



wwPDB EM Validation Summary Report ⓘ

May 12, 2025 – 09:43 PM EDT

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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.43.1

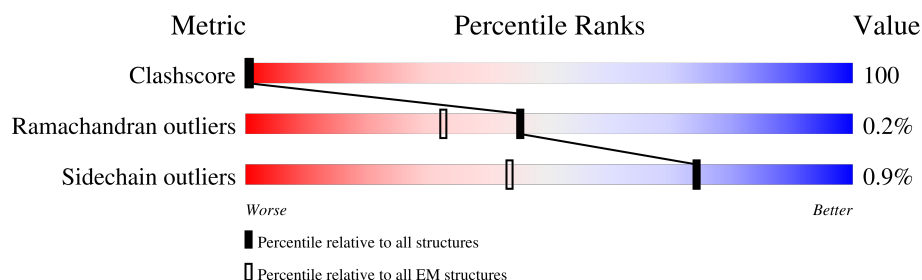
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

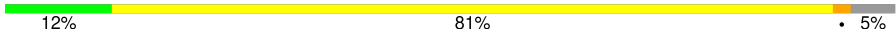
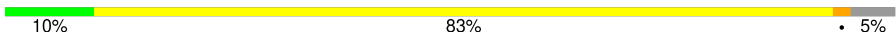



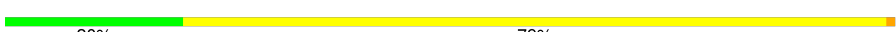


The reported resolution of this entry is 19.00 Å.

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)
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	843	
1	B	843	
2	C	375	
2	D	375	
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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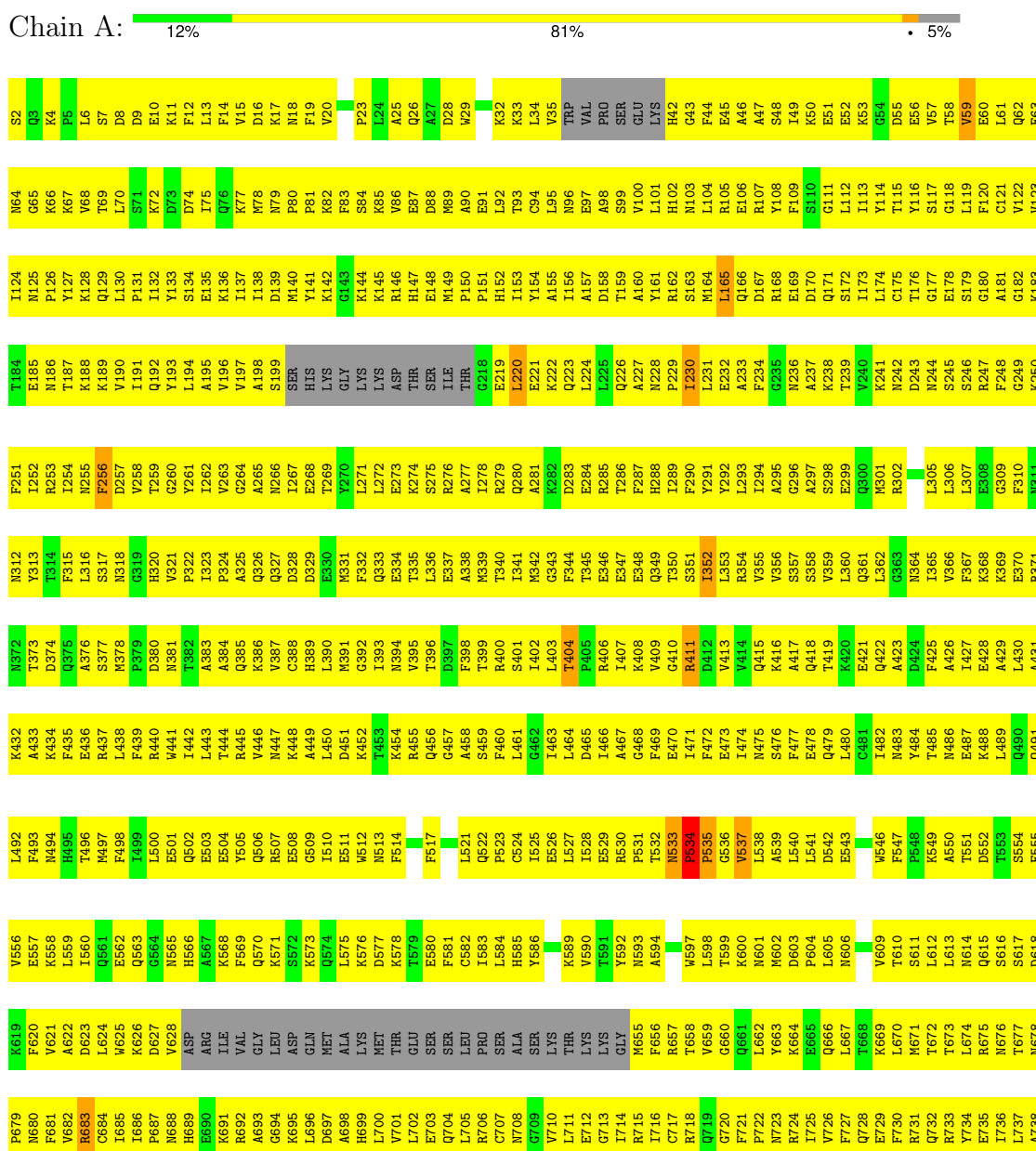
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Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	143	Total	C	N	O	S	0	0
			1161	727	189	235	10		

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



A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795	A796	A797	A798	A799	A800	A801
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Q802	C803	R804	G805	R806	Y807	A808	R809	K810	A811	F812	A813	K814	R815	Q816	Q817	Q818	L819	T820	A821	L822	K823	V824	I825	Q826	A831	K834	L835	R836	N837	W838	Q839	W840	W841	W842	R843	F844	T845	K846	V847	K848	P849	L850	L851
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● Molecule 1: Myosin, heavy chain 11, smooth muscle

Chain B: 10% 83% 5%

S2	Q3	K4	P5	L6	S7	D8	D9	E10	K11	F12	F13	L14	F15	D16	K17	N18	N21	N22	P23	L24	A25	Q26	A27	D28	W29	S30	A31	K32	K33	L34	V35	TRP	VAL	PRO	SER	GLU	LYS	H42	G43	F44	E45	A46	A47	S48	T49	K50	E51	E52	K53	G54	D55	E56	V57	T58	V59	E60	C61	L62	Q62
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B63	N64	G65	K66	K67	V68	T69	L70	S71	K72	D73	D74	I75	Q76	K77	M78	N79	P80	P81	K82	F83	S84	K85	Q86	E87	D88	N89	A90	E91	L92	C93	T94	L95	N96	E97	A98	S99	V100	L101	H102	N103	L104	E105	E106	R107	Y108	F109	G110	G111	L112	I113	Y114	T115	Y116	S117	G118	L119	F120	C121	L122	V122
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V123	I124	M125	P126	K127	K128	K129	L130	P131	I132	Y133	S134	E135	K136	I137	M138	D139	M140	Y141	K142	G143	K144	K145	A146	R147	E148	M149	P150	E151	H152	I153	V154	A155	I156	N157	D158	S159	A160	Y161	R162	S163	M164	E165	E166	D167	R168	E169	D170	Q171	S172	I173	C175	Y176	G177	E178	A181	G182	K183
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T184	E185	M186	T187	K188	K189	V190	I191	Q192	Y193	L194	A195	V196	V197	S198	S199	SER	HIS	LYS	GLY	LYS	ASP	THR	SER	I147	E148	M149	P150	E151	H152	I153	V154	A155	I156	N157	D158	S159	A160	Y161	R162	S163	M164	E165	E166	D167	R168	E169	D170	Q171	S172	I173	C175	Y176	G177	E178	A181	G182	K183
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F251	I252	R253	T254	N255	K256	D257	V258	T259	G260	Y261	T262	V263	G264	A265	A266	T267	T268	Y269	L270	L271	L272	E273	K274	S275	R276	A277	G278	R279	L280	K281	A282	T283	E284	R285	T286	F287	H288	L289	F290	Y291	E292	A293	K294	A295	G296	A297	S298	K299	Q300	N301	R302	D303	K304	L305	L306	L307	E308	G309	K310
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K311	N312	Y313	T314	F315	L316	S317	N318	G319	H320	V321	P322	K323	P324	A325	Q326	Q327	K328	D329	E330	K331	F332	Q333	E334	T335	L336	A337	A338	M339	S340	L341	K342	G343	F344	T345	E346	E347	E348	Q349	T350	S351	L352	R353	P354	V355	V356	S357	K358	V359	Q360	Q361	L362	K363	K364	L365	V366	F367	K368	K369	K432
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T373	D374	Q375	T376	S377	L378	P379	D380	N381	T382	A383	A384	Q385	K386	S387	C388	H389	L390	N391	G392	L393	N394	V395	T396	D397	F398	T399	R400	S401	L402	L403	T404	P405	R406	L407	V408	V409	G410	R411	D412	V413	V414	K415	A416	A417	K418	T419	K420	S421	Q422	A423	D424	F425	A426	L427	E428	A429	L430	A431	K432
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L433	K434	F435	A436	R437	L438	F439	R440	K441	L442	L443	T444	R445	V446	M447	K448	A449	L450	D451	K452	T453	K454	R455	Q456	S457	F458	L459	D460	L461	G462	L463	L464	D465	L466	A467	F468	F469	E470	L471	F472	E473	L474	N475	S476	F477	E478	Q479	L480	C481	Y484	T485	E486	A487	K488	L489	Q490	Q491	L492	F493	N494
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V495	T496	K497	F498	L499	L500	E501	Q502	E503	L504	Y505	H506	Q507	R508	E509	G510	L511	S512	W513	K514	L515	D516	F517	G518	L519	D520	L521	Q522	P523	L524	H525	L526	L527	K528	E529	R530	P531	L532	N533	P534	G535	V536	V537	L538	A539	N540	L541	D542	E543	P544	L545	C546	E547	C548	D549	D550	L551	F552	N553	S554	F555
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V556	E557	K558	L559	I560	Q561	E562	Q563	G564	N565	H566	A567	K568	F569	G570	K571	I572	S573	W574	K575	D576	K577	T578	L579	E580	F581	C582	L583	L584	H585	L586	A587	G588	K589	V590	T591	L592	L593	A594	S595	A596	V597	L598	T599	K600	N601	M602	D603	P604	E605	L606	Q607	N608	V609	T610	S611	L612	L613	L614	Q615
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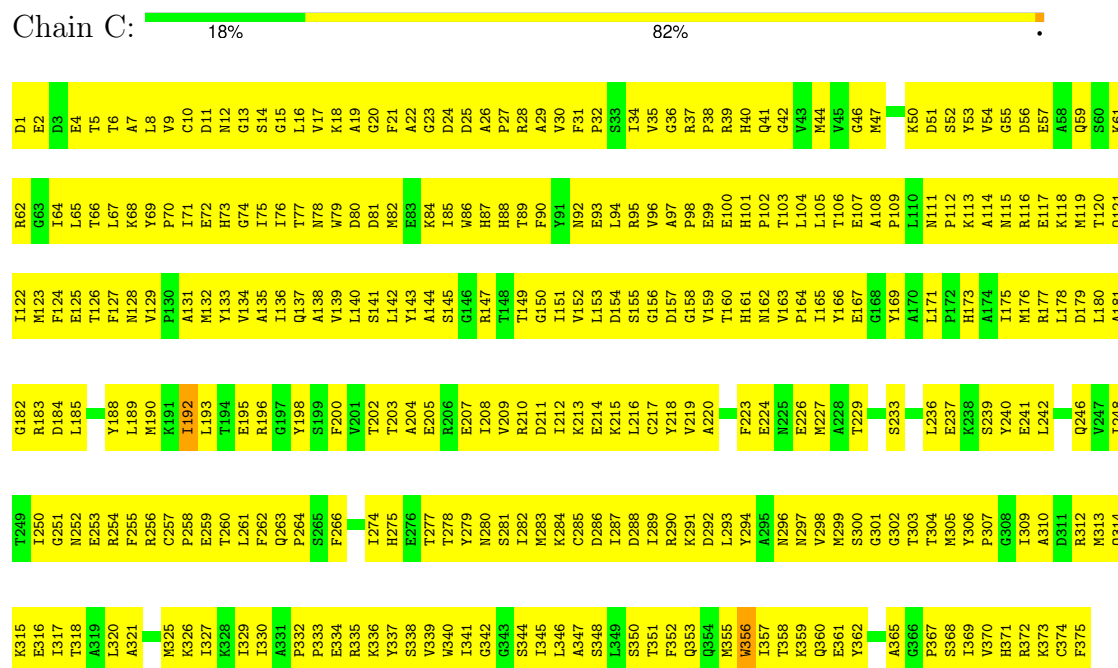
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N676	T677	N678	P679	N680	F681	V682	R683	G684	I685	H686	P687	N688	H689	E690	L691	VAL	GLY	L692	ASP	GLN	M693	A694	L695	L696	L697	L698	L699	L700	V701	L702	E703	Q704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735
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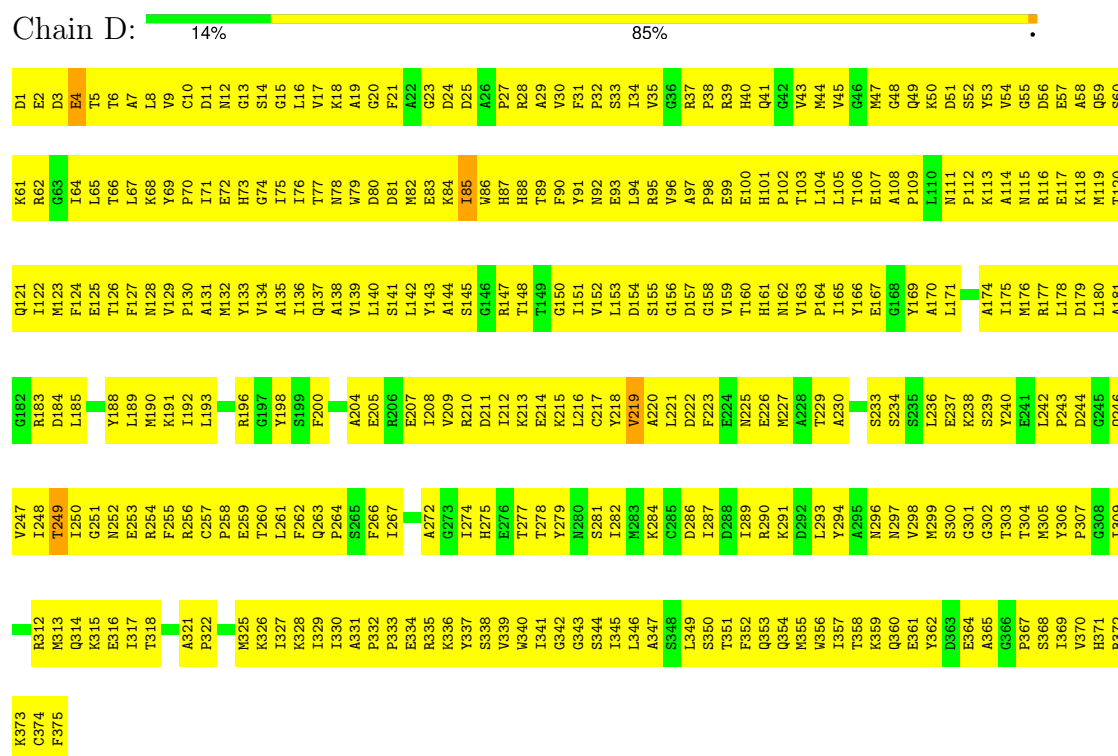
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L796	L797	F798	A799	N800	A801	Q802	C803	R804	G805	Y806	L807	A808	R809	K810	A811	F812	A813	K814	R815	Q816	Q817	K818	L819	M820	I825	Q826	N827	N828	C829	A830	A831	Y832	L833	K834	L835	R836	N837	W838	Q839	W840	W841	F844	T845	K846	V847	K848	P849	L850	L851
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- Molecule 2: Actin, alpha skeletal muscle

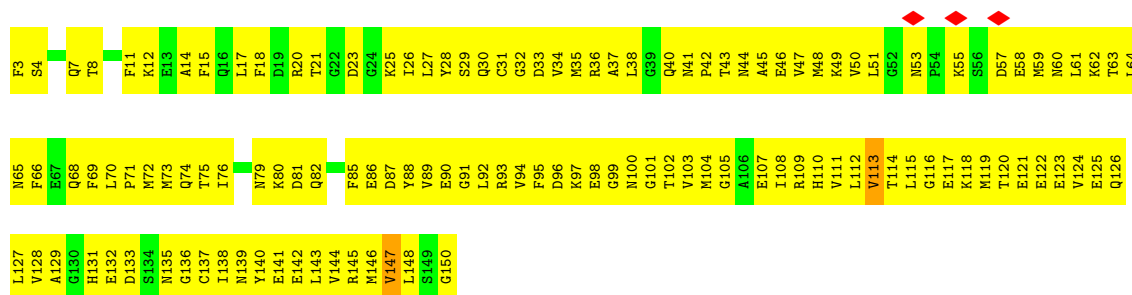


- Molecule 2: Actin, alpha skeletal muscle



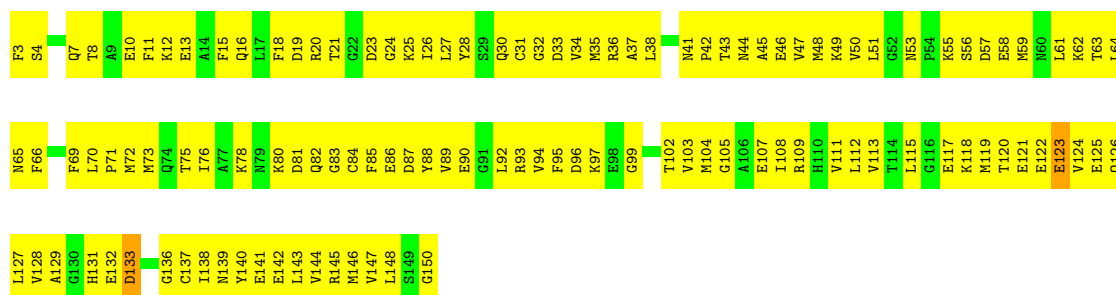
- Molecule 3: Myosin light polypeptide 6





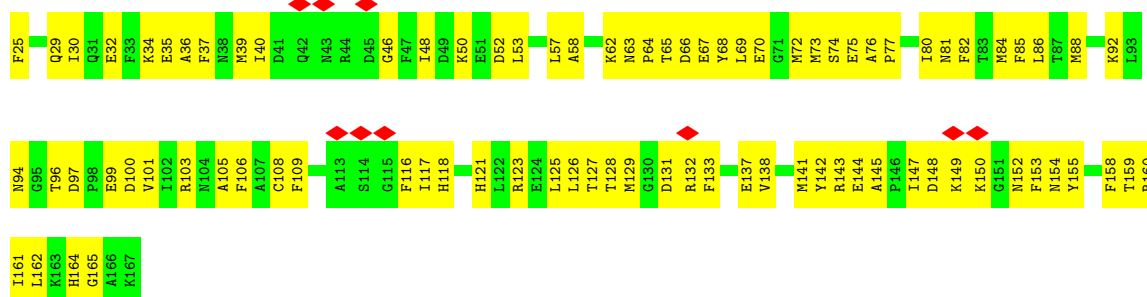
• Molecule 3: Myosin light polypeptide 6

Chain H: 20% 79%



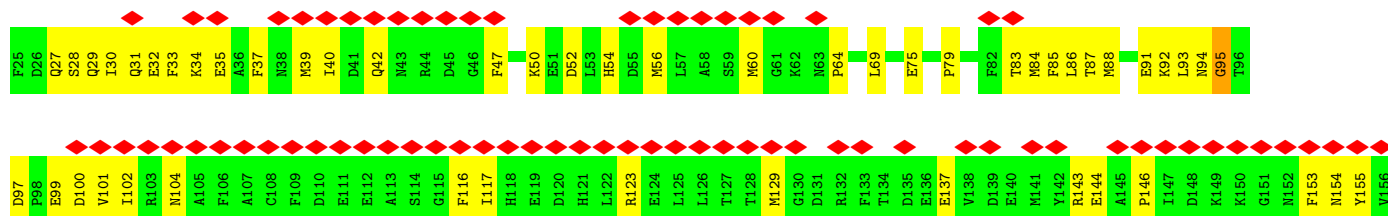
• Molecule 4: Myosin regulatory light chain 2, smooth muscle major isoform

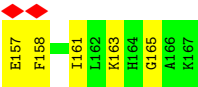
Chain F: 6% 40% 60%



• 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 (\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 (\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

Continued on next page...

Continued from previous page...

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%)	22	60
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%)	45	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%)	73	82
1	B	703/741 (95%)	695 (99%)	8 (1%)	70	80
2	C	318/318 (100%)	317 (100%)	1 (0%)	91	92
2	D	318/318 (100%)	315 (99%)	3 (1%)	75	83
3	E	127/127 (100%)	126 (99%)	1 (1%)	79	85
3	H	127/127 (100%)	125 (98%)	2 (2%)	58	73
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%)	74	83

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.

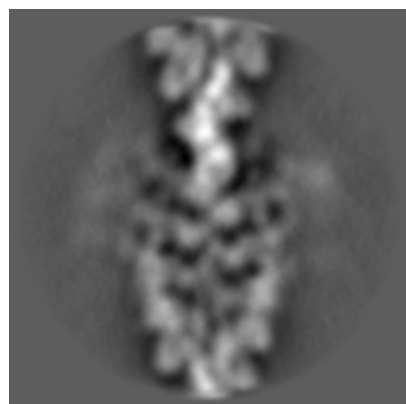
6 Map visualisation [i](#)

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.

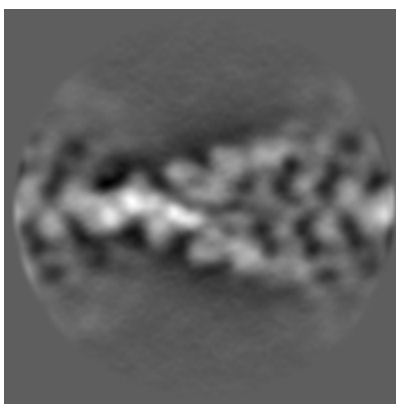
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

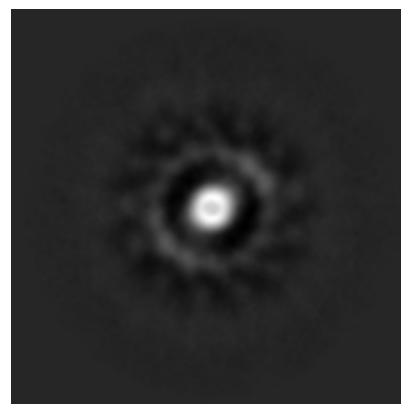
6.1.1 Primary map



X

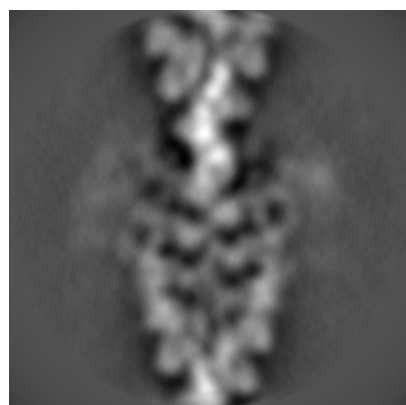


Y

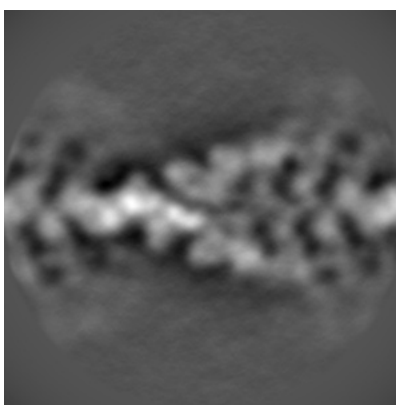


Z

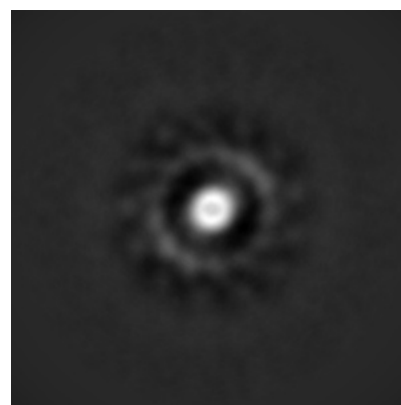
6.1.2 Raw map



X



Y



Z

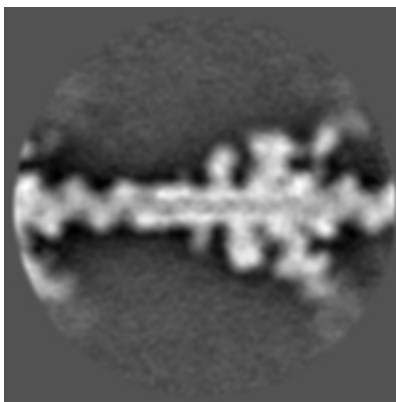
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

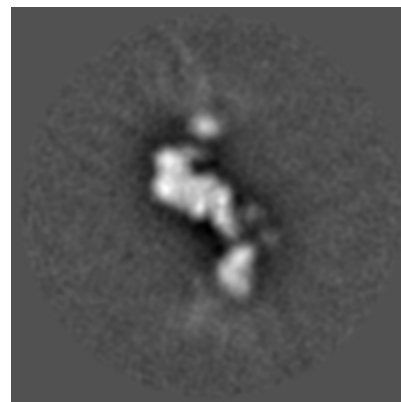
6.2.1 Primary map



X Index: 105

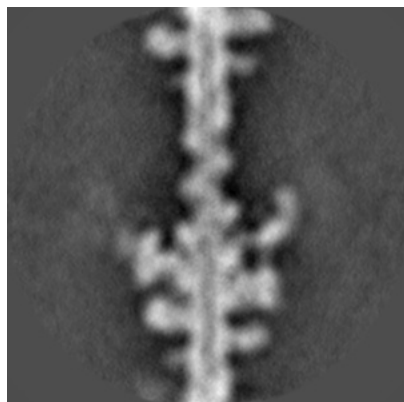


Y Index: 105

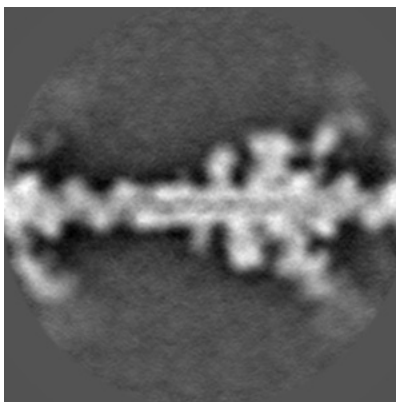


Z Index: 105

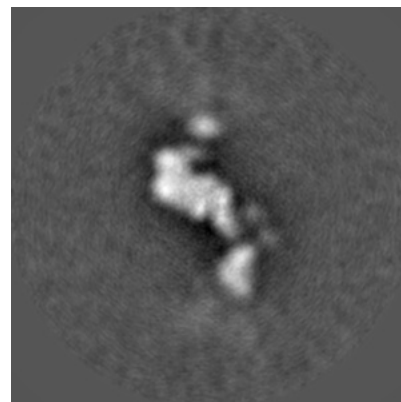
6.2.2 Raw map



X Index: 105



Y Index: 105



Z Index: 105

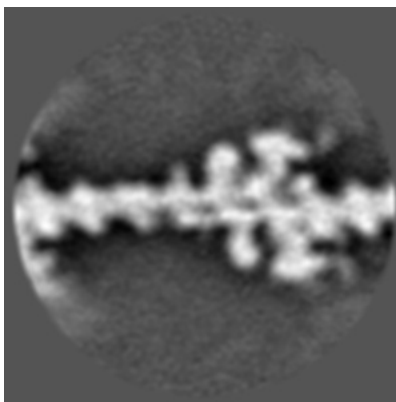
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

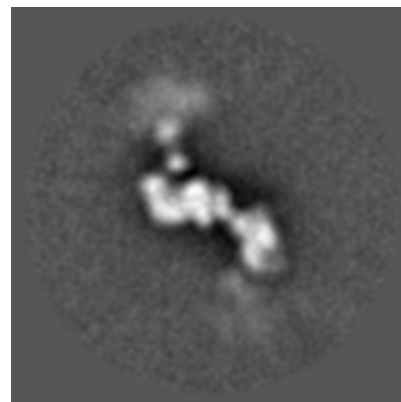
6.3.1 Primary map



X Index: 107

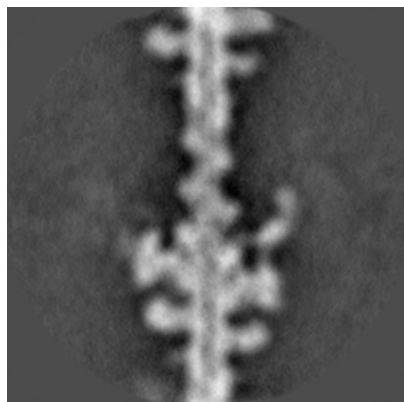


Y Index: 101

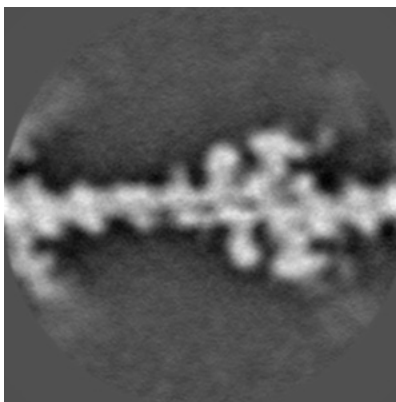


Z Index: 123

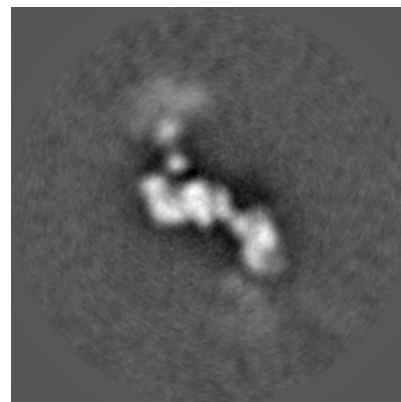
6.3.2 Raw map



X Index: 106



Y Index: 101

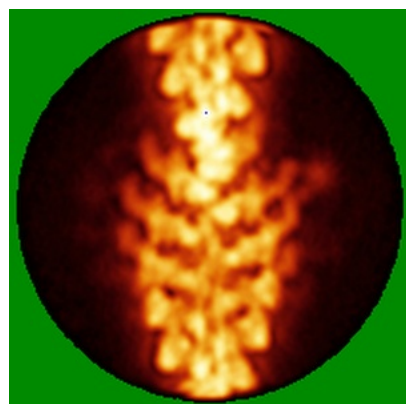


Z Index: 123

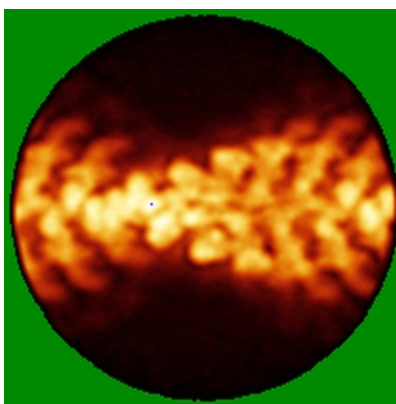
The images above show the largest variance slices of the map in three orthogonal directions.

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

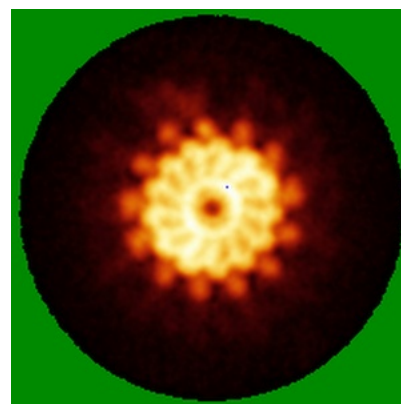
6.4.1 Primary map



X

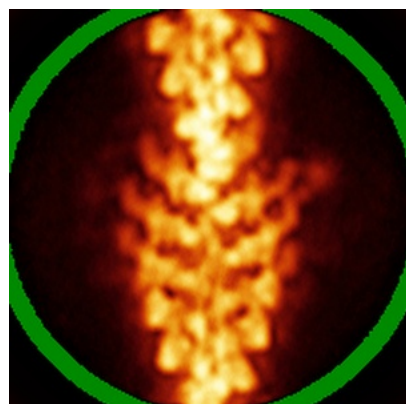


Y

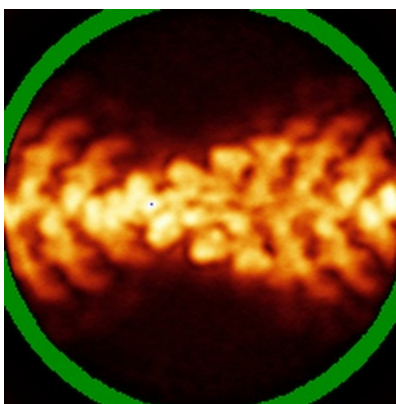


Z

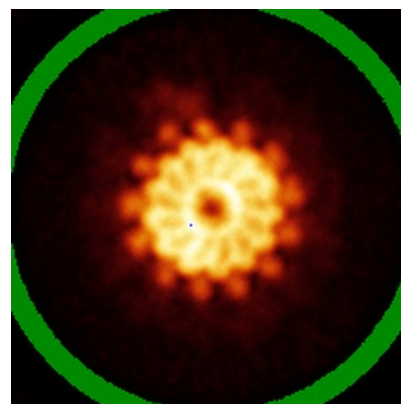
6.4.2 Raw map



X



Y



Z

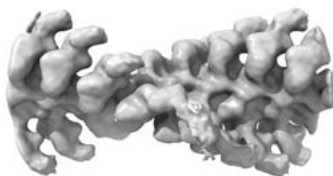
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



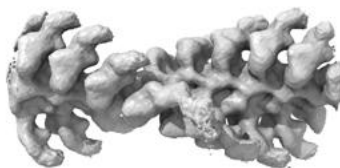
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0472. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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.

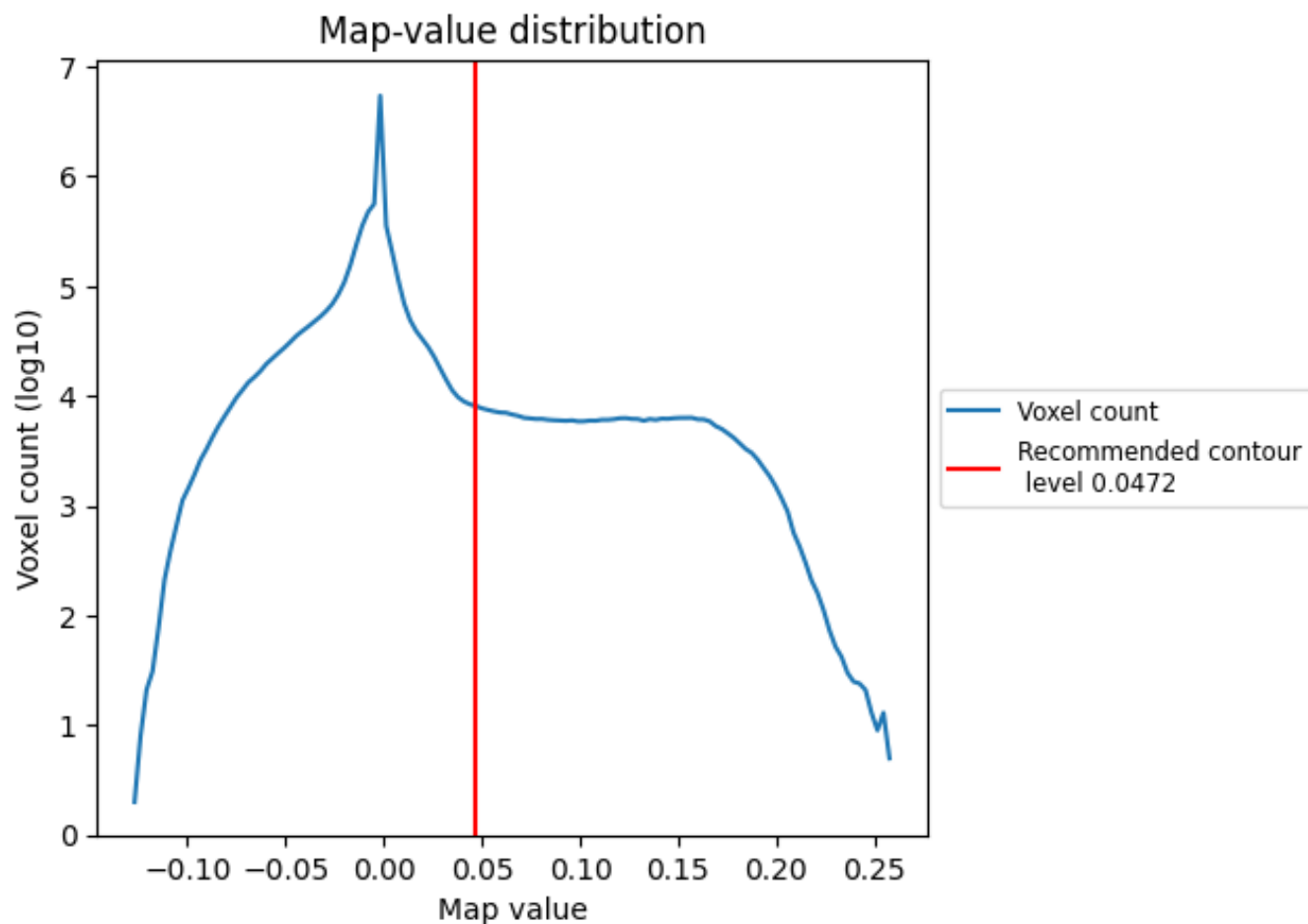
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

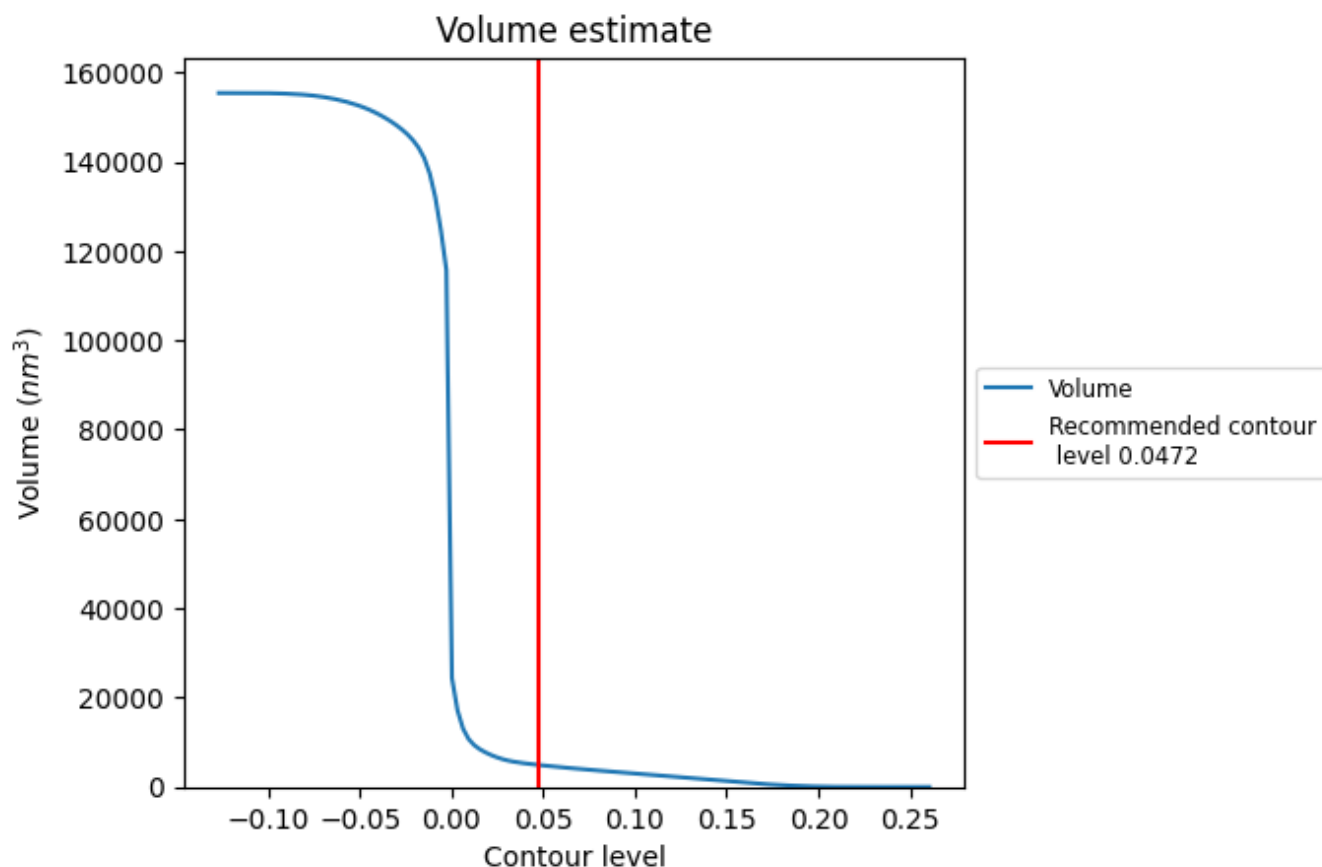
This section contains the results of statistical analysis of the map.

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.

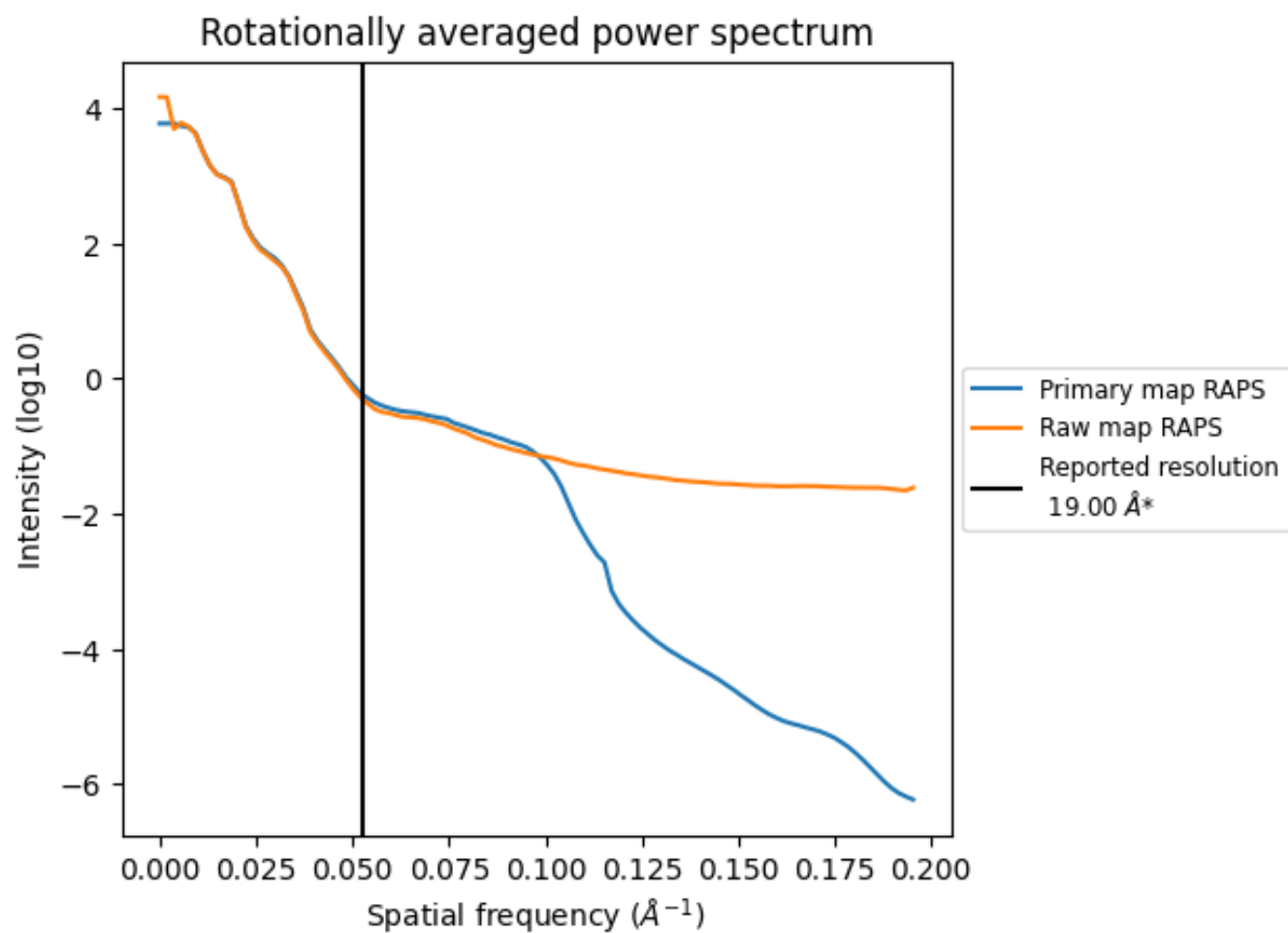
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4944 nm³; 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 ⓘ

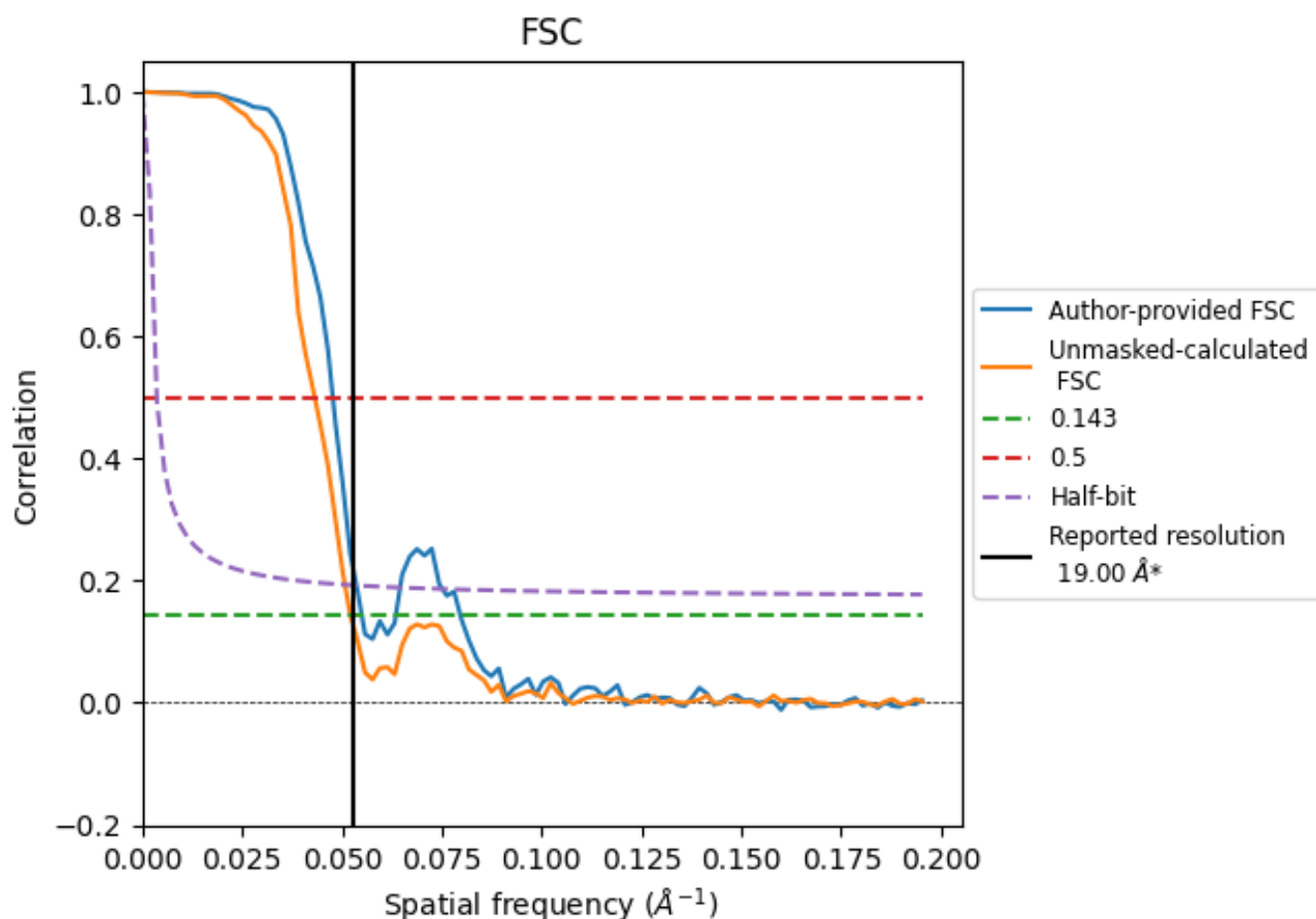


*Reported resolution corresponds to spatial frequency of 0.053 Å⁻¹

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](#)

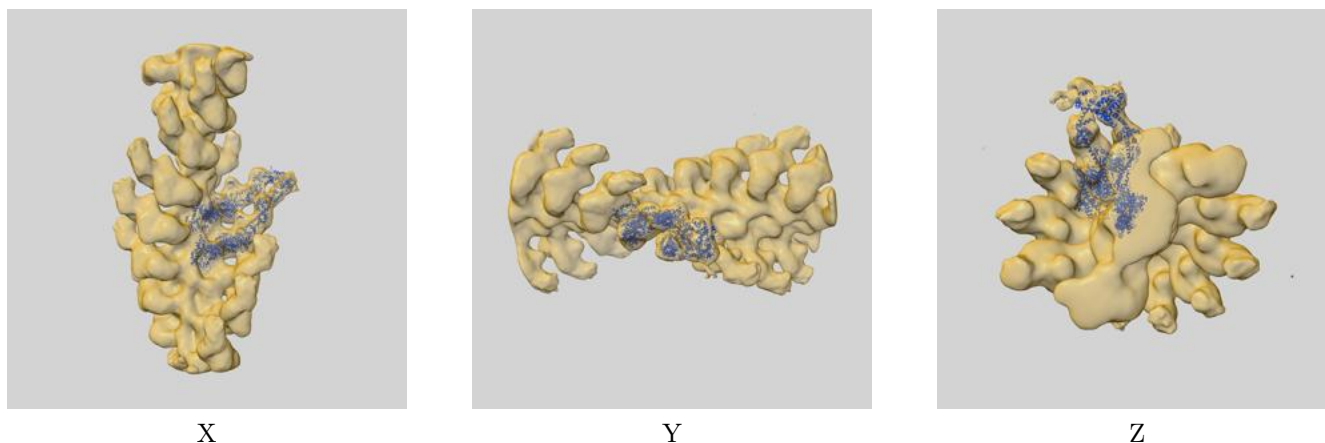
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	19.00	-	-
Author-provided FSC curve	18.18	20.96	18.62
Unmasked-calculated*	19.19	23.15	19.69

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

9 Map-model fit [i](#)

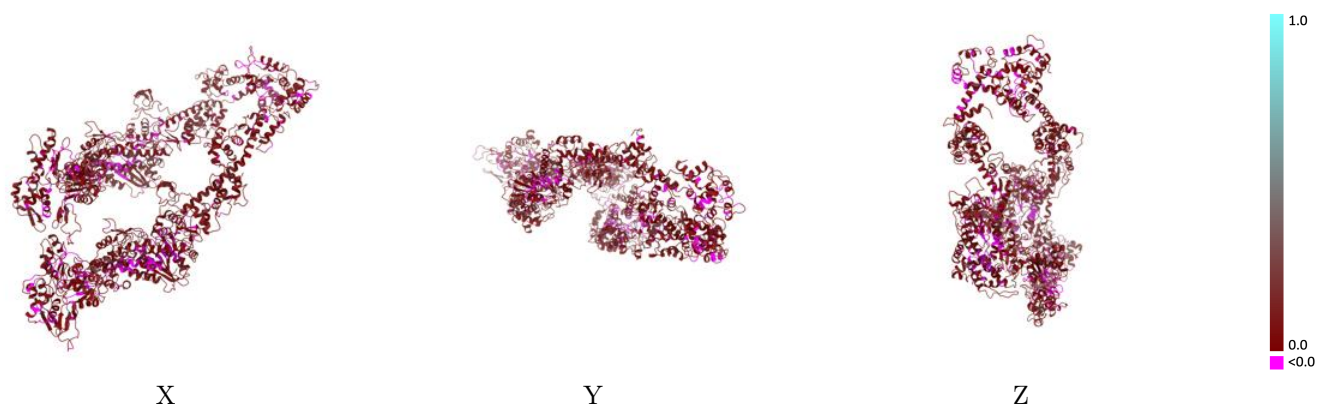
This section contains information regarding the fit between EMDB map EMD-29646 and PDB model 8SYF. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



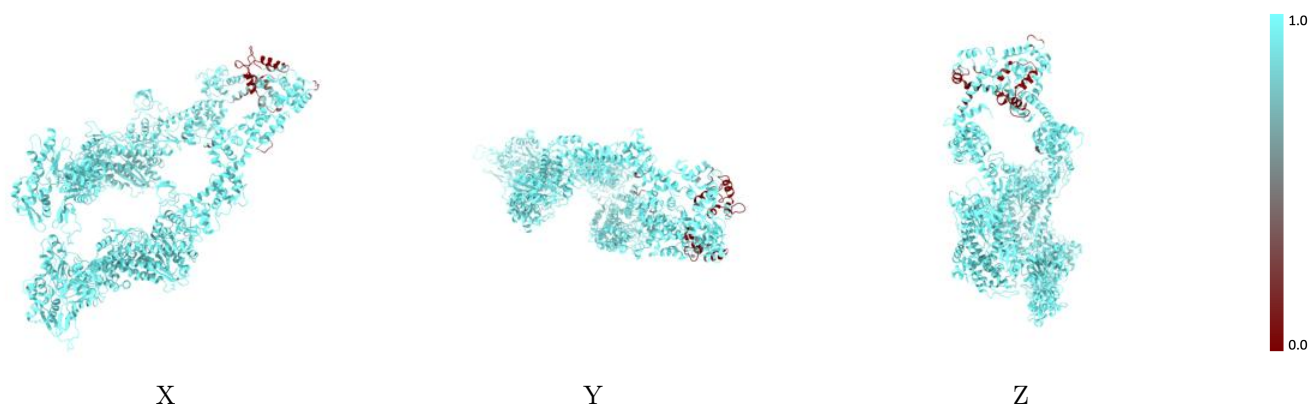
The images above show the 3D surface view of the map at the recommended contour level 0.0472 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



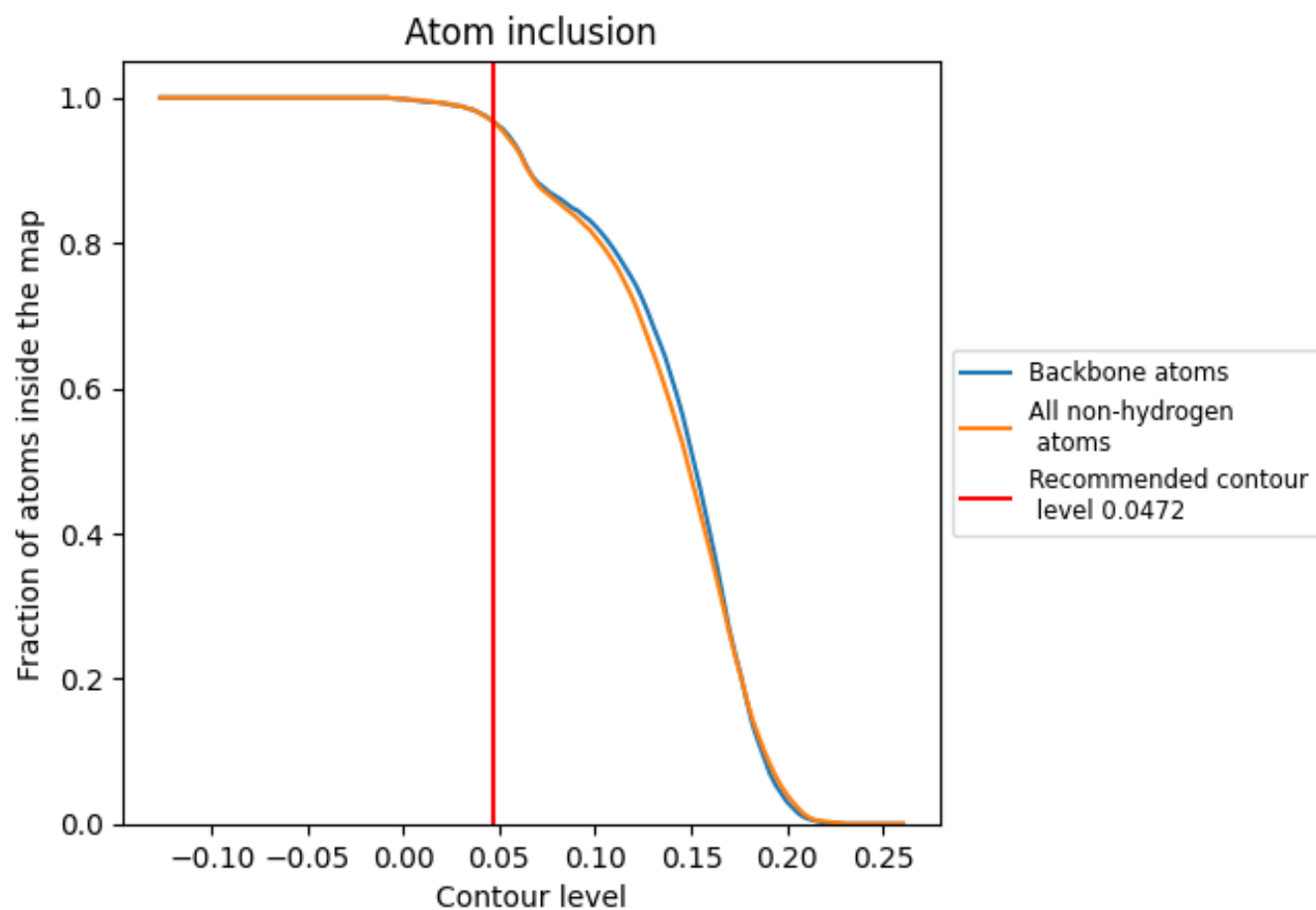
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0472).

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	<div></div> 0.9660	<div></div> 0.0800
A	<div></div> 0.9950	<div></div> 0.0810
B	<div></div> 1.0000	<div></div> 0.0810
C	<div></div> 1.0000	<div></div> 0.0740
D	<div></div> 1.0000	<div></div> 0.0790
E	<div></div> 0.9800	<div></div> 0.0890
F	<div></div> 0.9160	<div></div> 0.0870
G	<div></div> 0.4470	<div></div> 0.0570
H	<div></div> 0.9970	<div></div> 0.1000

1.0

0.0

<0.0