



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 08:11 pm GMT

PDB ID : 6EM3
EMDB ID : EMD-3888
Title : State A architectural model (Nsa1-TAP Flag-Ytm1) - Visualizing the assembly pathway of nucleolar pre-60S ribosomes
Authors : Kater, L.; Cheng, J.; Barrio-Garcia, C.; Hurt, E.; Beckmann, R.
Deposited on : 2017-10-01
Resolution : 3.20 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

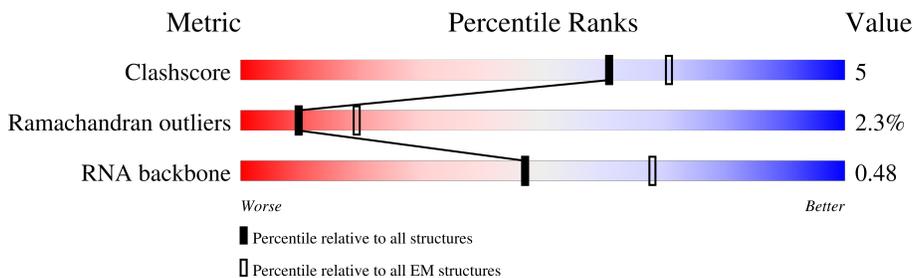
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



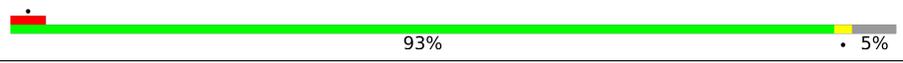
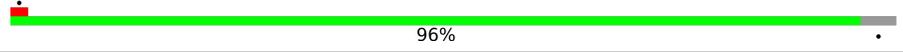
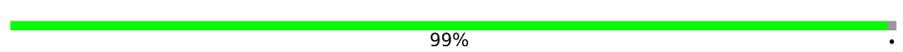
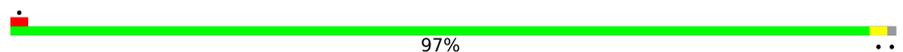
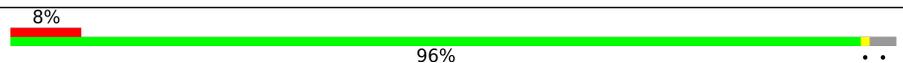
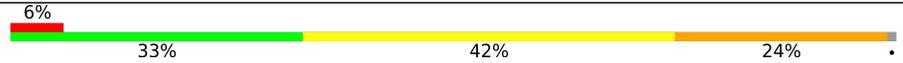
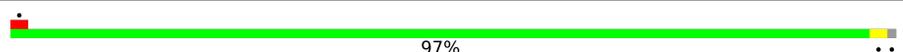
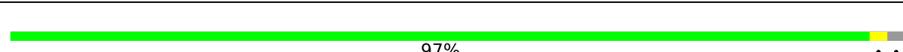
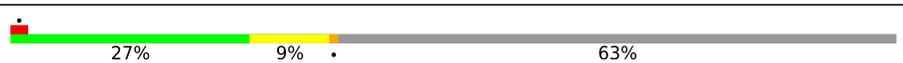
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
RNA backbone	4643	859

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	x	295	
2	F	244	
3	3	306	
4	4	278	
5	5	463	
6	A	291	
7	J	427	
8	v	231	

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Mol	Chain	Length	Quality of chain
9	C	362	 93% 5%
10	e	130	 96%
11	E	176	 86% 14%
12	f	107	 99%
13	G	256	 62% 38%
14	h	120	 97%
15	i	100	 72% 26%
16	j	88	 81% 19%
17	L	199	 53% 46%
18	M	138	 8% 96%
19	N	204	 86% 13%
20	O	199	 6% 33% 42% 24%
21	P	184	 62% 36%
22	Q	186	 70% 30%
23	S	172	 97%
24	Y	127	 97%
25	1	3396	 27% 9% 63%
26	2	158	 77% 21%
27	D	505	 37% 62%
28	K	376	 64% 35%
29	n	605	 52% 48%
30	o	220	 53% 47%
31	t	322	 76% 23%
32	6	232	 15% 12% 72%
33	B	807	 17% 82%

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 38436 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 Ribosome production factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	x	267	Total	C	N	O	0	0
			1068	534	267	267		

- Molecule 2 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	F	241	Total	C	N	O	0	0
			964	482	241	241		

- Molecule 3 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	3	173	Total	C	N	O	0	0
			692	346	173	173		

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	4	220	Total	C	N	O	0	0
			880	440	220	220		

- Molecule 5 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	5	385	Total	C	N	O	0	0
			1540	770	385	385		

- Molecule 6 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	A	145	Total	C	N	O	0	0
			580	290	145	145		

- Molecule 7 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	J	66	264	132	66	66	0	0

- Molecule 8 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	v	130	520	260	130	130	0	0

- Molecule 9 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	C	343	1372	686	343	343	0	0

- Molecule 10 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	e	125	500	250	125	125	0	0

- Molecule 11 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	E	151	604	302	151	151	0	0

- Molecule 12 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	f	106	424	212	106	106	0	0

- Molecule 13 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	G	159	636	318	159	159	0	0

- Molecule 14 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
14	h	119	Total	C	N	O	0	0
			476	238	119	119		

- Molecule 15 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms			AltConf	Trace	
15	i	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 16 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
16	j	71	Total	C	N	O	0	0
			284	142	71	71		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
17	L	108	Total	C	N	O	0	0
			432	216	108	108		

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
18	M	134	Total	C	N	O	0	0
			536	268	134	134		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
19	N	177	Total	C	N	O	0	0
			708	354	177	177		

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
20	O	197	Total	C	N	O	0	0
			788	394	197	197		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
21	P	117	Total	C	N	O	0	0
			468	234	117	117		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
22	Q	131	Total	C	N	O	0	0
			524	262	131	131		

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
23	S	170	Total	C	N	O	0	0
			680	340	170	170		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
24	Y	125	Total	C	N	O	0	0
			500	250	125	125		

- Molecule 25 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms			AltConf	Trace	
25	1	1250	Total	C	O	P	0	0
			15000	6250	7500	1250		

- Molecule 26 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms			AltConf	Trace	
26	2	157	Total	C	O	P	0	0
			1884	785	942	157		

- Molecule 27 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
27	D	194	Total	C	N	O	0	0
			776	388	194	194		

- Molecule 28 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
28	K	246	Total	C	N	O	0	0
			984	492	246	246		

- Molecule 29 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms			AltConf	Trace	
29	n	312	Total	C	N	O	0	0
			1248	624	312	312		

- Molecule 30 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms			AltConf	Trace	
30	o	116	Total	C	N	O	0	0
			464	232	116	116		

- Molecule 31 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms			AltConf	Trace	
31	t	248	Total	C	N	O	0	0
			992	496	248	248		

- Molecule 32 is a RNA chain called 5.8S ribosomal RNA.

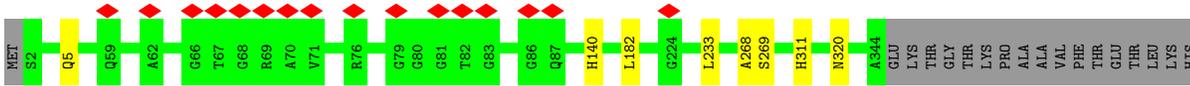
Mol	Chain	Residues	Atoms			AltConf	Trace	
32	6	65	Total	C	O	P	0	0
			780	325	390	65		

- Molecule 33 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms			AltConf	Trace	
33	B	143	Total	C	N	O	0	0
			572	286	143	143		



- Molecule 9: 60S ribosomal protein L4-A



ASP

- Molecule 10: 60S ribosomal protein L32



- Molecule 11: 60S ribosomal protein L6-A



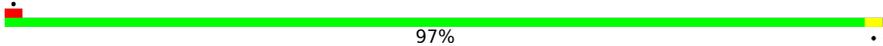
- Molecule 12: 60S ribosomal protein L33-A



- Molecule 13: 60S ribosomal protein L8-A



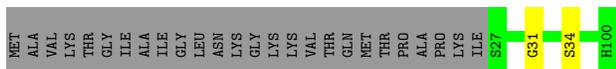
- Molecule 14: 60S ribosomal protein L35-A

Chain h:  97%



- Molecule 15: 60S ribosomal protein L36-B

Chain i:  72% 26%



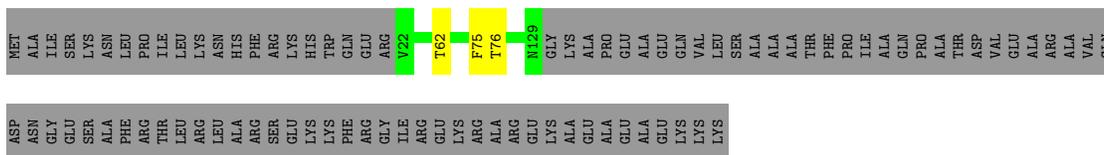
- Molecule 16: 60S ribosomal protein L37-A

Chain j:  81% 19%

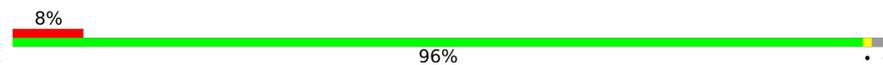


- Molecule 17: 60S ribosomal protein L13-A

Chain L:  53% 46%



- Molecule 18: 60S ribosomal protein L14-A

Chain M:  8% 96%



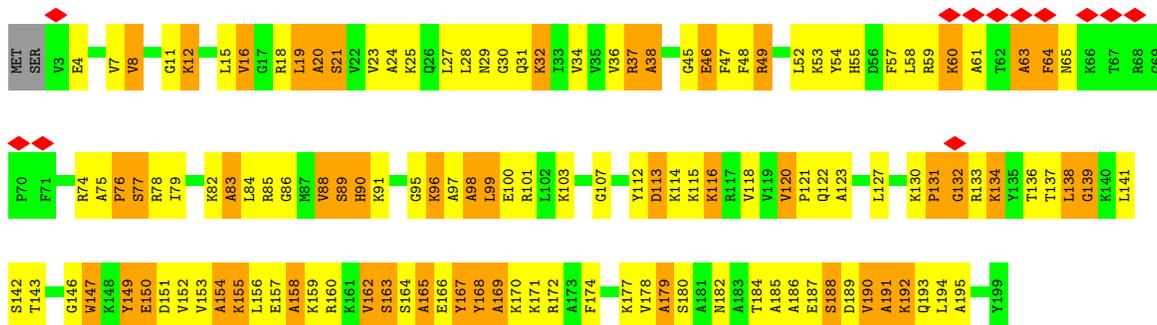
- Molecule 19: 60S ribosomal protein L15-A

Chain N:  86% 13%

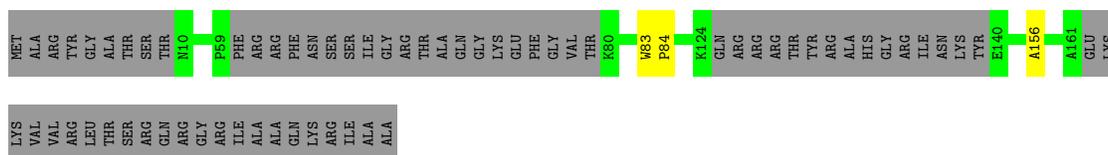


- Molecule 20: 60S ribosomal protein L16-A

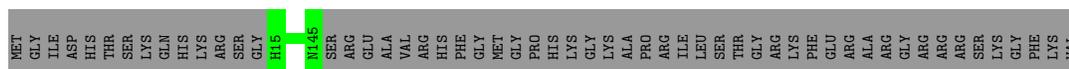
Chain O:  6% 33% 42% 24%



• Molecule 21: 60S ribosomal protein L17-A



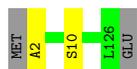
• Molecule 22: 60S ribosomal protein L18-A



• Molecule 23: 60S ribosomal protein L20-A

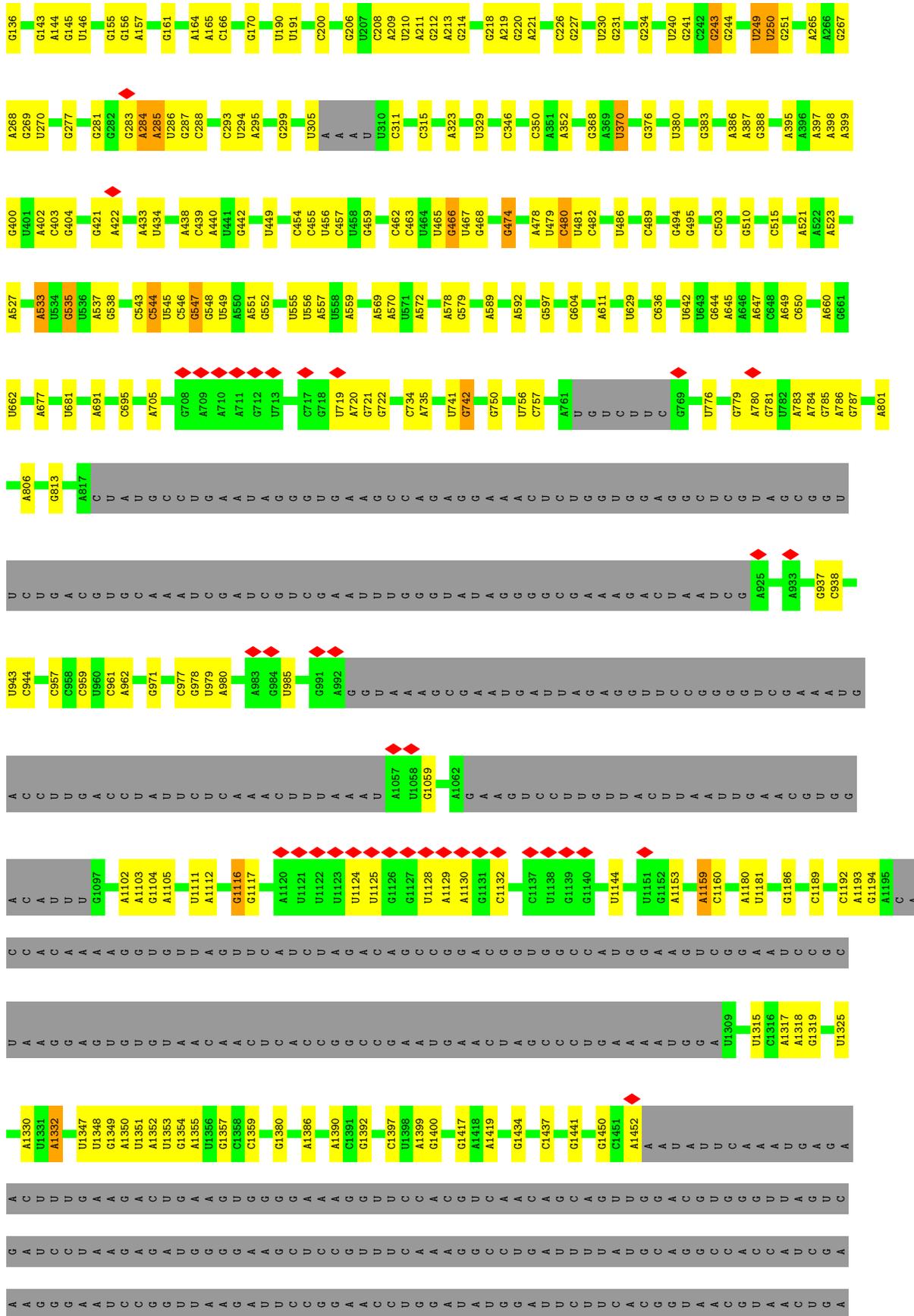


• Molecule 24: 60S ribosomal protein L26-A



• Molecule 25: 25S ribosomal RNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34453	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.121	Depositor
Minimum map value	-0.035	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.023	Depositor
Map size (\AA)	455.28, 455.28, 455.28	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.084, 1.084, 1.084	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	x	0.40	0/1064	0.67	0/1323
2	F	0.35	0/963	0.57	0/1202
3	3	0.36	0/691	0.63	0/862
4	4	0.29	0/878	0.75	2/1094 (0.2%)
5	5	0.36	0/1536	0.57	0/1913
6	A	0.43	0/577	0.60	0/716
7	J	0.41	0/263	0.58	0/327
8	v	0.34	0/517	0.53	0/641
9	C	0.37	0/1371	0.60	0/1712
10	e	0.35	0/499	0.58	0/622
11	E	0.35	0/602	0.58	0/749
12	f	0.32	0/423	0.57	0/527
13	G	0.37	0/634	0.61	0/789
14	h	0.36	0/475	0.55	0/592
15	i	0.38	0/295	0.57	0/367
16	j	0.36	0/283	0.59	0/352
17	L	0.36	0/431	0.61	0/537
18	M	0.34	0/535	0.55	0/667
19	N	0.35	0/706	0.55	0/879
20	O	0.25	0/787	0.41	0/982
21	P	0.34	0/465	0.55	0/576
22	Q	0.35	0/523	0.55	0/652
23	S	0.38	0/679	0.61	0/847
24	Y	0.33	0/499	0.55	0/622
25	1	0.24	0/16238	0.84	5/24952 (0.0%)
26	2	0.23	0/2034	0.85	1/3112 (0.0%)
27	D	0.63	0/773	0.66	0/961
28	K	0.58	0/982	0.63	0/1224
29	n	0.59	0/1244	0.57	0/1548
30	o	0.71	0/462	0.65	0/574
31	t	0.65	0/990	0.65	0/1234
32	6	0.70	0/843	0.99	1/1292 (0.1%)
33	B	0.61	0/570	0.69	0/709
All	All	0.37	0/39832	0.74	9/55156 (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.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	4	0	2
27	D	0	1
31	t	0	2
33	B	0	2
All	All	0	7

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	4	132	GLN	N-CA-C	-12.69	76.75	111.00
25	1	1102	A	C2'-C3'-O3'	7.41	125.81	109.50
25	1	649	A	C2'-C3'-O3'	6.41	123.95	113.70
4	4	133	LEU	N-CA-C	-6.29	94.03	111.00
26	2	114	G	C2'-C3'-O3'	6.12	123.49	113.70

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	4	135	TYR	Peptide
4	4	136	LEU	Peptide
27	D	396	PRO	Peptide
31	t	226	GLU	Peptide
31	t	270	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	x	1068	0	271	0	0
2	F	964	0	259	0	0
3	3	692	0	177	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	4	880	0	222	7	0
5	5	1540	0	421	1	0
6	A	580	0	142	14	0
7	J	264	0	64	10	0
8	v	520	0	139	0	0
9	C	1372	0	380	0	0
10	e	500	0	133	0	0
11	E	604	0	156	0	0
12	f	424	0	117	0	0
13	G	636	0	159	0	0
14	h	476	0	118	0	0
15	i	296	0	80	0	0
16	j	284	0	83	0	0
17	L	432	0	112	0	0
18	M	536	0	143	1	0
19	N	708	0	191	2	0
20	O	788	0	213	129	0
21	P	468	0	117	4	0
22	Q	524	0	137	0	0
23	S	680	0	170	1	0
24	Y	500	0	133	2	0
25	1	15000	0	7512	60	0
26	2	1884	0	949	5	0
27	D	776	0	199	2	0
28	K	984	0	248	3	0
29	n	1248	0	314	0	0
30	o	464	0	126	0	0
31	t	992	0	263	0	0
32	6	780	0	392	21	0
33	B	572	0	134	3	0
All	All	38436	0	14274	219	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 5.

The worst 5 of 219 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)
25:1:1:G:P	32:6:232:A:H3'	1.53	1.46
20:O:98:ALA:O	20:O:100:GLU:N	1.60	1.30
20:O:189:ASP:O	20:O:191:ALA:N	1.64	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:1:1:G:OP2	32:6:232:A:H3'	1.12	1.23
20:O:88:VAL:O	20:O:90:HIS:N	1.74	1.21

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	x	259/295 (88%)	220 (85%)	28 (11%)	11 (4%)	3	20
2	F	239/244 (98%)	227 (95%)	8 (3%)	4 (2%)	9	42
3	3	171/306 (56%)	148 (86%)	19 (11%)	4 (2%)	6	34
4	4	216/278 (78%)	197 (91%)	17 (8%)	2 (1%)	17	56
5	5	377/463 (81%)	356 (94%)	19 (5%)	2 (0%)	29	67
6	A	139/291 (48%)	123 (88%)	12 (9%)	4 (3%)	4	28
7	J	64/427 (15%)	61 (95%)	3 (5%)	0	100	100
8	v	124/231 (54%)	117 (94%)	7 (6%)	0	100	100
9	C	341/362 (94%)	304 (89%)	29 (8%)	8 (2%)	6	34
10	e	123/130 (95%)	116 (94%)	7 (6%)	0	100	100
11	E	147/176 (84%)	134 (91%)	13 (9%)	0	100	100
12	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
13	G	155/256 (60%)	142 (92%)	12 (8%)	1 (1%)	25	64
14	h	117/120 (98%)	109 (93%)	5 (4%)	3 (3%)	5	31
15	i	72/100 (72%)	67 (93%)	3 (4%)	2 (3%)	5	29
16	j	69/88 (78%)	68 (99%)	1 (1%)	0	100	100
17	L	106/199 (53%)	94 (89%)	9 (8%)	3 (3%)	5	29
18	M	132/138 (96%)	125 (95%)	6 (4%)	1 (1%)	19	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	N	173/204 (85%)	161 (93%)	12 (7%)	0	100	100
20	O	195/199 (98%)	81 (42%)	49 (25%)	65 (33%)	0	0
21	P	111/184 (60%)	106 (96%)	4 (4%)	1 (1%)	17	56
22	Q	129/186 (69%)	122 (95%)	7 (5%)	0	100	100
23	S	168/172 (98%)	155 (92%)	10 (6%)	3 (2%)	8	41
24	Y	123/127 (97%)	116 (94%)	7 (6%)	0	100	100
27	D	188/505 (37%)	174 (93%)	14 (7%)	0	100	100
28	K	242/376 (64%)	227 (94%)	15 (6%)	0	100	100
29	n	304/605 (50%)	280 (92%)	24 (8%)	0	100	100
30	o	112/220 (51%)	104 (93%)	8 (7%)	0	100	100
31	t	244/322 (76%)	214 (88%)	27 (11%)	3 (1%)	13	49
33	B	139/807 (17%)	125 (90%)	14 (10%)	0	100	100
All	All	5083/8118 (63%)	4571 (90%)	395 (8%)	117 (2%)	9	34

5 of 117 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	x	128	PHE
1	x	222	PRO
1	x	277	GLU
3	3	133	HIS
4	4	85	ALA

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	1	1238/3396 (36%)	279 (22%)	0
26	2	150/158 (94%)	29 (19%)	0
32	6	63/232 (27%)	31 (49%)	0
All	All	1451/3786 (38%)	339 (23%)	0

5 of 339 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	1	3	U
25	1	7	C
25	1	11	A
25	1	18	G
25	1	30	G

There are no RNA pucker outliers to report.

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 monosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
26	2	6
1	x	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	125:U	O3'	126:A	P	7.31
1	2	124:G	O3'	125:U	P	7.17
1	2	110:C	O3'	111:A	P	6.69
1	2	113:U	O3'	114:G	P	4.19

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	128:U	O3'	129:C	P	3.61

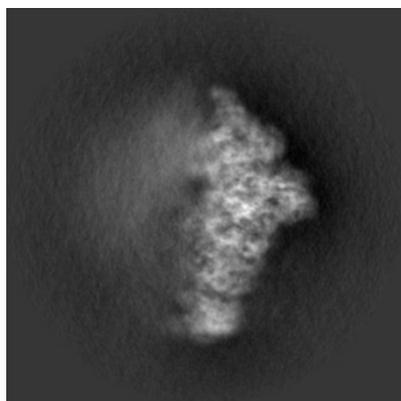
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3888. These allow visual inspection of the internal detail of the map and identification of artifacts.

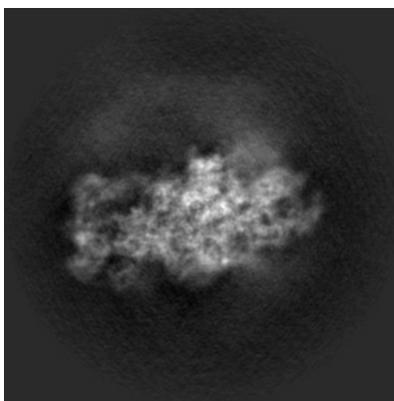
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

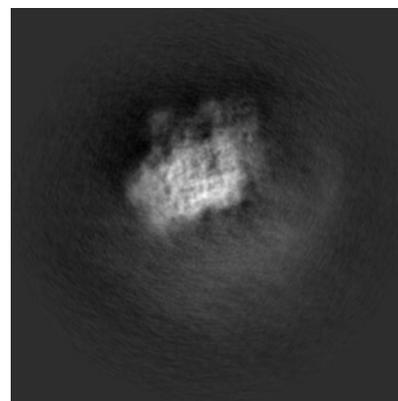
6.1.1 Primary map



X



Y

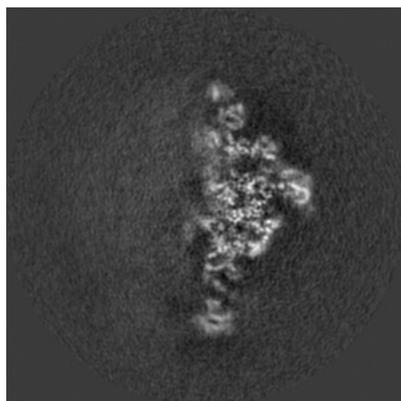


Z

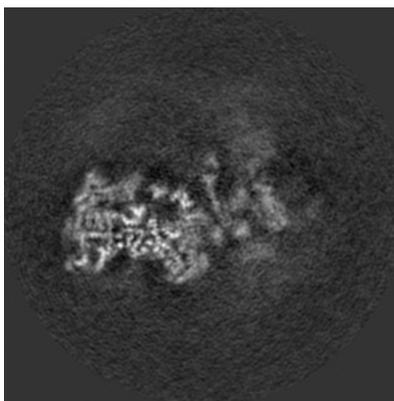
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

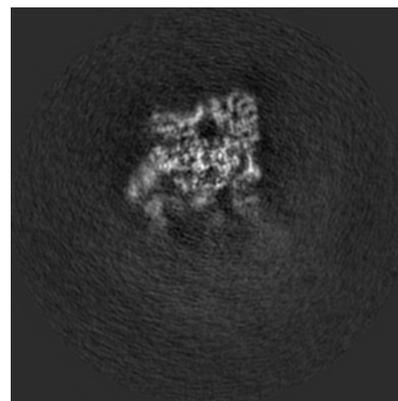
6.2.1 Primary map



X Index: 210



Y Index: 210

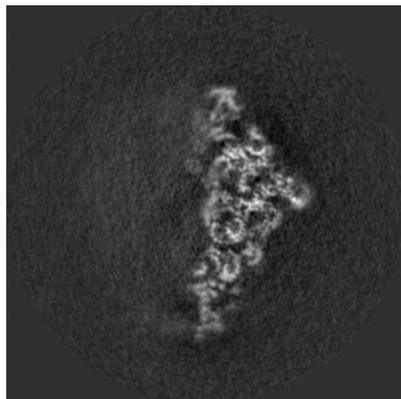


Z Index: 210

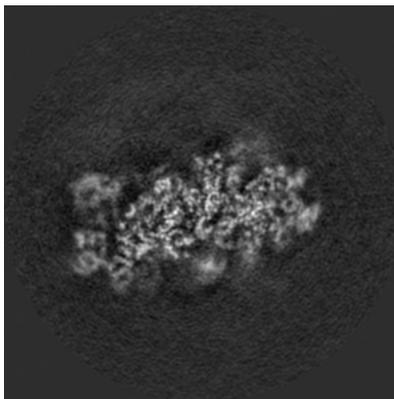
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

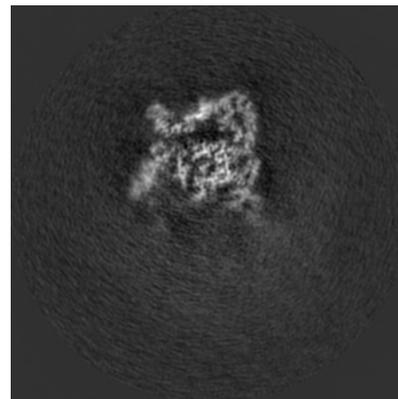
6.3.1 Primary map



X Index: 199



Y Index: 236



Z Index: 215

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.023. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

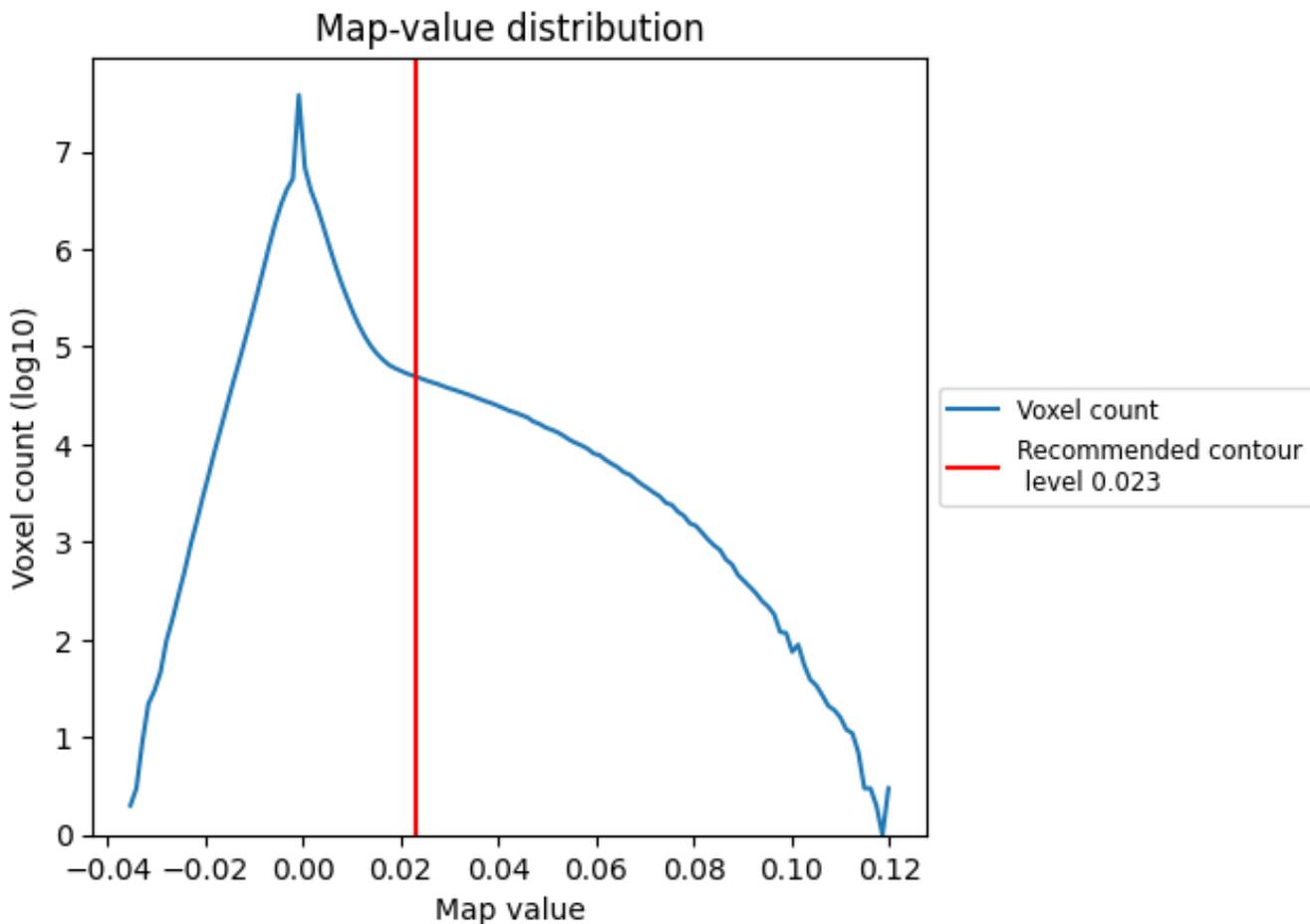
6.5 Mask visualisation

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

7 Map analysis [i](#)

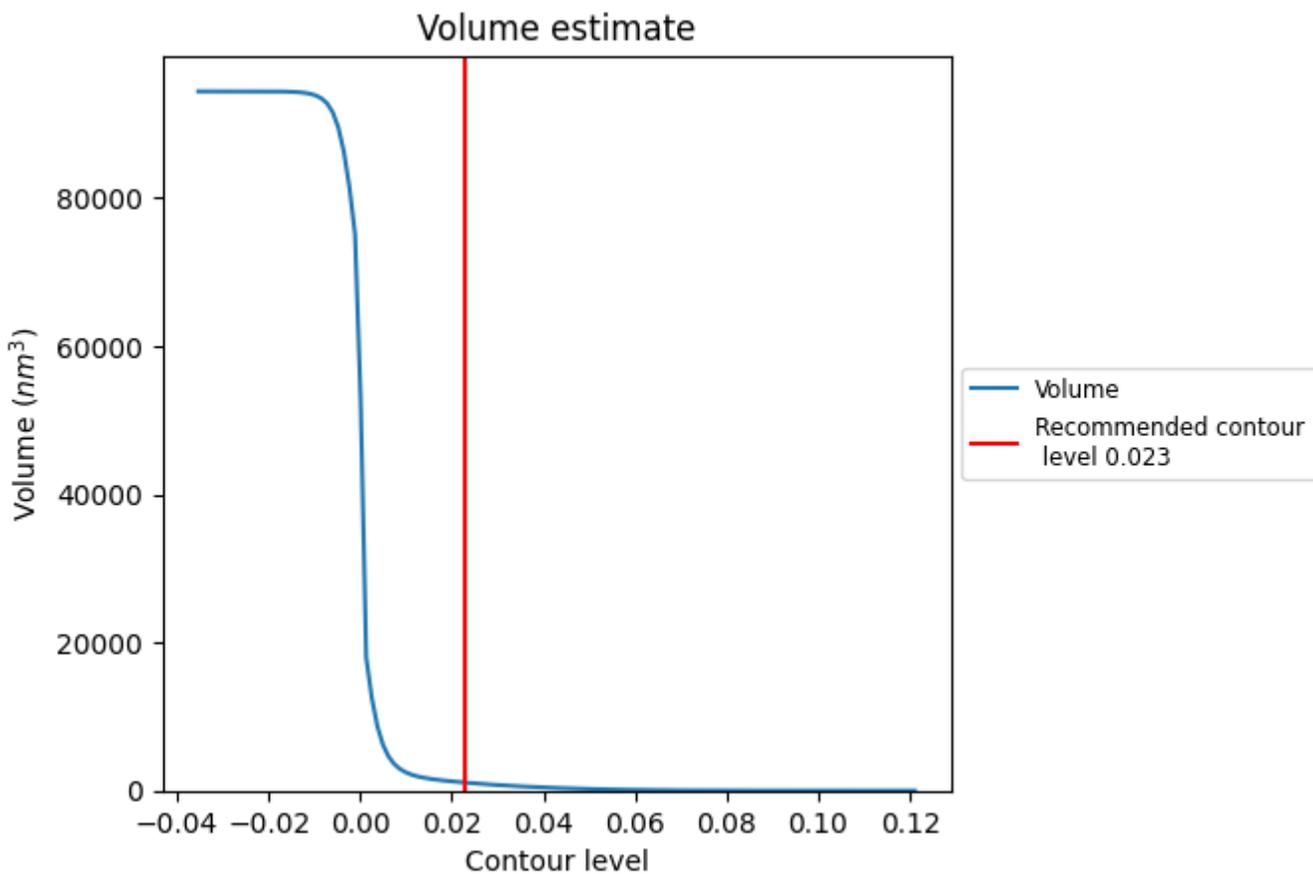
This section contains the results of statistical analysis of the map.

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.

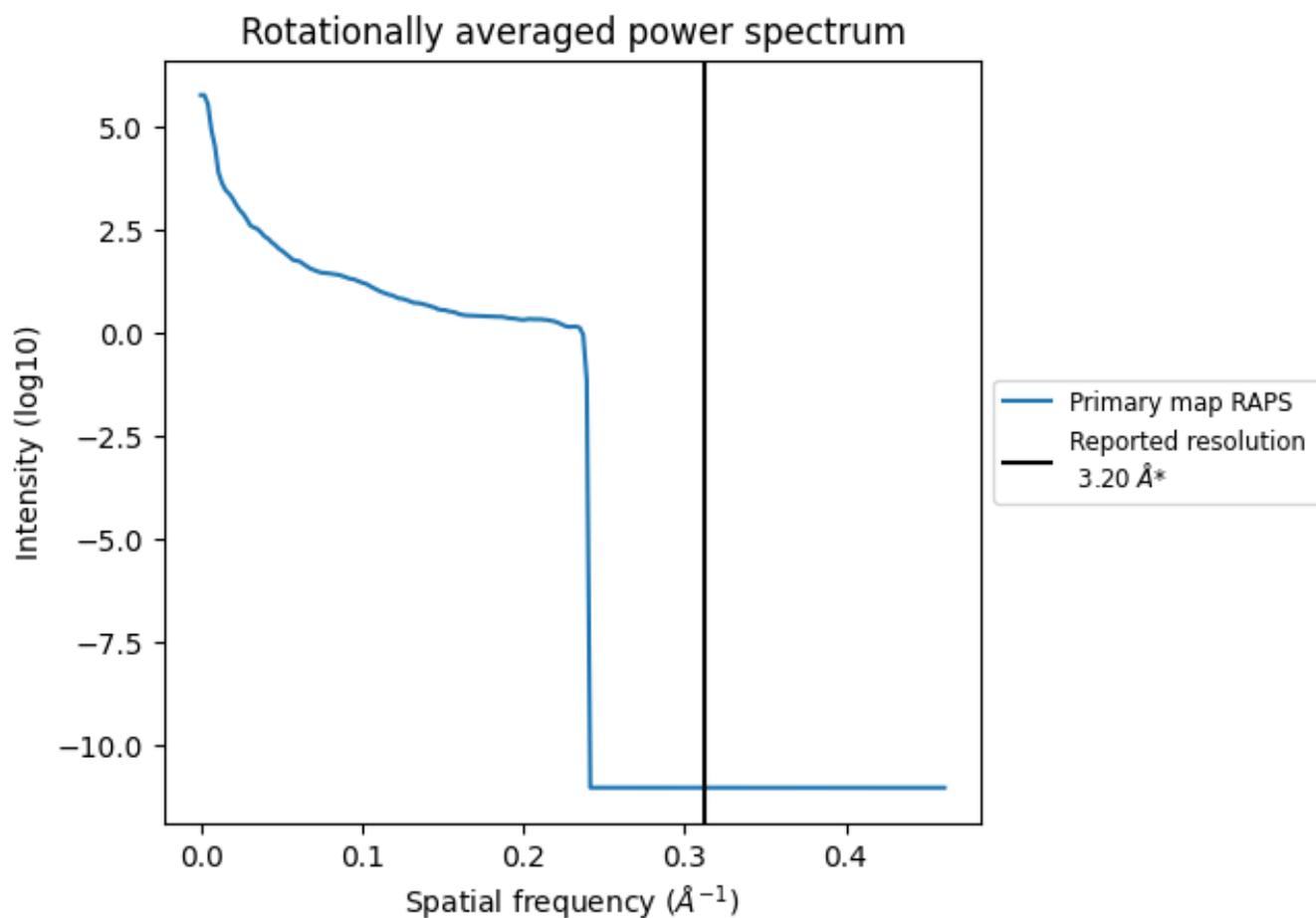
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1078 nm^3 ; this corresponds to an approximate mass of 974 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](#)

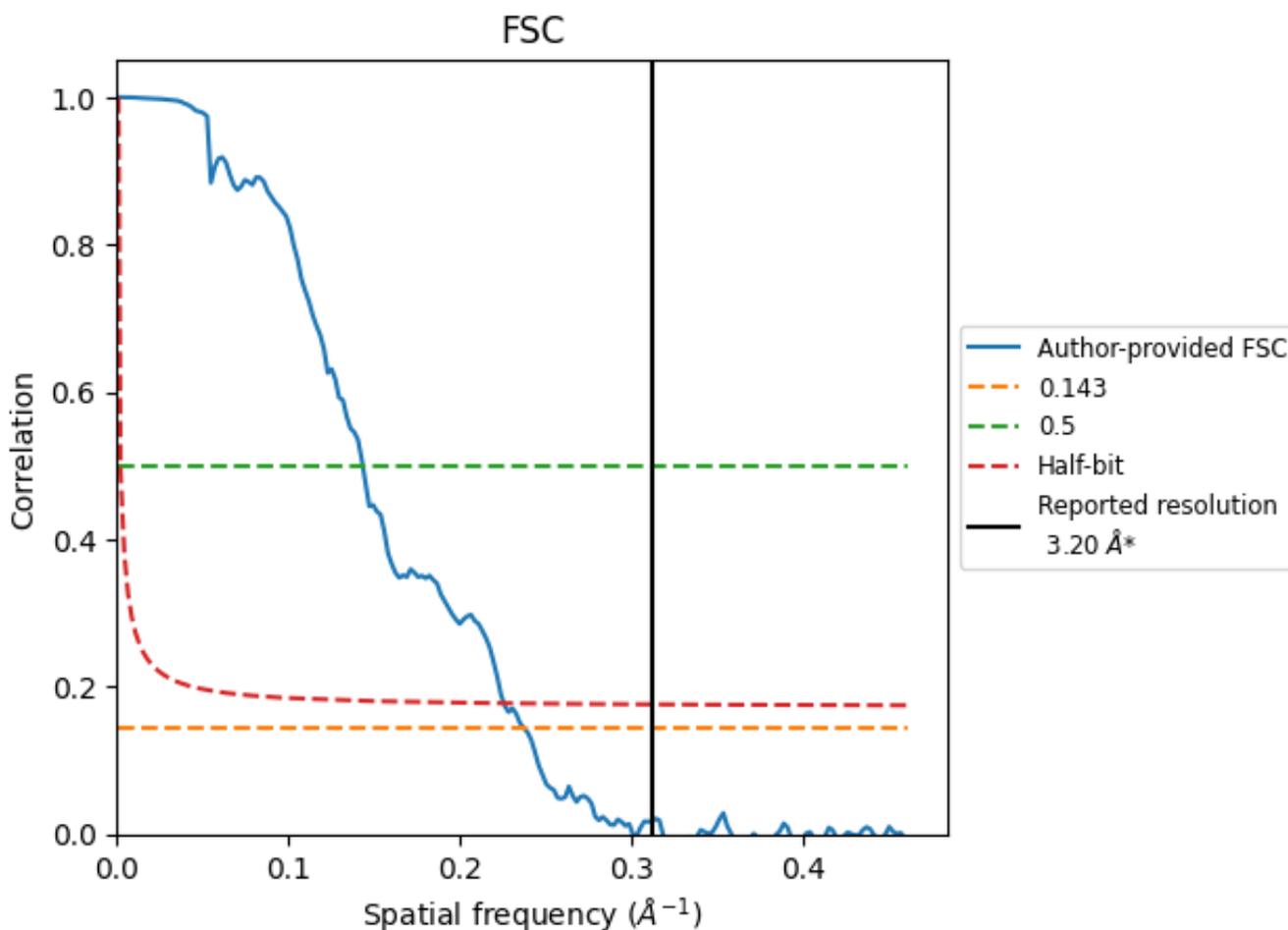


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

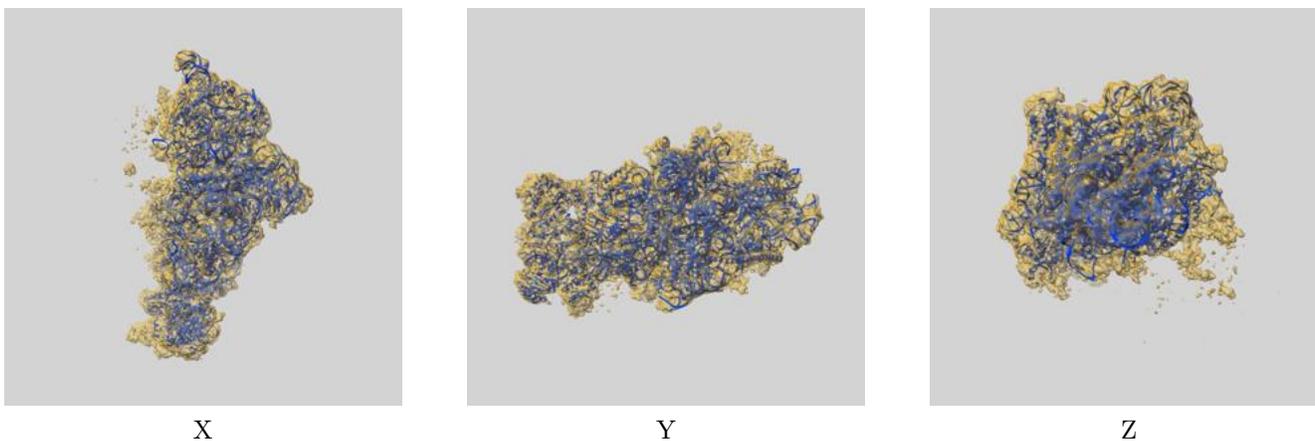
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.21	6.98	4.43
Unmasked-calculated*	-	-	-

*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 4.21 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

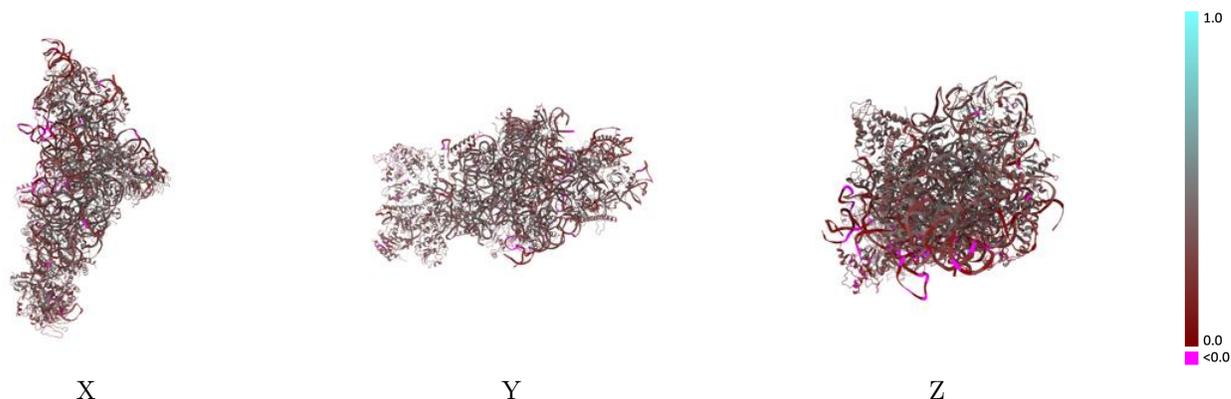
This section contains information regarding the fit between EMDB map EMD-3888 and PDB model 6EM3. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



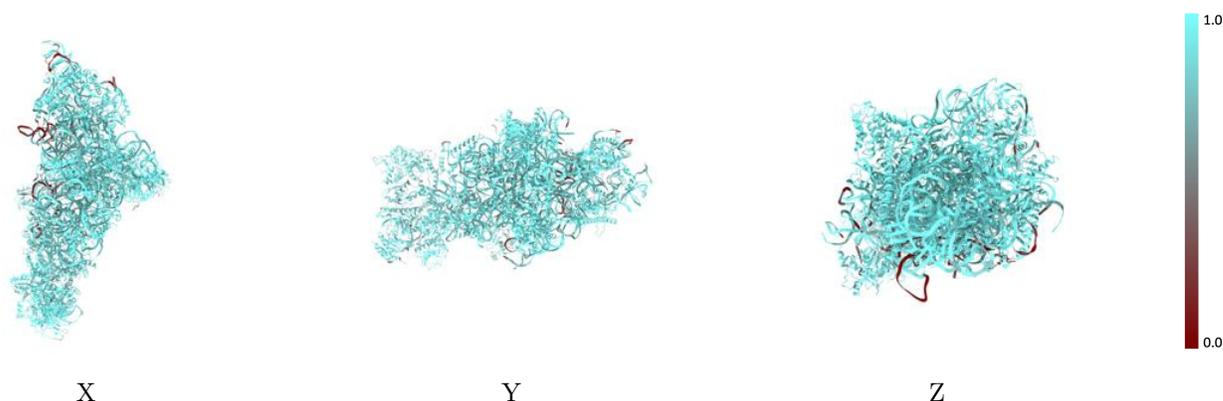
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



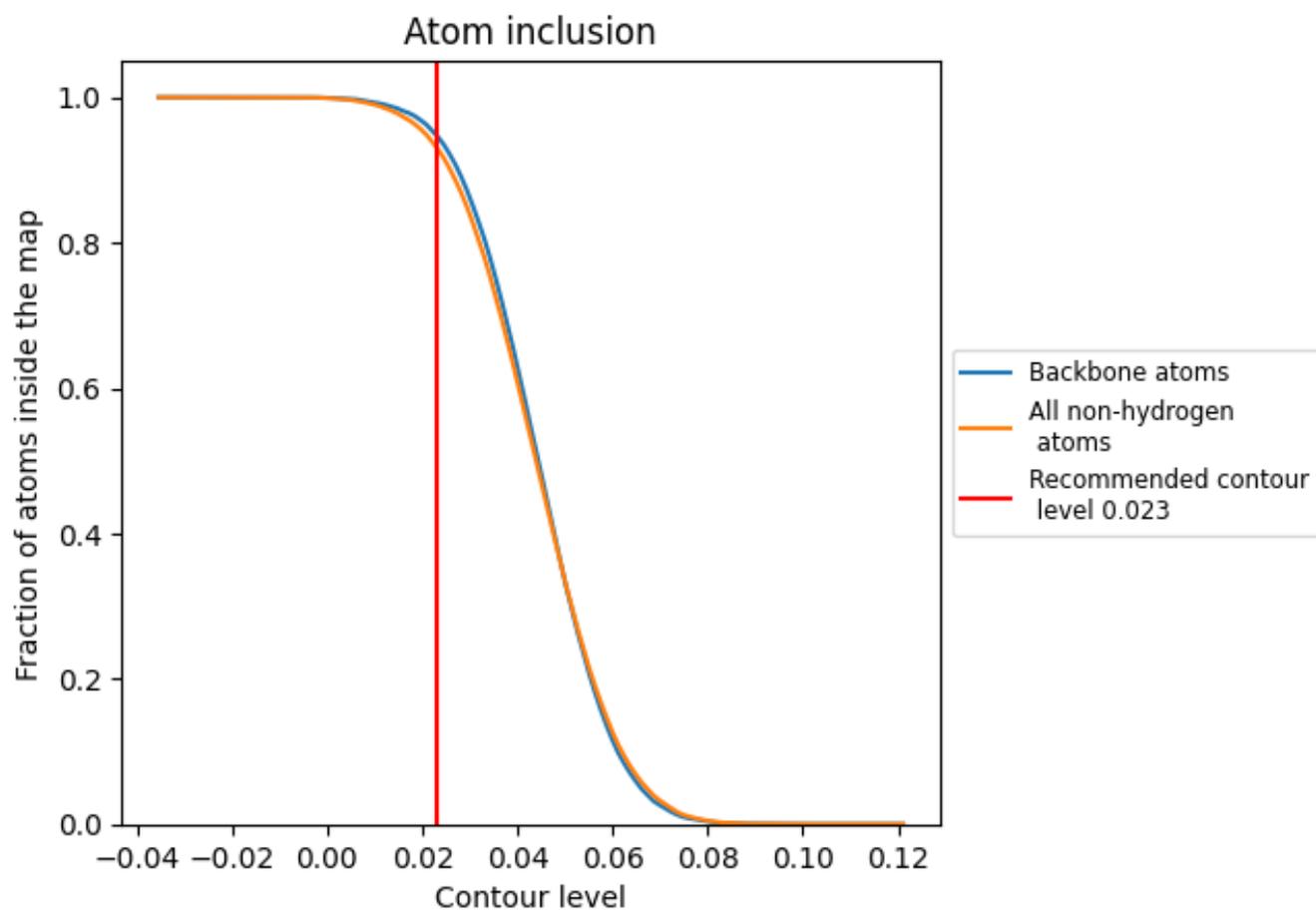
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9312	 0.3080
1	 0.8971	 0.2700
2	 0.9082	 0.2900
3	 0.9884	 0.3870
4	 0.9943	 0.3450
5	 0.9591	 0.3520
6	 0.9436	 0.2590
A	 0.9362	 0.2420
B	 0.9126	 0.3040
C	 0.9257	 0.3770
D	 0.9433	 0.3210
E	 0.9834	 0.3600
F	 0.9927	 0.3650
G	 0.9591	 0.3420
J	 0.8902	 0.1460
K	 0.9400	 0.3000
L	 0.9861	 0.3780
M	 0.9030	 0.3130
N	 0.9393	 0.3640
O	 0.9213	 0.3320
P	 0.9637	 0.3540
Q	 0.9885	 0.3900
S	 0.9647	 0.3150
Y	 0.9940	 0.3950
e	 0.9280	 0.4010
f	 0.9646	 0.3970
h	 0.9685	 0.3500
i	 0.9831	 0.2840
j	 0.9789	 0.3610
n	 0.9599	 0.2860
o	 0.9806	 0.3370
t	 0.9516	 0.2960
v	 0.9519	 0.3460
x	 0.9803	 0.3600

