wwPDB EM Validation Summary Report

Dec 2, 2024 – 11:20 PM JST

PDB ID	:	8YLR
EMDB ID	:	EMD-38668
Title	:	State 6 (S6) of yeast 80S ribosome bound to 2 tRNAs and eEF2 and eEF3 during tranlocation
Authors	:	Cheng, J.; Wu, C.L.; Li, J.X.; Zhang, X.Z.
Deposited on	:	2024-03-06
Resolution	:	3.90 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:

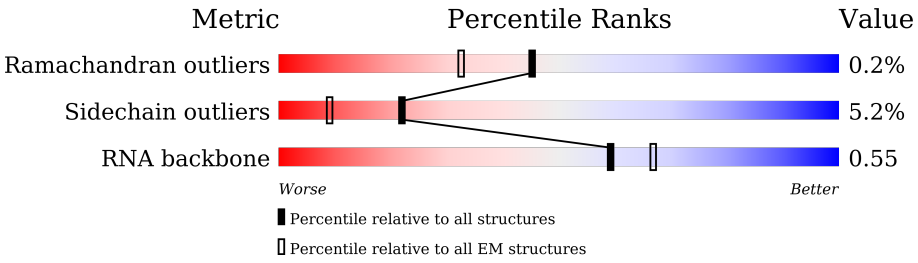
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 3.90 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2	1799	10% 72% 27% .
2	A	3394	. 79% 15% 6%
3	B	121	. 88% 12%
4	C	158	. 78% 22%
5	D	251	16% 96% .
6	F	361	9% 97% .
7	G	294	15% 97% .
8	H	175	14% 93% . 5%

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Mol	Chain	Length	Quality of chain
9	I	223	9% 97%
10	J	233	14% 97%
11	K	191	12% 96%
12	L	218	22% 94% 6%
13	M	169	21% 94% 6%
14	N	193	11% 97%
15	O	136	10% 98%
16	P	203	16% 93% 7%
17	Q	197	11% 94% 6%
18	R	183	10% 96%
19	S	185	13% 97%
20	T	188	19% 97%
21	U	171	8% 96%
22	V	159	12% 95%
23	W	100	20% 96%
24	X	136	19% 97%
25	Y	126	37% 97%
26	Z	121	13% 96%
27	a	125	8% 97%
28	b	135	8% 98%
29	c	148	10% 97%
30	d	58	21% 93% 7%
31	e	96	15% 97%
32	f	109	22% 97%
33	g	127	17% 96%

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Mol	Chain	Length	Quality of chain
34	h	106	9% 95% 5%
35	i	112	20% 93% 7%
36	j	119	12% 97%
37	k	99	10% 96%
38	l	81	10% 90% 10%
39	m	77	17% 94% 6%
40	n	50	24% 90% 10%
41	o	52	19% 90% 10%
42	p	25	20% 96%
43	q	103	20% 93% 7%
44	r	91	18% 95% 5%
45	t	75	67% 77% 23%
45	u	75	23% 76% 23%
46	v	1044	93% 92% 6%
47	x	842	61% 95% 5%
48	SA	222	62% 95% 5%
49	SC	92	62% 89% 11%
50	SD	121	83% 98%
51	SE	117	72% 91% 9%
52	SF	141	56% 95%
53	SH	145	52% 94% 6%
54	SI	143	59% 95% 5%
55	SJ	100	52% 98%
56	SK	108	38% 52% 7% 41%
57	SM	53	36% 89% 11%

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Mol	Chain	Length	Quality of chain
58	SN	73	86% 96%
59	SO	312	69% 96%
60	SQ	232	63% 91% 6%
61	SS	258	63% 95% 5%
62	ST	228	57% 94% 6%
63	SR	216	30% 96%
64	SV	200	38% 88% 6% 6%
65	SW	184	38% 92% 5%
66	SX	142	47% 90% 10%
67	SY	150	45% 95% 5%
68	SZ	127	61% 96%
69	Sa	87	54% 93% 7%
70	Sb	129	39% 96%
71	Sc	144	55% 95% 5%
72	Sd	134	53% 95% 5%
73	Se	94	40% 98%
74	Sf	81	52% 98%
75	Sg	60	58% 93% 7%
76	SG	121	50% 93% 7%
77	SP	206	36% 95% 5%
78	SU	184	46% 93% 7%
79	SL	63	76% 89% 11%
80	SB	206	70% 94% 6%
81	E	386	15% 95% 5%

2 Entry composition (i)

There are 81 unique types of molecules in this entry. The entry contains 216620 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
			Total	C	N	O	P		
1	2	1771	37739	16872	6683	12413	1771	0	0

- Molecule 2 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A	3192	68278	30498	12313	22275	3192	0	0

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

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

- Molecule 4 is a RNA chain called 5.8S rRNA.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL2A.

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL4A.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 8 is a protein called Large ribosomal subunit protein eL6B.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	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 10 is a protein called Large ribosomal subunit protein eL8A.

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

- Molecule 11 is a protein called Large ribosomal subunit protein uL6A.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL5B.

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

- Molecule 14 is a protein called Large ribosomal subunit protein eL13A.

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

- Molecule 15 is a protein called Large ribosomal subunit protein eL14A.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL15A.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL13A.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL22A.

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

- Molecule 19 is a protein called Large ribosomal subunit protein eL18A.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL19A.

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

- Molecule 21 is a protein called Large ribosomal subunit protein eL20A.

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

- Molecule 22 is a protein called Large ribosomal subunit protein eL21A.

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

- Molecule 23 is a protein called Large ribosomal subunit protein eL22A.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL14A.

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

- Molecule 25 is a protein called Large ribosomal subunit protein eL24A.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL24A.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL27A.

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

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL31A.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL33A.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL34A.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL29A.

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

- Molecule 37 is a protein called Large ribosomal subunit protein eL36A.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL37A.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL40A.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL41A.

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

- Molecule 43 is a protein called Large ribosomal subunit protein eL42A.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL43A.

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

- Molecule 45 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	75	Total	C	N	O	P	0	0
			1605	716	297	517	75		
45	u	74	Total	C	N	O	P	0	0
			1584	706	292	512	74		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	10	A	G	conflict	GB 176433
u	10	A	G	conflict	GB 176433

- Molecule 46 is a protein called Elongation factor 3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	977	Total	C	N	O	S	0	0
			7476	4726	1295	1418	37		

- Molecule 47 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	842	Total	C	N	O	S	0	0
			6559	4166	1124	1238	31		

- Molecule 48 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 49 is a protein called Small ribosomal subunit protein eS10A.

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

- Molecule 50 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS9A.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS13A.

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

- Molecule 54 is a protein called Small ribosomal subunit protein eS19A.

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

- Molecule 55 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 56 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SK	64	Total	C	N	O	0	0
			519	332	95	92		

- Molecule 57 is a protein called Small ribosomal subunit protein uS14A.

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

- Molecule 58 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SN	73	Total	C	N	O	S	0	0
			560	355	106	95	4		

- Molecule 59 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	225	Total	C	N	O	S	0	0
			1794	1137	329	324	4		

- Molecule 61 is a protein called Small ribosomal subunit protein eS4A.

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

- Molecule 62 is a protein called Small ribosomal subunit protein eS6A.

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

- Molecule 63 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 64 is a protein called Small ribosomal subunit protein eS8A.

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SW	178	Total	C	N	O	S	0	0
			1441	913	278	249	1		

- Molecule 66 is a protein called Small ribosomal subunit protein uS17A.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS11B.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS21A.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS8A.

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

- Molecule 71 is a protein called Small ribosomal subunit protein uS12A.

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

- Molecule 72 is a protein called Small ribosomal subunit protein eS24A.

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

- Molecule 73 is a protein called Small ribosomal subunit protein eS26A.

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

- Molecule 74 is a protein called Small ribosomal subunit protein eS27A.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS30A.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS17A.

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

- Molecule 77 is a protein called Small ribosomal subunit protein uS2A.

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

- Molecule 78 is a protein called Small ribosomal subunit protein eS7A.

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

- Molecule 79 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SL	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 80 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SB	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 81 is a protein called Large ribosomal subunit protein uL3.

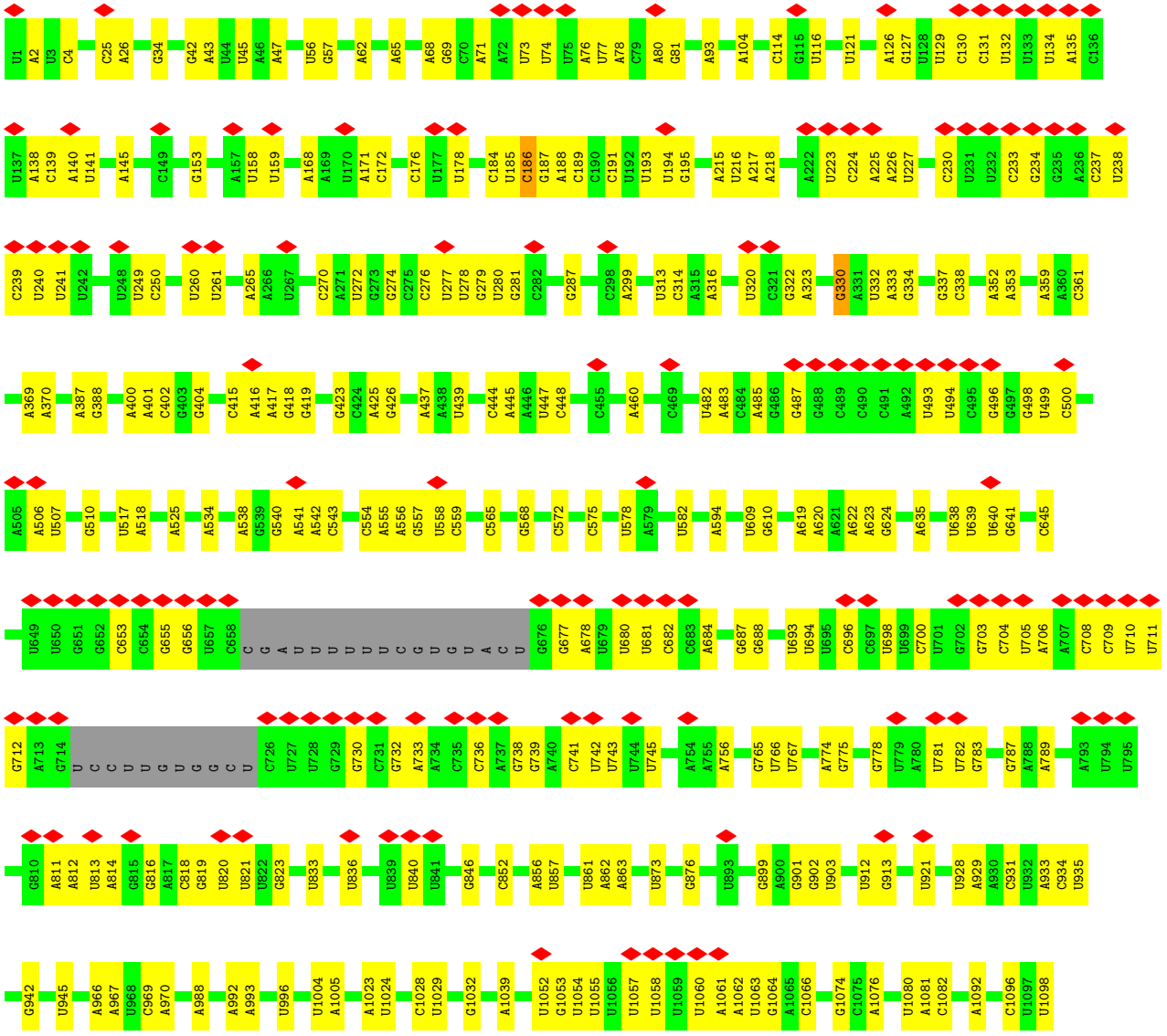
Mol	Chain	Residues	Atoms					AltConf	Trace
81	E	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

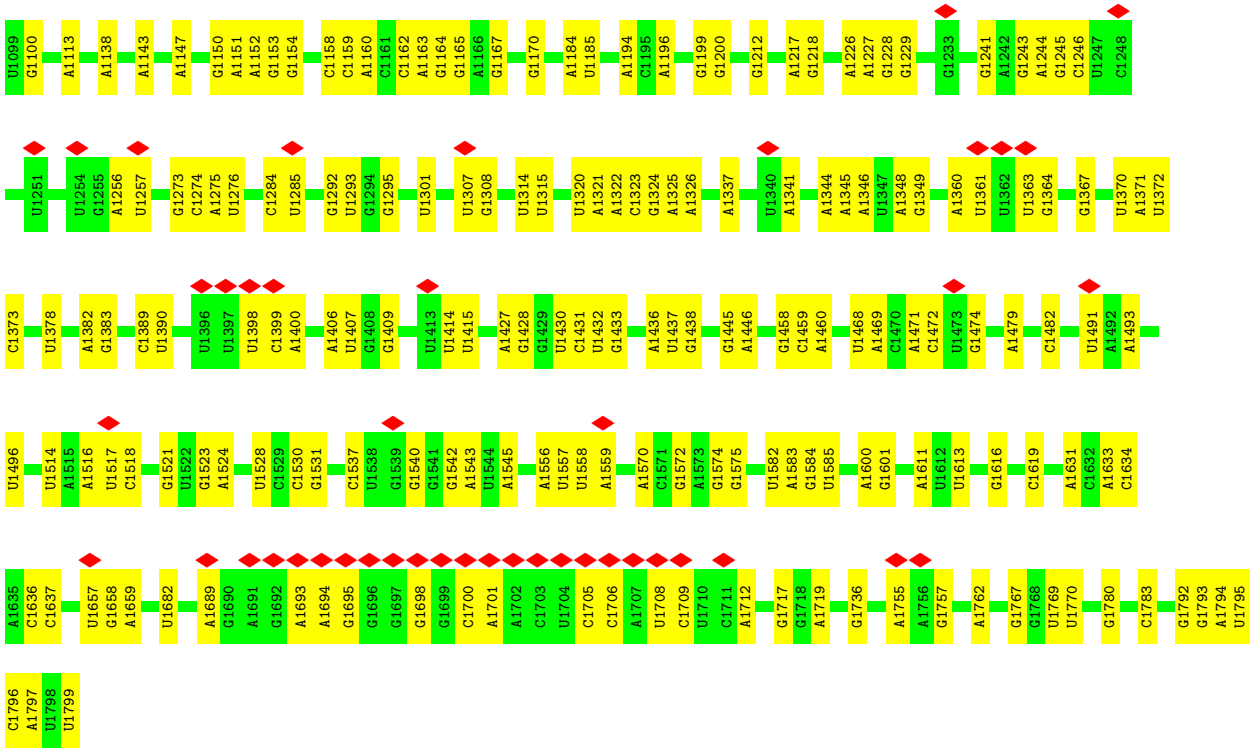
3 Residue-property plots (i)

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

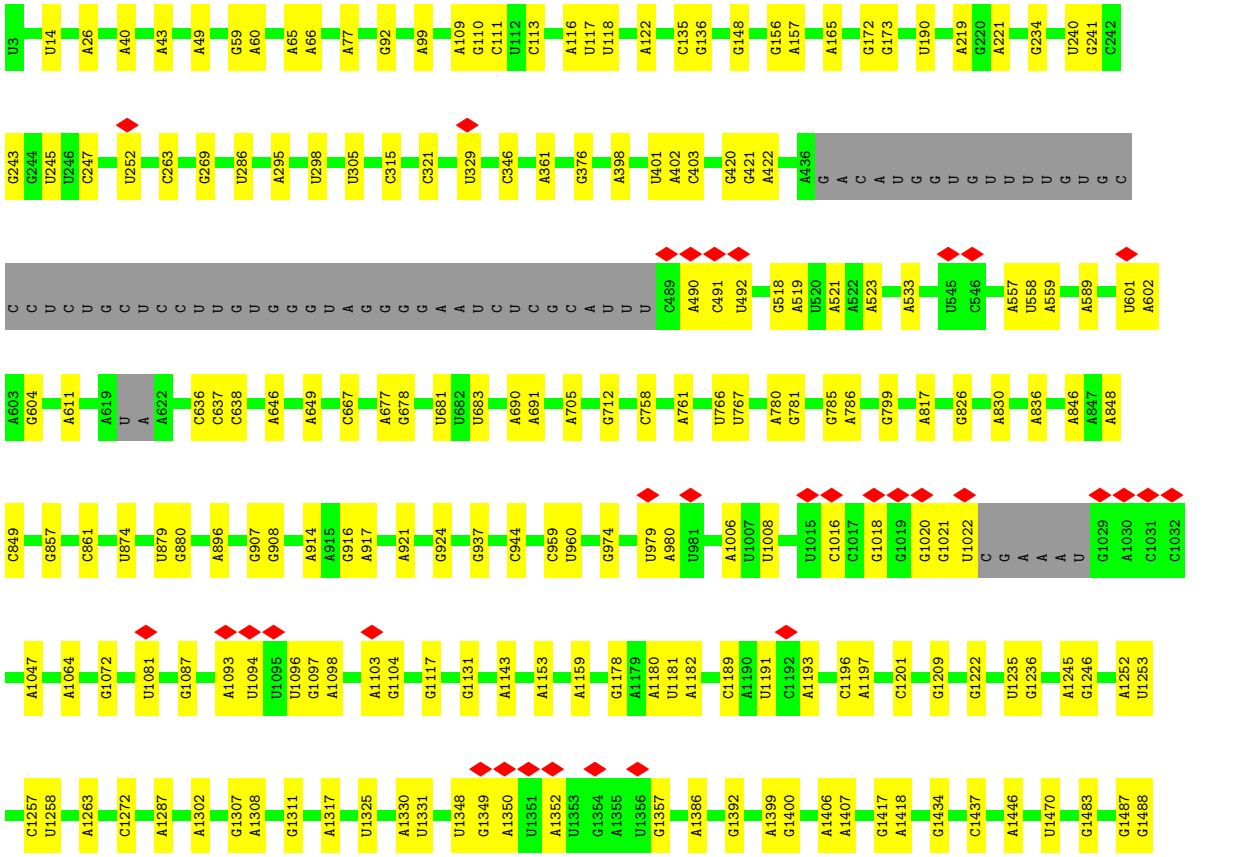
Chain 2:

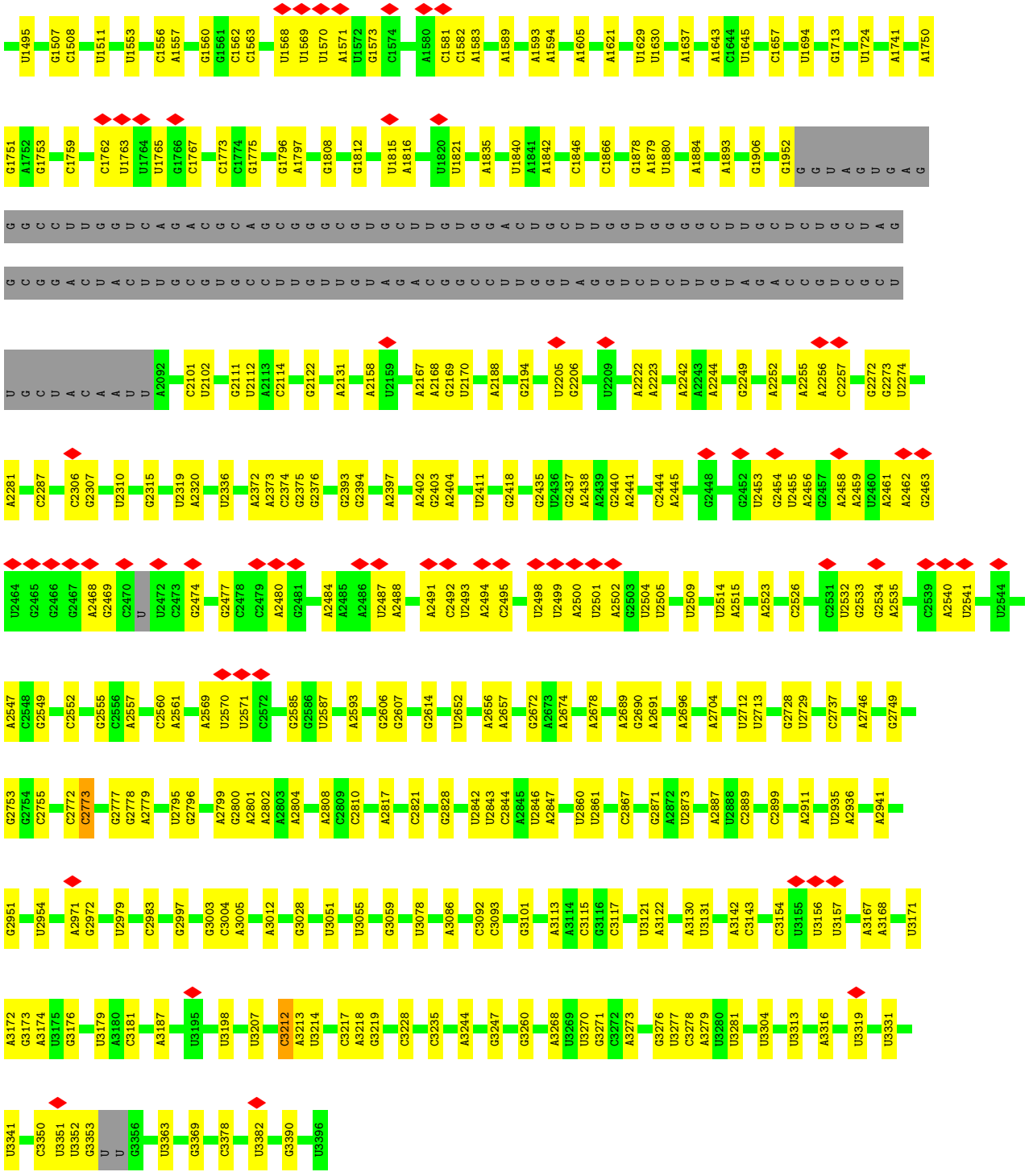




• Molecule 2: 25S rRNA

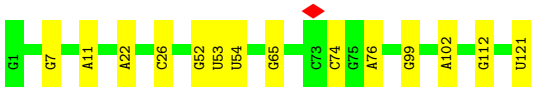
Chain A:





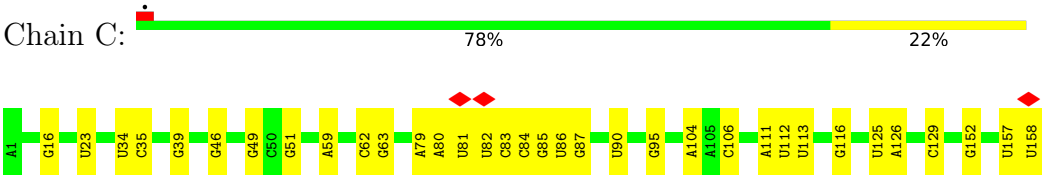
• Molecule 3: 5S rRNA

Chain B:



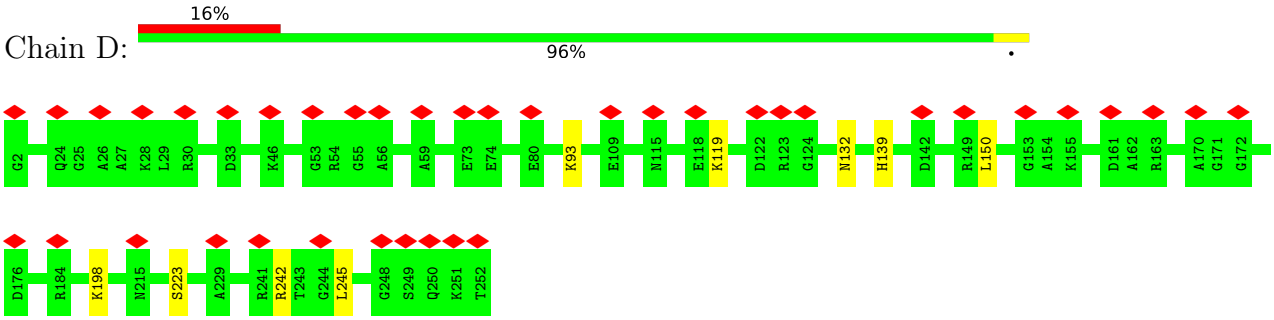
• Molecule 4: 5.8S rRNA

Chain C:



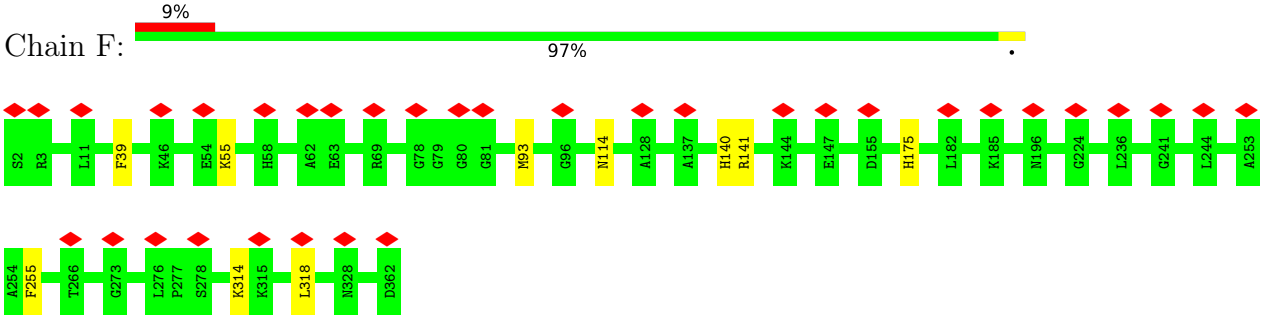
• Molecule 5: Large ribosomal subunit protein uL2A

Chain D:



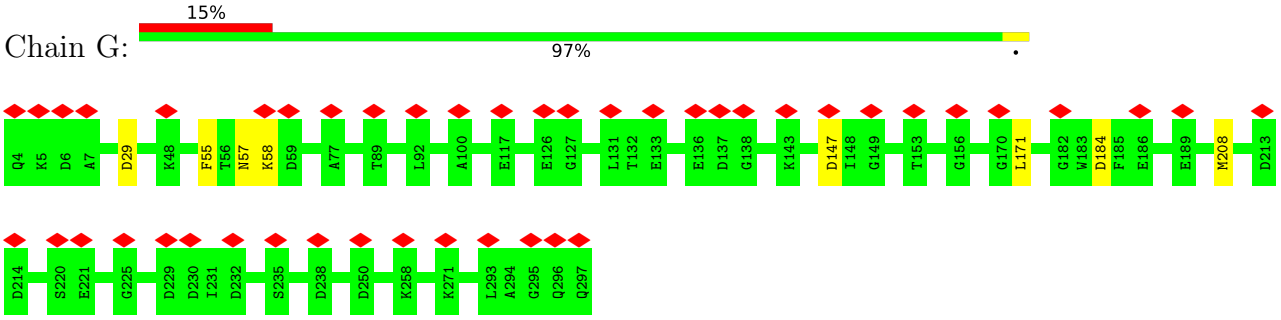
• Molecule 6: Large ribosomal subunit protein uL4A

Chain F:



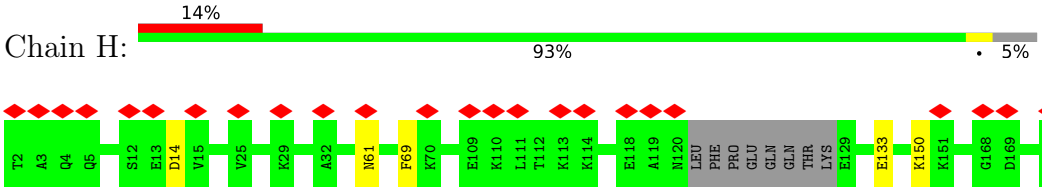
• Molecule 7: Large ribosomal subunit protein uL18

Chain G:



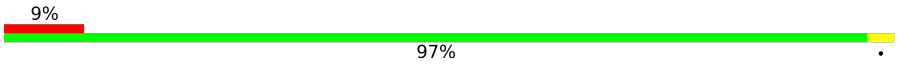
• Molecule 8: Large ribosomal subunit protein eL6B

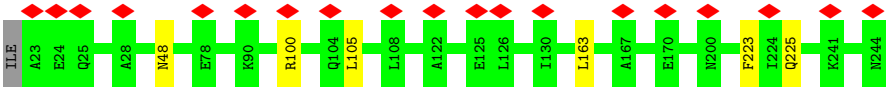
Chain H:



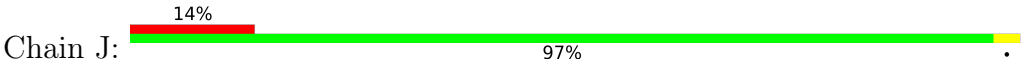
• Molecule 9: Large ribosomal subunit protein uL30A

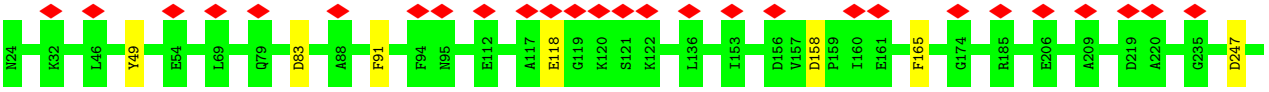
Chain I:

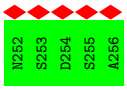




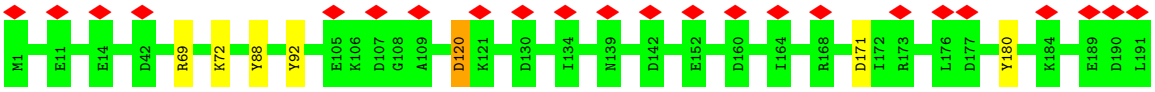
• Molecule 10: Large ribosomal subunit protein eL8A



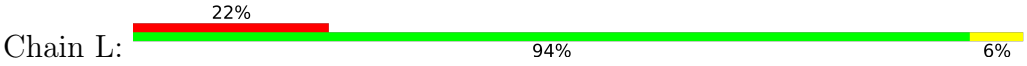


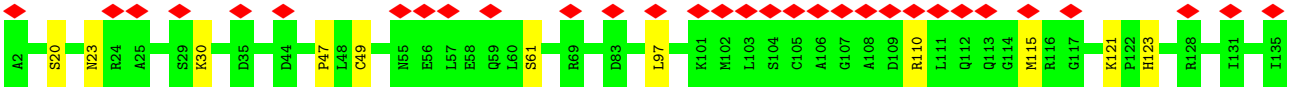


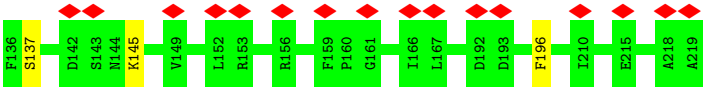
• Molecule 11: Large ribosomal subunit protein uL6A



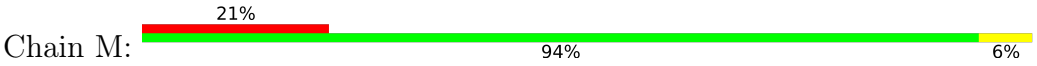
• Molecule 12: Large ribosomal subunit protein uL16

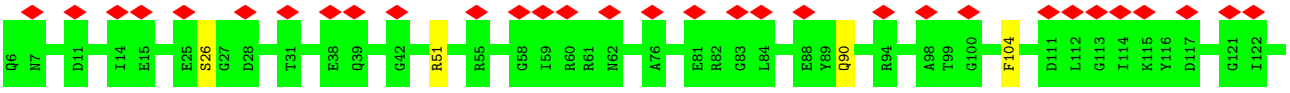


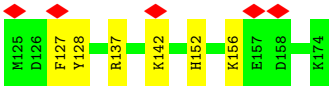




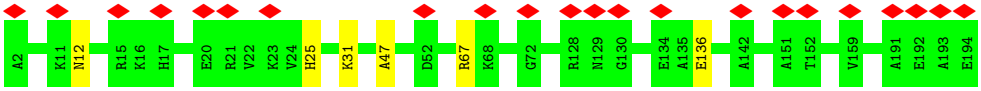
• Molecule 13: Large ribosomal subunit protein uL5B



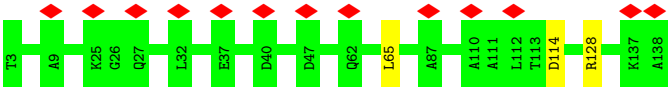




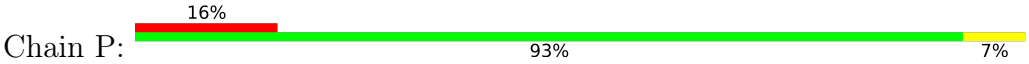
• Molecule 14: Large ribosomal subunit protein eL13A

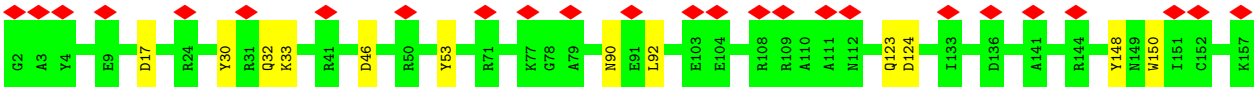


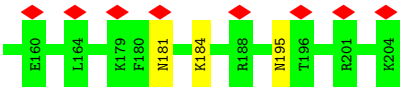
• Molecule 15: Large ribosomal subunit protein eL14A



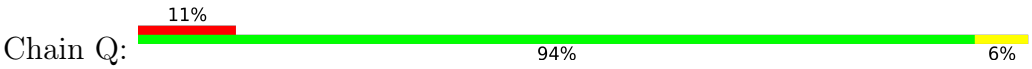
• Molecule 16: Large ribosomal subunit protein eL15A

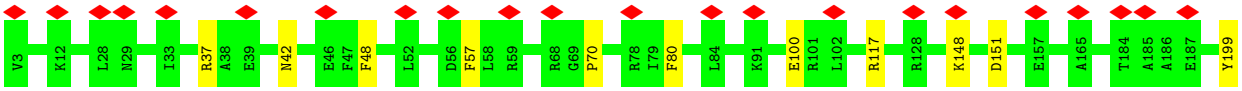




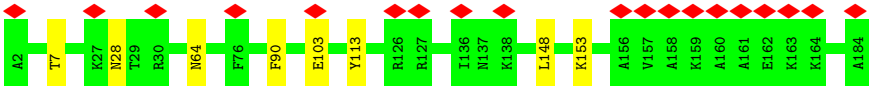


• Molecule 17: Large ribosomal subunit protein uL13A

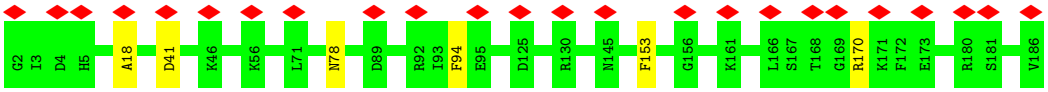




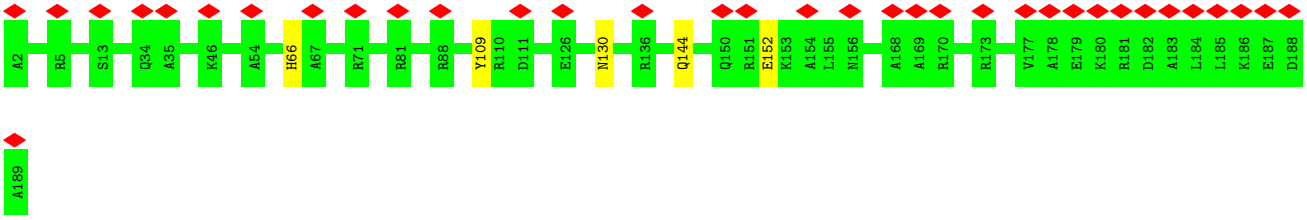
• Molecule 18: Large ribosomal subunit protein uL22A



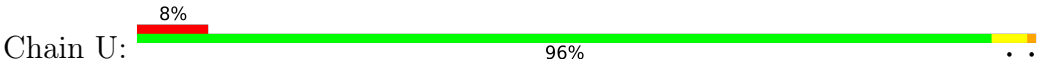
• Molecule 19: Large ribosomal subunit protein eL18A



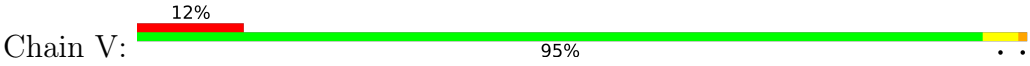
• Molecule 20: Large ribosomal subunit protein eL19A



• Molecule 21: Large ribosomal subunit protein eL20A



• Molecule 22: Large ribosomal subunit protein eL21A



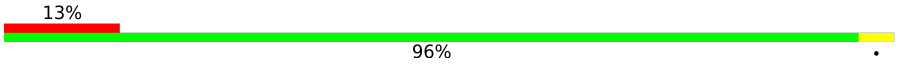
• Molecule 23: Large ribosomal subunit protein eL22A

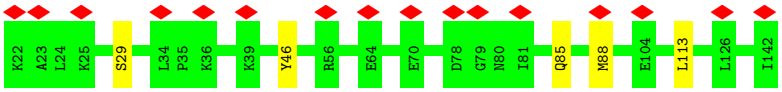
• Molecule 24: Large ribosomal subunit protein uL14A

• Molecule 25: Large ribosomal subunit protein eL24A

• Molecule 26: Large ribosomal subunit protein uL23

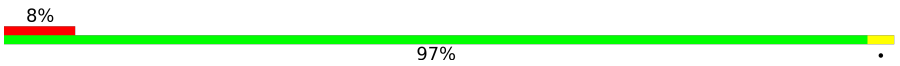
Chain Z:

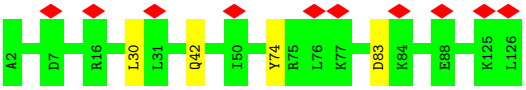




• Molecule 27: Large ribosomal subunit protein uL24A

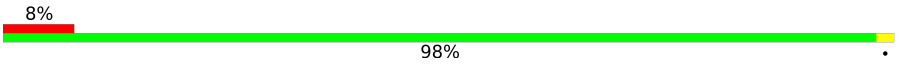
Chain a:

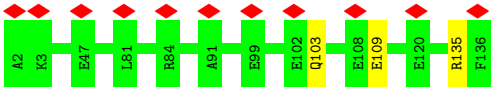




• Molecule 28: Large ribosomal subunit protein eL27A

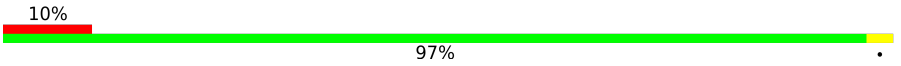
Chain b:

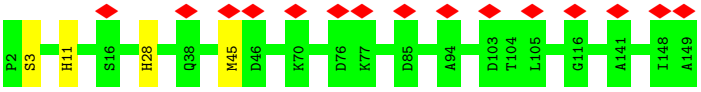




• Molecule 29: Large ribosomal subunit protein uL15

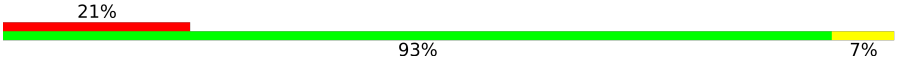
Chain c:

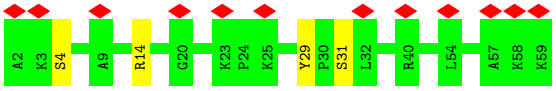




• Molecule 30: Large ribosomal subunit protein eL29

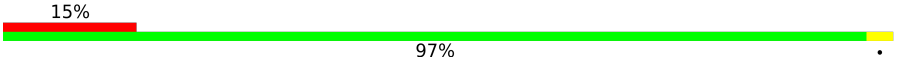
Chain d:

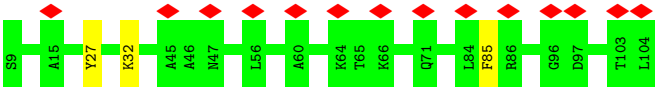




• Molecule 31: Large ribosomal subunit protein eL30

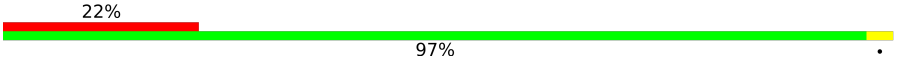
Chain e:

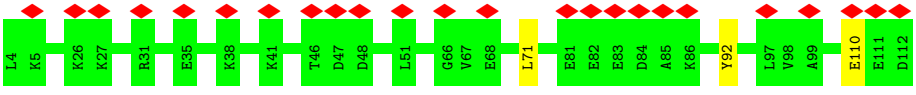




• Molecule 32: Large ribosomal subunit protein eL31A

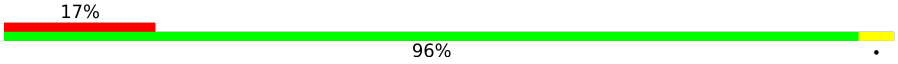
Chain f:

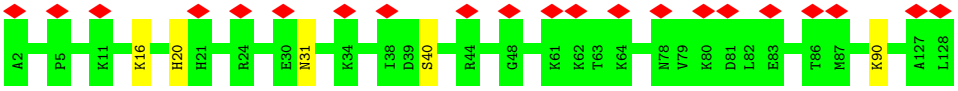




• Molecule 33: Large ribosomal subunit protein eL32

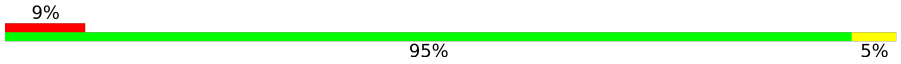
Chain g:

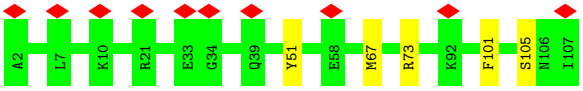




• Molecule 34: Large ribosomal subunit protein eL33A

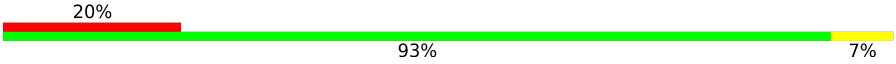
Chain h:

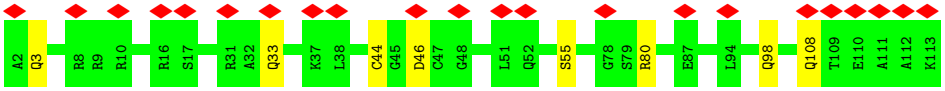




• Molecule 35: Large ribosomal subunit protein eL34A

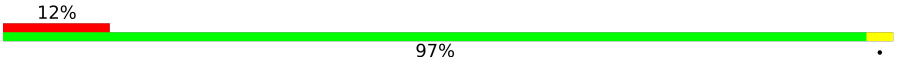
Chain i:

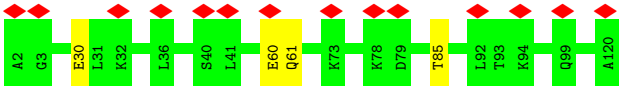




• Molecule 36: Large ribosomal subunit protein uL29A

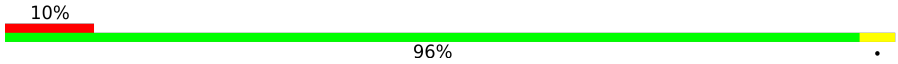
Chain j:

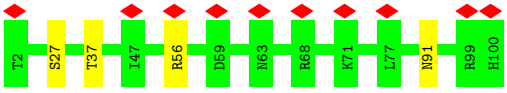




• Molecule 37: Large ribosomal subunit protein eL36A

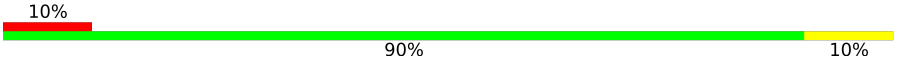
Chain k:

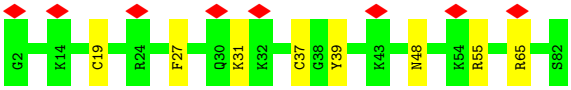




• Molecule 38: Large ribosomal subunit protein eL37A

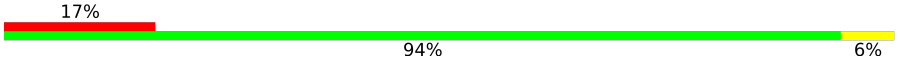
Chain l:

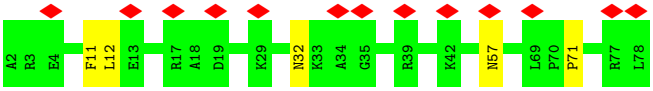




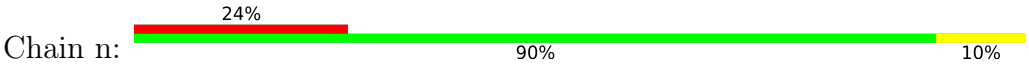
• Molecule 39: Large ribosomal subunit protein eL38

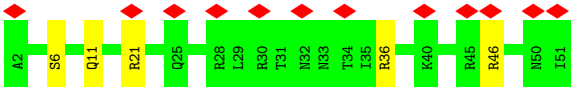
Chain m:



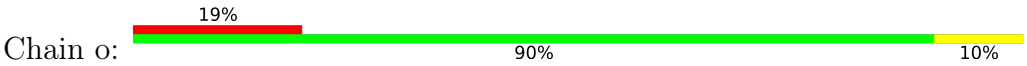


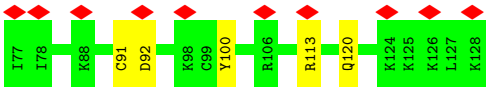
• Molecule 40: Large ribosomal subunit protein eL39



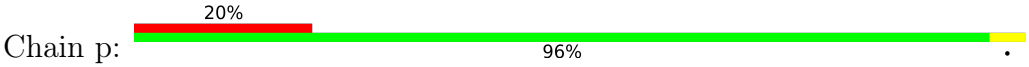


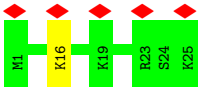
• Molecule 41: Large ribosomal subunit protein eL40A



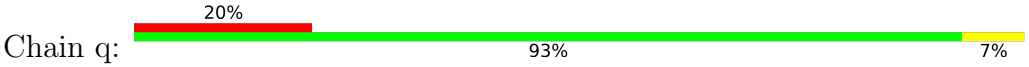


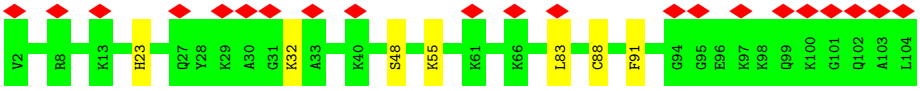
• Molecule 42: Large ribosomal subunit protein eL41A



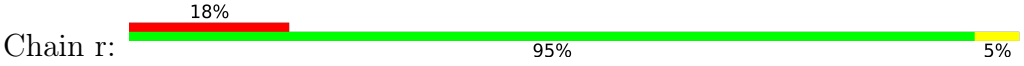


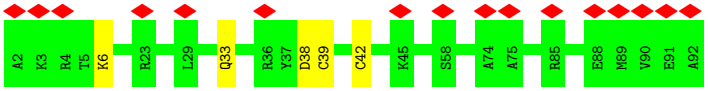
• Molecule 43: Large ribosomal subunit protein eL42A



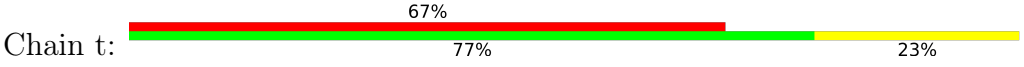


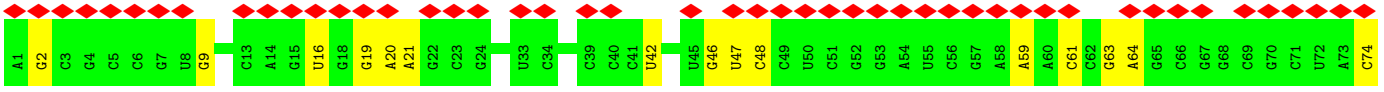
• Molecule 44: Large ribosomal subunit protein eL43A





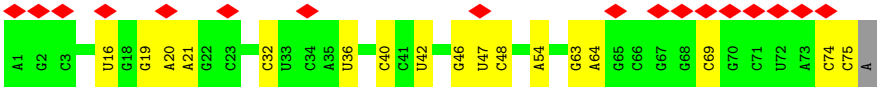
• Molecule 45: tRNA





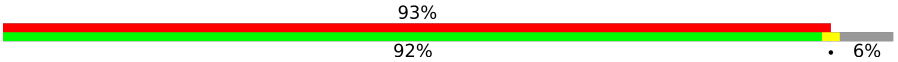
• Molecule 45: tRNA

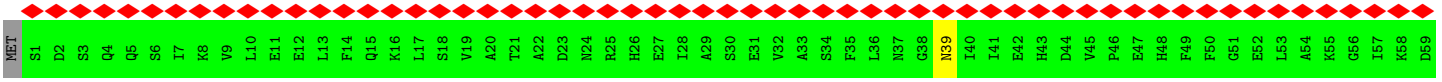
Chain u:

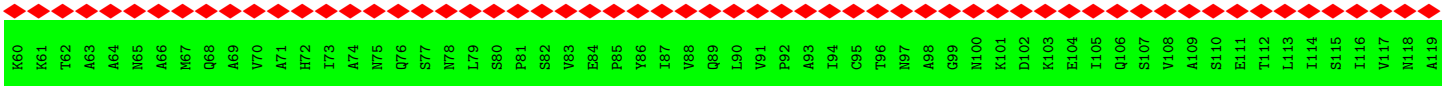


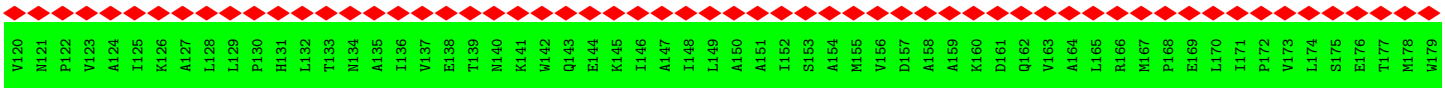
• Molecule 46: Elongation factor 3A

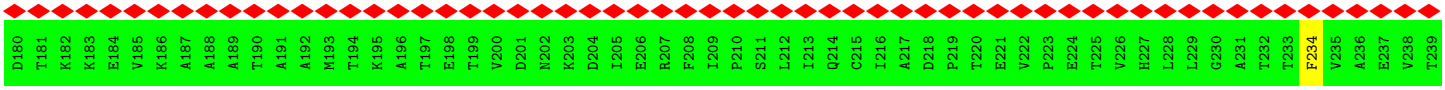
Chain v:

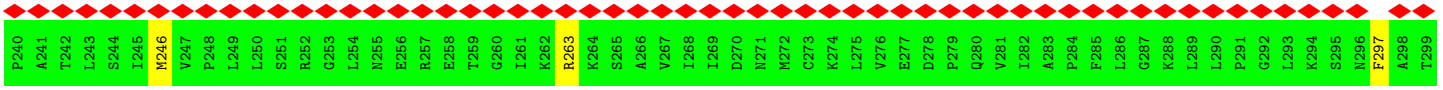


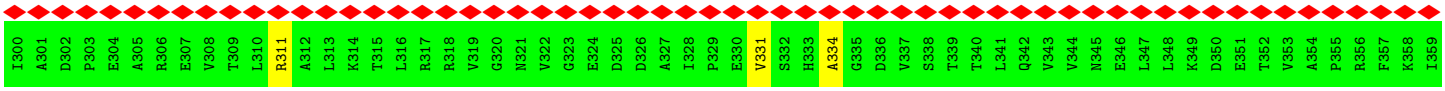


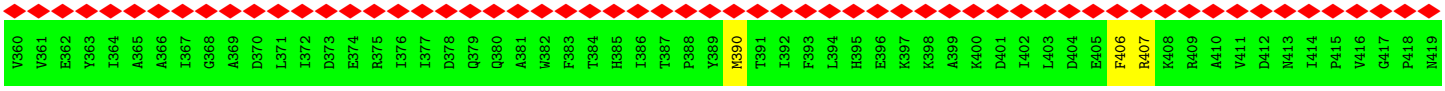


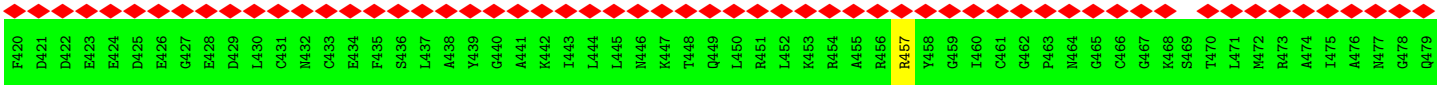


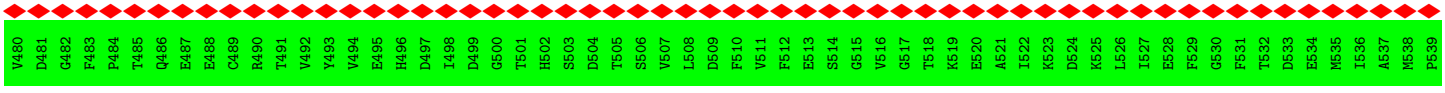


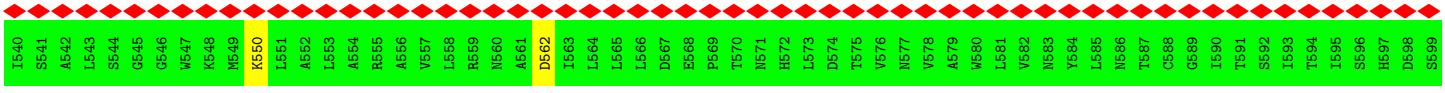


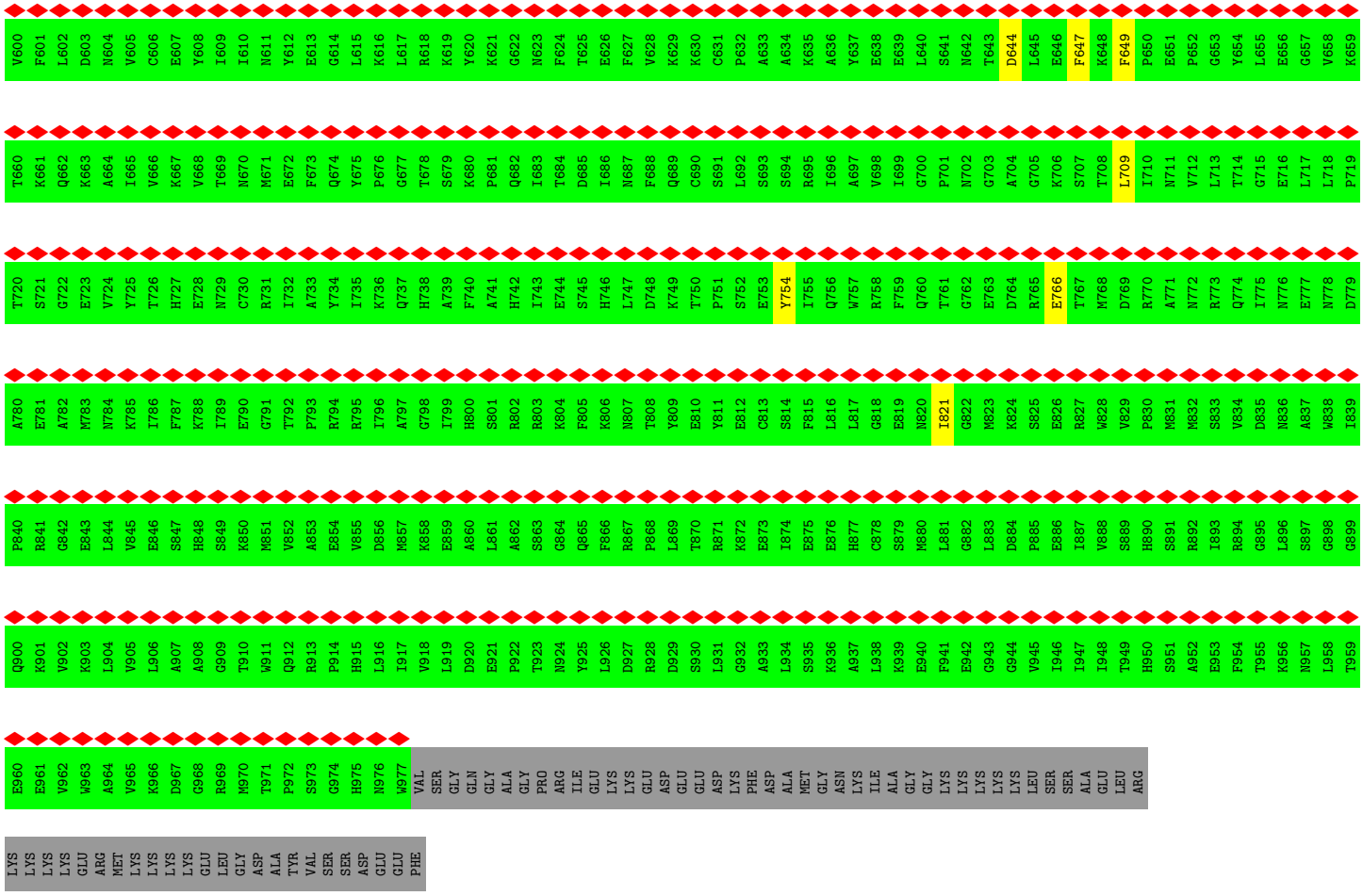






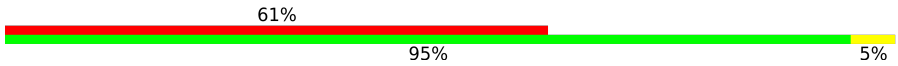


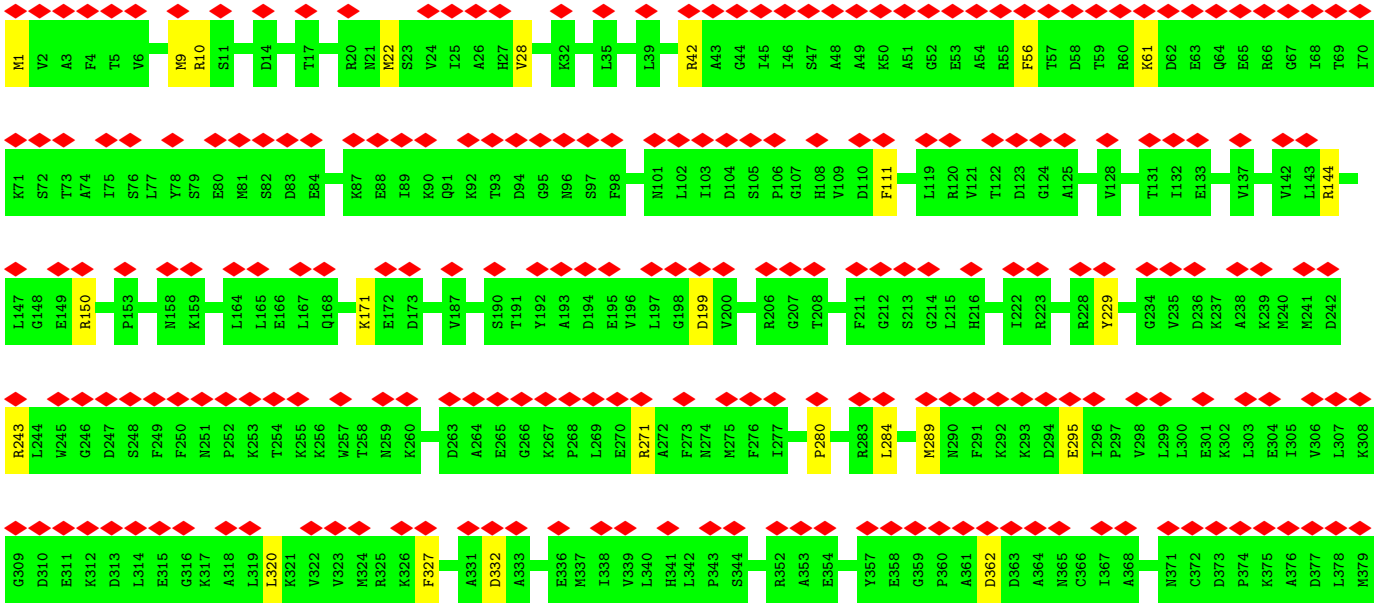


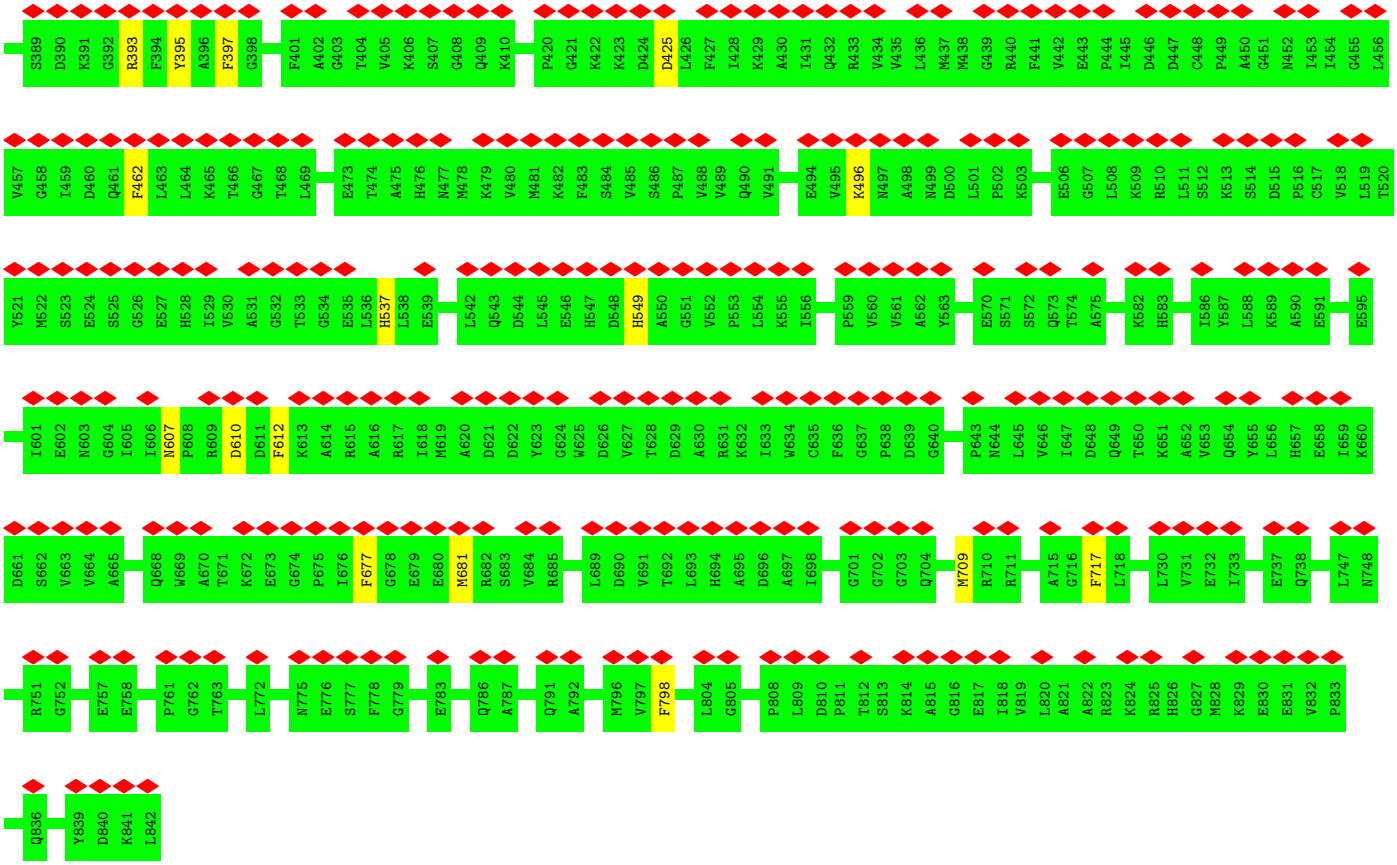


• Molecule 47: Elongation factor 2

Chain x:

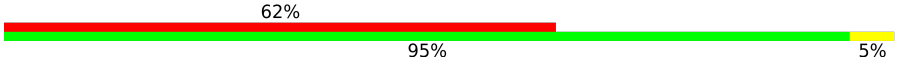


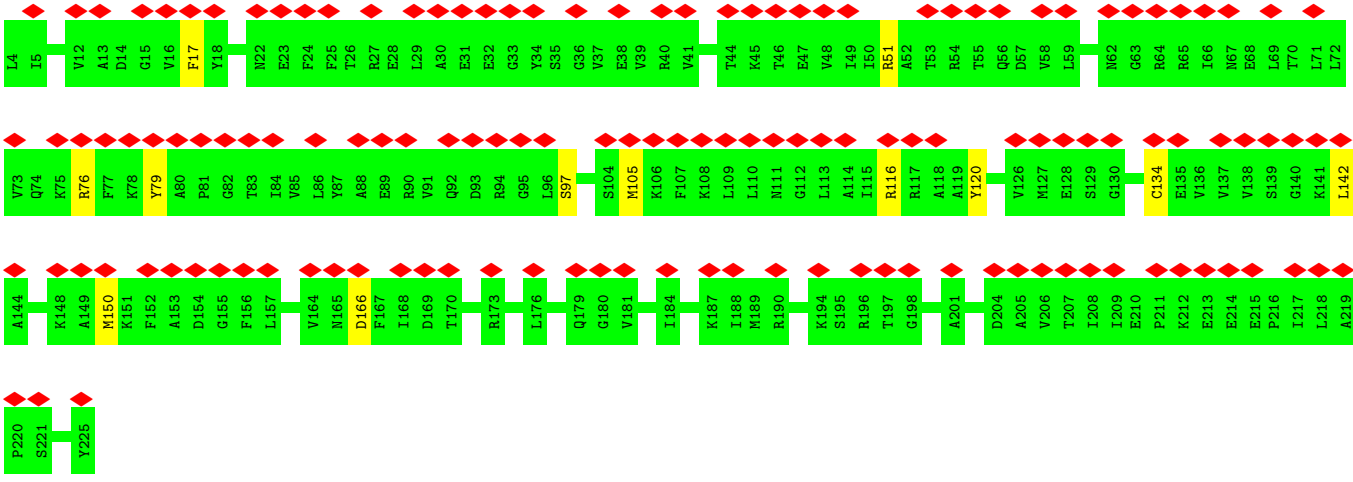




• Molecule 48: Small ribosomal subunit protein uS3

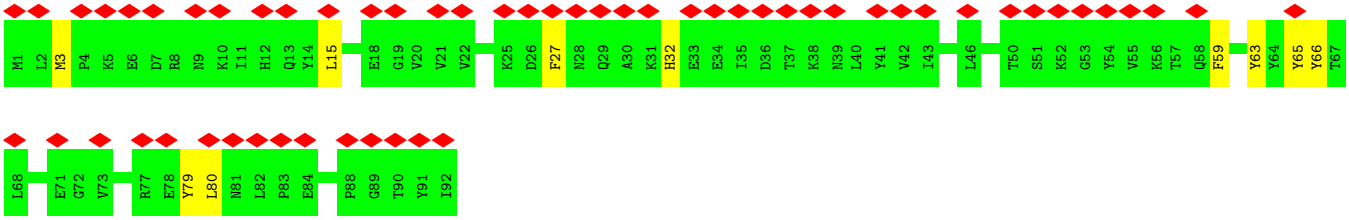
Chain SA:





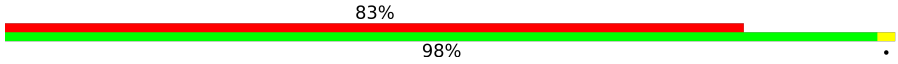
• Molecule 49: Small ribosomal subunit protein eS10A

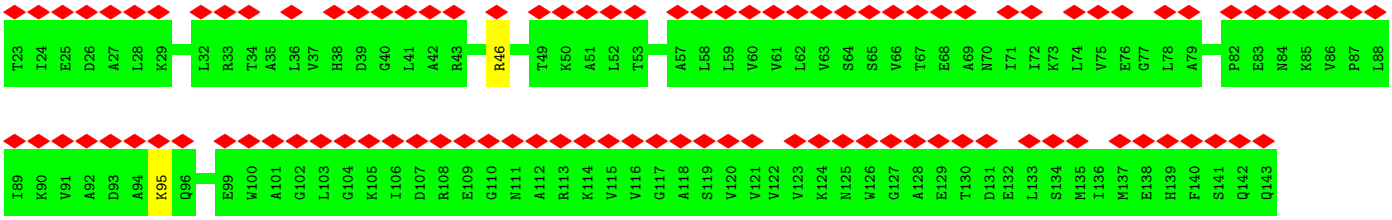
Chain SC:



• Molecule 50: Small ribosomal subunit protein eS12

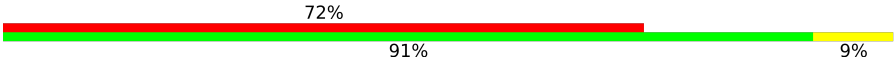
Chain SD:

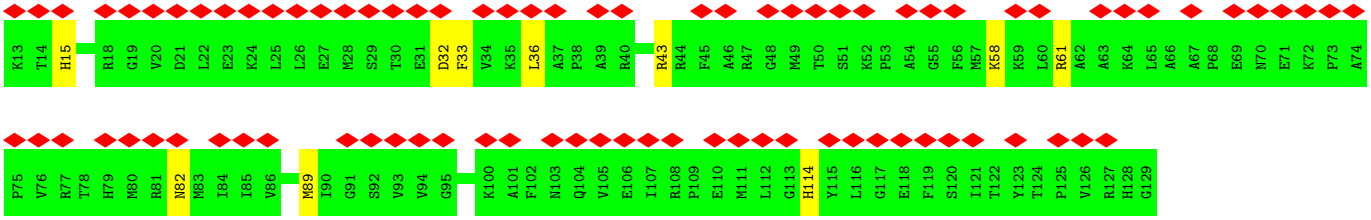




• Molecule 51: Small ribosomal subunit protein uS19

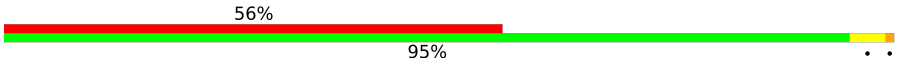
Chain SE:

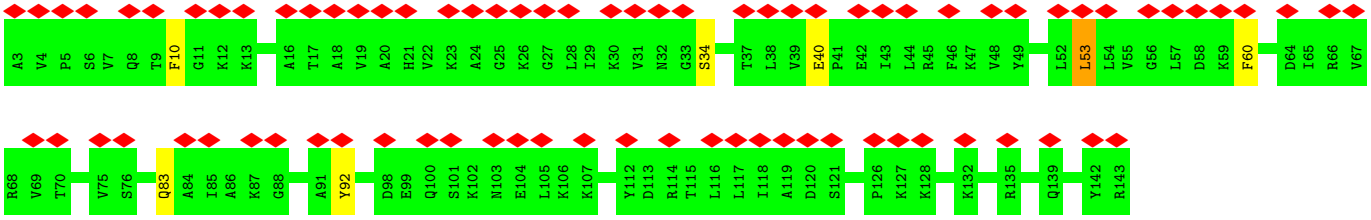




• Molecule 52: Small ribosomal subunit protein uS9A

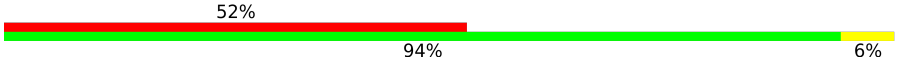
Chain SF:

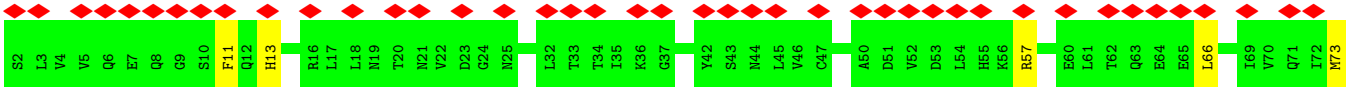


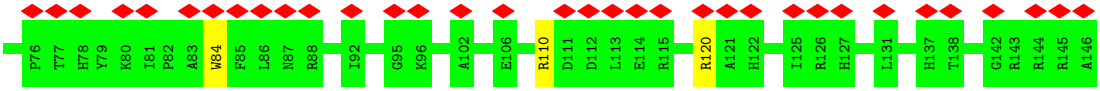


• Molecule 53: Small ribosomal subunit protein uS13A

Chain SH:

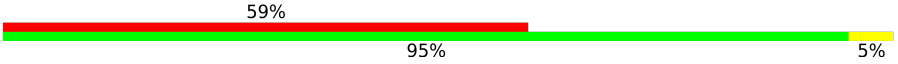


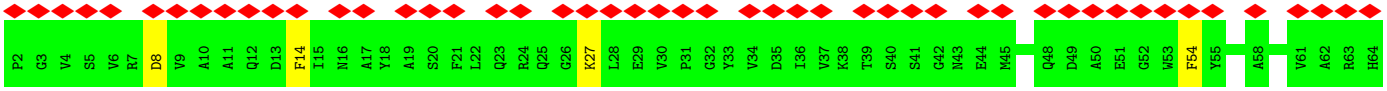


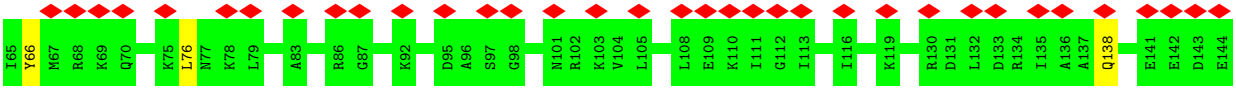


• Molecule 54: Small ribosomal subunit protein eS19A

Chain SI:

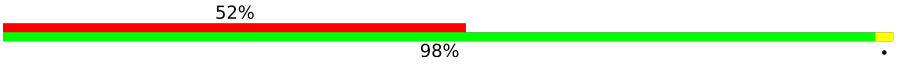


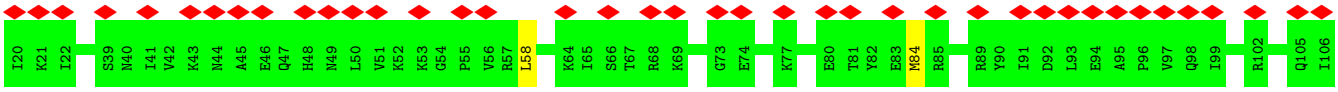


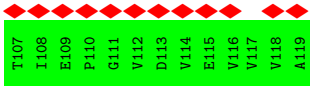


• Molecule 55: Small ribosomal subunit protein uS10

Chain SJ:

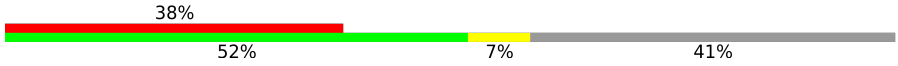


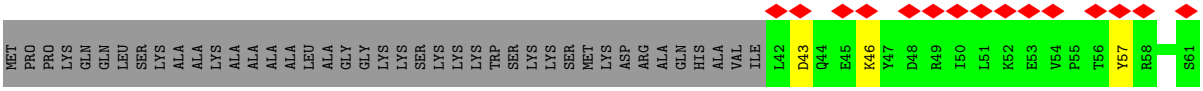


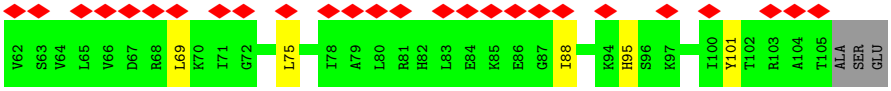


• Molecule 56: Small ribosomal subunit protein eS25A

Chain SK:

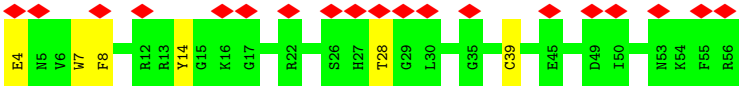






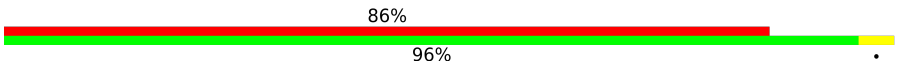
• Molecule 57: Small ribosomal subunit protein uS14A

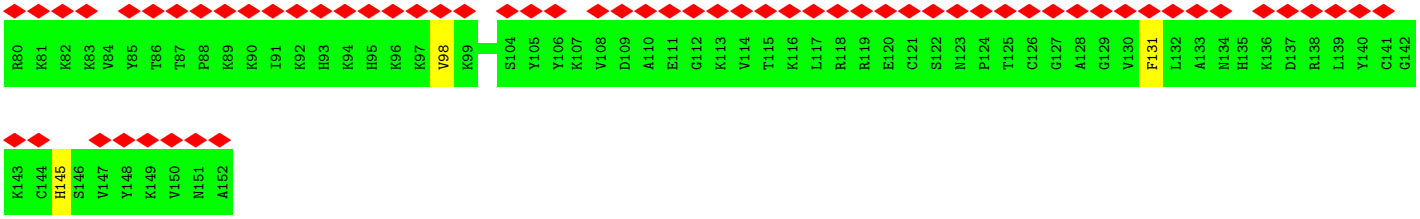
Chain SM:



• Molecule 58: Small ribosomal subunit protein eS31

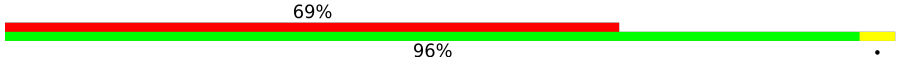
Chain SN:

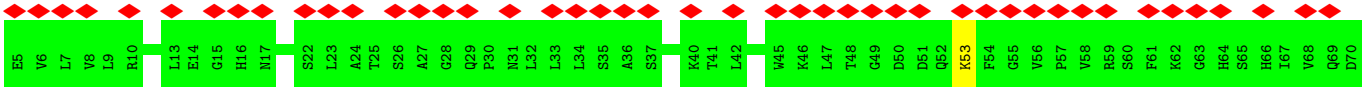


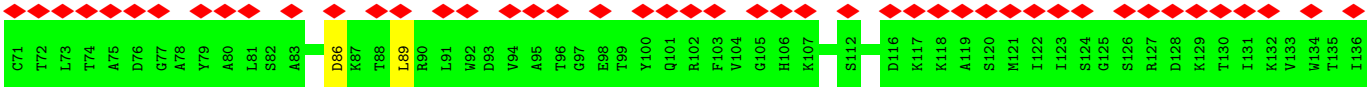


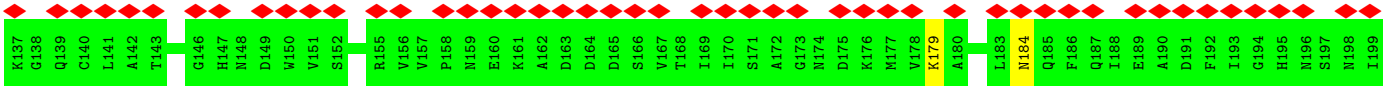
• Molecule 59: Small ribosomal subunit protein RACK1

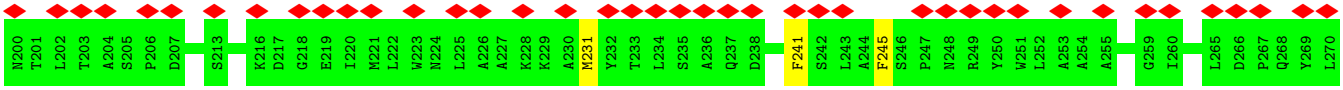
Chain SO:

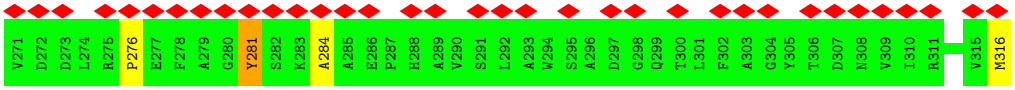






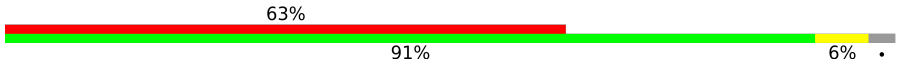


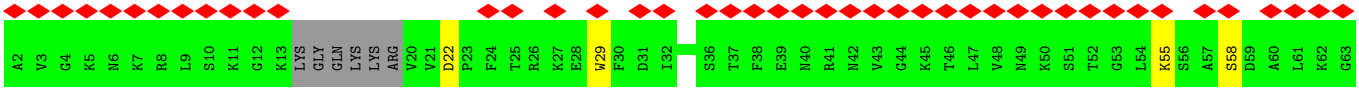


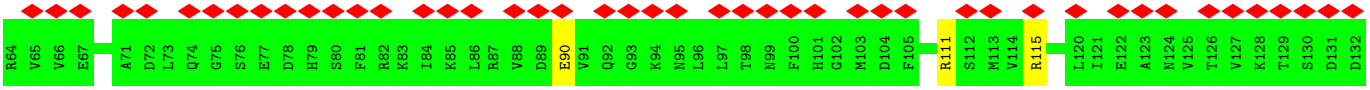


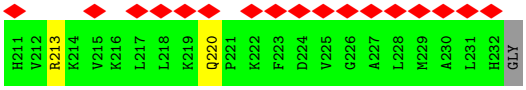
• Molecule 60: Small ribosomal subunit protein eS1A

Chain SQ:



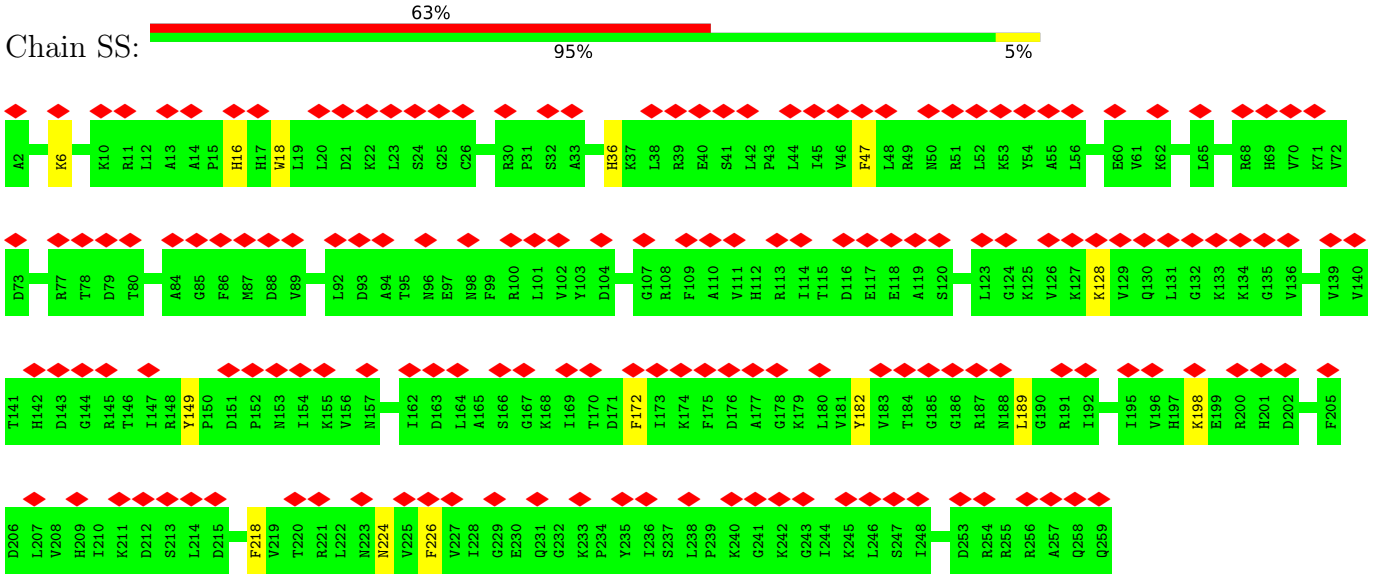






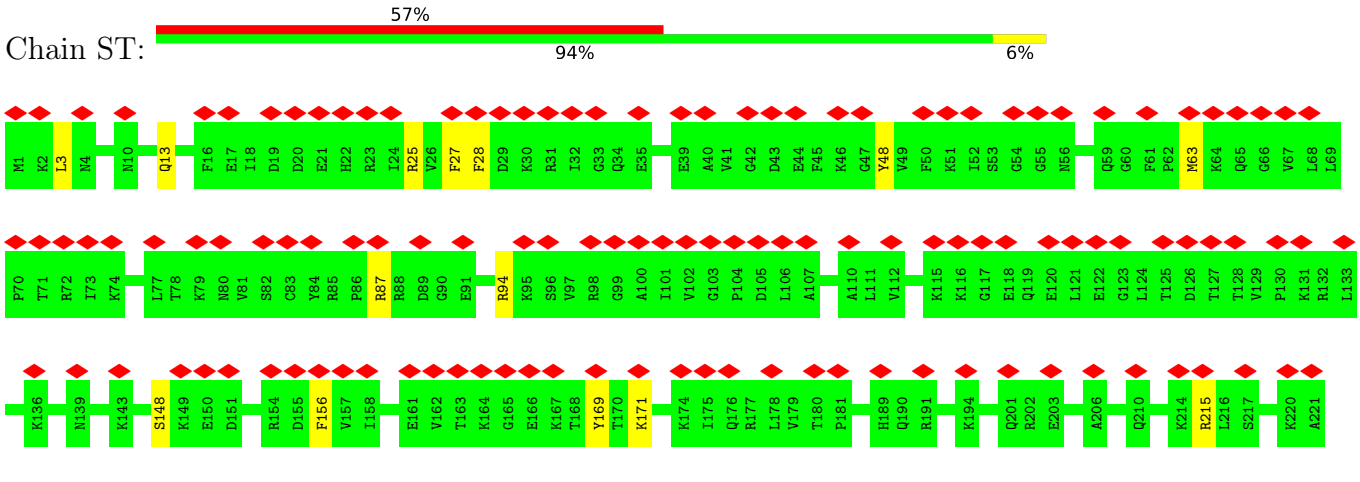
• Molecule 61: Small ribosomal subunit protein eS4A

Chain SS:



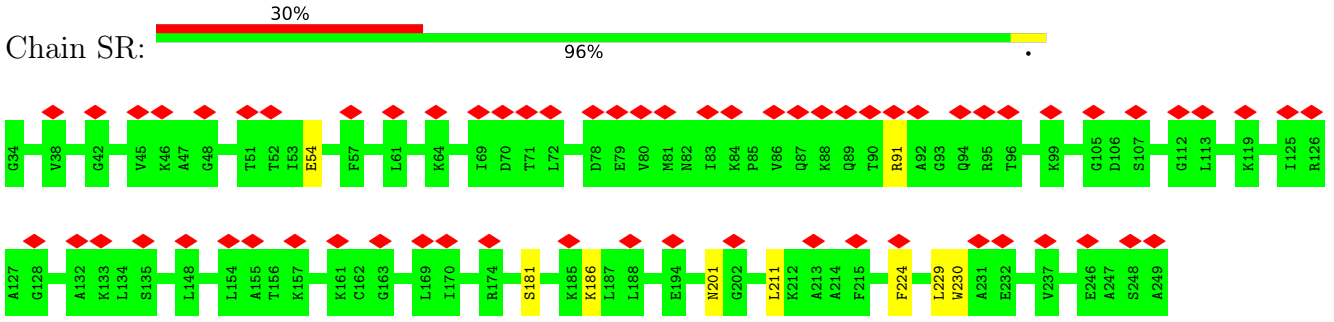
• Molecule 62: Small ribosomal subunit protein eS6A

Chain ST:



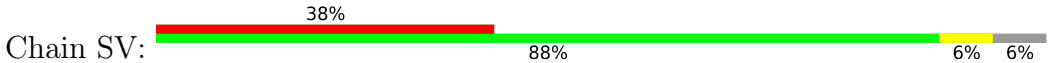
• Molecule 63: Small ribosomal subunit protein uS5

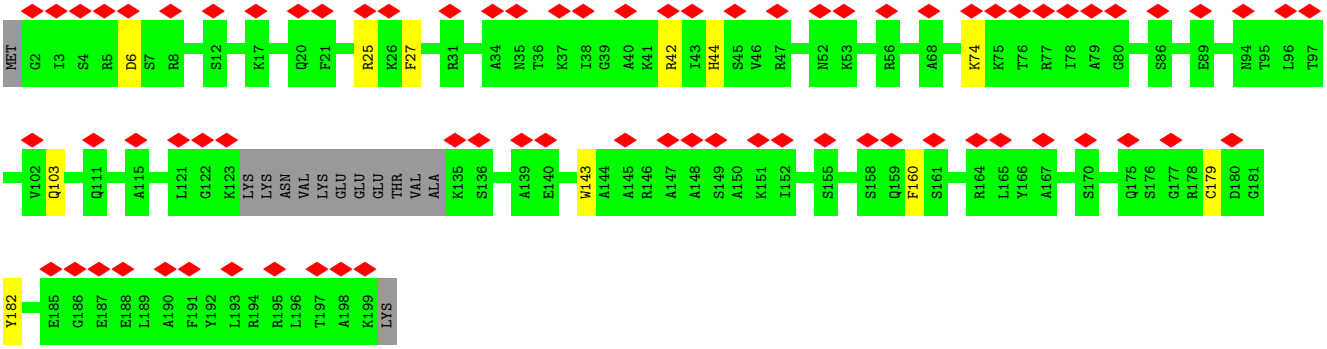
Chain SR:



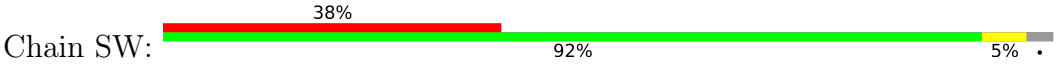
• Molecule 64: Small ribosomal subunit protein eS8A

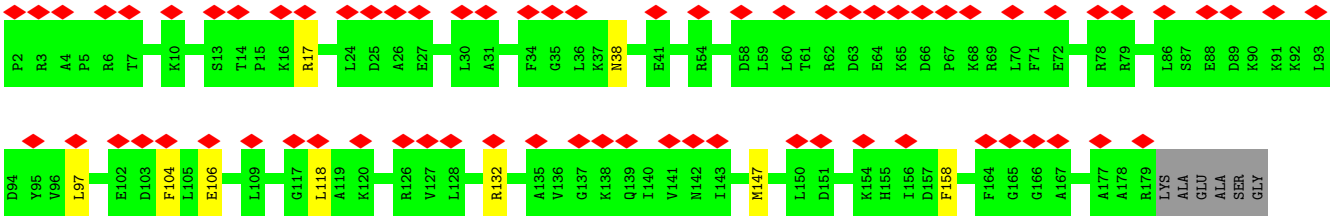
Chain SV:



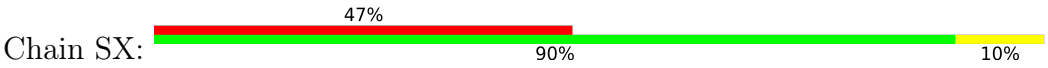


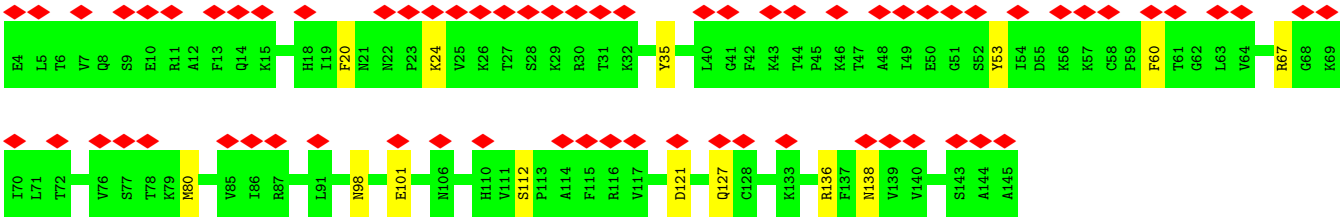
• Molecule 65: Small ribosomal subunit protein uS4A



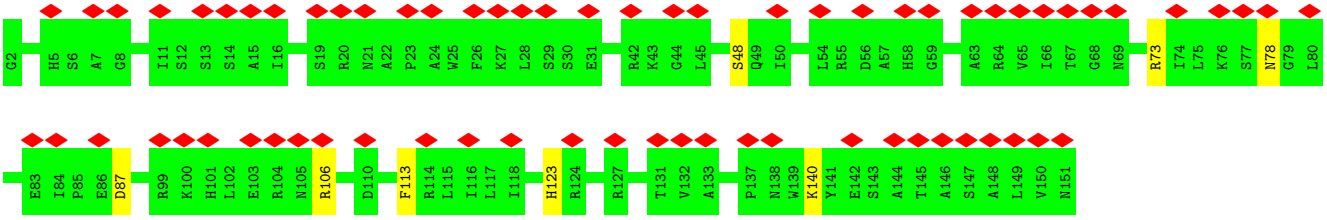


• Molecule 66: Small ribosomal subunit protein uS17A

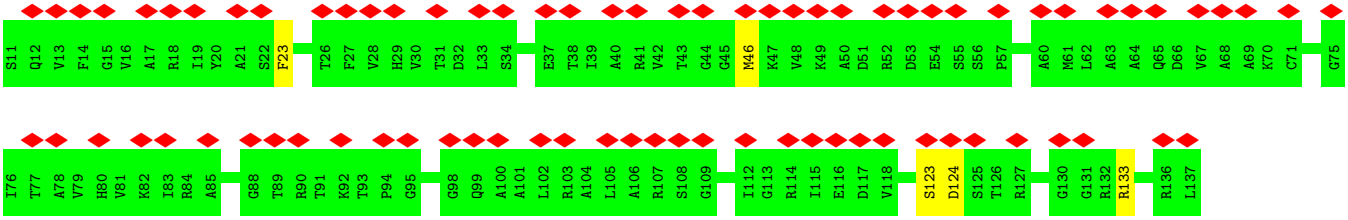




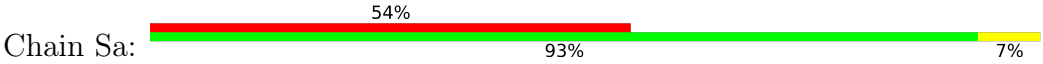
• Molecule 67: Small ribosomal subunit protein uS15

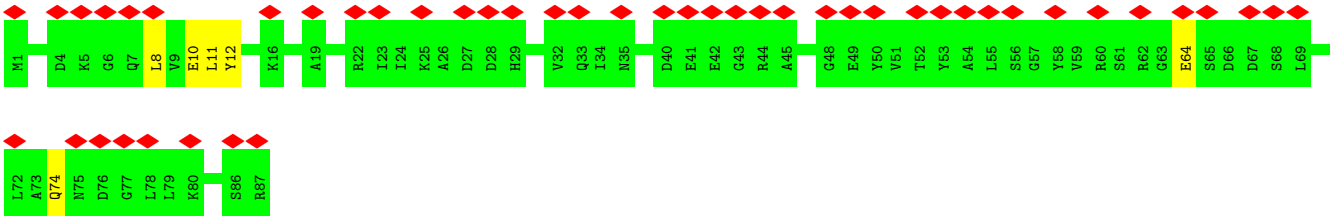


• Molecule 68: Small ribosomal subunit protein uS11B

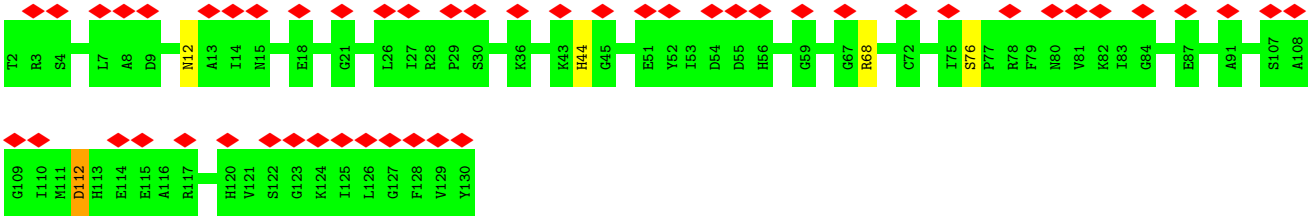


• Molecule 69: Small ribosomal subunit protein eS21A

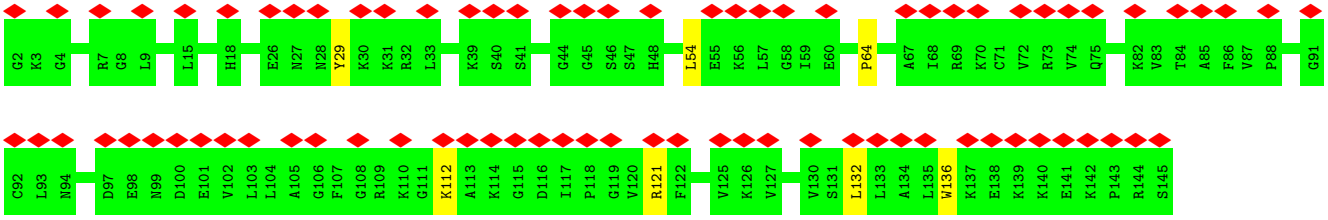




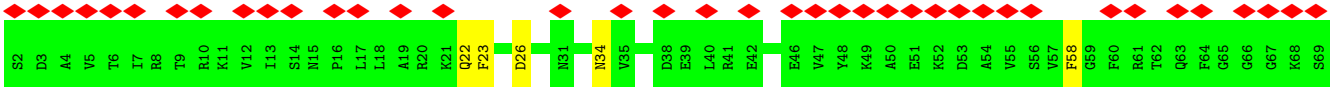
• Molecule 70: Small ribosomal subunit protein uS8A

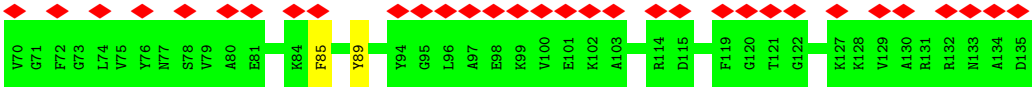


• Molecule 71: Small ribosomal subunit protein uS12A



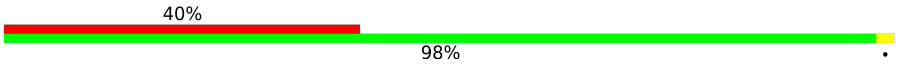
• Molecule 72: Small ribosomal subunit protein eS24A





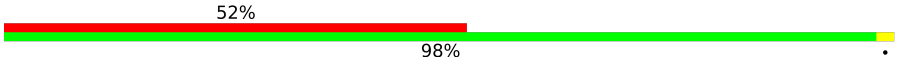
• Molecule 73: Small ribosomal subunit protein eS26A

Chain Se:



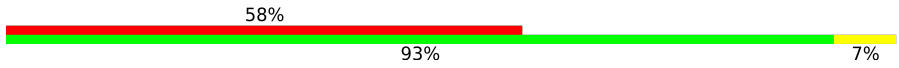
• Molecule 74: Small ribosomal subunit protein eS27A

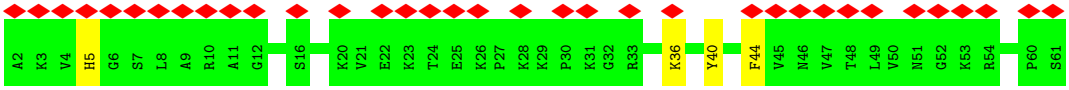
Chain Sf:



• Molecule 75: Small ribosomal subunit protein eS30A

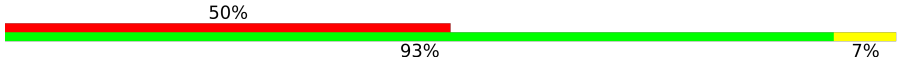
Chain Sg:

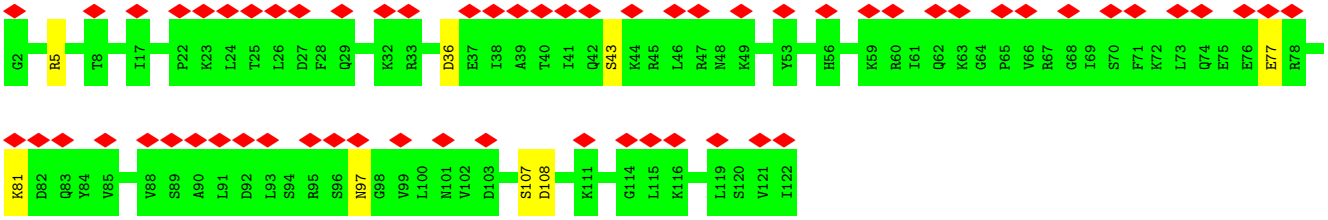




• Molecule 76: Small ribosomal subunit protein eS17A

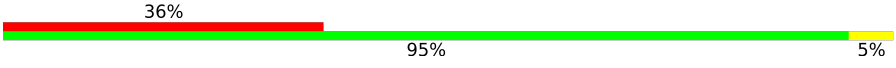
Chain SG:

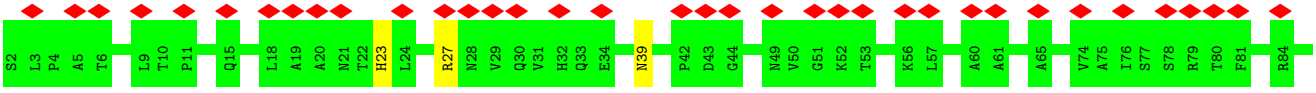


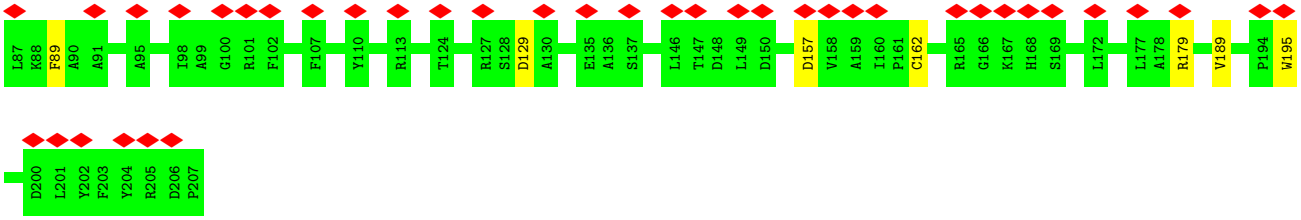


• Molecule 77: Small ribosomal subunit protein uS2A

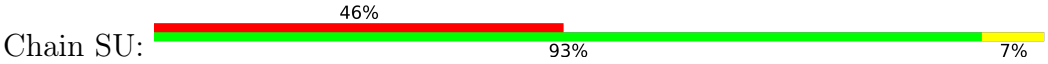
Chain SP:

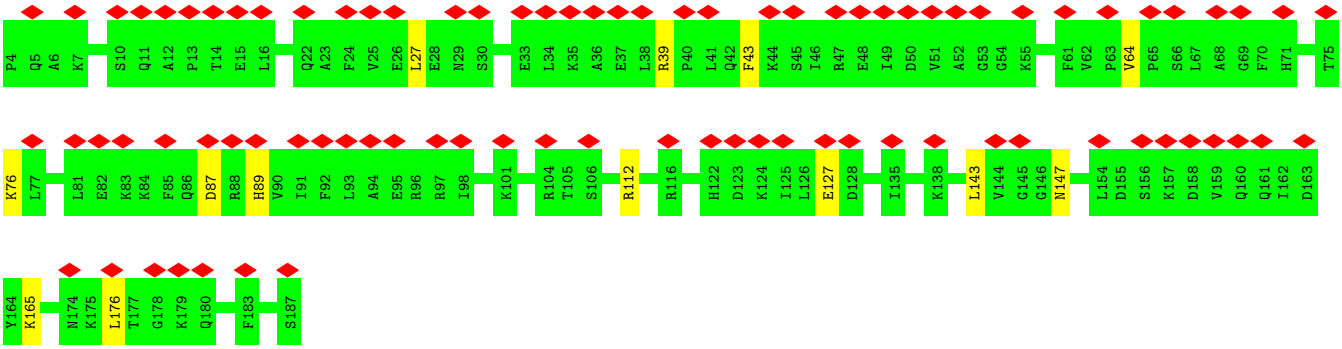




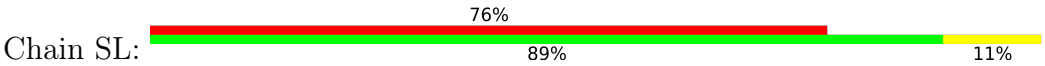


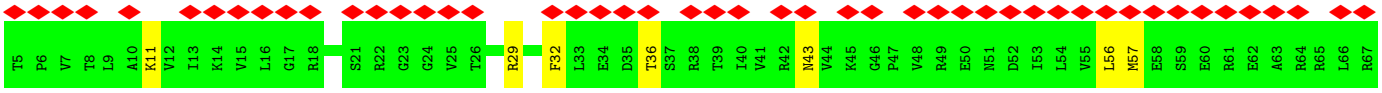
• Molecule 78: Small ribosomal subunit protein eS7A



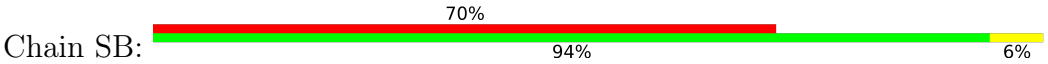


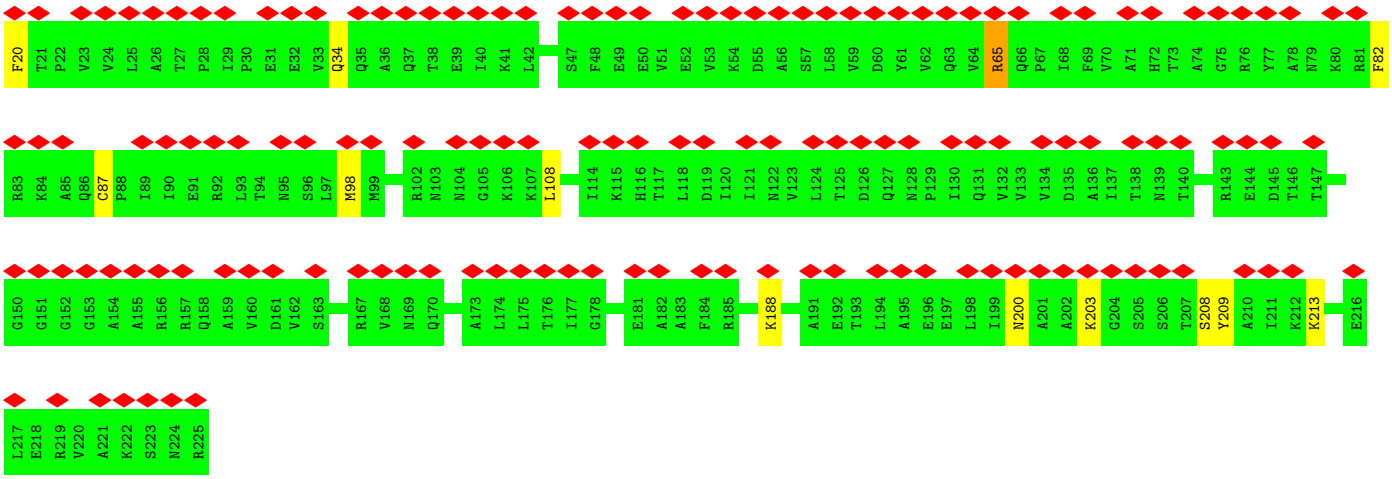
• Molecule 79: Small ribosomal subunit protein eS28A





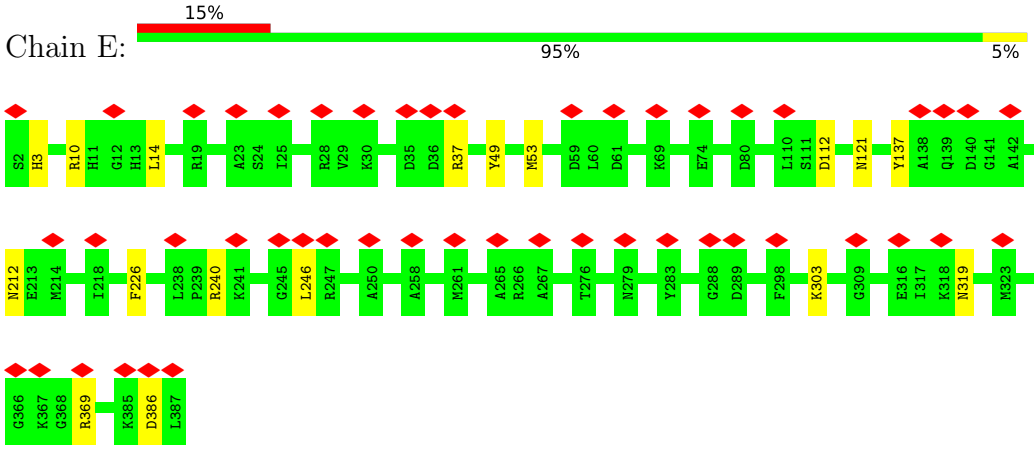
• Molecule 80: Small ribosomal subunit protein uS7





• Molecule 81: Large ribosomal subunit protein uL3

Chain E:


15%
95%
5%
S2 H3 R10 H11 G12 H13 L14 R19 A23 S24 I25 R28 Y29 K30 D35 D36 R37 Y49 M53 D59 L60 D61 K69 E74 D80 L110 S111 D112 N121 Y137 A138 Q139 D140 G141 A142 E145 R150 S156 A172 A204
N212 E213 M214 I218 F226 L238 P239 R240 K241 G245 L246 R247 A250 A258 M261 A265 R266 A267 T276 N279 Y283 G288 D289 F298 K303 G309 E316 I317 K318 N319 M323 R332 L338 R348 E352 E353 I359
G366 K367 G368 R369 K385 D386 L387

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11880	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	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	1.099	Depositor
Minimum map value	-0.558	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	528.0, 528.0, 528.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	2	0.18	0/42211	0.77	3/65773 (0.0%)
2	A	0.16	0/76425	0.74	7/119146 (0.0%)
3	B	0.15	0/2883	0.72	0/4491
4	C	0.17	0/3746	0.75	0/5832
5	D	0.26	0/1933	0.59	0/2598
6	F	0.25	0/2800	0.52	0/3790
7	G	0.25	0/2400	0.54	0/3239
8	H	0.25	0/1329	0.52	0/1794
9	I	0.25	0/1821	0.52	0/2451
10	J	0.26	0/1836	0.54	0/2481
11	K	0.25	0/1529	0.55	1/2060 (0.0%)
12	L	0.26	0/1801	0.58	0/2416
13	M	0.28	0/1367	0.65	0/1834
14	N	0.24	0/1568	0.57	0/2106
15	O	0.25	0/1068	0.55	0/1438
16	P	0.27	0/1757	0.64	0/2354
17	Q	0.27	0/1585	0.60	0/2128
18	R	0.26	0/1439	0.59	0/1938
19	S	0.25	0/1465	0.58	0/1965
20	T	0.26	0/1532	0.62	0/2043
21	U	0.26	0/1473	0.56	1/1980 (0.1%)
22	V	0.27	0/1296	0.60	1/1739 (0.1%)
23	W	0.26	0/812	0.57	1/1099 (0.1%)
24	X	0.26	0/1018	0.62	0/1369
25	Y	0.26	0/850	0.57	0/1152
26	Z	0.26	0/979	0.57	0/1321
27	a	0.25	0/995	0.60	0/1329
28	b	0.26	0/1106	0.54	0/1485
29	c	0.25	0/1200	0.55	0/1607
30	d	0.25	0/473	0.56	0/629
31	e	0.26	0/745	0.56	0/1001
32	f	0.28	0/890	0.63	0/1196
33	g	0.24	0/1034	0.53	0/1385
34	h	0.27	0/868	0.61	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	i	0.26	0/890	0.57	0/1189
36	j	0.27	0/978	0.63	1/1301 (0.1%)
37	k	0.25	0/772	0.54	0/1026
38	l	0.25	0/660	0.63	0/875
39	m	0.29	0/618	0.68	1/826 (0.1%)
40	n	0.34	0/443	0.73	0/588
41	o	0.25	0/416	0.62	0/553
42	p	0.26	0/230	0.82	0/296
43	q	0.26	0/836	0.54	0/1104
44	r	0.26	0/701	0.62	0/934
45	t	0.16	0/1795	0.75	0/2797
45	u	0.15	0/1771	0.77	0/2760
46	v	0.24	0/7611	0.50	0/10322
47	x	0.25	0/6685	0.54	2/9050 (0.0%)
48	SA	0.25	0/1754	0.57	0/2361
49	SC	0.27	0/769	0.63	0/1039
50	SD	0.23	0/883	0.51	0/1199
51	SE	0.26	0/936	0.60	0/1259
52	SF	0.26	0/1125	0.59	1/1510 (0.1%)
53	SH	0.24	0/1207	0.59	0/1623
54	SI	0.24	0/1130	0.54	0/1517
55	SJ	0.24	0/807	0.58	1/1091 (0.1%)
56	SK	0.27	0/526	0.66	0/706
57	SM	0.26	0/452	0.63	0/600
58	SN	0.27	0/571	0.61	0/768
59	SO	0.30	1/2436 (0.0%)	0.54	0/3318
60	SQ	0.25	0/1819	0.57	0/2442
61	SS	0.24	0/2097	0.55	0/2823
62	ST	0.24	0/1839	0.57	0/2460
63	SR	0.26	0/1656	0.59	1/2251 (0.0%)
64	SV	0.25	0/1501	0.57	0/2006
65	SW	0.25	0/1466	0.62	0/1966
66	SX	0.25	0/1168	0.57	0/1575
67	SY	0.24	0/1215	0.54	0/1638
68	SZ	0.24	0/901	0.58	0/1217
69	Sa	0.27	0/682	0.59	0/921
70	Sb	0.27	0/1038	0.63	1/1395 (0.1%)
71	Sc	0.25	0/1139	0.58	0/1518
72	Sd	0.25	0/1087	0.57	0/1449
73	Se	0.24	0/761	0.61	0/1016
74	Sf	0.25	0/620	0.55	0/838
75	Sg	0.24	0/480	0.54	0/639
76	SG	0.25	0/971	0.63	0/1303

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
77	SP	0.26	0/1644	0.56	0/2249
78	SU	0.25	0/1498	0.56	0/2019
79	SL	0.31	0/499	0.77	0/670
80	SB	0.29	0/1629	0.70	1/2202 (0.0%)
81	E	0.24	0/3146	0.55	0/4228
All	All	0.21	1/232092 (0.0%)	0.68	23/339774 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	SO	281	TYR	C-N	5.73	1.47	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	3212	C	N1-C2-O2	6.00	122.50	118.90
1	2	186	C	C2-N1-C1'	5.99	125.39	118.80
22	V	127	GLN	CA-CB-CG	5.95	126.50	113.40
2	A	2257	C	C2-N1-C1'	5.91	125.30	118.80
11	K	120	ASP	CB-CG-OD1	5.65	123.39	118.30

There are no chirality outliers.

There are no planarity outliers.

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	
5	D	249/251 (99%)	227 (91%)	22 (9%)	0	100	100
6	F	359/361 (99%)	345 (96%)	14 (4%)	0	100	100
7	G	292/294 (99%)	279 (96%)	13 (4%)	0	100	100
8	H	163/175 (93%)	153 (94%)	10 (6%)	0	100	100
9	I	220/223 (99%)	209 (95%)	11 (5%)	0	100	100
10	J	231/233 (99%)	221 (96%)	9 (4%)	1 (0%)	30	65
11	K	189/191 (99%)	177 (94%)	12 (6%)	0	100	100
12	L	216/218 (99%)	194 (90%)	21 (10%)	1 (0%)	25	60
13	M	167/169 (99%)	154 (92%)	13 (8%)	0	100	100
14	N	191/193 (99%)	180 (94%)	9 (5%)	2 (1%)	13	46
15	O	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
16	P	201/203 (99%)	195 (97%)	6 (3%)	0	100	100
17	Q	195/197 (99%)	190 (97%)	5 (3%)	0	100	100
18	R	181/183 (99%)	173 (96%)	8 (4%)	0	100	100
19	S	183/185 (99%)	175 (96%)	7 (4%)	1 (0%)	25	60
20	T	186/188 (99%)	185 (100%)	1 (0%)	0	100	100
21	U	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
22	V	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
23	W	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
24	X	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
25	Y	124/126 (98%)	108 (87%)	15 (12%)	1 (1%)	16	51
26	Z	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
27	a	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
28	b	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
29	c	146/148 (99%)	134 (92%)	12 (8%)	0	100	100
30	d	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
31	e	94/96 (98%)	88 (94%)	6 (6%)	0	100	100
32	f	107/109 (98%)	100 (94%)	7 (6%)	0	100	100
33	g	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
34	h	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
35	i	110/112 (98%)	103 (94%)	7 (6%)	0	100	100
36	j	117/119 (98%)	114 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	k	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
38	l	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
39	m	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
40	n	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
41	o	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
42	p	23/25 (92%)	23 (100%)	0	0	100	100
43	q	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
44	r	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
46	v	975/1044 (93%)	897 (92%)	75 (8%)	3 (0%)	37	70
47	x	840/842 (100%)	759 (90%)	79 (9%)	2 (0%)	44	75
48	SA	220/222 (99%)	206 (94%)	14 (6%)	0	100	100
49	SC	90/92 (98%)	78 (87%)	12 (13%)	0	100	100
50	SD	119/121 (98%)	97 (82%)	22 (18%)	0	100	100
51	SE	115/117 (98%)	97 (84%)	18 (16%)	0	100	100
52	SF	139/141 (99%)	132 (95%)	6 (4%)	1 (1%)	19	54
53	SH	143/145 (99%)	133 (93%)	10 (7%)	0	100	100
54	SI	141/143 (99%)	131 (93%)	10 (7%)	0	100	100
55	SJ	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
56	SK	62/108 (57%)	57 (92%)	4 (6%)	1 (2%)	8	37
57	SM	51/53 (96%)	43 (84%)	8 (16%)	0	100	100
58	SN	71/73 (97%)	47 (66%)	22 (31%)	2 (3%)	4	28
59	SO	310/312 (99%)	281 (91%)	26 (8%)	3 (1%)	13	46
60	SQ	221/232 (95%)	201 (91%)	20 (9%)	0	100	100
61	SS	256/258 (99%)	239 (93%)	17 (7%)	0	100	100
62	ST	226/228 (99%)	215 (95%)	10 (4%)	1 (0%)	30	65
63	SR	214/216 (99%)	197 (92%)	17 (8%)	0	100	100
64	SV	183/200 (92%)	178 (97%)	5 (3%)	0	100	100
65	SW	176/184 (96%)	166 (94%)	10 (6%)	0	100	100
66	SX	140/142 (99%)	130 (93%)	10 (7%)	0	100	100
67	SY	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
68	SZ	125/127 (98%)	115 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
69	Sa	85/87 (98%)	76 (89%)	8 (9%)	1 (1%)	11 43
70	Sb	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	16 51
71	Sc	142/144 (99%)	130 (92%)	11 (8%)	1 (1%)	19 54
72	Sd	132/134 (98%)	122 (92%)	10 (8%)	0	100 100
73	Se	92/94 (98%)	82 (89%)	10 (11%)	0	100 100
74	Sf	79/81 (98%)	76 (96%)	3 (4%)	0	100 100
75	Sg	58/60 (97%)	54 (93%)	4 (7%)	0	100 100
76	SG	119/121 (98%)	107 (90%)	12 (10%)	0	100 100
77	SP	204/206 (99%)	185 (91%)	17 (8%)	2 (1%)	13 46
78	SU	182/184 (99%)	173 (95%)	8 (4%)	1 (0%)	25 60
79	SL	61/63 (97%)	54 (88%)	7 (12%)	0	100 100
80	SB	204/206 (99%)	178 (87%)	26 (13%)	0	100 100
81	E	384/386 (100%)	363 (94%)	21 (6%)	0	100 100
All	All	12767/13071 (98%)	11873 (93%)	869 (7%)	25 (0%)	45 75

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	158	ASP
25	Y	81	PRO
52	SF	40	GLU
56	SK	88	ILE
70	Sb	76	SER

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	D	190/193 (98%)	181 (95%)	9 (5%)	22 47
6	F	288/288 (100%)	278 (96%)	10 (4%)	31 54
7	G	241/243 (99%)	233 (97%)	8 (3%)	33 56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	139/154 (90%)	134 (96%)	5 (4%)	30	54
9	I	186/187 (100%)	180 (97%)	6 (3%)	34	56
10	J	187/191 (98%)	181 (97%)	6 (3%)	34	56
11	K	168/171 (98%)	161 (96%)	7 (4%)	25	49
12	L	185/185 (100%)	172 (93%)	13 (7%)	12	36
13	M	145/147 (99%)	135 (93%)	10 (7%)	13	37
14	N	154/154 (100%)	150 (97%)	4 (3%)	41	61
15	O	107/107 (100%)	104 (97%)	3 (3%)	38	59
16	P	175/175 (100%)	160 (91%)	15 (9%)	8	31
17	Q	160/160 (100%)	149 (93%)	11 (7%)	13	37
18	R	138/145 (95%)	130 (94%)	8 (6%)	17	42
19	S	150/150 (100%)	145 (97%)	5 (3%)	33	56
20	T	152/153 (99%)	147 (97%)	5 (3%)	33	56
21	U	155/155 (100%)	148 (96%)	7 (4%)	23	48
22	V	135/136 (99%)	127 (94%)	8 (6%)	16	41
23	W	87/87 (100%)	84 (97%)	3 (3%)	32	55
24	X	104/104 (100%)	100 (96%)	4 (4%)	28	52
25	Y	56/108 (52%)	53 (95%)	3 (5%)	18	44
26	Z	104/105 (99%)	99 (95%)	5 (5%)	21	46
27	a	108/108 (100%)	104 (96%)	4 (4%)	29	53
28	b	112/115 (97%)	109 (97%)	3 (3%)	40	60
29	c	117/118 (99%)	113 (97%)	4 (3%)	32	55
30	d	46/46 (100%)	42 (91%)	4 (9%)	8	30
31	e	81/81 (100%)	78 (96%)	3 (4%)	29	53
32	f	92/96 (96%)	89 (97%)	3 (3%)	33	56
33	g	107/109 (98%)	102 (95%)	5 (5%)	22	47
34	h	90/90 (100%)	85 (94%)	5 (6%)	17	43
35	i	95/95 (100%)	87 (92%)	8 (8%)	9	32
36	j	104/104 (100%)	101 (97%)	3 (3%)	37	59
37	k	80/81 (99%)	76 (95%)	4 (5%)	20	45
38	l	67/67 (100%)	59 (88%)	8 (12%)	4	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
39	m	68/68 (100%)	64 (94%)	4 (6%)	16 41
40	n	45/45 (100%)	40 (89%)	5 (11%)	5 21
41	o	45/47 (96%)	40 (89%)	5 (11%)	5 21
42	p	22/23 (96%)	21 (96%)	1 (4%)	23 48
43	q	87/88 (99%)	80 (92%)	7 (8%)	10 33
44	r	71/71 (100%)	66 (93%)	5 (7%)	12 36
46	v	789/890 (89%)	771 (98%)	18 (2%)	45 64
47	x	715/715 (100%)	679 (95%)	36 (5%)	20 45
48	SA	182/182 (100%)	170 (93%)	12 (7%)	14 38
49	SC	77/85 (91%)	67 (87%)	10 (13%)	3 18
50	SD	88/98 (90%)	86 (98%)	2 (2%)	45 64
51	SE	95/98 (97%)	85 (90%)	10 (10%)	5 22
52	SF	117/117 (100%)	111 (95%)	6 (5%)	20 45
53	SH	127/128 (99%)	119 (94%)	8 (6%)	15 40
54	SI	115/115 (100%)	108 (94%)	7 (6%)	15 41
55	SJ	93/93 (100%)	92 (99%)	1 (1%)	70 79
56	SK	57/89 (64%)	50 (88%)	7 (12%)	4 19
57	SM	47/47 (100%)	41 (87%)	6 (13%)	3 18
58	SN	57/64 (89%)	56 (98%)	1 (2%)	54 71
59	SO	250/257 (97%)	241 (96%)	9 (4%)	30 54
60	SQ	200/205 (98%)	187 (94%)	13 (6%)	14 39
61	SS	220/220 (100%)	206 (94%)	14 (6%)	14 39
62	ST	189/195 (97%)	176 (93%)	13 (7%)	13 37
63	SR	175/175 (100%)	167 (95%)	8 (5%)	23 47
64	SV	148/161 (92%)	137 (93%)	11 (7%)	11 35
65	SW	153/157 (98%)	144 (94%)	9 (6%)	16 41
66	SX	126/127 (99%)	112 (89%)	14 (11%)	5 21
67	SY	127/127 (100%)	119 (94%)	8 (6%)	15 40
68	SZ	81/96 (84%)	76 (94%)	5 (6%)	15 40
69	Sa	71/74 (96%)	66 (93%)	5 (7%)	12 36
70	Sb	110/110 (100%)	106 (96%)	4 (4%)	30 54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
71	Sc	119/119 (100%)	113 (95%)	6 (5%)	20 45
72	Sd	112/112 (100%)	105 (94%)	7 (6%)	15 40
73	Se	81/81 (100%)	79 (98%)	2 (2%)	42 62
74	Sf	70/70 (100%)	68 (97%)	2 (3%)	37 59
75	Sg	50/51 (98%)	46 (92%)	4 (8%)	10 33
76	SG	105/110 (96%)	97 (92%)	8 (8%)	11 34
77	SP	170/173 (98%)	162 (95%)	8 (5%)	22 47
78	SU	163/165 (99%)	151 (93%)	12 (7%)	11 35
79	SL	56/56 (100%)	49 (88%)	7 (12%)	3 18
80	SB	173/173 (100%)	160 (92%)	13 (8%)	11 34
81	E	320/322 (99%)	302 (94%)	18 (6%)	17 43
All	All	10671/11007 (97%)	10111 (95%)	560 (5%)	22 45

5 of 560 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	SZ	133	ARG
71	Sc	121	ARG
68	SZ	124	ASP
78	SU	165	LYS
36	j	60	GLU

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

Mol	Chain	Res	Type
58	SN	123	ASN
62	ST	4	ASN
59	SO	31	ASN
60	SQ	148	ASN
67	SY	105	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1799 (98%)	471 (26%)	37 (2%)
2	A	3185/3394 (93%)	498 (15%)	6 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	B	120/121 (99%)	14 (11%)	1 (0%)
4	C	157/158 (99%)	33 (21%)	1 (0%)
45	t	74/75 (98%)	17 (22%)	0
45	u	73/75 (97%)	17 (23%)	0
All	All	5377/5622 (95%)	1050 (19%)	45 (0%)

5 of 1050 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 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1344	A
1	2	1636	C
1	2	1382	A
1	2	1557	U
2	A	1562	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 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.

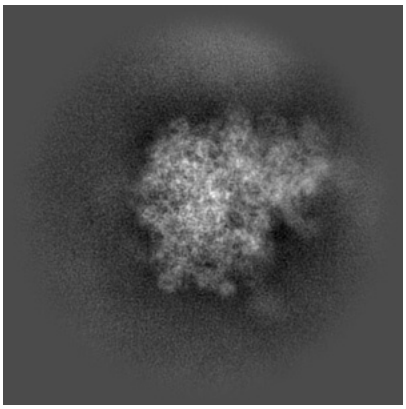
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-38668. These allow visual inspection of the internal detail of the map and identification of artifacts.

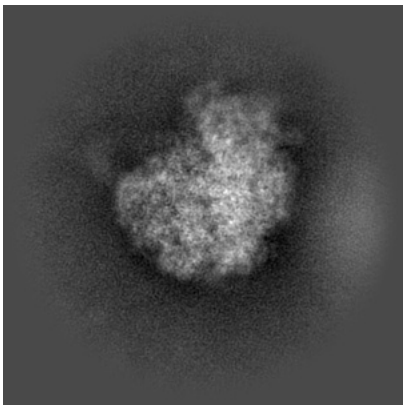
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

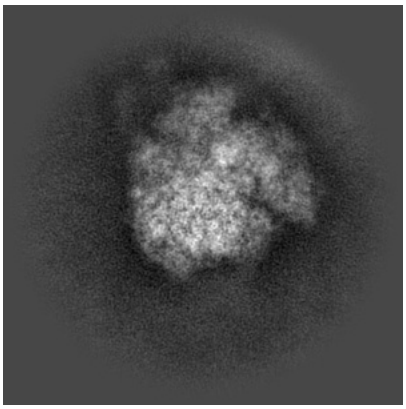
6.1.1 Primary map



X

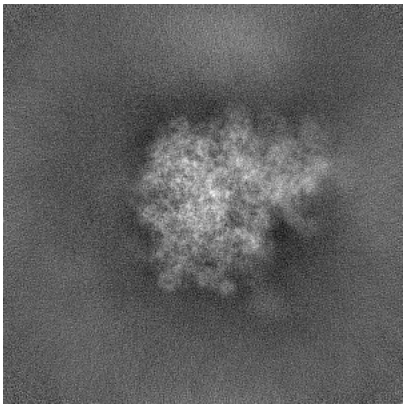


Y

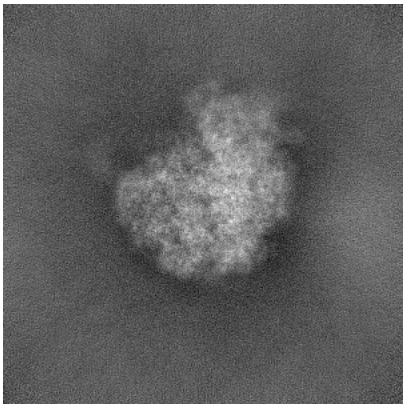


Z

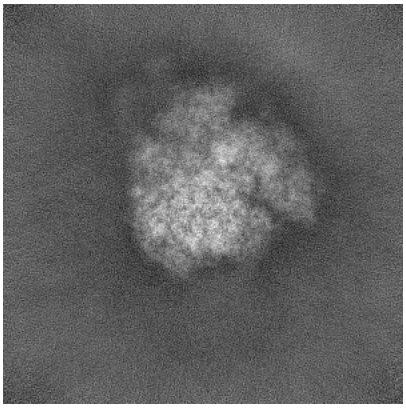
6.1.2 Raw map



X



Y

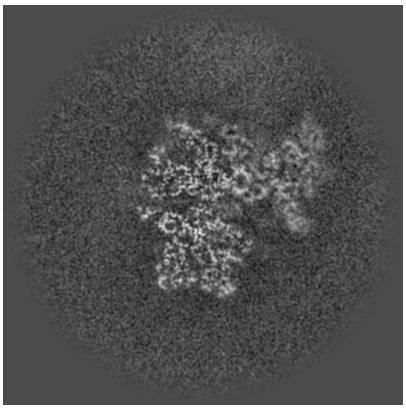


Z

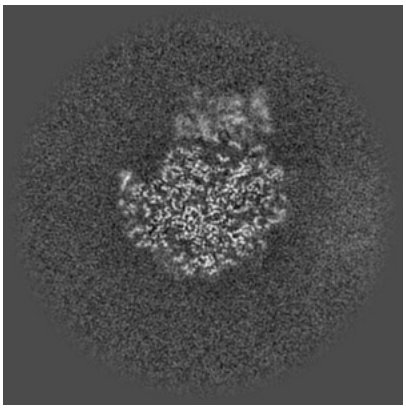
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

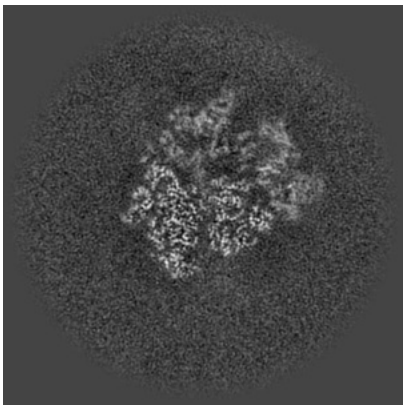
6.2.1 Primary map



X Index: 200

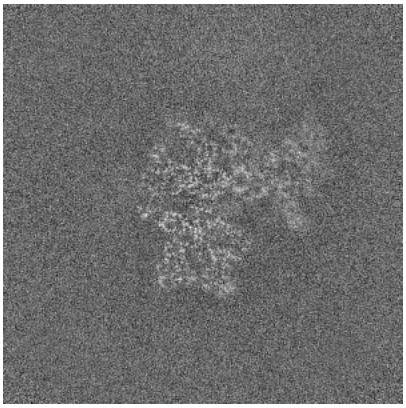


Y Index: 200

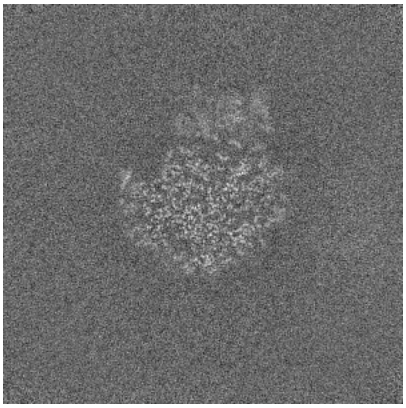


Z Index: 200

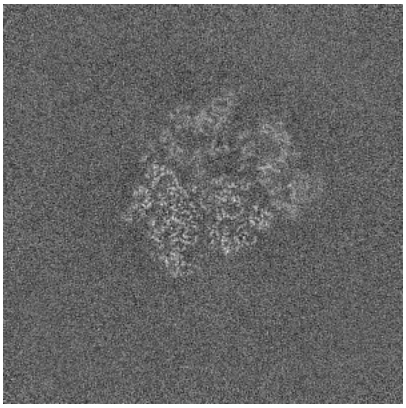
6.2.2 Raw map



X Index: 200



Y Index: 200

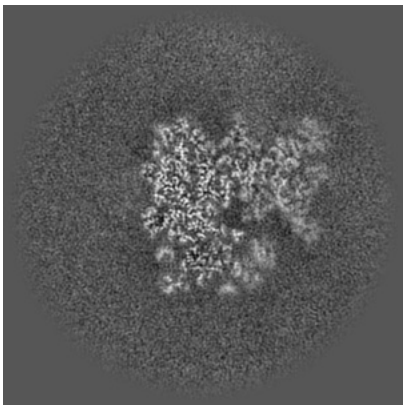


Z Index: 200

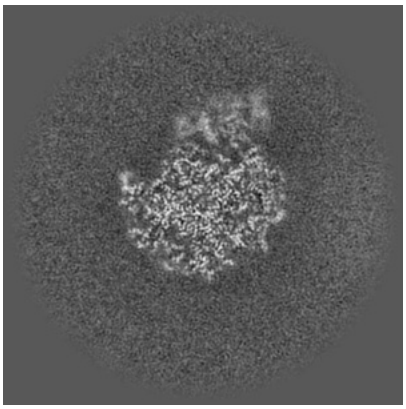
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

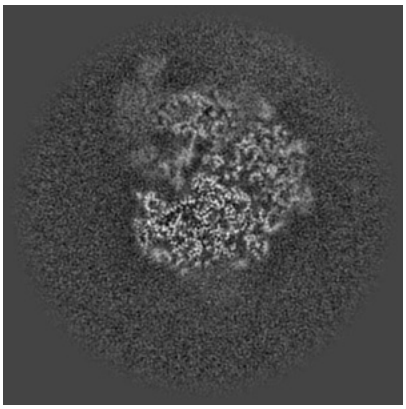
6.3.1 Primary map



X Index: 213

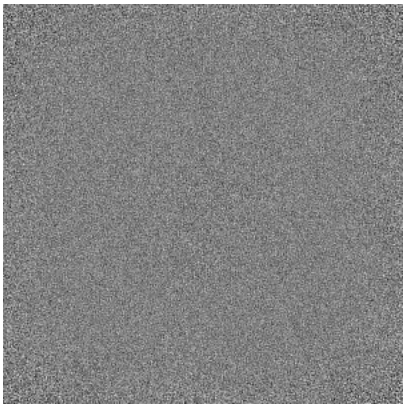


Y Index: 198

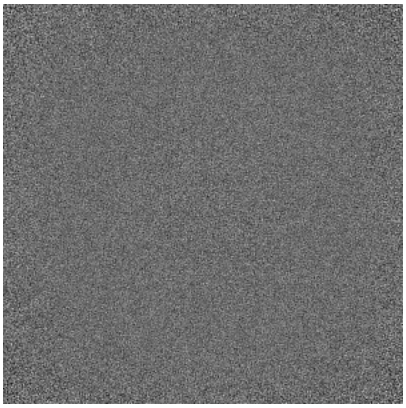


Z Index: 223

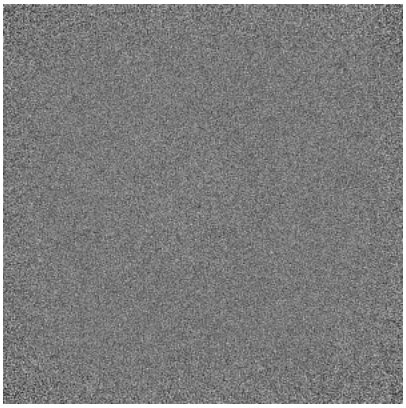
6.3.2 Raw map



X Index: 0



Y Index: 0

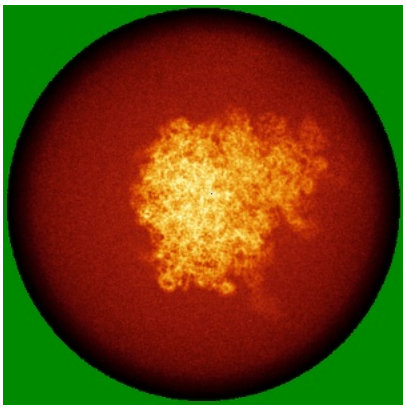


Z Index: 0

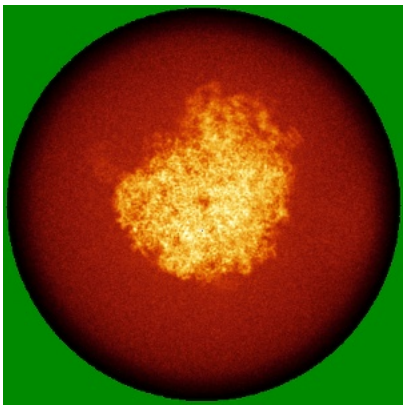
The images above show the largest variance slices of the map in three orthogonal directions.

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

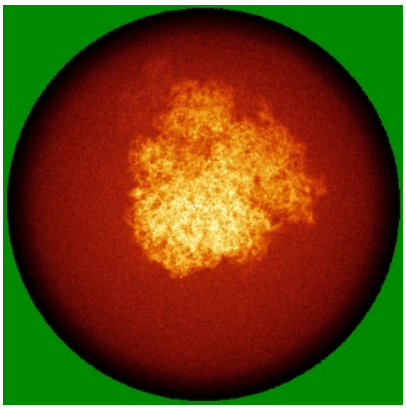
6.4.1 Primary map



X

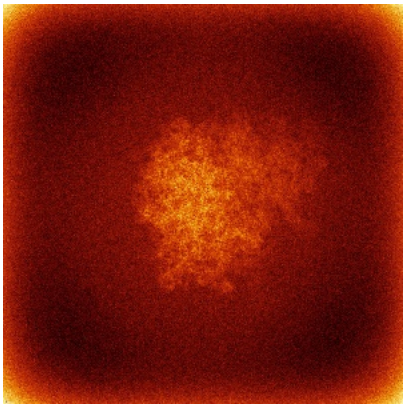


Y

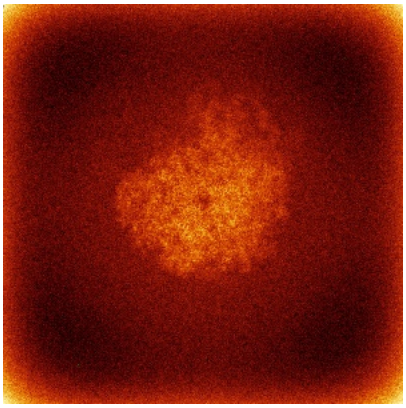


Z

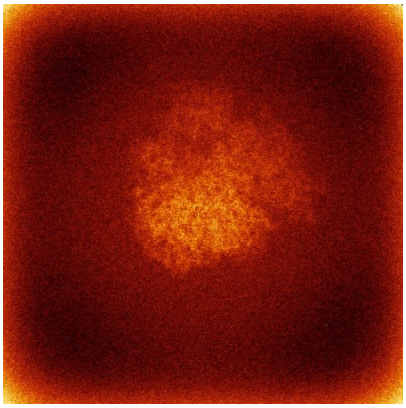
6.4.2 Raw map



X



Y

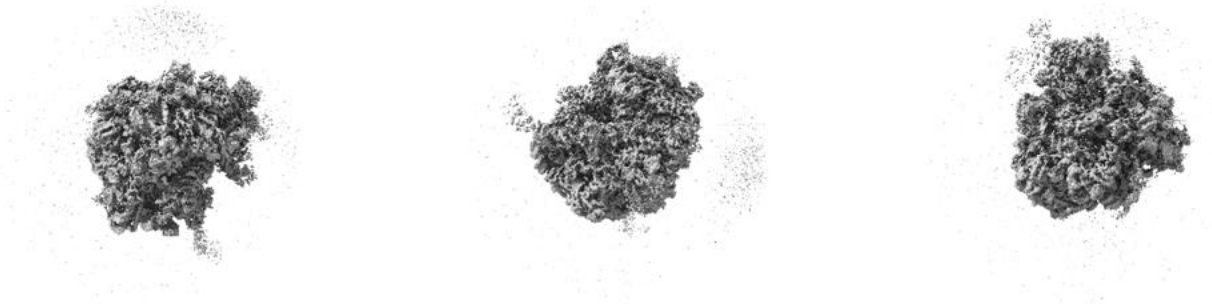


Z

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

6.5 Orthogonal surface views (i)

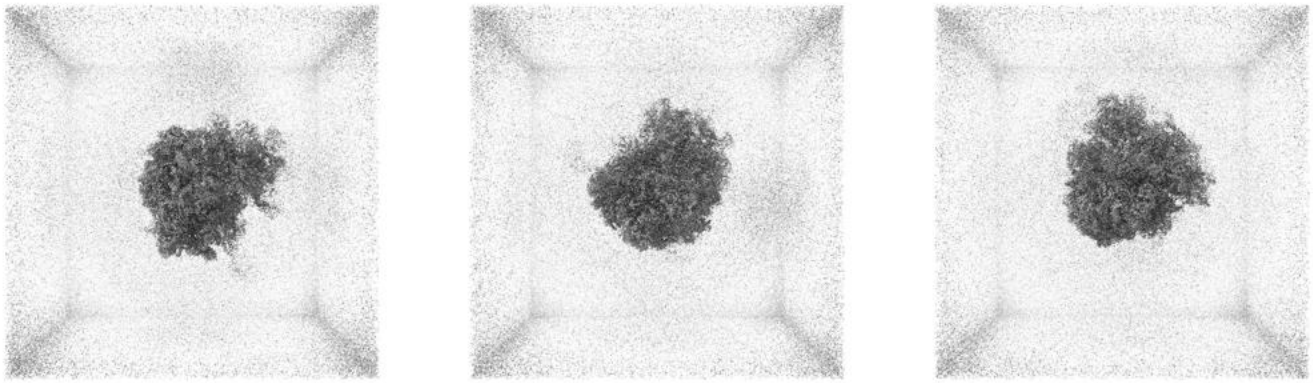
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.26. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

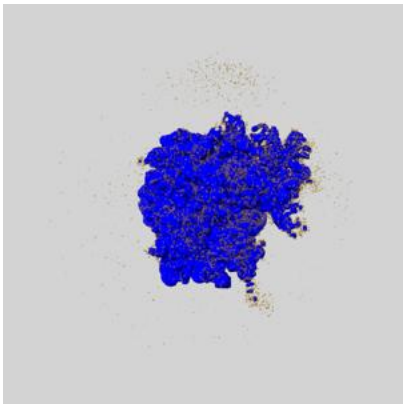
6.6 Mask visualisation (i)

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

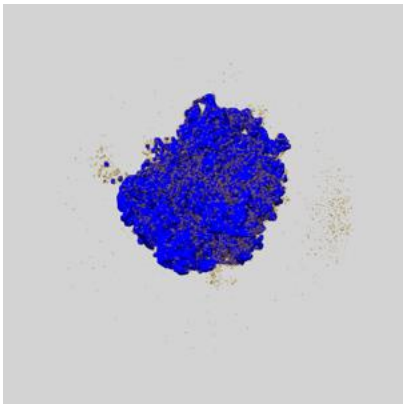
A mask typically either:

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

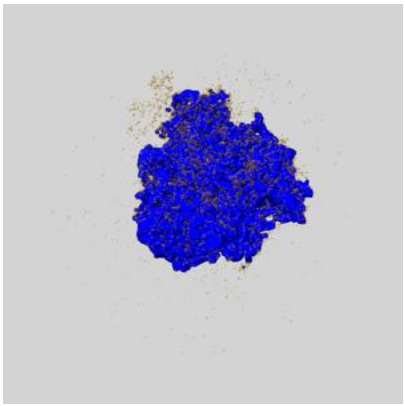
6.6.1 emd_38668_msk_1.map (i)



X



Y

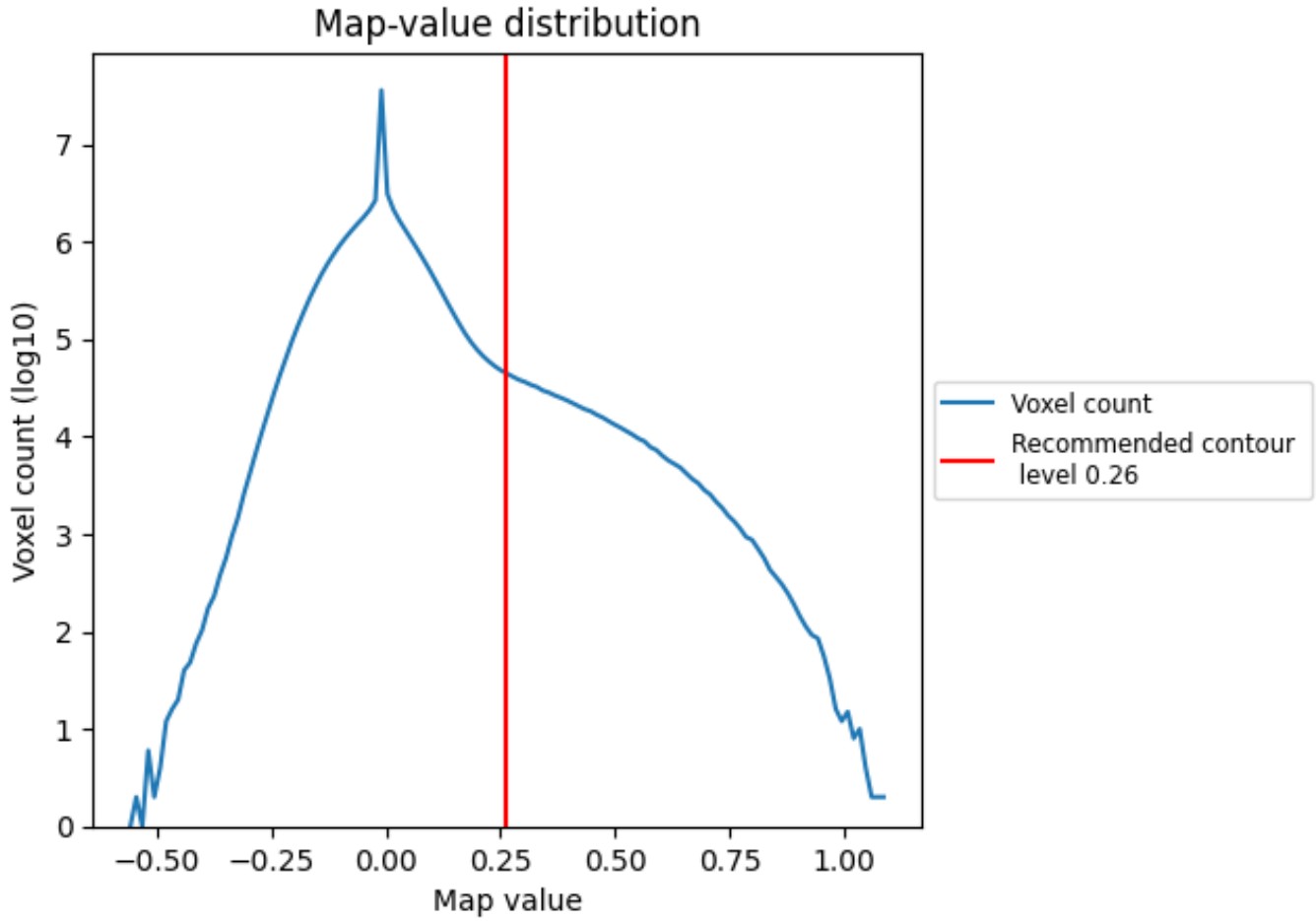


Z

7 Map analysis

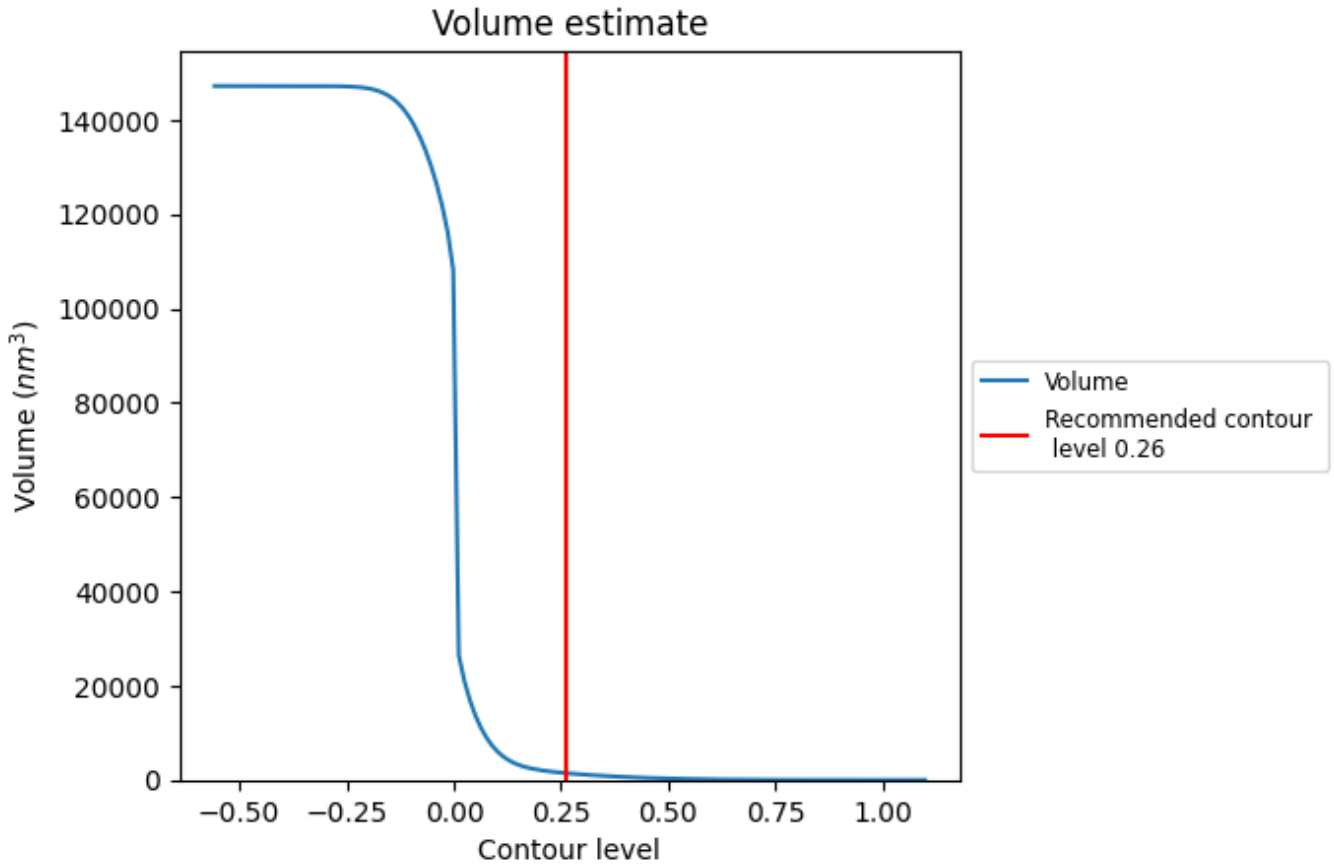
This section contains the results of statistical analysis of the map.

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.

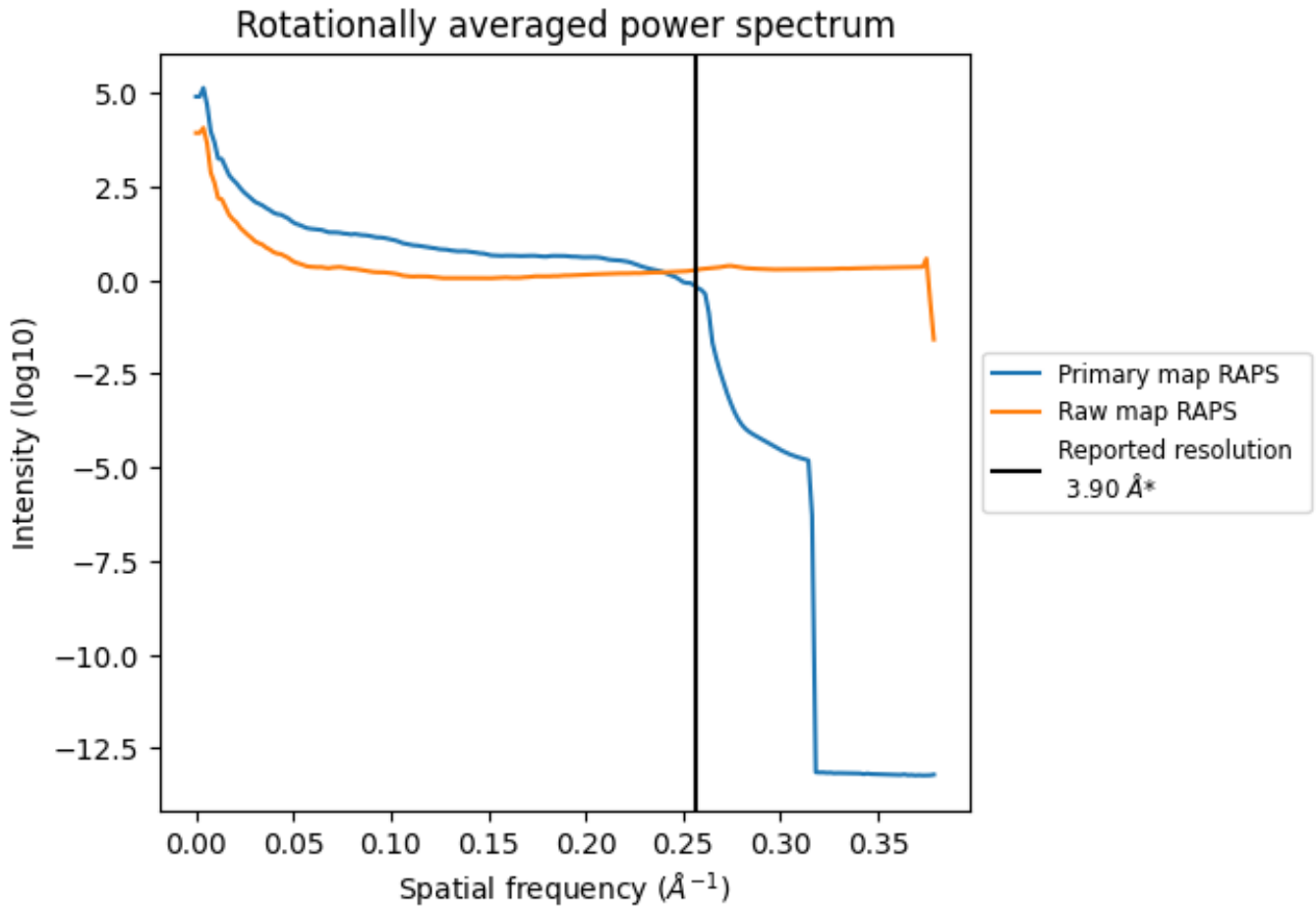
7.2 Volume estimate (i)



The volume at the recommended contour level is 1459 nm^3; this corresponds to an approximate mass of 1318 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)

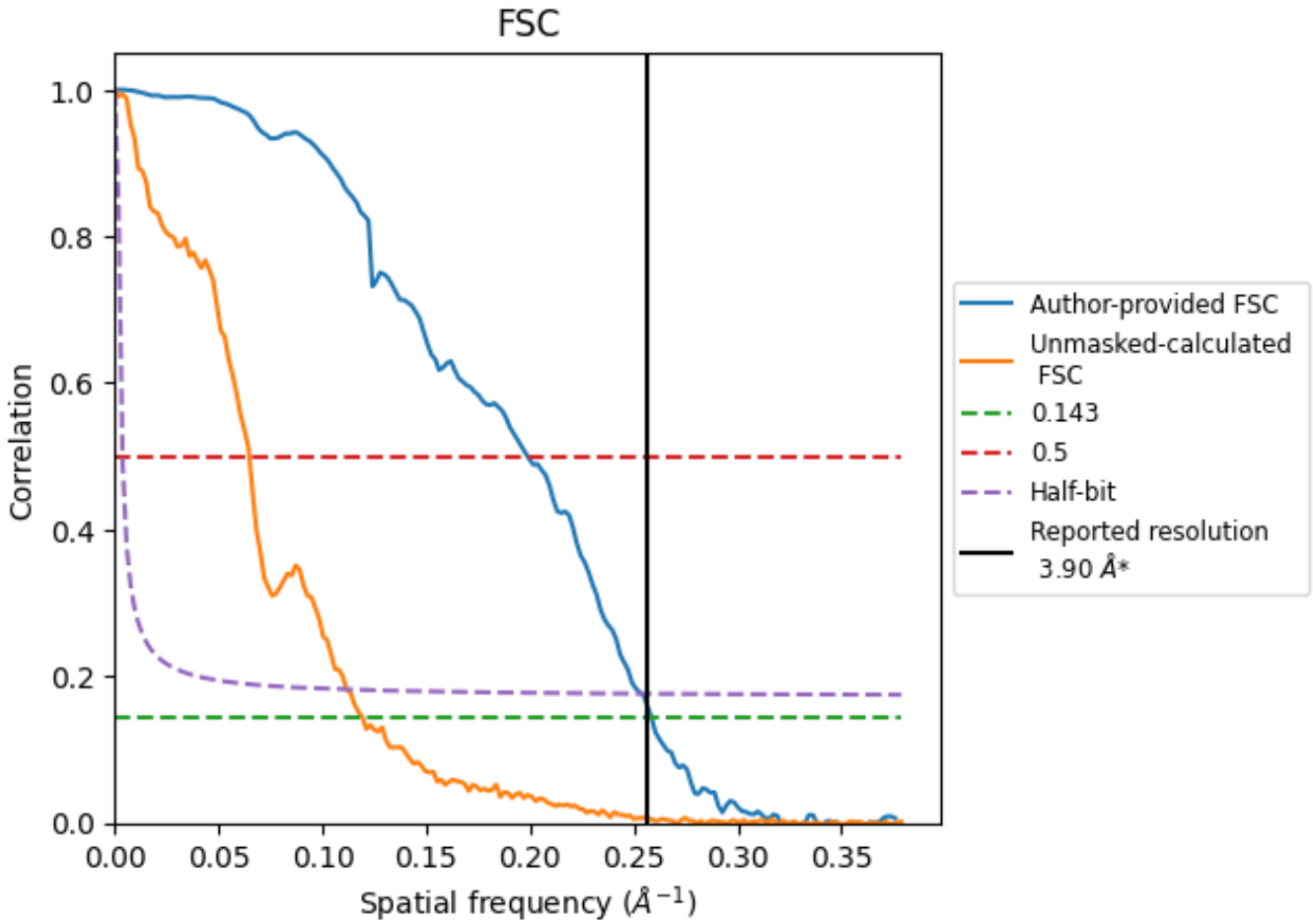


*Reported resolution corresponds to spatial frequency of 0.256 $Å^{-1}$

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 0.256 Å^{-1}

8.2 Resolution estimates (i)

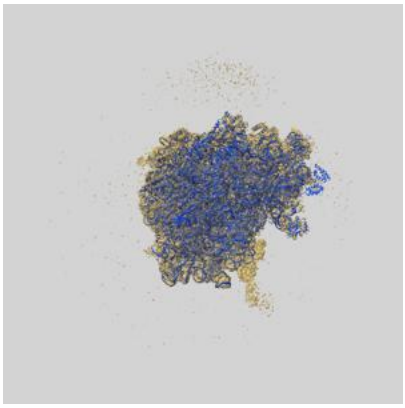
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.87	5.03	3.94
Unmasked-calculated*	8.38	15.43	8.95

*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 8.38 differs from the reported value 3.9 by more than 10 %

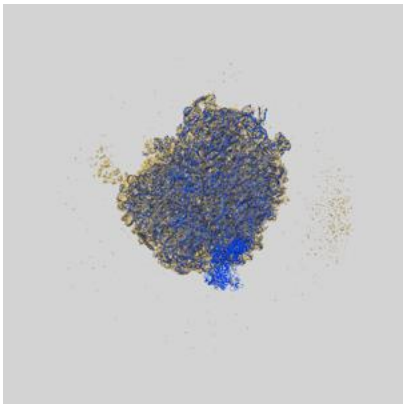
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-38668 and PDB model 8YLR. Per-residue inclusion information can be found in section 3 on page 18.

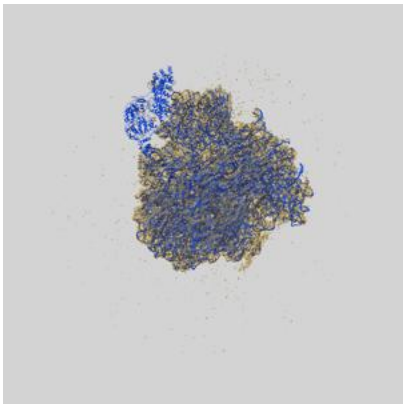
9.1 Map-model overlay



X



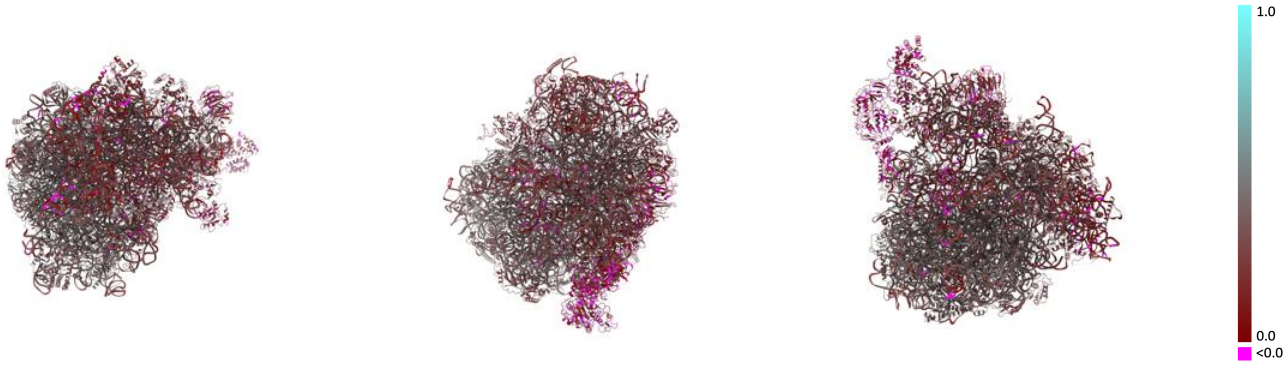
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.26 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.

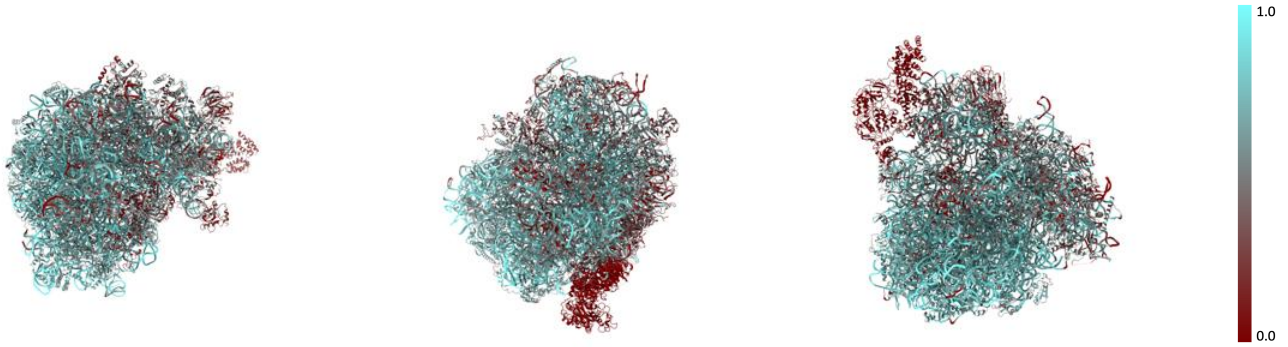
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

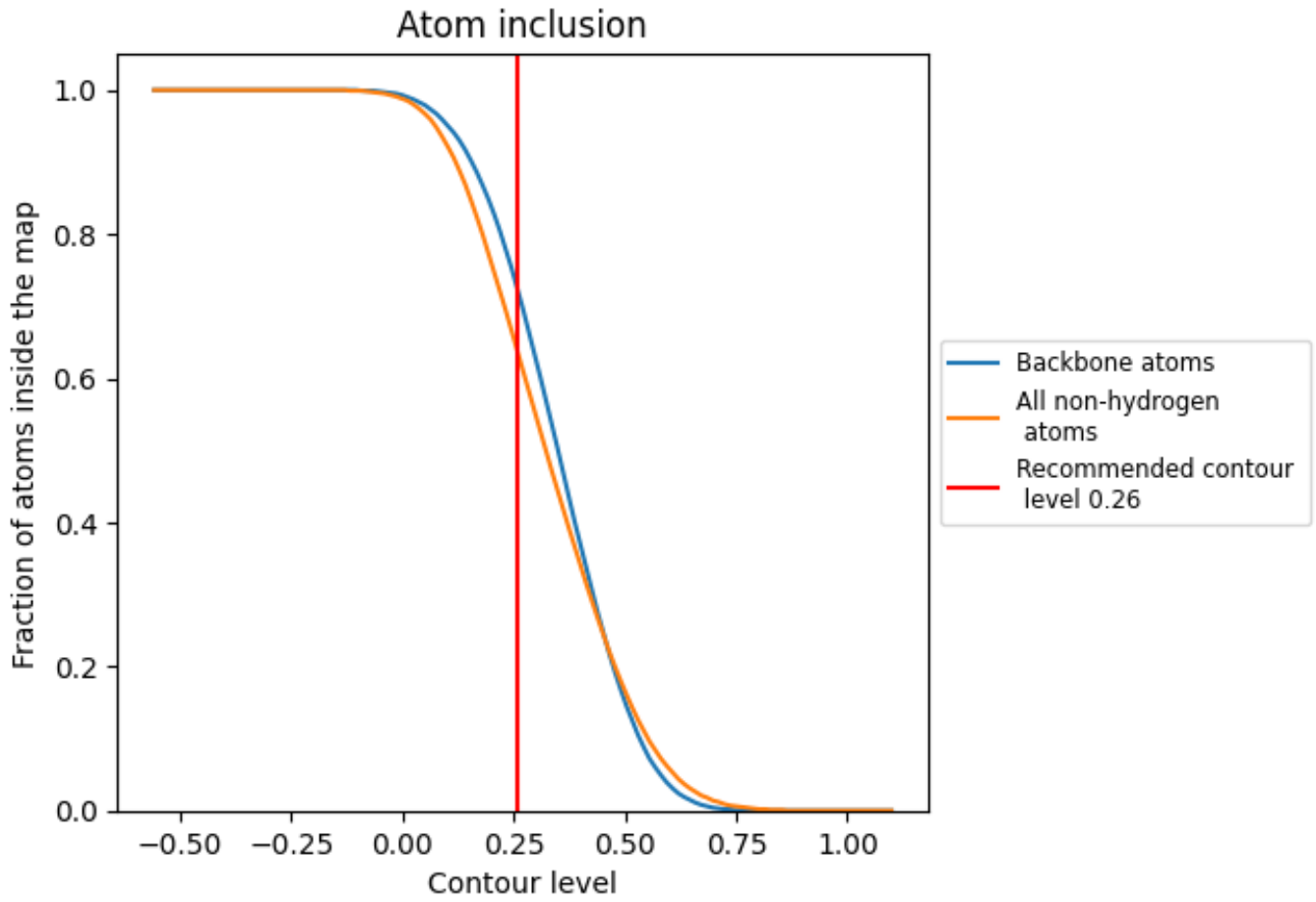
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.26).

9.4 Atom inclusion (i)



At the recommended contour level, 72% of all backbone atoms, 63% 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 (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6340	0.3220
2	0.7110	0.2750
A	0.8340	0.3660
B	0.8880	0.3710
C	0.8560	0.3830
D	0.5970	0.4190
E	0.6230	0.4050
F	0.6420	0.4070
G	0.6070	0.3380
H	0.6120	0.3760
I	0.6340	0.3800
J	0.6100	0.3630
K	0.6110	0.3740
L	0.5790	0.3590
M	0.5670	0.3110
N	0.6560	0.3950
O	0.6760	0.3830
P	0.6000	0.4110
Q	0.6350	0.3810
R	0.6110	0.3970
S	0.6150	0.4060
SA	0.3540	0.2780
SB	0.2940	0.2160
SC	0.3540	0.2490
SD	0.1790	0.1680
SE	0.2990	0.2650
SF	0.3580	0.2740
SG	0.4030	0.2290
SH	0.3650	0.2750
SI	0.3640	0.2550
SJ	0.3590	0.2840
SK	0.3100	0.2490
SL	0.2310	0.2190
SM	0.5080	0.3250
SN	0.1830	0.1620

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Chain	Atom inclusion	Q-score
SO	0.2870	0.1660
SP	0.4620	0.2770
SQ	0.3390	0.1880
SR	0.5150	0.3340
SS	0.3370	0.2550
ST	0.3780	0.2630
SU	0.4060	0.2690
SV	0.4540	0.3050
SW	0.4490	0.2830
SX	0.4080	0.3340
SY	0.4270	0.2890
SZ	0.3710	0.2060
Sa	0.4380	0.3040
Sb	0.4660	0.3200
Sc	0.3890	0.3270
Sd	0.3750	0.2260
Se	0.4670	0.3080
Sf	0.3990	0.2590
Sg	0.3620	0.2940
T	0.5950	0.3570
U	0.6280	0.4110
V	0.6020	0.4050
W	0.5770	0.3500
X	0.5640	0.3990
Y	0.5040	0.3160
Z	0.6200	0.3940
a	0.6440	0.3990
b	0.6230	0.3730
c	0.6590	0.4210
d	0.5800	0.3880
e	0.6040	0.3540
f	0.5710	0.3990
g	0.5860	0.4090
h	0.6630	0.4090
i	0.5560	0.4000
j	0.6290	0.3680
k	0.6390	0.3840
l	0.6380	0.4280
m	0.5780	0.3790
n	0.5450	0.3880
o	0.6060	0.4040
p	0.5430	0.3630

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Chain	Atom inclusion	Q-score
q	0.5640	0.4190
r	0.5770	0.3850
t	0.2710	0.1440
u	0.5570	0.1940
v	0.0150	0.1270
x	0.3320	0.2630