



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 11:27 PM UTC

PDB ID : 7TK2 / pdb_00007tk2
EMDB ID : EMD-25954
Title : Yeast ATP synthase State 1binding(a) with 10 mM ATP backbone model
Authors : Guo, H.; Rubinstein, J.L.
Deposited on : 2022-01-17
Resolution : 6.50 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

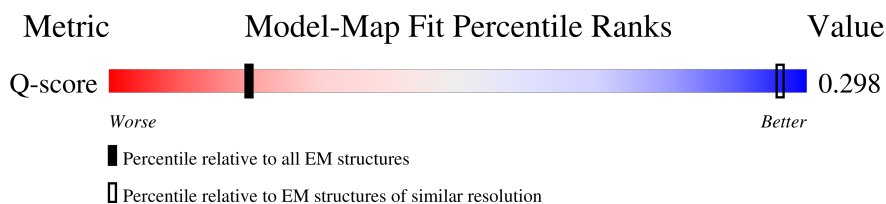
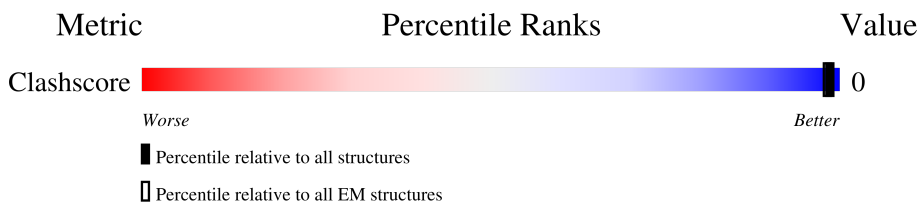
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

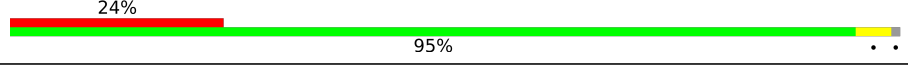
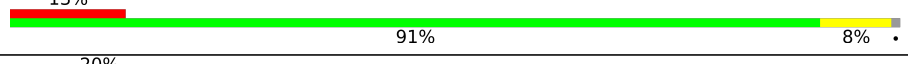
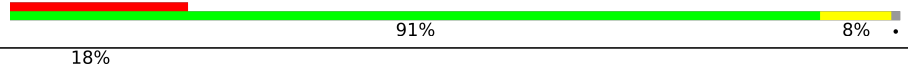
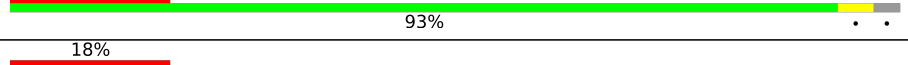
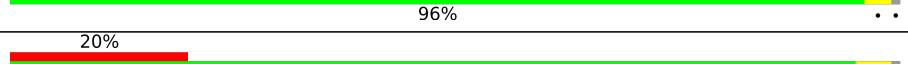
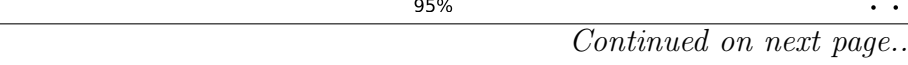
The reported resolution of this entry is 6.50 Å.

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	-
Q-score	-	25397	556 (6.00 - 7.00)

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	 24% 95% 8% ..
1	1	76	 13% 91% 8% ..
1	2	76	 20% 91% 8% ..
1	3	76	 18% 93% 8% ..
1	4	76	 18% 96% 8% ..
1	5	76	 20% 95% 8% ..

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Mol	Chain	Length	Quality of chain
1	6	76	20% 91% 7% .
1	7	76	25% 89% 7% .
1	8	76	17% 95% . .
1	9	76	26% 89% 8% .
2	A	510	. 90% 7% .
2	B	510	. 93% 6% .
2	C	510	. 91% 7% .
3	D	478	. 89% 9% .
3	E	478	5% 90% 8% .
3	F	478	. 88% 10% .
4	G	278	. 89% 6% 5%
5	H	138	. 79% 8% 13%
6	I	61	. 79% 21%
7	O	195	. 91% 5% .
8	T	249	. 86% . 10%
9	U	209	. 74% 26%
10	V	173	. 94% 5% .
11	W	95	5% 81% 8% 11%
12	X	92	7% 65% . 33%
13	Y	59	7% 63% 37%
14	Z	48	. 98% . .

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 20228 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, mitochondrial.

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	470	Total	C	N	O	0	0
			1880	940	470	470		
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

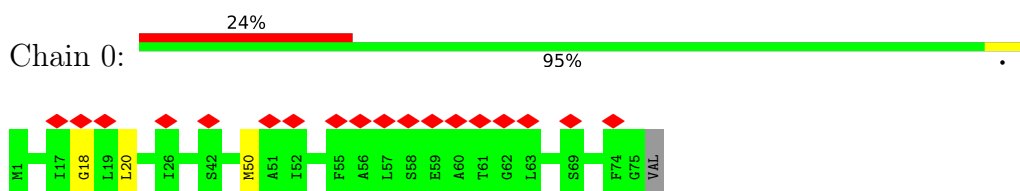
- Molecule 14 is a protein called ATP synthase protein 8.

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

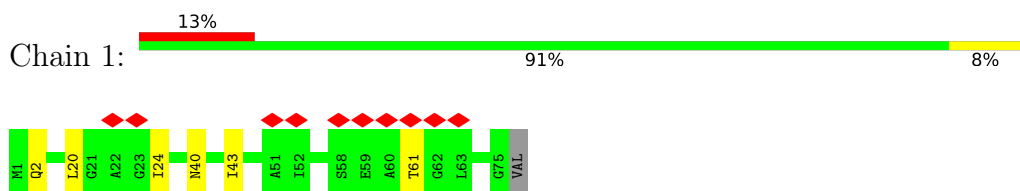
3 Residue-property plots [i](#)

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.

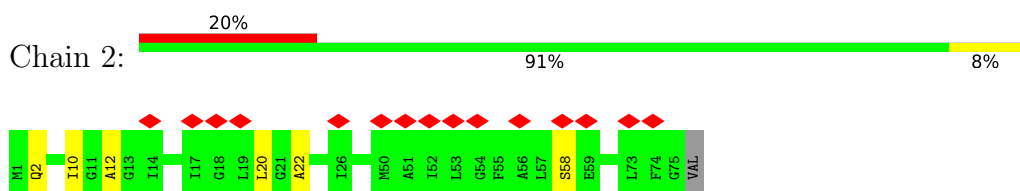
- Molecule 1: ATP synthase subunit 9, mitochondrial



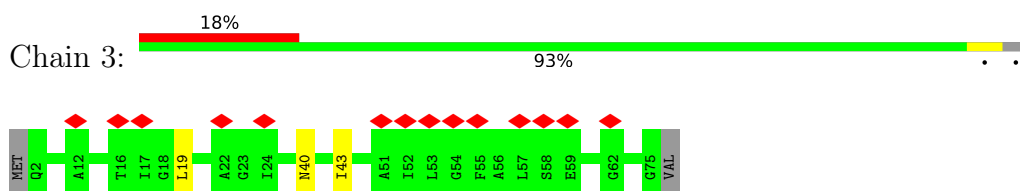
- Molecule 1: ATP synthase subunit 9, mitochondrial



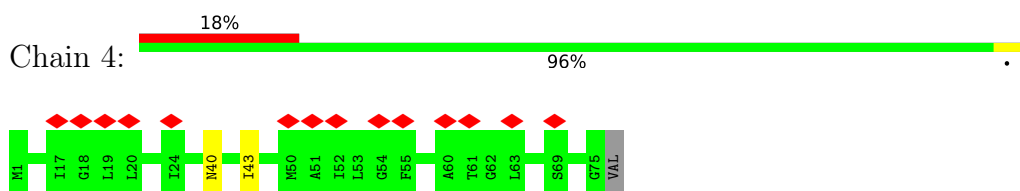
- Molecule 1: ATP synthase subunit 9, mitochondrial



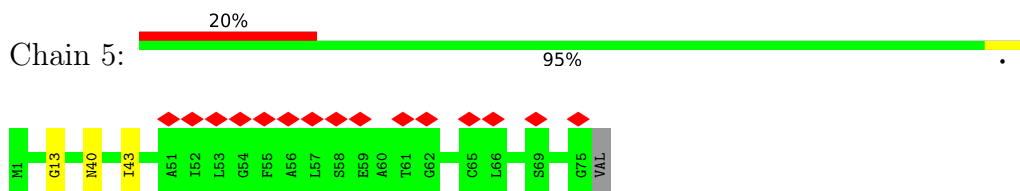
- Molecule 1: ATP synthase subunit 9, mitochondrial



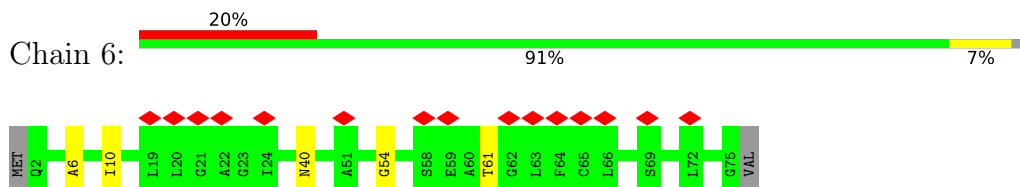
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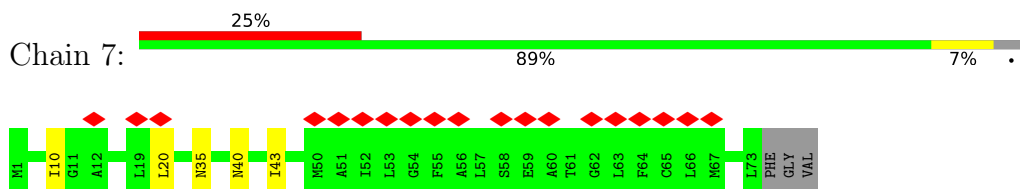
- Molecule 1: ATP synthase subunit 9, mitochondrial



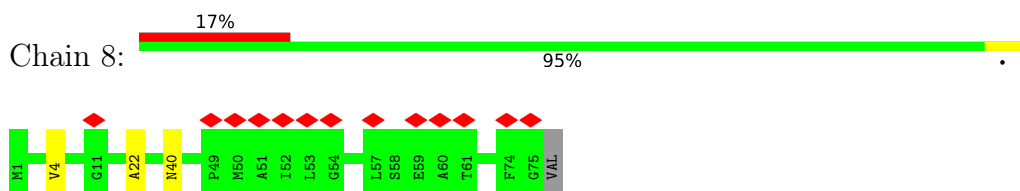
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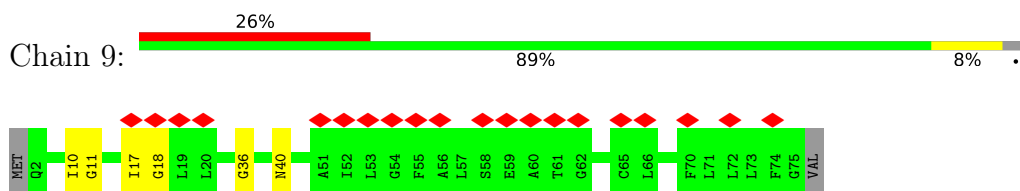
- Molecule 1: ATP synthase subunit 9, mitochondrial



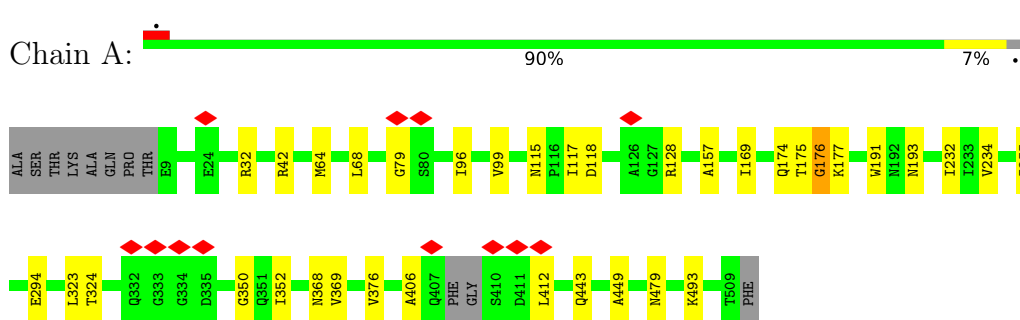
- Molecule 1: ATP synthase subunit 9, mitochondrial



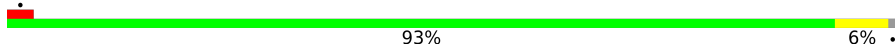
- Molecule 1: ATP synthase subunit 9, mitochondrial

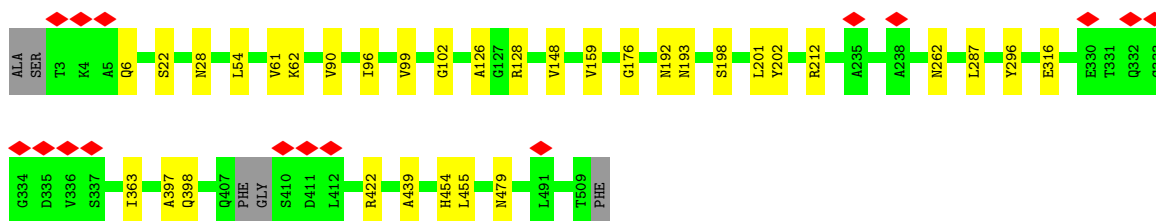


- Molecule 2: ATP synthase subunit alpha

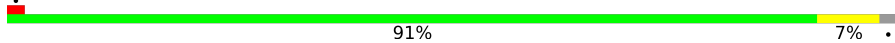


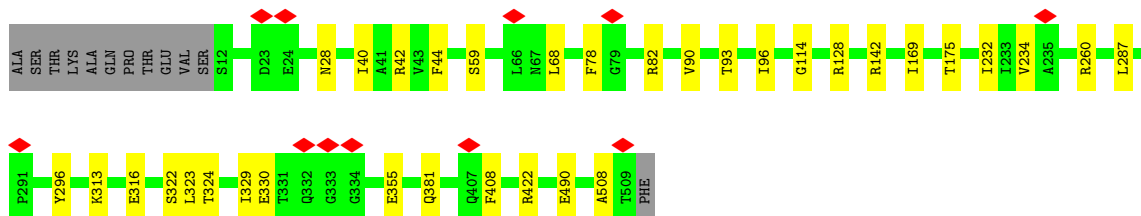
- Molecule 2: ATP synthase subunit alpha

Chain B:  93% 6%




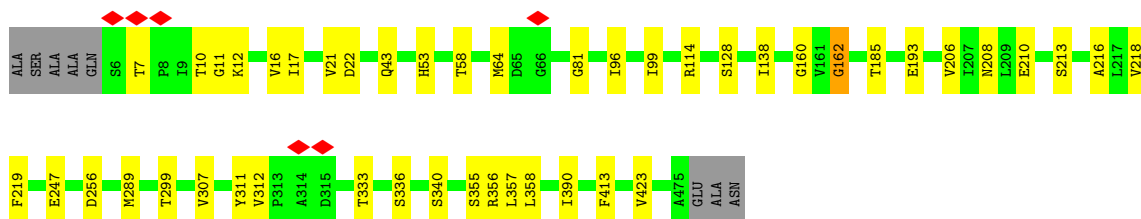
• Molecule 2: ATP synthase subunit alpha

Chain C:  91% 7%




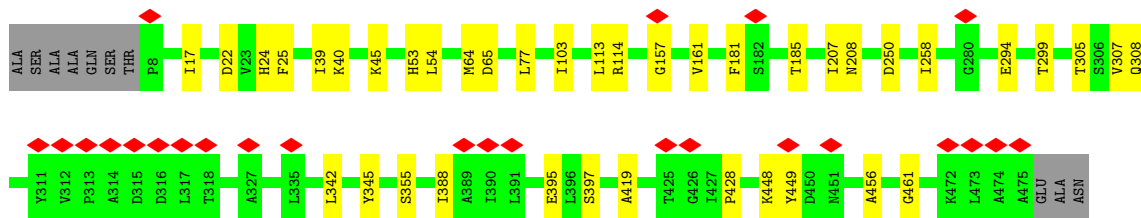
• Molecule 3: ATP synthase subunit beta

Chain D:  89% 9%




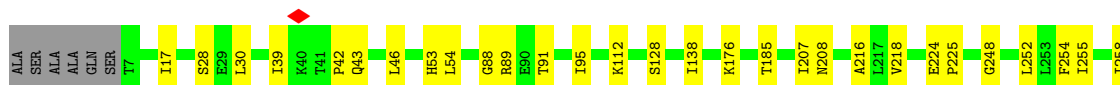
• Molecule 3: ATP synthase subunit beta

Chain E:  5% 90% 8%



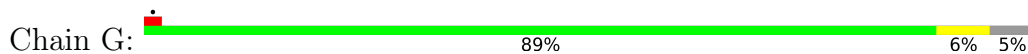
• Molecule 3: ATP synthase subunit beta

Chain F:  88% 10%

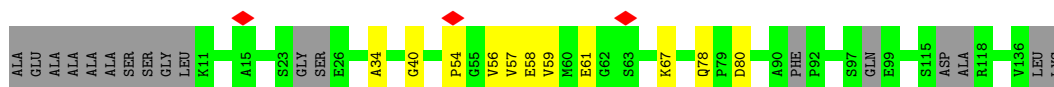
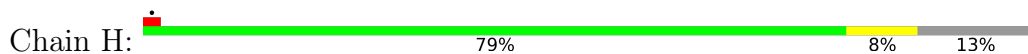




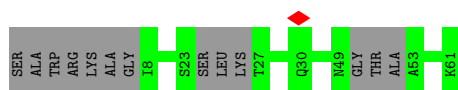
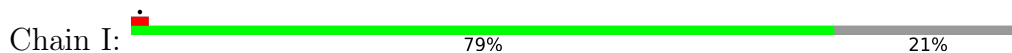
- Molecule 4: ATP synthase subunit gamma



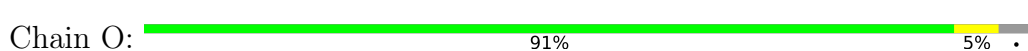
- Molecule 5: ATP synthase subunit delta



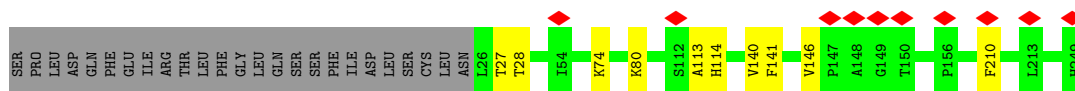
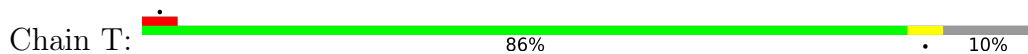
- Molecule 6: ATP synthase subunit epsilon



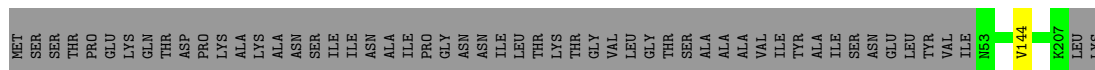
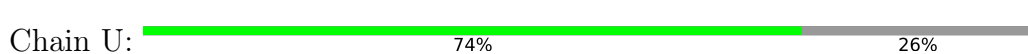
- Molecule 7: ATP synthase subunit 5



- Molecule 8: ATP synthase subunit a

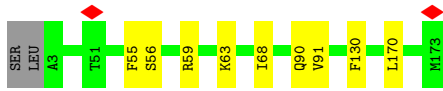


- Molecule 9: ATP synthase subunit 4




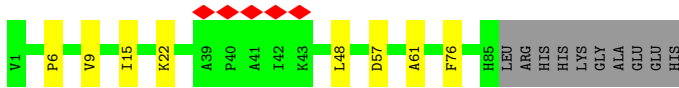
- Molecule 10: ATP synthase subunit d

Chain V:  94% 5%



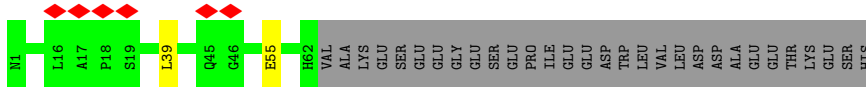
- Molecule 11: ATP synthase subunit f

Chain W:  5% 81% 8% 11%



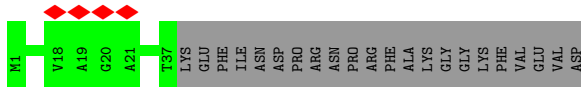
- Molecule 12: ATP synthase subunit H

Chain X:  7% 65% 1% 33%



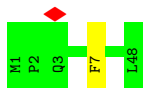
- Molecule 13: ATP synthase subunit J

Chain Y:  7% 63% 37%



- Molecule 14: ATP synthase protein 8

Chain Z:  98%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9369	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	103896	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.946	Depositor
Minimum map value	-0.590	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.116	Depositor
Recommended contour level	0.65	Depositor
Map size (\AA)	344.96, 344.96, 344.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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	2.08	6/372 (1.6%)
1	1	1.26	0/299	2.04	10/372 (2.7%)
1	2	1.23	0/299	2.18	12/372 (3.2%)
1	3	1.25	0/295	2.07	4/367 (1.1%)
1	4	1.25	0/299	2.09	2/372 (0.5%)
1	5	1.27	0/299	2.11	4/372 (1.1%)
1	6	1.25	0/295	2.22	8/367 (2.2%)
1	7	1.23	0/291	2.21	8/362 (2.2%)
1	8	1.21	0/299	2.20	4/372 (1.1%)
1	9	1.23	0/295	2.09	10/367 (2.7%)
2	A	1.59	1/1994 (0.1%)	1.89	47/2489 (1.9%)
2	B	1.56	0/2018	1.88	39/2519 (1.5%)
2	C	1.58	1/1991 (0.1%)	1.85	38/2487 (1.5%)
3	D	1.59	2/1879 (0.1%)	1.90	48/2347 (2.0%)
3	E	1.58	0/1871	1.91	43/2337 (1.8%)
3	F	1.60	1/1875 (0.1%)	1.89	49/2342 (2.1%)
4	G	1.52	0/1058	1.87	16/1319 (1.2%)
5	H	1.46	0/475	1.83	10/585 (1.7%)
6	I	1.38	0/190	1.71	0/231
7	O	1.24	0/747	1.83	9/932 (1.0%)
8	T	1.38	0/896	1.64	14/1117 (1.3%)
9	U	1.34	0/619	1.64	2/772 (0.3%)
10	V	1.51	0/684	1.77	9/852 (1.1%)
11	W	1.39	0/339	1.91	9/422 (2.1%)
12	X	1.46	0/247	2.08	3/307 (1.0%)
13	Y	1.27	0/147	1.69	0/182
14	Z	1.36	0/192	1.67	1/237 (0.4%)
All	All	1.49	5/20192 (0.0%)	1.90	405/25172 (1.6%)

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
3	D	0	1
5	H	0	1
All	All	0	10

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	391	LEU	CA-C	-7.00	1.49	1.53
3	D	11	GLY	CA-C	-5.89	1.46	1.51
3	D	312	VAL	CA-C	-5.87	1.48	1.53
2	A	157	ALA	CA-C	-5.60	1.48	1.52
2	C	322	SER	CA-C	-5.09	1.46	1.52

All (405) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	219	PHE	CA-C-N	9.26	129.09	122.33
3	D	219	PHE	C-N-CA	9.26	129.09	122.33
3	D	423	VAL	N-CA-C	-9.05	105.11	113.71
3	D	311	TYR	N-CA-C	-9.04	94.16	108.90
2	B	193	ASN	N-CA-C	-8.90	101.74	112.59
3	D	17	ILE	N-CA-C	-8.72	104.83	113.20
3	E	456	ALA	N-CA-C	-8.51	102.83	113.55
11	W	48	LEU	N-CA-C	-8.36	102.90	113.43
2	B	363	ILE	N-CA-C	-8.26	94.15	107.28
2	C	44	PHE	N-CA-C	-8.04	95.41	108.52
2	C	329	ILE	N-CA-C	-7.93	96.59	108.17
11	W	6	PRO	N-CA-C	7.93	120.38	110.70
11	W	15	ILE	N-CA-C	-7.90	106.20	113.71
3	F	225	PRO	CA-C-O	-7.82	115.27	120.90
2	B	192	ASN	N-CA-C	-7.82	103.77	113.38
8	T	80	LYS	N-CA-C	-7.77	103.32	114.12
2	C	82	ARG	N-CA-C	-7.74	102.76	112.90
3	F	43	GLN	N-CA-C	-7.71	103.94	112.72
2	A	479	ASN	N-CA-C	-7.67	103.93	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	99	VAL	N-CA-C	-7.63	102.93	109.19
3	E	39	ILE	N-CA-C	-7.61	96.76	107.80
2	A	350	GLY	N-CA-C	-7.61	104.72	111.95
3	E	103	ILE	N-CA-C	-7.48	105.55	112.43
8	T	140	VAL	N-CA-C	-7.48	103.99	111.77
3	F	336	SER	CA-C-N	7.33	130.11	120.28
3	F	336	SER	C-N-CA	7.33	130.11	120.28
3	E	17	ILE	N-CA-C	-7.28	97.36	107.99
3	D	7	THR	N-CA-C	-7.25	101.69	108.22
3	D	53	HIS	N-CA-C	-7.17	97.72	109.40
3	F	361	ALA	N-CA-C	-7.15	104.42	113.43
7	O	176	VAL	N-CA-C	-7.15	97.83	108.12
5	H	56	VAL	N-CA-C	-7.12	98.14	108.11
2	A	128	ARG	N-CA-C	-7.05	97.41	108.90
10	V	63	LYS	N-CA-C	-7.01	104.75	113.38
4	G	196	LYS	N-CA-C	-6.99	105.10	112.93
2	B	479	ASN	N-CA-C	-6.99	104.49	113.16
3	F	252	LEU	N-CA-C	-6.96	98.50	109.07
3	E	53	HIS	N-CA-C	-6.94	97.09	108.41
3	F	258	ILE	N-CA-C	-6.94	105.96	112.83
3	F	88	GLY	N-CA-C	-6.91	102.74	110.96
5	H	61	GLU	N-CA-C	-6.91	97.02	108.34
3	F	53	HIS	N-CA-C	-6.89	97.97	109.07
3	F	353	SER	N-CA-C	-6.86	98.59	109.23
7	O	192	GLU	N-CA-C	-6.86	104.59	114.12
1	4	43	ILE	CA-C-N	6.78	129.66	120.38
1	4	43	ILE	C-N-CA	6.78	129.66	120.38
3	E	258	ILE	N-CA-C	-6.77	104.89	113.22
3	F	54	LEU	N-CA-C	-6.77	104.64	113.17
3	D	289	MET	CA-C-N	6.73	127.45	119.98
3	D	289	MET	C-N-CA	6.73	127.45	119.98
10	V	68	ILE	N-CA-C	-6.73	103.67	111.00
3	D	96	ILE	N-CA-C	-6.69	97.80	108.90
2	A	323	LEU	N-CA-C	-6.68	98.09	109.24
2	C	313	LYS	N-CA-C	-6.67	98.11	109.24
3	F	218	VAL	N-CA-C	-6.66	98.54	108.46
2	B	262	ASN	N-CA-C	-6.63	104.81	113.17
2	C	355	GLU	CA-C-N	6.63	129.16	120.28
2	C	355	GLU	C-N-CA	6.63	129.16	120.28
7	O	147	VAL	N-CA-C	-6.62	97.44	106.85
8	T	146	VAL	N-CA-C	-6.62	100.52	107.60
2	B	6	GLN	N-CA-C	-6.62	100.53	108.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	40	ILE	N-CA-C	-6.61	98.61	108.12
2	A	64	MET	N-CA-C	-6.60	99.38	109.41
5	H	58	GLU	N-CA-C	-6.59	98.23	109.24
3	E	461	GLY	N-CA-C	-6.57	103.33	112.13
3	E	114	ARG	N-CA-C	-6.56	99.35	109.52
2	C	287	LEU	N-CA-C	-6.55	104.52	113.30
2	A	352	ILE	N-CA-C	-6.54	98.95	108.11
2	B	96	ILE	N-CA-C	-6.54	101.10	109.80
2	B	54	LEU	N-CA-C	-6.54	99.04	109.76
3	D	307	VAL	N-CA-C	-6.51	96.93	107.28
2	B	128	ARG	N-CA-C	-6.49	99.24	109.50
2	B	398	GLN	N-CA-C	-6.49	105.01	113.12
10	V	130	PHE	N-CA-C	-6.46	104.44	112.72
3	E	22	ASP	N-CA-C	-6.46	99.16	109.76
3	F	391	LEU	N-CA-C	-6.46	102.55	108.75
2	A	406	ALA	N-CA-C	-6.45	106.00	114.31
10	V	56	SER	N-CA-C	-6.44	102.93	111.24
1	0	20	LEU	CA-C-N	6.42	127.11	119.98
1	0	20	LEU	C-N-CA	6.42	127.11	119.98
3	E	181	PHE	N-CA-C	-6.42	99.81	108.86
2	A	324	THR	N-CA-C	-6.41	99.47	109.72
3	D	247	GLU	N-CA-C	-6.39	104.96	112.89
1	9	10	ILE	CA-C-N	6.39	127.19	120.03
1	9	10	ILE	C-N-CA	6.39	127.19	120.03
2	A	175	THR	N-CA-C	-6.37	106.22	112.97
2	C	234	VAL	N-CA-C	-6.36	99.27	108.17
7	O	101	PHE	N-CA-C	-6.35	103.43	112.13
2	C	90	VAL	N-CA-C	-6.35	99.00	108.46
3	E	208	ASN	N-CA-C	-6.34	97.73	108.26
3	E	161	VAL	N-CA-C	-6.33	105.52	112.80
3	F	138	ILE	N-CA-C	-6.32	99.26	108.11
3	F	208	ASN	N-CA-C	-6.32	98.69	109.24
4	G	164	ILE	N-CA-C	-6.29	98.60	108.86
2	B	62	LYS	N-CA-C	-6.28	99.79	109.52
1	6	6	ALA	CA-C-N	6.27	128.69	120.28
1	6	6	ALA	C-N-CA	6.27	128.69	120.28
2	B	148	VAL	N-CA-C	-6.26	99.40	108.17
3	E	299	THR	N-CA-C	-6.22	100.78	110.17
3	E	345	TYR	N-CA-C	-6.21	97.17	108.85
3	D	162	GLY	N-CA-C	-6.21	103.22	114.46
3	E	308	GLN	N-CA-C	-6.21	100.05	109.85
2	C	490	GLU	N-CA-C	-6.20	98.15	108.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	413	PHE	N-CA-C	-6.19	105.72	113.28
2	A	369	VAL	N-CA-C	-6.19	106.47	112.29
3	F	95	ILE	N-CA-C	-6.19	99.44	108.11
3	E	24	HIS	N-CA-C	-6.19	98.81	108.90
10	V	55	PHE	N-CA-C	-6.19	105.60	113.02
11	W	76	PHE	N-CA-C	-6.18	103.27	111.24
3	D	185	THR	N-CA-C	-6.16	98.96	109.24
2	A	193	ASN	CA-C-N	6.15	125.82	119.92
2	A	193	ASN	C-N-CA	6.15	125.82	119.92
2	A	294	GLU	CA-C-N	6.14	131.11	122.08
2	A	294	GLU	C-N-CA	6.14	131.11	122.08
4	G	100	ASN	N-CA-C	-6.14	105.83	113.38
4	G	168	ASP	N-CA-C	-6.13	101.92	109.65
1	1	43	ILE	CA-C-N	6.13	129.33	120.38
1	1	43	ILE	C-N-CA	6.13	129.33	120.38
2	B	61	VAL	N-CA-C	-6.13	98.86	108.86
2	A	234	VAL	N-CA-C	-6.13	99.76	108.58
1	7	43	ILE	CA-C-N	6.12	128.76	120.38
1	7	43	ILE	C-N-CA	6.12	128.76	120.38
4	G	171	SER	N-CA-C	-6.11	100.03	109.14
2	C	175	THR	N-CA-C	-6.11	102.19	110.68
3	D	299	THR	N-CA-C	-6.10	100.05	109.14
2	C	96	ILE	N-CA-C	-6.09	103.33	110.21
2	B	90	VAL	N-CA-C	-6.08	99.66	108.17
2	B	28	ASN	N-CA-C	-6.08	105.18	112.59
2	A	232	ILE	N-CA-C	-6.07	99.47	108.45
2	A	42	ARG	N-CA-C	-6.06	98.39	108.34
3	F	207	ILE	N-CA-C	-6.06	99.74	108.53
2	C	232	ILE	N-CA-C	-6.06	99.75	108.48
3	D	64	MET	N-CA-C	-6.03	103.87	112.13
1	2	10	ILE	CA-C-N	6.02	126.66	119.98
1	2	10	ILE	C-N-CA	6.02	126.66	119.98
2	A	376	VAL	N-CA-C	-6.01	107.13	112.90
2	C	93	THR	N-CA-C	-6.00	104.83	111.36
3	E	54	LEU	N-CA-C	-5.99	106.02	113.38
3	E	250	ASP	N-CA-C	-5.98	99.53	109.46
2	B	422	ARG	CA-C-N	5.96	126.59	119.98
2	B	422	ARG	C-N-CA	5.96	126.59	119.98
5	H	34	ALA	N-CA-C	-5.96	100.35	109.41
2	C	323	LEU	N-CA-C	-5.96	99.96	109.96
2	A	96	ILE	N-CA-C	-5.93	103.50	110.21
3	D	22	ASP	N-CA-C	-5.92	100.54	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	159	TYR	N-CA-C	-5.92	102.32	109.72
8	T	74	LYS	N-CA-C	-5.91	104.79	112.23
10	V	91	VAL	N-CA-C	-5.90	104.03	112.35
3	F	248	GLY	CA-C-N	5.89	129.07	120.71
3	F	248	GLY	C-N-CA	5.89	129.07	120.71
3	F	395	GLU	N-CA-C	-5.88	106.01	112.72
3	E	157	GLY	N-CA-C	-5.88	106.14	112.08
3	F	39	ILE	N-CA-C	-5.88	99.95	108.36
3	F	42	PRO	N-CA-C	-5.88	108.57	114.68
3	F	176	LYS	N-CA-C	-5.88	105.42	113.30
3	E	185	THR	N-CA-C	-5.87	99.62	109.07
2	C	59	SER	N-CA-C	-5.86	106.37	112.93
7	O	173	ASP	N-CA-C	-5.84	104.55	112.26
2	A	177	LYS	N-CA-C	-5.83	104.84	111.14
3	F	185	THR	N-CA-C	-5.80	98.96	108.76
3	F	224	GLU	CA-C-N	5.80	123.89	119.66
3	F	224	GLU	C-N-CA	5.80	123.89	119.66
3	F	128	SER	N-CA-C	-5.80	98.83	108.34
4	G	2	THR	N-CA-C	-5.79	104.89	111.14
2	A	115	ASN	N-CA-C	-5.79	102.32	110.31
3	D	333	THR	N-CA-C	-5.78	99.91	108.99
2	C	28	ASN	N-CA-C	-5.78	99.87	109.46
1	2	22	ALA	CA-C-N	5.76	126.38	119.98
1	2	22	ALA	C-N-CA	5.76	126.38	119.98
1	6	54	GLY	CA-C-N	5.76	127.93	120.44
1	6	54	GLY	C-N-CA	5.76	127.93	120.44
1	9	18	GLY	CA-C-N	5.76	128.57	120.28
1	9	18	GLY	C-N-CA	5.76	128.57	120.28
2	C	408	PHE	N-CA-C	-5.76	98.54	110.80
3	E	25	PHE	N-CA-C	-5.76	100.51	109.72
2	A	118	ASP	N-CA-C	-5.73	105.95	113.17
3	F	295	ARG	N-CA-C	-5.73	106.33	113.38
3	F	307	VAL	N-CA-C	-5.72	99.31	107.77
3	F	343	GLY	N-CA-C	-5.72	107.29	115.64
1	6	61	THR	CA-C-N	5.71	126.32	119.98
1	6	61	THR	C-N-CA	5.71	126.32	119.98
3	E	207	ILE	N-CA-C	-5.71	100.26	108.48
1	5	43	ILE	CA-C-N	5.71	128.50	120.28
1	5	43	ILE	C-N-CA	5.71	128.50	120.28
3	E	64	MET	N-CA-C	-5.71	105.98	113.12
2	C	42	ARG	N-CA-C	-5.71	98.21	108.48
3	F	89	ARG	N-CA-C	-5.70	106.09	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	O	144	SER	N-CA-C	-5.69	100.76	109.41
3	F	311	TYR	N-CA-C	-5.69	100.44	109.76
2	A	412	LEU	CA-C-N	5.68	132.39	121.54
2	A	412	LEU	C-N-CA	5.68	132.39	121.54
2	B	455	LEU	N-CA-C	-5.68	106.01	113.17
3	E	307	VAL	N-CA-C	-5.67	99.58	107.80
8	T	27	THR	CA-C-N	5.66	127.86	120.28
8	T	27	THR	C-N-CA	5.66	127.86	120.28
2	C	316	GLU	N-CA-C	-5.65	106.05	113.17
3	E	305	THR	N-CA-C	-5.65	100.49	109.59
4	G	129	SER	N-CA-C	-5.65	100.48	109.07
11	W	61	ALA	N-CA-C	-5.63	106.17	113.16
1	1	24	ILE	CA-C-N	5.63	126.19	119.94
1	1	24	ILE	C-N-CA	5.63	126.19	119.94
7	O	100	CYS	N-CA-C	-5.63	101.83	109.54
3	E	45	LYS	N-CA-C	-5.62	100.81	109.52
3	D	114	ARG	N-CA-C	-5.61	100.82	109.52
2	B	296	TYR	CA-C-N	5.60	126.84	119.84
2	B	296	TYR	C-N-CA	5.60	126.84	119.84
3	D	12	LYS	N-CA-C	-5.59	99.78	108.90
3	D	81	GLY	CA-C-N	5.59	125.59	119.89
3	D	81	GLY	C-N-CA	5.59	125.59	119.89
3	D	16	VAL	N-CA-C	-5.59	99.70	107.80
10	V	170	LEU	N-CA-C	-5.59	99.30	108.41
3	F	363	VAL	N-CA-C	-5.58	106.87	112.17
3	D	357	LEU	N-CA-C	-5.58	105.78	112.59
2	A	443	GLN	CA-C-N	5.58	123.75	120.24
2	A	443	GLN	C-N-CA	5.58	123.75	120.24
8	T	113	ALA	N-CA-C	-5.57	106.25	113.16
10	V	59	ARG	N-CA-C	-5.57	105.61	112.90
3	F	255	ILE	N-CA-C	-5.56	100.05	108.17
1	3	43	ILE	CA-C-N	5.56	128.50	120.38
1	3	43	ILE	C-N-CA	5.56	128.50	120.38
2	C	422	ARG	CA-C-N	5.55	126.14	119.98
2	C	422	ARG	C-N-CA	5.55	126.14	119.98
1	7	10	ILE	CA-C-N	5.55	126.14	119.98
1	7	10	ILE	C-N-CA	5.55	126.14	119.98
8	T	114	HIS	CA-C-N	5.55	128.75	120.31
8	T	114	HIS	C-N-CA	5.55	128.75	120.31
3	F	112	LYS	N-CA-C	-5.55	106.56	113.55
2	C	324	THR	N-CA-C	-5.54	101.14	109.95
3	F	46	LEU	N-CA-C	-5.54	99.87	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	T	141	PHE	N-CA-C	-5.53	106.49	113.18
1	3	19	LEU	CA-C-N	5.53	128.00	120.54
1	3	19	LEU	C-N-CA	5.53	128.00	120.54
2	C	508	ALA	N-CA-C	-5.52	100.54	108.60
4	G	75	VAL	N-CA-C	-5.52	99.87	108.86
2	B	22	SER	CA-C-N	5.52	127.61	120.44
2	B	22	SER	C-N-CA	5.52	127.61	120.44
2	A	32	ARG	N-CA-C	-5.51	98.94	108.69
3	F	284	THR	N-CA-C	-5.49	105.89	112.59
1	6	10	ILE	CA-C-N	5.47	126.05	119.98
1	6	10	ILE	C-N-CA	5.47	126.05	119.98
3	E	388	ILE	N-CA-C	-5.46	105.20	110.72
5	H	78	GLN	N-CA-C	-5.45	103.26	110.40
12	X	39	LEU	N-CA-C	-5.45	97.76	109.81
9	U	144	VAL	CA-C-N	5.45	127.53	120.44
9	U	144	VAL	C-N-CA	5.45	127.53	120.44
5	H	80	ASP	N-CA-C	-5.45	106.51	112.72
3	E	113	LEU	N-CA-C	-5.44	101.08	109.52
14	Z	7	PHE	N-CA-C	-5.42	105.89	112.88
3	E	65	ASP	CA-C-N	5.42	125.12	119.92
3	E	65	ASP	C-N-CA	5.42	125.12	119.92
3	E	395	GLU	N-CA-C	-5.42	106.52	113.02
2	C	169	ILE	N-CA-C	-5.42	100.08	107.99
11	W	9	VAL	N-CA-C	-5.42	99.84	107.75
2	A	191	TRP	CA-C-N	5.41	127.53	120.28
2	A	191	TRP	C-N-CA	5.41	127.53	120.28
2	B	201	LEU	N-CA-C	-5.41	100.36	109.07
3	F	356	ARG	N-CA-C	-5.41	106.18	112.89
2	B	316	GLU	CA-C-N	5.40	127.52	120.28
2	B	316	GLU	C-N-CA	5.40	127.52	120.28
2	A	68	LEU	N-CA-C	-5.40	99.72	108.52
2	A	176	GLY	N-CA-C	-5.40	100.38	113.18
3	D	208	ASN	N-CA-C	-5.40	99.88	109.06
11	W	57	ASP	N-CA-C	-5.40	102.53	110.52
2	B	159	VAL	CA-C-N	5.40	125.41	119.90
2	B	159	VAL	C-N-CA	5.40	125.41	119.90
3	E	428	PRO	CA-C-N	5.39	125.10	119.92
3	E	428	PRO	C-N-CA	5.39	125.10	119.92
4	G	166	TYR	N-CA-C	-5.39	100.50	107.73
4	G	86	SER	N-CA-C	-5.38	106.58	112.72
3	D	356	ARG	N-CA-C	-5.37	106.41	113.17
5	H	40	GLY	N-CA-C	-5.36	102.64	111.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	O	180	ILE	N-CA-C	-5.35	105.91	111.58
3	D	210	GLU	N-CA-C	-5.35	100.18	108.90
3	E	355	SER	N-CA-C	-5.35	101.16	109.24
8	T	210	PHE	CA-C-N	5.35	123.61	120.24
8	T	210	PHE	C-N-CA	5.35	123.61	120.24
2	A	255	ILE	CA-C-N	5.34	125.91	119.98
2	A	255	ILE	C-N-CA	5.34	125.91	119.98
3	D	58	THR	N-CA-C	-5.34	99.59	108.34
2	C	296	TYR	CA-C-N	5.33	126.08	120.11
2	C	296	TYR	C-N-CA	5.33	126.08	120.11
3	D	340	SER	CA-C-N	5.33	127.42	120.28
3	D	340	SER	C-N-CA	5.33	127.42	120.28
3	F	351	LEU	N-CA-C	-5.33	106.45	113.17
3	F	91	THR	N-CA-C	-5.33	106.46	113.17
4	G	137	ALA	CA-C-N	5.33	126.50	119.84
4	G	137	ALA	C-N-CA	5.33	126.50	119.84
3	D	216	ALA	N-CA-C	-5.32	101.44	109.85
3	E	449	TYR	N-CA-C	-5.32	104.13	110.41
1	9	17	ILE	CA-C-N	5.32	125.99	120.03
1	9	17	ILE	C-N-CA	5.32	125.99	120.03
1	1	2	GLN	CA-C-N	5.31	127.34	120.44
1	1	2	GLN	C-N-CA	5.31	127.34	120.44
2	C	330	GLU	N-CA-C	-5.30	99.88	108.52
3	F	17	ILE	N-CA-C	-5.30	99.62	107.51
1	9	36	GLY	CA-C-N	5.29	127.23	120.56
1	9	36	GLY	C-N-CA	5.29	127.23	120.56
2	C	78	PHE	N-CA-C	-5.29	106.51	113.17
1	7	20	LEU	CA-C-N	5.28	125.84	119.98
1	7	20	LEU	C-N-CA	5.28	125.84	119.98
1	8	4	VAL	CA-C-N	5.28	127.36	120.28
1	8	4	VAL	C-N-CA	5.28	127.36	120.28
2	B	176	GLY	N-CA-C	-5.27	105.72	114.48
2	C	142	ARG	N-CA-C	-5.27	101.68	110.17
7	O	160	LYS	N-CA-C	-5.27	98.17	109.81
2	B	479	ASN	CA-C-N	5.26	127.33	120.28
2	B	479	ASN	C-N-CA	5.26	127.33	120.28
3	F	30	LEU	N-CA-C	-5.26	101.43	109.64
2	A	449	ALA	CA-C-N	5.26	125.78	120.00
2	A	449	ALA	C-N-CA	5.26	125.78	120.00
3	D	193	GLU	CA-C-N	5.25	125.81	119.98
3	D	193	GLU	C-N-CA	5.25	125.81	119.98
2	A	368	ASN	N-CA-C	-5.25	100.62	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	336	SER	CA-C-N	5.25	127.31	120.28
3	D	336	SER	C-N-CA	5.25	127.31	120.28
2	B	287	LEU	N-CA-C	-5.24	106.93	113.38
3	F	392	GLY	N-CA-C	-5.24	103.31	111.12
2	C	68	LEU	N-CA-C	-5.24	103.81	111.30
3	F	421	ALA	N-CA-C	-5.23	106.58	113.17
1	7	35	ASN	CA-C-N	5.23	125.74	119.94
1	7	35	ASN	C-N-CA	5.23	125.74	119.94
3	D	99	ILE	N-CA-C	-5.23	106.79	112.80
2	A	169	ILE	N-CA-C	-5.22	98.47	109.34
1	8	22	ALA	CA-C-N	5.22	125.73	119.94
1	8	22	ALA	C-N-CA	5.22	125.73	119.94
1	1	61	THR	CA-C-N	5.21	125.77	119.98
1	1	61	THR	C-N-CA	5.21	125.77	119.98
2	B	212	ARG	N-CA-C	-5.21	105.77	111.82
3	E	77	LEU	N-CA-C	-5.21	100.53	109.24
8	T	28	THR	CA-C-N	5.21	127.27	120.28
8	T	28	THR	C-N-CA	5.21	127.27	120.28
2	B	198	SER	N-CA-C	-5.21	106.77	113.23
3	D	355	SER	N-CA-C	-5.21	101.44	109.52
1	2	2	GLN	CA-C-N	5.20	127.25	120.28
1	2	2	GLN	C-N-CA	5.20	127.25	120.28
3	D	218	VAL	N-CA-C	-5.20	98.53	109.34
3	D	43	GLN	N-CA-C	-5.19	106.18	112.88
1	2	20	LEU	CA-C-N	5.19	125.74	119.98
1	2	20	LEU	C-N-CA	5.19	125.74	119.98
1	2	12	ALA	CA-C-N	5.19	125.70	119.94
1	2	12	ALA	C-N-CA	5.19	125.70	119.94
2	A	79	GLY	CA-C-N	5.19	128.59	120.75
2	A	79	GLY	C-N-CA	5.19	128.59	120.75
2	A	117	ILE	N-CA-C	-5.19	107.69	112.83
4	G	176	GLU	N-CA-C	-5.18	101.10	109.40
2	B	202	TYR	N-CA-C	-5.17	98.83	107.99
3	E	294	GLU	N-CA-C	-5.17	106.89	114.39
12	X	55	GLU	CA-C-N	5.17	127.21	120.28
12	X	55	GLU	C-N-CA	5.17	127.21	120.28
2	A	493	LYS	CA-C-N	5.16	127.20	120.28
2	A	493	LYS	C-N-CA	5.16	127.20	120.28
3	D	128	SER	N-CA-C	-5.16	98.88	107.80
3	D	206	VAL	N-CA-C	-5.16	105.33	112.50
10	V	90	GLN	N-CA-C	-5.15	107.54	113.88
11	W	22	LYS	CA-C-N	5.15	127.14	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	W	22	LYS	C-N-CA	5.15	127.14	120.44
2	A	259	PHE	CA-C-N	5.15	127.44	120.44
2	A	259	PHE	C-N-CA	5.15	127.44	120.44
3	F	28	SER	N-CA-C	-5.15	107.00	113.28
3	D	10	THR	N-CA-C	-5.14	100.85	109.24
3	F	216	ALA	N-CA-C	-5.14	101.59	109.41
3	E	40	LYS	N-CA-C	-5.13	100.81	108.96
5	H	59	VAL	N-CA-C	-5.13	100.74	108.12
1	9	11	GLY	CA-C-N	5.12	127.10	120.44
1	9	11	GLY	C-N-CA	5.12	127.10	120.44
2	B	99	VAL	N-CA-C	-5.12	104.99	109.19
2	C	114	GLY	N-CA-C	-5.12	108.25	115.32
3	F	254	PHE	N-CA-C	-5.12	100.69	109.24
2	B	439	ALA	CA-C-N	5.12	127.13	120.28
2	B	439	ALA	C-N-CA	5.12	127.13	120.28
3	D	21	VAL	N-CA-C	-5.11	100.71	108.17
3	D	390	ILE	N-CA-C	-5.11	106.68	111.48
3	E	397	SER	CA-C-N	5.11	127.54	120.29
3	E	397	SER	C-N-CA	5.11	127.54	120.29
3	E	419	ALA	N-CA-C	5.09	116.83	111.28
5	H	57	VAL	N-CA-C	-5.09	100.57	108.86
2	B	397	ALA	N-CA-C	-5.08	106.67	112.92
1	0	18	GLY	CA-C-N	5.08	127.60	120.28
1	0	18	GLY	C-N-CA	5.08	127.60	120.28
2	A	290	PRO	N-CA-C	5.08	116.89	110.70
1	5	13	GLY	CA-C-N	5.07	127.41	120.46
1	5	13	GLY	C-N-CA	5.07	127.41	120.46
2	C	128	ARG	N-CA-C	-5.07	101.66	109.52
3	D	138	ILE	N-CA-C	-5.07	100.34	107.75
3	F	310	VAL	N-CA-C	-5.07	100.90	108.46
3	E	342	LEU	N-CA-C	-5.06	106.95	113.02
5	H	67	LYS	N-CA-C	5.06	117.32	107.71
2	A	265	HIS	N-CA-C	-5.05	101.69	109.52
2	B	454	HIS	N-CA-C	-5.05	106.89	113.16
1	1	20	LEU	CA-C-N	5.05	125.56	120.00
1	1	20	LEU	C-N-CA	5.05	125.56	120.00
4	G	101	ASP	N-CA-C	-5.05	106.80	113.17
3	E	448	LYS	N-CA-C	-5.05	106.96	113.02
3	D	358	LEU	N-CA-C	-5.05	99.05	107.99
3	F	394	ASP	N-CA-C	-5.04	106.82	113.17
4	G	165	PHE	N-CA-C	-5.03	101.55	109.50
1	0	50	MET	CA-C-N	5.03	127.02	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	50	MET	C-N-CA	5.03	127.02	120.28
3	D	213	SER	N-CA-C	-5.02	100.16	108.75
2	C	381	GLN	CA-C-N	5.01	127.22	120.50
2	C	381	GLN	C-N-CA	5.01	127.22	120.50
1	2	58	SER	CA-C-N	5.01	127.00	120.28
1	2	58	SER	C-N-CA	5.01	127.00	120.28
2	C	260	ARG	CA-C-N	5.00	126.99	120.28
2	C	260	ARG	C-N-CA	5.00	126.99	120.28

There are no chirality outliers.

All (10) 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
3	D	256	ASP	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	9	296	0	91	0	0
2	A	1996	0	570	1	0
2	B	2020	0	575	1	0
2	C	1992	0	572	0	0
3	D	1880	0	538	1	0
3	E	1872	0	537	0	0
3	F	1876	0	537	0	0
4	G	1060	0	277	1	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	20228	0	5731	4	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 (4) 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:D:160:GLY:C	3:D:162:GLY:H	2.19	0.51
2:B:102:GLY:HA3	2:B:126:ALA:H	1.81	0.44
2:A:174:GLN:C	2:A:176:GLY:H	2.26	0.43
4:G:80:ASP:H	4:G:134:GLY:HA3	1.86	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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.

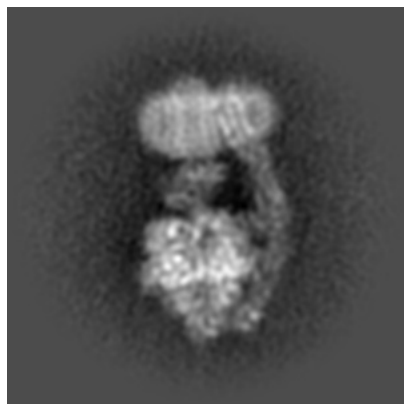
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25954. These allow visual inspection of the internal detail of the map and identification of artifacts.

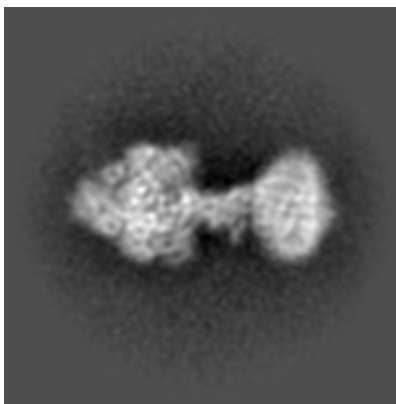
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

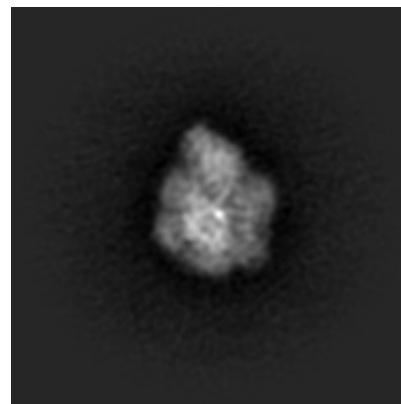
6.1.1 Primary map



X

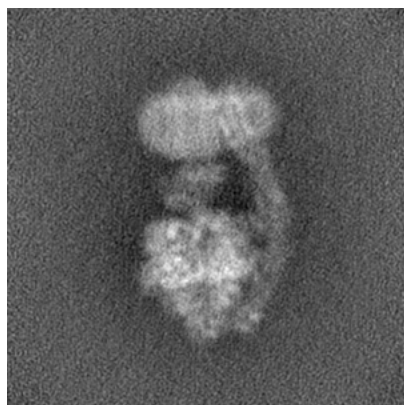


Y

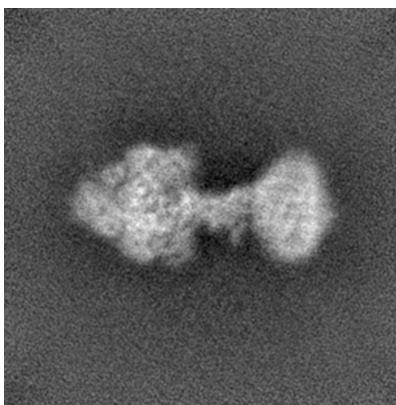


Z

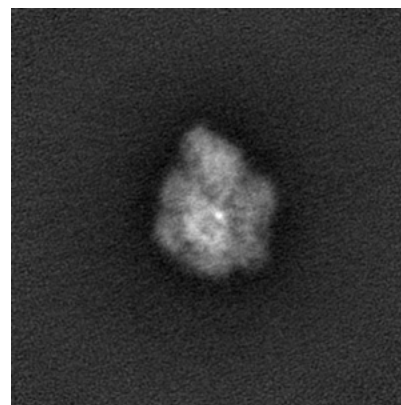
6.1.2 Raw map



X



Y

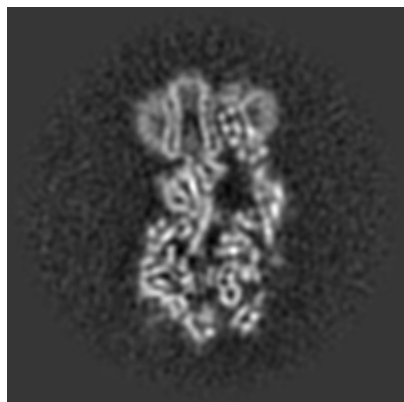


Z

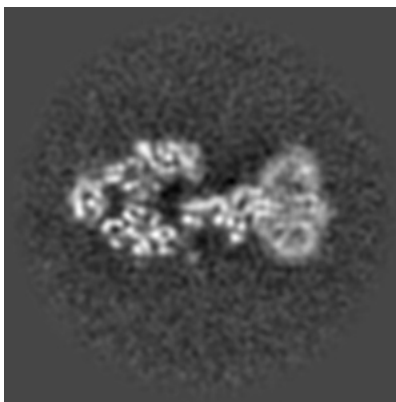
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

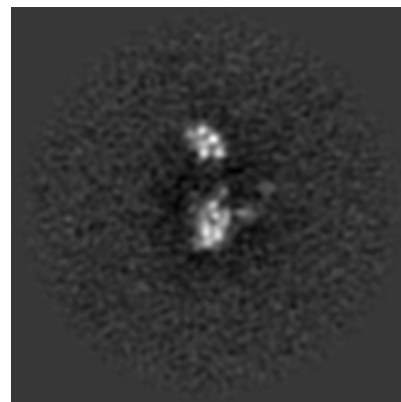
6.2.1 Primary map



X Index: 128

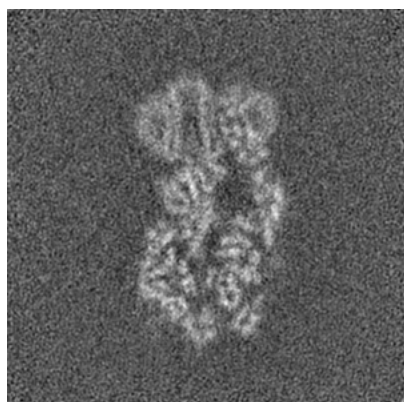


Y Index: 128

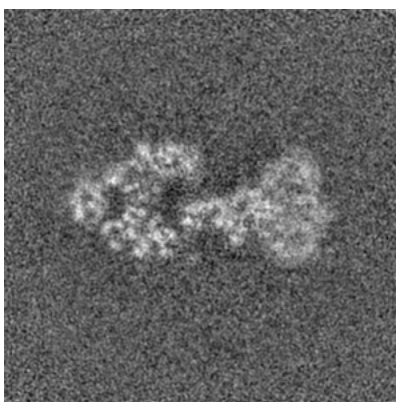


Z Index: 128

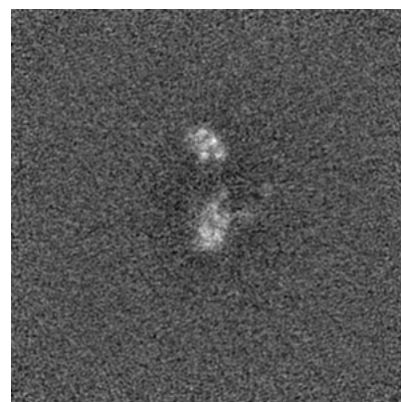
6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

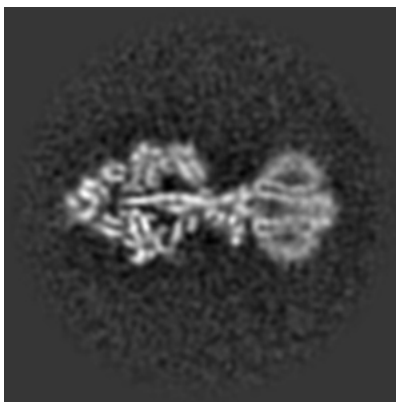
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

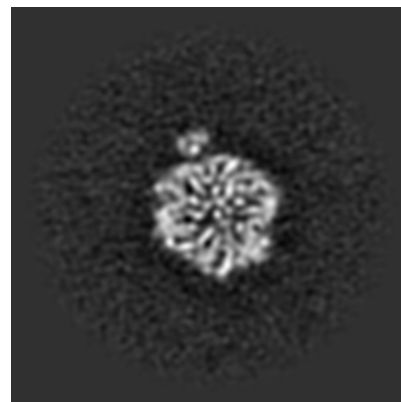
6.3.1 Primary map



X Index: 132

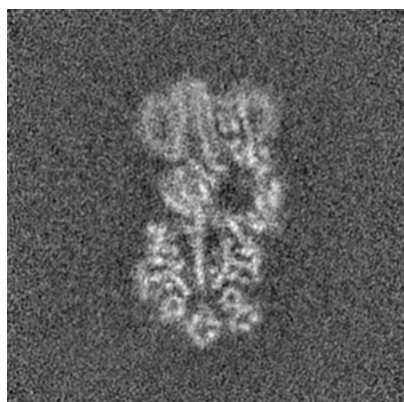


Y Index: 123

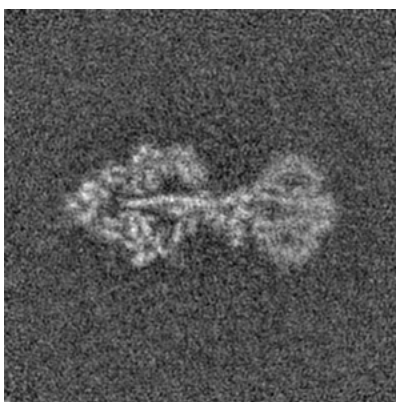


Z Index: 88

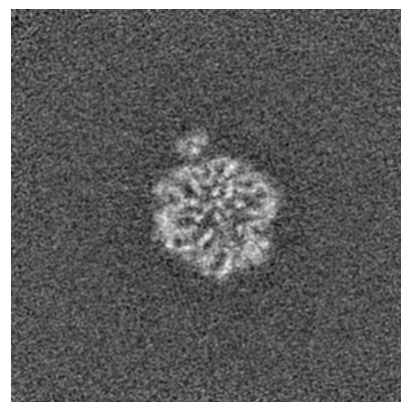
6.3.2 Raw map



X Index: 132



Y Index: 123

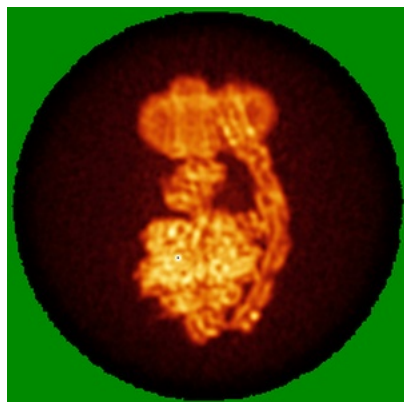


Z Index: 88

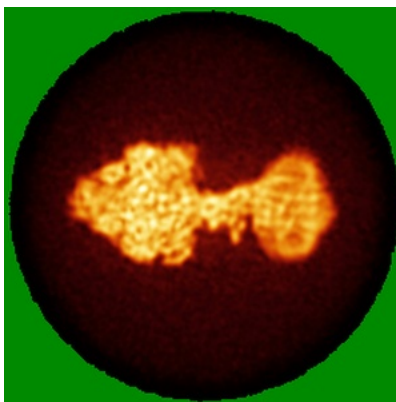
The images above show the largest variance slices of the map in three orthogonal directions.

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

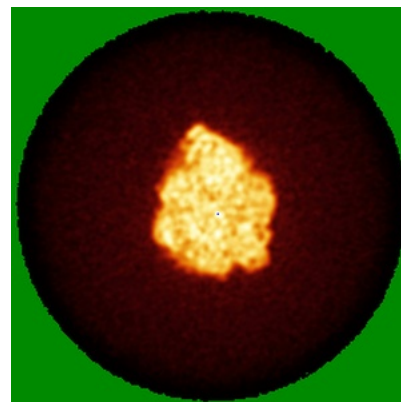
6.4.1 Primary map



X

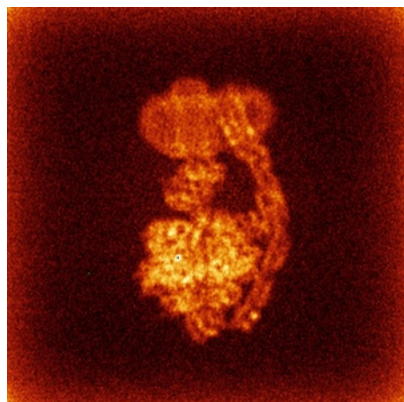


Y

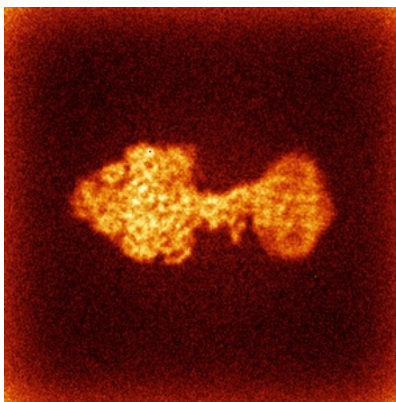


Z

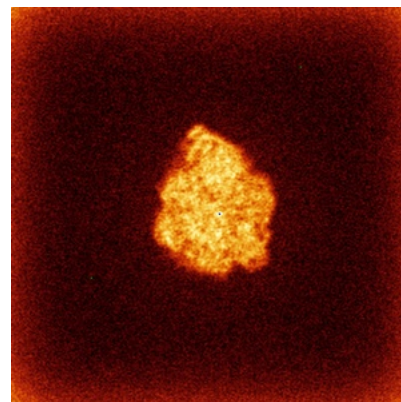
6.4.2 Raw map



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](#)

This section was not generated.

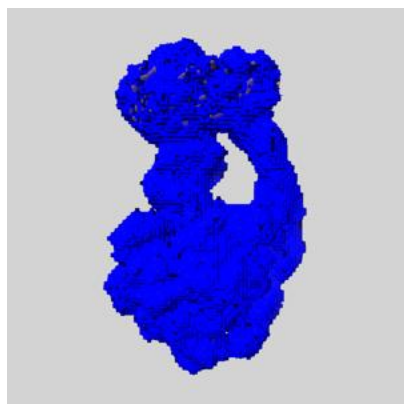
6.6 Mask visualisation [i](#)

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

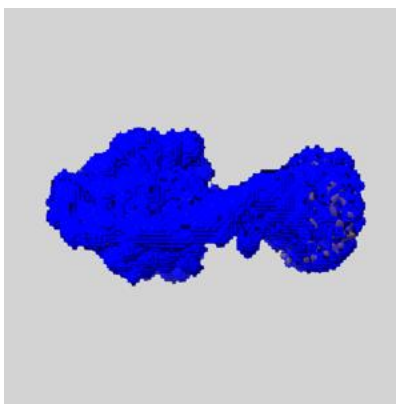
A mask typically either:

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

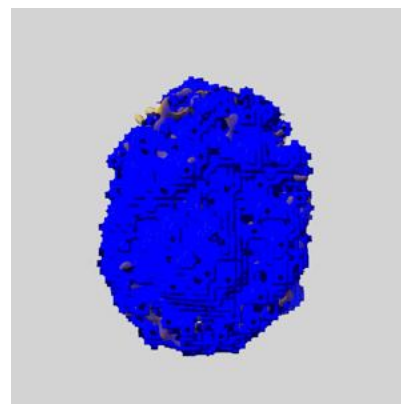
6.6.1 emd_25954_msk_1.map [i](#)



X



Y

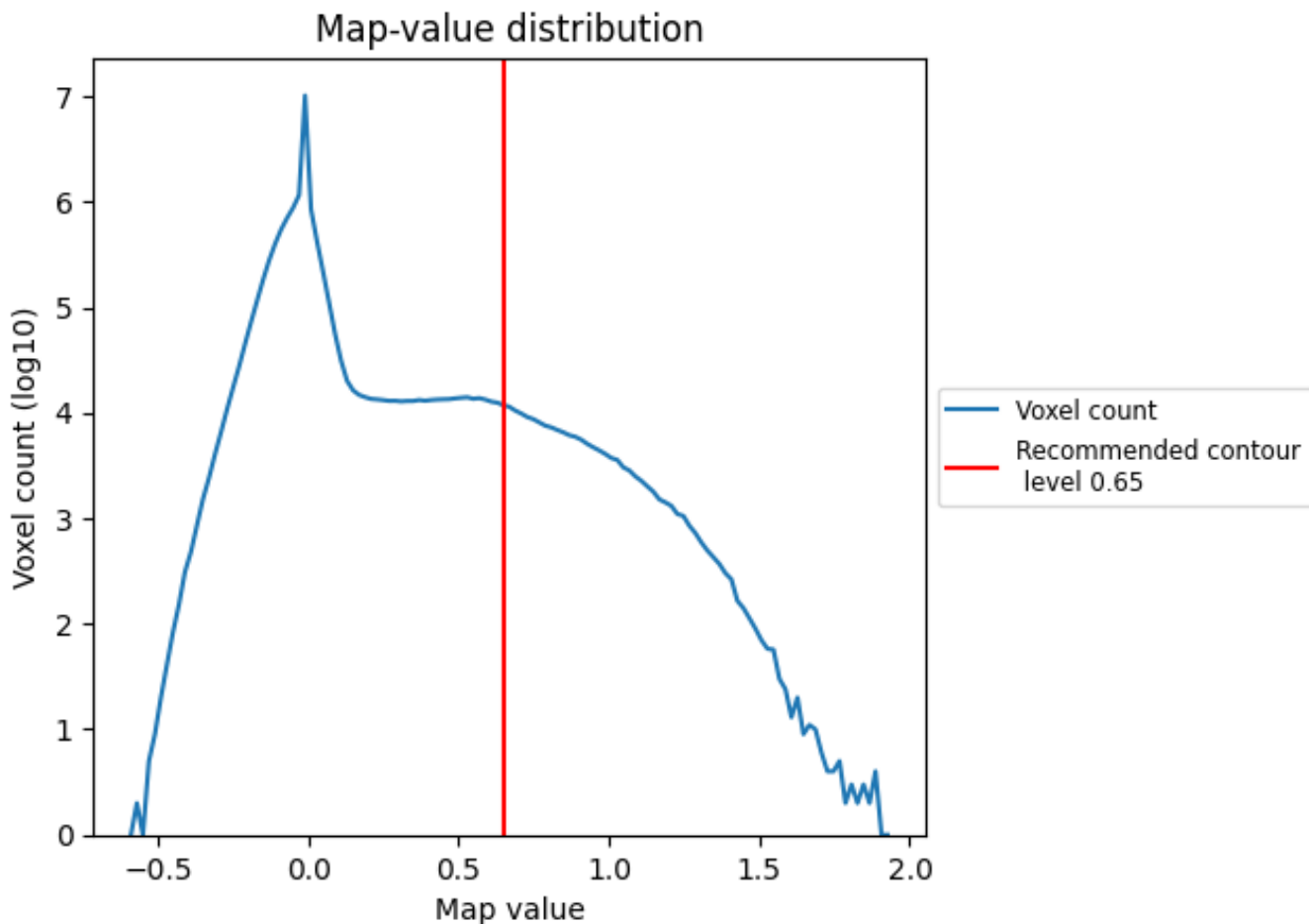


Z

7 Map analysis [i](#)

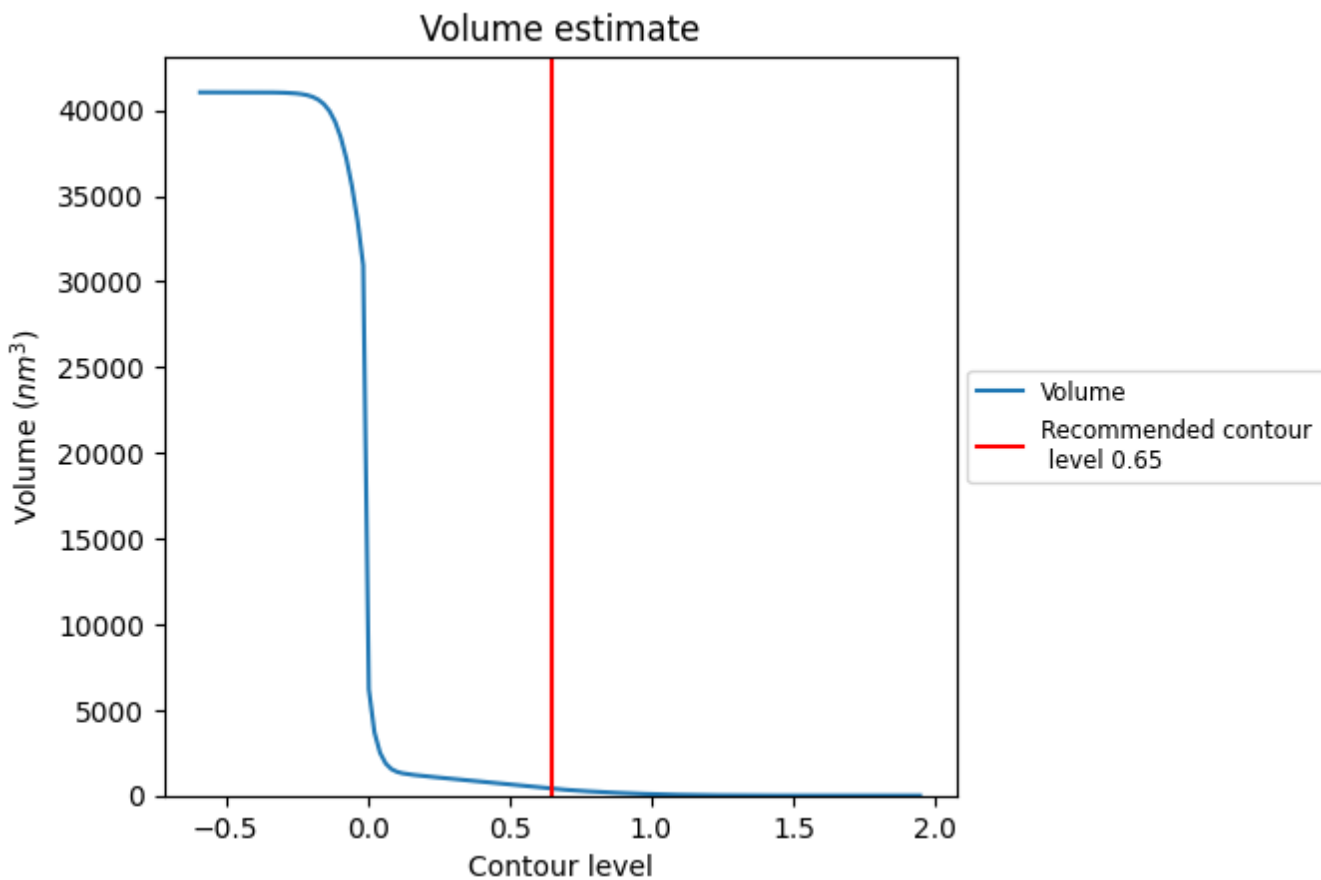
This section contains the results of statistical analysis of the map.

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.

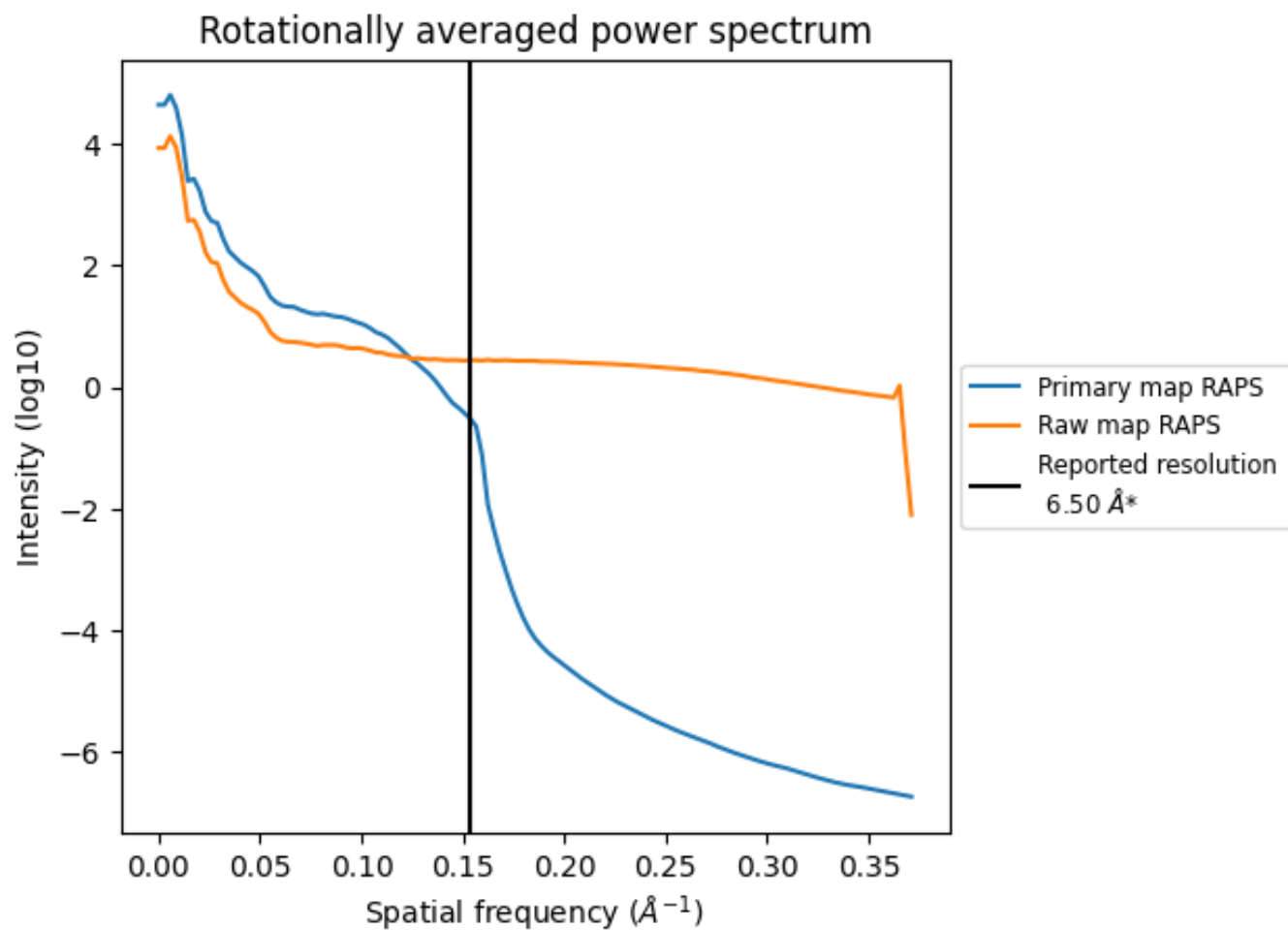
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 405 nm³; this corresponds to an approximate mass of 366 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](#)

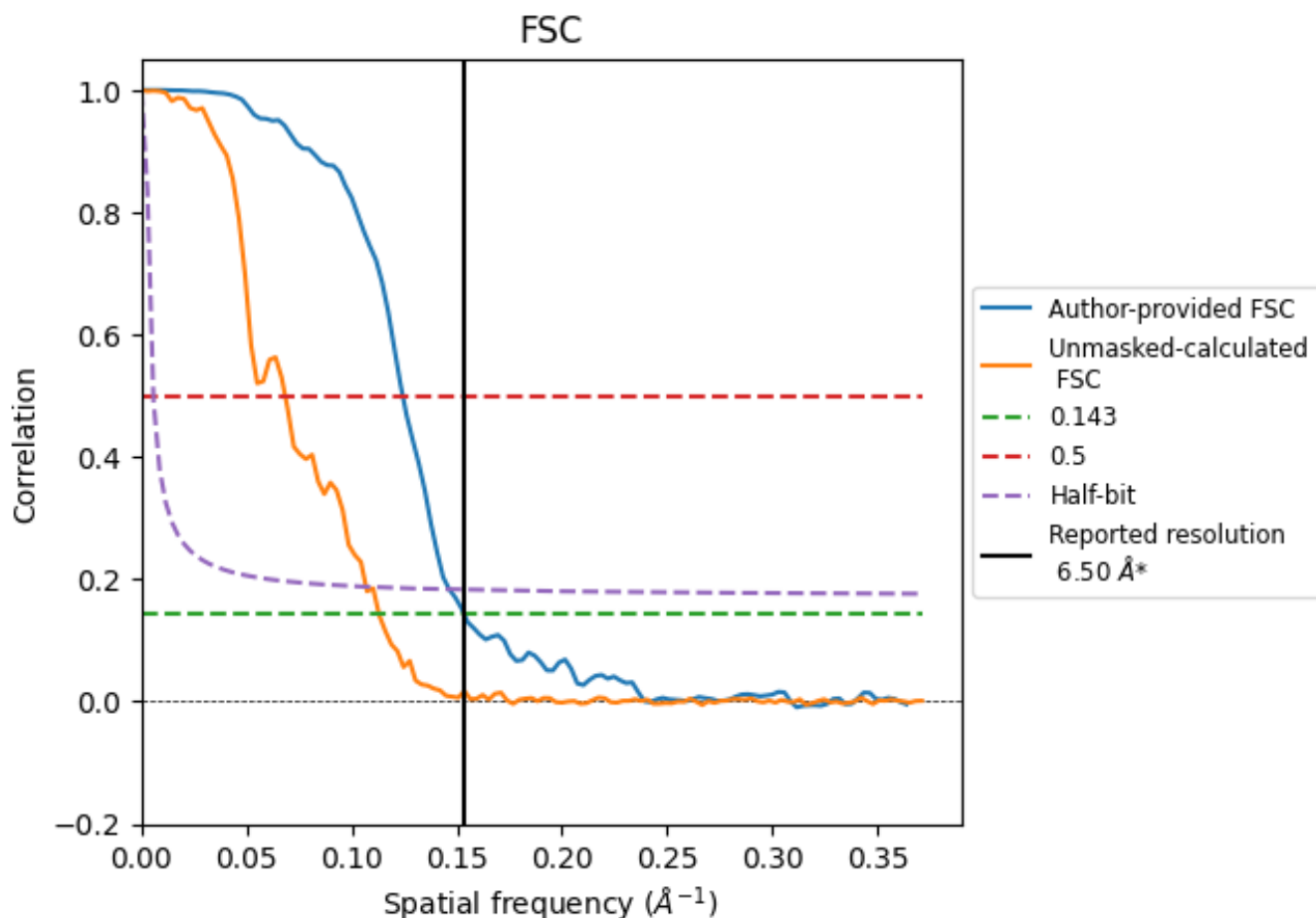


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

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 0.154 Å⁻¹

8.2 Resolution estimates [i](#)

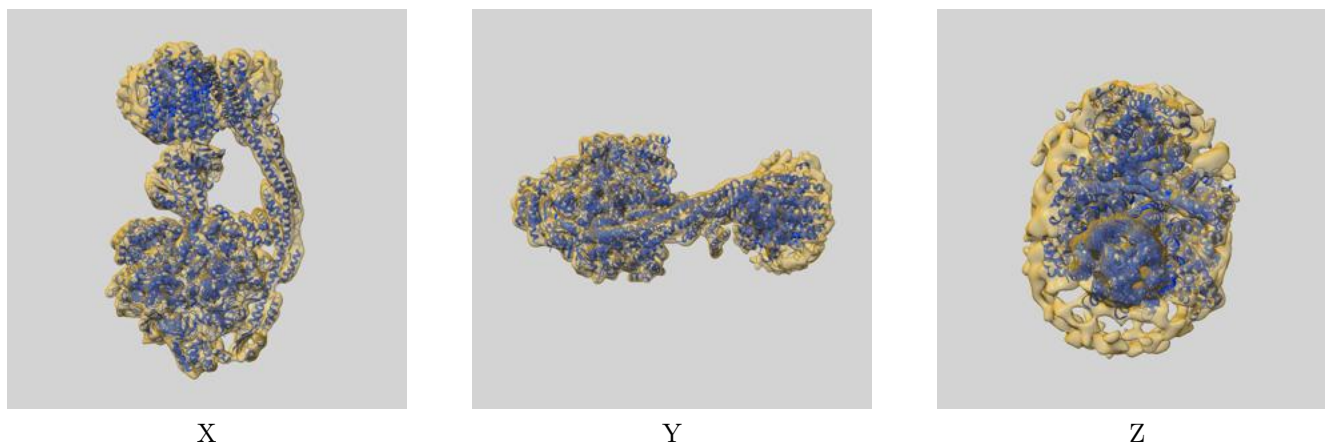
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	6.52	8.05	6.83
Unmasked-calculated*	8.86	14.62	9.36

*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 8.86 differs from the reported value 6.5 by more than 10 %

9 Map-model fit [i](#)

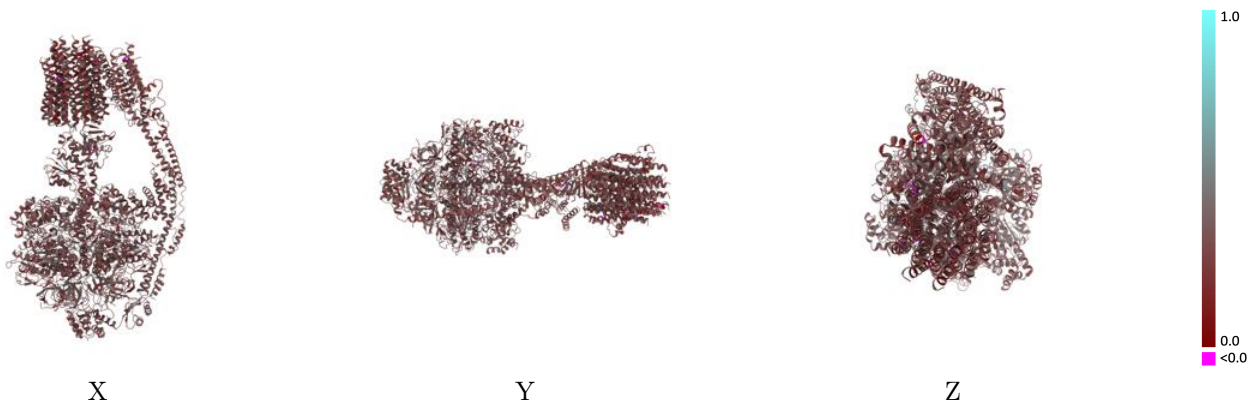
This section contains information regarding the fit between EMDB map EMD-25954 and PDB model 7TK2. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



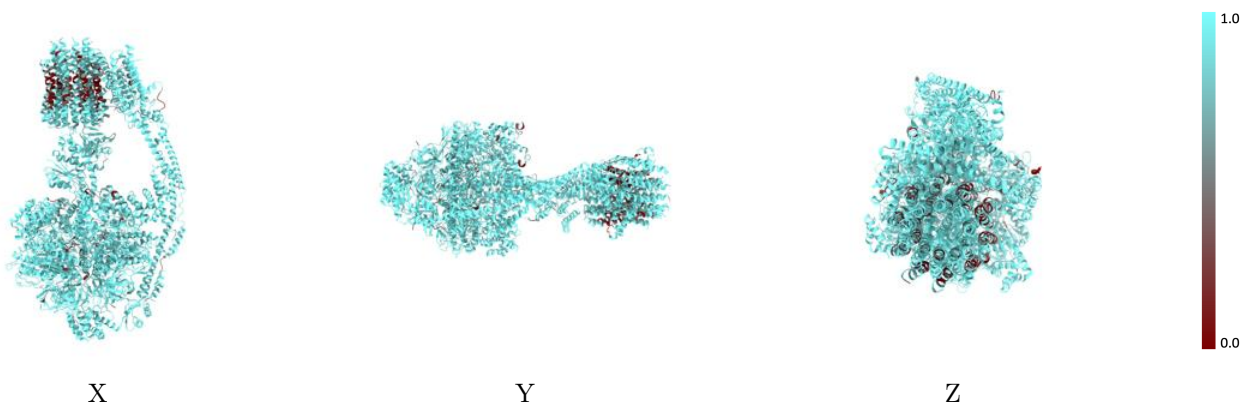
The images above show the 3D surface view of the map at the recommended contour level 0.65 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



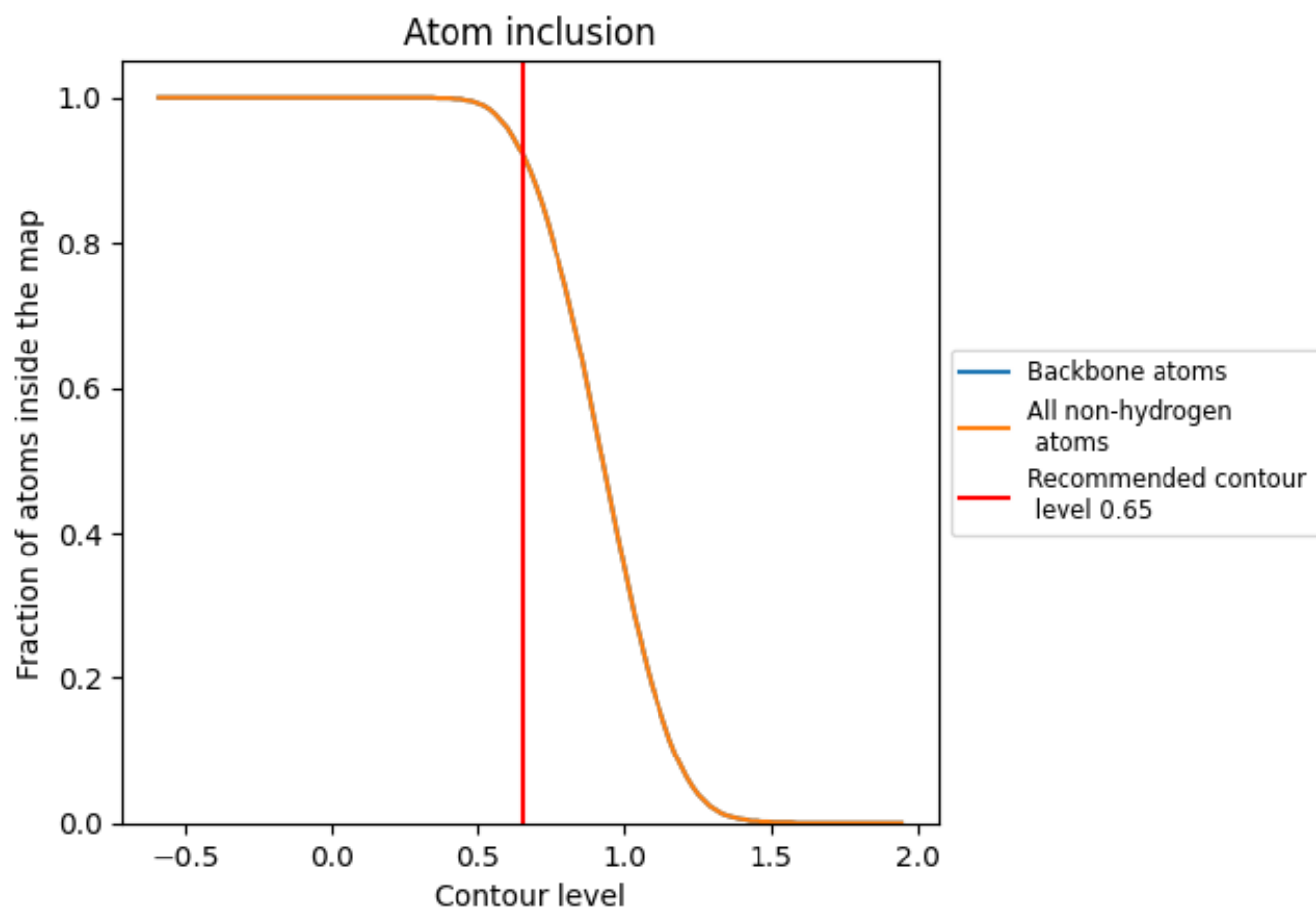
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.65).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.65) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9230	 0.2980
0	 0.7330	 0.2480
1	 0.7800	 0.2730
2	 0.7500	 0.2530
3	 0.7400	 0.2530
4	 0.7500	 0.2400
5	 0.7470	 0.2680
6	 0.7230	 0.2420
7	 0.6950	 0.2360
8	 0.7730	 0.2500
9	 0.7130	 0.2560
A	 0.9530	 0.3150
B	 0.9540	 0.3080
C	 0.9590	 0.3180
D	 0.9740	 0.3120
E	 0.9170	 0.3000
F	 0.9800	 0.3180
G	 0.9660	 0.3010
H	 0.9230	 0.2840
I	 0.9690	 0.2960
O	 0.9830	 0.3160
T	 0.9210	 0.2750
U	 0.9950	 0.2990
V	 0.9660	 0.2930
W	 0.9260	 0.2640
X	 0.8870	 0.3140
Y	 0.8580	 0.2560
Z	 0.9640	 0.2900

