



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 01:37 PM UTC

PDB ID : 8Z70 / pdb_00008z70
EMDB ID : EMD-38656
Title : State 1 (S1) of yeast 80S ribosome bound to 2 tRNAs during mRNA decoding
Authors : Cheng, J.; Wu, C.L.; Li, J.X.; Zhang, X.Z.
Deposited on : 2024-04-19
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

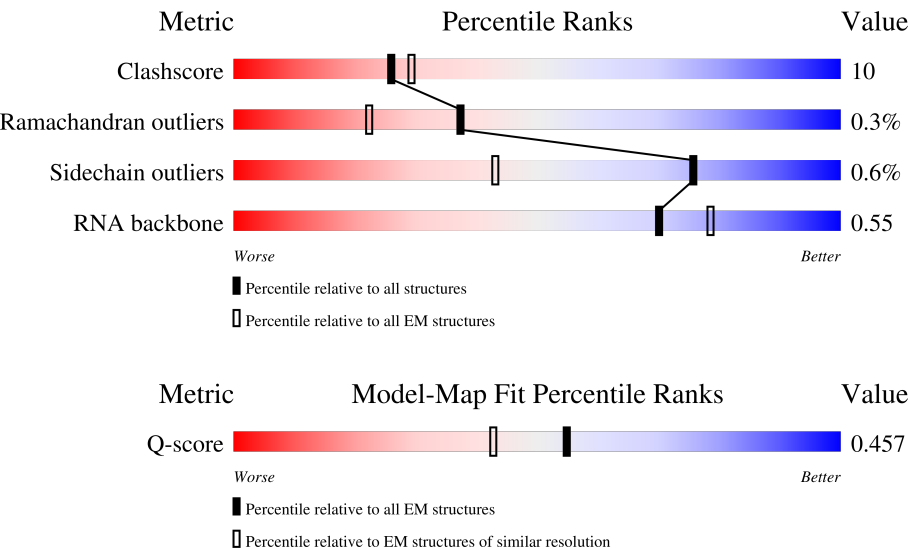
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	2	1799	
2	SA	222	
3	SB	206	

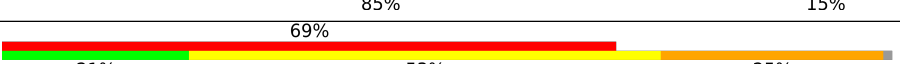
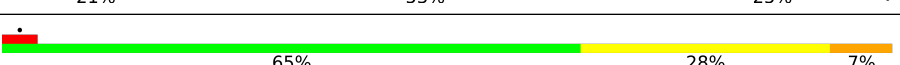
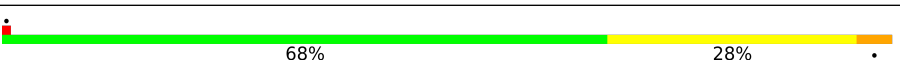
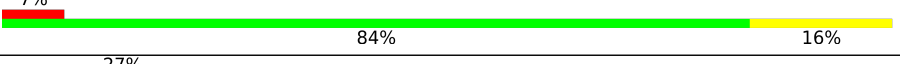
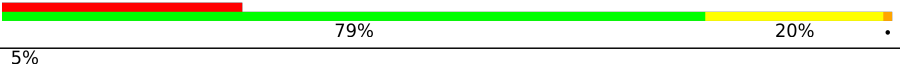
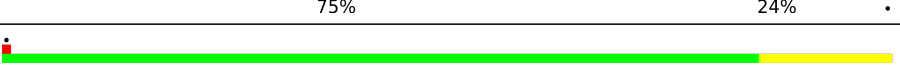
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	SC	92	
5	SD	121	
6	SE	117	
7	SF	141	
8	SG	121	
9	SH	145	
10	SI	143	
11	SJ	100	
12	SK	108	
13	SL	63	
14	SM	53	
15	SN	73	
16	SO	312	
17	SP	206	
18	SQ	232	
19	SR	216	
20	SS	258	
21	ST	228	
22	SU	184	
23	SV	200	
24	SW	184	
25	SX	142	
26	SY	150	
27	SZ	127	
28	Sa	87	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Sb	129	
30	Sc	144	
31	Sd	134	
32	Se	94	
33	Sf	81	
34	Sg	60	
35	s	77	
36	t	75	
37	B	121	
38	C	158	
39	T	188	
40	Y	126	
41	A	3394	
42	D	251	
43	E	386	
44	F	361	
45	G	294	
46	H	175	
47	I	223	
48	J	233	
49	K	191	
50	L	218	
51	M	169	
52	N	193	
53	O	136	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	P	203	
55	Q	197	
56	R	183	
57	S	185	
58	U	171	
59	V	159	
60	W	100	
61	X	136	
62	Z	121	
63	a	125	
64	b	135	
65	c	148	
66	d	58	
67	e	96	
68	f	109	
69	g	127	
70	h	106	
71	i	112	
72	j	119	
73	k	99	
74	l	81	
75	m	77	
76	n	50	
77	o	52	
78	p	25	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	q	103	 85%15%
80	r	91	 74%26%
81	x	462	 89%65%27%• • 5%

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 206049 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 2 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 3 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 4 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 5 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SD	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 6 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SE	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 7 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	SF	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 8 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SG	121	Total	C	N	O	S	0	0
			961	599	182	178	2		

- Molecule 9 is a protein called Small ribosomal subunit protein uS13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 10 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SI	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 11 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 12 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	SK	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 13 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SL	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SM	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 15 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SN	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 16 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SO	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 17 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SP	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 18 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SQ	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 19 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 20 is a protein called Small ribosomal subunit protein eS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 21 is a protein called Small ribosomal subunit protein eS6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	ST	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 22 is a protein called Small ribosomal subunit protein eS7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SU	184	Total	C	N	O		0	0
			1473	946	263	264			

- Molecule 23 is a protein called Small ribosomal subunit protein eS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SV	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 24 is a protein called Small ribosomal subunit protein uS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SW	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 25 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 26 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SY	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 27 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SZ	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Sa	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 29 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 30 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 31 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sd	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 32 is a protein called Small ribosomal subunit protein eS26A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Se	94	Total	C	N	O	S	0	0
			750	462	157	126	5		

- Molecule 33 is a protein called Small ribosomal subunit protein eS27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sf	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called Small ribosomal subunit protein eS30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sg	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 35 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	s	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 36 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	t	75	Total	C	N	O	P	0	0
			1606	716	297	518	75		

- Molecule 37 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 38 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 39 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	T	188	Total	C	N	O	0	0
			1515	932	323	260		

- Molecule 40 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Y	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

- Molecule 41 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A	3187	Total	C	N	O	P	0	0
			68170	30449	12289	22245	3187		

- Molecule 42 is a protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	D	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 43 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	E	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 44 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	F	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 45 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	G	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 46 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	H	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 47 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	I	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	22	ILE	THR	conflict	UNP P05737

- Molecule 48 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	J	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 49 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	K	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 50 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	L	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 51 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	M	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 52 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	N	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 53 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 54 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	P	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 55 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Q	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 56 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	R	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 57 is a protein called Large ribosomal subunit protein eL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 58 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	U	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 59 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	V	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 60 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 61 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	X	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 62 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 63 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	a	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 64 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	b	135	Total	C	N	O		0	0
			1080	701	199	180			

- Molecule 65 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	c	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 66 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	d	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 67 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	e	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 68 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 69 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	g	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 70 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	h	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 71 is a protein called Large ribosomal subunit protein eL34A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 72 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	j	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 73 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	k	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 74 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	l	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 75 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	m	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 76 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 77 is a protein called Large ribosomal subunit protein eL40A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	o	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 78 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	p	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 79 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	q	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 80 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	r	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 81 is a protein called Elongation factor 1-alpha 1.

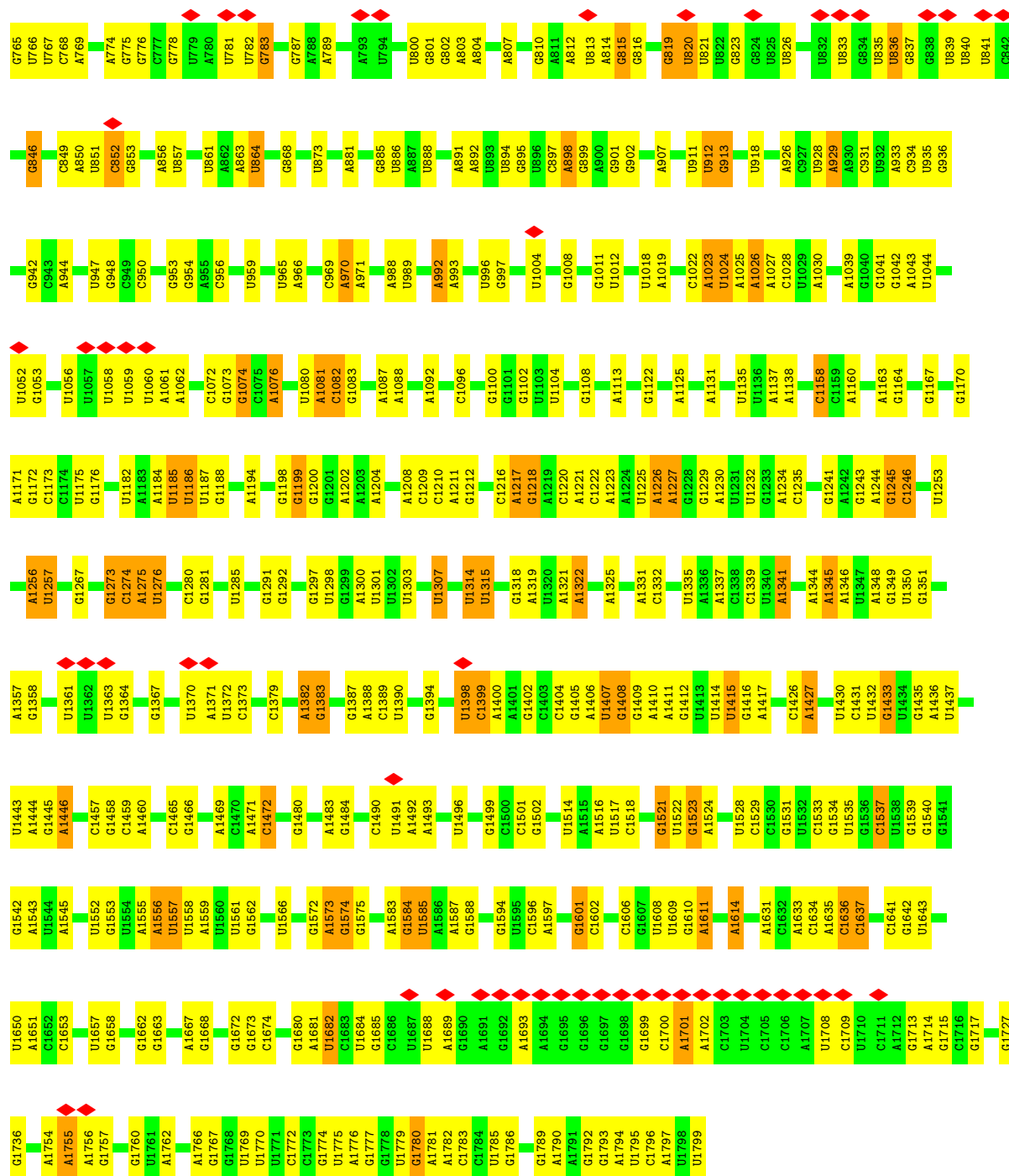
Mol	Chain	Residues	Atoms					AltConf	Trace
81	x	441	Total	C	N	O	S	0	0
			3379	2148	581	633	17		

3 Residue-property plots [i](#)

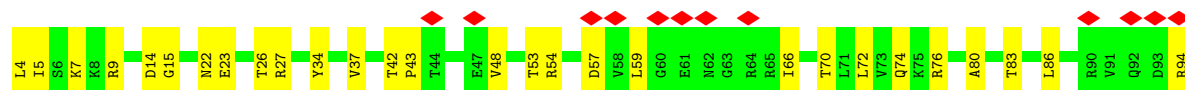
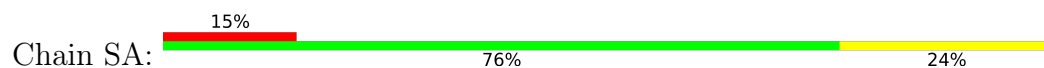
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

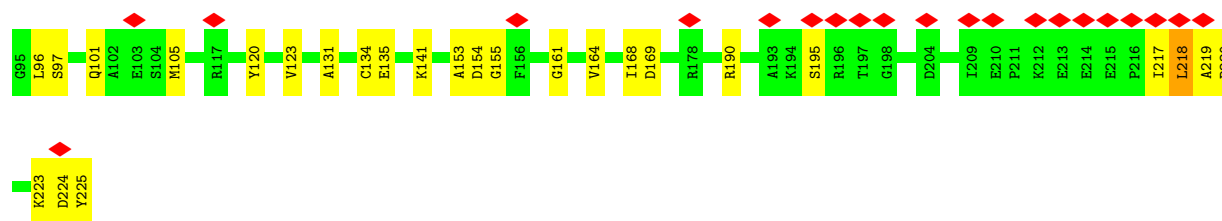
• Molecule 1: 18S rRNA



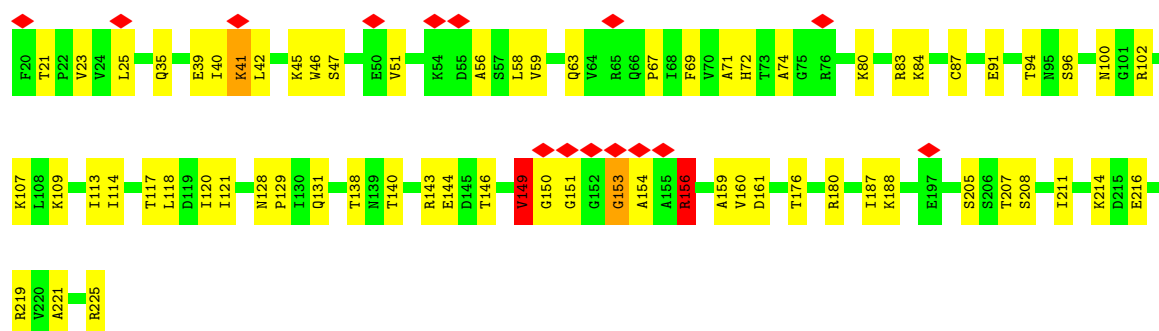


• Molecule 2: Small ribosomal subunit protein uS3

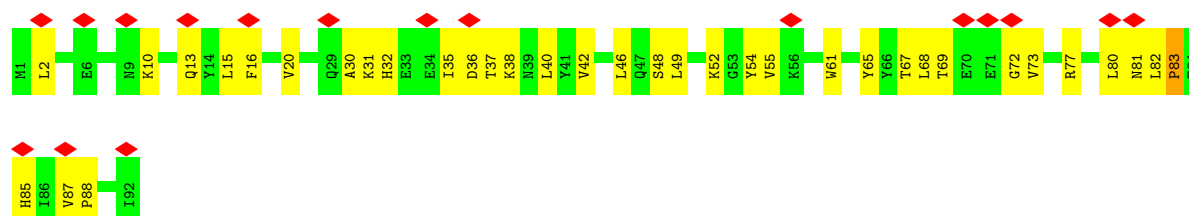




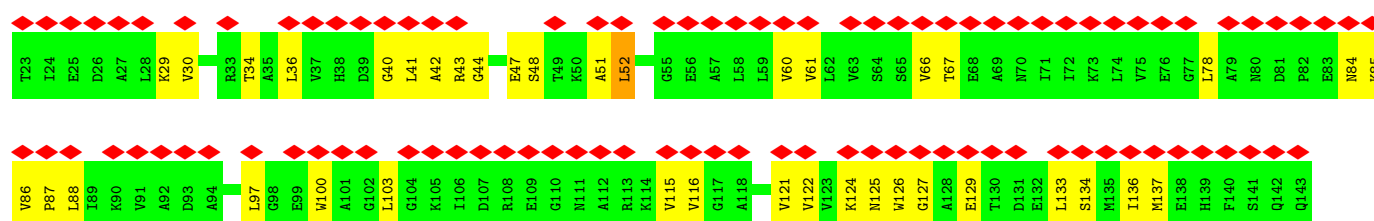
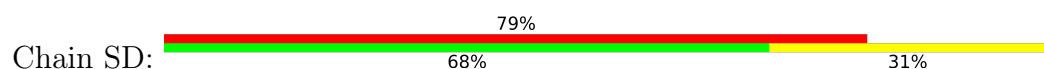
- Molecule 3: Small ribosomal subunit protein uS7



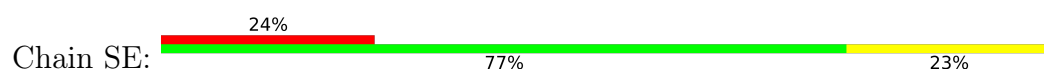
- Molecule 4: Small ribosomal subunit protein eS10A

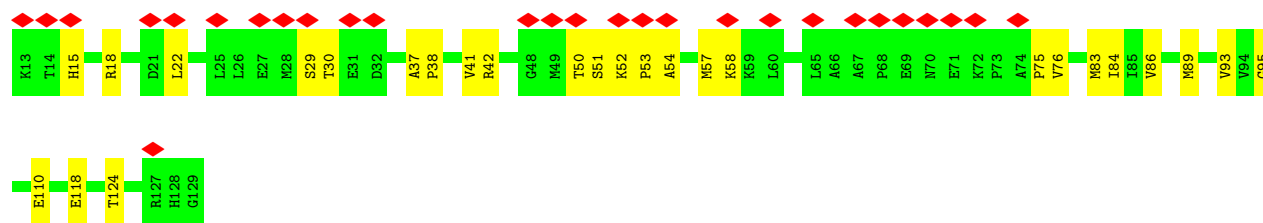


- Molecule 5: Small ribosomal subunit protein eS12

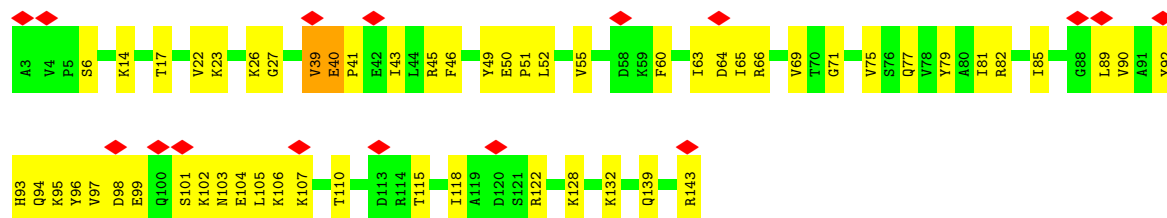


- Molecule 6: Small ribosomal subunit protein uS19

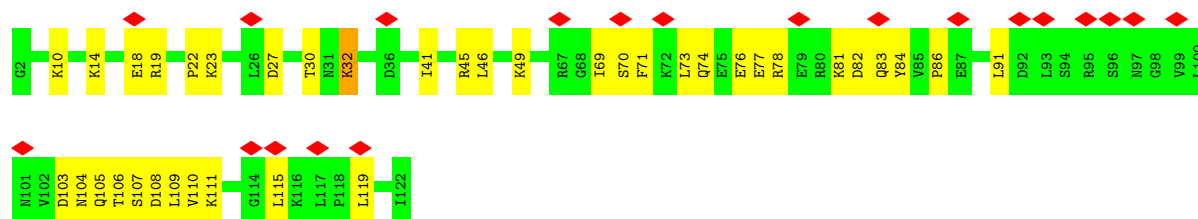




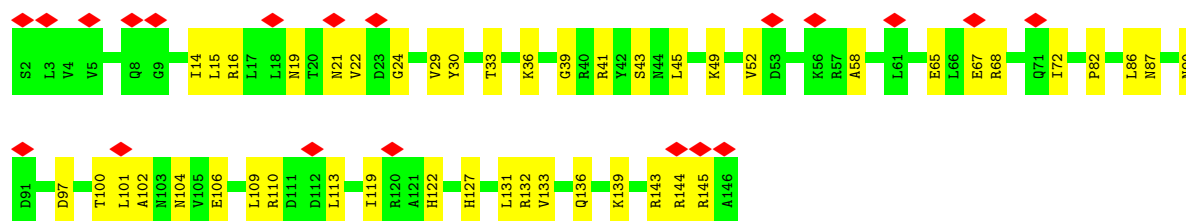
- Molecule 7: Small ribosomal subunit protein uS9A



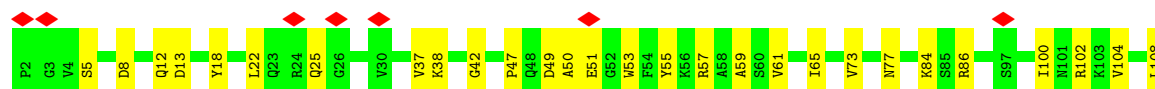
- Molecule 8: Small ribosomal subunit protein eS17A

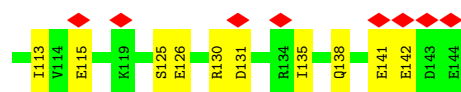


- Molecule 9: Small ribosomal subunit protein uS13A

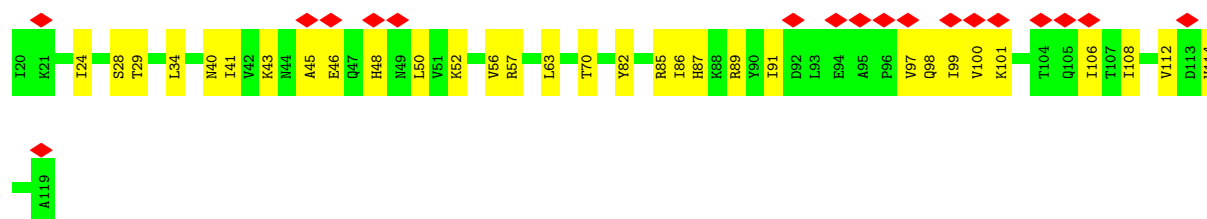


- Molecule 10: Small ribosomal subunit protein eS19A

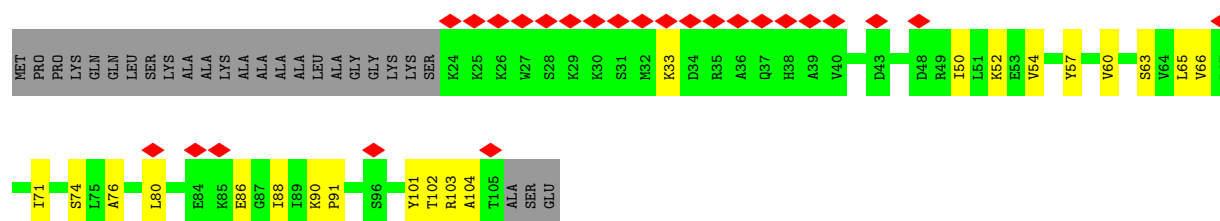




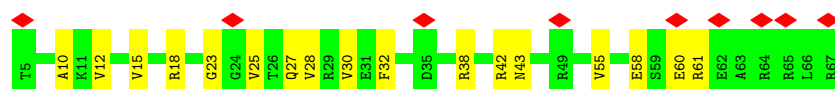
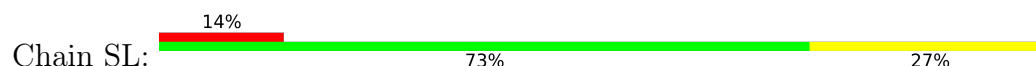
- Molecule 11: Small ribosomal subunit protein uS10



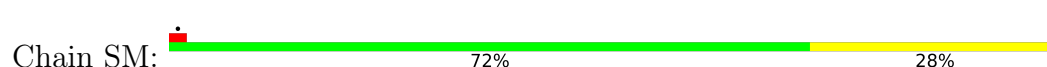
- Molecule 12: Small ribosomal subunit protein eS25A



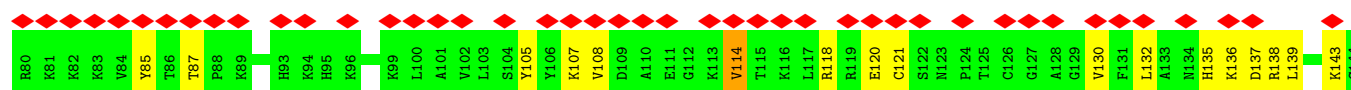
- Molecule 13: Small ribosomal subunit protein eS28A

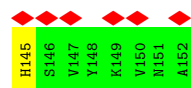


- Molecule 14: Small ribosomal subunit protein uS14A

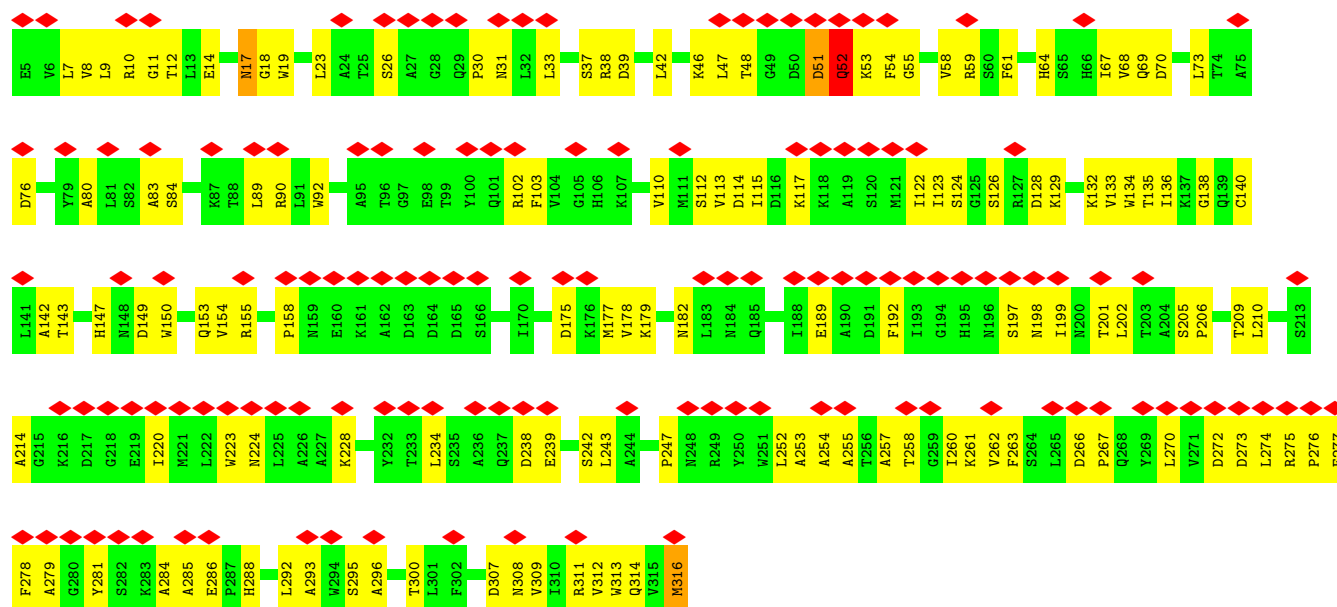


- Molecule 15: Small ribosomal subunit protein eS31

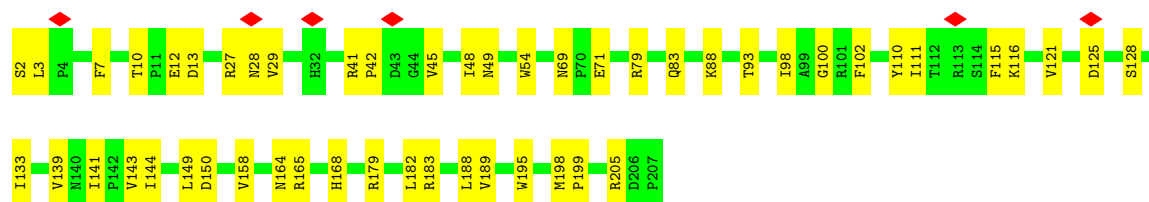
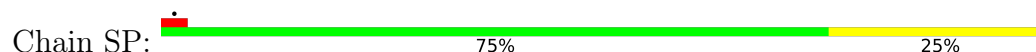




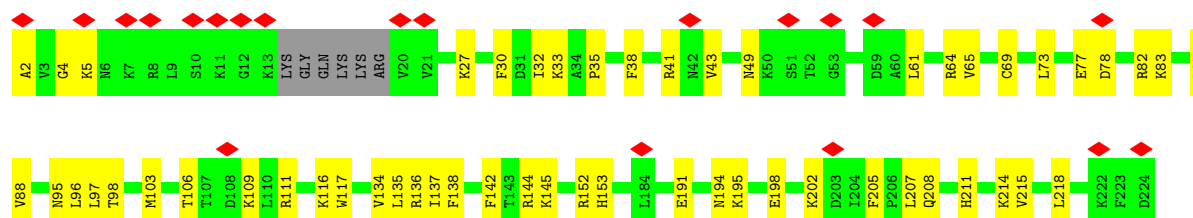
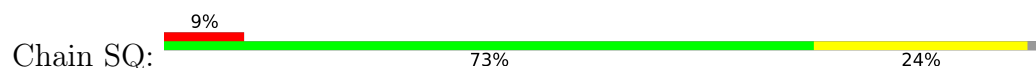
• Molecule 16: Small ribosomal subunit protein RACK1

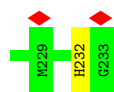


• Molecule 17: Small ribosomal subunit protein uS2A



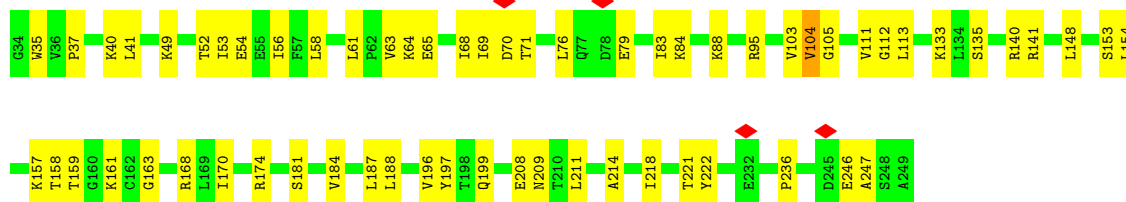
• Molecule 18: Small ribosomal subunit protein eS1A





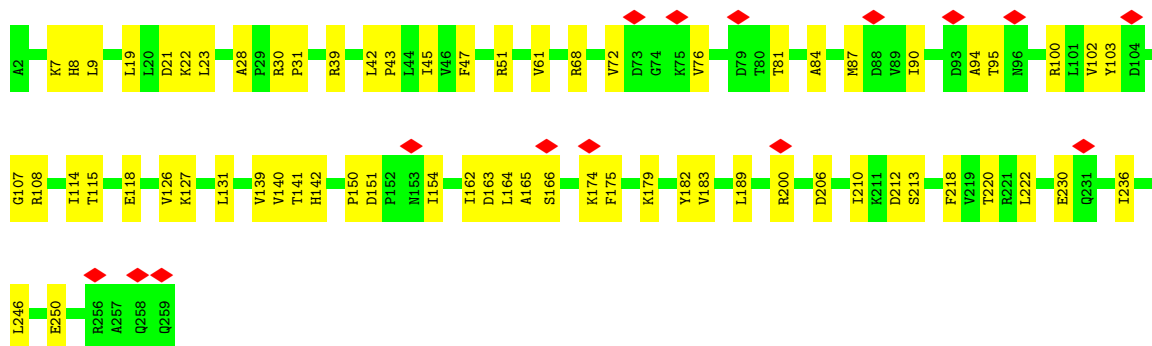
- Molecule 19: Small ribosomal subunit protein uS5

Chain SR: 71% 28%



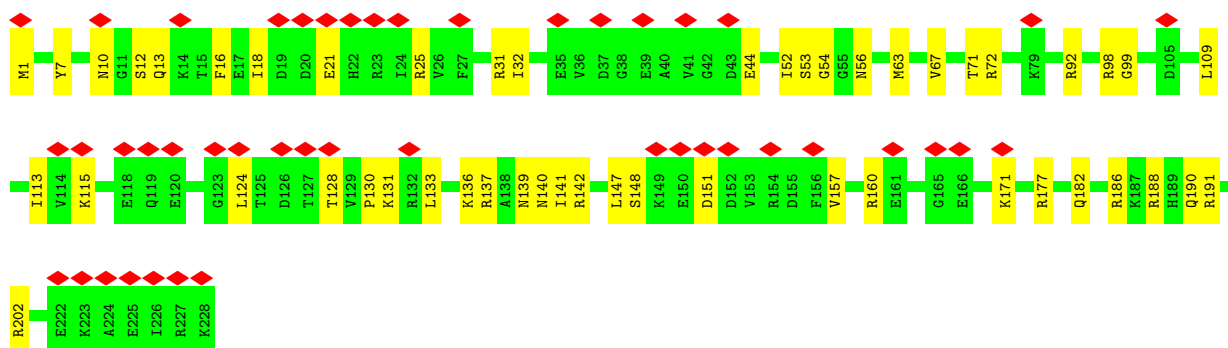
- Molecule 20: Small ribosomal subunit protein eS4A

Chain SS: 6% 74% 26%



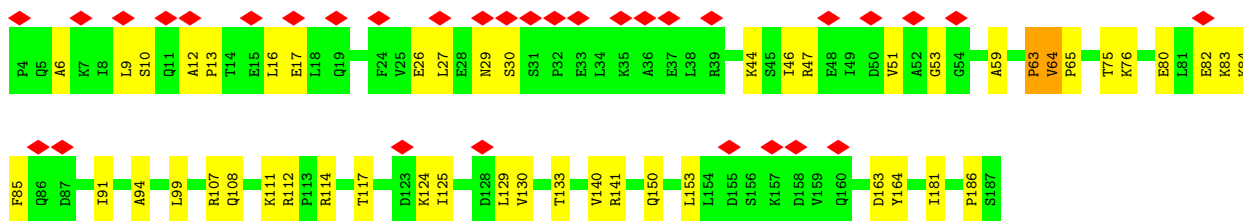
- Molecule 21: Small ribosomal subunit protein eS6A

Chain ST: 20% 78% 22%

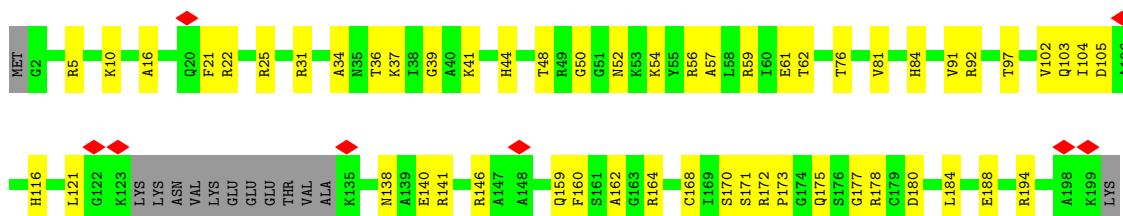


- Molecule 22: Small ribosomal subunit protein eS7A

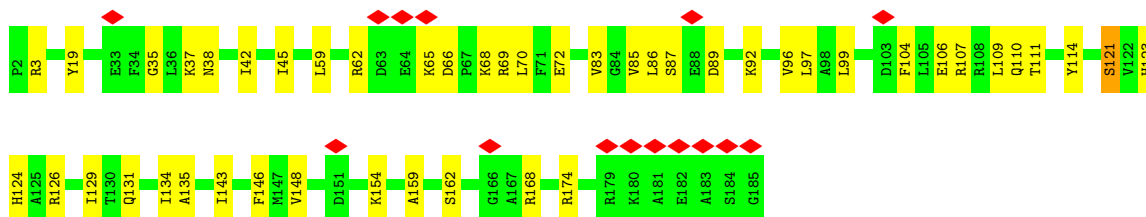
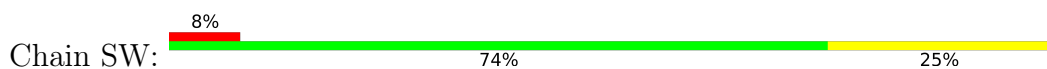
Chain SU: 17% 73% 26%



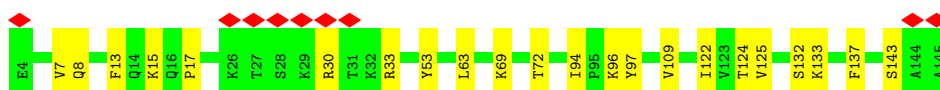
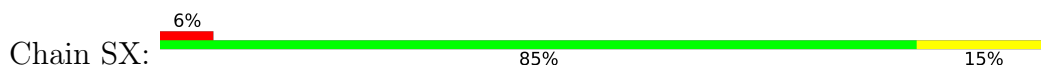
- Molecule 23: Small ribosomal subunit protein eS8A



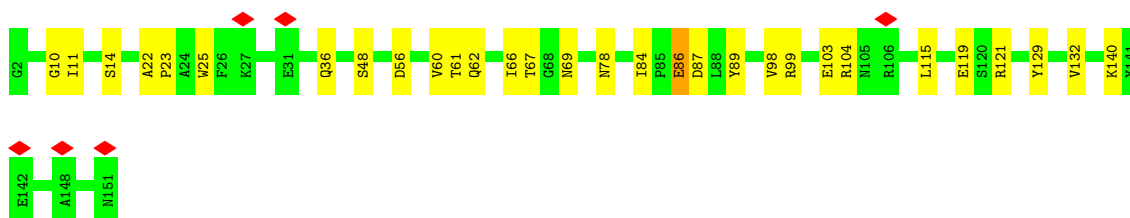
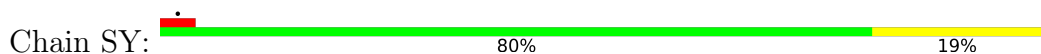
- Molecule 24: Small ribosomal subunit protein uS4A



- Molecule 25: Small ribosomal subunit protein uS17A

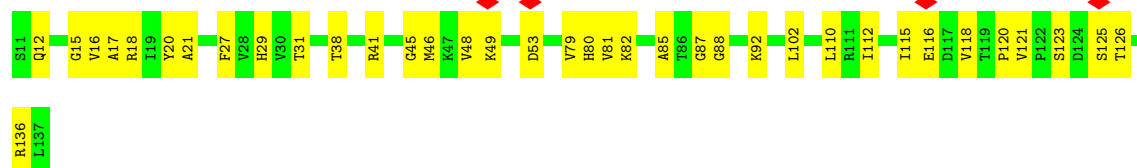


- Molecule 26: Small ribosomal subunit protein uS15



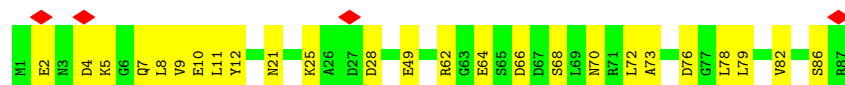
- Molecule 27: Small ribosomal subunit protein uS11B

Chain SZ:  71% 29%



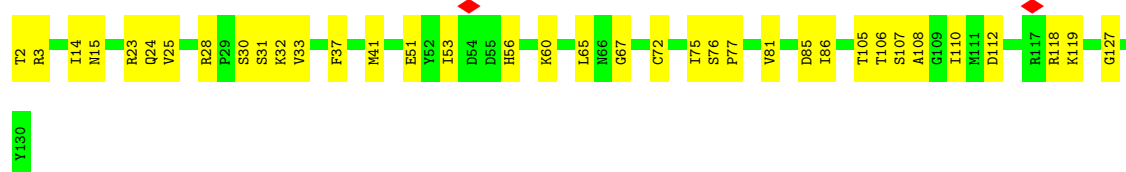
- Molecule 28: Small ribosomal subunit protein eS21A

Chain Sa:  5% 71% 29%



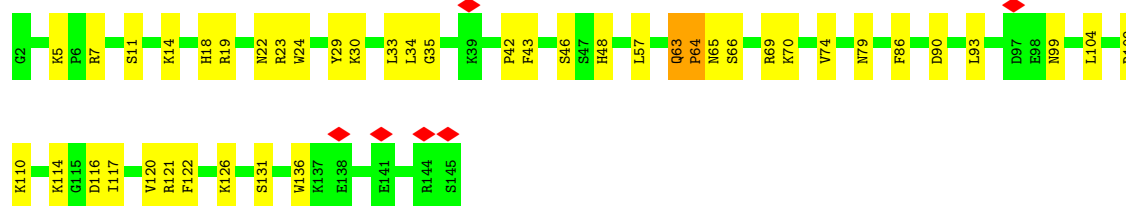
- Molecule 29: Small ribosomal subunit protein uS8A

Chain Sb:  72% 28%



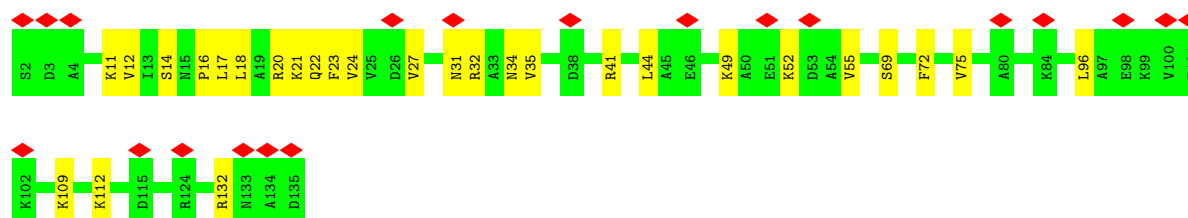
- Molecule 30: Small ribosomal subunit protein uS12A

Chain Sc:  70% 28%

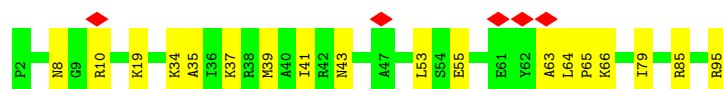
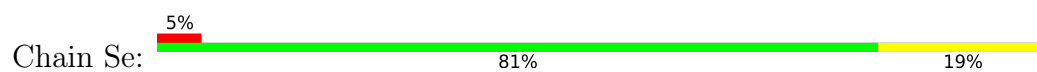


- Molecule 31: Small ribosomal subunit protein eS24A

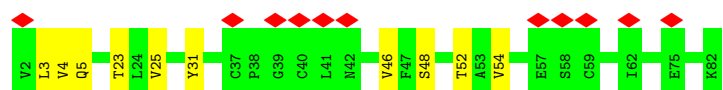
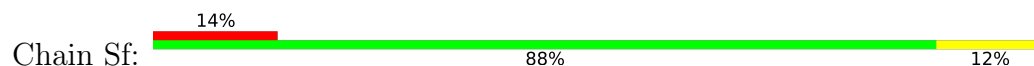
Chain Sd:  15% 79% 21%



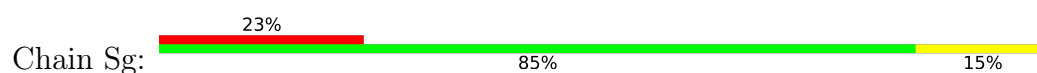
- Molecule 32: Small ribosomal subunit protein eS26A



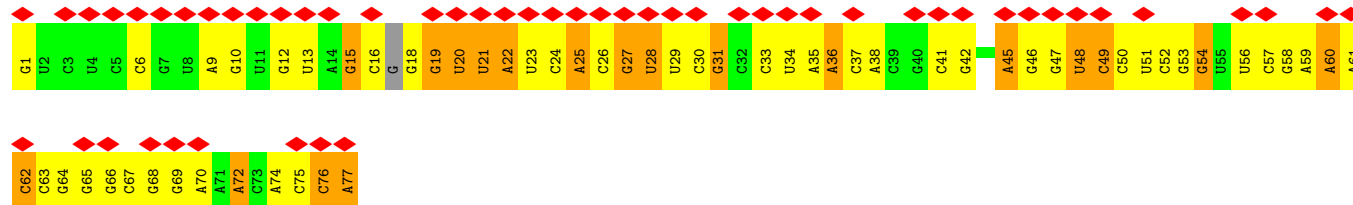
- Molecule 33: Small ribosomal subunit protein eS27A



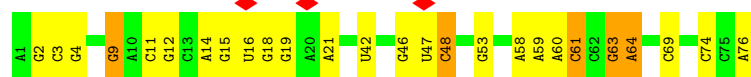
- Molecule 34: Small ribosomal subunit protein eS30A



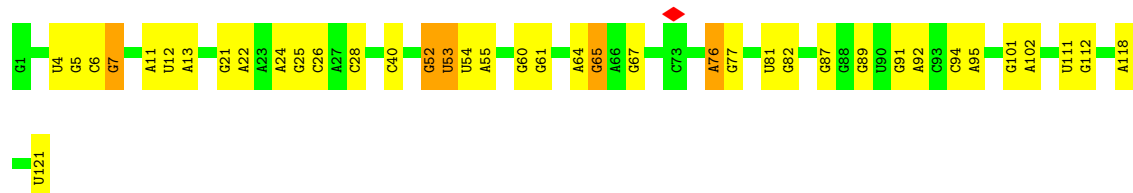
- Molecule 35: tRNA



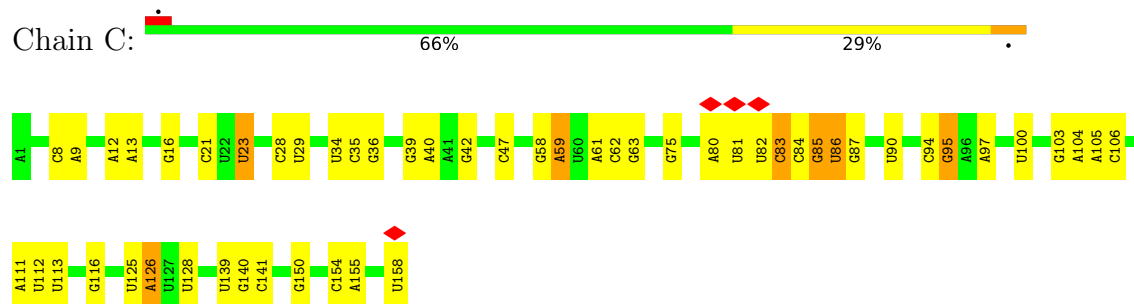
- Molecule 36: tRNA



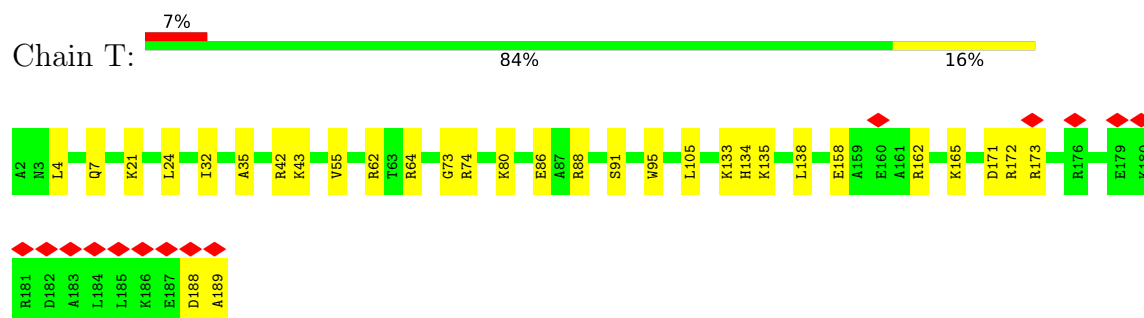
- Molecule 37: 5S rRNA



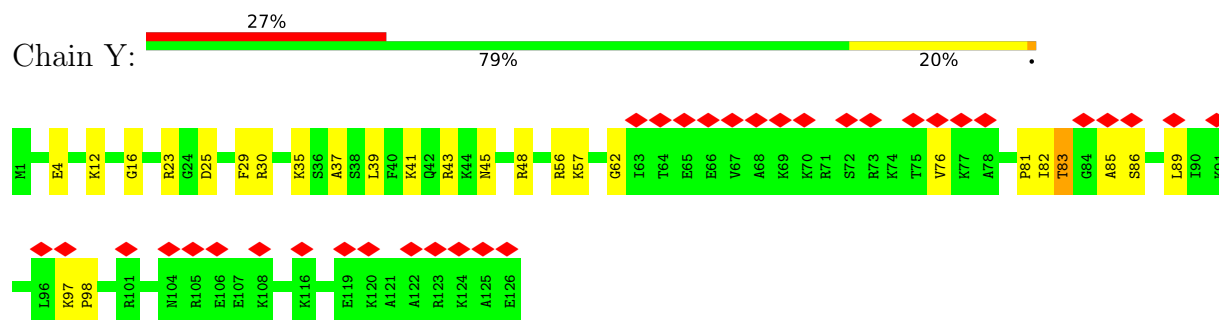
- Molecule 38: 5.8S rRNA



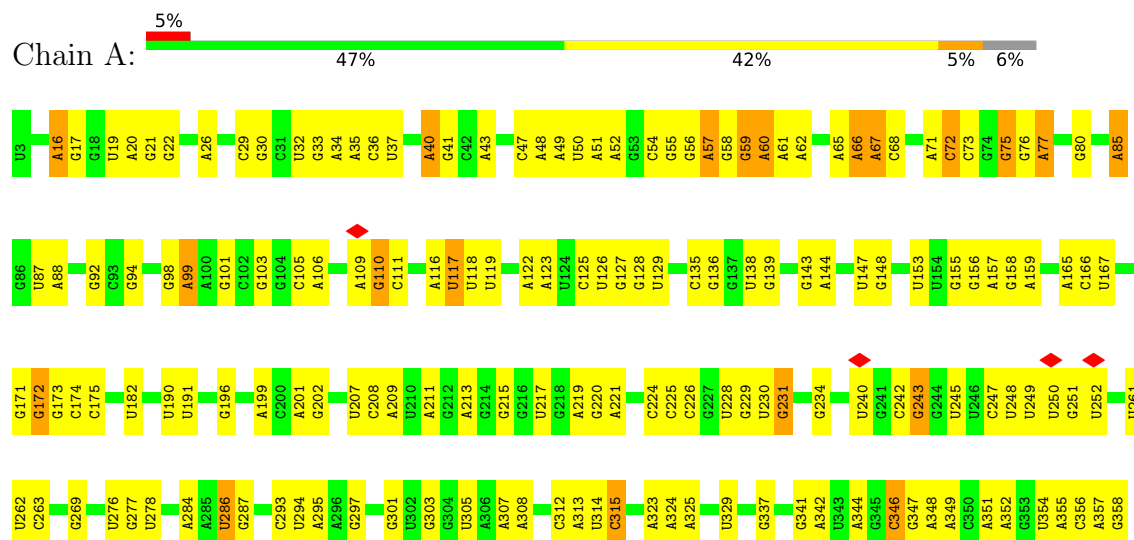
- Molecule 39: Large ribosomal subunit protein eL19A



- Molecule 40: Large ribosomal subunit protein eL24A

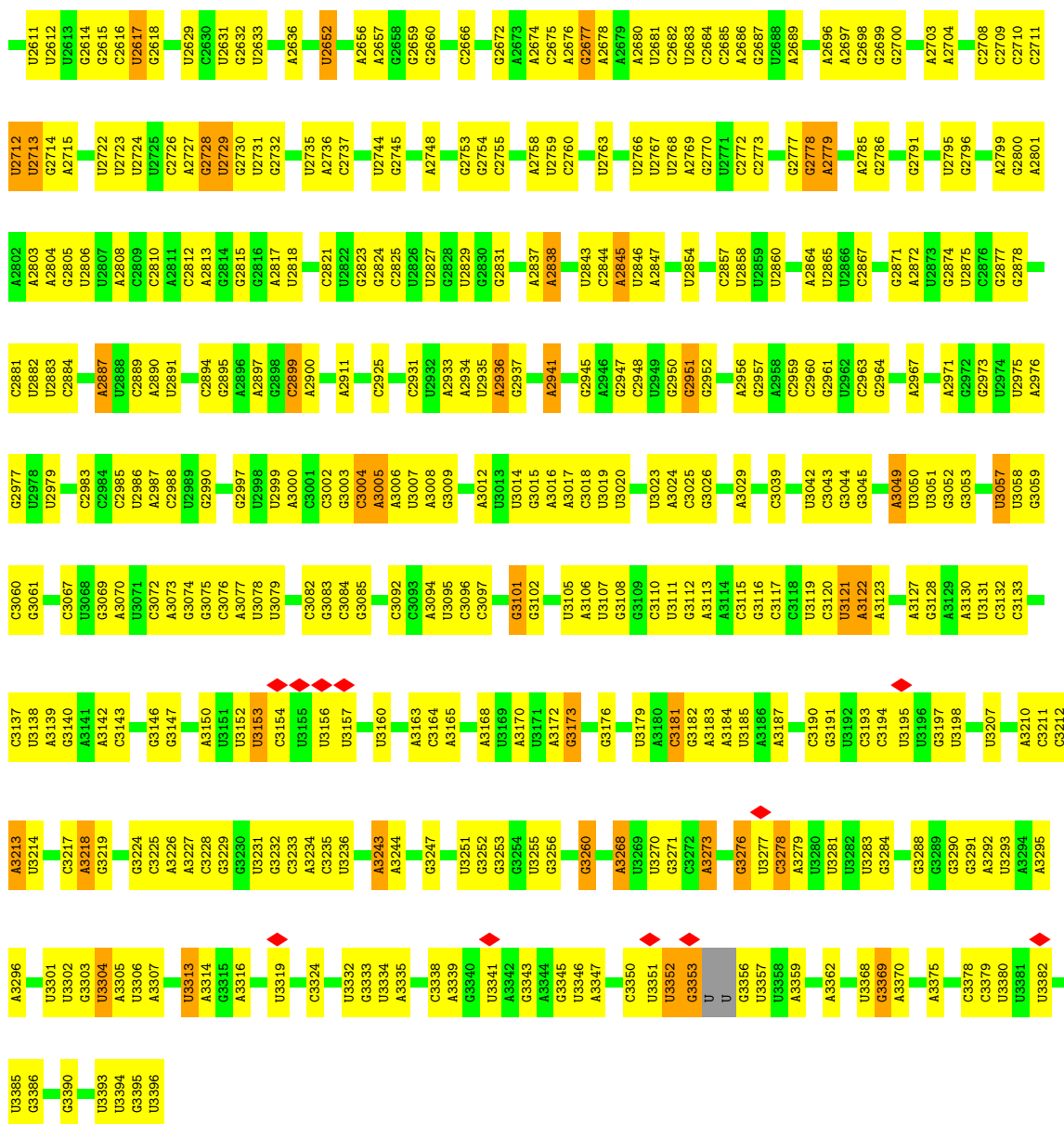


- Molecule 41: 25S rRNA



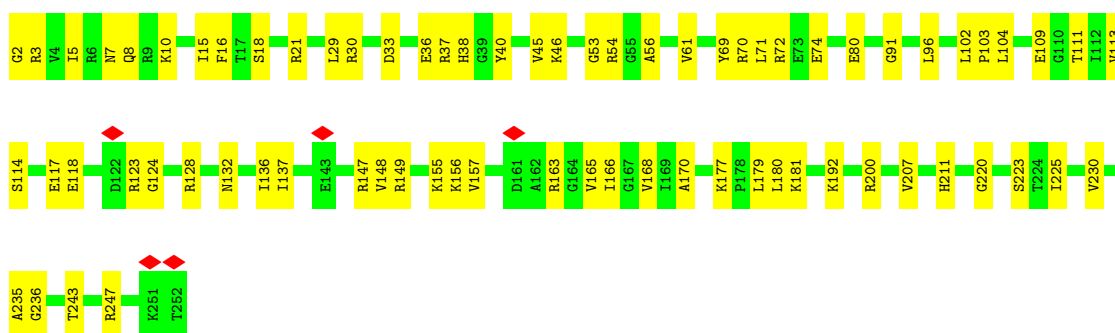


G2534	G2470	G2403	U2328	A2243	U2162	G	C	C1870	G1776	U1882	G1591	A1498
A2535	U2471	A2404	C2329	A2244	C2163	C	G	G1878	U1777	U1691	G1592	C1499
U2537	U2472	C2407	C2330	C2245	A2166	U	C	A1879	C1778	U1589	A1593	G1500
U2538	C2473	U2408	C2331	G2249	A2167	A	A	U1880	G1780	U1694	A1503	
C2539	G2474	U2411	G2335	G2250	A2168	A	U	A1881	U1785	U1695	G1507	
A2540	G2412	G2412	U2336	G2251	G2169	A	C	G1882	U1786	C1597	C1508	
G2413	C2476	A2413	C2337	A2252	U2170	U	C	A1883	A1787	G1598	A1509	
G2414	G2477	G2414	C2338	U2254	G2171	C	C	U1886	U1705	G1599		
C2415	C2478	C2415	C2339	A2255	A2172	G	A	U1887	C1709	U1600	G1525	
G2418	C2479	G2418	U2340	A2256	U2173	A	G	U1888	C1710	U1601	G1526	
U2423	A2480	U2423	A2341	C2257	G2177	A	C	U1889	C1711	A1602	U1527	
A2424	G2481	A2424	U2344	G2260	A2178	U	C	U1890	G1712	G1604	G1528	
U2427	U2482	U2427	U2345	U2261	A2179	G	C	A1895	G1713	A1605	A1529	
U2428	G2483	U2428	U2349	G2262	C2180	C	C	A1900	U1717	U1606		
G2429	A2484	G2429	C2350	C2263	C2181	C	C	U1901	G1718	U1533	U1534	
A2430	U2485	A2430	U2351	U2264	A2182	U	G	G1905	G1719	A1535		
A2431	A2486	A2431	U2352	U2265	A2183	G	G	G1906	U1724	G1543		
A2432	U2487	A2432	A2353	U2266	U2184	U	G	U1907	G1615	C1551		
U2433	A2488	U2433	G2354	U2267	G2185	G	C	A1908	G1616	G1552		
U2434	U2489	U2434	G2355	U2268	U2186	U	C	A1909	G1617	U1553		
G2435	C2489	G2435	U2356	U2269	A2188	A	U	A1910	G1728	U1554		
U2436	C2490	U2436	A2359	A2270	U2189	G	C	G1918	U1729	U1555		
G2437	A2491	G2437	G2360	A2271	U2190	C	C	G1919	G1733	C1556		
A2438	U2492	A2438	A2363	G2272	U2191	A	U	G1920	G1734	A1557		
A2439	C2493	A2439	U2364	U2273	U2192	C	U	A1921	U1735	A1558		
G2440	A2494	G2440	C2365	A2274	U2193	G	C	G1922	C1738	G1559		
A2441	G2495	A2441	U2366	A2275	C2195	C	G	U1923	U1740	G1560		
G2442	C2496	G2442	C2367	U2276	C2196	U	C	G1928	A1741	G1561		
A2443	U2497	A2443	A2368	A2280	U2205	C	A	G1929	U1742	C1562		
C2444	U2498	C2444	G2369	U2281	G2206	U	C	A1930	G1743	C1563		
A2445	U2499	A2445	U2370	G2282	A2207	G	C	U1931	C1822	C1644		
U2446	C2500	U2446	C2371	C2284	U2209	U	C	A1932	G1744	U1564		
A2447	U2501	A2447	A2372	U2294	U2209	A	U	U1933	U1745	G1565		
G2448	A2502	G2448	G2373	A2295	G2216	C	U	G1934	G1829	A1566		
A2449	U2503	A2449	U2374	A2296	U2217	C	C	U1935	G1747	U1567		
G2450	U2504	G2450	G2375	U2297	G2218	U	C	G1940	G1748	U1568		
C2451	U2505	C2451	C2376	U2298	G2219	C	C	U1941	A1750	U1569		
G2452	U2506	G2452	U2377	G2305	A2222	U	C	U1942	G1751	U1570		
U2453	U2507	U2453	U2388	C2306	A2223	C	G	G1948	C1756	A1571		
G2454	C2508	G2454	C2389	G2307	A2224	G	C	U1949	A1757	U1572		
U2455	U2509	U2455	A2390	C2308	U2225	U	C	U1950	G1758	G1573		
A2456	U2510	A2456	C2391	A2309	U2226	A	U	C1951	C1759	C1574		
G2457	A2511	G2457	G2392	U2310	C2227	C	C	G1952	C1762	G1575		
A2458	U2514	A2458	C2393	U2314	A2228	A	C	G	U1763	G1576		
U2459	A2515	U2459	G2394	G2315	A2229	C	C	U	G1577	U1578		
G2460	C2518	G2460	U2395	U2316	G2234	C	C	A	C1579	C1579		
A2461	U2519	A2461	G2396	G2317	C2235	G	C	U	U1672	A1580		
A2462	G2520	A2462	U2397	U2318	G2236	U	C	G	G1677	C1581		
G2463	U2521	G2463	A2398	A2320	G2237	C	C	U	G1678	C1582		
U2464	C2522	U2464	U2402	U2327	G2238	C	A	A	U1679	A1583		
A2523	A2523	A2523	A2402	U2241	U2241	C	G	G	G1680	A1586		
G2525	G2525	G2525		A2242	A2242	C	U					
C2526	G2526	C2526										
G2527	G2527	G2527										
U2528	U2531	U2531										
G2533	U2532	G2533										



- Molecule 42: Large ribosomal subunit protein uL2A

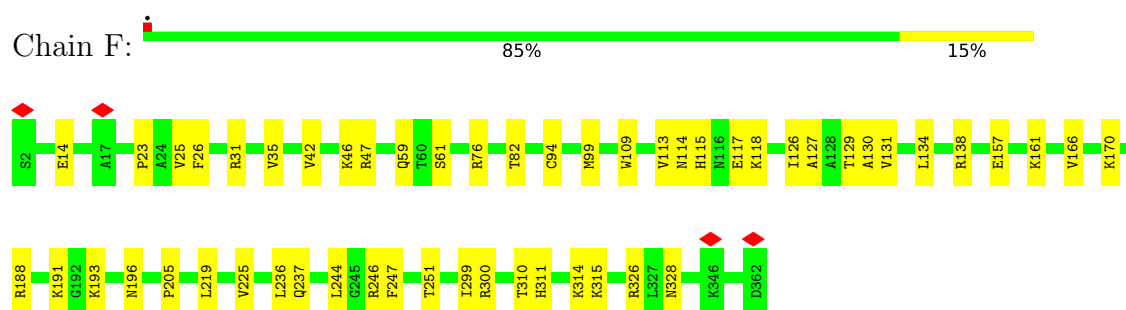
Chain D: 71% 29%



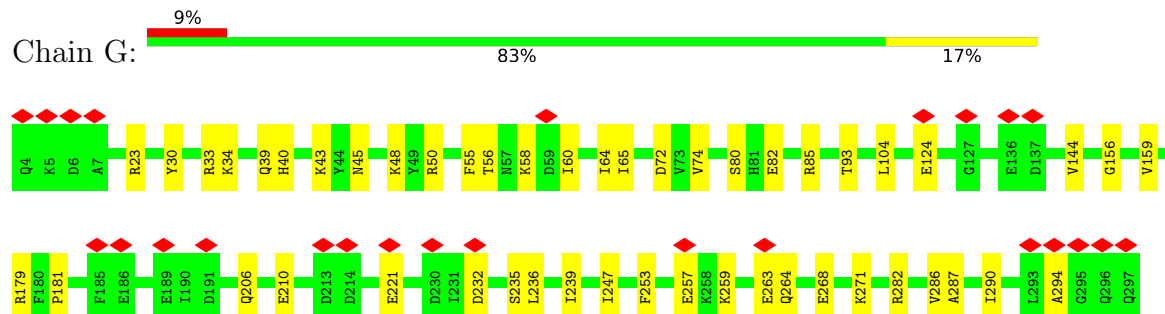
- Molecule 43: Large ribosomal subunit protein uL3



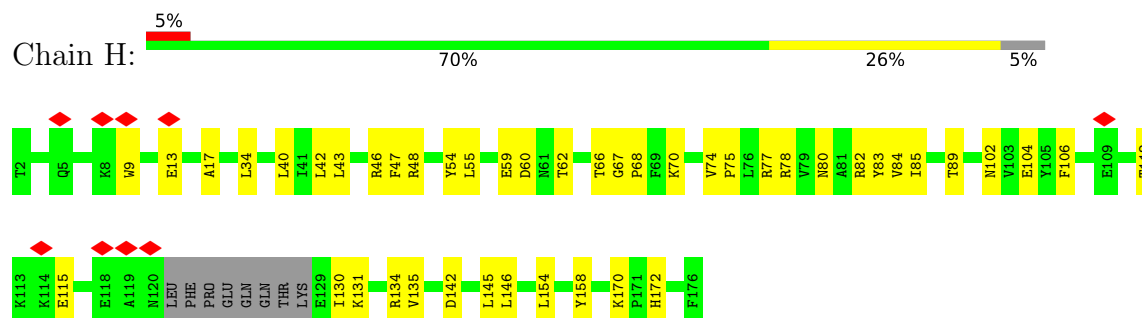
- Molecule 44: Large ribosomal subunit protein uL4A



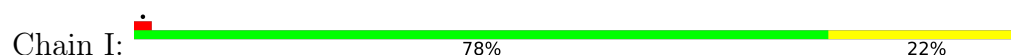
- Molecule 45: Large ribosomal subunit protein uL18



- Molecule 46: Large ribosomal subunit protein eL6B

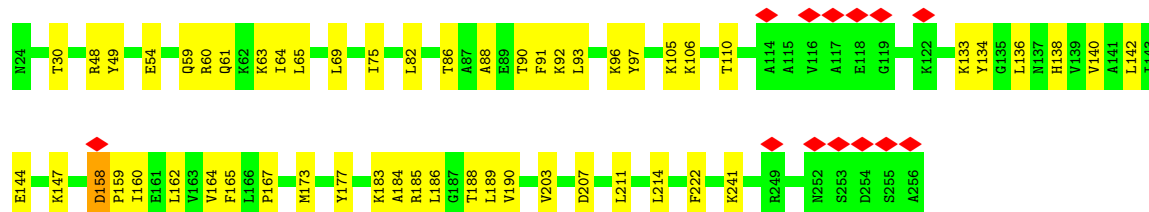
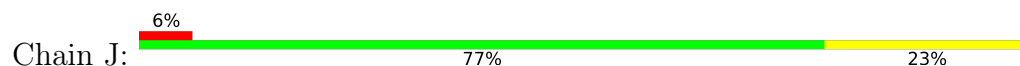


- Molecule 47: Large ribosomal subunit protein uL30A

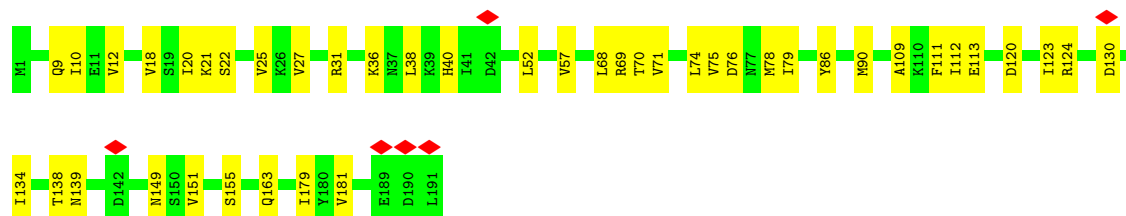
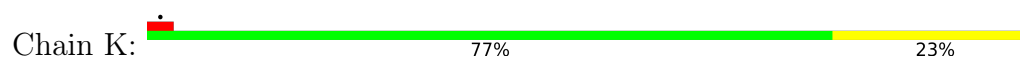




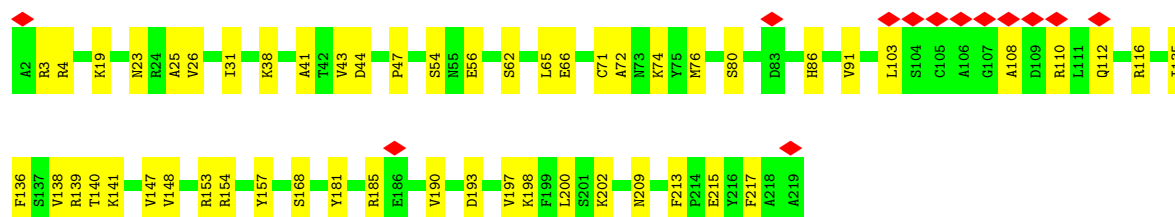
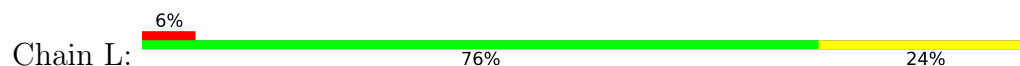
- Molecule 48: Large ribosomal subunit protein eL8A



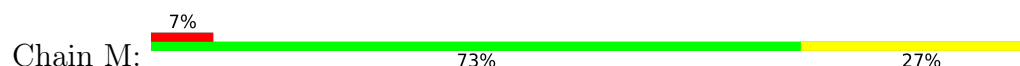
- Molecule 49: Large ribosomal subunit protein uL6A

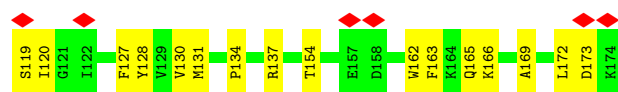


- Molecule 50: Large ribosomal subunit protein uL16

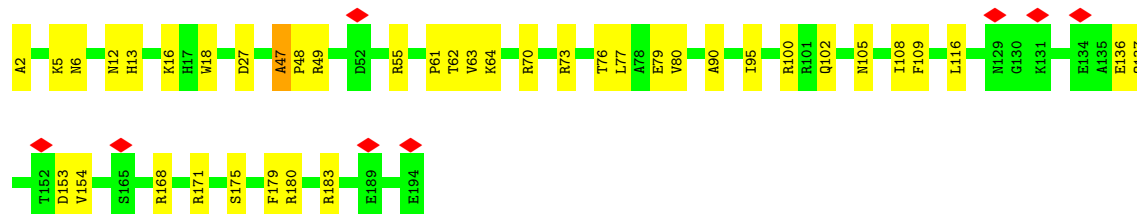
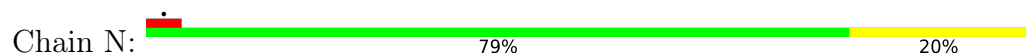


- Molecule 51: Large ribosomal subunit protein uL5B

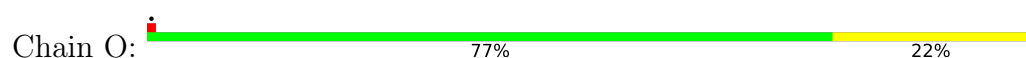




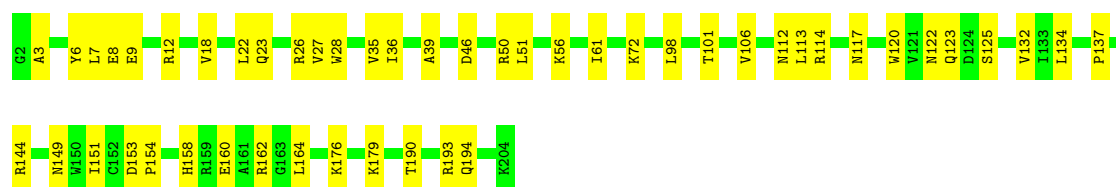
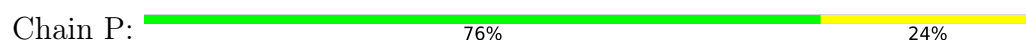
- Molecule 52: Large ribosomal subunit protein eL13A



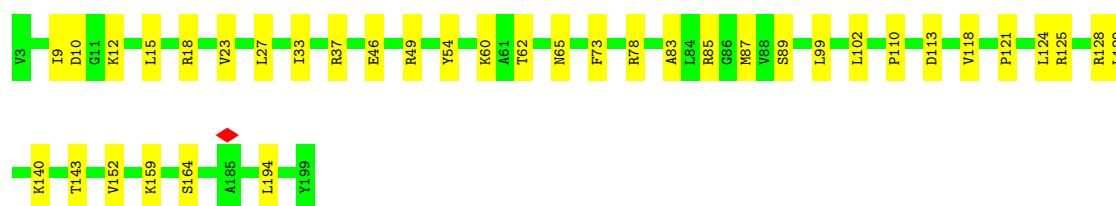
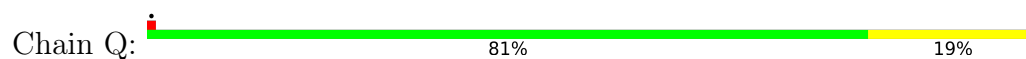
- Molecule 53: Large ribosomal subunit protein eL14A



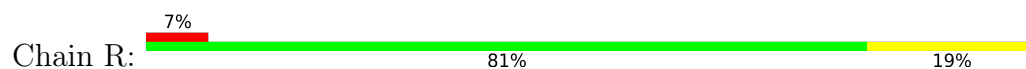
- Molecule 54: Large ribosomal subunit protein eL15A



- Molecule 55: Large ribosomal subunit protein uL13A



- Molecule 56: Large ribosomal subunit protein uL22A





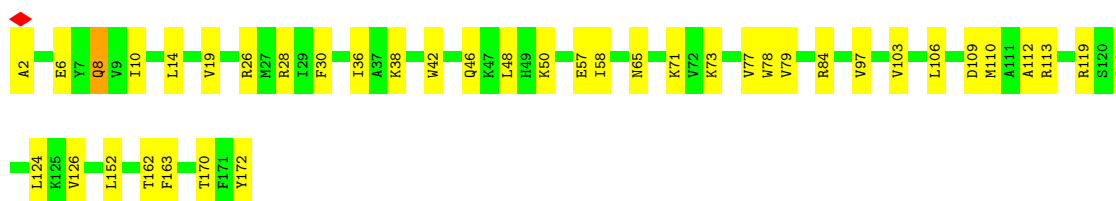
- Molecule 57: Large ribosomal subunit protein eL18A

Chain S: 79% 21%



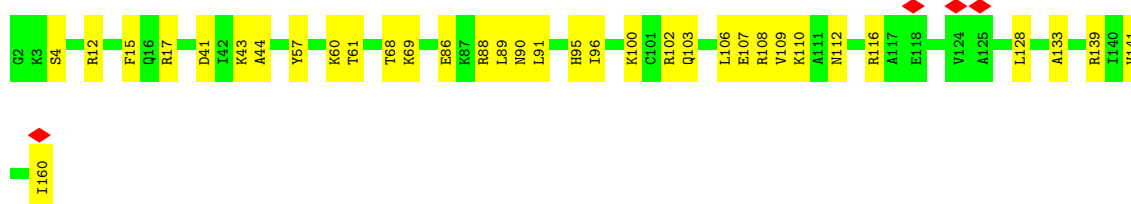
- Molecule 58: Large ribosomal subunit protein eL20A

Chain U: 77% 23%



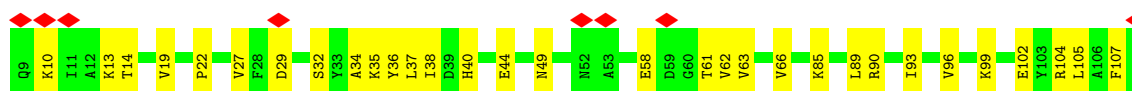
- Molecule 59: Large ribosomal subunit protein eL21A

Chain V: 79% 21%



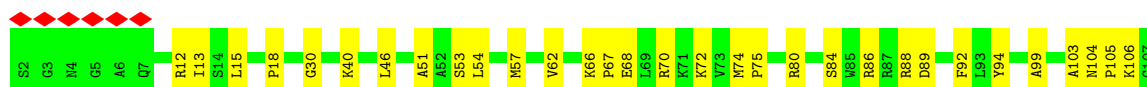
- Molecule 60: Large ribosomal subunit protein eL22A

Chain W: 8% 69% 31%



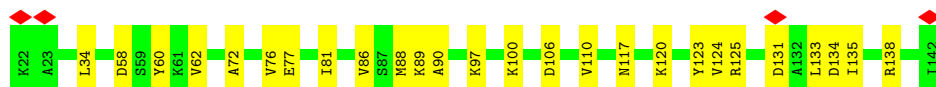
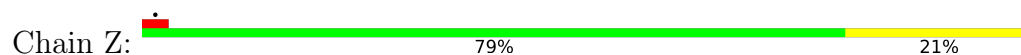
- Molecule 61: Large ribosomal subunit protein uL14A

Chain X: 72% 28%

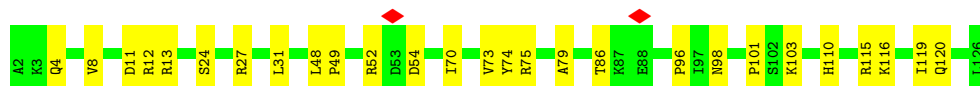
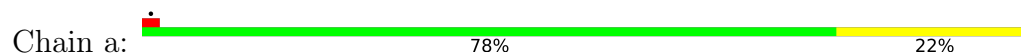




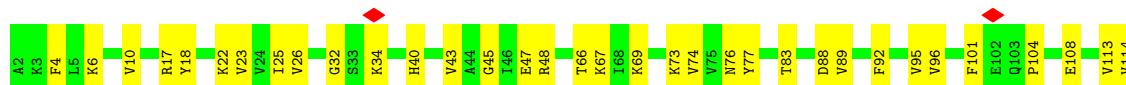
- Molecule 62: Large ribosomal subunit protein uL23



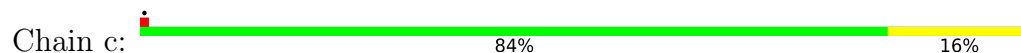
- Molecule 63: Large ribosomal subunit protein uL24A



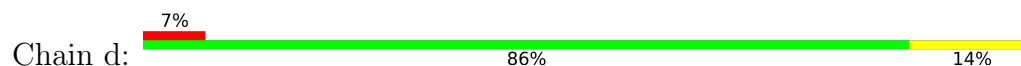
- Molecule 64: Large ribosomal subunit protein eL27A



- Molecule 65: Large ribosomal subunit protein uL15



- Molecule 66: Large ribosomal subunit protein eL29

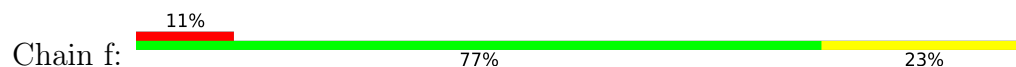


- Molecule 67: Large ribosomal subunit protein eL30

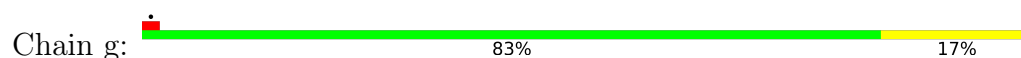




- Molecule 68: Large ribosomal subunit protein eL31A



- Molecule 69: Large ribosomal subunit protein eL32



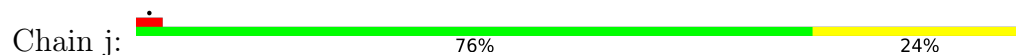
- Molecule 70: Large ribosomal subunit protein eL33A



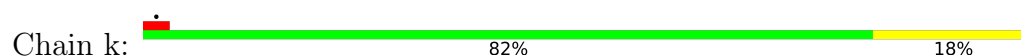
- Molecule 71: Large ribosomal subunit protein eL34A



- Molecule 72: Large ribosomal subunit protein uL29A



- Molecule 73: Large ribosomal subunit protein eL36A



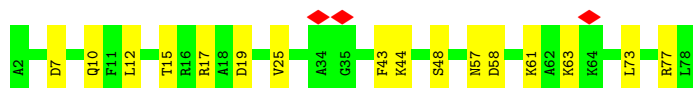
- Molecule 74: Large ribosomal subunit protein eL37A

Chain l:  72% 26%



- Molecule 75: Large ribosomal subunit protein eL38

Chain m:  79% 21%



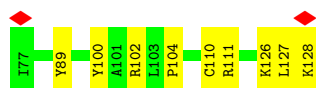
- Molecule 76: Large ribosomal subunit protein eL39

Chain n:  84% 16%



- Molecule 77: Large ribosomal subunit protein eL40A

Chain o:  83% 17%



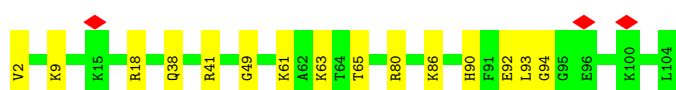
- Molecule 78: Large ribosomal subunit protein eL41A

Chain p:  60% 40%



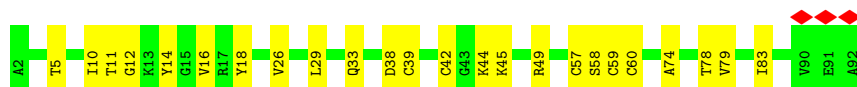
- Molecule 79: Large ribosomal subunit protein eL42A

Chain q:  85% 15%



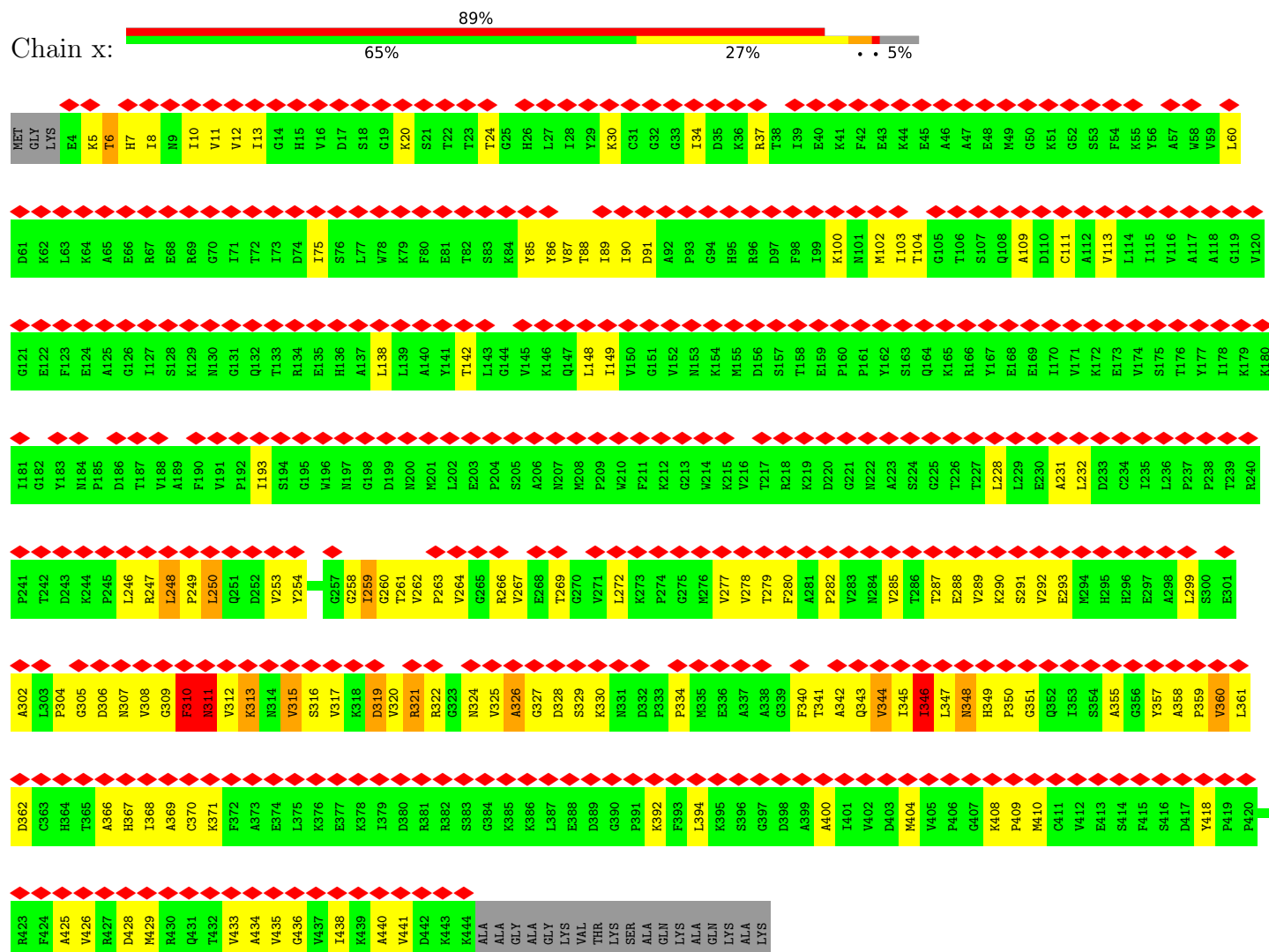
- Molecule 80: Large ribosomal subunit protein eL43A

Chain r:  74% 26%



● Molecule 81: Elongation factor 1-alpha 1

Chain x:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	150024	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.974	Depositor
Minimum map value	-1.157	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.23	Depositor
Map size ($\text{\AA}$)	528.0, 528.0, 528.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2	0.07	0/42211	0.17	0/65773
2	SA	0.16	0/1754	0.39	0/2361
3	SB	0.20	0/1625	0.42	0/2197
4	SC	0.12	0/769	0.35	0/1039
5	SD	0.15	0/883	0.49	0/1199
6	SE	0.13	0/936	0.36	0/1259
7	SF	0.18	0/1125	0.45	0/1510
8	SG	0.14	0/971	0.45	0/1303
9	SH	0.16	0/1207	0.39	1/1623 (0.1%)
10	SI	0.12	0/1130	0.34	0/1517
11	SJ	0.14	0/807	0.55	1/1091 (0.1%)
12	SK	0.17	0/661	0.54	0/888
13	SL	0.10	0/493	0.28	0/663
14	SM	0.12	0/452	0.36	0/600
15	SN	0.18	0/567	0.49	0/764
16	SO	0.18	0/2436	0.50	2/3318 (0.1%)
17	SP	0.11	0/1644	0.31	0/2249
18	SQ	0.14	0/1823	0.37	0/2447
19	SR	0.12	0/1656	0.35	0/2251
20	SS	0.11	0/2097	0.33	0/2823
21	ST	0.11	0/1839	0.32	0/2460
22	SU	0.17	0/1498	0.41	1/2019 (0.0%)
23	SV	0.13	0/1501	0.32	0/2006
24	SW	0.10	0/1504	0.30	0/2016
25	SX	0.10	0/1168	0.30	0/1575
26	SY	0.10	0/1215	0.27	0/1638
27	SZ	0.13	0/901	0.35	0/1217
28	Sa	0.13	0/682	0.42	0/921
29	Sb	0.10	0/1038	0.29	0/1395
30	Sc	0.16	0/1139	0.34	0/1518
31	Sd	0.12	0/1087	0.33	0/1449
32	Se	0.12	0/761	0.39	0/1016
33	Sf	0.09	0/620	0.28	0/838
34	Sg	0.10	0/480	0.28	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	s	0.11	0/1805	0.27	2/2809 (0.1%)
36	t	0.07	0/1796	0.16	0/2799
37	B	0.05	0/2883	0.11	0/4491
38	C	0.05	0/3746	0.12	0/5832
39	T	0.09	0/1532	0.29	0/2043
40	Y	0.10	0/850	0.30	0/1152
41	A	0.08	0/76303	0.19	0/118956
42	D	0.09	0/1933	0.26	0/2598
43	E	0.09	0/3146	0.26	0/4228
44	F	0.09	0/2800	0.26	0/3790
45	G	0.11	0/2400	0.30	0/3239
46	H	0.14	0/1329	0.35	0/1794
47	I	0.11	0/1821	0.27	0/2451
48	J	0.13	0/1836	0.34	0/2481
49	K	0.13	0/1529	0.34	0/2060
50	L	0.11	0/1801	0.29	0/2416
51	M	0.13	0/1367	0.38	0/1834
52	N	0.12	0/1568	0.29	0/2106
53	O	0.09	0/1068	0.22	0/1438
54	P	0.08	0/1757	0.22	0/2354
55	Q	0.13	0/1585	0.28	0/2128
56	R	0.14	0/1439	0.29	0/1938
57	S	0.10	0/1465	0.25	0/1965
58	U	0.09	0/1473	0.27	0/1980
59	V	0.11	0/1296	0.30	0/1739
60	W	0.13	0/812	0.42	0/1099
61	X	0.14	0/1018	0.33	0/1369
62	Z	0.10	0/979	0.32	0/1321
63	a	0.10	0/995	0.26	0/1329
64	b	0.12	0/1106	0.31	0/1485
65	c	0.09	0/1200	0.27	0/1607
66	d	0.09	0/473	0.24	0/629
67	e	0.12	0/745	0.33	0/1001
68	f	0.09	0/890	0.25	0/1196
69	g	0.07	0/1034	0.21	0/1385
70	h	0.10	0/868	0.26	0/1168
71	i	0.11	0/890	0.29	0/1189
72	j	0.15	0/978	0.36	1/1301 (0.1%)
73	k	0.10	0/772	0.28	0/1026
74	l	0.36	1/660 (0.2%)	0.47	0/875
75	m	0.14	0/618	0.34	0/826
76	n	0.09	0/443	0.24	0/588
77	o	0.12	0/416	0.34	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	p	0.13	0/230	0.36	0/296
79	q	0.09	0/836	0.26	0/1104
80	r	0.17	0/701	0.40	0/934
81	x	0.54	0/3449	0.82	5/4667 (0.1%)
All	All	0.12	1/221321 (0.0%)	0.27	13/325151 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
74	l	33	THR	C-N	5.71	1.41	1.33

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	x	311	ASN	CA-C-N	-7.95	107.66	121.97
81	x	311	ASN	C-N-CA	-7.95	107.66	121.97
11	SJ	101	LYS	N-CA-C	-7.19	103.71	114.64
35	s	76	C	C4'-C3'-O3'	6.83	119.65	109.40
16	SO	52	GLN	CA-C-N	-6.26	111.80	120.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37739	0	18988	436	0
2	SA	1729	0	1812	39	0
3	SB	1605	0	1669	52	0
4	SC	752	0	719	29	0
5	SD	875	0	878	27	0
6	SE	916	0	941	19	0
7	SF	1105	0	1166	64	0
8	SG	961	0	999	39	0
9	SH	1188	0	1218	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	SI	1112	0	1124	26	0
11	SJ	797	0	863	27	0
12	SK	651	0	682	15	0
13	SL	491	0	524	13	0
14	SM	442	0	432	12	0
15	SN	556	0	549	15	0
16	SO	2383	0	2332	115	0
17	SP	1603	0	1610	35	0
18	SQ	1798	0	1890	40	0
19	SR	1626	0	1715	41	0
20	SS	2056	0	2140	47	0
21	ST	1815	0	1894	44	0
22	SU	1473	0	1555	35	0
23	SV	1476	0	1501	47	0
24	SW	1479	0	1556	37	0
25	SX	1142	0	1209	13	0
26	SY	1192	0	1255	21	0
27	SZ	891	0	883	29	0
28	Sa	673	0	662	21	0
29	Sb	1021	0	1060	30	0
30	Sc	1121	0	1196	37	0
31	Sd	1073	0	1132	23	0
32	Se	750	0	799	18	0
33	Sf	610	0	633	8	0
34	Sg	472	0	521	9	0
35	s	1616	0	824	82	0
36	t	1606	0	816	9	0
37	B	2579	0	1304	28	0
38	C	3353	0	1695	33	0
39	T	1515	0	1606	29	0
40	Y	836	0	706	16	0
41	A	68170	0	34260	1138	0
42	D	1899	0	1957	57	0
43	E	3075	0	3142	70	0
44	F	2748	0	2859	40	0
45	G	2351	0	2294	33	0
46	H	1307	0	1377	39	0
47	I	1784	0	1862	33	0
48	J	1804	0	1877	40	0
49	K	1508	0	1572	27	0
50	L	1764	0	1804	42	0
51	M	1346	0	1370	34	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	N	1543	0	1608	30	0
53	O	1053	0	1149	26	0
54	P	1720	0	1779	41	0
55	Q	1555	0	1659	29	0
56	R	1416	0	1433	27	0
57	S	1441	0	1543	30	0
58	U	1437	0	1475	32	0
59	V	1272	0	1312	29	0
60	W	796	0	812	22	0
61	X	1003	0	1048	22	0
62	Z	964	0	1025	20	0
63	a	984	0	1075	20	0
64	b	1080	0	1122	31	0
65	c	1169	0	1211	19	0
66	d	462	0	491	7	0
67	e	737	0	792	18	0
68	f	876	0	912	14	0
69	g	1013	0	1077	19	0
70	h	850	0	880	21	0
71	i	880	0	945	23	0
72	j	969	0	1078	20	0
73	k	766	0	844	11	0
74	l	645	0	649	29	0
75	m	612	0	682	12	0
76	n	436	0	475	7	0
77	o	410	0	446	8	0
78	p	229	0	273	10	0
79	q	824	0	892	12	0
80	r	694	0	738	20	0
81	x	3379	0	3433	287	0
All	All	206049	0	152290	3519	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 3519 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:x:280:PHE:HB3	81:x:324:ASN:CG	1.48	1.35
35:s:77:A:C5	81:x:293:GLU:HG3	1.76	1.20
81:x:346:ILE:HA	81:x:434:ALA:CA	1.72	1.18

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:x:280:PHE:CD1	81:x:324:ASN:HB2	1.80	1.16
30:Sc:63:GLN:HB3	30:Sc:64:PRO:HD2	1.23	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SA	220/222 (99%)	208 (94%)	11 (5%)	1 (0%)	24	59
3	SB	204/206 (99%)	186 (91%)	13 (6%)	5 (2%)	4	27
4	SC	90/92 (98%)	76 (84%)	12 (13%)	2 (2%)	5	29
5	SD	119/121 (98%)	99 (83%)	20 (17%)	0	100	100
6	SE	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
7	SF	139/141 (99%)	130 (94%)	7 (5%)	2 (1%)	9	39
8	SG	119/121 (98%)	108 (91%)	11 (9%)	0	100	100
9	SH	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
10	SI	141/143 (99%)	132 (94%)	8 (6%)	1 (1%)	18	52
11	SJ	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
12	SK	80/108 (74%)	64 (80%)	14 (18%)	2 (2%)	4	27
13	SL	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
14	SM	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
15	SN	71/73 (97%)	49 (69%)	21 (30%)	1 (1%)	9	39
16	SO	310/312 (99%)	285 (92%)	24 (8%)	1 (0%)	36	68
17	SP	204/206 (99%)	191 (94%)	12 (6%)	1 (0%)	24	59
18	SQ	222/232 (96%)	203 (91%)	19 (9%)	0	100	100
19	SR	214/216 (99%)	204 (95%)	10 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	SS	256/258 (99%)	240 (94%)	16 (6%)	0	100	100
21	ST	226/228 (99%)	220 (97%)	5 (2%)	1 (0%)	30	62
22	SU	182/184 (99%)	170 (93%)	11 (6%)	1 (0%)	24	59
23	SV	183/200 (92%)	172 (94%)	11 (6%)	0	100	100
24	SW	182/184 (99%)	176 (97%)	6 (3%)	0	100	100
25	SX	140/142 (99%)	132 (94%)	7 (5%)	1 (1%)	18	52
26	SY	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
27	SZ	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
28	Sa	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
29	Sb	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	50
30	Sc	142/144 (99%)	136 (96%)	4 (3%)	2 (1%)	9	39
31	Sd	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
32	Se	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
33	Sf	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
34	Sg	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
39	T	186/188 (99%)	184 (99%)	2 (1%)	0	100	100
40	Y	124/126 (98%)	111 (90%)	11 (9%)	2 (2%)	7	36
42	D	249/251 (99%)	239 (96%)	10 (4%)	0	100	100
43	E	384/386 (100%)	370 (96%)	14 (4%)	0	100	100
44	F	359/361 (99%)	348 (97%)	11 (3%)	0	100	100
45	G	292/294 (99%)	279 (96%)	13 (4%)	0	100	100
46	H	163/175 (93%)	151 (93%)	12 (7%)	0	100	100
47	I	220/223 (99%)	216 (98%)	4 (2%)	0	100	100
48	J	231/233 (99%)	217 (94%)	13 (6%)	1 (0%)	30	62
49	K	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
50	L	216/218 (99%)	207 (96%)	9 (4%)	0	100	100
51	M	167/169 (99%)	157 (94%)	10 (6%)	0	100	100
52	N	191/193 (99%)	178 (93%)	11 (6%)	2 (1%)	12	45
53	O	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
54	P	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
55	Q	195/197 (99%)	189 (97%)	6 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	R	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
57	S	183/185 (99%)	175 (96%)	7 (4%)	1 (0%)	24	59
58	U	169/171 (99%)	161 (95%)	8 (5%)	0	100	100
59	V	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
60	W	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
61	X	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
62	Z	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
63	a	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
64	b	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
65	c	146/148 (99%)	138 (94%)	8 (6%)	0	100	100
66	d	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
67	e	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
68	f	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
69	g	125/127 (98%)	124 (99%)	1 (1%)	0	100	100
70	h	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
71	i	110/112 (98%)	104 (94%)	6 (6%)	0	100	100
72	j	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
73	k	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
74	l	79/81 (98%)	74 (94%)	5 (6%)	0	100	100
75	m	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
76	n	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
77	o	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
78	p	23/25 (92%)	23 (100%)	0	0	100	100
79	q	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
80	r	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
81	x	439/462 (95%)	405 (92%)	28 (6%)	6 (1%)	9	39
All	All	11416/11647 (98%)	10753 (94%)	629 (6%)	34 (0%)	37	68

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	SC	83	PRO
4	SC	88	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	SF	39	VAL
7	SF	40	GLU
12	SK	33	LYS

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	
2	SA	182/182 (100%)	182 (100%)	0	100	100
3	SB	172/173 (99%)	170 (99%)	2 (1%)	63	79
4	SC	77/85 (91%)	76 (99%)	1 (1%)	61	78
5	SD	88/98 (90%)	87 (99%)	1 (1%)	65	79
6	SE	95/98 (97%)	95 (100%)	0	100	100
7	SF	117/117 (100%)	117 (100%)	0	100	100
8	SG	105/110 (96%)	104 (99%)	1 (1%)	68	80
9	SH	127/128 (99%)	127 (100%)	0	100	100
10	SI	115/115 (100%)	114 (99%)	1 (1%)	70	81
11	SJ	93/93 (100%)	93 (100%)	0	100	100
12	SK	67/89 (75%)	67 (100%)	0	100	100
13	SL	55/56 (98%)	55 (100%)	0	100	100
14	SM	47/47 (100%)	46 (98%)	1 (2%)	47	71
15	SN	56/64 (88%)	56 (100%)	0	100	100
16	SO	250/257 (97%)	247 (99%)	3 (1%)	63	79
17	SP	170/173 (98%)	170 (100%)	0	100	100
18	SQ	200/205 (98%)	198 (99%)	2 (1%)	68	80
19	SR	175/175 (100%)	173 (99%)	2 (1%)	65	79
20	SS	220/220 (100%)	220 (100%)	0	100	100
21	ST	189/195 (97%)	189 (100%)	0	100	100
22	SU	163/165 (99%)	163 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	SV	148/161 (92%)	148 (100%)	0	100	100
24	SW	156/157 (99%)	155 (99%)	1 (1%)	78	84
25	SX	126/127 (99%)	126 (100%)	0	100	100
26	SY	127/127 (100%)	126 (99%)	1 (1%)	73	82
27	SZ	81/96 (84%)	80 (99%)	1 (1%)	63	79
28	Sa	71/74 (96%)	71 (100%)	0	100	100
29	Sb	110/110 (100%)	110 (100%)	0	100	100
30	Sc	119/119 (100%)	119 (100%)	0	100	100
31	Sd	112/112 (100%)	111 (99%)	1 (1%)	70	81
32	Se	81/81 (100%)	81 (100%)	0	100	100
33	Sf	70/70 (100%)	70 (100%)	0	100	100
34	Sg	50/51 (98%)	50 (100%)	0	100	100
39	T	152/153 (99%)	152 (100%)	0	100	100
40	Y	56/108 (52%)	56 (100%)	0	100	100
42	D	190/193 (98%)	190 (100%)	0	100	100
43	E	319/322 (99%)	316 (99%)	3 (1%)	70	81
44	F	288/288 (100%)	287 (100%)	1 (0%)	86	88
45	G	241/243 (99%)	239 (99%)	2 (1%)	73	82
46	H	139/154 (90%)	139 (100%)	0	100	100
47	I	186/187 (100%)	186 (100%)	0	100	100
48	J	187/191 (98%)	187 (100%)	0	100	100
49	K	168/171 (98%)	168 (100%)	0	100	100
50	L	185/185 (100%)	184 (100%)	1 (0%)	81	85
51	M	145/147 (99%)	144 (99%)	1 (1%)	76	83
52	N	154/154 (100%)	153 (99%)	1 (1%)	78	84
53	O	107/107 (100%)	106 (99%)	1 (1%)	70	81
54	P	175/175 (100%)	175 (100%)	0	100	100
55	Q	160/160 (100%)	160 (100%)	0	100	100
56	R	138/145 (95%)	138 (100%)	0	100	100
57	S	150/150 (100%)	149 (99%)	1 (1%)	76	83
58	U	155/155 (100%)	153 (99%)	2 (1%)	61	78

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	V	135/136 (99%)	134 (99%)	1 (1%)	76	83
60	W	87/87 (100%)	87 (100%)	0	100	100
61	X	104/104 (100%)	104 (100%)	0	100	100
62	Z	104/105 (99%)	104 (100%)	0	100	100
63	a	108/108 (100%)	108 (100%)	0	100	100
64	b	112/115 (97%)	111 (99%)	1 (1%)	70	81
65	c	117/118 (99%)	117 (100%)	0	100	100
66	d	46/46 (100%)	46 (100%)	0	100	100
67	e	81/81 (100%)	81 (100%)	0	100	100
68	f	92/96 (96%)	92 (100%)	0	100	100
69	g	107/109 (98%)	107 (100%)	0	100	100
70	h	90/90 (100%)	90 (100%)	0	100	100
71	i	95/95 (100%)	94 (99%)	1 (1%)	65	79
72	j	104/104 (100%)	103 (99%)	1 (1%)	68	80
73	k	80/81 (99%)	79 (99%)	1 (1%)	61	78
74	l	67/67 (100%)	66 (98%)	1 (2%)	57	76
75	m	68/68 (100%)	68 (100%)	0	100	100
76	n	45/45 (100%)	45 (100%)	0	100	100
77	o	45/47 (96%)	45 (100%)	0	100	100
78	p	22/23 (96%)	22 (100%)	0	100	100
79	q	87/88 (99%)	87 (100%)	0	100	100
80	r	71/71 (100%)	71 (100%)	0	100	100
81	x	366/379 (97%)	349 (95%)	17 (5%)	24	58
All	All	9542/9781 (98%)	9488 (99%)	54 (1%)	76	84

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	S	17	THR
73	k	21	THR
81	x	344	VAL
58	U	8	GLN
64	b	118	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
52	N	99	HIS
57	S	126	GLN
53	O	59	ASN
54	P	149	ASN
62	Z	80	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1799 (98%)	408 (23%)	40 (2%)
35	s	74/77 (96%)	32 (43%)	0
36	t	74/75 (98%)	18 (24%)	0
37	B	120/121 (99%)	9 (7%)	1 (0%)
38	C	157/158 (99%)	26 (16%)	1 (0%)
41	A	3180/3394 (93%)	506 (15%)	9 (0%)
All	All	5373/5624 (95%)	999 (18%)	51 (0%)

5 of 999 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	25	C
1	2	26	A
1	2	34	G

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1256	A
1	2	1557	U
41	A	3004	C
1	2	1273	G
1	2	1382	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

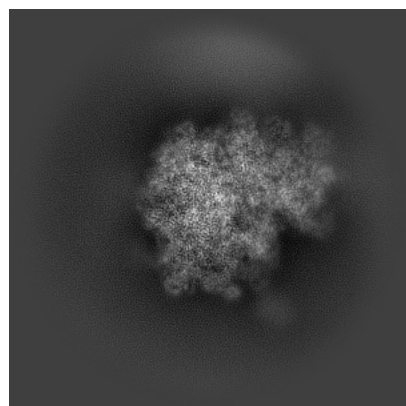
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38656. These allow visual inspection of the internal detail of the map and identification of artifacts.

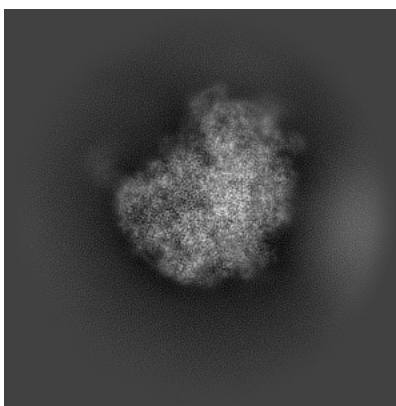
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

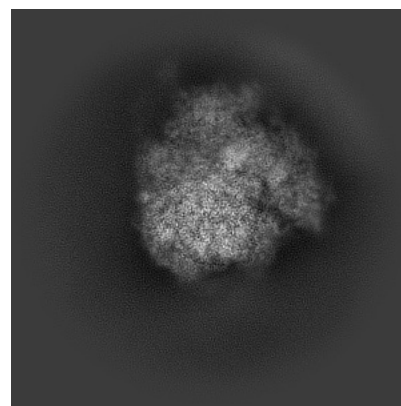
6.1.1 Primary map



X

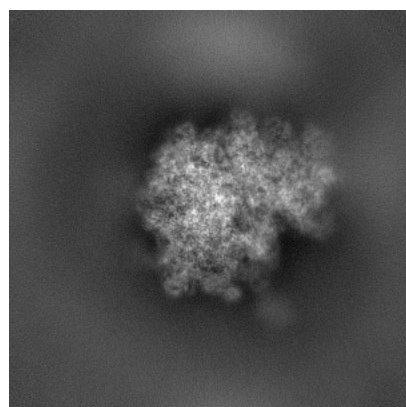


Y

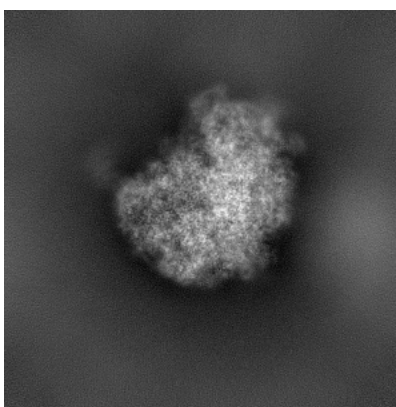


Z

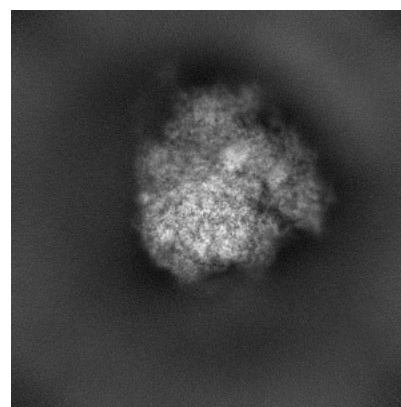
6.1.2 Raw map



X



Y

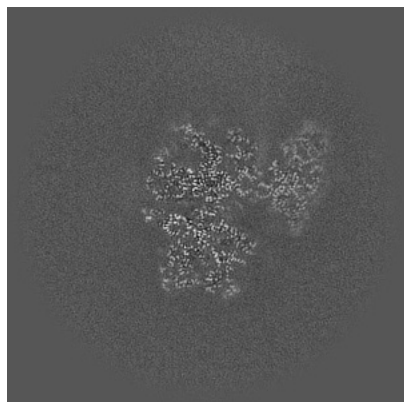


Z

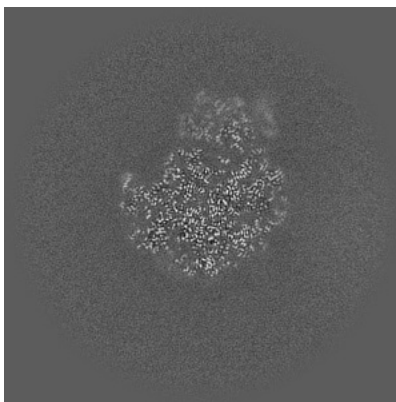
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

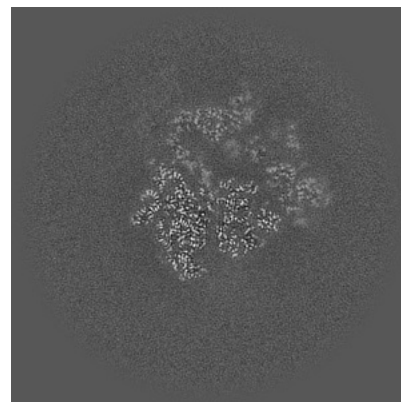
6.2.1 Primary map



X Index: 200

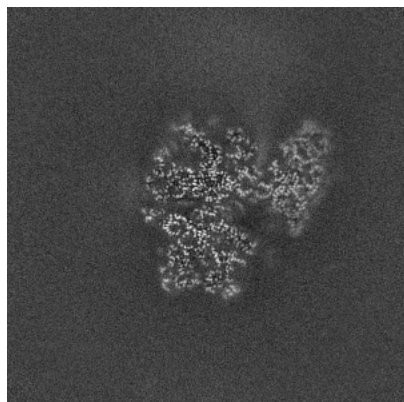


Y Index: 200

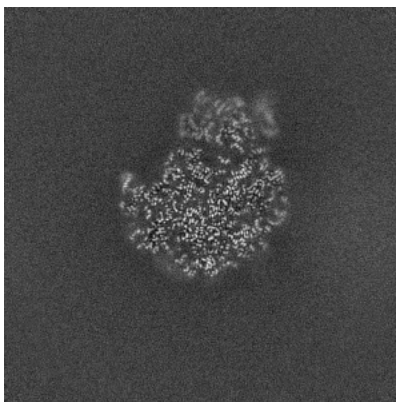


Z Index: 200

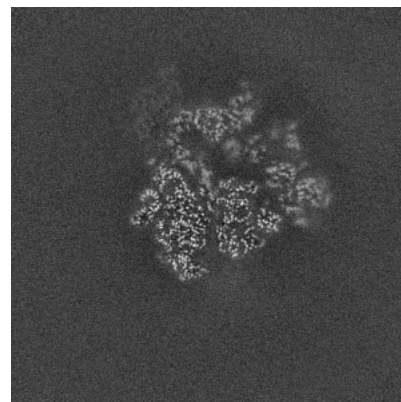
6.2.2 Raw map



X Index: 200



Y Index: 200

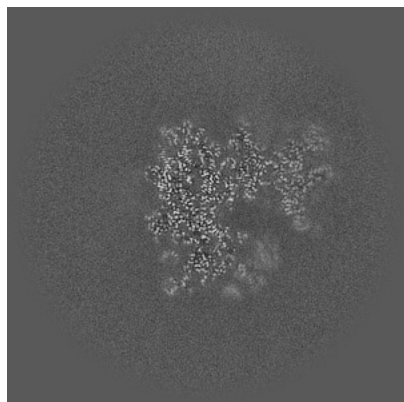


Z Index: 200

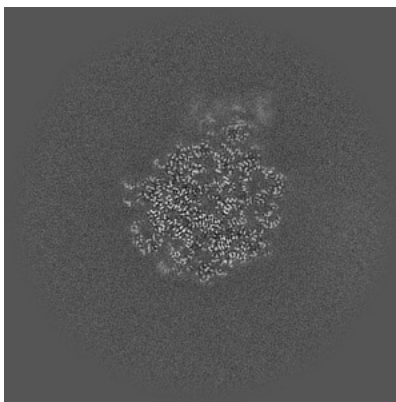
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

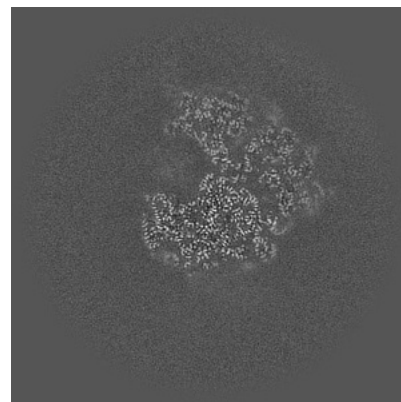
6.3.1 Primary map



X Index: 212

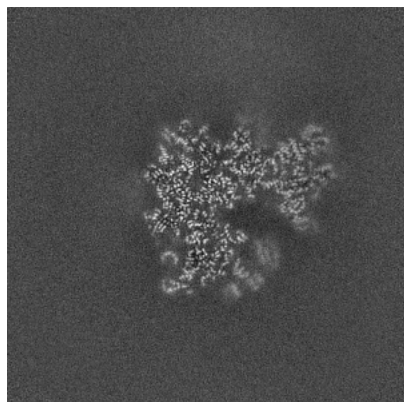


Y Index: 192

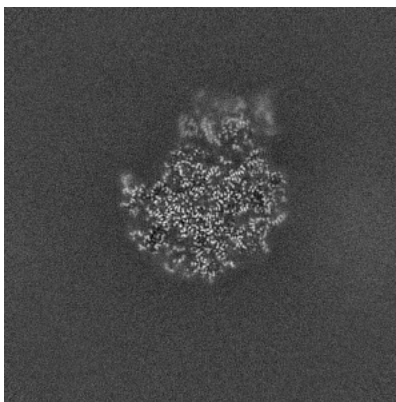


Z Index: 222

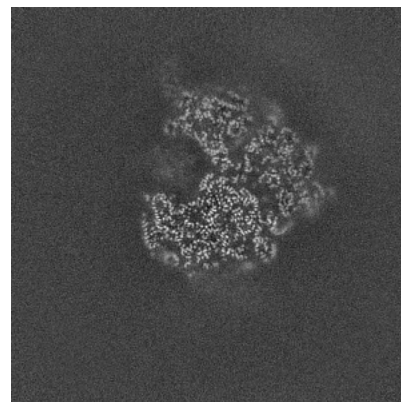
6.3.2 Raw map



X Index: 210



Y Index: 198

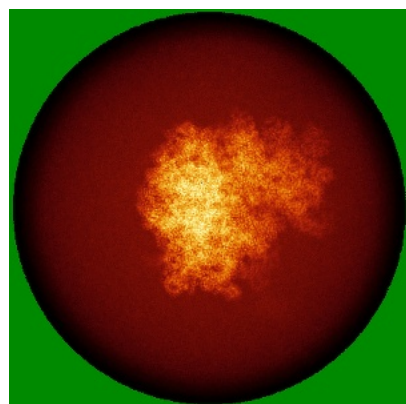


Z Index: 222

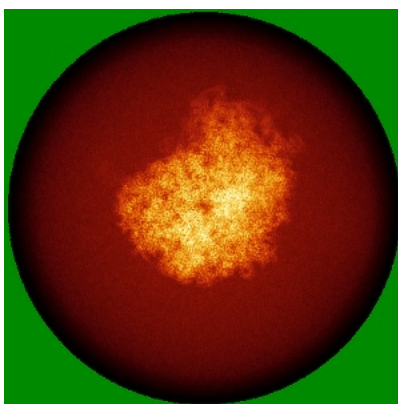
The images above show the largest variance slices of the map in three orthogonal directions.

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

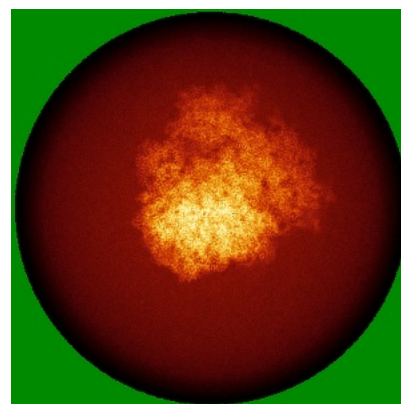
6.4.1 Primary map



X

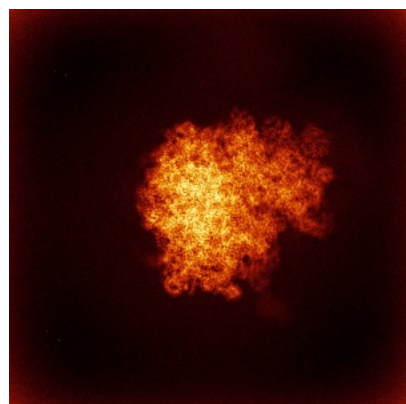


Y

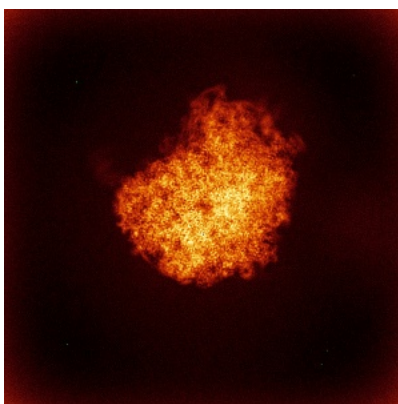


Z

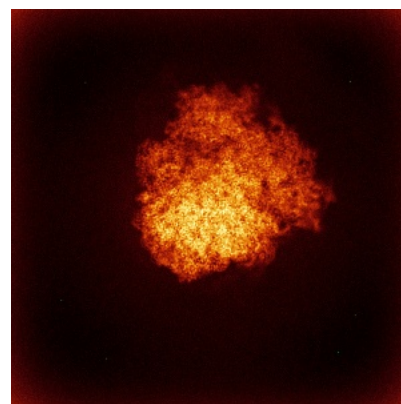
6.4.2 Raw map



X



Y

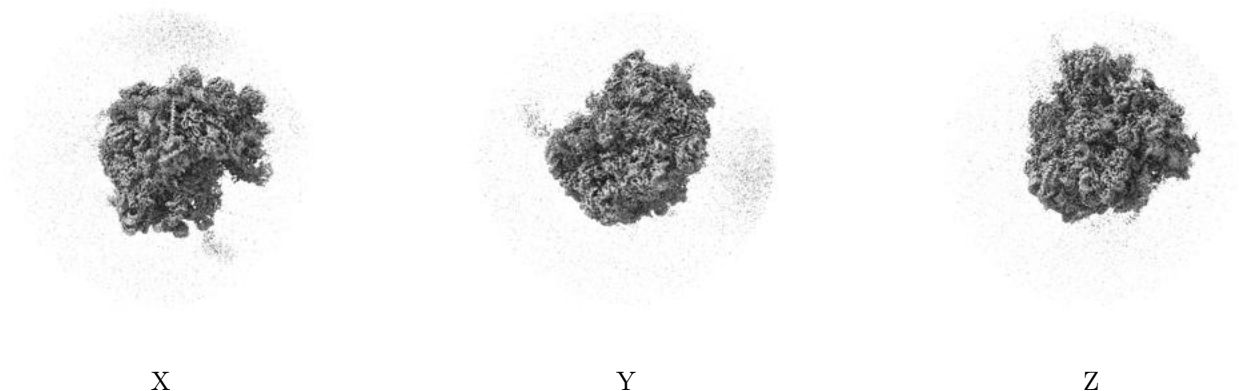


Z

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

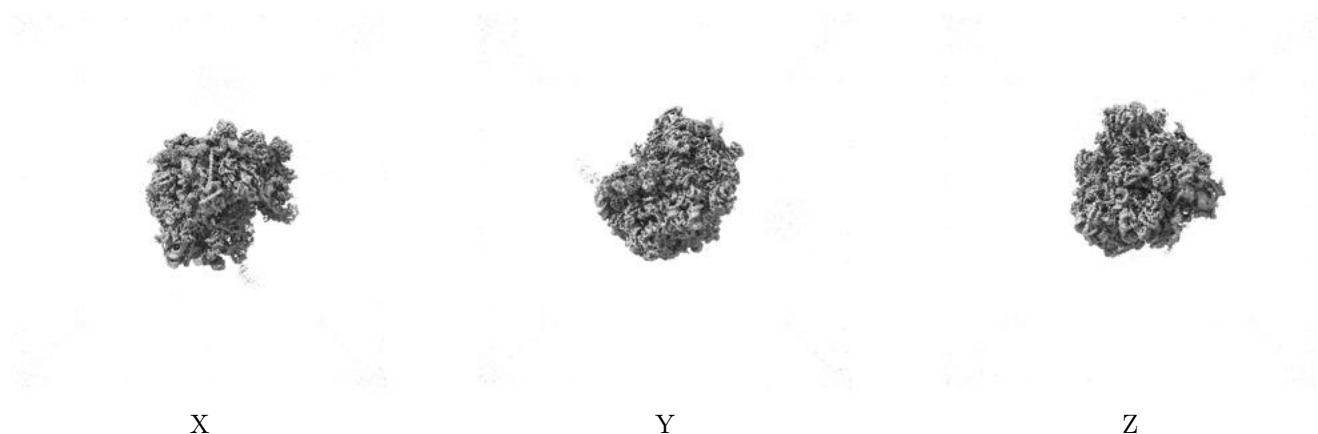
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.23. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

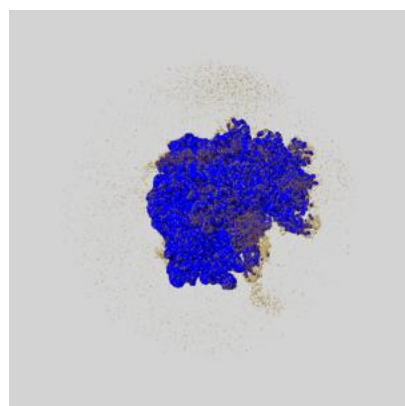
6.6 Mask visualisation [i](#)

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

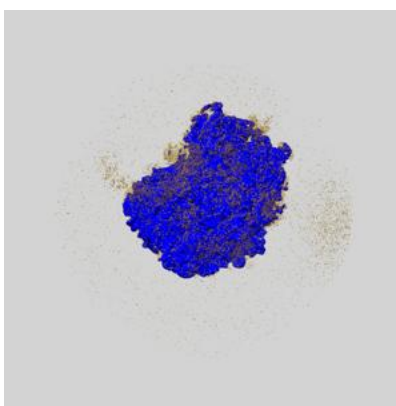
A mask typically either:

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

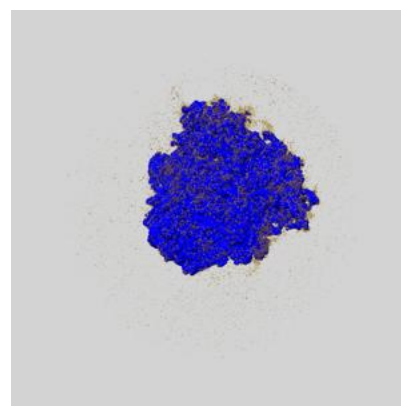
6.6.1 emd_38656_msk_1.map [i](#)



X



Y

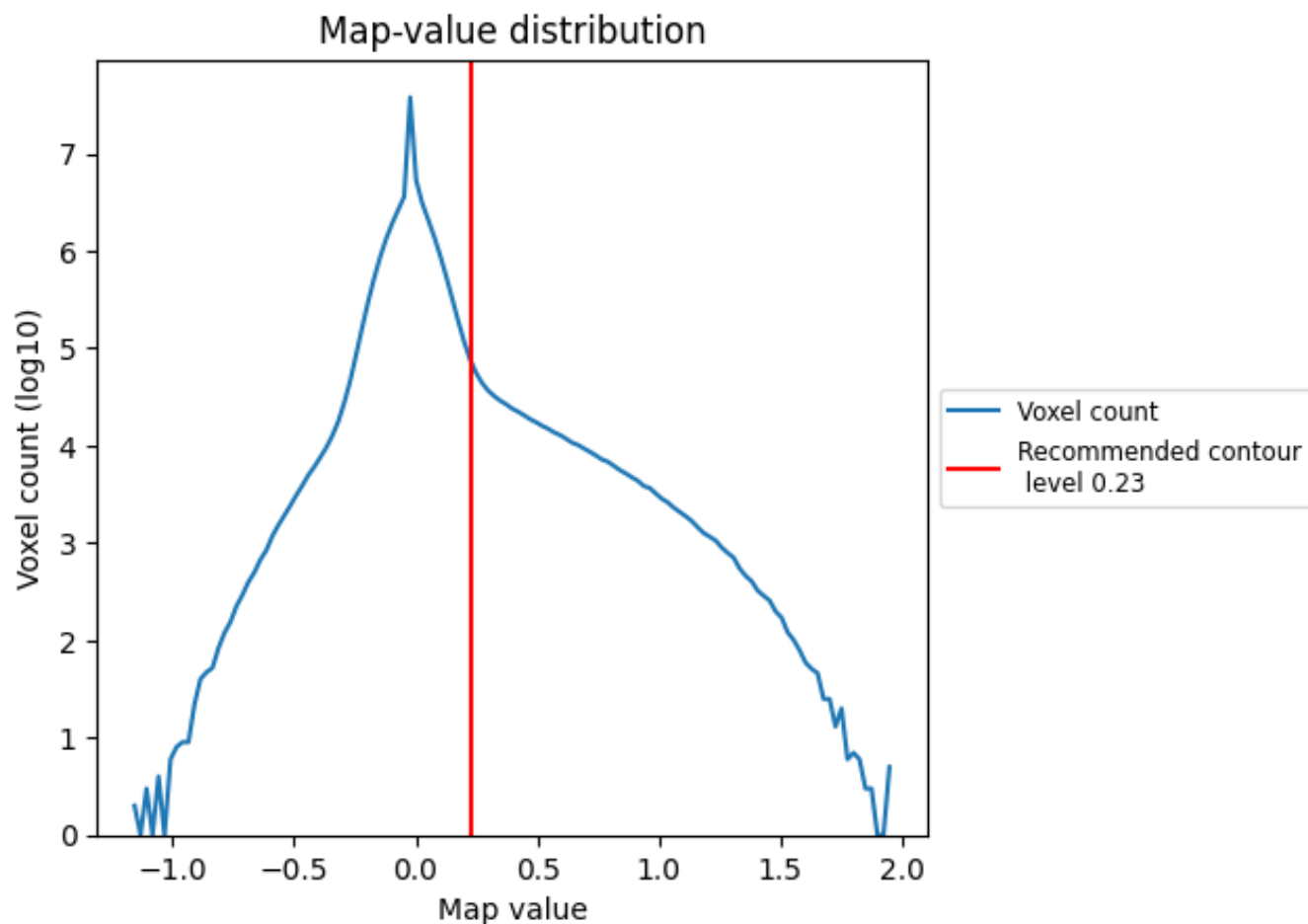


Z

7 Map analysis [i](#)

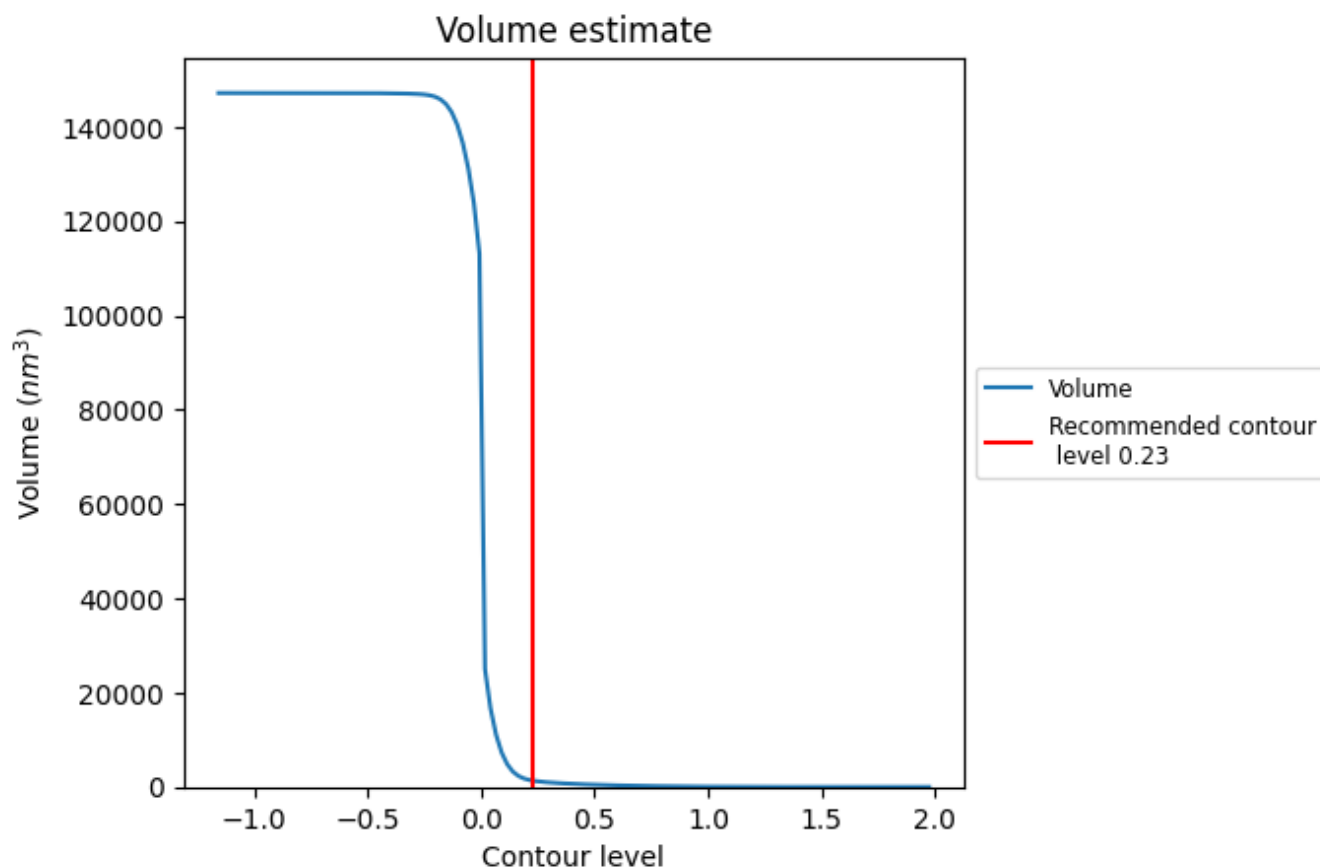
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

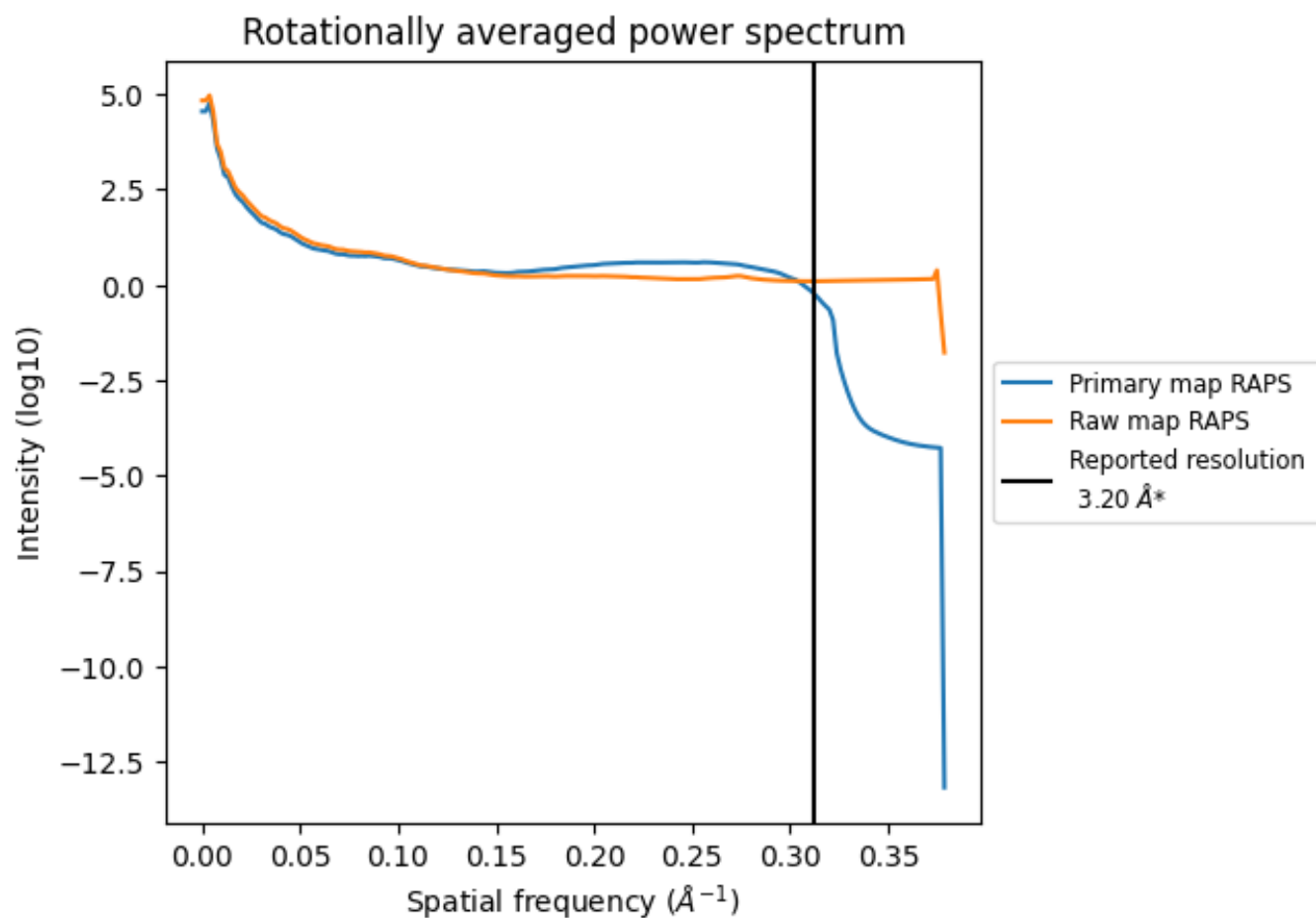
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1324 nm^3 ; this corresponds to an approximate mass of 1196 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

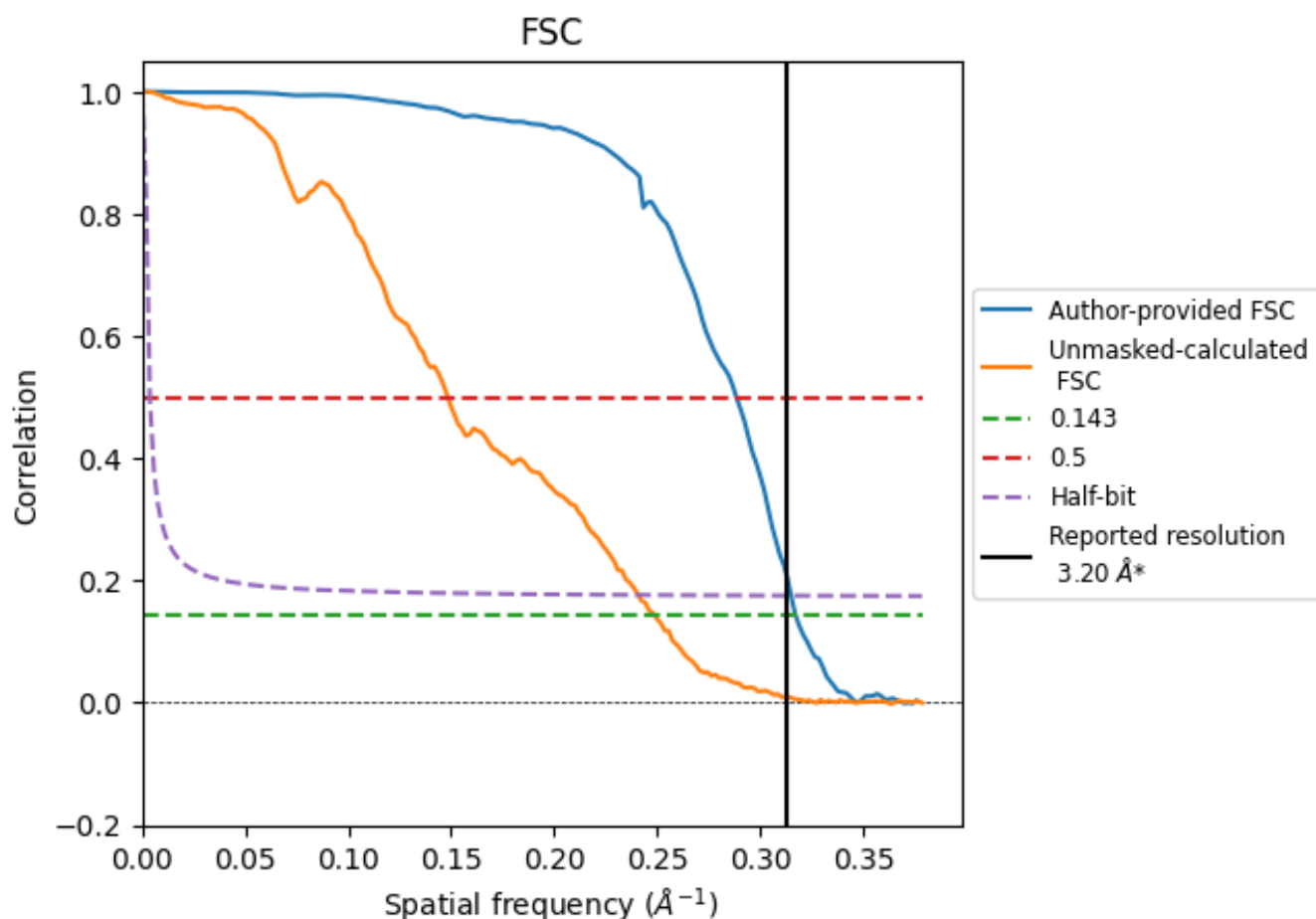


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

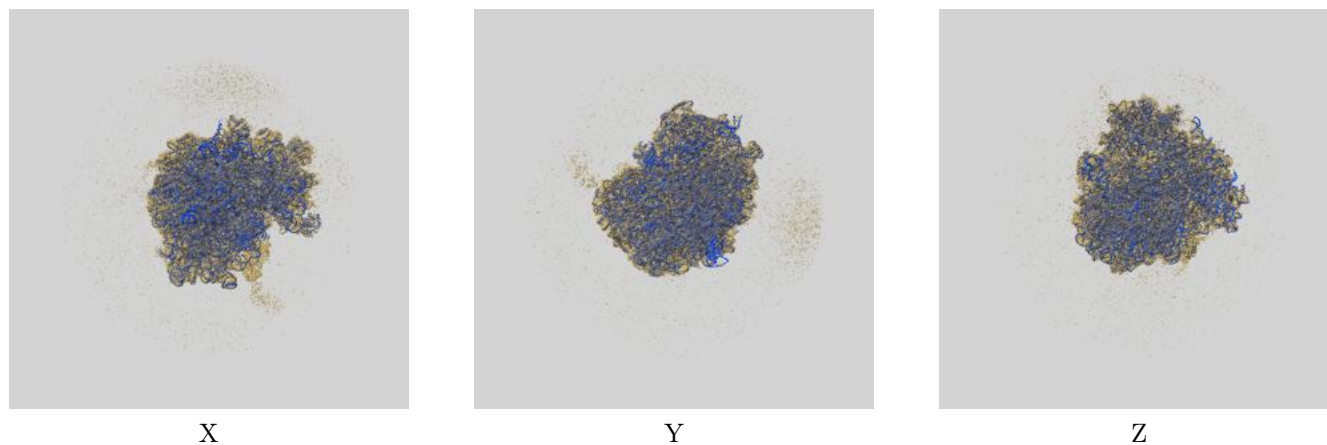
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.15	3.47	3.17
Unmasked-calculated*	4.02	6.74	4.15

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

9 Map-model fit [i](#)

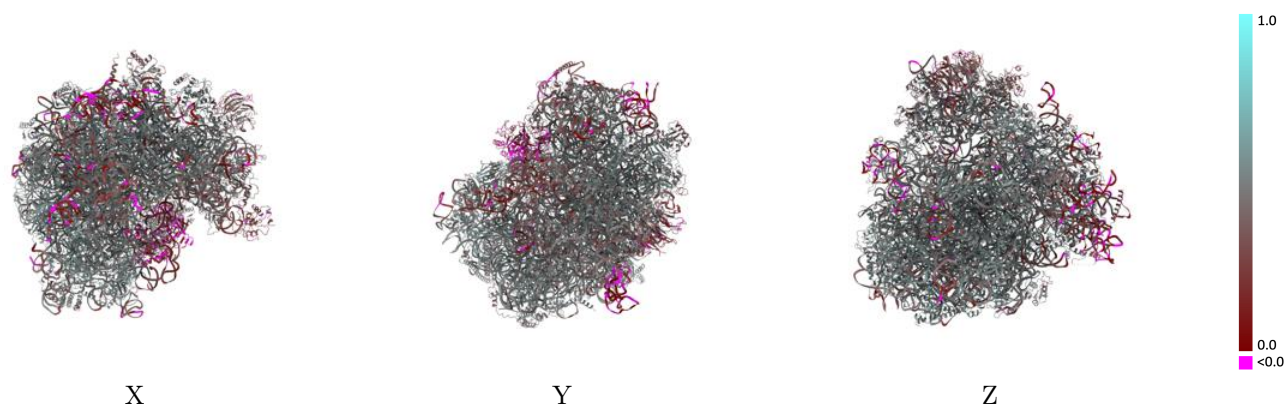
This section contains information regarding the fit between EMDB map EMD-38656 and PDB model 8Z70. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



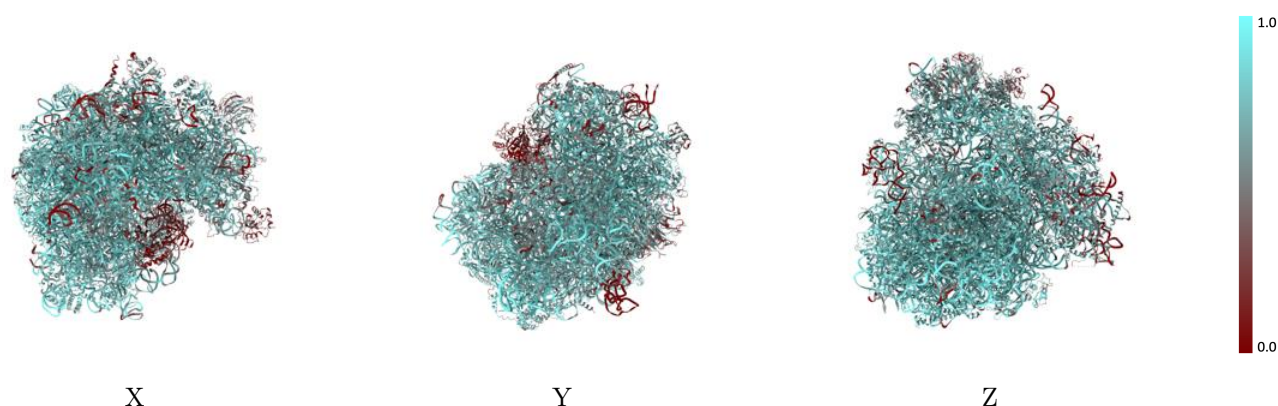
The images above show the 3D surface view of the map at the recommended contour level 0.23 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



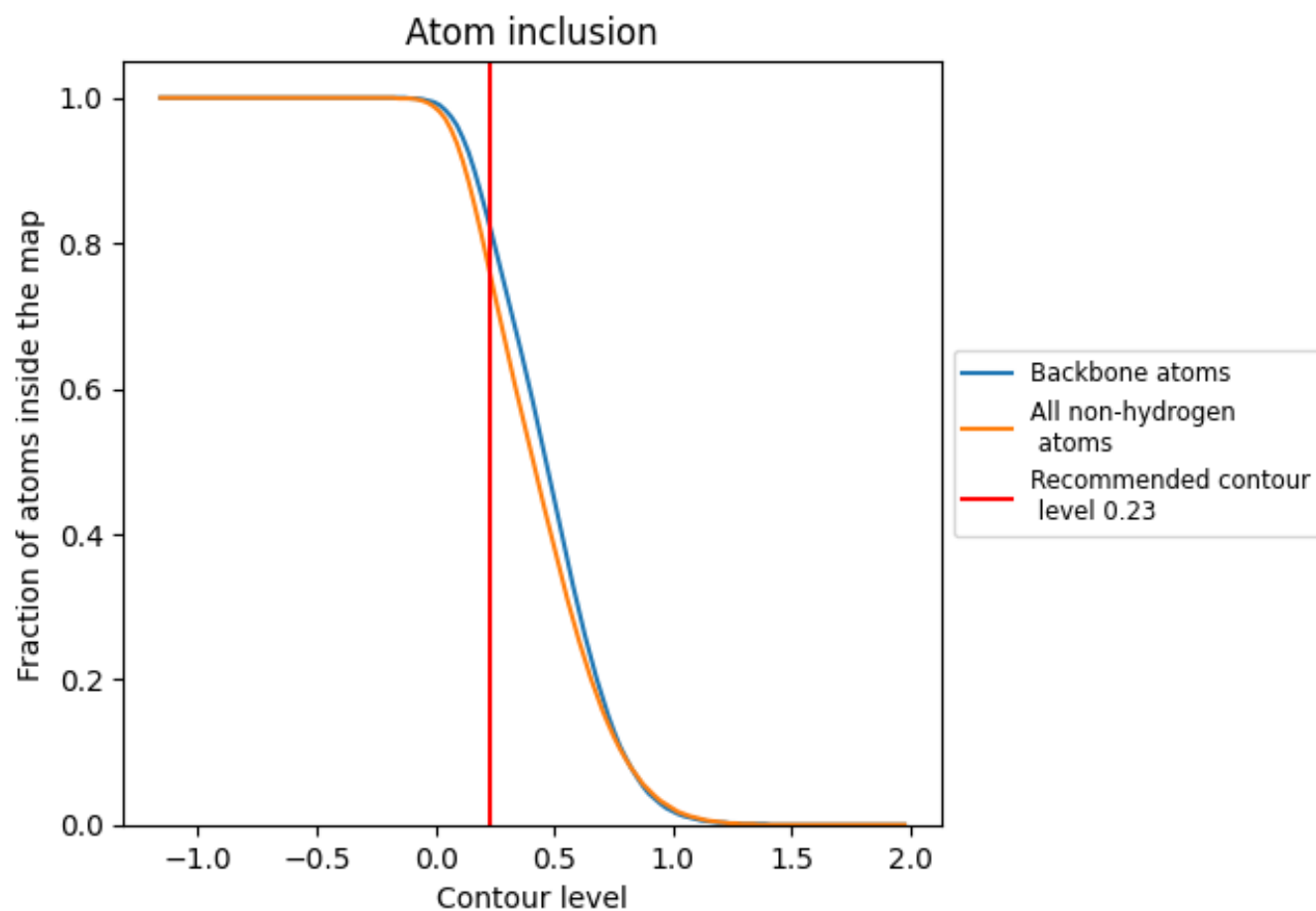
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.23).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 76% 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 (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7570	 0.4570
2	 0.7740	 0.4160
A	 0.8320	 0.4510
B	 0.9270	 0.5130
C	 0.9060	 0.5200
D	 0.7950	 0.5470
E	 0.8110	 0.5430
F	 0.7970	 0.5320
G	 0.7380	 0.4940
H	 0.7340	 0.4970
I	 0.8050	 0.5250
J	 0.7440	 0.4990
K	 0.7590	 0.5090
L	 0.7350	 0.5110
M	 0.6970	 0.4860
N	 0.7930	 0.5260
O	 0.7840	 0.5240
P	 0.8390	 0.5500
Q	 0.8100	 0.5270
R	 0.7900	 0.5350
S	 0.8190	 0.5440
SA	 0.5930	 0.4560
SB	 0.6340	 0.4680
SC	 0.5790	 0.4090
SD	 0.2640	 0.2440
SE	 0.5580	 0.4260
SF	 0.6510	 0.4540
SG	 0.6200	 0.4230
SH	 0.6240	 0.4660
SI	 0.6490	 0.4460
SJ	 0.6060	 0.4390
SK	 0.4920	 0.3650
SL	 0.5980	 0.4250
SM	 0.7540	 0.4940
SN	 0.3430	 0.2980



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SO	 0.4370	 0.2820
SP	 0.7180	 0.5080
SQ	 0.6620	 0.4950
SR	 0.7270	 0.5130
SS	 0.6750	 0.5030
ST	 0.5630	 0.4330
SU	 0.5800	 0.4420
SV	 0.7360	 0.5090
SW	 0.6650	 0.4730
SX	 0.7250	 0.5240
SY	 0.7270	 0.5210
SZ	 0.7480	 0.4970
Sa	 0.7240	 0.5020
Sb	 0.7560	 0.5250
Sc	 0.6940	 0.5180
Sd	 0.6170	 0.4500
Se	 0.7530	 0.4730
Sf	 0.6720	 0.4930
Sg	 0.5680	 0.4580
T	 0.7110	 0.5150
U	 0.7970	 0.5410
V	 0.7770	 0.5300
W	 0.6970	 0.4600
X	 0.7460	 0.5340
Y	 0.6690	 0.4550
Z	 0.7610	 0.5240
a	 0.7900	 0.5320
b	 0.8060	 0.5220
c	 0.8270	 0.5400
d	 0.7570	 0.5210
e	 0.7590	 0.5290
f	 0.7420	 0.5200
g	 0.8220	 0.5560
h	 0.8360	 0.5510
i	 0.7740	 0.5240
j	 0.7890	 0.5270
k	 0.7630	 0.5060
l	 0.8630	 0.5530
m	 0.7160	 0.4990
n	 0.7950	 0.5510
o	 0.7750	 0.5240
p	 0.8170	 0.5380

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
q	 0.7590	 0.5330
r	 0.7650	 0.5350
s	 0.3400	 0.2330
t	 0.7550	 0.4120
x	 0.1090	 0.0790