



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 12:13 AM UTC

PDB ID : 7TK6 / pdb_00007tk6
EMDB ID : EMD-25958
Title : Yeast ATP synthase State 1catalytic(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:

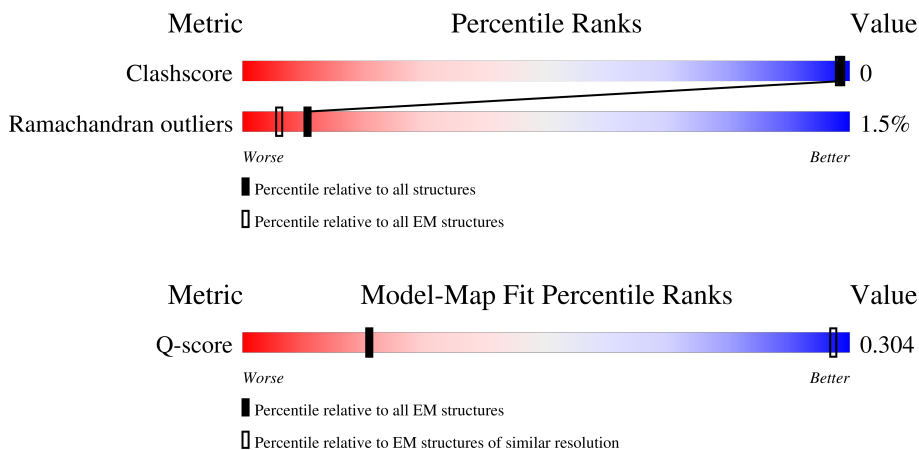
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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



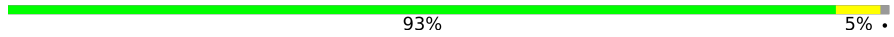

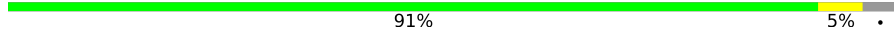
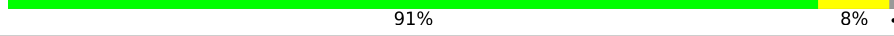
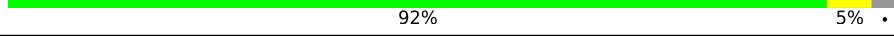



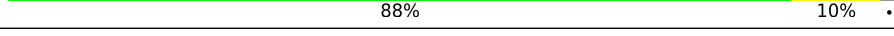


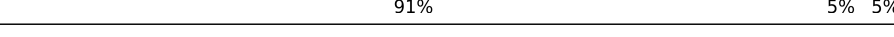

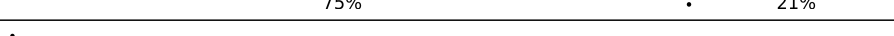


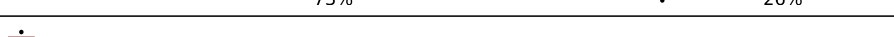

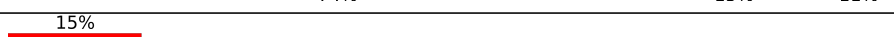



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	556 (6.00 - 7.00)

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	 93% 5% .
1	1	76	 7% 95% . .
1	2	76	 96% . .
1	3	76	 89% 8% .
1	4	76	 92% 7% .

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Mol	Chain	Length	Quality of chain
1	5	76	 93% 5%
1	6	76	 91% 7%
1	7	76	 91% 5%
1	8	76	 91% 8%
1	9	76	 92% 5%
2	A	510	 90% 7%
2	B	510	 90% 9%
2	C	510	 89% 8%
3	D	478	 88% 10%
3	E	478	 89% 9%
3	F	478	 88% 9%
4	G	278	 91% 5% 5%
5	H	138	 76% 11% 13%
6	I	61	 75% 21%
7	O	195	 88% 8%
8	T	249	 86% 10%
9	U	209	 73% 26%
10	V	173	 90% 9%
11	W	95	 74% 15% 11%
12	X	92	 64% 33% 15%
13	Y	59	 59% 37%
14	Z	48	 96%

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, mitochondrial.

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

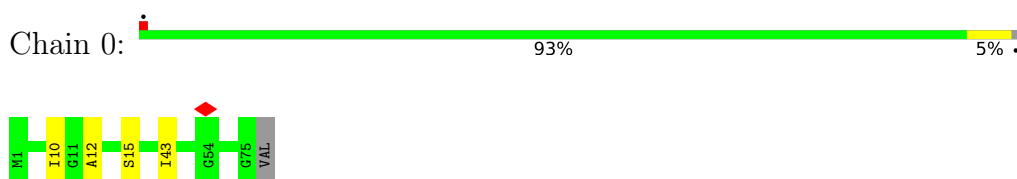
- Molecule 14 is a protein called ATP synthase protein 8.

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

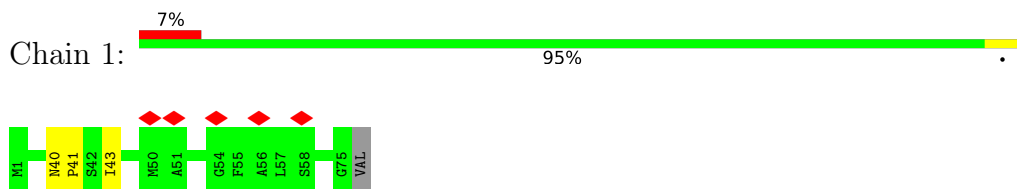
3 Residue-property plots [i](#)

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.

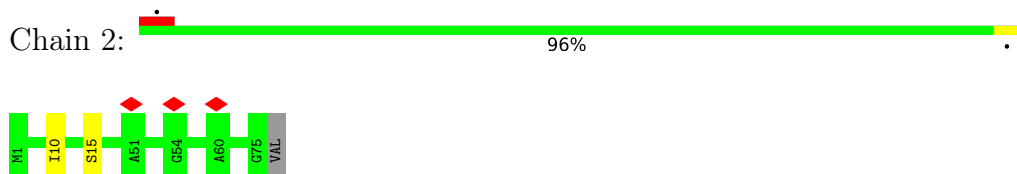
- Molecule 1: ATP synthase subunit 9, mitochondrial



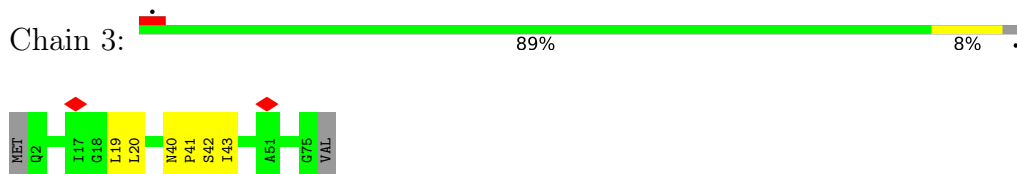
- Molecule 1: ATP synthase subunit 9, mitochondrial



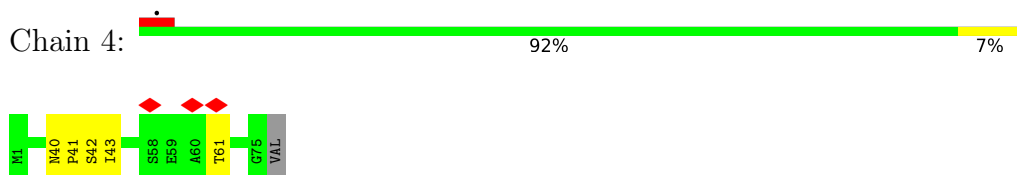
- Molecule 1: ATP synthase subunit 9, mitochondrial



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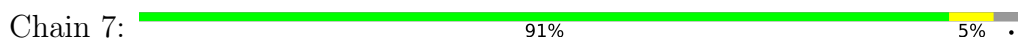
• Molecule 1: ATP synthase subunit 9, mitochondrial



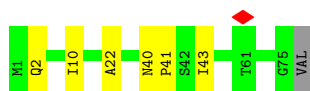
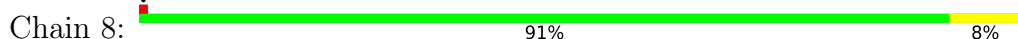
• Molecule 1: ATP synthase subunit 9, mitochondrial



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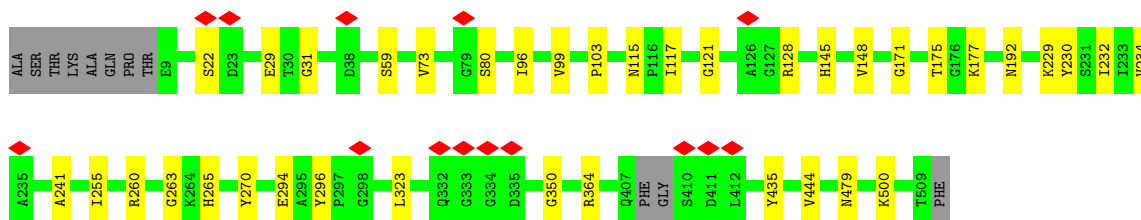
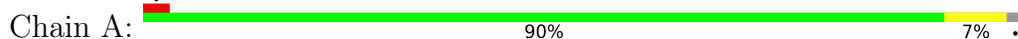
• Molecule 1: ATP synthase subunit 9, mitochondrial



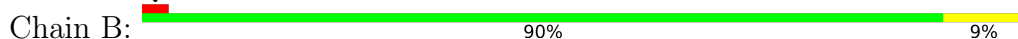
• Molecule 1: ATP synthase subunit 9, mitochondrial

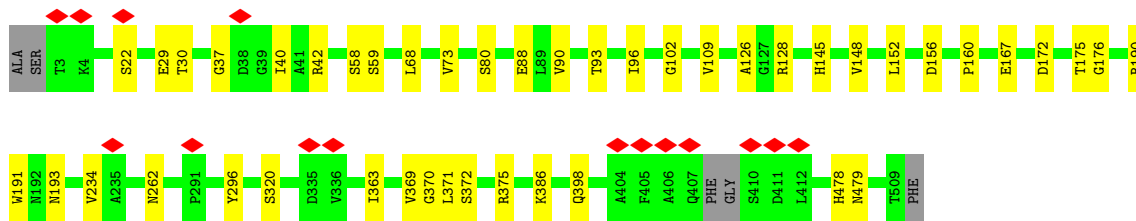


• Molecule 2: ATP synthase subunit alpha

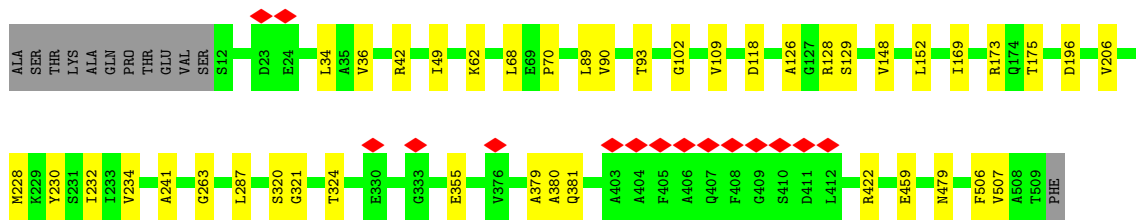
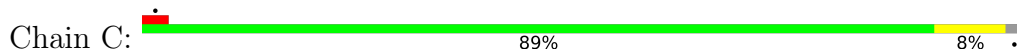


• Molecule 2: ATP synthase subunit alpha

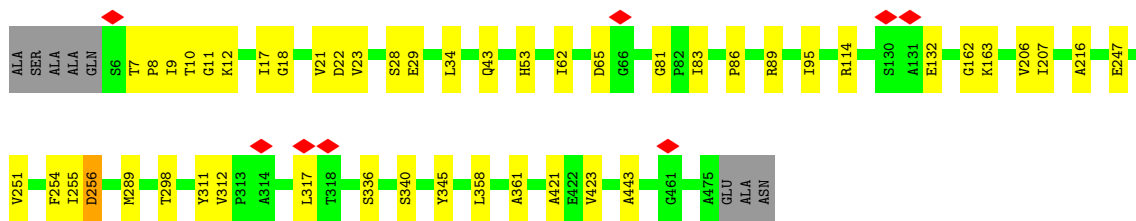
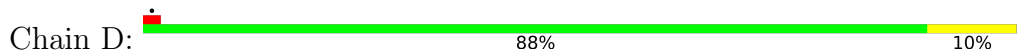




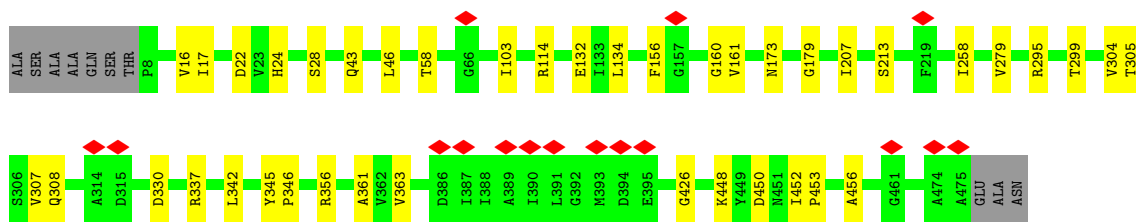
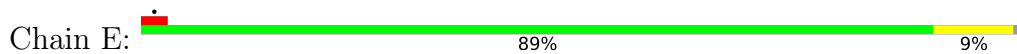
• Molecule 2: ATP synthase subunit alpha



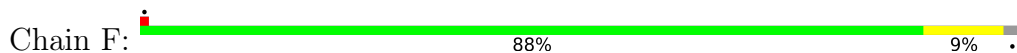
• Molecule 3: ATP synthase subunit beta

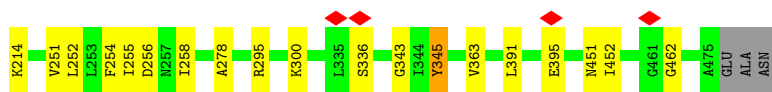


• Molecule 3: ATP synthase subunit beta

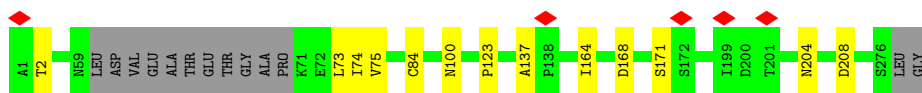
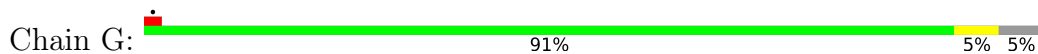


• Molecule 3: ATP synthase subunit beta

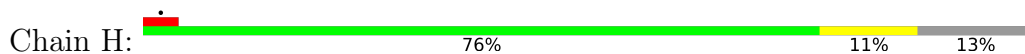




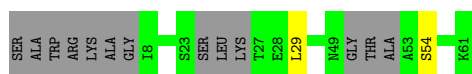
- Molecule 4: ATP synthase subunit gamma



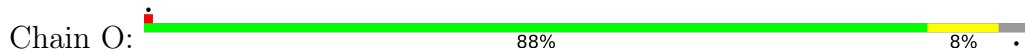
- Molecule 5: ATP synthase subunit delta



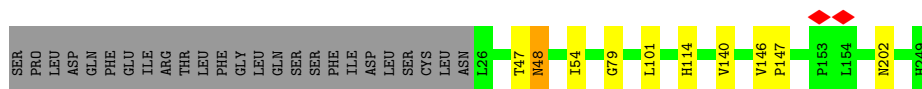
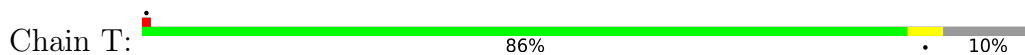
- Molecule 6: ATP synthase subunit epsilon



- Molecule 7: ATP synthase subunit 5, mitochondrial

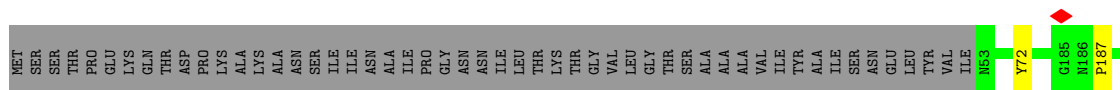


- Molecule 8: ATP synthase subunit a

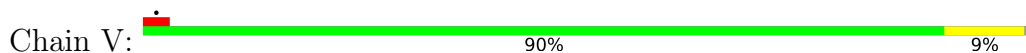


- Molecule 9: ATP synthase subunit 4

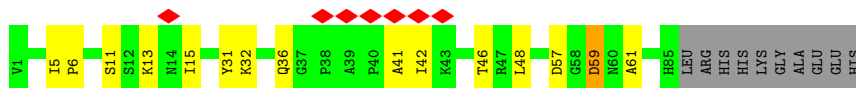
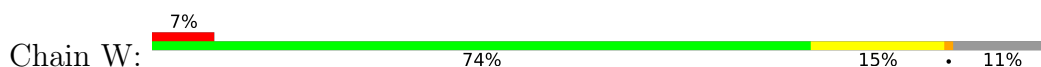




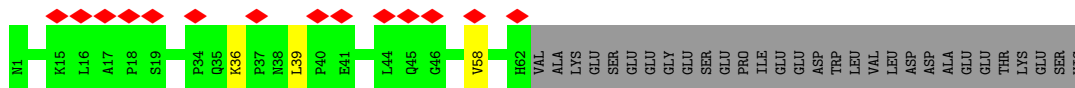
- Molecule 10: ATP synthase subunit d



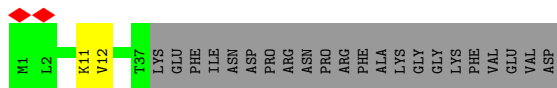
- Molecule 11: ATP synthase subunit f



- Molecule 12: ATP synthase subunit H



- Molecule 13: ATP synthase subunit J



- Molecule 14: ATP synthase protein 8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26797	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	1.738	Depositor
Minimum map value	-0.418	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.104	Depositor
Recommended contour level	0.6	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	1.28	0/299	2.05	8/372 (2.2%)
1	1	1.28	0/299	1.88	2/372 (0.5%)
1	2	1.28	0/299	2.02	4/372 (1.1%)
1	3	1.28	0/295	1.90	6/367 (1.6%)
1	4	1.29	0/299	2.07	4/372 (1.1%)
1	5	1.27	0/299	2.05	4/372 (1.1%)
1	6	1.26	0/295	2.14	6/367 (1.6%)
1	7	1.26	0/291	2.10	4/362 (1.1%)
1	8	1.28	0/299	2.14	8/372 (2.2%)
1	9	1.26	0/295	2.06	4/367 (1.1%)
2	A	1.56	0/1994	1.85	41/2489 (1.6%)
2	B	1.56	0/2018	1.85	43/2519 (1.7%)
2	C	1.54	0/1991	1.81	39/2487 (1.6%)
3	D	1.57	1/1879 (0.1%)	1.89	46/2347 (2.0%)
3	E	1.55	0/1871	1.90	41/2337 (1.8%)
3	F	1.57	1/1875 (0.1%)	1.85	41/2342 (1.8%)
4	G	1.48	0/1058	1.85	14/1319 (1.1%)
5	H	1.50	0/475	1.81	11/585 (1.9%)
6	I	1.44	0/190	1.69	0/231
7	O	1.51	0/747	1.85	13/932 (1.4%)
8	T	1.36	0/896	1.58	9/1117 (0.8%)
9	U	1.35	0/619	1.62	1/772 (0.1%)
10	V	1.43	0/684	1.79	11/852 (1.3%)
11	W	1.38	0/339	1.87	8/422 (1.9%)
12	X	1.36	0/247	1.90	2/307 (0.7%)
13	Y	1.35	0/147	1.72	1/182 (0.5%)
14	Z	1.37	0/192	1.66	2/237 (0.8%)
All	All	1.48	2/20192 (0.0%)	1.86	373/25172 (1.5%)

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
3	F	0	1
5	H	0	1
9	U	0	1
All	All	0	12

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	391	LEU	CA-C	-6.58	1.50	1.53
3	D	11	GLY	CA-C	-5.01	1.47	1.51

All (373) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	204	ASN	CA-C-N	10.77	127.02	120.24
4	G	204	ASN	C-N-CA	10.77	127.02	120.24
8	T	54	ILE	N-CA-C	-10.58	102.38	112.96
2	A	99	VAL	N-CA-C	-9.26	101.60	109.19
10	V	172	VAL	N-CA-C	-9.03	104.59	111.90
3	F	95	ILE	N-CA-C	-8.85	95.78	108.17
7	O	15	VAL	N-CA-C	-8.71	104.15	111.91
11	W	15	ILE	N-CA-C	-8.44	105.25	113.53
10	V	90	GLN	N-CA-C	-8.29	103.11	113.55
3	D	361	ALA	N-CA-C	-8.08	105.41	114.62
2	B	398	GLN	N-CA-C	-8.06	103.57	113.41
2	A	232	ILE	N-CA-C	-7.83	96.86	108.45
11	W	6	PRO	N-CA-C	7.79	120.20	110.70
11	W	57	ASP	N-CA-C	-7.77	95.60	108.34
5	H	61	GLU	N-CA-C	-7.76	95.61	108.34
3	D	423	VAL	N-CA-C	-7.67	106.42	113.71
10	V	163	TYR	N-CA-C	-7.61	104.02	113.38
5	H	56	VAL	N-CA-C	-7.59	97.48	108.11
10	V	25	THR	N-CA-C	-7.55	101.78	112.13
3	E	258	ILE	N-CA-C	-7.54	103.94	113.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	479	ASN	N-CA-C	-7.50	103.86	113.16
2	C	320	SER	N-CA-C	-7.50	103.75	113.12
2	B	37	GLY	N-CA-C	-7.34	102.11	111.72
2	B	190	ARG	N-CA-C	-7.31	103.50	113.30
2	B	193	ASN	N-CA-C	-7.27	102.71	113.61
2	C	234	VAL	N-CA-C	-7.25	98.02	108.17
5	H	41	VAL	N-CA-C	-7.24	97.67	108.46
5	H	69	PHE	N-CA-C	-7.24	97.10	108.90
3	E	304	VAL	N-CA-C	-7.12	102.30	110.05
4	G	168	ASP	N-CA-C	-7.10	100.70	109.65
3	E	103	ILE	N-CA-C	-7.10	105.90	112.43
7	O	180	ILE	N-CA-C	-7.08	104.07	111.58
3	E	307	VAL	N-CA-C	-7.06	98.29	108.17
2	B	42	ARG	N-CA-C	-7.03	96.80	108.34
10	V	164	LYS	N-CA-C	-7.03	104.58	113.72
2	B	175	THR	N-CA-C	-7.03	105.06	112.93
3	D	53	HIS	N-CA-C	-7.03	97.95	109.40
13	Y	12	VAL	N-CA-C	-7.02	104.92	111.45
3	E	356	ARG	N-CA-C	-7.01	104.76	113.38
3	E	160	GLY	N-CA-C	-7.00	106.14	114.48
8	T	140	VAL	N-CA-C	-7.00	104.50	111.77
3	E	43	GLN	N-CA-C	-6.98	104.68	112.57
11	W	61	ALA	N-CA-C	-6.92	104.58	113.16
3	E	305	THR	N-CA-C	-6.91	98.14	108.99
3	E	161	VAL	N-CA-C	-6.88	104.89	112.80
3	F	162	GLY	N-CA-C	-6.85	103.84	115.08
2	C	42	ARG	N-CA-C	-6.82	96.20	108.48
3	E	17	ILE	N-CA-C	-6.78	98.10	107.99
3	F	43	GLN	N-CA-C	-6.77	103.32	112.26
1	8	43	ILE	CA-C-N	6.77	129.66	120.38
1	8	43	ILE	C-N-CA	6.77	129.66	120.38
2	B	386	LYS	N-CA-C	-6.77	104.66	113.12
7	O	33	ILE	N-CA-C	-6.75	106.44	111.90
3	D	8	PRO	N-CA-C	-6.74	107.67	114.68
5	H	14	PHE	N-CA-C	-6.72	97.31	108.34
11	W	48	LEU	N-CA-C	-6.72	104.42	114.64
3	D	22	ASP	N-CA-C	-6.68	99.33	109.95
11	W	36	GLN	N-CA-C	-6.66	103.77	114.09
1	6	10	ILE	CA-C-N	6.65	127.36	119.98
1	6	10	ILE	C-N-CA	6.65	127.36	119.98
3	F	138	ILE	N-CA-C	-6.63	99.04	108.58
2	B	128	ARG	N-CA-C	-6.61	99.06	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	175	THR	N-CA-C	-6.60	103.27	112.25
2	B	234	VAL	N-CA-C	-6.56	99.02	108.53
3	D	12	LYS	N-CA-C	-6.53	98.26	108.90
2	A	296	TYR	N-CA-C	-6.52	101.07	110.40
2	A	364	ARG	N-CA-C	-6.52	96.59	108.85
2	B	96	ILE	N-CA-C	-6.47	102.90	110.21
4	G	2	THR	N-CA-C	-6.46	104.17	111.14
3	D	65	ASP	CA-C-N	6.41	126.19	120.10
3	D	65	ASP	C-N-CA	6.41	126.19	120.10
2	A	117	ILE	N-CA-C	-6.41	106.75	112.90
3	F	295	ARG	N-CA-C	-6.39	105.64	113.50
2	C	287	LEU	N-CA-C	-6.35	105.57	113.38
2	C	93	THR	N-CA-C	-6.34	104.37	111.28
3	D	89	ARG	N-CA-C	-6.34	105.20	114.39
3	E	22	ASP	N-CA-C	-6.31	99.44	109.59
3	D	289	MET	CA-C-N	6.30	126.98	119.98
3	D	289	MET	C-N-CA	6.30	126.98	119.98
1	0	43	ILE	CA-C-N	6.29	128.71	120.28
1	0	43	ILE	C-N-CA	6.29	128.71	120.28
2	B	296	TYR	CA-C-N	6.29	126.31	119.89
2	B	296	TYR	C-N-CA	6.29	126.31	119.89
3	F	252	LEU	N-CA-C	-6.27	99.54	109.07
7	O	101	PHE	N-CA-C	-6.26	104.60	112.93
7	O	55	HIS	N-CA-C	-6.24	106.27	114.31
3	D	336	SER	CA-C-N	6.21	128.61	120.28
3	D	336	SER	C-N-CA	6.21	128.61	120.28
3	D	251	VAL	N-CA-C	-6.21	100.96	108.53
2	B	22	SER	CA-C-N	6.19	128.49	120.44
2	B	22	SER	C-N-CA	6.19	128.49	120.44
3	D	10	THR	N-CA-C	-6.18	99.63	109.59
2	B	191	TRP	N-CA-C	-6.18	106.38	114.04
2	C	232	ILE	N-CA-C	-6.18	99.58	108.48
2	A	59	SER	N-CA-C	-6.15	105.53	113.16
10	V	87	LYS	N-CA-C	-6.13	105.75	113.72
3	E	308	GLN	N-CA-C	-6.12	100.19	109.85
1	7	24	ILE	CA-C-N	6.11	126.72	119.94
1	7	24	ILE	C-N-CA	6.11	126.72	119.94
3	E	450	ASP	N-CA-C	-6.11	105.47	113.17
2	A	265	HIS	N-CA-C	-6.10	100.06	109.52
3	F	255	ILE	N-CA-C	-6.10	99.27	108.17
2	B	40	ILE	N-CA-C	-6.09	98.94	108.81
2	C	507	VAL	N-CA-C	-6.09	104.03	112.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	156	ASP	N-CA-C	-6.09	104.69	113.21
5	H	40	GLY	N-CA-C	-6.09	101.46	111.38
8	T	48	ASN	N-CA-C	-6.08	97.85	110.80
3	D	95	ILE	N-CA-C	-6.06	99.69	108.36
3	E	453	PRO	CA-C-N	6.06	128.40	120.28
3	E	453	PRO	C-N-CA	6.06	128.40	120.28
3	D	311	TYR	N-CA-C	-6.06	99.03	108.90
2	C	355	GLU	CA-C-N	6.05	128.38	120.28
2	C	355	GLU	C-N-CA	6.05	128.38	120.28
3	D	254	PHE	N-CA-C	-6.04	98.80	109.06
10	V	56	SER	N-CA-C	-6.02	103.48	111.24
2	B	58	SER	N-CA-C	-6.00	106.21	112.93
1	1	43	ILE	CA-C-N	5.99	129.12	120.38
1	1	43	ILE	C-N-CA	5.99	129.12	120.38
3	D	17	ILE	N-CA-C	-5.98	96.90	109.34
2	A	177	LYS	N-CA-C	-5.98	104.84	111.36
1	9	10	ILE	CA-C-N	5.97	126.61	119.98
1	9	10	ILE	C-N-CA	5.97	126.61	119.98
2	A	255	ILE	CA-C-N	5.97	126.61	119.98
2	A	255	ILE	C-N-CA	5.97	126.61	119.98
2	A	148	VAL	N-CA-C	-5.96	100.48	108.35
1	4	43	ILE	CA-C-N	5.96	129.08	120.38
1	4	43	ILE	C-N-CA	5.96	129.08	120.38
2	B	262	ASN	N-CA-C	-5.96	105.66	113.17
3	D	23	VAL	N-CA-C	-5.96	99.12	108.95
2	C	479	ASN	N-CA-C	-5.95	105.85	113.23
2	B	93	THR	N-CA-C	-5.95	104.88	111.36
7	O	176	VAL	N-CA-C	-5.94	99.57	108.12
3	E	207	ILE	N-CA-C	-5.93	99.10	107.75
7	O	58	LEU	N-CA-C	-5.92	104.73	113.61
3	F	258	ILE	N-CA-C	-5.91	106.00	112.80
5	H	82	GLN	N-CA-C	-5.88	97.57	107.99
3	D	163	LYS	N-CA-C	-5.88	104.87	111.28
2	A	241	ALA	CA-C-N	5.87	127.04	120.06
2	A	241	ALA	C-N-CA	5.87	127.04	120.06
1	8	10	ILE	CA-C-N	5.86	127.47	120.14
1	8	10	ILE	C-N-CA	5.86	127.47	120.14
3	E	295	ARG	N-CA-C	-5.85	105.80	113.17
3	E	361	ALA	N-CA-C	-5.85	105.15	112.93
2	B	372	SER	N-CA-C	-5.84	99.66	109.07
5	H	45	HIS	N-CA-C	-5.83	98.91	108.76
2	A	444	VAL	CA-C-O	-5.81	113.91	118.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	320	SER	CA-C-N	5.80	125.61	120.10
2	B	320	SER	C-N-CA	5.80	125.61	120.10
3	E	24	HIS	N-CA-C	-5.79	99.76	109.07
10	V	157	LYS	N-CA-C	-5.77	97.75	108.02
3	D	216	ALA	N-CA-C	-5.75	100.77	109.85
8	T	79	GLY	N-CA-C	-5.74	104.70	112.57
3	E	114	ARG	N-CA-C	-5.74	100.62	109.52
3	F	17	ILE	N-CA-C	-5.73	98.89	107.37
5	H	58	GLU	N-CA-C	-5.73	99.67	109.24
7	O	192	GLU	N-CA-C	-5.73	104.86	112.94
8	T	146	VAL	N-CA-C	-5.72	101.36	107.77
2	A	350	GLY	N-CA-C	-5.72	106.52	111.95
3	D	312	VAL	N-CA-C	-5.71	101.49	107.60
3	E	58	THR	N-CA-C	-5.71	100.67	109.52
1	3	43	ILE	CA-C-N	5.71	128.72	120.38
1	3	43	ILE	C-N-CA	5.71	128.72	120.38
10	V	162	GLY	N-CA-C	-5.71	107.50	114.92
3	D	43	GLN	N-CA-C	-5.71	104.73	112.26
2	C	62	LYS	N-CA-C	-5.70	100.10	109.40
8	T	114	HIS	CA-C-N	5.70	128.98	120.31
8	T	114	HIS	C-N-CA	5.70	128.98	120.31
2	B	148	VAL	N-CA-C	-5.69	100.14	108.11
4	G	164	ILE	N-CA-C	-5.69	99.58	108.86
2	A	145	HIS	N-CA-C	-5.68	105.25	113.21
2	A	234	VAL	N-CA-C	-5.67	100.41	108.58
4	G	74	ILE	N-CA-C	-5.67	99.95	108.12
1	5	43	ILE	CA-C-N	5.67	128.65	120.38
1	5	43	ILE	C-N-CA	5.67	128.65	120.38
4	G	171	SER	N-CA-C	-5.67	100.70	109.14
2	C	206	VAL	N-CA-C	-5.66	100.18	108.11
2	C	90	VAL	N-CA-C	-5.66	100.03	108.46
1	6	54	GLY	CA-C-N	5.64	127.77	120.44
1	6	54	GLY	C-N-CA	5.64	127.77	120.44
10	V	26	ALA	N-CA-C	-5.62	104.31	113.19
2	B	371	LEU	N-CA-C	-5.62	106.20	113.16
2	C	175	THR	N-CA-C	-5.61	102.88	110.68
2	A	260	ARG	CA-C-N	5.61	128.25	120.29
2	A	260	ARG	C-N-CA	5.61	128.25	120.29
2	C	422	ARG	CA-C-N	5.61	126.20	119.98
2	C	422	ARG	C-N-CA	5.61	126.20	119.98
1	6	43	ILE	CA-C-N	5.60	128.06	120.38
1	6	43	ILE	C-N-CA	5.60	128.06	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	90	VAL	N-CA-C	-5.60	100.33	108.17
2	C	173	ARG	N-CA-C	5.60	118.70	110.30
4	G	208	ASP	N-CA-C	-5.59	106.13	113.12
2	C	148	VAL	N-CA-C	-5.58	99.51	107.77
2	C	381	GLN	CA-C-N	5.58	127.98	120.50
2	C	381	GLN	C-N-CA	5.58	127.98	120.50
2	C	36	VAL	N-CA-C	-5.58	100.98	108.35
3	E	46	LEU	N-CA-C	-5.58	99.33	108.76
2	B	30	THR	N-CA-C	-5.58	100.88	109.52
14	Z	5	VAL	N-CA-C	-5.57	102.63	108.15
3	D	247	GLU	N-CA-C	-5.57	106.48	113.72
3	D	256	ASP	N-CA-C	-5.57	100.61	109.07
3	E	452	ILE	CA-C-N	5.56	125.56	119.89
3	E	452	ILE	C-N-CA	5.56	125.56	119.89
7	O	98	LEU	N-CA-C	-5.56	105.27	113.61
3	F	53	HIS	N-CA-C	-5.55	100.14	109.07
3	D	62	ILE	N-CA-C	-5.51	100.53	108.53
3	D	317	LEU	CA-C-N	5.51	127.67	120.28
3	D	317	LEU	C-N-CA	5.51	127.67	120.28
5	H	13	GLN	N-CA-C	-5.51	99.91	108.90
2	C	34	LEU	N-CA-C	-5.50	107.82	114.75
3	F	153	ILE	N-CA-C	-5.50	100.53	108.89
2	B	152	LEU	N-CA-C	-5.50	99.45	108.41
3	F	206	VAL	N-CA-C	-5.48	105.18	110.72
2	A	294	GLU	CA-C-N	5.48	130.13	122.08
2	A	294	GLU	C-N-CA	5.48	130.13	122.08
7	O	151	LYS	N-CA-C	-5.47	99.75	109.06
3	F	345	TYR	N-CA-C	-5.47	96.60	108.74
3	F	46	LEU	N-CA-C	-5.47	99.99	108.90
2	A	80	SER	CA-C-N	5.46	127.60	120.28
2	A	80	SER	C-N-CA	5.46	127.60	120.28
2	B	68	LEU	N-CA-C	-5.45	99.84	108.73
3	E	456	ALA	N-CA-C	-5.45	106.63	113.28
3	F	336	SER	CA-C-N	5.45	128.13	120.28
3	F	336	SER	C-N-CA	5.45	128.13	120.28
3	E	426	GLY	N-CA-C	-5.43	107.61	115.27
1	3	19	LEU	CA-C-N	5.42	127.81	120.38
1	3	19	LEU	C-N-CA	5.42	127.81	120.38
2	C	68	LEU	N-CA-C	-5.42	99.57	108.41
3	F	163	LYS	N-CA-C	-5.42	105.37	111.28
3	E	448	LYS	N-CA-C	-5.42	106.44	113.16
3	F	112	LYS	N-CA-C	-5.41	99.27	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	255	ILE	N-CA-C	-5.41	100.05	108.86
2	C	128	ARG	N-CA-C	-5.40	101.15	109.52
3	D	114	ARG	N-CA-C	-5.40	101.31	109.85
10	V	63	LYS	N-CA-C	-5.40	106.06	113.30
3	F	395	GLU	N-CA-C	-5.40	104.30	112.99
2	B	73	VAL	N-CA-C	-5.39	100.42	108.46
2	C	118	ASP	N-CA-C	-5.38	106.48	113.16
8	T	47	THR	N-CA-C	-5.38	107.73	114.56
2	A	121	GLY	CA-C-N	5.37	125.37	119.90
2	A	121	GLY	C-N-CA	5.37	125.37	119.90
2	A	96	ILE	N-CA-C	-5.37	104.15	110.21
2	C	152	LEU	N-CA-C	-5.36	98.51	107.99
2	A	73	VAL	N-CA-C	-5.36	99.93	107.75
3	E	330	ASP	N-CA-C	-5.35	107.29	113.88
1	4	61	THR	CA-C-N	5.35	125.92	119.98
1	4	61	THR	C-N-CA	5.35	125.92	119.98
7	O	125	SER	N-CA-C	-5.35	100.99	108.96
3	E	337	ARG	N-CA-C	-5.35	106.60	113.23
2	B	172	ASP	CA-C-N	5.35	128.69	121.05
2	B	172	ASP	C-N-CA	5.35	128.69	121.05
2	B	109	VAL	N-CA-C	-5.34	101.95	109.21
3	D	345	TYR	N-CA-C	-5.34	96.89	108.74
2	C	506	PHE	N-CA-C	-5.33	106.08	112.59
1	0	15	SER	CA-C-N	5.33	127.95	120.28
1	0	15	SER	C-N-CA	5.33	127.95	120.28
2	A	128	ARG	N-CA-C	-5.32	100.23	108.90
2	B	80	SER	CA-C-N	5.31	127.40	120.28
2	B	80	SER	C-N-CA	5.31	127.40	120.28
2	C	228	MET	N-CA-C	-5.30	106.99	112.93
3	D	443	ALA	CA-C-N	5.27	127.20	120.56
3	D	443	ALA	C-N-CA	5.27	127.20	120.56
2	B	176	GLY	N-CA-C	-5.27	103.62	114.16
7	O	164	LYS	N-CA-C	-5.26	100.59	108.96
3	F	104	ASP	N-CA-C	-5.25	106.65	113.16
4	G	100	ASN	N-CA-C	-5.25	106.38	112.89
3	D	132	GLU	N-CA-C	-5.24	101.33	109.24
2	B	160	PRO	N-CA-C	-5.23	103.03	111.77
3	D	298	THR	N-CA-C	-5.23	100.00	108.41
1	2	10	ILE	CA-C-N	5.22	125.78	119.98
1	2	10	ILE	C-N-CA	5.22	125.78	119.98
2	C	196	ASP	CA-C-N	5.22	127.28	120.28
2	C	196	ASP	C-N-CA	5.22	127.28	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	80	GLY	CA-C-N	5.22	130.06	121.87
3	F	80	GLY	C-N-CA	5.22	130.06	121.87
2	A	31	GLY	N-CA-C	-5.21	103.49	111.10
14	Z	7	PHE	N-CA-C	-5.21	105.79	113.61
2	C	70	PRO	N-CA-C	-5.20	107.36	113.86
3	F	54	LEU	N-CA-C	-5.20	106.62	113.17
3	D	162	GLY	N-CA-C	-5.19	100.87	113.18
3	F	190	ARG	CA-C-N	5.19	127.24	120.28
3	F	190	ARG	C-N-CA	5.19	127.24	120.28
1	8	2	GLN	CA-C-N	5.19	127.23	120.28
1	8	2	GLN	C-N-CA	5.19	127.23	120.28
3	D	21	VAL	N-CA-C	-5.18	100.60	108.17
3	E	179	GLY	N-CA-C	-5.18	106.58	115.08
3	F	300	LYS	N-CA-C	-5.18	106.22	112.54
3	F	214	LYS	N-CA-C	-5.18	106.20	112.88
7	O	150	GLY	N-CA-C	-5.18	108.08	115.64
3	F	363	VAL	N-CA-C	-5.17	107.67	112.43
3	E	345	TYR	N-CA-C	-5.17	98.10	109.11
3	F	254	PHE	N-CA-C	-5.17	100.61	109.24
3	F	343	GLY	N-CA-C	-5.17	107.92	115.72
8	T	101	LEU	N-CA-C	-5.16	106.12	112.72
2	C	169	ILE	N-CA-C	-5.16	100.46	107.99
3	D	421	ALA	N-CA-C	-5.15	104.46	111.56
11	W	13	LYS	N-CA-C	-5.15	107.05	113.38
3	E	173	ASN	CA-C-N	5.13	127.49	120.46
3	E	173	ASN	C-N-CA	5.13	127.49	120.46
3	F	209	LEU	N-CA-C	-5.13	105.31	112.45
1	2	15	SER	CA-C-N	5.13	127.87	120.38
1	2	15	SER	C-N-CA	5.13	127.87	120.38
1	9	43	ILE	CA-C-N	5.13	127.15	120.28
1	9	43	ILE	C-N-CA	5.13	127.15	120.28
2	C	109	VAL	N-CA-C	-5.12	101.07	108.71
2	B	59	SER	N-CA-C	-5.12	106.88	113.02
11	W	59	ASP	N-CA-C	-5.11	99.92	110.80
3	E	156	PHE	N-CA-C	-5.11	101.53	109.24
3	F	115	LYS	CA-C-N	5.11	125.02	119.76
3	F	115	LYS	C-N-CA	5.11	125.02	119.76
2	C	380	ALA	N-CA-C	-5.10	106.74	113.17
3	F	35	ASN	N-CA-C	-5.10	103.95	110.53
3	D	340	SER	CA-C-N	5.09	128.05	120.31
3	D	340	SER	C-N-CA	5.09	128.05	120.31
2	C	89	LEU	N-CA-C	-5.08	101.98	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	270	TYR	N-CA-C	-5.08	100.44	108.73
4	G	84	CYS	N-CA-C	-5.08	106.33	112.88
9	U	72	TYR	N-CA-C	-5.08	106.17	112.93
2	A	192	ASN	CA-C-N	5.08	127.09	120.28
2	A	192	ASN	C-N-CA	5.08	127.09	120.28
2	C	129	SER	N-CA-C	-5.08	101.70	108.86
1	7	20	LEU	CA-C-N	5.08	125.62	119.98
1	7	20	LEU	C-N-CA	5.08	125.62	119.98
1	8	22	ALA	CA-C-N	5.07	125.57	119.94
1	8	22	ALA	C-N-CA	5.07	125.57	119.94
2	A	479	ASN	N-CA-C	-5.07	107.09	113.28
2	B	479	ASN	CA-C-N	5.07	127.08	120.28
2	B	479	ASN	C-N-CA	5.07	127.08	120.28
3	D	206	VAL	N-CA-C	-5.07	104.75	111.09
3	E	342	LEU	N-CA-C	-5.07	106.94	113.02
4	G	73	LEU	N-CA-C	-5.07	101.89	109.95
3	D	207	ILE	N-CA-C	-5.07	99.40	107.15
3	D	317	LEU	N-CA-C	-5.06	106.96	113.23
3	F	107	GLY	CA-C-N	5.06	126.16	119.84
3	F	107	GLY	C-N-CA	5.06	126.16	119.84
12	X	39	LEU	CA-C-N	5.06	125.05	119.89
12	X	39	LEU	C-N-CA	5.06	125.05	119.89
2	B	88	GLU	N-CA-C	-5.05	102.59	110.42
4	G	137	ALA	CA-C-N	5.05	126.15	119.84
4	G	137	ALA	C-N-CA	5.05	126.15	119.84
1	3	20	LEU	CA-C-N	5.05	125.55	120.00
1	3	20	LEU	C-N-CA	5.05	125.55	120.00
3	F	256	ASP	N-CA-C	-5.05	100.05	110.80
1	0	12	ALA	CA-C-N	5.05	125.54	119.94
1	0	12	ALA	C-N-CA	5.05	125.54	119.94
2	C	459	GLU	CA-C-N	5.04	127.04	120.28
2	C	459	GLU	C-N-CA	5.04	127.04	120.28
2	A	115	ASN	N-CA-C	-5.04	103.36	110.31
3	E	299	THR	N-CA-C	-5.04	102.56	110.17
2	A	323	LEU	N-CA-C	-5.03	100.08	110.80
2	C	324	THR	N-CA-C	-5.03	101.67	109.72
3	E	213	SER	N-CA-C	-5.03	102.62	110.42
2	A	263	GLY	N-CA-C	-5.03	108.38	114.92
2	B	363	ILE	N-CA-C	-5.03	98.79	107.24
3	F	452	ILE	CA-C-N	5.03	125.03	119.90
3	F	452	ILE	C-N-CA	5.03	125.03	119.90
3	D	18	GLY	CA-C-N	5.02	127.26	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	18	GLY	C-N-CA	5.02	127.26	120.38
3	F	79	THR	N-CA-C	-5.02	107.20	113.38
5	H	60	MET	N-CA-C	-5.02	100.27	108.76
2	A	171	GLY	CA-C-N	5.02	127.84	120.71
2	A	171	GLY	C-N-CA	5.02	127.84	120.71
3	E	363	VAL	N-CA-C	-5.02	107.40	112.17
3	E	134	LEU	N-CA-C	-5.02	100.23	108.41
4	G	75	VAL	N-CA-C	-5.02	100.68	108.86
3	F	114	ARG	N-CA-C	-5.02	100.99	109.07
1	0	10	ILE	CA-C-N	5.01	126.41	120.14
1	0	10	ILE	C-N-CA	5.01	126.41	120.14
1	5	61	THR	CA-C-N	5.01	125.54	119.98
1	5	61	THR	C-N-CA	5.01	125.54	119.98
3	E	132	GLU	CA-C-N	5.01	127.31	120.35
3	E	132	GLU	C-N-CA	5.01	127.31	120.35
2	A	500	LYS	CA-C-N	5.00	126.98	120.28
2	A	500	LYS	C-N-CA	5.00	126.98	120.28

There are no chirality outliers.

All (12) 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
3	F	345	TYR	Peptide
5	H	54	PRO	Peptide
9	U	187	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	1996	0	570	0	0
2	B	2020	0	575	1	0
2	C	1992	0	572	2	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	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	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)
2:C:102:GLY:HA3	2:C:126:ALA:H	1.70	0.57
2:C:263:GLY:HA2	2:C:321:GLY:H	1.78	0.48
2:B:102:GLY:HA3	2:B:126:ALA:H	1.78	0.47
3:D:7:THR:C	3:D:9:ILE:H	2.26	0.44

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	73/76 (96%)	72 (99%)	1 (1%)	0	100	100
1	1	73/76 (96%)	71 (97%)	1 (1%)	1 (1%)	9	40
1	2	73/76 (96%)	72 (99%)	1 (1%)	0	100	100
1	3	72/76 (95%)	69 (96%)	1 (1%)	2 (3%)	4	24
1	4	73/76 (96%)	70 (96%)	1 (1%)	2 (3%)	4	25
1	5	73/76 (96%)	71 (97%)	1 (1%)	1 (1%)	9	40
1	6	72/76 (95%)	70 (97%)	1 (1%)	1 (1%)	9	40
1	7	71/76 (93%)	69 (97%)	1 (1%)	1 (1%)	9	40
1	8	73/76 (96%)	70 (96%)	2 (3%)	1 (1%)	9	40
1	9	72/76 (95%)	69 (96%)	2 (3%)	1 (1%)	9	40
2	A	495/510 (97%)	468 (94%)	21 (4%)	6 (1%)	10	44
2	B	501/510 (98%)	476 (95%)	18 (4%)	7 (1%)	9	40
2	C	496/510 (97%)	476 (96%)	16 (3%)	4 (1%)	16	54
3	D	468/478 (98%)	439 (94%)	22 (5%)	7 (2%)	8	40
3	E	466/478 (98%)	440 (94%)	22 (5%)	4 (1%)	14	51
3	F	467/478 (98%)	430 (92%)	27 (6%)	10 (2%)	5	30
4	G	261/278 (94%)	251 (96%)	9 (3%)	1 (0%)	30	67
5	H	110/138 (80%)	105 (96%)	2 (2%)	3 (3%)	4	25
6	I	42/61 (69%)	38 (90%)	2 (5%)	2 (5%)	2	16
7	O	185/195 (95%)	171 (92%)	11 (6%)	3 (2%)	7	38
8	T	222/249 (89%)	210 (95%)	9 (4%)	3 (1%)	9	40
9	U	153/209 (73%)	152 (99%)	1 (1%)	0	100	100
10	V	169/173 (98%)	154 (91%)	10 (6%)	5 (3%)	3	22
11	W	83/95 (87%)	67 (81%)	8 (10%)	8 (10%)	0	7
12	X	60/92 (65%)	56 (93%)	2 (3%)	2 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	Y	35/59 (59%)	33 (94%)	1 (3%)	1 (3%)	3	23
14	Z	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
All	All	4984/5321 (94%)	4712 (94%)	196 (4%)	76 (2%)	11	40

All (76) 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	22	SER
2	A	229	LYS
2	C	379	ALA
3	D	358	LEU
3	F	451	ASN
5	H	36	SER
7	O	62	LEU
10	V	89	LEU
11	W	31	TYR
2	C	49	ILE
3	D	28	SER
3	D	29	GLU
3	D	81	GLY
3	E	28	SER
3	F	125	ALA
3	F	462	GLY
5	H	33	PRO
7	O	10	VAL
8	T	147	PRO
8	T	202	ASN
11	W	11	SER
11	W	41	ALA
11	W	59	ASP
12	X	58	VAL
2	A	230	TYR
2	B	167	GLU

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Mol	Chain	Res	Type
2	B	370	GLY
2	B	375	ARG
3	F	86	PRO
3	F	131	ALA
7	O	51	PRO
8	T	48	ASN
10	V	66	SER
11	W	42	ILE
2	A	435	TYR
2	B	29	GLU
2	B	478	HIS
3	D	34	LEU
3	E	346	PRO
6	I	29	LEU
6	I	54	SER
10	V	84	ASP
11	W	32	LYS
11	W	46	THR
12	X	36	LYS
2	A	29	GLU
2	A	103	PRO
2	B	145	HIS
2	C	230	TYR
2	C	241	ALA
3	E	16	VAL
3	F	81	GLY
3	F	161	VAL
3	F	278	ALA
4	G	123	PRO
10	V	55	PHE
13	Y	11	LYS
1	3	42	SER
1	4	42	SER
3	D	83	ILE
5	H	22	TYR
3	F	251	VAL
3	D	86	PRO
3	E	279	VAL
2	B	369	VAL
11	W	5	ILE
3	F	83	ILE
10	V	80	PRO

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.

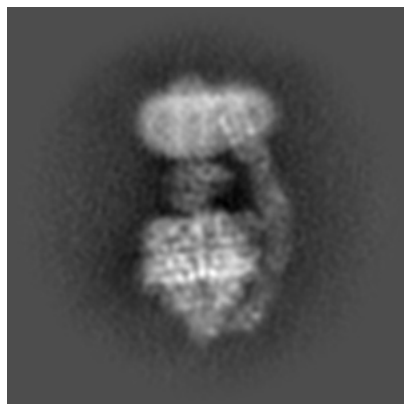
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25958. These allow visual inspection of the internal detail of the map and identification of artifacts.

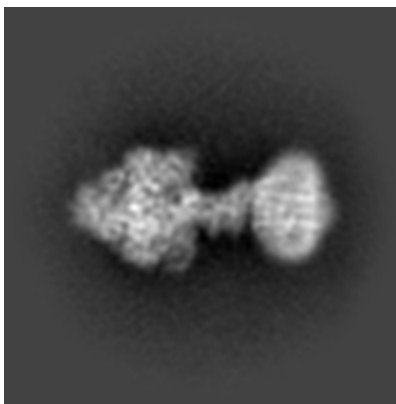
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

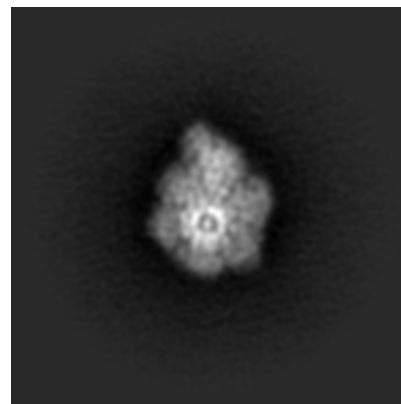
6.1.1 Primary map



X

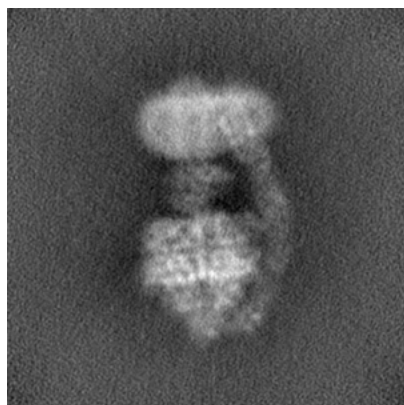


Y

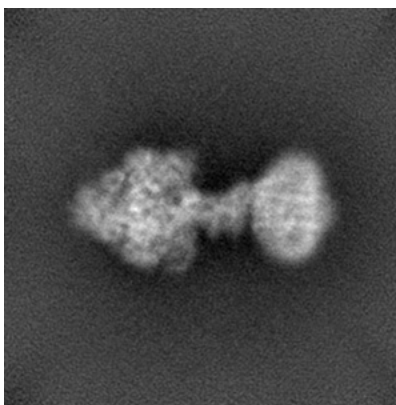


Z

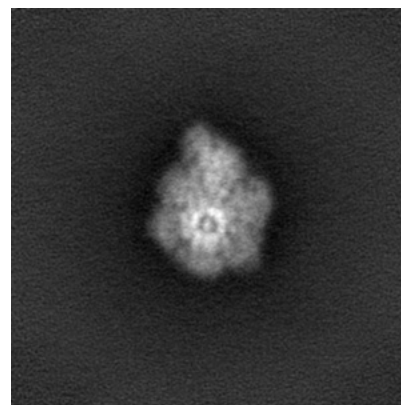
6.1.2 Raw map



X



Y

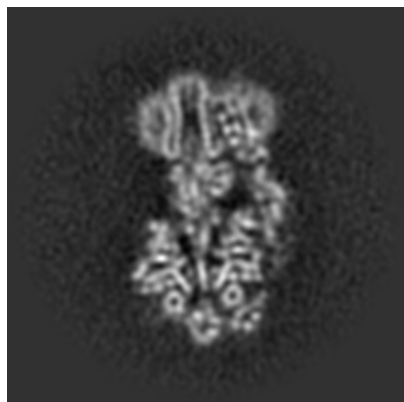


Z

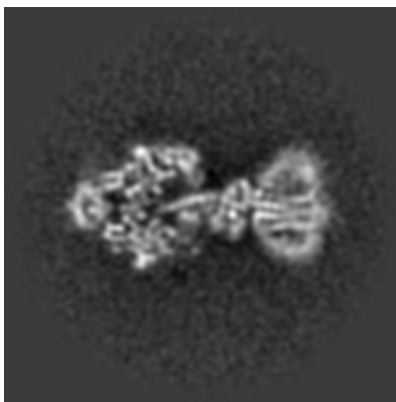
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

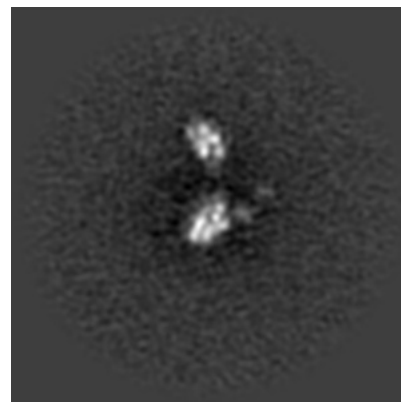
6.2.1 Primary map



X Index: 128

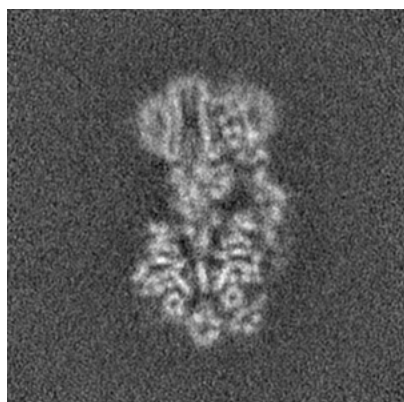


Y Index: 128

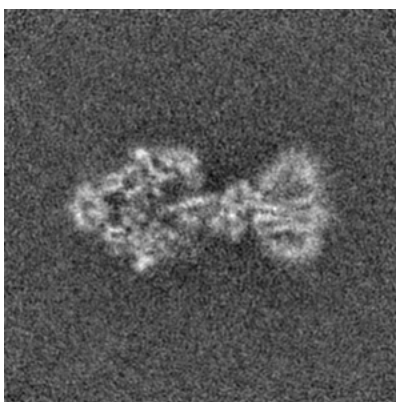


Z Index: 128

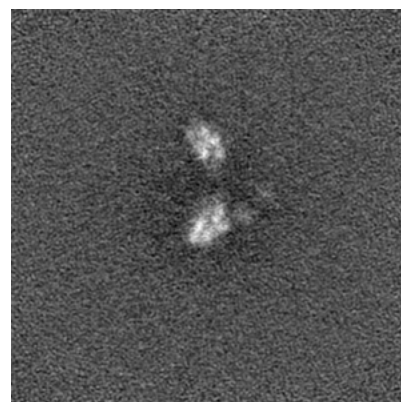
6.2.2 Raw map



X Index: 128



Y Index: 128

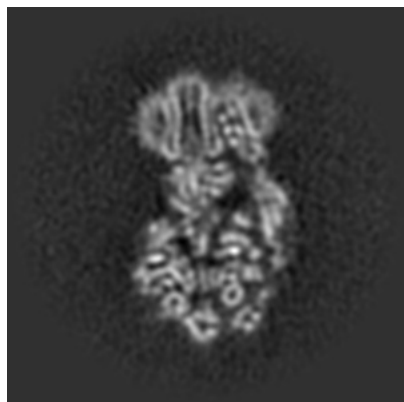


Z Index: 128

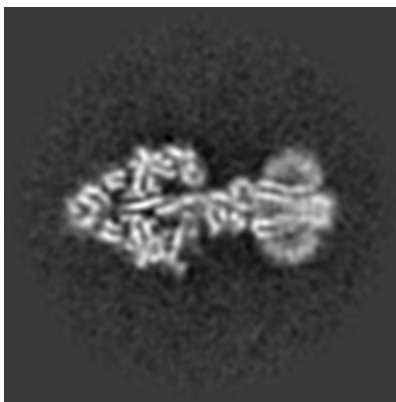
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

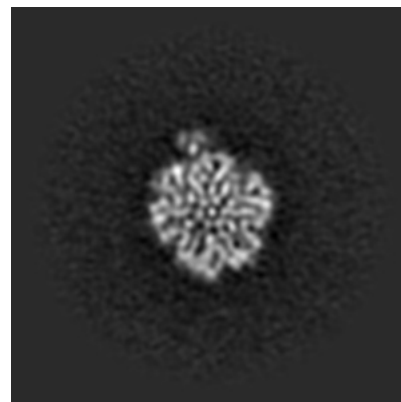
6.3.1 Primary map



X Index: 126

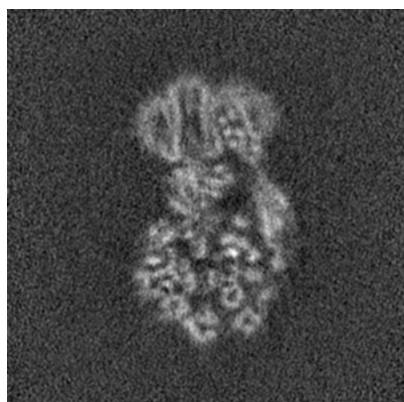


Y Index: 124

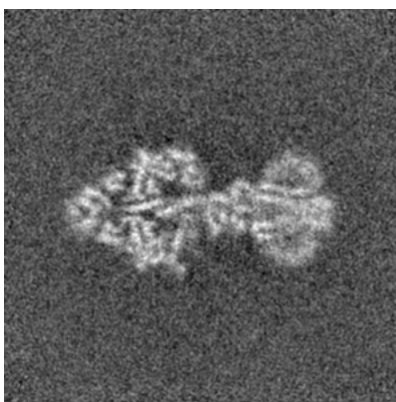


Z Index: 86

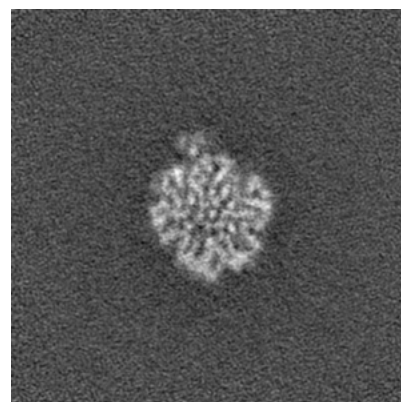
6.3.2 Raw map



X Index: 125



Y Index: 124

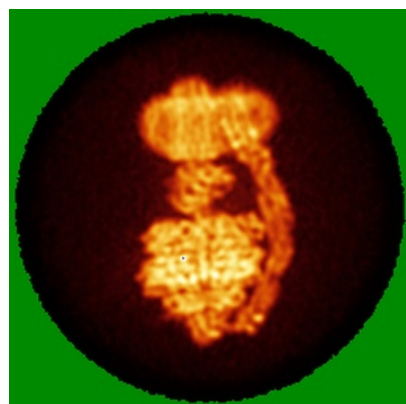


Z Index: 86

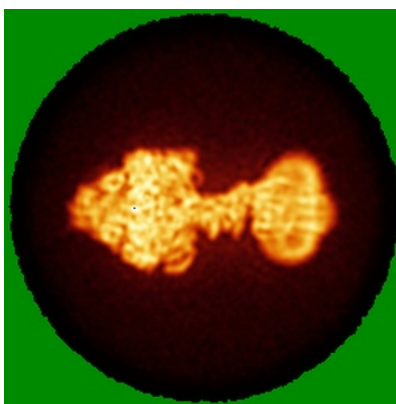
The images above show the largest variance slices of the map in three orthogonal directions.

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

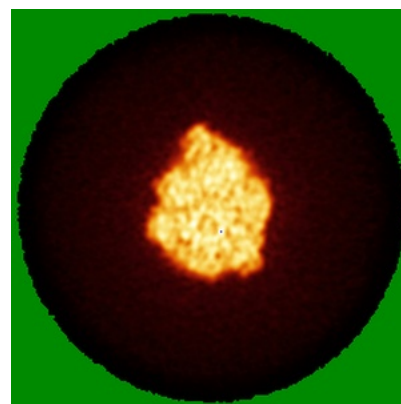
6.4.1 Primary map



X

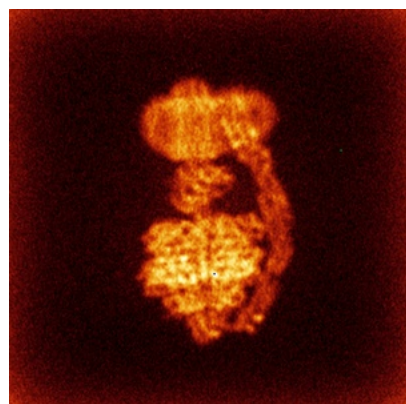


Y

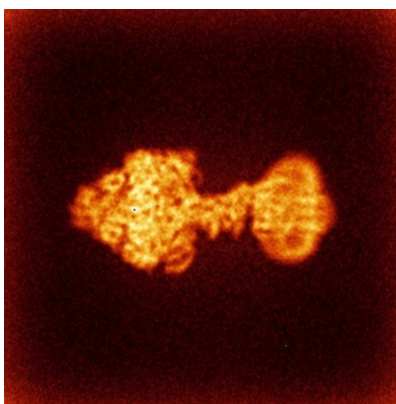


Z

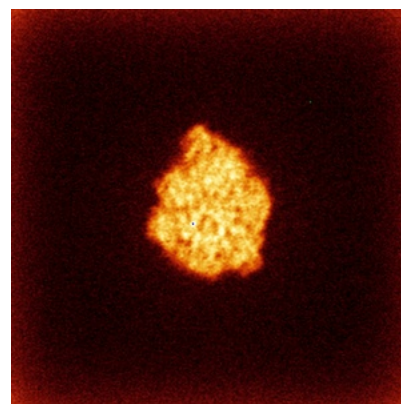
6.4.2 Raw map



X



Y

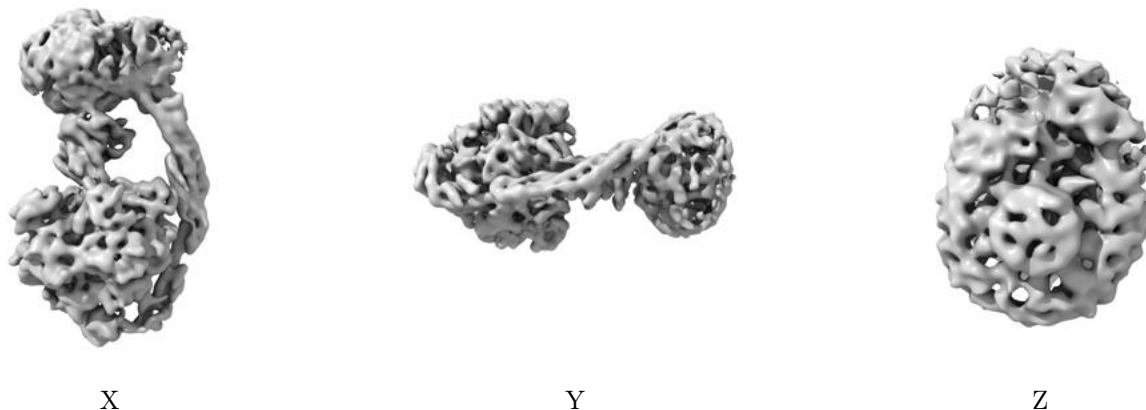


Z

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.

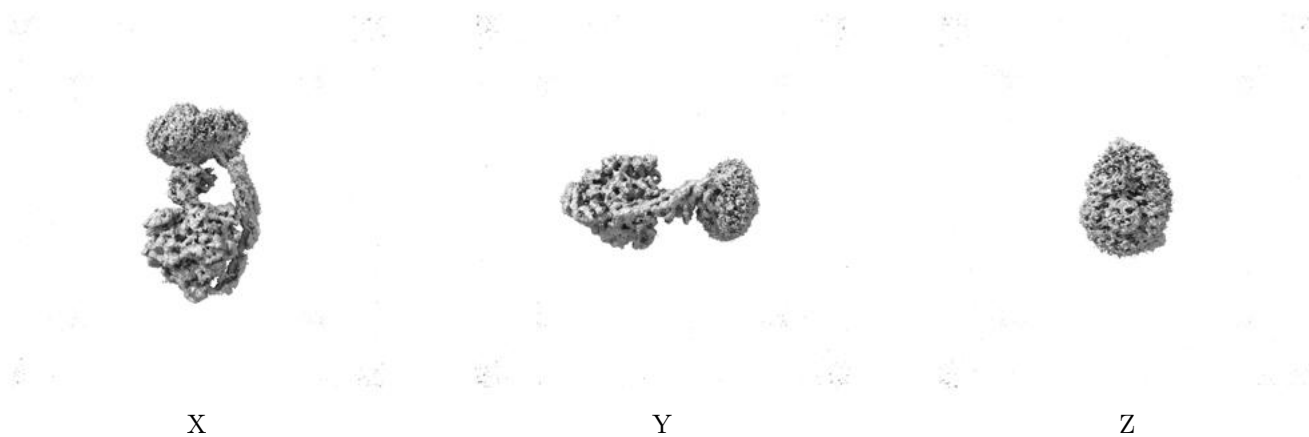
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

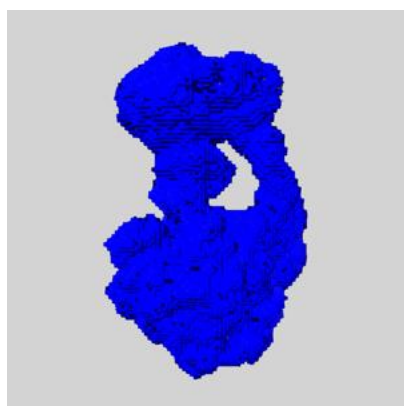
6.6 Mask visualisation [i](#)

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

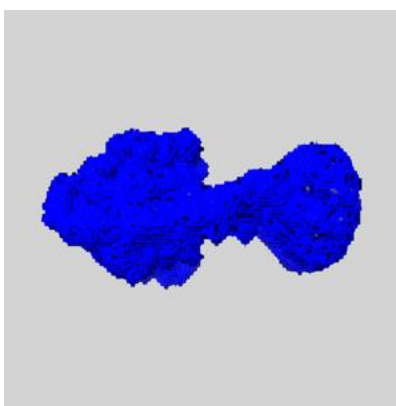
A mask typically either:

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

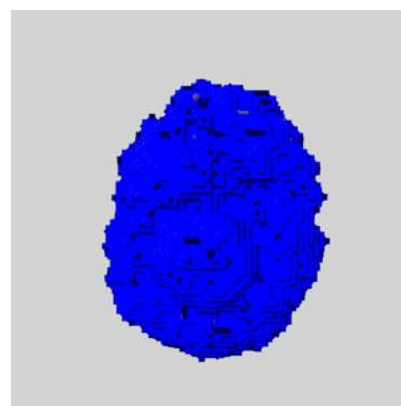
6.6.1 emd_25958_msk_1.map [i](#)



X



Y

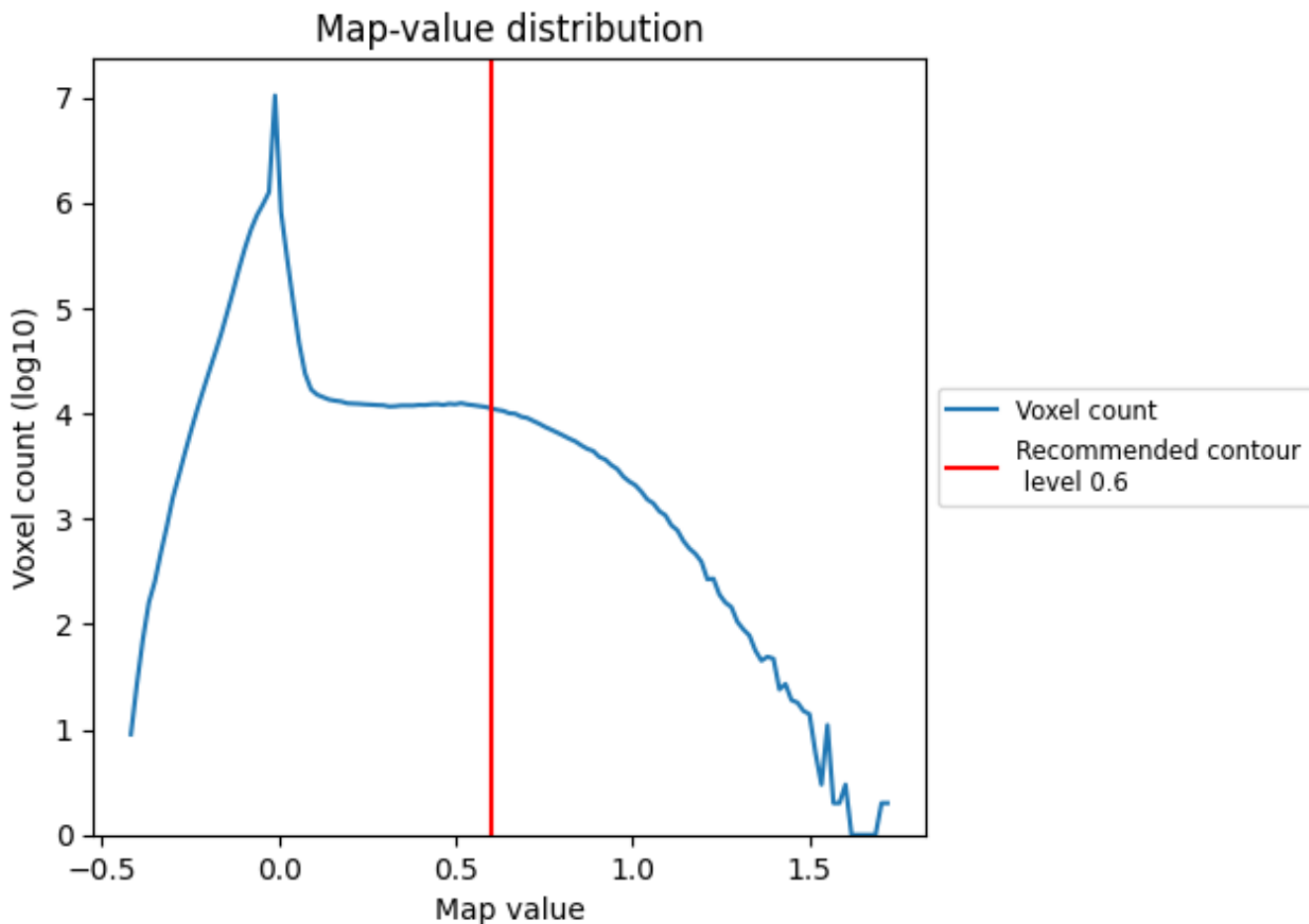


Z

7 Map analysis [i](#)

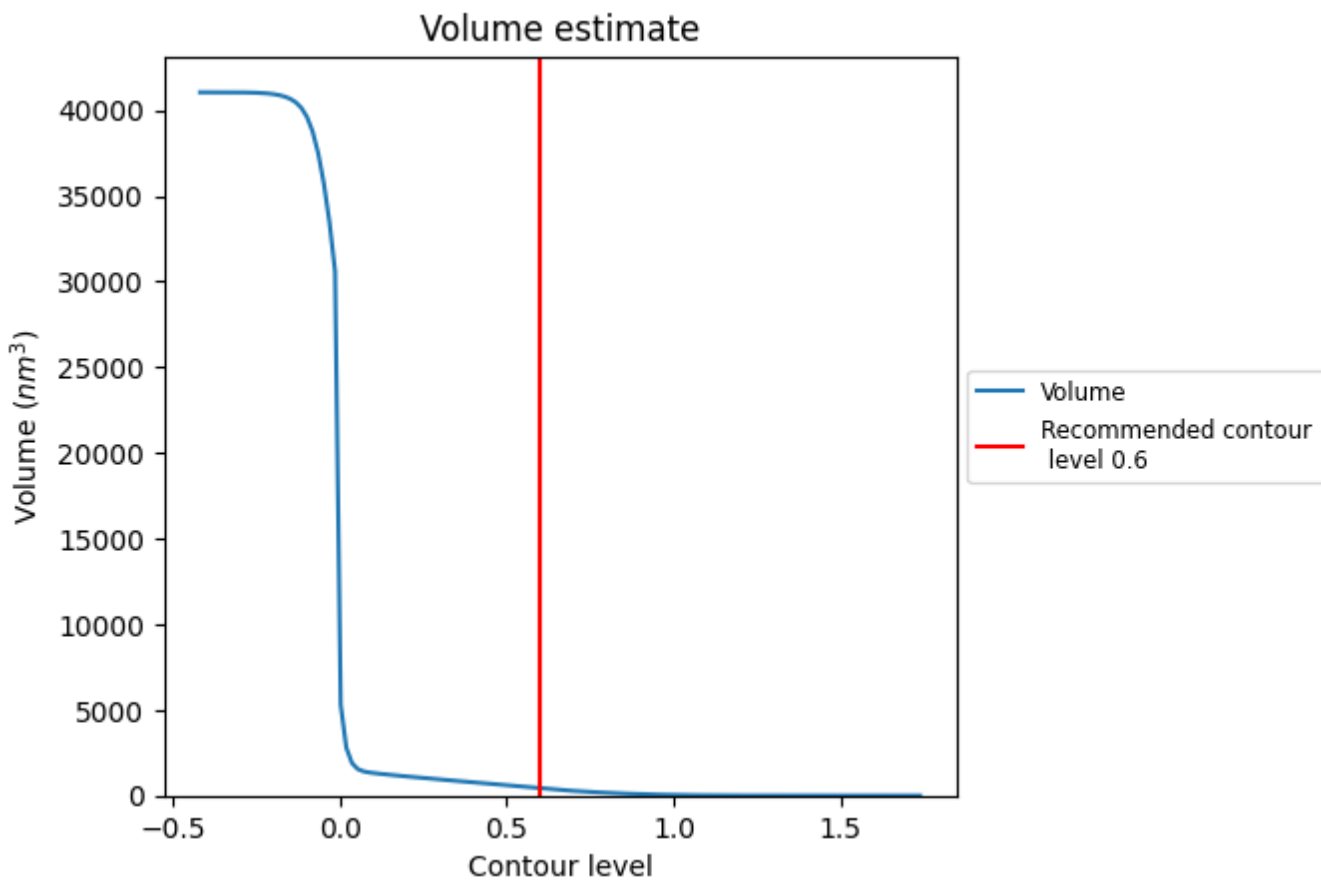
This section contains the results of statistical analysis of the map.

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.

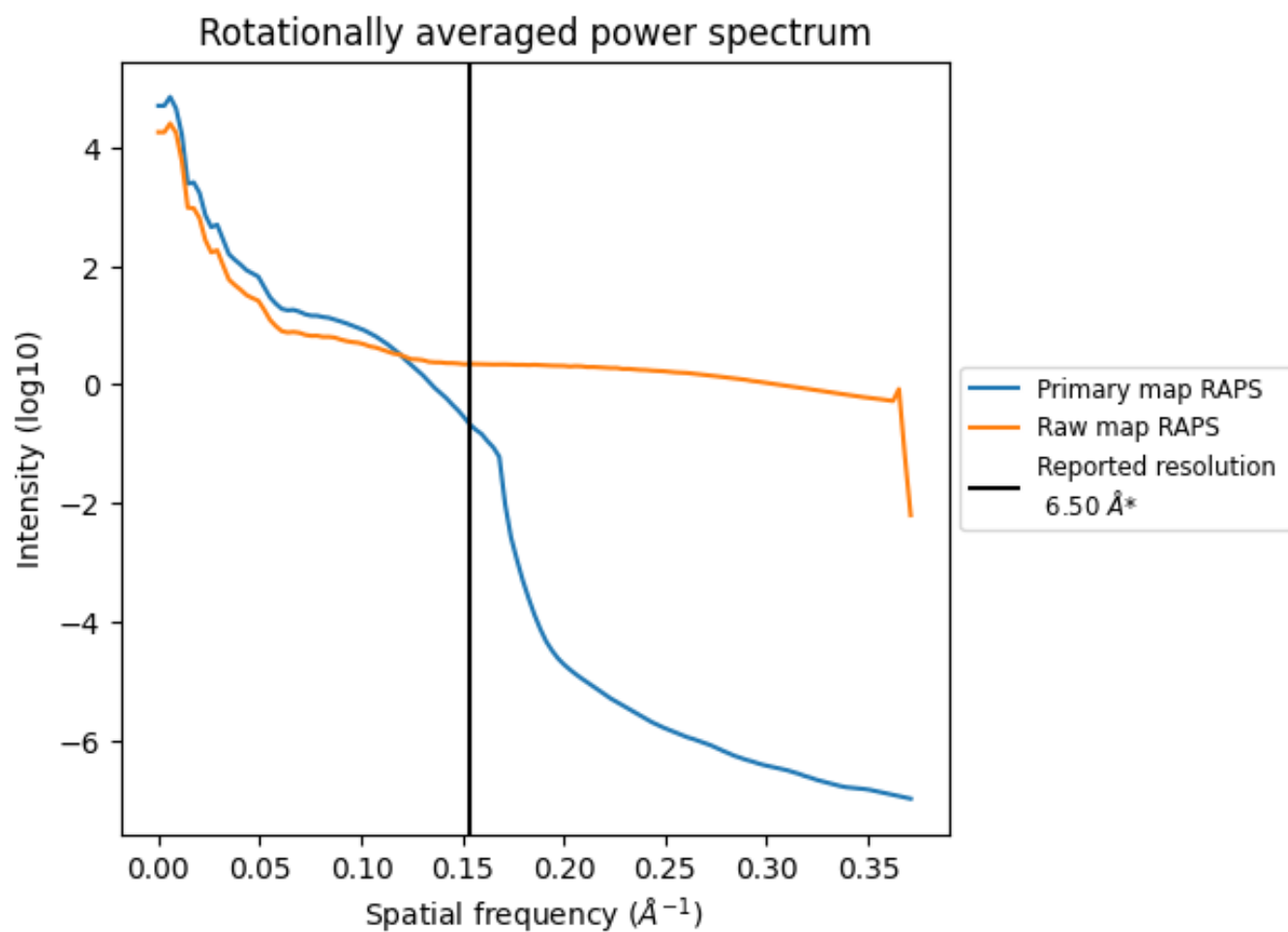
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 423 nm³; this corresponds to an approximate mass of 382 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](#)

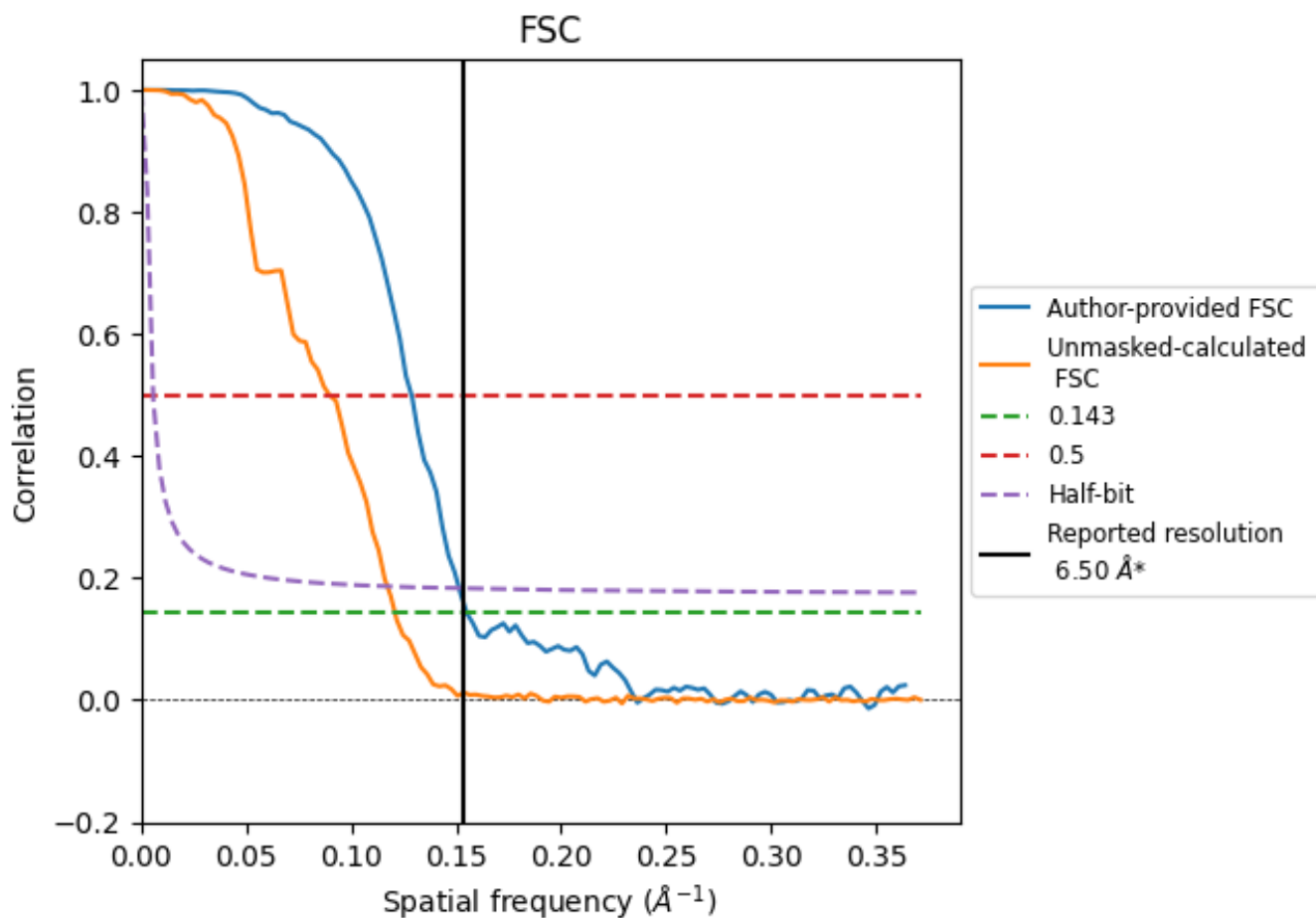


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

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](#)

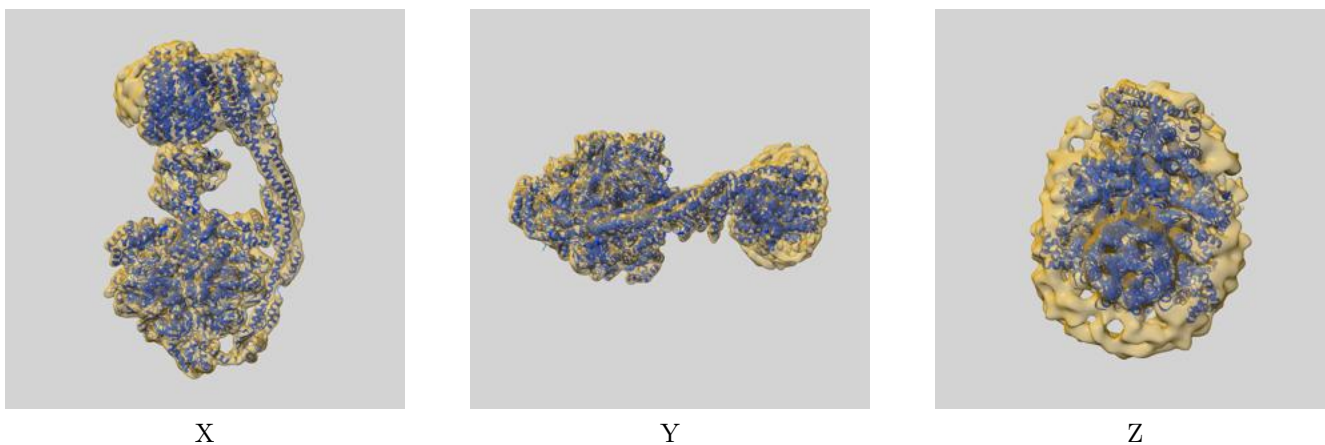
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	6.45	7.76	6.60
Unmasked-calculated*	8.28	11.16	8.53

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

9 Map-model fit [i](#)

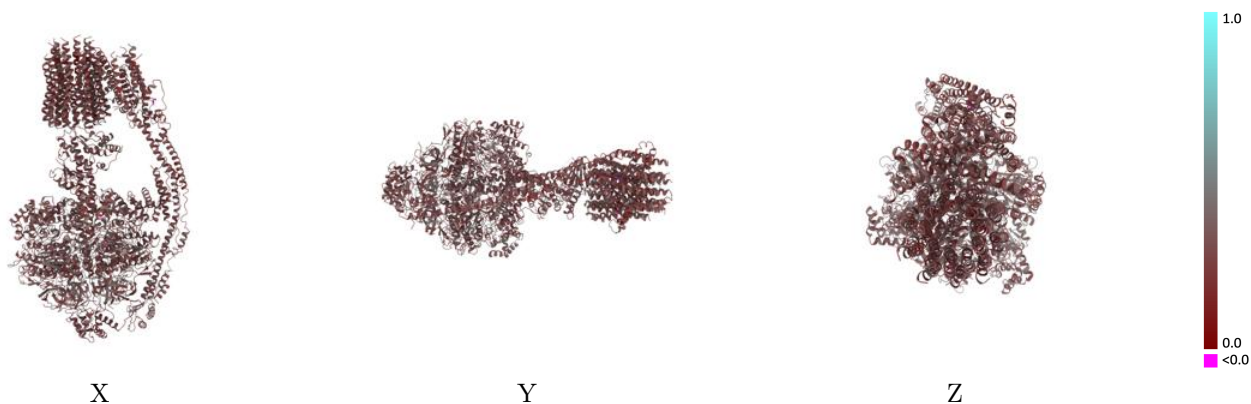
This section contains information regarding the fit between EMDB map EMD-25958 and PDB model 7TK6. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



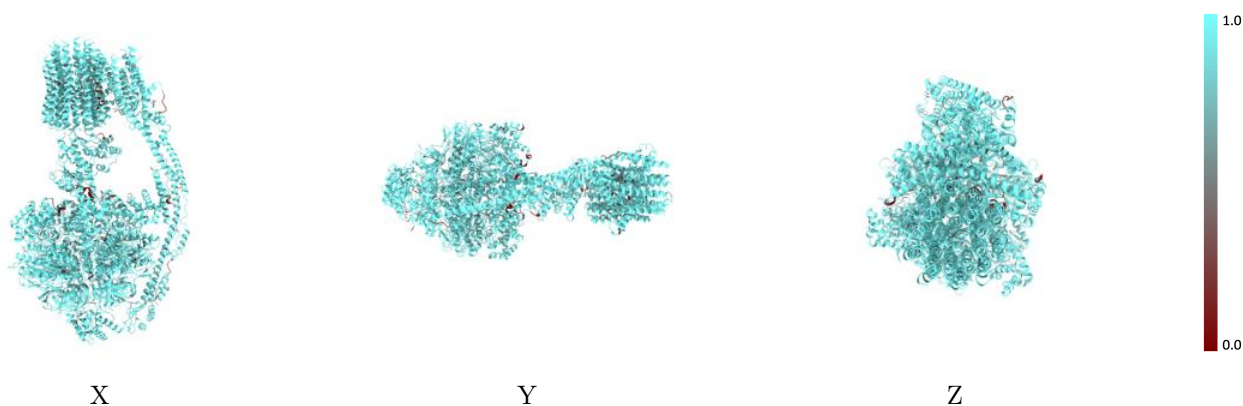
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



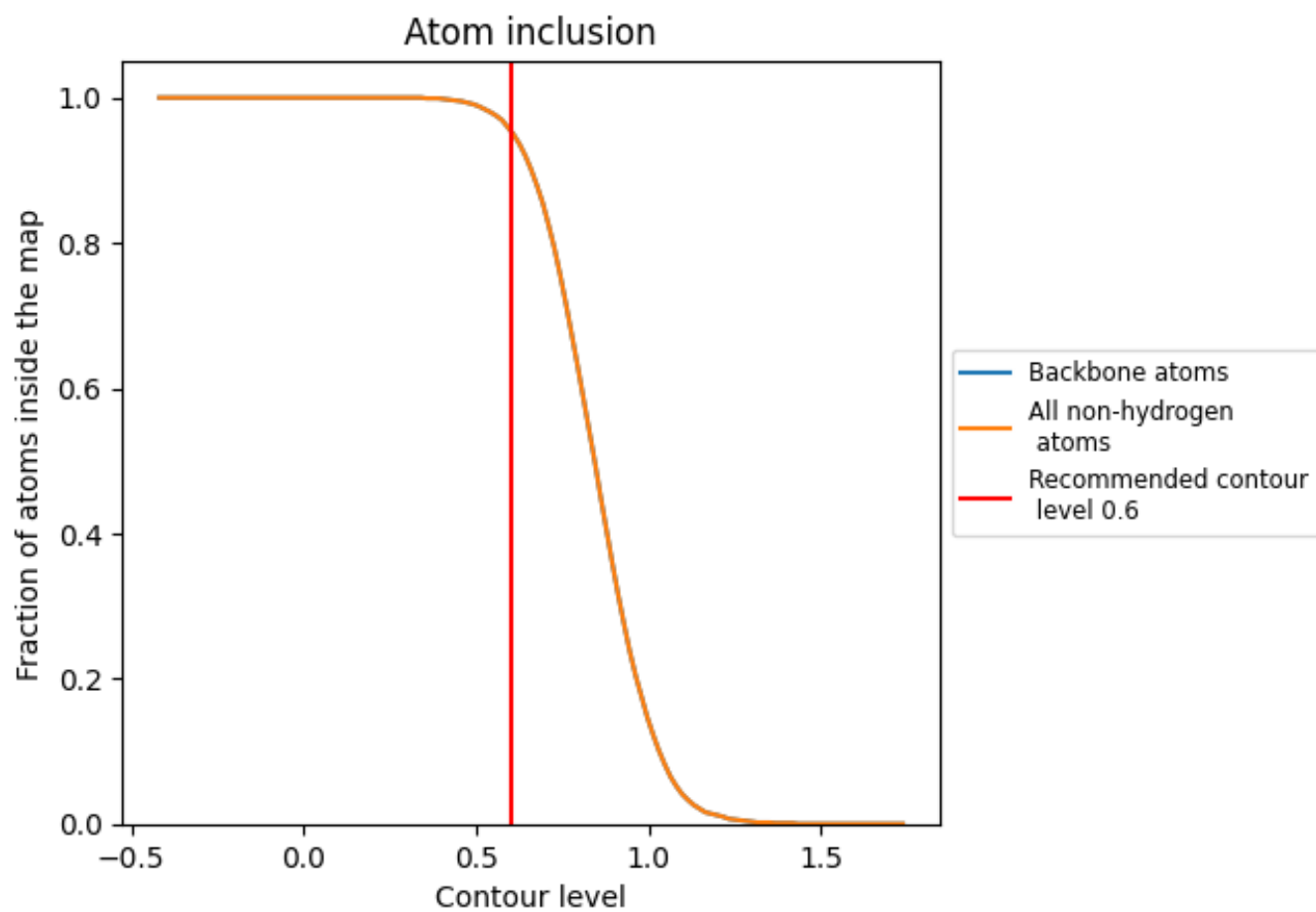
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.6).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.3040
0	 0.9600	 0.2690
1	 0.8900	 0.2720
2	 0.9570	 0.2800
3	 0.9760	 0.2780
4	 0.9330	 0.2720
5	 0.9800	 0.2650
6	 0.9900	 0.2850
7	 0.9830	 0.2770
8	 0.9770	 0.2830
9	 0.9730	 0.2760
A	 0.9560	 0.3200
B	 0.9560	 0.3160
C	 0.9390	 0.3120
D	 0.9650	 0.3200
E	 0.9530	 0.3150
F	 0.9650	 0.3220
G	 0.9580	 0.2980
H	 0.9230	 0.3090
I	 0.9790	 0.3180
O	 0.9720	 0.3020
T	 0.9730	 0.2860
U	 0.9940	 0.2950
V	 0.9520	 0.2840
W	 0.8940	 0.2510
X	 0.7460	 0.3110
Y	 0.9190	 0.2600
Z	 0.9790	 0.3000

