



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:02 AM UTC

PDB ID : 8Q84 / pdb_00008q84
EMDB ID : EMD-18246
Title : Outer kinetochore Dam1 protomer dimer Ndc80-Nuf2 coiled-coil complex
Authors : Muir, K.W.; Barford, D.
Deposited on : 2023-08-17
Resolution : 3.15 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.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

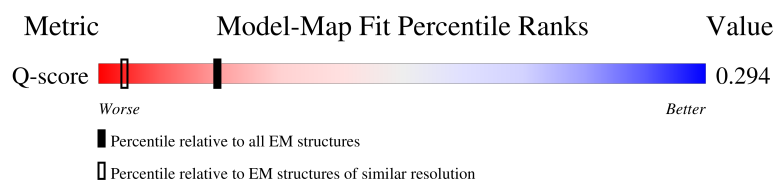
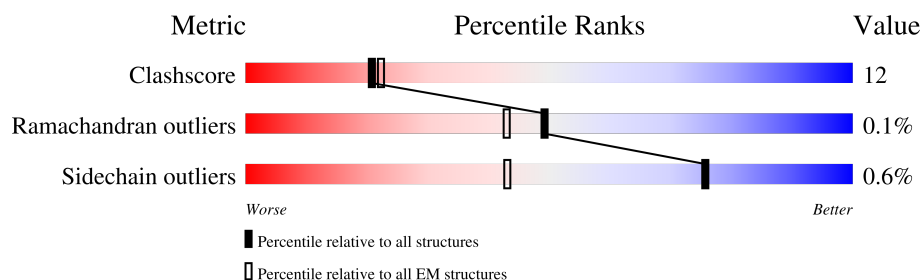
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.15 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.



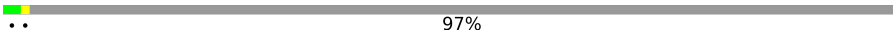
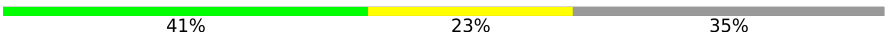
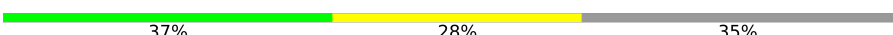
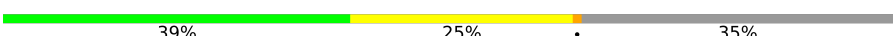
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14486 (2.65 - 3.65)

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	691	25% 42% 57%
1	F	691	26% 42% 57%
2	B	451	30% 52% 47%
2	G	451	31% 51% 48%

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Mol	Chain	Length	Quality of chain
3	I	343	
3	U	343	
3	e	343	
4	J	247	
4	V	247	
5	K	133	
5	W	133	
6	L	94	
6	X	94	
7	M	72	
7	Y	72	
8	N	94	
8	Z	94	
9	O	295	
9	a	295	
10	P	292	
10	b	292	
11	Q	69	
11	c	69	
12	R	165	
12	d	165	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 21802 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 Kinetochore protein NDC80.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	294	Total	C	N	O	0	0
			1463	875	294	294		
1	F	294	Total	C	N	O	0	0
			1463	875	294	294		

- Molecule 2 is a protein called Kinetochore protein NUF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	237	Total	C	N	O	0	0
			1180	706	237	237		
2	G	236	Total	C	N	O	0	0
			1175	703	236	236		

- Molecule 3 is a protein called DASH complex subunit DAM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	95	Total	C	N	O	S	0	0
			757	474	126	153	4		
3	U	95	Total	C	N	O	S	0	0
			757	474	126	153	4		
3	e	11	Total	C	N	O		0	0
			82	50	14	18			

- Molecule 4 is a protein called DASH complex subunit DUO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	117	Total	C	N	O	S	0	0
			935	580	167	185	3		
4	V	117	Total	C	N	O	S	0	0
			935	580	167	185	3		

- Molecule 5 is a protein called DASH complex subunit DAD2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	106	Total	C	N	O	S	0	0
			837	519	139	174	5		
5	W	106	Total	C	N	O	S	0	0
			837	519	139	174	5		

- Molecule 6 is a protein called DASH complex subunit DAD1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	61	Total	C	N	O	S	0	0
			485	304	79	101	1		
6	X	68	Total	C	N	O	S	0	0
			535	334	86	114	1		

- Molecule 7 is a protein called DASH complex subunit DAD4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	72	Total	C	N	O	S	0	0
			571	351	106	111	3		
7	Y	72	Total	C	N	O	S	0	0
			571	351	106	111	3		

- Molecule 8 is a protein called DASH complex subunit DAD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	92	Total	C	N	O	S	0	0
			744	461	130	152	1		
8	Z	94	Total	C	N	O	S	0	0
			761	471	132	156	2		

- Molecule 9 is a protein called DASH complex subunit SPC34.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	235	Total	C	N	O	S	0	0
			1929	1213	342	367	7		
9	a	234	Total	C	N	O	S	0	0
			1925	1211	341	366	7		

- Molecule 10 is a protein called DASH complex subunit ASK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	P	65	Total	C	N	O	S	0	0
			527	332	83	108	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	70	Total	C	N	O	S	0	0
			561	352	88	116	5		

- Molecule 11 is a protein called DASH complex subunit HSK3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Q	64	Total	C	N	O	S	0	0
			527	327	94	101	5		
11	c	64	Total	C	N	O	S	0	0
			527	327	94	101	5		

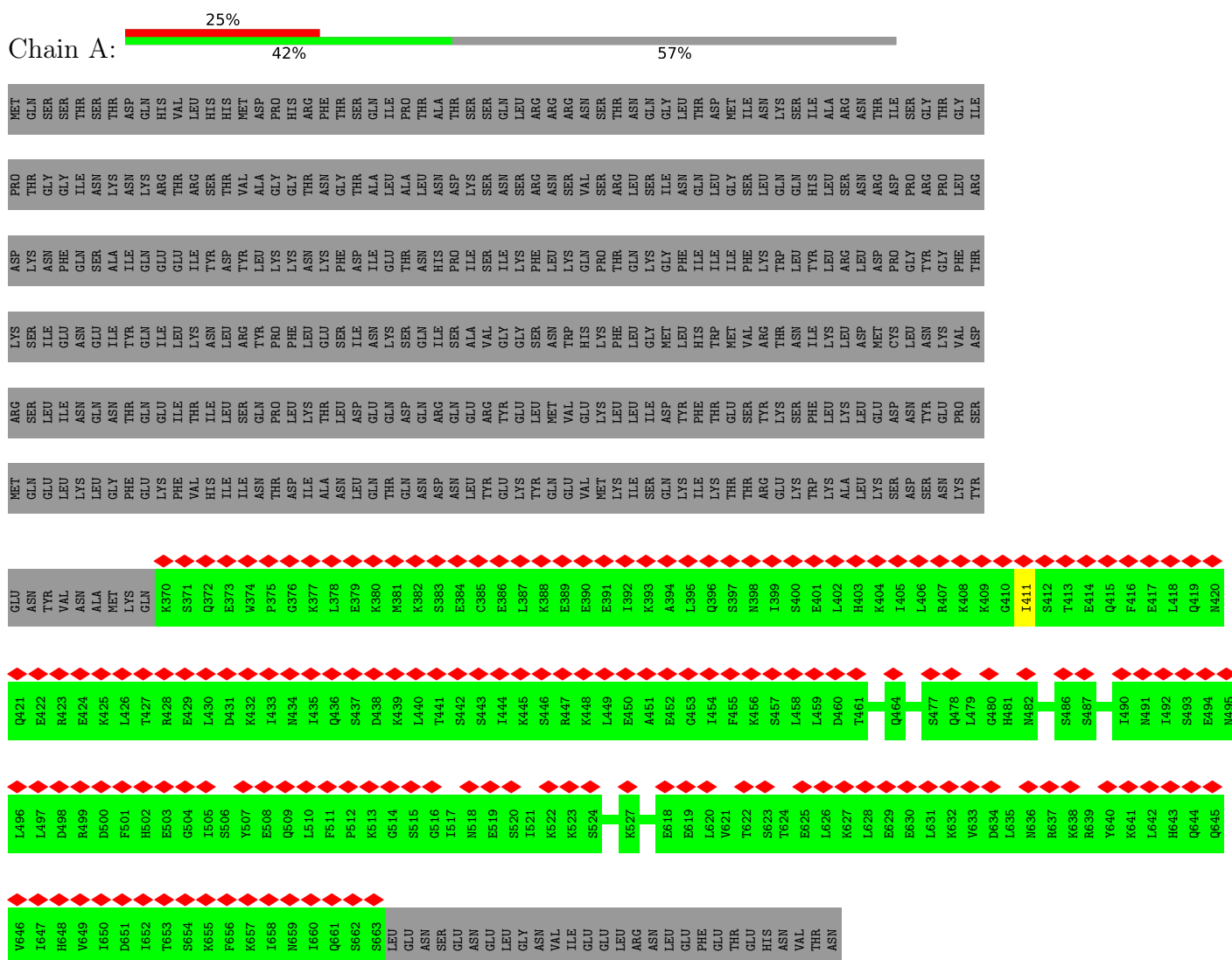
- Molecule 12 is a protein called DASH complex subunit SPC19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	108	Total	C	N	O	S	0	0
			859	532	149	172	6		
12	d	108	Total	C	N	O	S	0	0
			859	532	149	172	6		

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: Kinetochore protein NDC80



• Molecule 1: Kinetochore protein NDC80

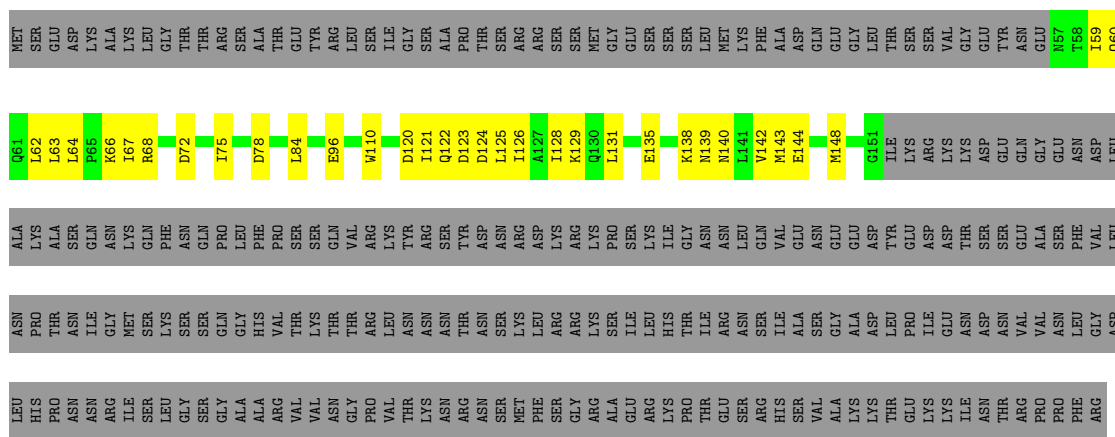


V646	I647	H648	V649	D651	I652	T653	S654	K655	F656	K657	T658	N659	I660	Q661	S662	S663	LEU	GLU	ASN	SER	GLU	ASN	GLU	LEU	GLY	ASN	VAL	ILE	GLU	GLU	GLU	LEU	ARG	ASN	LEU	GLU	PHE	THR	GLU	HIS	ASN	VAL	THR	ASN															
L496	L497	D498	R499	D500	F501	H502	S503	F504	S505	Y506	E508	Q509	L510	F511	P512	K513	G514	S515	S516	I517	N518	GLU	L519	S520	K523	S524	I525	L526	K527	R587	E619	T622	S623	T624	E625	L626	K627	L628	E629	E630	L631	K632	V633	D634	L635	N636	K637	K638	R639	Y640	K641	L642	H643	D644	D645				
Q421	E422	R423	E424	K425	L426	T427	R428	E429	L430	D431	K432	I433	N434	I435	Q436	S437	D438	K439	L440	T441	S442	S443	I444	K445	S446	R447	K448	L449	E450	A451	E452	G453	I454	F455	K456	S457	L458	L459	R463	D466	S467	S468	Q478	L479	G480	N484	D485	S486	S487	N491	I492	S493	E494	N495					
GLU	ASN	TYR	VAL	ASN	ALA	MET	LYS	GLN	K370	S371	Q372	E373	V374	P375	G376	K377	L378	E379	K380	M381	K382	S383	E384	K385	E386	L387	K388	E389	E390	E391	I392	K393	A394	L395	Q396	S397	N398	I399	S400	E401	L402	H403	K404	I405	L406	R407	K408	K409	G410	I411	S412	T413	E414	Q415	F416	E417	L418	Q419	N420

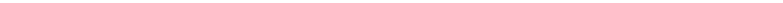
Chain B: 30% 52% 47%

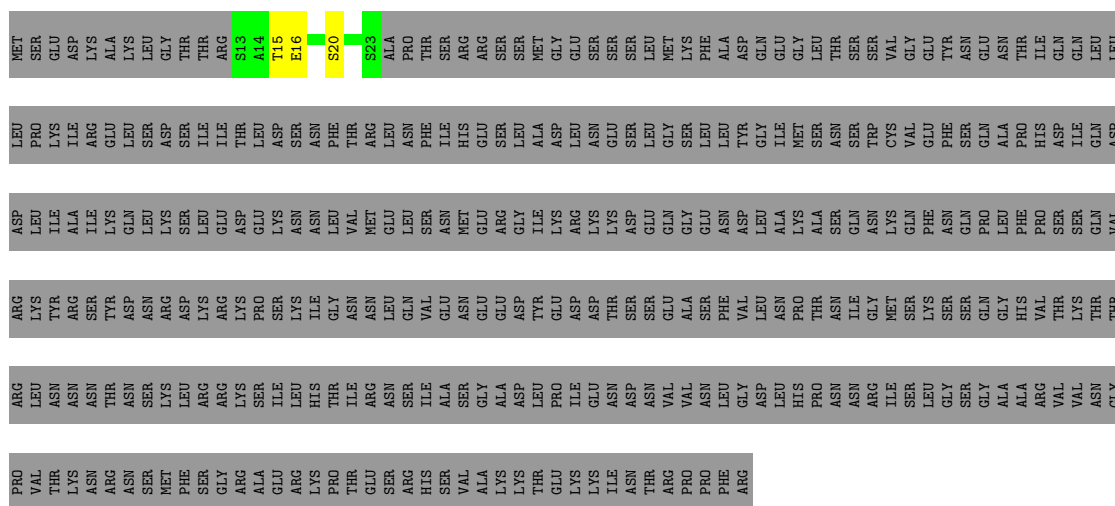
R241	R242	R243	R244	R245	R246	R247	R248	R249	R250	R251	R252	R253	R254	R255	R256	R257	R258	R259	R260	R261	R262	R263	R264	R265	R266	R267	R268	R269	R270	R271	R272	R273	R274	R275	R276	R277	R278	R279	R280	R281	R282	R283	R284	R285	R286	R287	R288	R289	R290	R291	R292	R293	R294	R295	R296	R297	R298	R299	R300	R301	R302	R303	R304	R305	R306	R307	R308	R309	R310	R311	R312	R313	R314	R315	R316	R317	R318	R319	R320	R321	R322	R323	R324	R325	R326	R327	R328	R329	R330	R331	R332	R333	R334	R335	R336	R337	R338	R339	R340	R341	R342	R343	R344	R345	R346	R347	R348	R349	R350	R351	R352	R353	R354	R355	R356	R357	R358	R359	R360	R361	R362	R363	R364	R365	R366	R367	R368	R369	R370	R371	R372	R373	R374	R375	R376	R377	R378	R379	R380	R381	R382	R383	R384	R385	R386	R387	R388	R389	R390	R391	R392	R393	R394	R395	R396	R397	R398	R399	R400	R401	R402	R403	R404	R405	R406	R407	R408	R409	R410	R411	R412	R413	R414	R415	R416	R417	R418	R419	R420	R421	R422	R423	R424	R425	R426	R427	R428	R429	R430	R431	R432	R433	R434	R435	R436	R437	R438	R439	R440	R441	R442	R443	R444	R445	R446	R447	R448	R449	R450	R451	R452	R453	R454	R455	R456	R457	R458	R459	R460	R461	R462	R463	R464	R465	R466	R467	R468	R469	R470	R471	R472	R473	R474	R475	R476	R477	R478	R479	R480	R481	R482	R483	R484	R485	R486	R487	R488	R489	R490	R491	R492	R493	R494	R495	R496	R497	R498	R499	R500	R501	R502	R503	R504	R505	R506	R507	R508	R509	R510	R511	R512	R513	R514	R515	R516	R517	R518	R519	R520	R521	R522	R523	R524	R525	R526	R527	R528	R529	R530	R531	R532	R533	R534	R535	R536	R537	R538	R539	R540	R541	R542	R543	R544	R545	R546	R547	R548	R549	R550	R551	R552	R553	R554	R555	R556	R557	R558	R559	R560	R561	R562	R563	R564	R565	R566	R567	R568	R569	R570	R571	R572	R573	R574	R575	R576	R577	R578	R579	R580	R581
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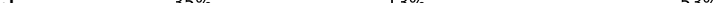


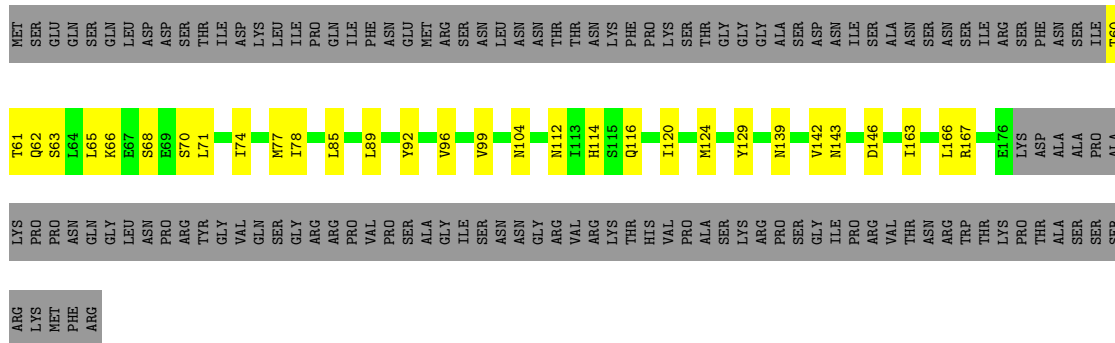
- Molecule 3: DASH complex subunit DAM1

Chain e:  97%



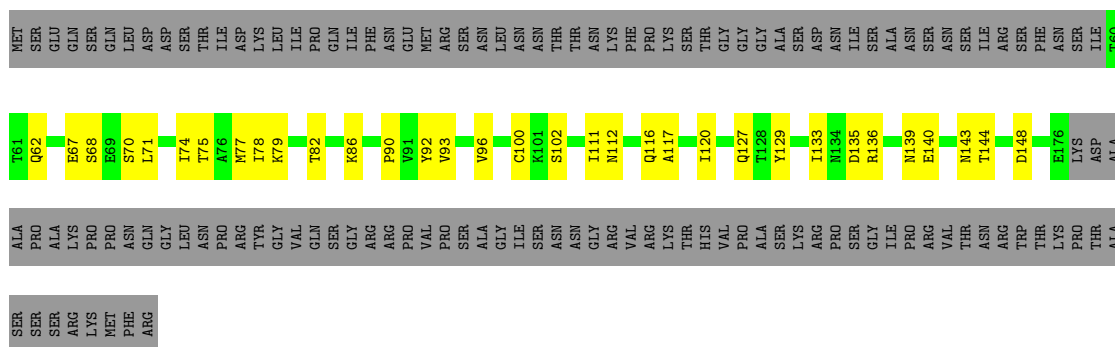
- Molecule 4: DASH complex subunit DUO1

Chain J:  35% 13% 53%



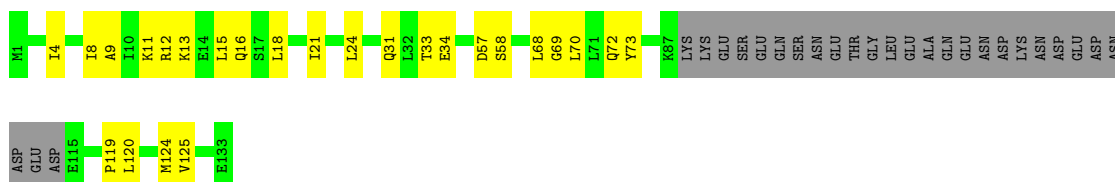
- Molecule 4: DASH complex subunit DUO1

Chain V: 34% 13% 53%



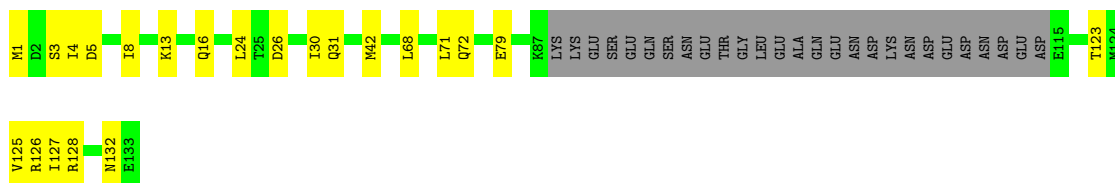
• Molecule 5: DASH complex subunit DAD2

Chain K: 61% 19% 20%



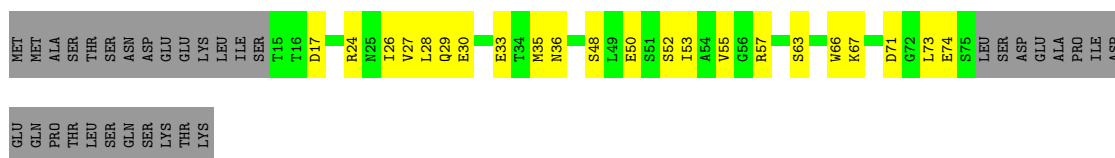
• Molecule 5: DASH complex subunit DAD2

Chain W: 63% 17% 20%



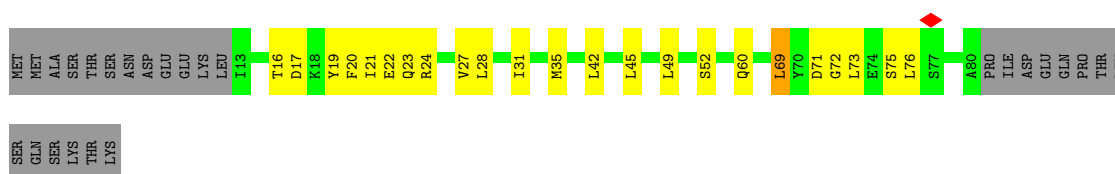
• Molecule 6: DASH complex subunit DAD1

Chain L: 41% 23% 35%



• Molecule 6: DASH complex subunit DAD1

Chain X: 48% 23% 28%



- Molecule 7: DASH complex subunit DAD4

Chain M:  56% 44%



- Molecule 7: DASH complex subunit DAD4

Chain Y:  64% 36%



- Molecule 8: DASH complex subunit DAD3

Chain N:  64% 34%



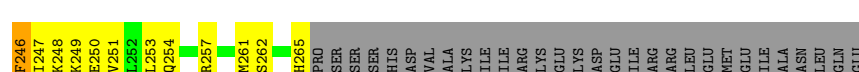
- Molecule 8: DASH complex subunit DAD3

Chain Z:  71% 29%



- Molecule 9: DASH complex subunit SPC34

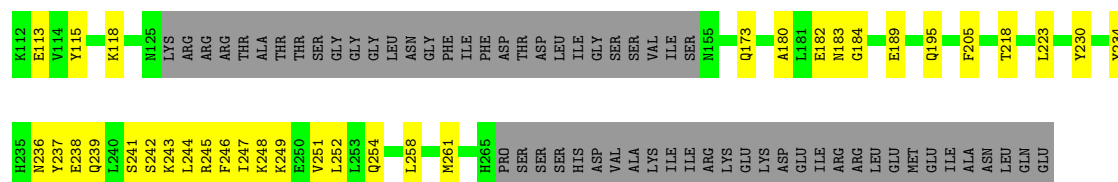
Chain O:  59% 20% 20%



- Molecule 9: DASH complex subunit SPC34

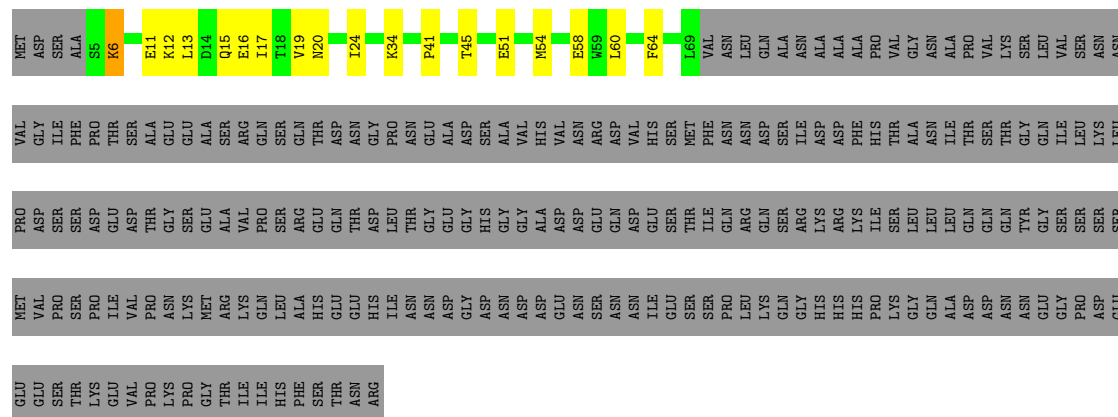
Chain a:  57% 23% 21%





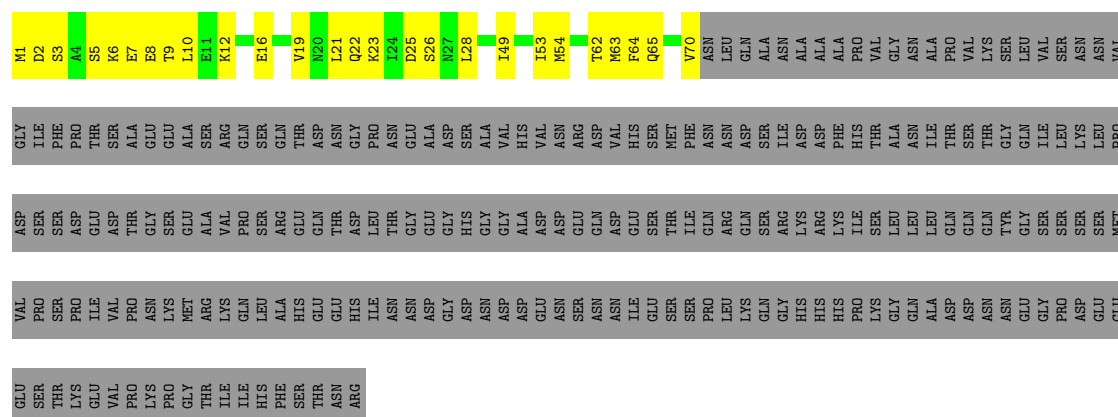
• Molecule 10: DASH complex subunit ASK1

Chain P: 16% 6% 78%



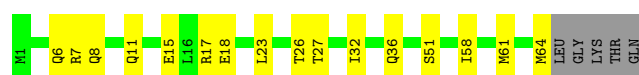
• Molecule 10: DASH complex subunit ASK1

Chain b: 15% 9% 76%



• Molecule 11: DASH complex subunit HSK3

Chain Q: 70% 23% 7%

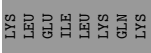
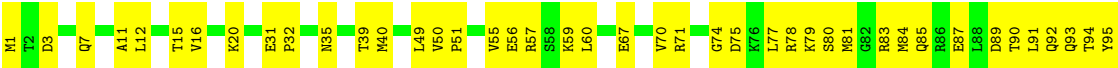
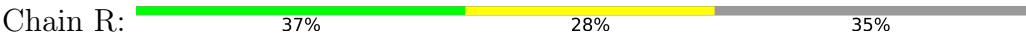


• Molecule 11: DASH complex subunit HSK3

Chain c: 72% 20% 7%



● Molecule 12: DASH complex subunit SPC19



● Molecule 12: DASH complex subunit SPC19



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	248732	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.815	Depositor
Minimum map value	-0.855	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0.13	0/1462	0.29	0/2041
1	F	0.13	0/1462	0.30	0/2041
2	B	0.14	0/1179	0.35	0/1646
2	G	0.15	0/1174	0.35	0/1639
3	I	0.18	0/766	0.48	0/1034
3	U	0.21	0/766	0.56	0/1034
3	e	0.19	0/82	0.41	0/109
4	J	0.17	0/945	0.41	0/1275
4	V	0.16	0/945	0.39	0/1275
5	K	0.18	0/844	0.47	0/1135
5	W	0.17	0/844	0.38	0/1135
6	L	0.16	0/490	0.38	0/662
6	X	0.21	0/540	0.53	0/730
7	M	0.17	0/577	0.42	0/779
7	Y	0.17	0/577	0.44	0/779
8	N	0.32	0/751	0.57	0/1007
8	Z	0.19	0/768	0.56	0/1029
9	O	0.16	0/1962	0.41	0/2638
9	a	0.14	0/1958	0.37	0/2633
10	P	0.15	0/535	0.35	0/722
10	b	0.19	0/569	0.43	0/768
11	Q	0.18	0/534	0.45	0/716
11	c	0.14	0/534	0.35	0/716
12	R	0.17	0/864	0.50	0/1161
12	d	0.18	0/864	0.52	0/1161
All	All	0.17	0/21992	0.42	0/29865

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1463	0	607	0	0
1	F	1463	0	607	1	0
2	B	1180	0	483	1	0
2	G	1175	0	481	2	0
3	I	757	0	753	21	0
3	U	757	0	753	27	0
3	e	82	0	79	4	0
4	J	935	0	952	33	0
4	V	935	0	952	31	0
5	K	837	0	837	30	0
5	W	837	0	837	21	0
6	L	485	0	475	18	0
6	X	535	0	522	23	0
7	M	571	0	578	28	0
7	Y	571	0	578	21	0
8	N	744	0	754	41	0
8	Z	761	0	772	30	0
9	O	1929	0	1929	63	0
9	a	1925	0	1926	61	0
10	P	527	0	513	21	0
10	b	561	0	548	25	0
11	Q	527	0	520	14	0
11	c	527	0	520	12	0
12	R	859	0	897	52	0
12	d	859	0	897	52	0
All	All	21802	0	18770	486	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 12.

The worst 5 of 486 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:W:24:LEU:HB3	12:d:12:LEU:HD22	1.61	0.82
9:a:182:GLU:OE2	9:a:183:ASN:ND2	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:V:127:GLN:HE22	12:d:32:PRO:HB3	1.47	0.79
8:N:18:GLN:HA	8:N:21:LEU:HD12	1.65	0.77
9:O:176:ARG:HB3	9:O:186:VAL:HG21	1.67	0.76

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	292/691 (42%)	291 (100%)	0	1 (0%)	36	64
1	F	292/691 (42%)	290 (99%)	1 (0%)	1 (0%)	36	64
2	B	235/451 (52%)	229 (97%)	6 (3%)	0	100	100
2	G	234/451 (52%)	228 (97%)	6 (3%)	0	100	100
3	I	93/343 (27%)	91 (98%)	2 (2%)	0	100	100
3	U	93/343 (27%)	92 (99%)	1 (1%)	0	100	100
3	e	9/343 (3%)	8 (89%)	1 (11%)	0	100	100
4	J	115/247 (47%)	113 (98%)	2 (2%)	0	100	100
4	V	115/247 (47%)	113 (98%)	2 (2%)	0	100	100
5	K	102/133 (77%)	100 (98%)	2 (2%)	0	100	100
5	W	102/133 (77%)	98 (96%)	4 (4%)	0	100	100
6	L	59/94 (63%)	59 (100%)	0	0	100	100
6	X	66/94 (70%)	63 (96%)	3 (4%)	0	100	100
7	M	70/72 (97%)	67 (96%)	3 (4%)	0	100	100
7	Y	70/72 (97%)	67 (96%)	3 (4%)	0	100	100
8	N	90/94 (96%)	79 (88%)	11 (12%)	0	100	100
8	Z	92/94 (98%)	85 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	O	231/295 (78%)	228 (99%)	3 (1%)	0	100	100
9	a	230/295 (78%)	222 (96%)	8 (4%)	0	100	100
10	P	63/292 (22%)	62 (98%)	1 (2%)	0	100	100
10	b	68/292 (23%)	67 (98%)	1 (2%)	0	100	100
11	Q	62/69 (90%)	60 (97%)	2 (3%)	0	100	100
11	c	62/69 (90%)	62 (100%)	0	0	100	100
12	R	106/165 (64%)	105 (99%)	1 (1%)	0	100	100
12	d	106/165 (64%)	105 (99%)	1 (1%)	0	100	100
All	All	3057/6235 (49%)	2984 (98%)	71 (2%)	2 (0%)	49	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	411	ILE
1	F	411	ILE

5.3.2 Protein sidechains [i](#)

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	
3	I	89/309 (29%)	89 (100%)	0	100	100
3	U	89/309 (29%)	88 (99%)	1 (1%)	65	75
3	e	9/309 (3%)	9 (100%)	0	100	100
4	J	109/222 (49%)	109 (100%)	0	100	100
4	V	109/222 (49%)	108 (99%)	1 (1%)	70	77
5	K	95/120 (79%)	95 (100%)	0	100	100
5	W	95/120 (79%)	94 (99%)	1 (1%)	65	75
6	L	56/87 (64%)	56 (100%)	0	100	100
6	X	62/87 (71%)	61 (98%)	1 (2%)	55	71
7	M	66/66 (100%)	66 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	Y	66/66 (100%)	65 (98%)	1 (2%)	57	72
8	N	87/89 (98%)	87 (100%)	0	100	100
8	Z	89/89 (100%)	89 (100%)	0	100	100
9	O	217/269 (81%)	215 (99%)	2 (1%)	70	77
9	a	217/269 (81%)	217 (100%)	0	100	100
10	P	62/259 (24%)	61 (98%)	1 (2%)	55	71
10	b	66/259 (26%)	66 (100%)	0	100	100
11	Q	58/62 (94%)	57 (98%)	1 (2%)	53	70
11	c	58/62 (94%)	58 (100%)	0	100	100
12	R	101/153 (66%)	101 (100%)	0	100	100
12	d	101/153 (66%)	99 (98%)	2 (2%)	48	68
All	All	1901/3581 (53%)	1890 (99%)	11 (1%)	76	81

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	X	69	LEU
7	Y	66	ASN
12	d	98	ASN
12	d	12	LEU
3	U	84	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
4	V	88	ASN
11	c	38	ASN
5	W	62	ASN
12	d	98	ASN
10	b	20	ASN

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.

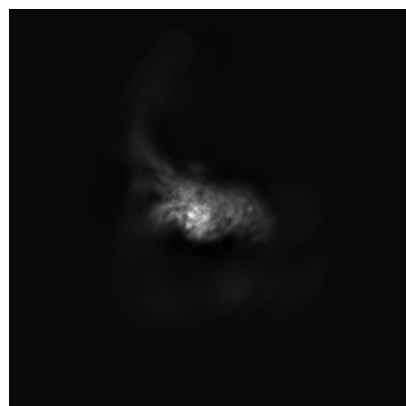
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18246. These allow visual inspection of the internal detail of the map and identification of artifacts.

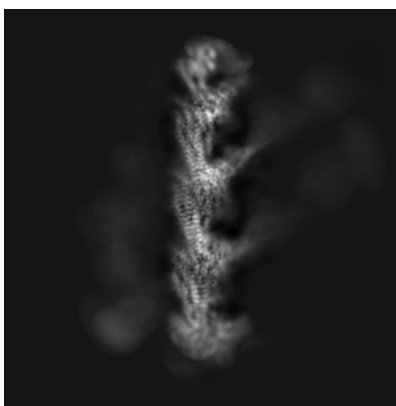
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

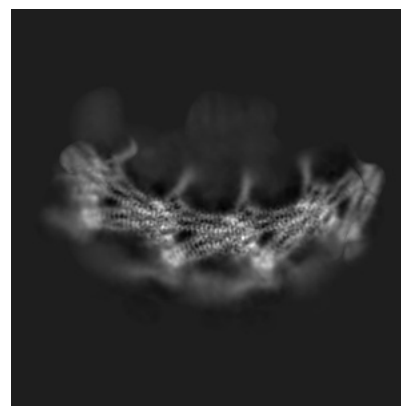
6.1.1 Primary map



X

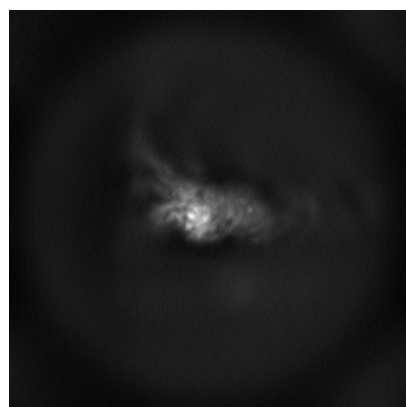


Y

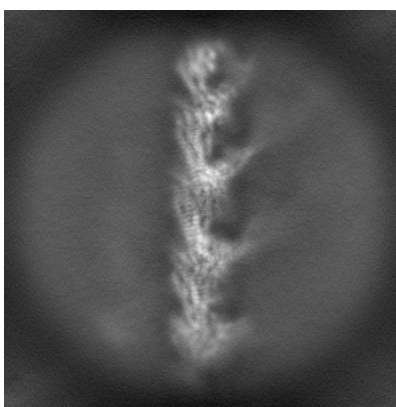


Z

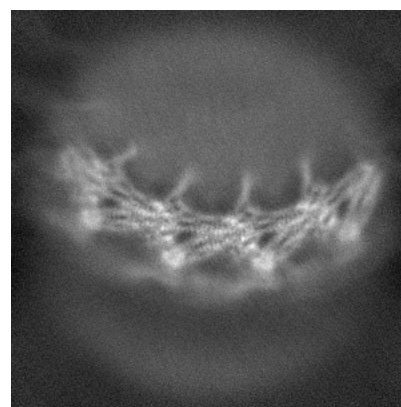
6.1.2 Raw map



X



Y

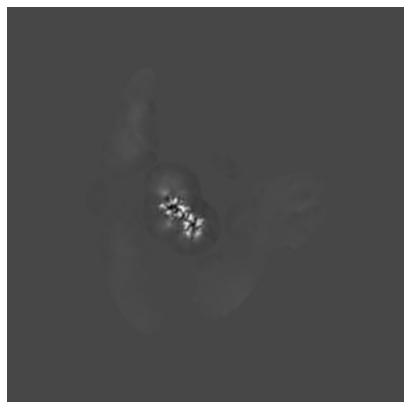


Z

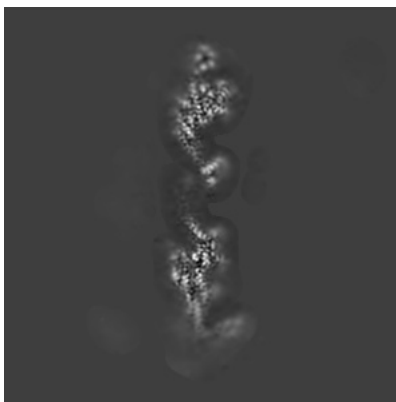
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 200



Y Index: 200

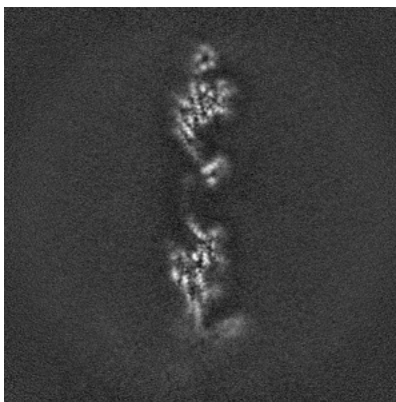


Z Index: 200

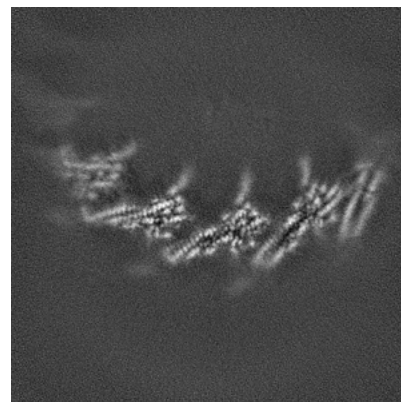
6.2.2 Raw map



X Index: 200



Y Index: 200

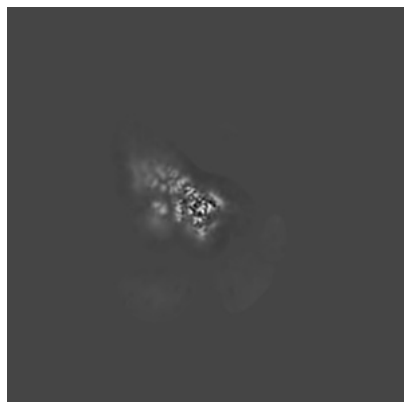


Z Index: 200

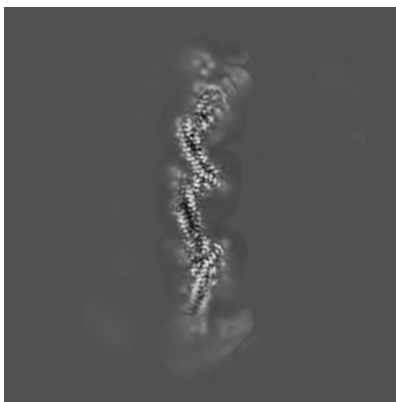
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

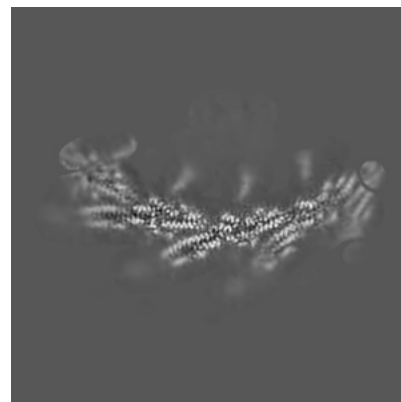
6.3.1 Primary map



X Index: 157

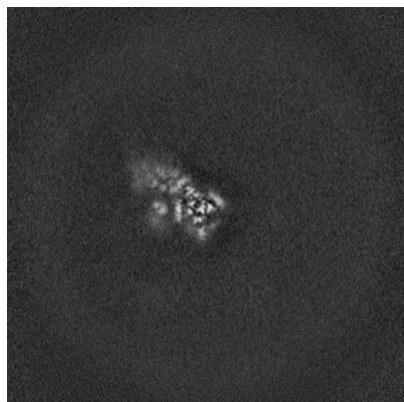


Y Index: 186

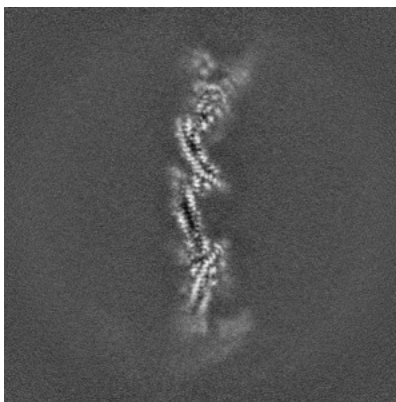


Z Index: 194

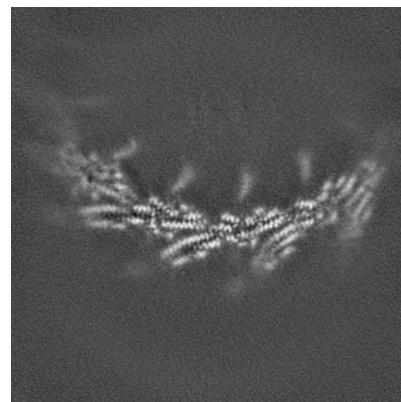
6.3.2 Raw map



X Index: 157



Y Index: 186

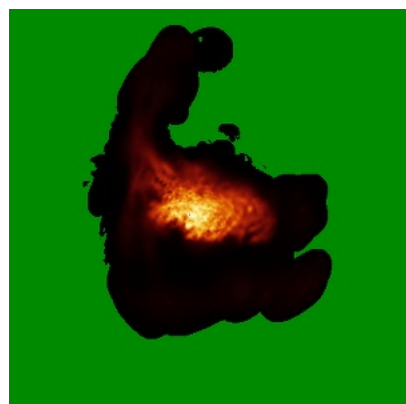


Z Index: 194

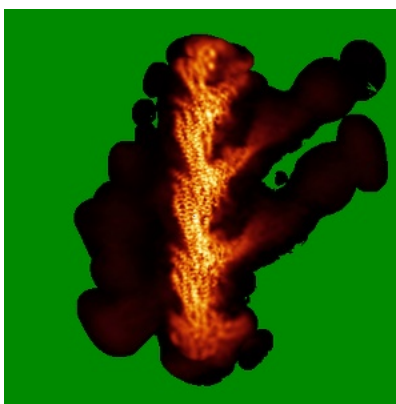
The images above show the largest variance slices of the map in three orthogonal directions.

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

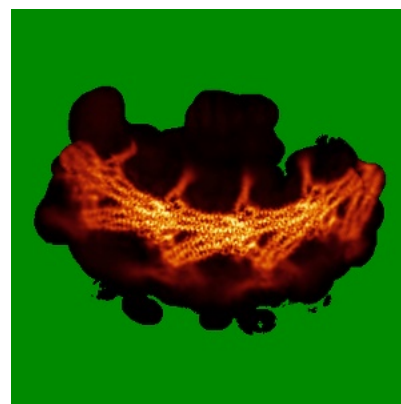
6.4.1 Primary map



X

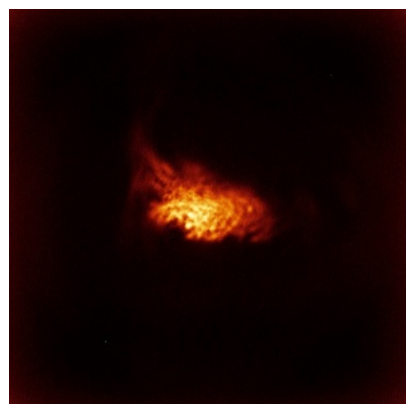


Y

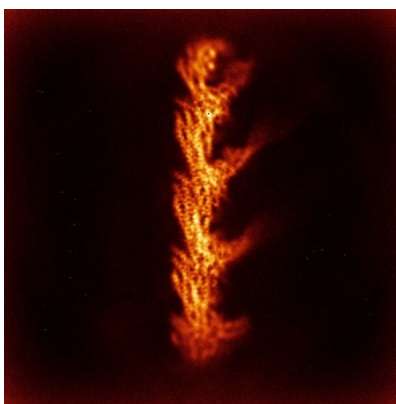


Z

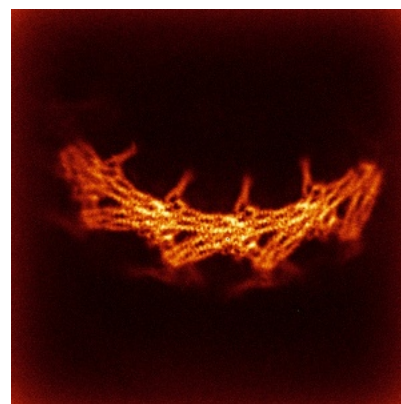
6.4.2 Raw map



X



Y

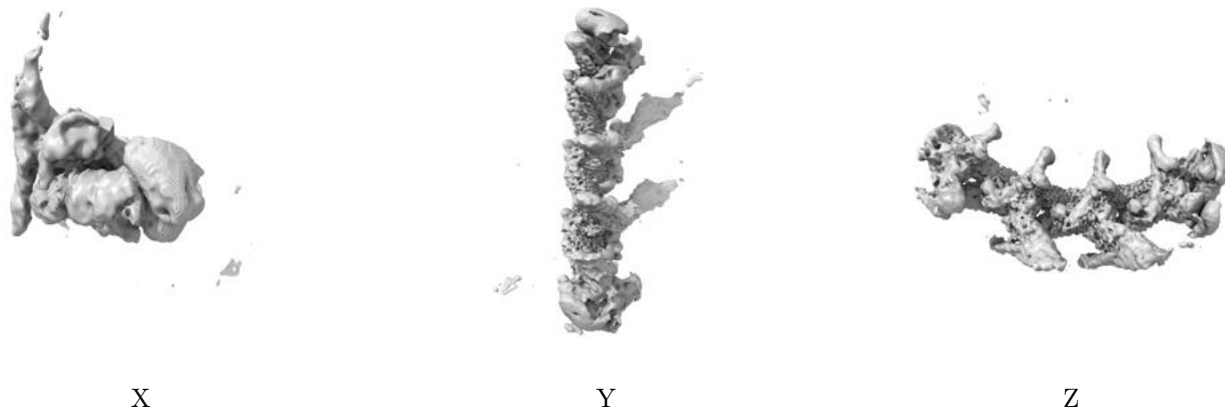


Z

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.

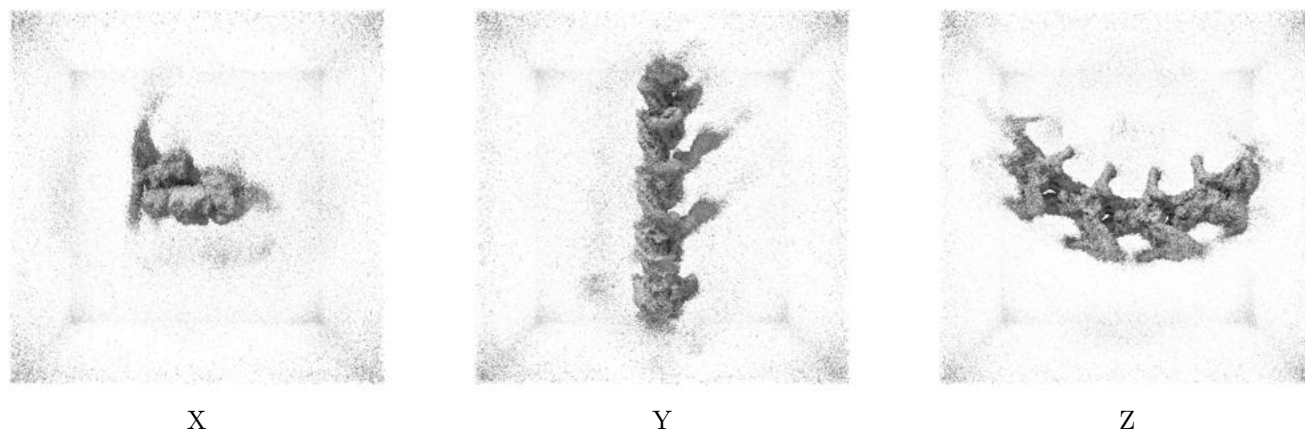
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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



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.

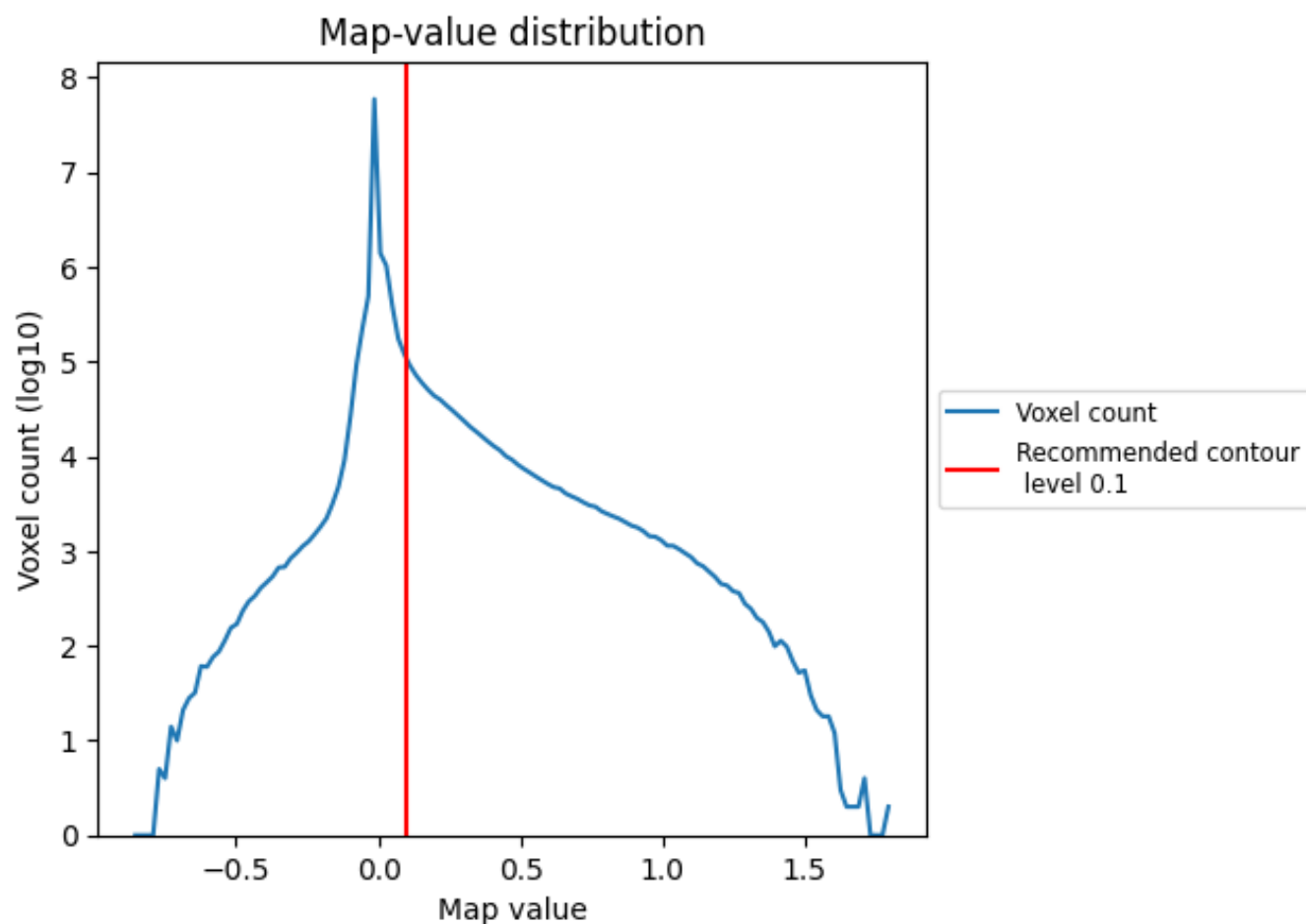
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

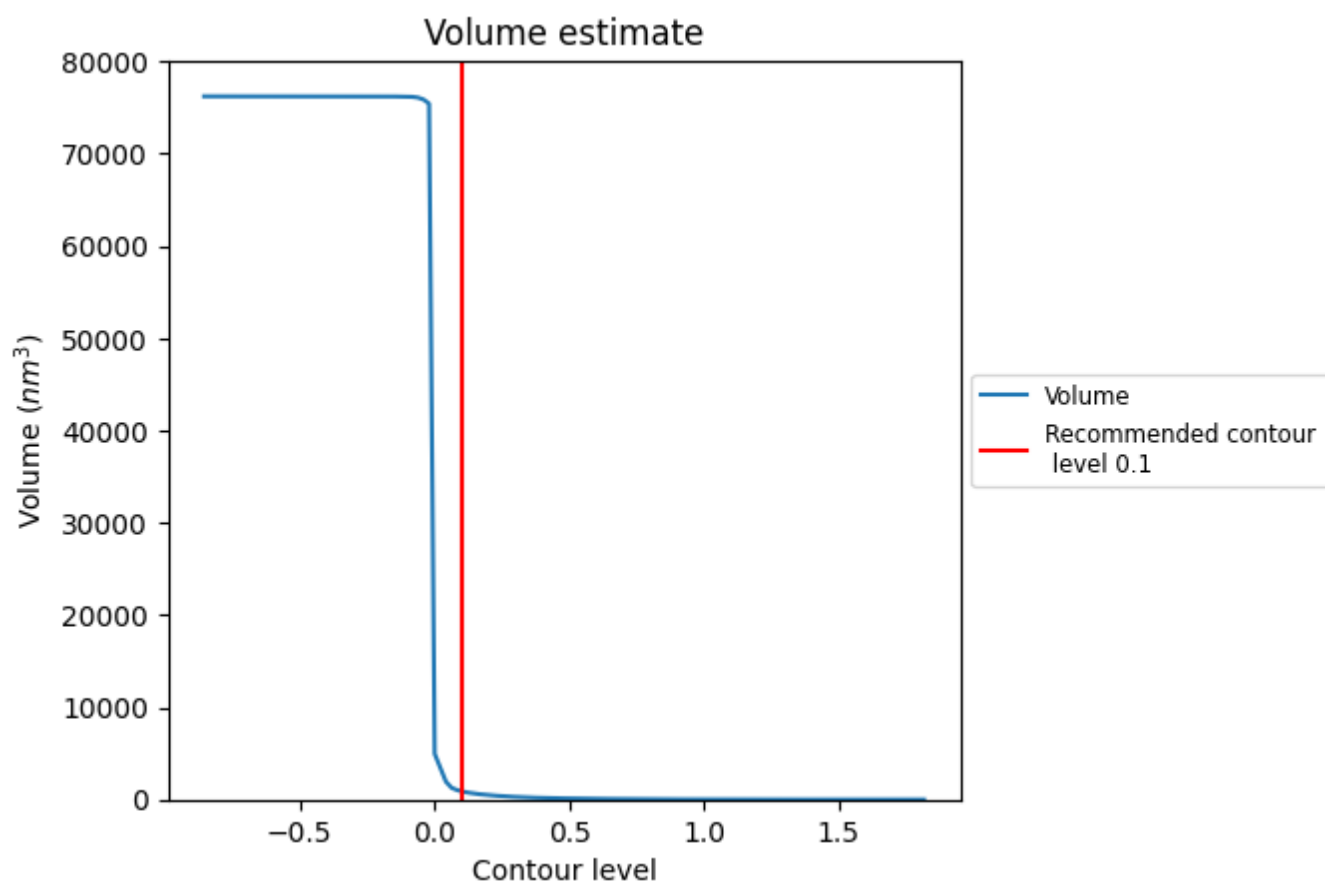
This section contains the results of statistical analysis of the map.

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.

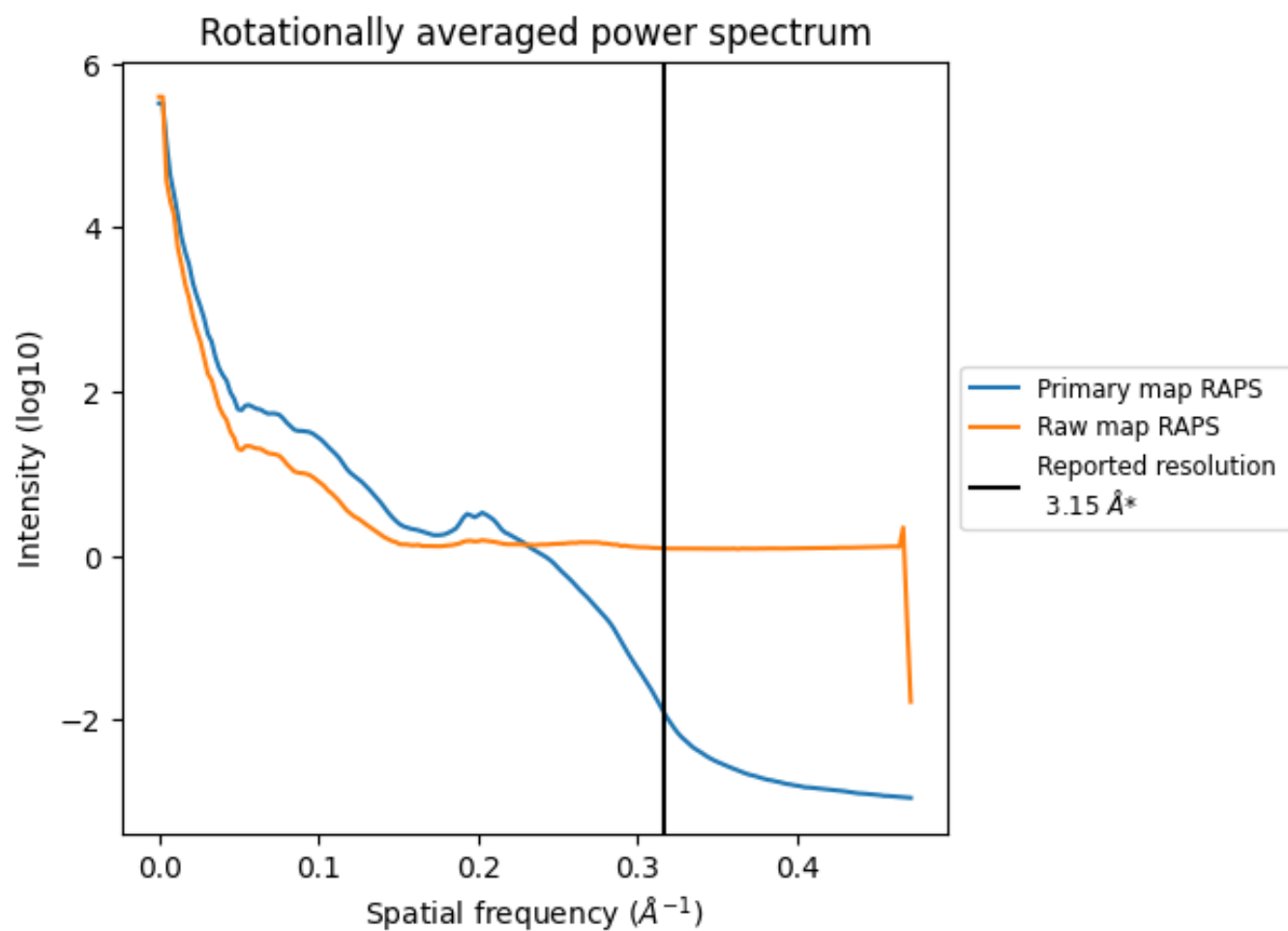
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 901 nm³; this corresponds to an approximate mass of 814 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 ⓘ

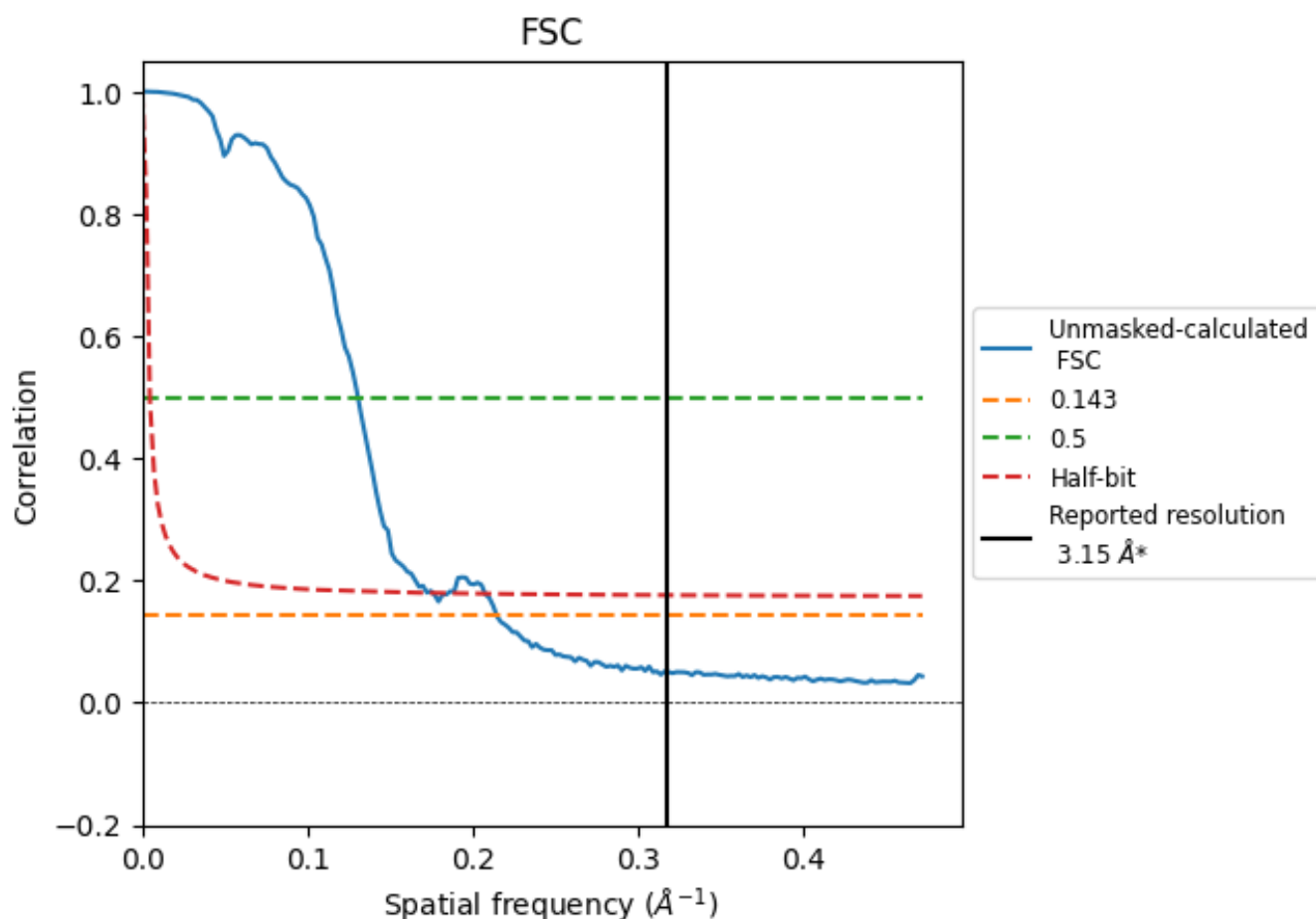


*Reported resolution corresponds to spatial frequency of $0.317 \text{ \AA}^{-1}$

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 0.317 Å⁻¹

8.2 Resolution estimates [i](#)

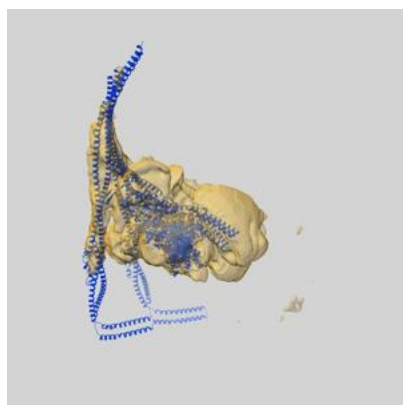
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.15	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.67	7.66	5.69

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.67 differs from the reported value 3.15 by more than 10 %

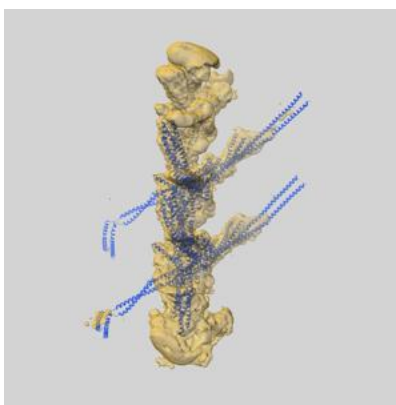
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18246 and PDB model 8Q84. Per-residue inclusion information can be found in section [3](#) on page [7](#).

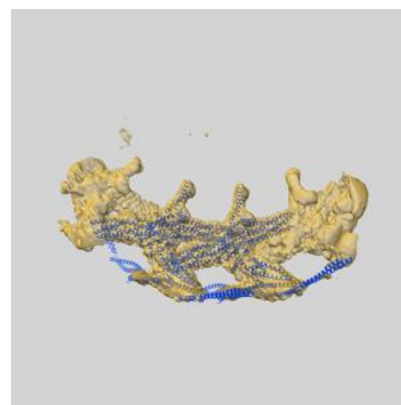
9.1 Map-model overlay [i](#)



X



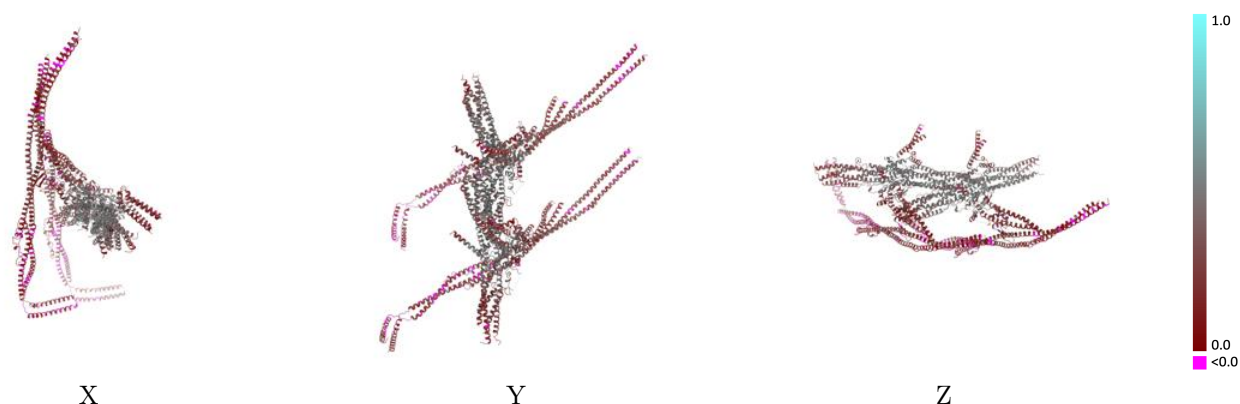
Y



Z

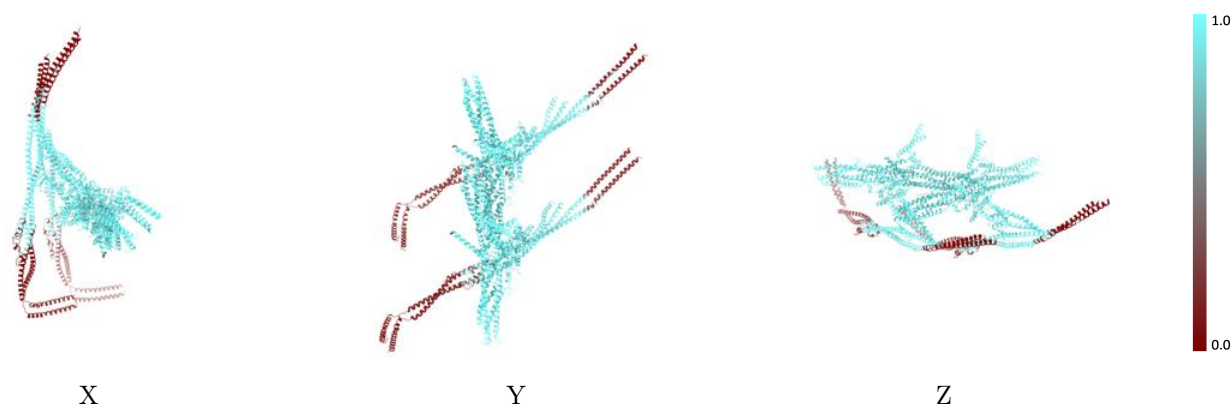
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



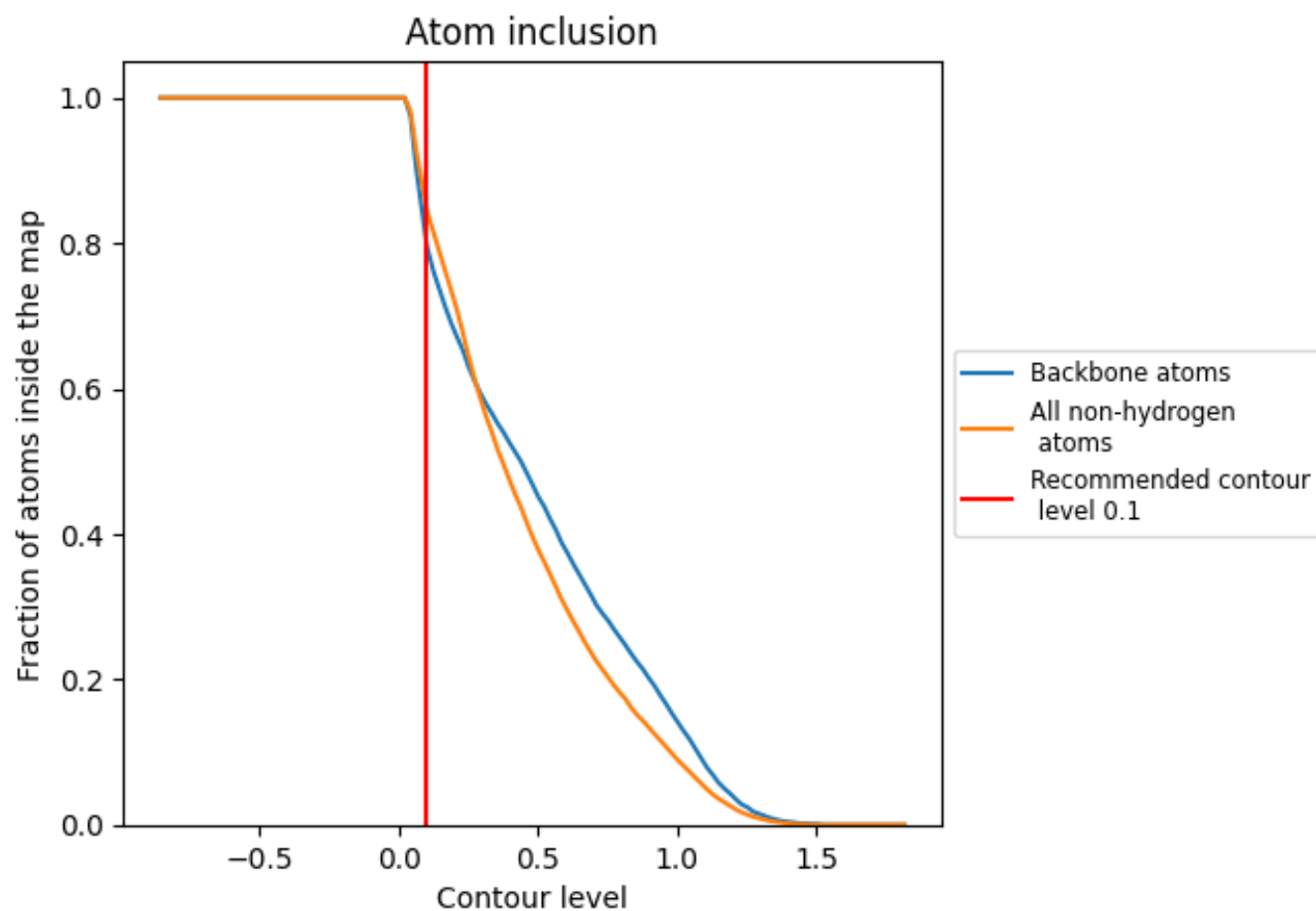
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 85% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8480	 0.2940
A	 0.4160	 0.1260
B	 0.4420	 0.1410
F	 0.3840	 0.1320
G	 0.4140	 0.1540
I	 0.9910	 0.3500
J	 0.9980	 0.3260
K	 0.9890	 0.4110
L	 0.9960	 0.4130
M	 0.9970	 0.4540
N	 0.9760	 0.3380
O	 0.9790	 0.2890
P	 1.0000	 0.4330
Q	 1.0000	 0.4430
R	 0.9940	 0.3240
U	 0.9960	 0.3210
V	 0.9950	 0.2900
W	 0.9950	 0.4120
X	 0.9740	 0.2880
Y	 1.0000	 0.4470
Z	 0.9800	 0.2990
a	 0.9880	 0.2590
b	 0.9890	 0.4140
c	 0.9960	 0.4640
d	 0.9940	 0.2970
e	 1.0000	 0.4850

