wwPDB EM Validation Summary Report (i)

Mar 10, 2025 – 12:24 PM EDT

PDB ID	:	9B0P
EMDB ID	:	EMD-44049
Title	:	In situ human Hibernating class1 80S ribosome
Authors	:	Wei, Z.; Yong, X.
Deposited on	:	2024-03-12
Resolution	:	2.82 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

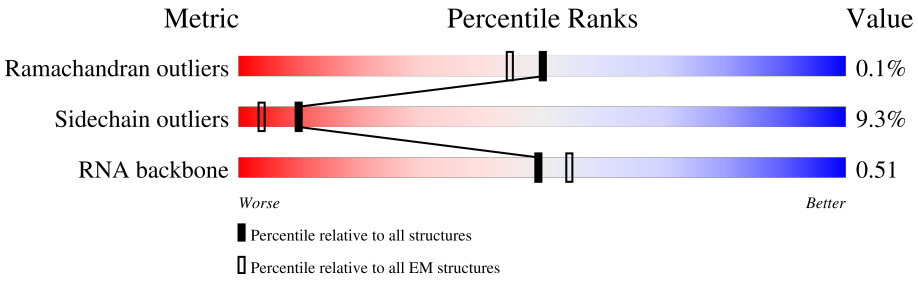
EMDB validation analysis	:	0.0.1.dev117
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

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 2.82 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	S2	1869	10% 67% 26% 7%
2	SD	227	27% 86% 14%
3	SF	189	30% 94% 6%
4	SK	98	41% 91% 8%
5	SP	121	35% 91% 9%
6	SQ	144	25% 87% 13%
7	SS	145	40% 89% 11%
8	ST	143	29% 91% 9%

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Mol	Chain	Length	Quality of chain
9	SU	104	43% 90% 10%
10	Sc	64	48% 88% 12%
11	Sd	55	5% 89% 11%
12	Sg	313	60% 88% 12%
13	SM	122	91% 89% 11%
14	SZ	75	59% 89% 11%
15	Sf	67	78% 90% 10%
16	CD	55	85% 95% 5%
17	SE	262	25% 86% 14%
18	SI	206	23% 87% 13%
19	SL	153	21% 89% 11%
20	SX	141	11% 90% 10%
21	SG	237	51% 89% 11%
22	SJ	185	26% 86% 14%
23	SY	131	50% 88% 12%
24	Se	58	43% 93% 7%
25	SA	221	17% 86% 14%
26	SB	214	32% 95% 5%
27	SH	189	54% 93% 5%
28	SV	83	23% 84% 16%
29	Sa	102	13% 92% 8%
30	SC	222	9% 92% 8%
31	SN	150	9% 91% 9%
32	SO	140	20% 89% 11%
33	SW	129	5% 94% 6%

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Mol	Chain	Length	Quality of chain
34	Sb	83	31% 89% 11%
35	L5	5070	7% 56% 17% 26%
36	L7	120	88% 12%
37	L8	156	80% 20%
38	LA	248	94% 6%
39	LB	402	94% 5%
40	LC	368	94% 6%
41	LD	293	5% 93% 7%
42	LE	247	11% 90% 5%
43	LF	225	96%
44	LG	241	12% 93% 7%
45	LH	190	94% 6%
46	LI	213	91% 5%
47	LJ	176	14% 92% 8%
48	LL	210	8% 92% 8%
49	LM	139	92% 7%
50	LN	203	98%
51	LO	201	96%
52	LP	153	92% 8%
53	LQ	187	93% 7%
54	LR	187	12% 93% 7%
55	LS	175	94% 6%
56	LT	159	91% 9%
57	LU	101	15% 89% 11%
58	LV	131	95% 5%

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Mol	Chain	Length	Quality of chain
59	LX	120	5% 95% 5%
60	LY	134	93% 7%
61	LZ	135	93% 7%
62	La	147	96%
63	Lb	121	15% 83% 7% 10%
64	Lc	98	7% 91% 9%
65	Ld	107	7% 92% 8%
66	Le	128	95% 5%
67	Lf	109	96%
68	Lg	114	91% 9%
69	Lh	122	92% 8%
70	Li	102	92% 8%
71	Lj	86	91% 9%
72	Lk	69	7% 90% 9%
73	Ll	50	92% 8%
74	Lm	52	92% 8%
75	Ln	24	92% 8%
76	Lo	105	7% 91% 9%
77	Lp	91	92% 8%
78	Lr	125	93% 7%
79	Lz	217	100% 92% 8%
80	CA	356	92% 90% 10%
81	Ls	196	56% 92% 8%
82	Lt	141	84% 94% 6%
83	CB	856	41% 89% 10%

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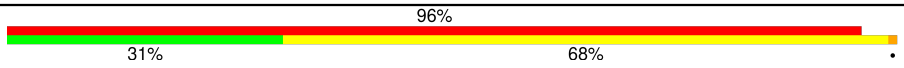
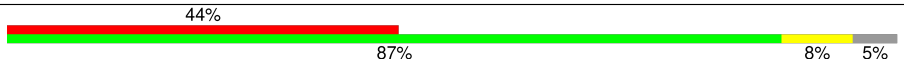
Mol	Chain	Length	Quality of chain
84	Et	75	
85	LW	124	

2 Entry composition (i)

There are 87 unique types of molecules in this entry. The entry contains 229857 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	S2	1740	36898	16459	6599	12101	1739	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	SD	227	1765	1125	317	315	8	0	0

- Molecule 3 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	SF	189	1495	934	284	270	7	0	0

- Molecule 4 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SK	98	827	539	148	134	6	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SP	121	985	623	185	170	7	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SQ	144	1142	726	216	197	3	0	0

- Molecule 7 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 8 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 9 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 10 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 11 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 12 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 13 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 14 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 15 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 16 is a protein called Serbp1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	CD	55	Total	C	N	O	0	0
			440	263	87	90		

- Molecule 17 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 18 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 19 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 20 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 21 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 22 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 23 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 24 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 25 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 26 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 27 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 28 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 29 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 30 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 31 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 32 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 33 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 34 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 35 is a RNA chain called 28S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		

- Molecule 36 is a RNA chain called 5S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 37 is a RNA chain called 5.8S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 38 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 39 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 40 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 42 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 43 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 44 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 45 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 46 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 47 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 48 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 49 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 50 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 51 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 52 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 53 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 54 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 55 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 56 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 57 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 58 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 59 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 61 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 62 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 63 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Lb	109	Total 876	C 546	N 189	O 137	S 4	0	0

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Lc	98	Total 764	C 485	N 135	O 138	S 6	0	0

- Molecule 65 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ld	107	Total 888	C 560	N 171	O 155	S 2	0	0

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Le	128	Total 1053	C 667	N 216	O 165	S 5	0	0

- Molecule 67 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lf	109	Total 876	C 555	N 174	O 144	S 3	0	0

- Molecule 68 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lg	114	Total 906	C 566	N 187	O 147	S 6	0	0

- Molecule 69 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Lh	122	Total 1015	C 641	N 205	O 168	S 1	0	0

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 71 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 74 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 75 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 76 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 78 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 79 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 80 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 81 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 82 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 83 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 84 is a RNA chain called E site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Et	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 85 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
86	S2	27	Total	Mg	0
			27	27	
86	SQ	1	Total	Mg	0
			1	1	
86	SG	1	Total	Mg	0
			1	1	
86	L5	210	Total	Mg	0
			210	210	
86	L7	3	Total	Mg	0
			3	3	
86	L8	6	Total	Mg	0
			6	6	
86	LA	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	
86	Le	1	Total	Mg	0
			1	1	
86	Lg	1	Total	Mg	0
			1	1	
86	Lj	1	Total	Mg	0
			1	1	

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

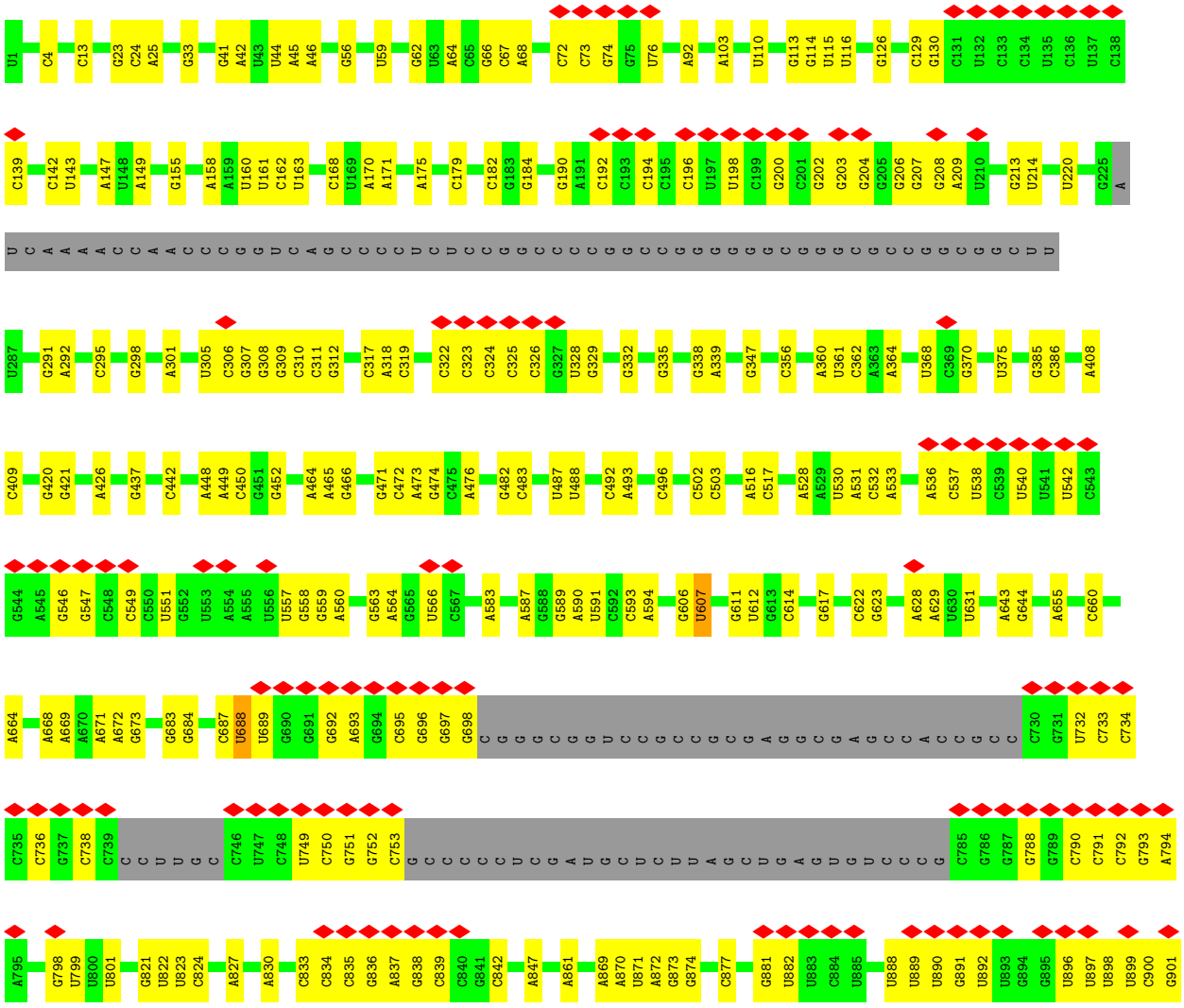
Mol	Chain	Residues	Atoms	AltConf
87	Sa	1	Total Zn 1 1	0
87	Lg	1	Total Zn 1 1	0
87	Lj	1	Total Zn 1 1	0
87	Lm	1	Total Zn 1 1	0
87	Lo	1	Total Zn 1 1	0
87	Lp	1	Total Zn 1 1	0

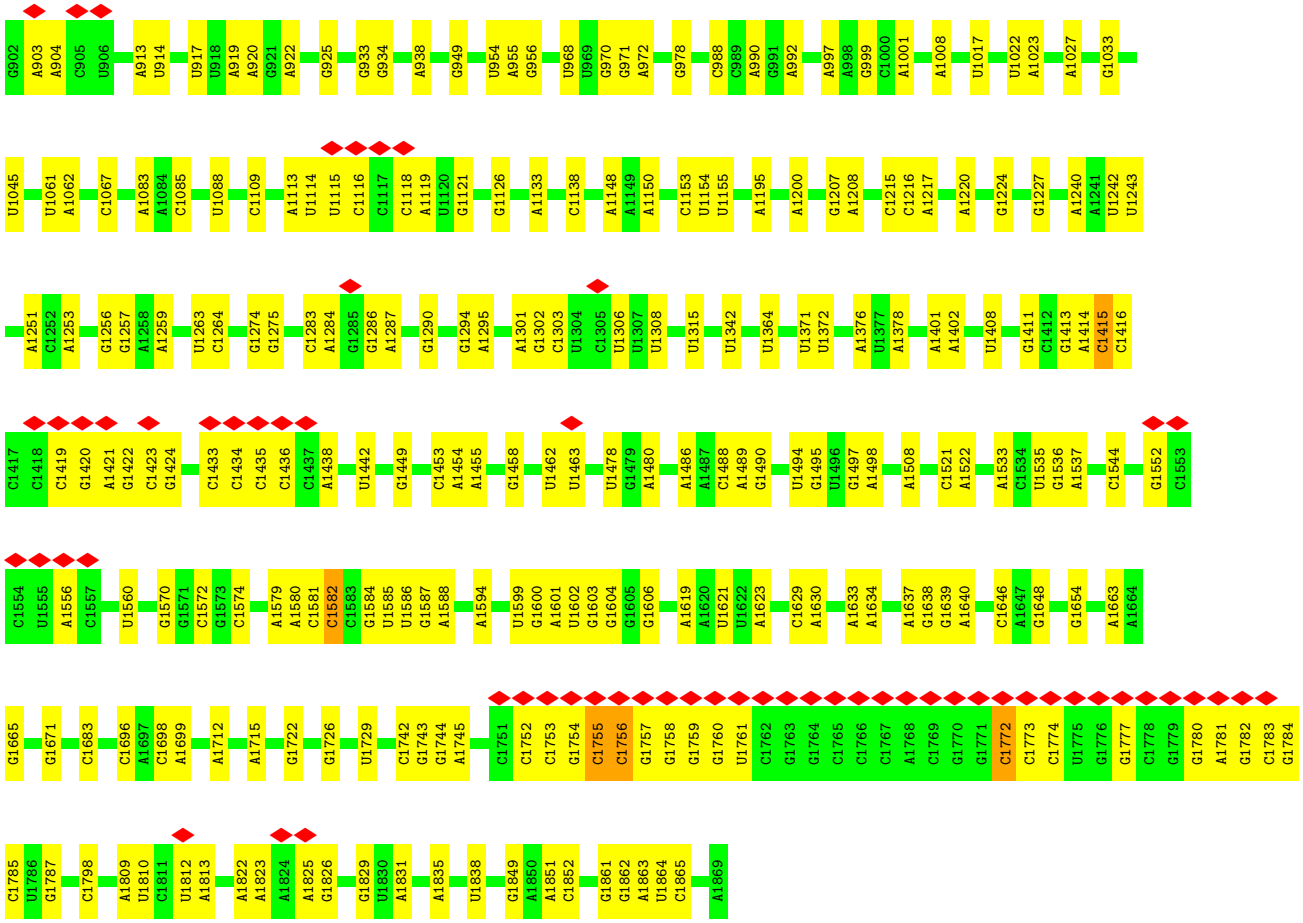
3 Residue-property plots (i)

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

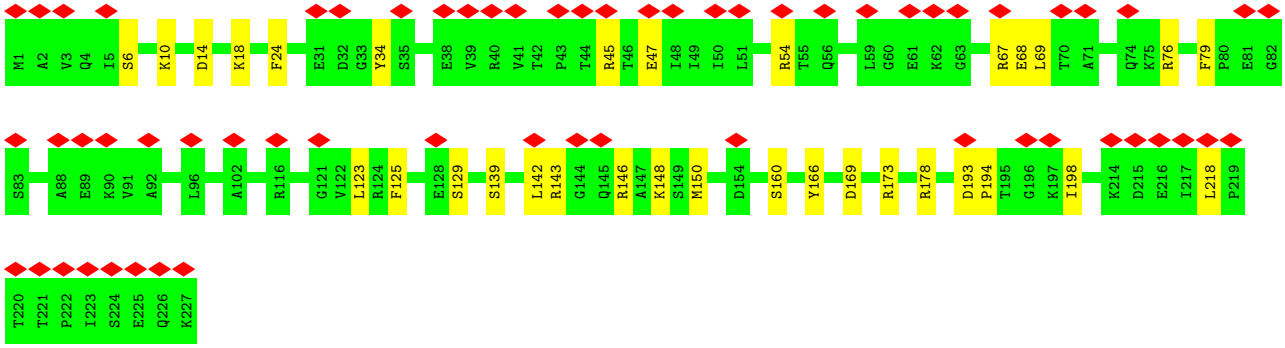
Chain S2:





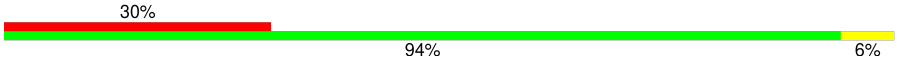
• Molecule 2: Small ribosomal subunit protein uS3

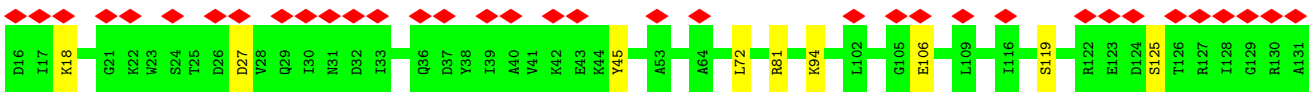
Chain SD:

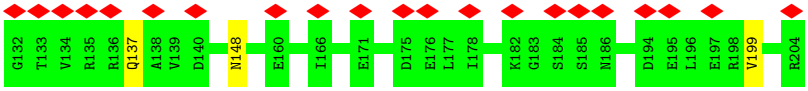


• Molecule 3: 40S ribosomal protein S5

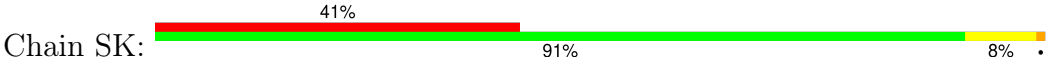
Chain SF:

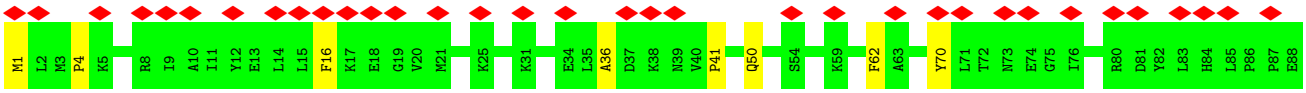


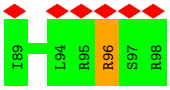




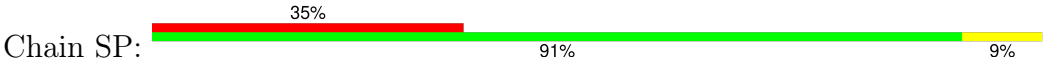
• Molecule 4: 40S ribosomal protein S10

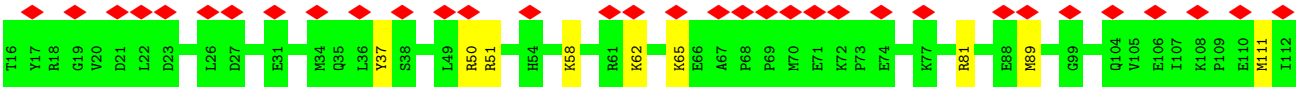


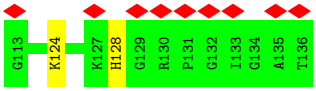




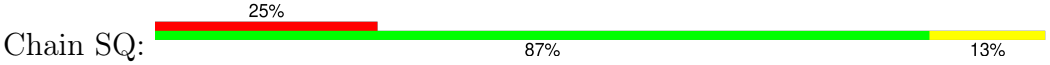
• Molecule 5: Small ribosomal subunit protein uS19

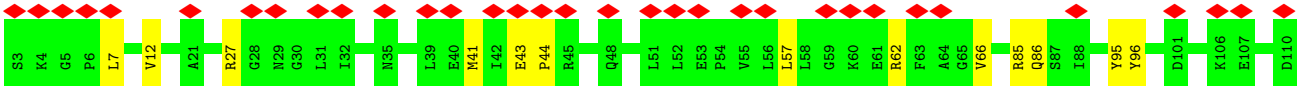




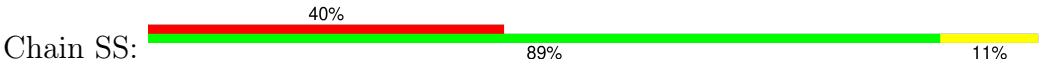


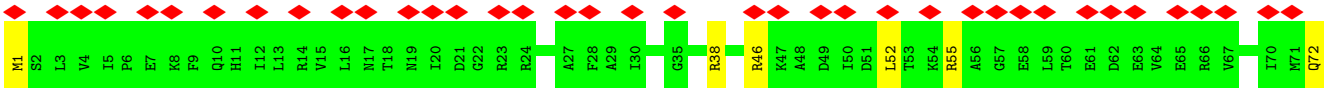
• Molecule 6: Small ribosomal subunit protein uS9





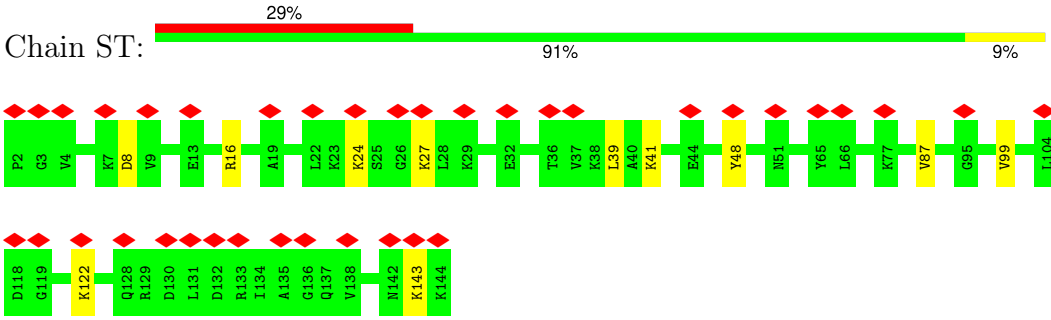
• Molecule 7: 40S ribosomal protein S18





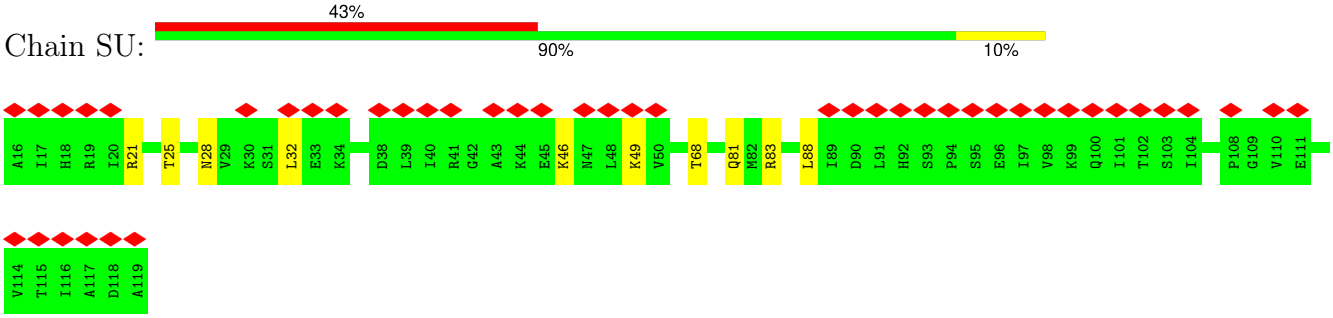
• Molecule 8: 40S ribosomal protein S19

Chain ST:



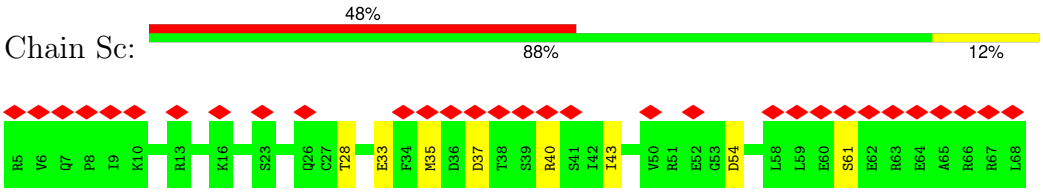
• Molecule 9: 40S ribosomal protein S20

Chain SU:



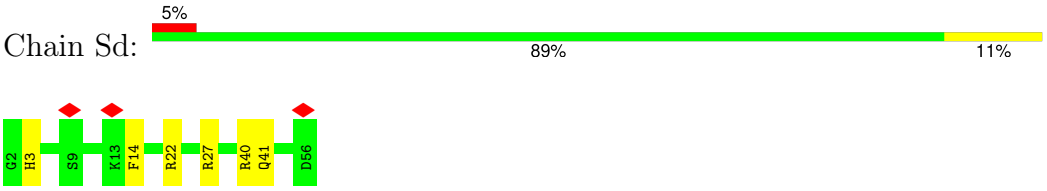
• Molecule 10: 40S ribosomal protein S28

Chain Sc:



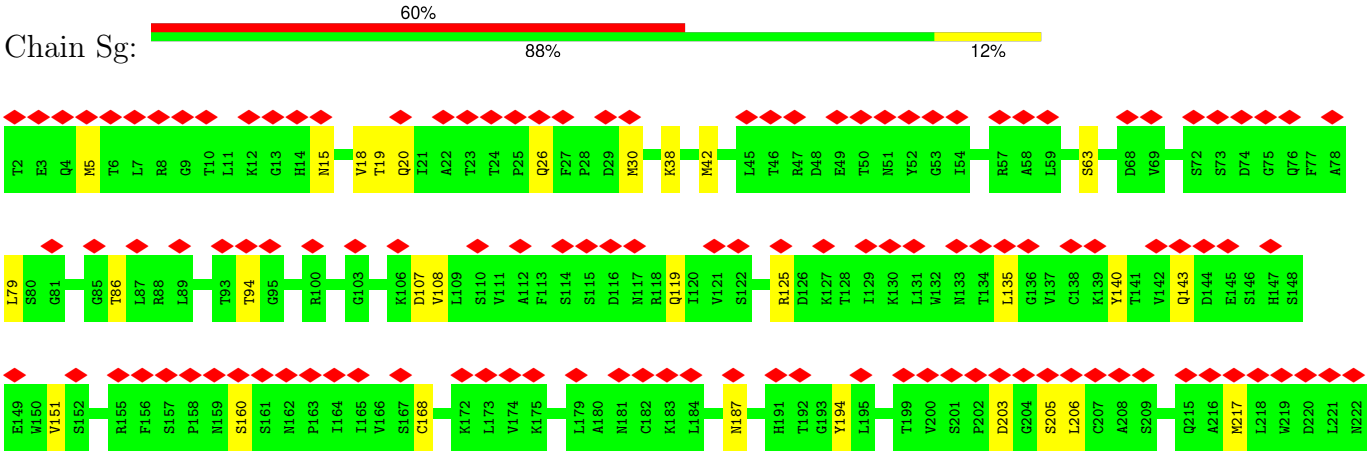
• Molecule 11: 40S ribosomal protein S29

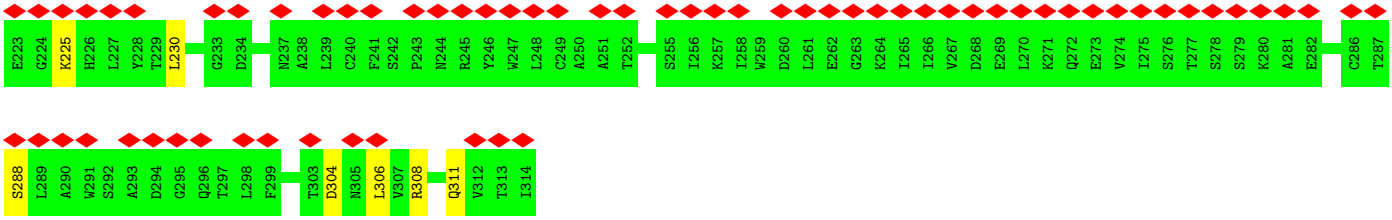
Chain Sd:



• Molecule 12: Receptor of activated protein C kinase 1

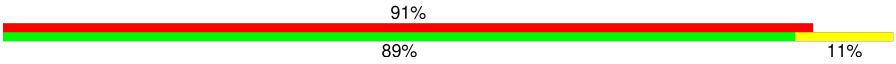
Chain Sg:

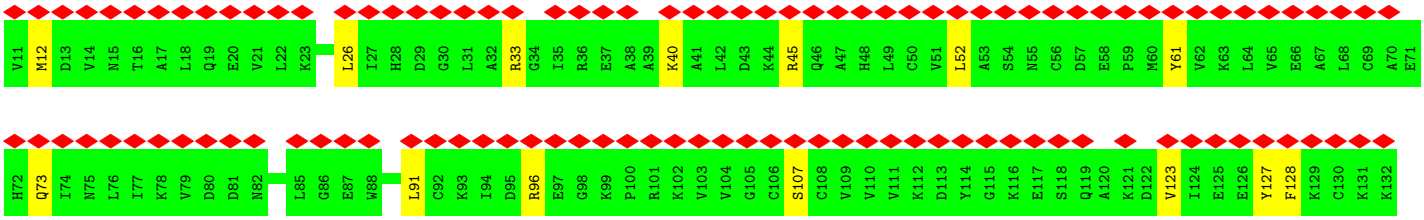




• Molecule 13: Small ribosomal subunit protein eS12

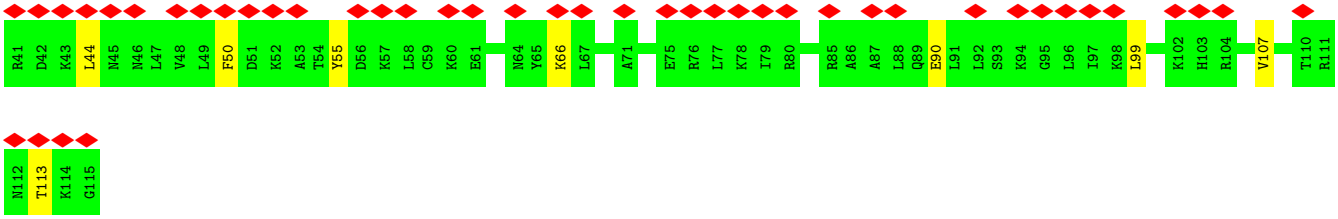
Chain SM:





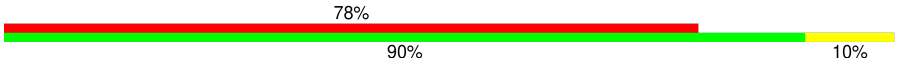
• Molecule 14: Small ribosomal subunit protein eS25

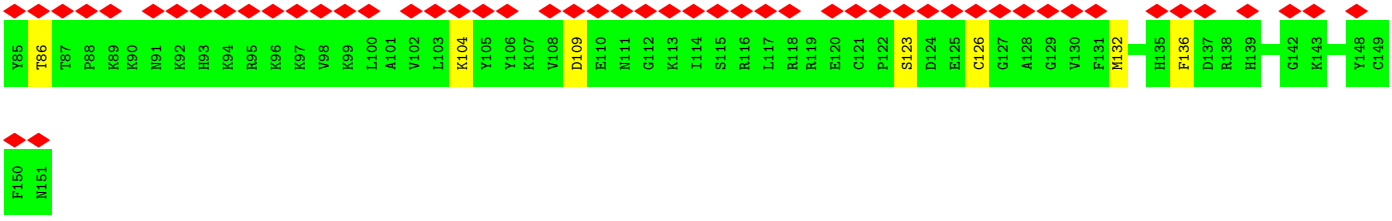
Chain SZ:



• Molecule 15: Ubiquitin-40S ribosomal protein S27a

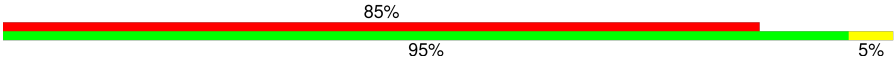
Chain Sf:

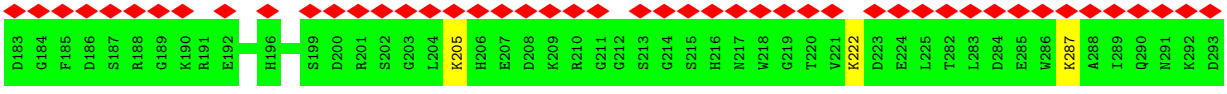




• Molecule 16: Serbp1

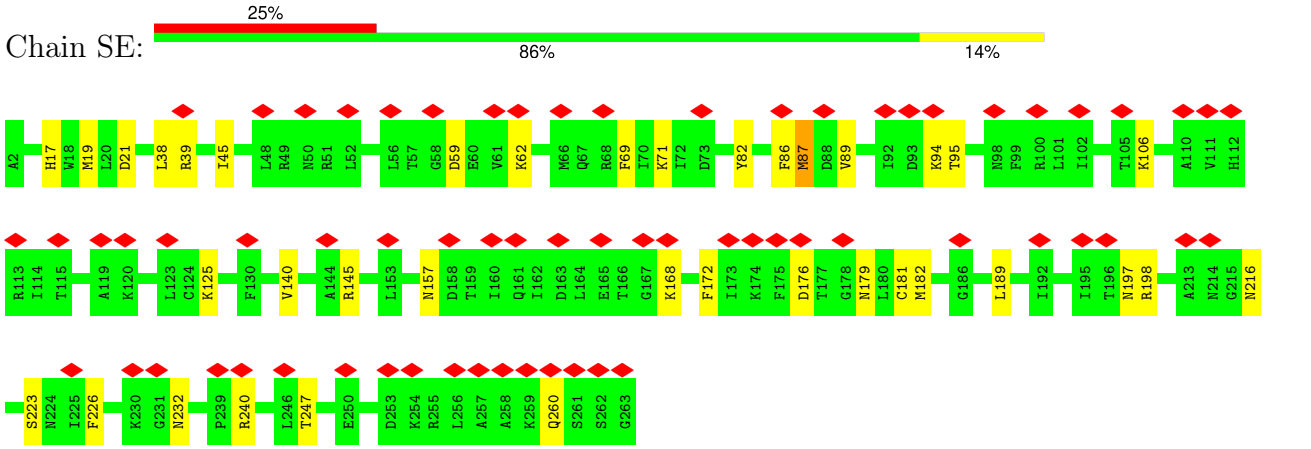
Chain CD:





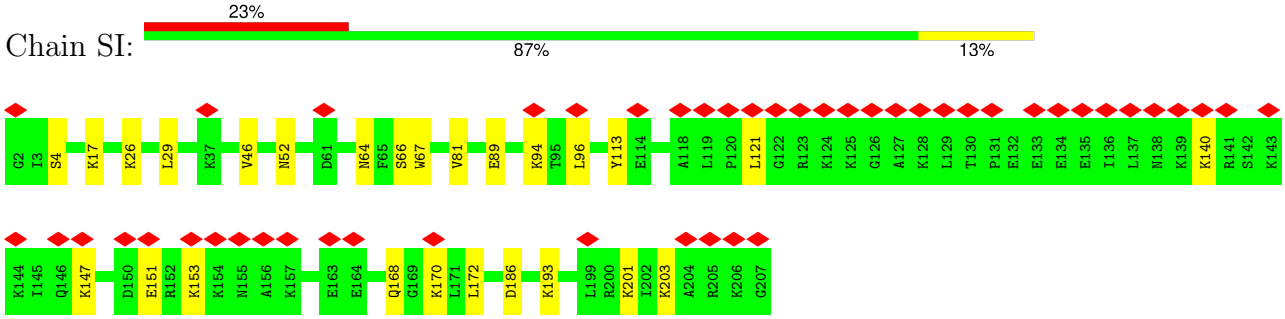
• Molecule 17: Small ribosomal subunit protein eS4, X isoform

Chain SE:



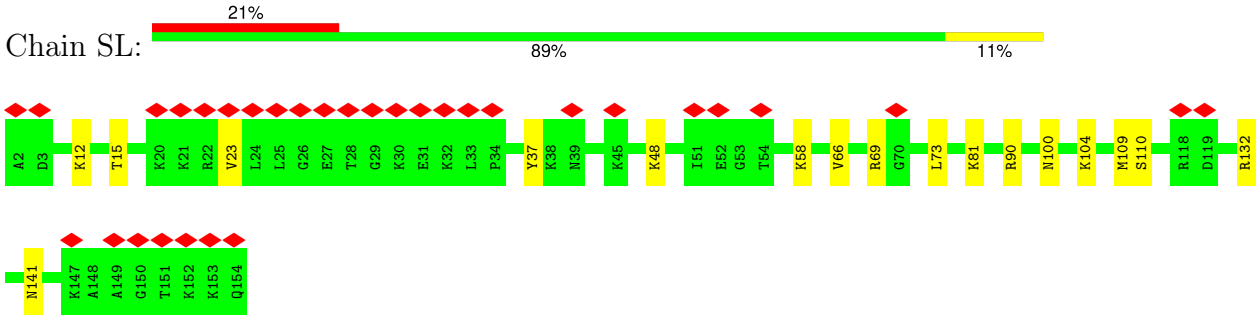
• Molecule 18: 40S ribosomal protein S8

Chain SI:



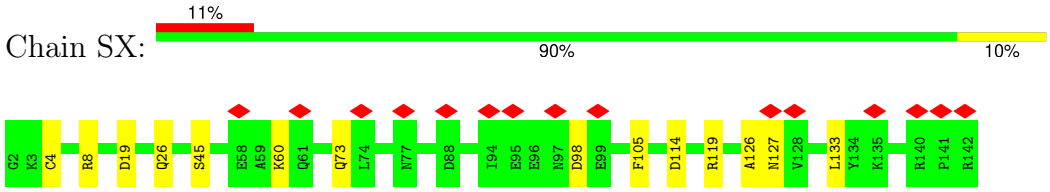
• Molecule 19: 40S ribosomal protein S11

Chain SL:



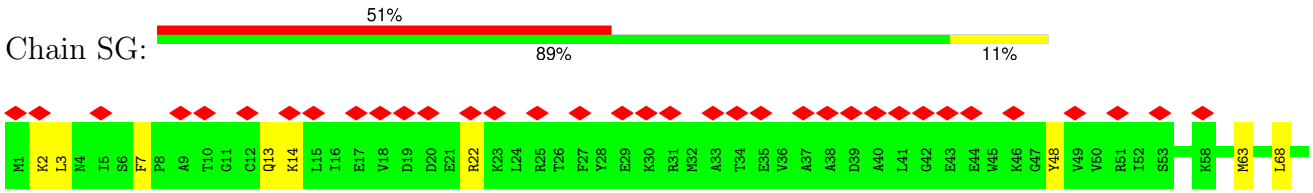
• Molecule 20: 40S ribosomal protein S23

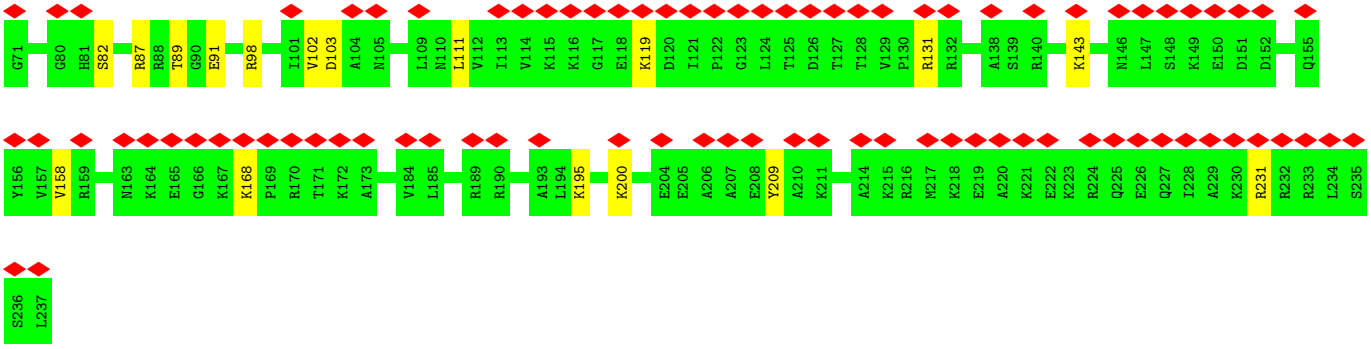
Chain SX:



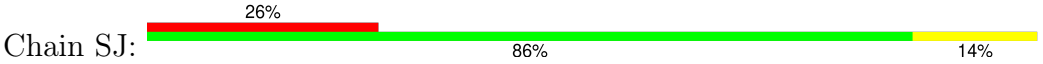
• Molecule 21: 40S ribosomal protein S6

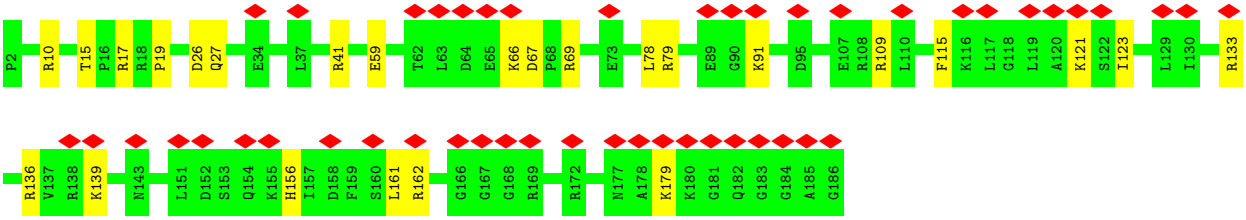
Chain SG:



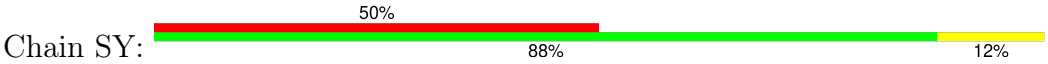


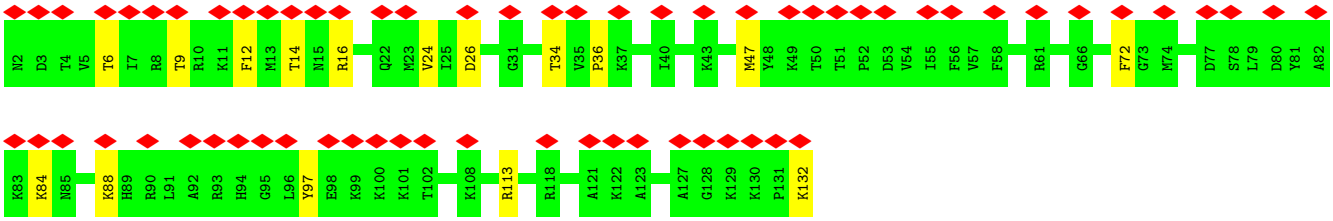
• Molecule 22: 40S ribosomal protein S9



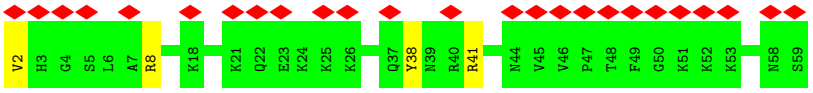


• Molecule 23: 40S ribosomal protein S24

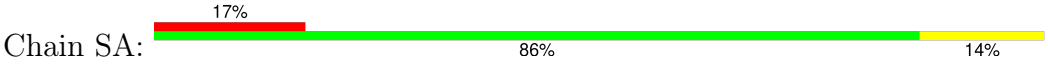


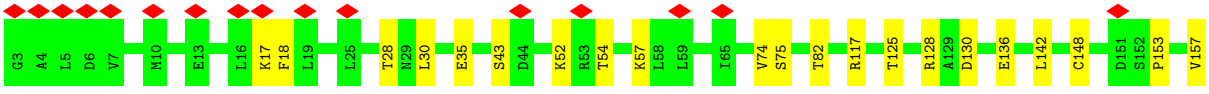


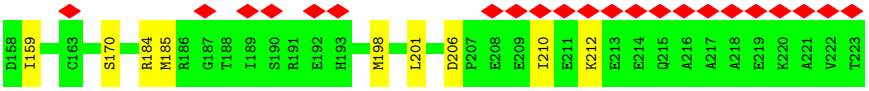
• Molecule 24: Small ribosomal subunit protein eS30



• Molecule 25: 40S ribosomal protein SA

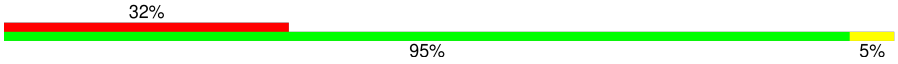


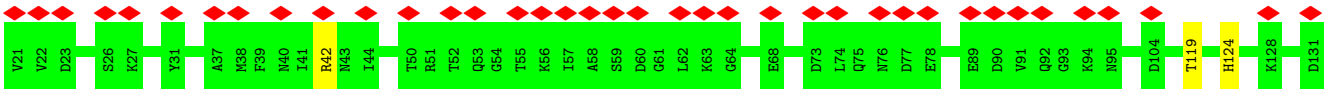


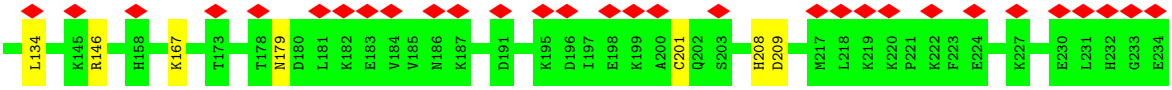


• Molecule 26: 40S ribosomal protein S3a

Chain SB:

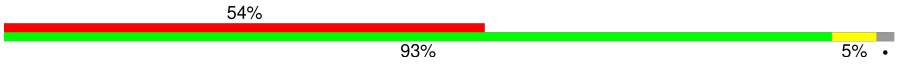


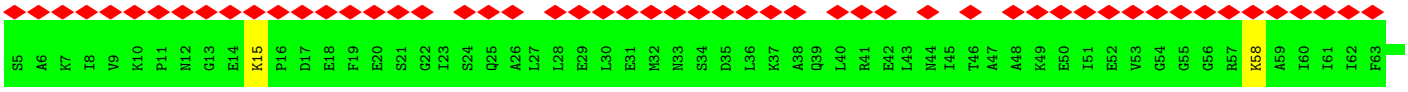


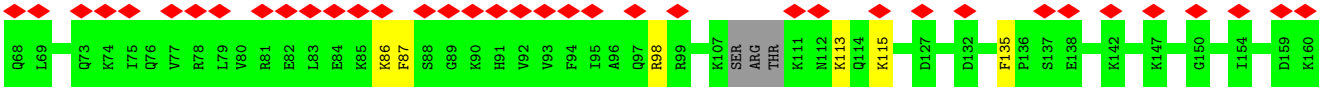


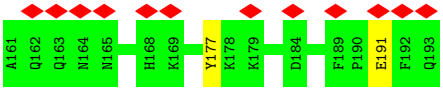
• Molecule 27: Small ribosomal subunit protein eS7

Chain SH:



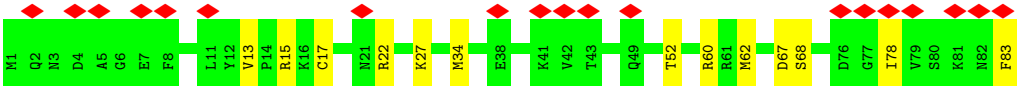






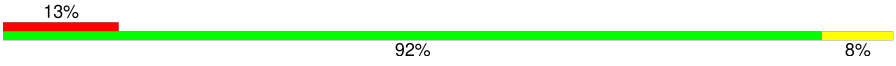
• Molecule 28: 40S ribosomal protein S21

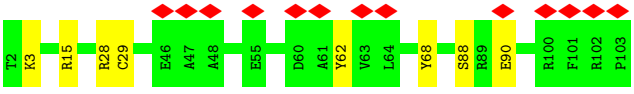
Chain SV:



• Molecule 29: 40S ribosomal protein S26

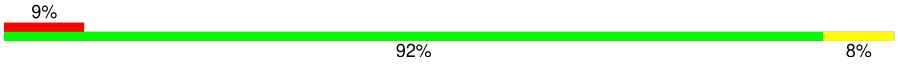
Chain Sa:

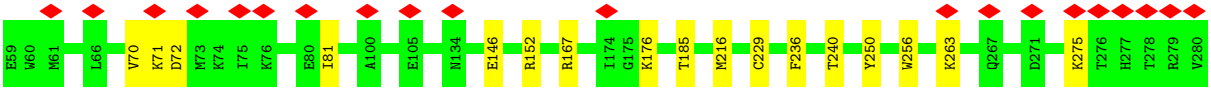




• Molecule 30: 40S ribosomal protein S2

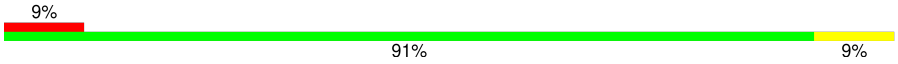
Chain SC:

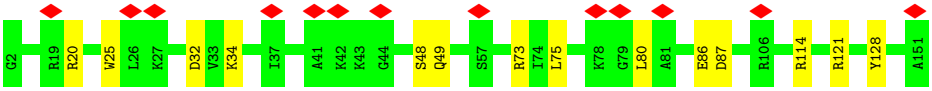




• Molecule 31: 40S ribosomal protein S13

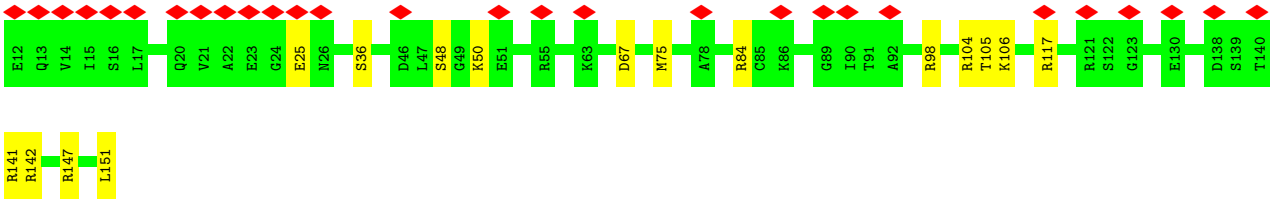
Chain SN:





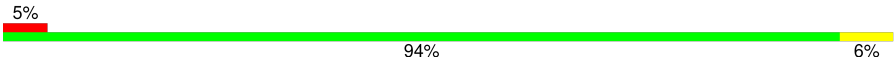
• Molecule 32: Small ribosomal subunit protein uS11

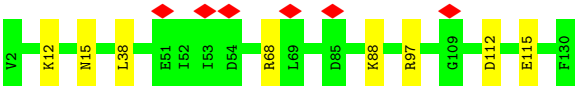
Chain SO:



• Molecule 33: 40S ribosomal protein S15a

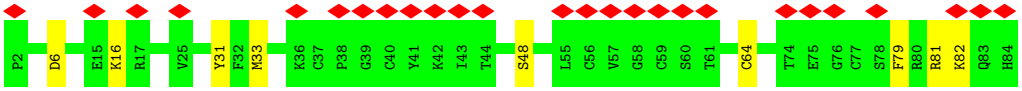
Chain SW:





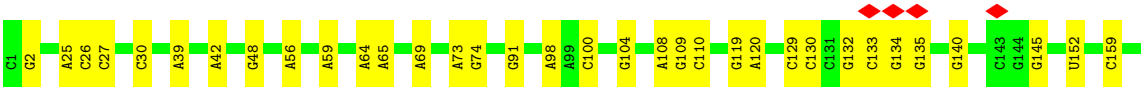
• Molecule 34: Small ribosomal subunit protein eS27

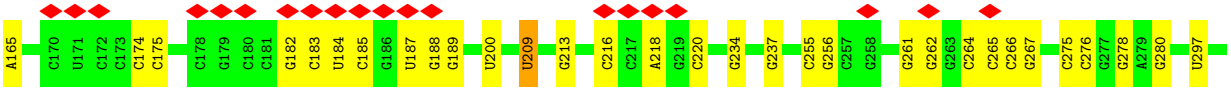
Chain Sb:

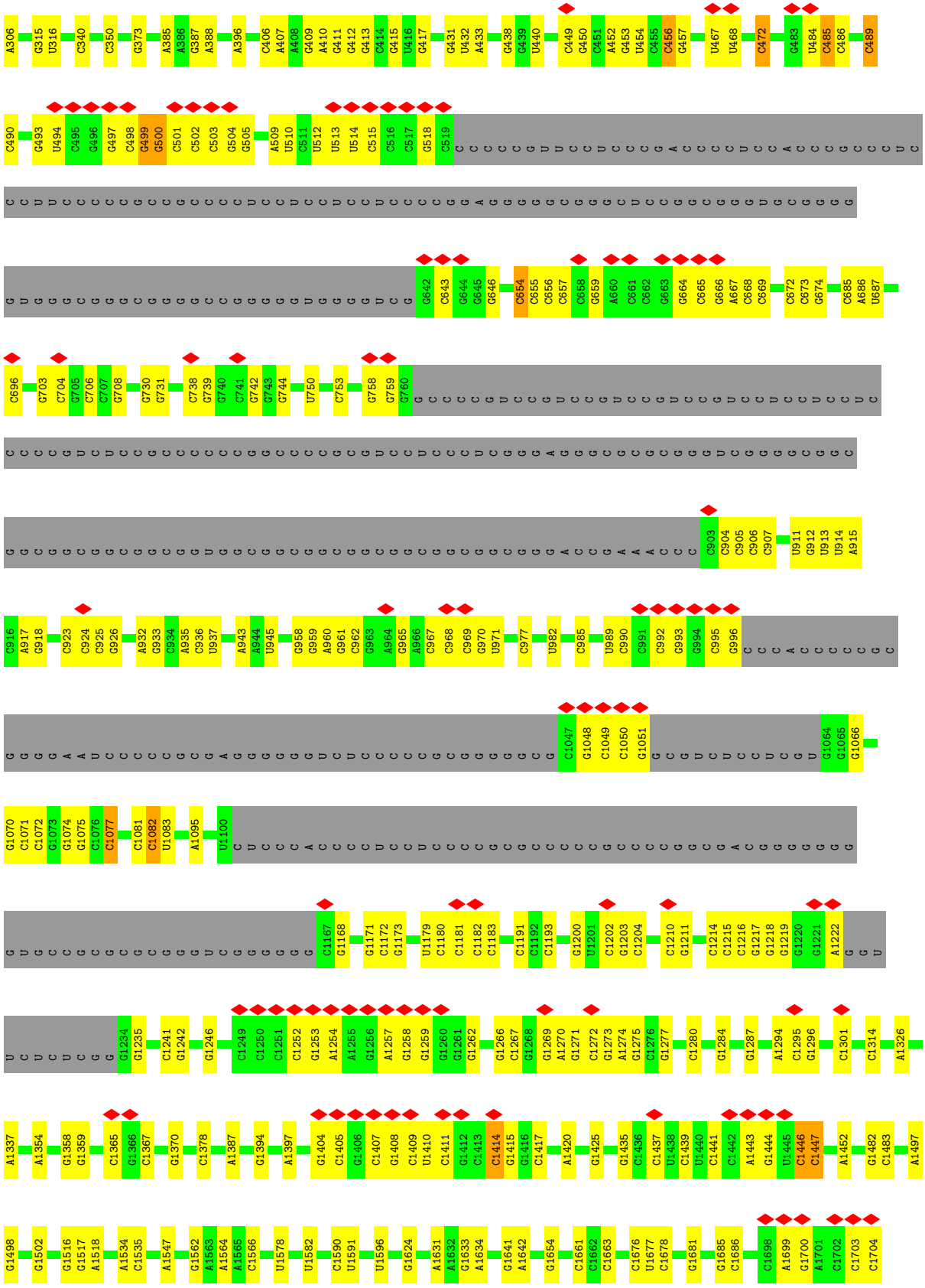


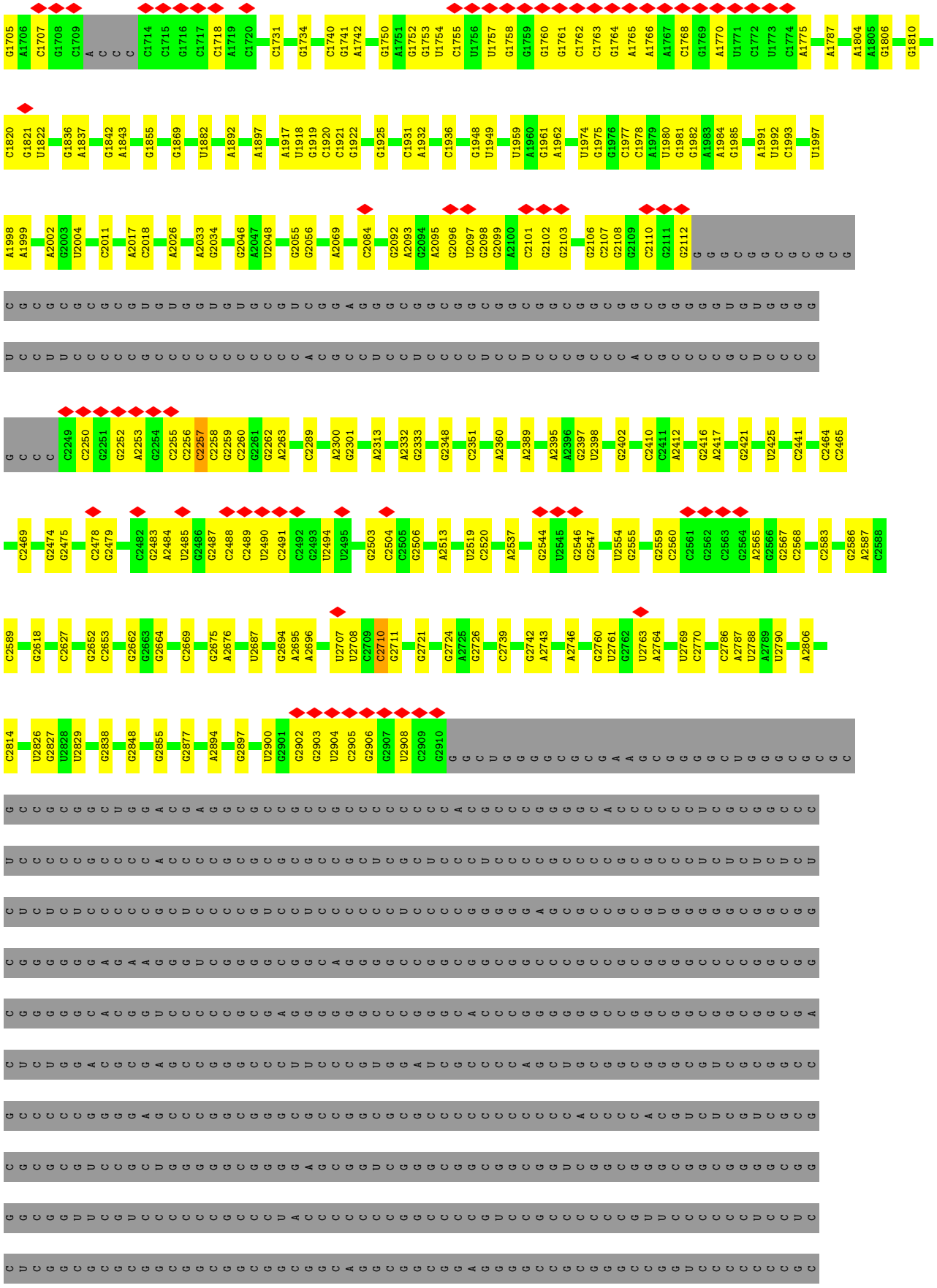
• Molecule 35: 28S rRNA [Homo sapiens]

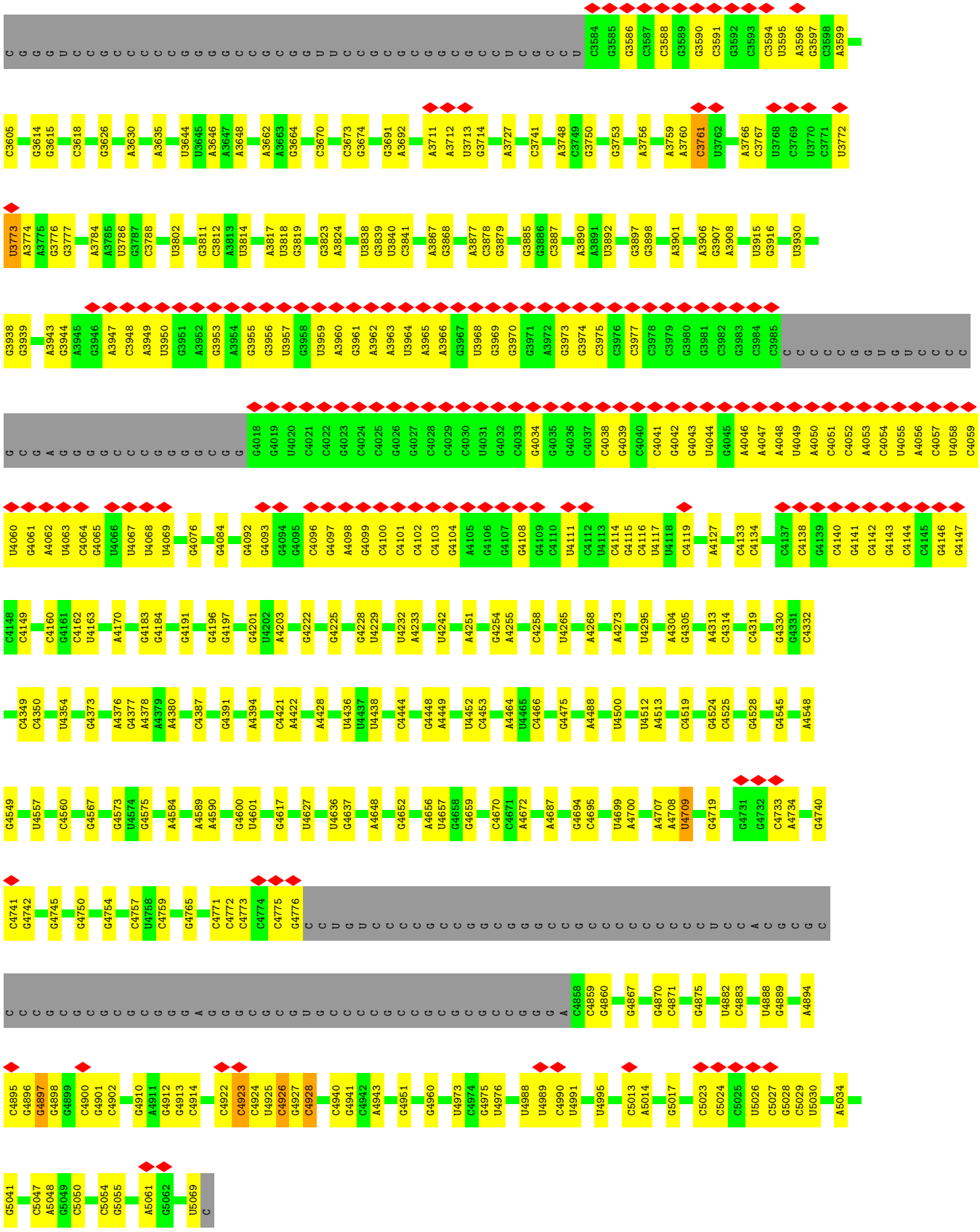
Chain L5:





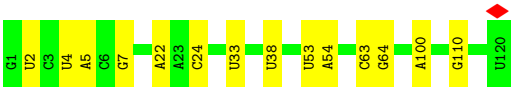






• Molecule 36: 5S rRNA [Homo sapiens]

Chain L7:

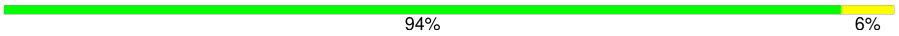


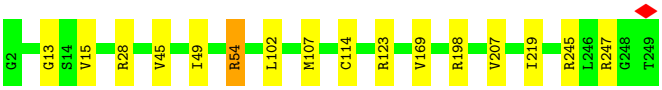
• Molecule 37: 5.8S rRNA [Homo sapiens]

Chain L8:

• Molecule 38: 60S ribosomal protein L8

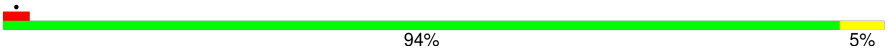
Chain LA:

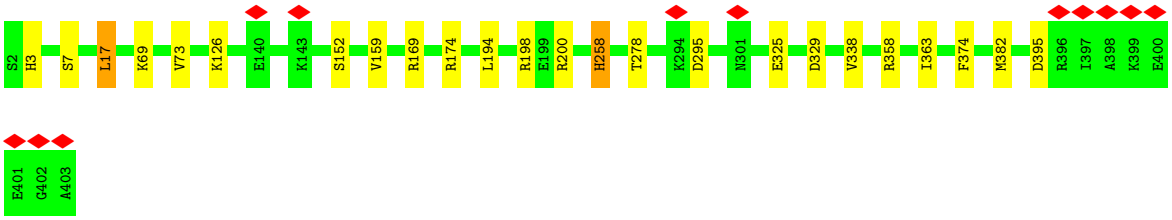




• Molecule 39: Large ribosomal subunit protein uL3

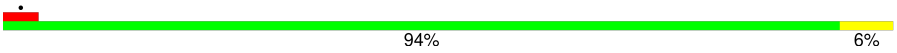
Chain LB:

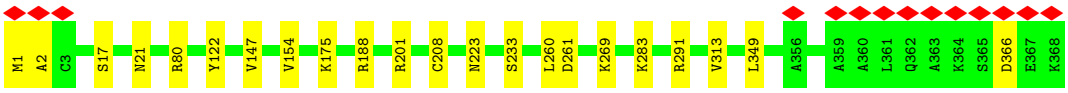




• Molecule 40: 60S ribosomal protein L4

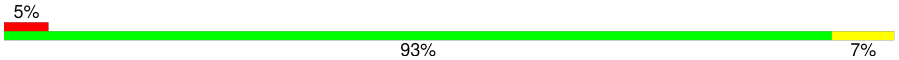
Chain LC:

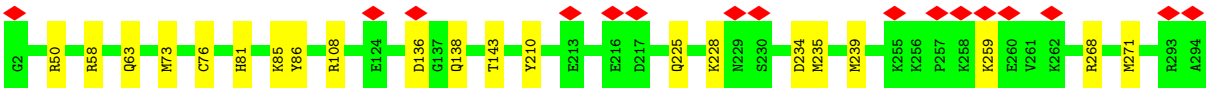




• Molecule 41: Large ribosomal subunit protein uL18

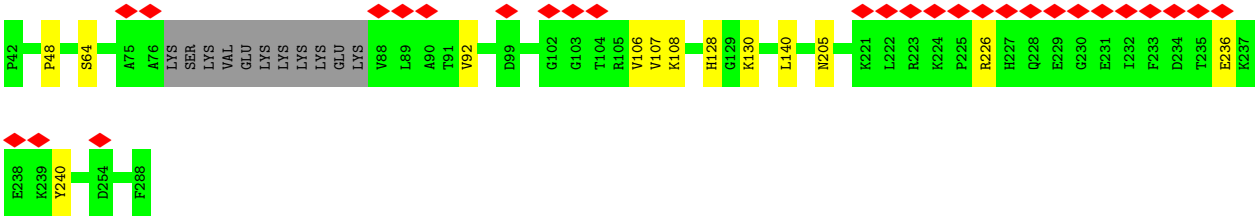
Chain LD:





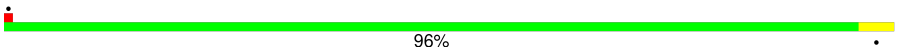
• Molecule 42: Large ribosomal subunit protein eL6

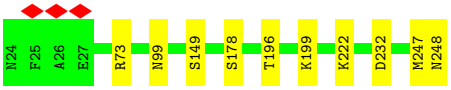
Chain LE:



• Molecule 43: 60S ribosomal protein L7

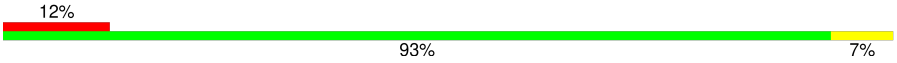
Chain LF:

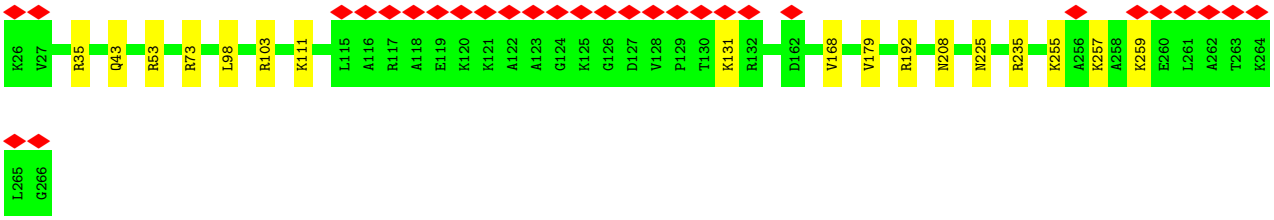




• Molecule 44: 60S ribosomal protein L7a

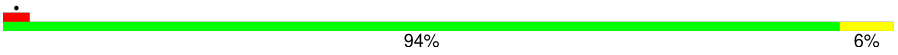
Chain LG:

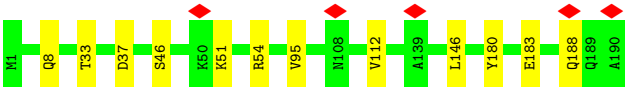




• Molecule 45: 60S ribosomal protein L9

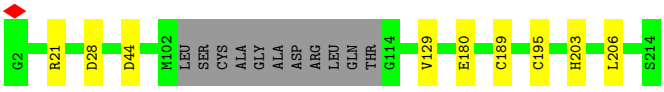
Chain LH:





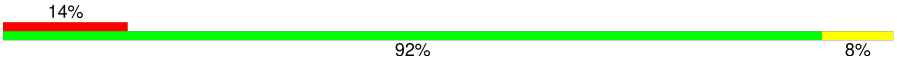
• Molecule 46: Ribosomal protein uL16-like

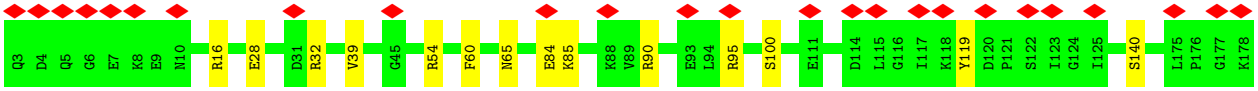
Chain LI:



• Molecule 47: 60S ribosomal protein L11

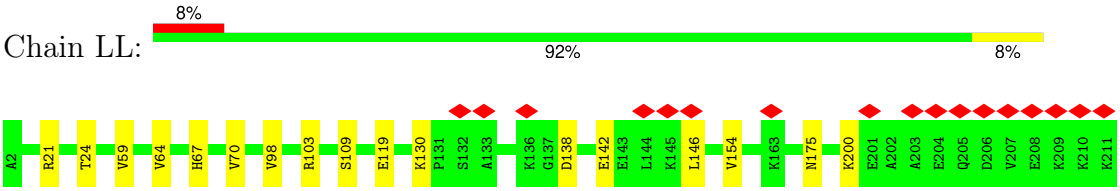
Chain LJ:





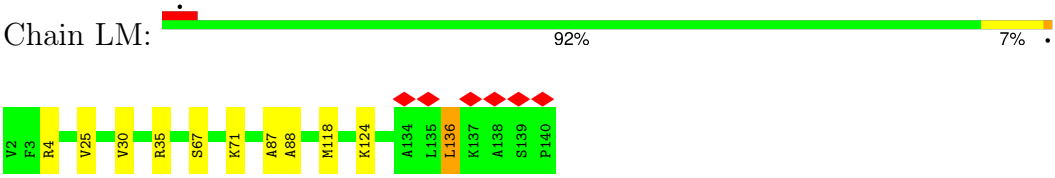
• Molecule 48: Large ribosomal subunit protein eL13

Chain LL:



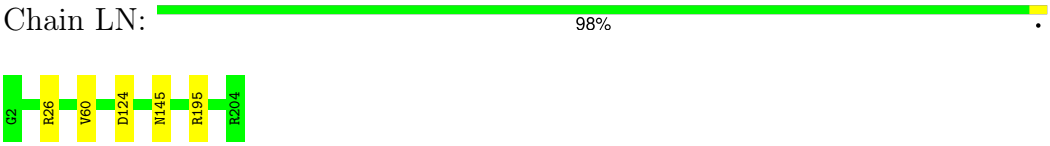
• Molecule 49: 60S ribosomal protein L14

Chain LM:



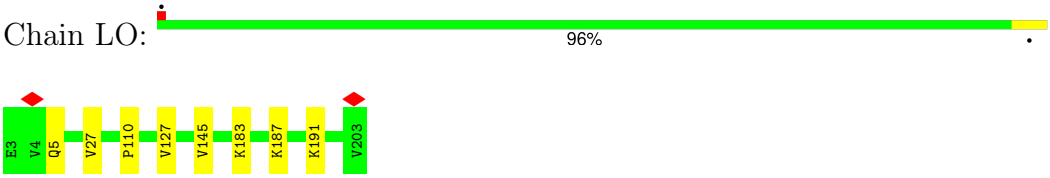
• Molecule 50: 60S ribosomal protein L15

Chain LN:



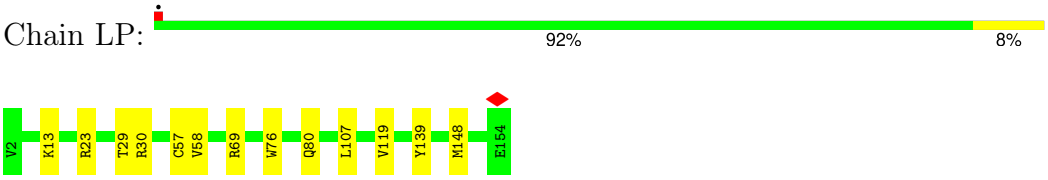
• Molecule 51: 60S ribosomal protein L13a

Chain LO:



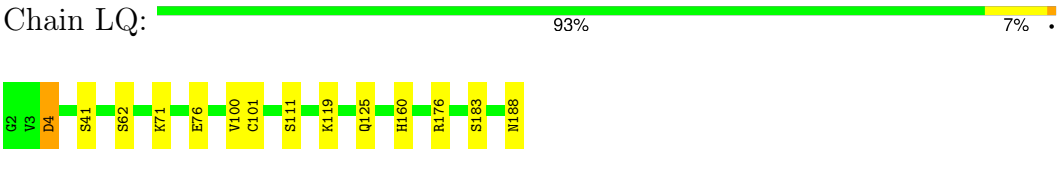
• Molecule 52: 60S ribosomal protein L17

Chain LP:



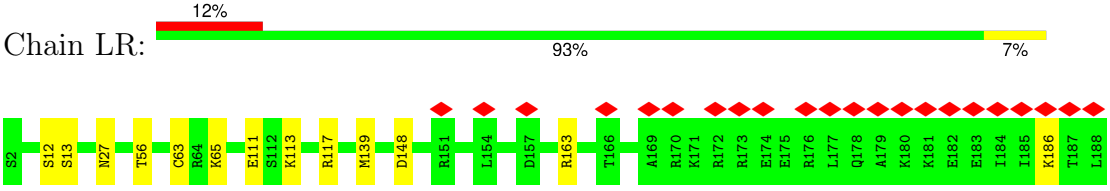
• Molecule 53: 60S ribosomal protein L18

Chain LQ:



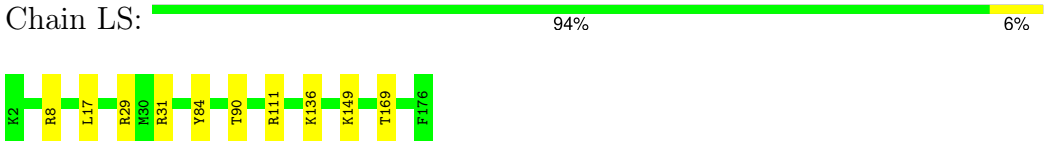
• Molecule 54: 60S ribosomal protein L19

Chain LR:



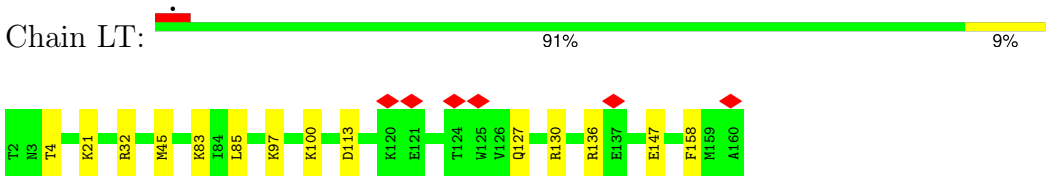
• Molecule 55: 60S ribosomal protein L18a

Chain LS:



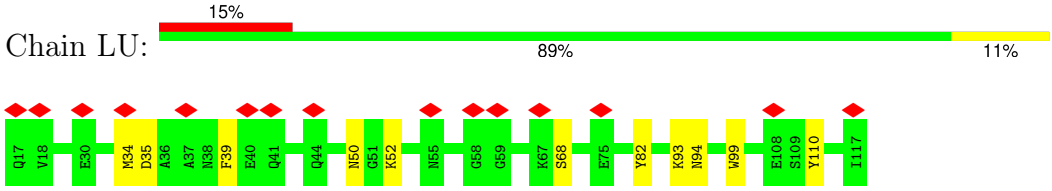
• Molecule 56: 60S ribosomal protein L21

Chain LT:



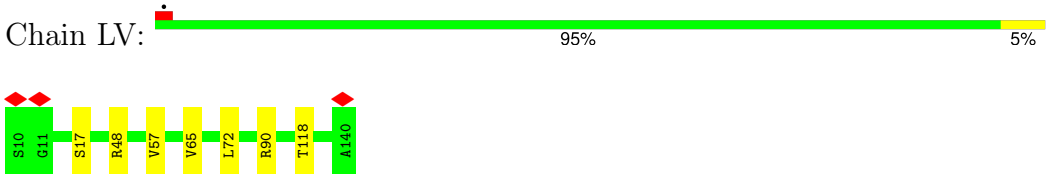
• Molecule 57: Heparin-binding protein HBp15

Chain LU:



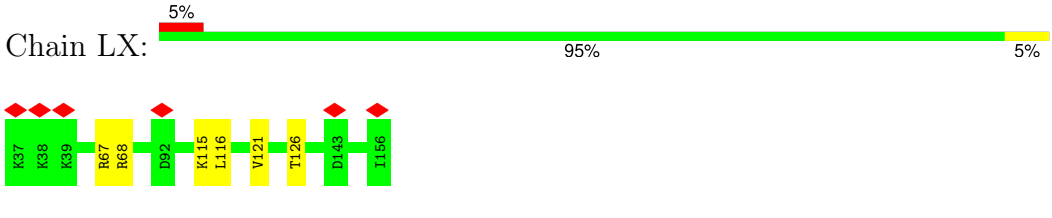
• Molecule 58: 60S ribosomal protein L23

Chain LV:



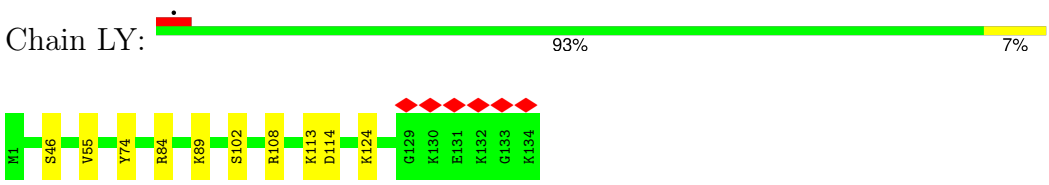
• Molecule 59: 60S ribosomal protein L23a

Chain LX:



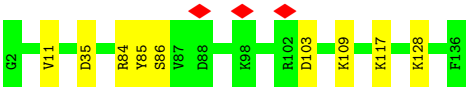
• Molecule 60: 60S ribosomal protein L26

Chain LY:



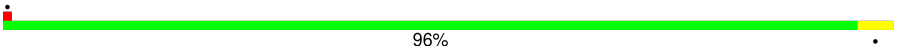
• Molecule 61: 60S ribosomal protein L27

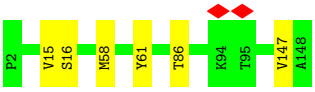
Chain LZ:



• Molecule 62: 60S ribosomal protein L27a

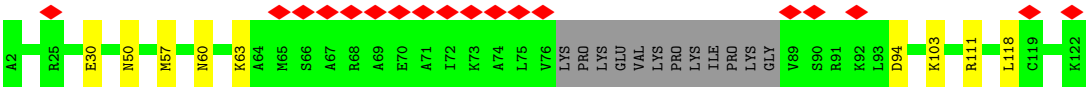
Chain La:





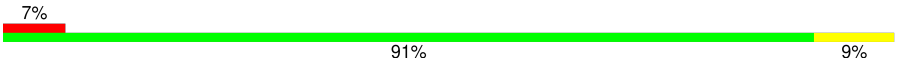
• Molecule 63: Large ribosomal subunit protein eL29

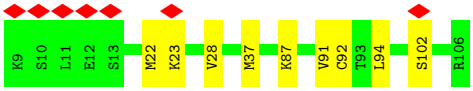
Chain Lb:



• Molecule 64: 60S ribosomal protein L30

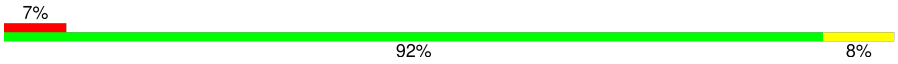
Chain Lc:

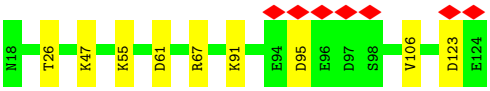




• Molecule 65: 60S ribosomal protein L31

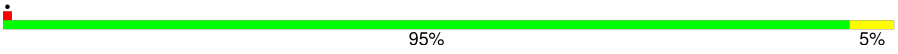
Chain Ld:

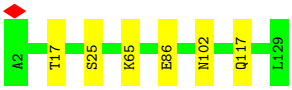




• Molecule 66: 60S ribosomal protein L32

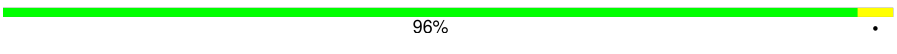
Chain Le:

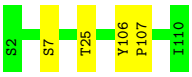




• Molecule 67: 60S ribosomal protein L35a

Chain Lf:





• Molecule 68: 60S ribosomal protein L34

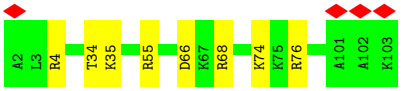
Chain Lg:

• Molecule 69: 60S ribosomal protein L35

Chain Lh:

• Molecule 70: 60S ribosomal protein L36

Chain Li:

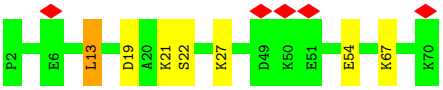


• Molecule 71: 60S ribosomal protein L37

Chain Lj:

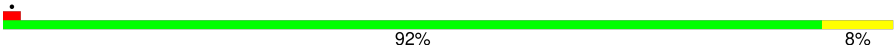
• Molecule 72: 60S ribosomal protein L38

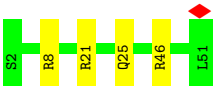
Chain Lk:



• Molecule 73: 60S ribosomal protein L39

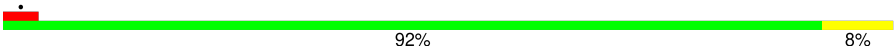
Chain Ll:





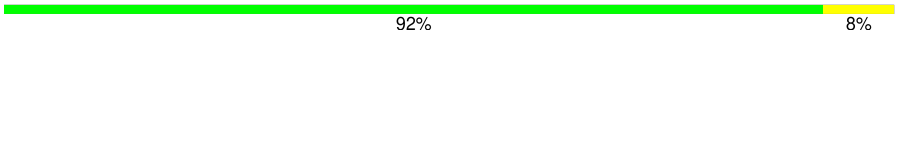
• Molecule 74: Large ribosomal subunit protein eL40

Chain Lm:



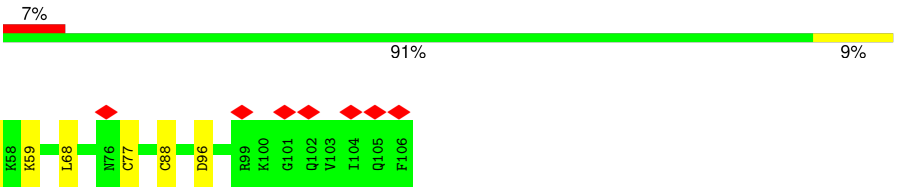
• Molecule 75: 60S ribosomal protein L41

Chain Ln:



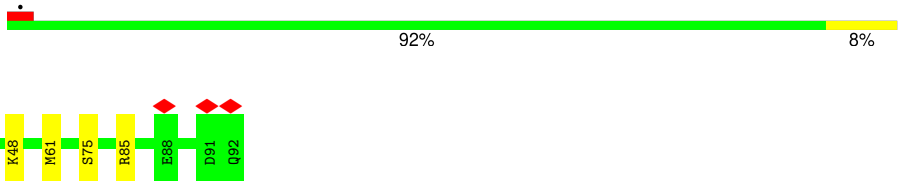
• Molecule 76: 60S ribosomal protein L36a

Chain Lo:



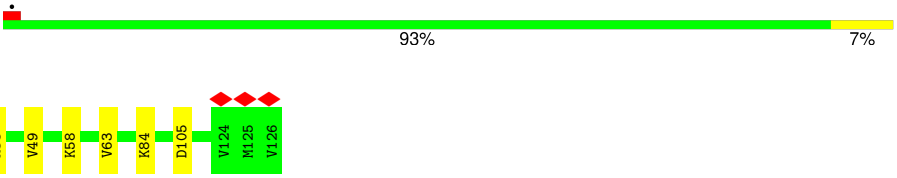
• Molecule 77: 60S ribosomal protein L37a

Chain Lp:



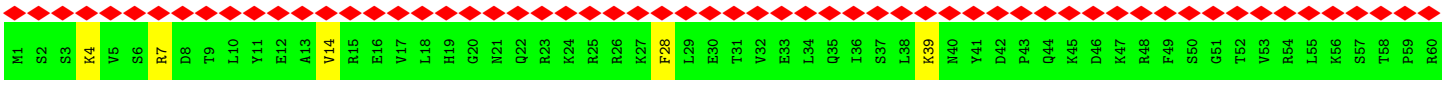
• Molecule 78: 60S ribosomal protein L28

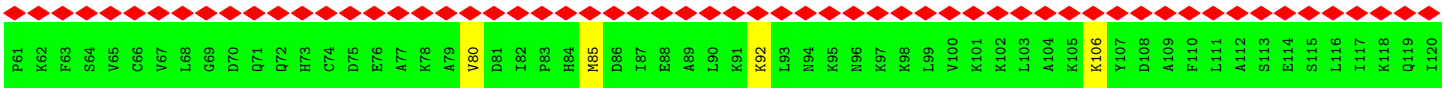
Chain Lr:

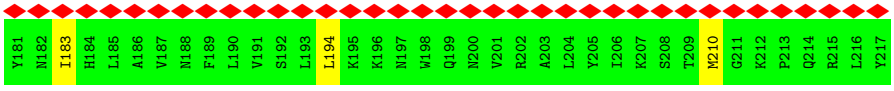


• Molecule 79: 60S ribosomal protein L10a

Chain Lz:

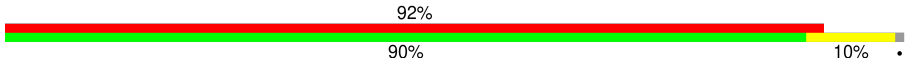


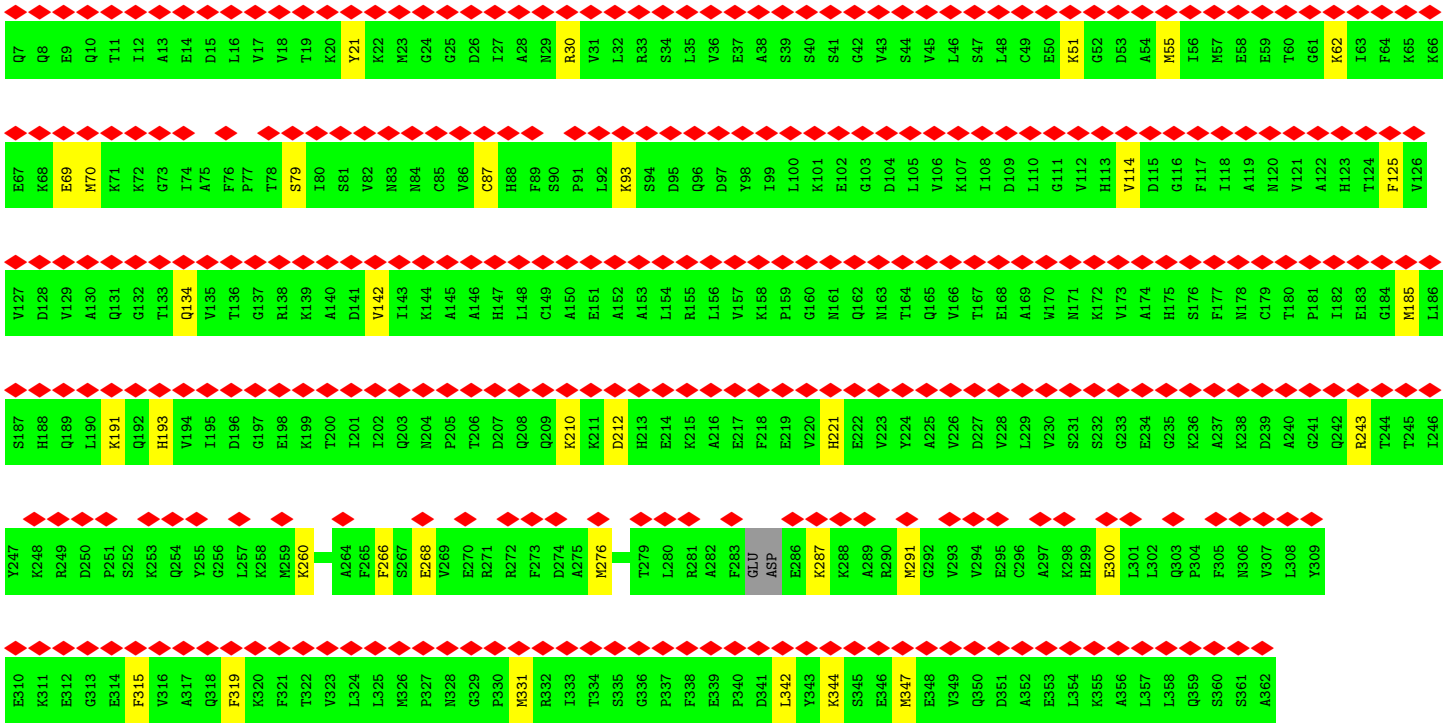




• Molecule 80: Proliferation-associated protein 2G4

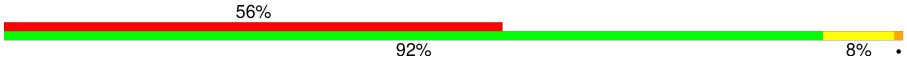
Chain CA:

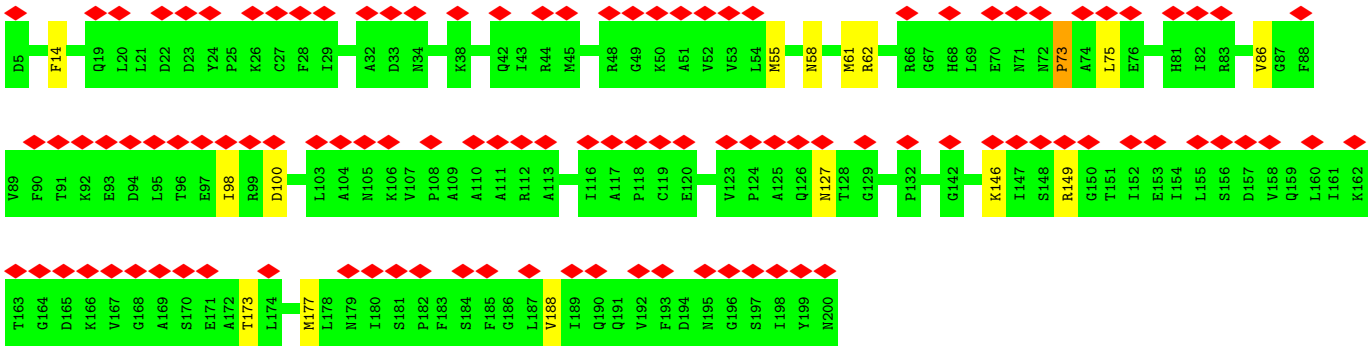




• Molecule 81: 60S acidic ribosomal protein P0

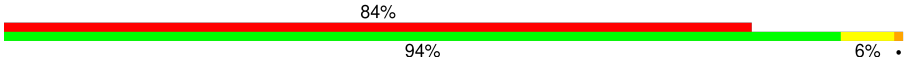
Chain Ls:

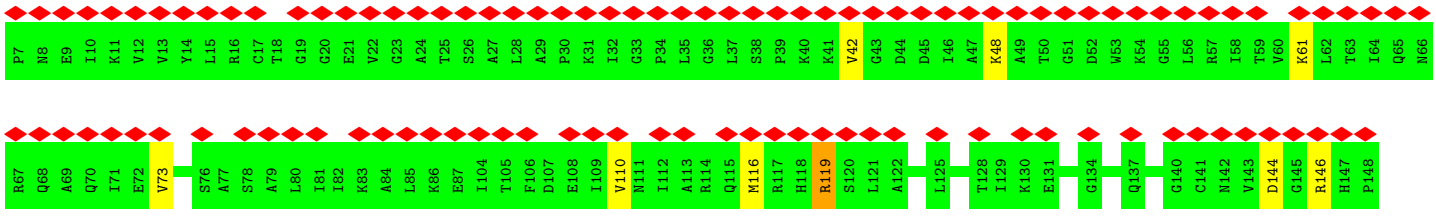


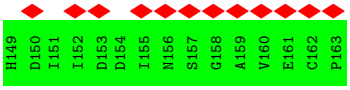


• Molecule 82: 60S ribosomal protein L12

Chain Lt:

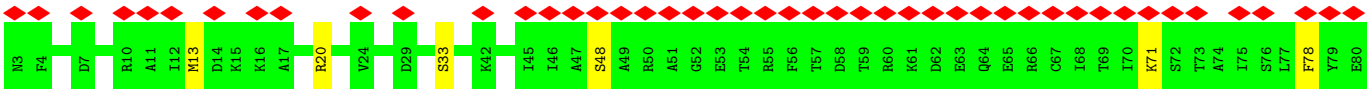


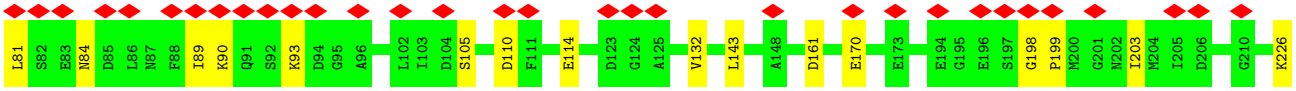


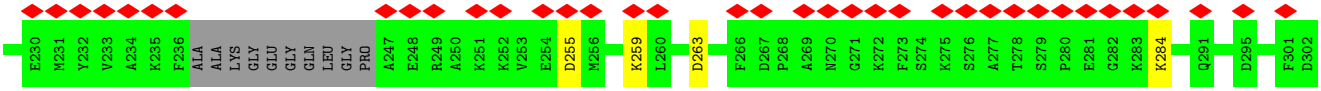


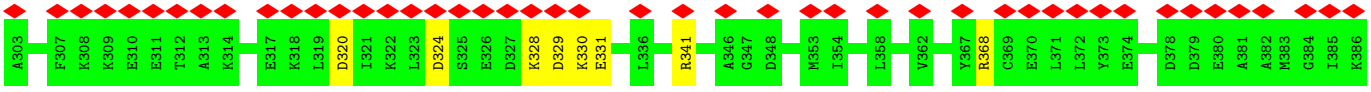
• Molecule 83: Elongation factor 2

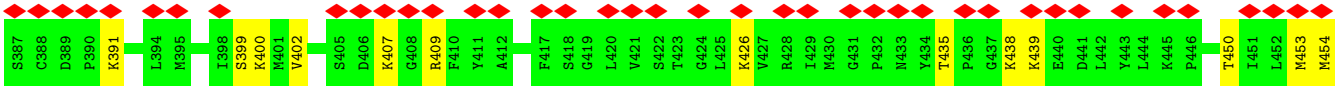
Chain CB:

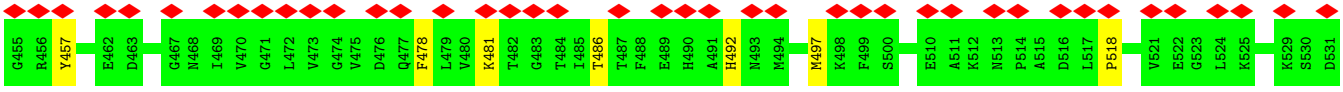


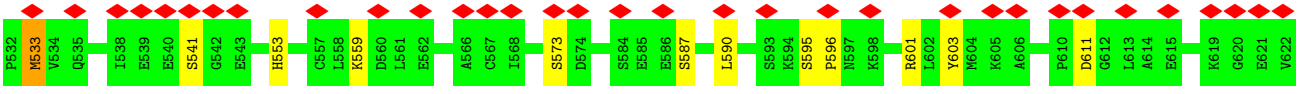


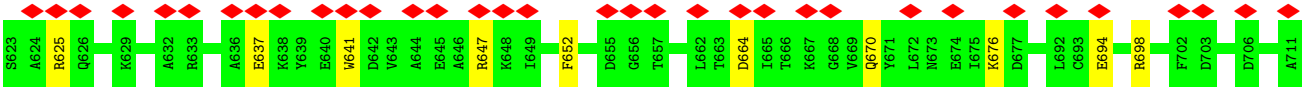


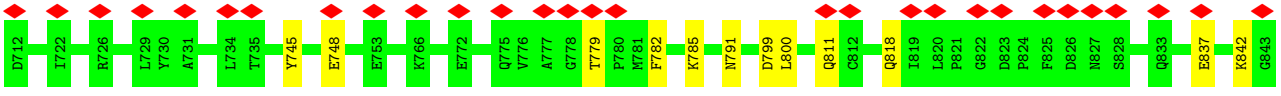


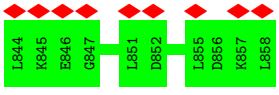






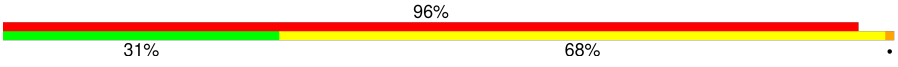


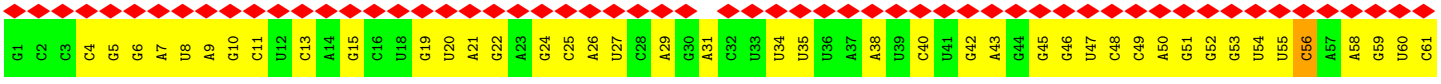


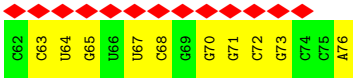


• Molecule 84: E site tRNA

Chain Et:

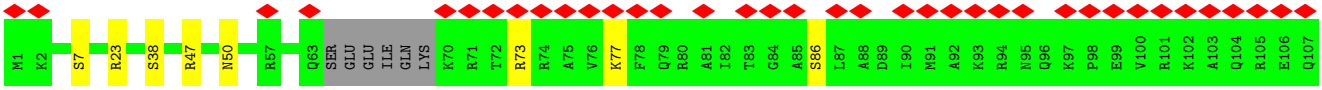


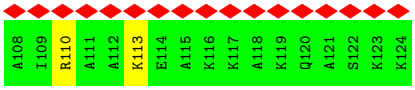




• Molecule 85: Ribosomal protein L24

Chain LW:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54349	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.246	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.029	Depositor
Map size (Å)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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	S2	0.25	0/41243	0.82	22/64259 (0.0%)
2	SD	0.57	2/1793 (0.1%)	1.00	6/2414 (0.2%)
3	SF	0.27	0/1516	0.60	0/2037
4	SK	0.32	0/851	0.69	2/1147 (0.2%)
5	SP	0.29	0/1003	0.70	0/1342
6	SQ	0.26	0/1160	0.62	0/1553
7	SS	0.26	0/1216	0.63	0/1628
8	ST	0.27	0/1131	0.65	1/1515 (0.1%)
9	SU	0.28	0/831	0.64	0/1115
10	Sc	0.27	0/508	0.72	0/680
11	Sd	0.27	0/470	0.64	0/623
12	Sg	0.26	0/2493	0.62	0/3394
13	SM	0.25	0/950	0.56	1/1275 (0.1%)
14	SZ	0.25	0/604	0.65	0/810
15	Sf	0.26	0/560	0.62	0/745
16	CD	0.24	0/447	0.53	0/592
17	SE	0.27	0/2118	0.65	2/2849 (0.1%)
18	SI	0.27	0/1715	0.61	0/2287
19	SL	0.26	0/1268	0.56	0/1696
20	SX	0.27	0/1116	0.59	1/1490 (0.1%)
21	SG	0.26	0/1946	0.64	0/2590
22	SJ	0.28	0/1550	0.63	0/2069
23	SY	0.51	2/1083 (0.2%)	1.04	3/1438 (0.2%)
24	Se	0.27	0/465	0.64	0/612
25	SA	0.29	0/1778	0.74	3/2416 (0.1%)
26	SB	0.26	0/1765	0.61	1/2362 (0.0%)
27	SH	0.27	0/1519	0.58	0/2033
28	SV	0.26	0/643	0.58	0/860
29	Sa	0.27	0/836	0.63	0/1121
30	SC	0.27	0/1762	0.57	0/2381
31	SN	0.26	0/1232	0.57	0/1656
32	SO	0.26	0/1062	0.63	0/1425

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	SW	0.28	0/1051	0.61	0/1406
34	Sb	0.28	0/665	0.64	0/891
35	L5	0.32	0/89313	0.85	90/139291 (0.1%)
36	L7	0.30	0/2861	0.77	0/4459
37	L8	0.31	0/3701	0.77	0/5766
38	LA	0.29	0/1936	0.61	0/2596
39	LB	0.27	0/3306	0.56	0/4424
40	LC	0.26	0/2981	0.58	2/4002 (0.0%)
41	LD	0.27	0/2428	0.53	0/3252
42	LE	0.27	0/1942	0.58	0/2606
43	LF	0.27	0/1905	0.56	0/2539
44	LG	0.27	0/1960	0.56	0/2637
45	LH	0.27	0/1537	0.60	1/2066 (0.0%)
46	LI	0.27	0/1673	0.55	0/2233
47	LJ	0.27	0/1433	0.61	0/1915
48	LL	0.26	0/1732	0.57	0/2315
49	LM	0.27	0/1161	0.56	1/1554 (0.1%)
50	LN	0.26	0/1746	0.59	0/2338
51	LO	0.27	0/1682	0.54	0/2250
52	LP	0.26	0/1268	0.54	0/1701
53	LQ	0.27	0/1537	0.62	1/2052 (0.0%)
54	LR	0.25	0/1581	0.60	0/2088
55	LS	0.27	0/1493	0.56	0/2003
56	LT	0.27	0/1326	0.55	0/1770
57	LU	0.29	0/839	0.63	0/1126
58	LV	0.28	0/993	0.55	0/1332
59	LX	0.27	0/1002	0.59	1/1345 (0.1%)
60	LY	0.26	0/1132	0.56	0/1504
61	LZ	0.28	0/1130	0.54	0/1507
62	La	0.26	0/1191	0.55	0/1591
63	Lb	0.25	0/889	0.58	1/1175 (0.1%)
64	Lc	0.26	0/774	0.51	0/1038
65	Ld	0.26	0/903	0.60	0/1216
66	Le	0.26	0/1071	0.55	0/1429
67	Lf	0.27	0/895	0.60	0/1198
68	Lg	0.26	0/916	0.59	0/1220
69	Lh	0.24	0/1023	0.57	0/1351
70	Li	0.29	0/843	0.60	0/1115
71	Lj	0.27	0/720	0.63	0/952
72	Lk	0.27	0/575	0.60	1/761 (0.1%)
73	Ll	0.24	0/454	0.59	0/599
74	Lm	0.25	0/435	0.55	0/575
75	Ln	0.24	0/231	0.73	0/294

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	Lo	0.28	0/876	0.60	0/1156
77	Lp	0.26	0/718	0.54	0/953
78	Lr	0.26	0/1017	0.59	0/1364
79	Lz	0.25	0/1769	0.55	1/2371 (0.0%)
80	CA	0.26	0/2810	0.53	0/3780
81	Ls	0.28	0/1519	0.58	1/2052 (0.0%)
82	Lt	0.26	0/1058	0.64	0/1430
83	CB	0.34	2/6734 (0.0%)	0.69	11/9094 (0.1%)
84	Et	0.29	0/1778	0.99	1/2767 (0.0%)
85	LW	0.27	0/979	0.61	0/1295
All	All	0.29	6/246126 (0.0%)	0.76	154/360158 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	SQ	0	1
20	SX	0	1
22	SJ	0	1
27	SH	0	1
28	SV	0	1
38	LA	0	2
39	LB	0	2
48	LL	0	1
49	LM	0	1
51	LO	0	1
56	LT	0	1
67	Lf	0	1
71	Lj	0	1
79	Lz	0	1
82	Lt	0	1
All	All	0	17

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	SD	194	PRO	CB-CG	16.48	2.32	1.50
2	SD	194	PRO	CG-CD	-10.98	1.14	1.50
83	CB	199	PRO	CB-CG	-10.54	0.97	1.50
83	CB	596	PRO	CG-CD	-10.29	1.16	1.50

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	SY	36	PRO	CG-CD	-9.77	1.18	1.50

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	SD	194	PRO	CA-N-CD	-24.25	77.55	111.50
2	SD	194	PRO	CB-CG-CD	-20.72	25.68	106.50
23	SY	36	PRO	N-CD-CG	-20.36	72.66	103.20
23	SY	36	PRO	CB-CG-CD	18.82	179.91	106.50
25	SA	153	PRO	CA-N-CD	-16.90	87.84	111.50

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
27	SH	15	LYS	Peptide
22	SJ	19	PRO	Peptide
6	SQ	43	GLU	Peptide
28	SV	78	ILE	Peptide
20	SX	126	ALA	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	SD	225/227 (99%)	206 (92%)	18 (8%)	1 (0%)	30 59
3	SF	187/189 (99%)	167 (89%)	20 (11%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	SK	96/98 (98%)	86 (90%)	8 (8%)	2 (2%)	5 19
5	SP	119/121 (98%)	107 (90%)	12 (10%)	0	100 100
6	SQ	142/144 (99%)	124 (87%)	17 (12%)	1 (1%)	19 46
7	SS	143/145 (99%)	138 (96%)	5 (4%)	0	100 100
8	ST	141/143 (99%)	130 (92%)	10 (7%)	1 (1%)	19 46
9	SU	102/104 (98%)	94 (92%)	8 (8%)	0	100 100
10	Sc	62/64 (97%)	47 (76%)	15 (24%)	0	100 100
11	Sd	53/55 (96%)	50 (94%)	3 (6%)	0	100 100
12	Sg	311/313 (99%)	271 (87%)	40 (13%)	0	100 100
13	SM	120/122 (98%)	107 (89%)	12 (10%)	1 (1%)	16 42
14	SZ	73/75 (97%)	59 (81%)	14 (19%)	0	100 100
15	Sf	65/67 (97%)	57 (88%)	8 (12%)	0	100 100
16	CD	51/55 (93%)	49 (96%)	2 (4%)	0	100 100
17	SE	260/262 (99%)	247 (95%)	13 (5%)	0	100 100
18	SI	204/206 (99%)	196 (96%)	8 (4%)	0	100 100
19	SL	151/153 (99%)	140 (93%)	11 (7%)	0	100 100
20	SX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	19 46
21	SG	235/237 (99%)	222 (94%)	13 (6%)	0	100 100
22	SJ	183/185 (99%)	171 (93%)	11 (6%)	1 (0%)	25 54
23	SY	129/131 (98%)	118 (92%)	11 (8%)	0	100 100
24	Se	56/58 (97%)	51 (91%)	5 (9%)	0	100 100
25	SA	219/221 (99%)	197 (90%)	22 (10%)	0	100 100
26	SB	212/214 (99%)	207 (98%)	5 (2%)	0	100 100
27	SH	182/189 (96%)	159 (87%)	23 (13%)	0	100 100
28	SV	81/83 (98%)	73 (90%)	8 (10%)	0	100 100
29	Sa	100/102 (98%)	89 (89%)	11 (11%)	0	100 100
30	SC	220/222 (99%)	204 (93%)	16 (7%)	0	100 100
31	SN	148/150 (99%)	143 (97%)	5 (3%)	0	100 100
32	SO	138/140 (99%)	126 (91%)	12 (9%)	0	100 100
33	SW	127/129 (98%)	125 (98%)	2 (2%)	0	100 100
34	Sb	81/83 (98%)	68 (84%)	13 (16%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	LA	246/248 (99%)	222 (90%)	24 (10%)	0	100	100
39	LB	400/402 (100%)	374 (94%)	26 (6%)	0	100	100
40	LC	366/368 (100%)	341 (93%)	25 (7%)	0	100	100
41	LD	291/293 (99%)	275 (94%)	16 (6%)	0	100	100
42	LE	232/247 (94%)	209 (90%)	23 (10%)	0	100	100
43	LF	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
44	LG	239/241 (99%)	226 (95%)	13 (5%)	0	100	100
45	LH	188/190 (99%)	172 (92%)	16 (8%)	0	100	100
46	LI	198/213 (93%)	188 (95%)	10 (5%)	0	100	100
47	LJ	174/176 (99%)	162 (93%)	12 (7%)	0	100	100
48	LL	208/210 (99%)	192 (92%)	16 (8%)	0	100	100
49	LM	137/139 (99%)	128 (93%)	8 (6%)	1 (1%)	19	46
50	LN	201/203 (99%)	192 (96%)	8 (4%)	1 (0%)	25	54
51	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
52	LP	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
53	LQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
54	LR	183/187 (98%)	177 (97%)	6 (3%)	0	100	100
55	LS	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
56	LT	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
57	LU	99/101 (98%)	85 (86%)	14 (14%)	0	100	100
58	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
59	LX	118/120 (98%)	115 (98%)	3 (2%)	0	100	100
60	LY	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
61	LZ	133/135 (98%)	122 (92%)	11 (8%)	0	100	100
62	La	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
63	Lb	105/121 (87%)	97 (92%)	8 (8%)	0	100	100
64	Lc	96/98 (98%)	88 (92%)	8 (8%)	0	100	100
65	Ld	105/107 (98%)	99 (94%)	6 (6%)	0	100	100
66	Le	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
67	Lf	107/109 (98%)	98 (92%)	8 (8%)	1 (1%)	14	39
68	Lg	112/114 (98%)	112 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	Lh	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
70	Li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
71	Lj	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
72	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
73	Ll	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
74	Lm	50/52 (96%)	50 (100%)	0	0	100	100
75	Ln	22/24 (92%)	22 (100%)	0	0	100	100
76	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
77	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
78	Lr	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
79	Lz	215/217 (99%)	168 (78%)	47 (22%)	0	100	100
80	CA	350/356 (98%)	335 (96%)	15 (4%)	0	100	100
81	Ls	194/196 (99%)	182 (94%)	11 (6%)	1 (0%)	25	54
82	Lt	137/141 (97%)	104 (76%)	32 (23%)	1 (1%)	19	46
83	CB	842/856 (98%)	789 (94%)	49 (6%)	4 (0%)	25	54
85	LW	114/124 (92%)	110 (96%)	4 (4%)	0	100	100
All	All	12971/13206 (98%)	12031 (93%)	923 (7%)	17 (0%)	50	76

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	SK	96	ARG
82	Lt	144	ASP
83	CB	407	LYS
83	CB	779	THR
20	SX	127	ASN

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	SD	190/190 (100%)	162 (85%)	28 (15%)	2 8
3	SF	159/159 (100%)	147 (92%)	12 (8%)	11 31
4	SK	89/89 (100%)	83 (93%)	6 (7%)	13 37
5	SP	107/107 (100%)	96 (90%)	11 (10%)	6 18
6	SQ	119/119 (100%)	102 (86%)	17 (14%)	2 8
7	SS	126/126 (100%)	110 (87%)	16 (13%)	3 11
8	ST	113/113 (100%)	102 (90%)	11 (10%)	6 20
9	SU	94/94 (100%)	84 (89%)	10 (11%)	5 17
10	Sc	57/57 (100%)	49 (86%)	8 (14%)	3 9
11	Sd	48/48 (100%)	42 (88%)	6 (12%)	3 12
12	Sg	272/272 (100%)	236 (87%)	36 (13%)	3 10
13	SM	102/104 (98%)	90 (88%)	12 (12%)	4 13
14	SZ	66/66 (100%)	58 (88%)	8 (12%)	4 13
15	Sf	60/60 (100%)	53 (88%)	7 (12%)	4 14
16	CD	46/46 (100%)	43 (94%)	3 (6%)	14 38
17	SE	224/224 (100%)	188 (84%)	36 (16%)	2 6
18	SI	178/178 (100%)	152 (85%)	26 (15%)	2 8
19	SL	137/137 (100%)	120 (88%)	17 (12%)	4 12
20	SX	113/113 (100%)	102 (90%)	11 (10%)	6 20
21	SG	207/207 (100%)	181 (87%)	26 (13%)	3 11
22	SJ	161/161 (100%)	138 (86%)	23 (14%)	2 8
23	SY	113/113 (100%)	98 (87%)	15 (13%)	3 10
24	Se	47/47 (100%)	43 (92%)	4 (8%)	8 26
25	SA	183/183 (100%)	156 (85%)	27 (15%)	2 7
26	SB	195/195 (100%)	186 (95%)	9 (5%)	23 53
27	SH	166/169 (98%)	157 (95%)	9 (5%)	18 46
28	SV	67/67 (100%)	55 (82%)	12 (18%)	1 4
29	Sa	89/89 (100%)	81 (91%)	8 (9%)	8 24
30	SC	188/188 (100%)	171 (91%)	17 (9%)	8 24
31	SN	130/130 (100%)	116 (89%)	14 (11%)	5 16
32	SO	110/110 (100%)	94 (86%)	16 (14%)	2 8
33	SW	112/112 (100%)	104 (93%)	8 (7%)	12 34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
34	Sb	75/75 (100%)	66 (88%)	9 (12%)	4 13
38	LA	190/190 (100%)	175 (92%)	15 (8%)	10 29
39	LB	348/348 (100%)	324 (93%)	24 (7%)	13 35
40	LC	306/306 (100%)	286 (94%)	20 (6%)	14 38
41	LD	246/247 (100%)	225 (92%)	21 (8%)	8 26
42	LE	209/220 (95%)	196 (94%)	13 (6%)	15 41
43	LF	194/194 (100%)	184 (95%)	10 (5%)	19 48
44	LG	203/205 (99%)	186 (92%)	17 (8%)	9 27
45	LH	169/169 (100%)	158 (94%)	11 (6%)	14 38
46	LI	172/180 (96%)	163 (95%)	9 (5%)	19 48
47	LJ	148/148 (100%)	134 (90%)	14 (10%)	7 21
48	LL	176/176 (100%)	160 (91%)	16 (9%)	7 23
49	LM	118/118 (100%)	109 (92%)	9 (8%)	11 31
50	LN	171/171 (100%)	167 (98%)	4 (2%)	45 77
51	LO	173/173 (100%)	166 (96%)	7 (4%)	27 58
52	LP	134/134 (100%)	121 (90%)	13 (10%)	6 20
53	LQ	164/164 (100%)	150 (92%)	14 (8%)	8 26
54	LR	166/166 (100%)	153 (92%)	13 (8%)	10 29
55	LS	156/156 (100%)	146 (94%)	10 (6%)	14 39
56	LT	139/139 (100%)	126 (91%)	13 (9%)	7 22
57	LU	91/91 (100%)	80 (88%)	11 (12%)	4 13
58	LV	101/101 (100%)	94 (93%)	7 (7%)	13 35
59	LX	108/108 (100%)	103 (95%)	5 (5%)	23 53
60	LY	124/124 (100%)	114 (92%)	10 (8%)	9 28
61	LZ	117/117 (100%)	108 (92%)	9 (8%)	10 30
62	La	120/120 (100%)	114 (95%)	6 (5%)	20 50
63	Lb	88/101 (87%)	80 (91%)	8 (9%)	7 23
64	Lc	83/83 (100%)	74 (89%)	9 (11%)	5 16
65	Ld	98/98 (100%)	89 (91%)	9 (9%)	7 23
66	Le	114/114 (100%)	108 (95%)	6 (5%)	19 47
67	Lf	88/88 (100%)	86 (98%)	2 (2%)	45 77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
68	Lg	98/98 (100%)	88 (90%)	10 (10%)	6 18
69	Lh	109/109 (100%)	99 (91%)	10 (9%)	7 23
70	Li	86/86 (100%)	78 (91%)	8 (9%)	7 22
71	Lj	73/73 (100%)	66 (90%)	7 (10%)	7 21
72	Lk	64/64 (100%)	57 (89%)	7 (11%)	5 16
73	Ll	47/47 (100%)	43 (92%)	4 (8%)	8 26
74	Lm	48/48 (100%)	44 (92%)	4 (8%)	9 27
75	Ln	23/23 (100%)	21 (91%)	2 (9%)	8 25
76	Lo	93/93 (100%)	84 (90%)	9 (10%)	6 20
77	Lp	74/74 (100%)	67 (90%)	7 (10%)	7 21
78	Lr	109/109 (100%)	100 (92%)	9 (8%)	9 27
79	Lz	195/196 (100%)	180 (92%)	15 (8%)	10 30
80	CA	303/305 (99%)	269 (89%)	34 (11%)	5 15
81	Ls	162/164 (99%)	147 (91%)	15 (9%)	7 22
82	Lt	112/115 (97%)	104 (93%)	8 (7%)	12 34
83	CB	722/728 (99%)	643 (89%)	79 (11%)	5 16
85	LW	97/103 (94%)	87 (90%)	10 (10%)	6 18
All	All	11272/11332 (100%)	10221 (91%)	1051 (9%)	10 22

5 of 1051 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
80	CA	260	LYS
81	Ls	188	VAL
80	CA	243	ARG
83	CB	842	LYS
27	SH	98	ARG

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

Mol	Chain	Res	Type
59	LX	94	ASN
83	CB	715	HIS
60	LY	72	GLN
78	Lr	70	GLN

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Mol	Chain	Res	Type
18	SI	87	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1716/1869 (91%)	477 (27%)	6 (0%)
35	L5	3705/5070 (73%)	865 (23%)	22 (0%)
36	L7	119/120 (99%)	14 (11%)	0
37	L8	155/156 (99%)	31 (20%)	0
84	Et	73/75 (97%)	52 (71%)	0
All	All	5768/7290 (79%)	1439 (24%)	28 (0%)

5 of 1439 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S2	4	C
1	S2	13	C
1	S2	23	G
1	S2	24	C
1	S2	25	A

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	L5	2033	A
35	L5	4913	G
35	L5	2675	G
35	L5	4061	G
35	L5	2416	G

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

Of 261 ligands modelled in this entry, 261 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
16	CD	1
82	Lt	1
84	Et	1
54	LR	1
1	S2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CD	225:LEU	C	282:THR	N	57.64
1	Lt	87:GLU	C	104:ILE	N	8.89
1	Et	16:C	O3'	18:U	P	5.86
1	LR	153:LYS	C	154:LEU	N	3.52
1	S2	1210:G	O3'	1211:G	P	3.00

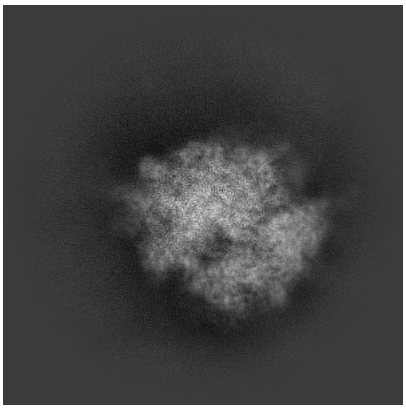
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-44049. These allow visual inspection of the internal detail of the map and identification of artifacts.

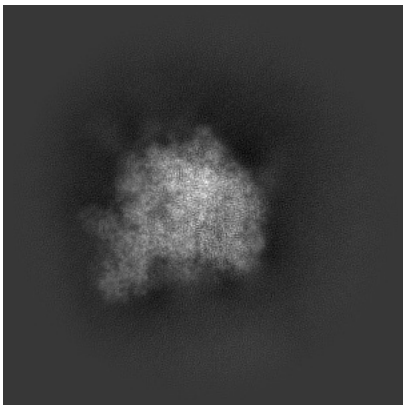
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

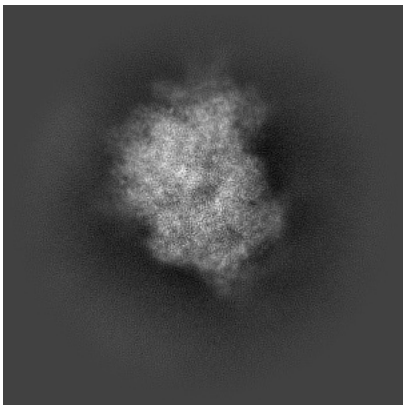
6.1.1 Primary map



X

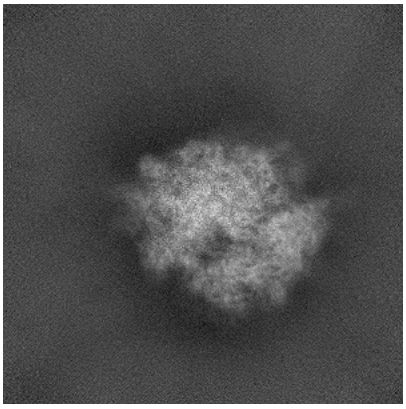


Y

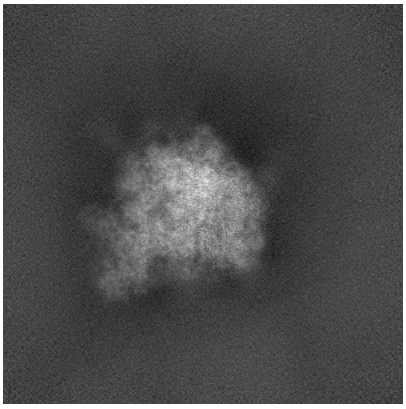


Z

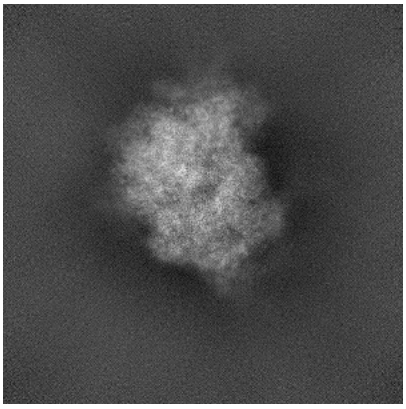
6.1.2 Raw map



X



Y

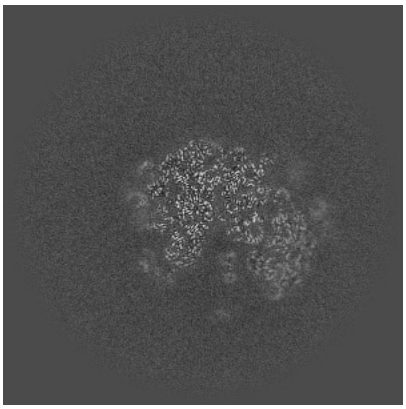


Z

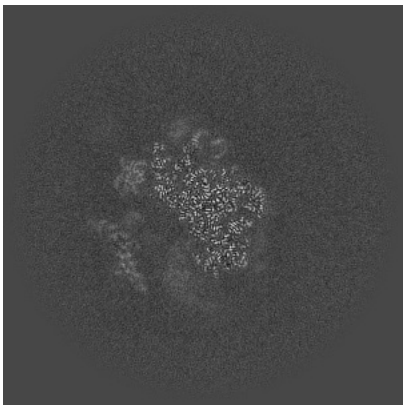
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

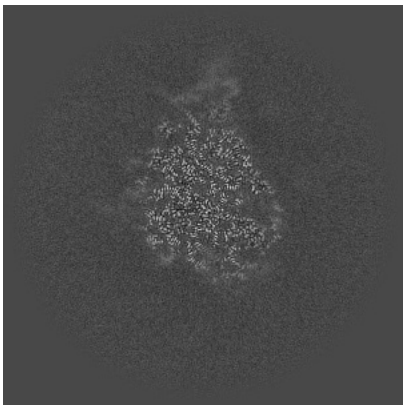
6.2.1 Primary map



X Index: 256

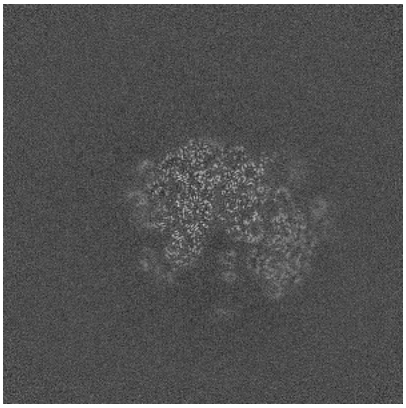


Y Index: 256

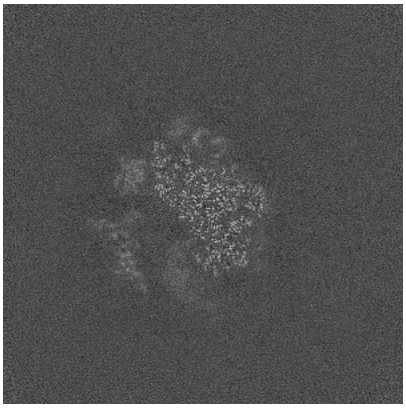


Z Index: 256

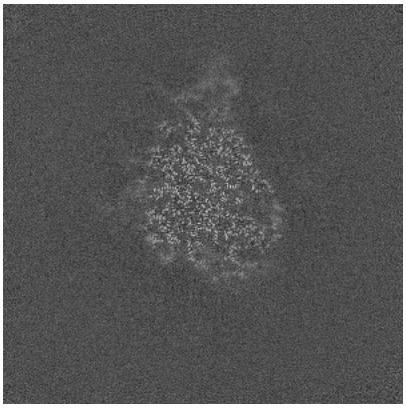
6.2.2 Raw map



X Index: 256



Y Index: 256

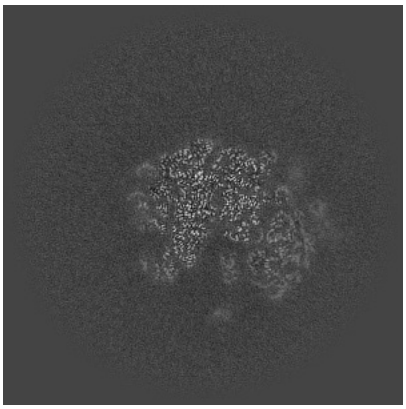


Z Index: 256

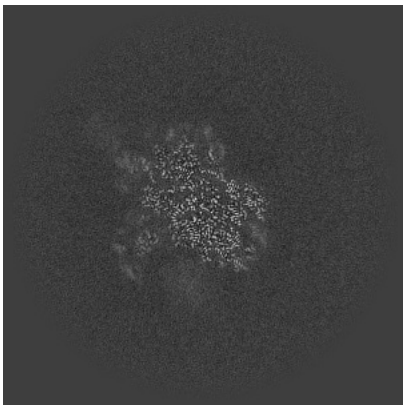
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

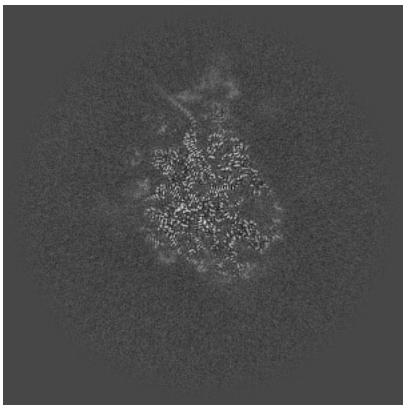
6.3.1 Primary map



X Index: 253

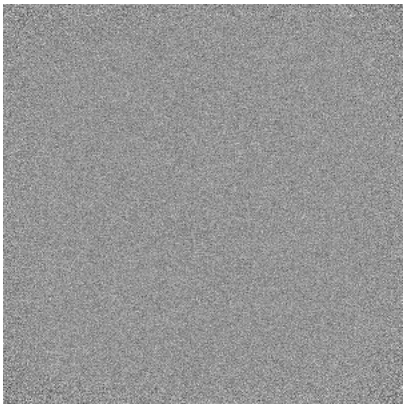


Y Index: 243

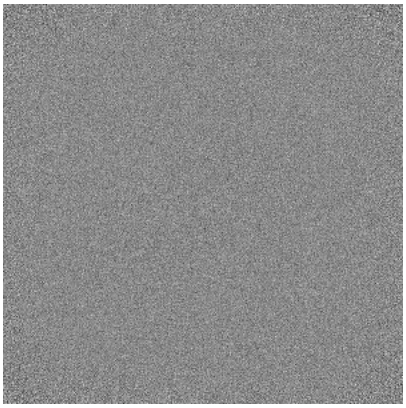


Z Index: 254

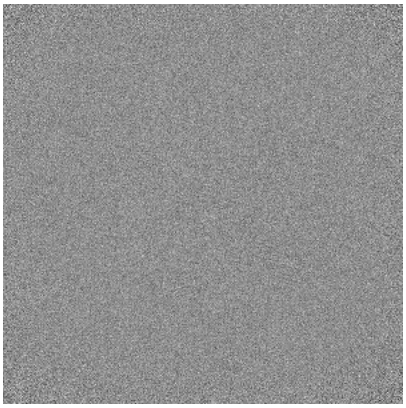
6.3.2 Raw map



X Index: 0



Y Index: 0

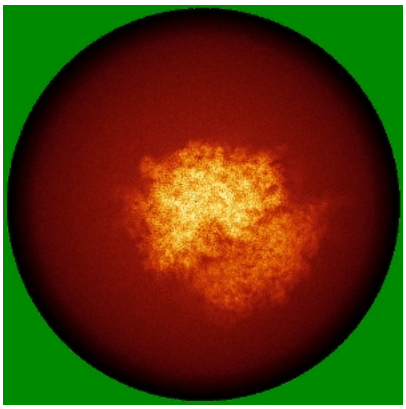


Z Index: 0

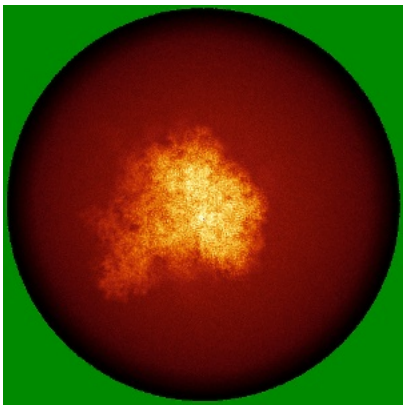
The images above show the largest variance slices of the map in three orthogonal directions.

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

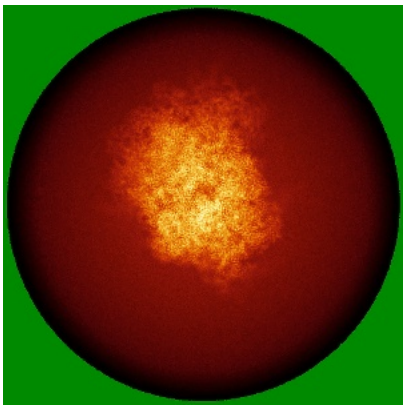
6.4.1 Primary map



X

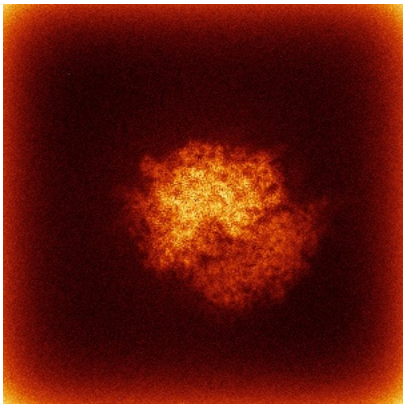


Y

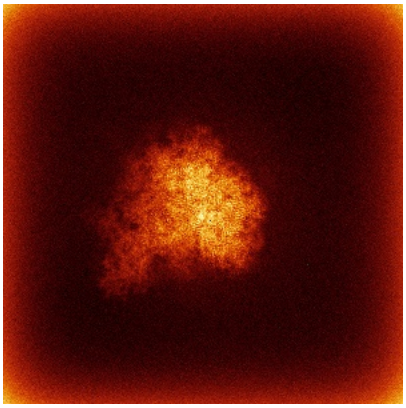


Z

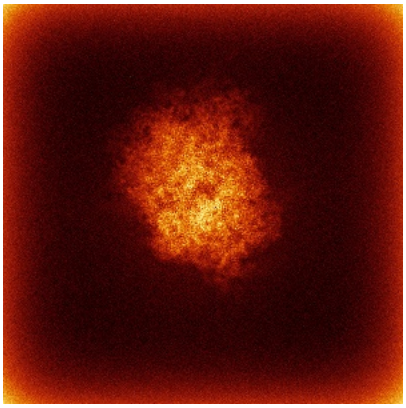
6.4.2 Raw map



X



Y

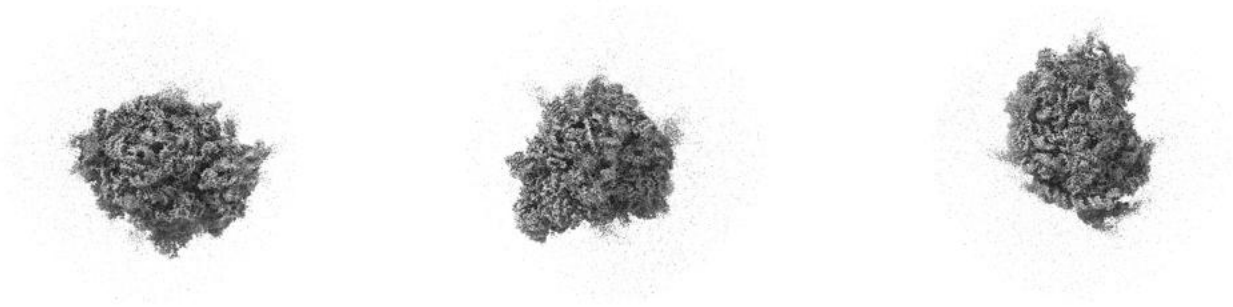


Z

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 0.029. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

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

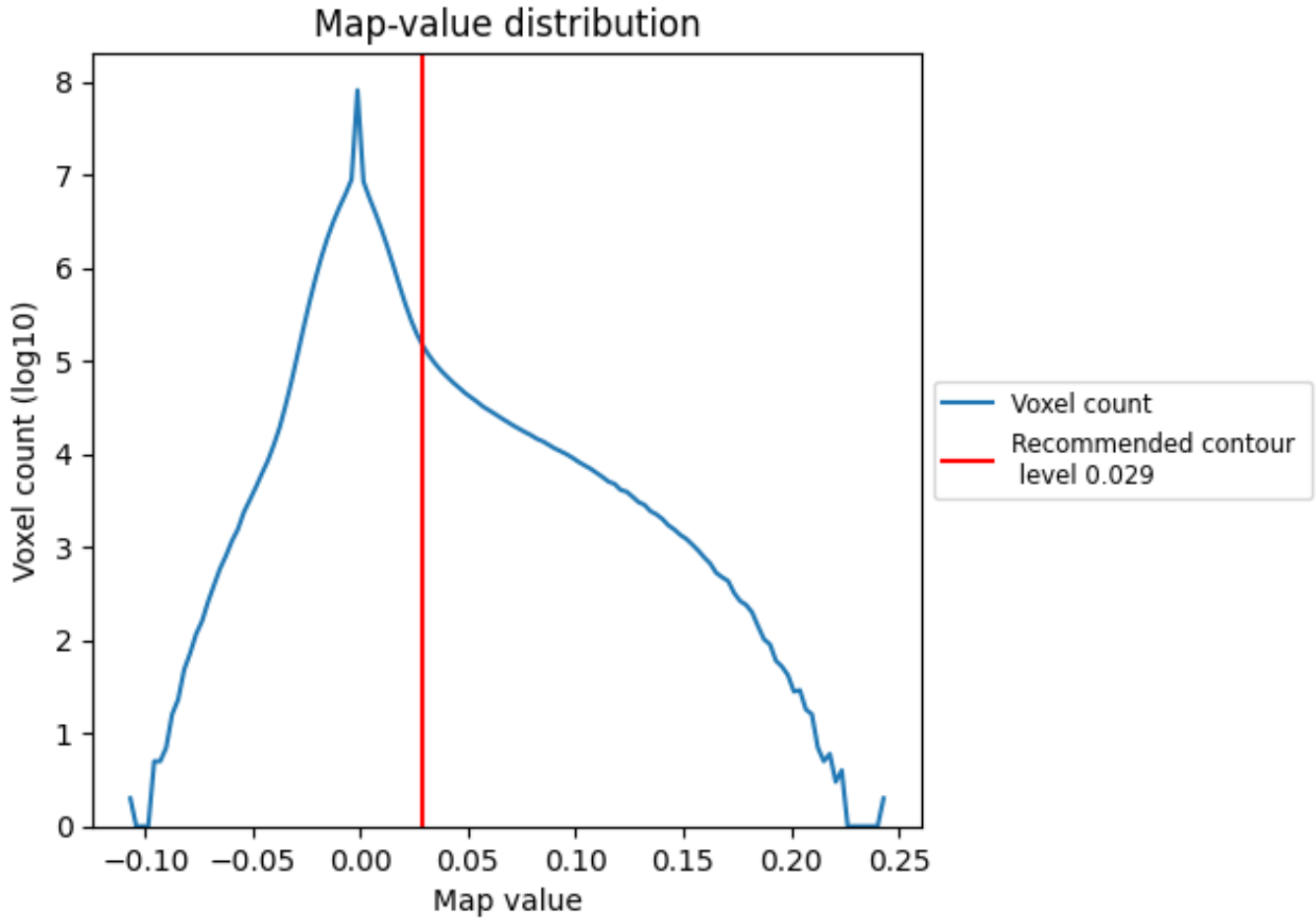
6.6 Mask visualisation (i)

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

7 Map analysis

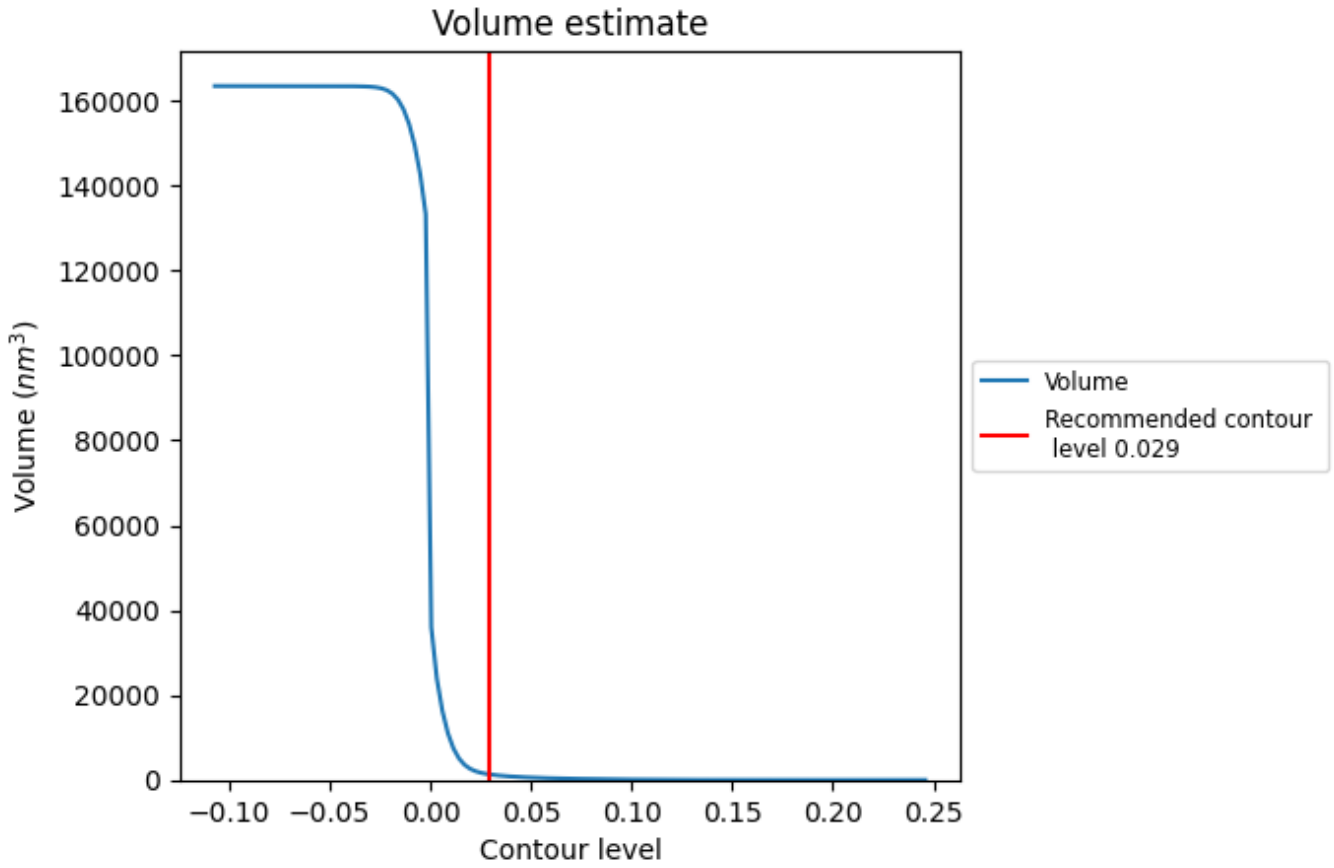
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

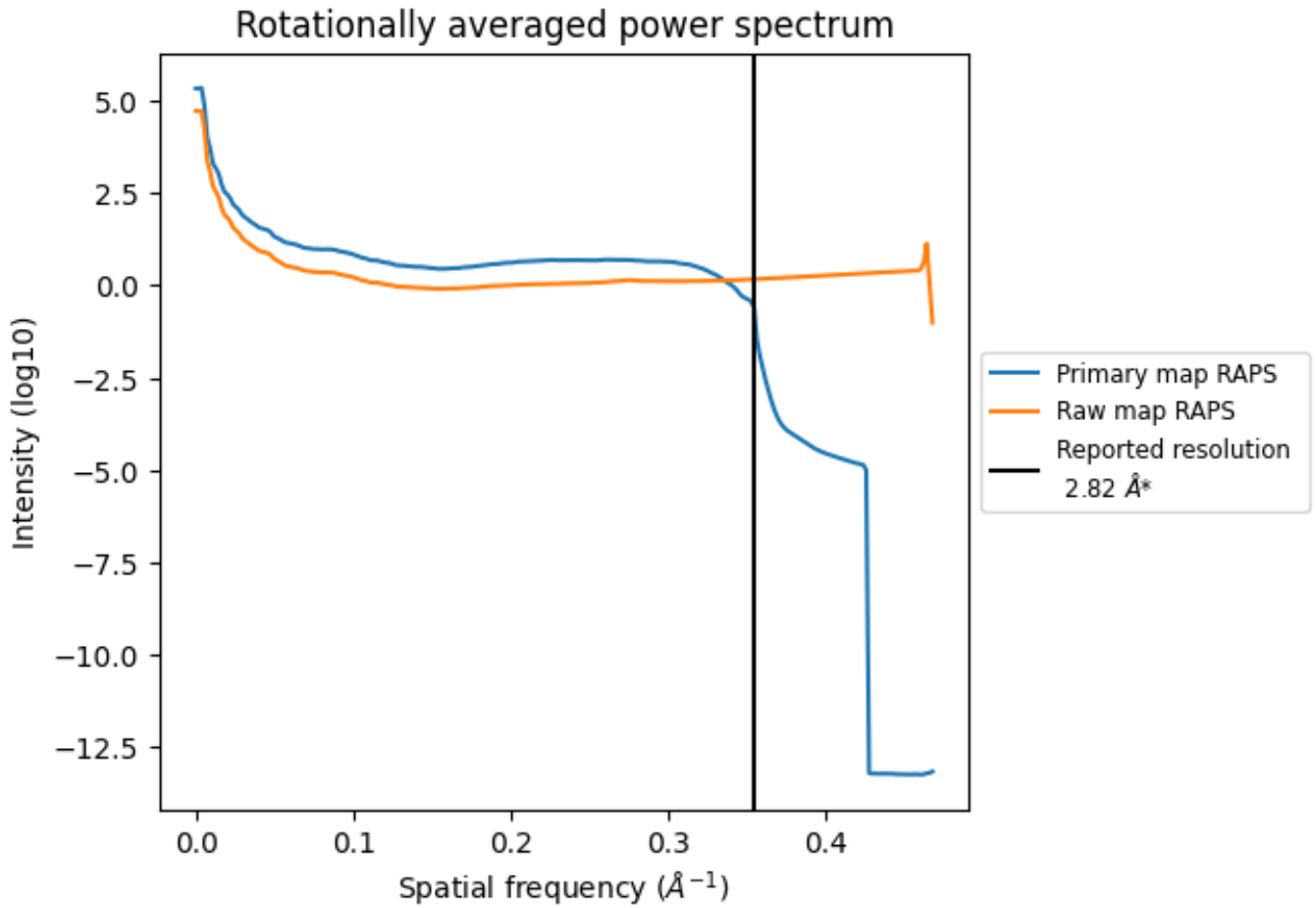
7.2 Volume estimate (i)



The volume at the recommended contour level is 1352 nm^3; this corresponds to an approximate mass of 1221 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)

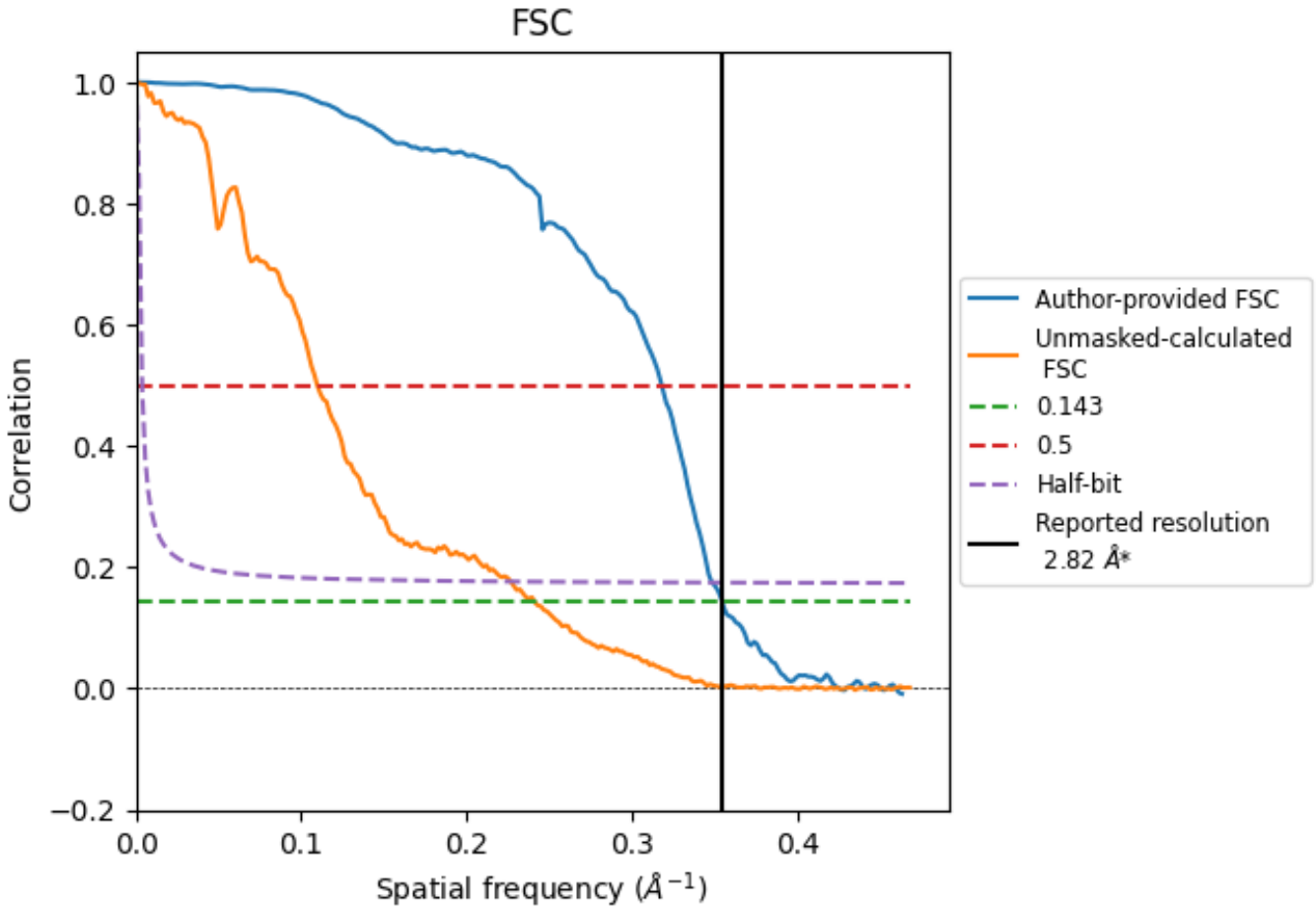


*Reported resolution corresponds to spatial frequency of 0.355 $Å^{-1}$

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 0.355 Å^{-1}

8.2 Resolution estimates (i)

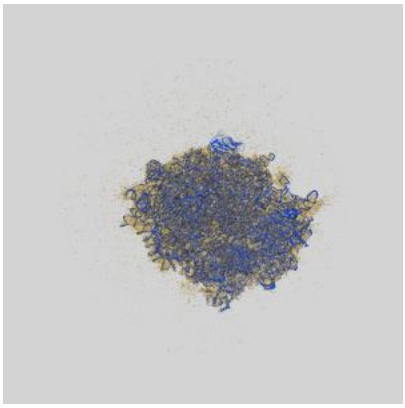
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.82	-	-
Author-provided FSC curve	2.82	3.14	2.87
Unmasked-calculated*	4.15	9.12	4.41

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.15 differs from the reported value 2.82 by more than 10 %

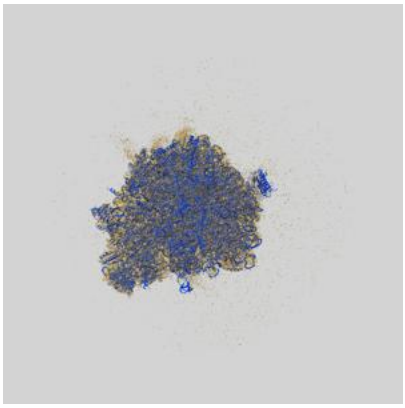
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-44049 and PDB model 9B0P. Per-residue inclusion information can be found in section 3 on page 21.

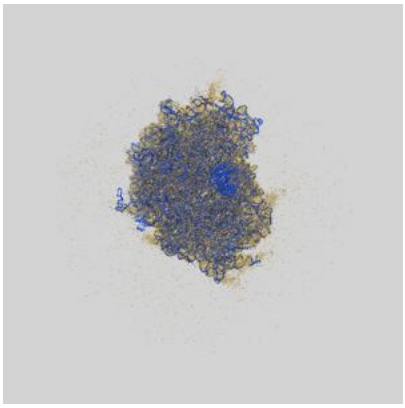
9.1 Map-model overlay



X



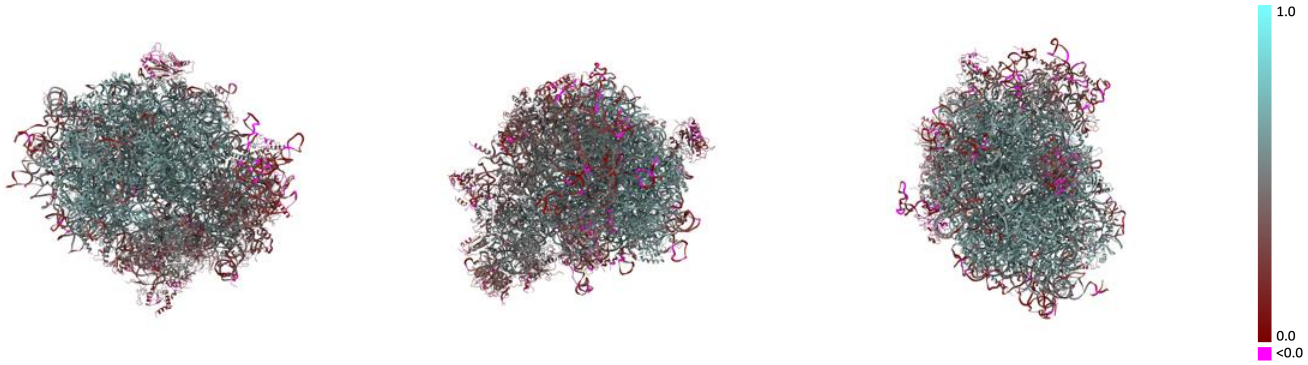
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.029 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

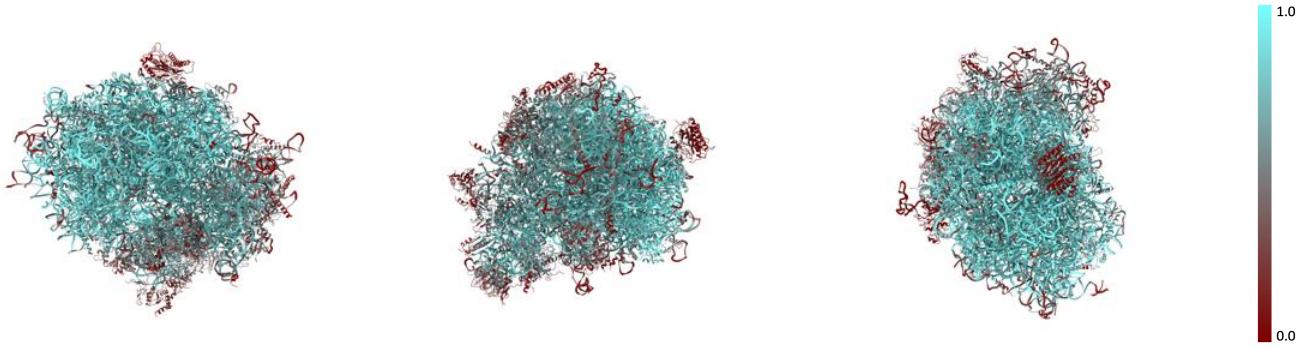
9.2 Q-score mapped to coordinate model



X Y Z

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

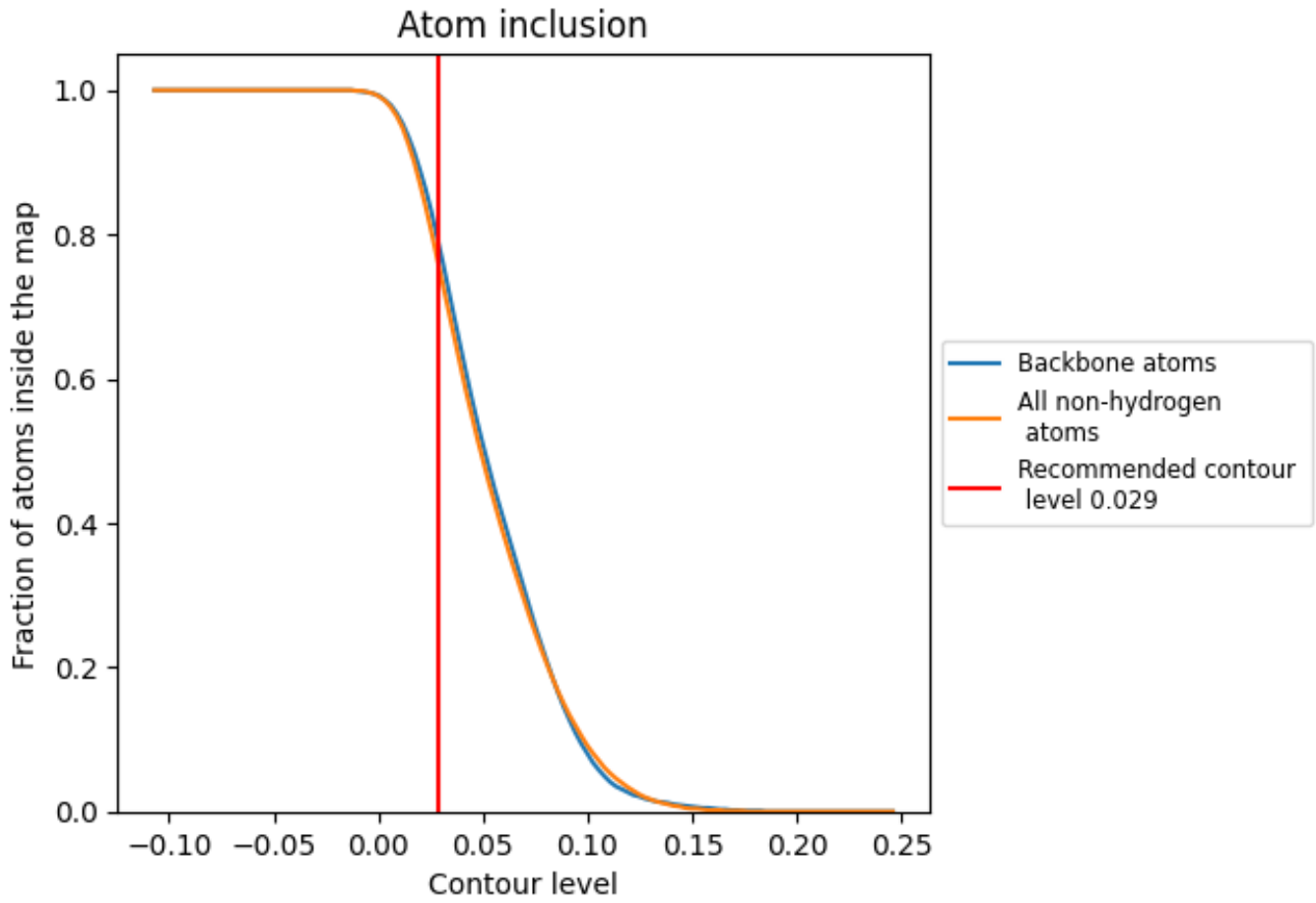
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.029).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.029) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7550	0.4860
CA	0.0940	0.2430
CB	0.4470	0.3890
CD	0.1870	0.2300
Et	0.1050	0.1280
L5	0.8610	0.5240
L7	0.9640	0.5920
L8	0.9120	0.5640
LA	0.9280	0.6110
LB	0.8790	0.5910
LC	0.8800	0.5910
LD	0.8080	0.5460
LE	0.7750	0.5210
LF	0.9120	0.6020
LG	0.7770	0.5310
LH	0.8410	0.5770
LI	0.8810	0.5920
LJ	0.6940	0.4780
LL	0.8250	0.5630
LM	0.8550	0.5720
LN	0.9550	0.6190
LO	0.9050	0.6010
LP	0.9010	0.6070
LQ	0.9270	0.6190
LR	0.7880	0.5260
LS	0.9210	0.6090
LT	0.8560	0.5750
LU	0.6630	0.4560
LV	0.8900	0.6020
LW	0.5270	0.3990
LX	0.8390	0.5720
LY	0.8530	0.5870
LZ	0.8460	0.5650
La	0.9250	0.6140
Lb	0.7430	0.5050

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Chain	Atom inclusion	Q-score
Lc	0.8340	0.5440
Ld	0.8310	0.5660
Le	0.9190	0.6110
Lf	0.9300	0.6120
Lg	0.8770	0.5850
Lh	0.8550	0.5880
Li	0.8460	0.5740
Lj	0.9240	0.6060
Lk	0.7150	0.5160
Ll	0.8840	0.5990
Lm	0.8820	0.5930
Ln	0.8950	0.6000
Lo	0.8420	0.5800
Lp	0.8770	0.5920
Lr	0.8860	0.5900
Ls	0.4070	0.3540
Lt	0.1790	0.1930
Lz	0.0230	0.1170
S2	0.7920	0.4390
SA	0.6040	0.4500
SB	0.5460	0.4020
SC	0.7030	0.4910
SD	0.5350	0.4080
SE	0.5270	0.3930
SF	0.5080	0.3800
SG	0.4150	0.3180
SH	0.3920	0.3070
SI	0.6060	0.4280
SJ	0.5590	0.4150
SK	0.4890	0.3780
SL	0.6390	0.4630
SM	0.1720	0.2100
SN	0.7120	0.4940
SO	0.6190	0.4470
SP	0.5330	0.4090
SQ	0.5660	0.4110
SS	0.4710	0.3780
ST	0.5320	0.3910
SU	0.5000	0.3670
SV	0.5920	0.4460
SW	0.7220	0.5080
SX	0.7080	0.5070

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Chain	Atom inclusion	Q-score
SY	0.3940	0.3160
SZ	0.3550	0.2990
Sa	0.7160	0.5010
Sb	0.5510	0.4130
Sc	0.4180	0.3150
Sd	0.7320	0.4860
Se	0.4600	0.3740
Sf	0.2420	0.2360
Sg	0.3690	0.3250