	B	703/741 (95%)	695 (99%)	8 (1%)	65	76
2	C	318/318 (100%)	317 (100%)	1 (0%)	86	86
2	D	318/318 (100%)	315 (99%)	3 (1%)	70	79
3	E	127/127 (100%)	126 (99%)	1 (1%)	73	80
3	H	127/127 (100%)	125 (98%)	2 (2%)	55	70
4	F	125/125 (100%)	125 (100%)	0	100	100
4	G	125/125 (100%)	125 (100%)	0	100	100
All	All	2546/2622 (97%)	2524 (99%)	22 (1%)	68	79

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	716	ILE
2	D	219	VAL
2	D	85	ILE
2	D	249	THR
1	A	753	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	353	GLN
4	F	29	GLN
2	D	49	GLN
2	D	296	ASN
4	G	42	GLN

5.3.3 RNA ⓘ

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.

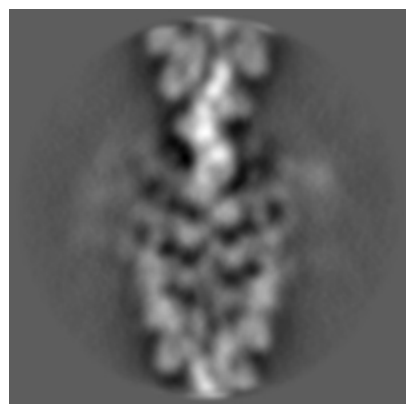
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29646. These allow visual inspection of the internal detail of the map and identification of artifacts.

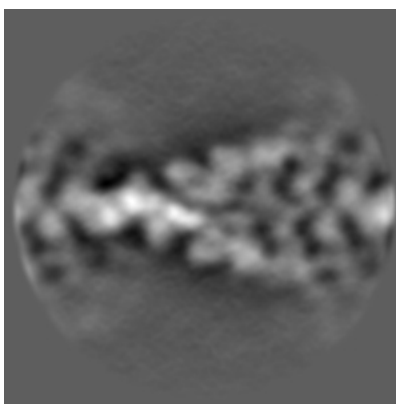
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

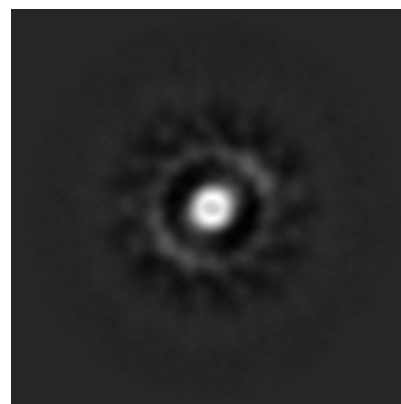
6.1.1 Primary map



X

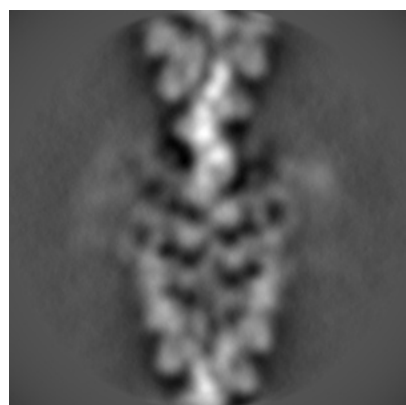


Y

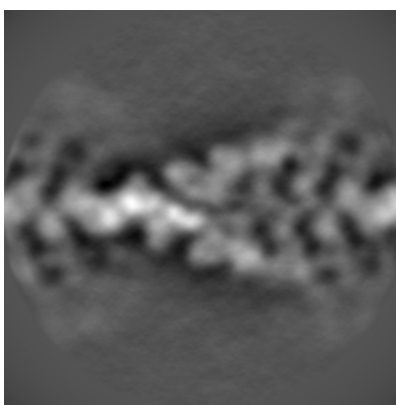


Z

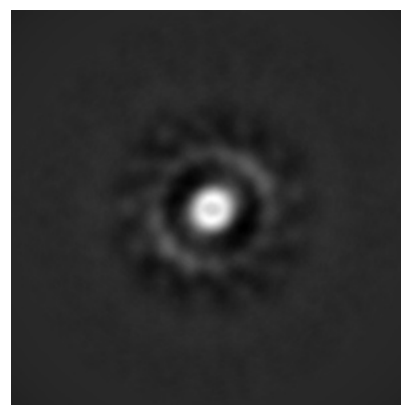
6.1.2 Raw map



X



Y



Z

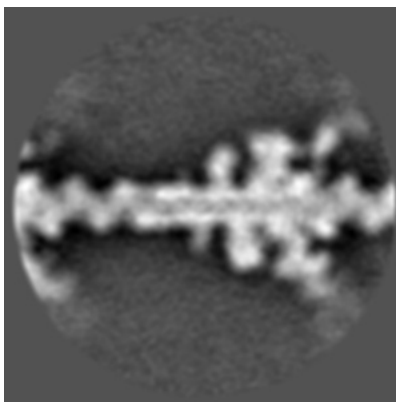
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

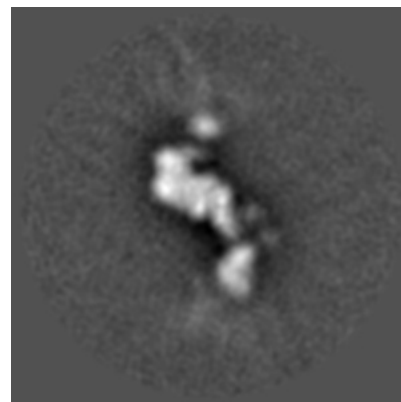
6.2.1 Primary map



X Index: 105

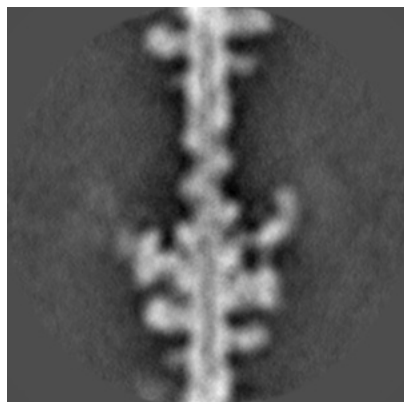


Y Index: 105

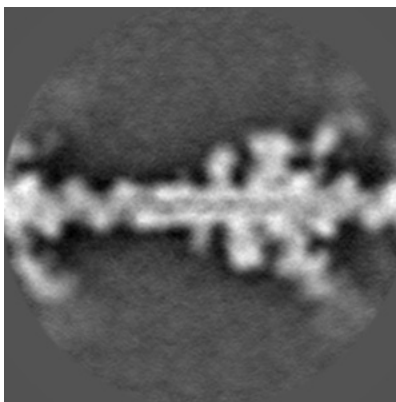


Z Index: 105

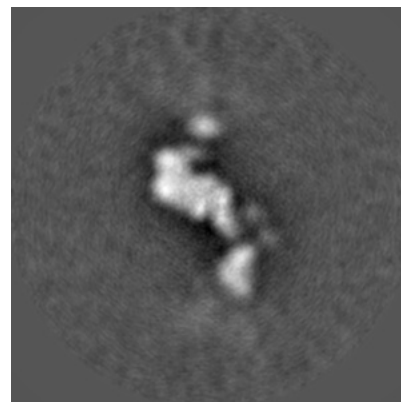
6.2.2 Raw map



X Index: 105



Y Index: 105



Z Index: 105

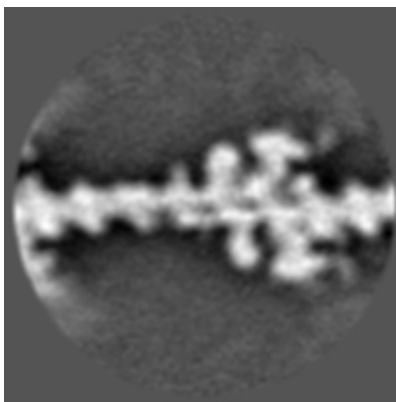
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

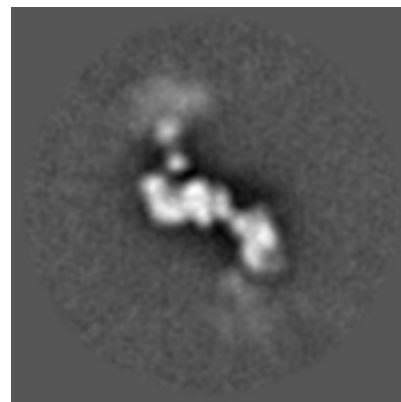
6.3.1 Primary map



X Index: 107

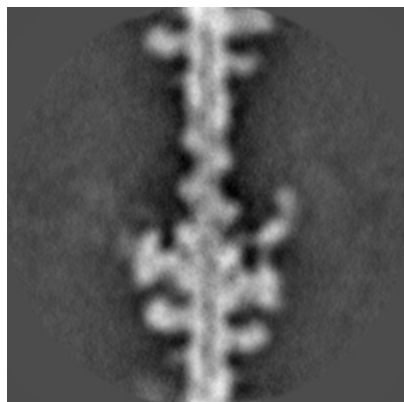


Y Index: 101

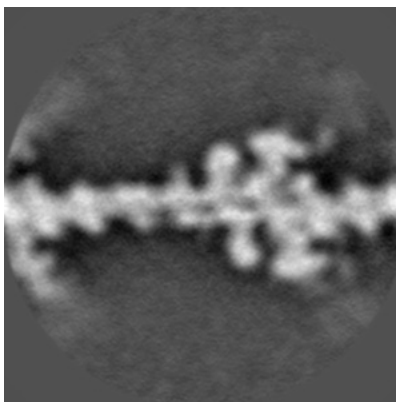


Z Index: 123

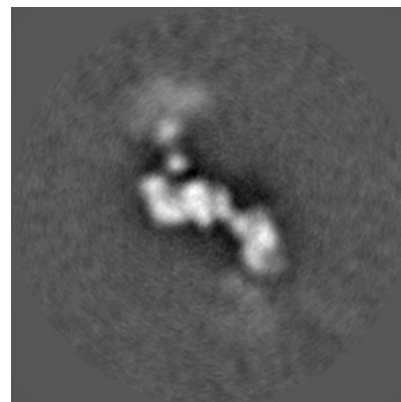
6.3.2 Raw map



X Index: 106



Y Index: 101

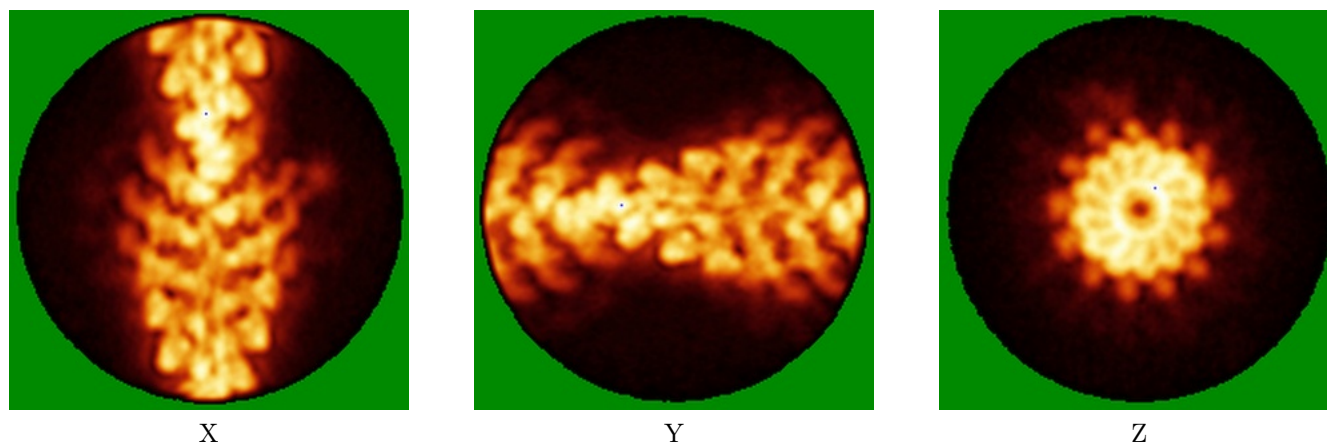


Z Index: 123

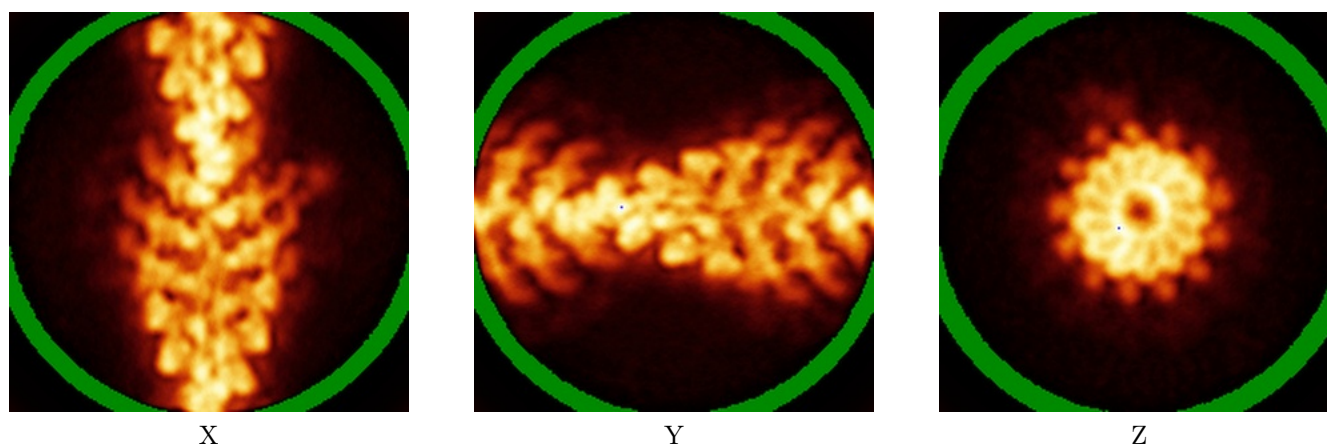
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

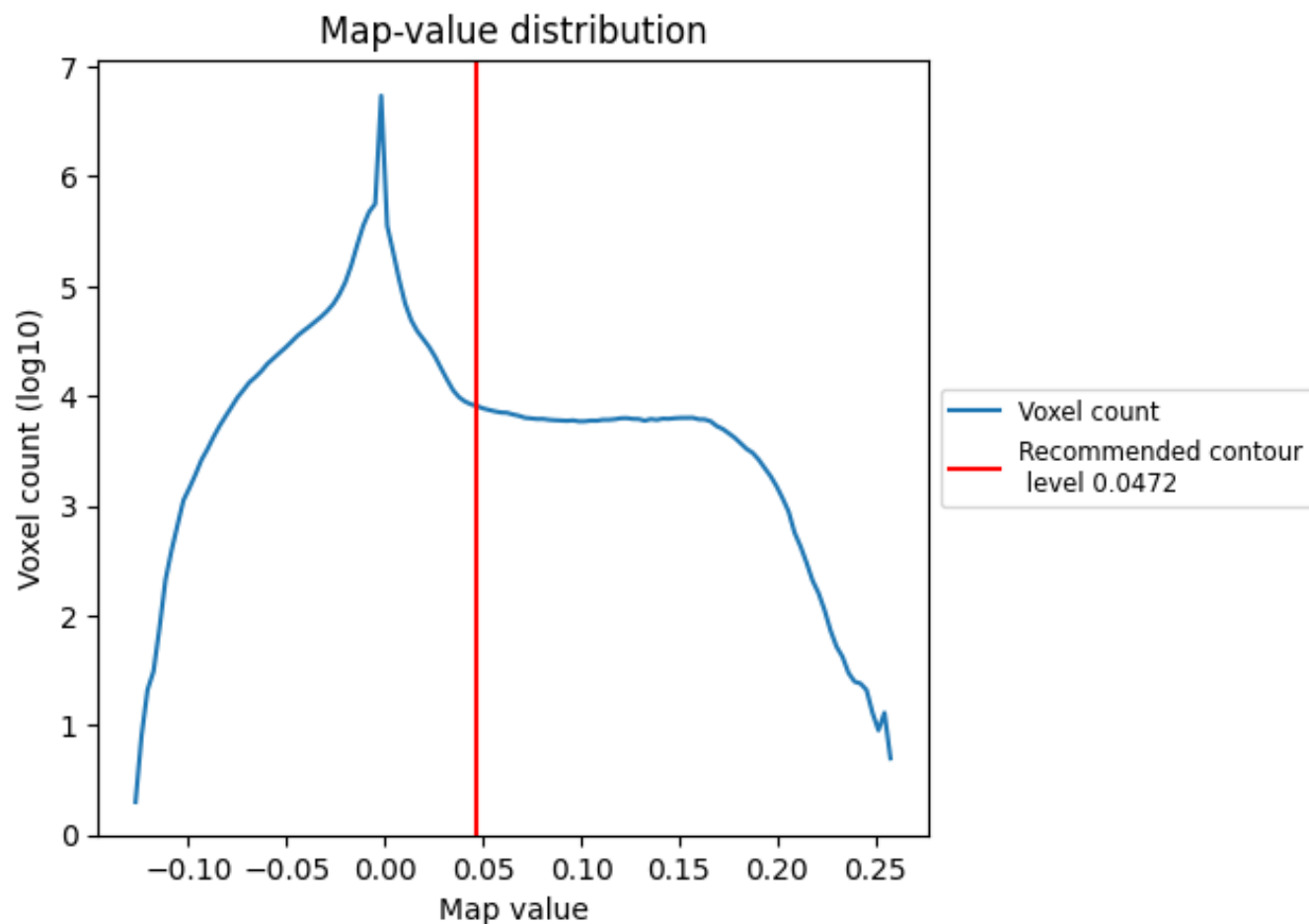
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

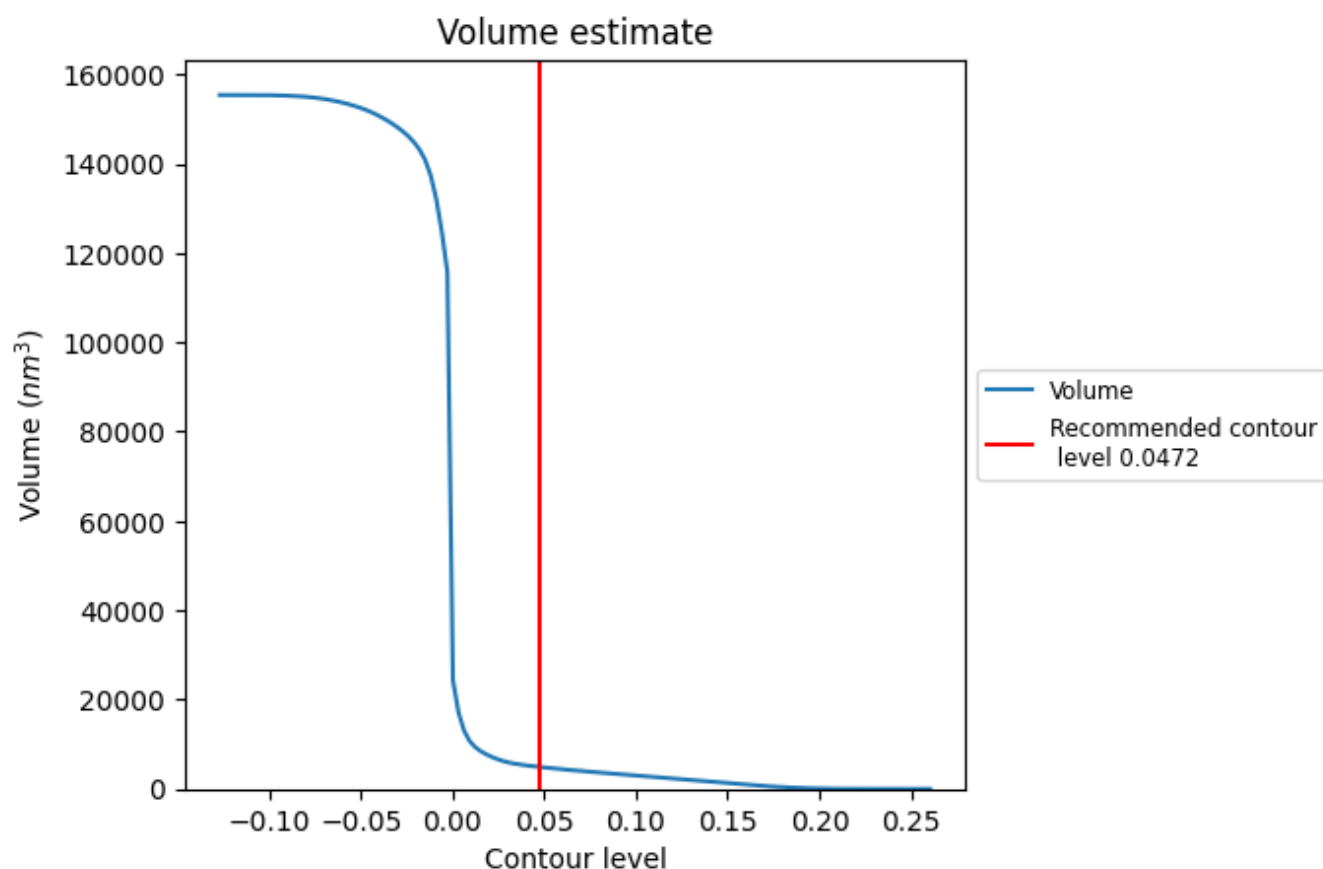
This section contains the results of statistical analysis of the map.

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.

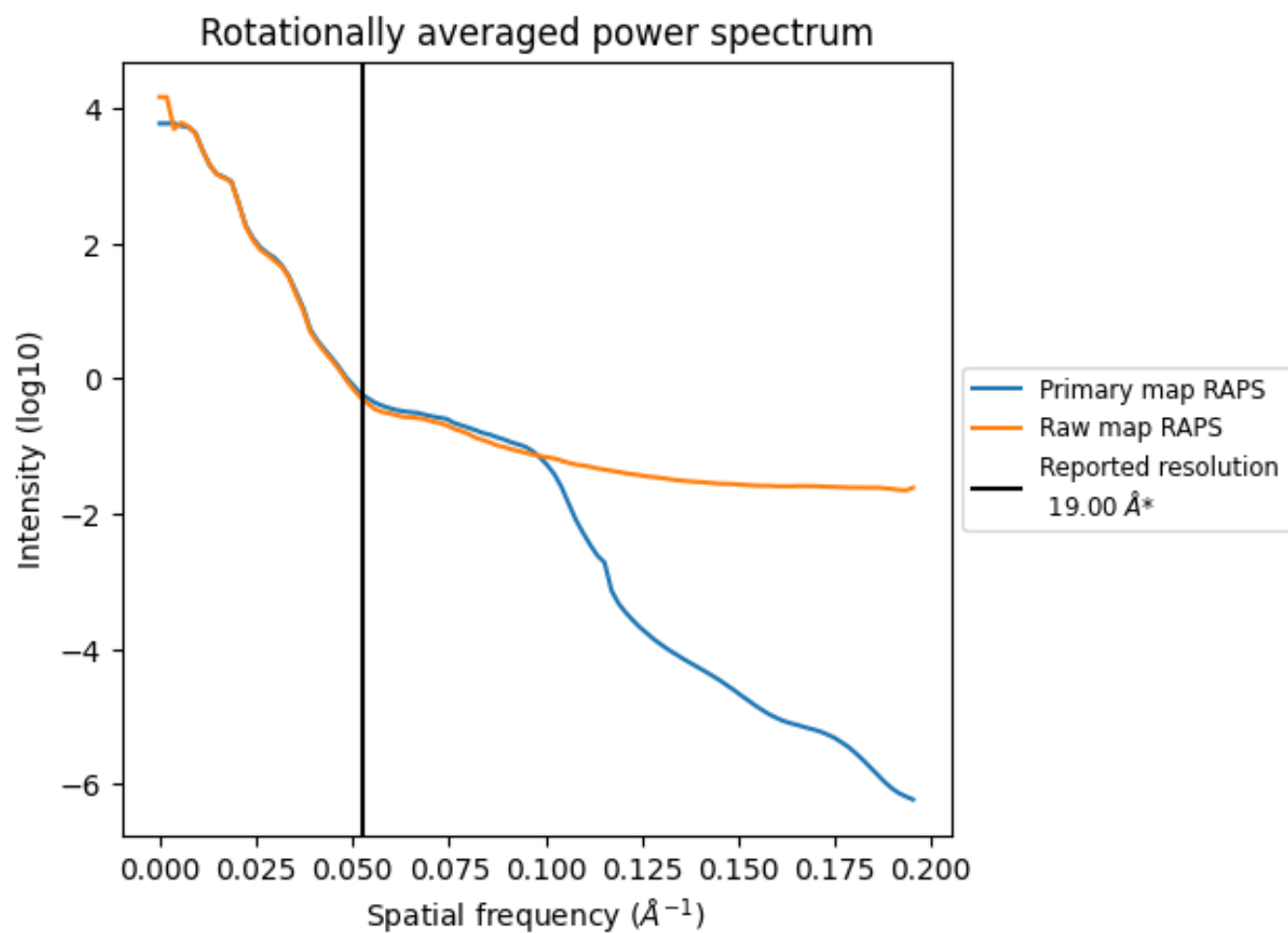
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4944 nm^3 ; this corresponds to an approximate mass of 4466 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 ⓘ

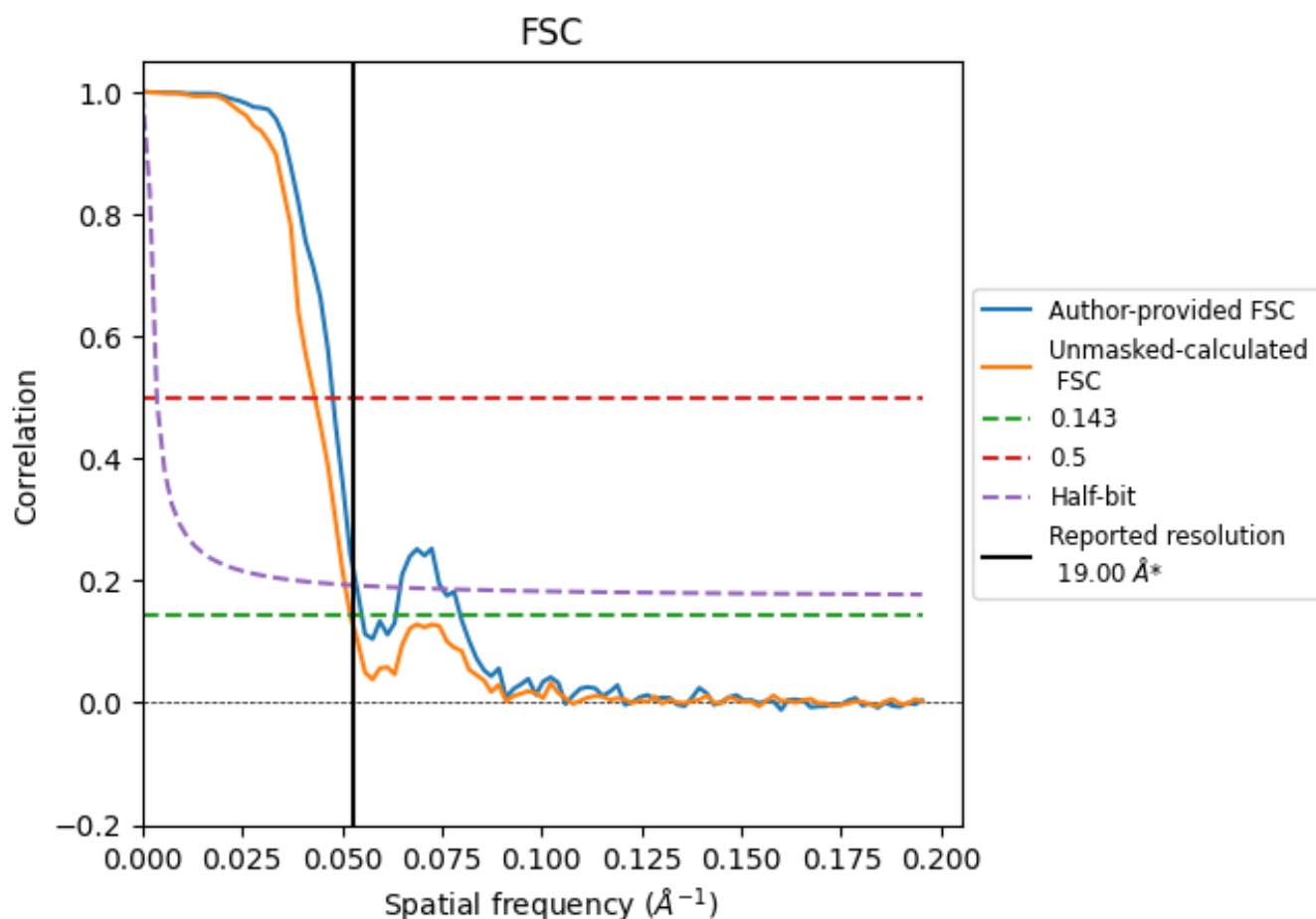


*Reported resolution corresponds to spatial frequency of 0.053 Å⁻¹

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 0.053 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	19.00	-	-
Author-provided FSC curve	18.18	20.96	18.62
Unmasked-calculated*	19.19	23.15	19.69

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

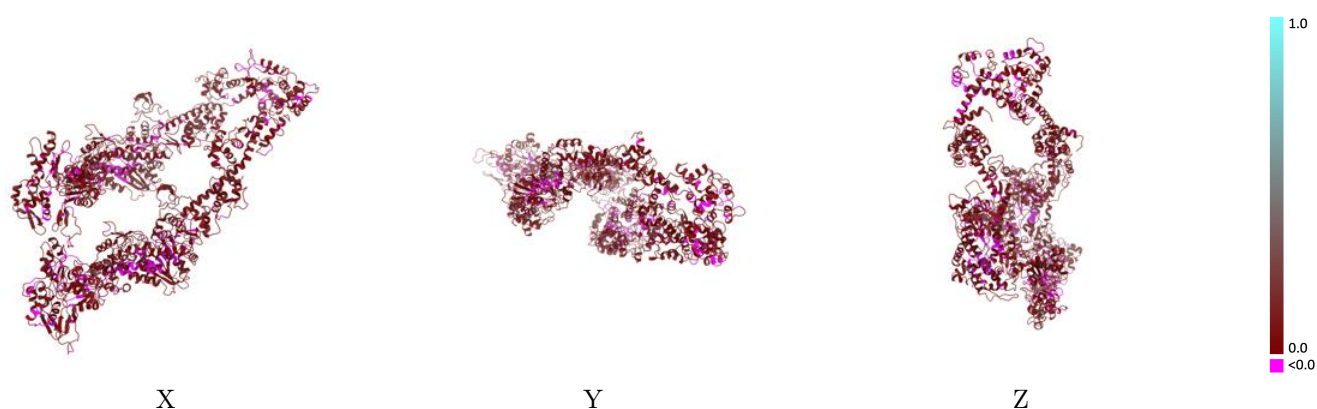
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29646 and PDB model 8SYF. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

This section was not generated.

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

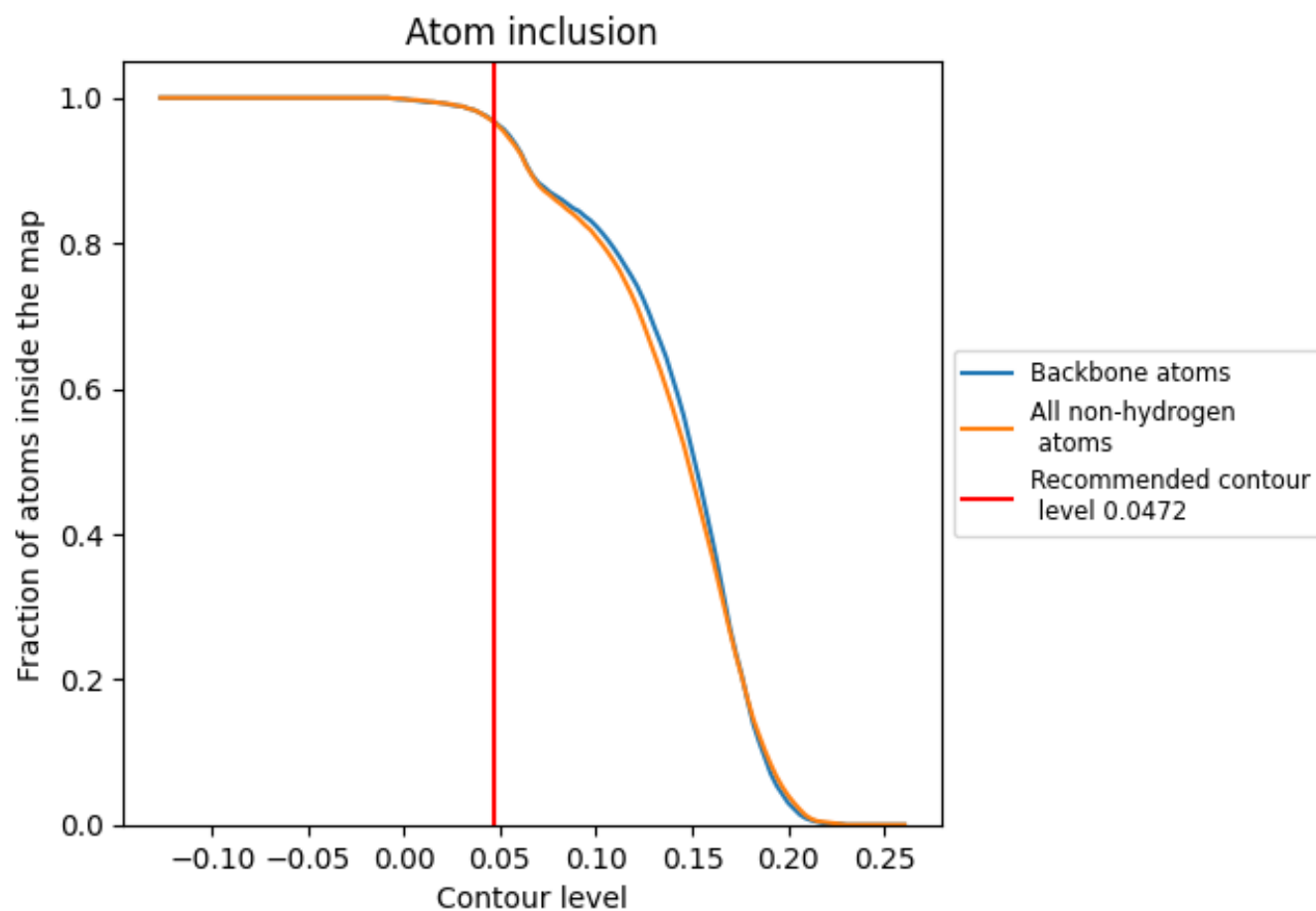


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.0472) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9660	0.0800
A	0.9950	0.0810
B	1.0000	0.0810
C	1.0000	0.0740
D	1.0000	0.0790
E	0.9800	0.0890
F	0.9160	0.0870
G	0.4470	0.0570
H	0.9970	0.1000

1.0

0.0

<0.0