



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 09:30 AM UTC

PDB ID : 7TK0 / pdb_00007tk0
EMDB ID : EMD-25948
Title : Yeast ATP synthase State 1catalytic(c) without exogenous ATP backbone model
Authors : Guo, H.; Rubinstein, J.L.
Deposited on : 2022-01-17
Resolution : 4.40 Å(reported)
Based on initial model : 2HLD

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:

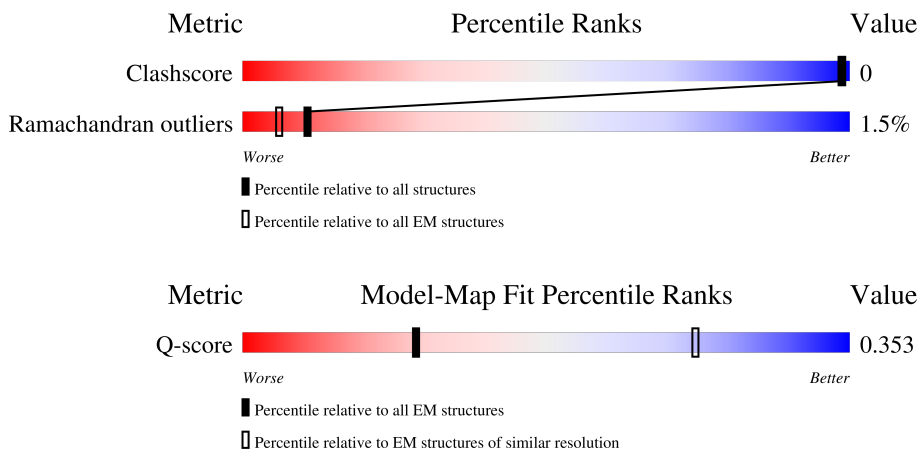
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	-
Q-score	-	25397	3132 (3.91 - 4.90)

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	0	76	 17% 91% 8% .
1	1	76	 17% 93% 5% .
1	2	76	 16% 97% ..
1	3	76	 24% 91% 7% .
1	4	76	 20% 93% 5% .

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Mol	Chain	Length	Quality of chain
1	5	76	17% 95% ...
1	6	76	21% 89% 8%
1	7	76	13% 88% 8%
1	8	76	14% 88% 11%
1	9	76	18% 89% 8%
2	A	510	91% 7%
2	B	510	92% 7%
2	C	510	91% 7%
3	D	478	5% 92% 5%
3	E	478	91% 7%
3	F	478	90% 8%
4	G	278	91% 5%
5	H	138	78% 9% 13%
6	I	61	7% 74% 5% 21%
7	O	195	86% 10%
8	T	249	85% 5% 10%
9	U	209	73% 26%
10	V	173	8% 89% 10%
11	W	95	8% 77% 13% 11%
12	X	92	14% 62% 5% 33%
13	Y	59	12% 61% 37%
14	Z	48	96%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 20220 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 ATP synthase subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	0	75	300	150	75	75	0	0
1	1	75	300	150	75	75	0	0
1	2	75	300	150	75	75	0	0
1	3	74	296	148	74	74	0	0
1	4	75	300	150	75	75	0	0
1	5	75	300	150	75	75	0	0
1	6	74	296	148	74	74	0	0
1	7	73	292	146	73	73	0	0
1	8	75	300	150	75	75	0	0
1	9	74	296	148	74	74	0	0

- Molecule 2 is a protein called ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	A	499	1996	998	499	499	0	0
2	B	505	2020	1010	505	505	0	0
2	C	498	1992	996	498	498	0	0

- Molecule 3 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	468	Total	C	N	O	0	0
			1872	936	468	468		
3	E	468	Total	C	N	O	0	0
			1872	936	468	468		
3	F	469	Total	C	N	O	0	0
			1876	938	469	469		

- Molecule 4 is a protein called ATP synthase subunit gamma.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	265	Total	C	N	O	0	0
			1060	530	265	265		

- Molecule 5 is a protein called ATP synthase subunit delta.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	120	Total	C	N	O	0	0
			480	240	120	120		

- Molecule 6 is a protein called ATP synthase subunit epsilon.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	I	48	Total	C	N	O	0	0
			193	96	48	49		

- Molecule 7 is a protein called ATP synthase subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	187	Total	C	N	O	0	0
			748	374	187	187		

- Molecule 8 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	T	224	Total	C	N	O	0	0
			897	448	224	225		

- Molecule 9 is a protein called ATP synthase subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	155	Total	C	N	O	0	0
			620	310	155	155		

- Molecule 10 is a protein called ATP synthase subunit d.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	V	171	685	342	171	172	0	0

- Molecule 11 is a protein called ATP synthase subunit f.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	W	85	340	170	85	85	0	0

- Molecule 12 is a protein called ATP synthase subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	X	62	248	124	62	62	0	0

- Molecule 13 is a protein called ATP synthase subunit J.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	Y	37	148	74	37	37	0	0

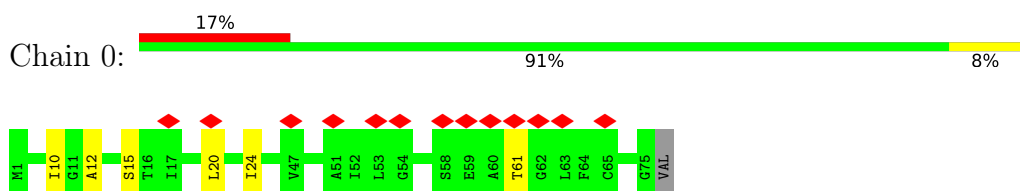
- Molecule 14 is a protein called ATP synthase protein 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	Z	48	193	96	48	49	0	0

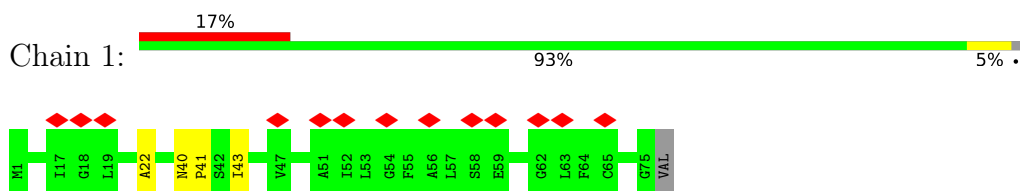
3 Residue-property plots [i](#)

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.

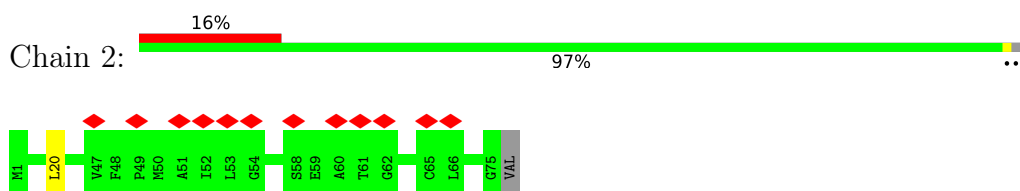
- Molecule 1: ATP synthase subunit 9



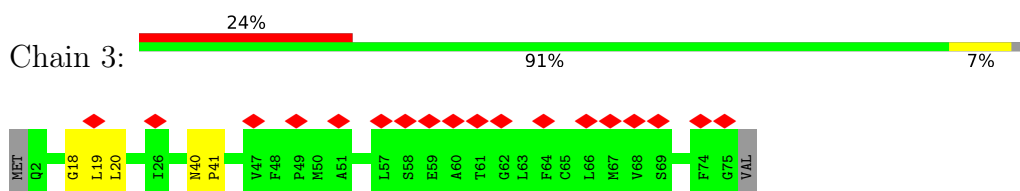
- Molecule 1: ATP synthase subunit 9



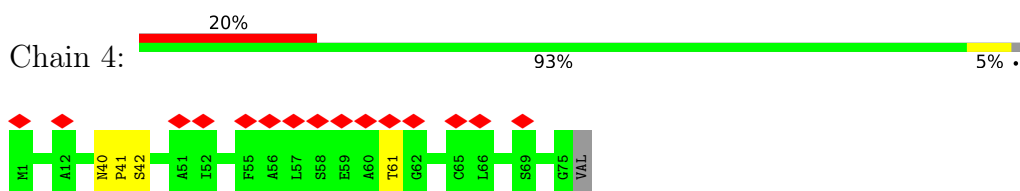
- Molecule 1: ATP synthase subunit 9



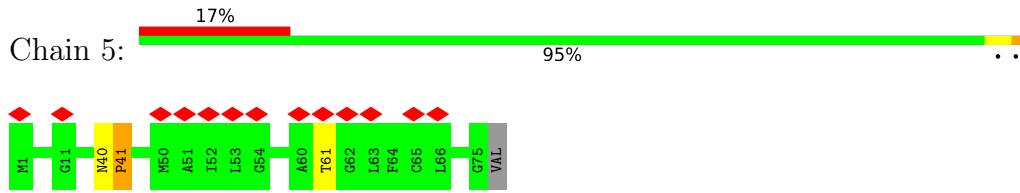
- Molecule 1: ATP synthase subunit 9



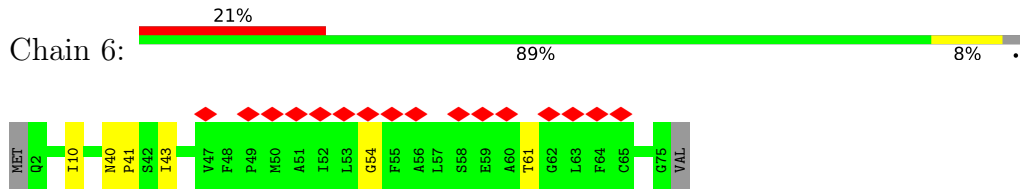
- Molecule 1: ATP synthase subunit 9



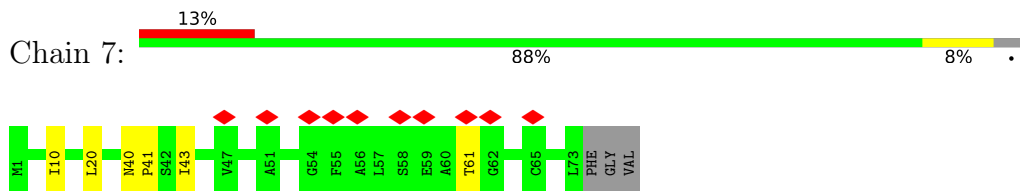
- Molecule 1: ATP synthase subunit 9



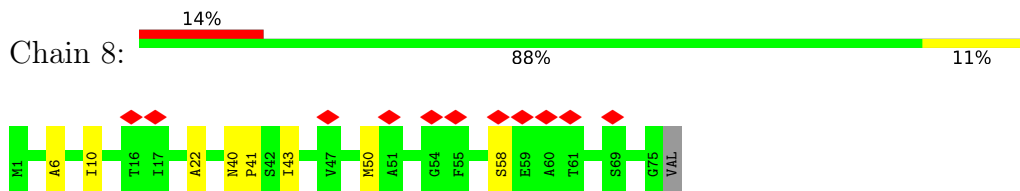
- Molecule 1: ATP synthase subunit 9



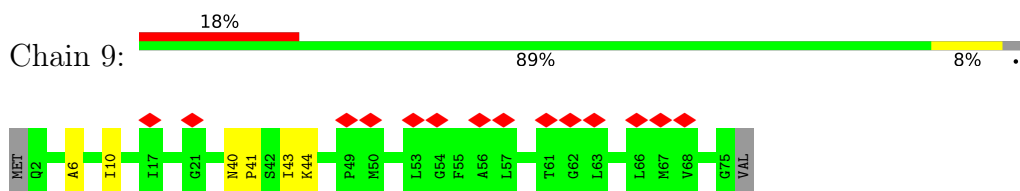
- Molecule 1: ATP synthase subunit 9



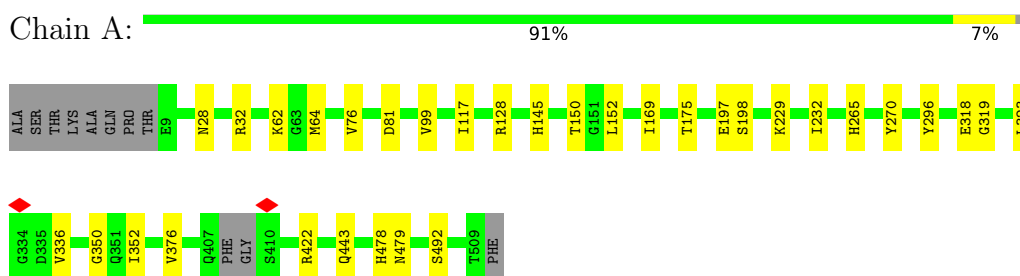
- Molecule 1: ATP synthase subunit 9




- Molecule 1: ATP synthase subunit 9

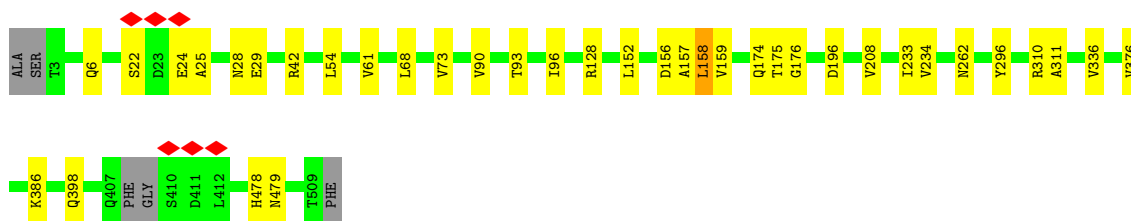


- Molecule 2: ATP synthase subunit alpha



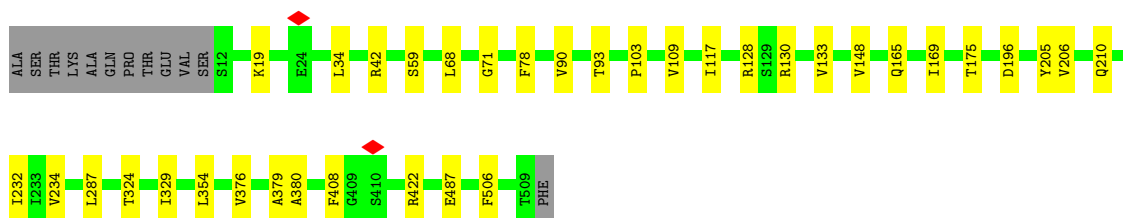
- Molecule 2: ATP synthase subunit alpha

Chain B:  92% 7%

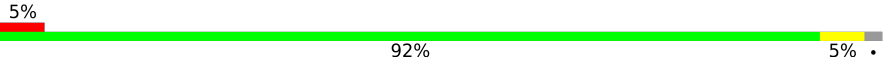


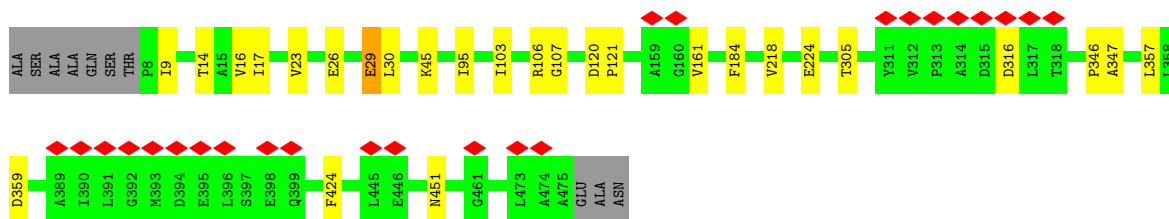
• Molecule 2: ATP synthase subunit alpha

Chain C:  91% 7%




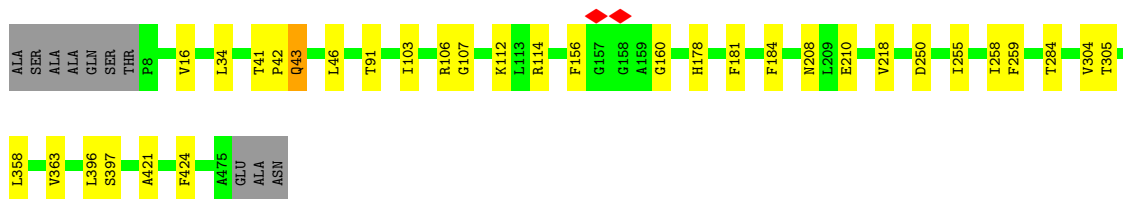
• Molecule 3: ATP synthase subunit beta

Chain D:  92% 5% 5%




• Molecule 3: ATP synthase subunit beta

Chain E:  91% 7%



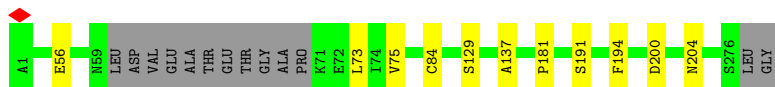
• Molecule 3: ATP synthase subunit beta

Chain F:  90% 8%

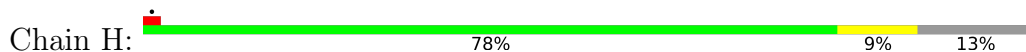




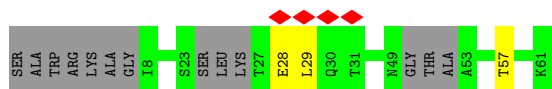
• Molecule 4: ATP synthase subunit gamma



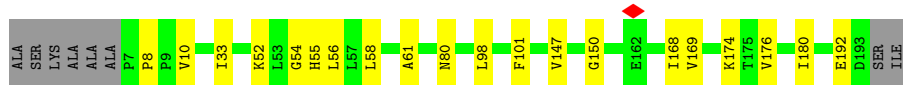
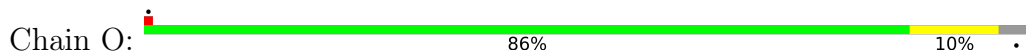
• Molecule 5: ATP synthase subunit delta



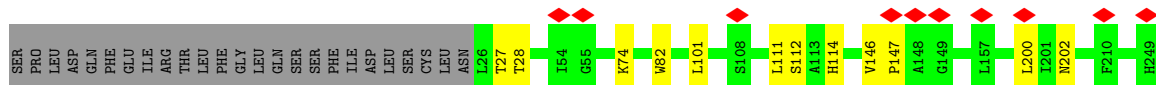
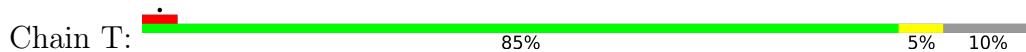
• Molecule 6: ATP synthase subunit epsilon



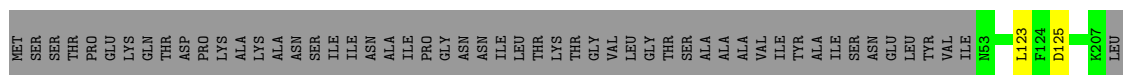
• Molecule 7: ATP synthase subunit 5



• Molecule 8: ATP synthase subunit a

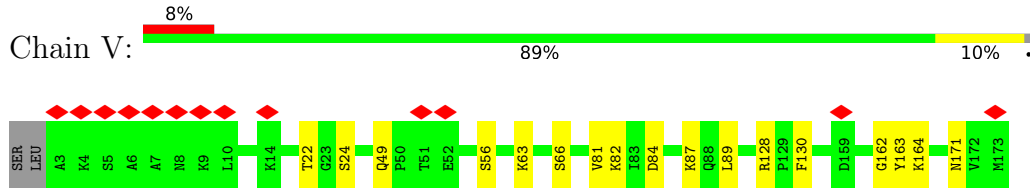


• Molecule 9: ATP synthase subunit 4

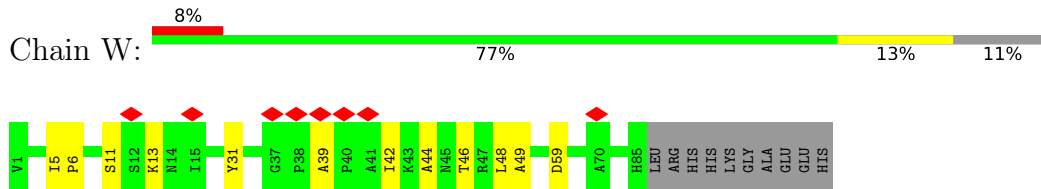


LYS

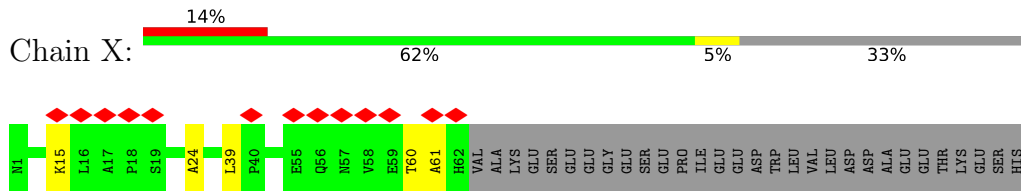
• Molecule 10: ATP synthase subunit d



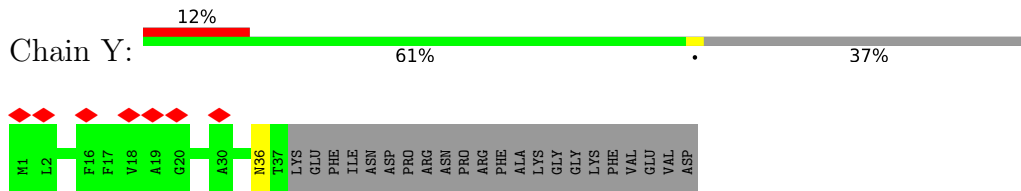
• Molecule 11: ATP synthase subunit f



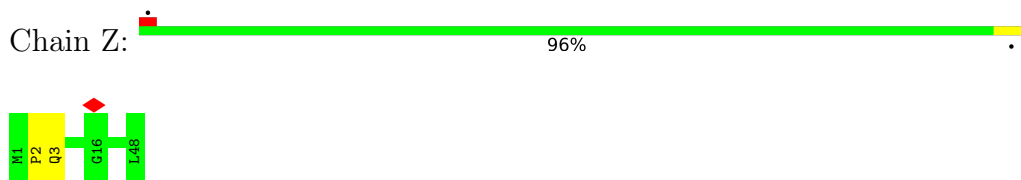
• Molecule 12: ATP synthase subunit H



• Molecule 13: ATP synthase subunit J



• Molecule 14: ATP synthase protein 8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10550	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	133843	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.898	Depositor
Minimum map value	-0.578	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.106	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	344.96, 344.96, 344.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3475, 1.3475, 1.3475	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	0	1.24	0/299	2.22	12/372 (3.2%)
1	1	1.26	0/299	1.99	4/372 (1.1%)
1	2	1.25	0/299	2.00	2/372 (0.5%)
1	3	1.29	0/295	1.96	6/367 (1.6%)
1	4	1.25	0/299	2.03	2/372 (0.5%)
1	5	1.25	0/299	2.05	3/372 (0.8%)
1	6	1.23	0/295	2.15	8/367 (2.2%)
1	7	1.22	0/291	2.05	8/362 (2.2%)
1	8	1.25	0/299	2.20	12/372 (3.2%)
1	9	1.24	0/295	2.10	7/367 (1.9%)
2	A	1.60	1/1994 (0.1%)	1.71	33/2489 (1.3%)
2	B	1.59	0/2018	1.75	26/2519 (1.0%)
2	C	1.60	0/1991	1.71	32/2487 (1.3%)
3	D	1.51	0/1871	1.75	30/2337 (1.3%)
3	E	1.60	0/1871	1.78	29/2337 (1.2%)
3	F	1.60	0/1875	1.72	30/2342 (1.3%)
4	G	1.50	0/1058	1.76	10/1319 (0.8%)
5	H	1.52	0/475	1.77	9/585 (1.5%)
6	I	1.32	0/190	1.74	0/231
7	O	1.60	0/747	1.83	18/932 (1.9%)
8	T	1.38	1/896 (0.1%)	1.59	10/1117 (0.9%)
9	U	1.36	0/619	1.71	4/772 (0.5%)
10	V	1.40	0/684	1.85	11/852 (1.3%)
11	W	1.33	0/339	1.88	5/422 (1.2%)
12	X	1.37	0/247	2.14	5/307 (1.6%)
13	Y	1.24	0/147	1.71	1/182 (0.5%)
14	Z	1.33	0/192	1.58	2/237 (0.8%)
All	All	1.50	2/20184 (0.0%)	1.80	319/25162 (1.3%)

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	1	0	1
1	3	0	1
1	4	0	1
1	5	0	1
1	6	0	1
1	7	0	1
1	8	0	1
1	9	0	1
5	H	0	1
All	All	0	9

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	478	HIS	CA-C	-5.65	1.48	1.53
8	T	111	LEU	CA-C	-5.05	1.49	1.52

All (319) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	376	VAL	N-CA-C	-10.89	103.02	111.62
2	B	398	GLN	N-CA-C	-9.45	101.89	113.41
7	O	180	ILE	N-CA-C	-8.96	102.08	111.58
3	F	95	ILE	N-CA-C	-8.72	95.91	108.11
3	E	258	ILE	N-CA-C	-8.55	102.70	113.22
2	B	96	ILE	N-CA-C	-8.21	100.94	110.21
3	E	112	LYS	N-CA-C	-7.90	100.82	111.96
3	E	304	VAL	N-CA-C	-7.83	101.52	110.05
2	B	234	VAL	N-CA-C	-7.77	97.26	108.53
2	A	479	ASN	N-CA-C	-7.68	103.91	113.28
4	G	204	ASN	CA-C-N	7.67	125.07	120.24
4	G	204	ASN	C-N-CA	7.67	125.07	120.24
3	F	258	ILE	N-CA-C	-7.62	105.29	112.83
8	T	146	VAL	N-CA-C	-7.56	99.13	108.05
5	H	61	GLU	N-CA-C	-7.48	96.07	108.34
4	G	137	ALA	N-CA-C	-7.35	100.81	110.07
5	H	56	VAL	N-CA-C	-7.34	97.83	108.11
2	A	352	ILE	N-CA-C	-7.33	97.57	108.12
7	O	33	ILE	N-CA-C	-7.25	105.57	111.81
2	A	232	ILE	N-CA-C	-7.25	97.72	108.45
3	E	305	THR	N-CA-C	-7.24	97.62	108.99
3	D	121	PRO	CA-C-O	-7.24	115.69	120.90
3	F	161	VAL	N-CA-C	-7.23	105.49	112.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	160	GLY	N-CA-C	-7.06	104.44	116.01
3	D	218	VAL	N-CA-C	-7.05	97.96	108.12
2	A	99	VAL	N-CA-C	-7.04	103.42	109.19
2	C	234	VAL	N-CA-C	-7.02	98.34	108.17
2	B	175	THR	N-CA-C	-7.02	103.17	112.72
2	A	175	THR	N-CA-C	-7.01	104.64	112.57
8	T	101	LEU	N-CA-C	-6.96	104.65	113.43
2	B	296	TYR	N-CA-C	-6.85	100.86	110.31
7	O	98	LEU	N-CA-C	-6.84	103.64	113.21
3	D	17	ILE	N-CA-C	-6.81	97.64	107.78
3	E	43	GLN	N-CA-C	-6.75	104.35	112.59
5	H	41	VAL	N-CA-C	-6.73	98.43	108.46
3	E	184	PHE	N-CA-C	-6.73	97.77	108.73
2	C	169	ILE	N-CA-C	-6.69	98.22	107.99
2	B	22	SER	N-CA-C	-6.67	106.09	114.56
7	O	56	LEU	N-CA-C	-6.67	105.18	113.38
3	E	114	ARG	N-CA-C	-6.64	99.22	109.52
3	D	16	VAL	N-CA-C	-6.63	97.95	107.77
3	D	26	GLU	N-CA-C	-6.63	105.10	113.72
10	V	56	SER	N-CA-C	-6.61	102.71	111.24
3	E	181	PHE	N-CA-C	-6.58	99.58	108.86
10	V	164	LYS	N-CA-C	-6.51	106.29	114.56
2	C	109	VAL	N-CA-C	-6.51	99.02	108.71
1	6	54	GLY	CA-C-N	6.50	128.89	120.44
1	6	54	GLY	C-N-CA	6.50	128.89	120.44
2	A	331	THR	N-CA-C	-6.49	99.11	109.76
3	E	363	VAL	N-CA-C	-6.49	106.46	112.43
7	O	174	LYS	N-CA-C	-6.47	97.83	108.76
2	B	479	ASN	N-CA-C	-6.46	105.15	113.16
1	8	43	ILE	CA-C-N	6.45	129.21	120.38
1	8	43	ILE	C-N-CA	6.45	129.21	120.38
3	D	161	VAL	N-CA-C	-6.42	106.26	112.29
3	E	106	ARG	N-CA-C	-6.41	105.42	112.72
7	O	147	VAL	N-CA-C	-6.39	97.99	107.51
7	O	176	VAL	N-CA-C	-6.39	98.92	108.12
3	E	208	ASN	N-CA-C	-6.37	97.18	108.13
2	C	175	THR	N-CA-C	-6.34	102.86	111.55
2	C	376	VAL	N-CA-C	-6.27	104.17	113.39
3	D	106	ARG	N-CA-C	-6.26	104.95	112.59
2	B	262	ASN	N-CA-C	-6.26	105.22	112.92
2	C	206	VAL	N-CA-C	-6.25	99.35	108.11
3	F	112	LYS	N-CA-C	-6.24	104.73	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	187	VAL	N-CA-C	-6.22	99.47	108.36
2	C	133	VAL	N-CA-C	-6.21	99.18	108.12
2	C	422	ARG	CA-C-N	6.17	126.83	119.98
2	C	422	ARG	C-N-CA	6.17	126.83	119.98
10	V	81	VAL	N-CA-C	-6.17	106.71	113.43
3	D	103	ILE	N-CA-C	-6.16	106.31	112.17
12	X	60	THR	N-CA-C	-6.15	105.72	113.72
5	H	42	LEU	N-CA-C	-6.14	97.43	108.48
3	E	250	ASP	N-CA-C	-6.14	99.19	109.07
3	F	106	ARG	N-CA-C	-6.14	105.11	112.59
3	F	23	VAL	N-CA-C	-6.13	99.41	108.85
3	F	103	ILE	N-CA-C	-6.12	105.69	113.22
4	G	73	LEU	N-CA-C	-6.11	100.23	109.95
3	F	153	ILE	N-CA-C	-6.09	99.64	108.89
2	B	61	VAL	N-CA-C	-6.08	103.43	110.05
2	C	506	PHE	N-CA-C	-6.06	103.12	110.88
3	F	222	MET	N-CA-C	-6.04	105.17	112.54
3	D	45	LYS	N-CA-C	-6.03	99.17	109.24
2	B	42	ARG	N-CA-C	-6.01	98.60	108.76
3	E	210	GLU	N-CA-C	-6.01	105.78	113.23
2	A	443	GLN	CA-C-N	6.01	124.02	120.24
2	A	443	GLN	C-N-CA	6.01	124.02	120.24
2	C	232	ILE	N-CA-C	-6.00	99.84	108.48
3	E	178	HIS	N-CA-C	-6.00	105.05	112.72
2	C	130	ARG	N-CA-C	-5.99	100.14	109.72
3	E	42	PRO	N-CA-C	-5.99	108.45	114.68
3	F	53	HIS	N-CA-C	-5.97	99.46	109.07
2	B	93	THR	N-CA-C	-5.97	104.86	111.36
4	G	75	VAL	N-CA-C	-5.94	99.18	108.86
7	O	8	PRO	CA-C-N	5.93	127.25	119.84
7	O	8	PRO	C-N-CA	5.93	127.25	119.84
2	A	64	MET	N-CA-C	-5.93	100.40	109.41
2	B	68	LEU	N-CA-C	-5.91	99.09	108.73
3	F	16	VAL	N-CA-C	-5.90	97.07	109.34
2	C	93	THR	N-CA-C	-5.89	104.94	111.36
2	A	296	TYR	N-CA-C	-5.88	101.98	110.40
7	O	52	LYS	N-CA-C	-5.88	100.12	109.59
2	A	150	THR	N-CA-C	-5.87	107.10	114.56
3	F	42	PRO	N-CA-C	-5.87	108.58	114.68
3	E	46	LEU	N-CA-C	-5.86	98.85	108.76
4	G	129	SER	N-CA-C	-5.85	100.18	109.07
2	C	287	LEU	N-CA-C	-5.84	106.19	113.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	208	VAL	N-CA-C	-5.83	100.08	108.48
2	B	310	ARG	N-CA-C	-5.80	100.22	109.96
1	8	58	SER	CA-C-N	5.79	128.03	120.28
1	8	58	SER	C-N-CA	5.79	128.03	120.28
3	E	284	THR	N-CA-C	-5.78	106.04	112.57
3	F	218	VAL	N-CA-C	-5.78	99.80	108.12
1	9	44	LYS	N-CA-C	5.78	117.58	111.28
8	T	74	LYS	N-CA-C	-5.78	104.95	112.23
2	A	152	LEU	N-CA-C	-5.77	99.01	108.41
3	F	252	LEU	N-CA-C	-5.75	100.32	109.07
11	W	49	ALA	N-CA-C	-5.75	105.15	111.82
1	9	43	ILE	CA-C-N	5.74	127.97	120.28
1	9	43	ILE	C-N-CA	5.74	127.97	120.28
7	O	192	GLU	N-CA-C	-5.74	105.01	113.61
3	E	255	ILE	N-CA-C	-5.72	99.53	108.86
3	E	156	PHE	N-CA-C	-5.72	100.37	109.23
3	D	14	THR	N-CA-C	-5.71	107.31	114.56
2	C	354	LEU	N-CA-C	-5.70	101.31	110.14
1	0	10	ILE	CA-C-N	5.69	127.25	120.14
1	0	10	ILE	C-N-CA	5.69	127.25	120.14
3	F	395	GLU	N-CA-C	-5.69	104.92	112.94
5	H	14	PHE	N-CA-C	-5.69	99.01	108.34
8	T	27	THR	CA-C-N	5.68	127.90	120.28
8	T	27	THR	C-N-CA	5.68	127.90	120.28
14	Z	2	PRO	N-CA-C	-5.68	106.61	114.27
7	O	168	ILE	N-CA-C	-5.67	99.89	108.17
2	C	329	ILE	N-CA-C	-5.67	99.96	108.12
5	H	69	PHE	N-CA-C	-5.66	99.68	108.90
3	F	185	THR	N-CA-C	-5.66	99.20	108.76
2	C	148	VAL	N-CA-C	-5.65	99.36	107.78
3	E	103	ILE	N-CA-C	-5.64	107.24	112.43
2	A	32	ARG	N-CA-C	-5.64	99.22	108.76
8	T	114	HIS	N-CA-C	-5.64	97.26	107.75
3	F	255	ILE	N-CA-C	-5.64	99.94	108.17
2	C	380	ALA	N-CA-C	-5.63	106.23	114.39
5	H	59	VAL	N-CA-C	-5.62	100.03	108.12
2	B	128	ARG	N-CA-C	-5.62	100.62	109.50
3	D	23	VAL	N-CA-C	-5.61	100.40	108.48
2	C	78	PHE	N-CA-C	-5.60	106.61	113.50
2	B	336	VAL	N-CA-C	-5.59	107.30	112.83
3	D	107	GLY	CA-C-N	5.58	125.59	119.90
3	D	107	GLY	C-N-CA	5.58	125.59	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	W	13	LYS	N-CA-C	-5.58	105.08	113.89
3	E	91	THR	N-CA-C	-5.56	106.26	113.16
1	9	6	ALA	CA-C-N	5.56	127.73	120.28
1	9	6	ALA	C-N-CA	5.56	127.73	120.28
1	7	20	LEU	CA-C-N	5.55	126.14	119.98
1	7	20	LEU	C-N-CA	5.55	126.14	119.98
2	A	350	GLY	N-CA-C	-5.55	106.68	111.95
3	F	43	GLN	N-CA-C	-5.55	104.93	112.26
4	G	84	CYS	N-CA-C	-5.53	103.68	110.65
11	W	48	LEU	N-CA-C	-5.53	105.53	114.09
10	V	87	LYS	N-CA-C	-5.52	106.38	114.39
2	B	73	VAL	N-CA-C	-5.52	100.24	108.46
12	X	39	LEU	CA-C-N	5.50	125.50	119.89
12	X	39	LEU	C-N-CA	5.50	125.50	119.89
7	O	101	PHE	N-CA-C	-5.50	105.68	112.72
2	C	42	ARG	N-CA-C	-5.49	98.59	108.48
3	D	359	ASP	CA-C-N	5.49	128.19	120.28
3	D	359	ASP	C-N-CA	5.49	128.19	120.28
10	V	171	ASN	N-CA-C	-5.49	100.45	109.40
7	O	150	GLY	N-CA-C	-5.49	106.62	115.08
2	A	270	TYR	N-CA-C	-5.49	99.79	108.73
2	B	54	LEU	N-CA-C	-5.47	100.33	109.24
3	F	54	LEU	N-CA-C	-5.43	106.33	113.17
2	A	128	ARG	N-CA-C	-5.43	100.06	108.90
2	A	318	GLU	N-CA-C	-5.42	106.54	112.72
3	D	120	ASP	CA-C-N	5.41	123.61	119.66
3	D	120	ASP	C-N-CA	5.41	123.61	119.66
3	F	220	GLY	N-CA-C	-5.41	100.36	113.18
10	V	22	THR	N-CA-C	-5.39	99.89	109.06
1	3	18	GLY	CA-C-N	5.39	128.25	120.38
1	3	18	GLY	C-N-CA	5.39	128.25	120.38
1	7	10	ILE	CA-C-N	5.39	125.96	119.98
1	7	10	ILE	C-N-CA	5.39	125.96	119.98
7	O	8	PRO	N-CA-C	5.38	117.27	110.70
8	T	28	THR	CA-C-N	5.38	127.49	120.28
8	T	28	THR	C-N-CA	5.38	127.49	120.28
3	E	424	PHE	N-CA-C	5.38	117.22	111.36
2	B	90	VAL	N-CA-C	-5.38	100.64	108.17
3	D	29	GLU	N-CA-C	-5.36	99.39	110.80
11	W	6	PRO	N-CA-C	5.35	117.23	110.70
2	B	152	LEU	N-CA-C	-5.35	99.56	108.34
3	F	17	ILE	N-CA-C	-5.35	99.45	107.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9	10	ILE	CA-C-N	5.35	125.92	119.98
1	9	10	ILE	C-N-CA	5.35	125.92	119.98
1	8	10	ILE	CA-C-N	5.34	125.91	119.98
1	8	10	ILE	C-N-CA	5.34	125.91	119.98
3	D	95	ILE	N-CA-C	-5.34	100.69	108.17
3	F	335	LEU	N-CA-C	-5.34	100.19	108.90
1	0	12	ALA	CA-C-N	5.34	125.87	119.94
1	0	12	ALA	C-N-CA	5.34	125.87	119.94
1	6	10	ILE	CA-C-N	5.33	125.90	119.98
1	6	10	ILE	C-N-CA	5.33	125.90	119.98
3	E	107	GLY	CA-C-N	5.33	126.50	119.84
3	E	107	GLY	C-N-CA	5.33	126.50	119.84
3	E	218	VAL	N-CA-C	-5.33	99.88	107.77
2	C	210	GLN	N-CA-C	-5.33	101.88	110.14
3	F	60	ARG	N-CA-C	-5.32	99.77	108.76
2	C	408	PHE	N-CA-C	-5.31	106.57	113.16
3	D	9	ILE	N-CA-C	-5.31	100.10	107.80
10	V	163	TYR	N-CA-C	-5.31	106.31	112.89
2	A	492	SER	N-CA-C	-5.30	102.67	110.52
7	O	55	HIS	N-CA-C	-5.30	106.86	113.38
2	A	62	LYS	N-CA-C	-5.29	101.94	110.14
7	O	58	LEU	N-CA-C	-5.29	106.50	113.17
3	D	184	PHE	N-CA-C	-5.29	100.55	109.07
1	0	15	SER	CA-C-N	5.29	127.90	120.28
1	0	15	SER	C-N-CA	5.29	127.90	120.28
3	D	224	GLU	CA-C-N	5.26	125.80	120.38
3	D	224	GLU	C-N-CA	5.26	125.80	120.38
2	C	68	LEU	N-CA-C	-5.26	97.12	107.69
7	O	169	VAL	N-CA-C	-5.25	100.88	108.71
8	T	200	LEU	N-CA-C	-5.25	107.05	113.50
1	0	20	LEU	CA-C-N	5.23	125.79	119.98
1	0	20	LEU	C-N-CA	5.23	125.79	119.98
1	0	61	THR	CA-C-N	5.22	125.78	119.98
1	0	61	THR	C-N-CA	5.22	125.78	119.98
1	6	61	THR	CA-C-N	5.22	125.77	119.98
1	6	61	THR	C-N-CA	5.22	125.77	119.98
2	A	169	ILE	N-CA-C	-5.22	98.49	109.34
4	G	200	ASP	N-CA-C	-5.21	100.40	108.90
3	D	30	LEU	CA-C-N	5.21	125.15	119.78
3	D	30	LEU	C-N-CA	5.21	125.15	119.78
2	B	386	LYS	N-CA-C	-5.21	106.61	113.12
2	A	76	VAL	N-CA-C	-5.20	100.89	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	265	HIS	N-CA-C	-5.19	101.47	109.52
2	B	6	GLN	N-CA-C	-5.19	100.45	108.55
1	4	61	THR	CA-C-N	5.19	125.74	119.98
1	4	61	THR	C-N-CA	5.19	125.74	119.98
3	D	424	PHE	CA-C-N	5.18	127.23	120.28
3	D	424	PHE	C-N-CA	5.18	127.23	120.28
1	5	41	PRO	N-CA-C	5.18	123.15	112.47
11	W	59	ASP	N-CA-C	-5.17	106.66	113.17
2	C	487	GLU	N-CA-C	5.16	116.99	111.36
5	H	60	MET	N-CA-C	-5.16	100.03	108.76
2	A	117	ILE	N-CA-C	-5.16	107.72	112.83
1	2	20	LEU	CA-C-N	5.16	125.70	119.98
1	2	20	LEU	C-N-CA	5.16	125.70	119.98
1	8	22	ALA	CA-C-N	5.15	125.66	119.94
1	8	22	ALA	C-N-CA	5.15	125.66	119.94
2	C	128	ARG	N-CA-C	-5.15	101.53	109.52
2	C	324	THR	N-CA-C	-5.15	101.77	109.95
3	F	275	ILE	N-CA-C	-5.14	103.91	108.95
1	0	24	ILE	CA-C-N	5.14	125.64	119.94
1	0	24	ILE	C-N-CA	5.14	125.64	119.94
1	7	43	ILE	CA-C-N	5.14	127.42	120.38
1	7	43	ILE	C-N-CA	5.14	127.42	120.38
5	H	45	HIS	N-CA-C	-5.13	101.39	109.50
3	D	357	LEU	N-CA-C	-5.13	105.74	112.41
10	V	49	GLN	N-CA-C	-5.13	102.40	110.14
3	F	207	ILE	N-CA-C	-5.12	101.03	108.36
10	V	24	SER	CA-C-N	5.12	127.15	120.28
10	V	24	SER	C-N-CA	5.12	127.15	120.28
1	1	43	ILE	CA-C-N	5.12	127.86	120.38
1	1	43	ILE	C-N-CA	5.12	127.86	120.38
2	A	422	ARG	CA-C-N	5.12	125.66	119.98
2	A	422	ARG	C-N-CA	5.12	125.66	119.98
1	8	6	ALA	CA-C-N	5.11	127.13	120.28
1	8	6	ALA	C-N-CA	5.11	127.13	120.28
2	B	233	ILE	N-CA-C	-5.11	100.95	108.11
2	A	197	GLU	N-CA-C	-5.11	106.73	113.17
2	B	156	ASP	N-CA-C	-5.11	99.92	110.80
2	B	158	LEU	N-CA-C	-5.11	99.92	110.80
1	8	50	MET	CA-C-N	5.11	127.13	120.28
1	8	50	MET	C-N-CA	5.11	127.13	120.28
2	C	90	VAL	N-CA-C	-5.11	100.85	108.46
8	T	112	SER	N-CA-C	-5.10	105.81	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	Y	36	ASN	N-CA-C	-5.10	100.86	109.07
14	Z	3	GLN	N-CA-C	-5.10	106.65	112.92
1	6	43	ILE	CA-C-N	5.09	127.36	120.38
1	6	43	ILE	C-N-CA	5.09	127.36	120.38
3	F	79	THR	N-CA-C	-5.07	107.14	113.38
10	V	63	LYS	N-CA-C	-5.07	107.12	113.72
2	A	198	SER	N-CA-C	-5.07	106.93	113.02
2	A	328	VAL	N-CA-C	-5.07	101.01	108.11
3	E	259	PHE	N-CA-C	-5.07	105.83	111.36
2	A	81	ASP	CA-C-N	5.07	127.07	120.28
2	A	81	ASP	C-N-CA	5.07	127.07	120.28
9	U	123	LEU	CA-C-N	5.07	127.03	120.44
9	U	123	LEU	C-N-CA	5.07	127.03	120.44
3	F	184	PHE	N-CA-C	-5.06	100.65	108.90
3	E	396	LEU	N-CA-C	-5.06	101.39	109.23
2	C	34	LEU	N-CA-C	-5.05	108.38	114.75
1	3	20	LEU	CA-C-N	5.04	125.55	120.00
1	3	20	LEU	C-N-CA	5.04	125.55	120.00
4	G	191	SER	CA-C-N	5.04	126.14	119.84
4	G	191	SER	C-N-CA	5.04	126.14	119.84
3	E	421	ALA	N-CA-C	-5.04	106.98	112.72
2	B	159	VAL	N-CA-C	-5.04	98.00	108.88
3	F	115	LYS	CA-C-N	5.03	124.94	119.76
3	F	115	LYS	C-N-CA	5.03	124.94	119.76
2	A	323	LEU	N-CA-C	-5.03	100.08	110.80
2	C	19	LYS	CA-C-N	5.03	125.56	119.98
2	C	19	LYS	C-N-CA	5.03	125.56	119.98
3	D	316	ASP	N-CA-C	-5.03	100.53	108.73
1	7	61	THR	CA-C-N	5.03	125.56	119.98
1	7	61	THR	C-N-CA	5.03	125.56	119.98
3	D	305	THR	N-CA-C	-5.02	101.05	109.24
12	X	24	ALA	CA-C-N	5.02	127.01	120.28
12	X	24	ALA	C-N-CA	5.02	127.01	120.28
1	5	61	THR	CA-C-N	5.02	125.55	119.98
1	5	61	THR	C-N-CA	5.02	125.55	119.98
1	1	22	ALA	CA-C-N	5.01	125.55	119.98
1	1	22	ALA	C-N-CA	5.01	125.55	119.98
2	A	336	VAL	N-CA-C	-5.01	107.03	112.80
2	C	117	ILE	N-CA-C	-5.01	108.24	113.10
9	U	125	ASP	CA-C-N	5.01	127.32	120.46
9	U	125	ASP	C-N-CA	5.01	127.32	120.46
1	3	19	LEU	CA-C-N	5.00	127.23	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3	19	LEU	C-N-CA	5.00	127.23	120.38
2	C	205	TYR	N-CA-C	-5.00	101.02	109.07

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	40	ASN	Peptide
1	3	40	ASN	Peptide
1	4	40	ASN	Peptide
1	5	40	ASN	Peptide
1	6	40	ASN	Peptide
1	7	40	ASN	Peptide
1	8	40	ASN	Peptide
1	9	40	ASN	Peptide
5	H	54	PRO	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	0	300	0	95	0	0
1	1	300	0	95	0	0
1	2	300	0	95	0	0
1	3	296	0	91	0	0
1	4	300	0	95	0	0
1	5	300	0	95	0	0
1	6	296	0	91	0	0
1	7	292	0	91	0	0
1	8	300	0	95	0	0
1	9	296	0	91	0	0
2	A	1996	0	570	0	0
2	B	2020	0	575	1	0
2	C	1992	0	572	0	0
3	D	1872	0	537	0	0
3	E	1872	0	537	1	0
3	F	1876	0	537	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	1060	0	277	0	0
5	H	480	0	122	0	0
6	I	193	0	43	0	0
7	O	748	0	205	0	0
8	T	897	0	248	0	0
9	U	620	0	158	0	0
10	V	685	0	173	0	0
11	W	340	0	92	0	0
12	X	248	0	61	0	0
13	Y	148	0	40	0	0
14	Z	193	0	49	0	0
All	All	20220	0	5730	2	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 0.

All (2) 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)
3:E:41:THR:C	3:E:43:GLN:H	2.27	0.42
2:B:174:GLN:C	2:B:176:GLY:H	2.27	0.41

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	0	73/76 (96%)	72 (99%)	1 (1%)	0	100 100
1	1	73/76 (96%)	70 (96%)	2 (3%)	1 (1%)	9 39
1	2	73/76 (96%)	72 (99%)	1 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	72/76 (95%)	70 (97%)	1 (1%)	1 (1%)	9	39
1	4	73/76 (96%)	70 (96%)	1 (1%)	2 (3%)	4	25
1	5	73/76 (96%)	70 (96%)	2 (3%)	1 (1%)	9	39
1	6	72/76 (95%)	70 (97%)	1 (1%)	1 (1%)	9	39
1	7	71/76 (93%)	69 (97%)	1 (1%)	1 (1%)	9	39
1	8	73/76 (96%)	70 (96%)	2 (3%)	1 (1%)	9	39
1	9	72/76 (95%)	69 (96%)	2 (3%)	1 (1%)	9	39
2	A	495/510 (97%)	476 (96%)	15 (3%)	4 (1%)	16	52
2	B	501/510 (98%)	469 (94%)	22 (4%)	10 (2%)	6	31
2	C	496/510 (97%)	470 (95%)	20 (4%)	6 (1%)	10	42
3	D	466/478 (98%)	446 (96%)	16 (3%)	4 (1%)	14	49
3	E	466/478 (98%)	441 (95%)	21 (4%)	4 (1%)	14	49
3	F	467/478 (98%)	431 (92%)	28 (6%)	8 (2%)	7	35
4	G	261/278 (94%)	248 (95%)	10 (4%)	3 (1%)	11	45
5	H	110/138 (80%)	103 (94%)	4 (4%)	3 (3%)	4	25
6	I	42/61 (69%)	38 (90%)	1 (2%)	3 (7%)	1	11
7	O	185/195 (95%)	169 (91%)	12 (6%)	4 (2%)	5	29
8	T	222/249 (89%)	208 (94%)	11 (5%)	3 (1%)	9	39
9	U	153/209 (73%)	152 (99%)	1 (1%)	0	100	100
10	V	169/173 (98%)	153 (90%)	9 (5%)	7 (4%)	2	18
11	W	83/95 (87%)	71 (86%)	5 (6%)	7 (8%)	0	9
12	X	60/92 (65%)	54 (90%)	4 (7%)	2 (3%)	3	21
13	Y	35/59 (59%)	34 (97%)	1 (3%)	0	100	100
14	Z	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
All	All	4982/5321 (94%)	4709 (94%)	196 (4%)	77 (2%)	11	38

All (77) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	41	PRO
1	3	41	PRO
1	4	41	PRO
1	5	41	PRO
1	6	41	PRO

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Mol	Chain	Res	Type
1	7	41	PRO
1	8	41	PRO
1	9	41	PRO
2	B	28	ASN
2	B	157	ALA
2	B	311	ALA
2	C	379	ALA
3	D	347	ALA
3	E	358	LEU
3	F	451	ASN
6	I	28	GLU
7	O	80	ASN
8	T	202	ASN
10	V	66	SER
10	V	130	PHE
11	W	11	SER
11	W	46	THR
2	B	158	LEU
2	C	165	GLN
3	D	451	ASN
3	E	34	LEU
3	E	397	SER
3	F	299	THR
3	F	359	ASP
5	H	33	PRO
5	H	88	ILE
10	V	82	LYS
11	W	31	TYR
11	W	42	ILE
12	X	61	ALA
2	B	25	ALA
2	B	29	GLU
2	B	376	VAL
2	C	59	SER
2	C	71	GLY
3	D	29	GLU
3	D	346	PRO
3	F	86	PRO
3	F	131	ALA
6	I	29	LEU
7	O	54	GLY
7	O	61	ALA

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Mol	Chain	Res	Type
8	T	147	PRO
10	V	84	ASP
10	V	162	GLY
12	X	15	LYS
2	A	229	LYS
2	B	24	GLU
2	B	478	HIS
3	F	214	LYS
3	F	301	LYS
4	G	194	PHE
7	O	10	VAL
10	V	89	LEU
11	W	44	ALA
2	A	28	ASN
2	A	145	HIS
2	B	196	ASP
2	C	103	PRO
2	C	196	ASP
3	E	16	VAL
4	G	56	GLU
1	4	42	SER
6	I	57	THR
8	T	82	TRP
10	V	128	ARG
4	G	181	PRO
5	H	17	PRO
2	A	319	GLY
3	F	302	GLY
11	W	5	ILE
11	W	39	ALA

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

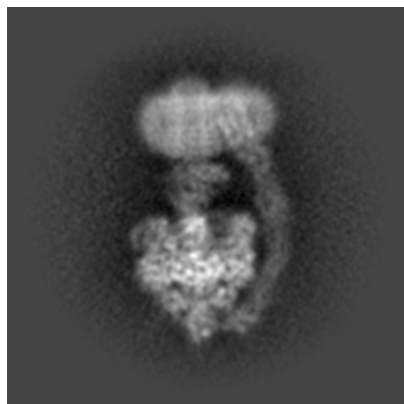
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25948. These allow visual inspection of the internal detail of the map and identification of artifacts.

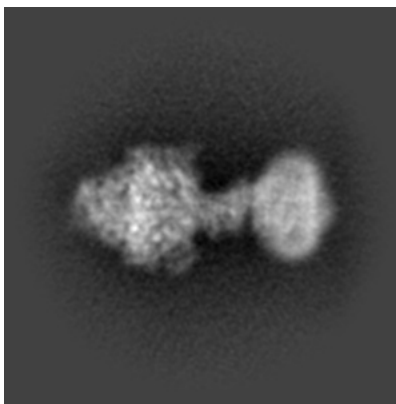
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

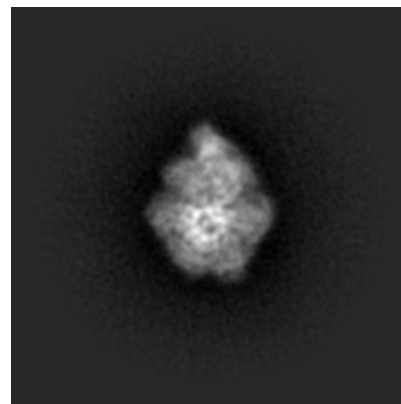
6.1.1 Primary map



X

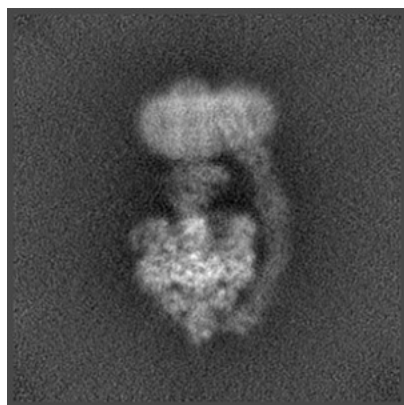


Y

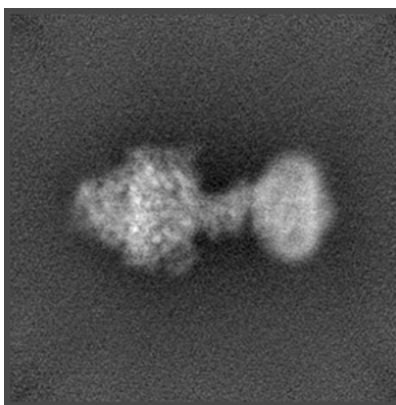


Z

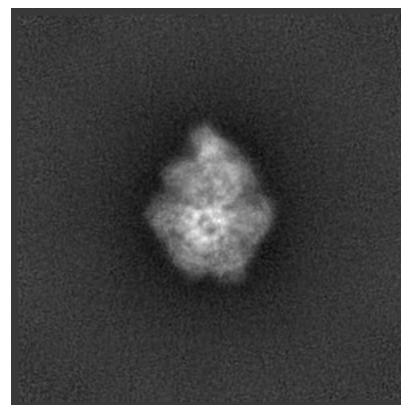
6.1.2 Raw map



X



Y

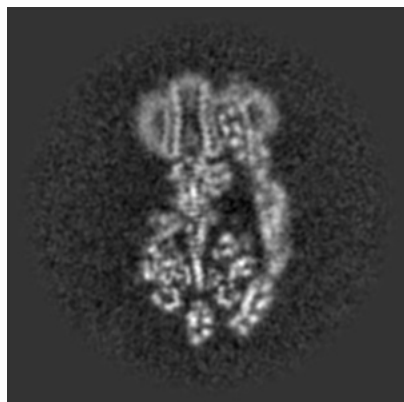


Z

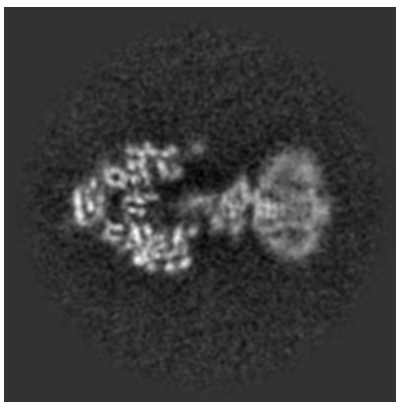
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

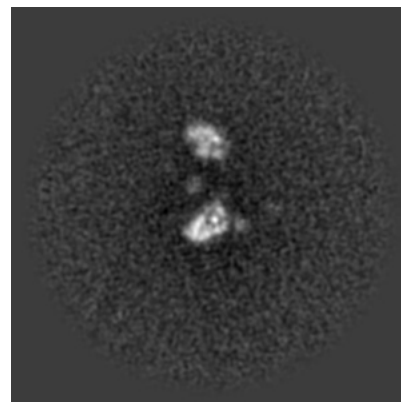
6.2.1 Primary map



X Index: 128

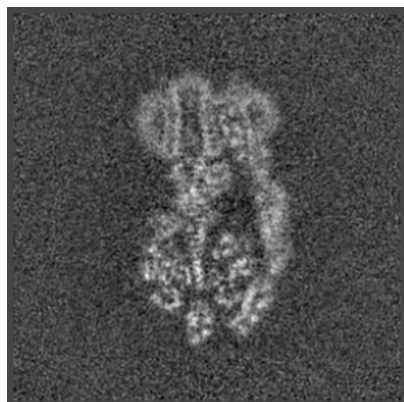


Y Index: 128

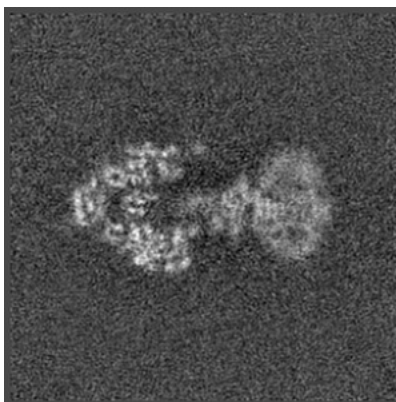


Z Index: 128

6.2.2 Raw map



X Index: 128



Y Index: 128

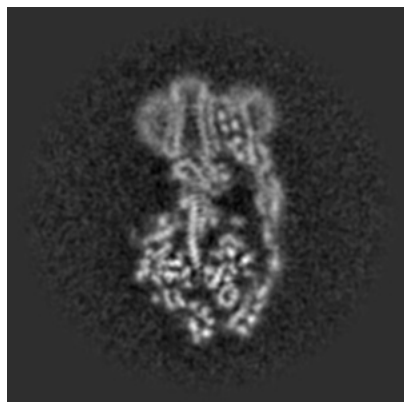


Z Index: 128

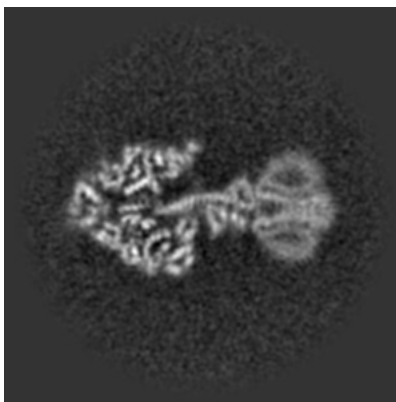
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

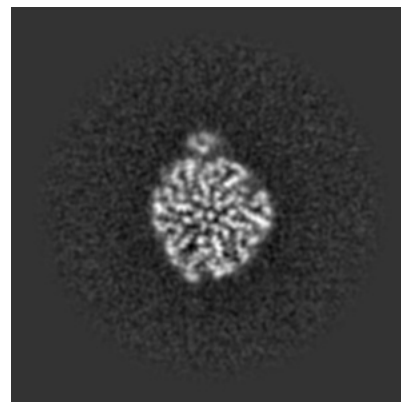
6.3.1 Primary map



X Index: 131



Y Index: 124

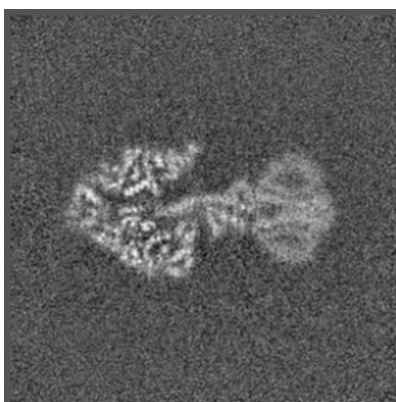


Z Index: 85

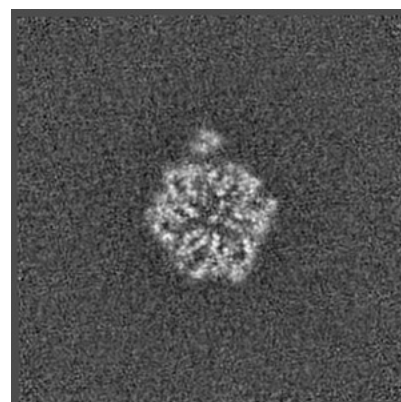
6.3.2 Raw map



X Index: 131



Y Index: 124

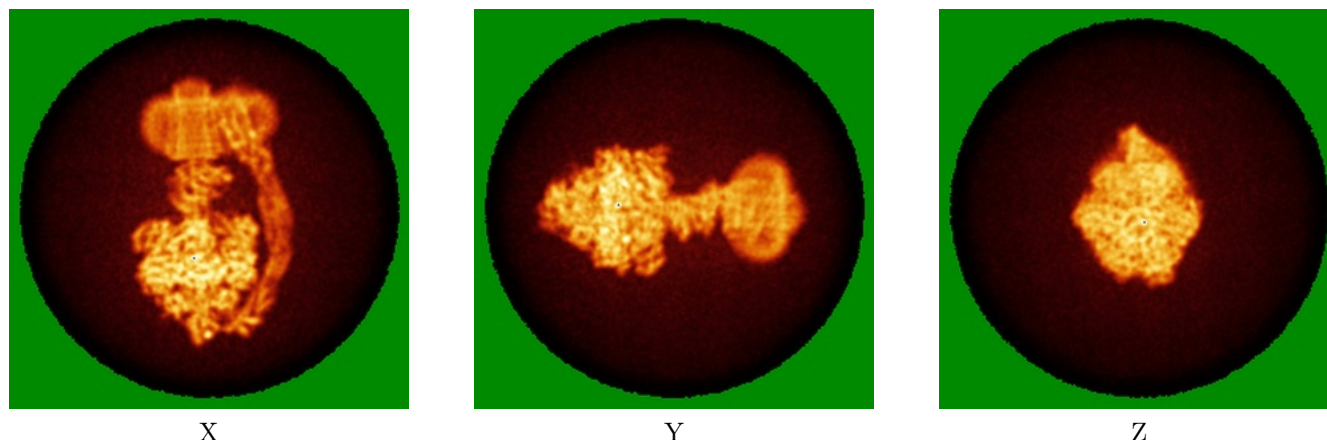


Z Index: 91

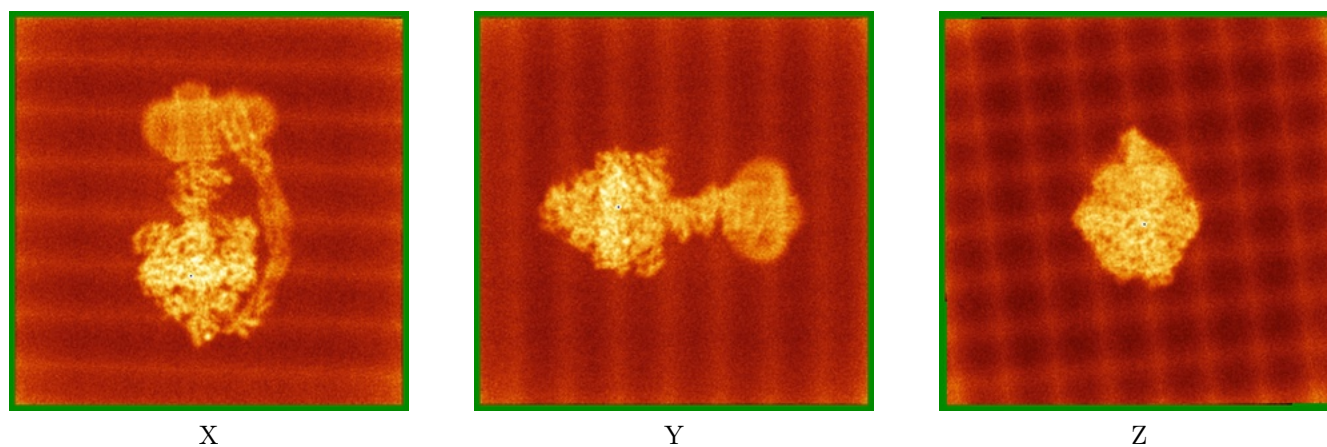
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



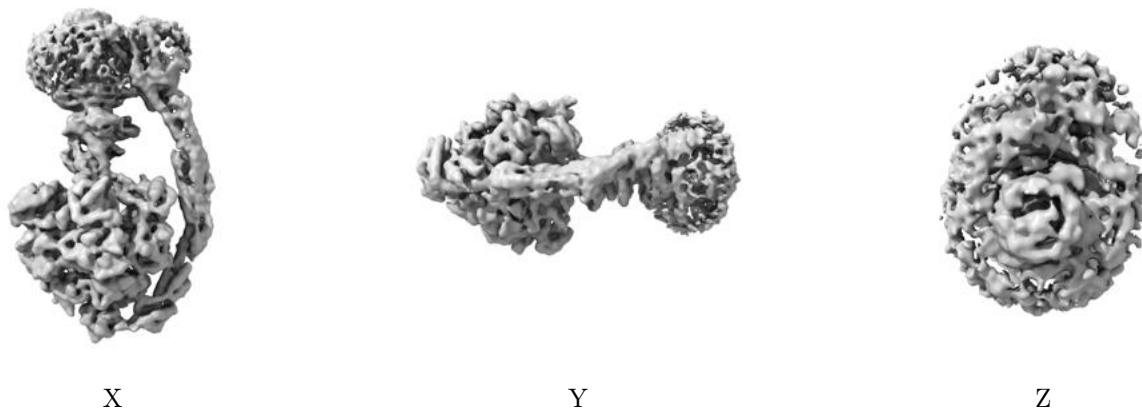
6.4.2 Raw map



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

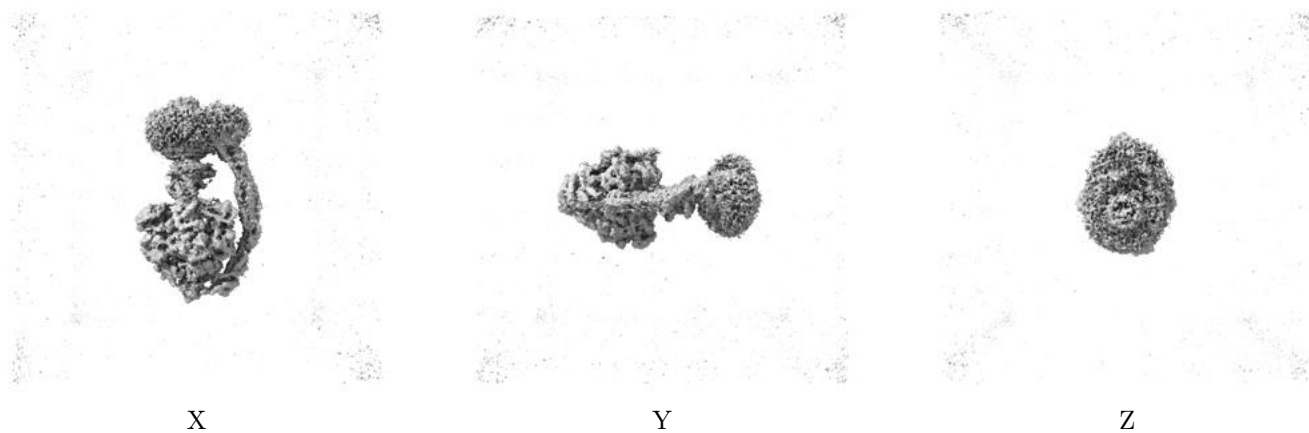
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. 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.

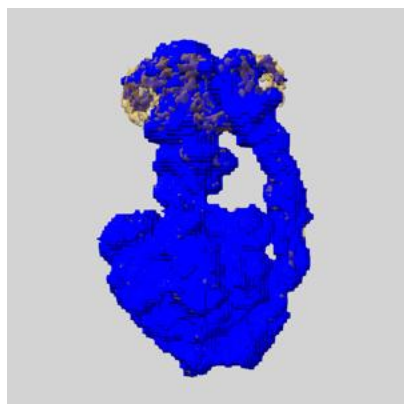
6.6 Mask visualisation [i](#)

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

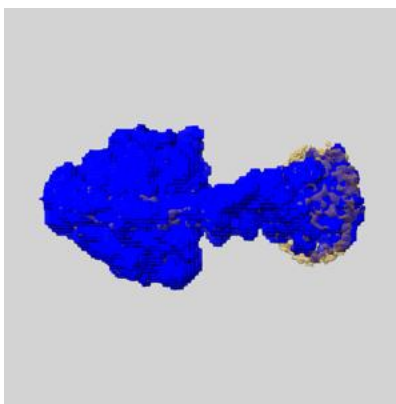
A mask typically either:

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

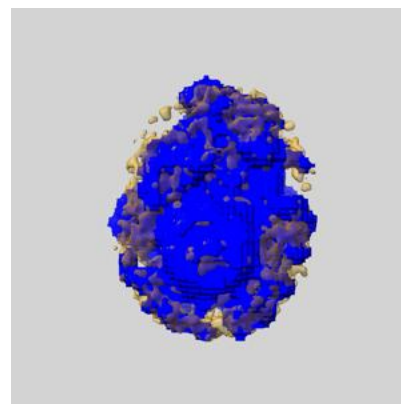
6.6.1 emd_25948_msk_1.map [i](#)



X



Y

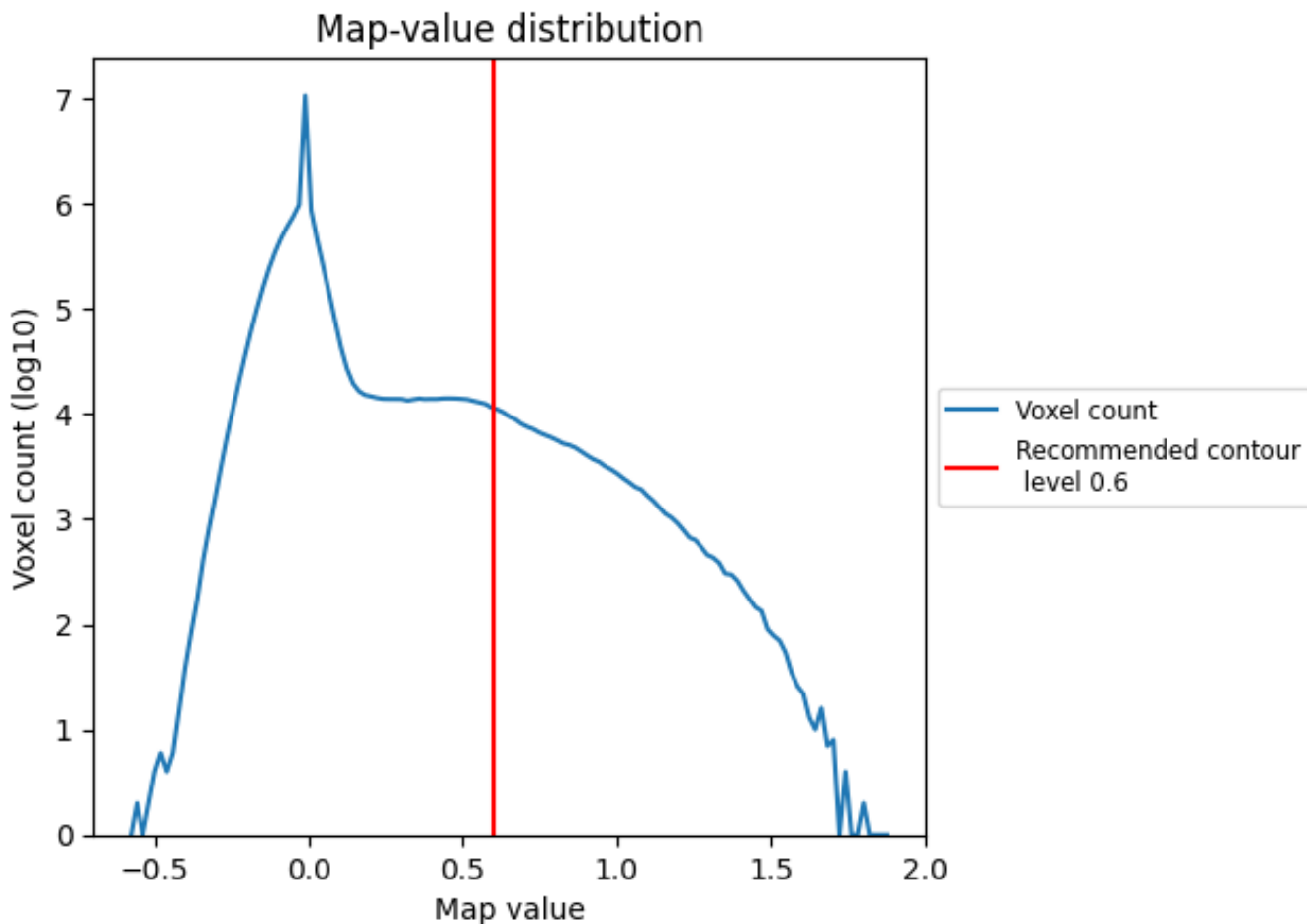


Z

7 Map analysis [i](#)

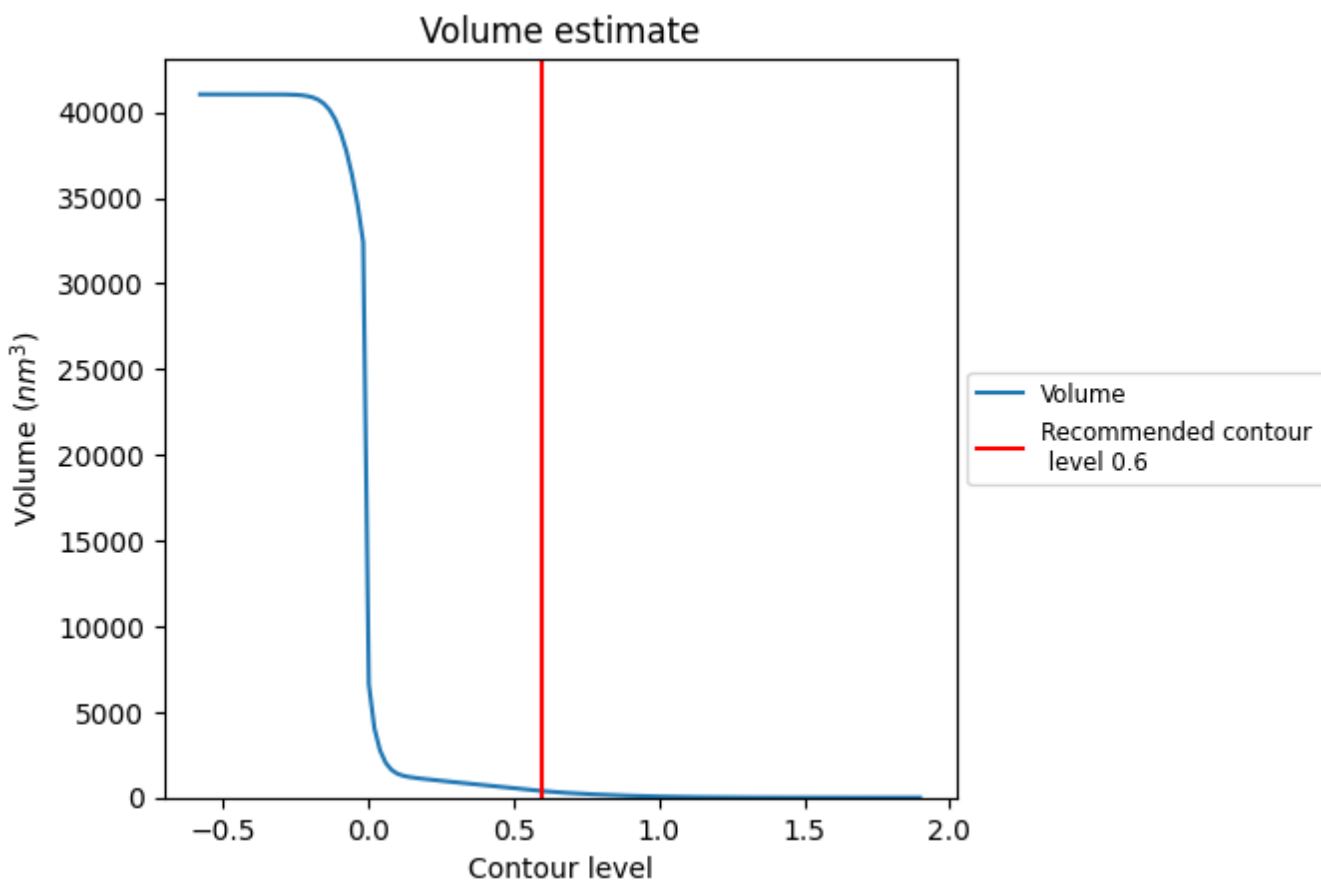
This section contains the results of statistical analysis of the map.

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.

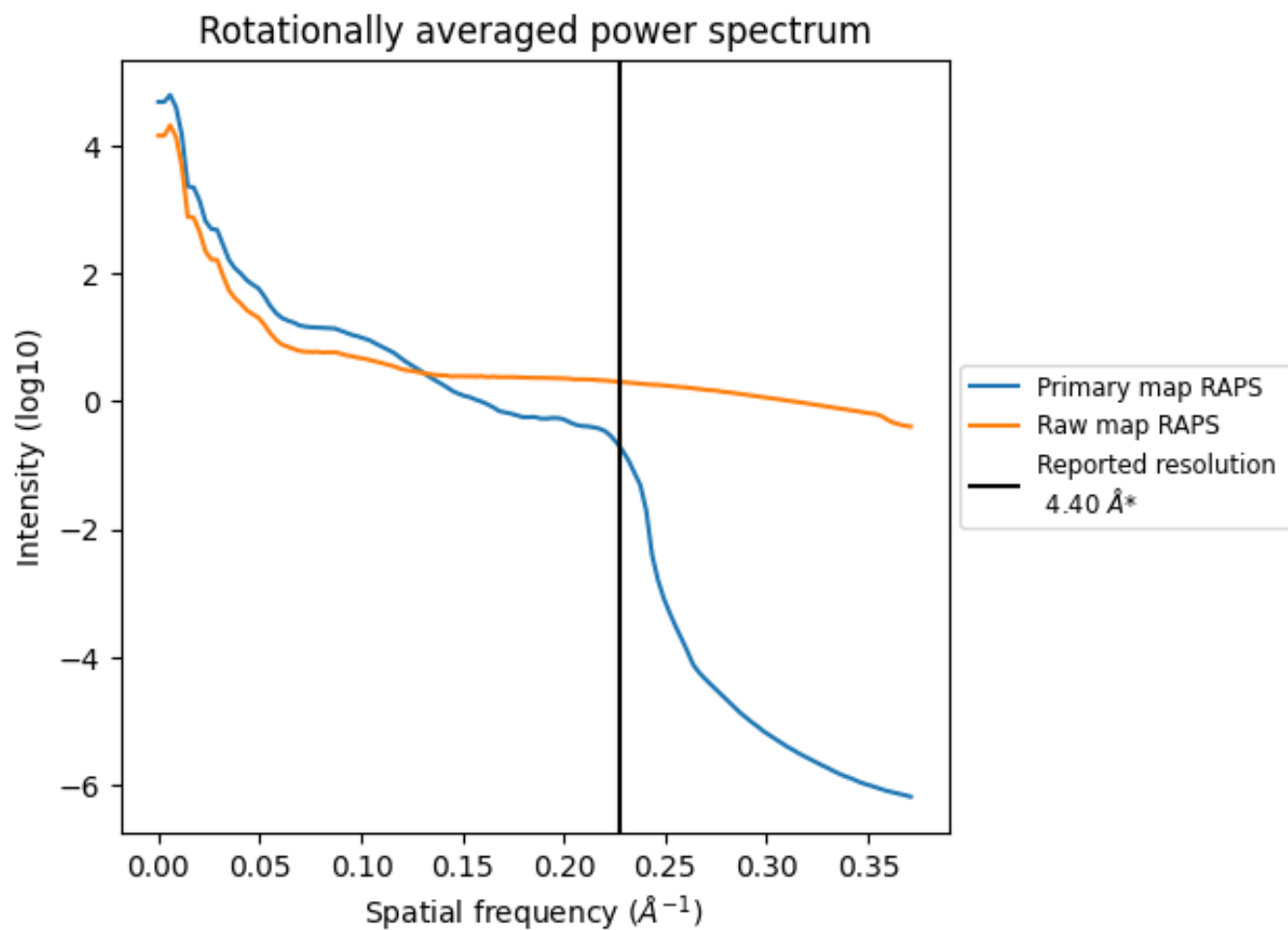
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 380 nm³; this corresponds to an approximate mass of 344 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

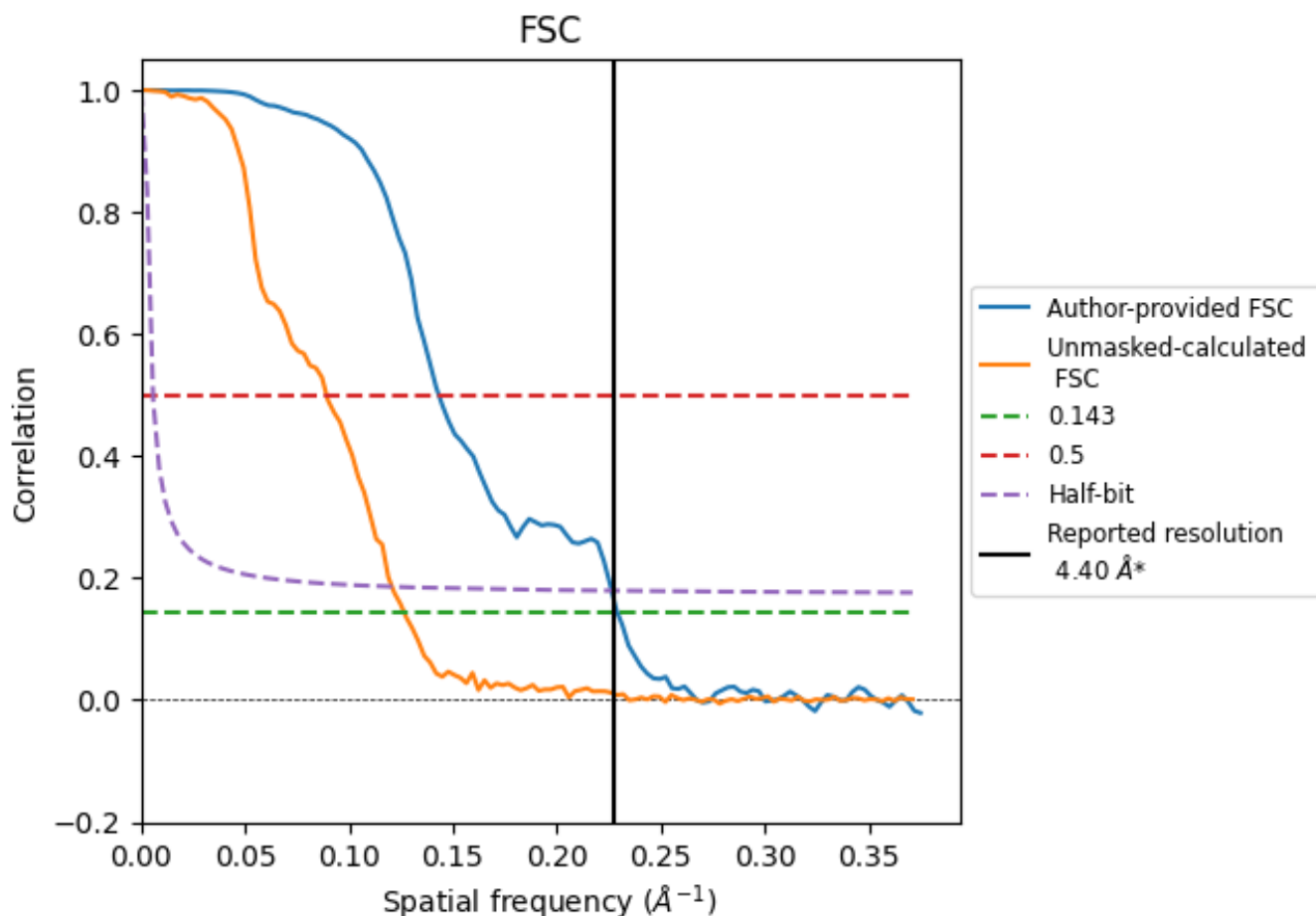


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

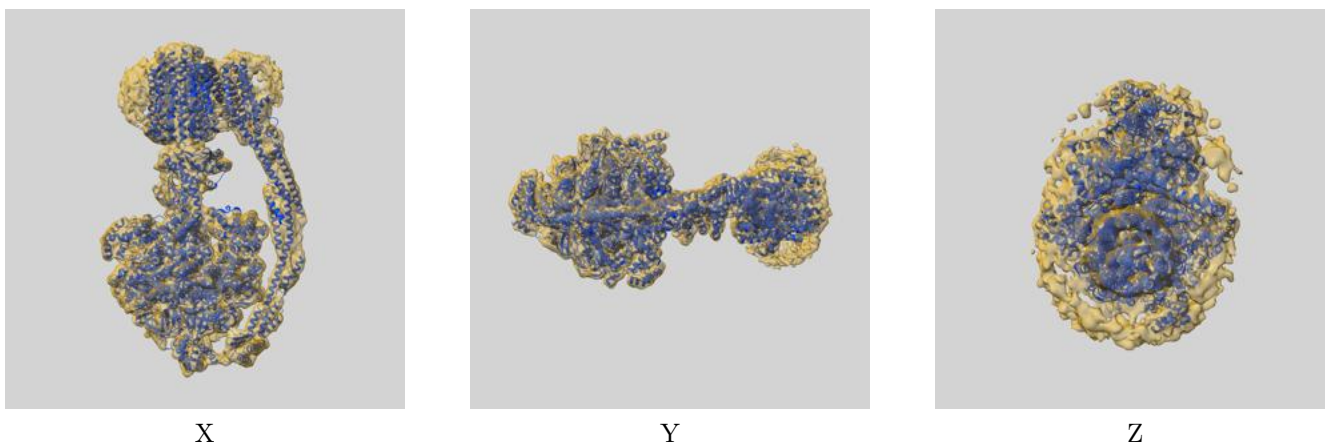
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.36	6.98	4.42
Unmasked-calculated*	7.91	11.21	8.29

*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 7.91 differs from the reported value 4.4 by more than 10 %

9 Map-model fit [i](#)

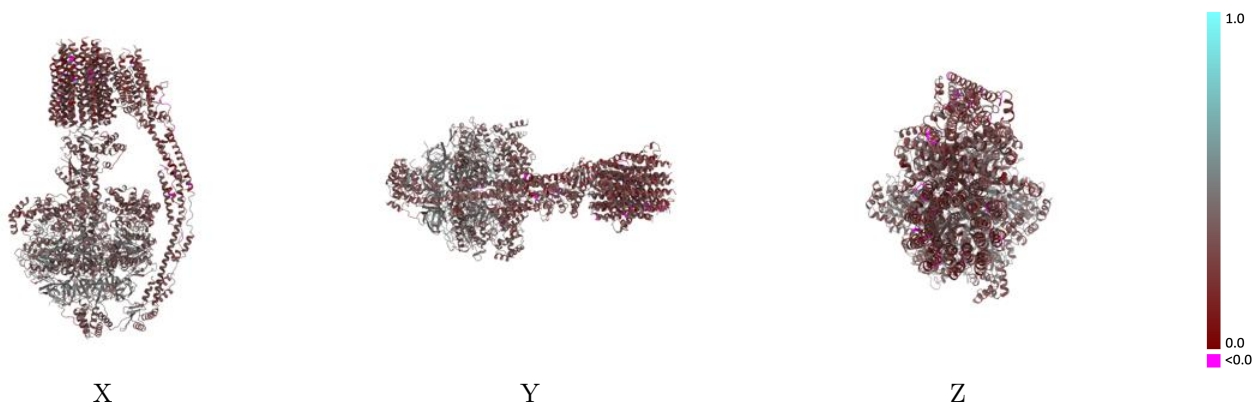
This section contains information regarding the fit between EMDB map EMD-25948 and PDB model 7TK0. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



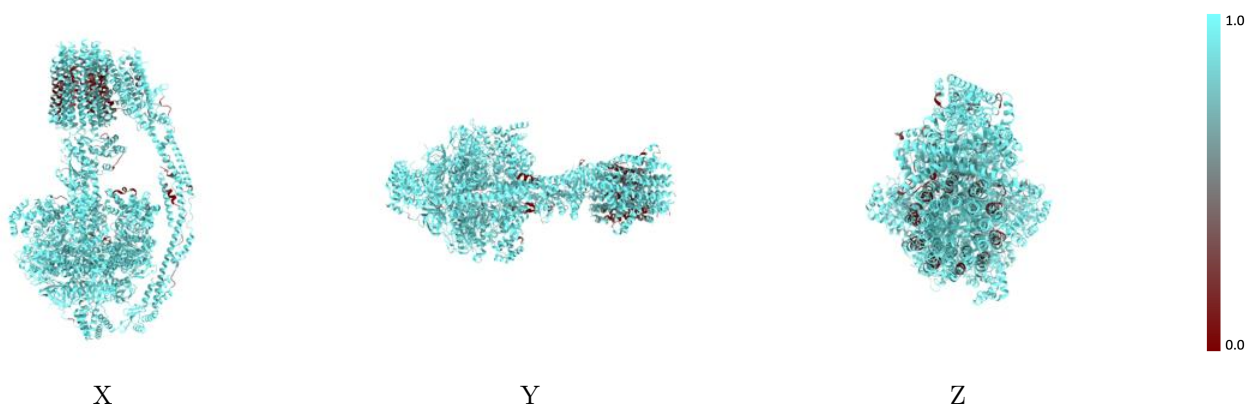
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



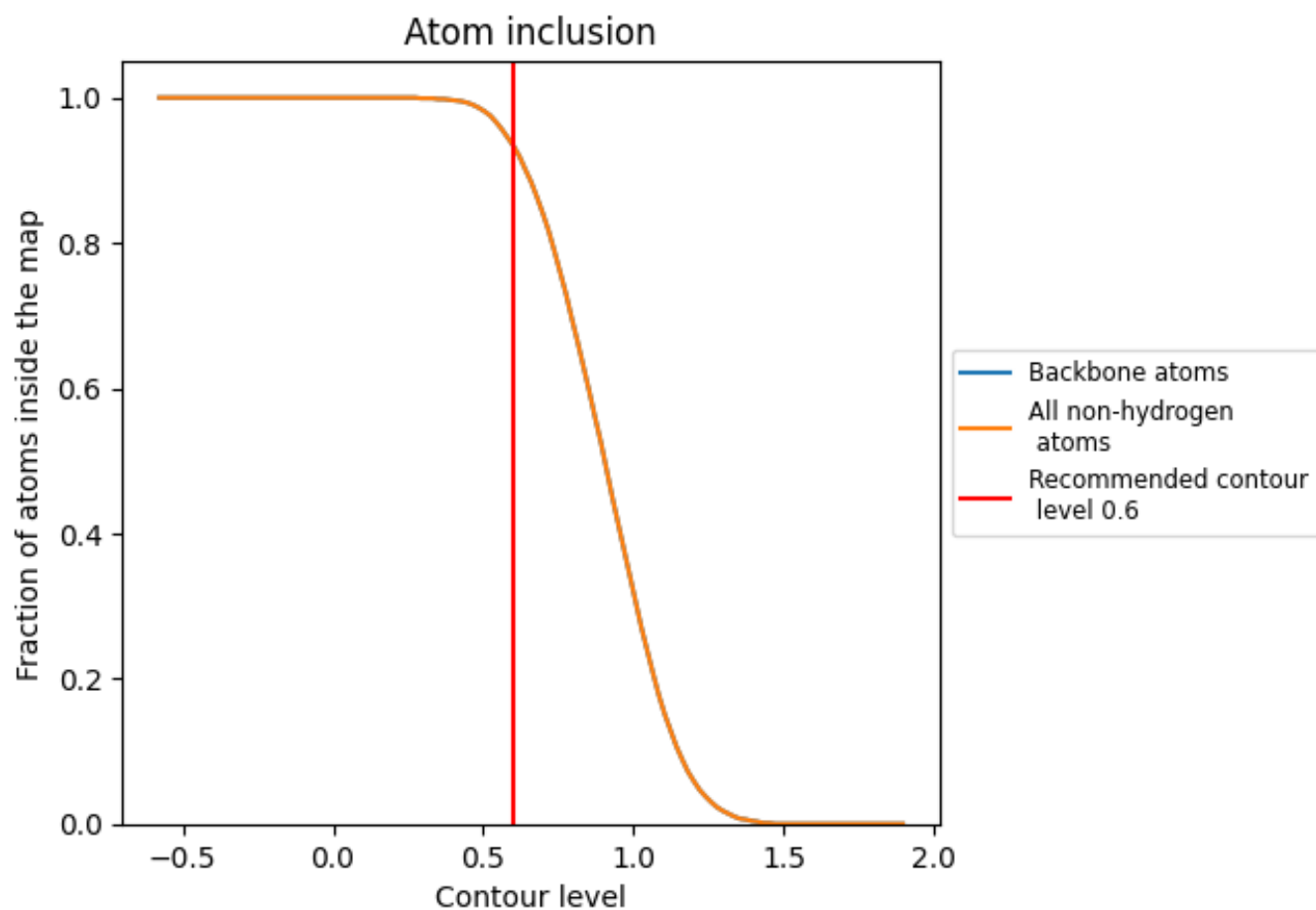
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.3530
0	 0.7600	 0.2630
1	 0.7630	 0.2740
2	 0.7800	 0.2640
3	 0.7200	 0.2330
4	 0.7300	 0.2660
5	 0.7470	 0.2440
6	 0.7370	 0.2300
7	 0.8150	 0.2520
8	 0.8130	 0.2470
9	 0.7970	 0.2560
A	 0.9900	 0.3980
B	 0.9790	 0.3960
C	 0.9860	 0.4010
D	 0.9230	 0.3860
E	 0.9880	 0.4060
F	 0.9980	 0.4180
G	 0.9780	 0.3400
H	 0.9350	 0.3390
I	 0.9020	 0.3070
O	 0.9910	 0.3510
T	 0.9240	 0.2870
U	 0.9860	 0.2970
V	 0.8900	 0.2860
W	 0.8500	 0.2220
X	 0.7500	 0.2850
Y	 0.7970	 0.2540
Z	 0.9590	 0.2780

