wwPDB EM Validation Summary Report (i)

Dec 1, 2021 – 04:03 pm GMT

PDB ID	:	7OH3
EMDB ID	:	EMD-12892
Title	:	Nog1-TAP associated immature ribosomal particle population B from S. cerevisiae
Authors	:	Milkereit, P.; Poell, G.
Deposited on	:	2021-05-08
Resolution	:	3.40 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 following versions of software and data (see references (1)) were used in the production of this report:

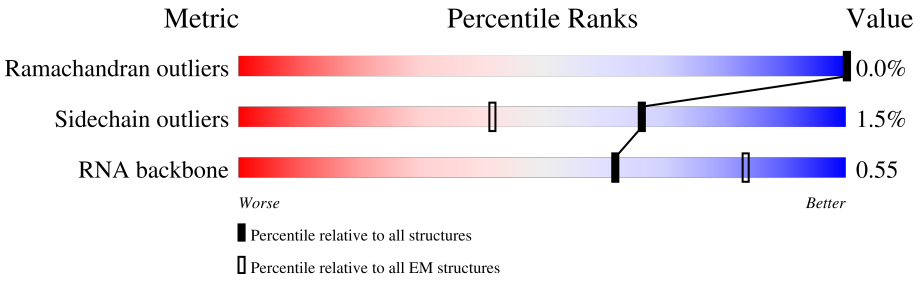
EMDB validation analysis	:	0.0.0.dev97
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 3.40 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% 19% 11%
2	2	158	79% 18%
3	3	121	83% 16%
4	5	120	40% 60% 39%
5	A	254	15% 77% 23%
6	B	387	11% 98%
7	C	362	7% 96%
8	D	297	8% 89% 10%

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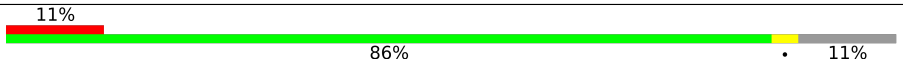
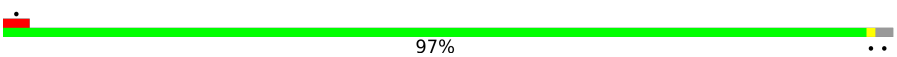
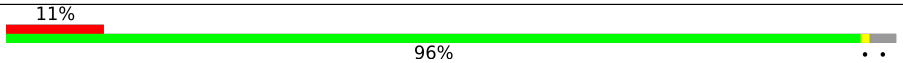
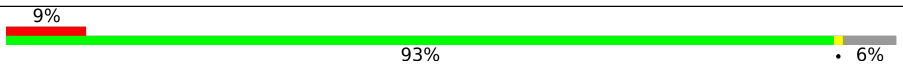
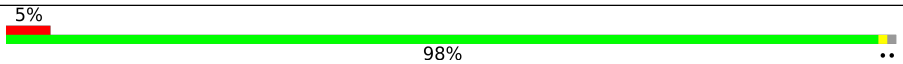
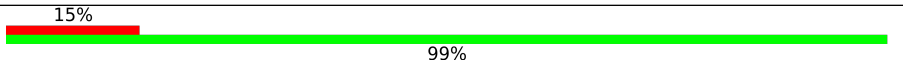
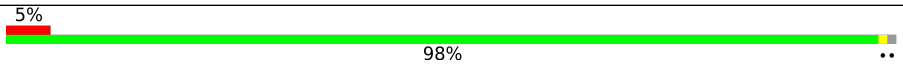
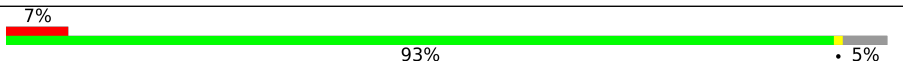
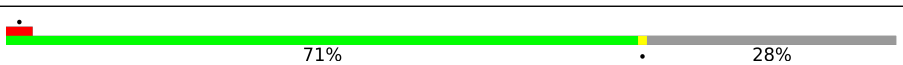
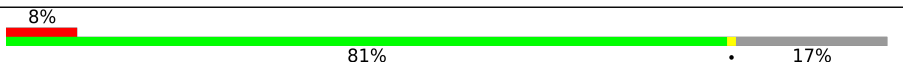
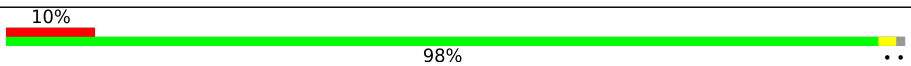
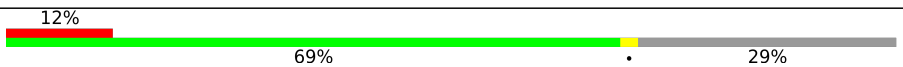
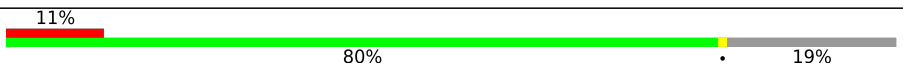
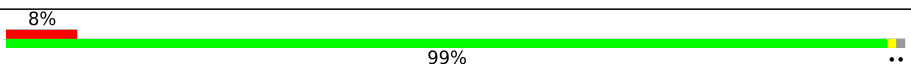
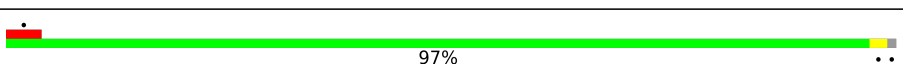
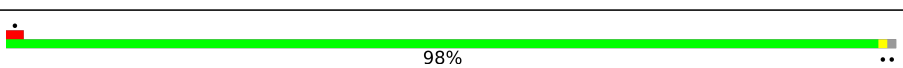
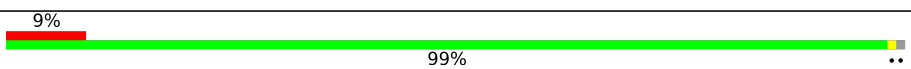
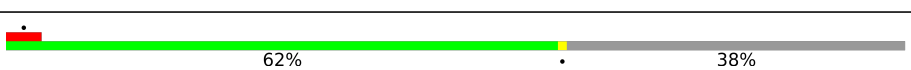
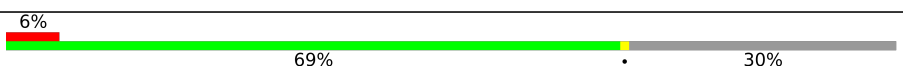
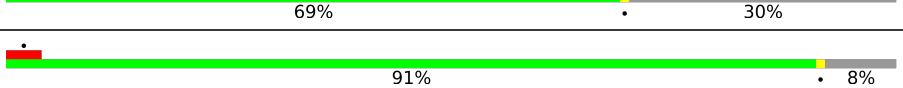
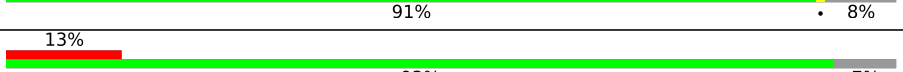
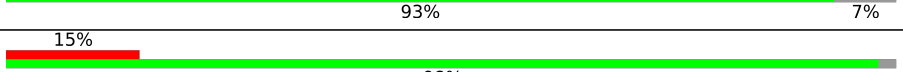
Mol	Chain	Length	Quality of chain
9	E	176	
10	F	244	
11	G	256	
12	H	191	
13	J	174	
14	L	199	
15	M	138	
16	N	204	
17	O	199	
18	P	184	
19	Q	186	
20	R	189	
21	S	172	
22	T	160	
23	U	121	
24	V	137	
25	W	236	
26	X	142	
27	Y	127	
28	Z	136	
29	a	149	
30	b	647	
31	c	105	
32	d	113	
33	e	130	

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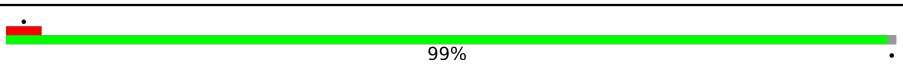
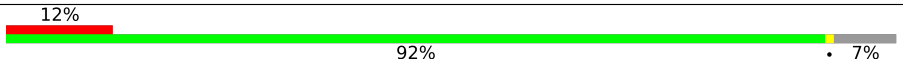
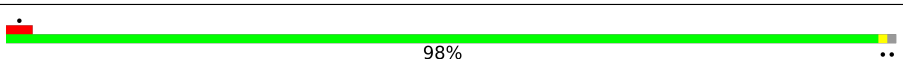
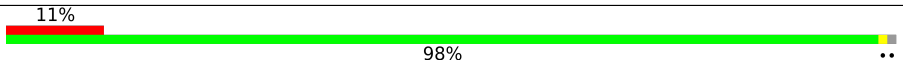
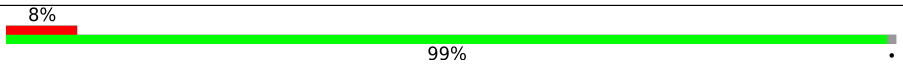
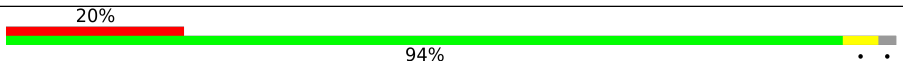
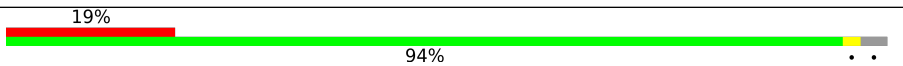
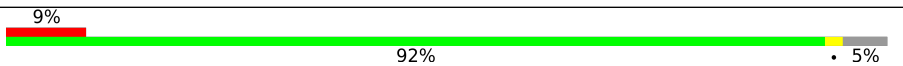
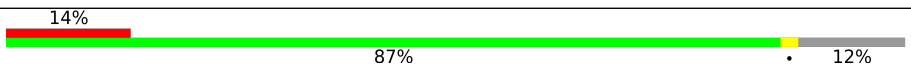
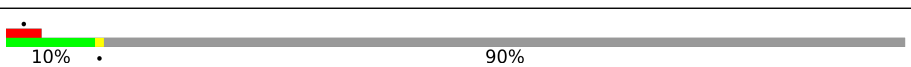
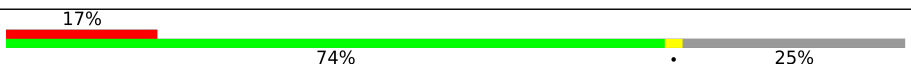
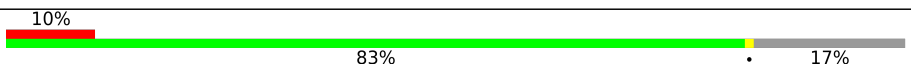
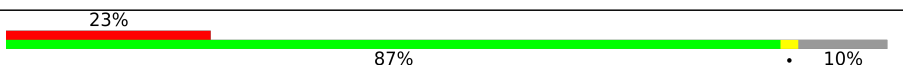
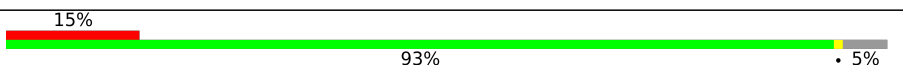
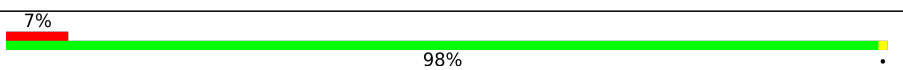
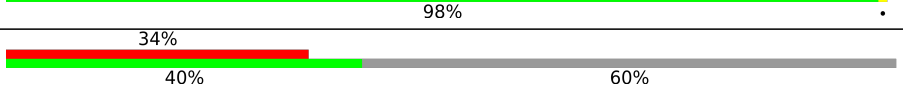
Mol	Chain	Length	Quality of chain
34	f	107	
35	g	121	
36	h	120	
37	i	100	
38	j	88	
39	k	78	
40	l	51	
41	m	486	
42	p	92	
43	r	261	
44	s	520	
45	u	199	
46	v	344	
47	w	203	
48	x	515	
49	y	245	
50	z	106	

2 Entry composition (i)

There are 52 unique types of molecules in this entry. The entry contains 240945 atoms, of which 104342 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	3013	96890	28804	32398	11667	21009	3012	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	155	4957	1473	1664	580	1085	155	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	73	1334	395	689	133	114	3	0	0

- Molecule 5 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
5	A	196	3098	954	1579	301	264	0	0

- Molecule 6 is a protein called 60S ribosomal protein L3.

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

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	C	352	Total	C	H	N	O	S	0	0
			5490	1691	2804	509	483	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	D	267	Total	C	H	N	O	S	0	0
			4266	1361	2114	379	410	2		

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	G	228	Total	C	H	N	O	S	0	0
			3668	1142	1884	320	319	3		

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	H	188	Total	C	H	N	O	S	0	0
			3059	948	1566	271	270	4		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	J	169	Total	C	H	N	O	S	0	0
			2738	847	1385	253	249	4		

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	O	197	Total	C	H	N	O	S	0	0
			3216	1003	1661	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	174	Total	C	H	N	O	0	0
			2798	857	1419	276	246		

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	T	113	Total	C	H	N	O	S	0	0
			1868	574	962	172	157	3		

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	98	Total	C	H	N	O	0	0
			1571	502	796	128	145		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 25 is a protein called Ribosome assembly factor MRT4.

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

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	X	117	Total	C	H	N	O	S	0	0
			1932	602	995	164	169	2		

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L28.

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

- Molecule 30 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	b	455	Total	C	H	N	O	S	0	0
			7450	2353	3755	640	684	18		

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	e	127	Total	C	H	N	O	S	0	0
			2111	647	1091	205	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	j	87	Total	C	H	N	O	S	0	0
			1369	414	688	148	114	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	70	Total	C	H	N	O	0	0
			1197	362	634	106	95		

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	m	469	Total	C	H	N	O	S	0	0
			7611	2381	3837	685	699	9		

- Molecule 42 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	p	87	Total	C	H	N	O	S	0	0
			1375	411	710	134	115	5		

- Molecule 43 is a protein called Ribosome biogenesis protein NSA2.

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

- Molecule 44 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	s	54	Total	C	H	N	O	S	0	0
			947	279	503	90	73	2		

- Molecule 45 is a protein called Ribosome biogenesis protein RLP24.

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

- Molecule 46 is a protein called Ribosome biogenesis protein RPF2.

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

- Molecule 47 is a protein called Regulator of ribosome biosynthesis.

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

- Molecule 48 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	x	488	Total	C	H	N	O	S	0	0
			7606	2398	3799	677	711	21		

- Molecule 49 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 50 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	42	Total	C	H	N	O	0	0
			699	206	364	69	60		

- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

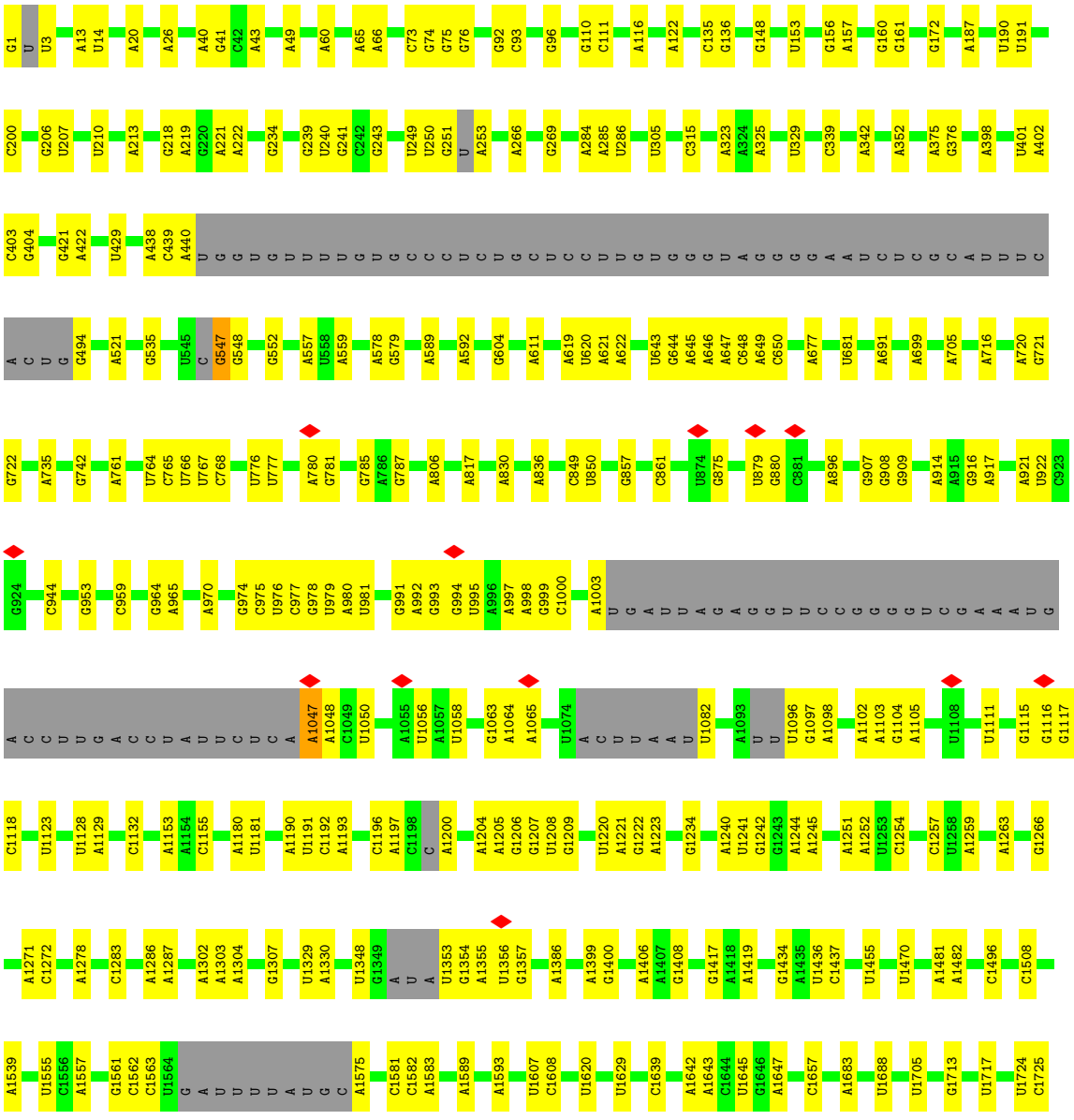
Mol	Chain	Residues	Atoms		AltConf
52	j	1	Total	Zn	0
			1	1	
52	p	1	Total	Zn	0
			1	1	
52	u	1	Total	Zn	0
			1	1	

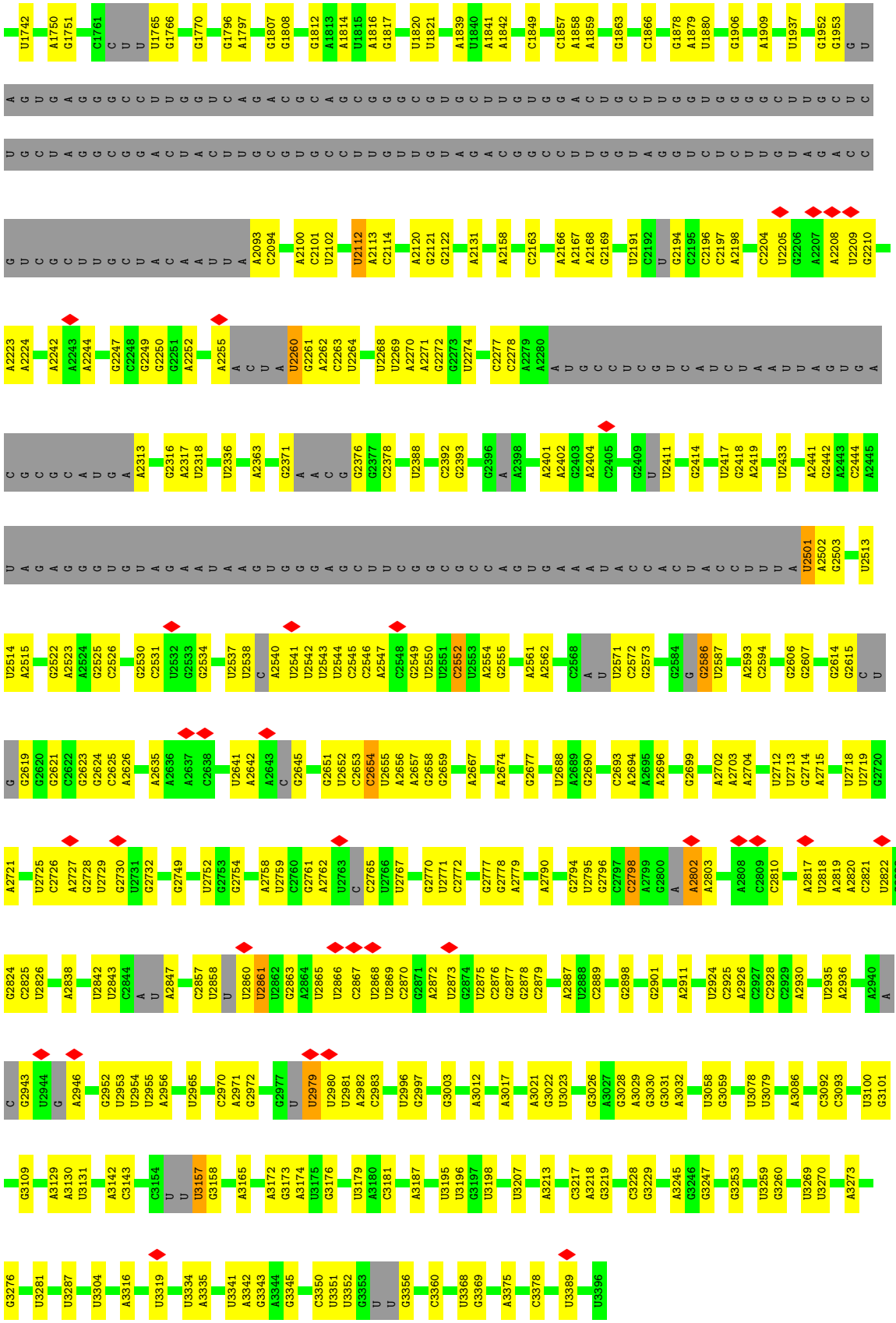
3 Residue-property plots (i)

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

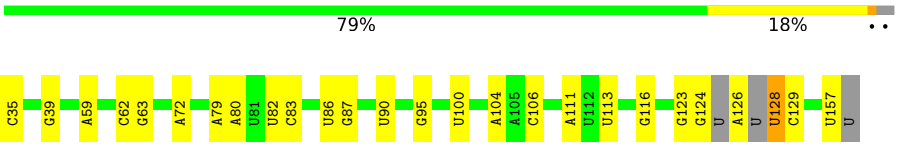
Chain 1:





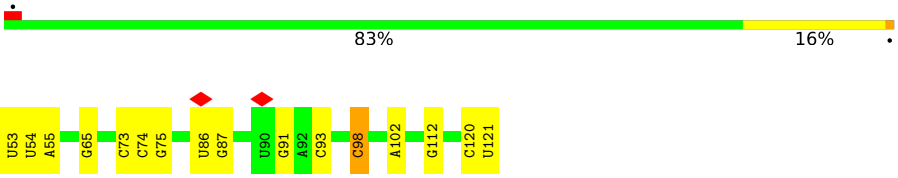
• Molecule 2: 5.8S rRNA

Chain 2:



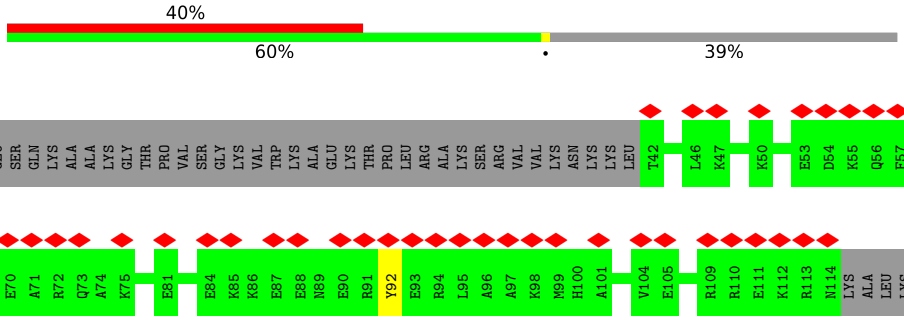
• Molecule 3: 5S rRNA

Chain 3:



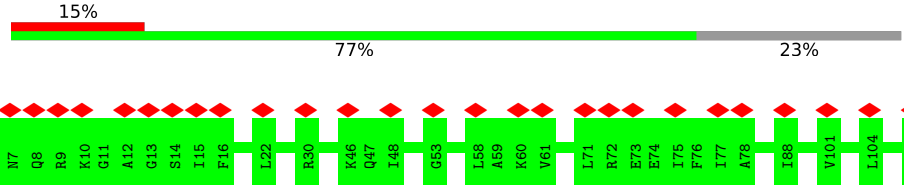
• Molecule 4: rRNA-processing protein CGR1

Chain 5:



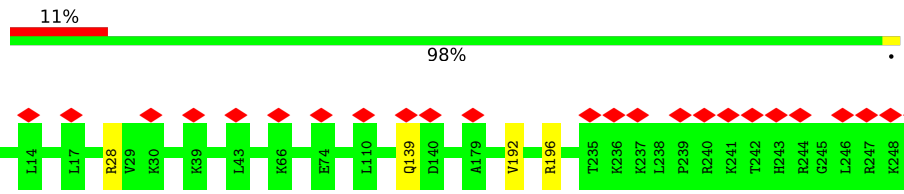
• Molecule 5: 60S ribosomal protein L2-A

Chain A:



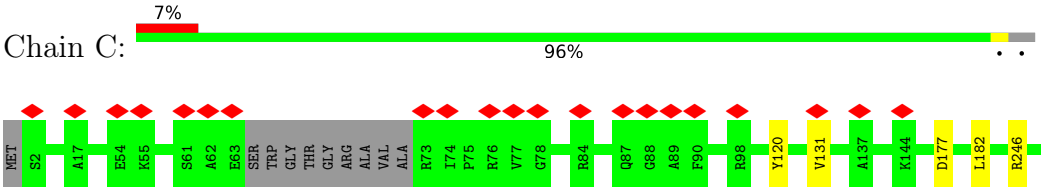
• Molecule 6: 60S ribosomal protein L3

Chain B:



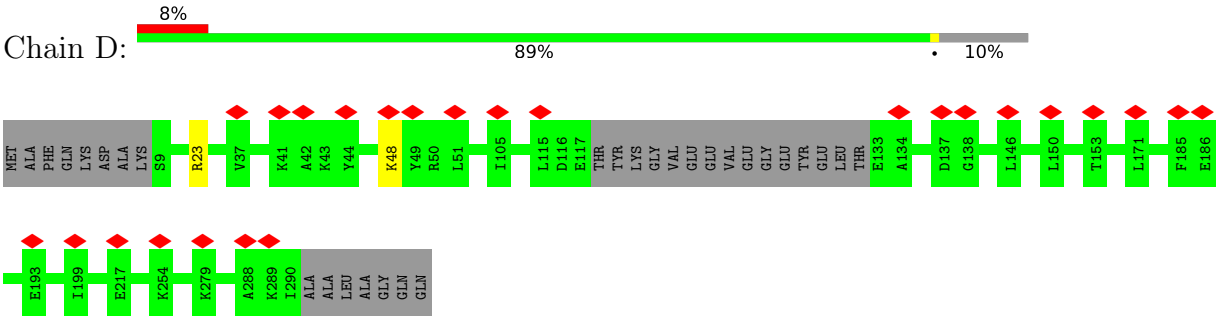
• Molecule 7: 60S ribosomal protein L4-A

Chain C:



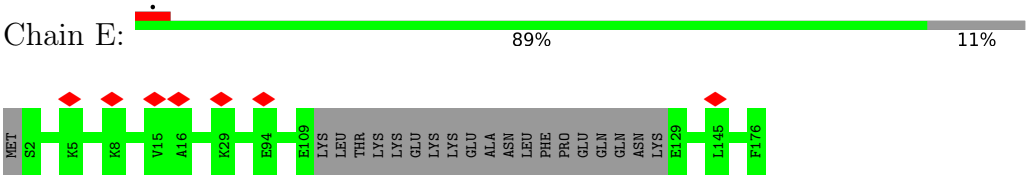
• Molecule 8: 60S ribosomal protein L5

Chain D:



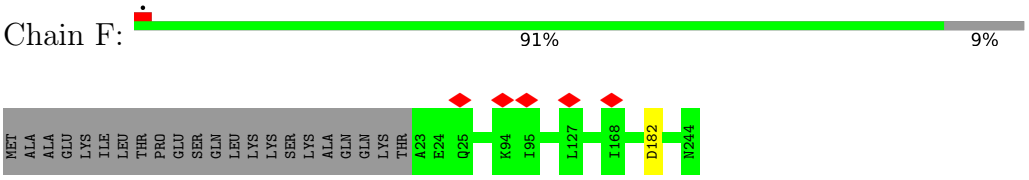
• Molecule 9: 60S ribosomal protein L6-A

Chain E:



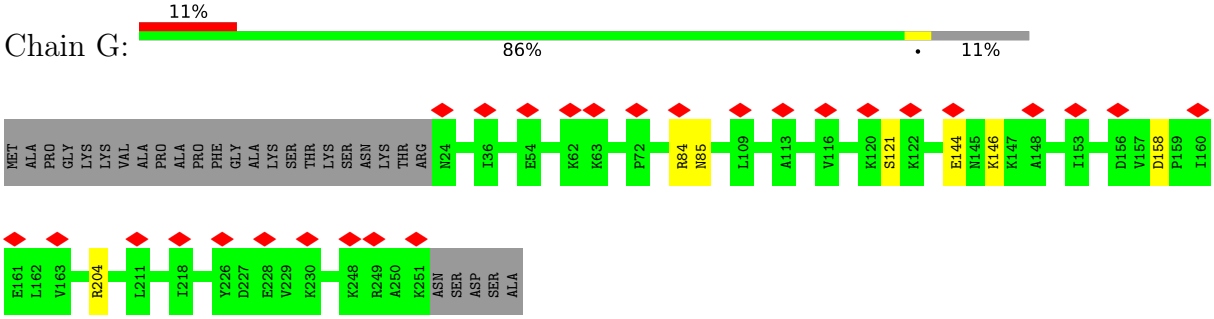
• Molecule 10: 60S ribosomal protein L7-A

Chain F:



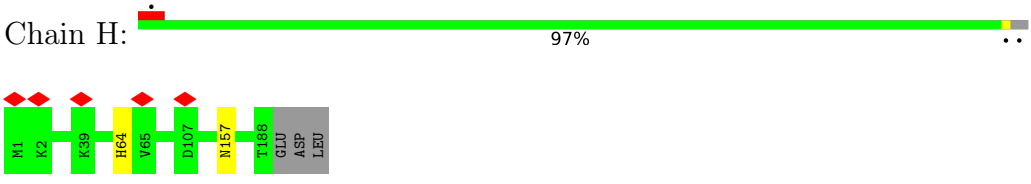
• Molecule 11: 60S ribosomal protein L8-A

Chain G:

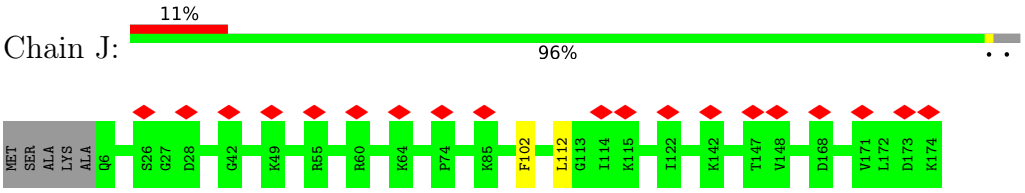


• Molecule 12: 60S ribosomal protein L9-A

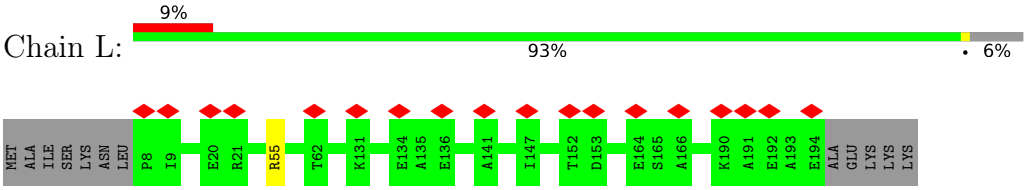
Chain H:



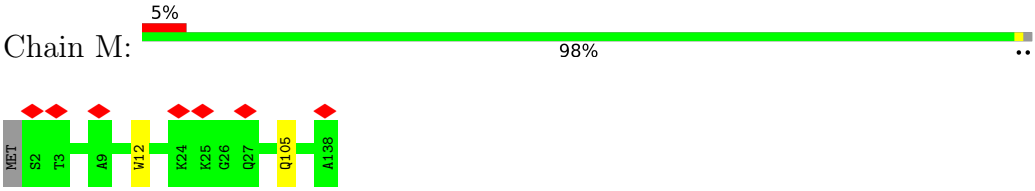
• Molecule 13: 60S ribosomal protein L11-A



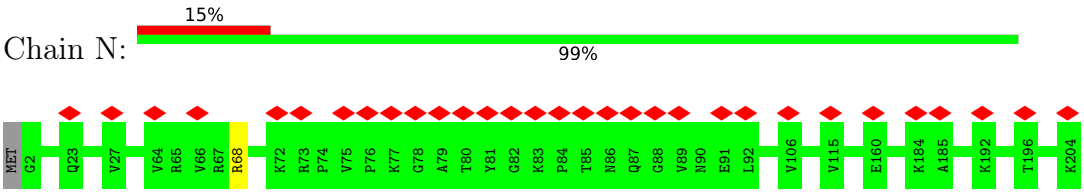
• Molecule 14: 60S ribosomal protein L13-A



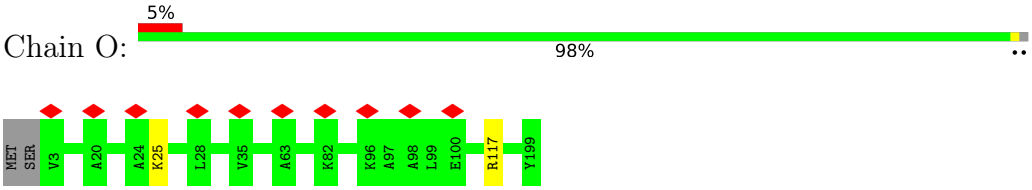
• Molecule 15: 60S ribosomal protein L14-A



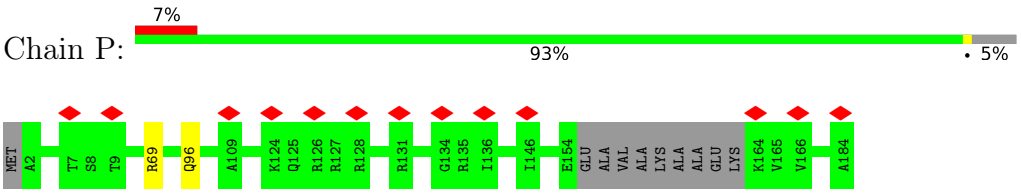
• Molecule 16: 60S ribosomal protein L15-A



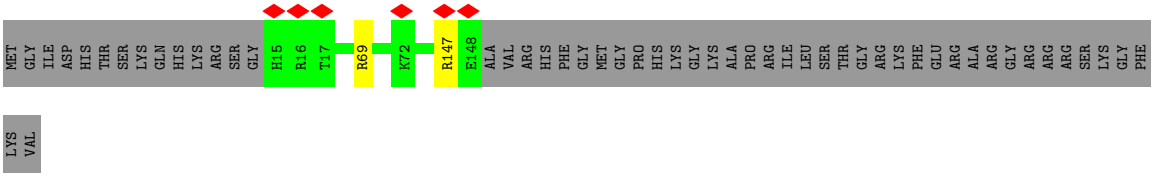
• Molecule 17: 60S ribosomal protein L16-A



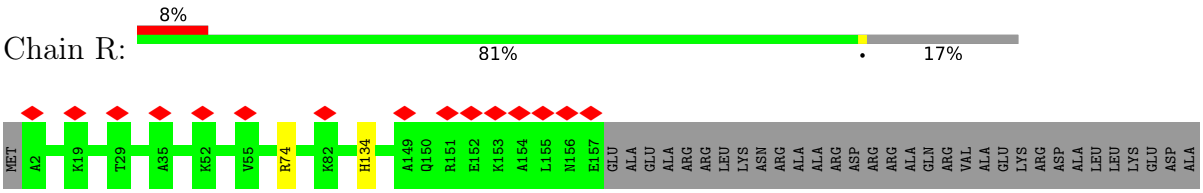
• Molecule 18: 60S ribosomal protein L17-A



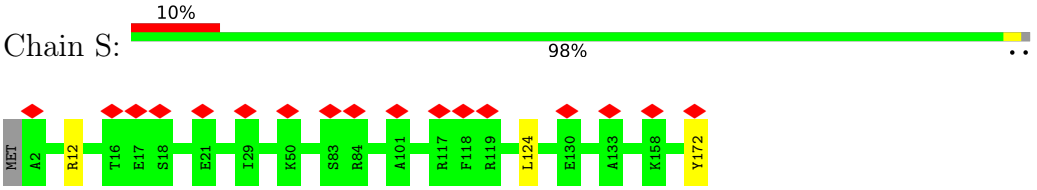
• Molecule 19: 60S ribosomal protein L18-A



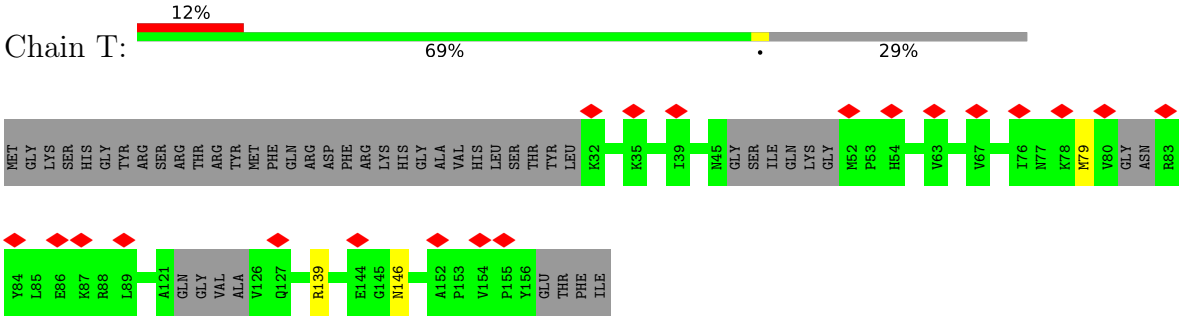
• Molecule 20: 60S ribosomal protein L19-A



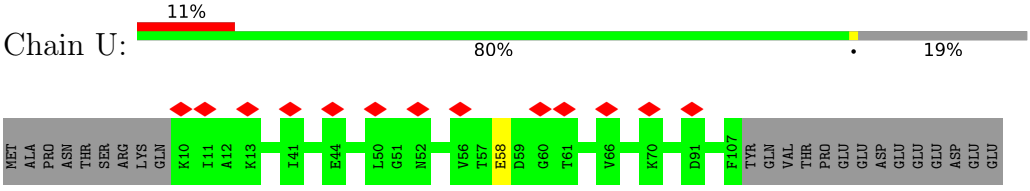
• Molecule 21: 60S ribosomal protein L20-A



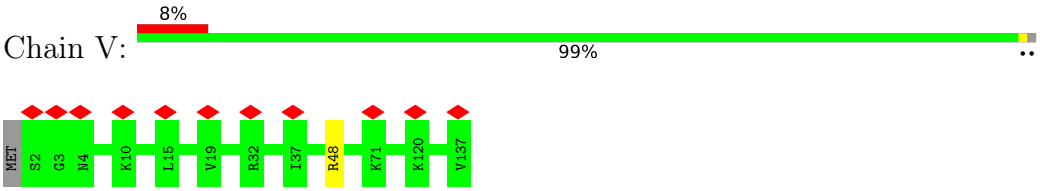
• Molecule 22: 60S ribosomal protein L21-A



• Molecule 23: 60S ribosomal protein L22-A

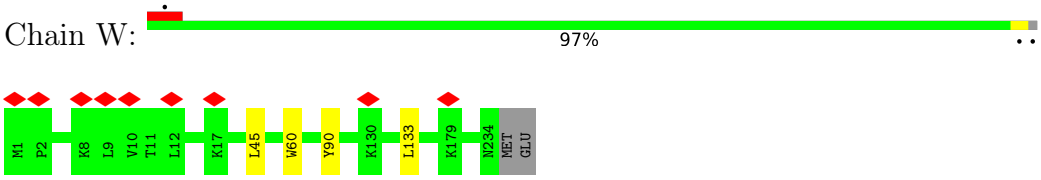


• Molecule 24: 60S ribosomal protein L23-A



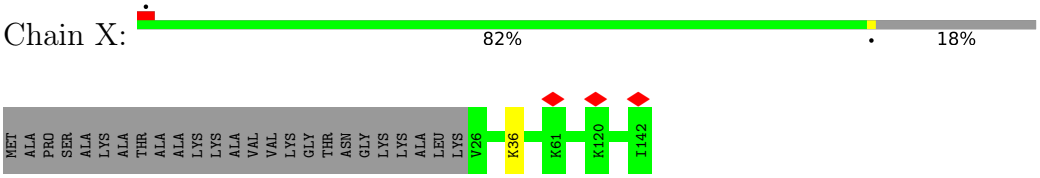
• Molecule 25: Ribosome assembly factor MRT4

Chain W:



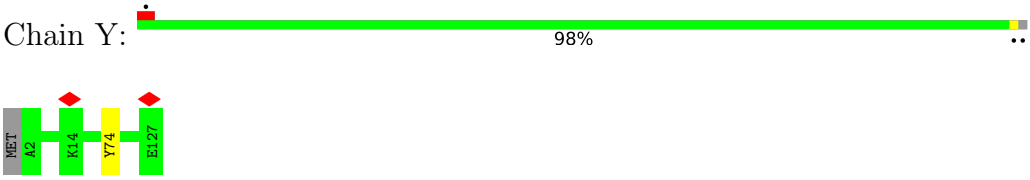
• Molecule 26: 60S ribosomal protein L25

Chain X:



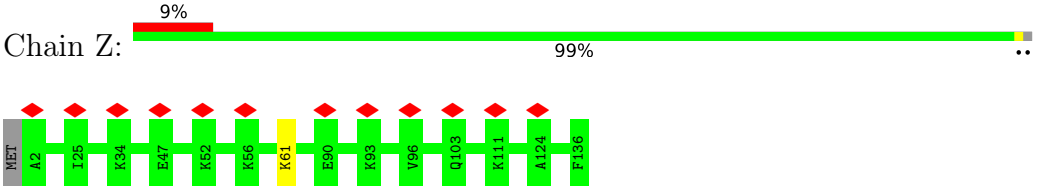
• Molecule 27: 60S ribosomal protein L26-A

Chain Y:



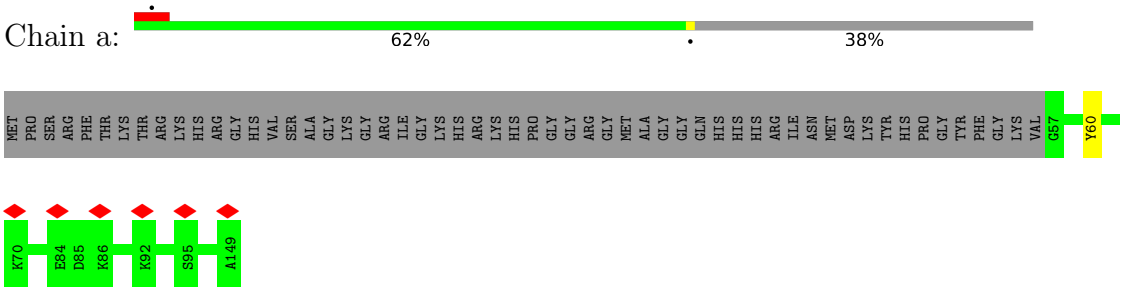
• Molecule 28: 60S ribosomal protein L27-A

Chain Z:



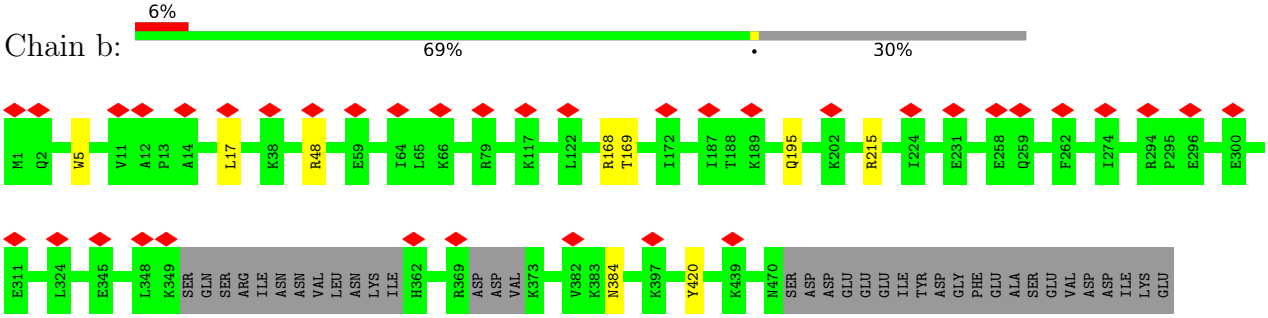
• Molecule 29: 60S ribosomal protein L28

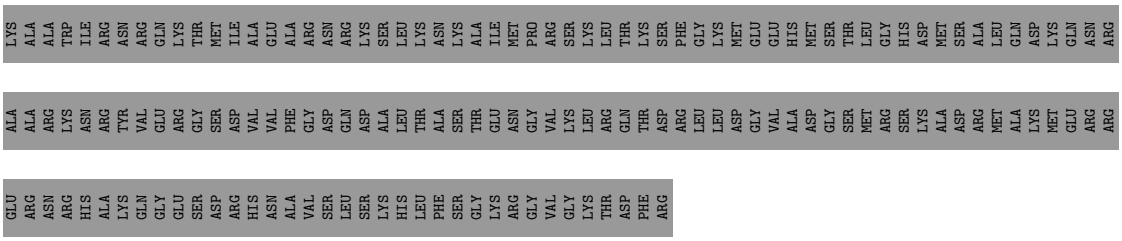
Chain a:



• Molecule 30: Nucleolar GTP-binding protein 1

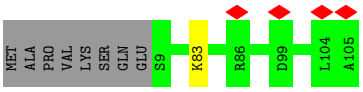
Chain b:





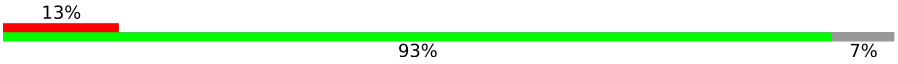
• Molecule 31: 60S ribosomal protein L30

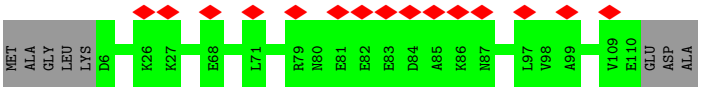
Chain c:



• Molecule 32: 60S ribosomal protein L31-A

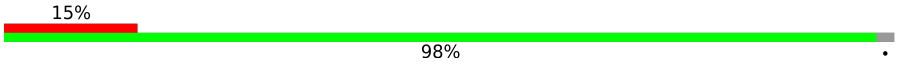
Chain d:

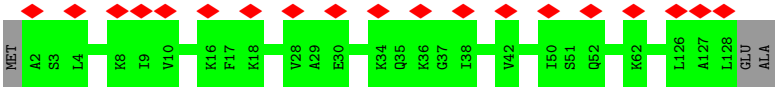




• Molecule 33: 60S ribosomal protein L32

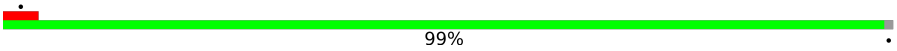
Chain e:

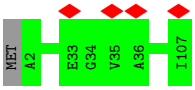




• Molecule 34: 60S ribosomal protein L33-A

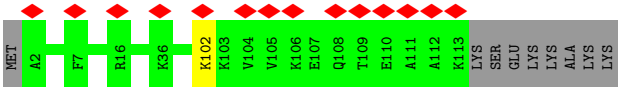
Chain f:





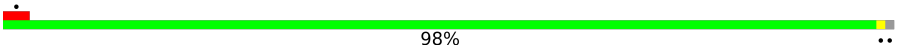
• Molecule 35: 60S ribosomal protein L34-A

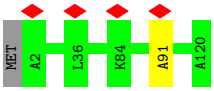
Chain g:



• Molecule 36: 60S ribosomal protein L35-A

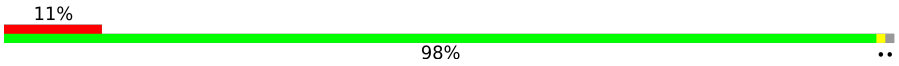
Chain h:

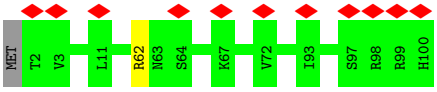




• Molecule 37: 60S ribosomal protein L36-A

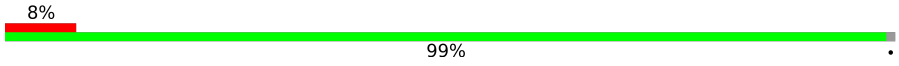
Chain i:

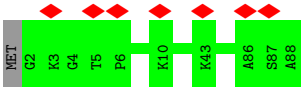




• Molecule 38: 60S ribosomal protein L37-A

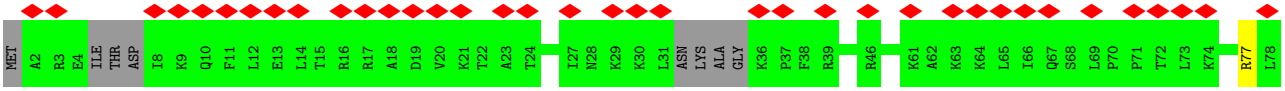
Chain j:





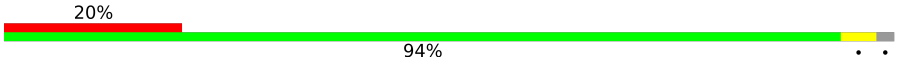
• Molecule 39: 60S ribosomal protein L38

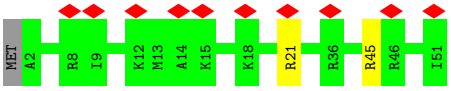
Chain k:



• Molecule 40: 60S ribosomal protein L39

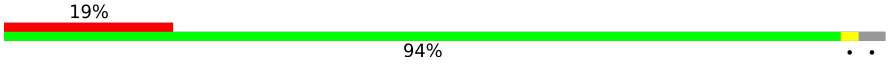
Chain l:

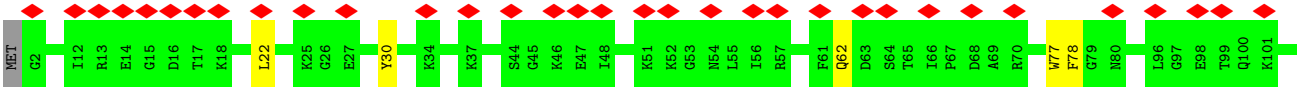


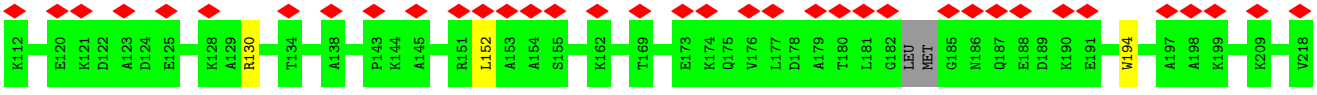


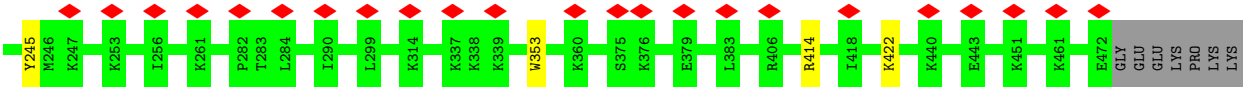
• Molecule 41: Nucleolar GTP-binding protein 2

Chain m:



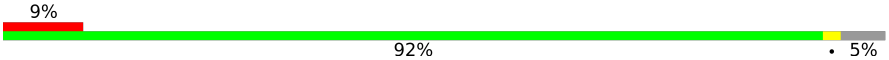


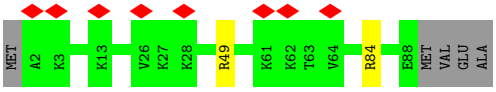




• Molecule 42: 60S ribosomal protein L43-A

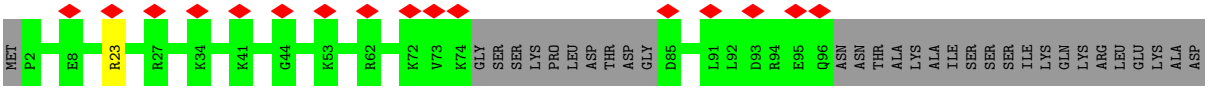
Chain p:

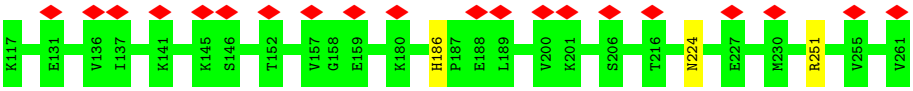




• Molecule 43: Ribosome biogenesis protein NSA2

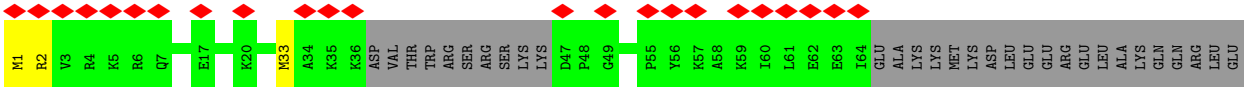
Chain r:



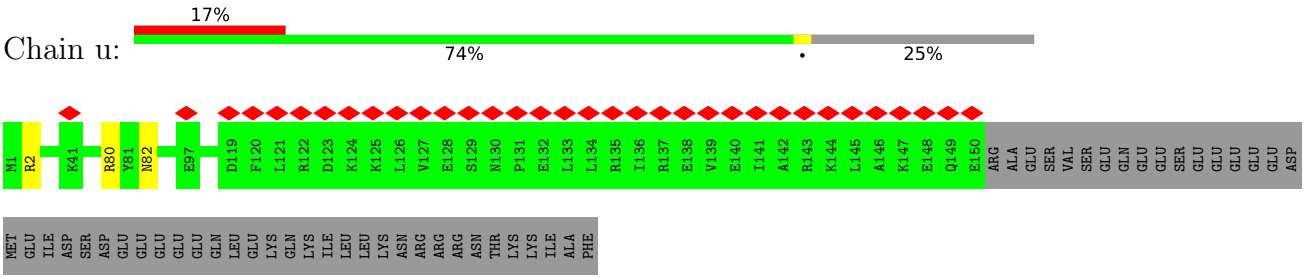


• Molecule 44: Nuclear GTP-binding protein NUG1

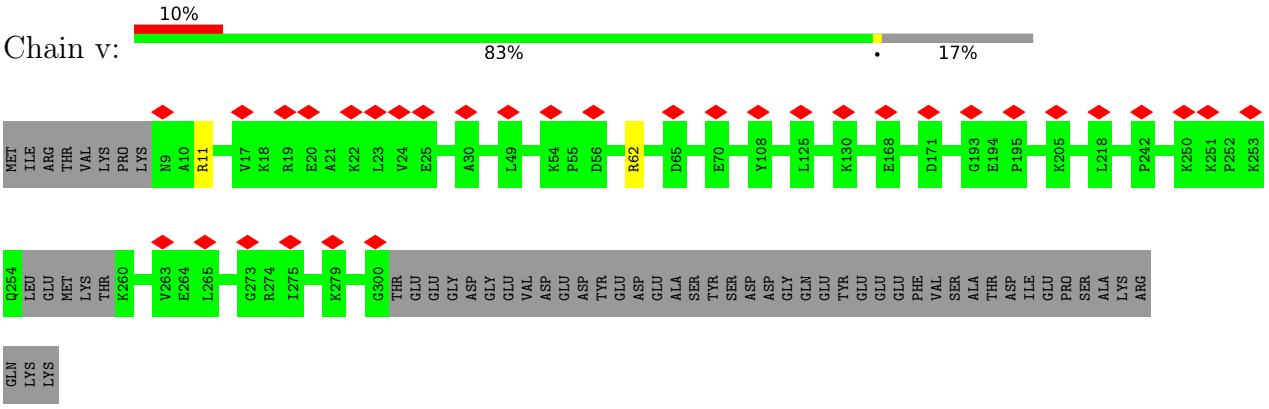
Chain s:



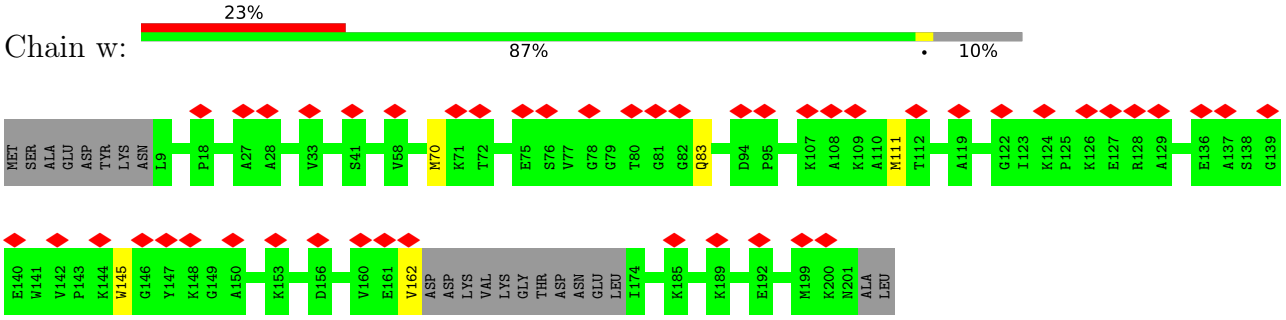
• Molecule 45: Ribosome biogenesis protein RLP24



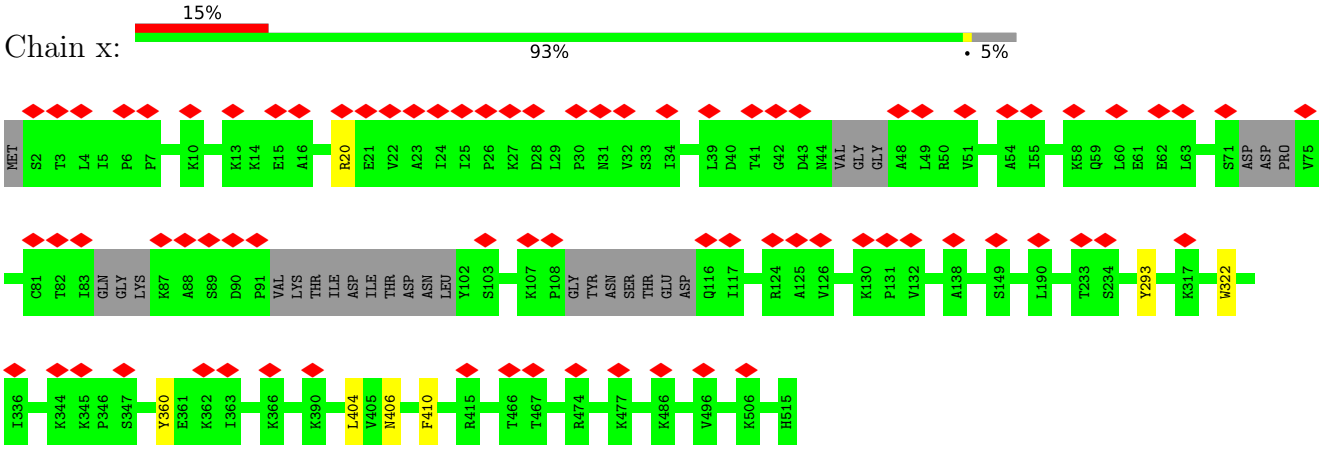
• Molecule 46: Ribosome biogenesis protein RPF2



• Molecule 47: Regulator of ribosome biosynthesis

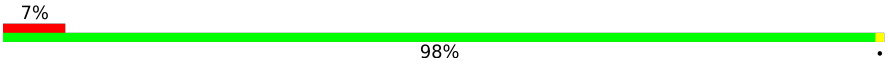


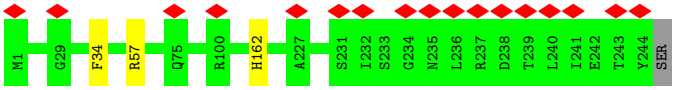
• Molecule 48: Ribosome assembly protein 4



• Molecule 49: Eukaryotic translation initiation factor 6

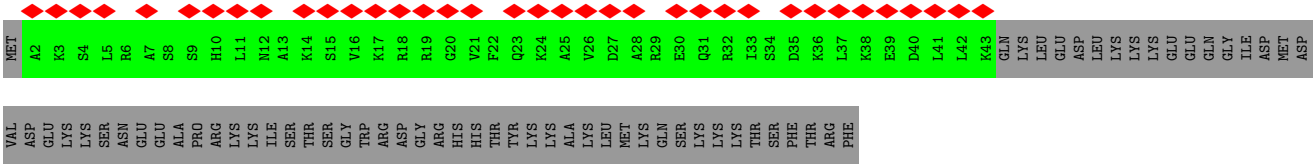
Chain y:





• Molecule 50: 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	18823	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	0.136	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.026	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	0/72171	0.74	44/112459 (0.0%)
2	2	0.16	0/3678	0.77	4/5722 (0.1%)
3	3	0.16	0/2883	0.78	6/4491 (0.1%)
4	5	0.24	0/649	0.37	0/848
5	A	0.24	0/1547	0.43	0/2079
6	B	0.24	0/3152	0.43	0/4239
7	C	0.24	0/2735	0.41	0/3700
8	D	0.24	0/2198	0.40	0/2964
9	E	0.25	0/1260	0.40	0/1694
10	F	0.25	0/1821	0.38	0/2451
11	G	0.24	0/1816	0.41	0/2450
12	H	0.24	0/1514	0.42	0/2039
13	J	0.24	0/1374	0.43	0/1842
14	L	0.24	0/1524	0.41	0/2046
15	M	0.23	0/1074	0.40	0/1446
16	N	0.23	0/1757	0.41	0/2354
17	O	0.24	0/1585	0.38	0/2128
18	P	0.24	0/1401	0.41	0/1881
19	Q	0.25	0/1050	0.42	0/1419
20	R	0.23	0/1275	0.39	0/1702
21	S	0.24	0/1473	0.41	0/1980
22	T	0.24	0/918	0.41	0/1229
23	U	0.25	0/790	0.43	0/1069
24	V	0.25	0/1018	0.42	0/1369
25	W	0.24	0/1918	0.41	0/2586
26	X	0.24	0/952	0.40	0/1285
27	Y	0.23	0/1004	0.39	0/1341
28	Z	0.24	0/1118	0.41	0/1497
29	a	0.25	0/751	0.39	0/1013
30	b	0.24	0/3764	0.40	0/5075
31	c	0.24	0/751	0.39	0/1008
32	d	0.23	0/870	0.39	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	e	0.23	0/1041	0.40	0/1394
34	f	0.25	0/868	0.42	0/1168
35	g	0.23	0/891	0.42	0/1191
36	h	0.24	0/978	0.39	0/1301
37	i	0.24	0/778	0.38	0/1034
38	j	0.25	0/696	0.42	0/923
39	k	0.25	0/567	0.42	0/754
40	l	0.24	0/443	0.41	0/588
41	m	0.23	0/3848	0.41	0/5181
42	p	0.24	0/672	0.45	0/895
43	r	0.24	0/1892	0.42	0/2528
44	s	0.24	0/448	0.39	0/585
45	u	0.24	0/1287	0.38	0/1711
46	v	0.24	0/2361	0.40	0/3153
47	w	0.23	0/1471	0.40	0/1980
48	x	0.23	0/3897	0.41	0/5282
49	y	0.23	0/1872	0.43	0/2548
50	z	0.24	0/336	0.33	0/443
All	All	0.20	0/146137	0.62	54/213233 (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
41	m	0	1

There are no bond length outliers.

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	3	98	C	C2-N1-C1'	7.20	126.72	118.80
1	1	1082	U	OP1-P-OP2	-6.81	109.39	119.60
1	1	2376	G	OP1-P-OP2	-6.80	109.39	119.60
1	1	3157	U	OP1-P-OP2	-6.80	109.40	119.60
1	1	2943	G	OP1-P-OP2	-6.80	109.41	119.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
41	m	77	TRP	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	71/120 (59%)	71 (100%)	0	0	100	100
5	A	194/254 (76%)	187 (96%)	7 (4%)	0	100	100
6	B	384/387 (99%)	362 (94%)	22 (6%)	0	100	100
7	C	348/362 (96%)	323 (93%)	24 (7%)	1 (0%)	41	72
8	D	263/297 (89%)	248 (94%)	15 (6%)	0	100	100
9	E	152/176 (86%)	145 (95%)	7 (5%)	0	100	100
10	F	220/244 (90%)	215 (98%)	5 (2%)	0	100	100
11	G	226/256 (88%)	213 (94%)	13 (6%)	0	100	100
12	H	186/191 (97%)	178 (96%)	8 (4%)	0	100	100
13	J	167/174 (96%)	155 (93%)	12 (7%)	0	100	100
14	L	185/199 (93%)	169 (91%)	16 (9%)	0	100	100
15	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
16	N	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
17	O	195/199 (98%)	195 (100%)	0	0	100	100
18	P	170/184 (92%)	166 (98%)	4 (2%)	0	100	100
19	Q	132/186 (71%)	130 (98%)	2 (2%)	0	100	100
20	R	154/189 (82%)	153 (99%)	1 (1%)	0	100	100
21	S	169/172 (98%)	160 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	T	105/160 (66%)	96 (91%)	9 (9%)	0	100	100
23	U	96/121 (79%)	95 (99%)	1 (1%)	0	100	100
24	V	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
25	W	232/236 (98%)	223 (96%)	9 (4%)	0	100	100
26	X	115/142 (81%)	112 (97%)	3 (3%)	0	100	100
27	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
28	Z	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
29	a	91/149 (61%)	89 (98%)	2 (2%)	0	100	100
30	b	449/647 (69%)	421 (94%)	28 (6%)	0	100	100
31	c	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
32	d	103/113 (91%)	100 (97%)	3 (3%)	0	100	100
33	e	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
34	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
35	g	110/121 (91%)	109 (99%)	1 (1%)	0	100	100
36	h	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	17	49
37	i	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
38	j	85/88 (97%)	84 (99%)	1 (1%)	0	100	100
39	k	64/78 (82%)	64 (100%)	0	0	100	100
40	l	48/51 (94%)	48 (100%)	0	0	100	100
41	m	465/486 (96%)	429 (92%)	35 (8%)	1 (0%)	47	78
42	p	85/92 (92%)	80 (94%)	5 (6%)	0	100	100
43	r	224/261 (86%)	206 (92%)	18 (8%)	0	100	100
44	s	50/520 (10%)	47 (94%)	3 (6%)	0	100	100
45	u	148/199 (74%)	143 (97%)	5 (3%)	0	100	100
46	v	283/344 (82%)	277 (98%)	6 (2%)	0	100	100
47	w	178/203 (88%)	168 (94%)	10 (6%)	0	100	100
48	x	476/515 (92%)	456 (96%)	20 (4%)	0	100	100
49	y	242/245 (99%)	236 (98%)	6 (2%)	0	100	100
50	z	40/106 (38%)	38 (95%)	2 (5%)	0	100	100
All	All	8170/9771 (84%)	7809 (96%)	358 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	h	91	ALA
41	m	78	PHE
7	C	131	VAL

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	67/106 (63%)	66 (98%)	1 (2%)	65	82
5	A	155/196 (79%)	154 (99%)	1 (1%)	86	94
6	B	322/323 (100%)	316 (98%)	6 (2%)	57	78
7	C	283/289 (98%)	278 (98%)	5 (2%)	59	79
8	D	223/245 (91%)	221 (99%)	2 (1%)	78	90
9	E	134/153 (88%)	134 (100%)	0	100	100
10	F	186/205 (91%)	185 (100%)	1 (0%)	88	94
11	G	187/208 (90%)	180 (96%)	7 (4%)	34	62
12	H	168/171 (98%)	166 (99%)	2 (1%)	71	85
13	J	147/150 (98%)	145 (99%)	2 (1%)	67	83
14	L	149/159 (94%)	148 (99%)	1 (1%)	84	92
15	M	108/109 (99%)	106 (98%)	2 (2%)	57	78
16	N	175/176 (99%)	174 (99%)	1 (1%)	86	94
17	O	160/162 (99%)	158 (99%)	2 (1%)	69	84
18	P	140/146 (96%)	138 (99%)	2 (1%)	67	83
19	Q	110/151 (73%)	108 (98%)	2 (2%)	59	79
20	R	129/154 (84%)	127 (98%)	2 (2%)	62	81
21	S	155/156 (99%)	152 (98%)	3 (2%)	57	78
22	T	99/137 (72%)	96 (97%)	3 (3%)	41	68
23	U	85/107 (79%)	84 (99%)	1 (1%)	71	85
24	V	104/105 (99%)	103 (99%)	1 (1%)	76	88
25	W	211/213 (99%)	207 (98%)	4 (2%)	57	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
26	X	102/118 (86%)	101 (99%)	1 (1%)	76 88
27	Y	109/110 (99%)	108 (99%)	1 (1%)	78 90
28	Z	115/116 (99%)	114 (99%)	1 (1%)	78 90
29	a	76/119 (64%)	75 (99%)	1 (1%)	69 84
30	b	409/573 (71%)	400 (98%)	9 (2%)	52 75
31	c	81/88 (92%)	80 (99%)	1 (1%)	71 85
32	d	92/97 (95%)	92 (100%)	0	100 100
33	e	109/111 (98%)	109 (100%)	0	100 100
34	f	90/91 (99%)	90 (100%)	0	100 100
35	g	95/103 (92%)	94 (99%)	1 (1%)	73 86
36	h	104/105 (99%)	104 (100%)	0	100 100
37	i	81/82 (99%)	80 (99%)	1 (1%)	71 85
38	j	70/71 (99%)	70 (100%)	0	100 100
39	k	63/69 (91%)	62 (98%)	1 (2%)	62 81
40	l	45/46 (98%)	43 (96%)	2 (4%)	28 58
41	m	413/428 (96%)	403 (98%)	10 (2%)	49 74
42	p	68/72 (94%)	66 (97%)	2 (3%)	42 69
43	r	203/229 (89%)	199 (98%)	4 (2%)	55 77
44	s	48/445 (11%)	45 (94%)	3 (6%)	18 47
45	u	133/180 (74%)	130 (98%)	3 (2%)	50 74
46	v	258/309 (84%)	256 (99%)	2 (1%)	81 91
47	w	161/179 (90%)	156 (97%)	5 (3%)	40 68
48	x	428/451 (95%)	421 (98%)	7 (2%)	62 81
49	y	210/211 (100%)	207 (99%)	3 (1%)	67 83
50	z	36/95 (38%)	36 (100%)	0	100 100
All	All	7096/8319 (85%)	6987 (98%)	109 (2%)	66 82

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	b	48	ARG
41	m	30	TYR
48	x	20	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	b	169	THR
35	g	102	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
45	u	82	ASN
49	y	82	GLN
46	v	9	ASN
48	x	116	GLN
13	J	150	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2987/3396 (87%)	579 (19%)	80 (2%)
2	2	153/158 (96%)	25 (16%)	2 (1%)
3	3	120/121 (99%)	17 (14%)	1 (0%)
All	All	3260/3675 (88%)	621 (19%)	83 (2%)

5 of 621 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	14	U
1	1	20	A
1	1	26	A
1	1	40	A

5 of 83 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2728	G
1	1	3078	U
1	1	2761	G
1	1	2869	U
1	1	3228	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.

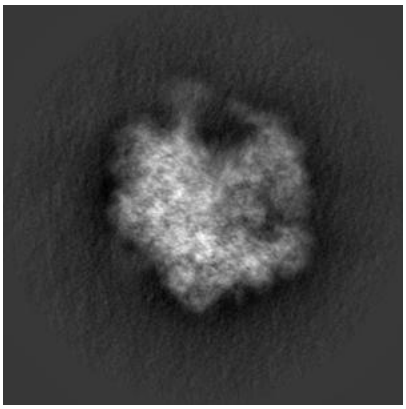
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12892. These allow visual inspection of the internal detail of the map and identification of artifacts.

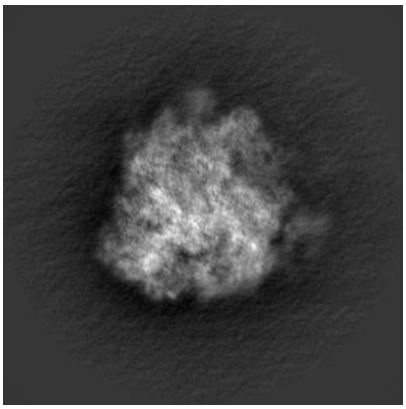
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

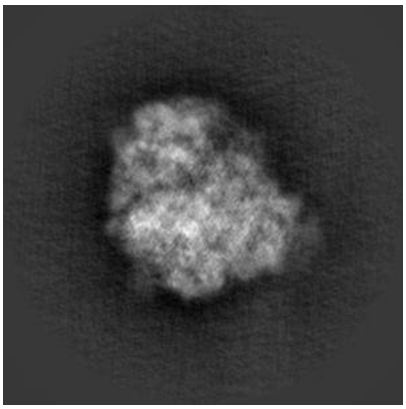
6.1.1 Primary map



X

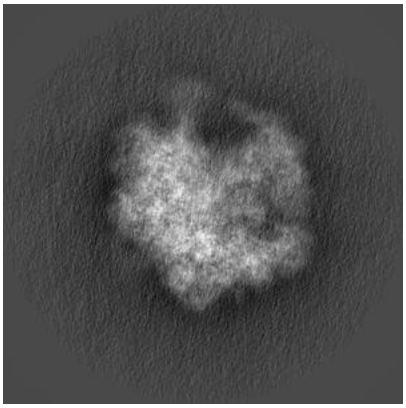


Y

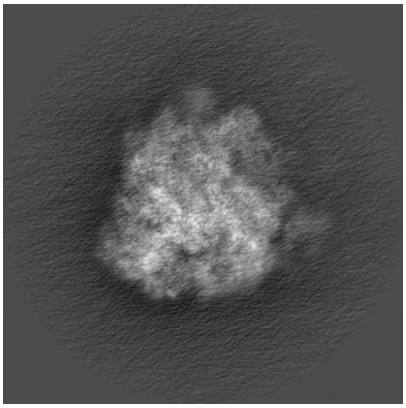


Z

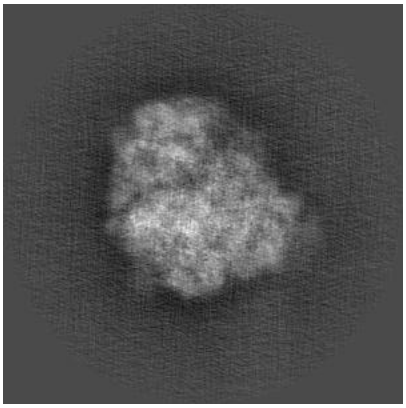
6.1.2 Raw map



X



Y

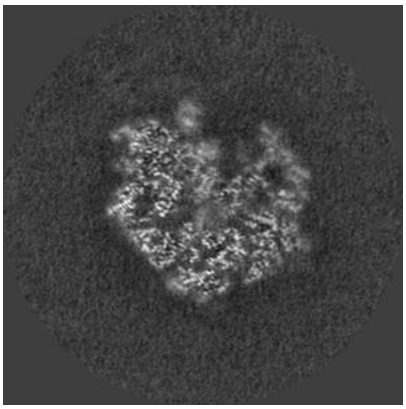


Z

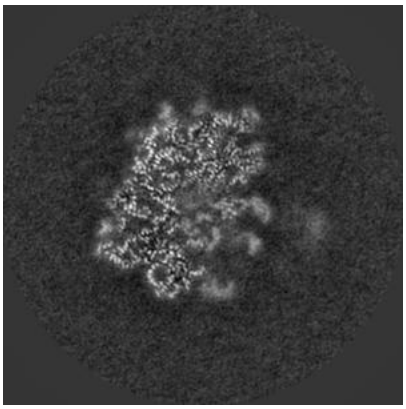
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

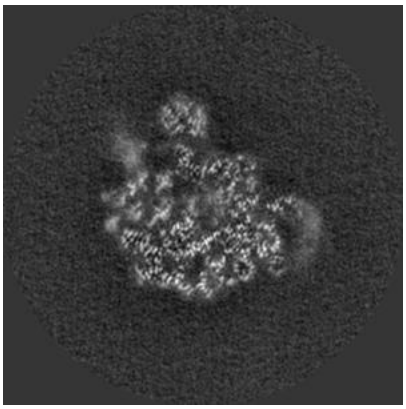
6.2.1 Primary map



X Index: 200

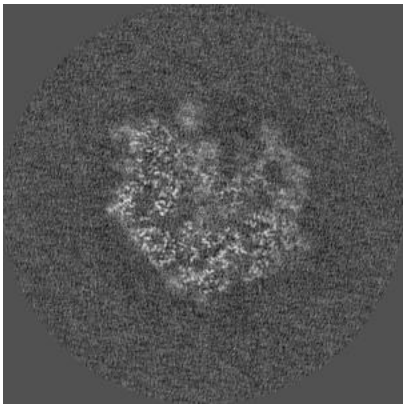


Y Index: 200

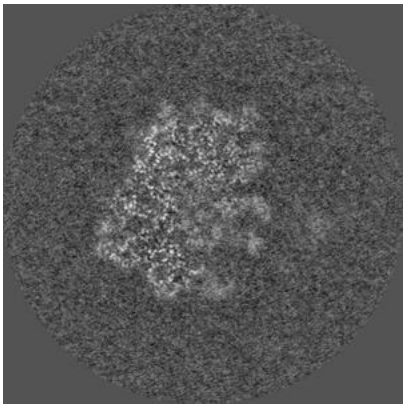


Z Index: 200

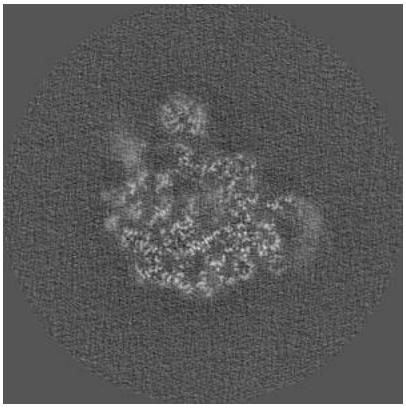
6.2.2 Raw map



X Index: 200



Y Index: 200

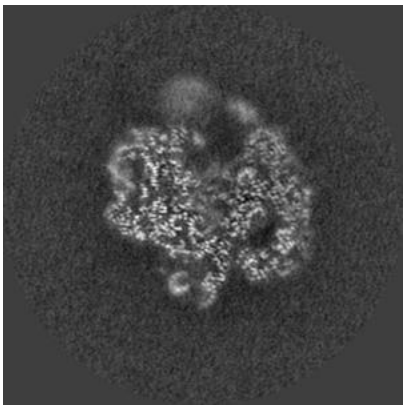


Z Index: 200

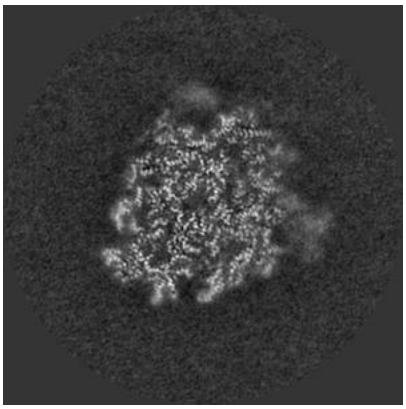
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

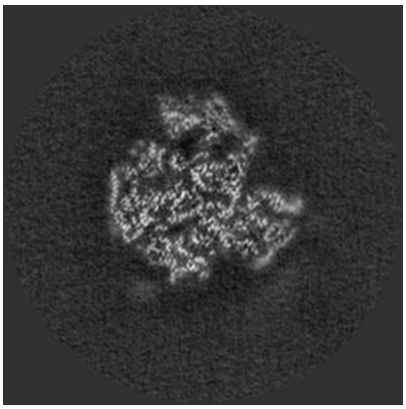
6.3.1 Primary map



X Index: 184

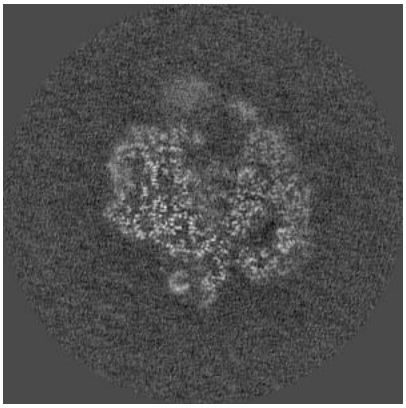


Y Index: 177

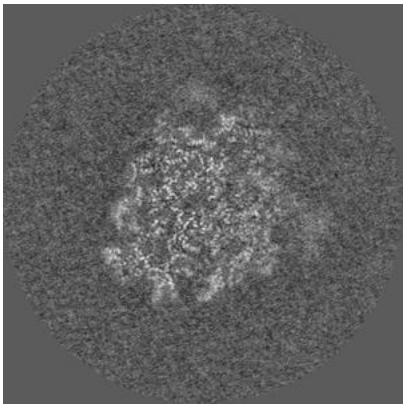


Z Index: 166

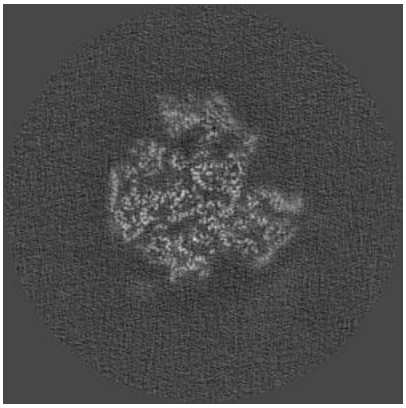
6.3.2 Raw map



X Index: 184



Y Index: 177



Z Index: 166

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

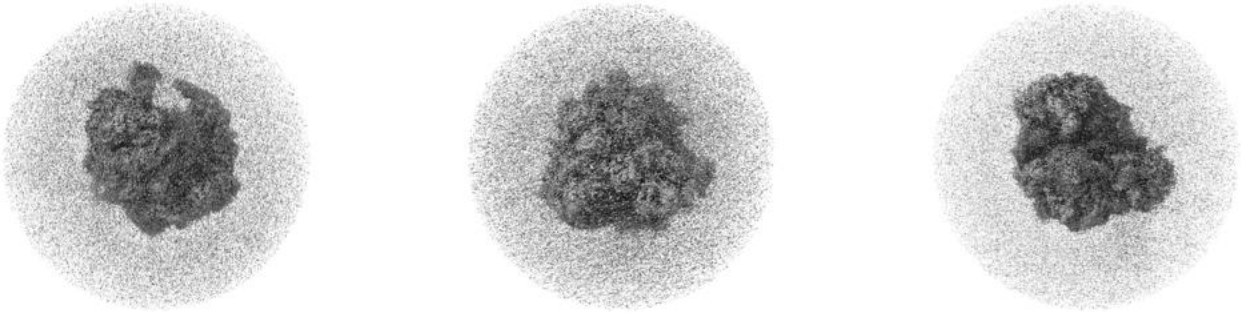
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

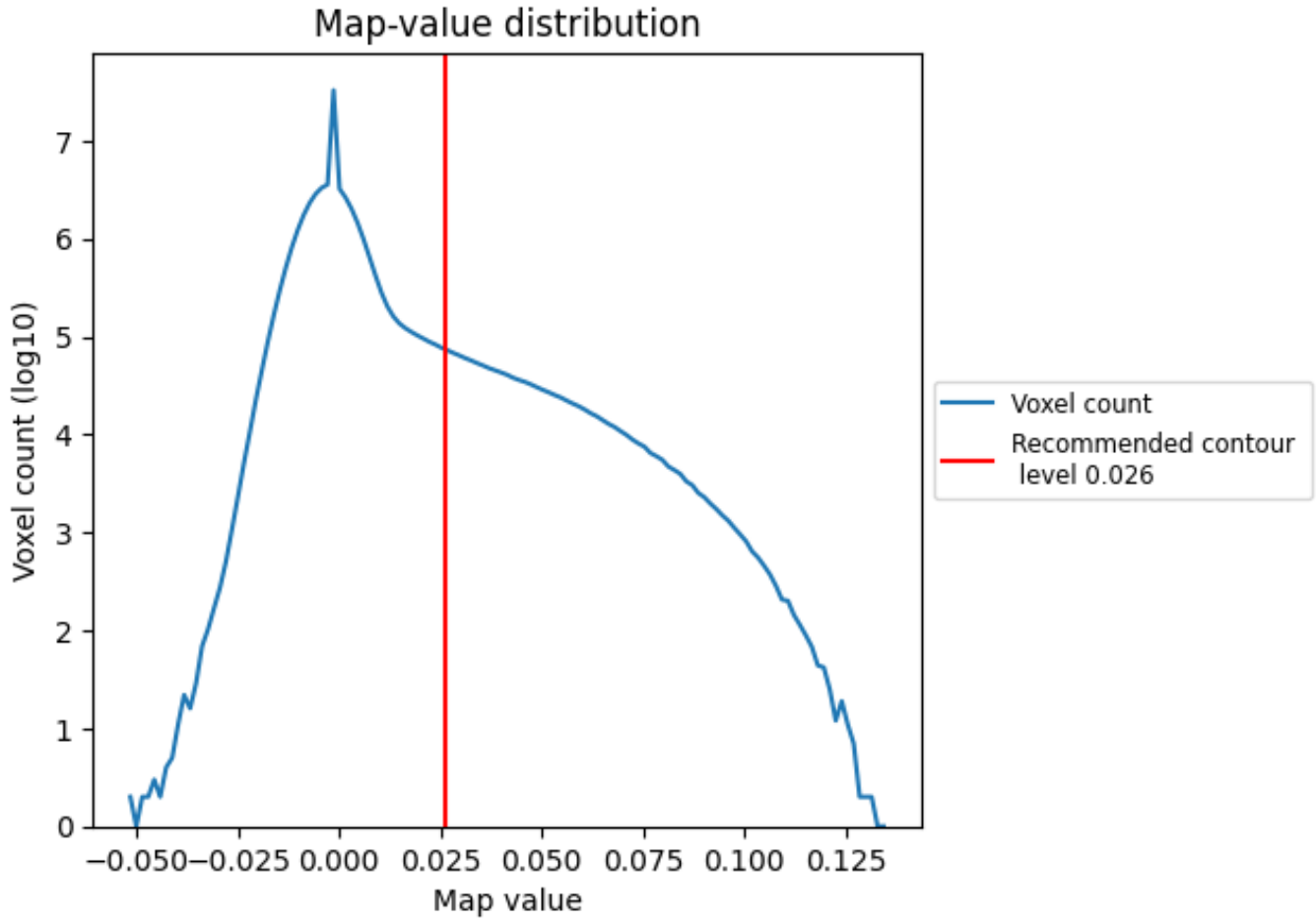
6.5 Mask visualisation (i)

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

7 Map analysis

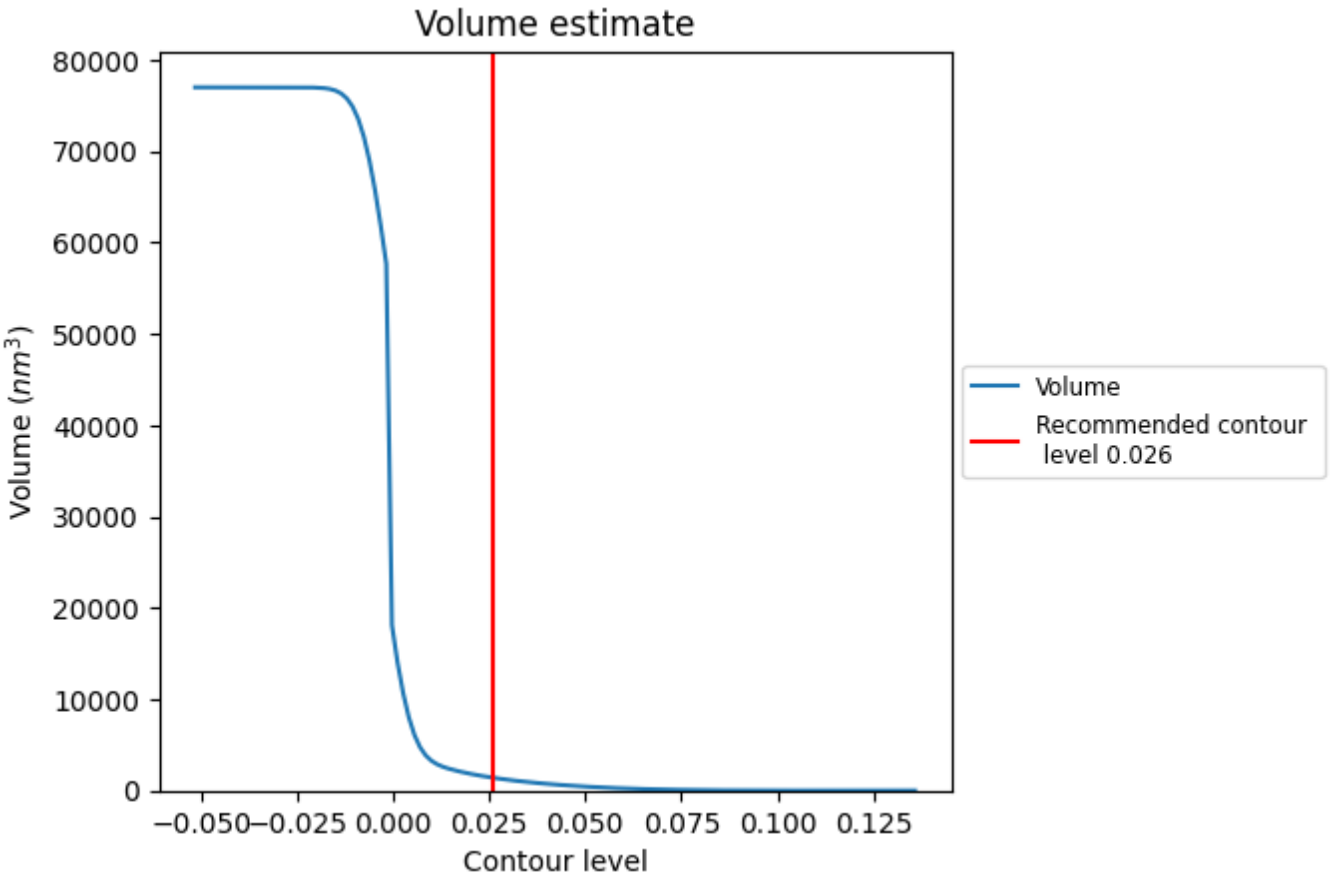
This section contains the results of statistical analysis of the map.

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.

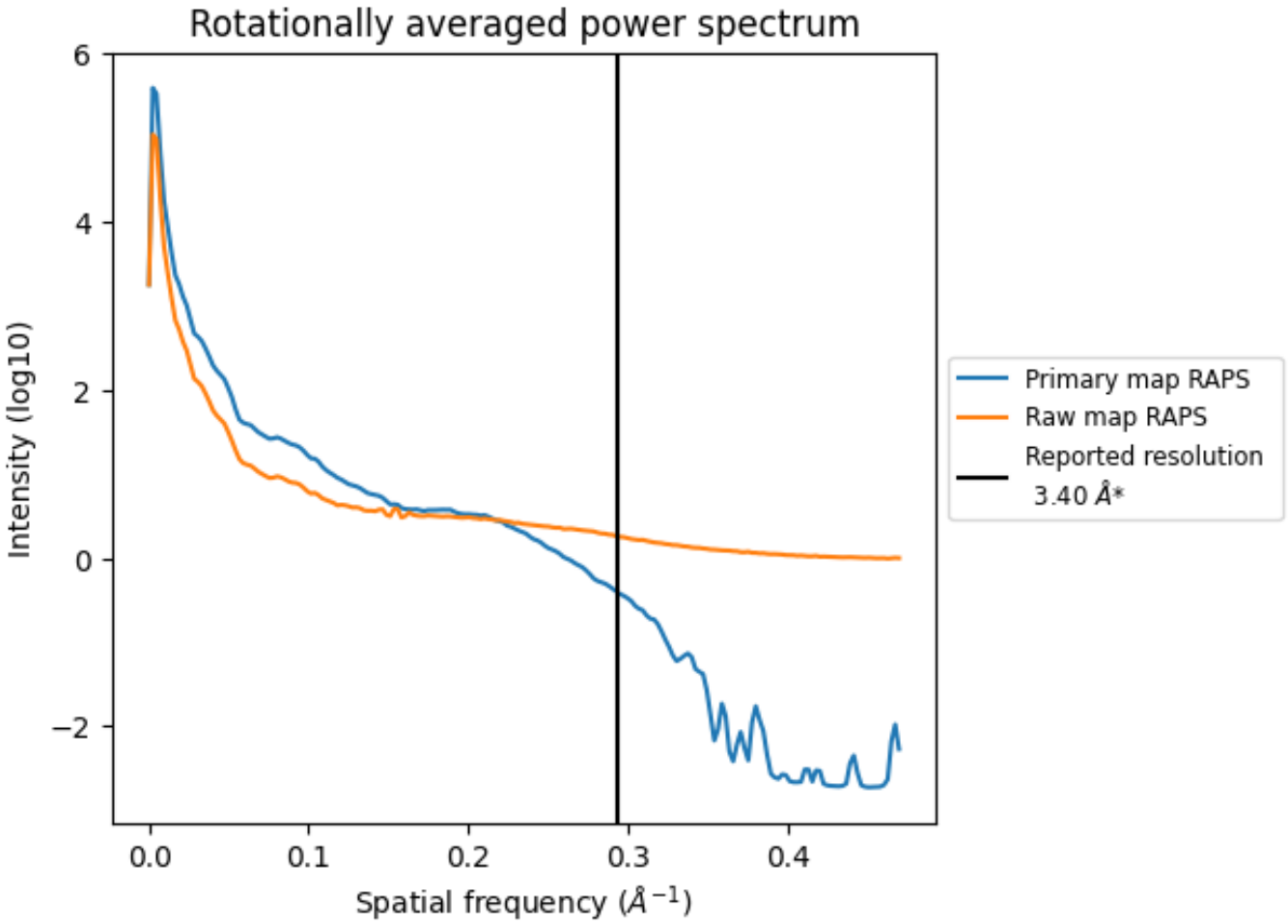
7.2 Volume estimate (i)



The volume at the recommended contour level is 1405 nm^3; this corresponds to an approximate mass of 1269 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)

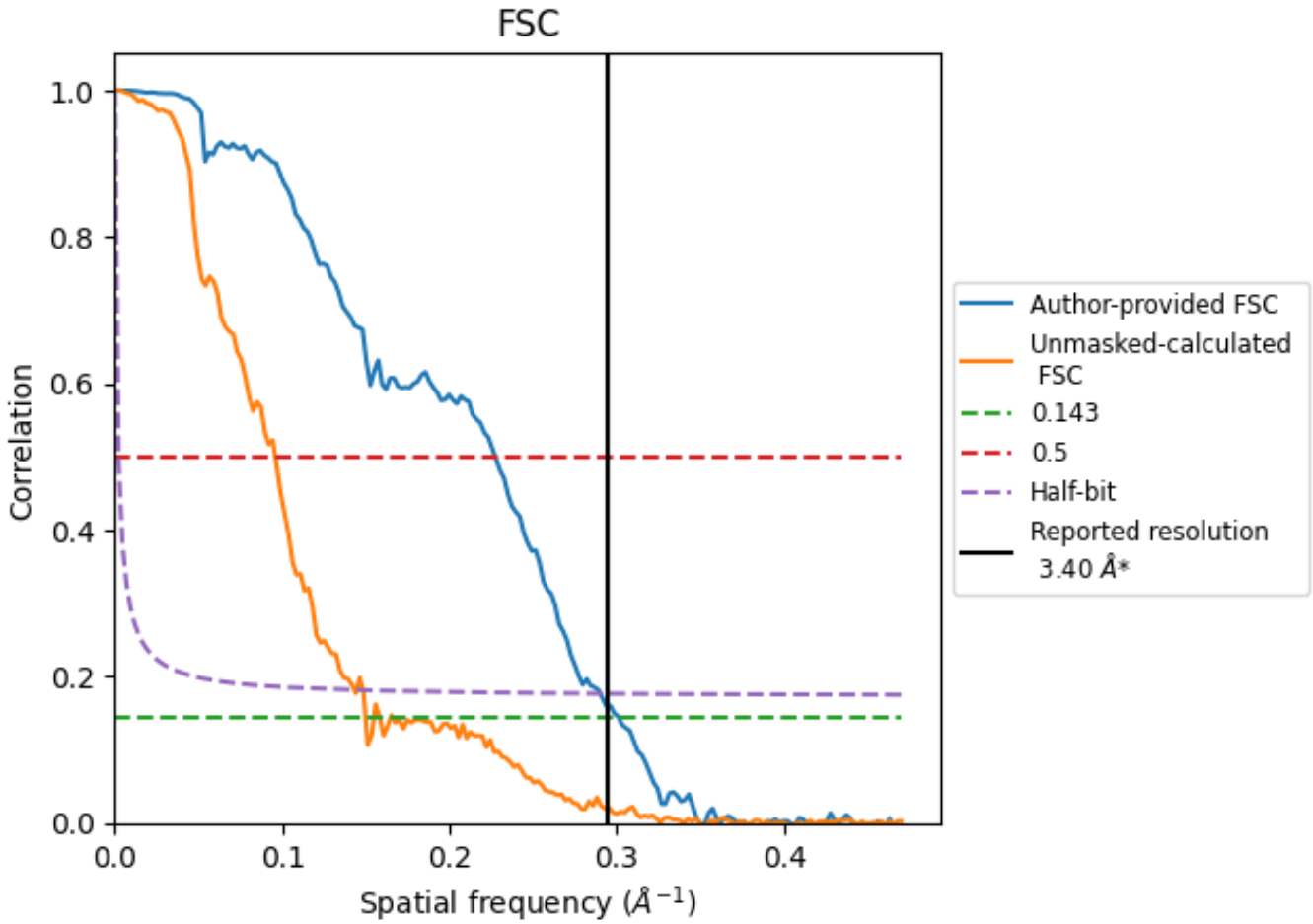


*Reported resolution corresponds to spatial frequency of 0.294 $Å^{-1}$

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 0.294 Å^{-1}

8.2 Resolution estimates (i)

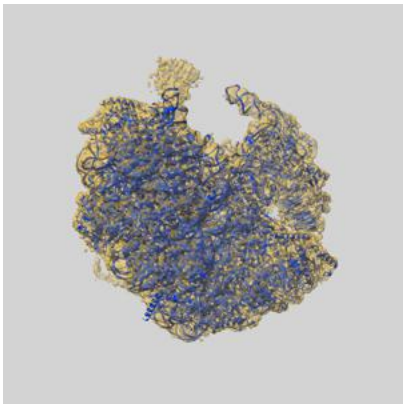
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.32	4.40	3.45
Unmasked-calculated*	6.67	10.43	6.98

*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 6.67 differs from the reported value 3.4 by more than 10 %

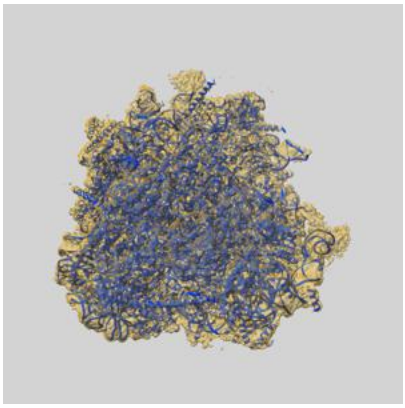
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12892 and PDB model 7OH3. Per-residue inclusion information can be found in section 3 on page 13.

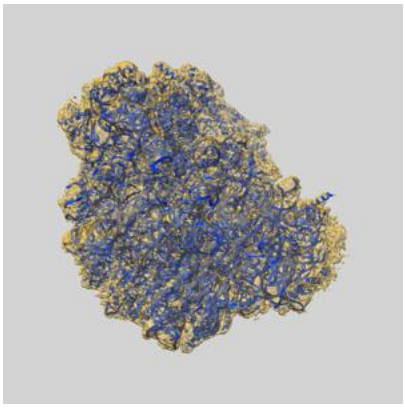
9.1 Map-model overlay



X



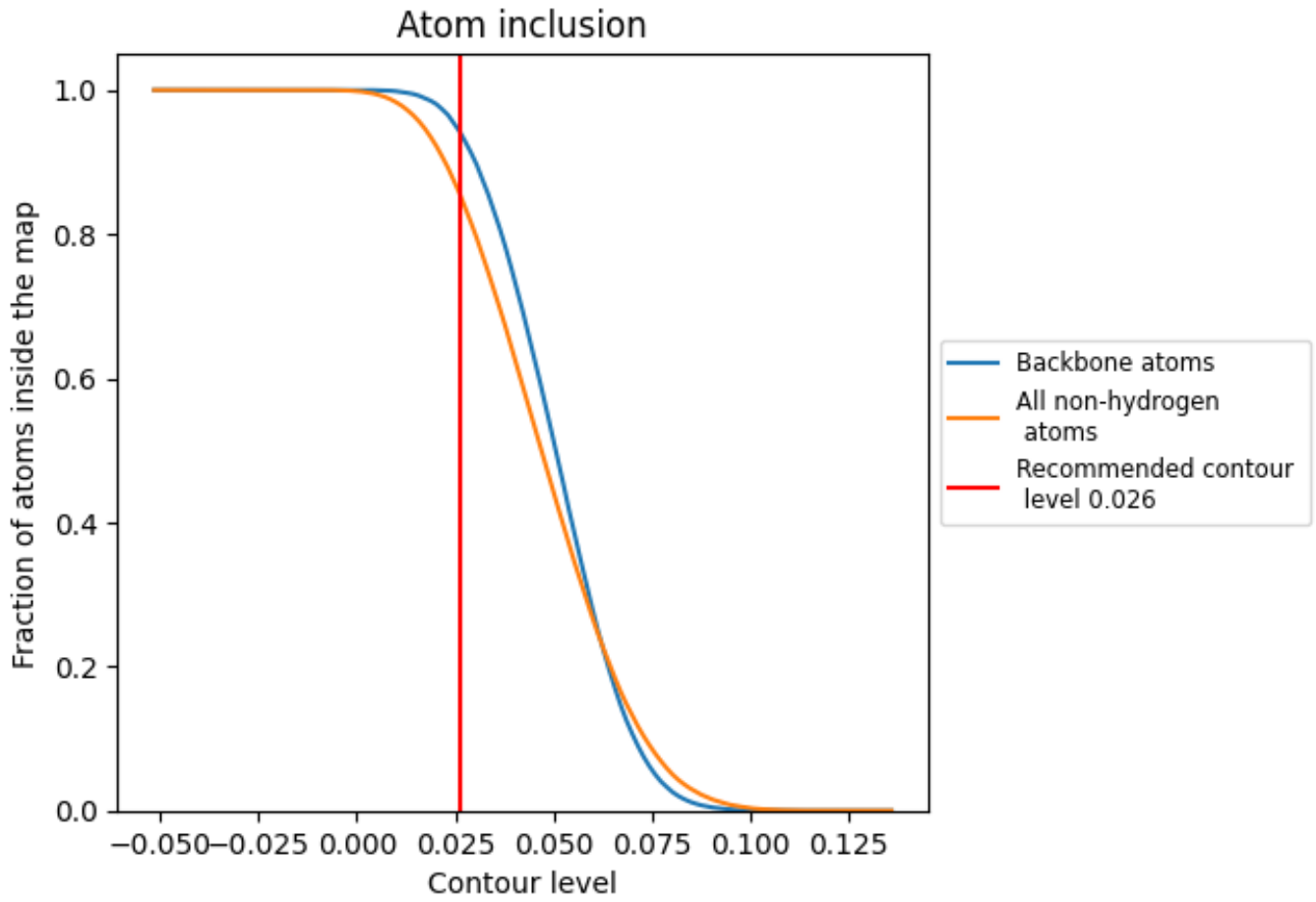
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.026 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 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.