



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 03:15 AM UTC

PDB ID : 7TKG / pdb_00007tkg
EMDB ID : EMD-25968
Title : Yeast ATP synthase State 2catalytic(a) with 10 mM ATP backbone model
Authors : Guo, H.; Rubinstein, J.L.
Deposited on : 2022-01-17
Resolution : 4.50 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:

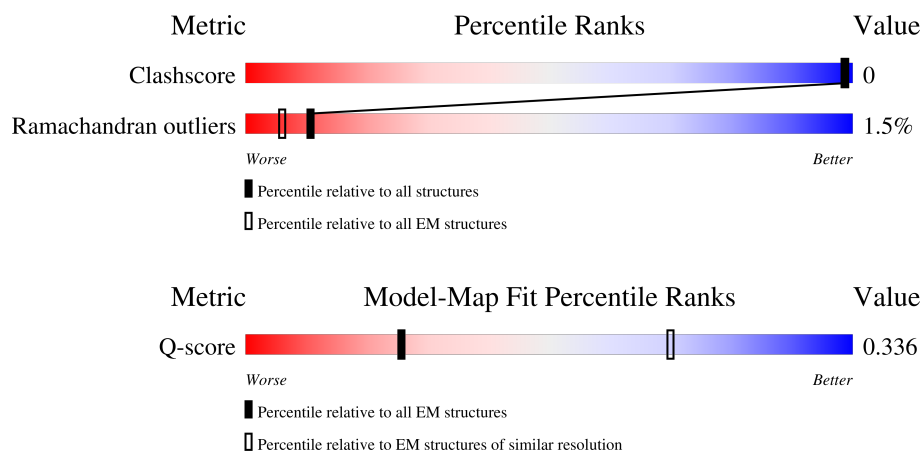
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.50 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	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	
1	1	76	
1	2	76	
1	3	76	
1	4	76	

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Mol	Chain	Length	Quality of chain
1	5	76	
1	6	76	
1	7	76	
1	8	76	
1	9	76	
2	A	510	
2	B	510	
2	C	510	
3	D	478	
3	E	478	
3	F	478	
4	G	278	
5	H	138	
6	I	61	
7	O	195	
8	T	249	
9	U	209	
10	V	173	
11	W	95	
12	X	92	
13	Y	59	
14	Z	48	

2 Entry composition

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.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A	501	Total	C	N	O	0	0
			2004	1002	501	501		
2	B	505	Total	C	N	O	0	0
			2020	1010	505	505		
2	C	496	Total	C	N	O	0	0
			1984	992	496	496		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	469	Total	C	N	O	0	0
			1876	938	469	469		
3	E	470	Total	C	N	O	0	0
			1880	940	470	470		
3	F	468	Total	C	N	O	0	0
			1872	936	468	468		

- 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
10	V	171	Total	C	N	O	0	0
			685	342	171	172		

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

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

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

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

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

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

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

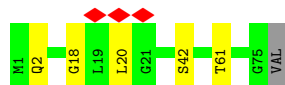
Mol	Chain	Residues	Atoms				AltConf	Trace
14	Z	48	Total	C	N	O	0	0
			193	96	48	49		

3 Residue-property plots [i](#)

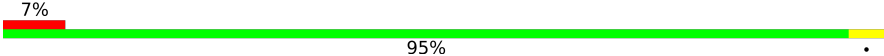
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

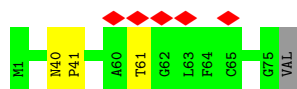
- Molecule 1: ATP synthase subunit 9

Chain 0:  92% 7%

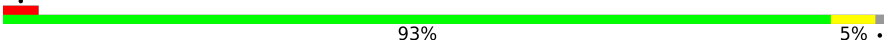


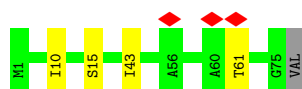
- Molecule 1: ATP synthase subunit 9

Chain 1:  7% 95%

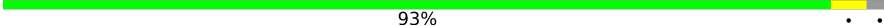


- Molecule 1: ATP synthase subunit 9

Chain 2:  93% 5%

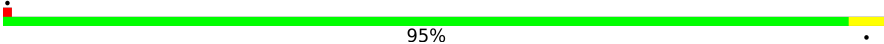


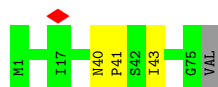
- Molecule 1: ATP synthase subunit 9

Chain 3:  93%

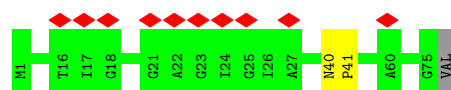


- Molecule 1: ATP synthase subunit 9

Chain 4:  95%



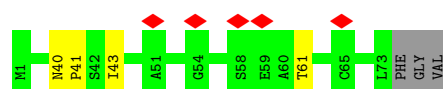
- Molecule 1: ATP synthase subunit 9



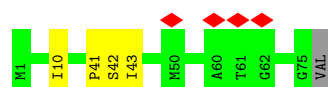
- Molecule 1: ATP synthase subunit 9



- Molecule 1: ATP synthase subunit 9



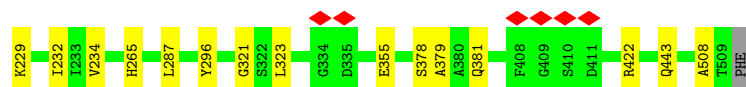
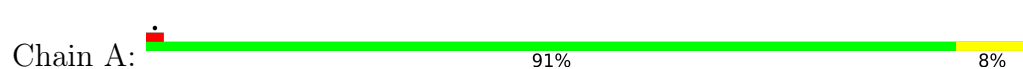
- Molecule 1: ATP synthase subunit 9



- Molecule 1: ATP synthase subunit 9



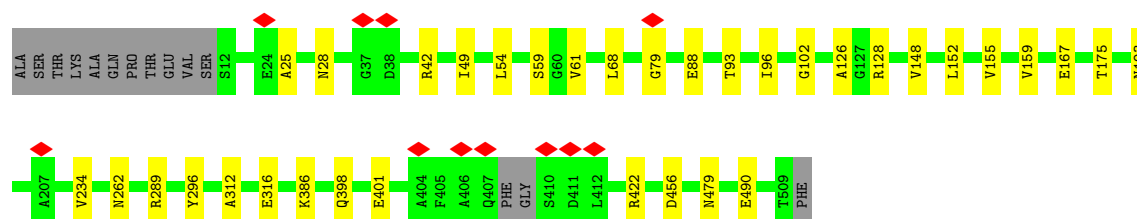
- Molecule 2: ATP synthase subunit alpha



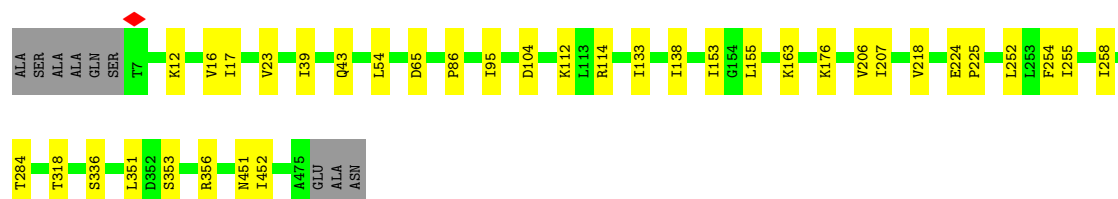
- Molecule 2: ATP synthase subunit alpha

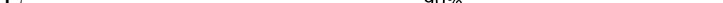
Sequence logo for the 1000bp upstream region of the T3 gene. The y-axis represents information content in bits (0.00 to 0.15). The x-axis shows amino acid positions from -1000 to +100. Amino acids are color-coded: red for high conservation, yellow for moderate, and grey for low. Red diamonds above the sequence indicate specific positions of interest.

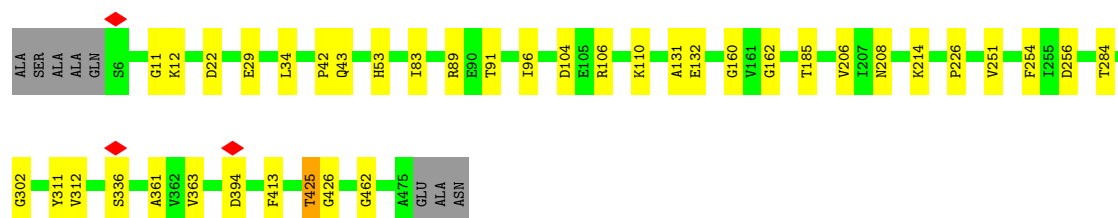
- Chain C: 90% 7%



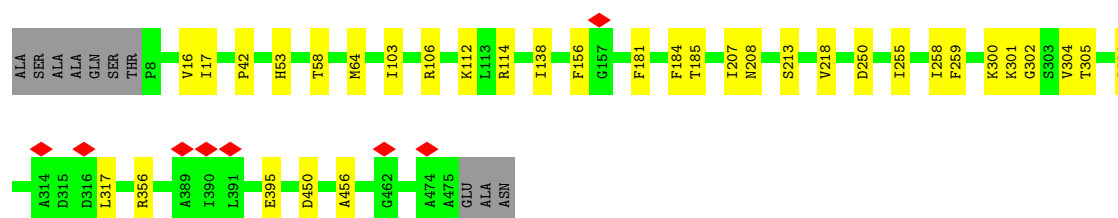
- Chain D: 91% 8%



- Chain E:  90% 8%

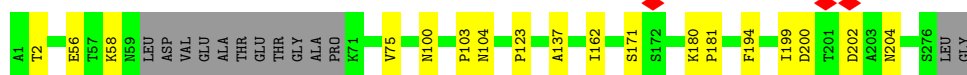


- Chain F: 91% 7% .



- Molecule 4: ATP synthase subunit gamma

Chain G:  89% 6% 5%



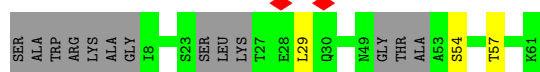
- Molecule 5: ATP synthase subunit delta

Chain H:  76% 11% 13%



- Molecule 6: ATP synthase subunit epsilon

Chain I:  74% 5% 21%



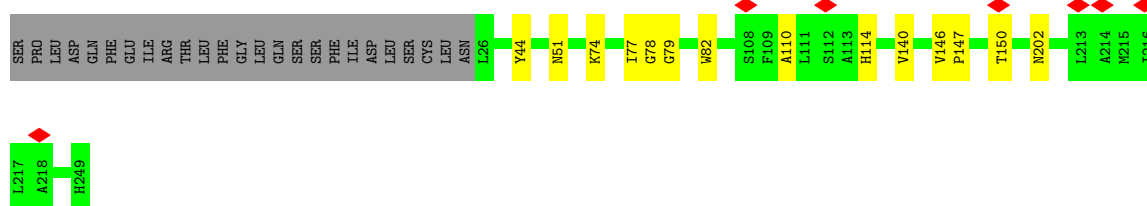
- Molecule 7: ATP synthase subunit 5

Chain O:  87% 9% 4%



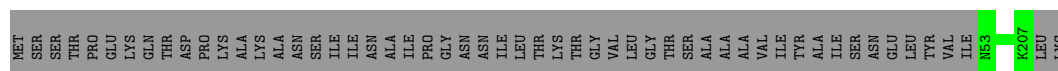
- Molecule 8: ATP synthase subunit a

Chain T:  84% 6% 10%

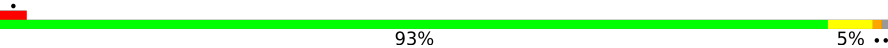


- Molecule 9: ATP synthase subunit 4

Chain U:  74% 26%



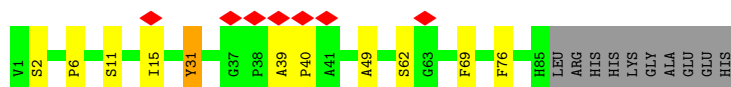
- Molecule 10: ATP synthase subunit d

Chain V:  93% 5% ..



- Molecule 11: ATP synthase subunit f

Chain W:  7% 78% 11% • 11%



- Molecule 12: ATP synthase subunit H

Chain X:  13% 63% • 33%

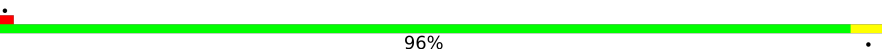


- Molecule 13: ATP synthase subunit J

Chain Y:  5% 61% • 37%



- Molecule 14: ATP synthase protein 8

Chain Z:  96% •



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32285	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	2.168	Depositor
Minimum map value	-0.608	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.114	Depositor
Recommended contour level	0.63	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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	1.26	0/299	2.11	8/372 (2.2%)
1	1	1.27	0/299	1.87	2/372 (0.5%)
1	2	1.28	0/299	1.97	8/372 (2.2%)
1	3	1.27	0/295	1.88	2/367 (0.5%)
1	4	1.28	0/299	1.96	2/372 (0.5%)
1	5	1.28	0/299	1.95	0/372
1	6	1.28	0/295	2.03	2/367 (0.5%)
1	7	1.26	0/291	2.03	4/362 (1.1%)
1	8	1.26	0/299	2.06	4/372 (1.1%)
1	9	1.26	0/295	2.00	4/367 (1.1%)
2	A	1.57	0/2003	1.77	38/2502 (1.5%)
2	B	1.56	0/2018	1.72	21/2519 (0.8%)
2	C	1.54	0/1982	1.74	32/2474 (1.3%)
3	D	1.58	0/1875	1.78	37/2342 (1.6%)
3	E	1.56	1/1879 (0.1%)	1.77	26/2347 (1.1%)
3	F	1.58	0/1871	1.80	35/2337 (1.5%)
4	G	1.47	0/1058	1.82	14/1319 (1.1%)
5	H	1.54	0/475	1.79	12/585 (2.1%)
6	I	1.36	0/190	1.73	0/231
7	O	1.56	0/747	1.80	15/932 (1.6%)
8	T	1.36	0/896	1.58	14/1117 (1.3%)
9	U	1.39	0/619	1.68	0/772
10	V	1.44	0/684	1.71	8/852 (0.9%)
11	W	1.37	0/339	1.86	8/422 (1.9%)
12	X	1.40	0/247	2.03	4/307 (1.3%)
13	Y	1.25	0/147	1.66	1/182 (0.5%)
14	Z	1.34	0/192	1.51	1/237 (0.4%)
All	All	1.49	1/20192 (0.0%)	1.79	302/25172 (1.2%)

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	9	0	1
2	B	0	1
3	E	0	1
5	H	0	1
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	11	GLY	CA-C	-6.09	1.47	1.52

All (302) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	V	67	VAL	N-CA-C	-13.91	100.50	113.71
4	G	204	ASN	CA-C-N	9.89	126.47	120.24
4	G	204	ASN	C-N-CA	9.89	126.47	120.24
2	B	175	THR	N-CA-C	-8.52	102.94	112.57
3	D	225	PRO	CA-C-O	-8.10	115.07	120.90
7	O	55	HIS	N-CA-C	-8.07	103.26	113.43
3	F	258	ILE	N-CA-C	-8.07	103.29	113.22
7	O	101	PHE	N-CA-C	-7.94	102.37	112.93
2	B	479	ASN	N-CA-C	-7.87	103.68	113.28
3	F	114	ARG	N-CA-C	-7.84	97.37	109.52
2	C	193	ASN	N-CA-C	-7.80	103.83	112.72
3	D	112	LYS	N-CA-C	-7.76	102.61	112.93
8	T	140	VAL	N-CA-C	-7.74	105.01	112.29
3	F	103	ILE	N-CA-C	-7.43	105.89	113.10
3	F	304	VAL	N-CA-C	-7.39	101.99	110.05
3	D	43	GLN	N-CA-C	-7.35	103.62	112.59
7	O	180	ILE	N-CA-C	-7.33	103.81	111.58
3	D	258	ILE	N-CA-C	-7.32	104.38	112.80
3	F	138	ILE	N-CA-C	-7.24	97.97	108.11
2	B	99	VAL	N-CA-C	-7.21	103.28	109.19
3	D	252	LEU	N-CA-C	-7.10	98.28	109.07
3	F	305	THR	N-CA-C	-7.07	97.89	108.99
2	C	96	ILE	N-CA-C	-6.99	102.31	110.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	204	ASN	N-CA-C	-6.99	104.07	112.59
3	E	312	VAL	N-CA-C	-6.91	100.21	107.60
2	C	93	THR	N-CA-C	-6.90	103.84	111.36
2	B	352	ILE	N-CA-C	-6.83	98.28	108.12
8	T	146	VAL	N-CA-C	-6.83	100.79	107.55
2	B	6	GLN	N-CA-C	-6.80	100.36	108.25
2	A	232	ILE	N-CA-C	-6.78	98.72	108.48
2	C	68	LEU	N-CA-C	-6.76	97.71	108.73
7	O	150	GLY	N-CA-C	-6.75	105.86	114.37
1	6	10	ILE	CA-C-N	6.71	127.43	119.98
1	6	10	ILE	C-N-CA	6.71	127.43	119.98
3	E	425	THR	N-CA-C	-6.71	96.51	110.80
2	C	175	THR	N-CA-C	-6.67	101.42	110.68
3	F	112	LYS	N-CA-C	-6.66	100.90	111.02
3	D	218	VAL	N-CA-C	-6.65	98.54	108.12
2	A	175	THR	N-CA-C	-6.64	101.44	110.68
2	C	456	ASP	N-CA-C	-6.59	104.71	112.89
5	H	40	GLY	N-CA-C	-6.59	100.63	111.38
3	E	208	ASN	N-CA-C	-6.58	98.47	109.07
10	V	133	LEU	N-CA-C	-6.55	96.84	110.80
2	C	398	GLN	N-CA-C	-6.55	105.42	113.41
2	B	128	ARG	N-CA-C	-6.52	98.27	108.90
2	C	296	TYR	N-CA-C	-6.52	101.85	110.07
3	D	224	GLU	CA-C-N	6.51	124.41	119.66
3	D	224	GLU	C-N-CA	6.51	124.41	119.66
3	D	176	LYS	N-CA-C	-6.47	105.42	113.38
2	A	234	VAL	N-CA-C	-6.47	99.11	108.17
5	H	17	PRO	N-CA-C	-6.38	105.21	113.57
3	E	53	HIS	N-CA-C	-6.38	99.00	109.40
3	D	54	LEU	N-CA-C	-6.37	105.14	113.17
3	E	89	ARG	N-CA-C	-6.33	104.82	113.30
2	A	109	VAL	N-CA-C	-6.31	99.31	108.71
3	D	356	ARG	N-CA-C	-6.28	105.58	113.18
3	D	163	LYS	N-CA-C	-6.28	104.44	111.28
5	H	69	PHE	N-CA-C	-6.25	98.71	108.90
1	2	10	ILE	CA-C-N	6.25	126.92	119.98
1	2	10	ILE	C-N-CA	6.25	126.92	119.98
2	A	169	ILE	N-CA-C	-6.24	98.89	107.99
2	B	232	ILE	N-CA-C	-6.24	99.22	108.45
5	H	61	GLU	N-CA-C	-6.20	98.17	108.34
5	H	41	VAL	N-CA-C	-6.19	99.21	108.12
2	B	177	LYS	N-CA-C	-6.18	104.62	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	255	ILE	N-CA-C	-6.18	98.79	108.86
4	G	2	THR	N-CA-C	-6.18	104.47	111.14
3	F	450	ASP	N-CA-C	-6.18	104.23	112.94
11	W	69	PHE	CA-C-N	6.18	128.56	120.28
11	W	69	PHE	C-N-CA	6.18	128.56	120.28
2	C	234	VAL	N-CA-C	-6.15	99.61	108.53
4	G	171	SER	N-CA-C	-6.14	99.99	109.14
3	F	395	GLU	N-CA-C	-6.09	105.02	112.88
2	A	379	ALA	N-CA-C	-6.06	105.81	112.72
2	A	381	GLN	CA-C-N	6.06	128.62	120.50
2	A	381	GLN	C-N-CA	6.06	128.62	120.50
3	D	39	ILE	N-CA-C	-6.06	99.68	108.17
4	G	162	ILE	N-CA-C	-6.06	100.35	108.35
3	D	65	ASP	CA-C-N	6.05	125.85	120.10
3	D	65	ASP	C-N-CA	6.05	125.85	120.10
3	E	363	VAL	N-CA-C	-6.04	106.87	112.43
2	A	68	LEU	N-CA-C	-6.01	98.61	108.41
10	V	88	GLN	N-CA-C	-6.01	98.74	108.41
4	G	100	ASN	N-CA-C	-6.01	105.60	113.17
7	O	98	LEU	N-CA-C	-6.00	105.26	113.30
2	C	128	ARG	N-CA-C	-6.00	100.02	109.50
2	C	490	GLU	N-CA-C	-5.98	99.64	108.79
2	C	262	ASN	N-CA-C	-5.97	105.75	113.16
3	D	17	ILE	N-CA-C	-5.97	98.53	107.37
7	O	33	ILE	N-CA-C	-5.97	107.06	111.90
3	D	138	ILE	N-CA-C	-5.94	99.85	108.17
3	D	114	ARG	N-CA-C	-5.94	99.51	109.07
4	G	202	ASP	N-CA-C	-5.92	105.24	112.88
7	O	192	GLU	N-CA-C	-5.91	105.84	113.16
2	A	206	VAL	N-CA-C	-5.90	99.99	108.48
2	C	479	ASN	N-CA-C	-5.89	106.09	113.28
3	F	208	ASN	N-CA-C	-5.86	97.61	107.99
2	A	443	GLN	N-CA-C	-5.86	106.67	113.88
7	O	17	GLY	N-CA-C	-5.83	106.56	115.66
3	E	206	VAL	N-CA-C	-5.80	104.71	110.62
7	O	176	VAL	N-CA-C	-5.80	99.70	108.17
3	D	153	ILE	N-CA-C	-5.79	100.09	108.89
2	A	118	ASP	N-CA-C	-5.78	106.27	113.38
1	2	43	ILE	CA-C-N	5.78	128.29	120.38
1	2	43	ILE	C-N-CA	5.78	128.29	120.38
8	T	44	TYR	N-CA-C	-5.77	108.05	114.62
3	F	185	THR	N-CA-C	-5.76	99.79	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	12	LYS	N-CA-C	-5.76	99.51	108.90
2	B	148	VAL	N-CA-C	-5.75	99.93	108.45
2	A	422	ARG	CA-C-N	5.75	126.36	119.98
2	A	422	ARG	C-N-CA	5.75	126.36	119.98
3	D	284	THR	N-CA-C	-5.74	105.59	112.59
3	E	413	PHE	N-CA-C	-5.73	105.79	112.89
5	H	56	VAL	N-CA-C	-5.72	100.10	108.11
14	Z	7	PHE	N-CA-C	-5.72	105.96	113.17
2	A	355	GLU	CA-C-N	5.71	127.93	120.28
2	A	355	GLU	C-N-CA	5.71	127.93	120.28
2	A	96	ILE	N-CA-C	-5.71	102.21	109.80
3	F	58	THR	N-CA-C	-5.71	100.67	109.52
8	T	110	ALA	CA-C-N	5.71	127.92	120.28
8	T	110	ALA	C-N-CA	5.71	127.92	120.28
3	D	16	VAL	N-CA-C	-5.70	97.47	109.34
3	F	356	ARG	N-CA-C	-5.70	106.19	113.02
5	H	60	MET	N-CA-C	-5.69	99.14	108.76
7	O	7	PRO	CA-C-N	5.69	126.24	120.38
7	O	7	PRO	C-N-CA	5.69	126.24	120.38
7	O	151	LYS	N-CA-C	-5.69	99.13	108.41
8	T	150	THR	N-CA-C	-5.67	103.11	108.22
1	0	18	GLY	CA-C-N	5.66	128.43	120.28
1	0	18	GLY	C-N-CA	5.66	128.43	120.28
10	V	90	GLN	N-CA-C	-5.66	106.92	113.88
2	C	386	LYS	N-CA-C	-5.65	106.06	113.12
3	E	361	ALA	N-CA-C	-5.64	105.50	112.72
2	A	142	ARG	N-CA-C	-5.64	100.78	109.52
3	F	42	PRO	N-CA-C	-5.62	106.83	113.86
5	H	14	PHE	N-CA-C	-5.62	99.73	108.90
2	A	78	PHE	N-CA-C	-5.60	105.66	112.88
3	F	308	GLN	N-CA-C	-5.59	100.85	109.52
2	A	70	PRO	N-CA-C	-5.59	107.36	114.35
2	A	296	TYR	N-CA-C	-5.58	102.74	109.72
3	D	23	VAL	N-CA-C	-5.57	100.30	108.99
3	E	42	PRO	N-CA-C	-5.54	108.92	114.68
4	G	180	LYS	N-CA-C	-5.51	103.26	108.22
3	F	456	ALA	N-CA-C	-5.51	106.56	113.28
2	B	381	GLN	N-CA-C	-5.50	101.62	110.14
3	D	255	ILE	N-CA-C	-5.50	100.15	108.17
7	O	179	SER	N-CA-C	-5.49	101.84	110.36
3	E	284	THR	N-CA-C	-5.49	105.89	112.59
2	C	422	ARG	CA-C-N	5.49	126.03	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	422	ARG	C-N-CA	5.49	126.03	119.94
3	F	17	ILE	N-CA-C	-5.47	100.01	107.99
3	D	336	SER	CA-C-N	5.46	128.14	120.28
3	D	336	SER	C-N-CA	5.46	128.14	120.28
11	W	62	SER	N-CA-C	-5.46	101.68	110.14
3	D	206	VAL	N-CA-C	-5.46	105.21	110.72
3	E	22	ASP	N-CA-C	-5.44	101.30	109.95
2	B	234	VAL	N-CA-C	-5.43	100.77	108.58
2	C	61	VAL	N-CA-C	-5.42	100.67	108.42
2	C	42	ARG	N-CA-C	-5.42	99.61	108.76
3	E	96	ILE	N-CA-C	-5.42	100.53	108.11
8	T	74	LYS	N-CA-C	-5.41	105.41	112.23
3	F	250	ASP	N-CA-C	-5.40	100.50	109.46
7	O	50	ASN	N-CA-C	-5.39	97.62	109.11
8	T	79	GLY	N-CA-C	-5.39	105.43	111.63
2	B	265	HIS	N-CA-C	-5.38	101.35	109.85
5	H	39	ILE	N-CA-C	-5.37	100.46	108.46
3	F	395	GLU	CA-C-N	5.37	128.33	120.71
3	F	395	GLU	C-N-CA	5.37	128.33	120.71
1	1	61	THR	CA-C-N	5.36	125.93	119.98
1	1	61	THR	C-N-CA	5.36	125.93	119.98
3	F	181	PHE	N-CA-C	-5.36	101.30	108.86
3	D	353	SER	N-CA-C	-5.36	100.57	108.99
2	B	142	ARG	N-CA-C	-5.35	100.67	109.40
1	4	43	ILE	CA-C-N	5.35	128.19	120.38
1	4	43	ILE	C-N-CA	5.35	128.19	120.38
3	F	302	GLY	N-CA-C	-5.33	103.46	111.19
2	B	96	ILE	N-CA-C	-5.33	104.19	110.21
13	Y	2	LEU	N-CA-C	-5.32	106.56	112.57
3	F	259	PHE	N-CA-C	-5.32	105.56	111.36
2	C	28	ASN	N-CA-C	-5.32	100.50	108.96
1	7	61	THR	CA-C-N	5.32	125.88	119.98
1	7	61	THR	C-N-CA	5.32	125.88	119.98
10	V	167	PHE	N-CA-C	-5.32	98.91	108.48
2	B	121	GLY	CA-C-N	5.32	126.48	119.84
2	B	121	GLY	C-N-CA	5.32	126.48	119.84
3	D	351	LEU	N-CA-C	-5.32	106.47	113.17
3	E	336	SER	CA-C-N	5.31	127.40	120.28
3	E	336	SER	C-N-CA	5.31	127.40	120.28
11	W	6	PRO	CA-C-O	-5.30	112.87	120.56
11	W	49	ALA	N-CA-C	-5.30	105.56	112.23
2	A	54	LEU	N-CA-C	-5.29	100.55	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	323	LEU	N-CA-C	-5.29	100.68	109.46
3	F	300	LYS	N-CA-C	-5.29	106.67	113.02
3	E	185	THR	N-CA-C	-5.28	99.84	108.76
2	C	289	ARG	N-CA-C	-5.28	103.42	110.07
3	F	156	PHE	N-CA-C	-5.27	101.06	109.23
3	E	254	PHE	N-CA-C	-5.27	99.36	108.69
3	E	91	THR	N-CA-C	-5.27	106.87	113.72
4	G	75	VAL	N-CA-C	-5.27	100.27	108.86
3	D	95	ILE	N-CA-C	-5.26	100.74	108.11
1	2	15	SER	CA-C-N	5.26	127.85	120.28
1	2	15	SER	C-N-CA	5.26	127.85	120.28
5	H	13	GLN	N-CA-C	-5.26	98.66	108.02
1	0	61	THR	CA-C-N	5.25	125.81	119.98
1	0	61	THR	C-N-CA	5.25	125.81	119.98
2	A	205	TYR	N-CA-C	-5.25	100.63	109.07
2	A	265	HIS	N-CA-C	-5.24	101.15	109.59
2	C	79	GLY	CA-C-N	5.24	128.67	120.75
2	C	79	GLY	C-N-CA	5.24	128.67	120.75
10	V	55	PHE	N-CA-C	-5.24	106.73	113.02
1	9	10	ILE	CA-C-N	5.24	125.79	119.98
1	9	10	ILE	C-N-CA	5.24	125.79	119.98
2	A	42	ARG	N-CA-C	-5.24	99.05	108.48
5	H	58	GLU	N-CA-C	-5.24	100.50	109.24
3	D	207	ILE	N-CA-C	-5.22	100.23	108.23
10	V	132	GLU	CA-C-N	5.22	131.51	121.54
10	V	132	GLU	C-N-CA	5.22	131.51	121.54
3	F	64	MET	N-CA-C	-5.21	106.87	114.12
3	F	317	LEU	N-CA-C	-5.21	106.16	112.88
2	B	114	GLY	N-CA-C	-5.21	107.39	115.67
2	C	159	VAL	N-CA-C	-5.20	102.03	107.60
4	G	199	ILE	CA-C-N	5.20	131.48	121.54
4	G	199	ILE	C-N-CA	5.20	131.48	121.54
3	F	106	ARG	N-CA-C	-5.20	107.10	112.93
7	O	30	ASN	N-CA-C	-5.20	106.78	113.23
2	C	316	GLU	CA-C-N	5.20	127.24	120.28
2	C	316	GLU	C-N-CA	5.20	127.24	120.28
2	C	401	GLU	CA-C-N	5.20	127.58	120.46
2	C	401	GLU	C-N-CA	5.20	127.58	120.46
2	B	176	GLY	N-CA-C	-5.19	100.87	113.18
2	A	173	ARG	N-CA-C	5.19	117.76	110.23
3	D	12	LYS	N-CA-C	-5.19	101.47	109.52
11	W	31	TYR	N-CA-C	-5.19	99.75	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	7	43	ILE	CA-C-N	5.19	127.49	120.38
1	7	43	ILE	C-N-CA	5.19	127.49	120.38
4	G	137	ALA	CA-C-N	5.18	126.32	119.84
4	G	137	ALA	C-N-CA	5.18	126.32	119.84
2	A	40	ILE	N-CA-C	-5.17	100.11	107.77
2	A	64	MET	N-CA-C	-5.17	103.86	110.53
3	E	214	LYS	N-CA-C	-5.17	106.82	112.72
2	C	88	GLU	N-CA-C	-5.17	102.41	110.42
3	D	155	LEU	N-CA-C	-5.17	100.27	109.06
3	F	184	PHE	N-CA-C	-5.16	100.32	108.73
3	D	254	PHE	N-CA-C	-5.16	100.62	109.24
3	E	251	VAL	N-CA-C	-5.16	101.63	108.96
12	X	2	VAL	CA-C-N	5.14	127.04	120.56
12	X	2	VAL	C-N-CA	5.14	127.04	120.56
3	F	213	SER	N-CA-C	-5.14	100.52	108.90
3	E	226	PRO	CA-C-N	5.13	125.68	119.98
3	E	226	PRO	C-N-CA	5.13	125.68	119.98
8	T	51	ASN	CA-C-N	5.13	128.50	120.75
8	T	51	ASN	C-N-CA	5.13	128.50	120.75
1	0	20	LEU	CA-C-N	5.13	125.67	119.98
1	0	20	LEU	C-N-CA	5.13	125.67	119.98
1	9	24	ILE	CA-C-N	5.12	125.62	119.94
1	9	24	ILE	C-N-CA	5.12	125.62	119.94
5	H	16	LEU	N-CA-C	-5.11	100.58	108.55
8	T	150	THR	CA-C-N	5.11	125.11	119.90
8	T	150	THR	C-N-CA	5.11	125.11	119.90
1	2	61	THR	CA-C-N	5.10	125.61	120.00
1	2	61	THR	C-N-CA	5.10	125.61	120.00
2	A	287	LEU	N-CA-C	-5.10	106.74	113.17
11	W	76	PHE	N-CA-C	-5.10	104.66	111.24
3	E	106	ARG	N-CA-C	-5.10	106.90	113.02
3	D	104	ASP	N-CA-C	-5.10	106.75	113.17
2	B	323	LEU	N-CA-C	-5.10	99.95	110.80
1	3	43	ILE	CA-C-N	5.09	127.82	120.38
1	3	43	ILE	C-N-CA	5.09	127.82	120.38
1	8	43	ILE	CA-C-N	5.09	127.35	120.38
1	8	43	ILE	C-N-CA	5.09	127.35	120.38
2	C	25	ALA	N-CA-C	-5.08	100.61	108.90
3	D	452	ILE	CA-C-N	5.08	125.08	119.89
3	D	452	ILE	C-N-CA	5.08	125.08	119.89
2	B	64	MET	N-CA-C	-5.08	101.64	109.52
2	A	508	ALA	N-CA-C	-5.08	100.90	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	301	LYS	N-CA-C	-5.07	107.16	113.55
1	8	10	ILE	CA-C-N	5.07	126.47	120.14
1	8	10	ILE	C-N-CA	5.07	126.47	120.14
2	C	152	LEU	N-CA-C	-5.06	100.16	108.41
3	F	207	ILE	N-CA-C	-5.06	99.23	107.28
8	T	82	TRP	N-CA-C	-5.06	100.02	110.80
2	A	227	ALA	N-CA-C	-5.06	107.16	113.38
3	E	43	GLN	N-CA-C	-5.05	105.59	112.26
2	C	54	LEU	N-CA-C	-5.05	101.01	109.24
3	F	218	VAL	N-CA-C	-5.05	100.30	107.77
8	T	114	HIS	N-CA-C	-5.05	97.55	107.69
2	C	148	VAL	N-CA-C	-5.04	101.22	108.53
1	0	2	GLN	CA-C-N	5.04	127.03	120.28
1	0	2	GLN	C-N-CA	5.04	127.03	120.28
12	X	39	LEU	CA-C-N	5.04	125.03	119.89
12	X	39	LEU	C-N-CA	5.04	125.03	119.89
11	W	15	ILE	N-CA-C	-5.03	108.93	113.71
3	D	318	THR	N-CA-C	-5.03	107.20	113.38
3	F	53	HIS	N-CA-C	-5.03	100.22	108.41
2	A	130	ARG	N-CA-C	-5.02	101.69	109.72
2	A	152	LEU	N-CA-C	-5.02	100.99	109.07
2	A	196	ASP	CA-C-N	5.01	127.00	120.28
2	A	196	ASP	C-N-CA	5.01	127.00	120.28
2	B	263	GLY	N-CA-C	-5.01	108.37	115.43
3	E	311	TYR	N-CA-C	-5.01	100.73	108.90
2	A	62	LYS	N-CA-C	-5.00	101.24	109.40
2	A	128	ARG	N-CA-C	-5.00	101.77	109.52

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	9	40	ASN	Peptide
2	B	29	GLU	Peptide
3	E	256	ASP	Peptide
5	H	54	PRO	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	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	2004	0	575	0	0
2	B	2020	0	575	0	0
2	C	1984	0	567	1	0
3	D	1876	0	537	0	0
3	E	1880	0	538	1	0
3	F	1872	0	537	0	0
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	20228	0	5731	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)
2:C:102:GLY:HA3	2:C:126:ALA:H	1.80	0.47
3:E:160:GLY:C	3:E:162:GLY:H	2.28	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%)	71 (97%)	1 (1%)	1 (1%)	9	39
1	1	73/76 (96%)	70 (96%)	2 (3%)	1 (1%)	9	39
1	2	73/76 (96%)	71 (97%)	2 (3%)	0	100	100
1	3	72/76 (95%)	70 (97%)	1 (1%)	1 (1%)	9	39
1	4	73/76 (96%)	70 (96%)	2 (3%)	1 (1%)	9	39
1	5	73/76 (96%)	71 (97%)	1 (1%)	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%)	1 (1%)	2 (3%)	4	25
1	9	72/76 (95%)	69 (96%)	2 (3%)	1 (1%)	9	39
2	A	499/510 (98%)	477 (96%)	17 (3%)	5 (1%)	12	47
2	B	501/510 (98%)	473 (94%)	24 (5%)	4 (1%)	16	53
2	C	492/510 (96%)	468 (95%)	19 (4%)	5 (1%)	12	47
3	D	467/478 (98%)	437 (94%)	27 (6%)	3 (1%)	21	58
3	E	468/478 (98%)	432 (92%)	24 (5%)	12 (3%)	4	26
3	F	466/478 (98%)	446 (96%)	19 (4%)	1 (0%)	43	77
4	G	261/278 (94%)	243 (93%)	10 (4%)	8 (3%)	3	22
5	H	110/138 (80%)	105 (96%)	3 (3%)	2 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	I	42/61 (69%)	36 (86%)	3 (7%)	3 (7%)	1	11
7	O	185/195 (95%)	163 (88%)	18 (10%)	4 (2%)	5	29
8	T	222/249 (89%)	211 (95%)	7 (3%)	4 (2%)	6	33
9	U	153/209 (73%)	152 (99%)	1 (1%)	0	100	100
10	V	169/173 (98%)	155 (92%)	10 (6%)	4 (2%)	4	27
11	W	83/95 (87%)	70 (84%)	8 (10%)	5 (6%)	1	13
12	X	60/92 (65%)	53 (88%)	5 (8%)	2 (3%)	3	21
13	Y	35/59 (59%)	33 (94%)	2 (6%)	0	100	100
14	Z	46/48 (96%)	42 (91%)	3 (6%)	1 (2%)	5	29
All	All	4984/5321 (94%)	4697 (94%)	214 (4%)	73 (2%)	11	38

All (73) 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
1	7	41	PRO
1	8	41	PRO
1	9	41	PRO
2	A	229	LYS
2	B	30	THR
2	C	59	SER
3	D	451	ASN
3	E	29	GLU
3	E	110	LYS
7	O	81	LEU
10	V	24	SER
10	V	133	LEU
11	W	2	SER
11	W	39	ALA
12	X	58	VAL
14	Z	3	GLN
1	0	42	SER
2	C	49	ILE
3	D	133	ILE
3	E	131	ALA

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Mol	Chain	Res	Type
3	E	462	GLY
4	G	56	GLU
4	G	58	LYS
6	I	29	LEU
6	I	54	SER
7	O	51	PRO
7	O	61	ALA
11	W	11	SER
11	W	31	TYR
2	A	49	ILE
2	A	378	SER
2	B	29	GLU
2	B	145	HIS
2	B	230	TYR
2	C	312	ALA
3	D	86	PRO
3	E	104	ASP
3	E	132	GLU
3	E	425	THR
3	E	426	GLY
5	H	22	TYR
5	H	33	PRO
3	E	34	LEU
3	F	16	VAL
4	G	104	ASN
4	G	194	PHE
4	G	200	ASP
7	O	10	VAL
8	T	202	ASN
10	V	130	PHE
2	A	165	GLN
2	C	167	GLU
3	E	394	ASP
4	G	103	PRO
8	T	147	PRO
1	8	42	SER
4	G	123	PRO
12	X	31	TRP
11	W	40	PRO
3	E	83	ILE
3	E	302	GLY
10	V	81	VAL

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Mol	Chain	Res	Type
2	A	321	GLY
4	G	181	PRO
6	I	57	THR
2	C	155	VAL
8	T	78	GLY
8	T	77	ILE

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.

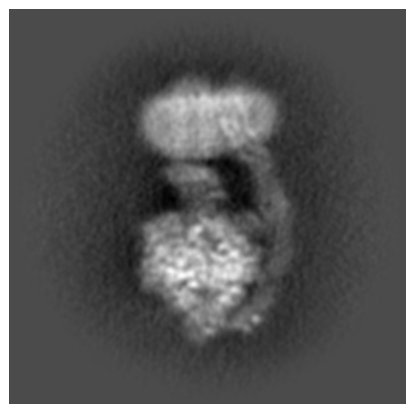
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25968. These allow visual inspection of the internal detail of the map and identification of artifacts.

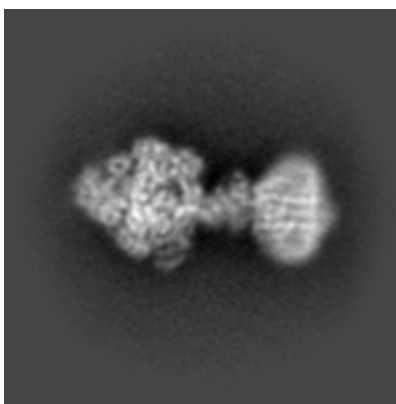
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

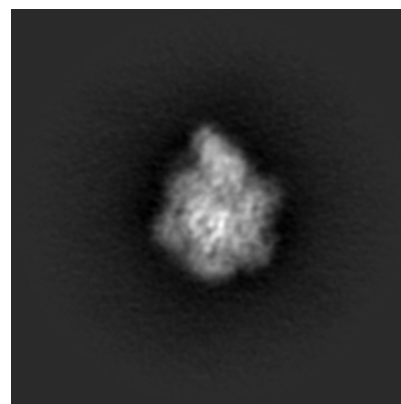
6.1.1 Primary map



X

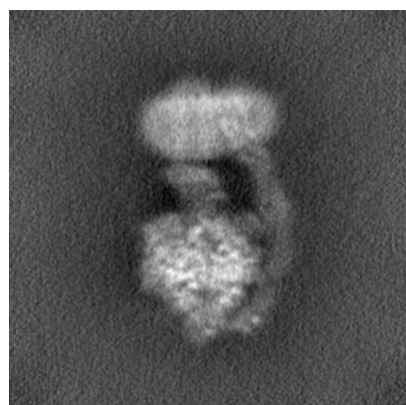


Y

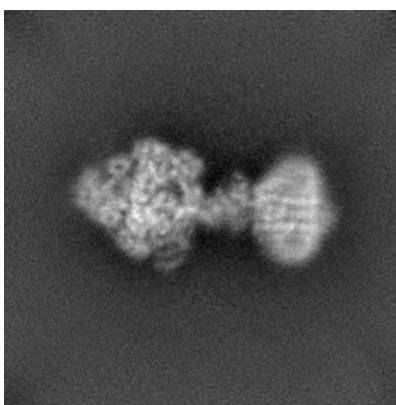


Z

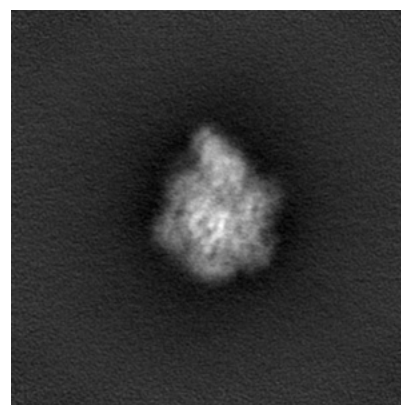
6.1.2 Raw map



X



Y

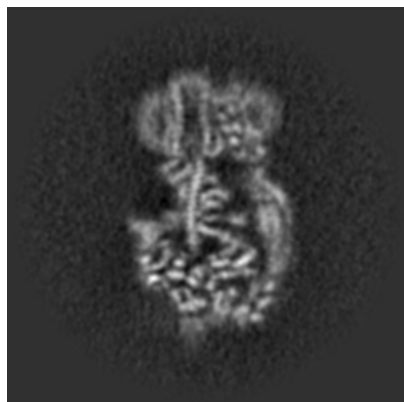


Z

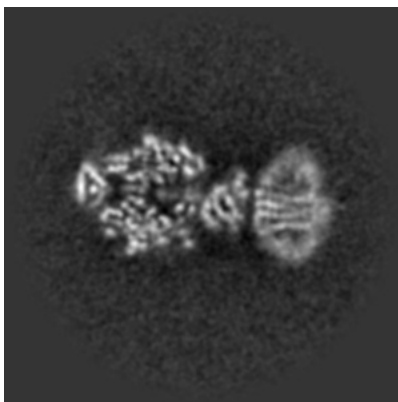
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

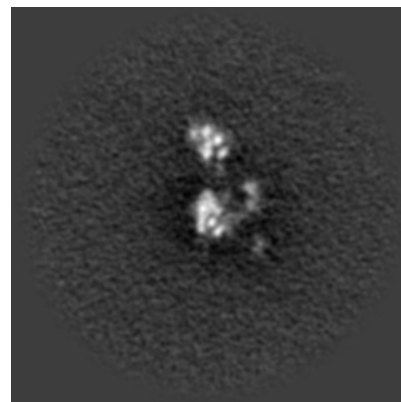
6.2.1 Primary map



X Index: 128

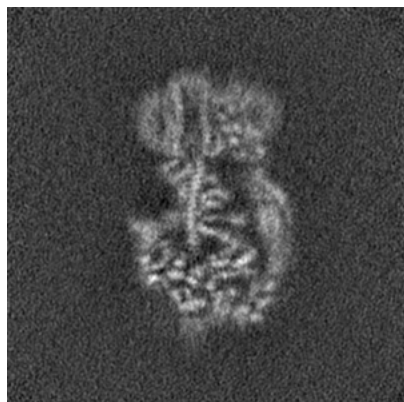


Y Index: 128

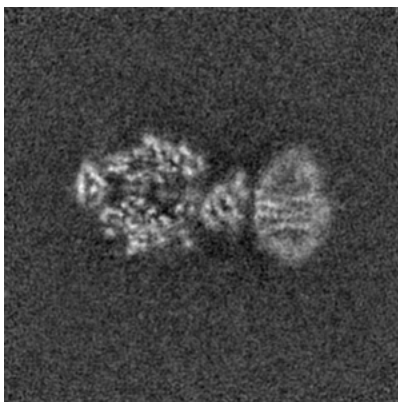


Z Index: 128

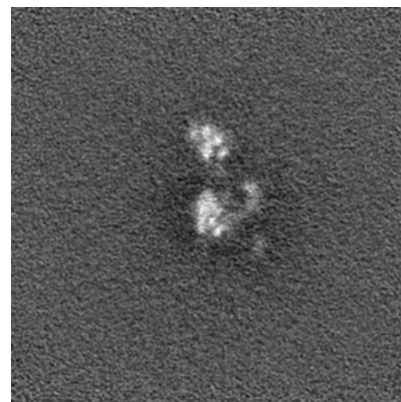
6.2.2 Raw map



X Index: 128



Y Index: 128

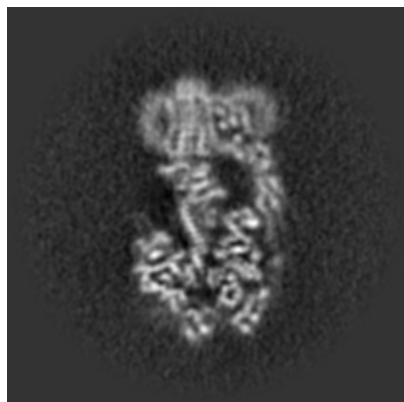


Z Index: 128

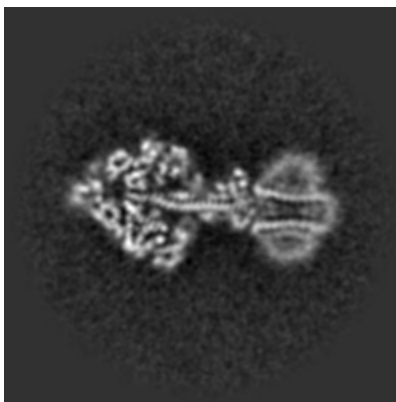
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

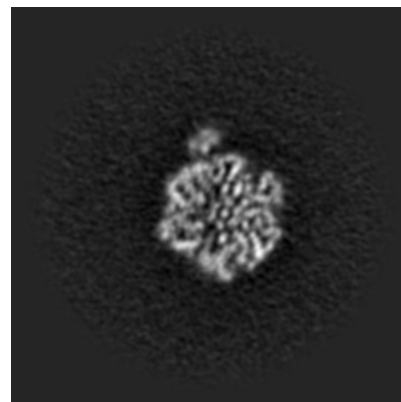
6.3.1 Primary map



X Index: 134

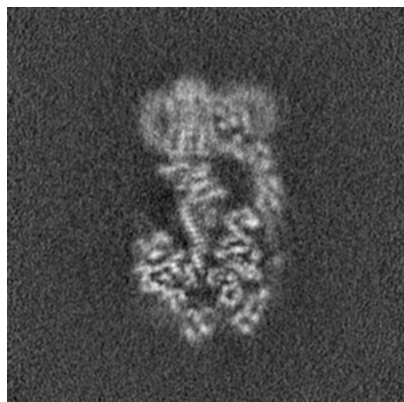


Y Index: 118

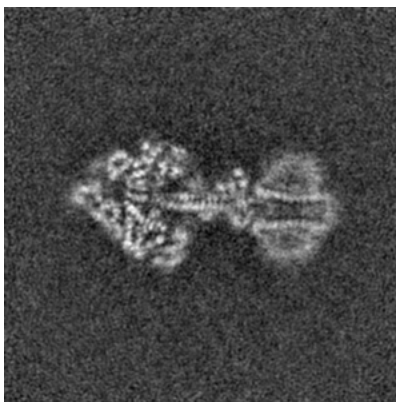


Z Index: 88

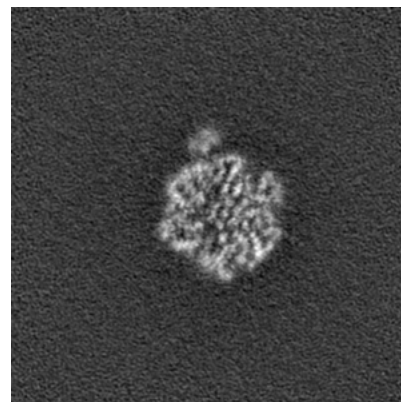
6.3.2 Raw map



X Index: 134



Y Index: 117

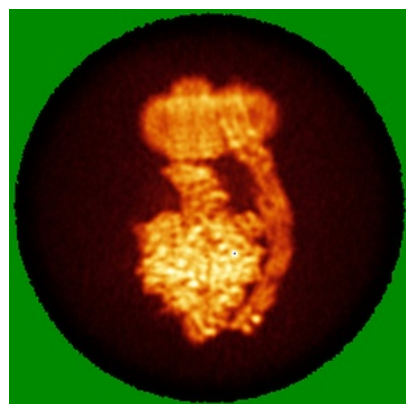


Z Index: 88

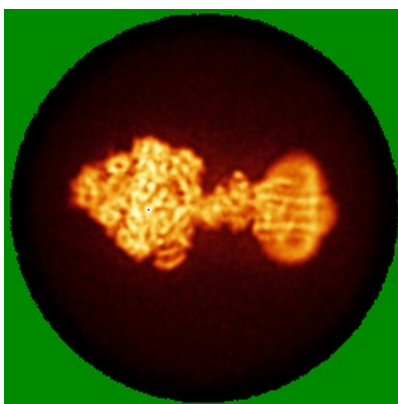
The images above show the largest variance slices of the map in three orthogonal directions.

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

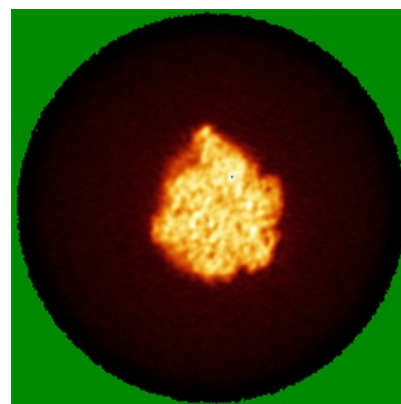
6.4.1 Primary map



X

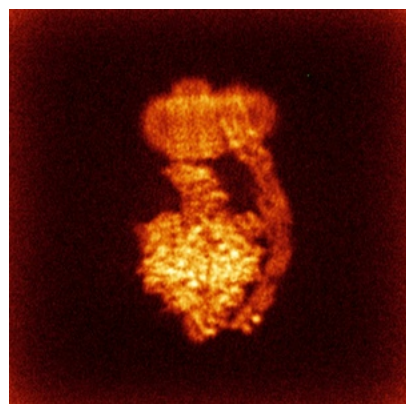


Y

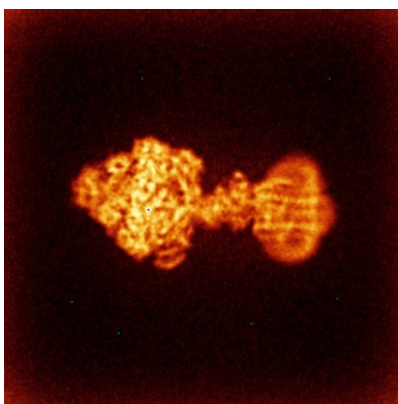


Z

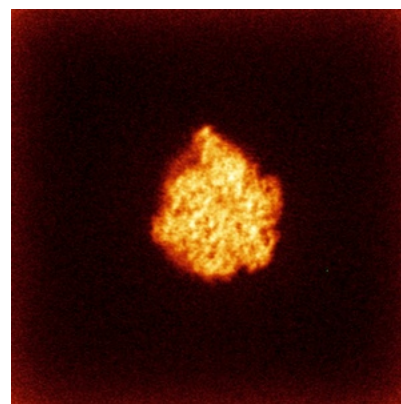
6.4.2 Raw map



X



Y

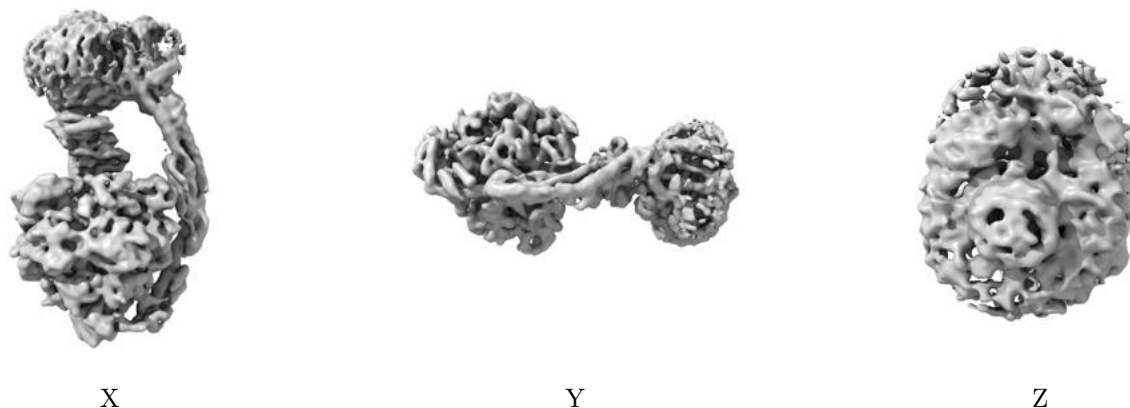


Z

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.

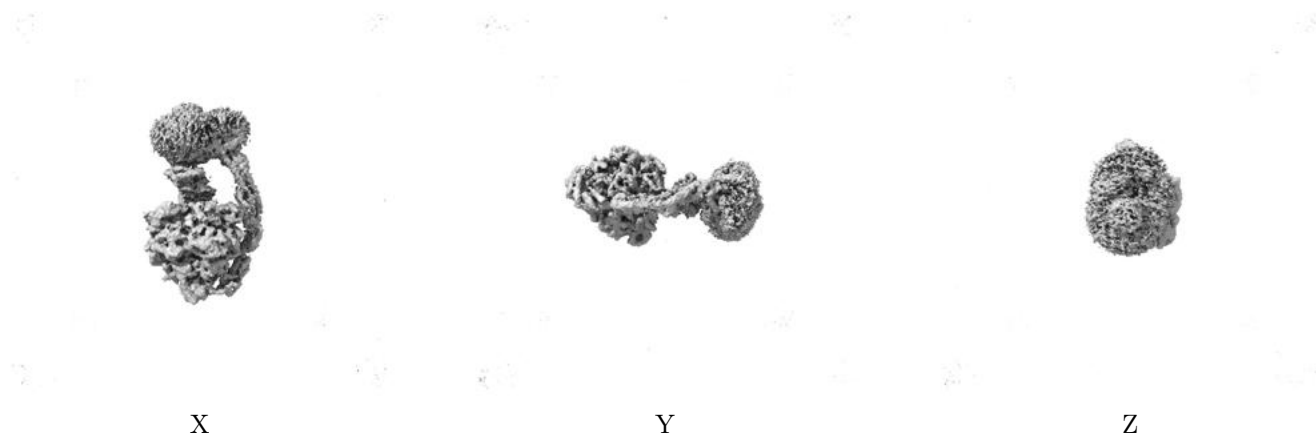
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.63. 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.

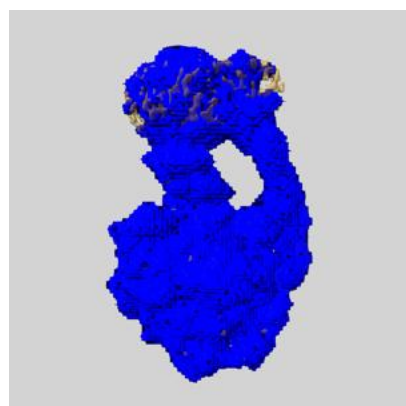
6.6 Mask visualisation [i](#)

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

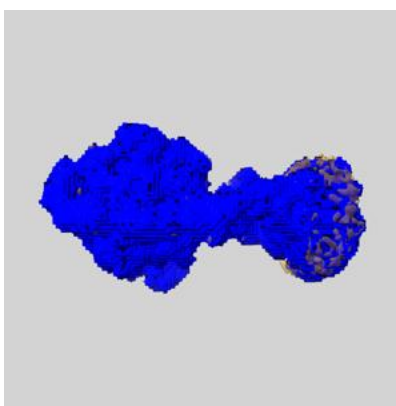
A mask typically either:

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

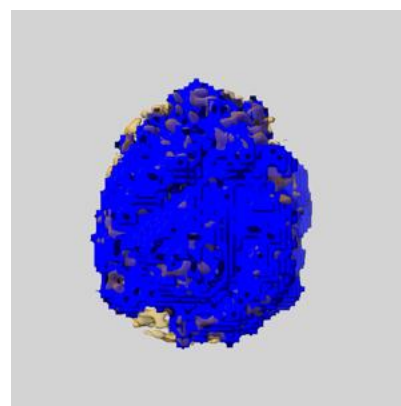
6.6.1 emd_25968_msk_1.map [i](#)



X



Y

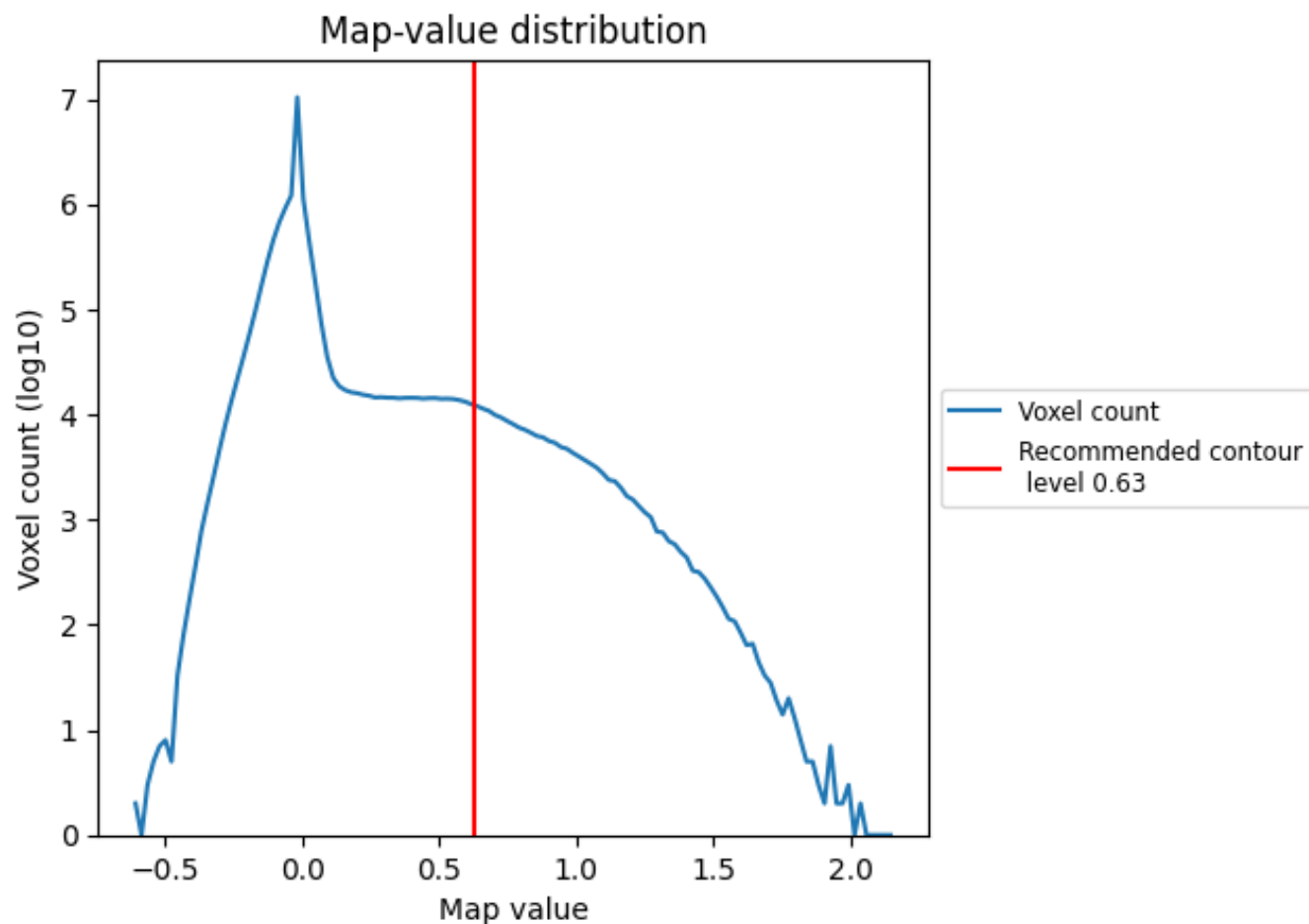


Z

7 Map analysis [i](#)

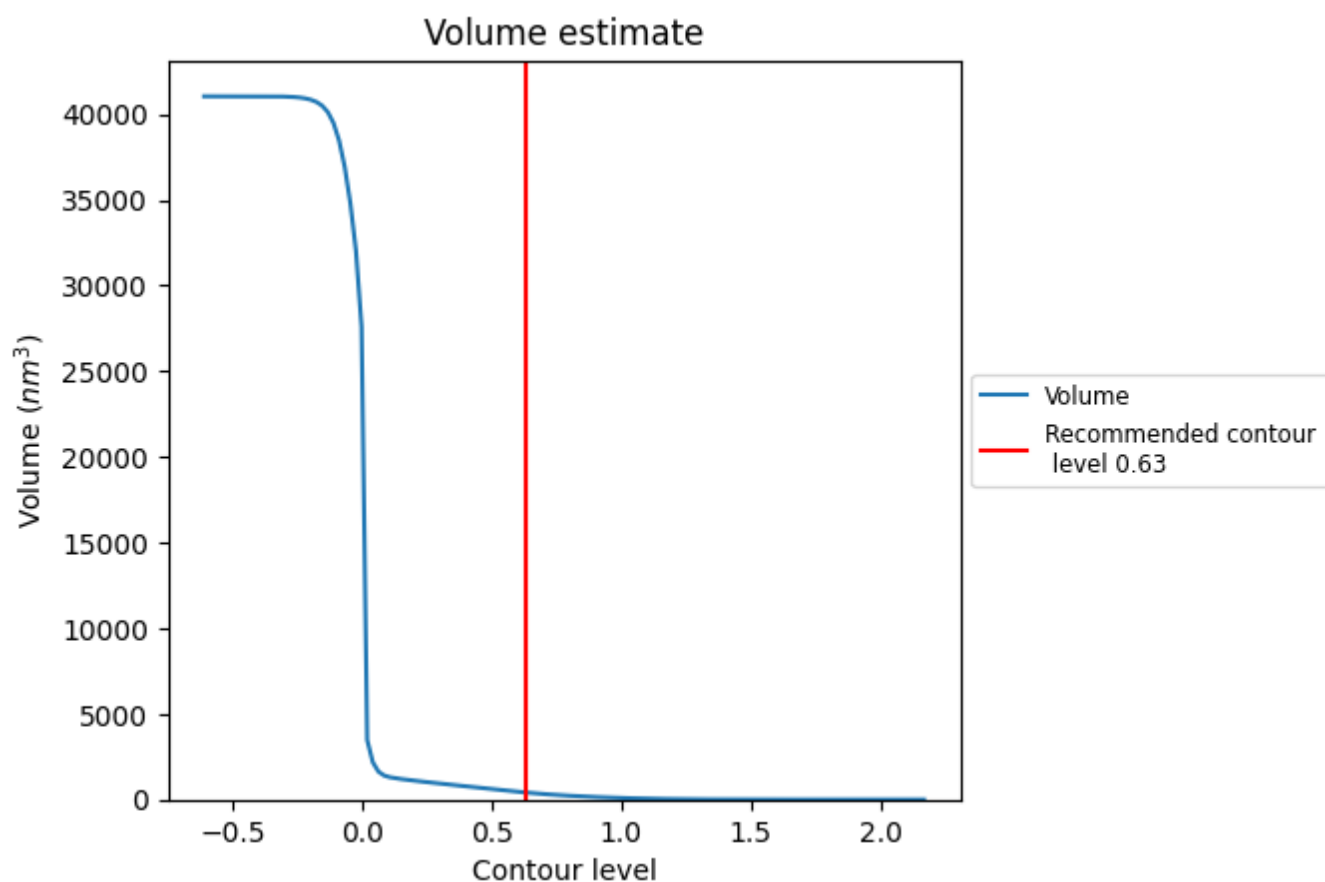
This section contains the results of statistical analysis of the map.

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.

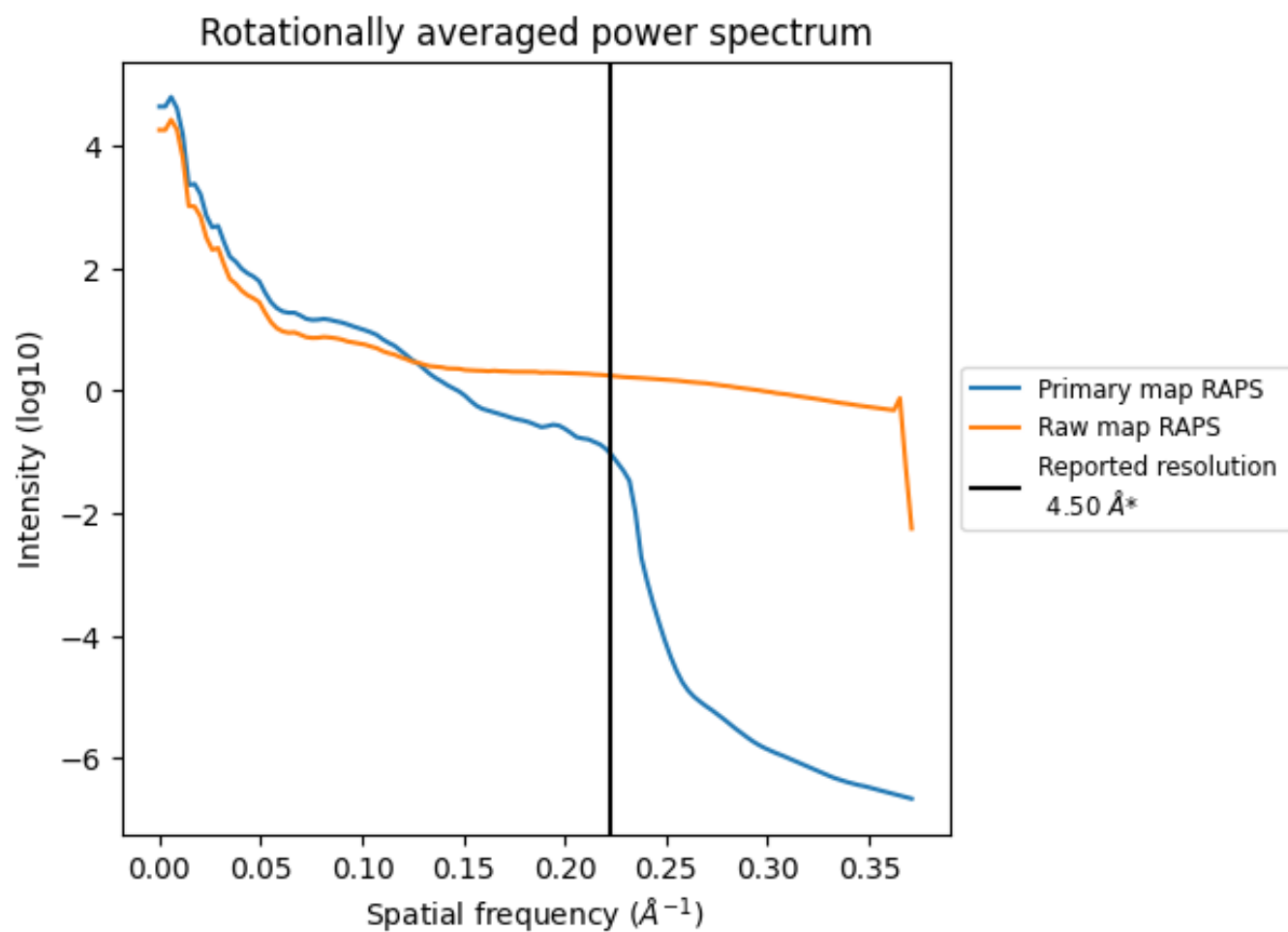
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 415 nm³; this corresponds to an approximate mass of 375 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

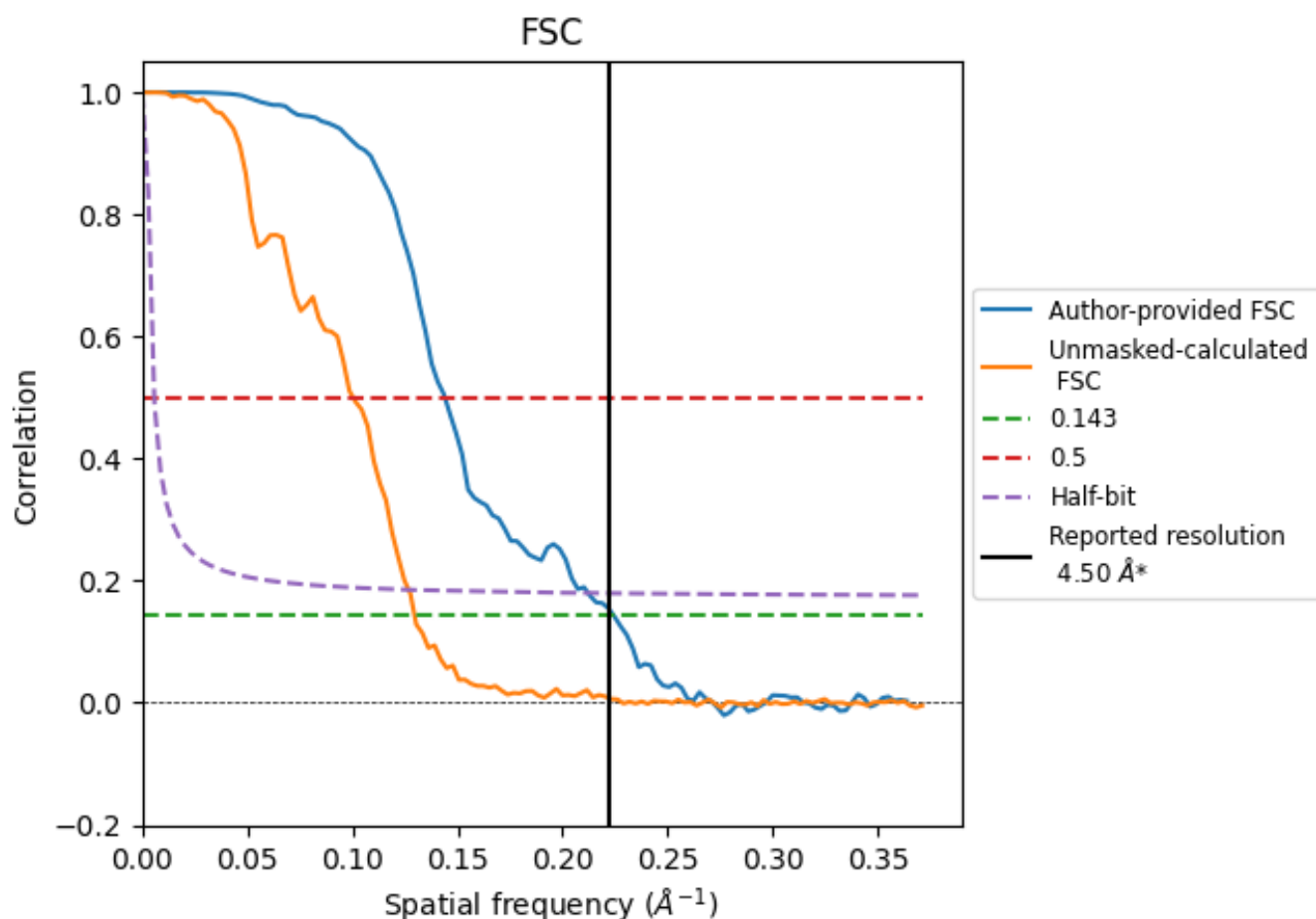


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 0.222 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.46	6.94	4.71
Unmasked-calculated*	7.72	9.97	7.89

*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 7.72 differs from the reported value 4.5 by more than 10 %

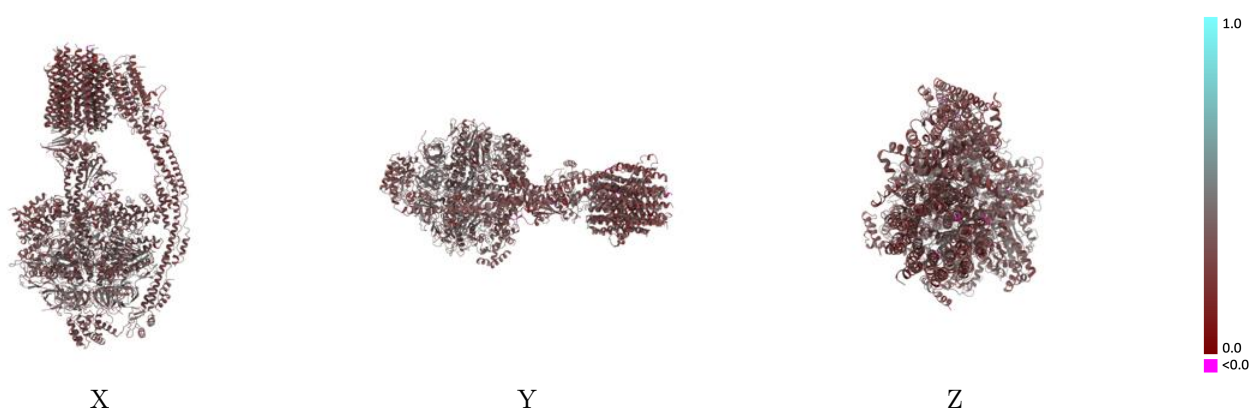
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25968 and PDB model 7TKG. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

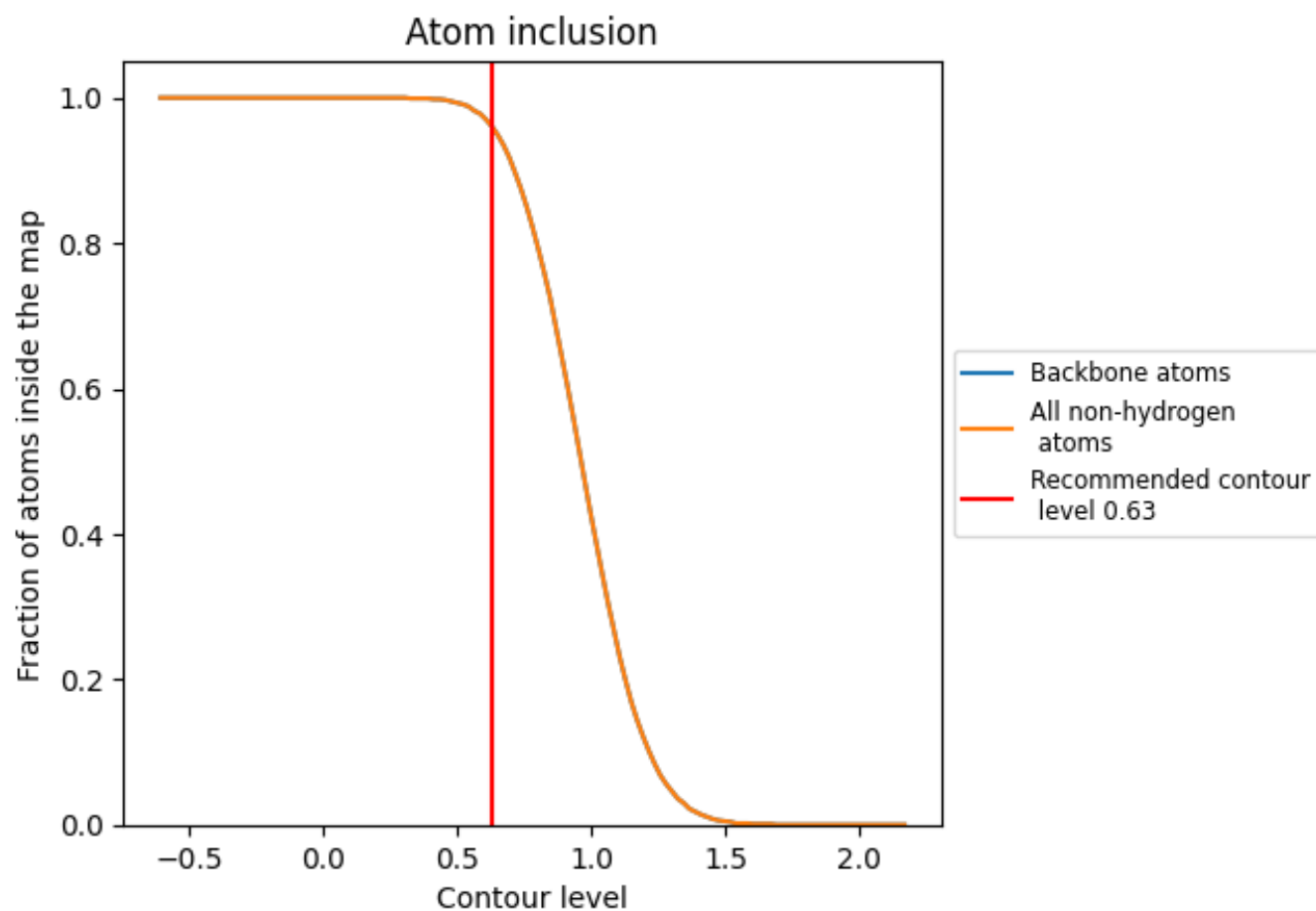


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.63) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9600	 0.3360
0	 0.8870	 0.2750
1	 0.9170	 0.2860
2	 0.9200	 0.2740
3	 0.9430	 0.2910
4	 0.9500	 0.2840
5	 0.8230	 0.2790
6	 0.9150	 0.2800
7	 0.9110	 0.2750
8	 0.9100	 0.2730
9	 0.9290	 0.2810
A	 0.9770	 0.3720
B	 0.9820	 0.3630
C	 0.9630	 0.3550
D	 0.9910	 0.3770
E	 0.9800	 0.3610
F	 0.9700	 0.3560
G	 0.9790	 0.3280
H	 0.9560	 0.3580
I	 0.9430	 0.3170
O	 0.9910	 0.3260
T	 0.9410	 0.2940
U	 0.9950	 0.2990
V	 0.9400	 0.2980
W	 0.8850	 0.2450
X	 0.7700	 0.2770
Y	 0.9120	 0.2860
Z	 0.9690	 0.2870

