



Full wwPDB EM Validation Report ⓘ

Jan 1, 2025 – 10:55 AM EST

PDB ID : 8TID
EMDB ID : EMD-41284
Title : Combined linker domain of N-DRC and associated proteins Tetrahymena
Authors : Ghanaeian, A.G.; Majhi, S.M.; McCaffrey, C.M.; Nami, B.N.; Black, C.B.;
Yang, S.K.; Legal, T.L.; Papoulas, O.P.; Janowska, M.J.; Valente-Paterno,
M.V.; Marcotte, E.M.; Wloga, D.W.; Bui, K.H.
Deposited on : 2023-07-19
Resolution : 3.60 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

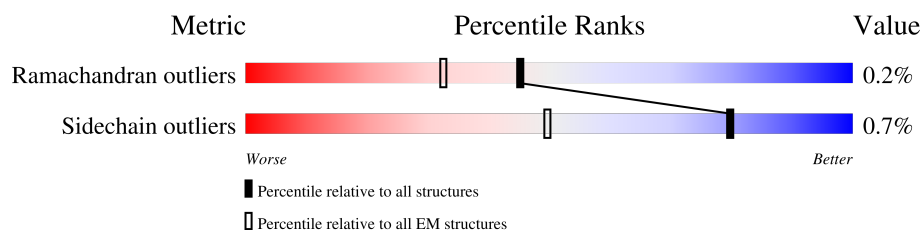
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

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 3.60 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)
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	826	
2	B	506	
3	C	575	
4	D	472	
5	E	468	
6	F	461	
7	G	345	
8	H	852	
9	I	185	

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Mol	Chain	Length	Quality of chain
9	i	185	
10	J	372	
11	K	434	
12	L	862	
13	M	644	
14	N	963	
14	n	963	
15	O	893	
15	o	893	
16	P	794	
17	Q	202	
17	R	202	
18	S	187	
18	s	187	
19	T	361	
20	U	597	
20	V	597	
21	W	1308	
22	Z	1079	
23	g	195	
24	w	1293	

2 Entry composition [i](#)

There are 24 unique types of molecules in this entry. The entry contains 123416 atoms, of which 12979 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
1	A	458	Total	C	N	O	S	0	0
			3929	2479	695	734	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	460	Total	C	N	O	S	0	0
			3873	2427	697	733	16		

- Molecule 3 is a protein called LRRC48 protein.

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	461	Total	C	H	N	O	S	0	0
			6572	2431	2704	672	756	9		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	464	Total	C	H	N	O	S	0	0
			6424	2418	2565	678	754	9		

- Molecule 6 is a protein called Flagellar associated protein.

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

- Molecule 7 is a protein called Kinase domain protein.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 13 is a protein called Cilia- and flagella-associated protein 91.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	164	Total	C	N	O	S	0	0
			1373	851	259	260	3		

- Molecule 14 is a protein called Flagella associated protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	434	Total	C	H	N	O	S	0	0
			5707	2237	2099	650	709	12		
14	n	208	Total	C	H	N	O	S	0	0
			3483	1076	1740	312	352	3		

- Molecule 15 is a protein called Coiled-coil protein, putative.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	430	Total	C	H	N	O	S	0	0
			5711	2223	2107	653	721	7		
15	o	205	Total	C	H	N	O	S	0	0
			3470	1063	1764	302	334	7		

- Molecule 16 is a protein called DUF4201 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	631	Total	C	N	O	S	0	0
			5310	3305	956	1034	15		

- Molecule 17 is a protein called Calmodulin 7-2.

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

- Molecule 18 is a protein called Coiled-coil domain-containing protein 153.

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

- Molecule 19 is a protein called Flagellar associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	335	Total	C	N	O	S	0	0
			2782	1740	489	548	5		

- Molecule 20 is a protein called L-shape (Unknown-protein).

Mol	Chain	Residues	Atoms				AltConf	Trace
20	U	597	Total	C	N	O	0	0
			2985	1791	597	597		
20	V	594	Total	C	N	O	0	0
			2970	1782	594	594		

- Molecule 21 is a protein called WD40 domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	1171	Total	C	N	O	S	0	0
			9536	5994	1665	1830	47		

- Molecule 22 is a protein called EF hand protein.

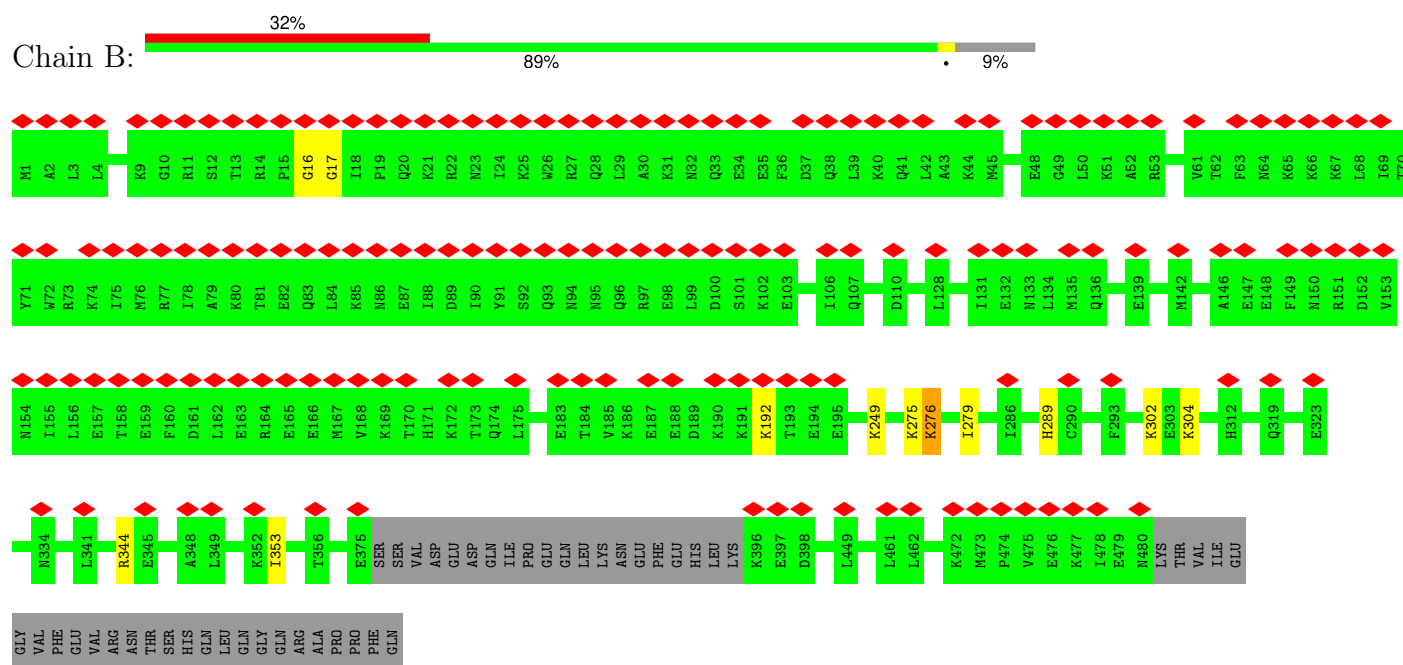
Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	830	Total	C	N	O	S	0	0
			6730	4277	1134	1286	33		

- Molecule 23 is a protein called CFAP20.

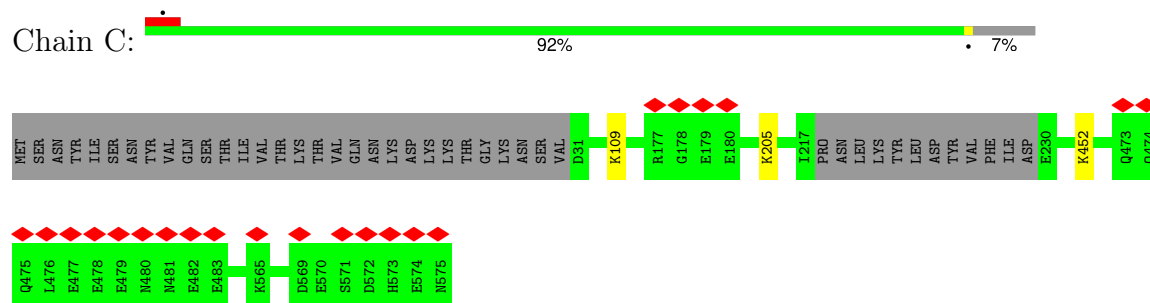
Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	187	Total	C	N	O	S	0	0
			1556	1003	269	277	7		

- Molecule 24 is a protein called WD40 domain protein.

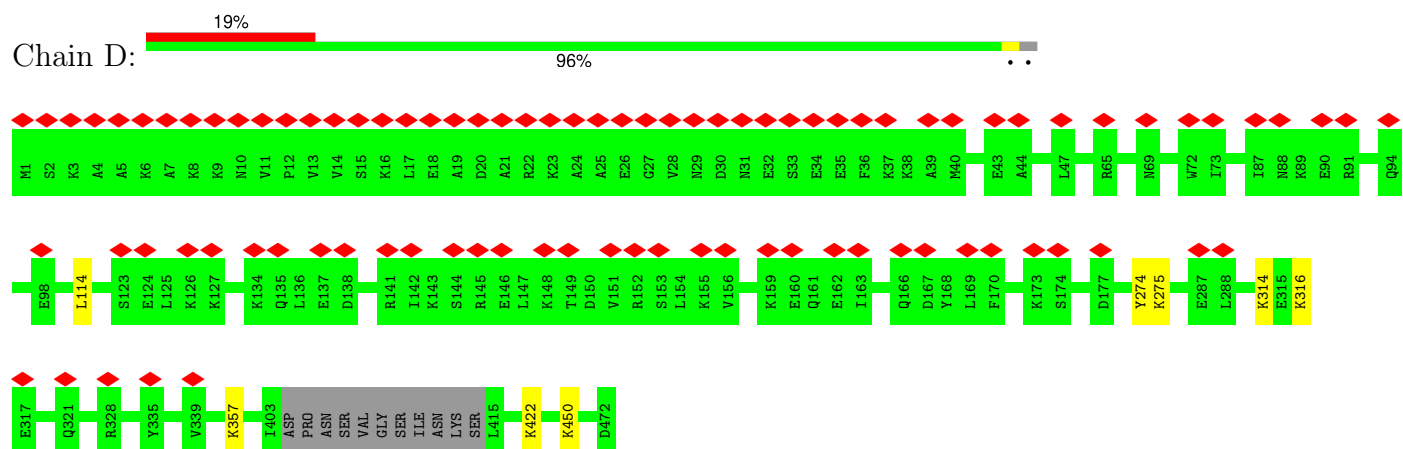
Mol	Chain	Residues	Atoms					AltConf	Trace
24	w	1192	Total	C	N	O	S	0	0
			9832	6196	1691	1893	52		



• Molecule 3: LRRC48 protein

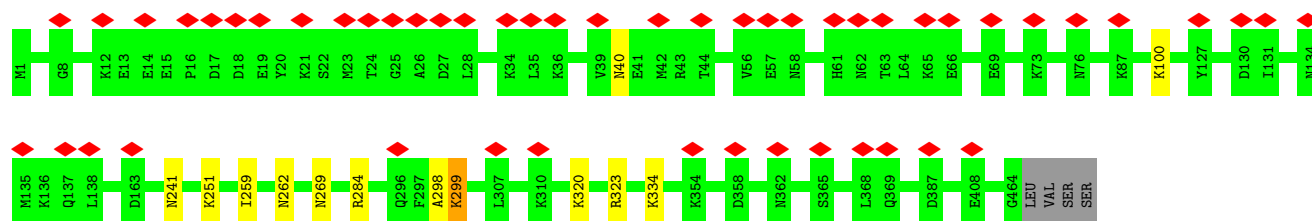


• Molecule 4: Growth-arrest-specific microtubule-binding protein



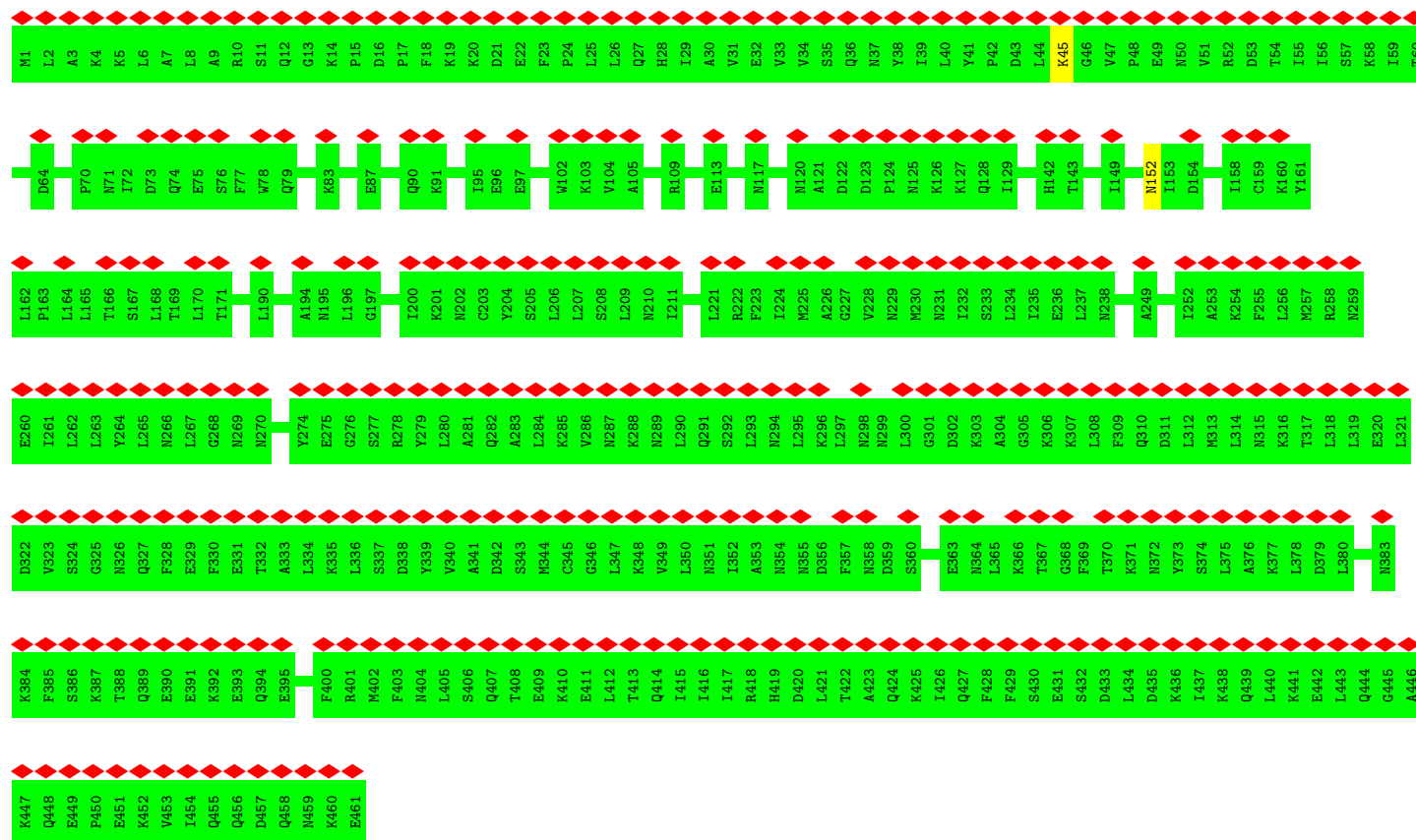
• Molecule 5: Growth-arrest-specific microtubule-binding protein





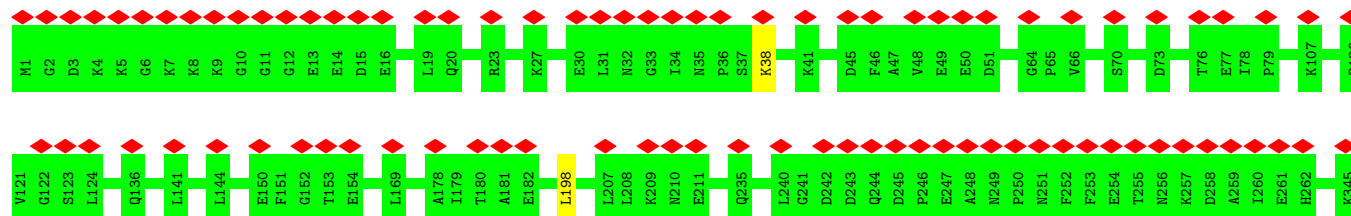
• Molecule 6: Flagellar associated protein

Chain F: 72%
100%



• Molecule 7: Kinase domain protein

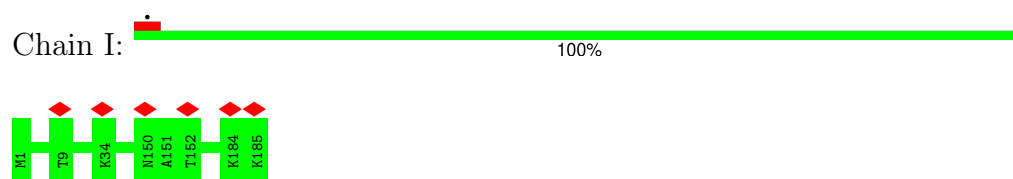
Chain G: 25%
99%



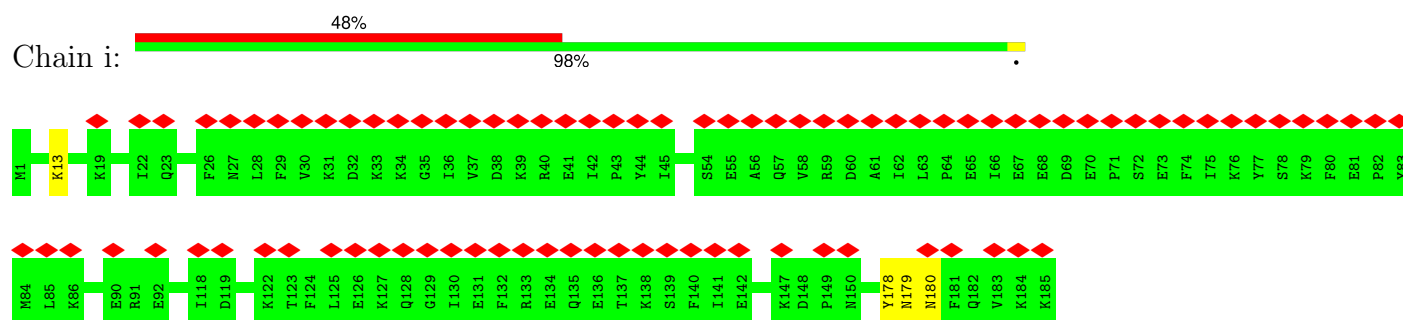
• Molecule 8: Coiled-coil lobo-like protein, putative



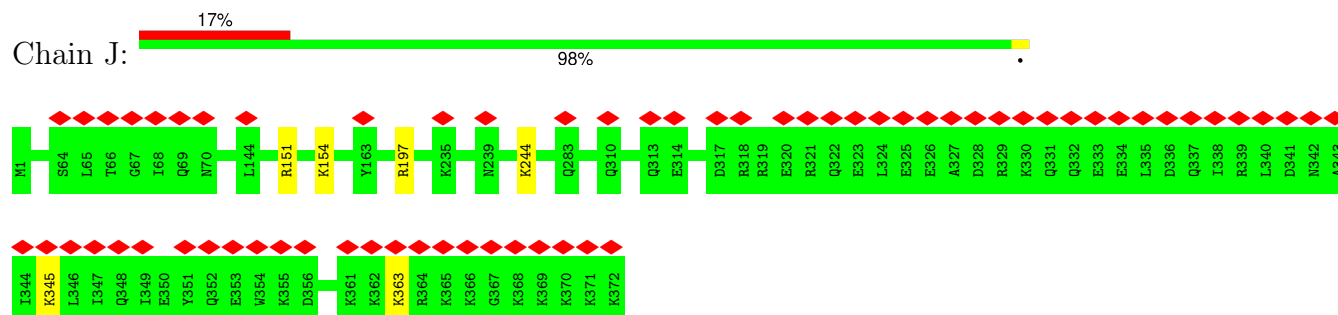
- Molecule 9: EF-hand calcium-binding domain protein



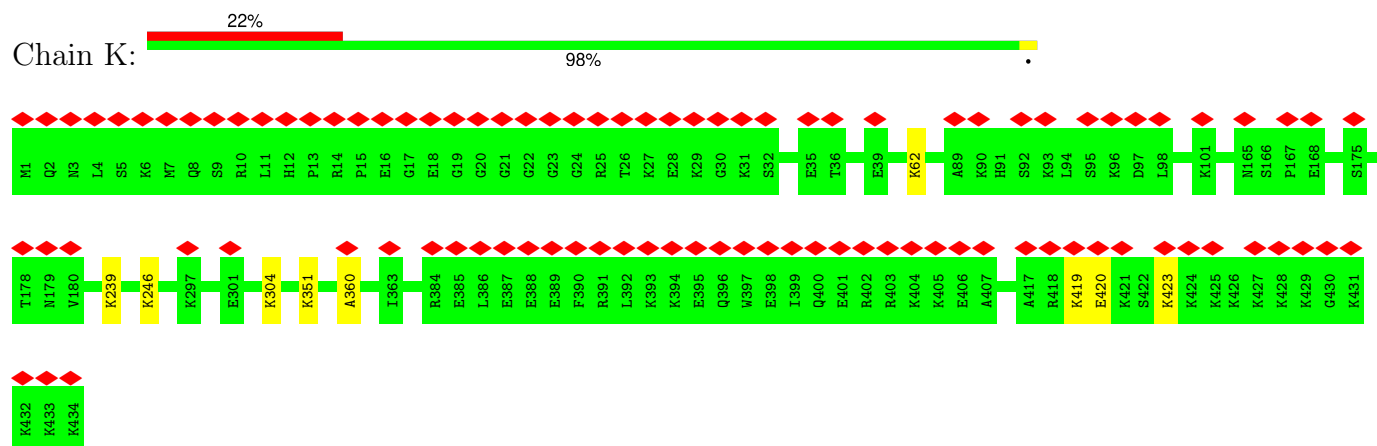
- Molecule 9: EF-hand calcium-binding domain protein



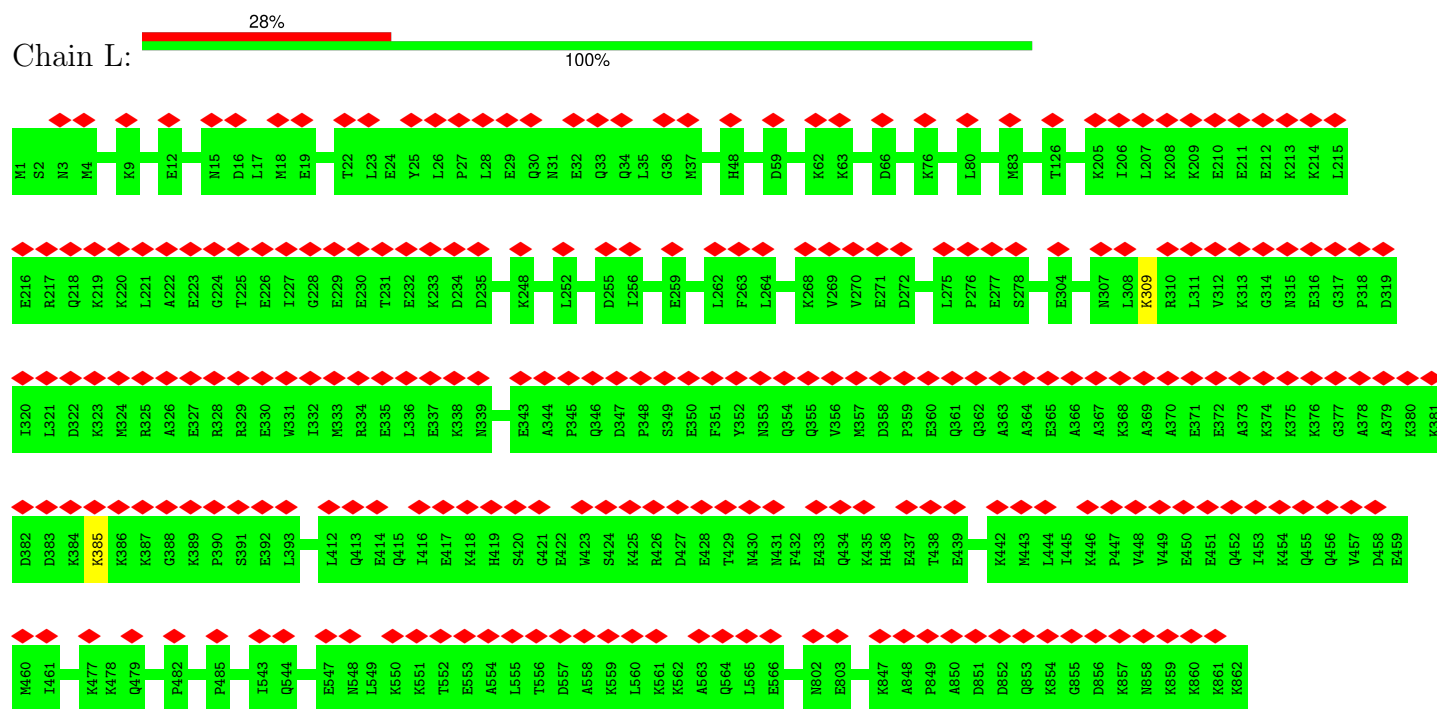
- Molecule 10: Dynein regulatory complex protein 9



- Molecule 11: Dynein regulatory complex protein 10

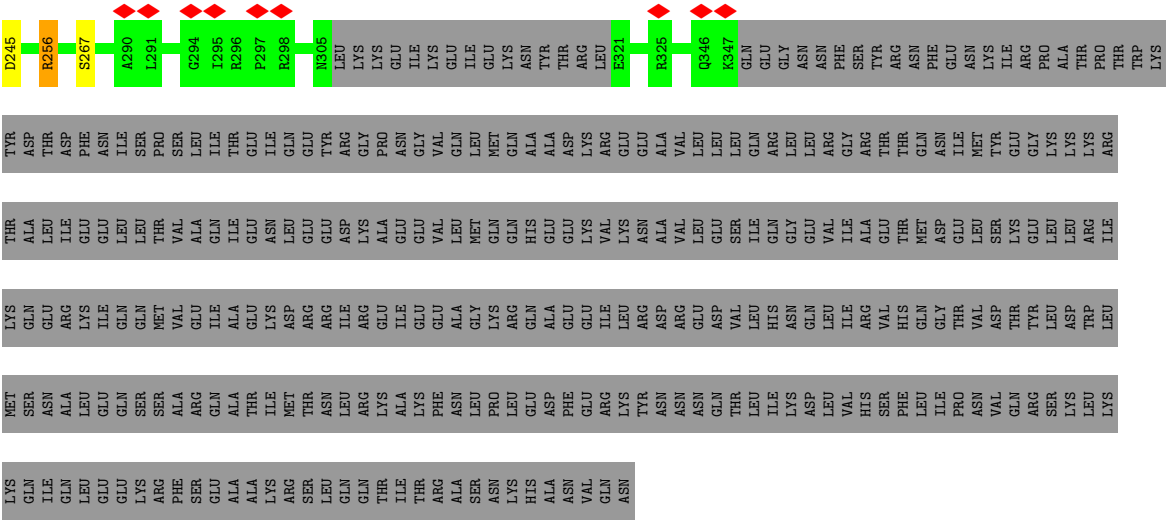


- Molecule 12: AAA family ATPase CDC48 subfamily protein

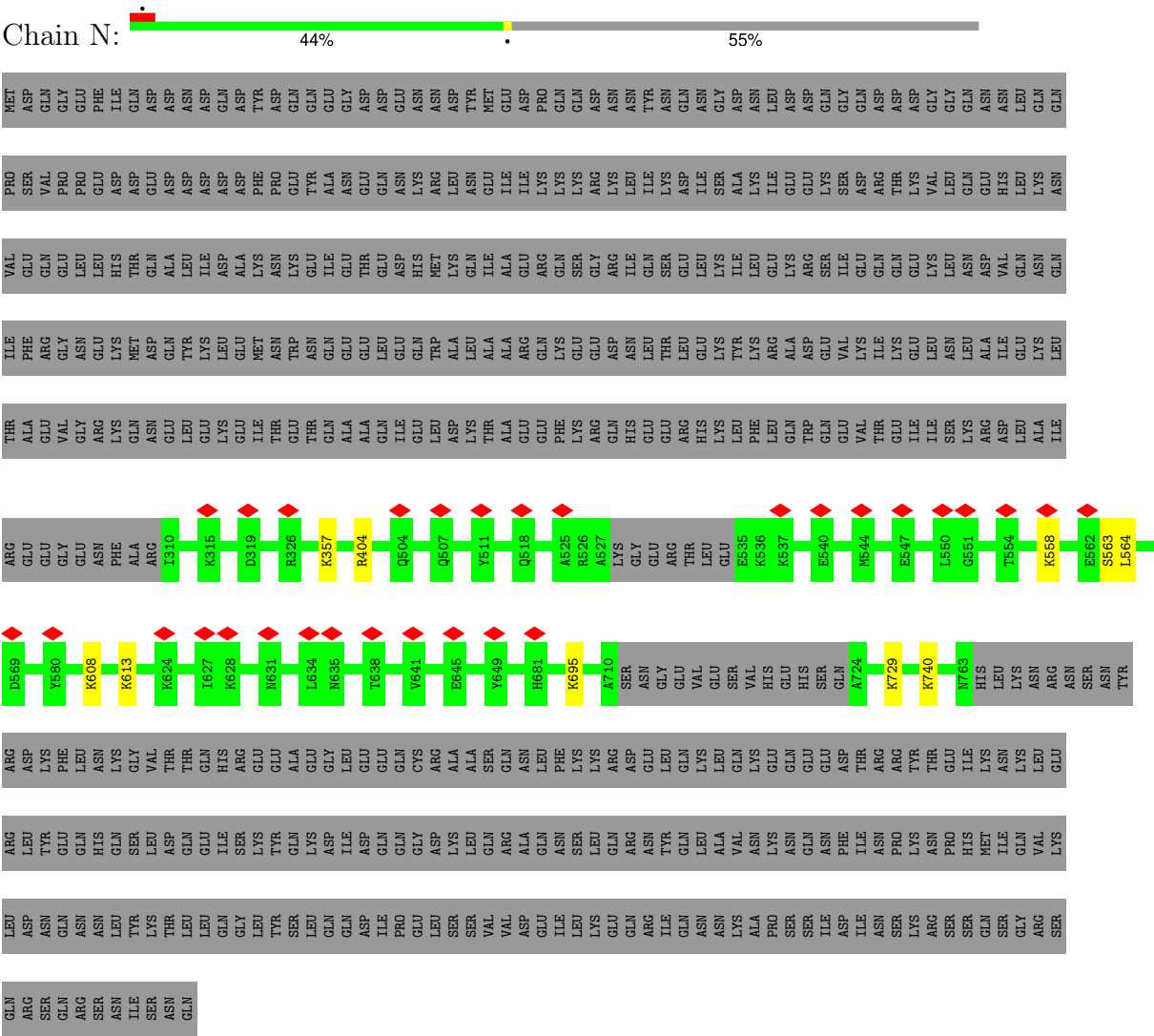


- Molecule 13: Cilia- and flagella-associated protein 91



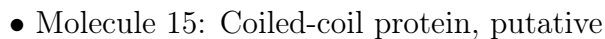


● Molecule 14: Flagella associated protein

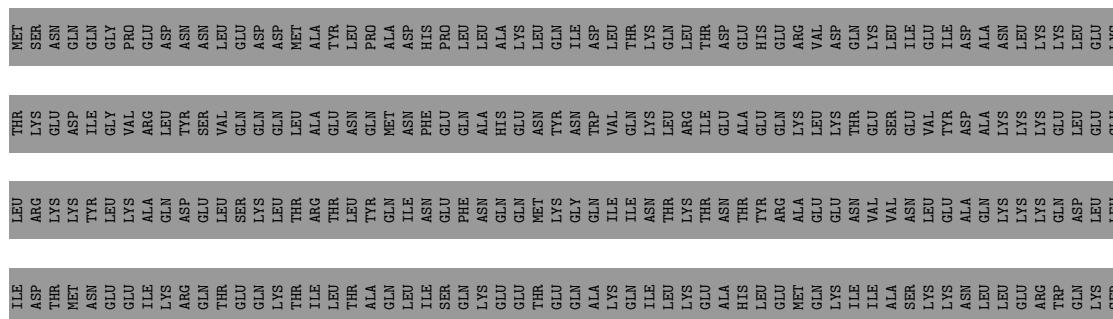


● Molecule 14: Flagella associated protein

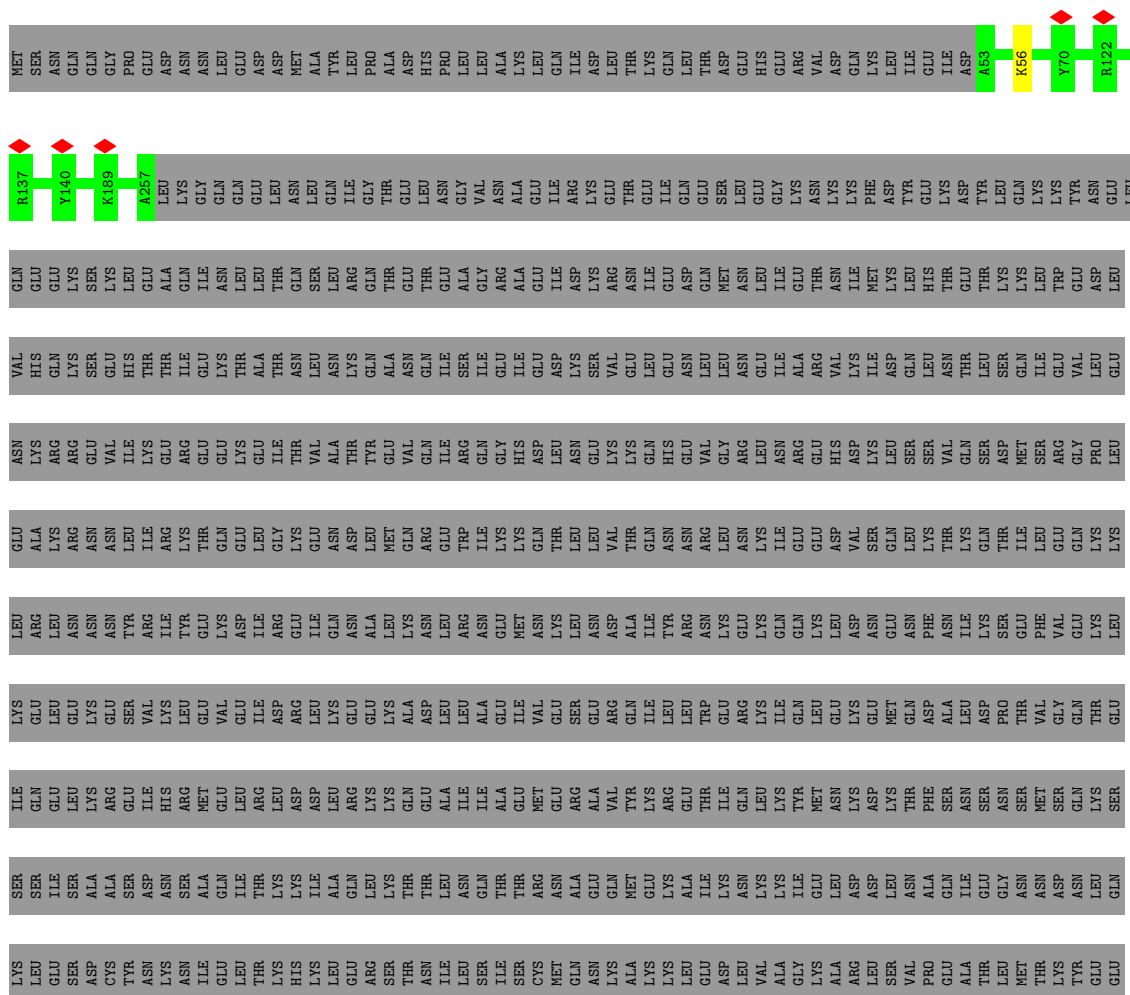
Response	Percentage
Yes, the U.S. is a democracy	22%
No, the U.S. is not a democracy	78%



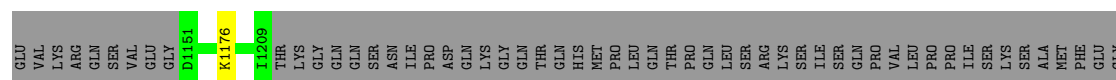
Frequency	Percentage
Often	47%
Not often	52%

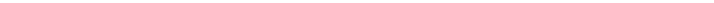


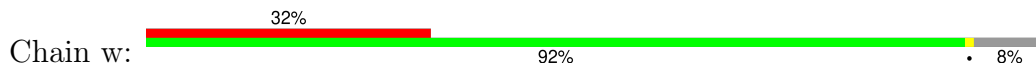
- Molecule 15: Coiled-coil protein, putative



M1	D2	N3	T4	G5	K6	L7	Q10	L11	V12	T13	L14	N15	D16	G17	L18	P22	E25	H33	L34	Y35	Q36	D37	F38	Q39	K40	F41	F42	S43	E44	E45	K46	K47	Q48	Q49	Y50	Q51	N52	A55	L56	R59	D60	N61	D62	T75	S76	V77	N78	D101	K121
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Chain Z:  7% 77% 23%





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	NONE	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	3.497	Depositor
Minimum map value	-1.582	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.240	Depositor
Recommended contour level	0.545	Depositor
Map size (\AA)	1293.28, 1293.28, 1293.28	wwPDB
Map dimensions	472, 472, 472	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.74, 2.74, 2.74	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.82	12/3988 (0.3%)	0.50	0/5310
2	B	0.57	3/3918 (0.1%)	0.57	3/5221 (0.1%)
3	C	0.25	0/4482	0.43	0/6008
4	D	0.81	6/3911 (0.2%)	0.50	0/5225
5	E	0.97	1/3903 (0.0%)	0.53	3/5211 (0.1%)
6	F	0.25	0/3768	0.43	0/5071
7	G	0.24	0/2821	0.43	1/3772 (0.0%)
8	H	1.20	8/6994 (0.1%)	0.51	2/9419 (0.0%)
9	I	0.26	0/1586	0.41	0/2128
9	i	0.26	0/1586	0.43	0/2128
10	J	0.24	0/3173	0.49	0/4219
11	K	0.24	0/3620	0.45	0/4803
12	L	0.25	0/7234	0.42	0/9693
13	M	0.27	0/1387	0.55	0/1843
14	N	0.30	0/3633	0.50	0/4835
14	n	0.26	0/1759	0.47	0/2350
15	O	0.28	0/3625	0.52	0/4840
15	o	0.29	0/1719	0.47	0/2295
16	P	0.26	0/5379	0.50	1/7204 (0.0%)
17	Q	0.27	0/1705	0.43	0/2290
17	R	0.24	0/1705	0.45	0/2290
18	S	0.24	0/1552	0.44	0/2057
18	s	0.23	0/1552	0.45	0/2057
19	T	0.25	0/2798	0.46	0/3711
21	W	0.24	0/9685	0.45	0/13007
22	Z	0.25	0/6876	0.48	0/9303
23	g	0.27	0/1591	0.57	0/2149
24	w	0.25	0/9986	0.45	0/13371
All	All	0.58	30/105936 (0.0%)	0.47	10/141810 (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	1
2	B	0	4
4	D	0	1
5	E	0	2
8	H	0	1
9	i	0	3
10	J	0	1
11	K	0	2
15	O	0	1
17	Q	0	1
20	V	0	1
21	W	0	1
All	All	0	19

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	295	TYR	CD1-CE1	59.37	2.28	1.39
5	E	259	ILE	CB-CG2	57.89	3.32	1.52
1	A	295	TYR	CD2-CE2	55.10	2.22	1.39
8	H	8	TYR	CD2-CE2	53.55	2.19	1.39
8	H	8	TYR	CD1-CE1	51.13	2.16	1.39
1	A	295	TYR	CE2-CZ	40.77	1.91	1.38
1	A	295	TYR	CE1-CZ	39.62	1.90	1.38
8	H	8	TYR	CE2-CZ	34.78	1.83	1.38
8	H	8	TYR	CE1-CZ	34.55	1.83	1.38
4	D	274	TYR	CD1-CE1	30.74	1.85	1.39
1	A	295	TYR	CG-CD1	29.85	1.77	1.39
1	A	295	TYR	CG-CD2	28.97	1.76	1.39
8	H	8	TYR	CG-CD2	27.63	1.75	1.39
8	H	8	TYR	CG-CD1	27.20	1.74	1.39
2	B	353	ILE	CG1-CD1	26.41	3.32	1.50
4	D	274	TYR	CD2-CE2	21.66	1.71	1.39
1	A	680	PHE	CE1-CZ	17.72	1.71	1.37
1	A	680	PHE	CE2-CZ	17.40	1.70	1.37
1	A	680	PHE	CD1-CE1	16.87	1.73	1.39
1	A	680	PHE	CD2-CE2	16.61	1.72	1.39
8	H	6	GLY	N-CA	16.26	1.70	1.46
4	D	274	TYR	CE1-CZ	15.10	1.58	1.38
2	B	289	HIS	CB-CG	14.75	1.76	1.50
4	D	274	TYR	CG-CD2	14.56	1.58	1.39
4	D	274	TYR	CE2-CZ	14.50	1.57	1.38
4	D	274	TYR	CG-CD1	14.20	1.57	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	680	PHE	CG-CD1	11.49	1.55	1.38
1	A	680	PHE	CG-CD2	11.35	1.55	1.38
2	B	289	HIS	CA-CB	7.47	1.70	1.53
8	H	5	GLU	C-N	6.60	1.45	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	5	GLU	C-N-CA	15.37	154.58	122.30
2	B	289	HIS	CA-CB-CG	12.06	134.10	113.60
8	H	6	GLY	N-CA-C	8.42	134.15	113.10
5	E	259	ILE	CA-CB-CG2	7.79	126.47	110.90
16	P	701	LEU	CA-CB-CG	7.20	131.86	115.30
5	E	259	ILE	CG1-CB-CG2	5.78	124.11	111.40
2	B	289	HIS	N-CA-CB	5.37	120.27	110.60
7	G	198	LEU	CA-CB-CG	5.12	127.08	115.30
2	B	276	LYS	CD-CE-NZ	5.06	123.33	111.70
5	E	259	ILE	CA-CB-CG1	-5.02	101.46	111.00

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	291	ASP	Peptide
2	B	16	GLY	Peptide
2	B	17	GLY	Peptide
2	B	275	LYS	Peptide
2	B	276	LYS	Peptide
4	D	314	LYS	Peptide
5	E	298	ALA	Peptide
5	E	40	ASN	Peptide
8	H	7	GLY	Peptide
10	J	363	LYS	Peptide
11	K	420	GLU	Peptide
11	K	423	LYS	Peptide
15	O	515	TRP	Peptide
17	Q	168	ASN	Peptide
20	V	538	UNK	Peptide
21	W	1050	ILE	Peptide
9	i	178	TYR	Peptide
9	i	179	ASN	Peptide
9	i	180	ASN	Peptide

5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	454/826 (55%)	417 (92%)	35 (8%)	2 (0%)	30	63
2	B	456/506 (90%)	405 (89%)	50 (11%)	1 (0%)	44	73
3	C	529/575 (92%)	500 (94%)	29 (6%)	0	100	100
4	D	457/472 (97%)	435 (95%)	21 (5%)	1 (0%)	44	73
5	E	462/468 (99%)	419 (91%)	40 (9%)	3 (1%)	22	55
6	F	459/461 (100%)	440 (96%)	19 (4%)	0	100	100
7	G	343/345 (99%)	318 (93%)	25 (7%)	0	100	100
8	H	816/852 (96%)	752 (92%)	64 (8%)	0	100	100
9	I	183/185 (99%)	177 (97%)	6 (3%)	0	100	100
9	i	183/185 (99%)	172 (94%)	11 (6%)	0	100	100
10	J	370/372 (100%)	346 (94%)	23 (6%)	1 (0%)	37	67
11	K	432/434 (100%)	403 (93%)	27 (6%)	2 (0%)	25	59
12	L	860/862 (100%)	819 (95%)	41 (5%)	0	100	100
13	M	160/644 (25%)	140 (88%)	17 (11%)	3 (2%)	6	35
14	N	428/963 (44%)	419 (98%)	7 (2%)	2 (0%)	25	59
14	n	206/963 (21%)	206 (100%)	0	0	100	100
15	O	424/893 (48%)	411 (97%)	10 (2%)	3 (1%)	19	53
15	o	203/893 (23%)	203 (100%)	0	0	100	100
16	P	625/794 (79%)	591 (95%)	34 (5%)	0	100	100
17	Q	200/202 (99%)	184 (92%)	16 (8%)	0	100	100
17	R	200/202 (99%)	184 (92%)	15 (8%)	1 (0%)	25	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	S	185/187 (99%)	176 (95%)	8 (4%)	1 (0%)	25	59
18	s	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
19	T	329/361 (91%)	326 (99%)	3 (1%)	0	100	100
21	W	1165/1308 (89%)	1117 (96%)	47 (4%)	1 (0%)	48	79
22	Z	828/1079 (77%)	754 (91%)	72 (9%)	2 (0%)	44	73
23	g	185/195 (95%)	145 (78%)	40 (22%)	0	100	100
24	w	1186/1293 (92%)	1141 (96%)	43 (4%)	2 (0%)	44	73
All	All	12513/16707 (75%)	11779 (94%)	709 (6%)	25 (0%)	45	73

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	237	LYS
2	B	279	ILE
5	E	241	ASN
5	E	299	LYS
10	J	154	LYS
11	K	360	ALA
11	K	419	LYS
14	N	564	LEU
18	S	57	LEU
22	Z	765	SER
24	w	1005	SER
1	A	185	PHE
5	E	100	LYS
13	M	245	ASP
13	M	267	SER
14	N	563	SER
15	O	516	ILE
15	O	517	LYS
22	Z	774	ASP
24	w	515	VAL
15	O	514	GLU
13	M	256	ARG
4	D	114	LEU
17	R	22	PRO
21	W	994	ILE

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	434/766 (57%)	431 (99%)	3 (1%)	81	90
2	B	430/473 (91%)	425 (99%)	5 (1%)	67	82
3	C	499/540 (92%)	496 (99%)	3 (1%)	84	92
4	D	428/438 (98%)	423 (99%)	5 (1%)	67	82
5	E	430/434 (99%)	422 (98%)	8 (2%)	52	73
6	F	414/414 (100%)	412 (100%)	2 (0%)	86	93
7	G	310/310 (100%)	309 (100%)	1 (0%)	91	96
8	H	759/786 (97%)	756 (100%)	3 (0%)	89	95
9	I	170/170 (100%)	170 (100%)	0	100	100
9	i	170/170 (100%)	169 (99%)	1 (1%)	84	92
10	J	350/350 (100%)	346 (99%)	4 (1%)	70	83
11	K	403/403 (100%)	398 (99%)	5 (1%)	67	82
12	L	776/776 (100%)	774 (100%)	2 (0%)	91	96
13	M	147/590 (25%)	146 (99%)	1 (1%)	81	90
14	N	394/884 (45%)	386 (98%)	8 (2%)	50	72
14	n	189/884 (21%)	189 (100%)	0	100	100
15	O	405/829 (49%)	400 (99%)	5 (1%)	67	82
15	o	188/829 (23%)	187 (100%)	1 (0%)	86	93
16	P	589/733 (80%)	580 (98%)	9 (2%)	60	78
17	Q	189/189 (100%)	189 (100%)	0	100	100
17	R	189/189 (100%)	188 (100%)	1 (0%)	86	93
18	S	172/172 (100%)	172 (100%)	0	100	100
18	s	172/172 (100%)	171 (99%)	1 (1%)	84	92
19	T	309/335 (92%)	304 (98%)	5 (2%)	58	76
21	W	1070/1200 (89%)	1065 (100%)	5 (0%)	86	93
22	Z	761/994 (77%)	759 (100%)	2 (0%)	91	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	g	175/182 (96%)	174 (99%)	1 (1%)	84	92
24	w	1103/1201 (92%)	1097 (100%)	6 (0%)	86	93
All	All	11625/15413 (75%)	11538 (99%)	87 (1%)	80	90

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	LYS
1	A	312	ARG
1	A	355	LYS
2	B	192	LYS
2	B	249	LYS
2	B	302	LYS
2	B	304	LYS
2	B	344	ARG
3	C	109	LYS
3	C	205	LYS
3	C	452	LYS
4	D	275	LYS
4	D	316	LYS
4	D	357	LYS
4	D	422	LYS
4	D	450	LYS
5	E	251	LYS
5	E	262	ASN
5	E	269	ASN
5	E	284	ARG
5	E	299	LYS
5	E	320	LYS
5	E	323	ARG
5	E	334	LYS
6	F	45	LYS
6	F	152	ASN
7	G	38	LYS
8	H	708	LYS
8	H	714	LYS
8	H	718	LYS
10	J	151	ARG
10	J	197	ARG
10	J	244	LYS
10	J	345	LYS

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Mol	Chain	Res	Type
11	K	62	LYS
11	K	239	LYS
11	K	246	LYS
11	K	304	LYS
11	K	351	LYS
12	L	309	LYS
12	L	385	LYS
13	M	256	ARG
14	N	357	LYS
14	N	404	ARG
14	N	558	LYS
14	N	608	LYS
14	N	613	LYS
14	N	695	LYS
14	N	729	LYS
14	N	740	LYS
15	O	280	ARG
15	O	281	LYS
15	O	556	ASN
15	O	619	LYS
15	O	626	ARG
16	P	488	LYS
16	P	547	LYS
16	P	554	LYS
16	P	581	LYS
16	P	598	LYS
16	P	618	LYS
16	P	696	ARG
16	P	706	LYS
16	P	713	LYS
17	R	121	LYS
19	T	108	LYS
19	T	189	LYS
19	T	217	LYS
19	T	271	LYS
19	T	350	ARG
21	W	98	LYS
21	W	128	LYS
21	W	342	LYS
21	W	1093	LYS
21	W	1176	LYS
22	Z	377	LYS

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Mol	Chain	Res	Type
22	Z	799	LYS
23	g	113	ARG
9	i	13	LYS
15	o	56	LYS
18	s	156	LYS
24	w	331	LYS
24	w	361	LYS
24	w	787	LYS
24	w	920	LYS
24	w	966	ASN
24	w	1186	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (137) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	38	ASN
1	A	133	GLN
1	A	147	GLN
1	A	287	GLN
1	A	326	HIS
1	A	688	GLN
1	A	731	GLN
2	B	127	HIS
2	B	211	ASN
2	B	252	GLN
2	B	406	ASN
2	B	407	ASN
2	B	430	GLN
2	B	466	HIS
3	C	48	ASN
3	C	104	HIS
3	C	107	ASN
3	C	211	ASN
3	C	238	GLN
3	C	255	GLN
3	C	332	HIS
3	C	374	ASN
3	C	545	ASN
4	D	219	GLN
4	D	268	GLN
4	D	326	GLN

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Mol	Chain	Res	Type
4	D	345	GLN
4	D	360	GLN
4	D	367	GLN
4	D	440	HIS
5	E	58	ASN
5	E	106	GLN
5	E	215	HIS
5	E	305	GLN
5	E	361	ASN
5	E	405	GLN
6	F	71	ASN
6	F	269	ASN
6	F	310	GLN
6	F	354	ASN
6	F	424	GLN
7	G	197	ASN
7	G	235	GLN
7	G	263	ASN
7	G	289	ASN
8	H	231	ASN
8	H	332	ASN
8	H	527	HIS
8	H	573	ASN
9	I	164	GLN
10	J	54	GLN
10	J	139	GLN
10	J	206	GLN
10	J	231	GLN
10	J	252	HIS
11	K	155	ASN
11	K	212	HIS
11	K	337	ASN
11	K	350	GLN
12	L	31	ASN
12	L	73	HIS
12	L	297	HIS
12	L	501	ASN
12	L	534	GLN
12	L	582	GLN
12	L	626	HIS
13	M	175	GLN
13	M	184	GLN

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Mol	Chain	Res	Type
13	M	198	GLN
14	N	507	GLN
14	N	604	GLN
14	N	612	GLN
14	N	643	ASN
14	N	673	HIS
15	O	377	HIS
15	O	465	GLN
15	O	525	GLN
15	O	543	GLN
15	O	569	ASN
15	O	576	ASN
15	O	592	GLN
15	O	653	GLN
16	P	148	ASN
16	P	239	GLN
16	P	274	ASN
16	P	307	GLN
16	P	320	GLN
16	P	342	GLN
16	P	486	ASN
16	P	490	GLN
16	P	535	GLN
16	P	576	ASN
16	P	608	GLN
16	P	722	ASN
17	Q	48	GLN
17	Q	51	GLN
17	R	32	HIS
17	R	36	GLN
17	R	48	GLN
18	S	165	GLN
19	T	182	ASN
19	T	186	GLN
19	T	195	GLN
19	T	216	ASN
19	T	299	GLN
21	W	7	HIS
21	W	268	GLN
21	W	333	GLN
21	W	384	GLN
21	W	489	HIS

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Mol	Chain	Res	Type
21	W	492	GLN
21	W	629	GLN
21	W	772	ASN
21	W	1098	GLN
21	W	1192	ASN
22	Z	341	GLN
22	Z	485	GLN
22	Z	713	ASN
22	Z	805	HIS
22	Z	862	GLN
23	g	7	GLN
23	g	23	GLN
23	g	131	GLN
23	g	157	HIS
9	i	170	HIS
9	i	180	ASN
24	w	168	HIS
24	w	192	GLN
24	w	317	GLN
24	w	468	HIS
24	w	731	ASN
24	w	1065	GLN
24	w	1094	GLN
24	w	1109	GLN
24	w	1126	HIS
24	w	1178	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.

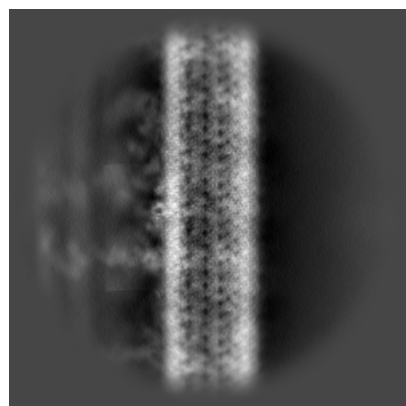
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41284. These allow visual inspection of the internal detail of the map and identification of artifacts.

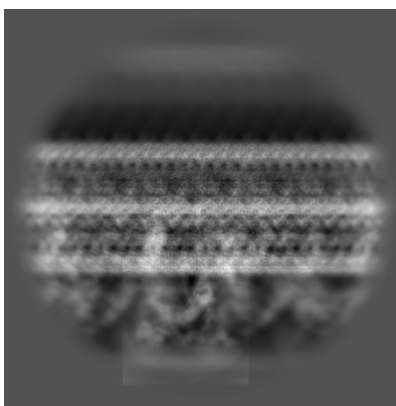
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

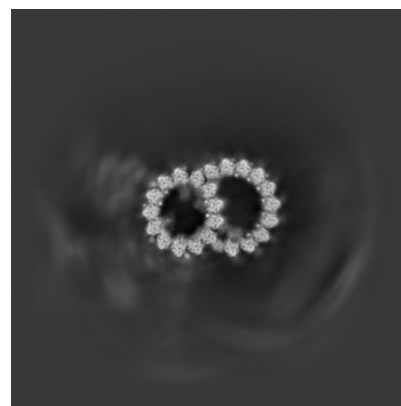
6.1.1 Primary map



X

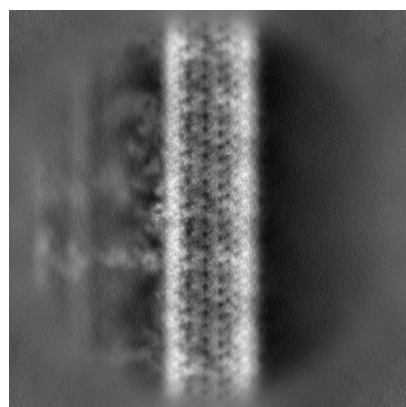


Y

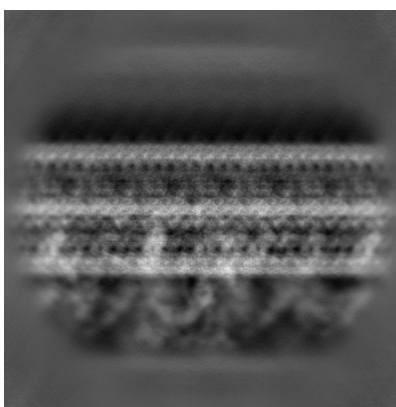


Z

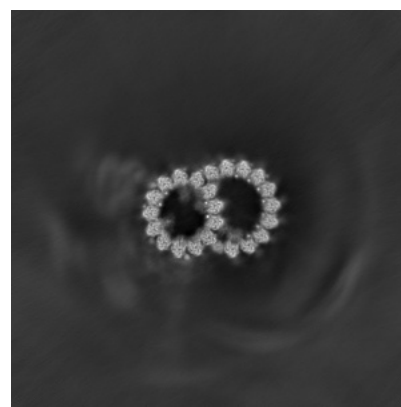
6.1.2 Raw map



X



Y

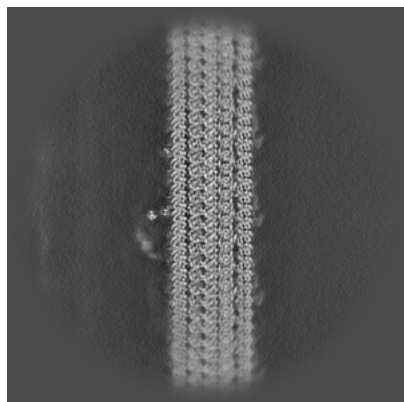


Z

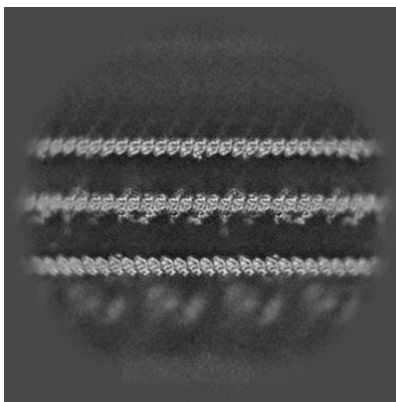
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

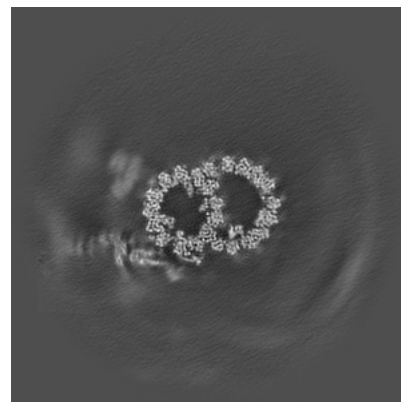
6.2.1 Primary map



X Index: 236

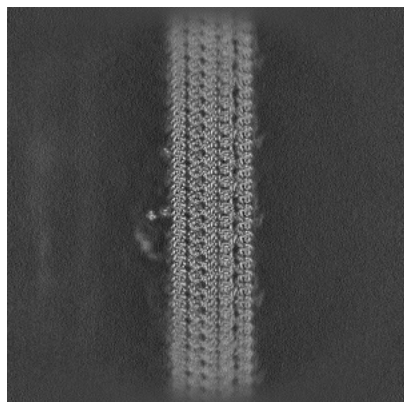


Y Index: 236

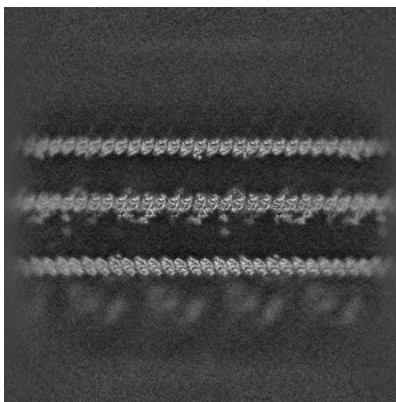


Z Index: 236

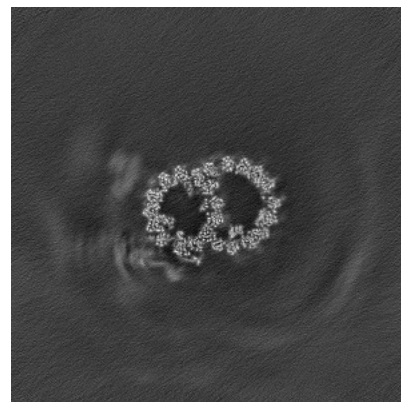
6.2.2 Raw map



X Index: 235



Y Index: 235

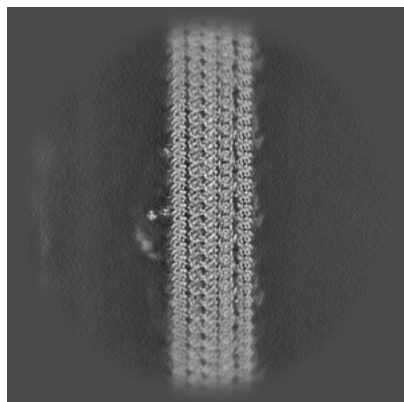


Z Index: 235

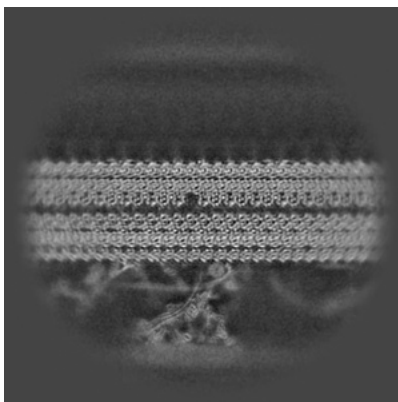
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

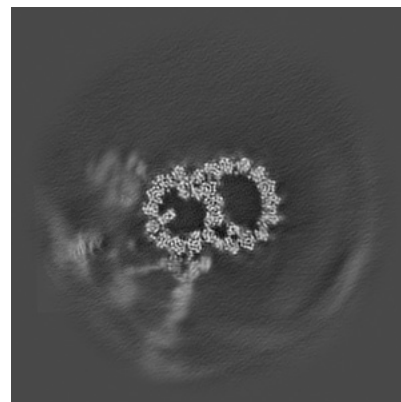
6.3.1 Primary map



X Index: 236

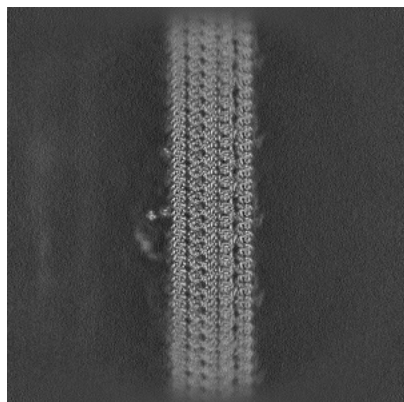


Y Index: 192

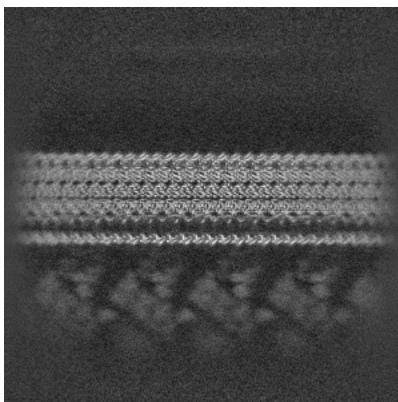


Z Index: 180

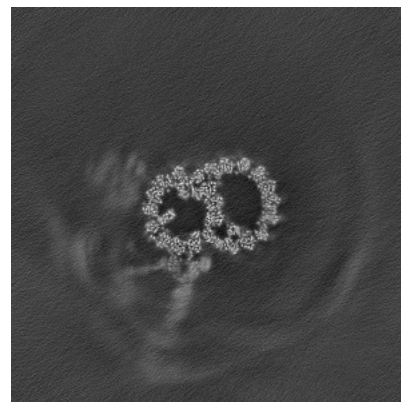
6.3.2 Raw map



X Index: 235



Y Index: 280

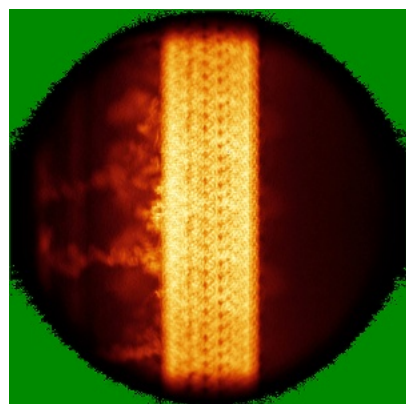


Z Index: 179

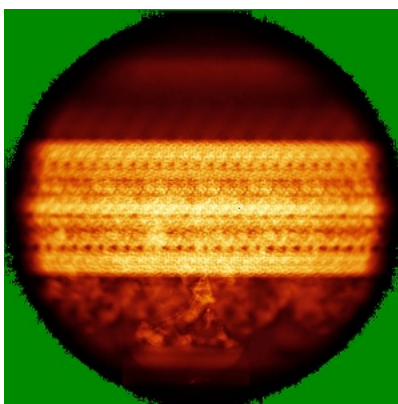
The images above show the largest variance slices of the map in three orthogonal directions.

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

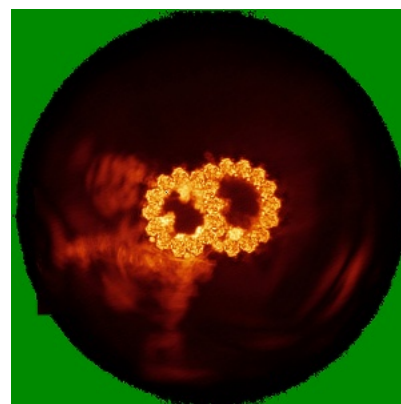
6.4.1 Primary map



X

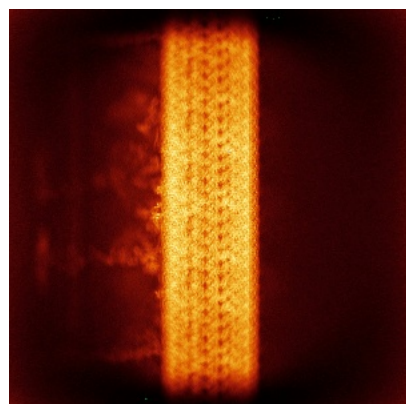


Y

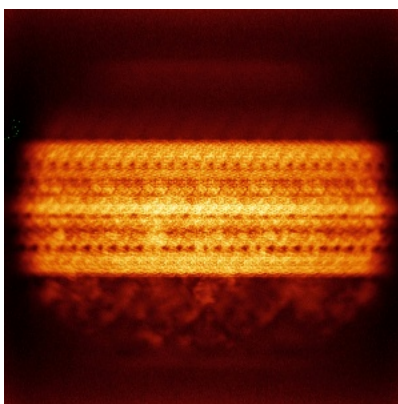


Z

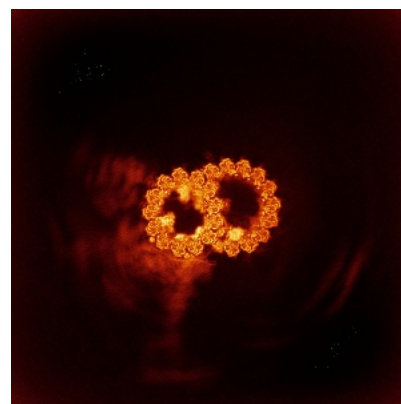
6.4.2 Raw map



X



Y

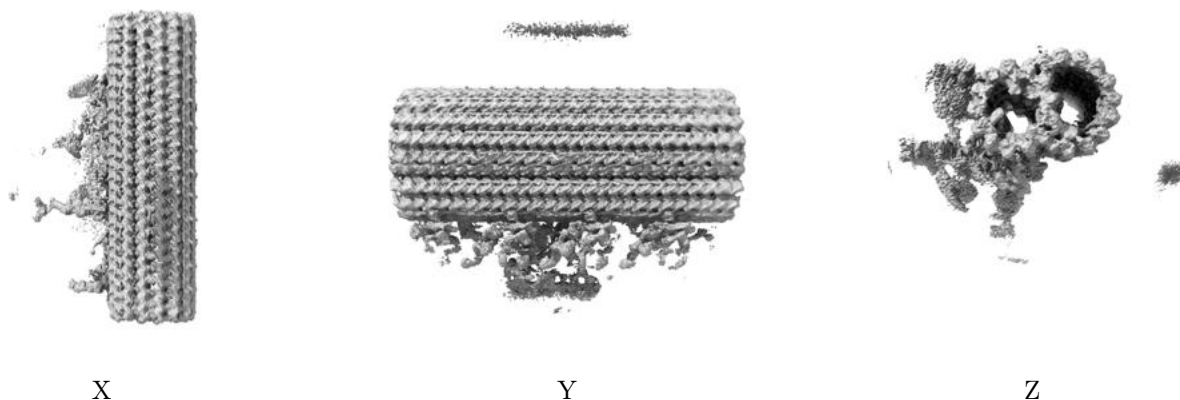


Z

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.

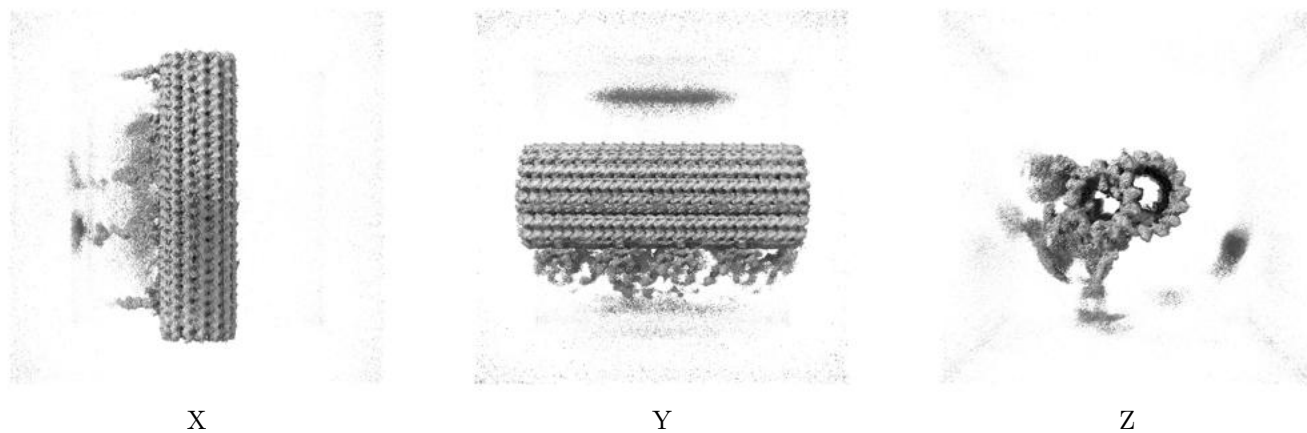
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.545. 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.

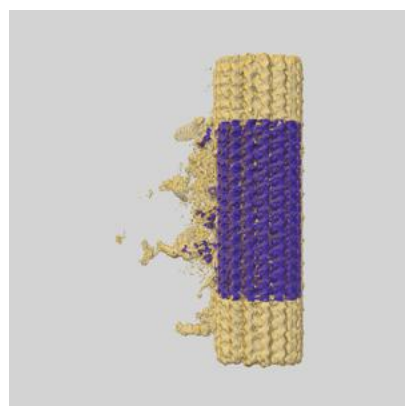
6.6 Mask visualisation [i](#)

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

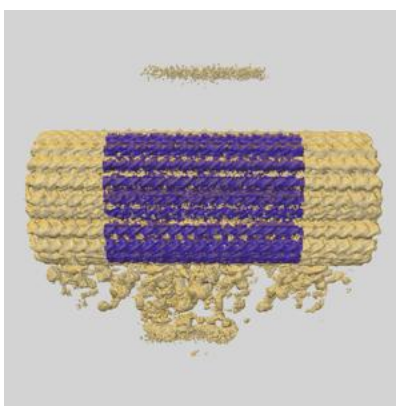
A mask typically either:

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

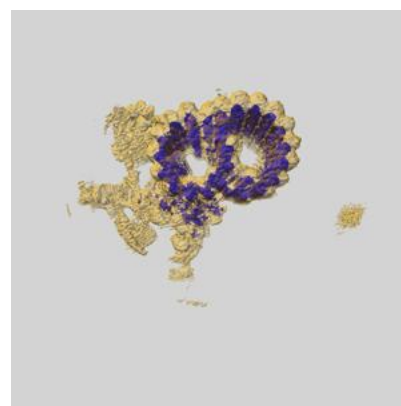
6.6.1 emd_41284_msk_1.map [i](#)



X



Y

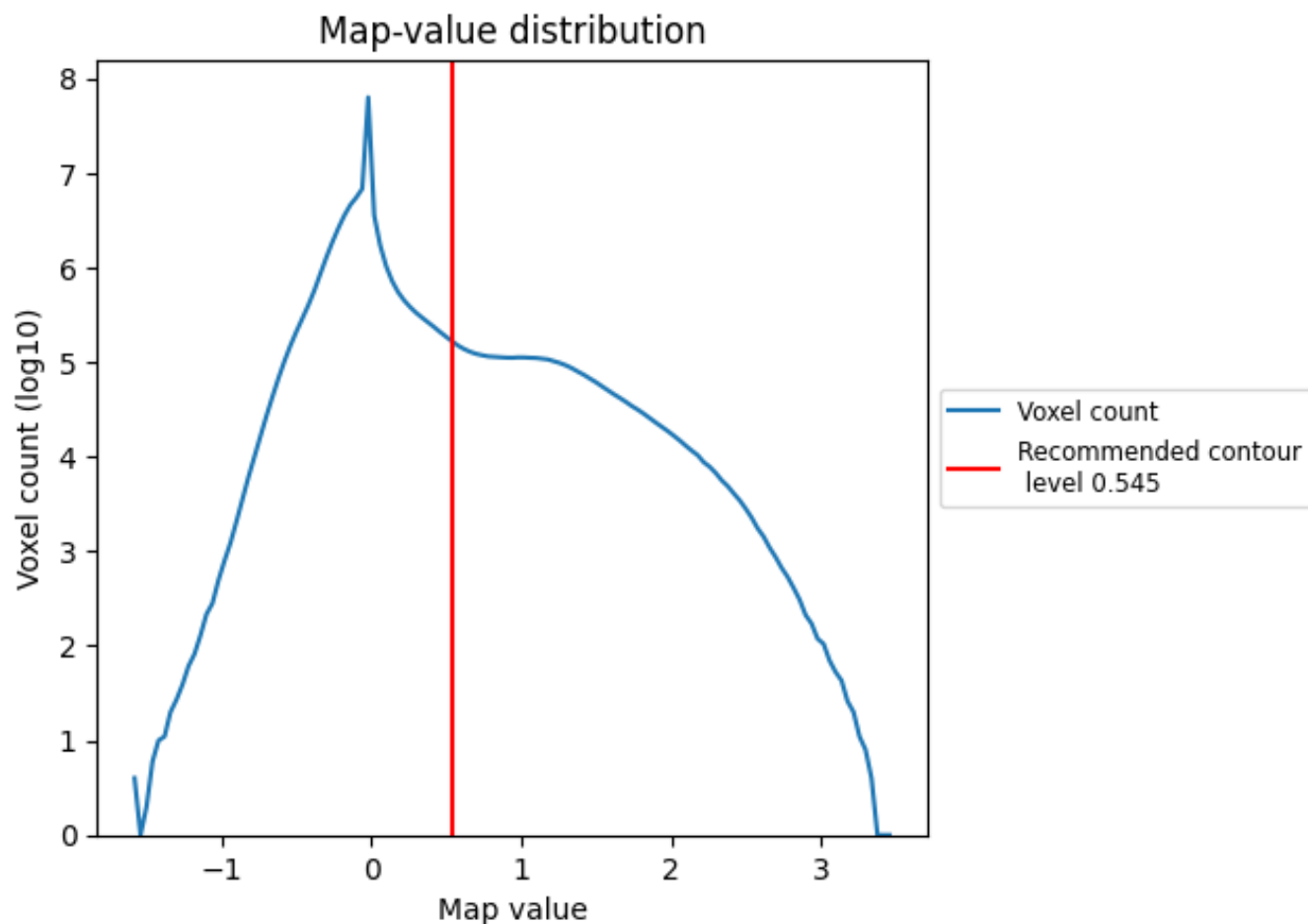


Z

7 Map analysis [i](#)

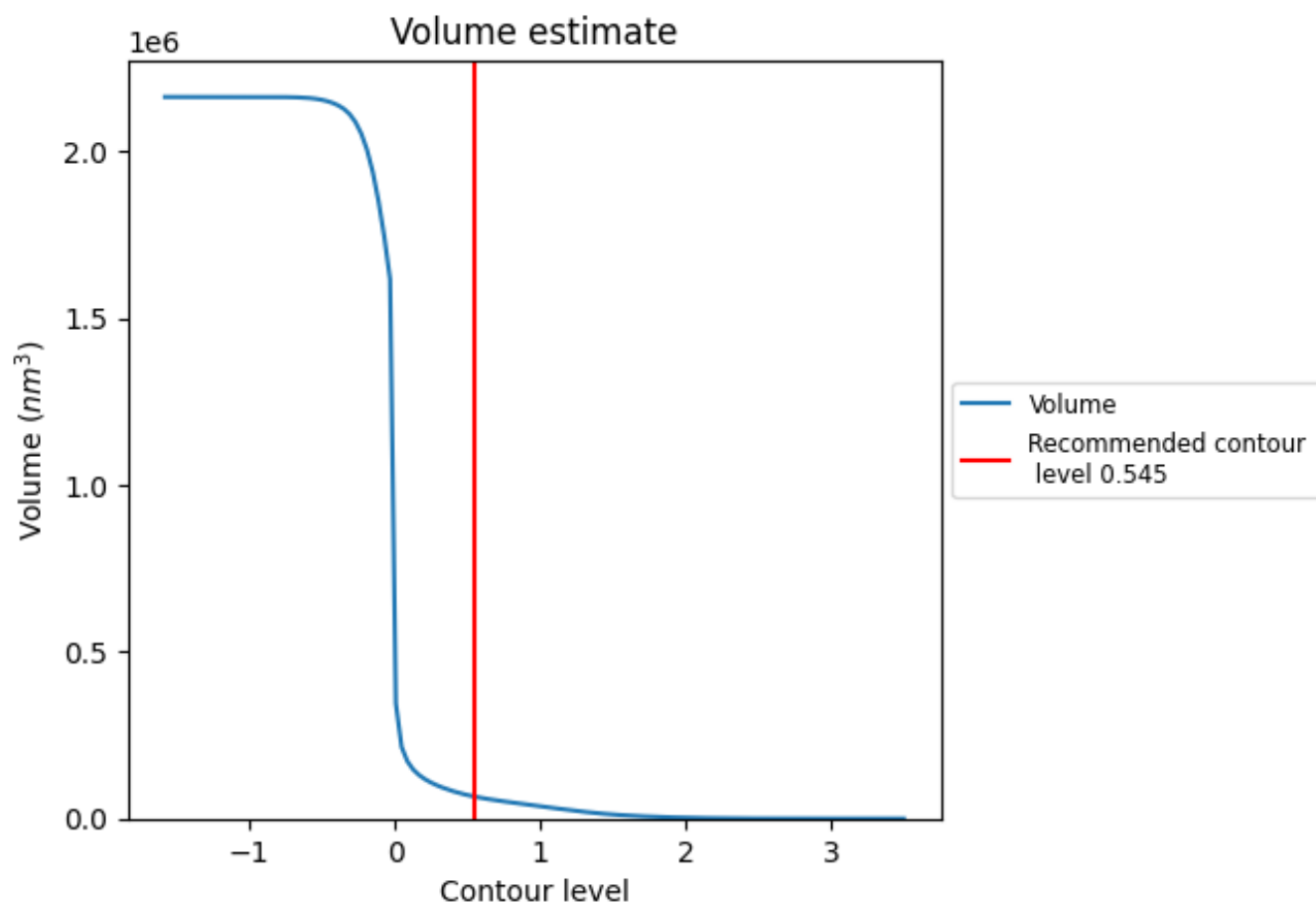
This section contains the results of statistical analysis of the map.

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.

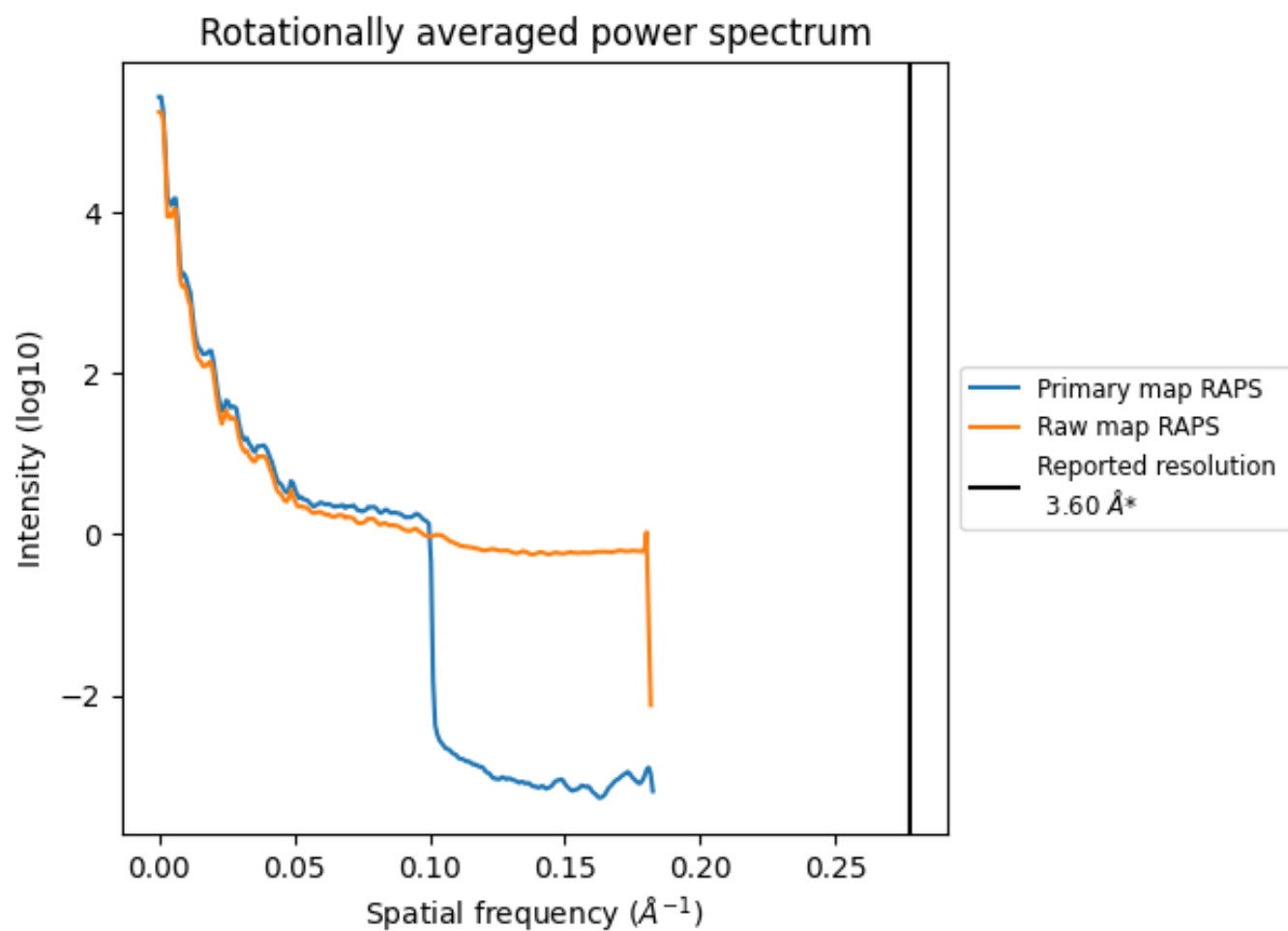
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66091 nm³; this corresponds to an approximate mass of 59702 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](#)

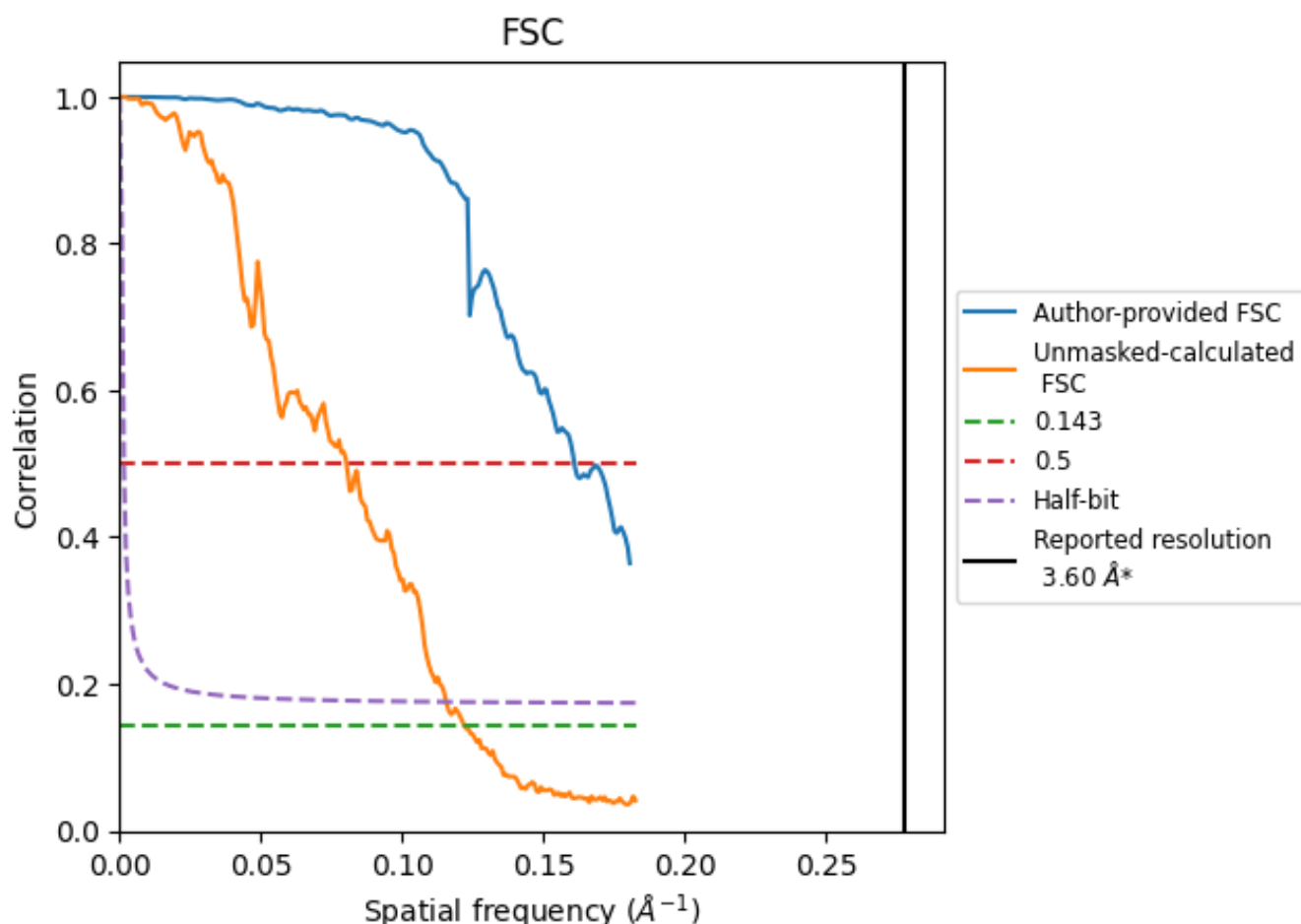


*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

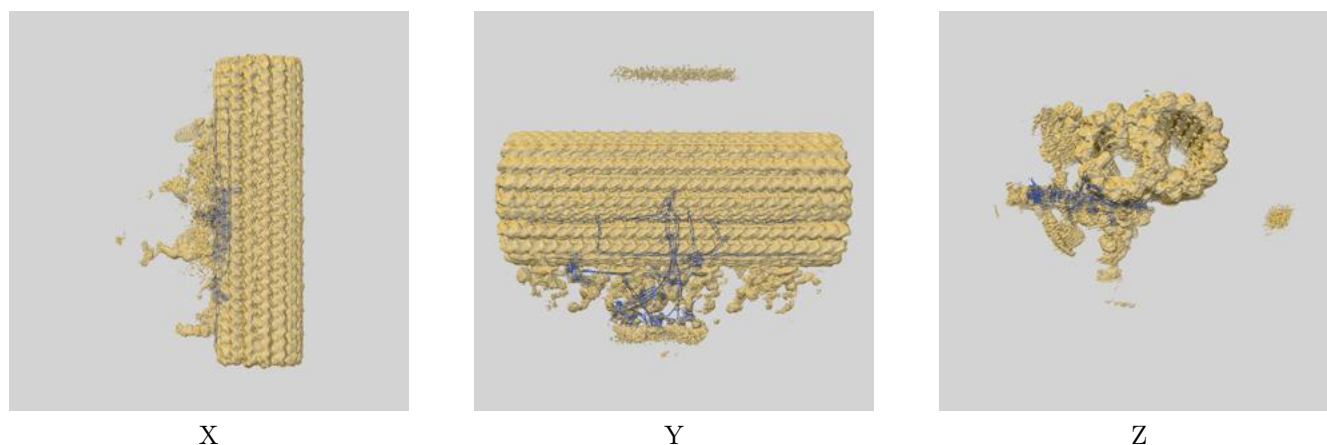
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.60
Author-provided FSC curve	-	6.22	-	-
Unmasked-calculated*	8.20	12.45	8.65	-

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

9 Map-model fit [i](#)

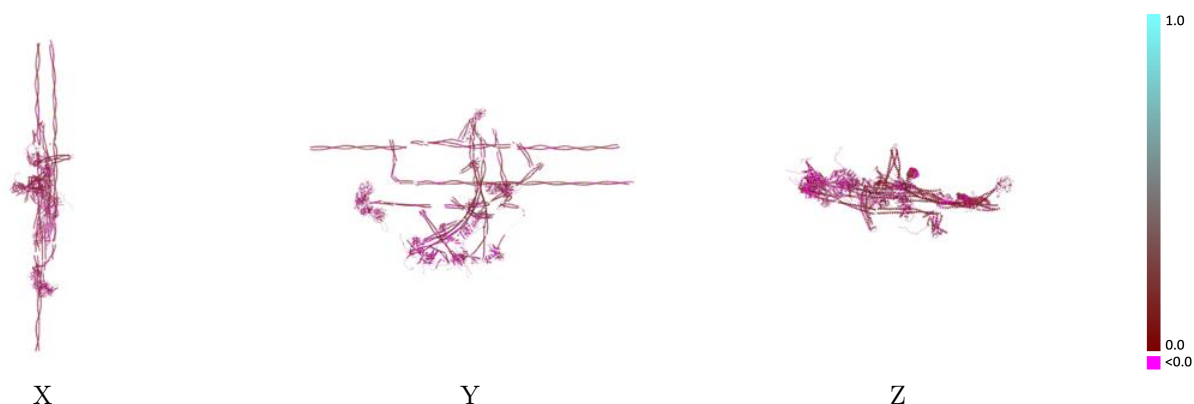
This section contains information regarding the fit between EMDB map EMD-41284 and PDB model 8TID. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



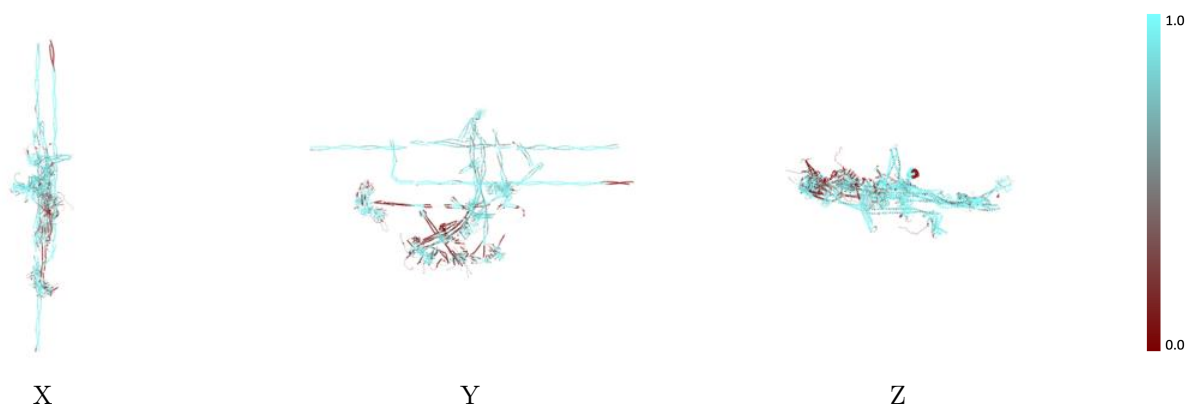
The images above show the 3D surface view of the map at the recommended contour level 0.545 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



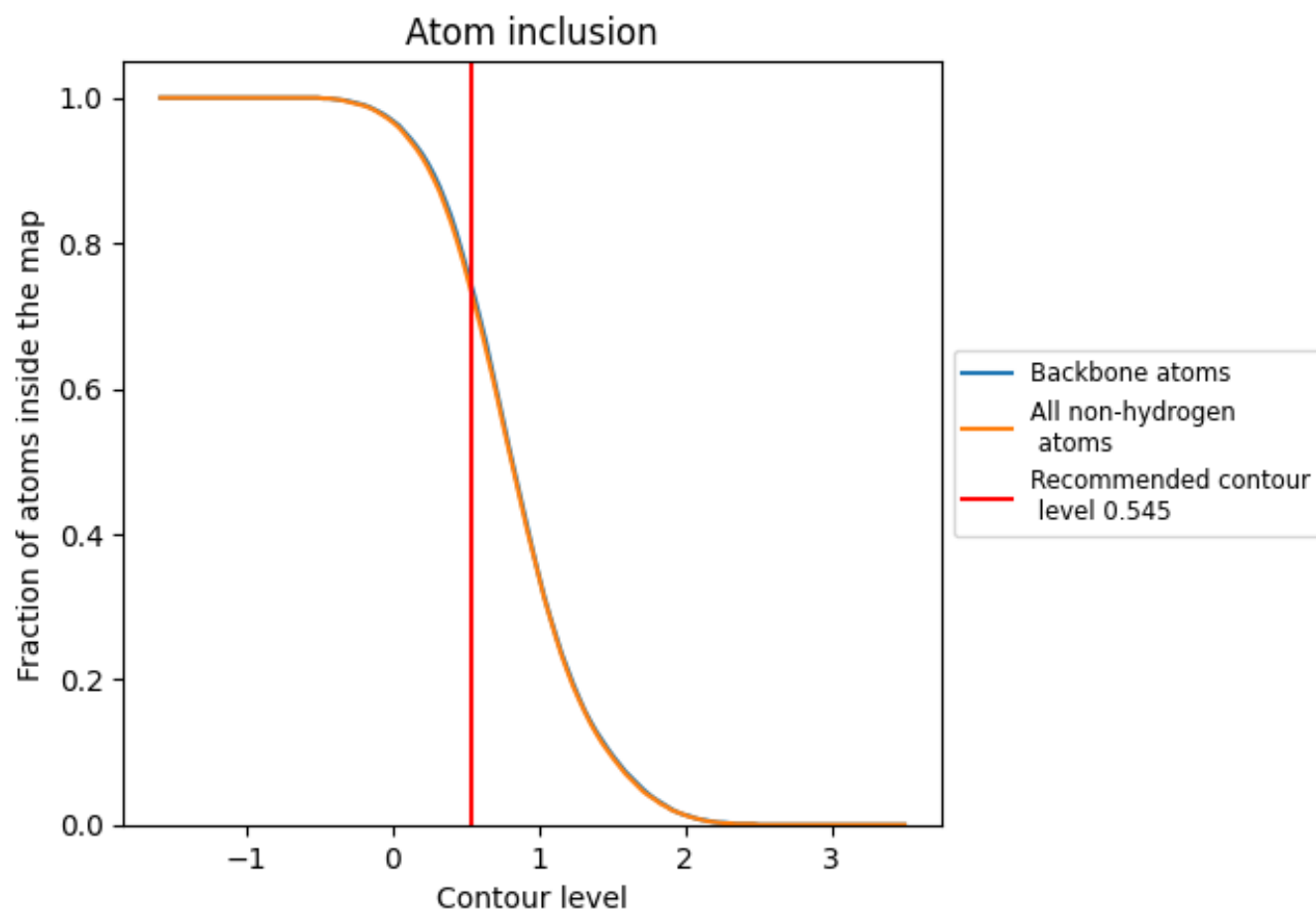
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.545).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 73% 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 (0.545) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7290	 0.0720
A	 0.6230	 0.0950
B	 0.5970	 0.0830
C	 0.9270	 0.0770
D	 0.7550	 0.0730
E	 0.8160	 0.0820
F	 0.2470	 0.0370
G	 0.7240	 0.0260
H	 0.7160	 0.0520
I	 0.9500	 0.0550
J	 0.7650	 0.0910
K	 0.7430	 0.0850
L	 0.6950	 0.0270
M	 0.8070	 0.1190
N	 0.8400	 0.0930
O	 0.8500	 0.1080
P	 0.7040	 0.0780
Q	 0.7370	 0.0350
R	 0.5740	 0.0500
S	 0.2970	 0.0610
T	 0.7580	 0.0850
U	 0.8690	 0.1310
V	 0.8790	 0.1240
W	 0.6990	 0.0670
Z	 0.8920	 0.0660
g	 0.8900	 0.0900
i	 0.5020	 0.0310
n	 0.8830	 0.0990
o	 0.9210	 0.1230
s	 0.2660	 0.0440
w	 0.6180	 0.0630

