wwPDB EM Validation Summary Report (i)

Jul 3, 2024 – 05:22 am BST

PDB ID	:	7OHQ
EMDB ID	:	EMD-12905
Title	:	Nog1-TAP associated immature ribosomal particle population C from S. cerevisiae
Authors	:	Milkereit, P.; Poell, G.
Deposited on	:	2021-05-11
Resolution	:	3.10 Å(reported)
Based on initial model	:	3JCT

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 (i) 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 (i)) were used in the production of this report:

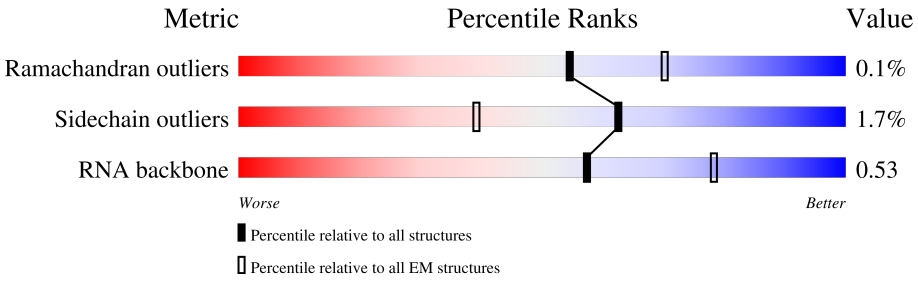
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.10 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
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 <=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	1	3396	70% 20% 10%
2	2	158	82% 18%
3	3	121	84% 16%
4	5	120	25% 41% 58%
5	6	232	18% 10% 72%
6	A	254	83% 17%
7	B	387	98%
8	C	362	98%

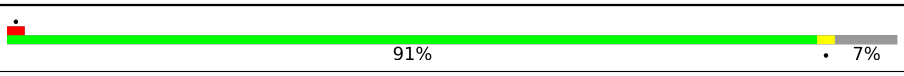
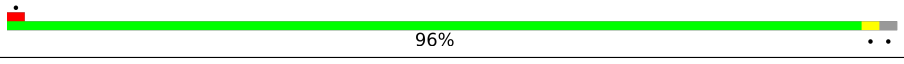
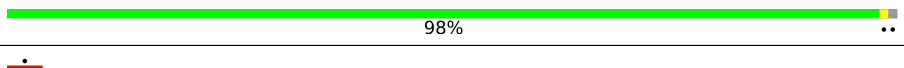
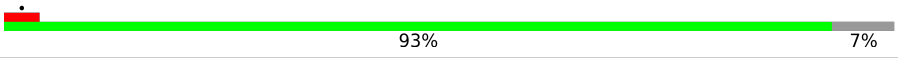
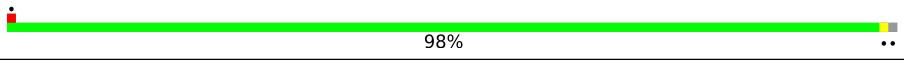
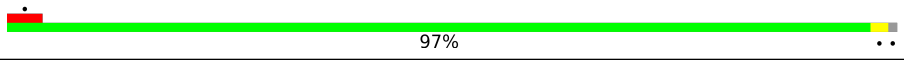
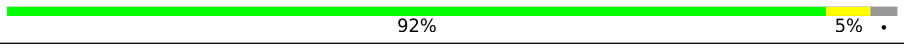
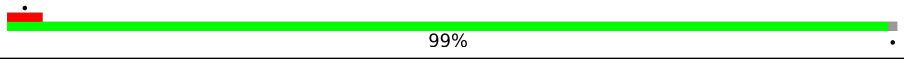
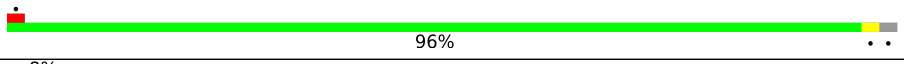
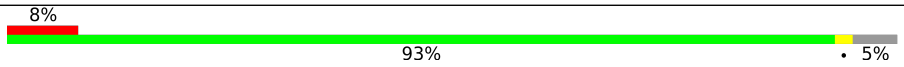
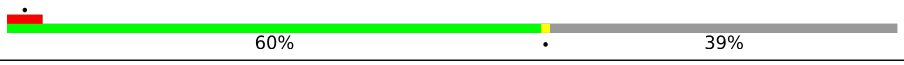
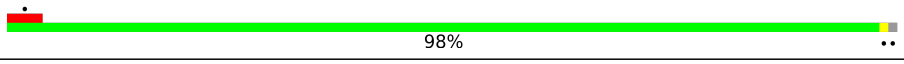
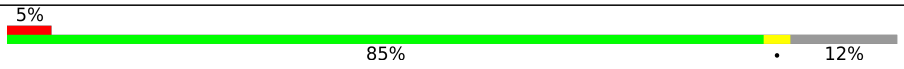
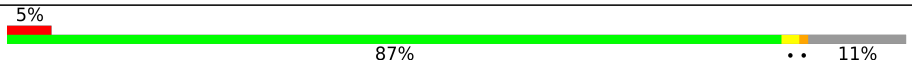
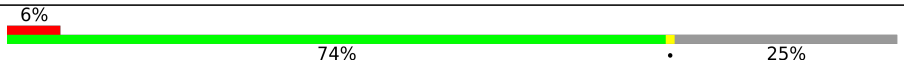
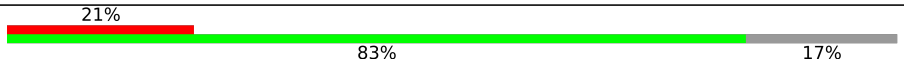
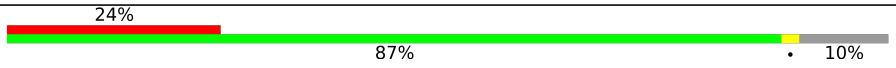
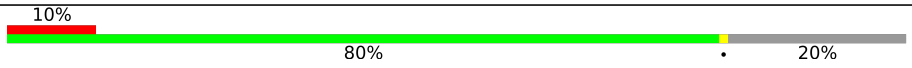
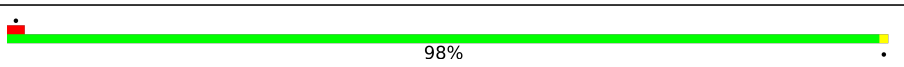
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	D	297	25% 86% 12%
10	E	176	88% 11%
11	F	244	90% 9%
12	G	256	90% 9%
13	H	191	99%
14	J	174	95%
15	K	376	65% 33%
16	L	199	92% 6%
17	M	138	99%
18	N	204	98%
19	O	199	98%
20	P	184	94%
21	Q	186	72% 28%
22	R	189	81% 17%
23	S	172	97%
24	T	160	12% 71% 28%
25	U	121	81% 17%
26	V	137	99%
27	W	236	96%
28	X	142	97%
29	Y	127	98%
30	Z	136	98%
31	a	149	62% 38%
32	b	647	81% 17%
33	c	105	91% 8%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	d	113	
35	e	130	
36	f	107	
37	g	121	
38	h	120	
39	i	100	
40	j	88	
41	k	78	
42	l	51	
43	m	486	
44	n	605	
45	o	220	
46	p	92	
47	q	455	
48	r	261	
49	s	520	
50	t	322	
51	u	199	
52	v	344	
53	w	203	
54	x	515	
55	y	245	
56	z	106	

2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 264865 atoms, of which 115934 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 RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
1	1	3053	98146	29178	32819	11796	21300	3053	0	0

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
2	2	158	5048	1500	1695	586	1109	158	0	0

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
3	3	121	3883	1152	1304	461	845	121	0	0

- Molecule 4 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	5	51	927	280	475	86	85	1	0	0

- Molecule 5 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
5	6	65	2061	614	691	228	463	65	0	0

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	A	212	3314	1021	1684	325	283	1	0	0

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	B	386	Total	C	H	N	O	S	0	0
			6247	1956	3166	584	533	8		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	C	361	Total	C	H	N	O	S	0	0
			5613	1730	2864	522	494	3		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	D	261	Total	C	H	N	O	S	0	0
			4178	1335	2066	372	403	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	E	156	Total	C	H	N	O	S	0	0
			2567	800	1328	222	216	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	F	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	G	233	Total	C	H	N	O	S	0	0
			3726	1159	1909	326	329	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	H	191	Total	C	H	N	O	S	0	0
			3105	963	1587	274	277	4		

- Molecule 14 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	J	169	Total	C	H	N	O	S	0	0
			2737	847	1384	253	249	4		

- Molecule 15 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	K	252	Total	C	H	N	O	S	0	0
			4153	1312	2121	336	381	3		

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	187	Total	C	H	N	O	0	0
			3057	934	1558	307	258		

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	M	137	Total	C	H	N	O	S	0	0
			2214	678	1155	200	179	2		

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	N	203	Total	C	H	N	O	S	0	0
			3500	1077	1780	361	281	1		

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	O	197	Total	C	H	N	O	S	0	0
			3215	1003	1660	289	262	1		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	177	Total	C	H	N	O	0	0
			2845	871	1443	280	251		

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	Q	134	Total	C	H	N	O	S	0	0
			2151	659	1116	196	179	1		

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	156	Total	C	H	N	O	0	0
			2601	781	1343	265	212		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
23	S	171	Total	C	H	N	O	S	0	0
			2913	925	1476	266	243	3		

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	T	116	Total	C	H	N	O	S	0	0
			1902	584	978	176	161	3		

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	101	Total	C	H	N	O	0	0
			1617	519	816	131	151		

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	V	136	Total	C	H	N	O	S	0	0
			2052	628	1049	189	179	7		

- Molecule 27 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	W	234	Total	C	H	N	O	S	0	0
			3806	1194	1921	323	362	6		

- Molecule 28 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	X	141	Total	C	H	N	O	S	0	0
			2288	705	1188	196	197	2		

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	126	Total	C	H	N	O	0	0
			2075	625	1082	192	176		

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	135	Total	C	H	N	O	0	0
			2248	710	1156	202	180		

- Molecule 31 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	93	Total	C	H	N	O	S	0	0
			1512	479	777	130	125	1		

- Molecule 32 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	537	Total	C	H	N	O	S	0	0
			8784	2760	4427	763	811	23		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	c	97	Total	C	H	N	O	S	0	0
			1541	479	798	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	d	105	Total	C	H	N	O	S	0	0
			1761	544	905	163	148	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	e	127	Total	C	H	N	O	S	0	0
			2112	647	1092	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	g	112	Total	C	H	N	O	S	0	0
			1831	546	950	179	152	4		

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	h	119	Total	C	H	N	O	S	0	0
			2048	615	1079	186	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	i	99	Total	C	H	N	O	S	0	0
			1621	481	850	156	132	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	j	85	Total	C	H	N	O	S	0	0
			1348	408	678	146	111	5		

- Molecule 41 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	77	Total	C	H	N	O	0	0
			1295	391	683	115	106		

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	l	50	Total	C	H	N	O	S	0	0
			912	272	476	97	65	2		

- Molecule 43 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	m	461	Total	C	H	N	O	S	0	0
			7508	2350	3788	675	686	9		

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	n	371	Total	C	H	N	O	S	0	0
			6139	1963	3109	523	534	10		

- Molecule 45 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	o	133	Total	C	H	N	O	S	0	0
			2267	716	1160	198	189	4		

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	p	91	Total	C	H	N	O	S	0	0
			1434	429	740	138	121	6		

- Molecule 47 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	q	147	Total	C	H	N	O	S	0	0
			2501	778	1268	222	232	1		

- Molecule 48 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	r	230	Total	C	H	N	O	S	0	0
			3827	1177	1967	352	324	7		

- Molecule 49 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	s	53	Total	C	H	N	O	S	0	0
			935	274	499	90	70	2		

- Molecule 50 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	t	287	Total	C	H	N	O	S	0	0
			4762	1459	2456	427	417	3		

- Molecule 51 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	u	150	Total	C	H	N	O	S	0	0
			2582	793	1317	253	210	9		

- Molecule 52 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	287	Total	C	H	N	O	S	0	0
			4718	1482	2400	408	412	16		

- Molecule 53 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	w	182	Total	C	H	N	O	S	0	0
			2960	911	1512	261	271	5		

- Molecule 54 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	x	413	Total	C	H	N	O	S	0	0
			6438	2030	3207	583	598	20		

- Molecule 55 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	y	244	Total	C	H	N	O	S	0	0
			3685	1146	1836	319	377	7		

- Molecule 56 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	46	Total	C	H	N	O	0	0
			772	228	402	75	67		

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	b	1	Total	Mg	0
			1	1	
57	m	1	Total	Mg	0
			1	1	

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

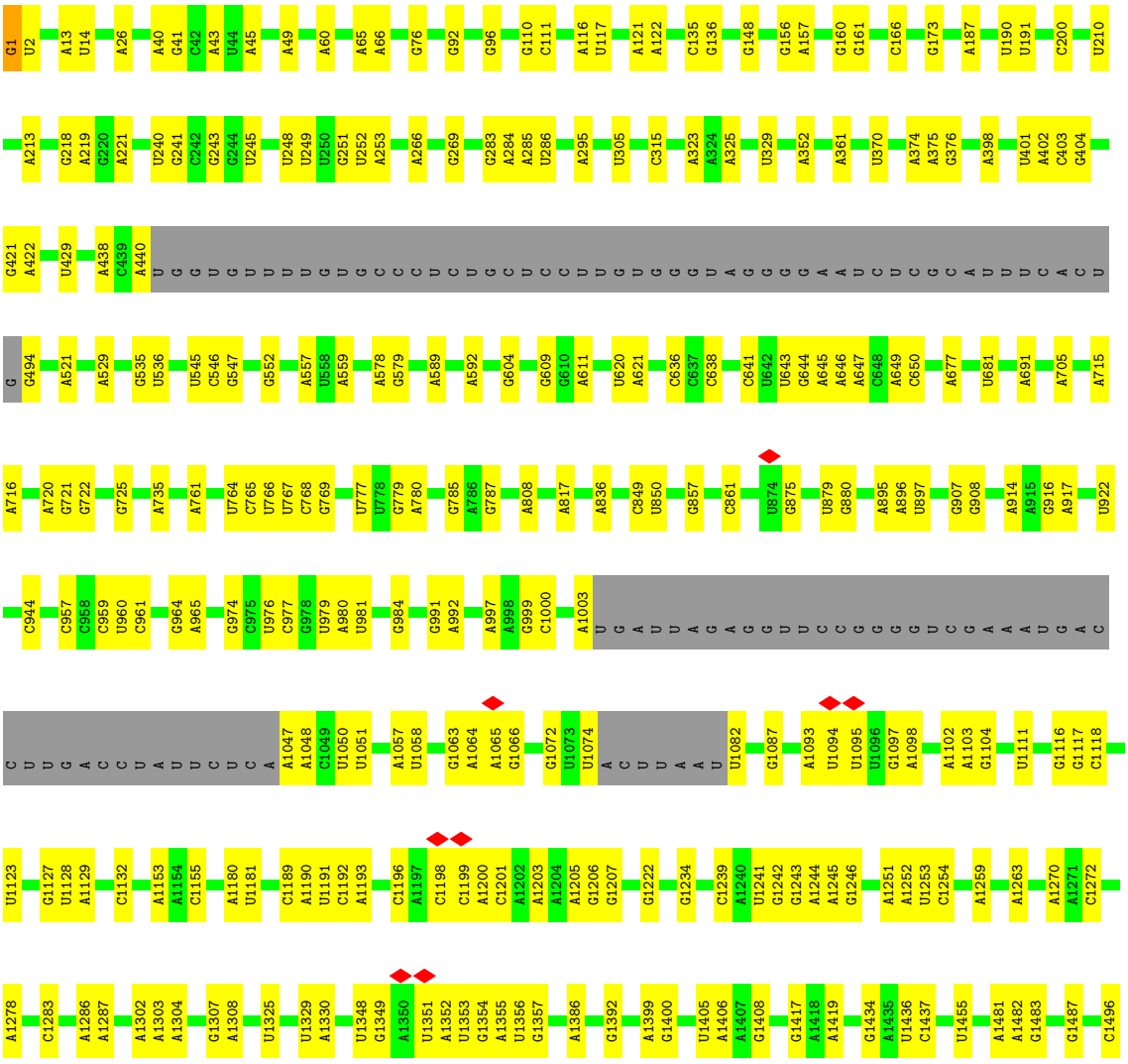
Mol	Chain	Residues	Atoms		AltConf
58	j	1	Total	Zn	0
			1	1	
58	p	1	Total	Zn	0
			1	1	
58	u	1	Total	Zn	0
			1	1	

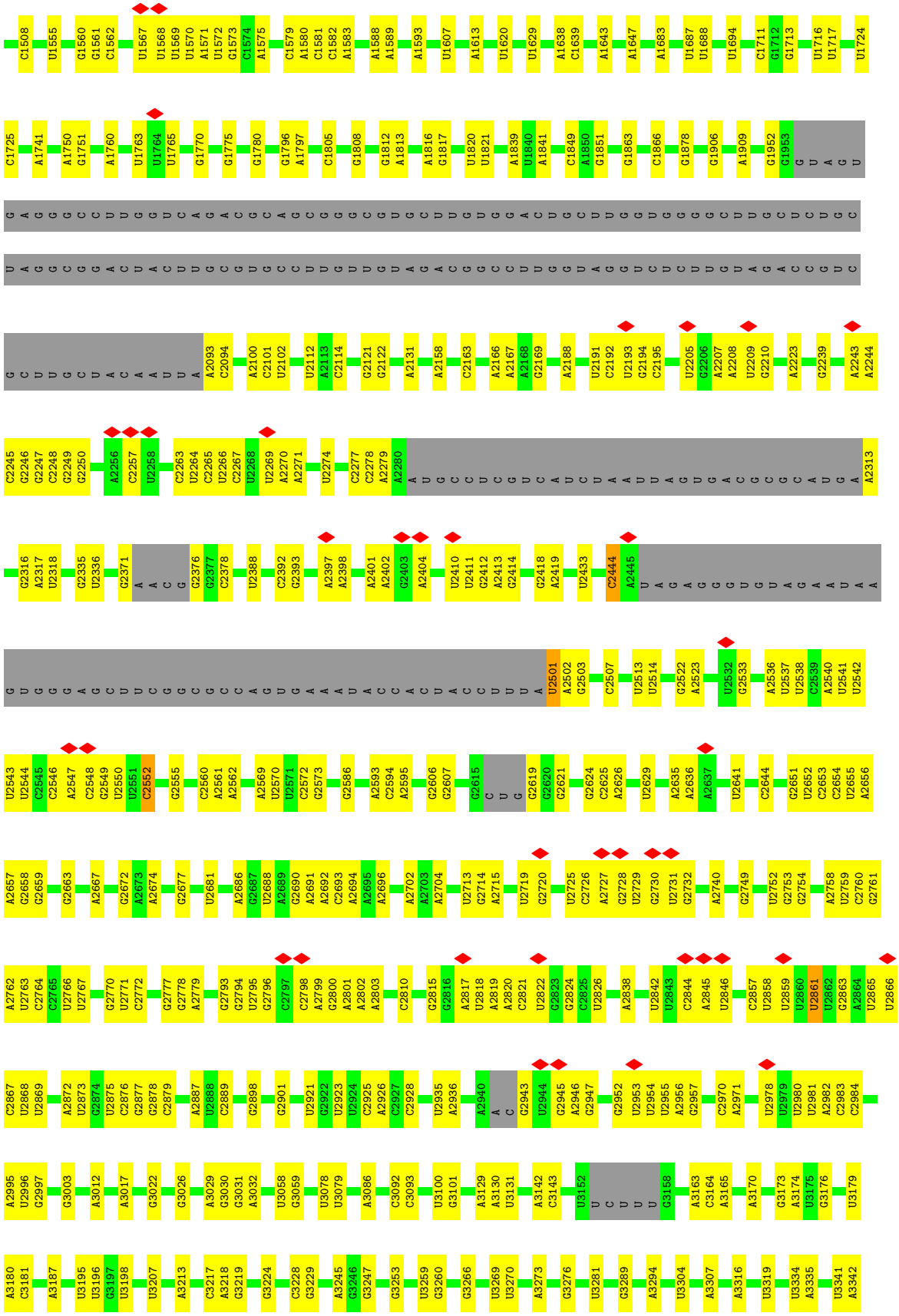
3 Residue-property plots (i)

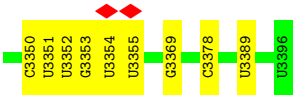
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 25S rRNA

Chain 1:

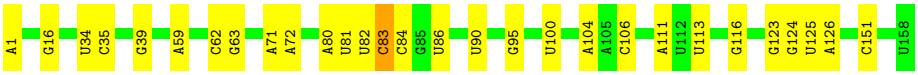






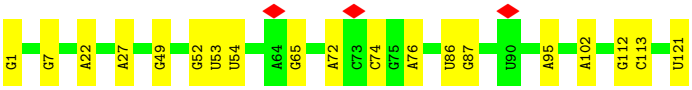
• Molecule 2: 5.8S rRNA

Chain 2:



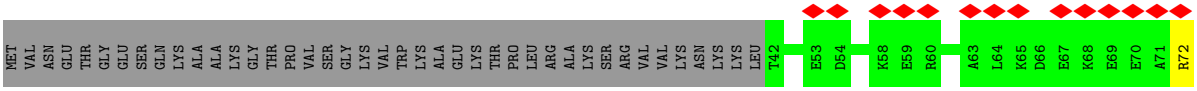
• Molecule 3: 5S rRNA

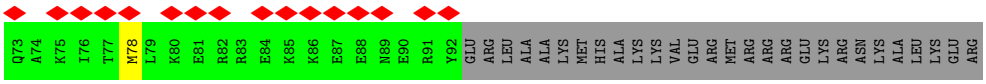
Chain 3:



• Molecule 4: rRNA-processing protein CGR1

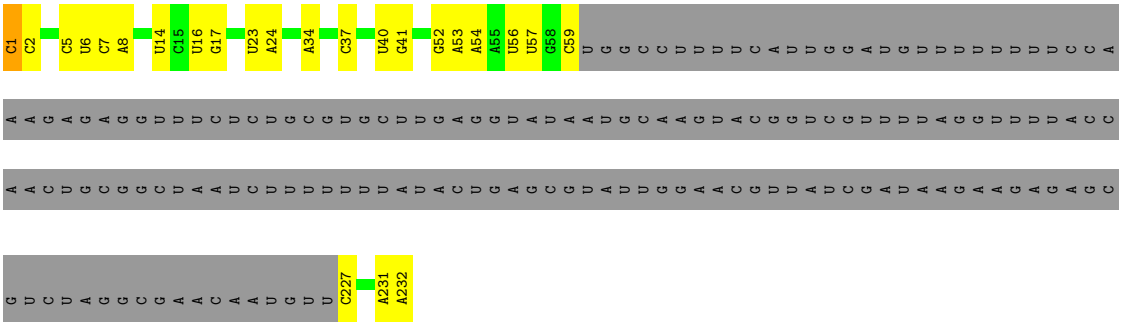
Chain 5:





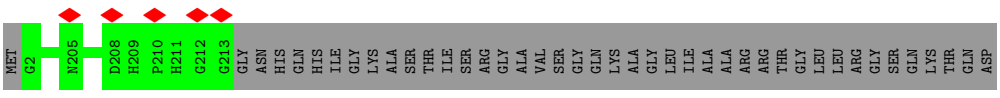
• Molecule 5: ITS2

Chain 6:



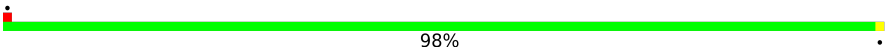
• Molecule 6: 60S ribosomal protein L2-A

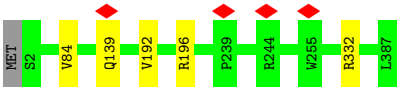
Chain A:



• Molecule 7: 60S ribosomal protein L3

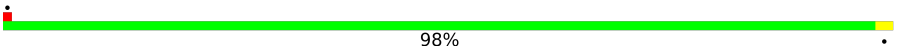
Chain B:

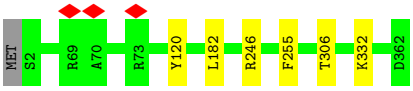




• Molecule 8: 60S ribosomal protein L4-A

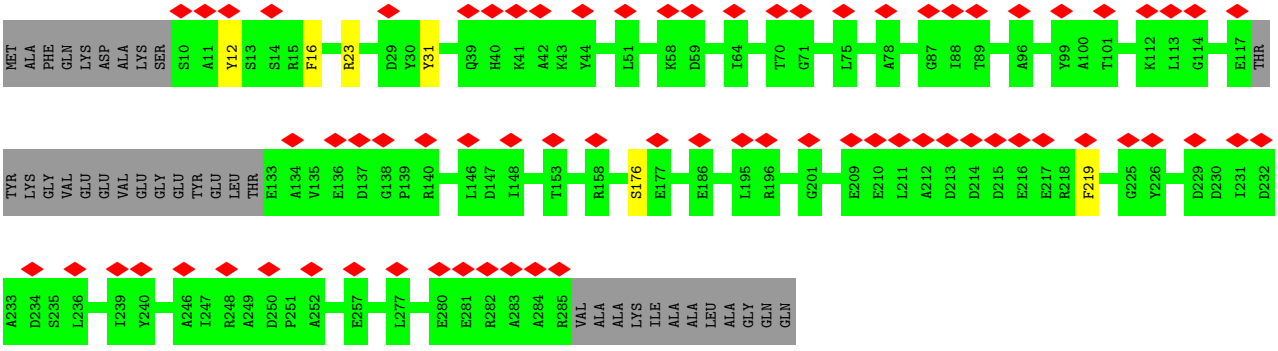
Chain C:





• Molecule 9: 60S ribosomal protein L5

Chain D:



• Molecule 10: 60S ribosomal protein L6-A

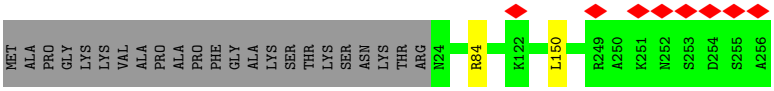
Chain E:

• Molecule 11: 60S ribosomal protein L7-A

Chain F:

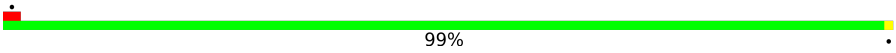
• Molecule 12: 60S ribosomal protein L8-A

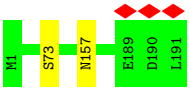
Chain G:



• Molecule 13: 60S ribosomal protein L9-A

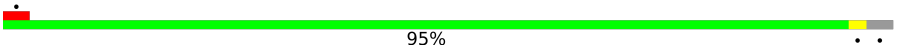
Chain H:

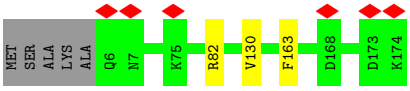




• Molecule 14: 60S ribosomal protein L11-A

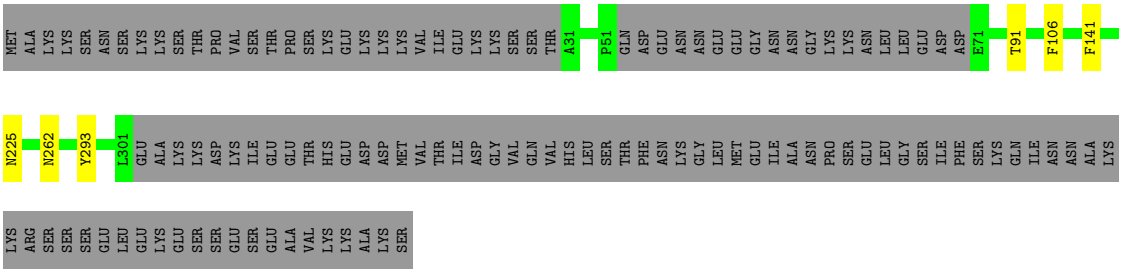
Chain J:





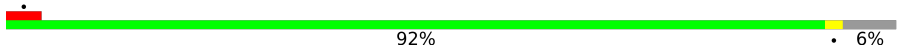
• Molecule 15: Proteasome-interacting protein CIC1

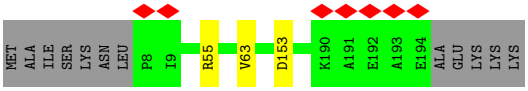
Chain K:



• Molecule 16: 60S ribosomal protein L13-A

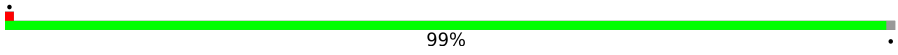
Chain L:





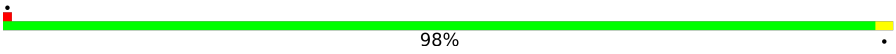
• Molecule 17: 60S ribosomal protein L14-A

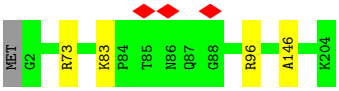
Chain M:



• Molecule 18: 60S ribosomal protein L15-A

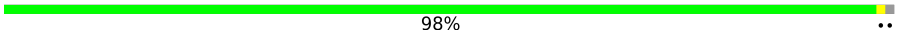
Chain N:

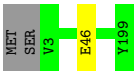




• Molecule 19: 60S ribosomal protein L16-A

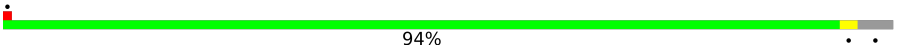
Chain O:

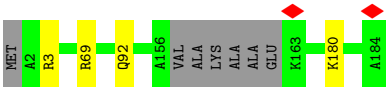




• Molecule 20: 60S ribosomal protein L17-A

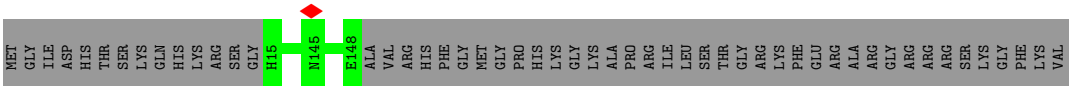
Chain P:





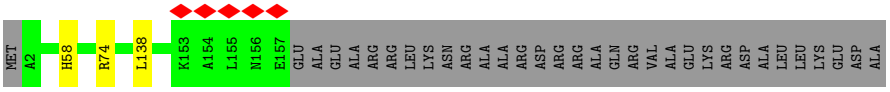
• Molecule 21: 60S ribosomal protein L18-A

Chain Q:



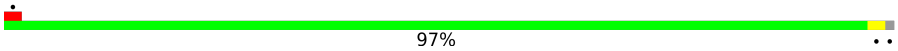
• Molecule 22: 60S ribosomal protein L19-A

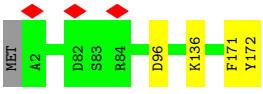
Chain R:



• Molecule 23: 60S ribosomal protein L20-A

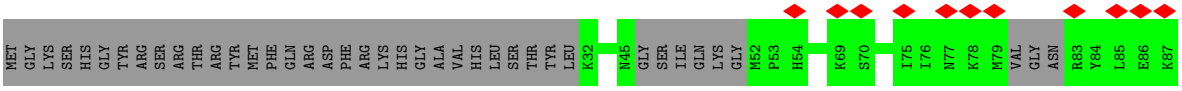
Chain S:





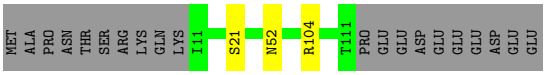
• Molecule 24: 60S ribosomal protein L21-A

Chain T:



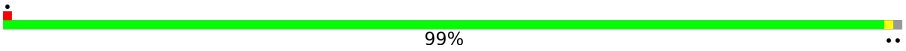
• Molecule 25: 60S ribosomal protein L22-A

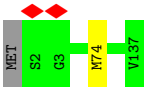
Chain U:



• Molecule 26: 60S ribosomal protein L23-A

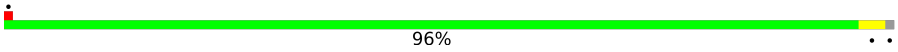
Chain V:





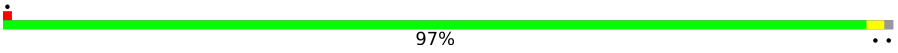
• Molecule 27: Ribosome assembly factor MRT4

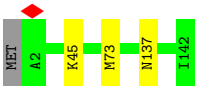
Chain W:



• Molecule 28: 60S ribosomal protein L25

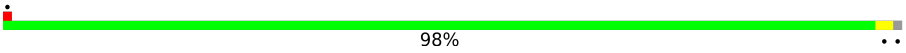
Chain X:





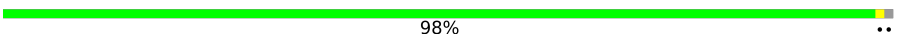
• Molecule 29: 60S ribosomal protein L26-A

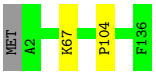
Chain Y:



• Molecule 30: 60S ribosomal protein L27-A

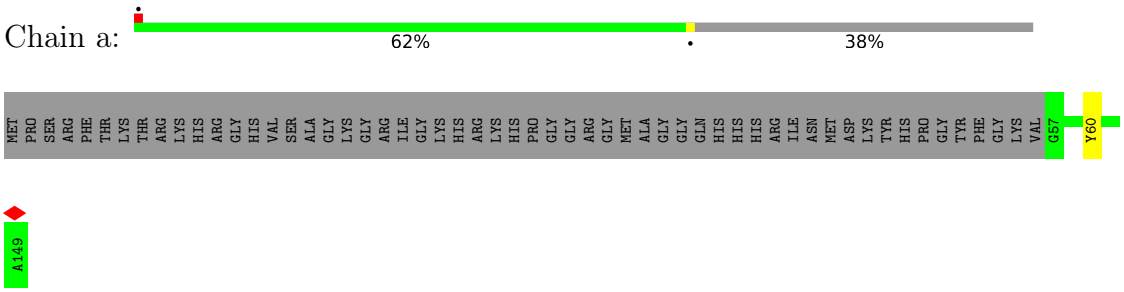
Chain Z:





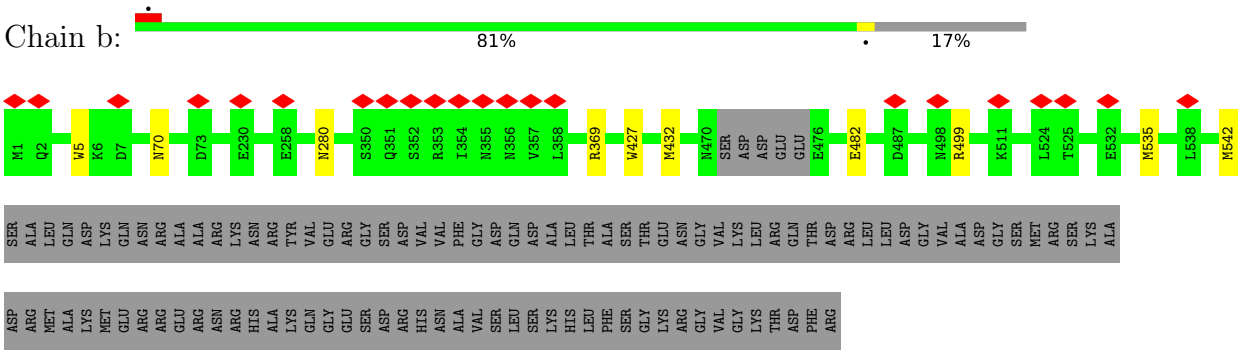
• Molecule 31: 60S ribosomal protein L28

Chain a:



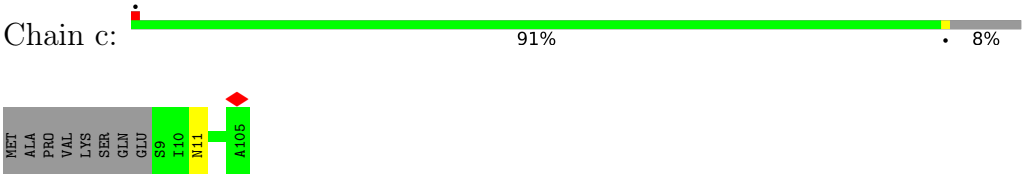
• Molecule 32: Nucleolar GTP-binding protein 1

Chain b:



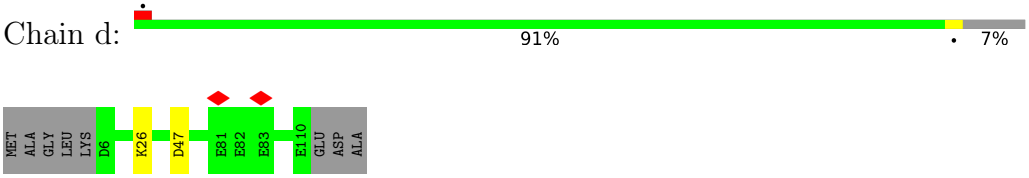
• Molecule 33: 60S ribosomal protein L30

Chain c:



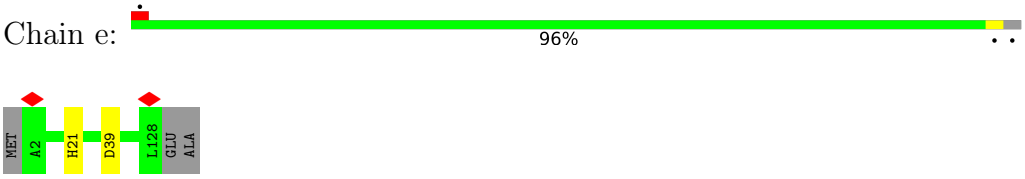
• Molecule 34: 60S ribosomal protein L31-A

Chain d:



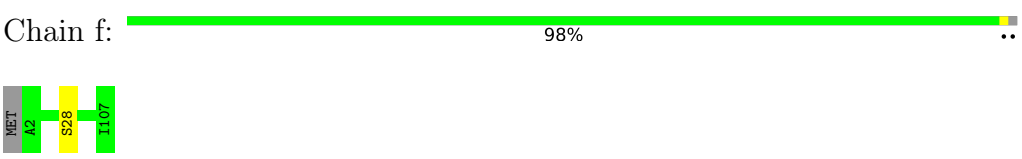
• Molecule 35: 60S ribosomal protein L32

Chain e:



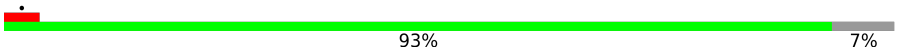
• Molecule 36: 60S ribosomal protein L33-A

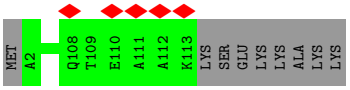
Chain f:



• Molecule 37: 60S ribosomal protein L34-A

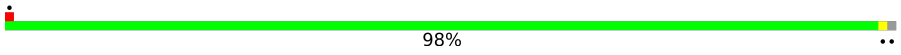
Chain g:

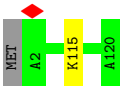




• Molecule 38: 60S ribosomal protein L35-A

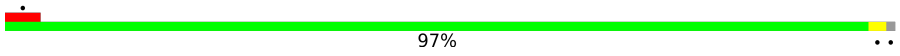
Chain h:

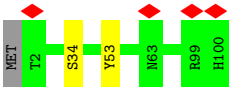




• Molecule 39: 60S ribosomal protein L36-A

Chain i:



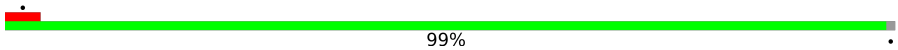


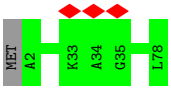
• Molecule 40: 60S ribosomal protein L37-A

Chain j:

• Molecule 41: 60S ribosomal protein L38

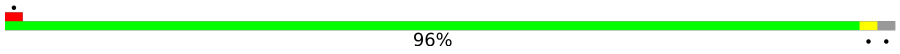
Chain k:

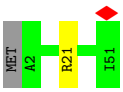




• Molecule 42: 60S ribosomal protein L39

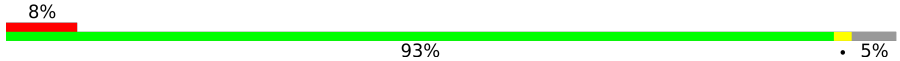
Chain l:

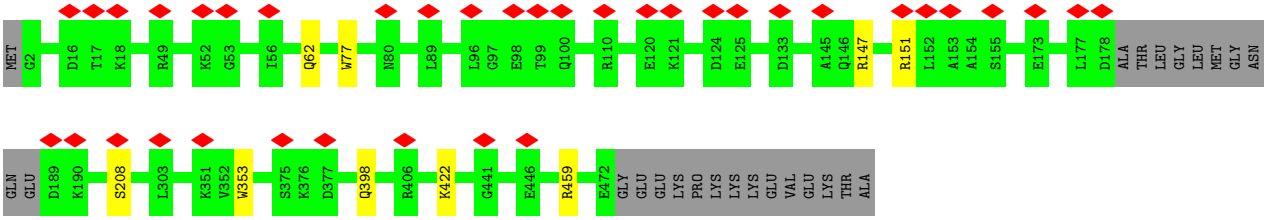




• Molecule 43: Nucleolar GTP-binding protein 2

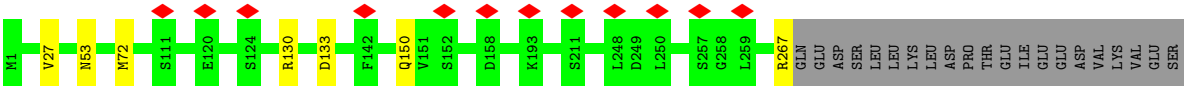
Chain m:

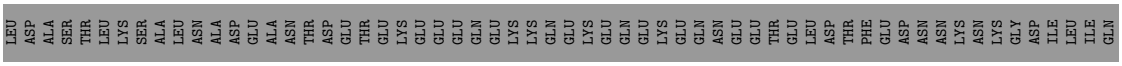


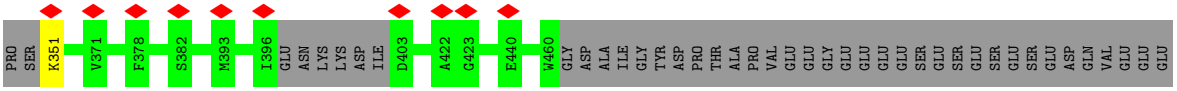


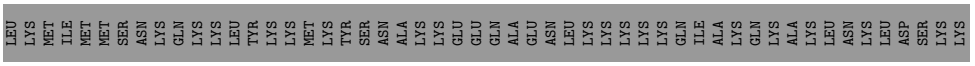
• Molecule 44: Pescadillo homolog

Chain n:







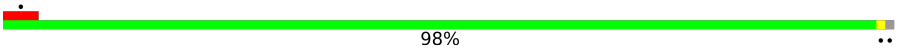


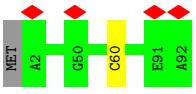
• Molecule 45: Ribosome biogenesis protein 15

Chain o:

• Molecule 46: 60S ribosomal protein L43-A

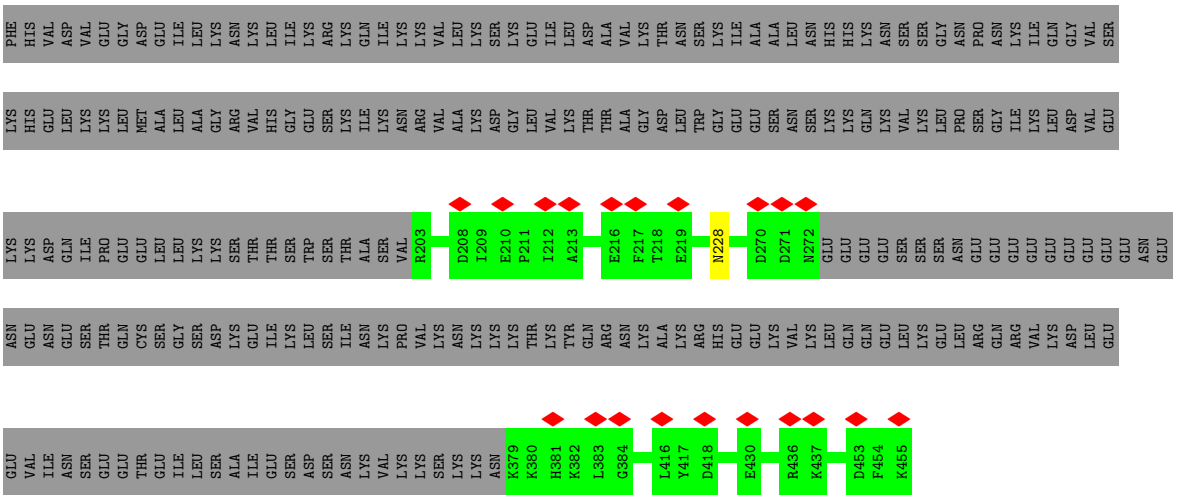
Chain p:



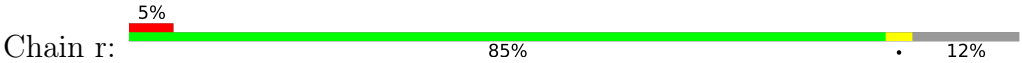


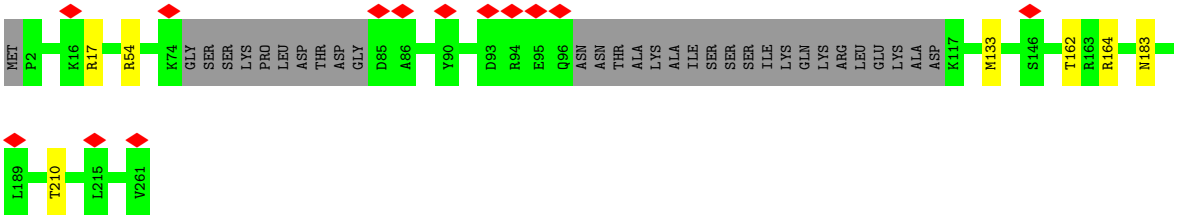
• Molecule 47: Ribosome biogenesis protein NOP53

Chain q:

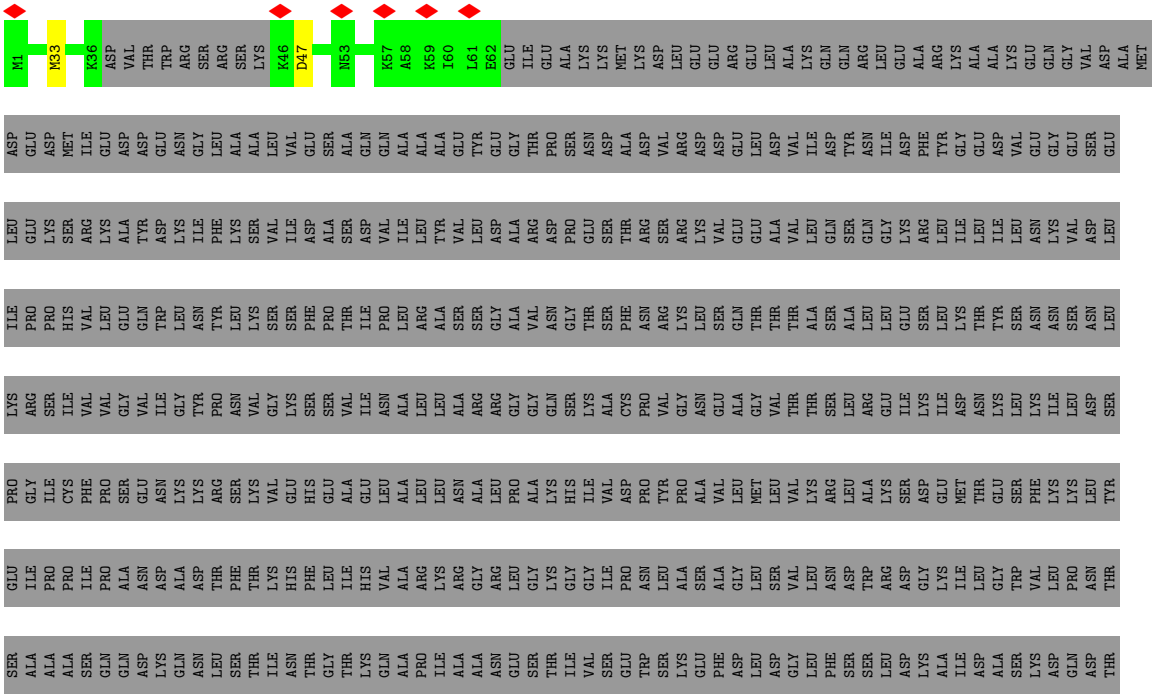


• Molecule 48: Ribosome biogenesis protein NSA2



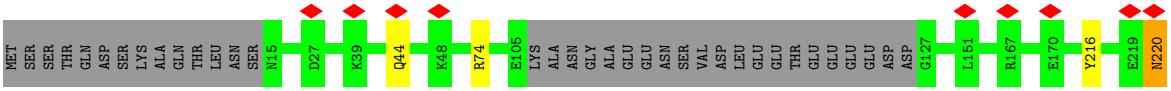


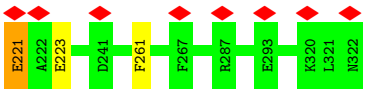
• Molecule 49: Nuclear GTP-binding protein NUG1



• Molecule 50: Ribosome biogenesis protein RLP7

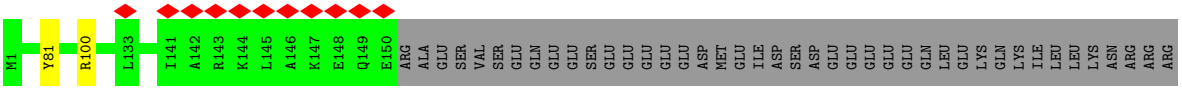
Chain t:





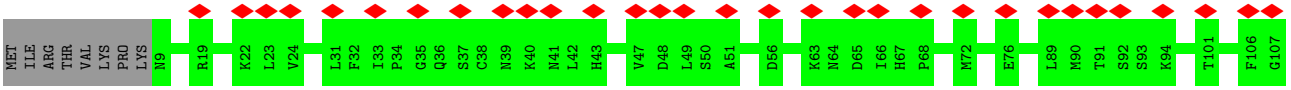
• Molecule 51: Ribosome biogenesis protein RLP24

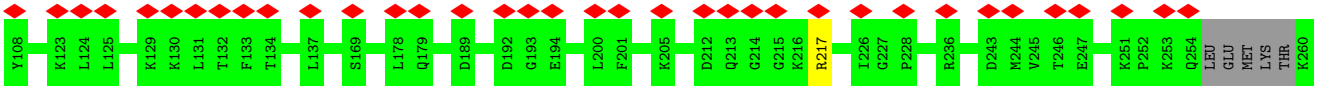
Chain u:

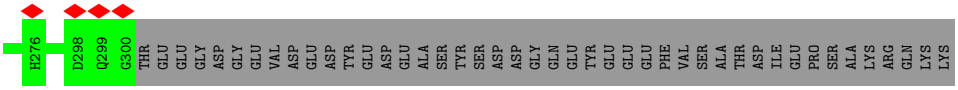


• Molecule 52: Ribosome biogenesis protein RPF2

Chain v:

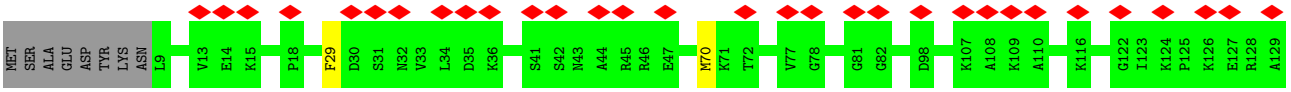


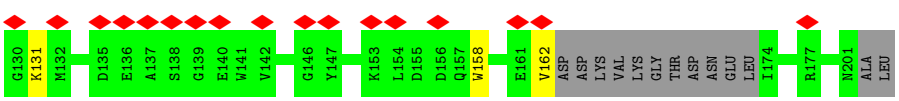




• Molecule 53: Regulator of ribosome biosynthesis

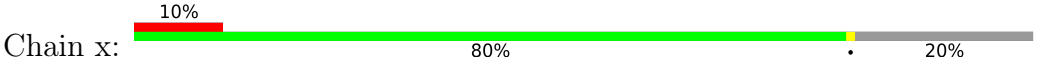
Chain w:

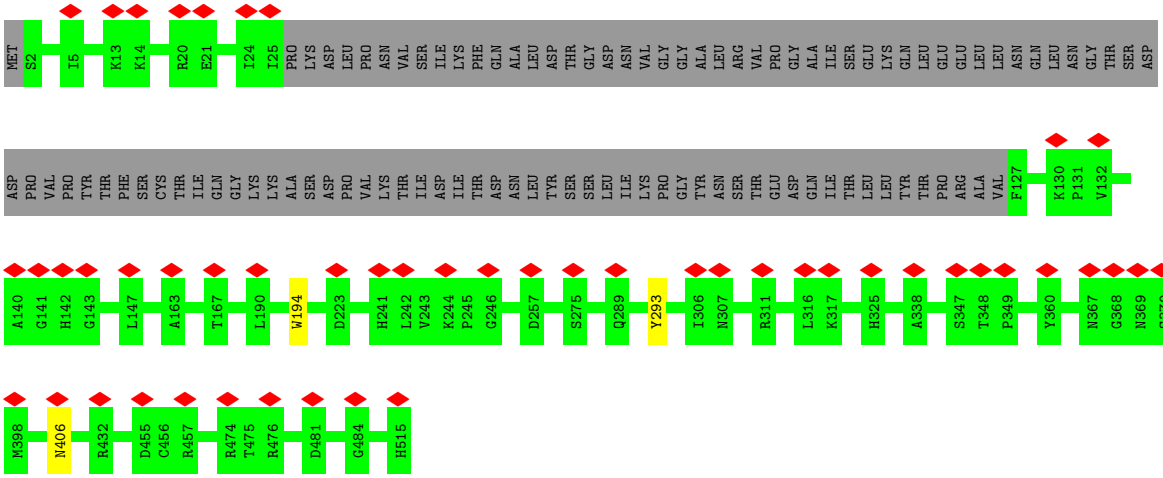




• Molecule 54: Ribosome assembly protein 4

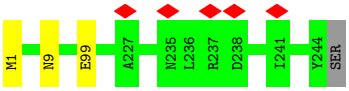
Chain x:





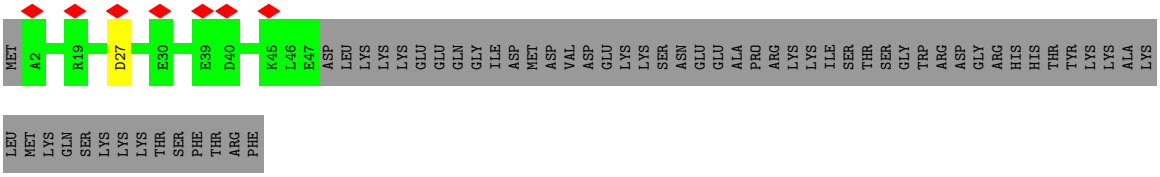
• Molecule 55: Eukaryotic translation initiation factor 6

Chain y:



• Molecule 56: UPF0642 protein YBL028C

Chain z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34162	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 ($e^-/Å^2$)	84.67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.165	Depositor
Minimum map value	-0.045	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.021	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	1	0.16	0/73123	0.74	30/113993 (0.0%)
2	2	0.16	0/3746	0.76	2/5832 (0.0%)
3	3	0.15	0/2883	0.75	1/4491 (0.0%)
4	5	0.25	0/455	0.35	0/596
5	6	0.17	0/1527	0.77	3/2371 (0.1%)
6	A	0.24	0/1662	0.44	0/2236
7	B	0.24	0/3152	0.43	0/4239
8	C	0.24	0/2801	0.42	0/3792
9	D	0.24	0/2158	0.40	0/2910
10	E	0.25	0/1260	0.42	0/1694
11	F	0.25	0/1821	0.41	0/2451
12	G	0.25	0/1849	0.42	0/2495
13	H	0.24	0/1539	0.43	0/2073
14	J	0.24	0/1374	0.43	0/1842
15	K	0.24	0/2066	0.42	0/2789
16	L	0.24	0/1524	0.43	0/2046
17	M	0.23	0/1074	0.41	0/1446
18	N	0.26	0/1757	0.43	0/2354
19	O	0.25	0/1585	0.39	0/2128
20	P	0.24	0/1424	0.42	0/1911
21	Q	0.25	0/1050	0.41	0/1419
22	R	0.23	0/1275	0.39	0/1702
23	S	0.24	0/1473	0.42	0/1980
24	T	0.25	0/937	0.44	0/1256
25	U	0.25	0/817	0.42	0/1108
26	V	0.25	0/1018	0.42	0/1369
27	W	0.24	0/1918	0.42	0/2586
28	X	0.24	0/1116	0.41	0/1503
29	Y	0.24	0/1004	0.40	0/1341
30	Z	0.26	0/1118	0.43	0/1497
31	a	0.25	0/751	0.40	0/1013
32	b	0.24	0/4435	0.40	0/5971

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	c	0.24	0/751	0.40	0/1008
34	d	0.23	0/870	0.41	0/1168
35	e	0.23	0/1041	0.41	0/1394
36	f	0.25	0/868	0.45	0/1168
37	g	0.23	0/891	0.40	0/1191
38	h	0.24	0/978	0.38	0/1301
39	i	0.23	0/778	0.38	0/1034
40	j	0.25	0/685	0.41	0/908
41	k	0.26	0/618	0.44	0/826
42	l	0.23	0/443	0.41	0/588
43	m	0.24	0/3794	0.43	0/5108
44	n	0.24	0/3101	0.40	0/4187
45	o	0.24	0/1129	0.40	0/1502
46	p	0.24	0/701	0.45	0/934
47	q	0.23	0/1254	0.42	0/1675
48	r	0.24	0/1892	0.44	0/2528
49	s	0.25	0/440	0.40	0/573
50	t	0.24	0/2333	0.43	0/3128
51	u	0.25	0/1287	0.40	0/1711
52	v	0.25	0/2361	0.42	0/3153
53	w	0.24	0/1471	0.40	0/1980
54	x	0.23	0/3313	0.42	0/4490
55	y	0.23	0/1872	0.44	0/2548
56	z	0.24	0/371	0.34	0/489
All	All	0.20	0/158934	0.62	36/231026 (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
11	F	0	1
30	Z	0	1
32	b	0	1
43	m	0	1
50	t	0	2
All	All	0	6

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	2376	G	OP1-P-OP2	-6.80	109.39	119.60
1	1	1082	U	OP1-P-OP2	-6.79	109.41	119.60
2	2	1	A	OP1-P-OP2	-6.79	109.41	119.60
1	1	2501	U	OP1-P-OP2	-6.78	109.43	119.60
5	6	1	C	OP1-P-OP2	-6.77	109.45	119.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	F	158	LYS	Peptide
30	Z	104	PRO	Peptide
32	b	369	ARG	Peptide
43	m	77	TRP	Peptide
50	t	220	ASN	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
4	5	49/120 (41%)	49 (100%)	0	0	100	100
6	A	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
7	B	384/387 (99%)	358 (93%)	26 (7%)	0	100	100
8	C	359/362 (99%)	336 (94%)	23 (6%)	0	100	100
9	D	257/297 (86%)	246 (96%)	11 (4%)	0	100	100
10	E	152/176 (86%)	145 (95%)	7 (5%)	0	100	100
11	F	220/244 (90%)	210 (96%)	9 (4%)	1 (0%)	29	64

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	G	231/256 (90%)	212 (92%)	19 (8%)	0	100	100
13	H	189/191 (99%)	177 (94%)	12 (6%)	0	100	100
14	J	167/174 (96%)	152 (91%)	15 (9%)	0	100	100
15	K	248/376 (66%)	231 (93%)	17 (7%)	0	100	100
16	L	185/199 (93%)	174 (94%)	10 (5%)	1 (0%)	29	64
17	M	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
18	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	29	64
19	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
20	P	173/184 (94%)	168 (97%)	5 (3%)	0	100	100
21	Q	132/186 (71%)	131 (99%)	1 (1%)	0	100	100
22	R	154/189 (82%)	147 (96%)	7 (4%)	0	100	100
23	S	169/172 (98%)	160 (95%)	9 (5%)	0	100	100
24	T	110/160 (69%)	98 (89%)	12 (11%)	0	100	100
25	U	99/121 (82%)	95 (96%)	4 (4%)	0	100	100
26	V	134/137 (98%)	129 (96%)	5 (4%)	0	100	100
27	W	232/236 (98%)	219 (94%)	12 (5%)	1 (0%)	34	69
28	X	139/142 (98%)	133 (96%)	6 (4%)	0	100	100
29	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
30	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
31	a	91/149 (61%)	86 (94%)	5 (6%)	0	100	100
32	b	533/647 (82%)	490 (92%)	43 (8%)	0	100	100
33	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
34	d	103/113 (91%)	97 (94%)	6 (6%)	0	100	100
35	e	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
36	f	104/107 (97%)	95 (91%)	9 (9%)	0	100	100
37	g	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
38	h	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
39	i	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
40	j	83/88 (94%)	78 (94%)	5 (6%)	0	100	100
41	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
42	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
43	m	457/486 (94%)	420 (92%)	36 (8%)	1 (0%)	47 79
44	n	365/605 (60%)	340 (93%)	25 (7%)	0	100 100
45	o	131/220 (60%)	123 (94%)	8 (6%)	0	100 100
46	p	89/92 (97%)	80 (90%)	9 (10%)	0	100 100
47	q	143/455 (31%)	130 (91%)	13 (9%)	0	100 100
48	r	224/261 (86%)	199 (89%)	25 (11%)	0	100 100
49	s	49/520 (9%)	46 (94%)	3 (6%)	0	100 100
50	t	283/322 (88%)	261 (92%)	20 (7%)	2 (1%)	22 57
51	u	148/199 (74%)	143 (97%)	5 (3%)	0	100 100
52	v	283/344 (82%)	270 (95%)	13 (5%)	0	100 100
53	w	178/203 (88%)	174 (98%)	4 (2%)	0	100 100
54	x	409/515 (79%)	391 (96%)	18 (4%)	0	100 100
55	y	242/245 (99%)	229 (95%)	13 (5%)	0	100 100
56	z	44/106 (42%)	44 (100%)	0	0	100 100
All	All	9407/11749 (80%)	8864 (94%)	536 (6%)	7 (0%)	54 83

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	F	159	GLN
50	t	220	ASN
50	t	221	GLU
18	N	146	ALA
43	m	208	SER

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain 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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	5	48/106 (45%)	46 (96%)	2 (4%)	30 62
6	A	166/196 (85%)	166 (100%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	B	322/323 (100%)	317 (98%)	5 (2%)	62	84
8	C	288/289 (100%)	282 (98%)	6 (2%)	53	79
9	D	219/245 (89%)	213 (97%)	6 (3%)	44	74
10	E	134/153 (88%)	133 (99%)	1 (1%)	84	93
11	F	186/205 (91%)	185 (100%)	1 (0%)	88	94
12	G	191/208 (92%)	189 (99%)	2 (1%)	76	90
13	H	171/171 (100%)	169 (99%)	2 (1%)	71	88
14	J	147/150 (98%)	144 (98%)	3 (2%)	55	80
15	K	233/346 (67%)	227 (97%)	6 (3%)	46	74
16	L	149/159 (94%)	147 (99%)	2 (1%)	69	87
17	M	108/109 (99%)	108 (100%)	0	100	100
18	N	175/176 (99%)	172 (98%)	3 (2%)	60	83
19	O	160/162 (99%)	159 (99%)	1 (1%)	86	94
20	P	142/146 (97%)	138 (97%)	4 (3%)	43	73
21	Q	110/151 (73%)	110 (100%)	0	100	100
22	R	129/154 (84%)	126 (98%)	3 (2%)	50	77
23	S	155/156 (99%)	151 (97%)	4 (3%)	46	74
24	T	100/137 (73%)	98 (98%)	2 (2%)	55	80
25	U	88/107 (82%)	85 (97%)	3 (3%)	37	69
26	V	104/105 (99%)	103 (99%)	1 (1%)	76	90
27	W	211/213 (99%)	205 (97%)	6 (3%)	43	73
28	X	117/118 (99%)	114 (97%)	3 (3%)	46	74
29	Y	109/110 (99%)	107 (98%)	2 (2%)	59	82
30	Z	115/116 (99%)	114 (99%)	1 (1%)	78	91
31	a	76/119 (64%)	75 (99%)	1 (1%)	69	87
32	b	482/573 (84%)	473 (98%)	9 (2%)	57	81
33	c	81/88 (92%)	80 (99%)	1 (1%)	71	88
34	d	92/97 (95%)	90 (98%)	2 (2%)	52	78
35	e	109/111 (98%)	107 (98%)	2 (2%)	59	82
36	f	90/91 (99%)	89 (99%)	1 (1%)	73	89
37	g	95/103 (92%)	95 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	h	104/105 (99%)	103 (99%)	1 (1%)	76 90
39	i	81/82 (99%)	79 (98%)	2 (2%)	47 75
40	j	69/71 (97%)	65 (94%)	4 (6%)	20 51
41	k	68/69 (99%)	68 (100%)	0	100 100
42	l	45/46 (98%)	44 (98%)	1 (2%)	52 78
43	m	408/428 (95%)	401 (98%)	7 (2%)	60 83
44	n	334/548 (61%)	326 (98%)	8 (2%)	49 76
45	o	118/199 (59%)	115 (98%)	3 (2%)	47 75
46	p	71/72 (99%)	70 (99%)	1 (1%)	67 86
47	q	137/420 (33%)	136 (99%)	1 (1%)	84 93
48	r	203/229 (89%)	196 (97%)	7 (3%)	37 69
49	s	47/445 (11%)	45 (96%)	2 (4%)	29 62
50	t	256/287 (89%)	251 (98%)	5 (2%)	55 80
51	u	133/180 (74%)	131 (98%)	2 (2%)	65 85
52	v	258/309 (84%)	257 (100%)	1 (0%)	91 96
53	w	161/179 (90%)	156 (97%)	5 (3%)	40 70
54	x	361/451 (80%)	358 (99%)	3 (1%)	81 92
55	y	210/211 (100%)	207 (99%)	3 (1%)	67 86
56	z	40/95 (42%)	39 (98%)	1 (2%)	47 75
All	All	8206/10119 (81%)	8064 (98%)	142 (2%)	62 83

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	r	133	MET
48	r	210	THR
53	w	29	PHE
23	S	136	LYS
23	S	96	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
32	b	356	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	r	256	ASN
34	d	57	GLN
44	n	53	ASN
51	u	5	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3044/3396 (89%)	615 (20%)	78 (2%)
2	2	157/158 (99%)	27 (17%)	2 (1%)
3	3	120/121 (99%)	16 (13%)	2 (1%)
5	6	64/232 (27%)	21 (32%)	5 (7%)
All	All	3385/3907 (86%)	679 (20%)	87 (2%)

5 of 679 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	13	A
1	1	14	U
1	1	26	A
1	1	40	A

5 of 87 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2728	G
1	1	3195	U
1	1	2761	G
1	1	2868	U
1	1	3350	C

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)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

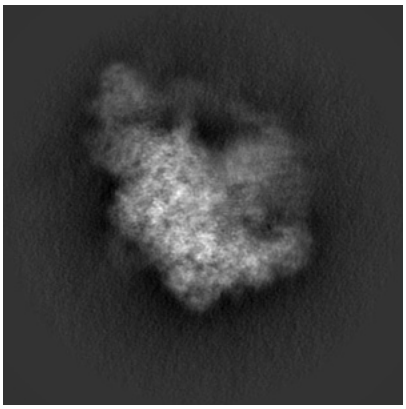
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12905. These allow visual inspection of the internal detail of the map and identification of artifacts.

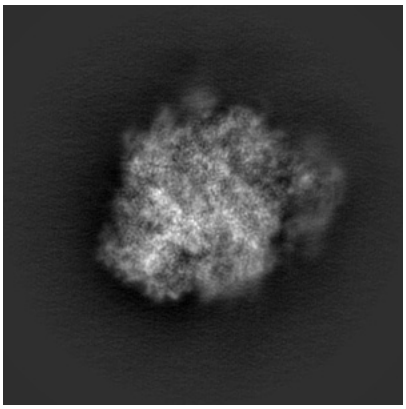
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

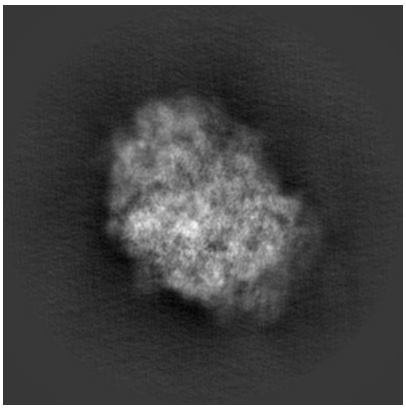
6.1.1 Primary map



X

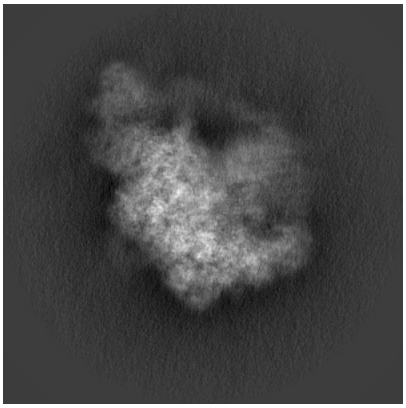


Y

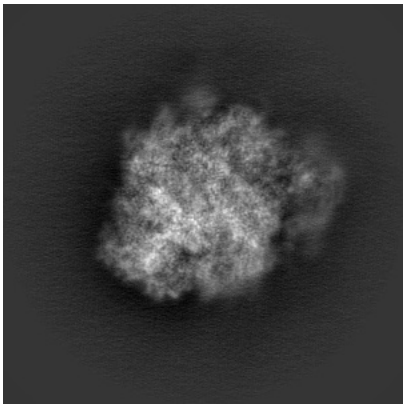


Z

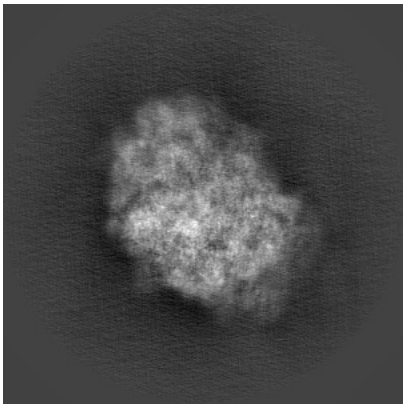
6.1.2 Raw map



X



Y

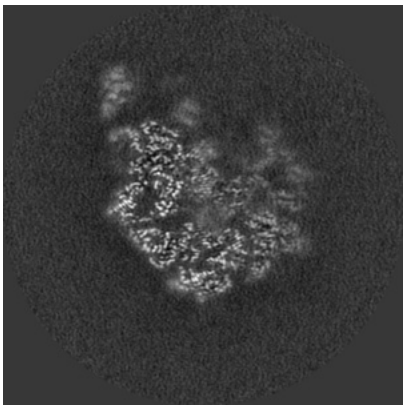


Z

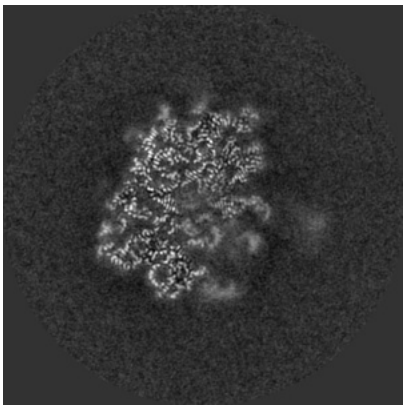
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

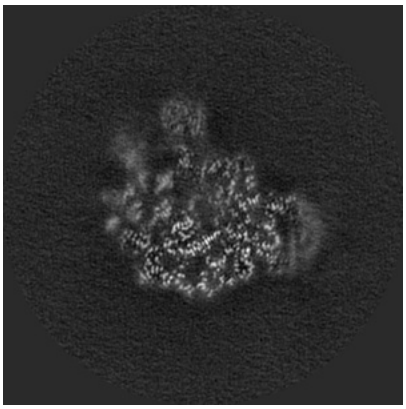
6.2.1 Primary map



X Index: 200

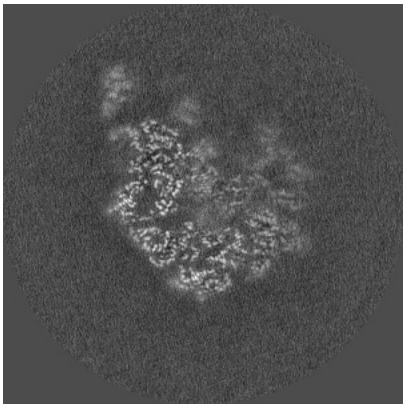


Y Index: 200

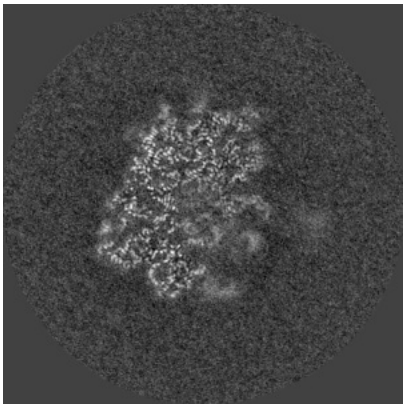


Z Index: 200

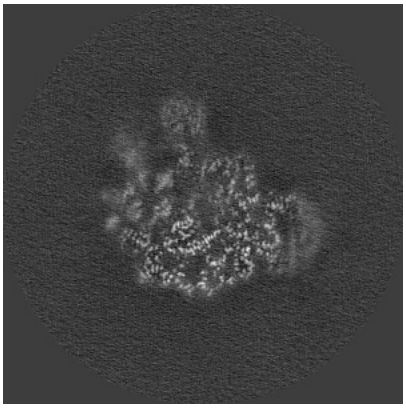
6.2.2 Raw map



X Index: 200



Y Index: 200

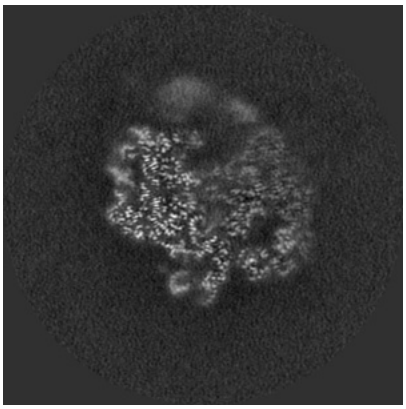


Z Index: 200

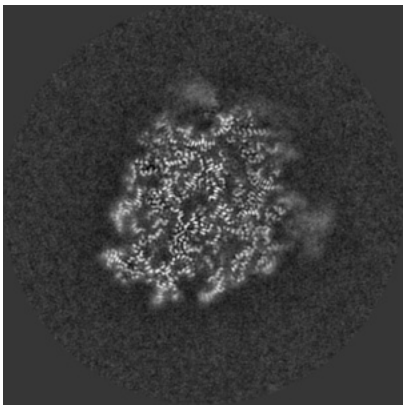
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

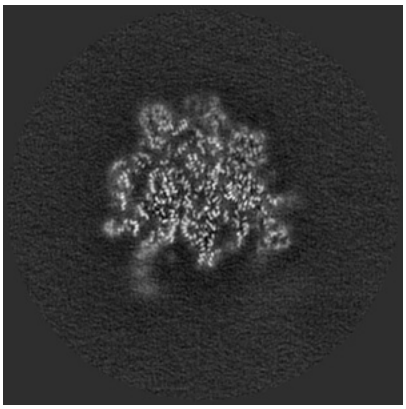
6.3.1 Primary map



X Index: 183

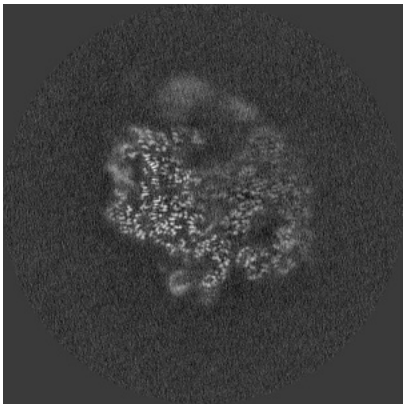


Y Index: 178

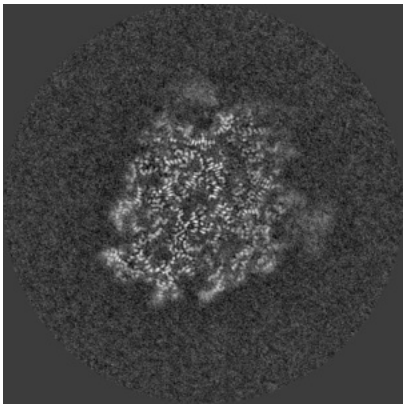


Z Index: 153

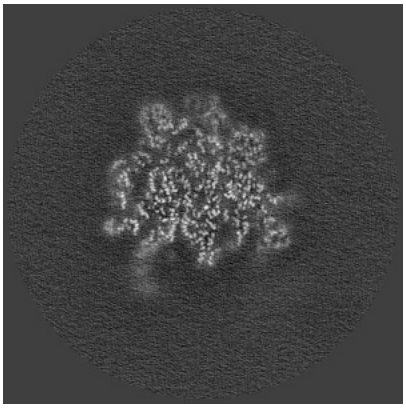
6.3.2 Raw map



X Index: 184



Y Index: 178

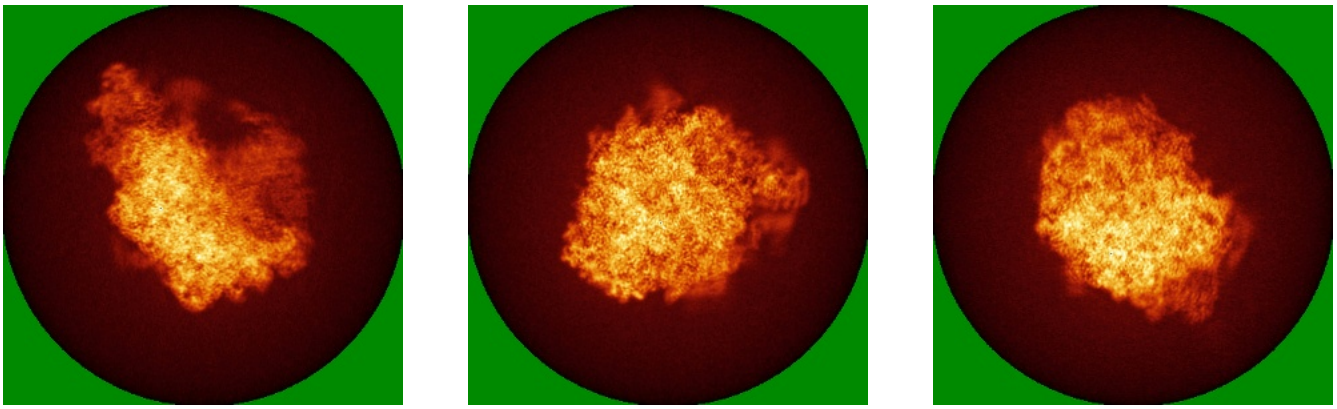


Z Index: 153

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

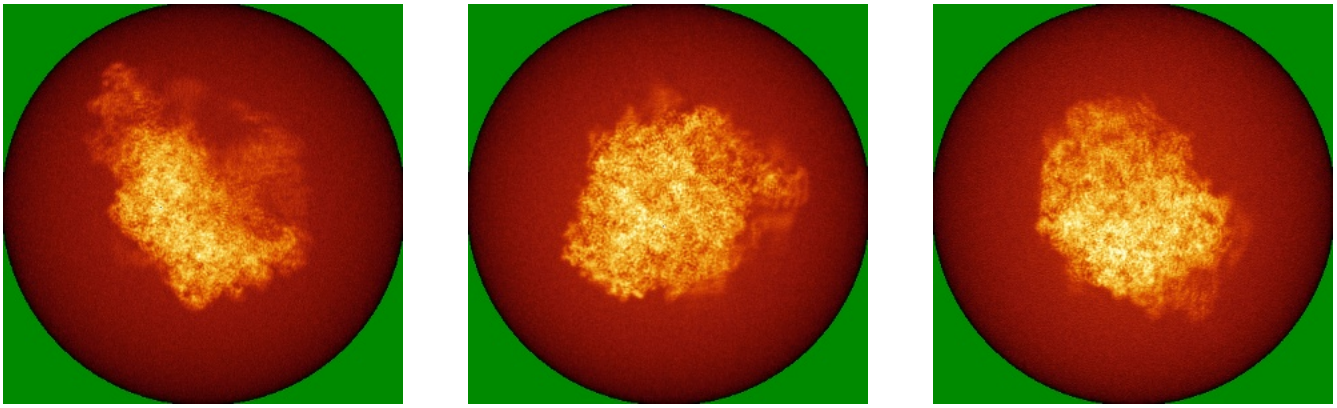
6.4 Orthogonal standard-deviation projections (False-color) (i)

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.

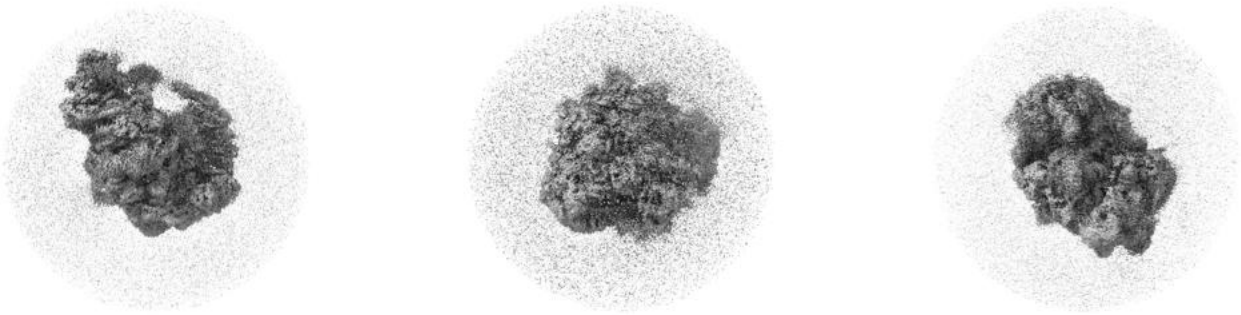
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.021. 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



X Y Z

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.

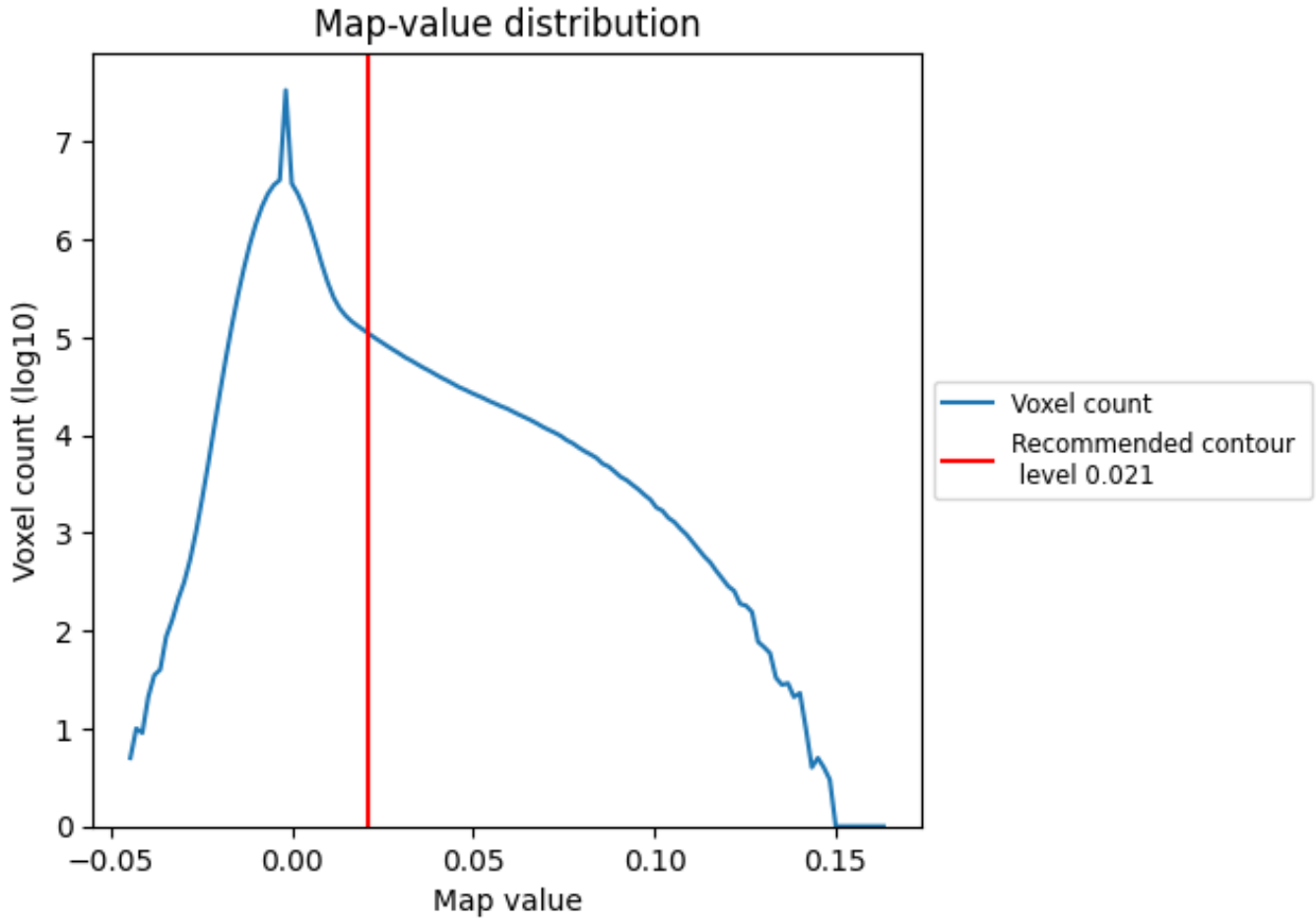
6.6 Mask visualisation (i)

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

7 Map analysis

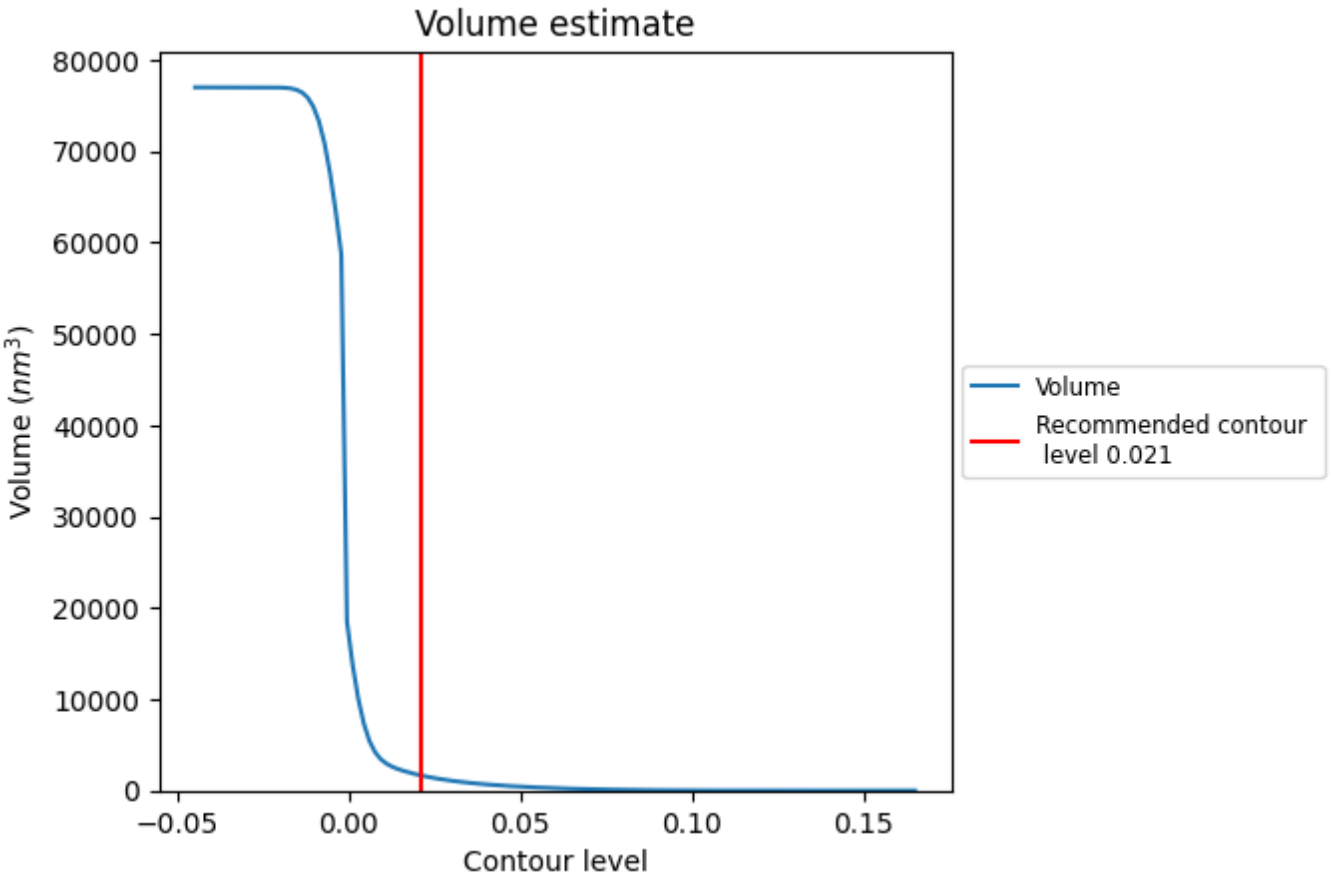
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

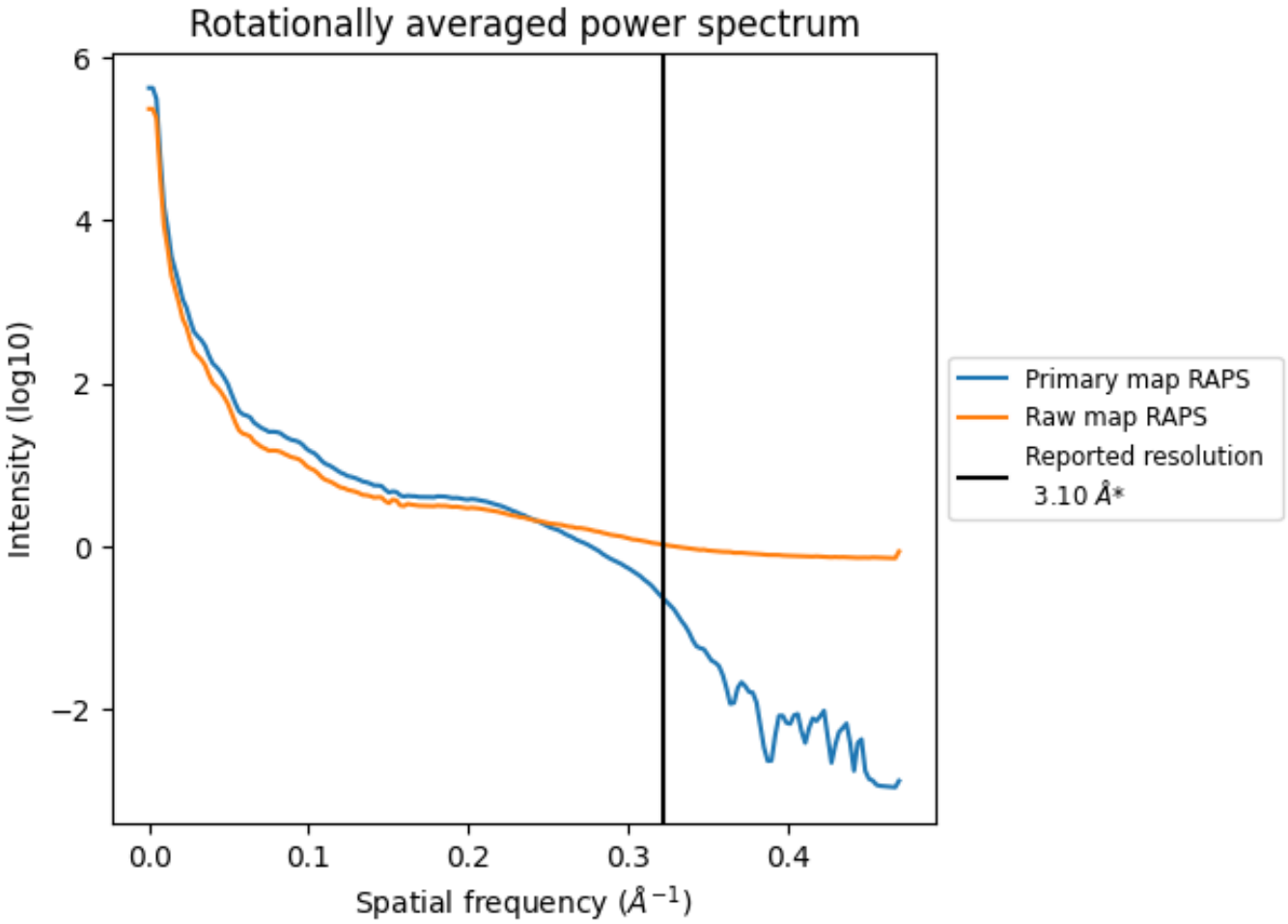
7.2 Volume estimate (i)



The volume at the recommended contour level is 1666 nm^3; this corresponds to an approximate mass of 1505 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)

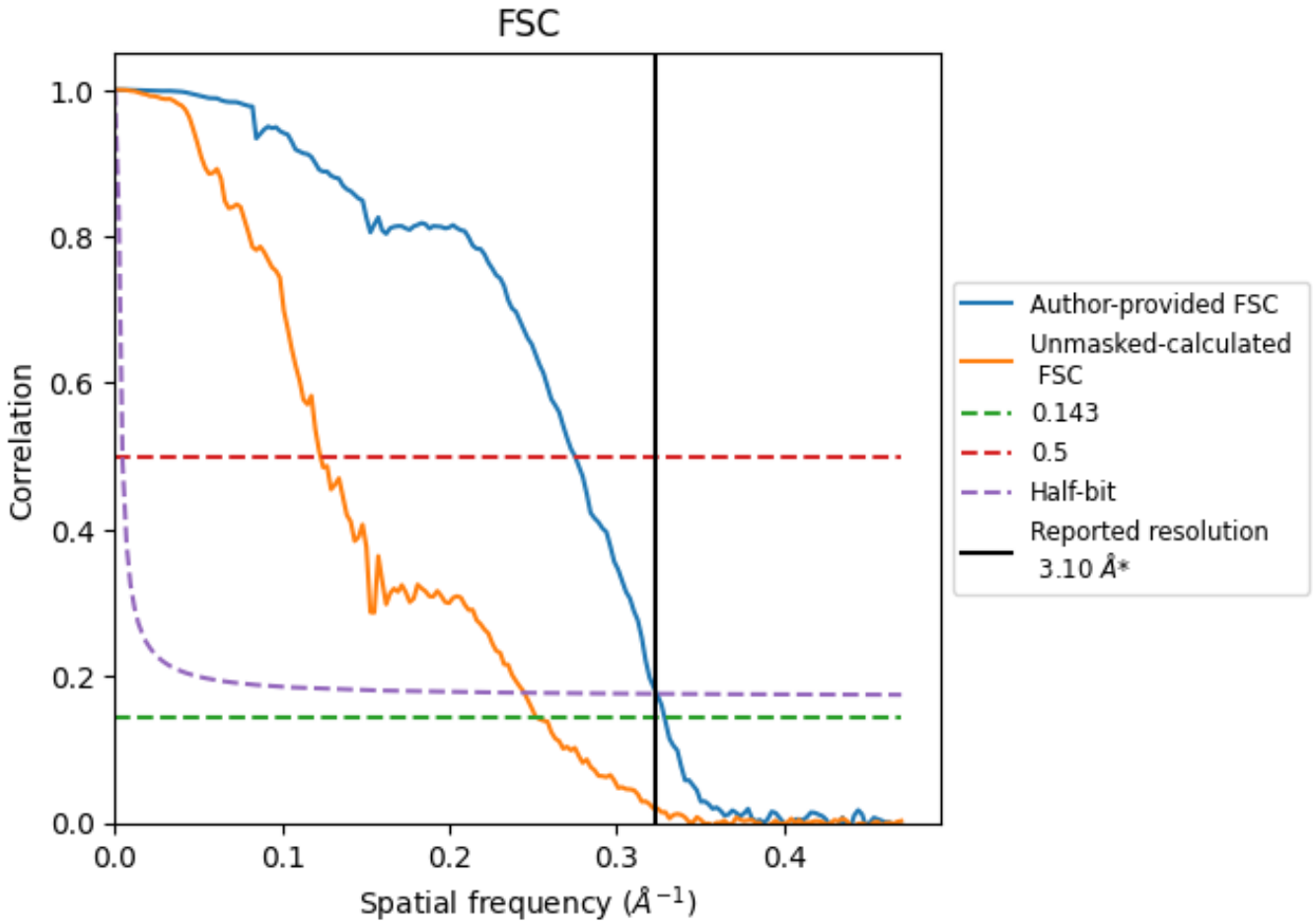


*Reported resolution corresponds to spatial frequency of 0.323 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8.2 Resolution estimates (i)

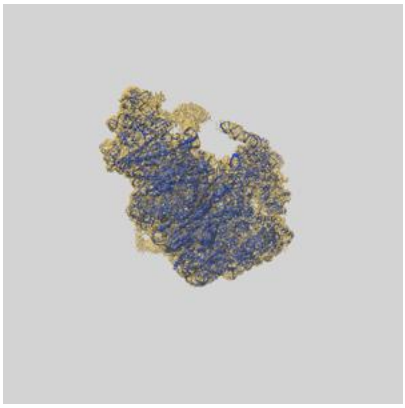
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.04	3.64	3.09
Unmasked-calculated*	3.96	8.13	4.08

*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 3.96 differs from the reported value 3.1 by more than 10 %

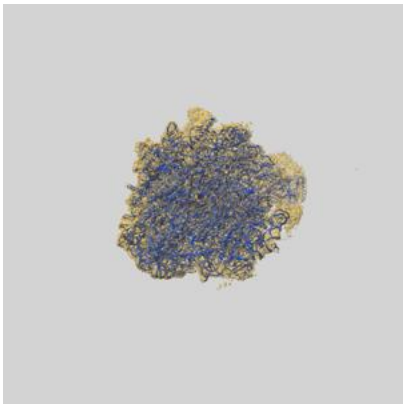
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12905 and PDB model 7OHQ. Per-residue inclusion information can be found in section 3 on page 14.

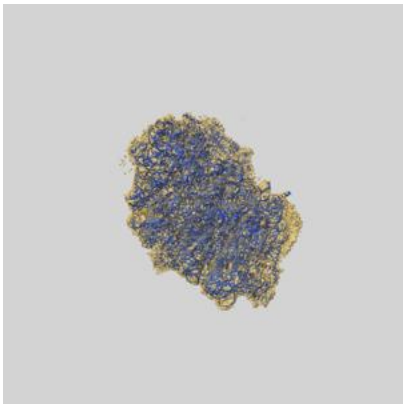
9.1 Map-model overlay



X



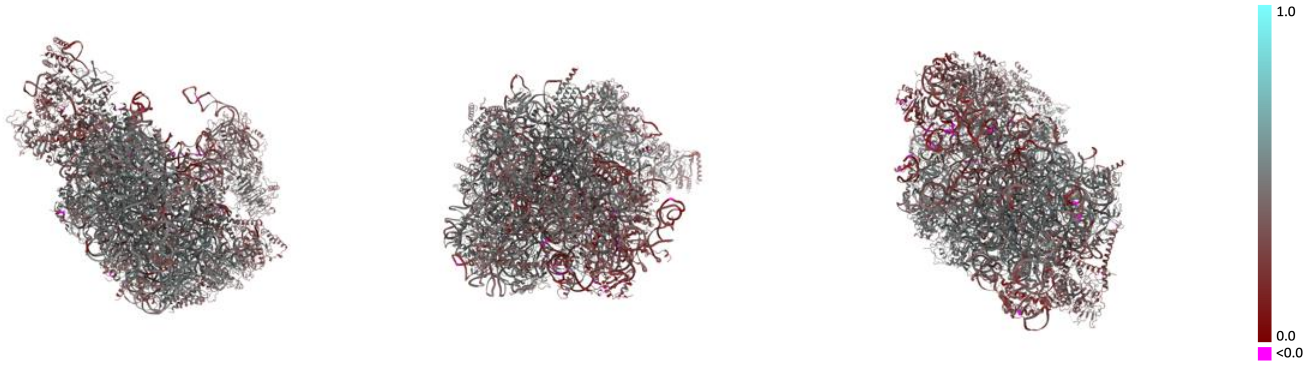
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.021 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.

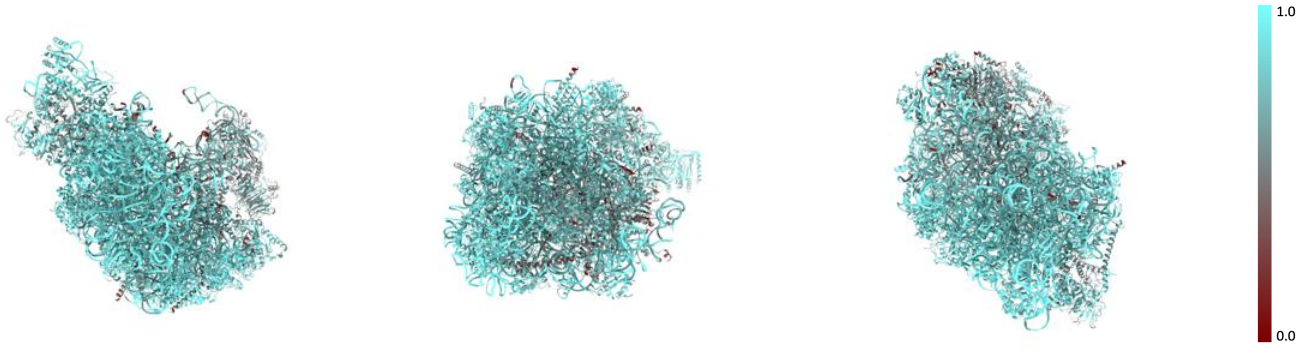
9.2 Q-score mapped to coordinate model



X Y Z

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.

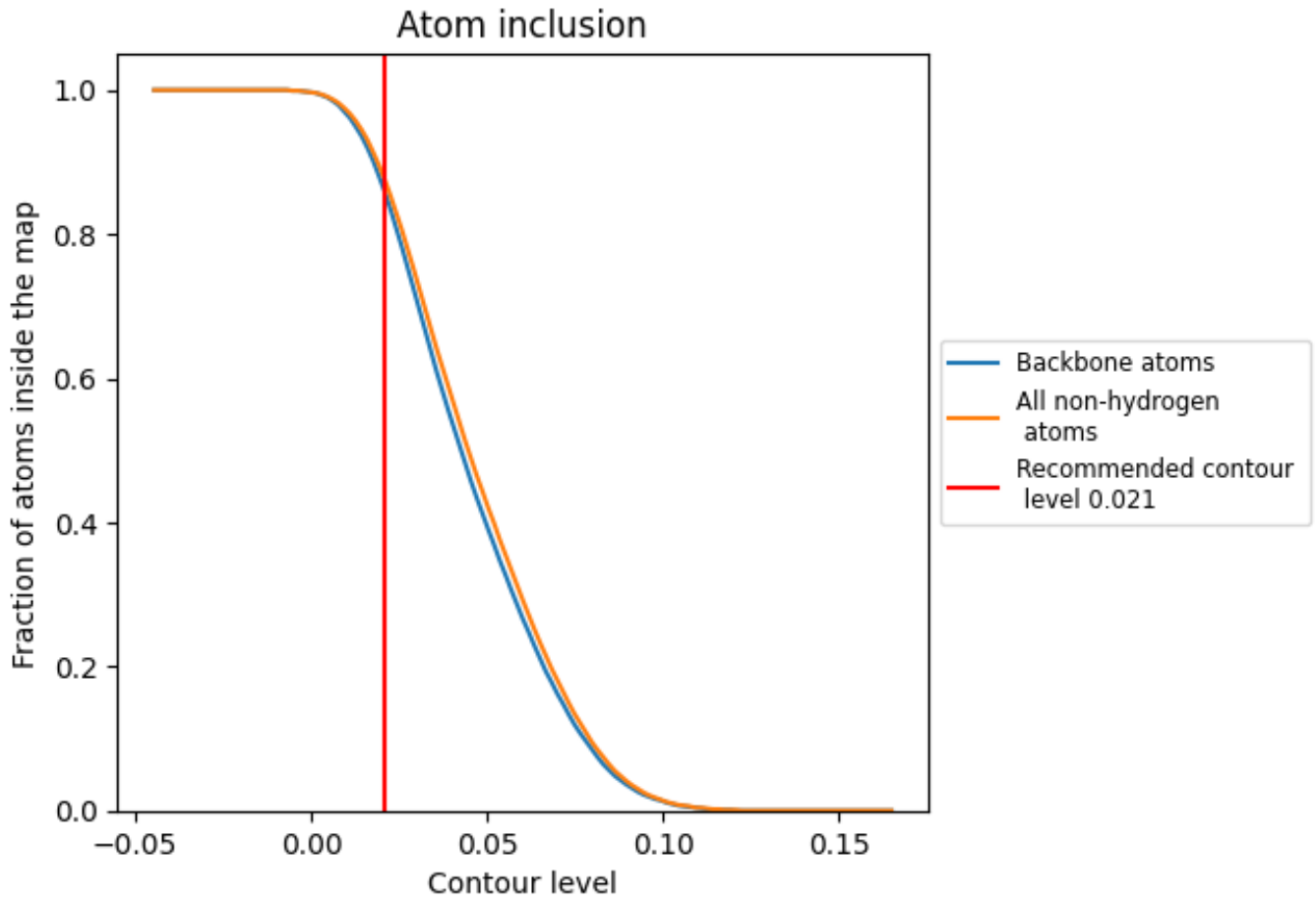
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.021).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 87% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8740	0.4170
1	0.9350	0.4130
2	0.9650	0.4520
3	0.8170	0.2760
5	0.4060	0.3030
6	0.9490	0.3430
A	0.8330	0.4950
B	0.9060	0.4830
C	0.9010	0.4850
D	0.5710	0.3230
E	0.9200	0.4710
F	0.8970	0.4610
G	0.8210	0.4330
H	0.8650	0.4550
J	0.8020	0.2580
K	0.8690	0.3340
L	0.8770	0.4590
M	0.9020	0.4760
N	0.8720	0.4900
O	0.9130	0.4980
P	0.8920	0.4910
Q	0.8920	0.4770
R	0.8630	0.4700
S	0.8710	0.4460
T	0.6870	0.3660
U	0.8840	0.4050
V	0.8920	0.4860
W	0.8530	0.3920
X	0.8780	0.4840
Y	0.9220	0.4890
Z	0.8890	0.4450
a	0.8780	0.4650
b	0.7950	0.3960
c	0.9060	0.4650
d	0.8660	0.4800

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	0.8850	0.5040
f	0.9240	0.5200
g	0.8560	0.4790
h	0.9070	0.4650
i	0.8230	0.4390
j	0.9260	0.5020
k	0.7750	0.4200
l	0.8770	0.4790
m	0.7340	0.4130
n	0.7430	0.3810
o	0.8580	0.3770
p	0.8580	0.4650
q	0.6570	0.3280
r	0.7600	0.4280
s	0.6480	0.4110
t	0.7300	0.3400
u	0.8420	0.4370
v	0.5730	0.3560
w	0.5790	0.3370
x	0.6480	0.3860
y	0.8930	0.4510
z	0.5940	0.4060