



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 02:27 AM UTC

PDB ID : 8TH8 / pdb_00008th8
EMDB ID : EMD-41251
Title : Linker domain of Nexin-dynein regulatory complex from *Tetrahymena thermophila*
Authors : Ghanaeian, A.G.; Bui, K.H.
Deposited on : 2023-07-14
Resolution : 7.40 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:

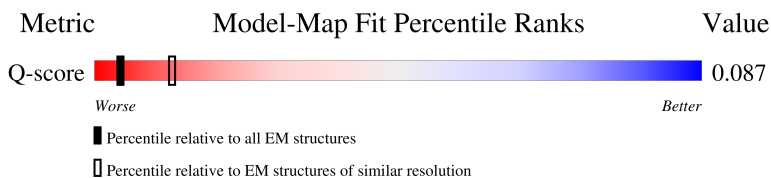
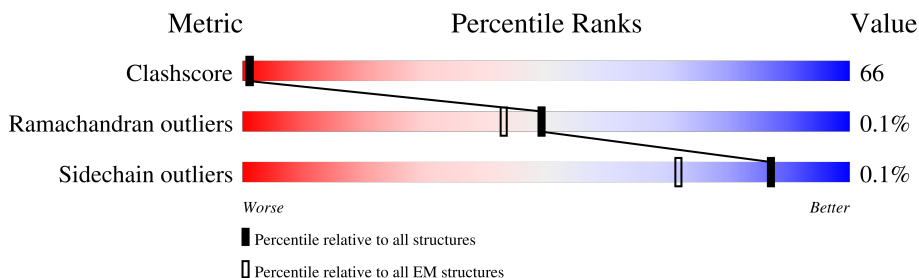
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 7.40 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	412 (6.90 - 7.90)

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	826	<p>11% 24% 65%</p>
2	B	506	<p>15% 39% 45%</p>
3	C	575	<p>29% 63% 7%</p>
4	D	472	<p>10% 44% 18% 38%</p>

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Mol	Chain	Length	Quality of chain
5	E	468	
6	F	461	
7	G	345	
8	H	852	
9	I	185	
9	i	185	
10	J	372	
11	K	434	
12	L	862	
13	P	794	
14	Q	202	
14	R	202	
15	S	187	
15	s	187	

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 58466 atoms, of which 5024 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 Dynein regulatory complex protein 1/2 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	290	2460	1524	439	483	14	0	0

- Molecule 2 is a protein called Coiled-coil protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	276	2329	1451	421	447	10	0	0

- Molecule 3 is a protein called LRRC48 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	533	4433	2771	760	890	12	0	0

- Molecule 4 is a protein called Growth-arrest-specific microtubule-binding protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	292	4976	1536	2515	435	482	8	0	0

- Molecule 5 is a protein called Growth-arrest-specific microtubule-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	E	291	4952	1528	2509	430	478	7	0	0

- Molecule 6 is a protein called Flagellar associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	461	3714	2351	632	714	17	0	0

- Molecule 7 is a protein called Kinase domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	345	2780	1763	474	527	16	0	0

- Molecule 8 is a protein called Coiled-coil lobo-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	820	6857	4318	1192	1314	33	0	0

- Molecule 9 is a protein called EF-hand calcium-binding domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	185	1553	1002	244	301	6	0	0
9	i	185	1553	1002	244	301	6	0	0

- Molecule 10 is a protein called Dynein regulatory complex protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	372	3151	1949	574	620	8	0	0

- Molecule 11 is a protein called Dynein regulatory complex protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	434	3588	2229	647	699	13	0	0

- Molecule 12 is a protein called AAA family ATPase CDC48 subfamily protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	862	7102	4513	1213	1345	31	0	0

- Molecule 13 is a protein called DUF4201 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	P	305	2576	1624	442	502	8	0	0

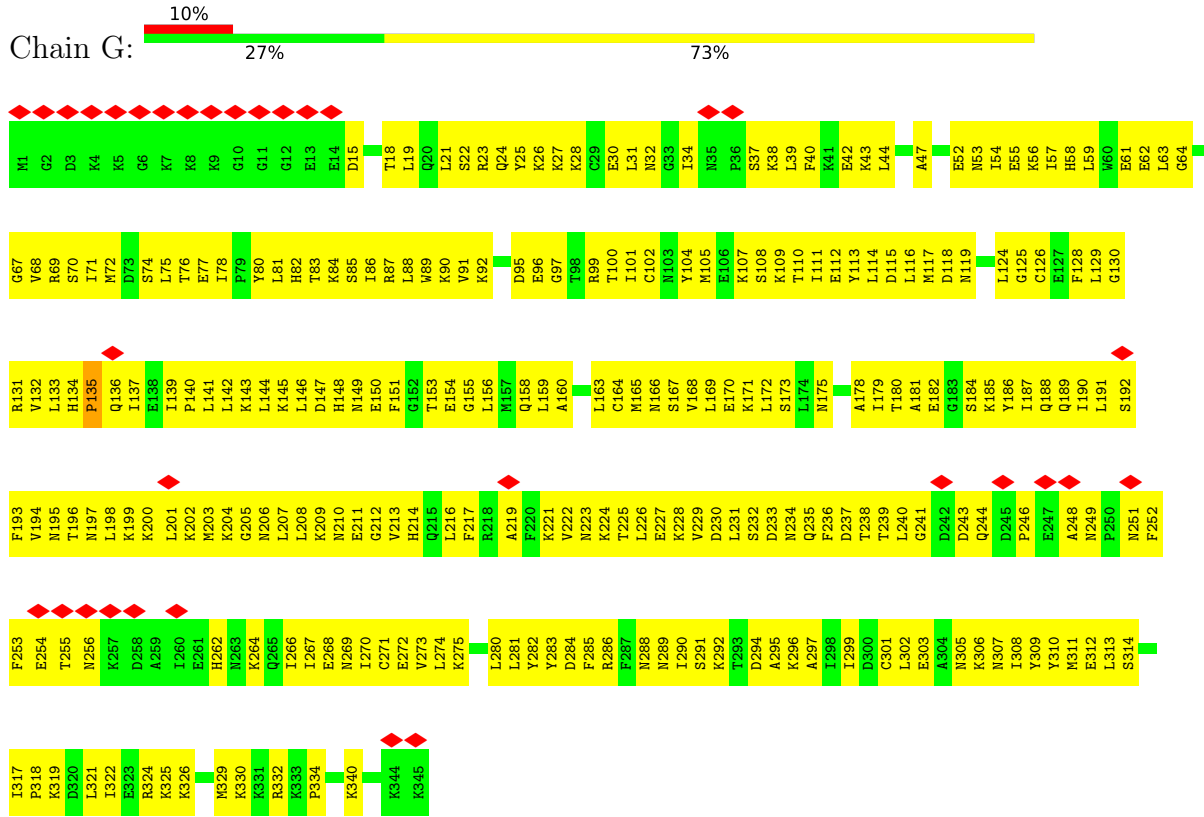
- Molecule 14 is a protein called Calmodulin 7-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	Q	202	1679	1061	276	338	4	0	0
14	R	202	1679	1061	276	338	4	0	0

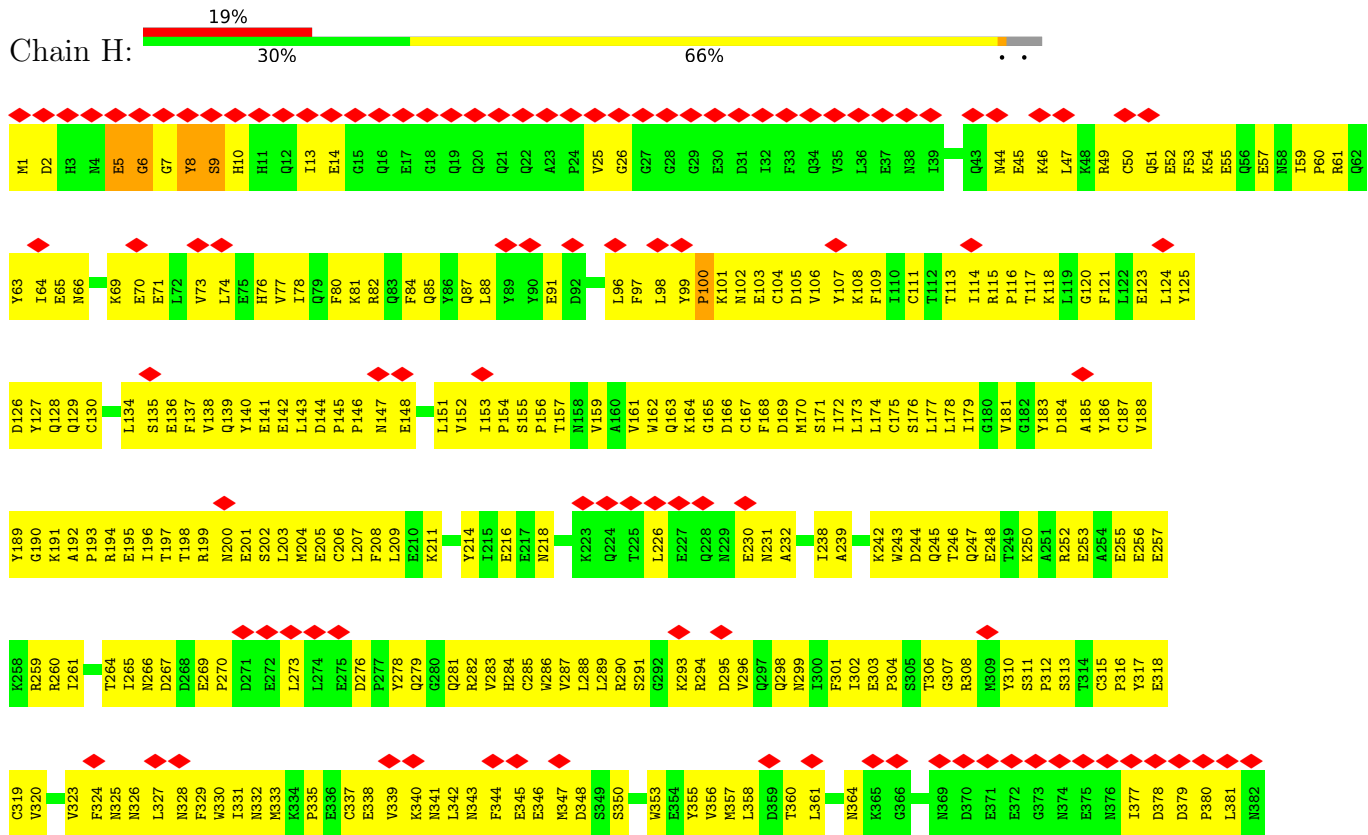
- Molecule 15 is a protein called Coiled-coil domain-containing protein 153.

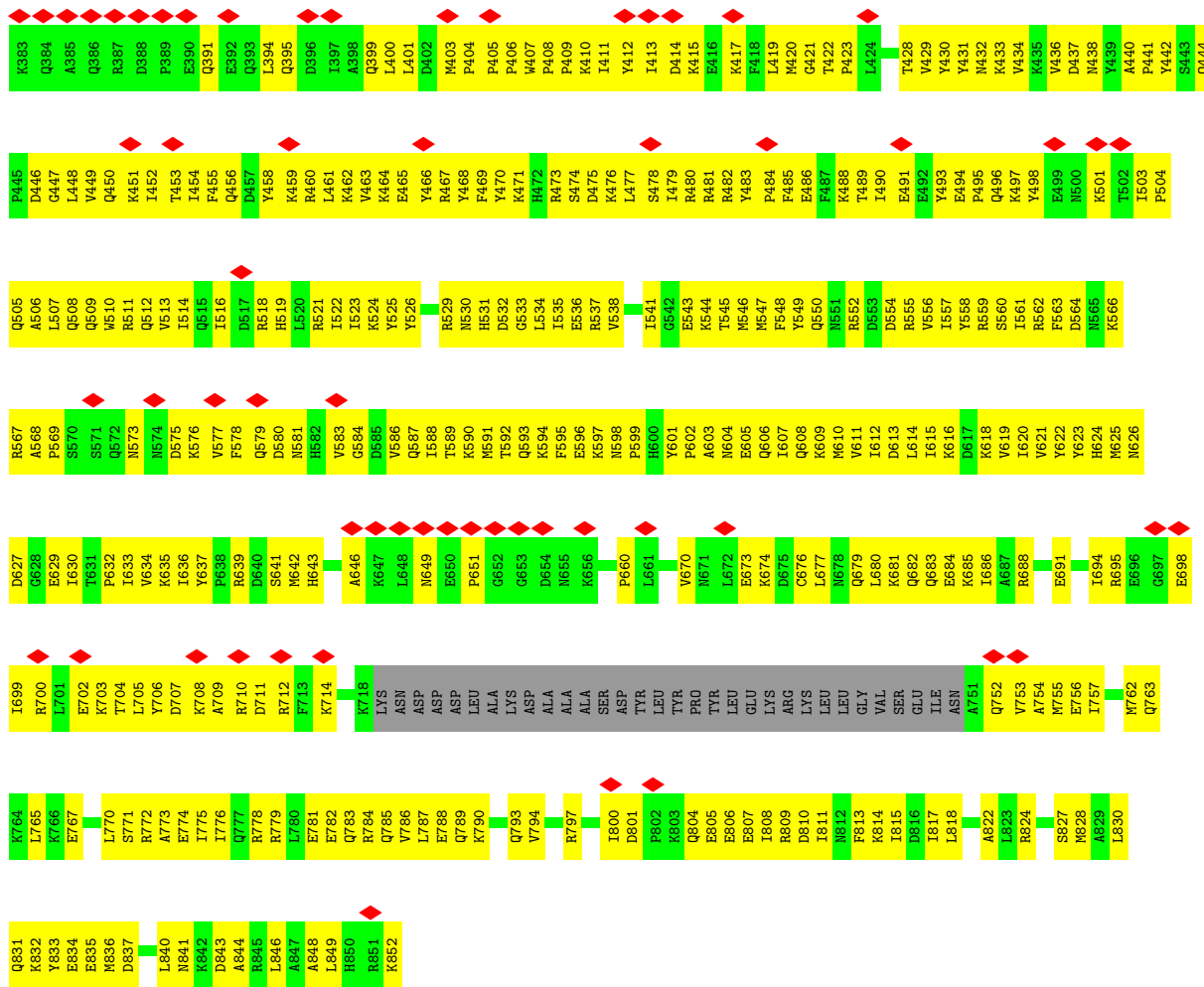
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	S	187	1542	943	274	314	11	0	0
15	s	187	1542	943	274	314	11	0	0

• Molecule 7: Kinase domain protein

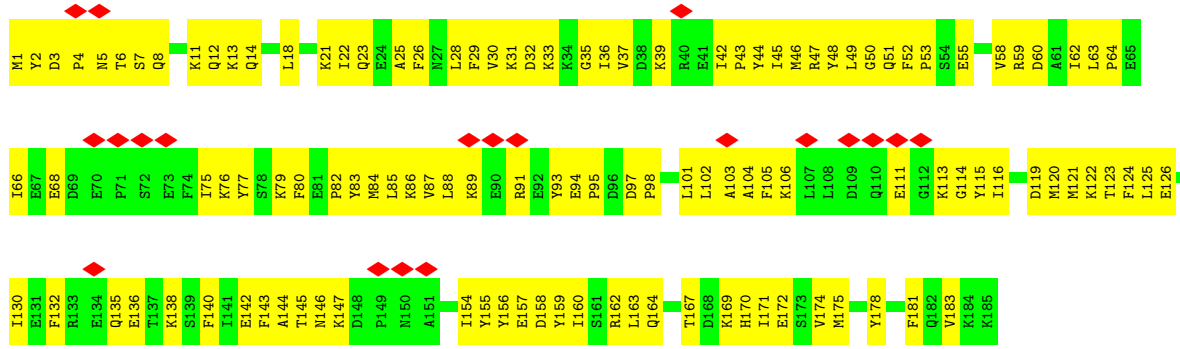


• Molecule 8: Coiled-coil lobo-like protein, putative



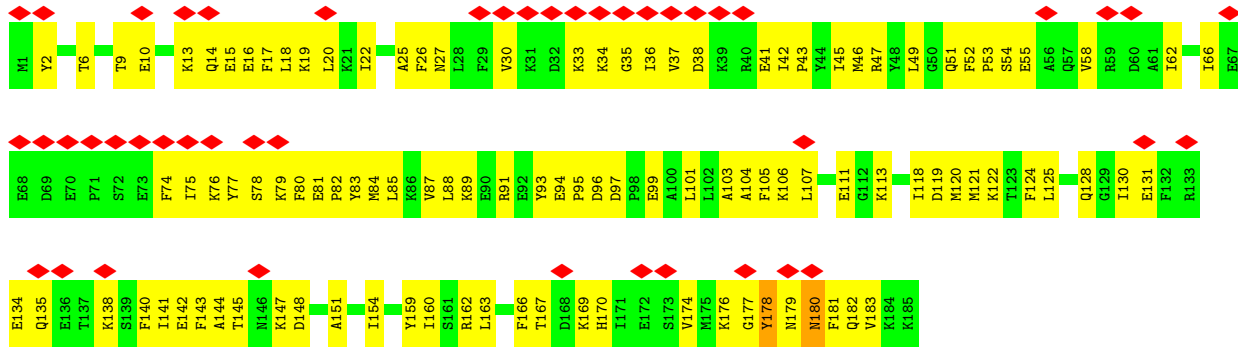


• Molecule 9: EF-hand calcium-binding domain protein

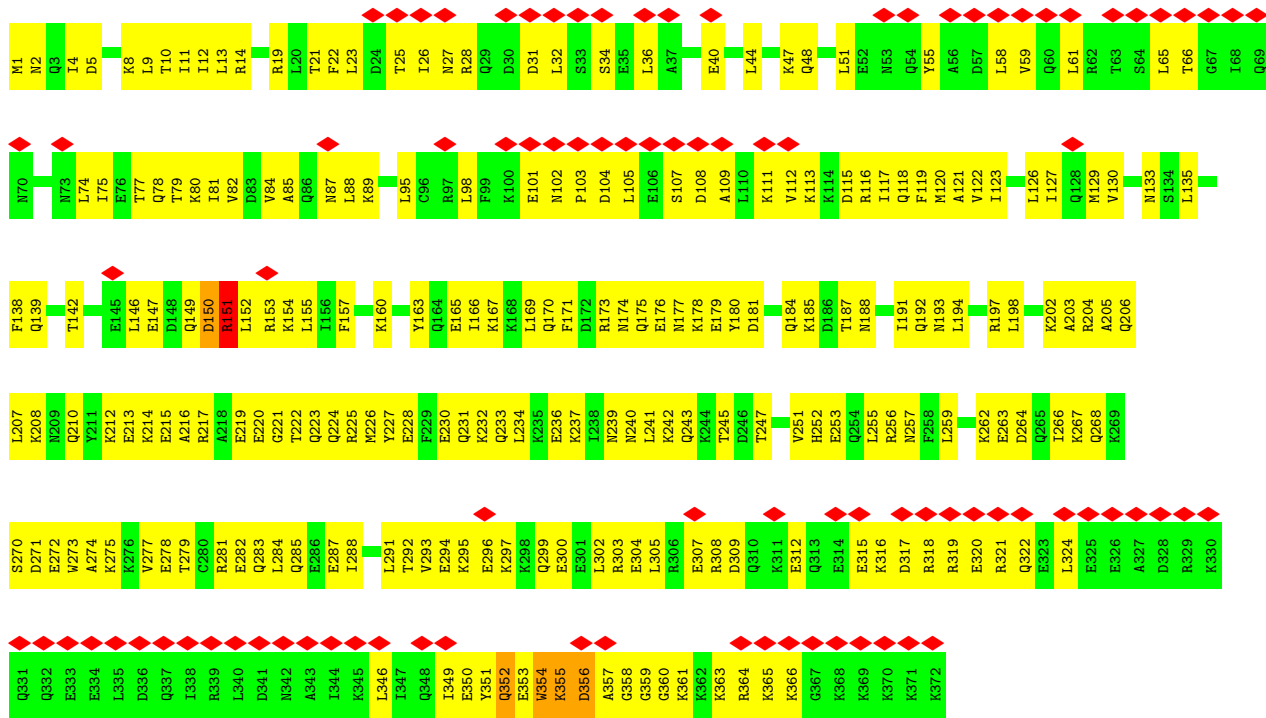


• Molecule 9: EF-hand calcium-binding domain protein

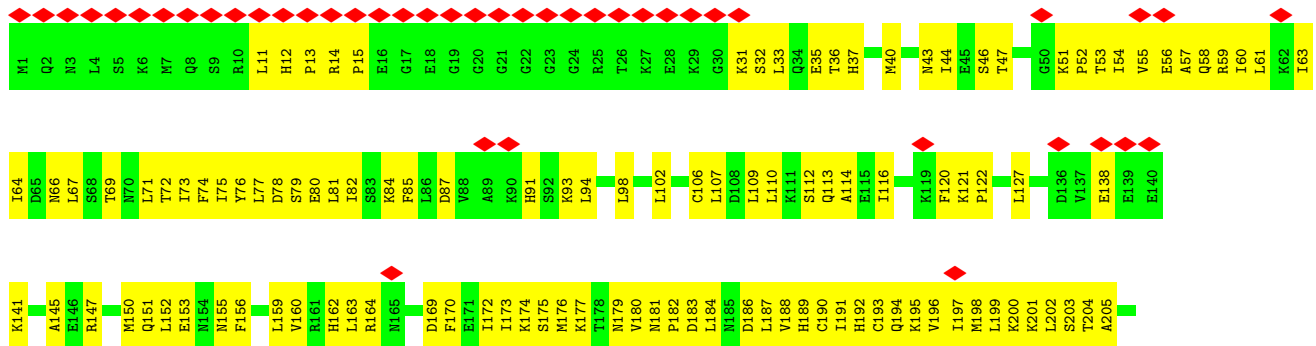


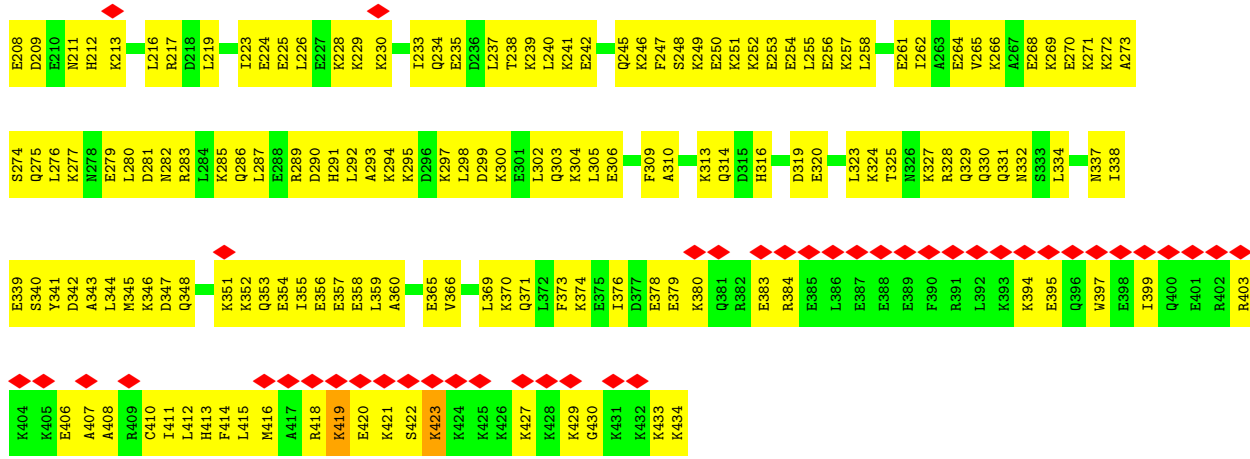


• Molecule 10: Dynein regulatory complex protein 9

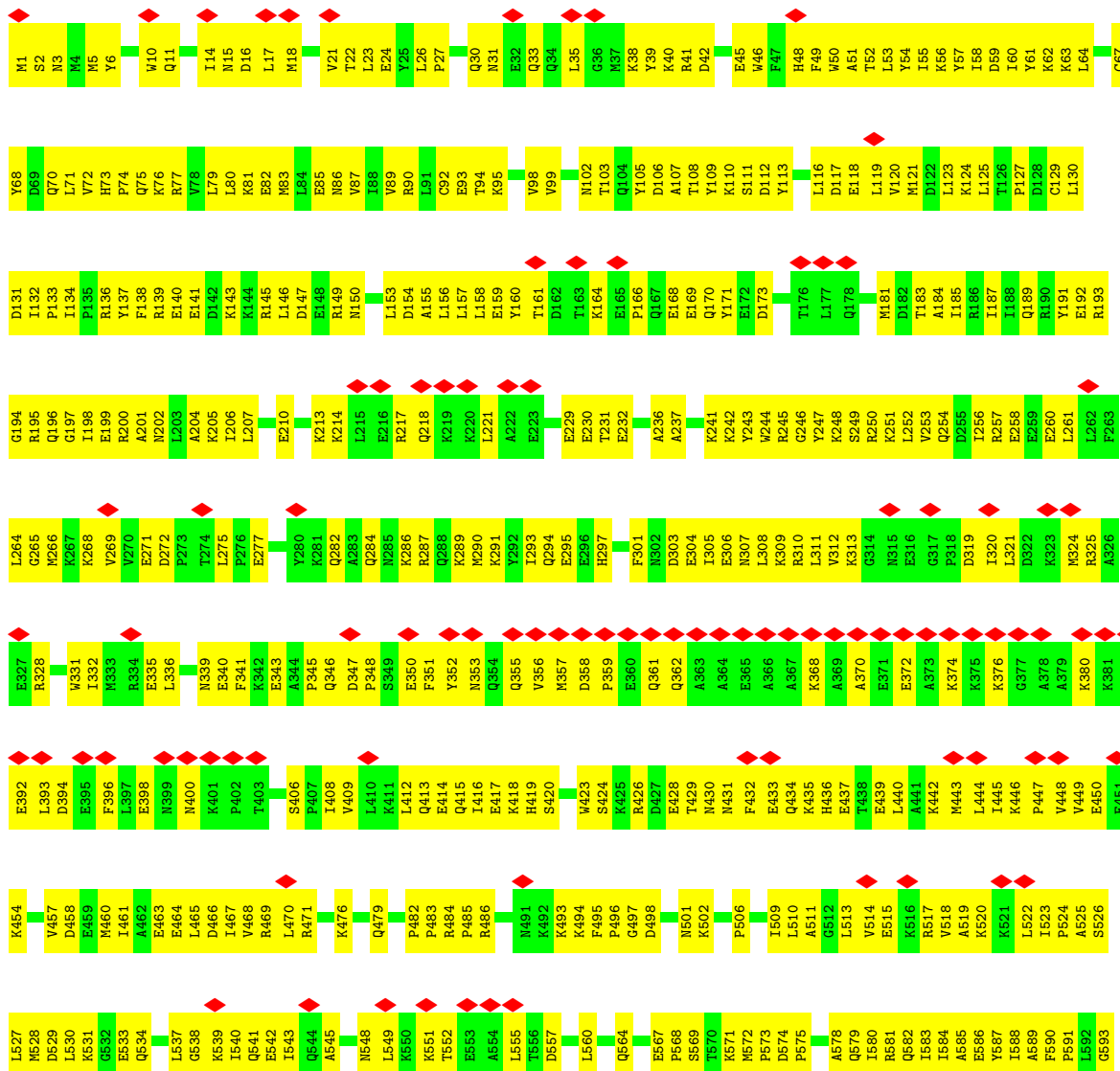


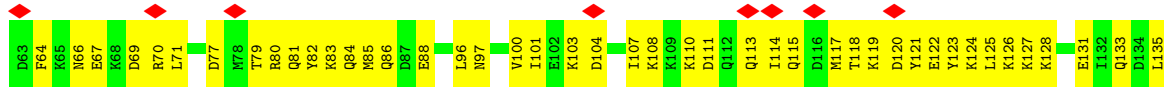
• Molecule 11: Dynein regulatory complex protein 10



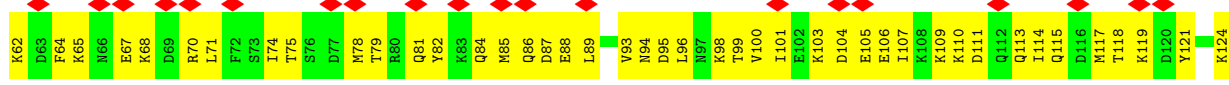
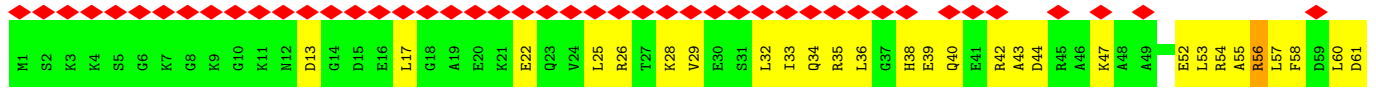


● Molecule 12: AAA family ATPase CDC48 subfamily protein





• Molecule 15: Coiled-coil domain-containing protein 153



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	211502	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.174	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0217	Depositor
Map size (\AA)	706.92, 578.14, 569.92	wwPDB
Map dimensions	258, 211, 208	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.74, 2.74, 2.74	Depositor

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.14	0/2485	0.37	0/3301
2	B	0.21	0/2356	0.52	3/3138 (0.1%)
3	C	0.13	0/4482	0.31	0/6008
4	D	0.16	0/2487	0.38	0/3314
5	E	0.20	0/2470	0.43	2/3290 (0.1%)
6	F	0.12	0/3768	0.30	0/5071
7	G	0.13	0/2821	0.33	1/3772 (0.0%)
8	H	0.68	8/6994 (0.1%)	0.46	4/9419 (0.0%)
9	I	0.08	0/1586	0.22	0/2128
9	i	0.09	0/1586	0.26	0/2128
10	J	0.41	2/3173 (0.1%)	0.66	5/4219 (0.1%)
11	K	0.15	0/3620	0.36	0/4803
12	L	0.19	1/7234 (0.0%)	0.34	3/9693 (0.0%)
13	P	0.15	0/2623	0.39	1/3530 (0.0%)
14	Q	1.30	6/1705 (0.4%)	0.56	3/2290 (0.1%)
14	R	0.15	0/1705	0.36	0/2290
15	S	0.11	0/1552	0.27	0/2057
15	s	0.14	0/1552	0.39	1/2057 (0.0%)
All	All	0.38	17/54199 (0.0%)	0.40	23/72508 (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
2	B	0	1
4	D	0	1
8	H	0	2
9	i	0	2
10	J	0	2
11	K	0	3
14	Q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	12

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	8	TYR	CD2-CE2	26.99	2.19	1.38
14	Q	38	PHE	CD1-CE1	26.10	2.17	1.38
8	H	8	TYR	CD1-CE1	25.82	2.16	1.38
14	Q	38	PHE	CD2-CE2	24.22	2.11	1.38
14	Q	38	PHE	CE1-CZ	23.46	2.09	1.38

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	355	LYS	CA-C-N	22.24	155.12	121.99
10	J	355	LYS	C-N-CA	22.24	155.12	121.99
8	H	5	GLU	CA-C-N	16.60	153.94	121.41
8	H	5	GLU	C-N-CA	16.60	153.94	121.41
12	L	765	PRO	N-CD-CG	-13.65	82.72	103.20

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	229	TYR	Peptide
4	D	113	HIS	Peptide
8	H	7	GLY	Peptide
8	H	9	SER	Peptide
10	J	352	GLN	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	2460	0	2474	427	0
2	B	2329	0	2374	479	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	4433	0	4443	690	0
4	D	2461	2515	2515	127	0
5	E	2443	2509	2509	212	0
6	F	3714	0	3768	614	0
7	G	2780	0	2863	565	0
8	H	6857	0	6740	1012	0
9	I	1553	0	1535	202	0
9	i	1553	0	1535	244	0
10	J	3151	0	3245	482	0
11	K	3588	0	3732	547	0
12	L	7102	0	7205	1012	0
13	P	2576	0	2526	614	0
14	Q	1679	0	1659	350	0
14	R	1679	0	1659	390	0
15	S	1542	0	1557	191	0
15	s	1542	0	1557	199	0
All	All	53442	5024	53896	7091	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 66.

The worst 5 of 7091 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)
8:H:8:TYR:CD2	8:H:8:TYR:CG	1.74	1.67
8:H:8:TYR:CG	8:H:8:TYR:CD1	1.74	1.66
8:H:8:TYR:CE1	8:H:8:TYR:CZ	1.83	1.59
8:H:8:TYR:CZ	8:H:8:TYR:CE2	1.83	1.59
8:H:6:GLY:N	8:H:6:GLY:CA	1.70	1.55

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	288/826 (35%)	275 (96%)	11 (4%)	2 (1%)	18	56
2	B	274/506 (54%)	243 (89%)	31 (11%)	0	100	100
3	C	529/575 (92%)	505 (96%)	24 (4%)	0	100	100
4	D	290/472 (61%)	284 (98%)	5 (2%)	1 (0%)	36	72
5	E	289/468 (62%)	277 (96%)	12 (4%)	0	100	100
6	F	459/461 (100%)	424 (92%)	35 (8%)	0	100	100
7	G	343/345 (99%)	321 (94%)	22 (6%)	0	100	100
8	H	816/852 (96%)	729 (89%)	87 (11%)	0	100	100
9	I	183/185 (99%)	181 (99%)	2 (1%)	0	100	100
9	i	183/185 (99%)	174 (95%)	9 (5%)	0	100	100
10	J	370/372 (100%)	349 (94%)	20 (5%)	1 (0%)	36	72
11	K	432/434 (100%)	394 (91%)	37 (9%)	1 (0%)	43	78
12	L	860/862 (100%)	823 (96%)	37 (4%)	0	100	100
13	P	303/794 (38%)	283 (93%)	20 (7%)	0	100	100
14	Q	200/202 (99%)	181 (90%)	18 (9%)	1 (0%)	24	63
14	R	200/202 (99%)	180 (90%)	20 (10%)	0	100	100
15	S	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
15	s	185/187 (99%)	183 (99%)	2 (1%)	0	100	100
All	All	6389/8115 (79%)	5981 (94%)	402 (6%)	6 (0%)	49	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	LYS
4	D	114	LEU
11	K	419	LYS
1	A	236	GLU
10	J	150	ASP

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	
1	A	238/766 (31%)	238 (100%)	0	100	100
2	B	258/473 (54%)	257 (100%)	1 (0%)	84	84
3	C	499/540 (92%)	499 (100%)	0	100	100
4	D	272/438 (62%)	272 (100%)	0	100	100
5	E	272/434 (63%)	272 (100%)	0	100	100
6	F	414/414 (100%)	414 (100%)	0	100	100
7	G	310/310 (100%)	310 (100%)	0	100	100
8	H	759/786 (97%)	759 (100%)	0	100	100
9	I	170/170 (100%)	170 (100%)	0	100	100
9	i	170/170 (100%)	170 (100%)	0	100	100
10	J	350/350 (100%)	347 (99%)	3 (1%)	70	79
11	K	403/403 (100%)	403 (100%)	0	100	100
12	L	776/776 (100%)	776 (100%)	0	100	100
13	P	284/733 (39%)	284 (100%)	0	100	100
14	Q	189/189 (100%)	189 (100%)	0	100	100
14	R	189/189 (100%)	189 (100%)	0	100	100
15	S	172/172 (100%)	172 (100%)	0	100	100
15	s	172/172 (100%)	171 (99%)	1 (1%)	78	83
All	All	5897/7485 (79%)	5892 (100%)	5 (0%)	87	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	110	ASP
10	J	150	ASP
10	J	151	ARG
10	J	153	ARG
15	s	56	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
8	H	682	GLN

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Mol	Chain	Res	Type
12	L	307	ASN
10	J	192	GLN
12	L	11	GLN
12	L	655	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

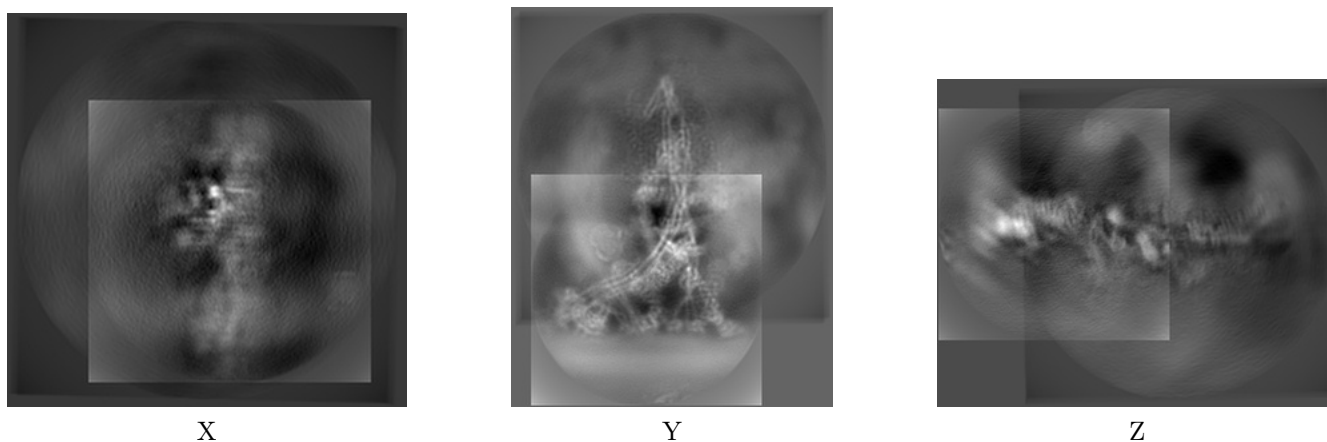
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41251. These allow visual inspection of the internal detail of the map and identification of artifacts.

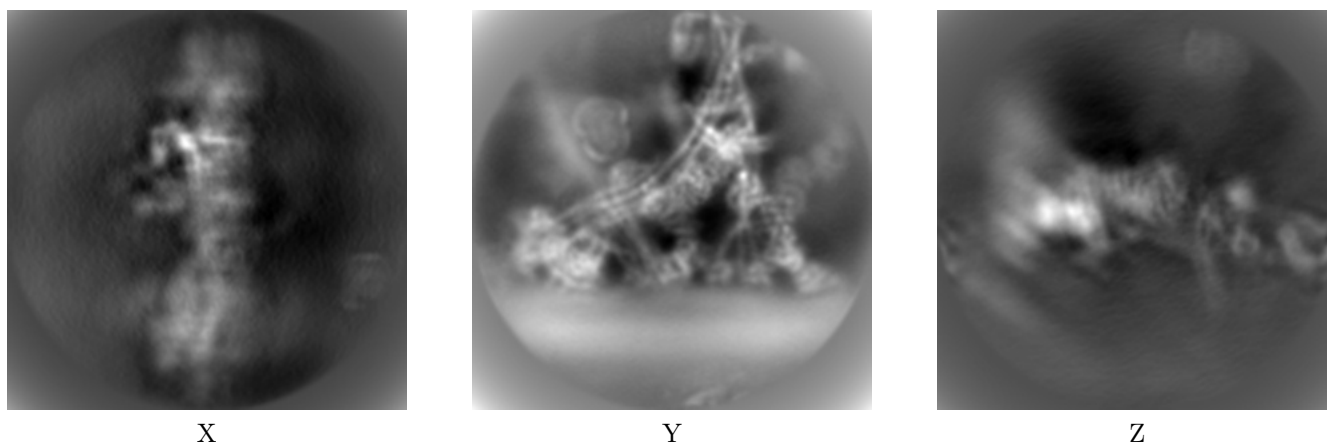
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



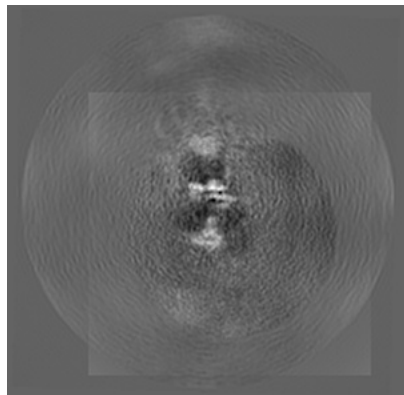
6.1.2 Raw map



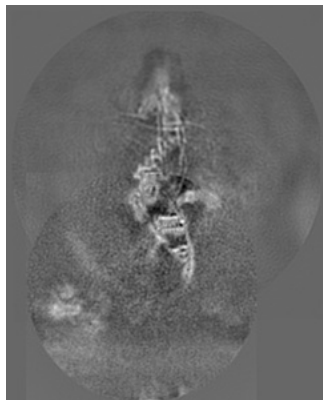
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

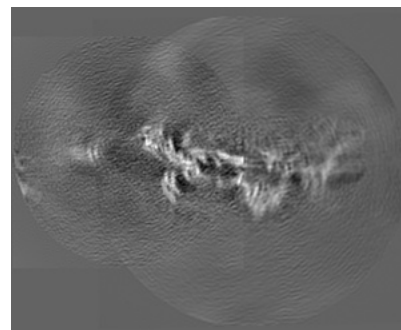
6.2.1 Primary map



X Index: 129

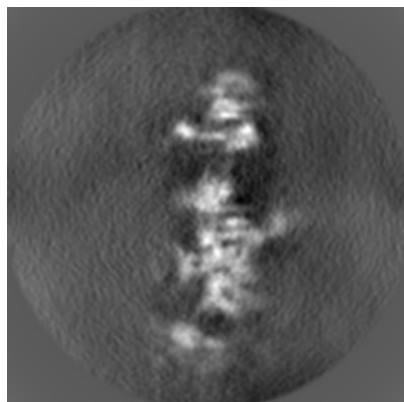


Y Index: 105

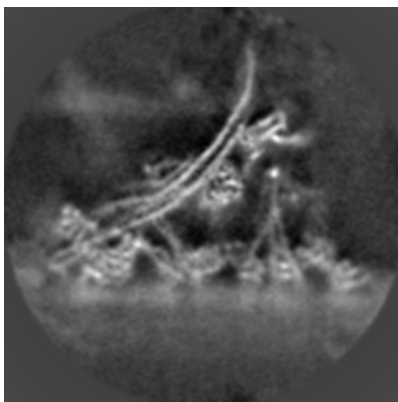


Z Index: 104

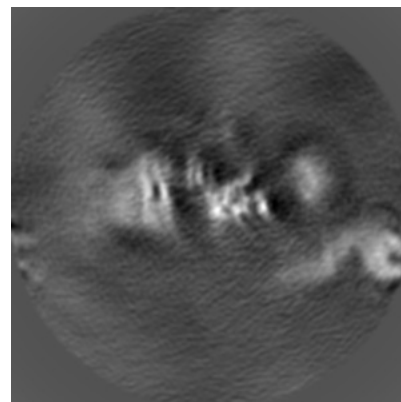
6.2.2 Raw map



X Index: 75



Y Index: 75

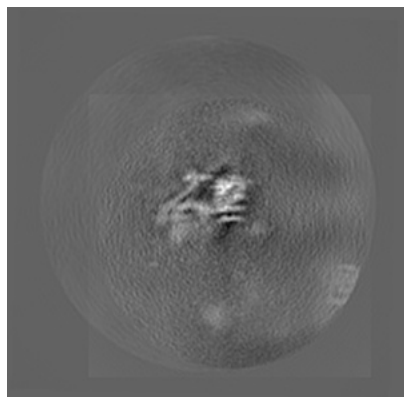


Z Index: 75

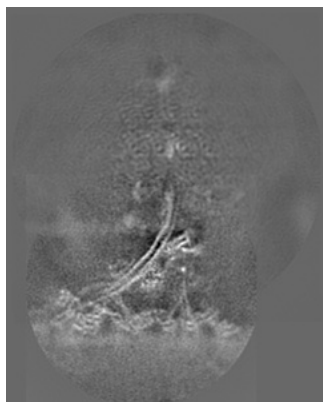
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

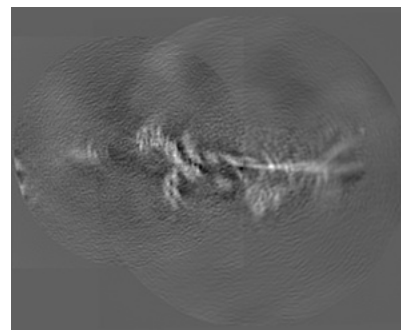
6.3.1 Primary map



X Index: 105

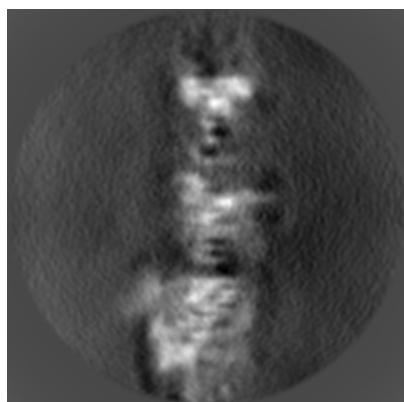


Y Index: 117

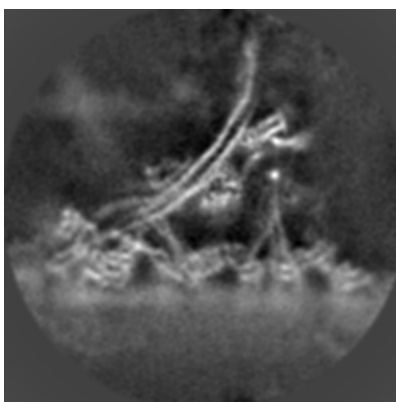


Z Index: 102

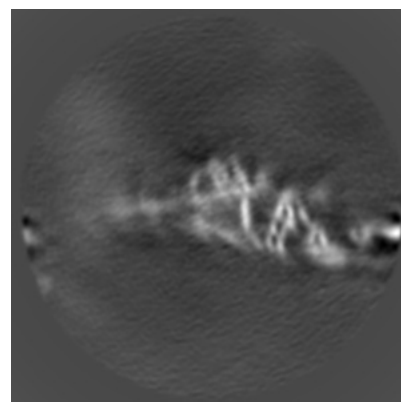
6.3.2 Raw map



X Index: 56



Y Index: 74

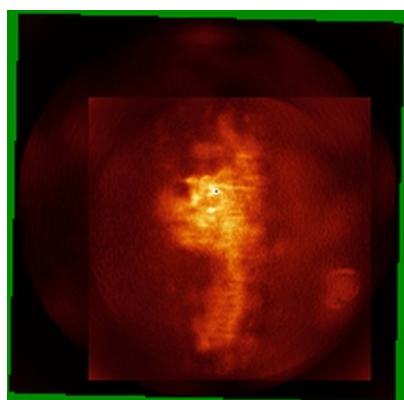


Z Index: 101

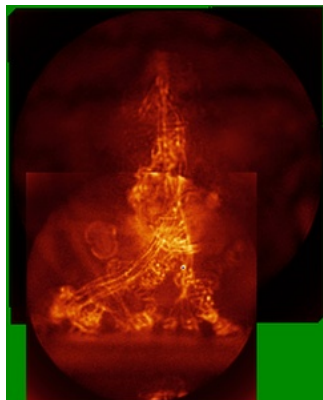
The images above show the largest variance slices of the map in three orthogonal directions.

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

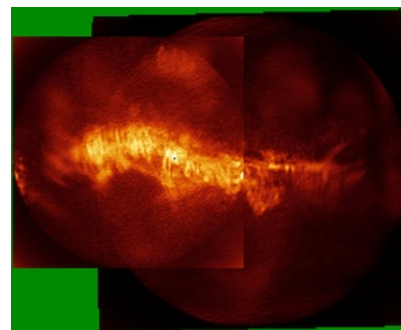
6.4.1 Primary map



X

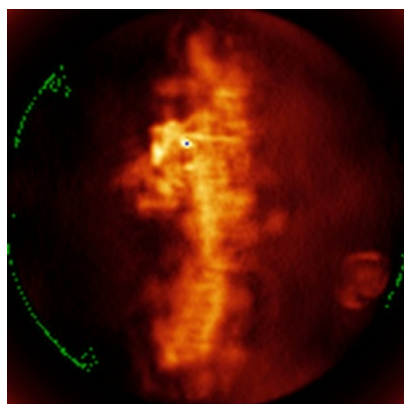


Y

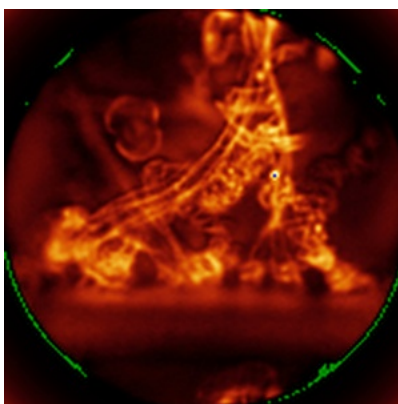


Z

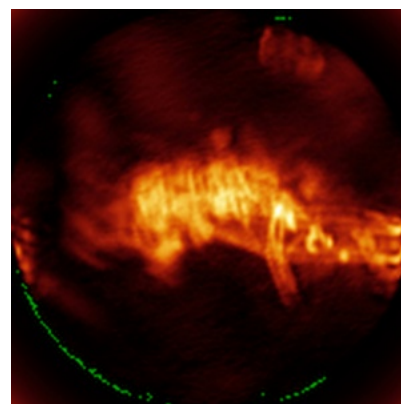
6.4.2 Raw map



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 0.0217. 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.

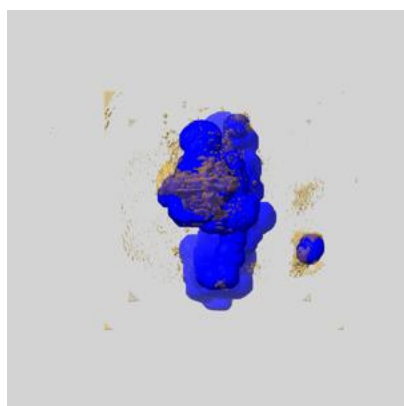
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

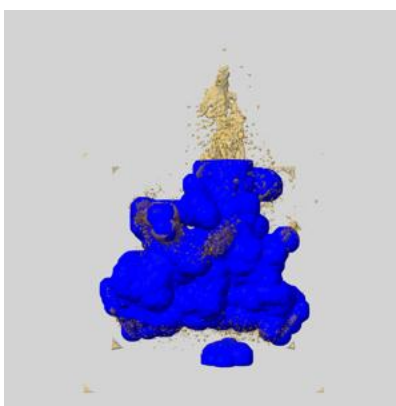
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

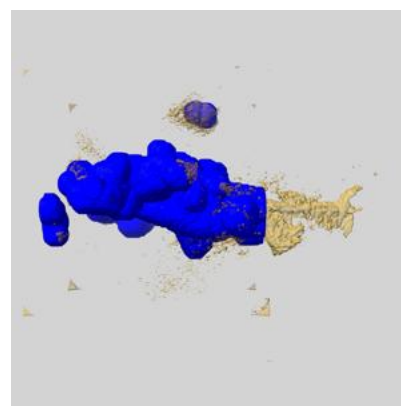
6.6.1 emd_41251_msk_1.map [i](#)



X



Y

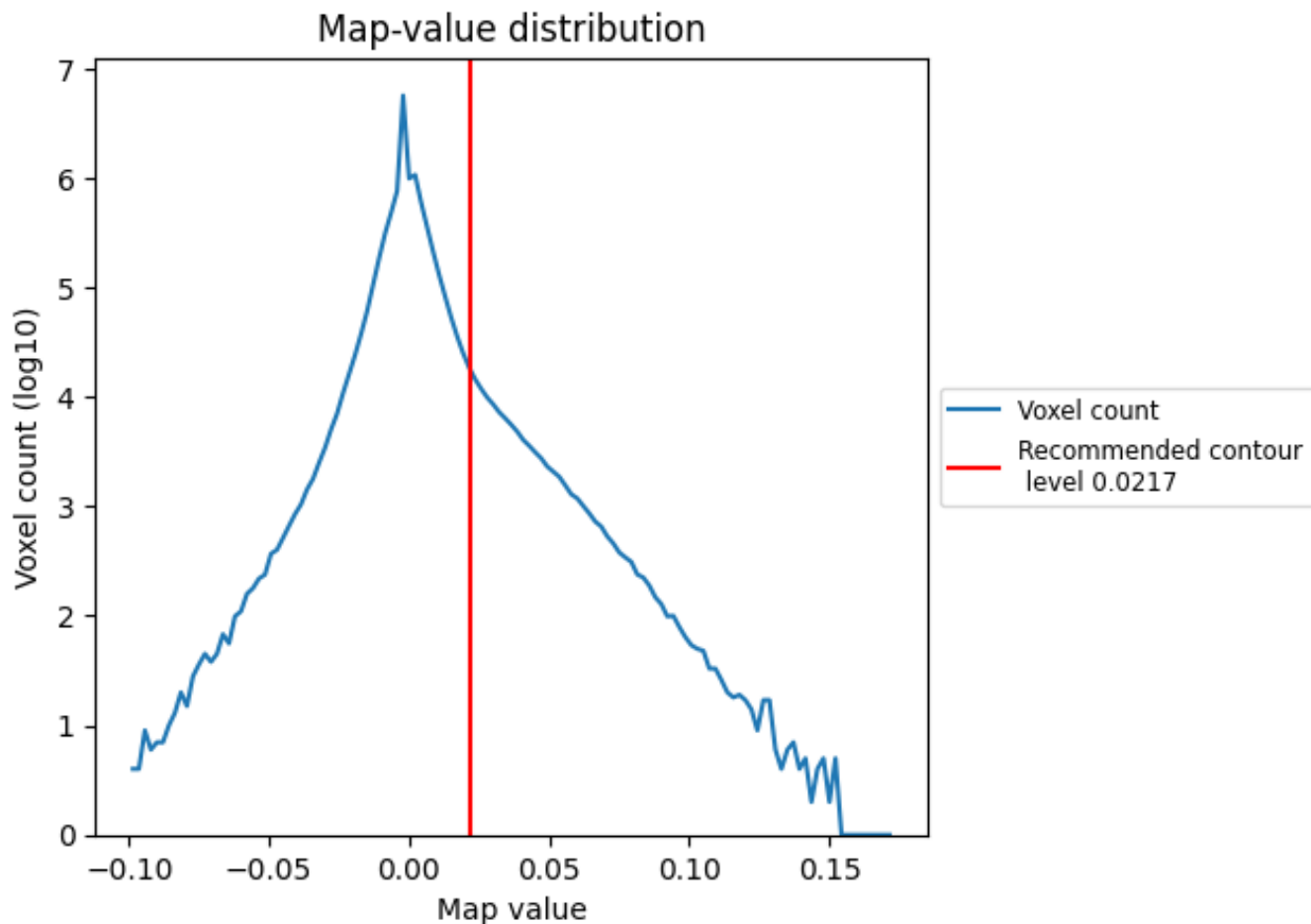


Z

7 Map analysis [i](#)

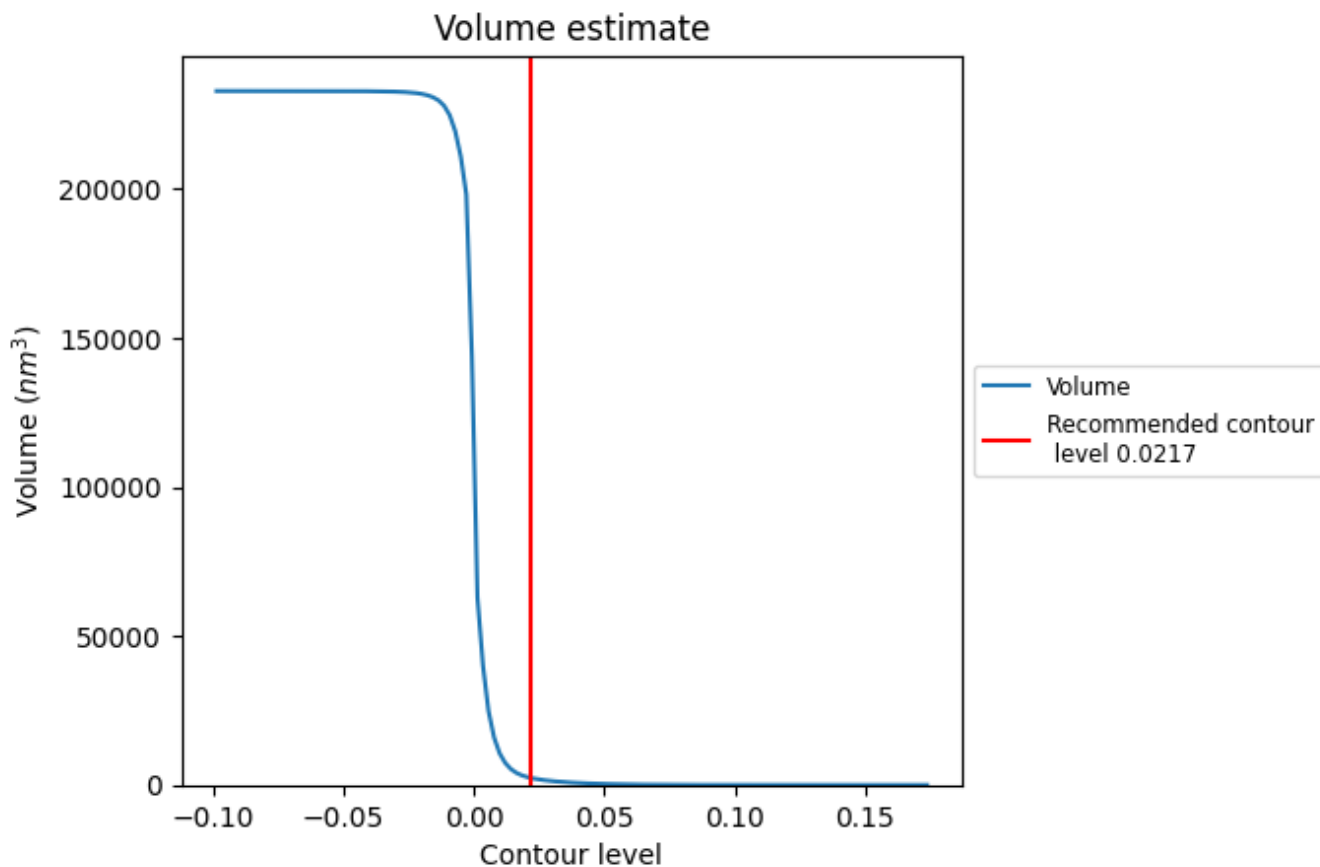
This section contains the results of statistical analysis of the map.

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 2392 nm³; this corresponds to an approximate mass of 2161 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

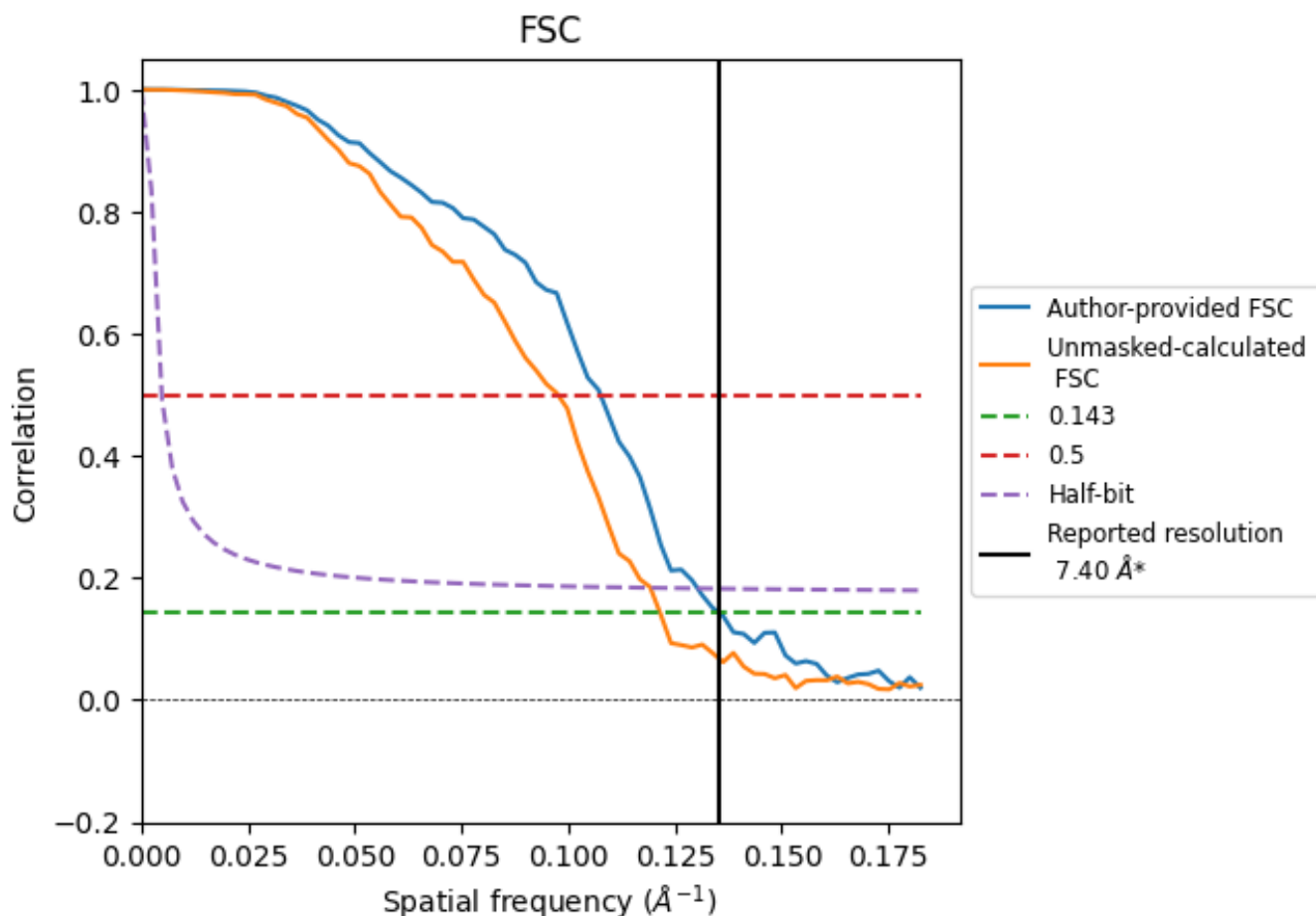
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation [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 0.135 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	7.40
Author-provided FSC curve	7.39	9.30	7.67	-
Unmasked-calculated*	8.23	10.25	8.38	-

*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-41251 and PDB model 8TH8. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

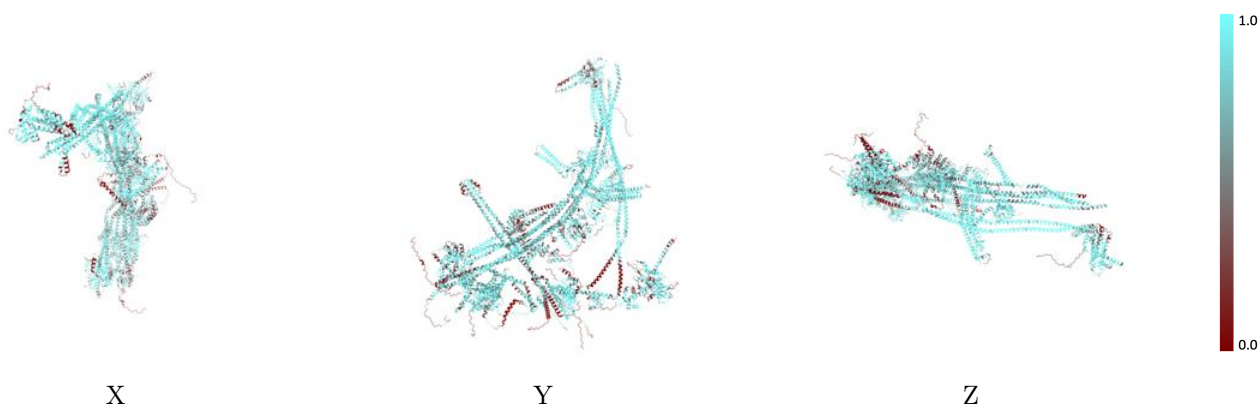
This section was not generated.

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



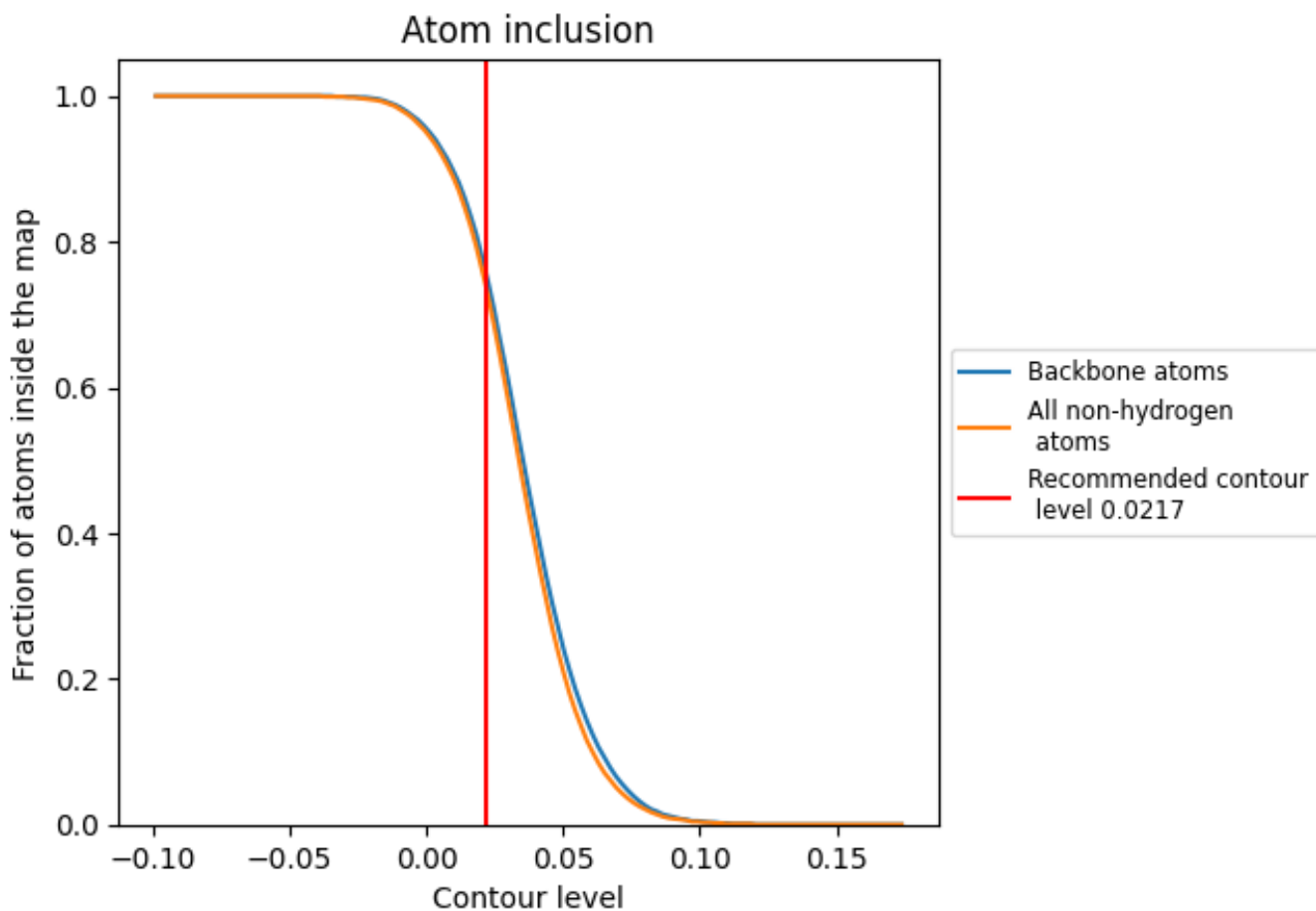
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0217).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 74% 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 (0.0217) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7420	 0.0870
A	 0.8020	 0.1410
B	 0.6920	 0.1080
C	 0.8960	 0.1310
D	 0.7720	 0.1100
E	 0.7300	 0.0830
F	 0.5790	 0.0990
G	 0.8340	 0.0890
H	 0.7290	 0.0720
I	 0.8710	 0.0610
J	 0.6900	 0.0730
K	 0.7400	 0.0670
L	 0.7820	 0.0980
P	 0.7140	 0.0590
Q	 0.6980	 0.0600
R	 0.7690	 0.0630
S	 0.5770	 0.0790
i	 0.7130	 0.0500
s	 0.4810	 0.0570

