



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 11:42 PM UTC

PDB ID : 8T9D / pdb_00008t9d
EMDB ID : EMD-41107
Title : CryoEM structure of TR-TRAP
Authors : Zhao, H.; Asturias, F.
Deposited on : 2023-06-23
Resolution : 4.66 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

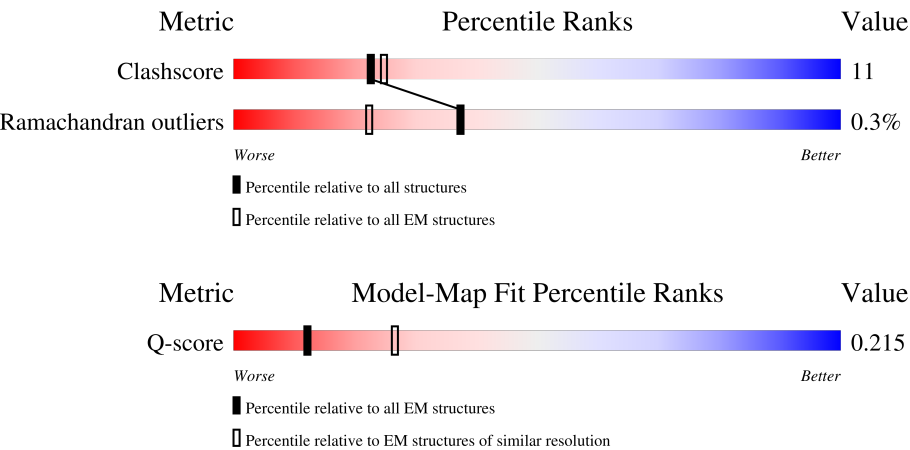
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.66 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.



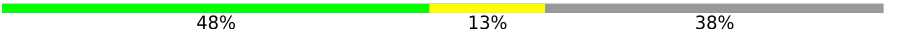
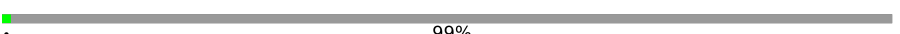
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	2028 (4.16 - 5.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1581	
2	B	270	
3	C	246	
4	D	233	
5	E	268	

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Mol	Chain	Length	Quality of chain
6	F	146	
7	G	135	
8	H	117	
9	I	1454	
10	J	788	
11	K	877	
12	L	651	
13	M	208	
14	O	212	
15	P	144	
16	Q	200	
17	R	1368	
18	S	989	
19	T	747	
20	V	311	
21	W	178	
22	X	200	
23	Y	178	
24	Z	131	
25	a	20	
26	9	2174	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 49136 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 Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	467	Total	C	N	O	0	0
			2354	1405	476	473		

- Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	158	Total	C	N	O	0	0
			793	475	158	160		

- Molecule 3 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	178	Total	C	N	O	0	0
			931	564	185	182		

- Molecule 4 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	161	Total	C	N	O	0	0
			801	479	161	161		

- Molecule 5 is a protein called Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	181	Total	C	N	O	S	0	0
			902	537	181	183	1		

- Molecule 6 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	73	Total	C	N	O	S	0	0
			379	228	74	76	1		

- Molecule 7 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	122	Total	C	N	O	0	0
			608	362	123	123		

- Molecule 8 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	105	Total	C	N	O	S	0	0
			583	354	116	112	1		

- Molecule 9 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	1102	Total	C	N	O	S	0	0
			6855	4319	1271	1245	20		

- Molecule 10 is a protein called Mediator of RNA polymerase II transcription subunit 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	167	Total	C	N	O	S	0	0
			1176	753	216	203	4		

- Molecule 11 is a protein called Mediator of RNA polymerase II transcription subunit 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	732	Total	C	N	O	S	0	0
			5037	3245	903	866	23		

- Molecule 12 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	543	Total	C	N	O	S	0	0
			3393	2134	632	622	5		

- Molecule 13 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	180	Total	C	N	O	S	0	0
			1146	729	218	197	2		

- Molecule 14 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	174	Total	C	N	O	S	0	0
			1022	645	180	193	4		

- Molecule 15 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	114	Total	C	N	O		0	0
			568	340	114	114			

- Molecule 16 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	131	Total	C	N	O		0	0
			759	467	145	147			

- Molecule 17 is a protein called Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	1294	Total	C	N	O	S	0	0
			9758	6300	1684	1721	53		

- Molecule 18 is a protein called Mediator of RNA polymerase II transcription subunit 24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	901	Total	C	N	O	S	0	0
			5888	3751	1061	1049	27		

- Molecule 19 is a protein called Mediator of RNA polymerase II transcription subunit 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	192	Total	C	N	O	S	0	0
			1302	837	223	237	5		

- Molecule 20 is a protein called Mediator of RNA polymerase II transcription subunit 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	270	Total	C	N	O	S	0	0
			1683	1067	307	306	3		

- Molecule 21 is a protein called Mediator of RNA polymerase II transcription subunit 28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	118	Total	C	N	O	S	0	0
			781	489	146	144	2		

- Molecule 22 is a protein called Mediator of RNA polymerase II transcription subunit 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	123	Total	C	N	O	S	0	0
			842	530	150	159	3		

- Molecule 23 is a protein called Mediator of RNA polymerase II transcription subunit 30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	132	Total	C	N	O	S	0	0
			839	523	167	146	3		

- Molecule 24 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	103	Total	C	N	O		0	0
			516	308	103	105			

- Molecule 25 is a protein called Unknown Peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	20	Total	C	N	O		0	0
			100	60	20	20			

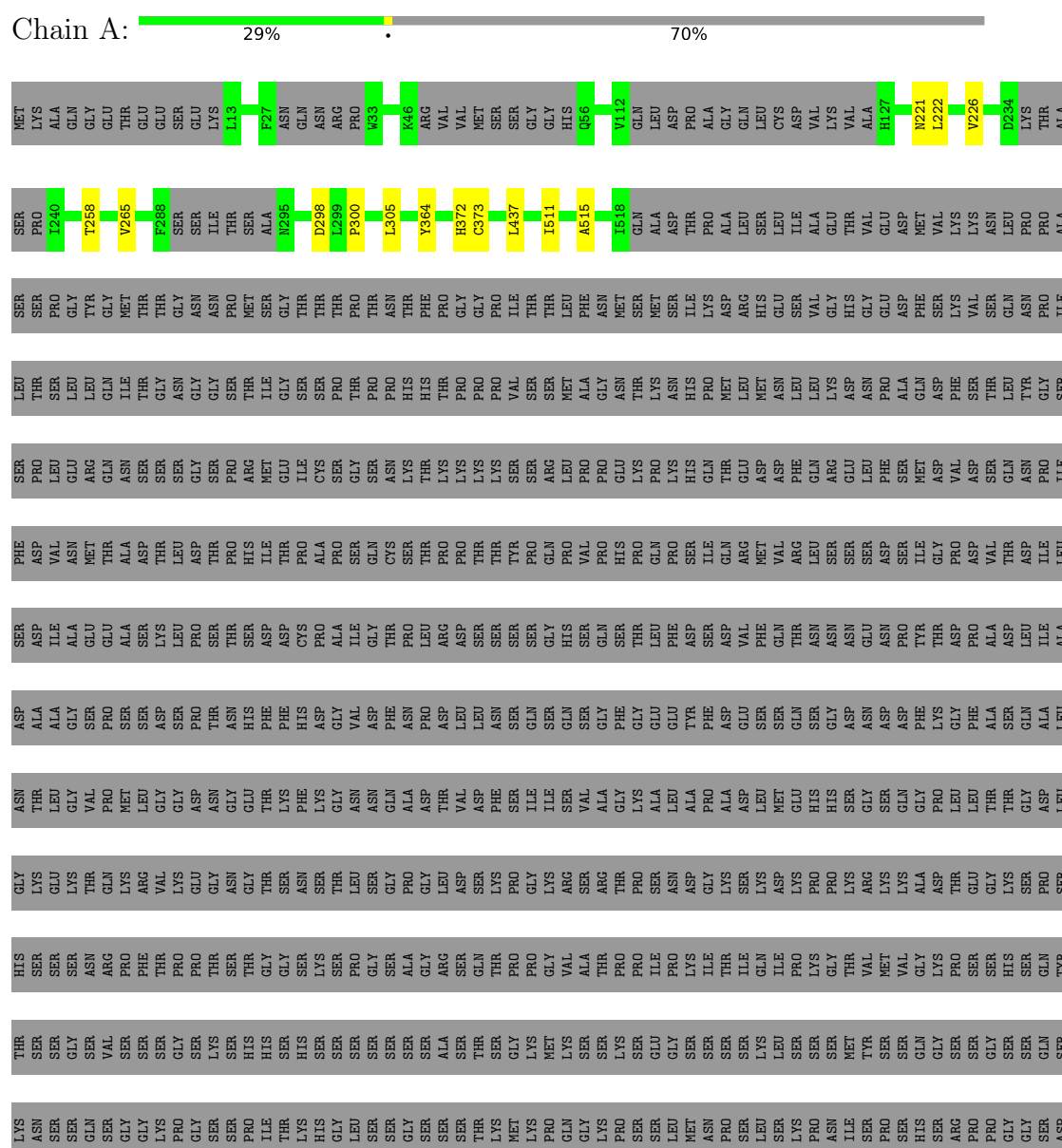
- Molecule 26 is a protein called Mediator of RNA polymerase II transcription subunit 13.

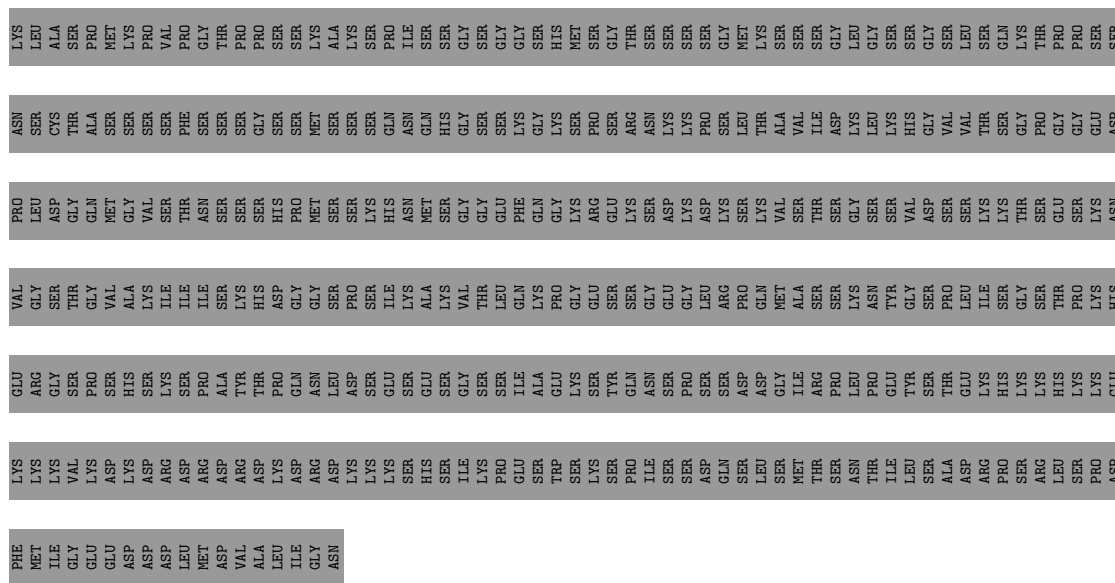
Mol	Chain	Residues	Atoms					AltConf	Trace
26	9	24	Total	C	N	O		0	0
			120	72	24	24			

3 Residue-property plots

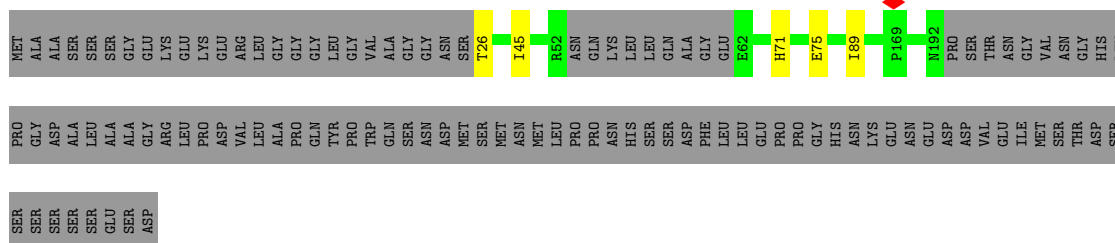
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Mediator of RNA polymerase II transcription subunit 1

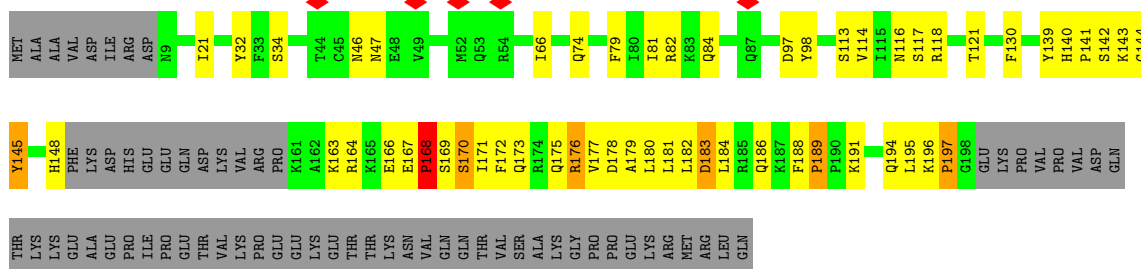




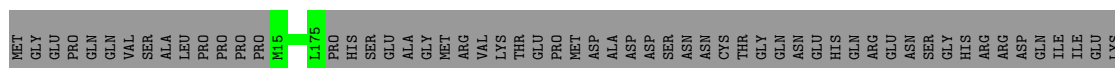
- Molecule 2: Mediator of RNA polymerase II transcription subunit 4

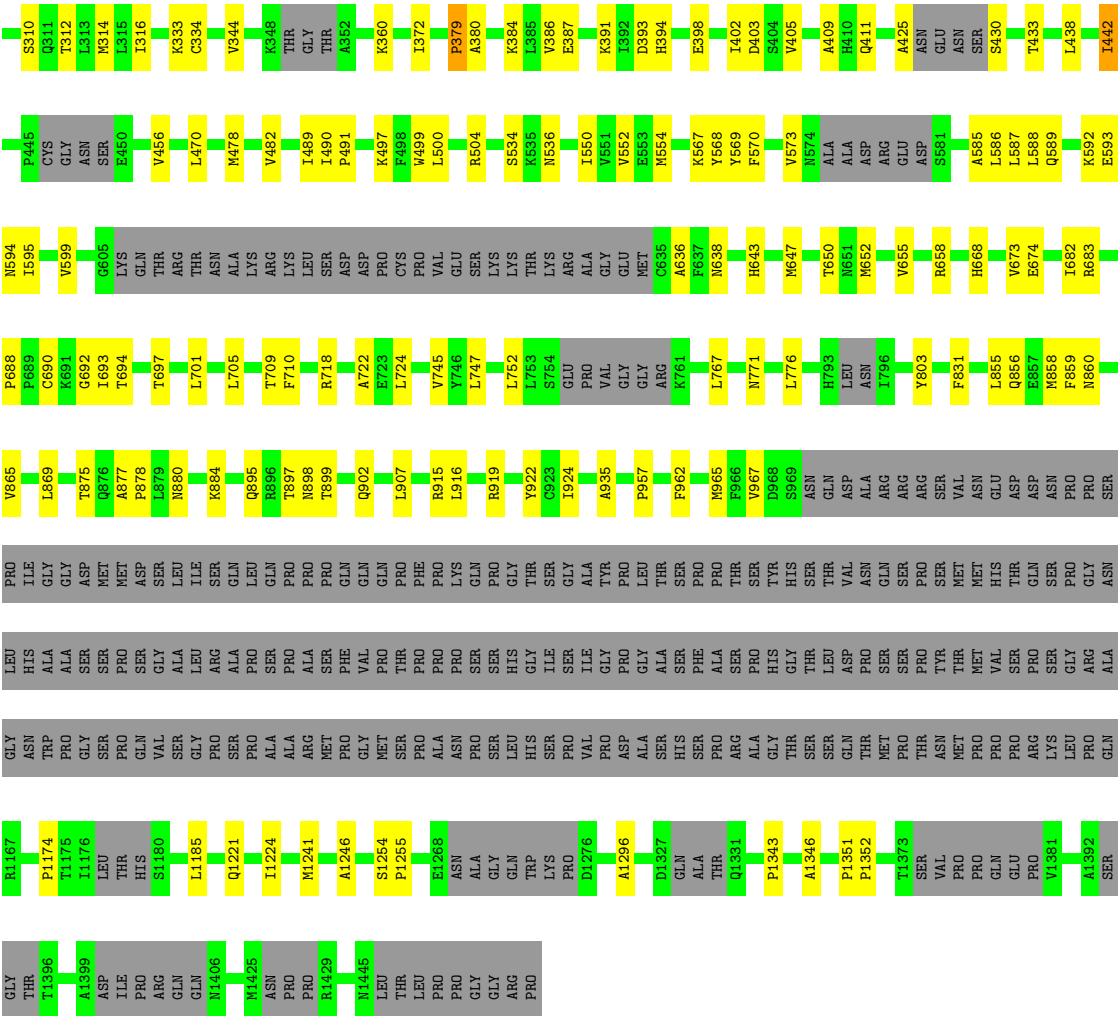


- Molecule 3: Mediator of RNA polymerase II transcription subunit 6

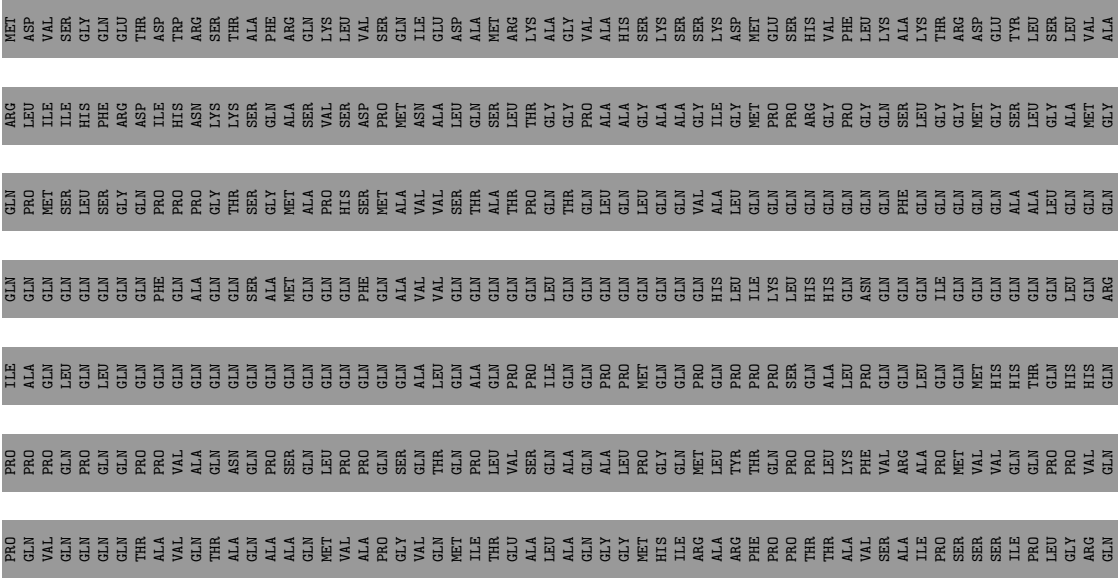


- Molecule 4: Mediator of RNA polymerase II transcription subunit 7





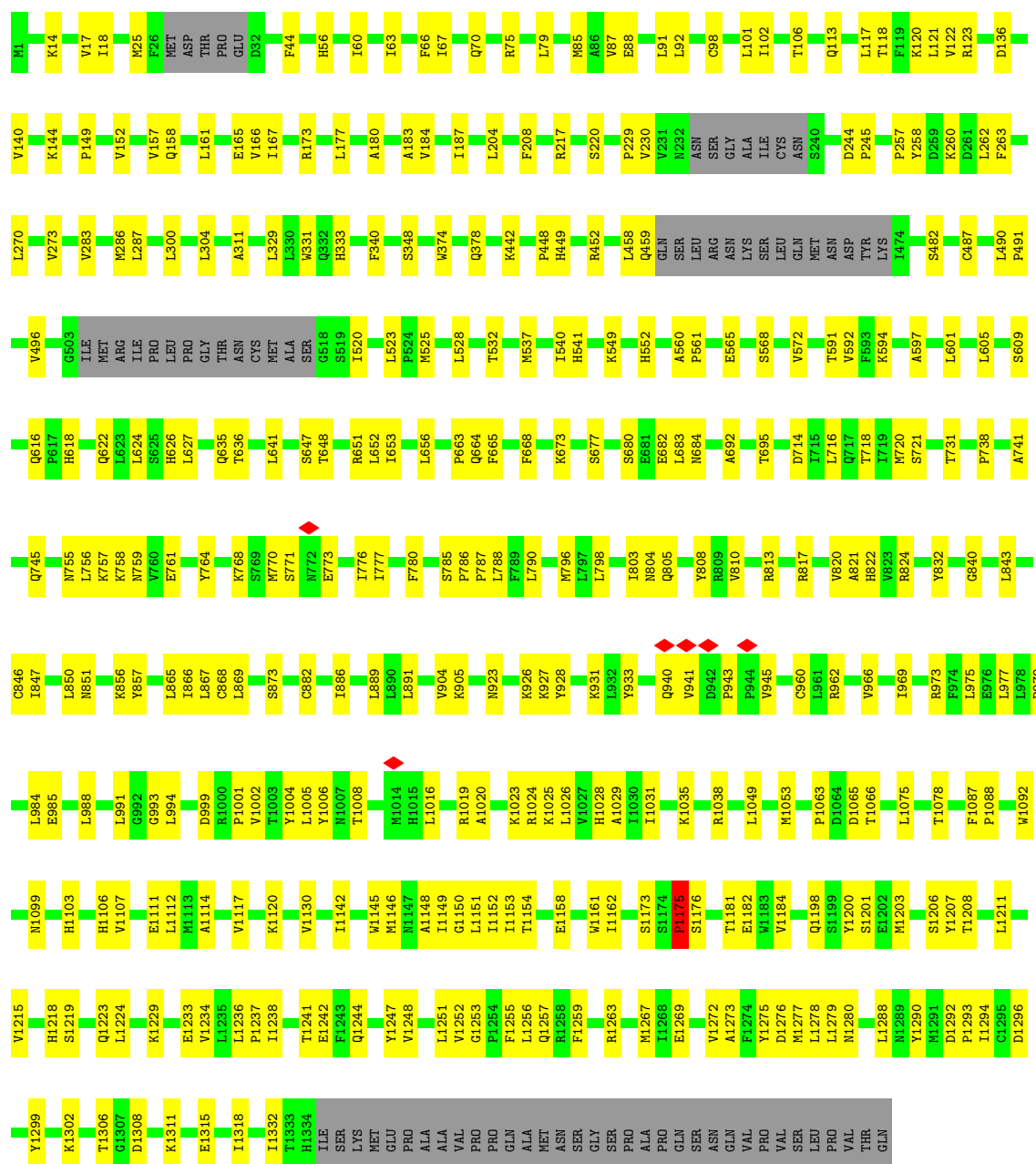
• Molecule 10: Mediator of RNA polymerase II transcription subunit 15



SER
ALA
ASP
GLY
LEU
SER
SER
ALA
PRO
LEU
LEU
LEU
SER
SER
PRO
GLU
PRO
SER
SER
ALA
GLY
PRO
LEU
GLN
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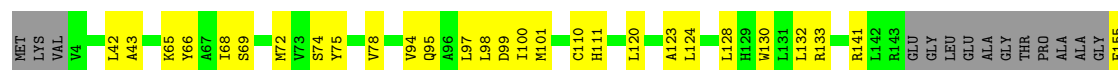
• Molecule 17: Mediator of RNA polymerase II transcription subunit 23

Chain R: 70% 24% 5%

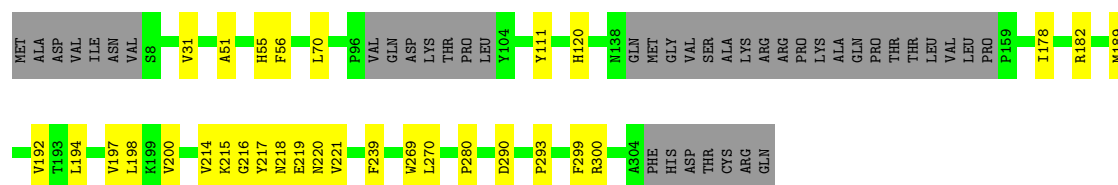


• Molecule 18: Mediator of RNA polymerase II transcription subunit 24

Chain S: 78% 14% 9%

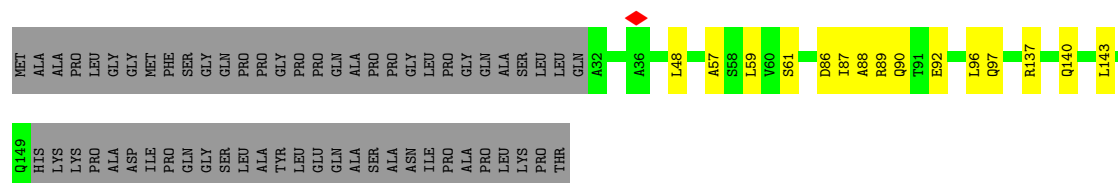


Chain V:  77% 10% 13%



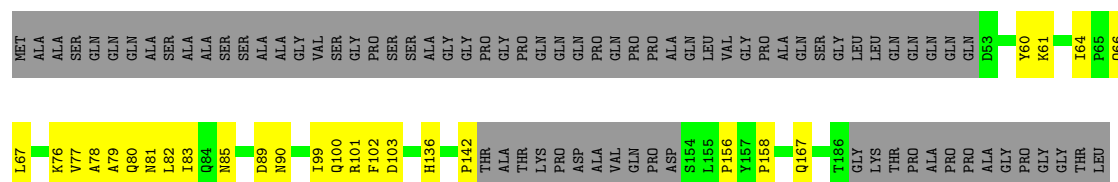
- Molecule 21: Mediator of RNA polymerase II transcription subunit 28

Chain W:  58% 8% 34%



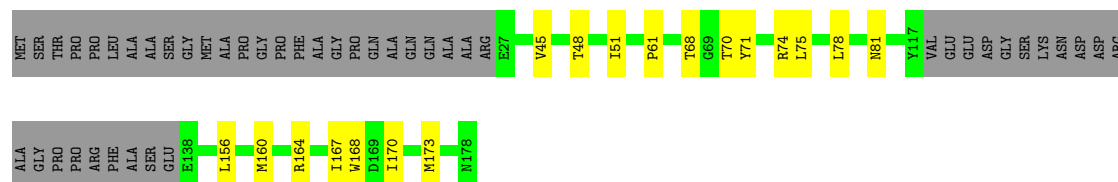
- Molecule 22: Mediator of RNA polymerase II transcription subunit 29

Chain X:  48% 13% 38%



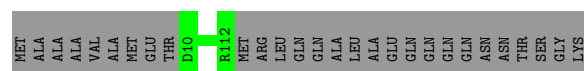
- Molecule 23: Mediator of RNA polymerase II transcription subunit 30

Chain Y:  64% 10% 26%



- Molecule 24: Mediator of RNA polymerase II transcription subunit 31

Chain Z:  79% 21%



- Molecule 25: Unknown Peptide

Chain a:  90% 10%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31505	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	35000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.563	Depositor
Minimum map value	-0.198	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	621.60004, 621.60004, 621.60004	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.11, 1.11, 1.11	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.16	0/2348	0.47	0/3260
2	B	0.12	0/791	0.31	0/1100
3	C	0.83	2/933 (0.2%)	1.30	8/1289 (0.6%)
4	D	0.12	0/800	0.34	0/1116
5	E	0.16	0/900	0.46	0/1252
6	F	0.12	0/377	0.34	0/521
7	G	0.09	0/607	0.30	0/845
8	H	0.15	0/585	0.66	1/805 (0.1%)
9	I	0.17	0/6977	0.52	2/9621 (0.0%)
10	J	0.19	0/1212	0.58	0/1678
11	K	0.20	0/5145	0.60	4/7058 (0.1%)
12	L	0.19	0/3451	0.54	3/4749 (0.1%)
13	M	0.16	0/1169	0.45	0/1598
14	O	0.15	0/1036	0.47	0/1424
15	P	0.09	0/566	0.29	0/788
16	Q	0.13	0/763	0.51	0/1053
17	R	0.17	0/10006	0.54	1/13665 (0.0%)
18	S	0.16	0/6009	0.54	0/8258
19	T	0.20	0/1340	0.55	1/1842 (0.1%)
20	V	0.15	0/1721	0.52	0/2377
21	W	0.17	0/793	0.48	0/1086
22	X	0.15	0/855	0.43	0/1172
23	Y	0.16	0/848	0.50	0/1160
24	Z	0.13	0/515	0.41	0/718
26	9	1.18	0/119	1.48	3/165 (1.8%)
All	All	0.21	2/49866 (0.0%)	0.55	23/68600 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

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Mol	Chain	#Chirality outliers	#Planarity outliers
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Mol	Chain	#Chirality outliers	#Planarity outliers
8	H	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	189	PRO	N-CA	11.28	1.69	1.46
3	C	188	PHE	C-N	10.40	1.45	1.33

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	188	PHE	CA-C-N	20.83	141.83	120.38
3	C	188	PHE	C-N-CA	20.83	141.83	120.38
3	C	170	SER	CA-C-N	10.05	140.07	121.97
3	C	170	SER	C-N-CA	10.05	140.07	121.97
3	C	168	PRO	CA-N-CD	-9.52	98.68	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	82	SER	Peptide
8	H	85	SER	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2354	0	1078	12	0
2	B	793	0	374	7	0
3	C	931	0	479	94	0
4	D	801	0	327	0	0
5	E	902	0	408	14	0
6	F	379	0	182	6	0
7	G	608	0	260	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	583	0	357	15	0
9	I	6855	0	5052	110	0
10	J	1176	0	1036	37	0
11	K	5037	0	4491	187	0
12	L	3393	0	2495	78	0
13	M	1146	0	845	11	0
14	O	1022	0	684	7	0
15	P	568	0	286	0	0
16	Q	759	0	459	29	0
17	R	9758	0	9145	244	0
18	S	5888	0	4727	112	0
19	T	1302	0	1025	21	0
20	V	1683	0	1190	23	0
21	W	781	0	618	10	0
22	X	842	0	710	31	0
23	Y	839	0	637	18	0
24	Z	516	0	227	0	0
25	a	100	0	23	1	0
26	9	120	0	43	8	0
All	All	49136	0	37158	975	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 11.

The worst 5 of 975 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:130:PHE:CE2	16:Q:62:HIS:CB	1.82	1.57
19:T:209:PRO:CD	19:T:210:PRO:HD2	1.19	1.57
3:C:189:PRO:N	3:C:189:PRO:CA	1.69	1.53
19:T:209:PRO:HD2	19:T:210:PRO:CD	1.08	1.53
3:C:118:ARG:HA	5:E:112:LYS:CB	1.03	1.50

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	A	455/1581 (29%)	430 (94%)	25 (6%)	0	100	100
2	B	154/270 (57%)	151 (98%)	3 (2%)	0	100	100
3	C	174/246 (71%)	118 (68%)	51 (29%)	5 (3%)	3	23
4	D	159/233 (68%)	153 (96%)	6 (4%)	0	100	100
5	E	177/268 (66%)	161 (91%)	16 (9%)	0	100	100
6	F	69/146 (47%)	67 (97%)	2 (3%)	0	100	100
7	G	120/135 (89%)	119 (99%)	1 (1%)	0	100	100
8	H	101/117 (86%)	92 (91%)	6 (6%)	3 (3%)	3	22
9	I	1068/1454 (74%)	958 (90%)	110 (10%)	0	100	100
10	J	165/788 (21%)	144 (87%)	21 (13%)	0	100	100
11	K	710/877 (81%)	598 (84%)	109 (15%)	3 (0%)	30	67
12	L	527/651 (81%)	460 (87%)	66 (12%)	1 (0%)	43	78
13	M	176/208 (85%)	162 (92%)	14 (8%)	0	100	100
14	O	164/212 (77%)	145 (88%)	19 (12%)	0	100	100
15	P	110/144 (76%)	108 (98%)	2 (2%)	0	100	100
16	Q	129/200 (64%)	123 (95%)	6 (5%)	0	100	100
17	R	1284/1368 (94%)	1127 (88%)	155 (12%)	2 (0%)	43	78
18	S	889/989 (90%)	802 (90%)	86 (10%)	1 (0%)	48	83
19	T	184/747 (25%)	171 (93%)	13 (7%)	0	100	100
20	V	264/311 (85%)	226 (86%)	37 (14%)	1 (0%)	30	67
21	W	116/178 (65%)	113 (97%)	3 (3%)	0	100	100
22	X	119/200 (60%)	115 (97%)	4 (3%)	0	100	100
23	Y	128/178 (72%)	120 (94%)	8 (6%)	0	100	100
24	Z	101/131 (77%)	100 (99%)	1 (1%)	0	100	100
26	9	22/2174 (1%)	6 (27%)	7 (32%)	9 (41%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7565/13806 (55%)	6769 (90%)	771 (10%)	25 (0%)	37	72

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	168	PRO
3	C	176	ARG
8	H	86	SER
11	K	835	PRO
26	9	621	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.

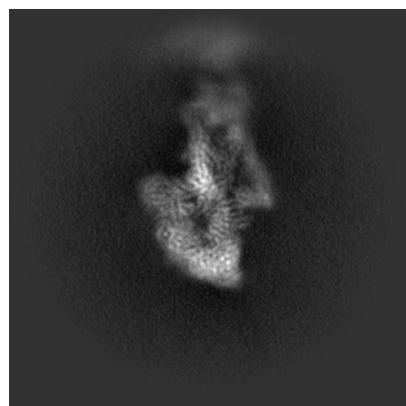
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41107. These allow visual inspection of the internal detail of the map and identification of artifacts.

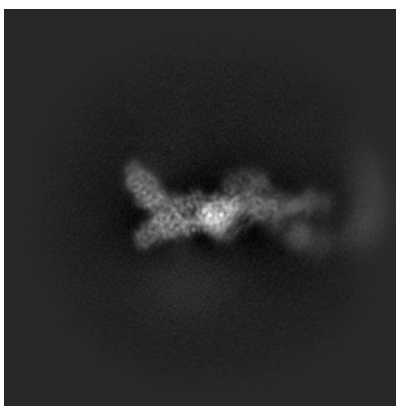
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

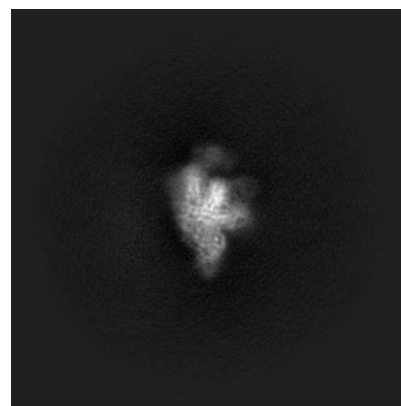
6.1.1 Primary map



X



Y

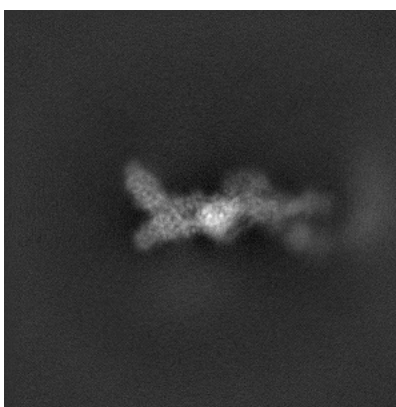


Z

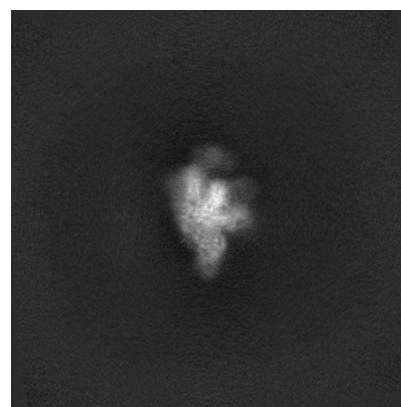
6.1.2 Raw map



X



Y

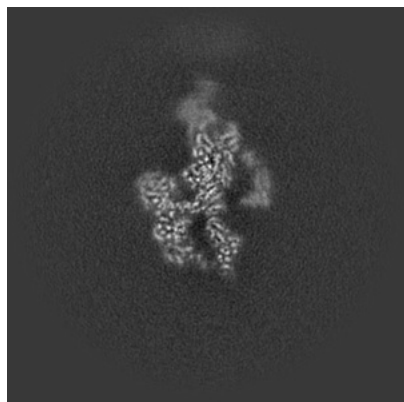


Z

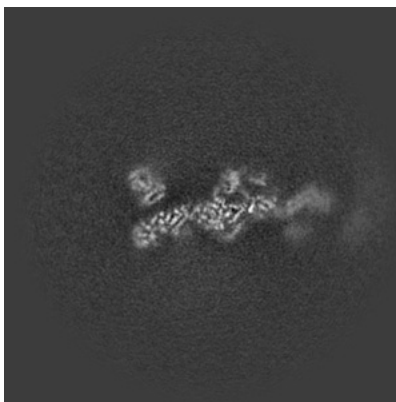
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

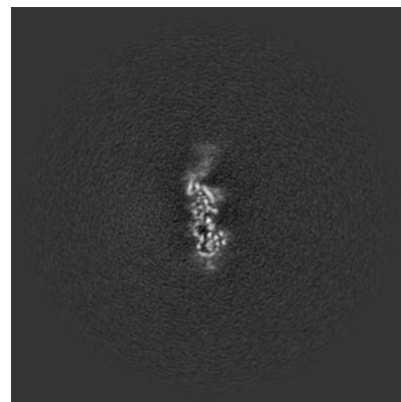
6.2.1 Primary map



X Index: 280

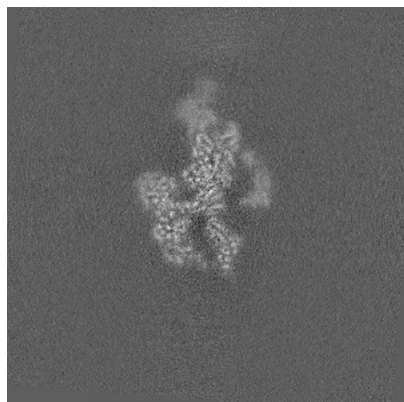


Y Index: 280

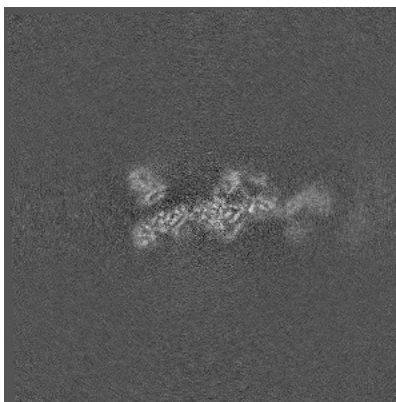


Z Index: 280

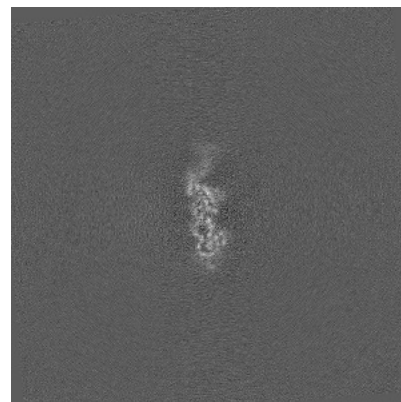
6.2.2 Raw map



X Index: 280



Y Index: 280

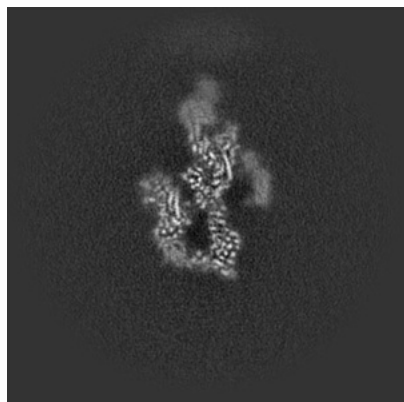


Z Index: 280

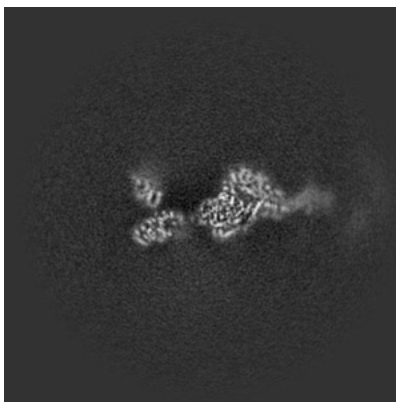
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

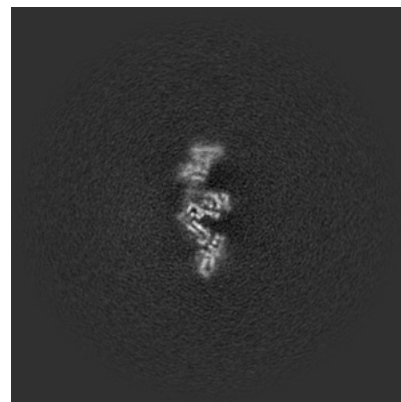
6.3.1 Primary map



X Index: 286

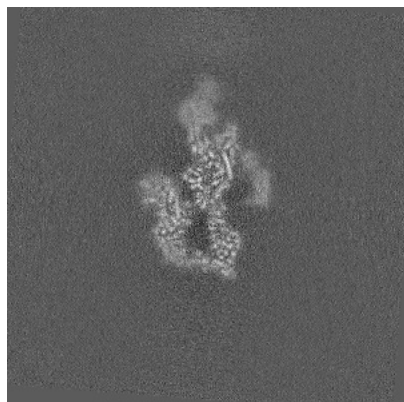


Y Index: 270

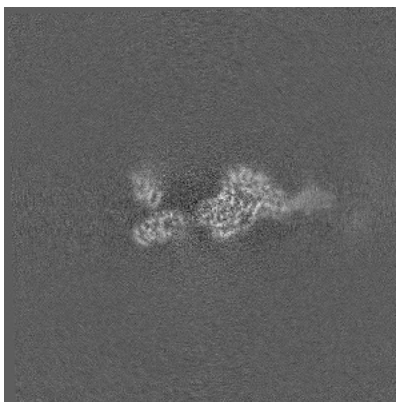


Z Index: 297

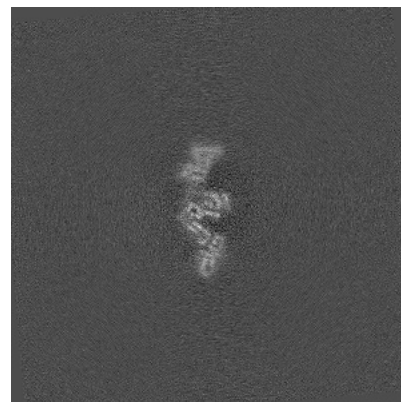
6.3.2 Raw map



X Index: 285



Y Index: 270

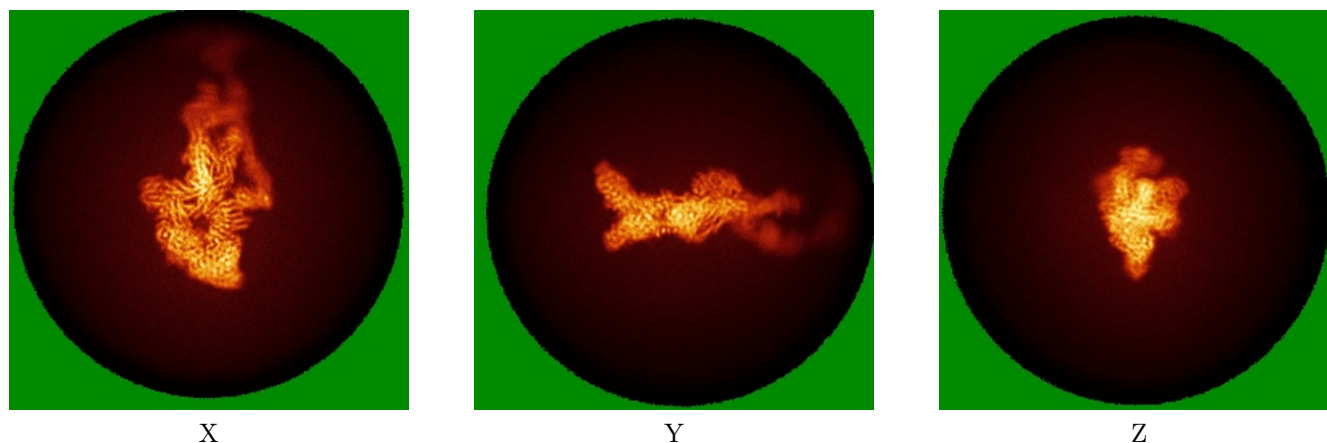


Z Index: 297

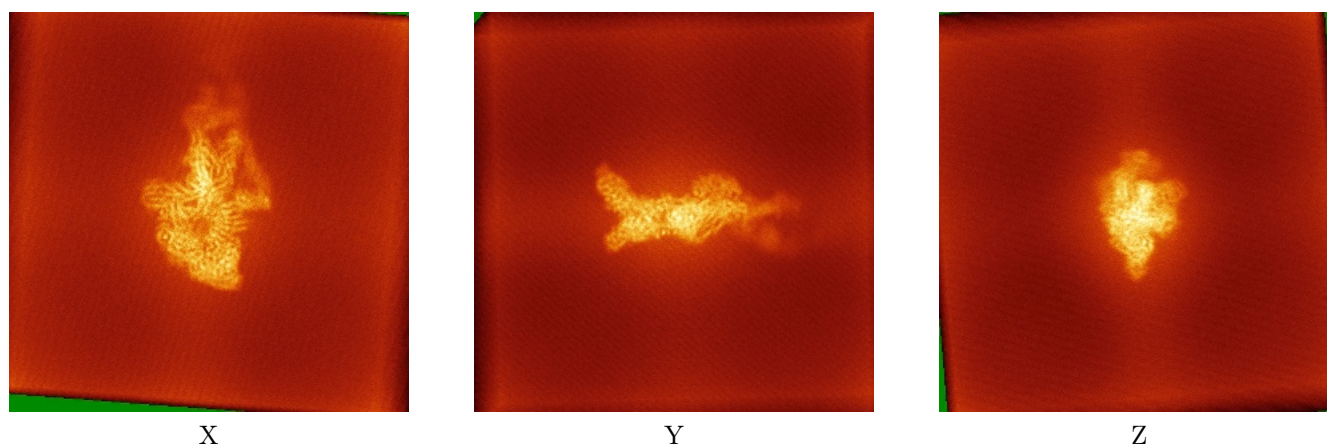
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

This section was not generated.

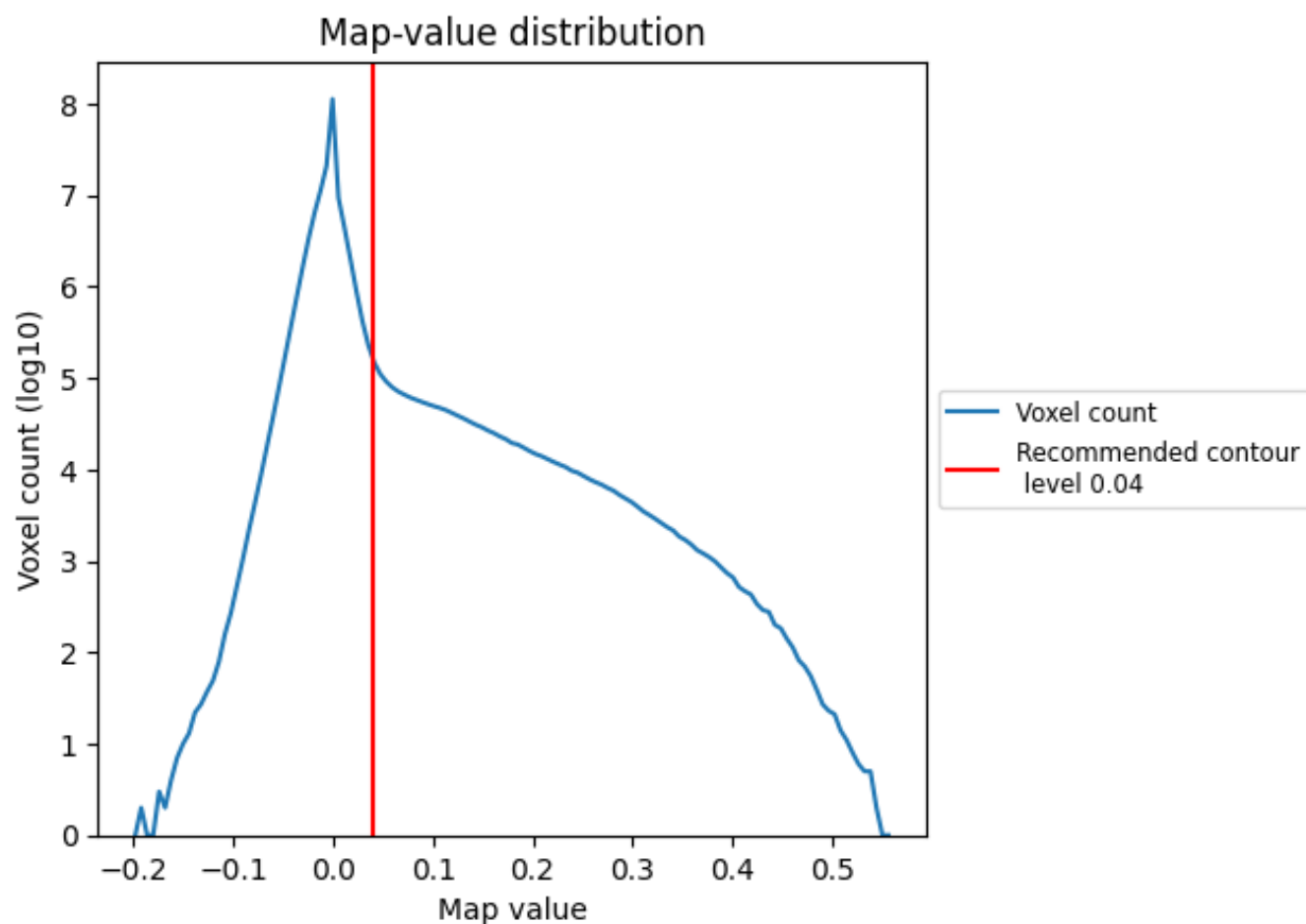
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

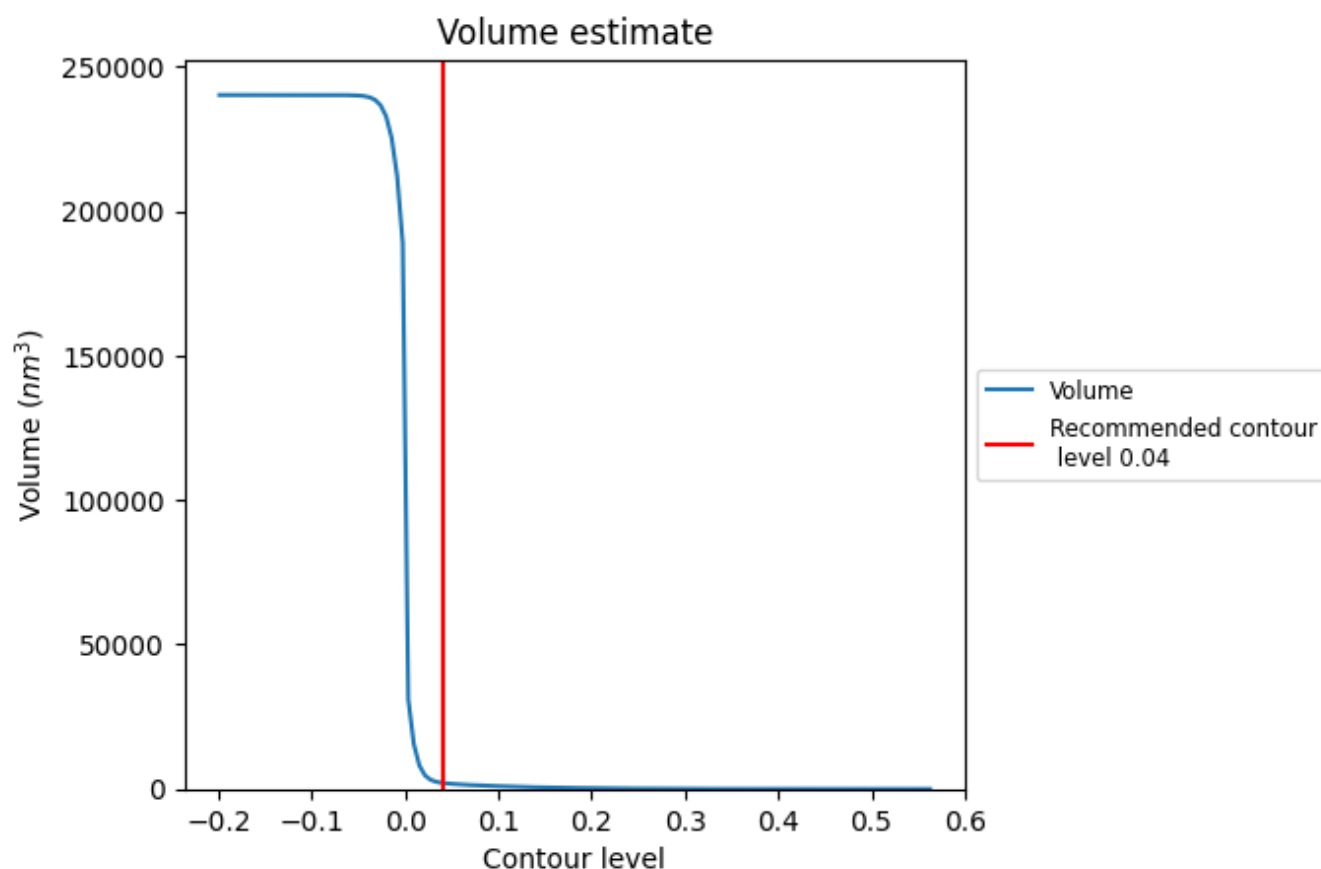
This section contains the results of statistical analysis of the map.

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.

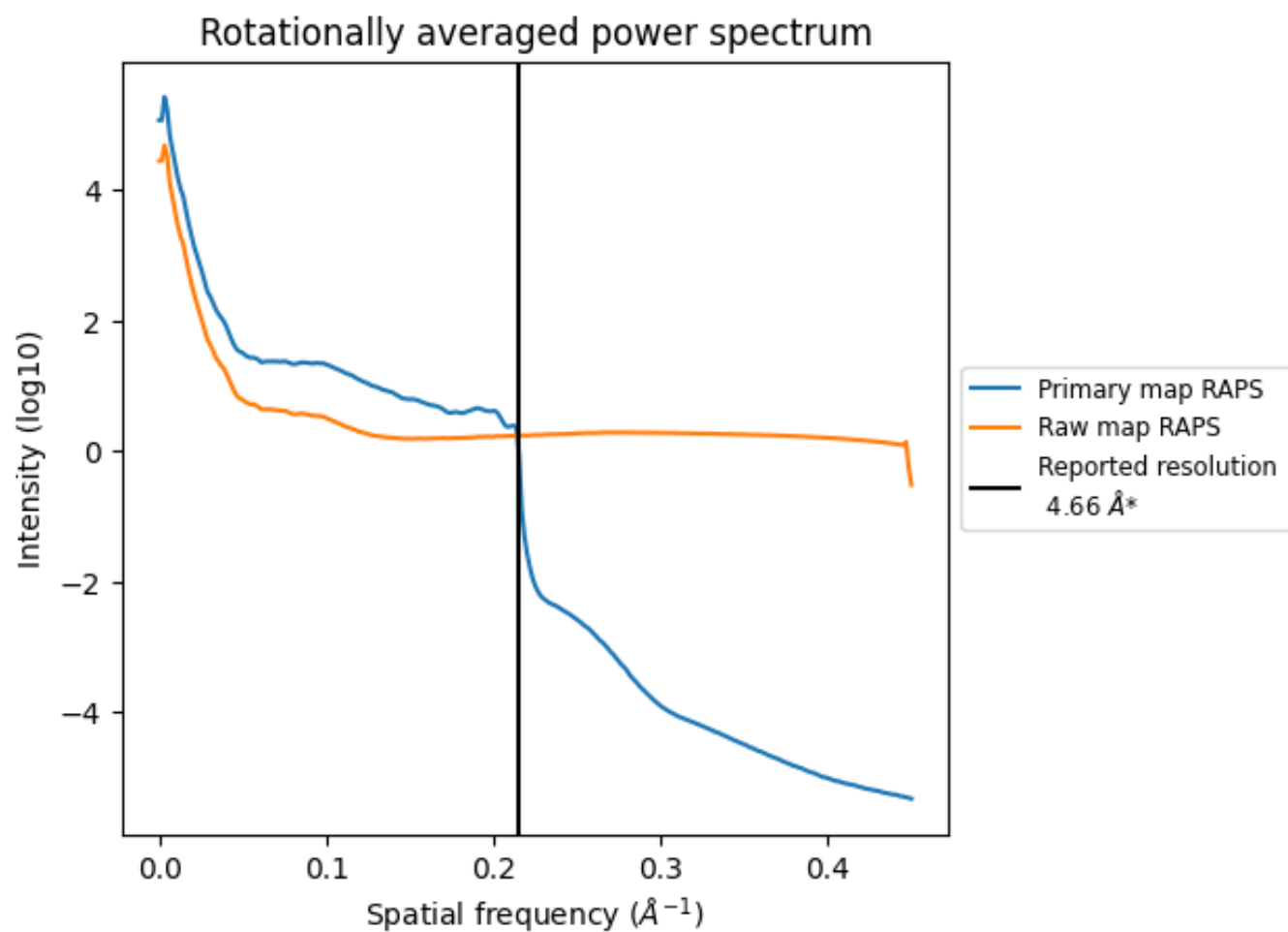
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2101 nm^3 ; this corresponds to an approximate mass of 1898 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 ⓘ

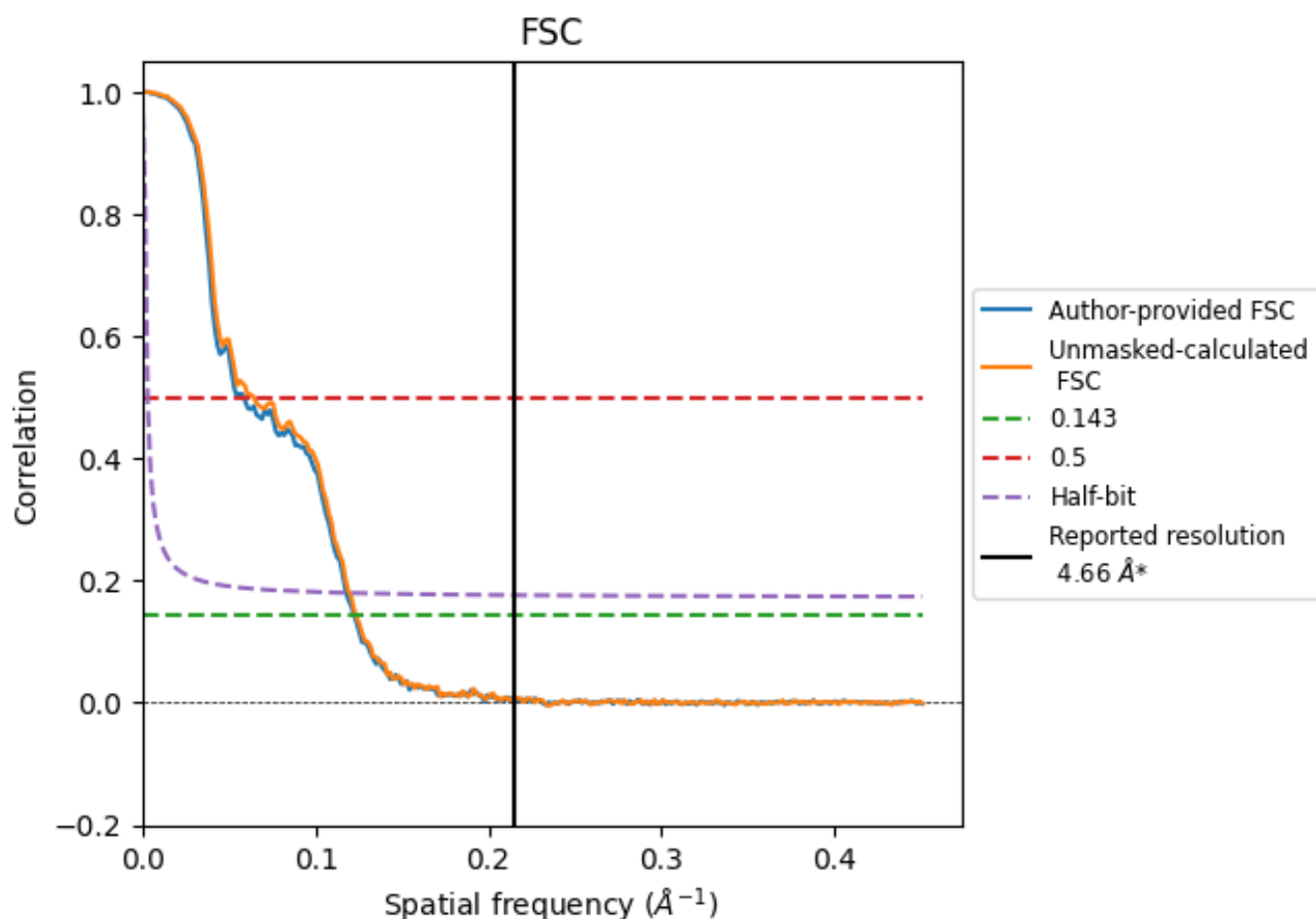


*Reported resolution corresponds to spatial frequency of 0.215 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.215 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.66	-	-
Author-provided FSC curve	8.18	17.06	8.47
Unmasked-calculated*	8.10	15.55	8.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 8.18 differs from the reported value 4.66 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.10 differs from the reported value 4.66 by more than 10 %

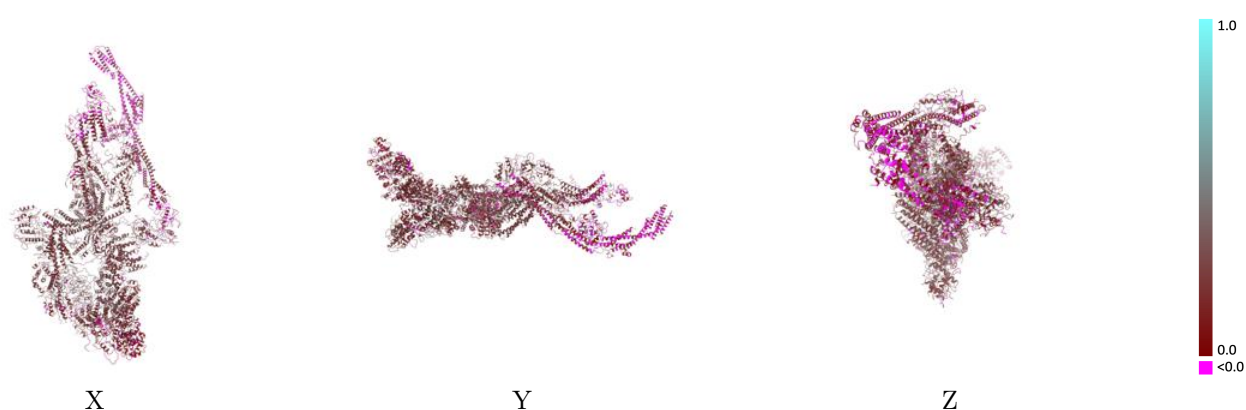
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41107 and PDB model 8T9D. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

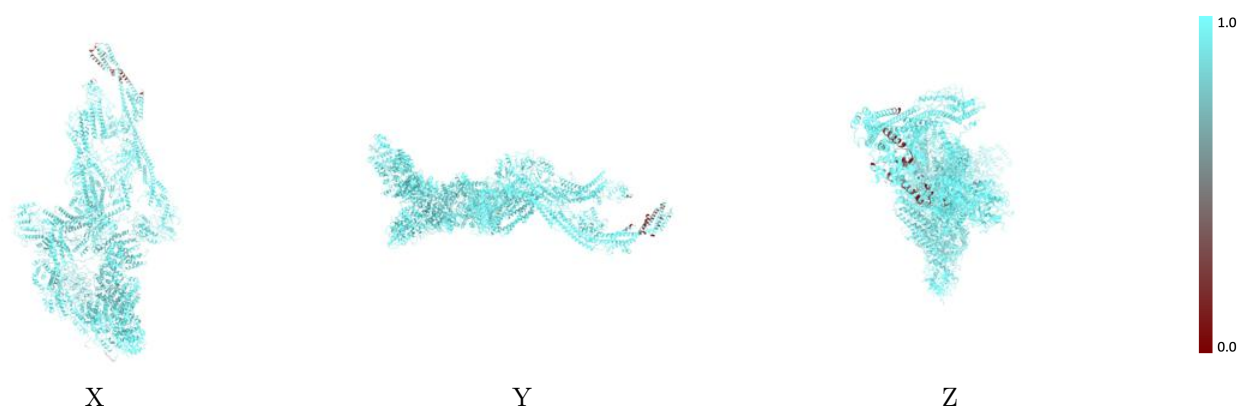
This section was not generated.

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



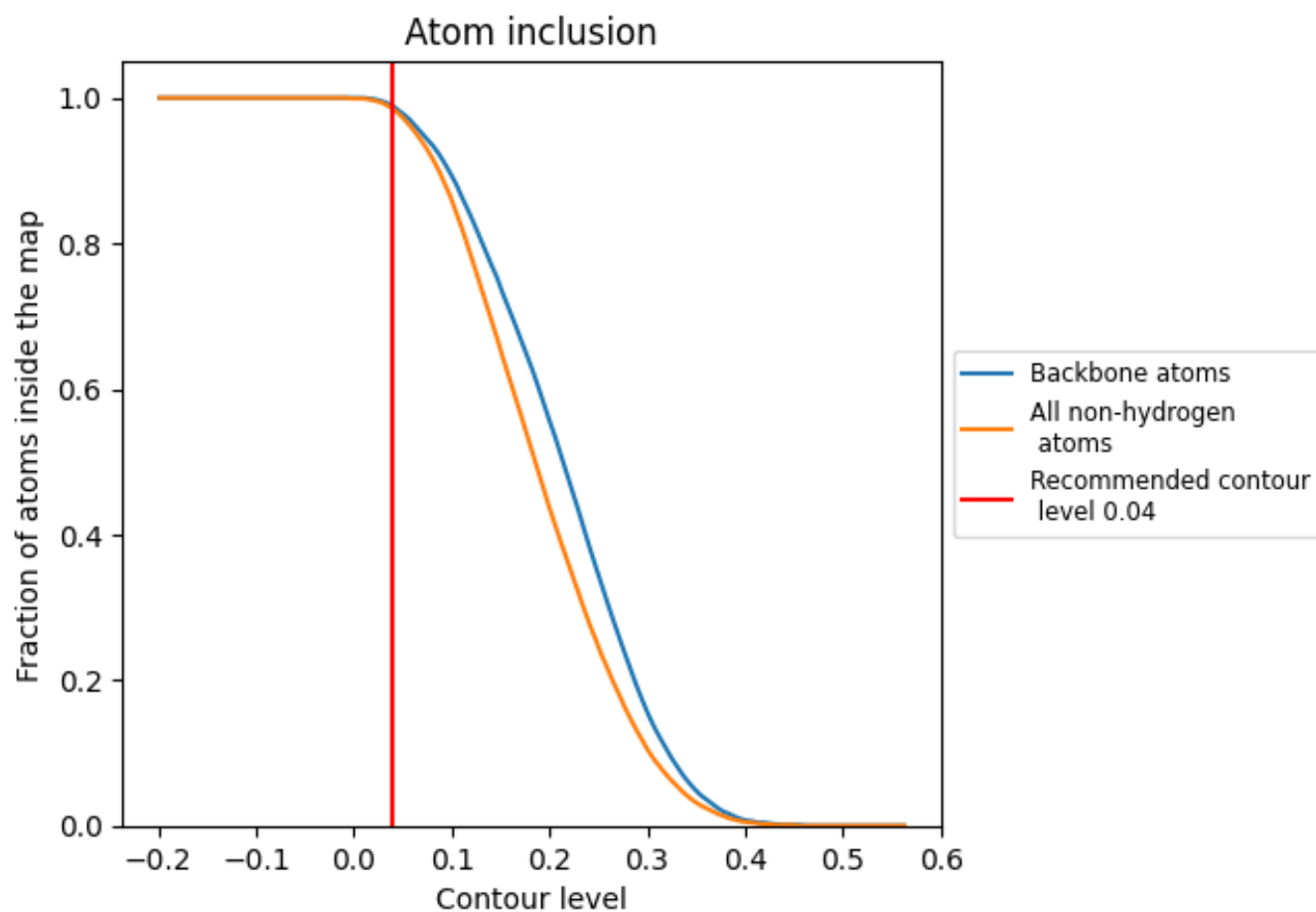
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9850	 0.2150
9	 1.0000	 0.2220
A	 0.9970	 0.1740
B	 0.9950	 0.1190
C	 0.9630	 0.1290
D	 0.9950	 0.0790
E	 0.9950	 0.1370
F	 1.0000	 0.1670
G	 0.7220	 0.0500
H	 0.9970	 0.1930
I	 0.9800	 0.2420
J	 0.9910	 0.2480
K	 0.9890	 0.2450
L	 0.9880	 0.2410
M	 0.9990	 0.2300
O	 1.0000	 0.2760
P	 0.9600	 0.0750
Q	 0.9930	 0.1920
R	 0.9840	 0.1950
S	 0.9920	 0.2380
T	 0.9950	 0.2050
V	 0.9960	 0.3020
W	 0.9910	 0.2380
X	 1.0000	 0.2500
Y	 0.9990	 0.2570
Z	 0.9940	 0.0880
a	 1.0000	 0.2080

